



MOTIFSIM - MOTIF SIMilarity Detection Tool

Version 2.2

INPUT

Input Parameters		
Number of files:	1	
Number of top significant motifs:	5	
Number of best matches:	5	
Similarity cutoff >=	0.5	
Matching motif database:	None	
Motif tree:	Yes	
Combined similar motifs:	Yes	
Output file type:	All	
Output file format:	All	
Input files and motif counts		
File name	Count of motifs	Dataset number
U20230328-stremeR.txt	365	1

RESULTS

Top 5 Significant Motifs - Global Matching (Highest to Lowest)
There is no global matching for 1 motif file.

Significant Motifs - Global and Local Matching (Highest to Lowest)

Dataset #: 1 Motif ID: 318 Motif name: Motif 318

Original motif Consensus sequence: CAGCCCCG



Reverse complement motif Consensus sequence: CGGGGCTG



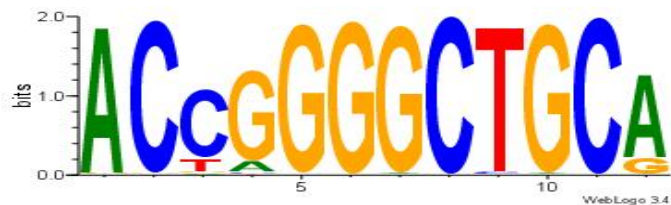
Best Matches for Significant Motif ID 318 (Highest to Lowest)

Dataset #:	1
Motif ID:	88
Motif name:	Motif 88
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	3
Number of overlap:	8
Similarity score:	0.00509921

Alignment:
 ACCGGGGCTGCA
 --CGGGGCTG--

Original motif Consensus sequence: ACCGGGGCTGCA

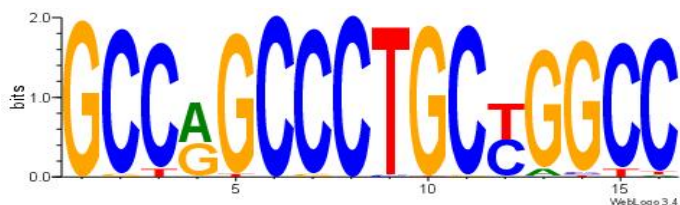
Reverse complement motif Consensus sequence: TGCAGCCCCGGT



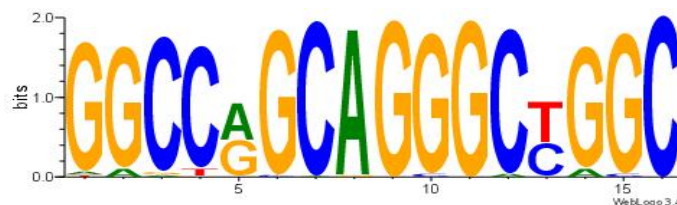
Dataset #: 1
 Motif ID: 183
 Motif name: Motif 183
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 8
 Similarity score: 0.0248687

Alignment:
 GCCRGCCTGCYGGCC
 --CAGCCCG-----

Original motif Consensus sequence: GCCRGCCTGCYGGCC



Reverse complement motif Consensus sequence: GGCCMGCAGGGCKGGC



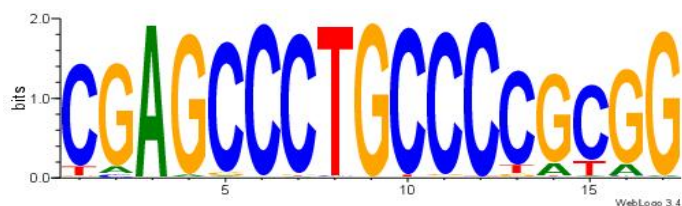
Dataset #: 1

Motif ID: 78
 Motif name: Motif 78
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 4
 Number of overlap: 8
 Similarity score: 0.026456

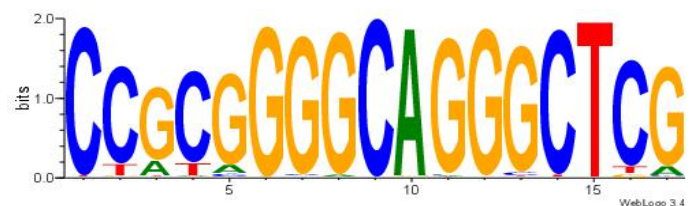
Alignment:

CGAGCCCTGCCCGCGG
 -----CAGCCCG----

Original motif Consensus sequence: CGAGCCCTGCCCGCGG



Reverse complement motif Consensus sequence: CCGCGGGGCAGGGCTCG



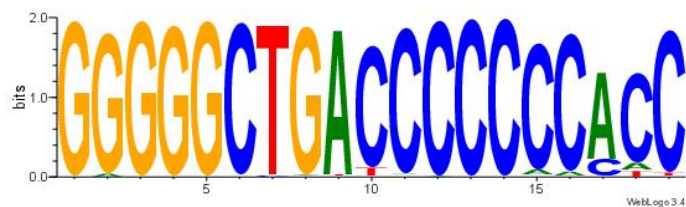
Dataset #: 1
 Motif ID: 92
 Motif name: Motif 92
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 12
 Number of overlap: 8

Similarity score: 0.0266885

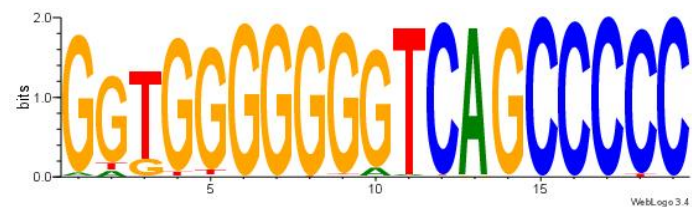
Alignment:

GGGGGCTGACCCCCCACC
-----CGGGGCTG

Original motif Consensus sequence: GGGGGCTGACCCCCCACC



Reverse complement motif Consensus sequence:
GGTGGGGGGGTCAGCCCC



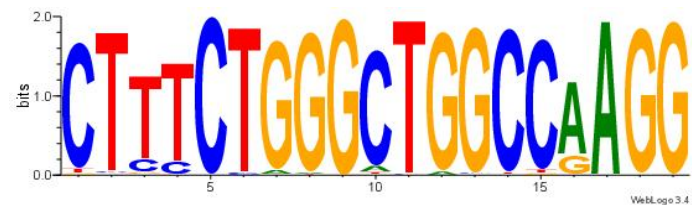
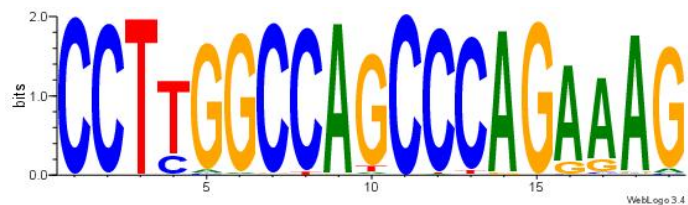
Dataset #: 1
Motif ID: 122
Motif name: Motif 122
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 8
Number of overlap: 8
Similarity score: 0.0291045

Alignment:

CTTTCTGGGCTGGCCAAGG
----CGGGGCTG-----

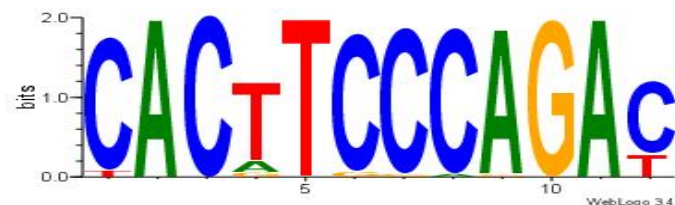
Original motif Consensus sequence: CCTTGGCCAGCCCAGAAAG

Reverse complement motif Consensus sequence:
CTTTCTGGGCTGGCCAAGG

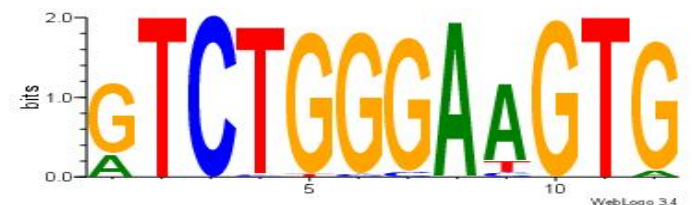


Dataset #: 1 Motif ID: 156 Motif name: Motif 156

Original motif Consensus sequence: CACTTCCCAGAC



Reverse complement motif Consensus sequence: GTCTGGGAAGTG

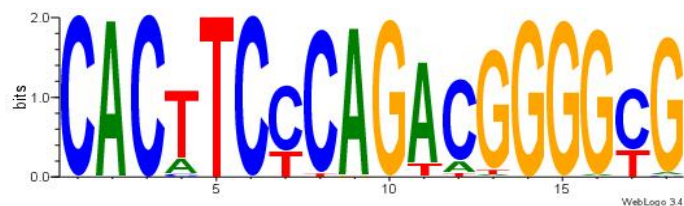


Best Matches for Significant Motif ID 156 (Highest to Lowest)

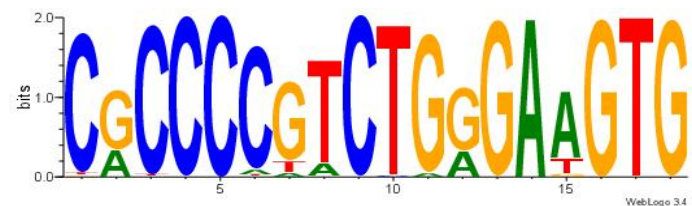
Dataset #:	1
Motif ID:	27
Motif name:	Motif 27
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	7
Number of overlap:	12
Similarity score:	0.00564821

Alignment:
 CACTTCCCAGACGGGGCG
 CACTTCCCAGAC-----

Original motif Consensus sequence: CACTTCCCAGACGGGGCG



Reverse complement motif Consensus sequence: CGCCCCGTCTGGGAAGTG

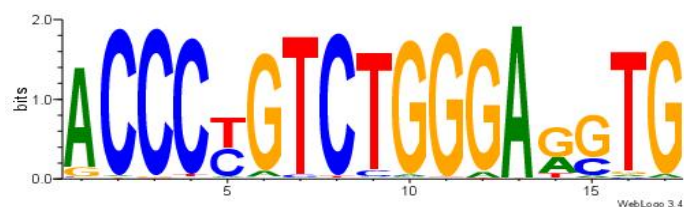


Dataset #: 1
Motif ID: 95
Motif name: Motif 95
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 6
Number of overlap: 12
Similarity score: 0.0183065

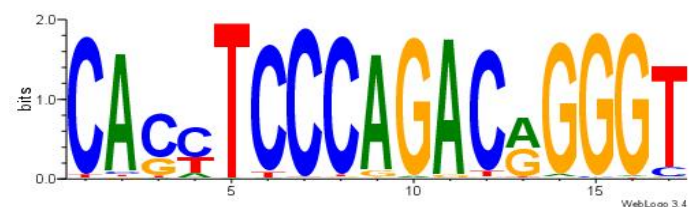
Alignment:

```
CACCTCCCAGACMGGGT  
-----CACTTCCCAGAC
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Original motif Consensus sequence: ACCYGTCTGGGAGGTG



Reverse complement motif Consensus sequence: CACCTCCCAGACMGGGT

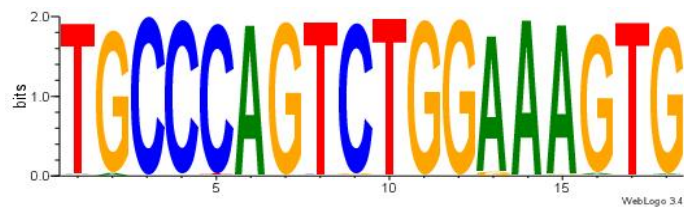


Dataset #: 1
 Motif ID: 45
 Motif name: Motif 45
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 12
 Similarity score: 0.0205412

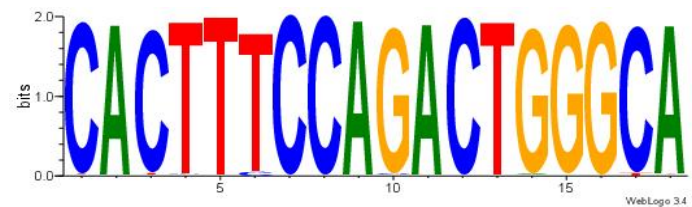
Alignment:

TGCCCAGTCTGGAAAGTG
 GTCTGGGAAGTG-----

Original motif Consensus sequence: TGCCCAGTCTGGAAAGTG



Reverse complement motif Consensus sequence: CACTTCCAGACTGGGCA



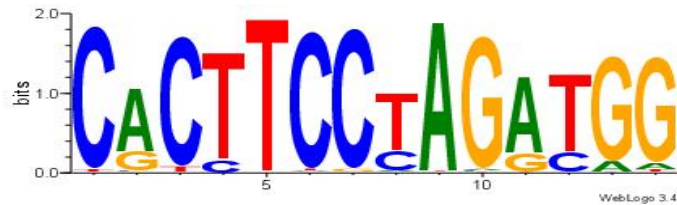
Dataset #: 1
 Motif ID: 74
 Motif name: Motif 74
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3

Number of overlap: 12
Similarity score: 0.0315299

Alignment:

CACTTCCTAGATGG
CACTTCCCAGAC--

Original motif Consensus sequence: CACTTCCTAGATGG



Reverse complement motif Consensus sequence: CCATCTAGGAAGT



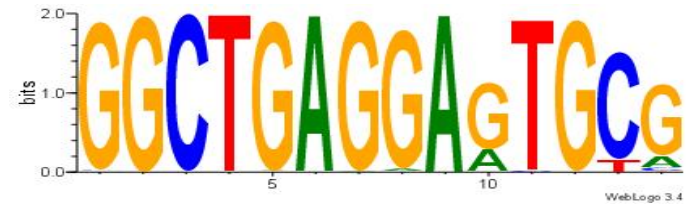
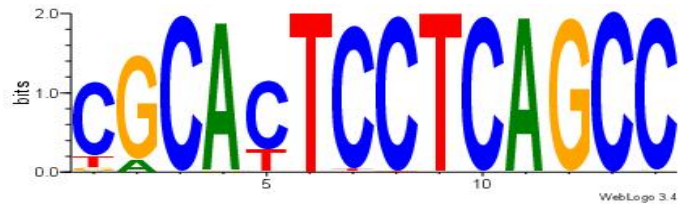
Dataset #: 1
Motif ID: 72
Motif name: Motif 72
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 12
Similarity score: 0.0670258

Alignment:

CGCACTCCTCAGCC
--CACTTCCCAGAC

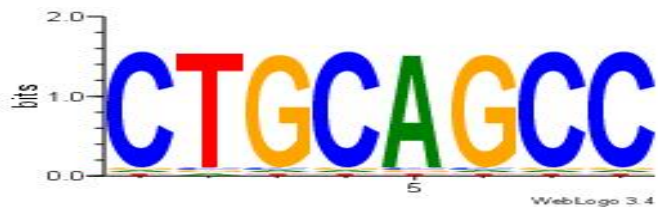
Original motif Consensus sequence: CGCACTCCTCAGCC

Reverse complement motif Consensus sequence: GGCTGAGGAGTGC



Dataset #: 1 Motif ID: 338 Motif name: Motif 338

Original motif Consensus sequence: CTGCAGCC



Reverse complement motif Consensus sequence: GGCTGCAG

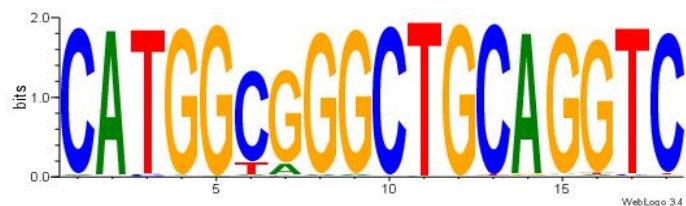


Best Matches for Significant Motif ID 338 (Highest to Lowest)

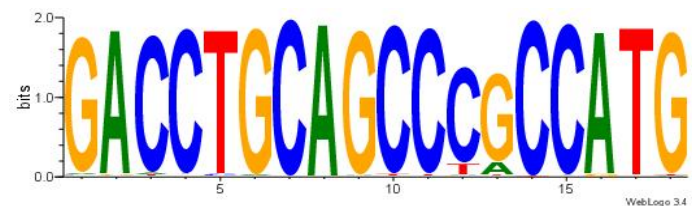
Dataset #:	1
Motif ID:	68
Motif name:	Motif 68
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	4
Number of overlap:	8
Similarity score:	0.0130204

Alignment:
 CATGGCGGGCTGCAGGTC
 ---GGCTGCAG-----

Original motif Consensus sequence: CATGGCGGGCTGCAGGTC



Reverse complement motif Consensus sequence: GACCTGCAGCCCGCCATG



Dataset #: 1
Motif ID: 219
Motif name: Motif 219
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 8
Similarity score: 0.0154581

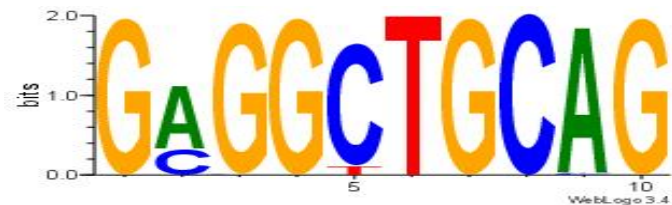
Alignment:

CTGCAGCCTC
CTGCAGCC--

Original motif Consensus sequence: CTGCAGCCTC



Reverse complement motif Consensus sequence: GAGGCTGCAG

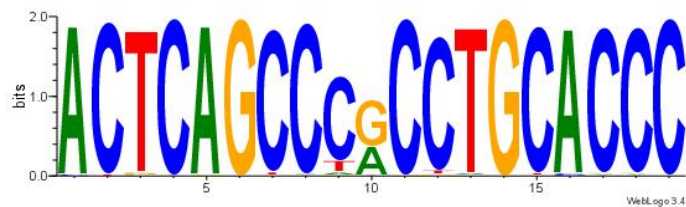


Dataset #: 1
 Motif ID: 149
 Motif name: Motif 149
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 12
 Number of overlap: 8
 Similarity score: 0.0406936

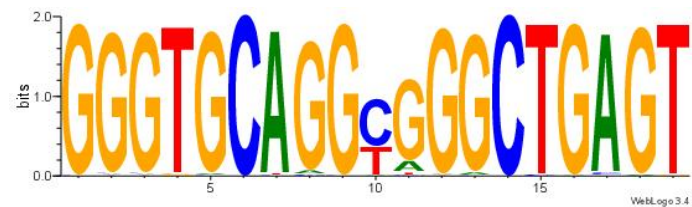
Alignment:

GGGTGCAGGMGGGCTGAGT
 GGCTGCAG-----

Original motif Consensus sequence: ACTCAGCCRCCTGCACCC



Reverse complement motif Consensus sequence: GGGTGCAGGMGGGCTGAGT

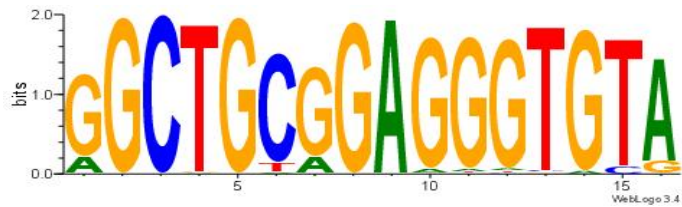


Dataset #: 1
 Motif ID: 89
 Motif name: Motif 89
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 9

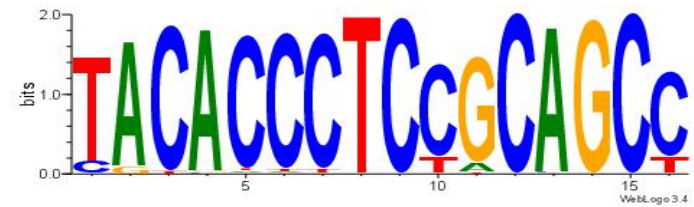
Number of overlap: 8
Similarity score: 0.0413146

Alignment:
TACACCCTCCGCAGCC
CTGCAGCC-----

Original motif Consensus sequence: GGCTGCGGAGGGTGTA



Reverse complement motif Consensus sequence:
TACACCCTCCGCAGCC

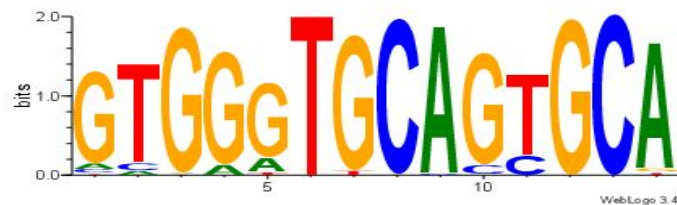
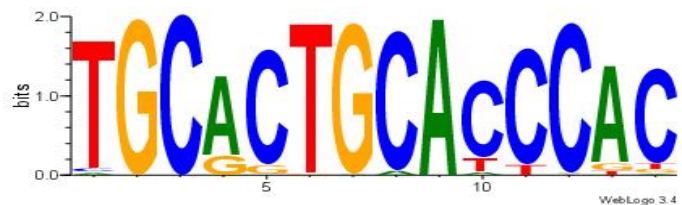


Dataset #: 1
Motif ID: 220
Motif name: Motif 220
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 3
Number of overlap: 8
Similarity score: 0.0415555

Alignment:
GTGGGTGCAGTGCA
--GGCTGCAG----

Original motif Consensus sequence: TGCACTGCACCCAC

Reverse complement motif Consensus sequence: GTGGGTGCAGTGCA

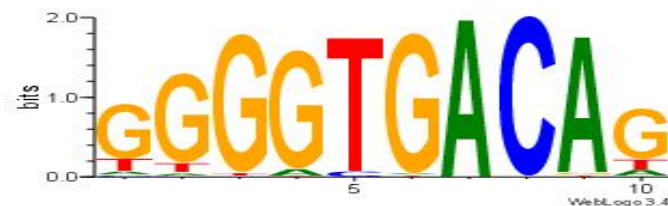


Dataset #: 1 Motif ID: 146 Motif name: Motif 146

Original motif Consensus sequence: CTGTCACCCC



Reverse complement motif Consensus sequence: GGGGTGACAG

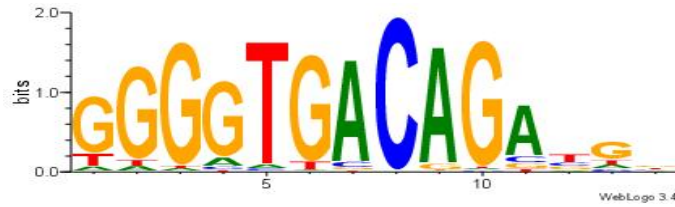


Best Matches for Significant Motif ID 146 (Highest to Lowest)

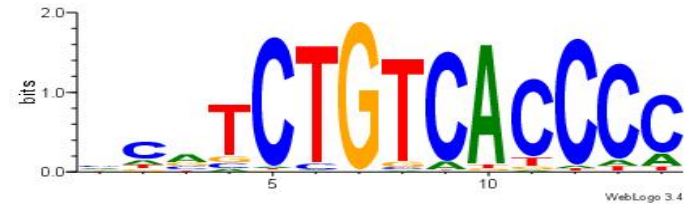
Dataset #:	1
Motif ID:	1
Motif name:	Motif 1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	10
Similarity score:	0.00304976

Alignment:
GGGGTGACAGABGB
----GGGGTGACAG

Original motif Consensus sequence: GGGGTGACAGABGB



Reverse complement motif Consensus sequence: BCVTCTGTCACCC



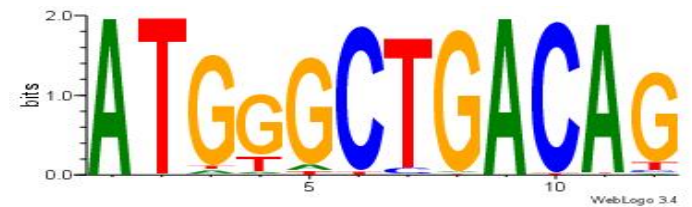
Dataset #: 1
Motif ID: 209
Motif name: Motif 209
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 10
Similarity score: 0.021009

Alignment:
CTGTCAGCCCAT
CTGTCACCC--

Original motif Consensus sequence: CTGTCAGCCCAT



Reverse complement motif Consensus sequence: ATGGGCTGACAG

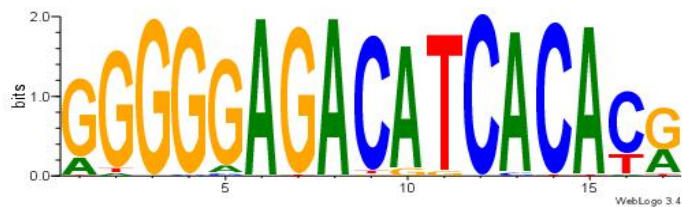


Dataset #: 1
 Motif ID: 279
 Motif name: Motif 279
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 7
 Number of overlap: 10
 Similarity score: 0.0415588

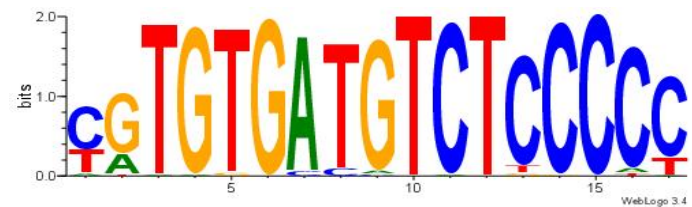
Alignment:

MGTGTGATGTCTCCCC
 -----CTGTCACCCC-

Original motif Consensus sequence: GGGGGAGACATCACACR



Reverse complement motif Consensus sequence: MGTGTGATGTCTCCCC

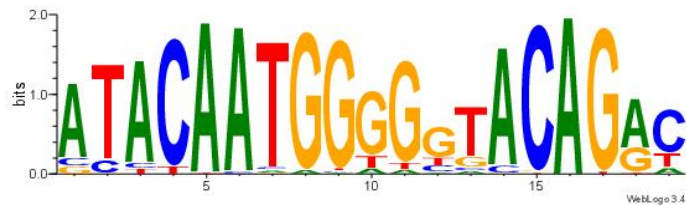


Dataset #: 1
 Motif ID: 193
 Motif name: Motif 193
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3

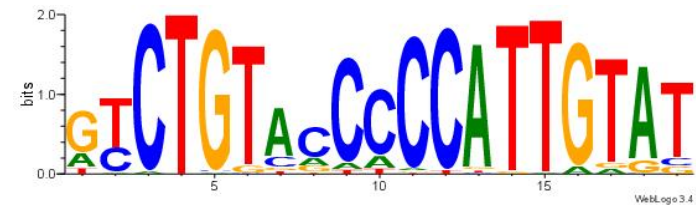
Number of overlap: 10
Similarity score: 0.0448872

Alignment:
ATACAATGGGGGTACAGRC
-----GGGGTGACAG--

Original motif Consensus sequence: ATACAATGGGGGTACAGRC



Reverse complement motif Consensus sequence:
GKCTGTACCCCCATTGTAT

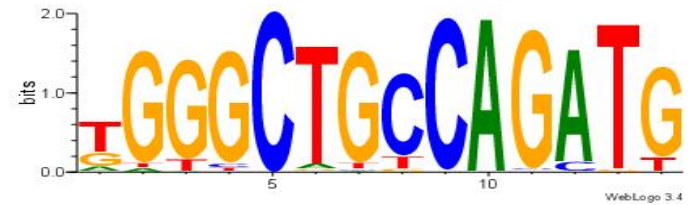
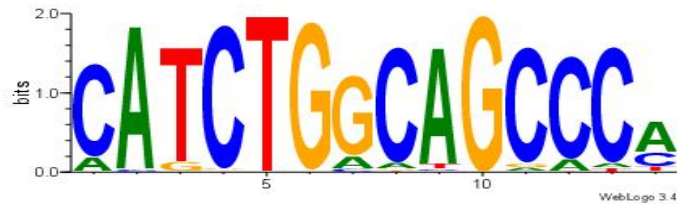


Dataset #: 1
Motif ID: 205
Motif name: Motif 205
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 2
Number of overlap: 10
Similarity score: 0.0451314

Alignment:
TGGGCTGCCAGATG
-GGGGTGACAG---

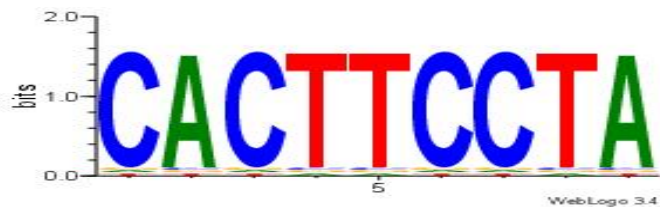
Original motif Consensus sequence: CATCTGGCAGCCCA

Reverse complement motif Consensus sequence: TGGGCTGCCAGAT



Dataset #: 1 Motif ID: 113 Motif name: Motif 113

Original motif Consensus sequence: CACTTCCTA



Reverse complement motif Consensus sequence: TAGGAAGTG

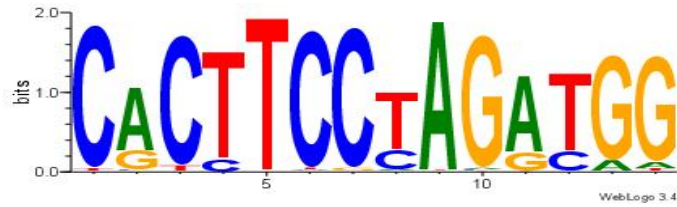


Best Matches for Significant Motif ID 113 (Highest to Lowest)

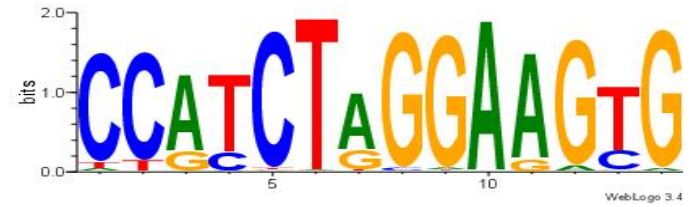
Dataset #:	1
Motif ID:	74
Motif name:	Motif 74
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	9
Similarity score:	0.0147795

Alignment:
 CCATCTAGGAAGTG
 -----TAGGAAGTG

Original motif Consensus sequence: CACTTCCTAGATGG



Reverse complement motif Consensus sequence: CCATCTAGGAAGT

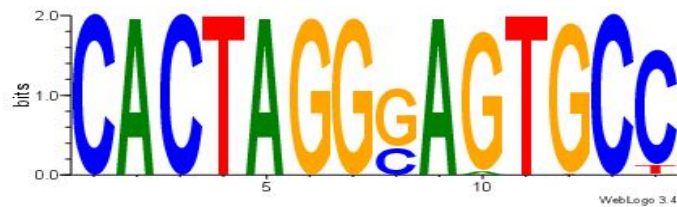


Dataset #: 1
Motif ID: 153
Motif name: Motif 153
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 3
Number of overlap: 9
Similarity score: 0.0332374

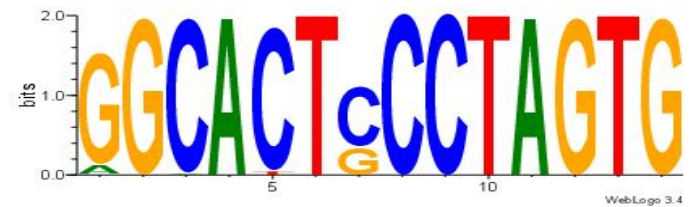
Alignment:

GGCACTCCCTAGTG
--CACTTCCTA----

Original motif Consensus sequence: CACTAGGGAGTGCC



Reverse complement motif Consensus sequence: GGCACTCCCTAGTG

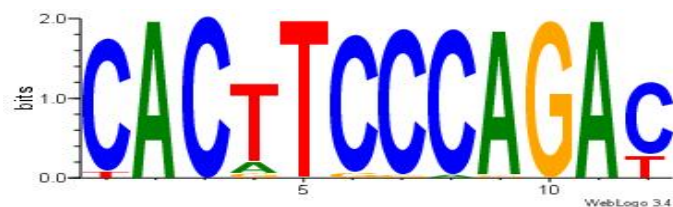


Dataset #: 1
 Motif ID: 156
 Motif name: Motif 156
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 4
 Number of overlap: 9
 Similarity score: 0.0333368

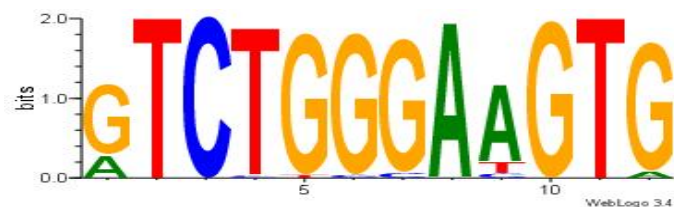
Alignment:

GTCTGGGAAGTG
 ---TAGGAAGTG

Original motif Consensus sequence: CACTTCCCAGAC



Reverse complement motif Consensus sequence: GTCTGGGAAGTG



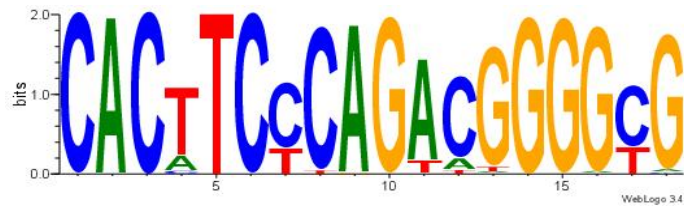
Dataset #: 1
 Motif ID: 27
 Motif name: Motif 27
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 9

Similarity score: 0.0419916

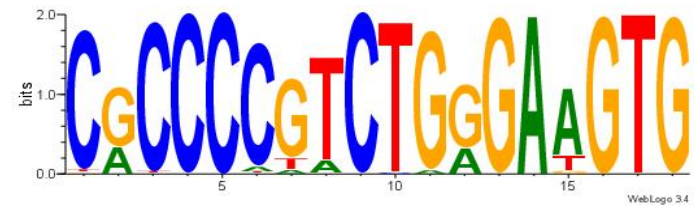
Alignment:

CACTTCCCAGACGGGGCG
CACTTCCTA-----

Original motif Consensus sequence: CACTTCCCAGACGGGGCG



Reverse complement motif Consensus sequence: CGCCCCGTCTGGGAAGTG



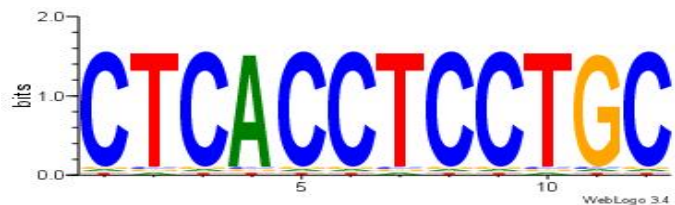
Dataset #: 1
Motif ID: 339
Motif name: Motif 339
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 3
Number of overlap: 9
Similarity score: 0.0431985

Alignment:

GCAGGAGGTGAG
-TAGGAAGTG--

Original motif Consensus sequence: CTCACCTCCTGC

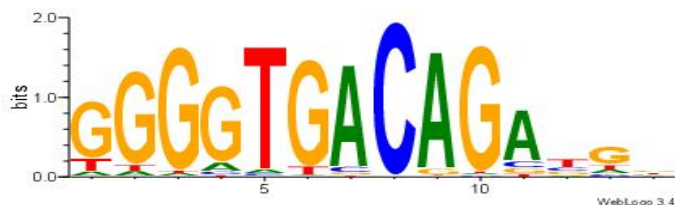
Reverse complement motif Consensus sequence: GCAGGAGGTGAG



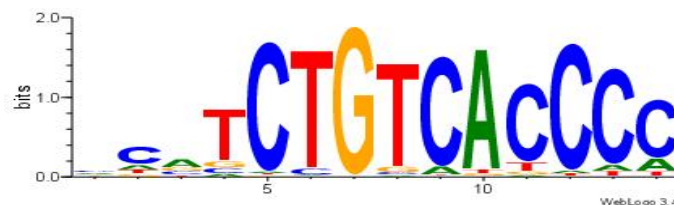
Best Matches for Each Motif (Highest to Lowest)

Dataset #: 1 Motif ID: 1 Motif name: Motif 1

Original motif Consensus sequence: GGGGTGACAGABGB



Reverse complement motif Consensus sequence: BCVTCTGTACCCG



Best Matches for Motif ID 1 (Highest to Lowest)

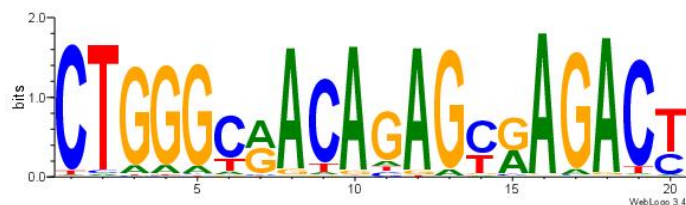
Dataset #:	1
Motif ID:	29
Motif name:	Motif 29
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	14

Similarity score: 0.0644652

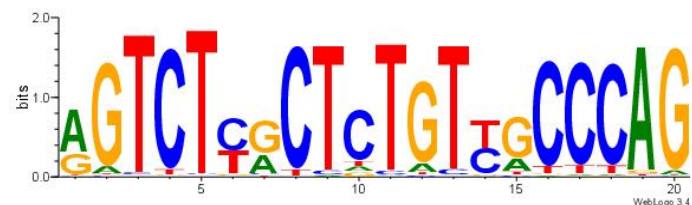
Alignment:

CTGGGCRACAGAGYRAGACY
-GGGGTGACAGABGB-----

Original motif Consensus sequence: CTGGGCRACAGAGYRAGACY



Reverse complement motif Consensus sequence: MGTCTMKCTCTGKGGCCAG



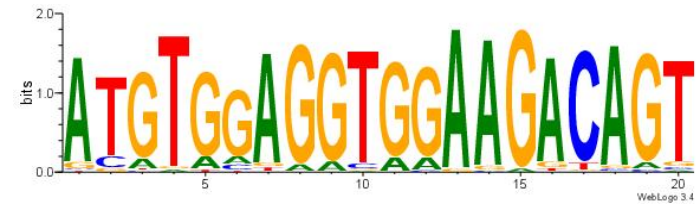
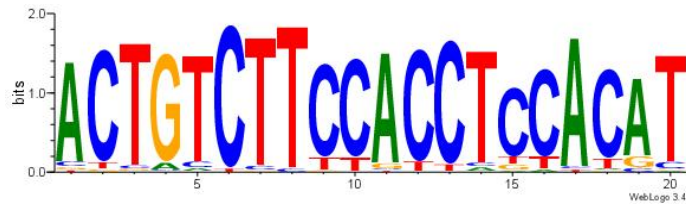
Dataset #: 1
Motif ID: 178
Motif name: Motif 178
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 6
Number of overlap: 14
Similarity score: 0.0767787

Alignment:

ACTGTCTTCCACCTCCACAT
-BCVTCTGTACCCC-----

Original motif Consensus sequence: ACTGTCTTCCACCTCCACAT

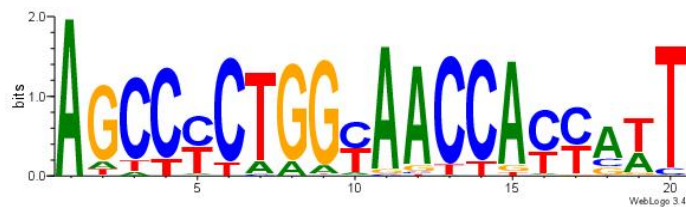
Reverse complement motif Consensus sequence: ATGTGGAGGTGGAAGACAGT



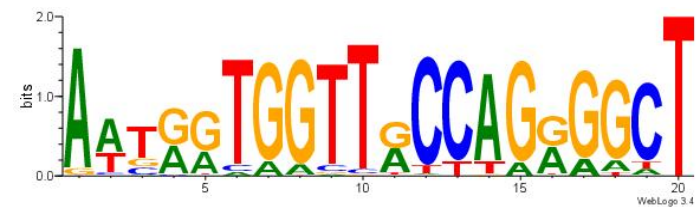
Dataset #: 1
 Motif ID: 139
 Motif name: Motif 139
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 6
 Number of overlap: 14
 Similarity score: 0.0824915

Alignment:
 AGCCYCTGGYAACCAYYAWT
 -BCVTCTGTCACCCC-----

Original motif Consensus sequence: AGCCYCTGGYAACCAYYAWT



Reverse complement motif Consensus sequence: AWTKKTGGTTKCCAGKGGCT



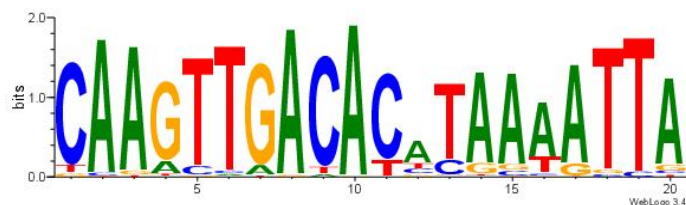
Dataset #: 1

Motif ID: 357
 Motif name: Motif 357
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 14
 Similarity score: 0.0825056

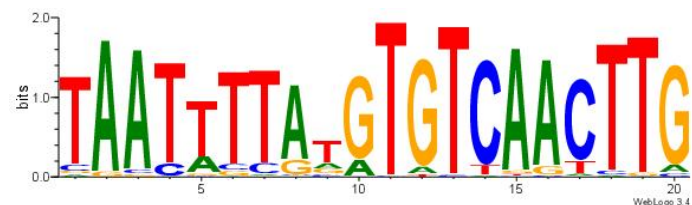
Alignment:

TAATTTTATGTGTCAACTTG
 -----BCVTCTGTCACCCC-

Original motif Consensus sequence: CAAGTTGACACATAAAATTA



Reverse complement motif Consensus sequence: TAATTTTATGTGTCAACTTG



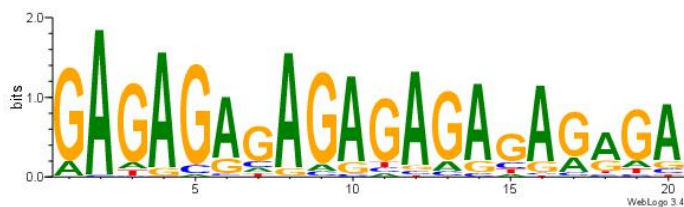
Dataset #: 1
 Motif ID: 109
 Motif name: Motif 109
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 14

Similarity score: 0.0851234

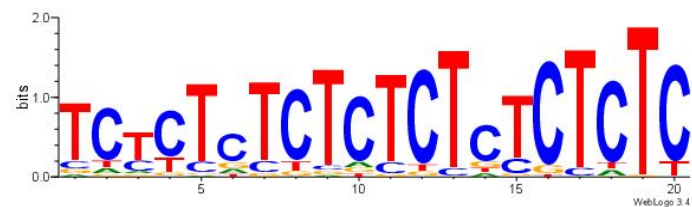
Alignment:

GAGAGAGAGAGAGAGAGAGA
---GGGGTGACAGABGB---

Original motif Consensus sequence: GAGAGAGAGAGAGAGAGA



Reverse complement motif Consensus sequence:
TCTCTCTCTCTCTCTCTC



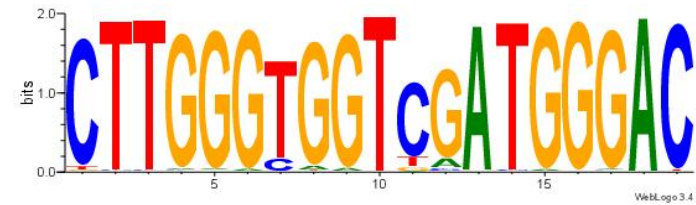
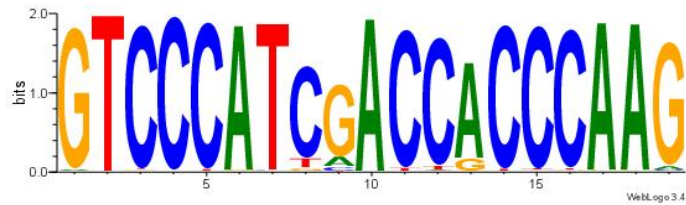
Dataset #: 1
Motif ID: 53
Motif name: Motif 53
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 4
Number of overlap: 14
Similarity score: 0.0864815

Alignment:

CTTGGGTGGTCGATGGGAC
--GGGGTGACAGABGB---

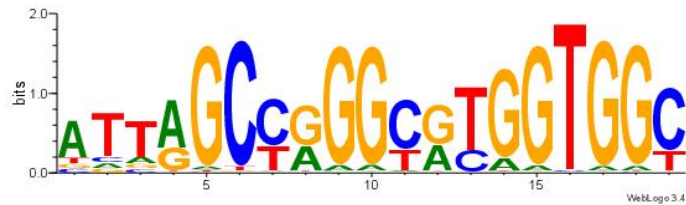
Original motif Consensus sequence: GTCCCATCGACCACCCAAG

Reverse complement motif Consensus sequence:
CTTGGGTGGTCGATGGGAC

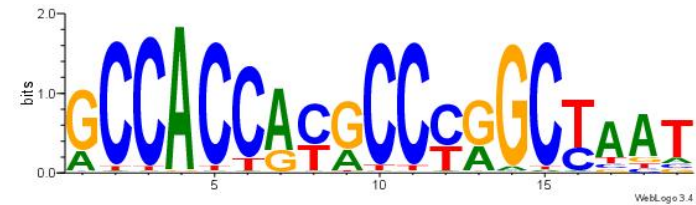


Dataset #: 1 Motif ID: 2 Motif name: Motif 2

Original motif Consensus sequence: ATTAGCYRGGCRTGGTGGC



Reverse complement motif Consensus sequence: GCCACcAMGCCMKGCTAAT



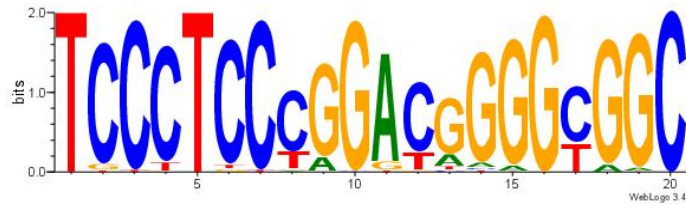
Best Matches for Motif ID 2 (Highest to Lowest)

Dataset #:	1
Motif ID:	155
Motif name:	Motif 155
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	19
Similarity score:	0.0936692

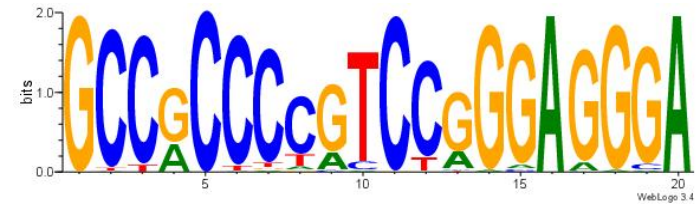
Alignment:

TCCCTCCCGGACGGGGYGGC
-ATTAGCYRGGCRTGGTGGC

Original motif Consensus sequence: TCCCTCCCGGACGGGGYGGC



Reverse complement motif Consensus sequence:
GCCKCCCCGTCCGGGAGGGA



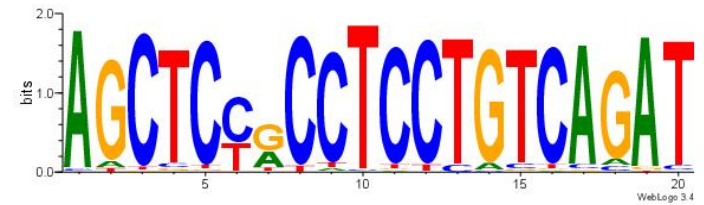
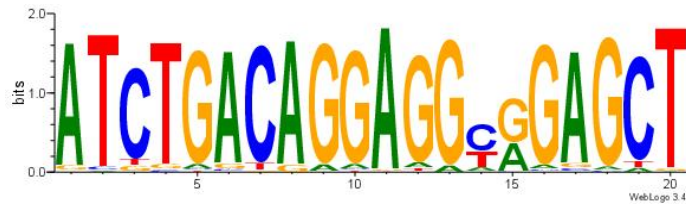
Dataset #: 1
Motif ID: 165
Motif name: Motif 165
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 19
Similarity score: 0.109865

Alignment:

AGCTCMKCCTCCTGTCAGAT
-GCCACCAMGCCMKGCTAAT

Original motif Consensus sequence: ATCTGACAGGAGGYRGAGCT

Reverse complement motif Consensus sequence:
AGCTCMKCCTCCTGTCAGAT

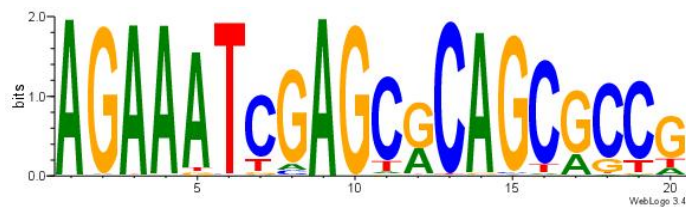


Dataset #: 1
 Motif ID: 65
 Motif name: Motif 65
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 19
 Similarity score: 0.112387

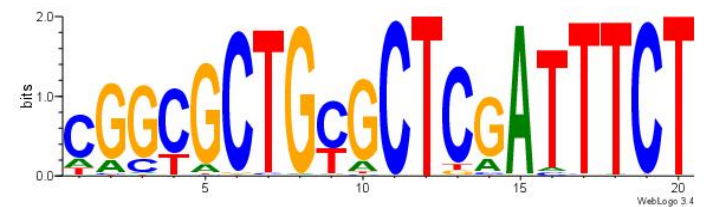
Alignment:

AGAAATCGAGCRCAGCGCCG
 ATTAGCYRGGCRTGGTGGC-

Original motif Consensus sequence: AGAAATCGAGCRCAGCGCCG



Reverse complement motif Consensus sequence: CGGCGCTGMGCTCGATTCT



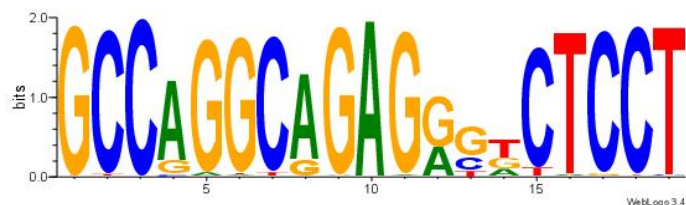
Dataset #: 1

Motif ID: 43
 Motif name: Motif 43
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 19
 Similarity score: 0.116369

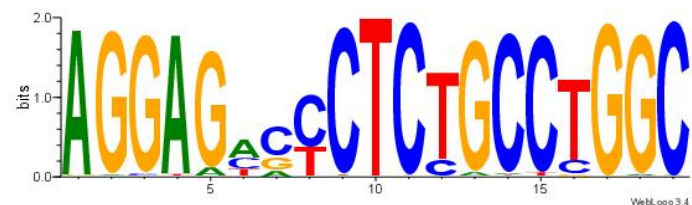
Alignment:

GCCAGGCAGAGRGKCTCCT
 GCCACCAMGCCMKGCTAAT

Original motif Consensus sequence: GCCAGGCAGAGRGKCTCCT



Reverse complement motif Consensus sequence: AGGAGRCMCTCTGCCTGGC



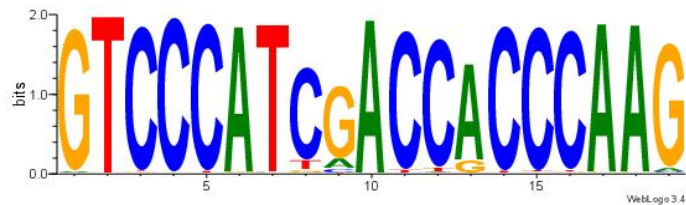
Dataset #: 1
 Motif ID: 53
 Motif name: Motif 53
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 19

Similarity score: 0.116437

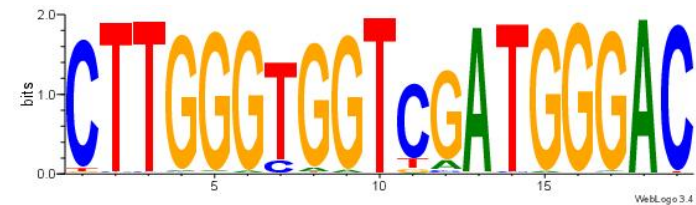
Alignment:

CTTGGGTGGTCGATGGGAC
ATTAGCYRGGCRTGGTGGC

Original motif Consensus sequence: GTCCCATCGACCACCCAAG

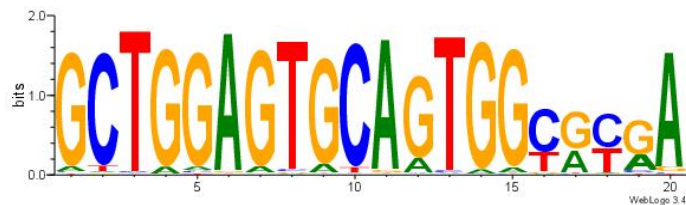


Reverse complement motif Consensus sequence: CTTGGGTGGTCGATGGGAC

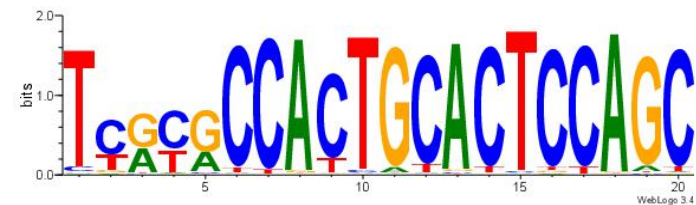


Dataset #: 1 Motif ID: 3 Motif name: Motif 3

Original motif Consensus sequence: GCTGGAGTGCAGTGGCRYGA



Reverse complement motif Consensus sequence: TCKMGCCACTGCACTCCAGC



Best Matches for Motif ID 3 (Highest to Lowest)

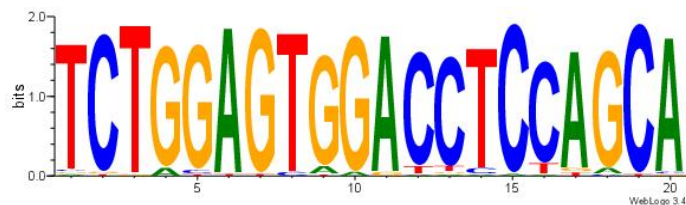
Dataset #:	1
Motif ID:	350
Motif name:	Motif 350
Matching format of first motif:	Original Motif

Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 20
Similarity score: 0.100707

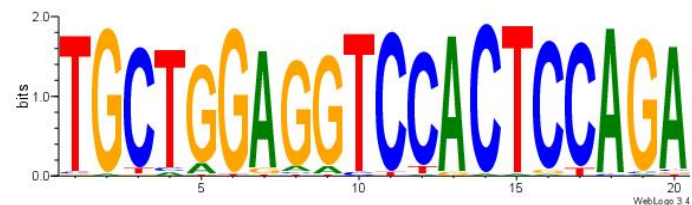
Alignment:

TCTGGAGTGGACCTCCAGCA
GCTGGAGTGCAGTGGCRYGA

Original motif Consensus sequence: TCTGGAGTGGACCTCCAGCA



Reverse complement motif Consensus sequence:
TGCTGGAGGTCCACTCCAGA

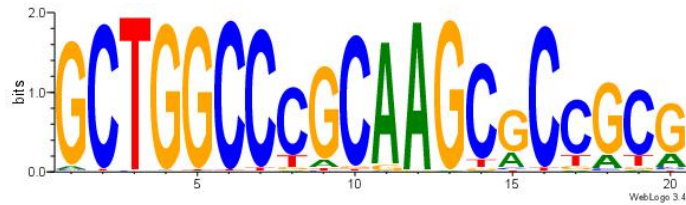


Dataset #: 1
Motif ID: 100
Motif name: Motif 100
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 20
Similarity score: 0.113987

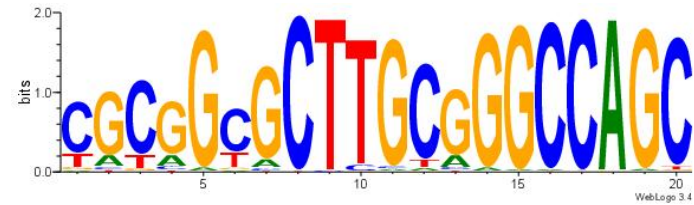
Alignment:

GCTGGCCCGCAAGCGCCGCG
GCTGGAGTGCAGTGGCRYGA

Original motif Consensus sequence: GCTGGCCCGCAAGCGCCGCG



Reverse complement motif Consensus sequence:
CGCGGCGCTTGCGGGCCAGC

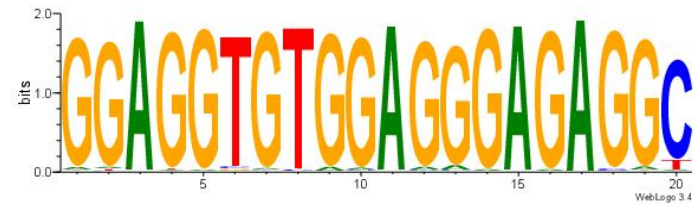
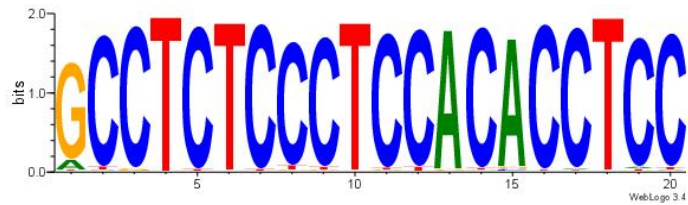


Dataset #: 1
Motif ID: 105
Motif name: Motif 105
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 20
Similarity score: 0.116177

Alignment:
GGAGGTGTGGAGGGAGAGGC
GCTGGAGTGCAGTGGCRYGA

Original motif Consensus sequence: GCCTCTCCCTCCACACCTCC

Reverse complement motif Consensus sequence:
GGAGGTGTGGAGGGAGAGGC

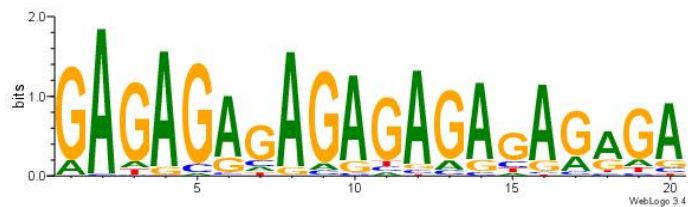


Dataset #: 1
 Motif ID: 109
 Motif name: Motif 109
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.122582

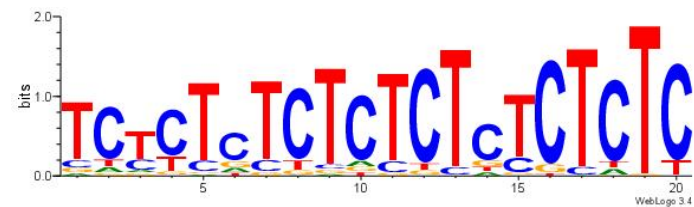
Alignment:

TCTCTCTCTCTCTCTCTCTC
 TCKMGCCACTGCACTCCAGC

Original motif Consensus sequence: GAGAGAGAGAGAGAGAGAGA



Reverse complement motif Consensus sequence: TCTCTCTCTCTCTCTCTC



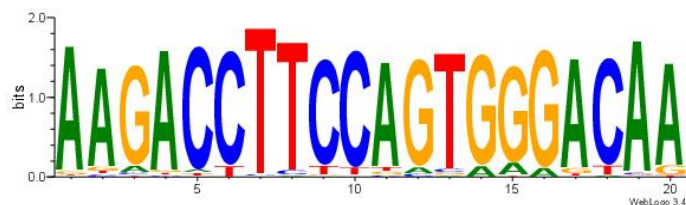
Dataset #: 1

Motif ID: 292
 Motif name: Motif 292
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.122944

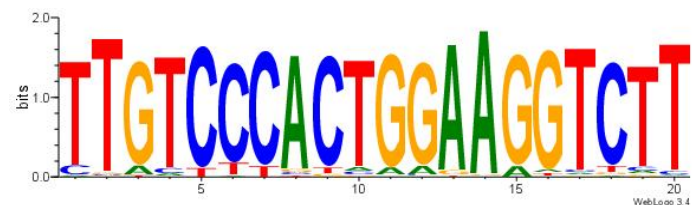
Alignment:

AAGACCTTCCAGTGGGACAA
 GCTGGAGTGCAGTGGCRYGA

Original motif Consensus sequence: AAGACCTTCCAGTGGGACAA

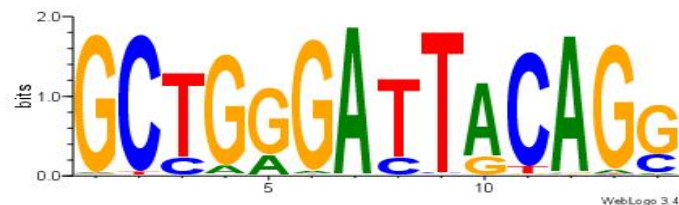


Reverse complement motif Consensus sequence: TTGTCCCCTGGAAGGTCTT



Dataset #: 1 Motif ID: 4 Motif name: Motif 4

Original motif Consensus sequence: GCTGGATTACAGG



Reverse complement motif Consensus sequence: CCTGTAATCCAG



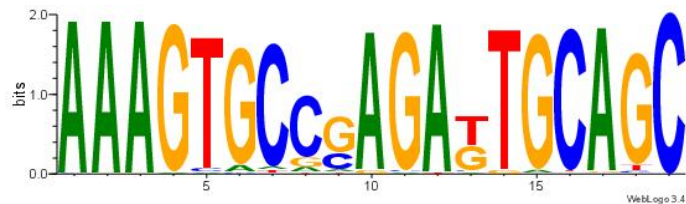
Best Matches for Motif ID 4 (Highest to Lowest)

Dataset #: 1
Motif ID: 191
Motif name: Motif 191
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 14
Similarity score: 0.0598063

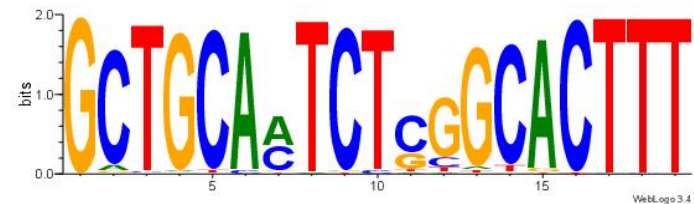
Alignment:

```
AAAGTGCCGAGAKTGCAGC  
-----GCTGGGATTACAGG
```

Original motif Consensus sequence: AAAGTGCCGAGAKTGCAGC



Reverse complement motif Consensus sequence:
GCTGCARTCTCGGCACTTT



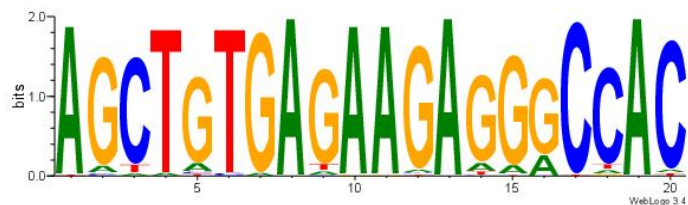
Dataset #: 1
Motif ID: 294
Motif name: Motif 294
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement

Direction: Forward
 Position number: 6
 Number of overlap: 14
 Similarity score: 0.0659358

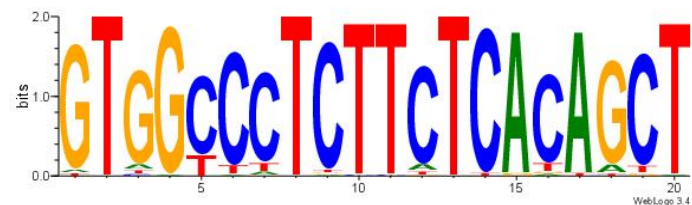
Alignment:

GTGGCCCTCTTCTCACAGCT
 -----CCTGTAATCCCAGC-

Original motif Consensus sequence: AGCTGTGAGAAGAGGGCCAC



Reverse complement motif Consensus sequence: GTGGCCCTCTTCTCACAGCT

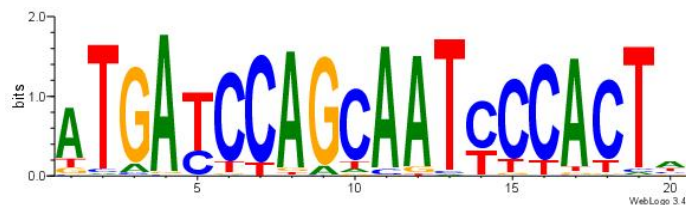


Dataset #: 1
 Motif ID: 115
 Motif name: Motif 115
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 14
 Similarity score: 0.0789579

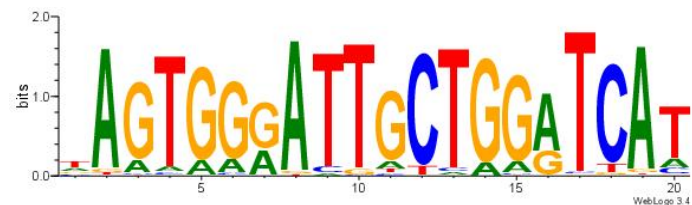
Alignment:

HAGTGGKATTGCTGGATCAT
 -GCTGGGATTACAGG-----

Original motif Consensus sequence: ATGATCCAGCAATYCCACTH



Reverse complement motif Consensus sequence: HAGTGGKATTGCTGGATCAT

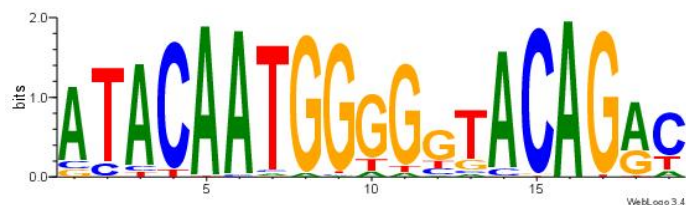


Dataset #: 1
Motif ID: 193
Motif name: Motif 193
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2
Number of overlap: 14
Similarity score: 0.0825729

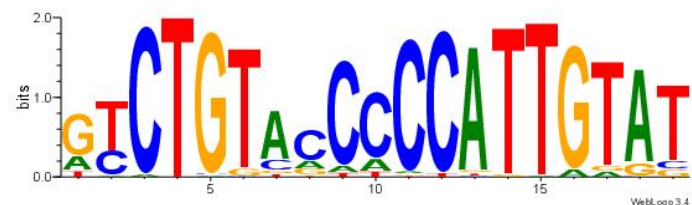
Alignment:

ATACAATGGGGGTACAGRC
----GCTGGGATTACAGG--

Original motif Consensus sequence: ATACAATGGGGGTACAGRC



Reverse complement motif Consensus sequence: GKCTGTACCCCATTTGTAT

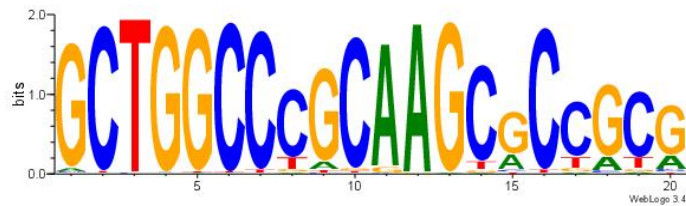


Dataset #: 1
 Motif ID: 100
 Motif name: Motif 100
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 6
 Number of overlap: 14
 Similarity score: 0.0827625

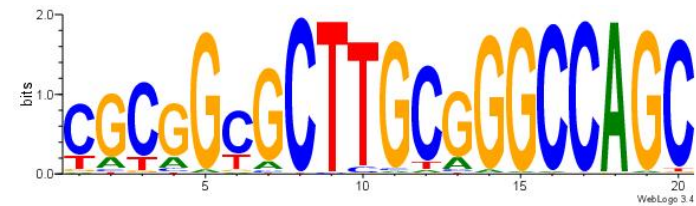
Alignment:

CGCGGCGCTTGC GGGCCAGC
 -GCTGGGATTACAGG-----

Original motif Consensus sequence: GCTGGCCCGCAAGCGCCGCG



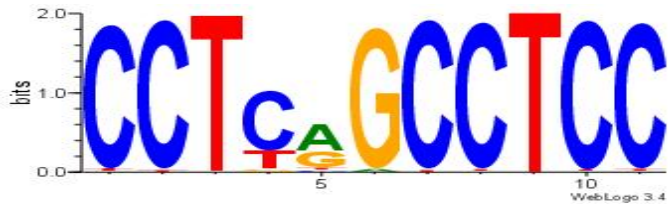
Reverse complement motif Consensus sequence: CGCGGCGCTTGC GGGCCAGC



Dataset #: 1 Motif ID: 5 Motif name: Motif 5

Original motif Consensus sequence: CCTCRGCCTCC

Reverse complement motif Consensus sequence: GGAGGCKGAGG

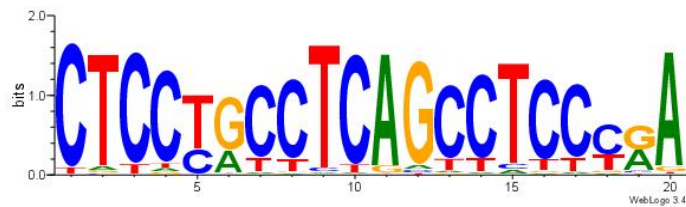


Best Matches for Motif ID 5 (Highest to Lowest)

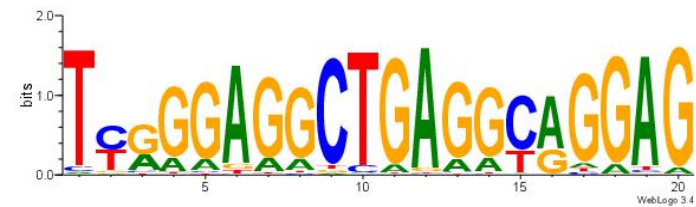
Dataset #: 1
 Motif ID: 26
 Motif name: Motif 26
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 7
 Number of overlap: 11
 Similarity score: 0.0355603

Alignment:
 CTCCTGCCTCAGCCTCCCRA
 -----CCTCRGCCTCC----

Original motif Consensus sequence: CTCCTGCCTCAGCCTCCCRA



Reverse complement motif Consensus sequence: TMGGGAGGCTGAGGCAGGAG

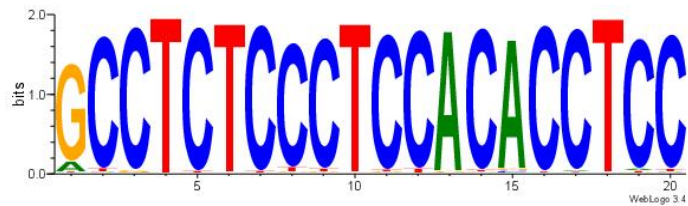


Dataset #: 1
 Motif ID: 105
 Motif name: Motif 105
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 11
 Similarity score: 0.0494199

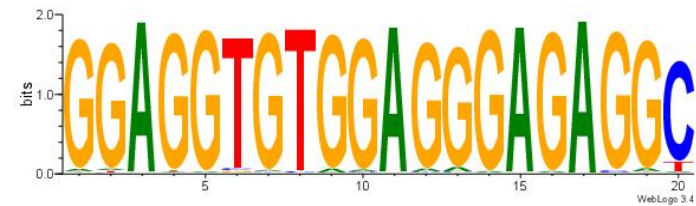
Alignment:

GCCTCTCCCTCCACACCTCC
 -CCTCRGCCTCC-----

Original motif Consensus sequence: GCCTCTCCCTCCACACCTCC



Reverse complement motif Consensus sequence: GGAGGTGTGGAGGGAGAGGC



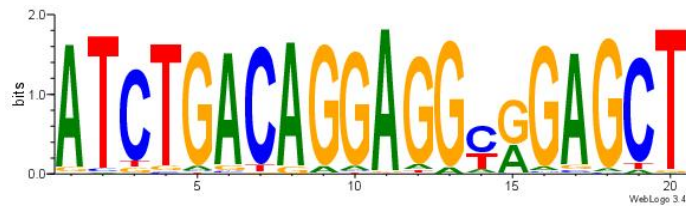
Dataset #: 1
 Motif ID: 165
 Motif name: Motif 165
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2

Number of overlap: 11
Similarity score: 0.0544617

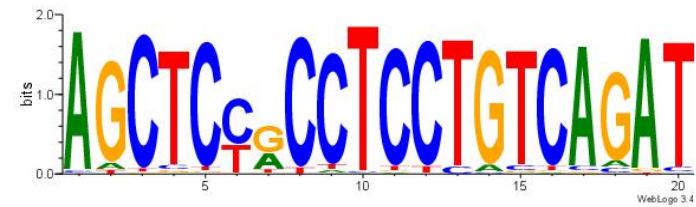
Alignment:

AGCTCMKCCTCCTGTCAGAT
-CCTCRGCCTCC-----

Original motif Consensus sequence: ATCTGACAGGAGGYRGAGCT



Reverse complement motif Consensus sequence:
AGCTCMKCCTCCTGTCAGAT



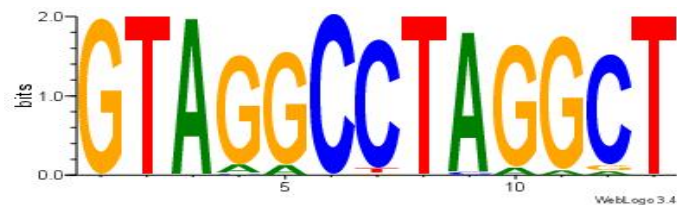
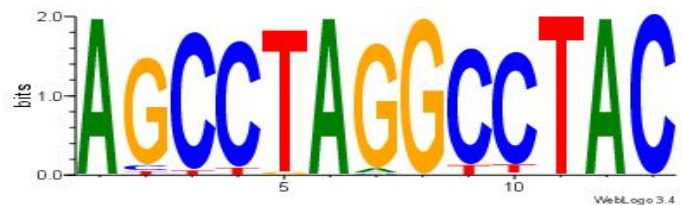
Dataset #: 1
Motif ID: 273
Motif name: Motif 273
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 3
Number of overlap: 11
Similarity score: 0.0616596

Alignment:

AGCCTAGGCCTAC
--CCTCRGCCTCC

Original motif Consensus sequence: AGCCTAGGCCTAC

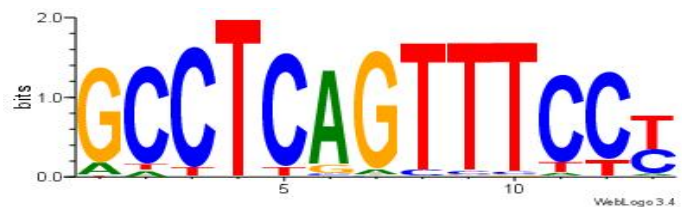
Reverse complement motif Consensus sequence: GTAGGCCTAGGCT



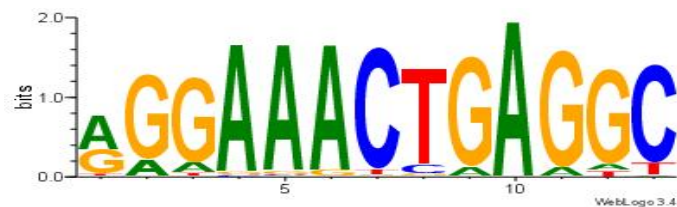
Dataset #: 1
 Motif ID: 47
 Motif name: Motif 47
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 11
 Similarity score: 0.0620118

Alignment:
 GCCTCAGTTTCCY
 -CCTCRGCCTCC-

Original motif Consensus sequence: GCCTCAGTTTCCY

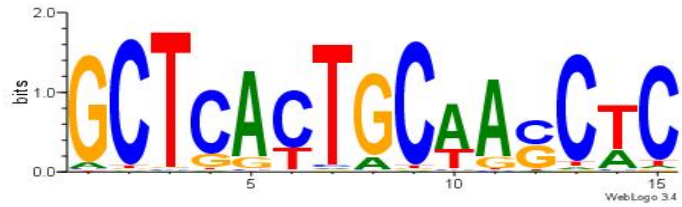


Reverse complement motif Consensus sequence: MGGAAACTGAGGC

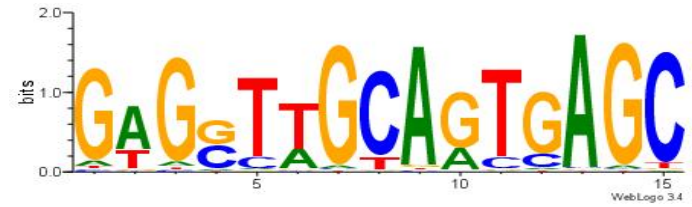


Dataset #: 1 Motif ID: 6 Motif name: Motif 6

Original motif Consensus sequence: GCTCACTGCAASCTC



Reverse complement motif Consensus sequence: GAGSTTGCAGTGA



Best Matches for Motif ID 6 (Highest to Lowest)

Dataset #:	1
Motif ID:	178
Motif name:	Motif 178
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	6
Number of overlap:	15
Similarity score:	0.0768829

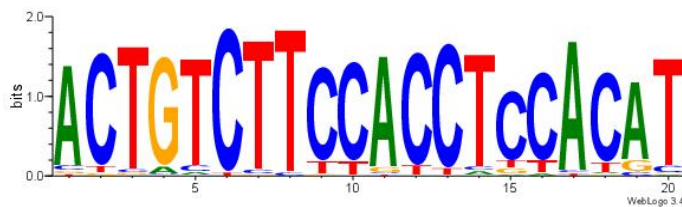
Alignment:

```

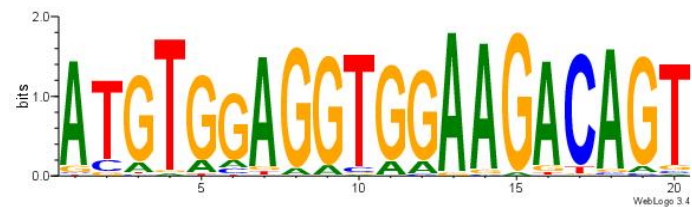
ATGTGGAGGTGGAAGACAGT
-----GAGSTTGCAGTGAGC

```

Original motif Consensus sequence: ACTGTCTTCCACCTCCACAT



Reverse complement motif Consensus sequence: ATGTGGAGGTGGAAGACAGT

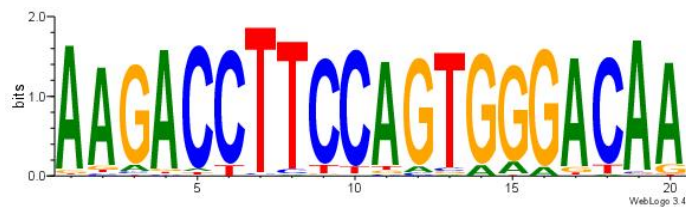


Dataset #: 1
 Motif ID: 292
 Motif name: Motif 292
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 15
 Similarity score: 0.0774202

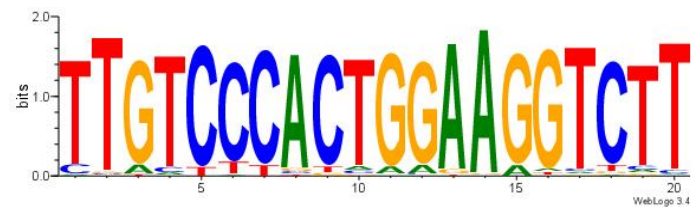
Alignment:

AAGACCTTCCAGTGGGACAA
 --GAGSTTGCAGTGAGC---

Original motif Consensus sequence: AAGACCTTCCAGTGGGACAA



Reverse complement motif Consensus sequence: TTGTCCTTGGAAAGGTCTT



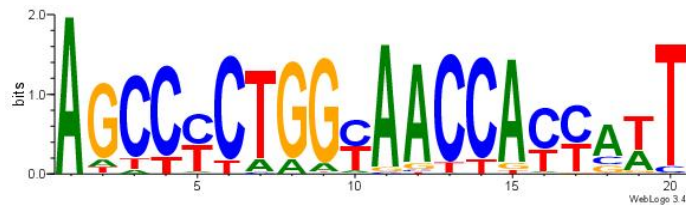
Dataset #: 1
 Motif ID: 139
 Motif name: Motif 139
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 5

Number of overlap: 15
Similarity score: 0.0892327

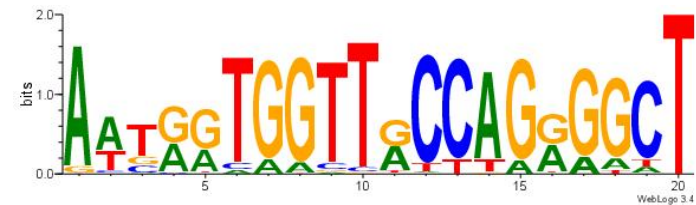
Alignment:

AWTKKTGGTTKCCAGKGGCT
----GAGSTTGCAGTGAGC-

Original motif Consensus sequence: AGCCYCTGGYAACCAYYAWT



Reverse complement motif Consensus sequence:
AWTKKTGGTTKCCAGKGGCT

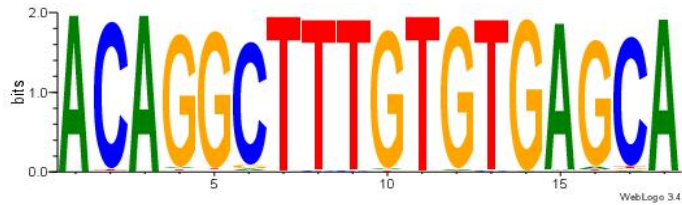


Dataset #: 1
Motif ID: 159
Motif name: Motif 159
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 2
Number of overlap: 15
Similarity score: 0.0907441

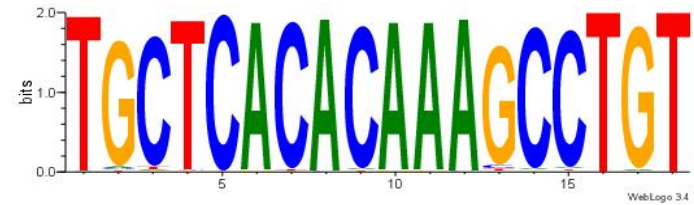
Alignment:

TGCTCACACAAAGCCTGT
-GCTCACTGCAASCTC--

Original motif Consensus sequence: ACAGGCTTTGTGTGAGCA



Reverse complement motif Consensus sequence: TGCTCACACAAAGCCTGT

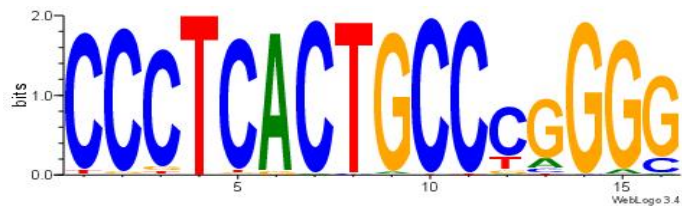


Dataset #: 1
Motif ID: 136
Motif name: Motif 136
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 15
Similarity score: 0.091144

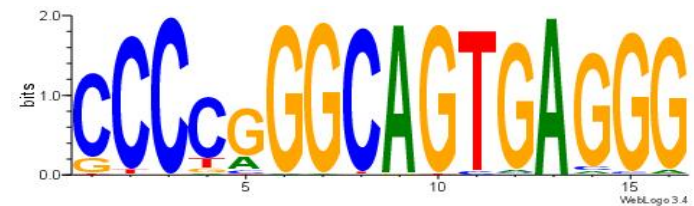
Alignment:

CCCCGGGCAGTGAGGG
GAGSTTGCAGTGAGC-

Original motif Consensus sequence: CCCTCACTGCCcGGGG

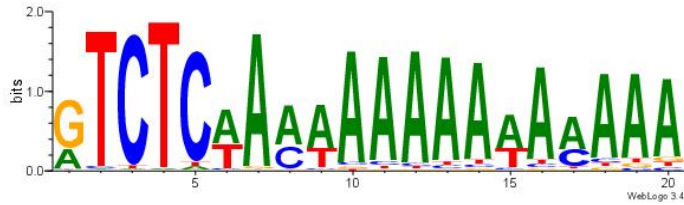


Reverse complement motif Consensus sequence: CCCCggGCAGTGAGGG

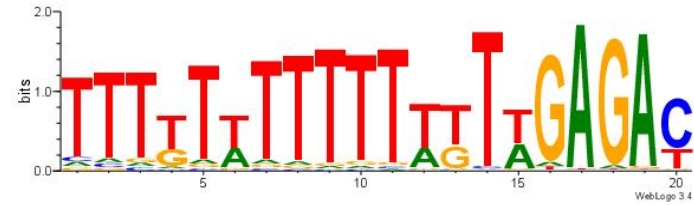


Dataset #: 1 Motif ID: 7 Motif name: Motif 7

Original motif Consensus sequence: GTCTCWAMAAAAAWAMAAA



Reverse complement motif Consensus sequence: TTTYTWTTTTTYYTWGAGAC



Best Matches for Motif ID 7 (Highest to Lowest)

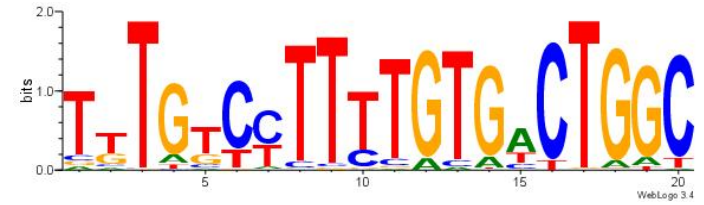
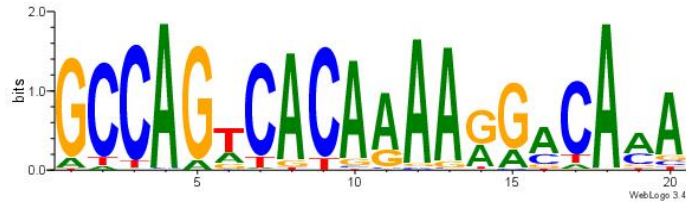
Dataset #:	1
Motif ID:	145
Motif name:	Motif 145
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	20
Similarity score:	0.0958672

Alignment:

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GCCAGTCACAAAARGACAMA  
GTCTCWAMAAAAAWAMAAA
```

Original motif Consensus sequence: GCCAGTCACAAAARGACAMA

Reverse complement motif Consensus sequence: TYTTCMTTTTTGTGACTGGC

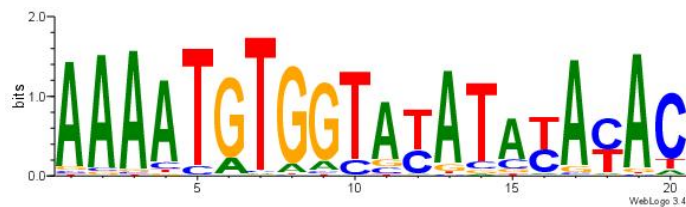


Dataset #: 1
 Motif ID: 83
 Motif name: Motif 83
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.124077

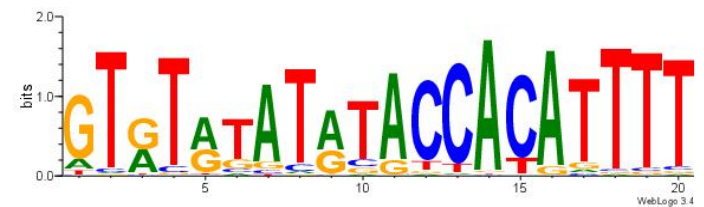
Alignment:

GTKTMTATMTACCACATTTT
 GTCTCWAMAAAAAWAMAAA

Original motif Consensus sequence: AAAATGTGGTAYATAYAYAC



Reverse complement motif Consensus sequence: GTKTMTATMTACCACATTTT



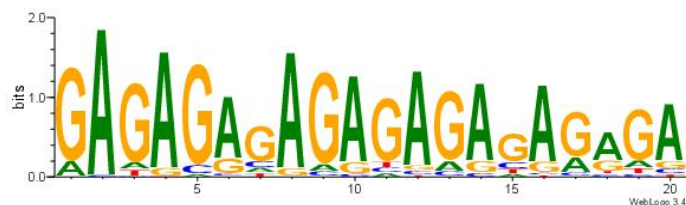
Dataset #: 1

Motif ID: 109
 Motif name: Motif 109
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.127162

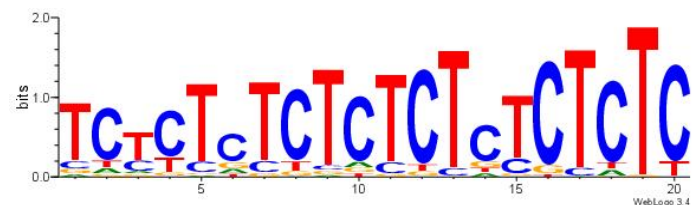
Alignment:

GAGAGAGAGAGAGAGAGAGA
 GTCTCWAMAAAAAWAMAAA

Original motif Consensus sequence: GAGAGAGAGAGAGAGAGA



Reverse complement motif Consensus sequence: TCTCTCTCTCTCTCTCTC



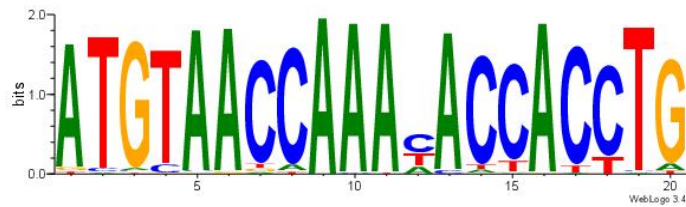
Dataset #: 1
 Motif ID: 336
 Motif name: Motif 336
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 20

Similarity score: 0.127593

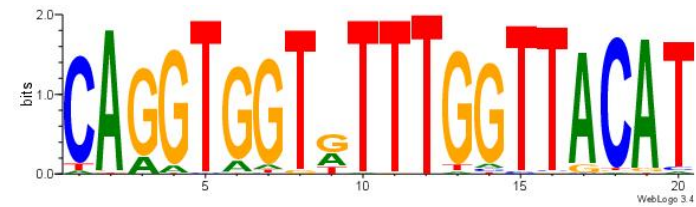
Alignment:

ATGTAACCAAAYACCACCTG
GTCTCWAMAAAAAWAMAAA

Original motif Consensus sequence: ATGTAACCAAAYACCACCTG



Reverse complement motif Consensus sequence:
CAGGTGGTKTTTGGTTACAT



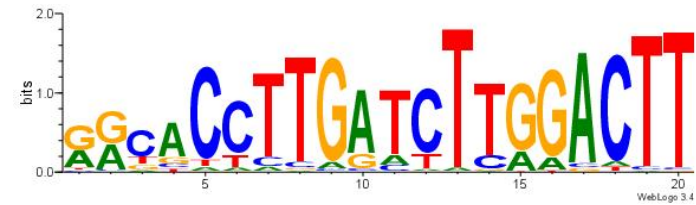
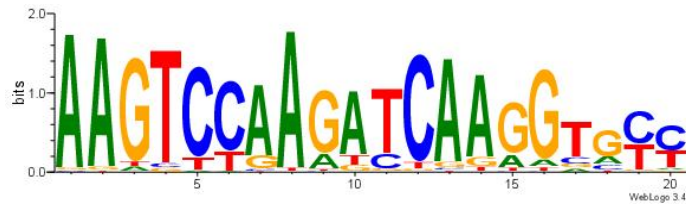
Dataset #: 1
Motif ID: 119
Motif name: Motif 119
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 20
Similarity score: 0.129755

Alignment:

KKCACCTTGATCTTGGACTT
TTYTWTTTTTYYTWGAGAC

Original motif Consensus sequence: AAGTCCAAGATCAAGGTGY

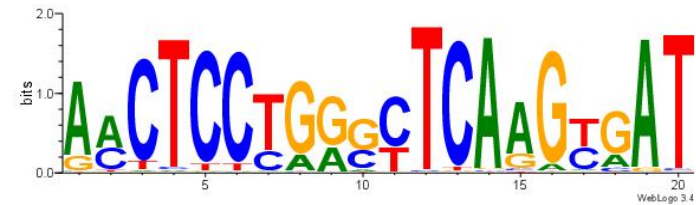
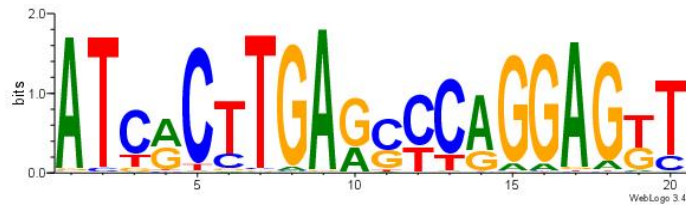
Reverse complement motif Consensus sequence:
KKCACCTTGATCTTGGACTT



Dataset #: 1 Motif ID: 8 Motif name: Motif 8

Original motif Consensus sequence: ATCRCTTGAGSYCAGGAGKT

Reverse complement motif Consensus sequence: ARCTCCTGKSCTCAAGKGAT



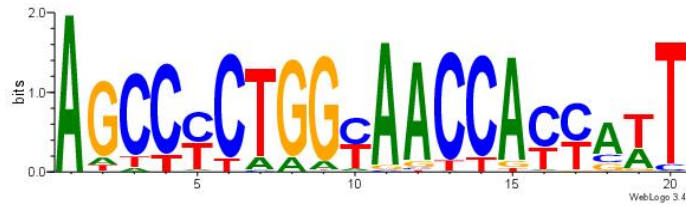
Best Matches for Motif ID 8 (Highest to Lowest)

Dataset #:	1
Motif ID:	139
Motif name:	Motif 139
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	20
Similarity score:	0.0757564

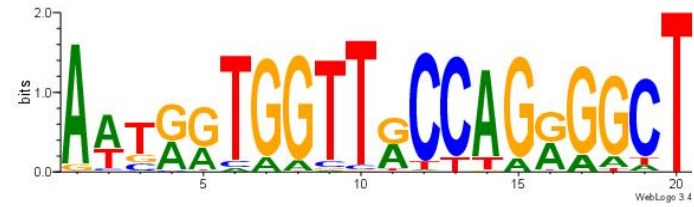
Alignment:

AGCCYCTGGYAACCAYYAWT
ARCTCCTGKSCTCAAGKGAT

Original motif Consensus sequence: AGCCYCTGGYAACCAYYAWT



Reverse complement motif Consensus sequence:
AWTKKTGGTTKCCAGGGCT

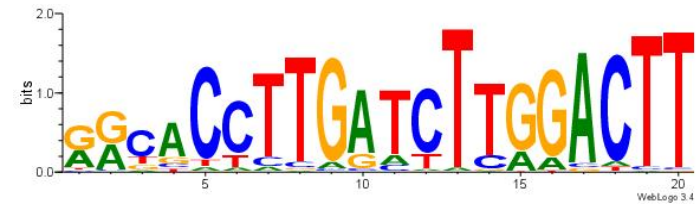
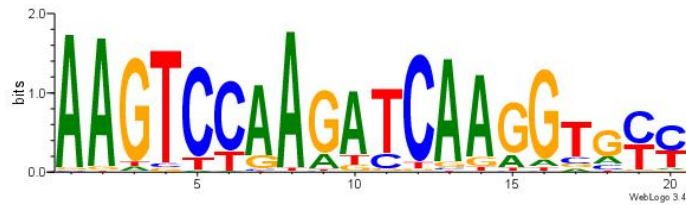


Dataset #: 1
Motif ID: 119
Motif name: Motif 119
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 20
Similarity score: 0.0854742

Alignment:
KKCACCTTGATCTTGGACTT
ATCRCTTGAGSYCAGGAGKT

Original motif Consensus sequence: AAGTCCAAGATCAAGGTGY

Reverse complement motif Consensus sequence:
KKCACCTTGATCTTGGACTT

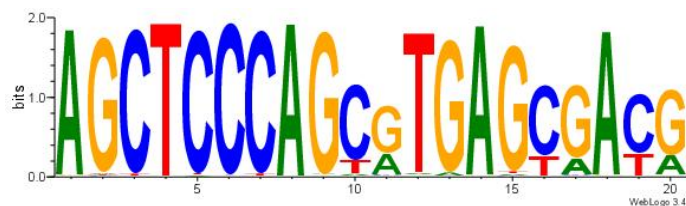


Dataset #: 1
 Motif ID: 48
 Motif name: Motif 48
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.0875132

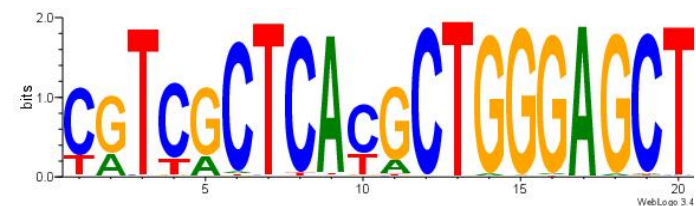
Alignment:

CGTCGCTCACGCTGGGAGCT
 ATCRCTTGAGSYCAGGAGKT

Original motif Consensus sequence: AGCTCCCAGCGTGAGCGACG



Reverse complement motif Consensus sequence: CGTCGCTCACGCTGGGAGCT



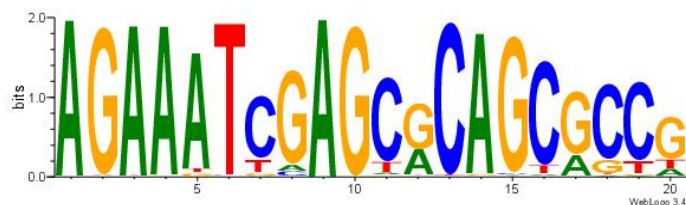
Dataset #: 1

Motif ID: 65
 Motif name: Motif 65
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.0919085

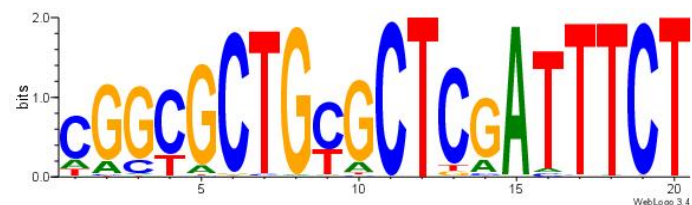
Alignment:

CGGCGCTGMGCTCGATTTCT
 ARCTCCTGKSCTCAAGKGAT

Original motif Consensus sequence: AGAAATCGAGCRCAGCGCCG



Reverse complement motif Consensus sequence: CGGCGCTGMGCTCGATTTCT



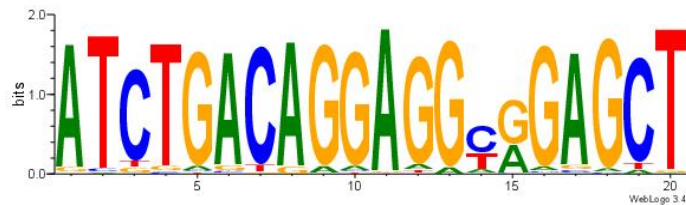
Dataset #: 1
 Motif ID: 165
 Motif name: Motif 165
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 20

Similarity score: 0.0931628

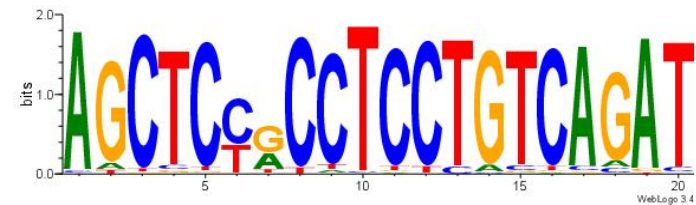
Alignment:

AGCTCMKCCTCCTGTCAGAT
ARCTCCTGKSCTCAAGKGAT

Original motif Consensus sequence: ATCTGACAGGAGGYRGAGCT



Reverse complement motif Consensus sequence: AGCTCMKCCTCCTGTCAGAT

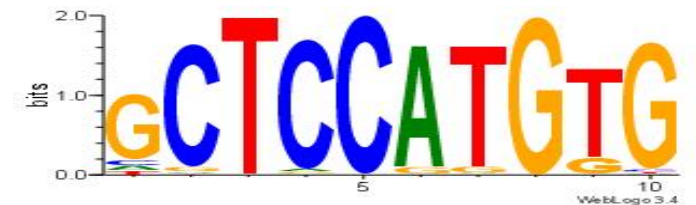


Dataset #: 1 Motif ID: 9 Motif name: Motif 9

Original motif Consensus sequence: CACATGGAGC



Reverse complement motif Consensus sequence: GCTCCATGTG



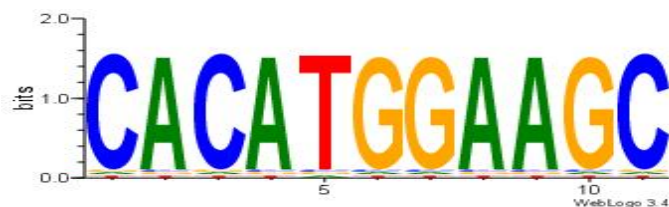
Best Matches for Motif ID 9 (Highest to Lowest)

Dataset #:	1
Motif ID:	353
Motif name:	Motif 353
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement

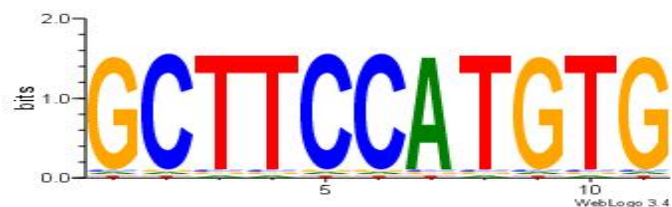
Direction: Forward
Position number: 2
Number of overlap: 10
Similarity score: 0.0442841

Alignment:
GCTTCCATGTG
-GCTCCATGTG

Original motif Consensus sequence: CACATGGAAGC



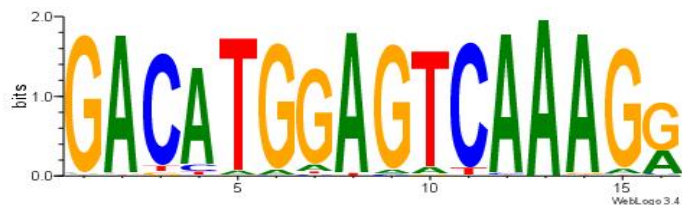
Reverse complement motif Consensus sequence: GCTTCCATGTG



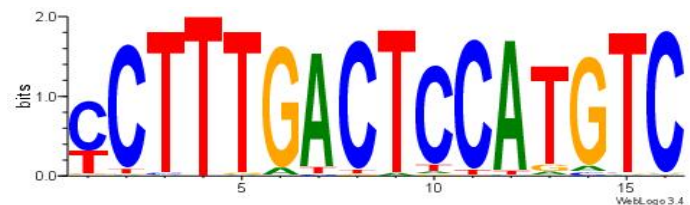
Dataset #: 1
Motif ID: 326
Motif name: Motif 326
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 7
Number of overlap: 10
Similarity score: 0.0461936

Alignment:
GACATGGAGTCAAAGG
CACATGGAGC-----

Original motif Consensus sequence: GACATGGAGTCAAAGG



Reverse complement motif Consensus sequence: CCTTTGACTCCATGTC

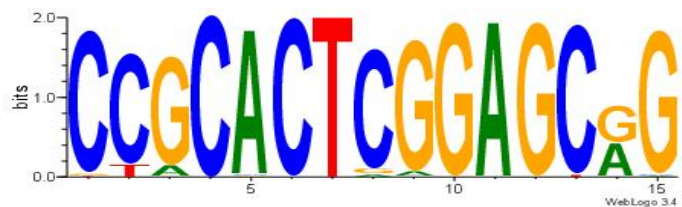


Dataset #: 1
Motif ID: 128
Motif name: Motif 128
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 4
Number of overlap: 10
Similarity score: 0.0487399

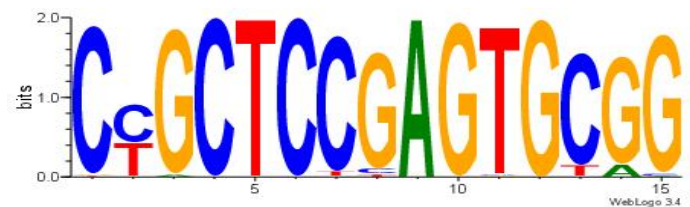
Alignment:

CMGCTCCGAGTGCGG
--GCTCCATGTG---

Original motif Consensus sequence: CCGCACTCGGAGCRG



Reverse complement motif Consensus sequence: CMGCTCCGAGTGCGG

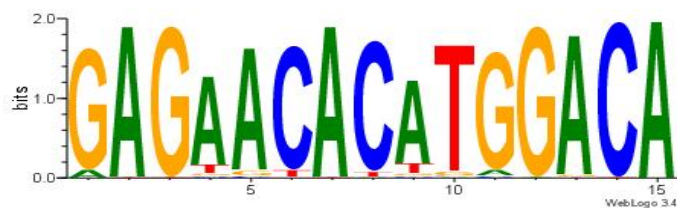


Dataset #: 1
 Motif ID: 257
 Motif name: Motif 257
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 6
 Number of overlap: 10
 Similarity score: 0.0488667

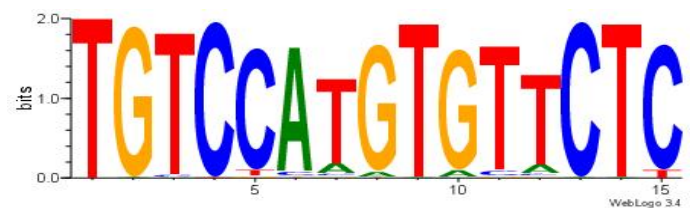
Alignment:

TGTCCATGTGTTCTC
 GCTCCATGTG-----

Original motif Consensus sequence: GAGAACACATGGACA



Reverse complement motif Consensus sequence: TGTCCATGTGTTCTC



Dataset #: 1
 Motif ID: 320
 Motif name: Motif 320
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 10

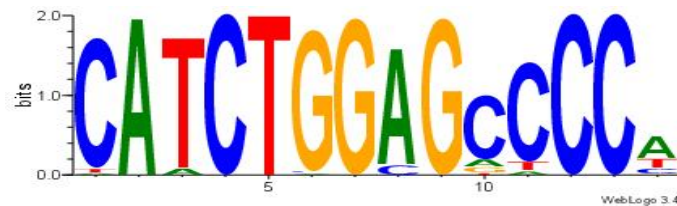
Similarity score: 0.048999

Alignment:

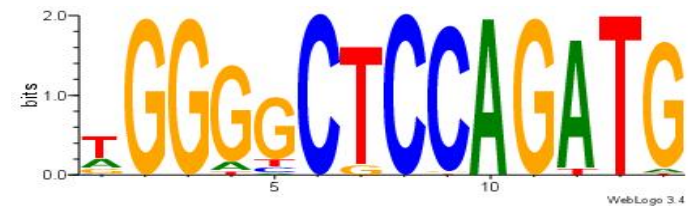
CATCTGGAGCCCCA

CACATGGAGC-----

Original motif Consensus sequence: CATCTGGAGCCCCA

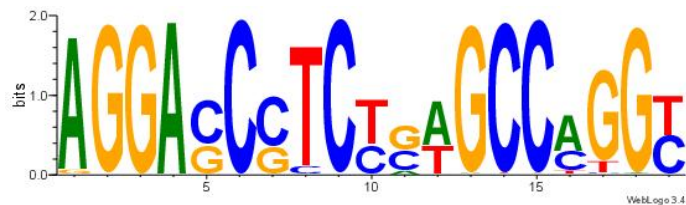


Reverse complement motif Consensus sequence: TGGGGCTCCAGATG

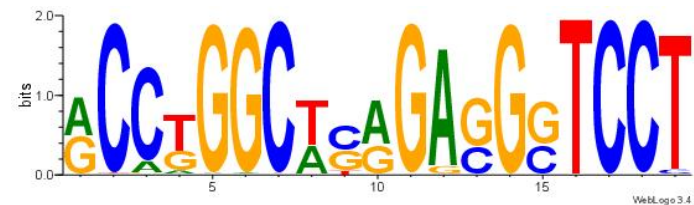


Dataset #: 1 Motif ID: 10 Motif name: Motif 10

Original motif Consensus sequence: AGGASCSTCYSWGCCMGGY



Reverse complement motif Consensus sequence: MCCYGGCWSMGASGSTCCT



Best Matches for Motif ID 10 (Highest to Lowest)

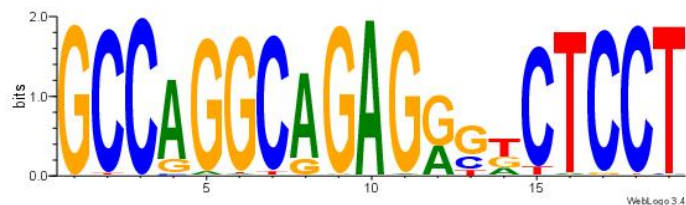
Dataset #:	1
Motif ID:	43
Motif name:	Motif 43
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif

Direction: Backward
 Position number: 1
 Number of overlap: 19
 Similarity score: 0.0458009

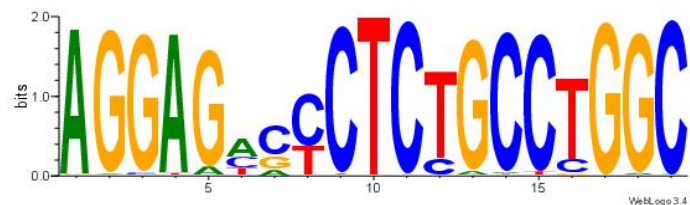
Alignment:

GCCAGGCAGAGRGKCTCCT
 MCCYGGCWSMGASGSTCCT

Original motif Consensus sequence: GCCAGGCAGAGRGKCTCCT



Reverse complement motif Consensus sequence: AGGAGRCMCTCTGCCTGGC

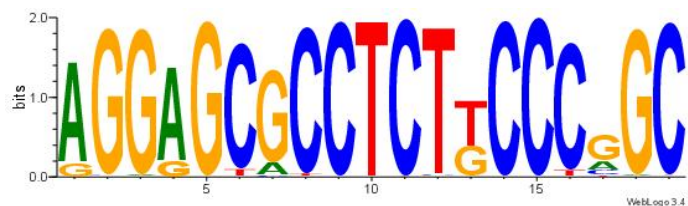


Dataset #: 1
 Motif ID: 30
 Motif name: Motif 30
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 19
 Similarity score: 0.0489869

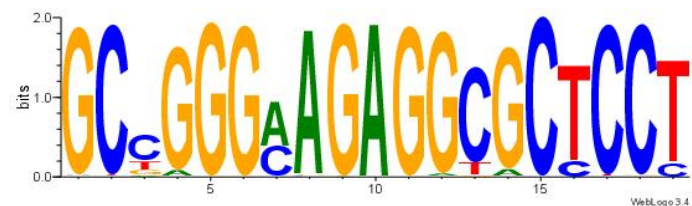
Alignment:

AGGAGCGCCTCTKCCCGGC
 AGGASCSTCYSWGCCMGY

Original motif Consensus sequence: AGGAGCGCTCTKCCCGGC



Reverse complement motif Consensus sequence: GCCGGGRAGAGGCGCTCCT

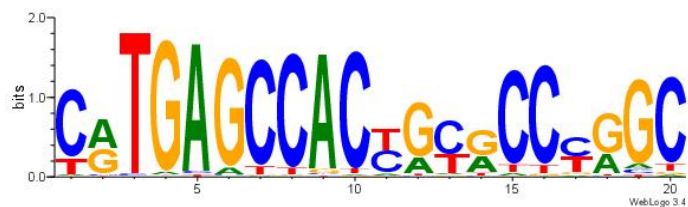


Dataset #: 1
Motif ID: 56
Motif name: Motif 56
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 19
Similarity score: 0.0576721

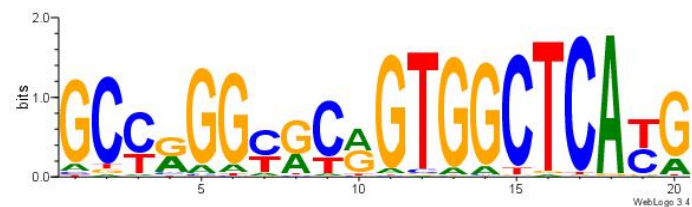
Alignment:

CRTGAGCCACYGYRCCYGGC
-AGGASCSTCYSWGCCMGY

Original motif Consensus sequence: CRTGAGCCACYGYRCCYGGC



Reverse complement motif Consensus sequence: GCCKGGMKCMGTGGCTCAKG

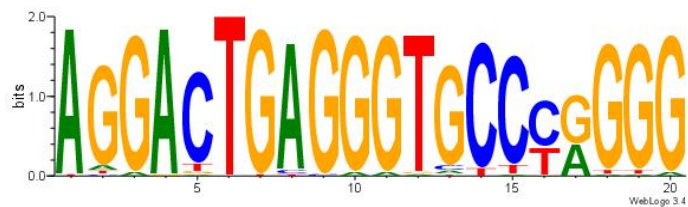


Dataset #: 1
 Motif ID: 312
 Motif name: Motif 312
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 19
 Similarity score: 0.0673069

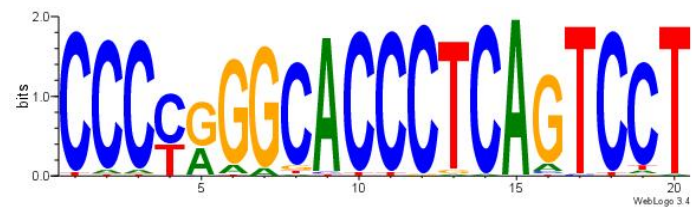
Alignment:

CCCMKGGCACCCCTCAGTCCT
 -MCCYGGCWSMGASGSTCCT

Original motif Consensus sequence: AGGACTGAGGGTGCCYRGGG



Reverse complement motif Consensus sequence: CCCMKGGCACCCCTCAGTCCT



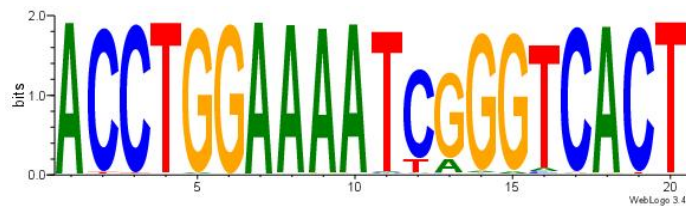
Dataset #: 1
 Motif ID: 14
 Motif name: Motif 14
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2

Number of overlap: 19
Similarity score: 0.0821184

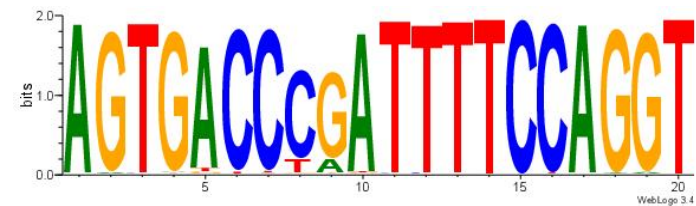
Alignment:

AGTGACCCGATTTTCCAGGT
-AGGASCSTCYSWGCCMGY

Original motif Consensus sequence: ACCTGGAAAATCGGGTCACT



Reverse complement motif Consensus sequence: AGTGACCCGATTTTCCAGGT



Dataset #: 1 Motif ID: 11 Motif name: Motif 11

Original motif Consensus sequence: CTC AAGGTCC



Reverse complement motif Consensus sequence: TGGACCTTGAG



Best Matches for Motif ID 11 (Highest to Lowest)

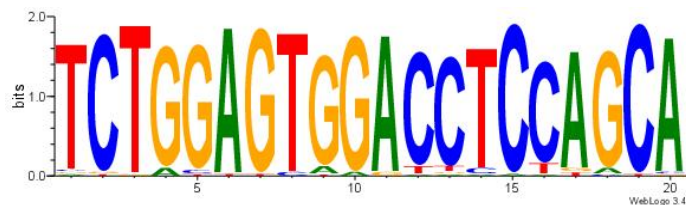
Dataset #: 1
Motif ID: 350
Motif name: Motif 350
Matching format of first motif: Original Motif

Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 8
 Number of overlap: 11
 Similarity score: 0.0546726

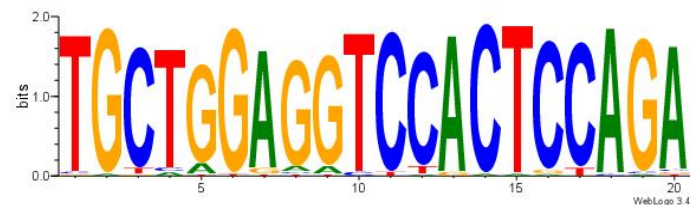
Alignment:

TGCTGGAGGTCCACTCCAGA
 --CTCAAGGTCCA-----

Original motif Consensus sequence: TCTGGAGTGGACCTCCAGCA



Reverse complement motif Consensus sequence:
 TGCTGGAGGTCCACTCCAGA

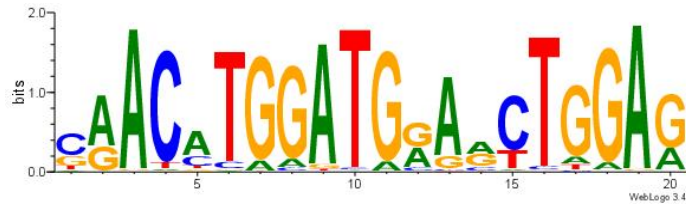


Dataset #: 1
 Motif ID: 104
 Motif name: Motif 104
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 10
 Number of overlap: 11
 Similarity score: 0.054717

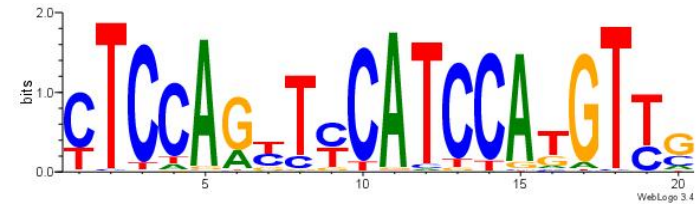
Alignment:

CTCCAGKTMCATCCATGTTG
 CTCAAGGTCCA-----

Original motif Consensus sequence: CAACATGGATGRARCTGGAG



Reverse complement motif Consensus sequence:
 CTCCAGKTMCATCCATGTTG

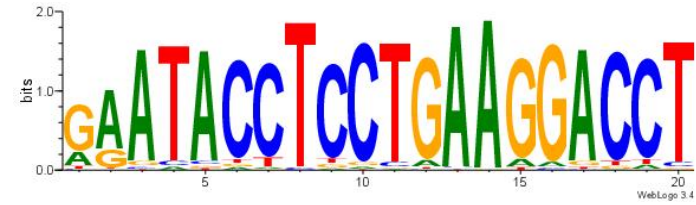
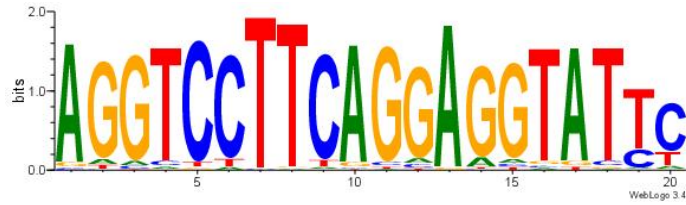


Dataset #:	1
Motif ID:	179
Motif name:	Motif 179
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	11
Similarity score:	0.0579649

Alignment:
 AGGTCCTTCAGGAGGTATTC
 TGGACCTTGAG-----

Original motif Consensus sequence: AGGTCCTTCAGGAGGTATTC

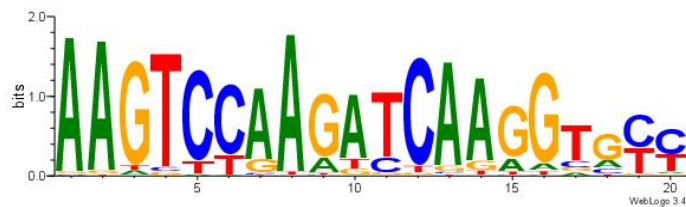
Reverse complement motif Consensus sequence:
 GAATACCTCCTGAAGGACCT



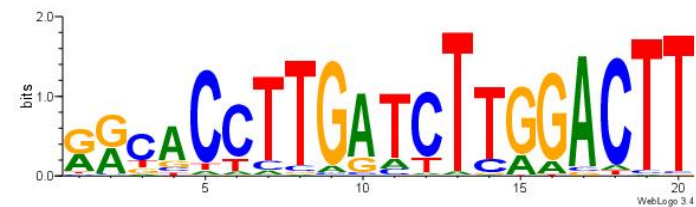
Dataset #: 1
 Motif ID: 119
 Motif name: Motif 119
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 10
 Number of overlap: 11
 Similarity score: 0.0624438

Alignment:
 KKCACCTTGATCTTGGACTT
 TGGACCTTGAG-----

Original motif Consensus sequence: AAGTCCAAGATCAAGGTGYY



Reverse complement motif Consensus sequence: KKCACCTTGATCTTGGACTT



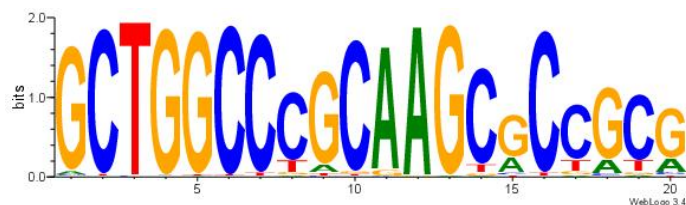
Dataset #: 1

Motif ID: 100
 Motif name: Motif 100
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 8
 Number of overlap: 11
 Similarity score: 0.0683174

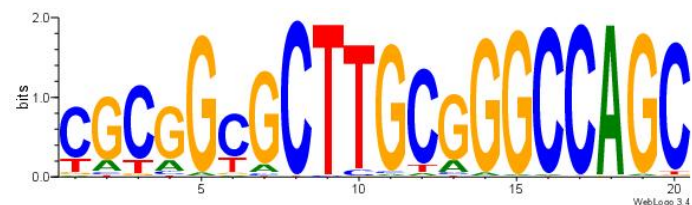
Alignment:

CGCGGCGCTTGC GGGCCAGC
 --TGGACCTTGAG-----

Original motif Consensus sequence: GCTGGCCCGCAAGCGCCGCG

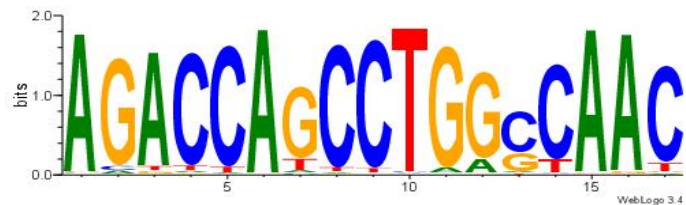


Reverse complement motif Consensus sequence: CGCGGCGCTTGC GGGCCAGC

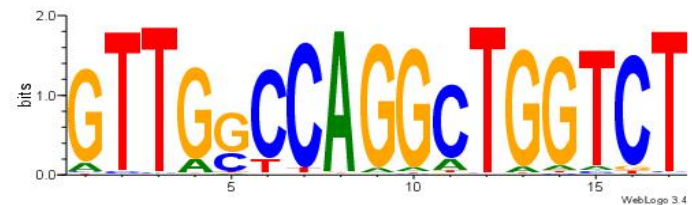


Dataset #: 1 Motif ID: 12 Motif name: Motif 12

Original motif Consensus sequence: AGACCAGCCTGGCCAAC



Reverse complement motif Consensus sequence: GTTGCCAGGCTGGTCT



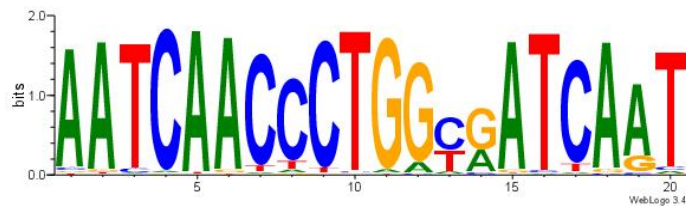
Best Matches for Motif ID 12 (Highest to Lowest)

Dataset #: 1
Motif ID: 170
Motif name: Motif 170
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 17
Similarity score: 0.0789836

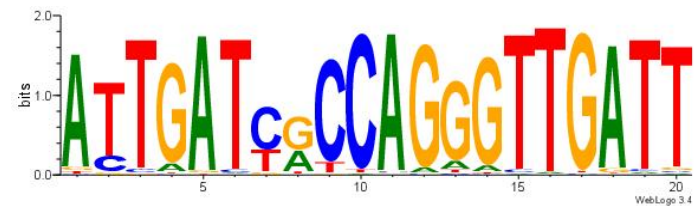
Alignment:

```
ATTGATMKCCAGGGTTGATT  
---GTTGGCCAGGCTGGTCT
```

Original motif Consensus sequence: AATCAACCCTGGYRATCAAT



Reverse complement motif Consensus sequence:
ATTGATMKCCAGGGTTGATT



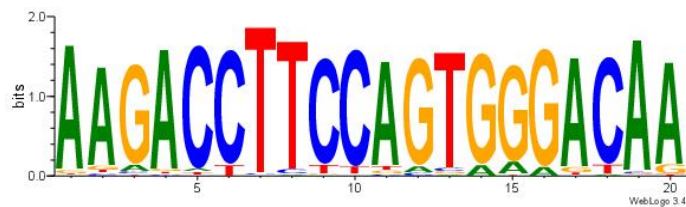
Dataset #: 1
Motif ID: 292
Motif name: Motif 292
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif

Direction: Backward
Position number: 3
Number of overlap: 17
Similarity score: 0.0836974

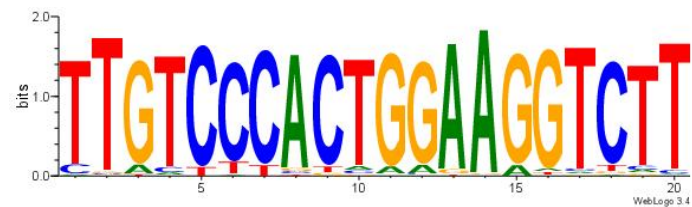
Alignment:

AAGACCTTCCAGTGGGACAA
-AGACCAGCCTGGCCAAC--

Original motif Consensus sequence: AAGACCTTCCAGTGGGACAA



Reverse complement motif Consensus sequence: TTGTCCCAGTGGGACAA

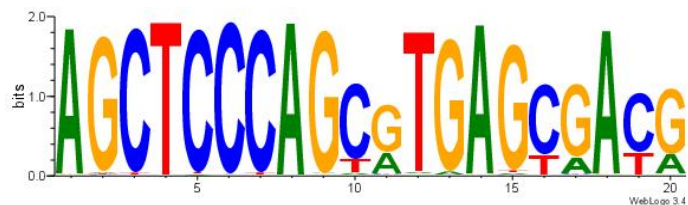


Dataset #: 1
Motif ID: 48
Motif name: Motif 48
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2
Number of overlap: 17
Similarity score: 0.0879397

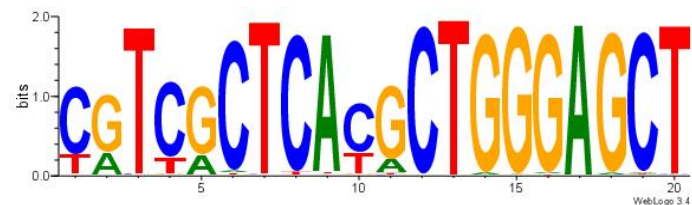
Alignment:

AGCTCCCAGCGTGAGCGACG
--AGACCAGCCTGGCCAAC-

Original motif Consensus sequence: AGCTCCCAGCGTGAGCGACG



Reverse complement motif Consensus sequence: CGTCGCTCACGCTGGGAGCT

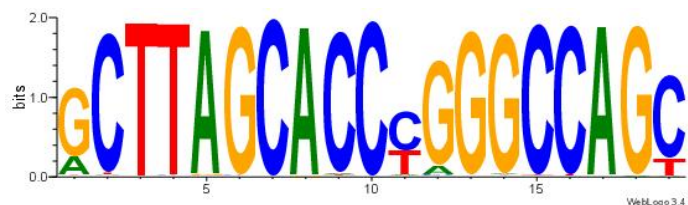


Dataset #: 1
Motif ID: 82
Motif name: Motif 82
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 3
Number of overlap: 17
Similarity score: 0.0890409

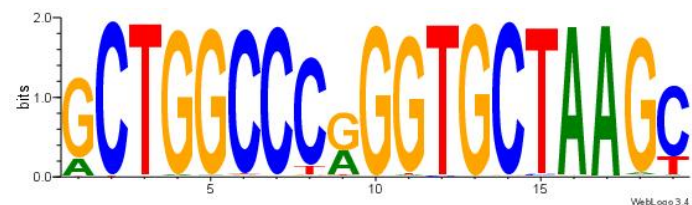
Alignment:

GCTGGCCCKGGTGCTAAGC
GTTGGCCAGGCTGGTCT--

Original motif Consensus sequence: GCTTAGCACCCGGGCCAGC



Reverse complement motif Consensus sequence: GCTGGCCCKGGTGCTAAGC

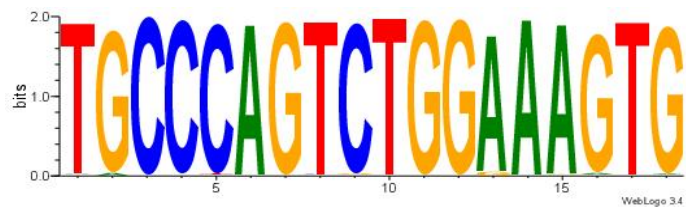


Dataset #: 1
 Motif ID: 45
 Motif name: Motif 45
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 17
 Similarity score: 0.0937553

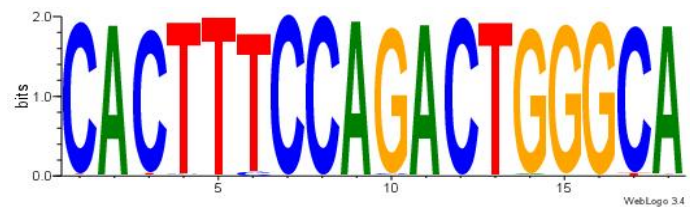
Alignment:

CACTTTCCAGACTGGGCA
 -GTTGGCCAGGCTGGTCT

Original motif Consensus sequence: TGCCCAGTCTGGAAAGTG



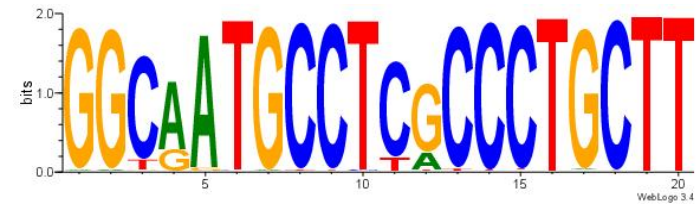
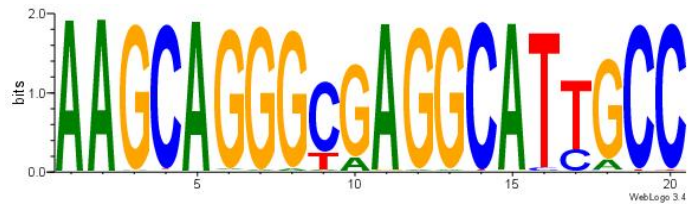
Reverse complement motif Consensus sequence: CACTTTCCAGACTGGGCA



Dataset #: 1 Motif ID: 13 Motif name: Motif 13

Original motif Consensus sequence: AAGCAGGGCGAGGCATTGCC

Reverse complement motif Consensus sequence: GGCAATGCCTCGCCCTGCTT

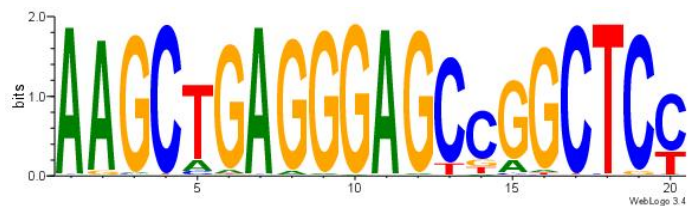


Best Matches for Motif ID 13 (Highest to Lowest)

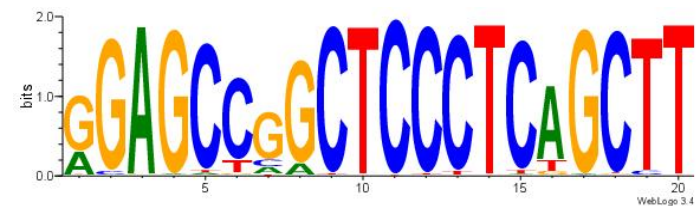
Dataset #: 1
 Motif ID: 96
 Motif name: Motif 96
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.0876504

Alignment:
 AAGCTGAGGGAGCCGGCTCC
 AAGCAGGGCGAGGCATTGCC

Original motif Consensus sequence: AAGCTGAGGGAGCCGGCTCC



Reverse complement motif Consensus sequence: GGAGCCGGCTCCCTCAGCTT

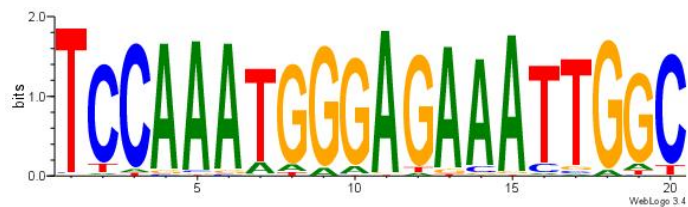


Dataset #: 1
 Motif ID: 235
 Motif name: Motif 235
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.115324

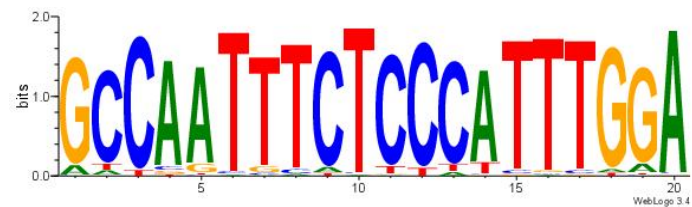
Alignment:

TCCAAATGGGAGAAATTGGC
 AAGCAGGGCGAGGCATTGCC

Original motif Consensus sequence: TCCAAATGGGAGAAATTGGC



Reverse complement motif Consensus sequence: GCCAATTTCTCCCATTGGGA



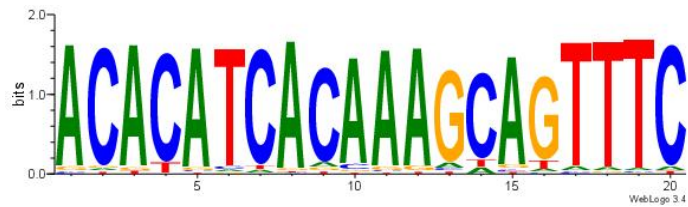
Dataset #: 1
 Motif ID: 202
 Motif name: Motif 202
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1

Number of overlap: 20
Similarity score: 0.115526

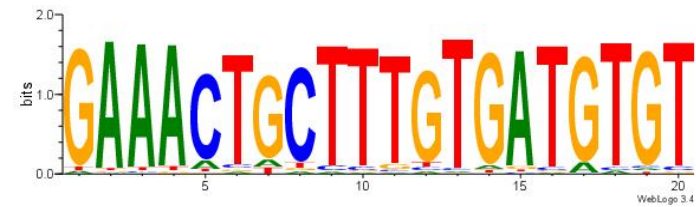
Alignment:

ACACATCACAAAGCAGTTTC
AAGCAGGGCGAGGCATTGCC

Original motif Consensus sequence: ACACATCACAAAGCAGTTTC



Reverse complement motif Consensus sequence:
GAAACTGCTTTGTGATGTGT

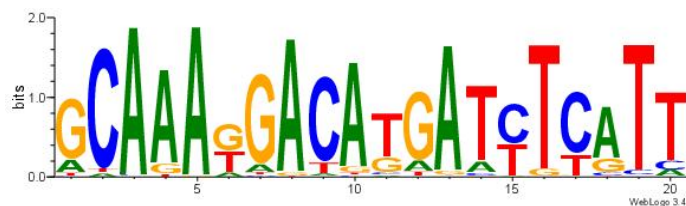


Dataset #: 1
Motif ID: 99
Motif name: Motif 99
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 20
Similarity score: 0.119281

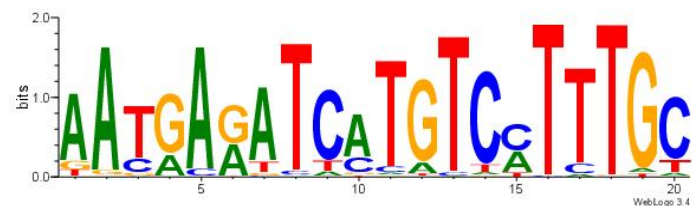
Alignment:

AATGAKATCATGTCYTTTGC
AAGCAGGGCGAGGCATTGCC

Original motif Consensus sequence: GCAAAGACATGATYTCATT



Reverse complement motif Consensus sequence: AATGAKATCATGTCTTTGC

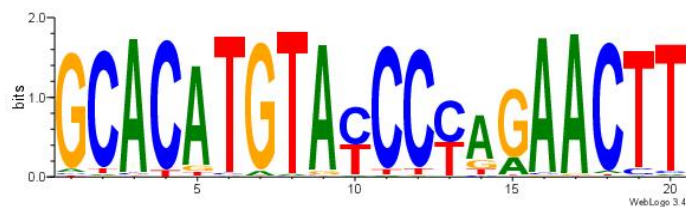


Dataset #: 1
Motif ID: 225
Motif name: Motif 225
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 20
Similarity score: 0.120924

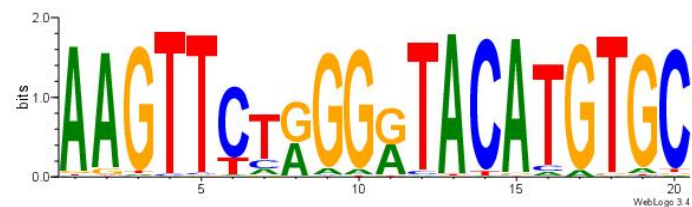
Alignment:

GCACATGTAYCCYAGAACTT
GGCAATGCCTCGCCCTGCTT

Original motif Consensus sequence: GCACATGTAYCCYAGAACTT

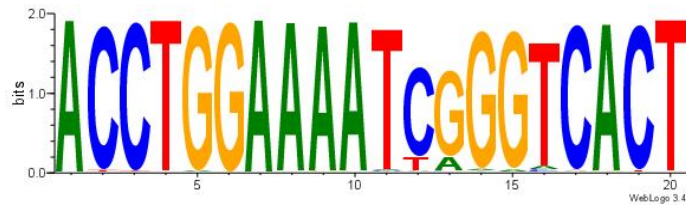


Reverse complement motif Consensus sequence: AAGTTCTKGGKTACATGTGC

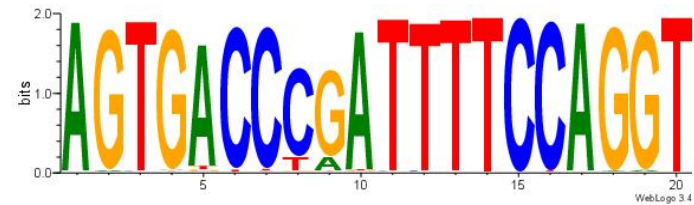


Dataset #: 1 Motif ID: 14 Motif name: Motif 14

Original motif Consensus sequence: ACCTGGAAAATCGGGTCACT



Reverse complement motif Consensus sequence: AGTGACCCGATTTTCCAGGT



Best Matches for Motif ID 14 (Highest to Lowest)

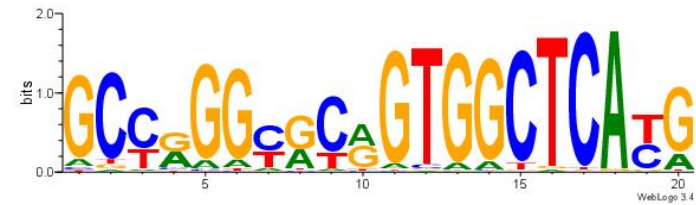
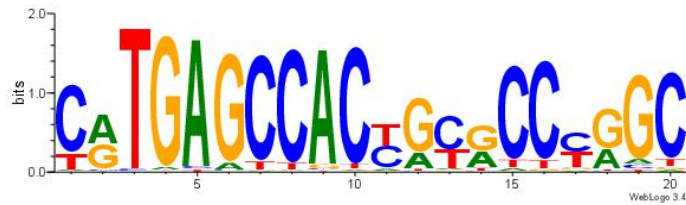
Dataset #:	1
Motif ID:	56
Motif name:	Motif 56
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	20
Similarity score:	0.120636

Alignment:

```
GCKKGGMKCMGTGGCTCAKG  
ACCTGGAAAATCGGGTCACT
```

Original motif Consensus sequence: CRTGAGCCACYGYRCCYGGC

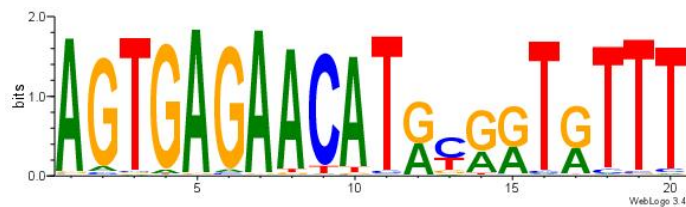
Reverse complement motif Consensus sequence: GCKKGGMKCMGTGGCTCAKG



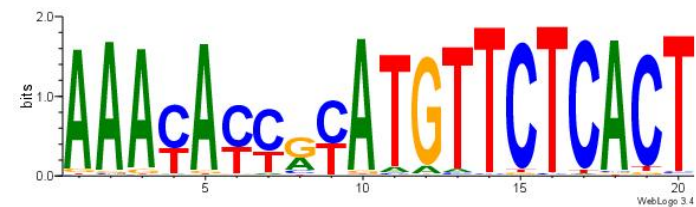
Dataset #: 1
 Motif ID: 63
 Motif name: Motif 63
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.12936

Alignment:
 AAAMAMMKMATGTTCTCACT
 AGTGACCCGATTTTCCAGGT

Original motif Consensus sequence: AGTGAGAACATRYRRTRTTT



Reverse complement motif Consensus sequence: AAAMAMMKMATGTTCTCACT



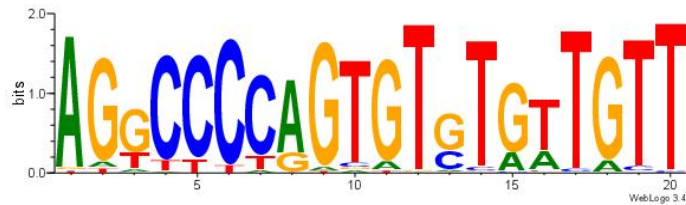
Dataset #: 1

Motif ID: 176
 Motif name: Motif 176
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.133601

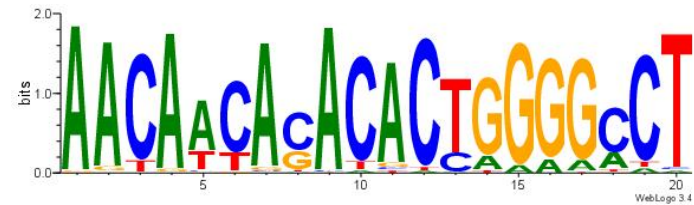
Alignment:

AACAACASACTGGGGCCT
 ACCTGGAAAATCGGGTCACT

Original motif Consensus sequence: AGGCCCCAGTGTSTGTTGTT



Reverse complement motif Consensus sequence: AACAACASACTGGGGCCT



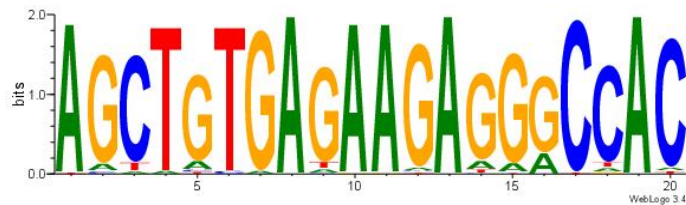
Dataset #: 1
 Motif ID: 294
 Motif name: Motif 294
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 20

Similarity score: 0.133651

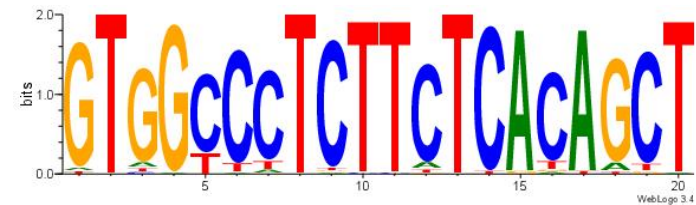
Alignment:

GTGGCCCTCTTCTCACAGCT
AGTGACCCGATTTTCCAGGT

Original motif Consensus sequence: AGCTGTGAGAAGAGGGCCAC



Reverse complement motif Consensus sequence:
GTGGCCCTCTTCTCACAGCT



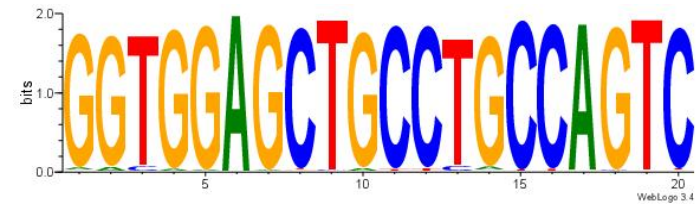
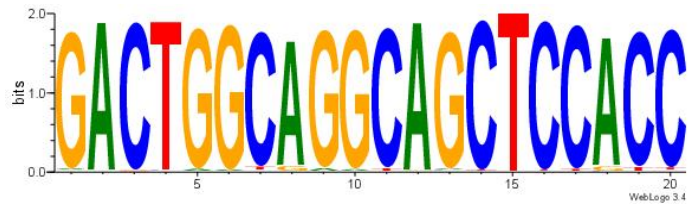
Dataset #: 1
Motif ID: 52
Motif name: Motif 52
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 20
Similarity score: 0.134283

Alignment:

GGTGGAGCTGCCTGCCAGTC
AGTGACCCGATTTTCCAGGT

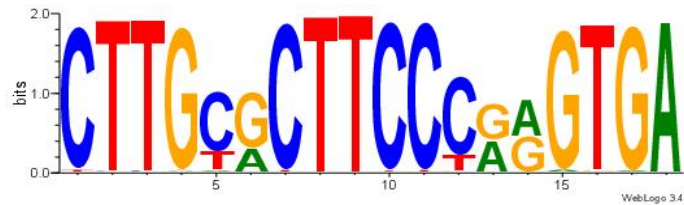
Original motif Consensus sequence: GACTGGCAGGCAGCTCCACC

Reverse complement motif Consensus sequence:
GGTGGAGCTGCCTGCCAGTC

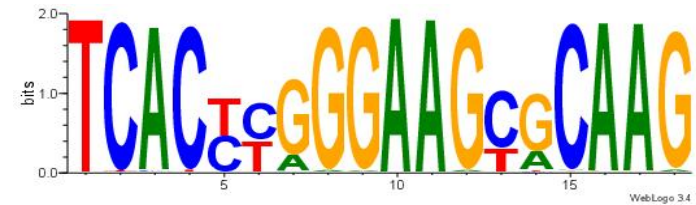


Dataset #: 1 Motif ID: 15 Motif name: Motif 15

Original motif Consensus sequence: CTTGCGCTCCRRGTGA



Reverse complement motif Consensus sequence: TCACKMGGGAAGCGCAAG



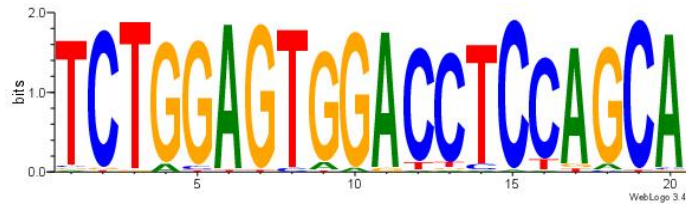
Best Matches for Motif ID 15 (Highest to Lowest)

Dataset #:	1
Motif ID:	350
Motif name:	Motif 350
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	18
Similarity score:	0.112624

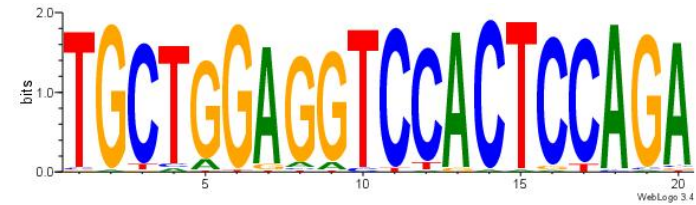
Alignment:

TCTGGAGTGGACCTCCAGCA
TCACKMGGGAAGCGCAAG--

Original motif Consensus sequence: TCTGGAGTGGACCTCCAGCA



Reverse complement motif Consensus sequence:
TGCTGGAGGTCCACTCCAGA

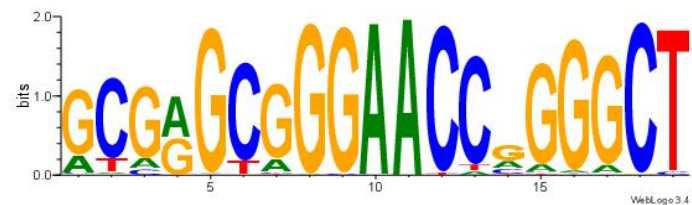
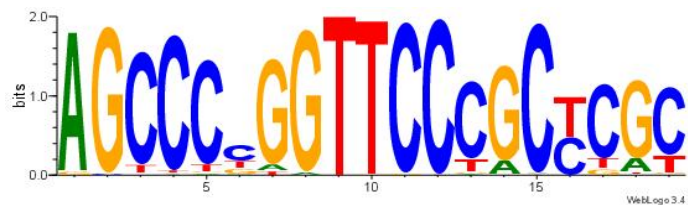


Dataset #: 1
Motif ID: 164
Motif name: Motif 164
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 2
Number of overlap: 18
Similarity score: 0.117199

Alignment:
GCGMGCGGGAACCGGGGCT
TCACKMGGGAAGCGCAAG-

Original motif Consensus sequence: AGCCCCGGTTCCCGCYCGC

Reverse complement motif Consensus sequence:
GCGMGCGGGAACCGGGGCT



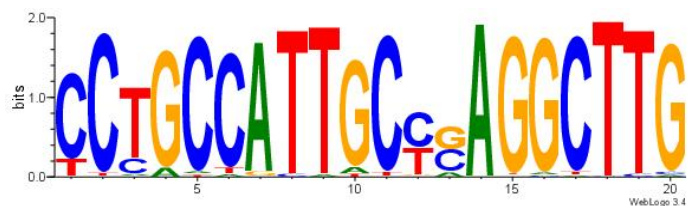
Dataset #: 1
 Motif ID: 196
 Motif name: Motif 196
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 18
 Similarity score: 0.117616

Alignment:

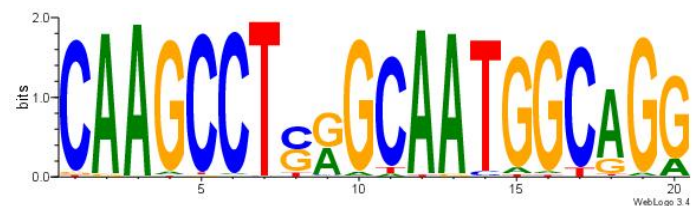
```

CAAGCCTSKGCAATGGCAGG
--TCACKMGGGAAGCGCAAG
  
```

Original motif Consensus sequence: CCTGCCATTGCYSAGGCTTG



Reverse complement motif Consensus sequence: CAAGCCTSKGCAATGGCAGG



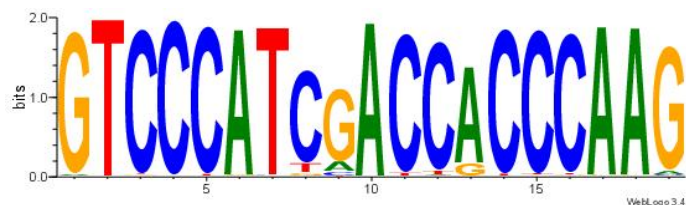
Dataset #: 1

Motif ID: 53
 Motif name: Motif 53
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 18
 Similarity score: 0.117943

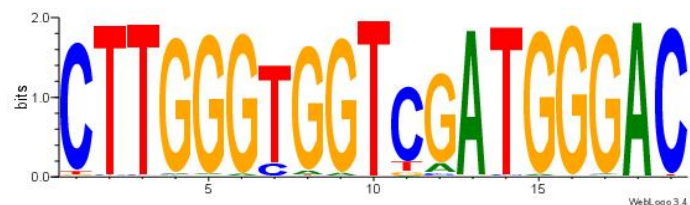
Alignment:

CTTGGGTGGTCGATGGGAC
 CTTGCGCTTCCCRRGTGA-

Original motif Consensus sequence: GTCCCATCGACCACCCAAG



Reverse complement motif Consensus sequence: CTTGGGTGGTCGATGGGAC



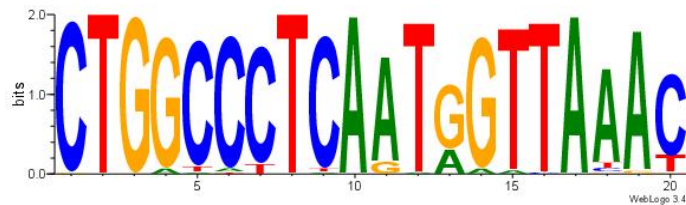
Dataset #: 1
 Motif ID: 332
 Motif name: Motif 332
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 18

Similarity score: 0.118862

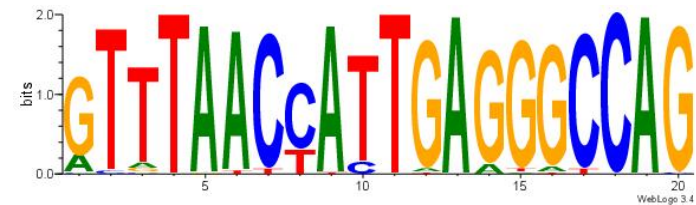
Alignment:

CTGGCCCTCAATGGTTAAAC
CTTGCGCTTCCCRRGTGA--

Original motif Consensus sequence: CTGGCCCTCAATGGTTAAAC

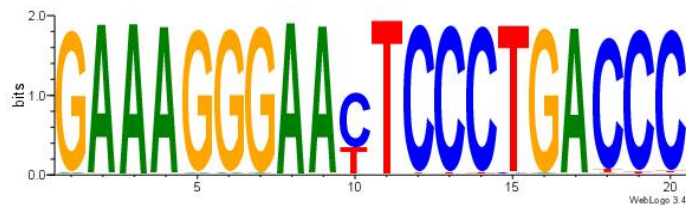


Reverse complement motif Consensus sequence: GTTTAACCATTGAGGGCCAG

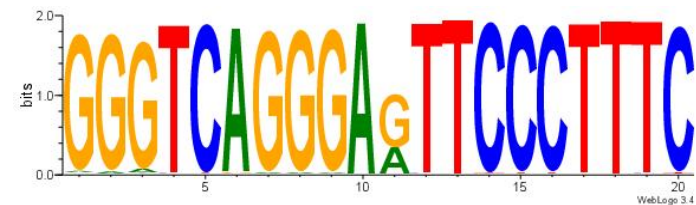


Dataset #: 1 Motif ID: 16 Motif name: Motif 16

Original motif Consensus sequence: GAAAGGGA ACTCCCTGACCC



Reverse complement motif Consensus sequence: GGGTCAGGGA GTTCCCTTTC



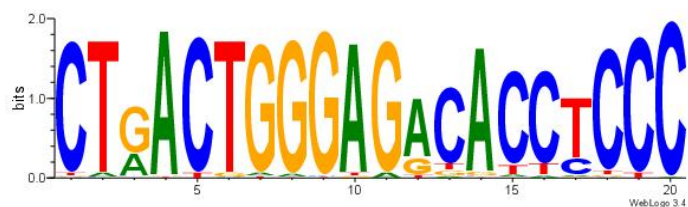
Best Matches for Motif ID 16 (Highest to Lowest)

Dataset #: 1
Motif ID: 293
Motif name: Motif 293
Matching format of first motif: Reverse Complement

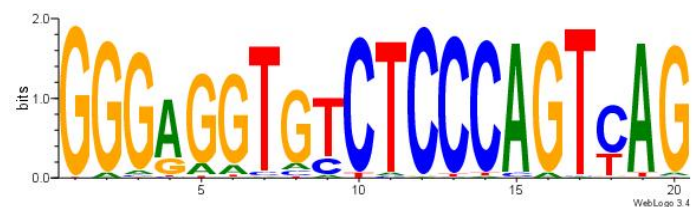
Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.122102

Alignment:
 CTGACTGGGAGACACCTCCC
 GGGTCAGGGAGTTCCTTTC

Original motif Consensus sequence: CTGACTGGGAGACACCTCCC



Reverse complement motif Consensus sequence:
 GGGAGGTGTCTCCAGTCAG

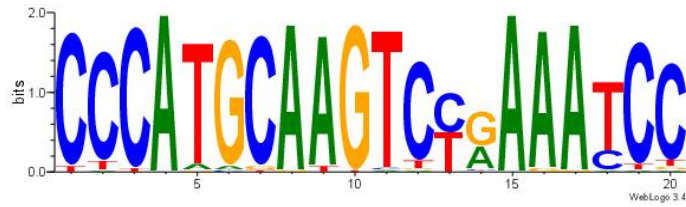


Dataset #: 1
 Motif ID: 310
 Motif name: Motif 310
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.12749

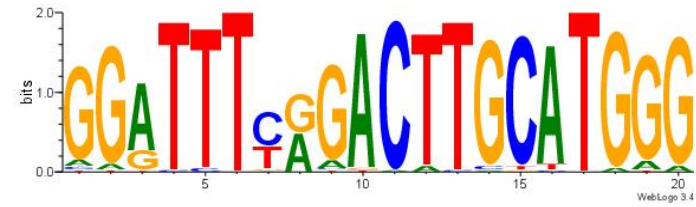
Alignment:

CCCATGCAAGTCYRAAATCC
GAAAGGGA ACTCCCTGACCC

Original motif Consensus sequence: CCCATGCAAGTCYRAAATCC



Reverse complement motif Consensus sequence:
GGATTTMKGACTTGCATGGG



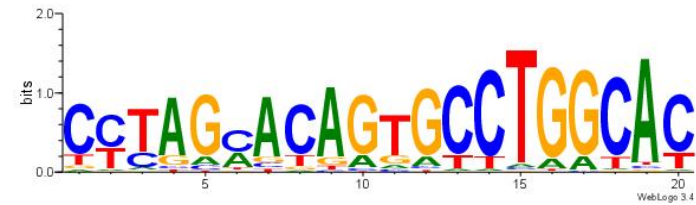
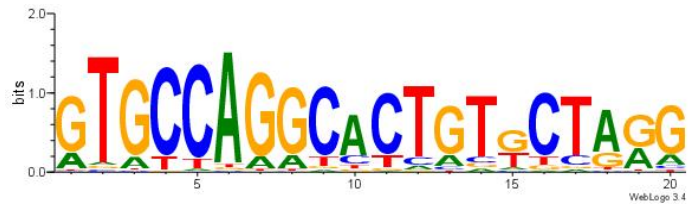
Dataset #:	1
Motif ID:	76
Motif name:	Motif 76
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	20
Similarity score:	0.129322

Alignment:

CMTAGYACAGTGCCTGGCAC
GAAAGGGA ACTCCCTGACCC

Original motif Consensus sequence: GTGCCAGGCACTGKCTARG

Reverse complement motif Consensus sequence:
CMTAGYACAGTGCCTGGCAC

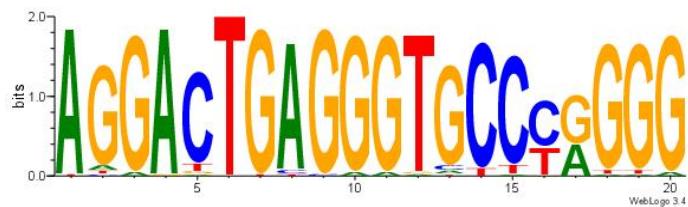


Dataset #: 1
 Motif ID: 312
 Motif name: Motif 312
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.129551

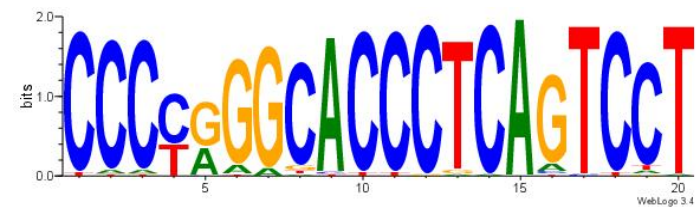
Alignment:

CCCMKGGCACCCTCAGTCCT
 GAAAGGGA ACTCCCTGACCC

Original motif Consensus sequence: AGGACTGAGGGTGCCYRGGG



Reverse complement motif Consensus sequence: CCCMKGGCACCCTCAGTCCT



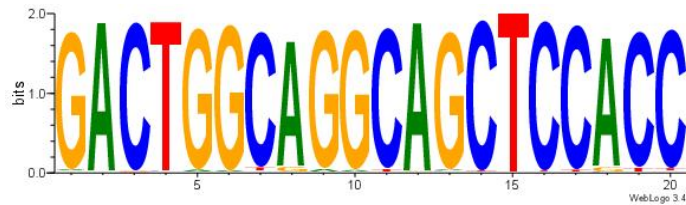
Dataset #: 1

Motif ID: 52
 Motif name: Motif 52
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.133875

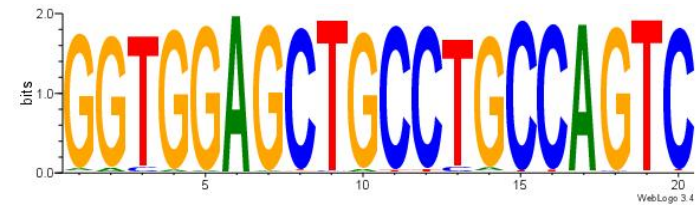
Alignment:

GGTGGAGCTGCCTGCCAGTC
 GGGTCAGGGAGTTCCTTTC

Original motif Consensus sequence: GACTGGCAGGCAGCTCCACC

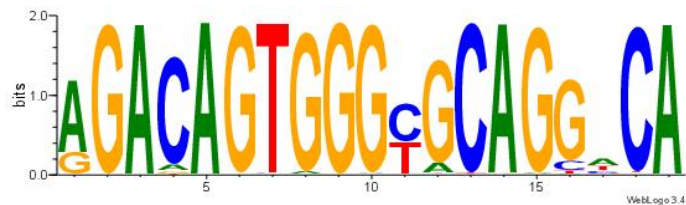


Reverse complement motif Consensus sequence: GGTGGAGCTGCCTGCCAGTC

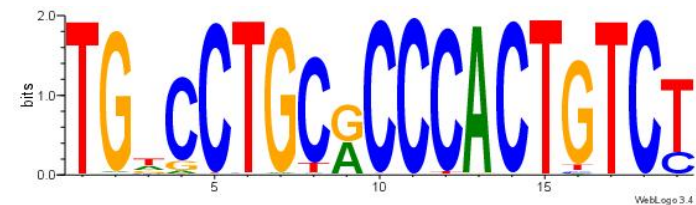


Dataset #: 1 Motif ID: 17 Motif name: Motif 17

Original motif Consensus sequence: AGACAGTGGGcGCAGG CA



Reverse complement motif Consensus sequence: TGHCTGCKCCCACTGTCT



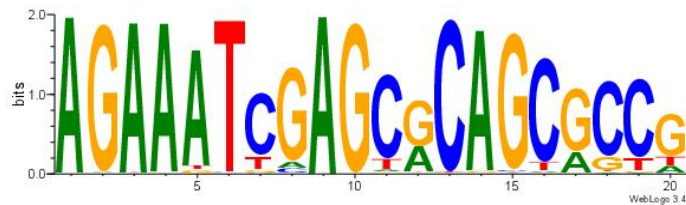
Best Matches for Motif ID 17 (Highest to Lowest)

Dataset #: 1
Motif ID: 65
Motif name: Motif 65
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 2
Number of overlap: 19
Similarity score: 0.0792941

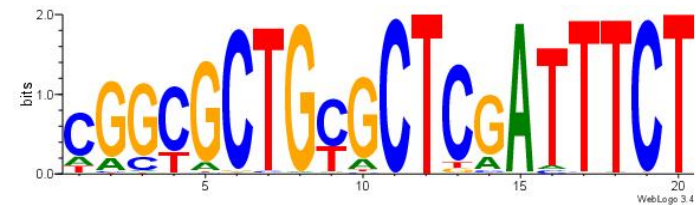
Alignment:

```
CGGCGCTGMGCTCGATTTCT  
-TGHCC TGCKCCCACTGTCT
```

Original motif Consensus sequence: AGAAATCGAGCRCAGCGCCG



Reverse complement motif Consensus sequence: CGGCGCTGMGCTCGATTTCT



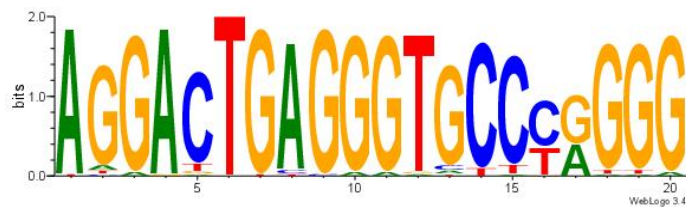
Dataset #: 1
Motif ID: 312
Motif name: Motif 312
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif

Direction: Backward
Position number: 1
Number of overlap: 19
Similarity score: 0.0967987

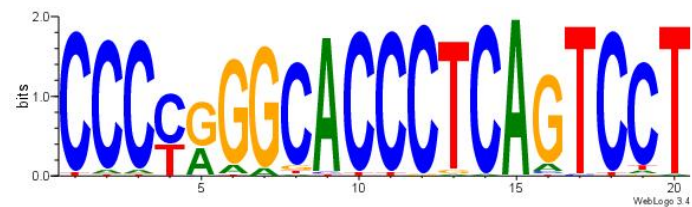
Alignment:

AGGACTGAGGGTGCCYRGGG
-AGACAGTGGGYGCAGGHCA

Original motif Consensus sequence: AGGACTGAGGGTGCCYRGGG



Reverse complement motif Consensus sequence: CCCMKGGCACCCCTCAGTCCT

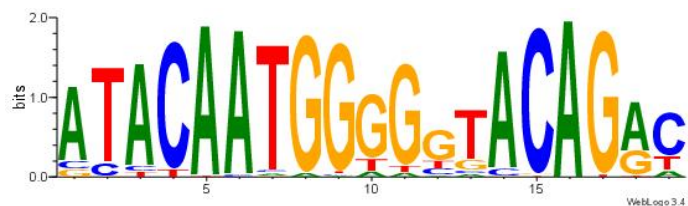


Dataset #: 1
Motif ID: 193
Motif name: Motif 193
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 19
Similarity score: 0.0971018

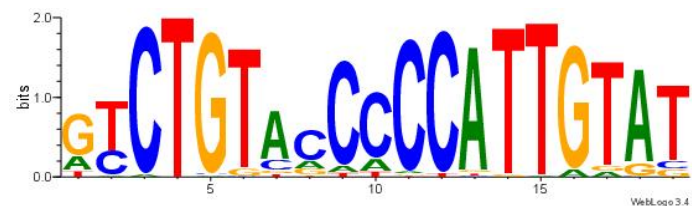
Alignment:

GKCTGTACCCCATTTGTAT
TGHCTGCKCCCACTGTCT

Original motif Consensus sequence: ATACAATGGGGTACAGRC



Reverse complement motif Consensus sequence: GKCTGTACCCCCATTGTAT

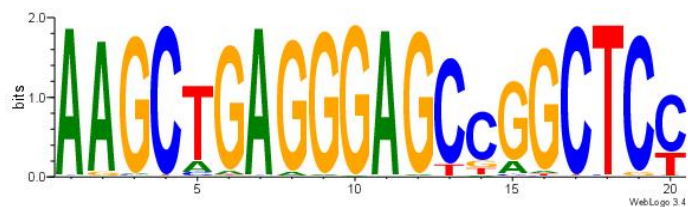


Dataset #: 1
Motif ID: 96
Motif name: Motif 96
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 19
Similarity score: 0.0996968

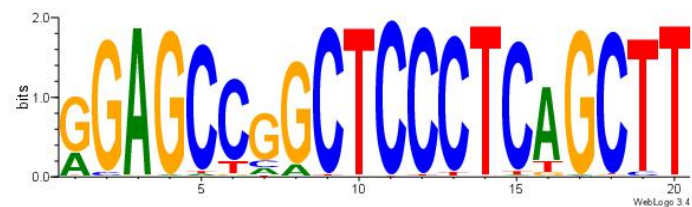
Alignment:

GGAGCCGGCTCCCTCAGCTT
-TGHCCCTGCKCCCCTGTCT

Original motif Consensus sequence: AAGCTGAGGGAGCCGGCTCC



Reverse complement motif Consensus sequence: GGAGCCGGCTCCCTCAGCTT

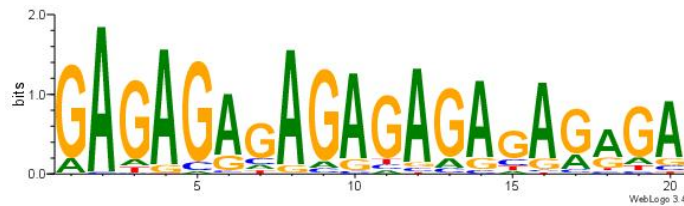


Dataset #: 1
 Motif ID: 109
 Motif name: Motif 109
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 19
 Similarity score: 0.101245

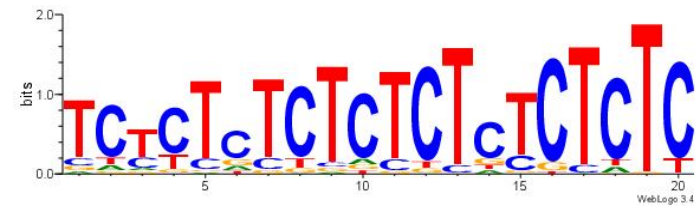
Alignment:

TCTCTCTCTCTCTCTCTCTC
 TGHCCCTGCKCCCCTGTCT-

Original motif Consensus sequence: GAGAGAGAGAGAGAGAGA



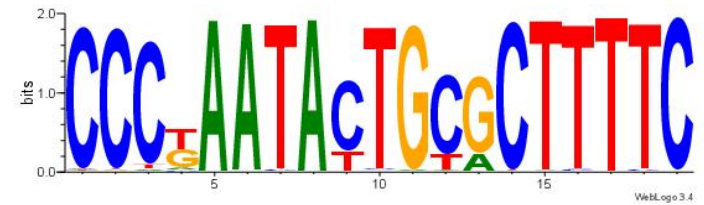
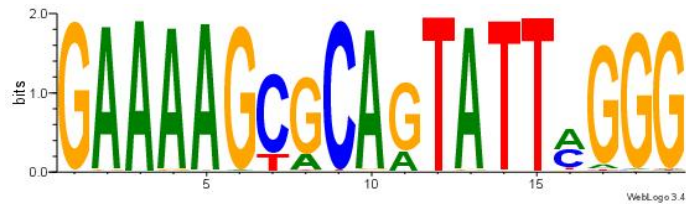
Reverse complement motif Consensus sequence: TCTCTCTCTCTCTCTCTC



Dataset #: 1 Motif ID: 18 Motif name: Motif 18

Original motif Consensus sequence: GAAAAGCGCAGTATTMGGG

Reverse complement motif Consensus sequence: CCCYAATACTGCGCTTTTC

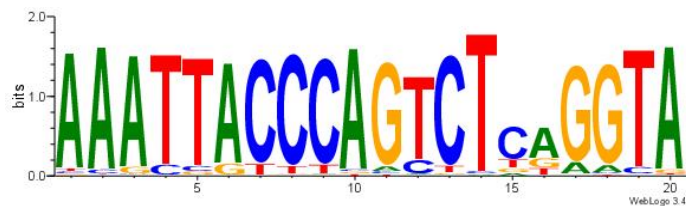


Best Matches for Motif ID 18 (Highest to Lowest)

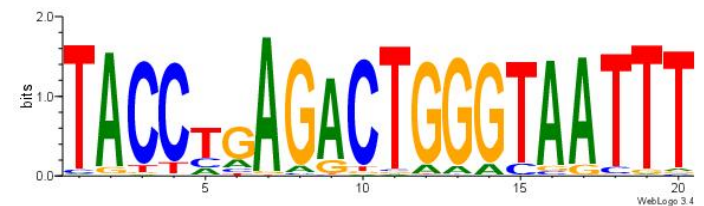
Dataset #: 1
 Motif ID: 160
 Motif name: Motif 160
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 19
 Similarity score: 0.112986

Alignment:
 AAATTACCCAGTCTCAGGTA
 GAAAAGCGCAGTATTMGGG-

Original motif Consensus sequence: AAATTACCCAGTCTCAGGTA



Reverse complement motif Consensus sequence: TACCTGAGACTGGGTAATTT

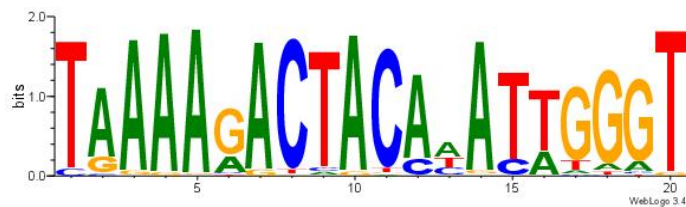


Dataset #: 1
 Motif ID: 195
 Motif name: Motif 195
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 19
 Similarity score: 0.113548

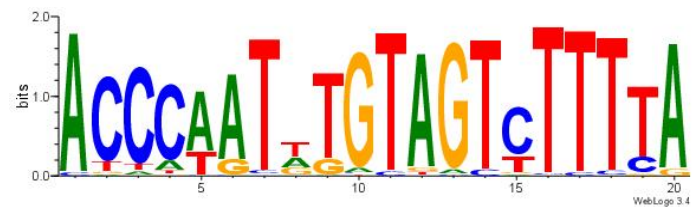
Alignment:

ACCCAATWTGTAGTCTTTTA
 -CCCYAATACTGCGCTTTTC

Original motif Consensus sequence: TAAAAGACTACAWATTGGGT



Reverse complement motif Consensus sequence: ACCCAATWTGTAGTCTTTTA



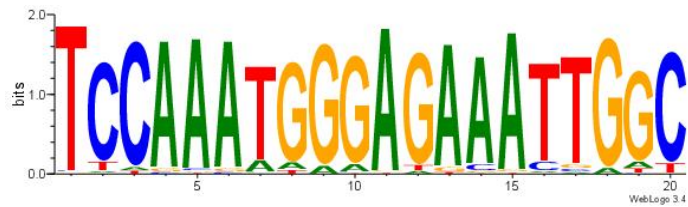
Dataset #: 1
 Motif ID: 235
 Motif name: Motif 235
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1

Number of overlap: 19
Similarity score: 0.12058

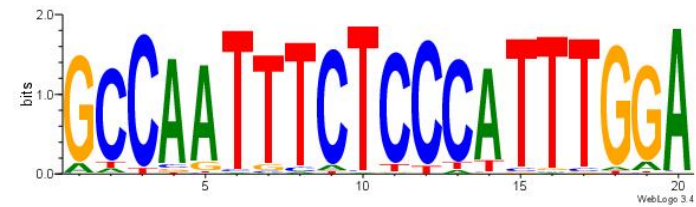
Alignment:

GCCAATTTCTCCCATTGGA
CCCYAATACTGCGCTTTTC-

Original motif Consensus sequence: TCCAATGGGAGAAATTGGC



Reverse complement motif Consensus sequence:
GCCAATTTCTCCCATTGGA

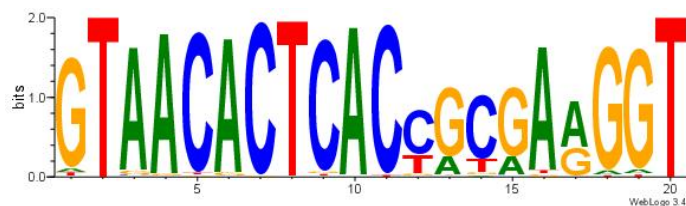


Dataset #: 1
Motif ID: 201
Motif name: Motif 201
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2
Number of overlap: 19
Similarity score: 0.124626

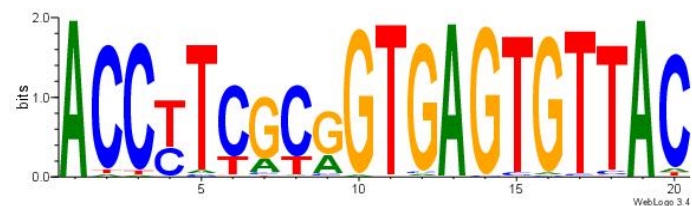
Alignment:

GTAACACTCACCGCGARGGT
GAAAAGCGCAGTATTMGGG-

Original motif Consensus sequence: GTAACACTCACCGCGARGGT



Reverse complement motif Consensus sequence: ACCKTCGCGGTGAGTGTTAC

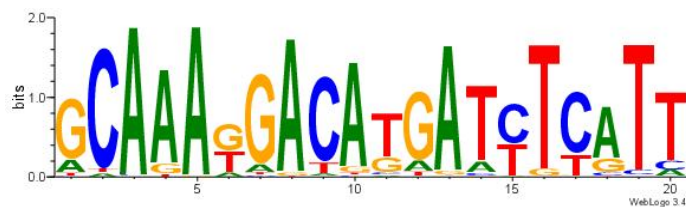


Dataset #: 1
Motif ID: 99
Motif name: Motif 99
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2
Number of overlap: 19
Similarity score: 0.125732

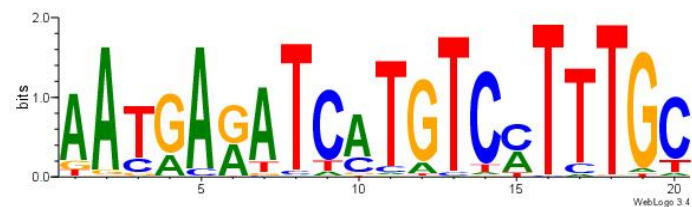
Alignment:

GCAAAGACATGATYTCATT
GAAAAGCGCAGTATTMGGG-

Original motif Consensus sequence: GCAAAGACATGATYTCATT

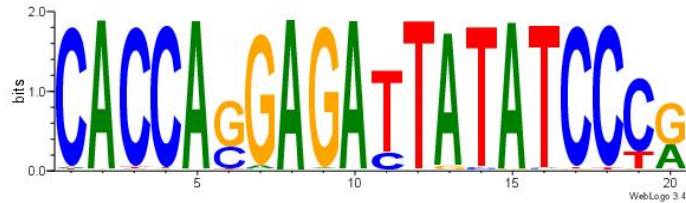


Reverse complement motif Consensus sequence: AATGAKATCATGTCYTTTGC

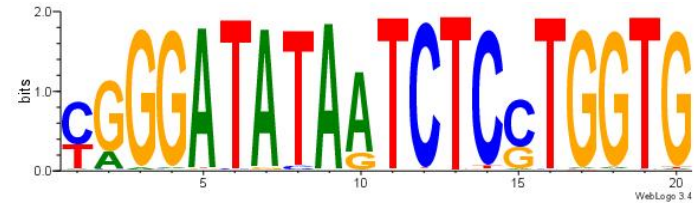


Dataset #: 1 Motif ID: 19 Motif name: Motif 19

Original motif Consensus sequence: CACCAGGAGATTATATCCCR



Reverse complement motif Consensus sequence: MGGGATATAATCTCCTGGTG



Best Matches for Motif ID 19 (Highest to Lowest)

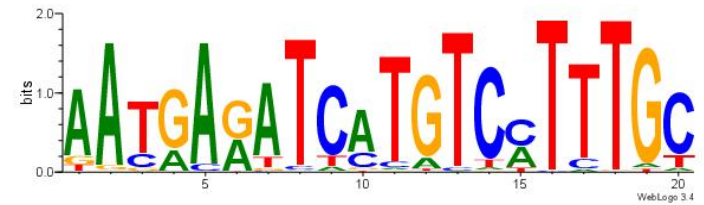
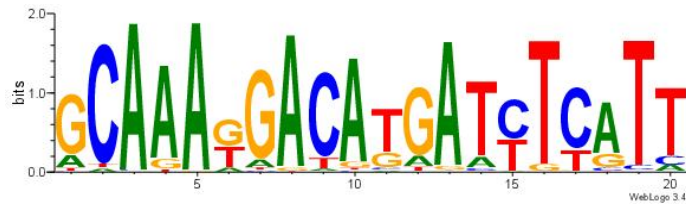
Dataset #:	1
Motif ID:	99
Motif name:	Motif 99
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	20
Similarity score:	0.11753

Alignment:

```
AATGAKATCATGTCYTTTGC  
MGGGATATAATCTCCTGGTG
```

Original motif Consensus sequence: GCAAAGACATGATYTCATT

Reverse complement motif Consensus sequence: AATGAKATCATGTCYTTTGC

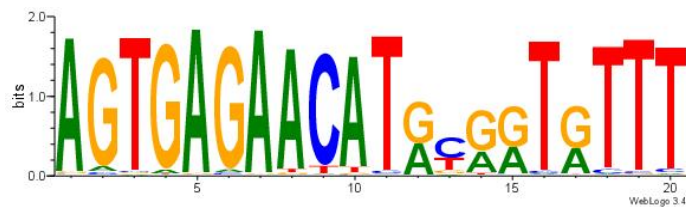


Dataset #: 1
 Motif ID: 63
 Motif name: Motif 63
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.126684

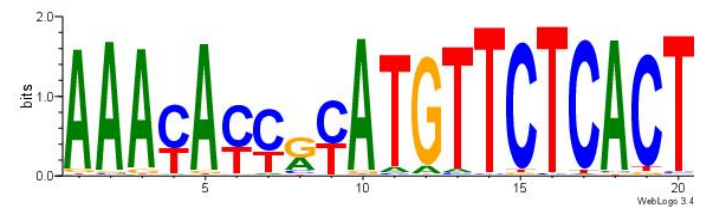
Alignment:

AGTGAGAACATRYRRTRTTT
 MGGGATATAATCTCCTGGTG

Original motif Consensus sequence: AGTGAGAACATRYRRTRTTT



Reverse complement motif Consensus sequence: AAAMAMMKMATGTTCTCACT



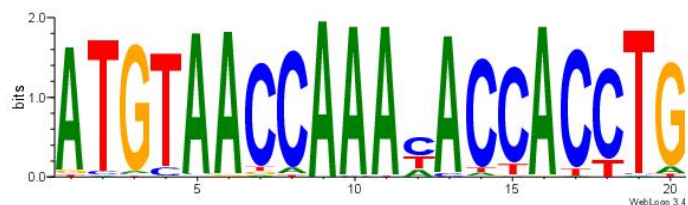
Dataset #: 1

Motif ID: 336
 Motif name: Motif 336
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.137442

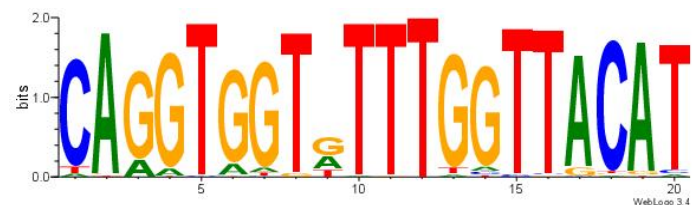
Alignment:

ATGTAACCAAAYACCACCTG
 MGGGATATAATCTCCTGGTG

Original motif Consensus sequence: ATGTAACCAAAYACCACCTG



Reverse complement motif Consensus sequence: CAGGTGGTKTTTGGTTACAT



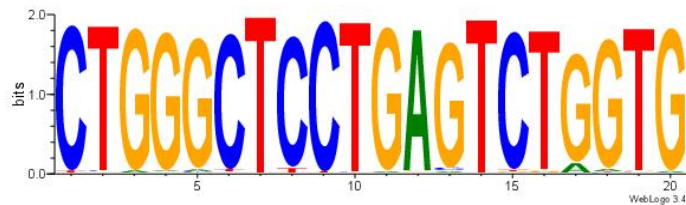
Dataset #: 1
 Motif ID: 67
 Motif name: Motif 67
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 20

Similarity score: 0.137843

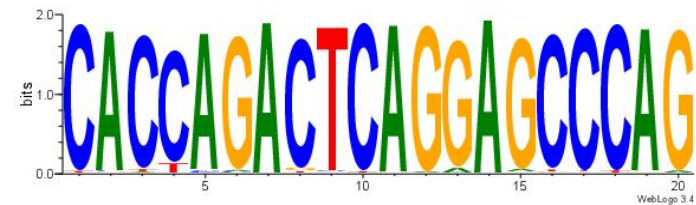
Alignment:

CTGGGCTCCTGAGTCTGGTG
MGGGATATAATCTCCTGGTG

Original motif Consensus sequence: CTGGGCTCCTGAGTCTGGTG



Reverse complement motif Consensus sequence:
CACCAGACTCAGGAGCCCAG



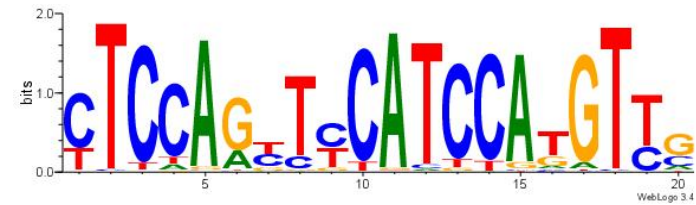
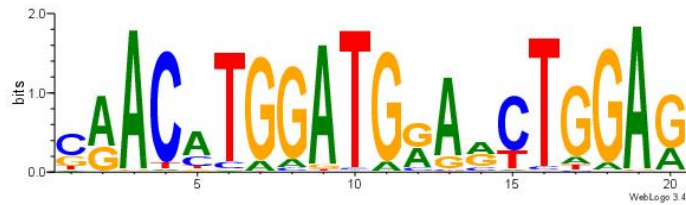
Dataset #: 1
Motif ID: 104
Motif name: Motif 104
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 20
Similarity score: 0.139054

Alignment:

CTCCAGKTMCATCCATGTTG
CACCAGGAGATTATATCCCR

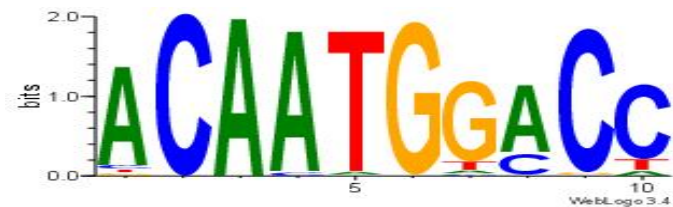
Original motif Consensus sequence: CAACATGGATGRARCTGGAG

Reverse complement motif Consensus sequence:
CTCCAGKTMCATCCATGTTG

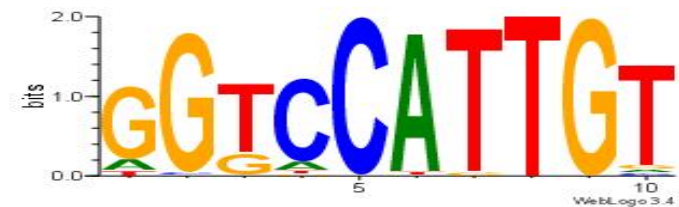


Dataset #: 1 Motif ID: 20 Motif name: Motif 20

Original motif Consensus sequence: ACAATGGACC



Reverse complement motif Consensus sequence: GTCCATTGT

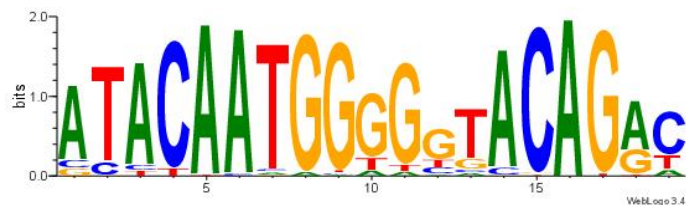


Best Matches for Motif ID 20 (Highest to Lowest)

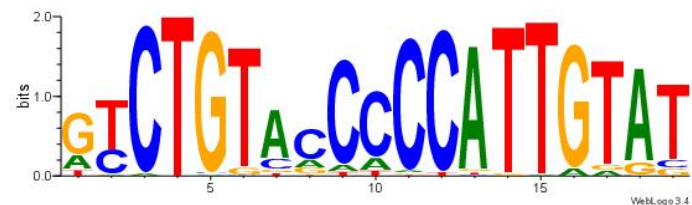
Dataset #:	1
Motif ID:	193
Motif name:	Motif 193
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	3
Number of overlap:	10
Similarity score:	0.0500147

Alignment:
 GKCTGTACCCCATTTGTAT
 -----GGTCCATTGT--

Original motif Consensus sequence: ATACAATGGGGTACAGRC



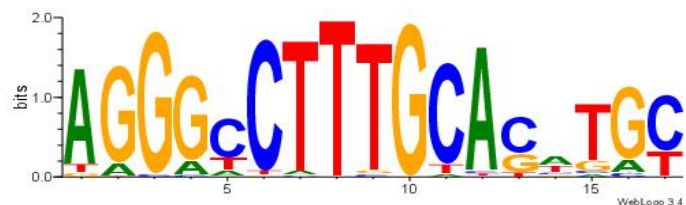
Reverse complement motif Consensus sequence: GKCTGTACCCCATTTGTAT



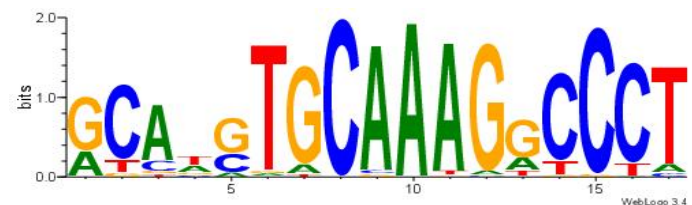
Dataset #: 1
Motif ID: 322
Motif name: Motif 322
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 7
Number of overlap: 10
Similarity score: 0.059291

Alignment:
GCAWSTGCAAAGGCCCT
-----ACAATGGACC-

Original motif Consensus sequence: AGGGCCTTTGCASWTGC



Reverse complement motif Consensus sequence: GCAWSTGCAAAGGCCCT

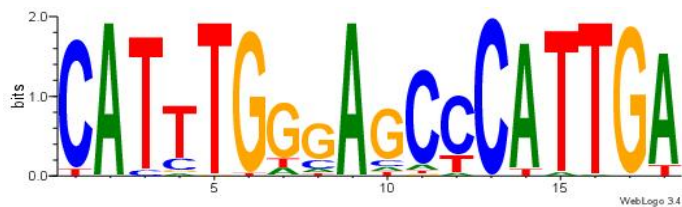


Dataset #: 1
 Motif ID: 284
 Motif name: Motif 284
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 10
 Similarity score: 0.0608949

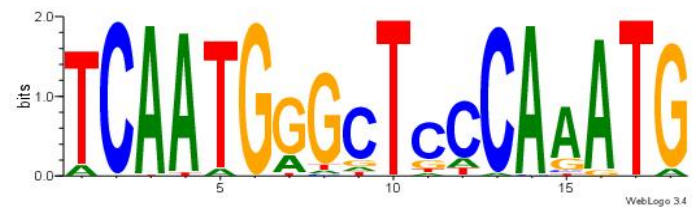
Alignment:

CATTGGGAGCCCATTGA
 -----GGTCCATTGT

Original motif Consensus sequence: CATTGGGAGCCCATTGA



Reverse complement motif Consensus sequence: TCAATGGGCTCCCAAATG



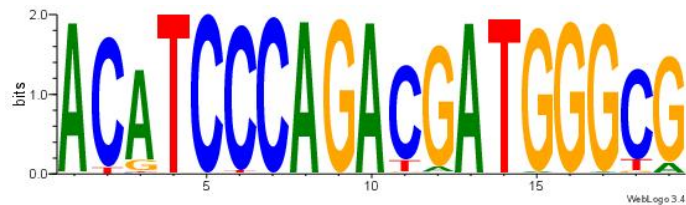
Dataset #: 1
 Motif ID: 36
 Motif name: Motif 36
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1

Number of overlap: 10
Similarity score: 0.0668018

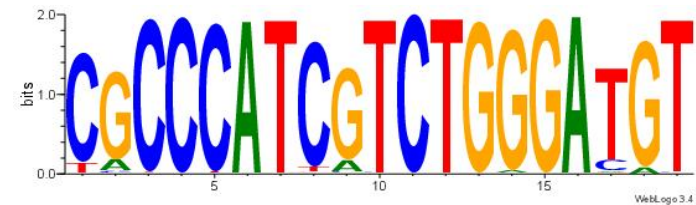
Alignment:

CGCCCATCGTCTGGGATGT
GGTCCATTGT-----

Original motif Consensus sequence: ACATCCCAGACGATGGGCG



Reverse complement motif Consensus sequence:
CGCCCATCGTCTGGGATGT



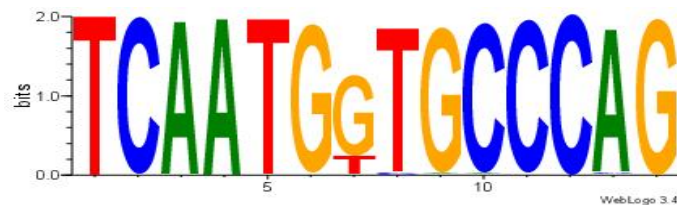
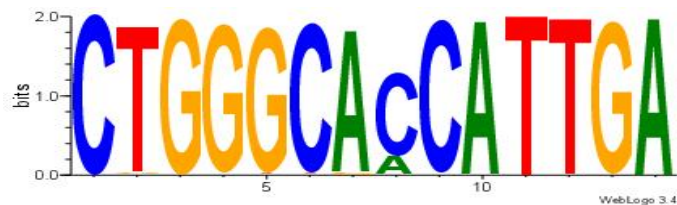
Dataset #: 1
Motif ID: 147
Motif name: Motif 147
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 10
Similarity score: 0.0697279

Alignment:

TCAATGGTGCCCAG
ACAATGGACC----

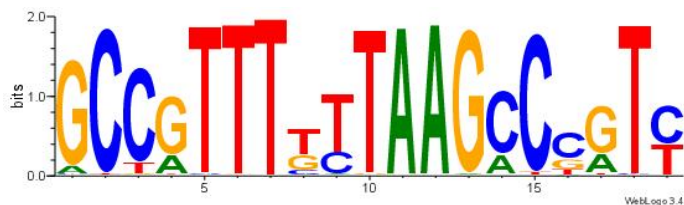
Original motif Consensus sequence: CTGGGCACCATTGA

Reverse complement motif Consensus sequence: TCAATGGTGCCCCA

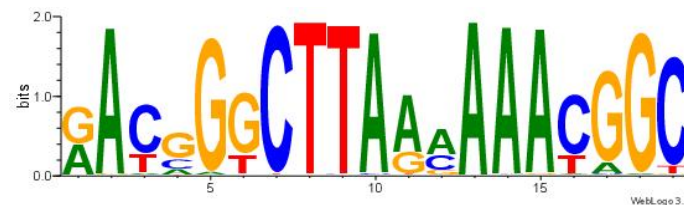


Dataset #: 1 Motif ID: 21 Motif name: Motif 21

Original motif Consensus sequence: GCCGTTTKTTAAGCCCGTY



Reverse complement motif Consensus sequence: KACGGGCTTAARAAACGGC



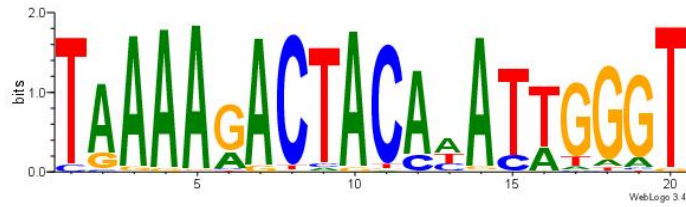
Best Matches for Motif ID 21 (Highest to Lowest)

Dataset #:	1
Motif ID:	195
Motif name:	Motif 195
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	19
Similarity score:	0.116692

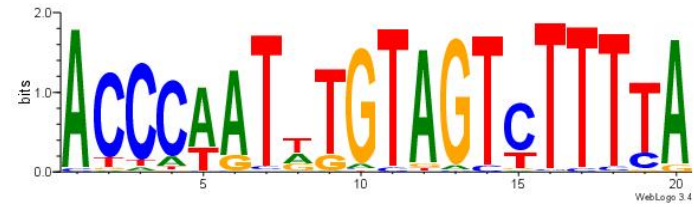
Alignment:

TAAAAGACTACAWATTGGGT
KACGGGCTTAARAAACGGC-

Original motif Consensus sequence: TAAAAGACTACAWATTGGGT



Reverse complement motif Consensus sequence:
ACCCAATWTGTAGTCTTTTA

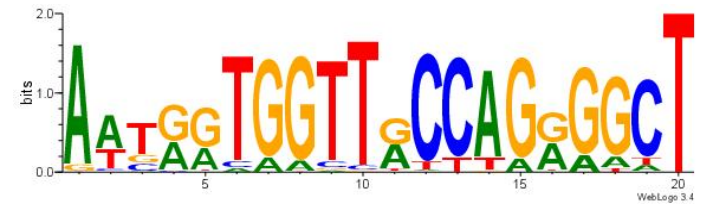
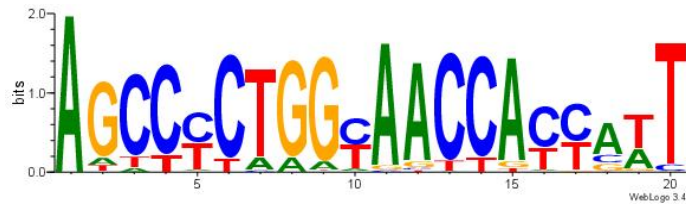


Dataset #: 1
Motif ID: 139
Motif name: Motif 139
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 2
Number of overlap: 19
Similarity score: 0.119179

Alignment:
AGCCYCTGGYAACCAYYAWT
-GCCGTTTKTTAAGCCCGTY

Original motif Consensus sequence: AGCCYCTGGYAACCAYYAWT

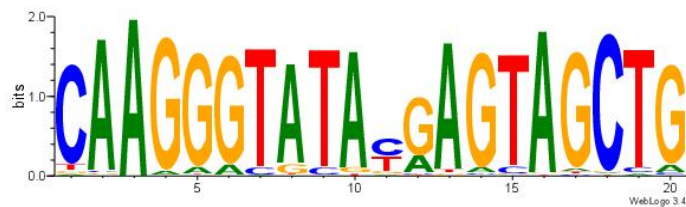
Reverse complement motif Consensus sequence:
AWTKKTGGTTKCCAGKGGCT



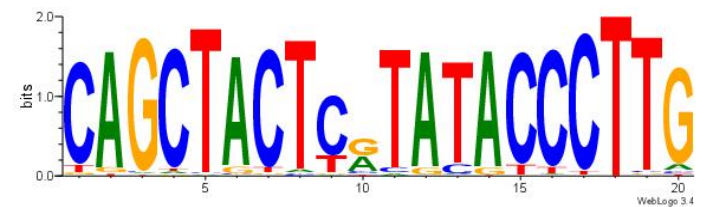
Dataset #: 1
 Motif ID: 194
 Motif name: Motif 194
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 19
 Similarity score: 0.119838

Alignment:
 CAAGGGTATAYGAGTAGCTG
 KACGGGCTTAARAAACGGC-

Original motif Consensus sequence: CAAGGGTATAYGAGTAGCTG



Reverse complement motif Consensus sequence: CAGCTACTCKTATACCCTTG



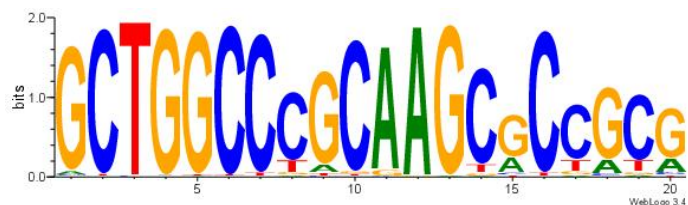
Dataset #: 1

Motif ID: 100
 Motif name: Motif 100
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 19
 Similarity score: 0.120266

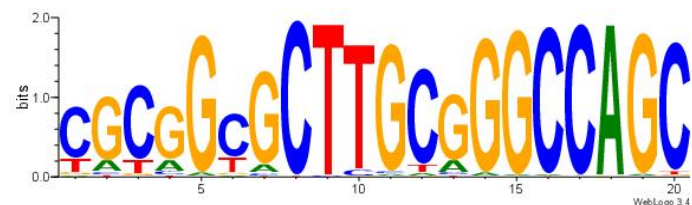
Alignment:

CGCGGCGCTTGC GGGCCAGC
 -KACGGGCTTAARAAACGGC

Original motif Consensus sequence: GCTGGCCCGCAAGCGCCGCG



Reverse complement motif Consensus sequence: CGCGGCGCTTGC GGGCCAGC



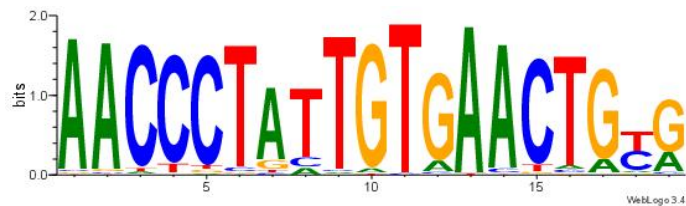
Dataset #: 1
 Motif ID: 242
 Motif name: Motif 242
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 19

Similarity score: 0.122834

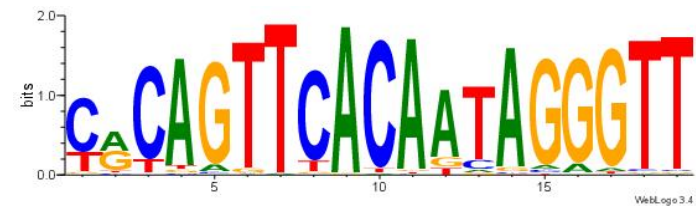
Alignment:

CMCAGTTCACAATAGGGTT
GCCGTTTKTTAAGCCCGTY

Original motif Consensus sequence: AACCTATTGTGAACTGYG



Reverse complement motif Consensus sequence: CMCAGTTCACAATAGGGTT

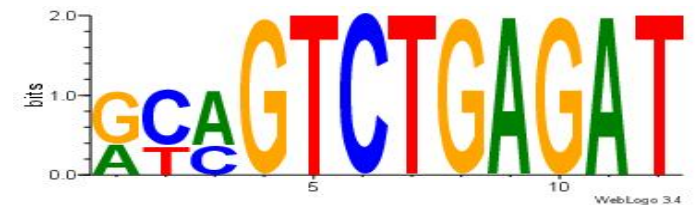


Dataset #: 1 Motif ID: 22 Motif name: Motif 22

Original motif Consensus sequence: ATCTCAGACKRY



Reverse complement motif Consensus sequence: KMRGTCTGAGAT



Best Matches for Motif ID 22 (Highest to Lowest)

Dataset #:	1
Motif ID:	36
Motif name:	Motif 36
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif

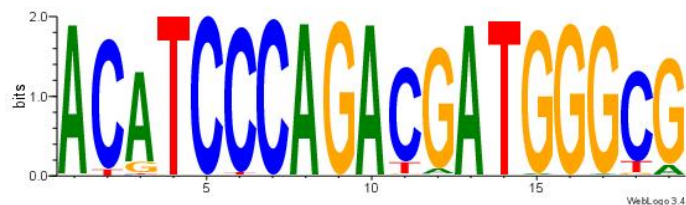
Direction: Backward
Position number: 6
Number of overlap: 12
Similarity score: 0.0496789

Alignment:

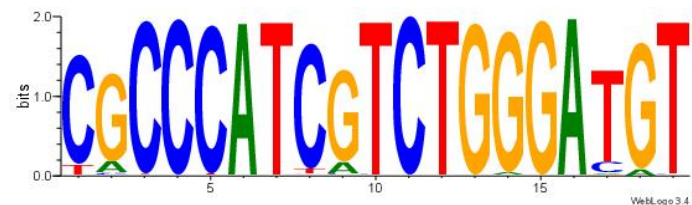
ACATCCCAGACGATGGGCG

--ATCTCAGACKRY-----

Original motif Consensus sequence: ACATCCCAGACGATGGGCG



Reverse complement motif Consensus sequence: CGCCCATCGTCTGGGATGT



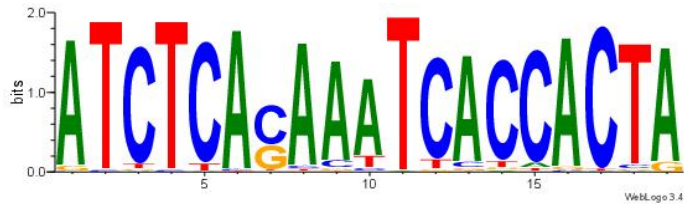
Dataset #: 1
Motif ID: 261
Motif name: Motif 261
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 12
Similarity score: 0.0600848

Alignment:

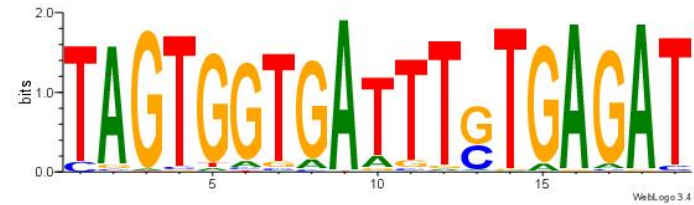
TAGTGGTGATTTSTGAGAT

-----KMRGTCTGAGAT

Original motif Consensus sequence: ATCTCASAAATCACCCTA



Reverse complement motif Consensus sequence: TAGTGGTGAATTTGAGAT

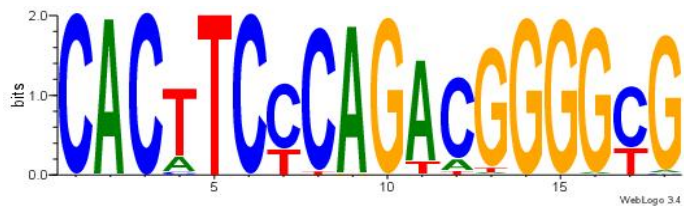


Dataset #: 1
Motif ID: 27
Motif name: Motif 27
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 4
Number of overlap: 12
Similarity score: 0.0627798

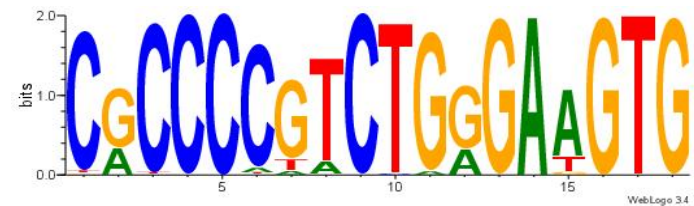
Alignment:

CACTTCCCAGACGGGGCG
---ATCTCAGACKRY---

Original motif Consensus sequence: CACTTCCCAGACGGGGCG



Reverse complement motif Consensus sequence: CGCCCCGTCTGGGAAGTG

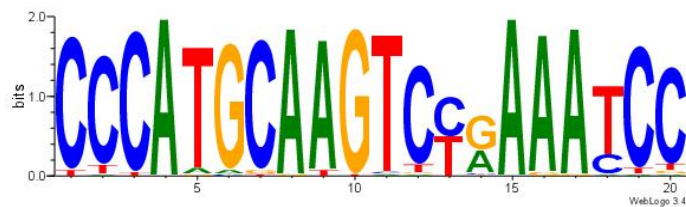


Dataset #: 1
 Motif ID: 310
 Motif name: Motif 310
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 7
 Number of overlap: 12
 Similarity score: 0.0718284

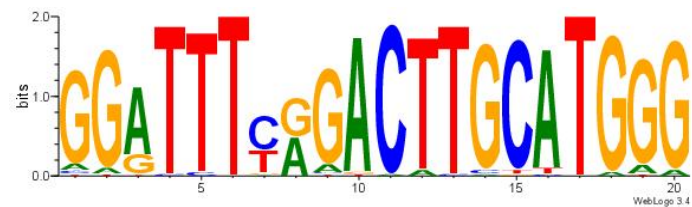
Alignment:

CCCATGCAAGTCYRAAATCC
 -----KMRGTCTGAGAT--

Original motif Consensus sequence: CCCATGCAAGTCYRAAATCC



Reverse complement motif Consensus sequence: GGATTTMKGACTTGCATGGG



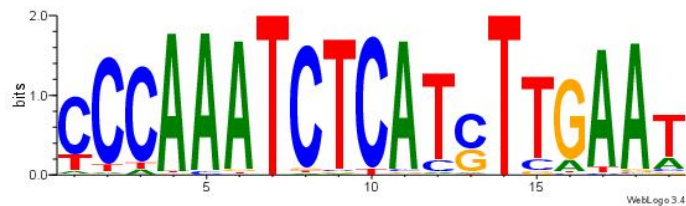
Dataset #: 1
 Motif ID: 227
 Motif name: Motif 227
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3

Number of overlap: 12
Similarity score: 0.0718827

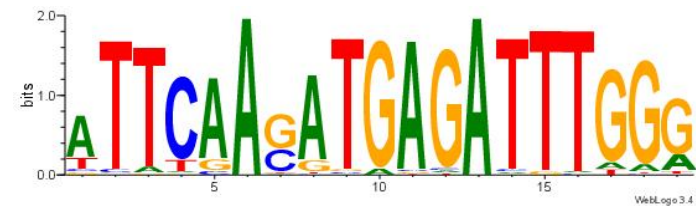
Alignment:

ATTCAASATGAGATTTGGG
--KMRGTCTGAGAT-----

Original motif Consensus sequence: CCCAAATCTCATSTTGAAT

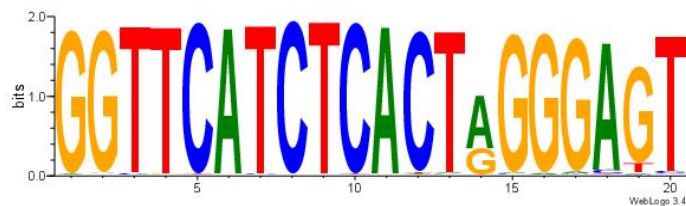


Reverse complement motif Consensus sequence: ATTCAASATGAGATTTGGG

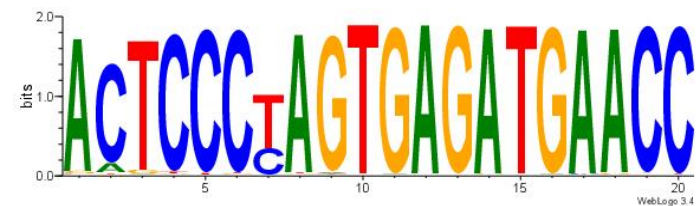


Dataset #: 1 Motif ID: 23 Motif name: Motif 23

Original motif Consensus sequence: GGTTTCATCTCACTAGGGAGT



Reverse complement motif Consensus sequence: ACTCCCTAGTGAGATGAACC



Best Matches for Motif ID 23 (Highest to Lowest)

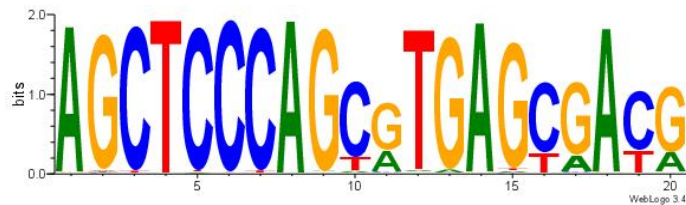
Dataset #: 1
Motif ID: 48
Motif name: Motif 48

Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	20
Similarity score:	0.116157

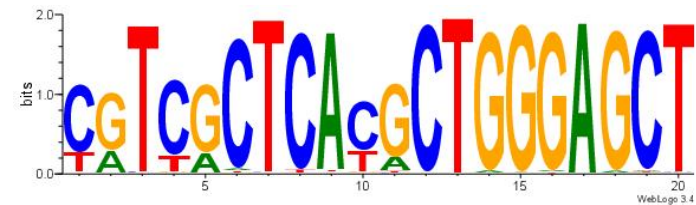
Alignment:

```
AGCTCCCAGCGTGAGCGACG
ACTCCCTAGTGAGATGAACC
```

Original motif Consensus sequence: AGCTCCCAGCGTGAGCGACG



Reverse complement motif Consensus sequence: CGTCGCTCAGCTGGGAGCT

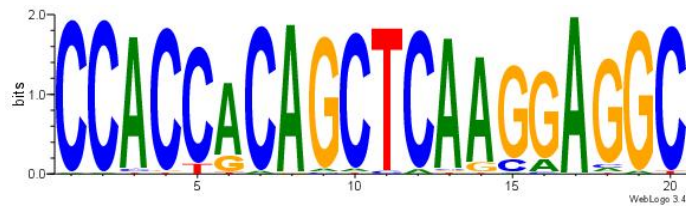


Dataset #:	1
Motif ID:	331
Motif name:	Motif 331
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	20
Similarity score:	0.123973

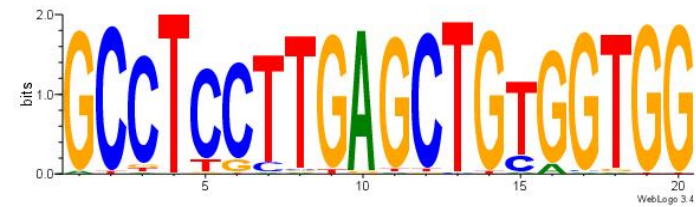
Alignment:

GCCTCCTTGAGCTGTGGTGG
GGTTCATCTCACTAGGGAGT

Original motif Consensus sequence: CCACCACAGCTCAAGGAGGC



Reverse complement motif Consensus sequence:
GCCTCCTTGAGCTGTGGTGG



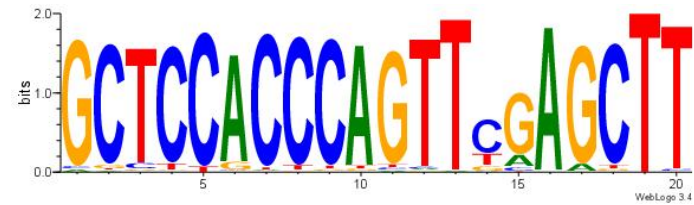
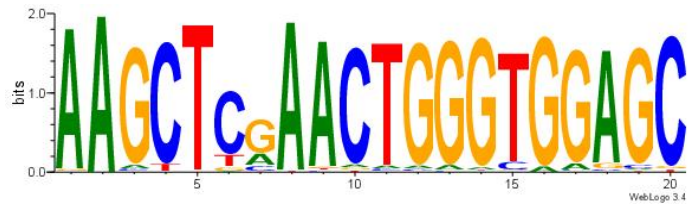
Dataset #:	1
Motif ID:	321
Motif name:	Motif 321
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	20
Similarity score:	0.124427

Alignment:

GCTCCACCCAGTTCGAGCTT
GGTTCATCTCACTAGGGAGT

Original motif Consensus sequence: AAGCTCGAACTGGGTGGAGC

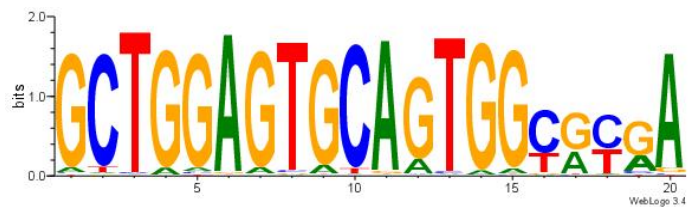
Reverse complement motif Consensus sequence:
GCTCCACCCAGTTCGAGCTT



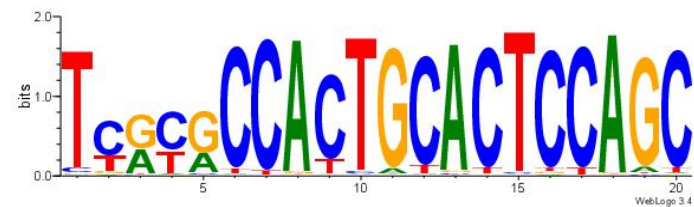
Dataset #: 1
 Motif ID: 3
 Motif name: Motif 3
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.127278

Alignment:
 TCKMGCCACTGCACTCCAGC
 ACTCCCTAGTGAGATGAACC

Original motif Consensus sequence: GCTGGAGTGCAGTGGCRYGA



Reverse complement motif Consensus sequence: TCKMGCCACTGCACTCCAGC



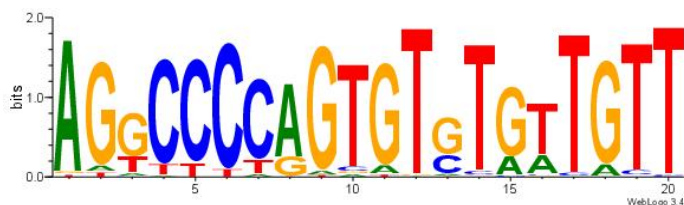
Dataset #: 1

Motif ID: 176
 Motif name: Motif 176
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.129596

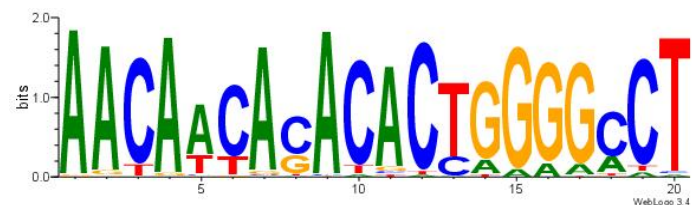
Alignment:

AACACASACTGGGGCCT
 GGTTCATCTACTAGGGAGT

Original motif Consensus sequence: AGGCCCCAGTGTSTGTTGTT

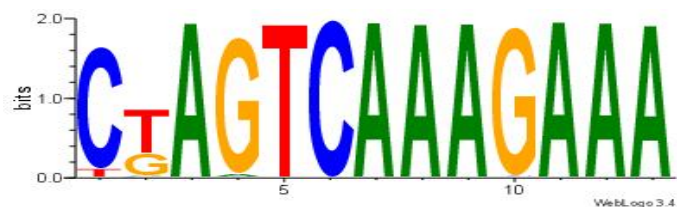


Reverse complement motif Consensus sequence: AACACASACTGGGGCCT

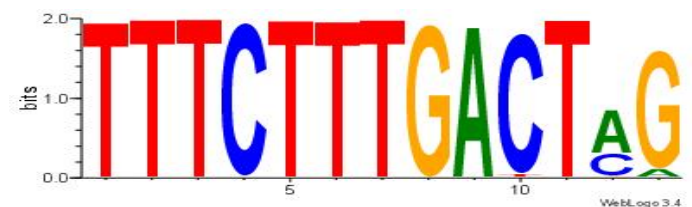


Dataset #: 1 Motif ID: 24 Motif name: Motif 24

Original motif Consensus sequence: CKAGTCAAAGAAA



Reverse complement motif Consensus sequence: TTTCTTTGACTAG



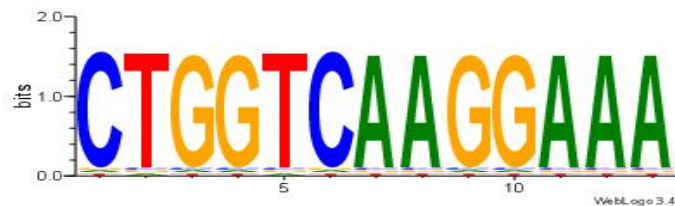
Best Matches for Motif ID 24 (Highest to Lowest)

Dataset #: 1
Motif ID: 274
Motif name: Motif 274
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 13
Similarity score: 0.0524968

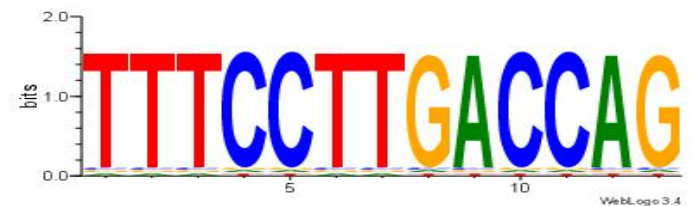
Alignment:

CTGGTCAAGGAAA
CKAGTCAAAGAAA

Original motif Consensus sequence: CTGGTCAAGGAAA



Reverse complement motif Consensus sequence: TTTCTTGACCAG



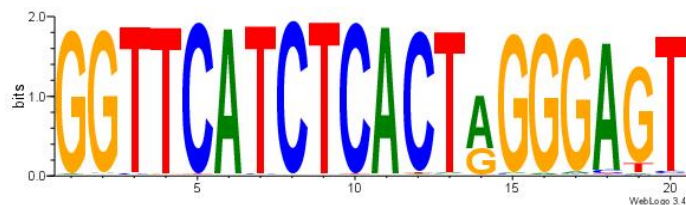
Dataset #: 1
Motif ID: 23
Motif name: Motif 23
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement

Direction: Backward
 Position number: 6
 Number of overlap: 13
 Similarity score: 0.0775612

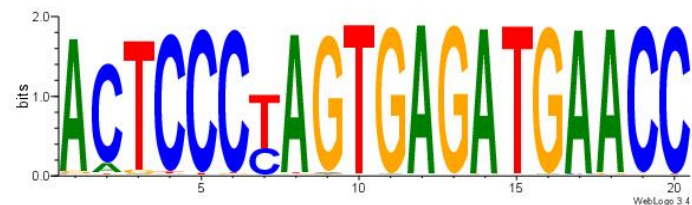
Alignment:

ACTCCCTAGTGAGATGAACC
 --CKAGTCAAAGAAA-----

Original motif Consensus sequence: GGTTCACTCTCACTAGGGAGT



Reverse complement motif Consensus sequence: ACTCCCTAGTGAGATGAACC

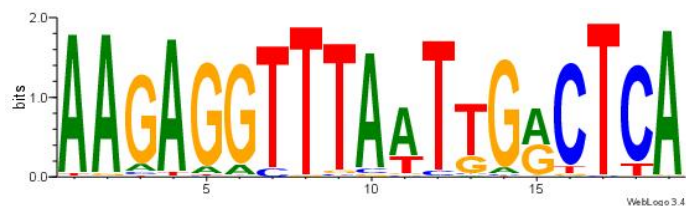


Dataset #: 1
 Motif ID: 129
 Motif name: Motif 129
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 13
 Similarity score: 0.0797194

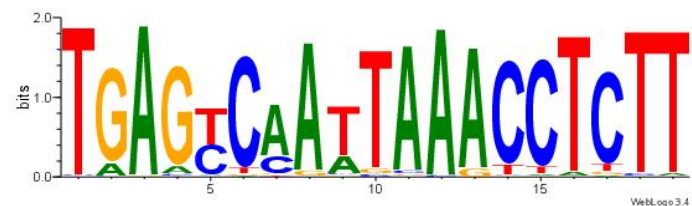
Alignment:

TGAGKCAATTAAACCTCTT
 CKAGTCAAAGAAA-----

Original motif Consensus sequence: AAGAGGTTTAATTGRCTCA



Reverse complement motif Consensus sequence: TGAGKCAATTAACCTCTT

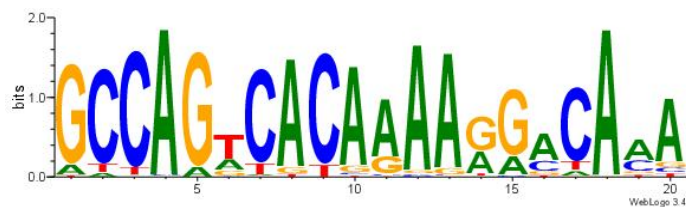


Dataset #: 1
Motif ID: 145
Motif name: Motif 145
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 7
Number of overlap: 13
Similarity score: 0.0798508

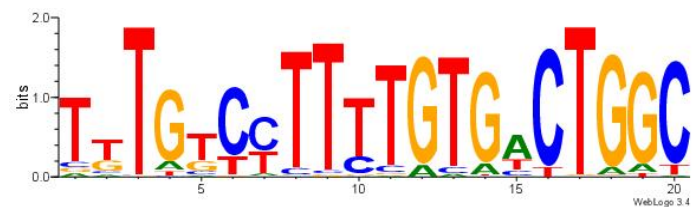
Alignment:

GCCAGTCACAAAARGACAMA
-CKAGTCAAAGAAA-----

Original motif Consensus sequence: GCCAGTCACAAAARGACAMA



Reverse complement motif Consensus sequence: TYTGTCTTTTTGTGACTGGC

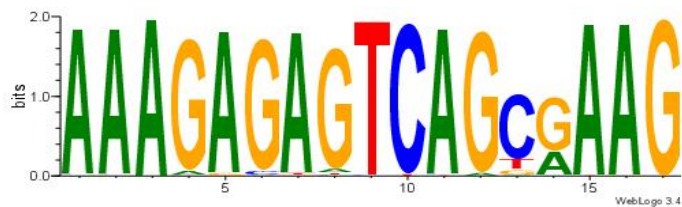


Dataset #: 1
 Motif ID: 148
 Motif name: Motif 148
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 5
 Number of overlap: 13
 Similarity score: 0.0937628

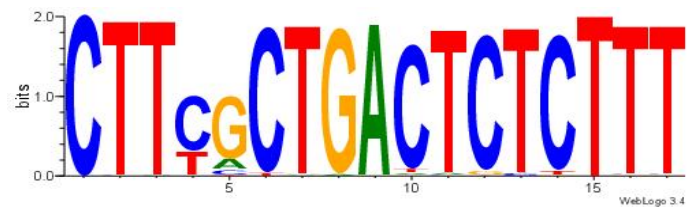
Alignment:

AAAGAGAGTCAGCGAAG
 ----CKAGTCAAAGAAA

Original motif Consensus sequence: AAAGAGAGTCAGCGAAG



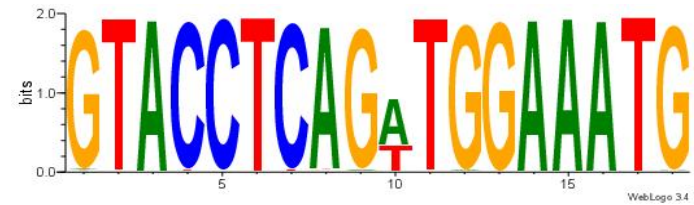
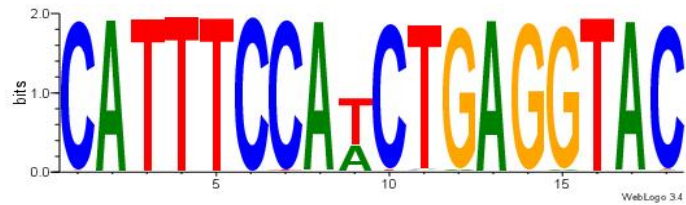
Reverse complement motif Consensus sequence: CTTGCTGACTCTCTTT



Dataset #: 1 Motif ID: 25 Motif name: Motif 25

Original motif Consensus sequence: CATTCCA WCTGAGGTAC

Reverse complement motif Consensus sequence: GTACCTCAGWTGGAAATG

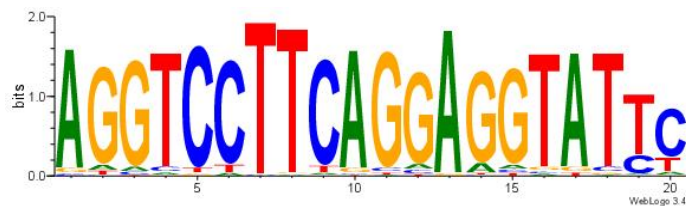


Best Matches for Motif ID 25 (Highest to Lowest)

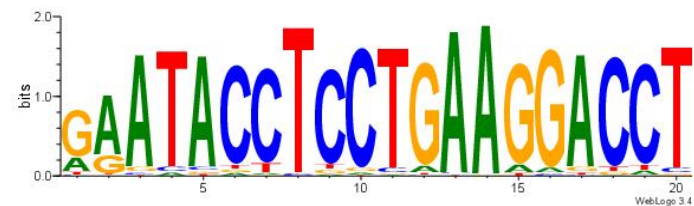
Dataset #: 1
 Motif ID: 179
 Motif name: Motif 179
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 18
 Similarity score: 0.0987898

Alignment:
 GAATACCTCCTGAAGGACCT
 CATTTCCTGAGGTAC--

Original motif Consensus sequence: AGGTCCTCAGGAGGTATTC



Reverse complement motif Consensus sequence: GAATACCTCCTGAAGGACCT

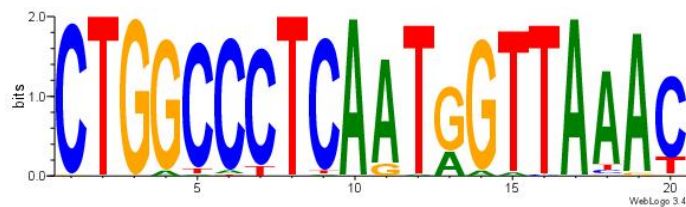


Dataset #: 1
 Motif ID: 332
 Motif name: Motif 332
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 18
 Similarity score: 0.110707

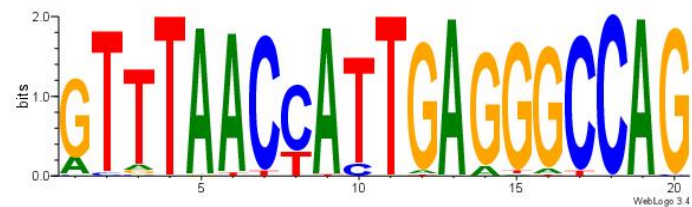
Alignment:

GTTTAACCATTGAGGGCCAG
 CATTTCcAwCTGAGGTAC--

Original motif Consensus sequence: CTGGCCCTCAATGGTTAAAC



Reverse complement motif Consensus sequence: GTTTAACCATTGAGGGCCAG



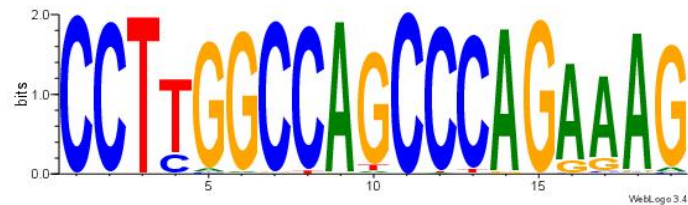
Dataset #: 1
 Motif ID: 122
 Motif name: Motif 122
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1

Number of overlap: 18
Similarity score: 0.117106

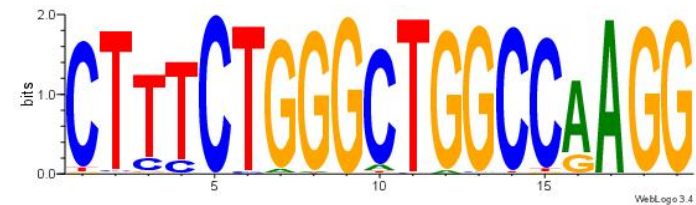
Alignment:

CCTTGCCAGCCCAGAAAG
-CATTTCWCTGAGGTAC

Original motif Consensus sequence: CCTTGCCAGCCCAGAAAG



Reverse complement motif Consensus sequence:
CTTCTGGGCTGGCCAAGG

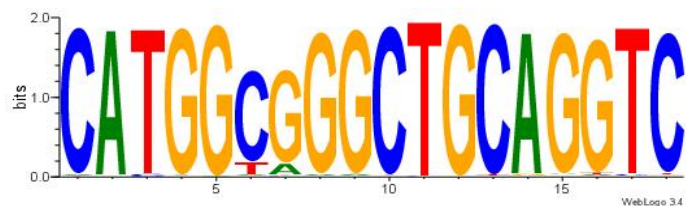


Dataset #: 1
Motif ID: 68
Motif name: Motif 68
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 18
Similarity score: 0.118191

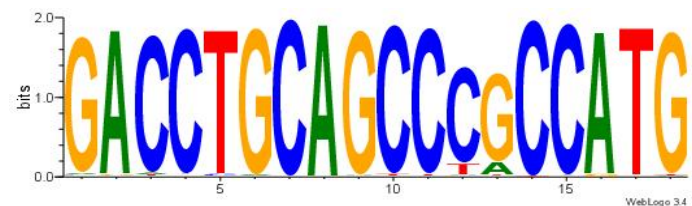
Alignment:

CATGGCGGGCTGCAGGTC
CATTTCWCTGAGGTAC

Original motif Consensus sequence: CATGGCGGGCTGCAGGTC



Reverse complement motif Consensus sequence: GACCTGCAGCCCGCCATG

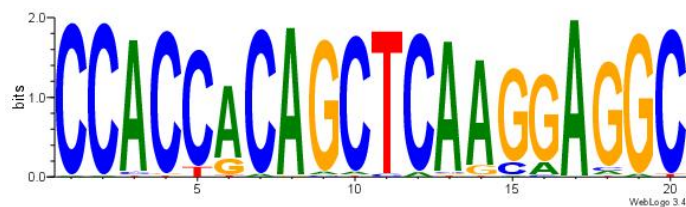


Dataset #: 1
Motif ID: 331
Motif name: Motif 331
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 3
Number of overlap: 18
Similarity score: 0.118723

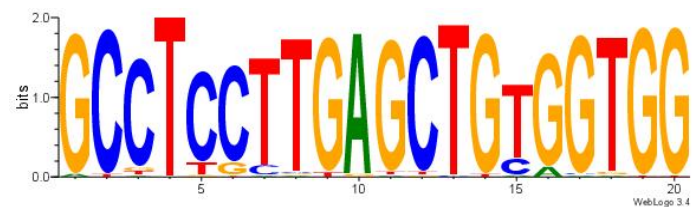
Alignment:

CCACCACAGCTCAAGGAGGC
GTACCTCAGWTGGAAATG--

Original motif Consensus sequence: CCACCACAGCTCAAGGAGGC

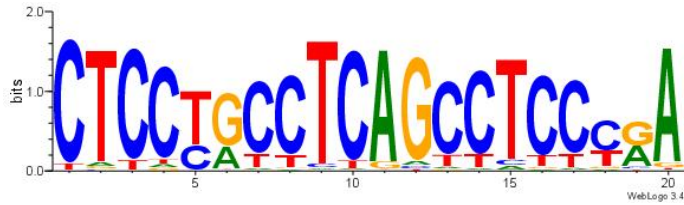


Reverse complement motif Consensus sequence: GCCTCCTTGAGCTGTGGTGG

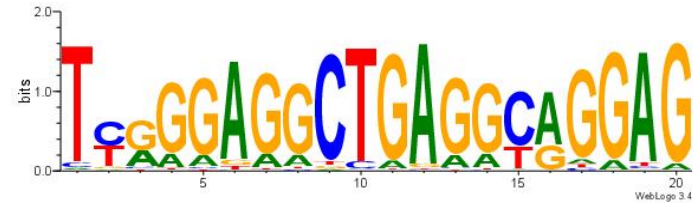


Dataset #: 1 Motif ID: 26 Motif name: Motif 26

Original motif Consensus sequence: CTCCTGCCTCAGCCTCCCRA



Reverse complement motif Consensus sequence: TMGGGAGGCTGAGGCAGGAG



Best Matches for Motif ID 26 (Highest to Lowest)

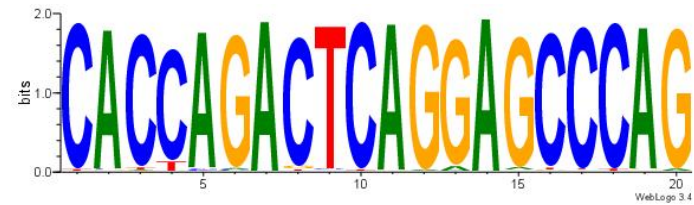
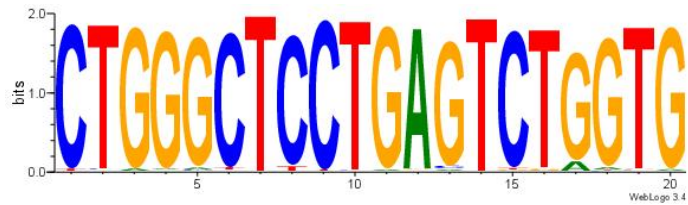
Dataset #:	1
Motif ID:	67
Motif name:	Motif 67
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	20
Similarity score:	0.0991184

Alignment:

```
CACCAGACTCAGGAGCCCAG  
CTCCTGCCTCAGCCTCCCRA
```

Original motif Consensus sequence: CTGGGCTCCTGAGTCTGGTG

Reverse complement motif Consensus sequence: CACCAGACTCAGGAGCCCAG

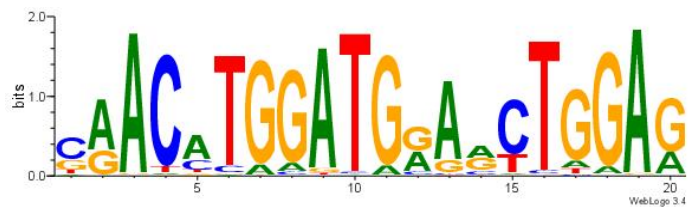


Dataset #: 1
 Motif ID: 104
 Motif name: Motif 104
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.111358

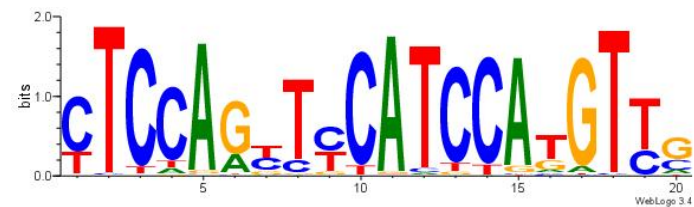
Alignment:

CAACATGGATGRARCTGGAG
 TMGGGAGGCTGAGGCAGGAG

Original motif Consensus sequence: CAACATGGATGRARCTGGAG



Reverse complement motif Consensus sequence: CTCCAGKTCATCCATGTTG



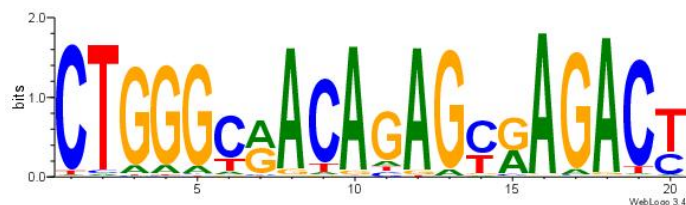
Dataset #: 1

Motif ID: 29
 Motif name: Motif 29
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.113787

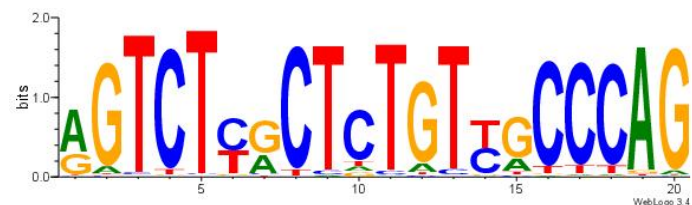
Alignment:

MGTCTMKCTCTGTKGCCCAG
 CTCCTGCCTCAGCCTCCRA

Original motif Consensus sequence: CTGGGCRACAGAGYRAGACY



Reverse complement motif Consensus sequence: MGTCTMKCTCTGTKGCCCAG



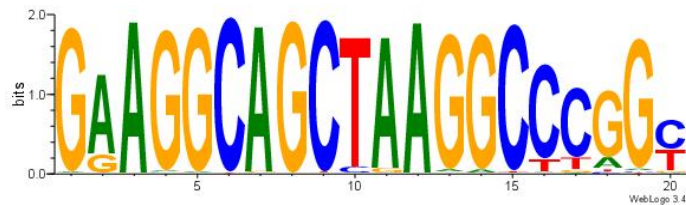
Dataset #: 1
 Motif ID: 64
 Motif name: Motif 64
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 20

Similarity score: 0.115298

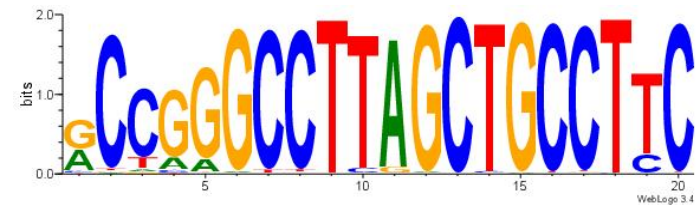
Alignment:

GAAGGCAGCTAAGGCCGGY
TMGGGAGGCTGAGGCAGGAG

Original motif Consensus sequence: GAAGGCAGCTAAGGCCGGY



Reverse complement motif Consensus sequence:
KCCGGGCCCTTAGCTGCCTTC



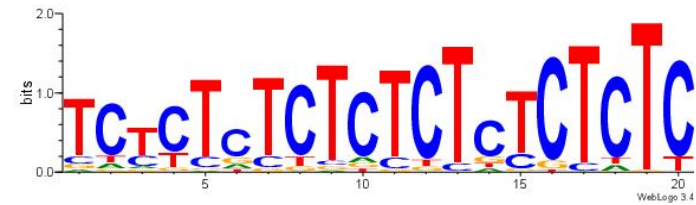
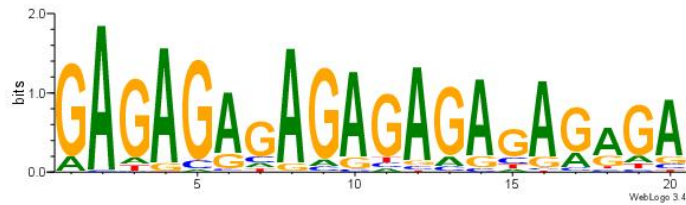
Dataset #: 1
Motif ID: 109
Motif name: Motif 109
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 20
Similarity score: 0.121771

Alignment:

GAGAGAGAGAGAGAGAGAGA
TMGGGAGGCTGAGGCAGGAG

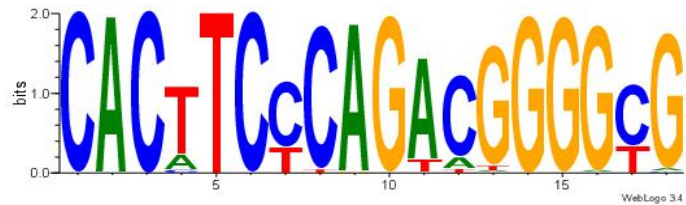
Original motif Consensus sequence: GAGAGAGAGAGAGAGAGA

Reverse complement motif Consensus sequence:
TCTCTCTCTCTCTCTCTC

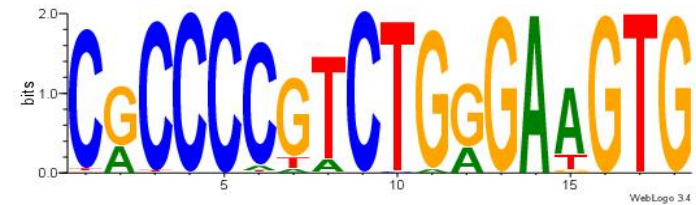


Dataset #: 1 Motif ID: 27 Motif name: Motif 27

Original motif Consensus sequence: CACTTCCCAGACGGGGCG



Reverse complement motif Consensus sequence: CGCCCCGTCTGGGAAGTG



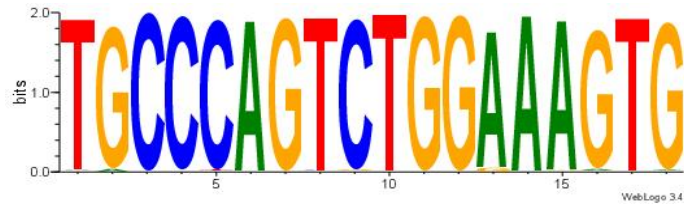
Best Matches for Motif ID 27 (Highest to Lowest)

Dataset #:	1
Motif ID:	45
Motif name:	Motif 45
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	18
Similarity score:	0.0413095

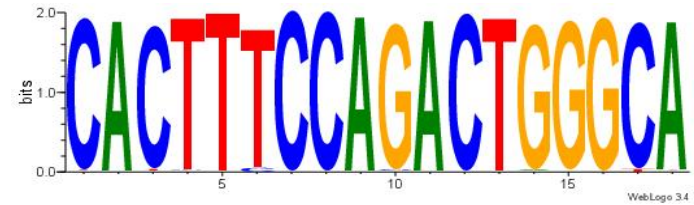
Alignment:

CACTTTCCAGACTGGGCA
CACTTCCCAGACGGGGCG

Original motif Consensus sequence: TGCCCAGTCTGGAAAGTG



Reverse complement motif Consensus sequence:
CACTTTCCAGACTGGGCA



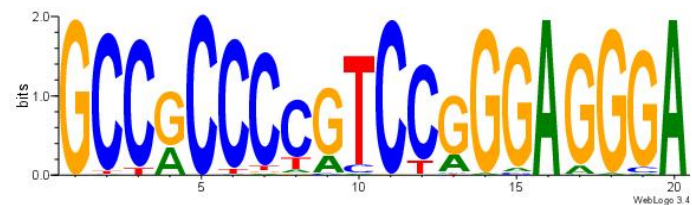
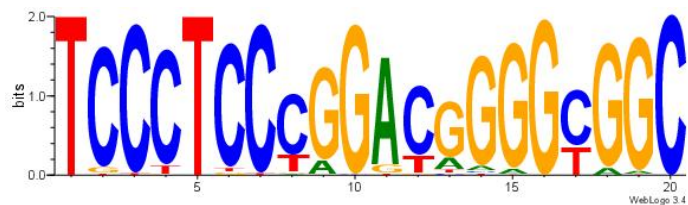
Dataset #: 1
Motif ID: 155
Motif name: Motif 155
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 3
Number of overlap: 18
Similarity score: 0.0525092

Alignment:

TCCCTCCCGGACGGGGYGGC
CACTTCCCAGACGGGGCG--

Original motif Consensus sequence: TCCCTCCCGGACGGGGYGGC

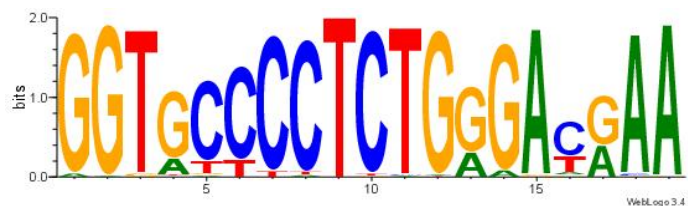
Reverse complement motif Consensus sequence:
GCCKCCCCGTCCGGGAGGGA



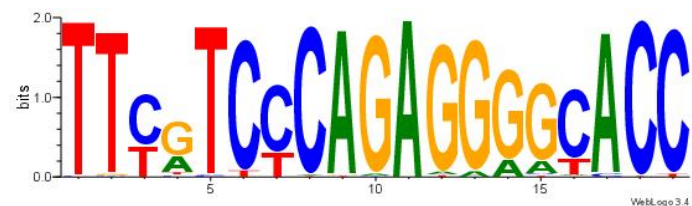
Dataset #: 1
 Motif ID: 260
 Motif name: Motif 260
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 18
 Similarity score: 0.0884142

Alignment:
 GGTGCCCTCTGGGACRAA
 -CGCCCCGTCTGGGAAGTG

Original motif Consensus sequence: GGTGCCCTCTGGGACRAA



Reverse complement motif Consensus sequence: TTMGTCCCAGAGGGGCACC



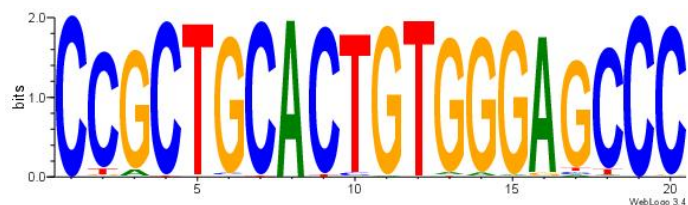
Dataset #: 1

Motif ID: 144
 Motif name: Motif 144
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 18
 Similarity score: 0.0977824

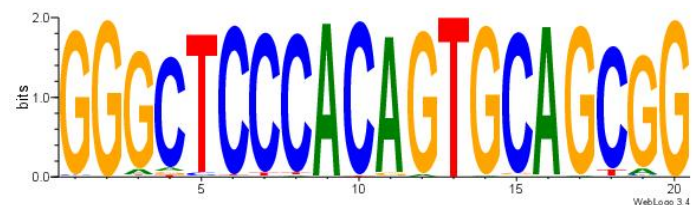
Alignment:

GGGCTCCCACAGTGCAGCGG
 -CGCCCCGTCTGGGAAGTG-

Original motif Consensus sequence: CCGCTGCACTGTGGGAGCCC



Reverse complement motif Consensus sequence: GGGCTCCCACAGTGCAGCGG



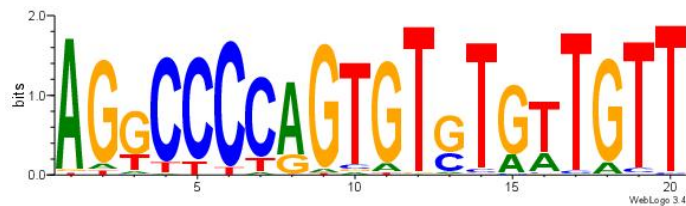
Dataset #: 1
 Motif ID: 176
 Motif name: Motif 176
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 18

Similarity score: 0.0995243

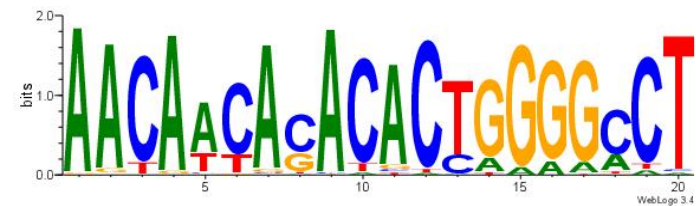
Alignment:

```
AGGCCCCAGTGTSTGTTGTT
--CGCCCCGTCTGGGAAGTG
```

Original motif Consensus sequence: AGGCCCCAGTGTSTGTTGTT

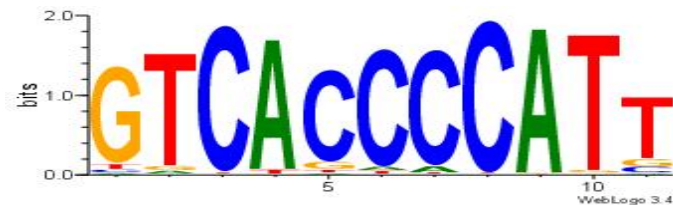


Reverse complement motif Consensus sequence: AACACASACTGGGGCCT

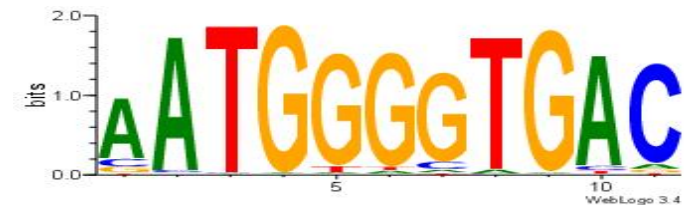


Dataset #: 1 Motif ID: 28 Motif name: Motif 28

Original motif Consensus sequence: GTCACCCCAT



Reverse complement motif Consensus sequence: AATGGGGTGAC



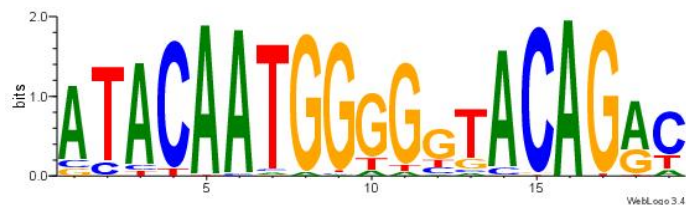
Best Matches for Motif ID 28 (Highest to Lowest)

Dataset #:	1
Motif ID:	193
Motif name:	Motif 193
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif

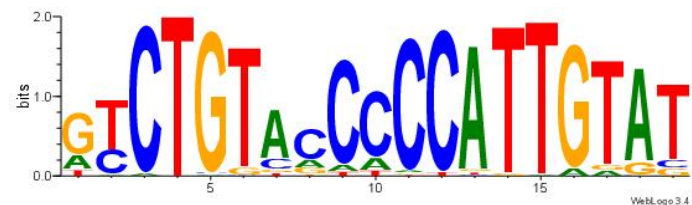
Direction: Forward
Position number: 5
Number of overlap: 11
Similarity score: 0.0423623

Alignment:
ATACAATGGGGGTACAGRC
----AATGGGGTGAC----

Original motif Consensus sequence: ATACAATGGGGGTACAGRC



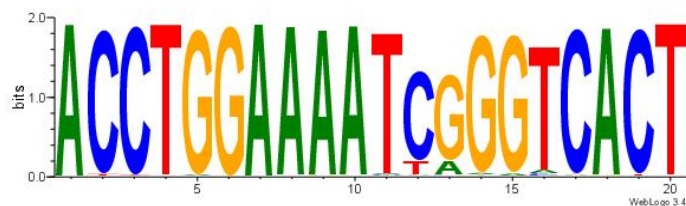
Reverse complement motif Consensus sequence: GKCTGTACCCCATTTGTAT



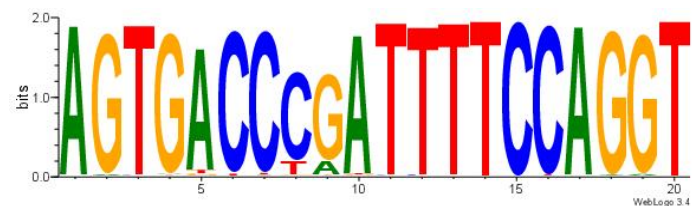
Dataset #: 1
Motif ID: 14
Motif name: Motif 14
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 2
Number of overlap: 11
Similarity score: 0.0486677

Alignment:
ACCTGGAAAATCGGGTCACT
-AATGGGGTGAC-----

Original motif Consensus sequence: ACCTGGAAAATCGGGTCACT



Reverse complement motif Consensus sequence: AGTGACCCGATTTTCCAGGT

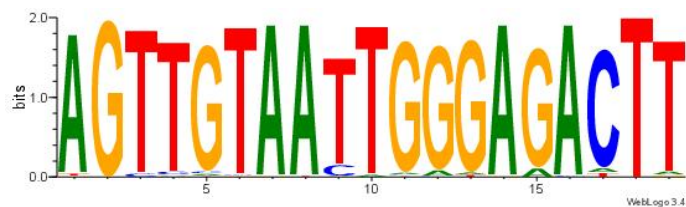


Dataset #: 1
Motif ID: 232
Motif name: Motif 232
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 7
Number of overlap: 11
Similarity score: 0.0491797

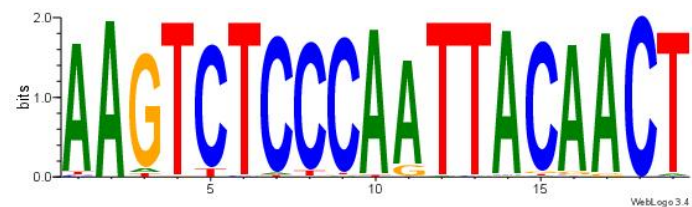
Alignment:

AGTTGTAATTGGGAGACTT
-----AATGGGGTGAC--

Original motif Consensus sequence: AGTTGTAATTGGGAGACTT



Reverse complement motif Consensus sequence: AAGTCTCCCAATTACAAC

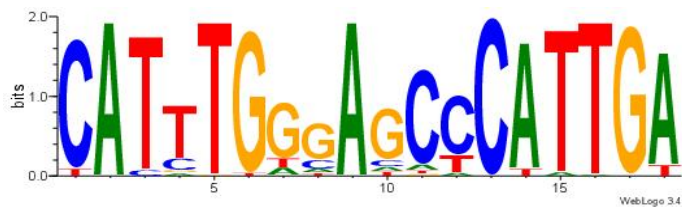


Dataset #: 1
 Motif ID: 284
 Motif name: Motif 284
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 11
 Similarity score: 0.0587499

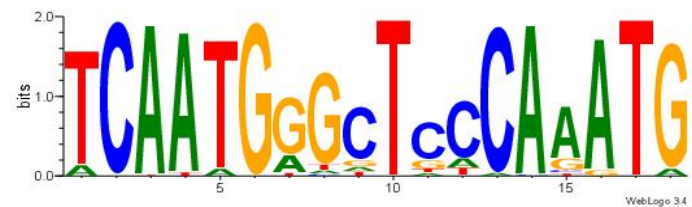
Alignment:

CATTGGGAGCCCATTGA
 -----GTCACCCATT--

Original motif Consensus sequence: CATTGGGAGCCCATTGA



Reverse complement motif Consensus sequence: TCAATGGGCTCCCAAATG



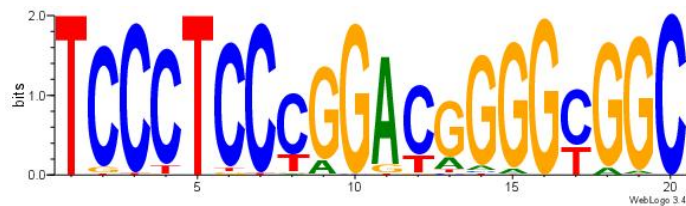
Dataset #: 1
 Motif ID: 155
 Motif name: Motif 155
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 10

Number of overlap: 11
 Similarity score: 0.0773836

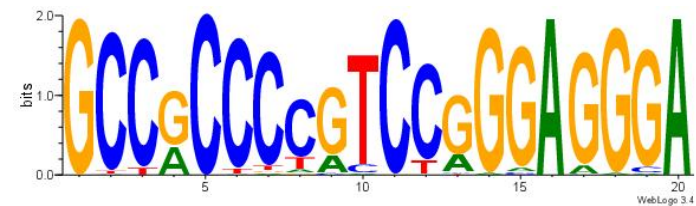
Alignment:

TCCCTCCCGGACGGGGYGGC
 -----AATGGGGTGAC

Original motif Consensus sequence: TCCCTCCCGGACGGGGYGGC

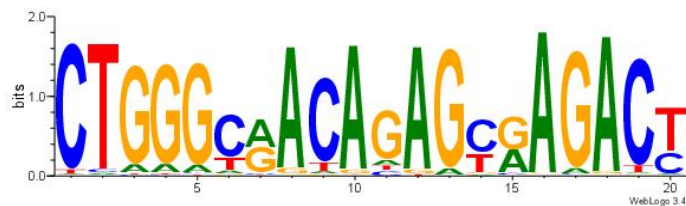


Reverse complement motif Consensus sequence:
 GCCKCCCCGTCCGGGAGGGA

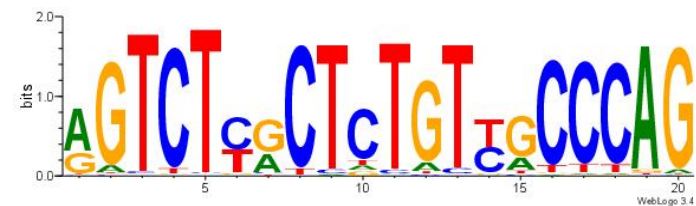


Dataset #: 1 Motif ID: 29 Motif name: Motif 29

Original motif Consensus sequence: CTGGGCRACAGAGYRAGACY



Reverse complement motif Consensus sequence:
 MGTCTMKCTCTGKGCCAG



Best Matches for Motif ID 29 (Highest to Lowest)

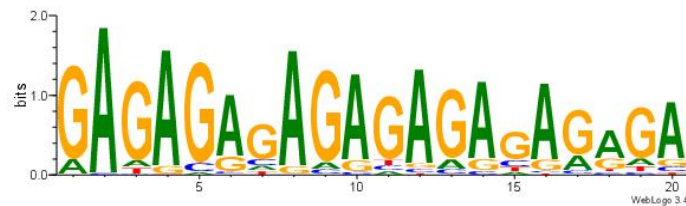
Dataset #: 1
 Motif ID: 109
 Motif name: Motif 109

Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	20
Similarity score:	0.0944011

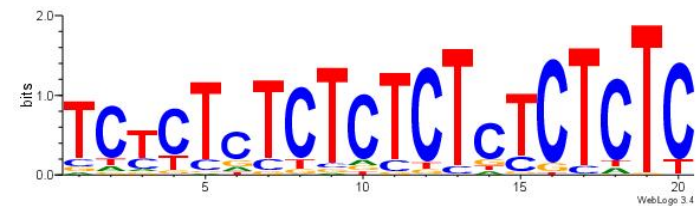
Alignment:

```
TCTCTCTCTCTCTCTCTCTC
MGTCTMKCTCTGTKGCCAG
```

Original motif Consensus sequence: GAGAGAGAGAGAGAGAGA



Reverse complement motif Consensus sequence: TCTCTCTCTCTCTCTCTC

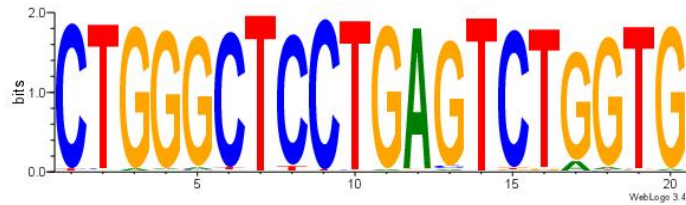


Dataset #:	1
Motif ID:	67
Motif name:	Motif 67
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	20
Similarity score:	0.100789

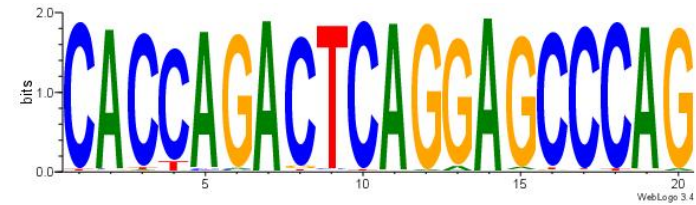
Alignment:

CTGGGCTCCTGAGTCTGGTG
CTGGGCRACAGAGYRAGACY

Original motif Consensus sequence: CTGGGCTCCTGAGTCTGGTG



Reverse complement motif Consensus sequence:
CACCAGACTCAGGAGCCCAG



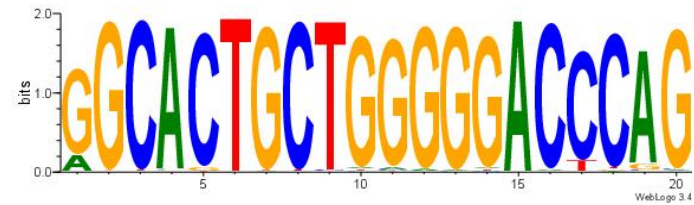
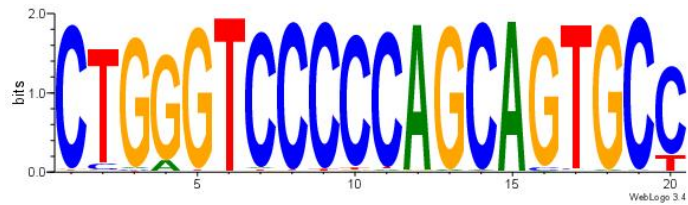
Dataset #:	1
Motif ID:	84
Motif name:	Motif 84
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	20
Similarity score:	0.103081

Alignment:

CTGGGTCCCCCAGCAGTGCC
CTGGGCRACAGAGYRAGACY

Original motif Consensus sequence: CTGGGTCCCCCAGCAGTGCC

Reverse complement motif Consensus sequence:
GGCACTGCTGGGGGACCCAG

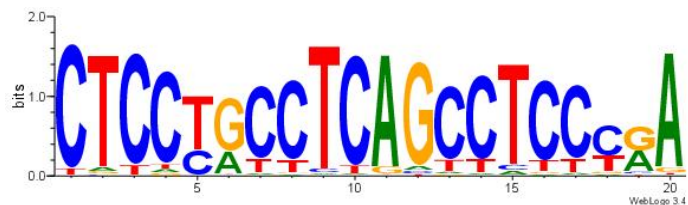


Dataset #: 1
 Motif ID: 26
 Motif name: Motif 26
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.108553

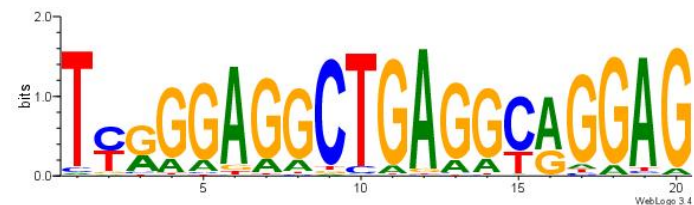
Alignment:

TMGGGAGGCTGAGGCAGGAG
 CTGGGCRACAGAGYRAGACY

Original motif Consensus sequence: CTCCTGCCTCAGCCTCCRA



Reverse complement motif Consensus sequence: TMGGGAGGCTGAGGCAGGAG



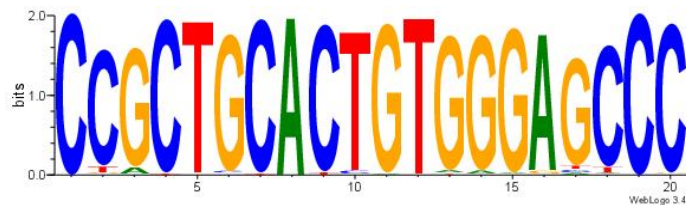
Dataset #: 1

Motif ID: 144
 Motif name: Motif 144
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.11235

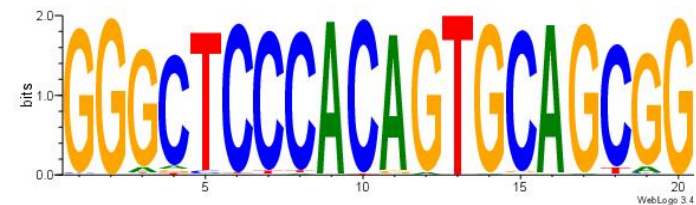
Alignment:

GGGCTCCCACAGTGCAGCGG
 MGTCTMKCTCTGTKGCCAG

Original motif Consensus sequence: CCGCTGCACTGTGGGAGCCC

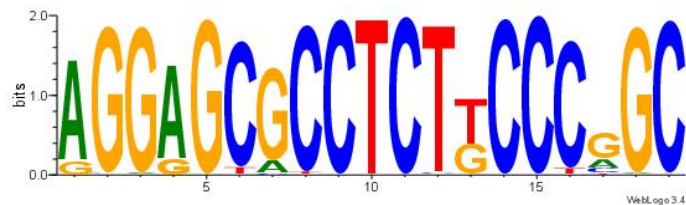


Reverse complement motif Consensus sequence: GGGCTCCCACAGTGCAGCGG

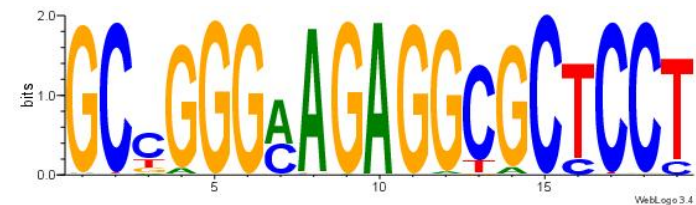


Dataset #: 1 Motif ID: 30 Motif name: Motif 30

Original motif Consensus sequence: AGGAGCGCCTCTKCCCGGC



Reverse complement motif Consensus sequence: GCCGGGAGAGGCCTCT



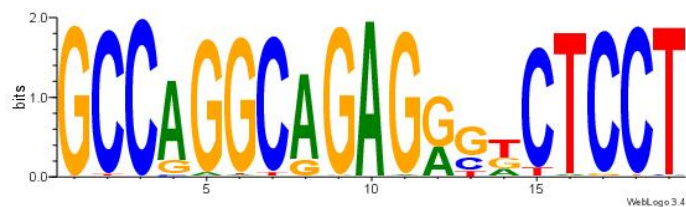
Best Matches for Motif ID 30 (Highest to Lowest)

Dataset #: 1
Motif ID: 43
Motif name: Motif 43
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 19
Similarity score: 0.0399316

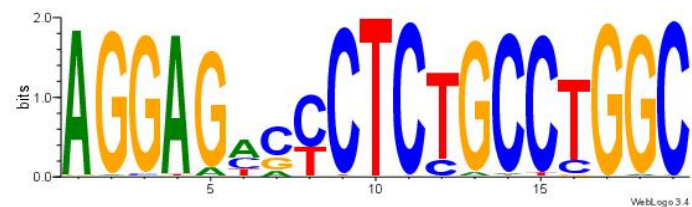
Alignment:

```
AGGAGRCMCTCTGCCTGGC  
AGGAGCGCCTCTKCCCGGC
```

Original motif Consensus sequence: GCCAGGCAGAGRGKCTCCT



Reverse complement motif Consensus sequence:
AGGAGRCMCTCTGCCTGGC



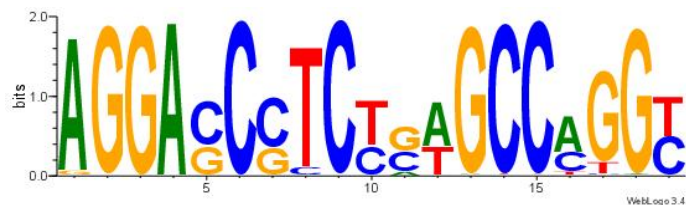
Dataset #: 1
Motif ID: 10
Motif name: Motif 10
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif

Direction: Forward
Position number: 1
Number of overlap: 19
Similarity score: 0.0610031

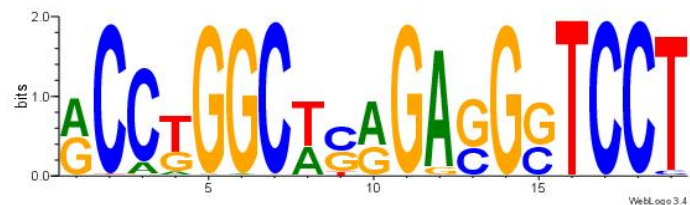
Alignment:

AGGASCSTCYSWGCCMGGY
AGGAGCGCCTCTKCCCGGC

Original motif Consensus sequence: AGGASCSTCYSWGCCMGGY



Reverse complement motif Consensus sequence: MCCYGGCWSMGASGSTCCT

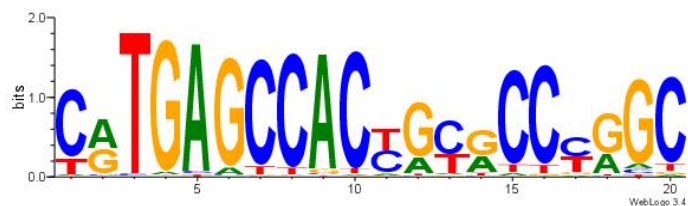


Dataset #: 1
Motif ID: 56
Motif name: Motif 56
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 2
Number of overlap: 19
Similarity score: 0.077695

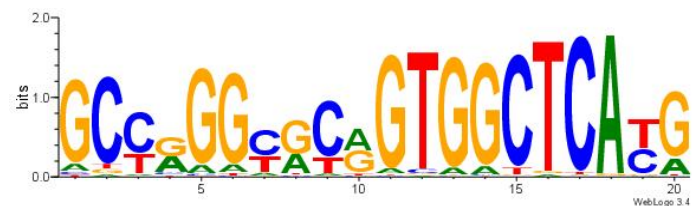
Alignment:

CRTGAGCCACYGYRCCYGGC
-AGGAGCGCCTCTKCCCGGC

Original motif Consensus sequence: CRTGAGCCACYGYRCCYGGC



Reverse complement motif Consensus sequence: GCCKGGMKCMGTGGCTCAKG

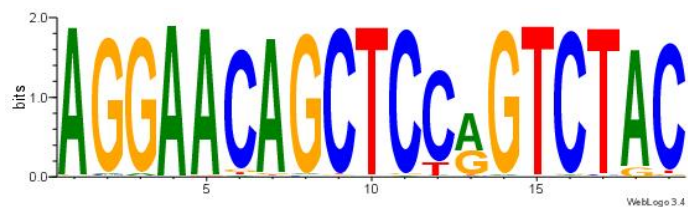


Dataset #: 1
Motif ID: 62
Motif name: Motif 62
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 19
Similarity score: 0.0937137

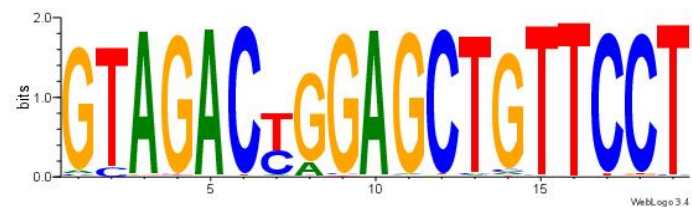
Alignment:

AGGAACAGCTCCRGCTCTAC
AGGAGCGCCTCTKCCCGGC

Original motif Consensus sequence: AGGAACAGCTCCRGCTCTAC



Reverse complement motif Consensus sequence: GTAGACKGGAGCTGTTCCCT

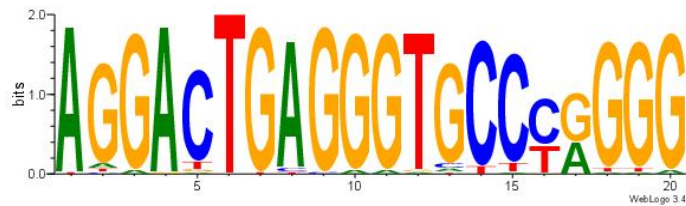


Dataset #: 1
 Motif ID: 312
 Motif name: Motif 312
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 19
 Similarity score: 0.0942612

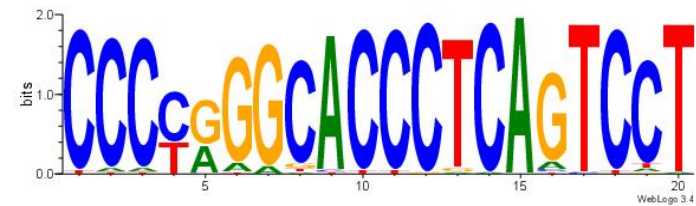
Alignment:

AGGACTGAGGGTGCCYRGGG
 AGGAGCGCCTCTKCCCGGC-

Original motif Consensus sequence: AGGACTGAGGGTGCCYRGGG



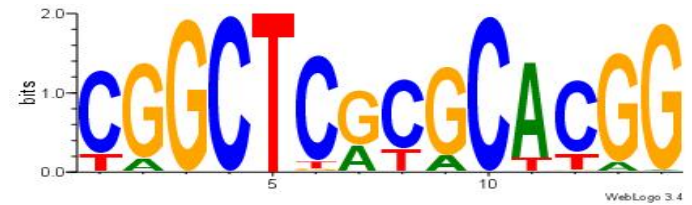
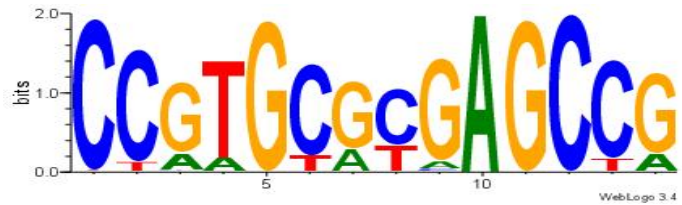
Reverse complement motif Consensus sequence: CCCMKGCCACCCTCAGTCCT



Dataset #: 1 Motif ID: 31 Motif name: Motif 31

Original motif Consensus sequence: CCGTGCGCGAGCCG

Reverse complement motif Consensus sequence: CGGCTCGCGCACCG

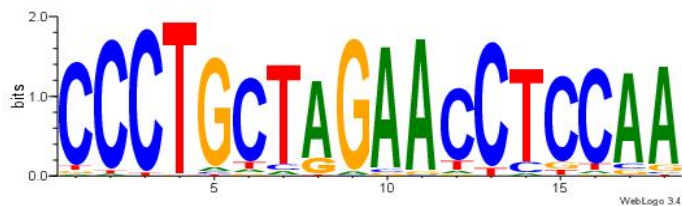


Best Matches for Motif ID 31 (Highest to Lowest)

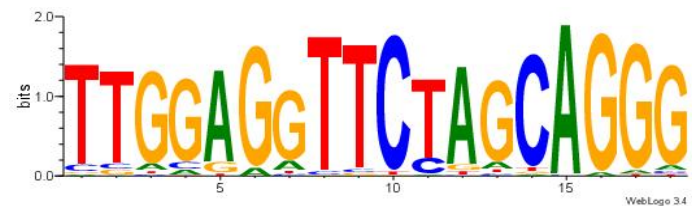
Dataset #: 1
 Motif ID: 299
 Motif name: Motif 299
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0.0706247

Alignment:
 TTGGAGGTTCTAGCAGGG
 ----CGGCTCGCGCACGG

Original motif Consensus sequence: CCCTGCTAGAACCTCCAA



Reverse complement motif Consensus sequence: TTGGAGGTTCTAGCAGGG

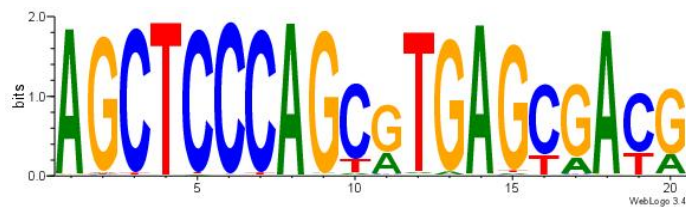


Dataset #: 1
 Motif ID: 48
 Motif name: Motif 48
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 14
 Similarity score: 0.0742371

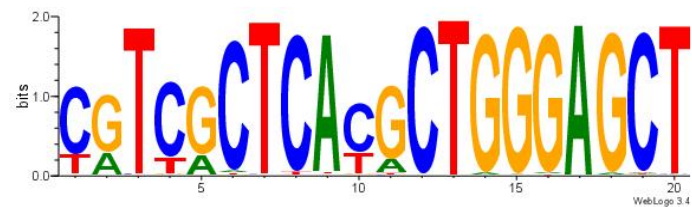
Alignment:

AGCTCCCAGCGTGAGCGACG
 ----CCGTGCGCGAGCCG--

Original motif Consensus sequence: AGCTCCCAGCGTGAGCGACG



Reverse complement motif Consensus sequence: CGTCGCTCAGCTGGGAGCT



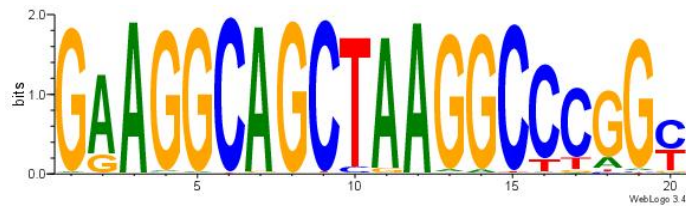
Dataset #: 1
 Motif ID: 64
 Motif name: Motif 64
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2

Number of overlap: 14
Similarity score: 0.0791073

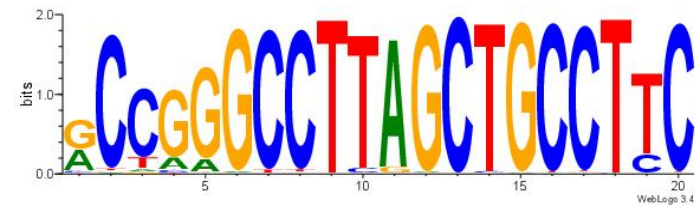
Alignment:

KCCGGGCCTTAGCTGCCTTC
-CCGTGCGCGAGCCG-----

Original motif Consensus sequence: GAAGGCAGCTAAGGCCGGC



Reverse complement motif Consensus sequence: KCCGGGCCTTAGCTGCCTTC

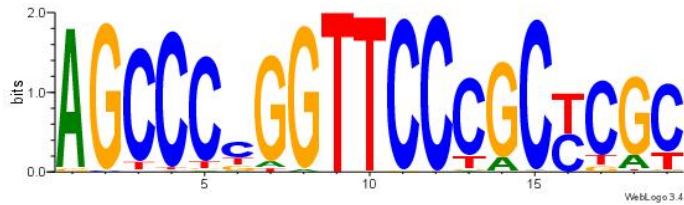


Dataset #: 1
Motif ID: 164
Motif name: Motif 164
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 14
Similarity score: 0.0804139

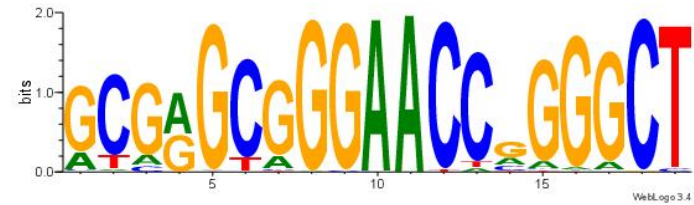
Alignment:

GCGMGCGGGAACCGGGGCT
CCGTGCGCGAGCCG-----

Original motif Consensus sequence: AGCCCCGGTTCCCGCYCGC



Reverse complement motif Consensus sequence: GCGMCGGGAACCGGGGCT

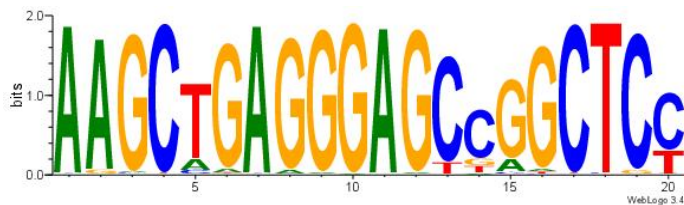


Dataset #: 1
Motif ID: 96
Motif name: Motif 96
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 2
Number of overlap: 14
Similarity score: 0.0852899

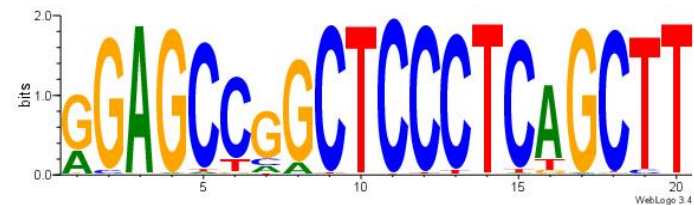
Alignment:

```
GGAGCCGGCTCCCTCAGCTT  
-----CGGCTCGCGCACGG--
```

Original motif Consensus sequence: AAGCTGAGGGAGCCGGCTCC



Reverse complement motif Consensus sequence: GGAGCCGGCTCCCTCAGCTT

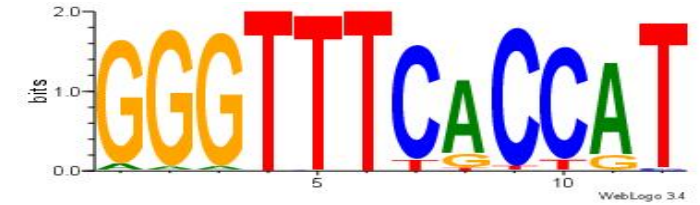


Dataset #: 1 Motif ID: 32 Motif name: Motif 32

Original motif Consensus sequence: ATGGTGAAACCC



Reverse complement motif Consensus sequence: GGGTTTCACCAT



Best Matches for Motif ID 32 (Highest to Lowest)

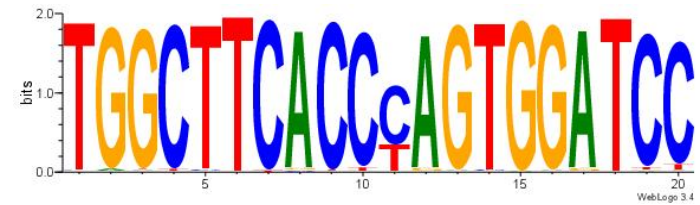
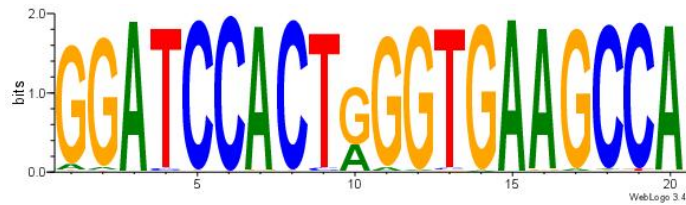
Dataset #:	1
Motif ID:	61
Motif name:	Motif 61
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	9
Number of overlap:	12
Similarity score:	0.0712132

Alignment:

```
TGGCTTCACCCAGTGGATCC  
GGGTTTCACCAT-----
```

Original motif Consensus sequence: GGATCCACTGGGTGAAGCCA

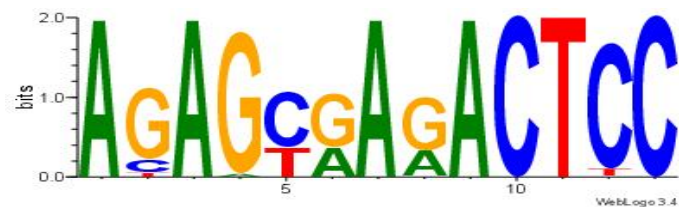
Reverse complement motif Consensus sequence:
TGGCTTCACCCAGTGGATCC



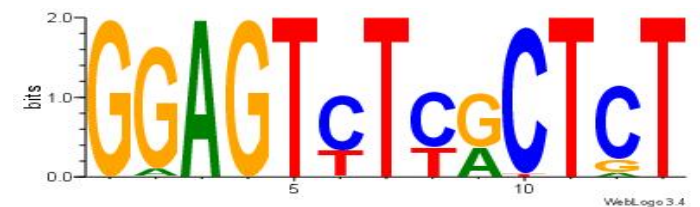
Dataset #: 1
 Motif ID: 204
 Motif name: Motif 204
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 12
 Similarity score: 0.0785008

Alignment:
 AGAGYRAGACTCC
 ATGGTGAAACCC-

Original motif Consensus sequence: AGAGYRAGACTCC



Reverse complement motif Consensus sequence: GGAGTCTMKCTCT



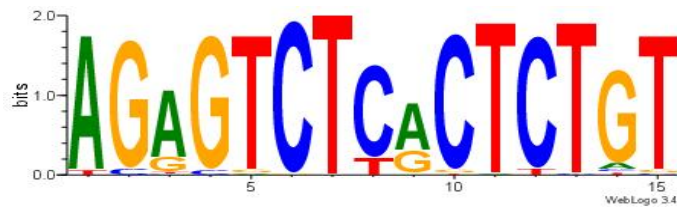
Dataset #: 1
 Motif ID: 253

Motif name:	Motif 253
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	12
Similarity score:	0.0802664

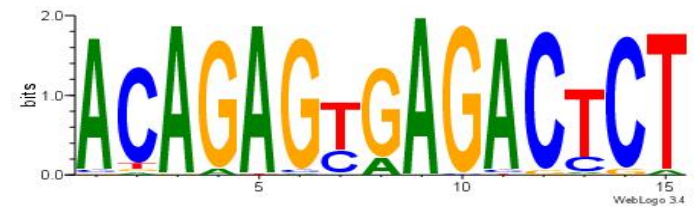
Alignment:

```
AGAGTCTCACTCTGT
-GGGTTTCACCAT--
```

Original motif Consensus sequence: AGAGTCTCACTCTGT



Reverse complement motif Consensus sequence: ACAGAGTGAGACT

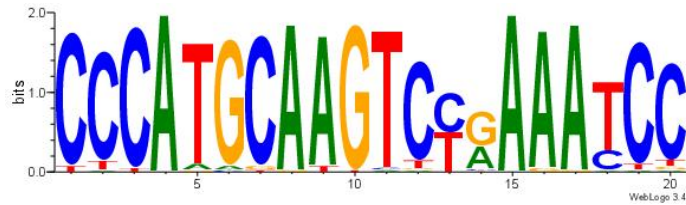


Dataset #:	1
Motif ID:	310
Motif name:	Motif 310
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	12
Similarity score:	0.0852091

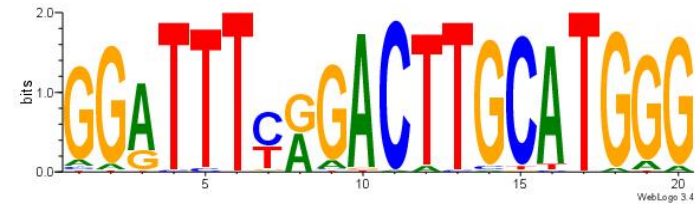
Alignment:

```
CCCATGCAAGTCYRAAATCC  
-----ATGGTGAAACCC
```

Original motif Consensus sequence: CCCATGCAAGTCYRAAATCC



Reverse complement motif Consensus sequence:
GGATTTMKGACTTGCATGGG



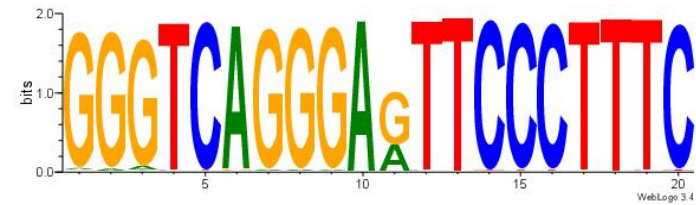
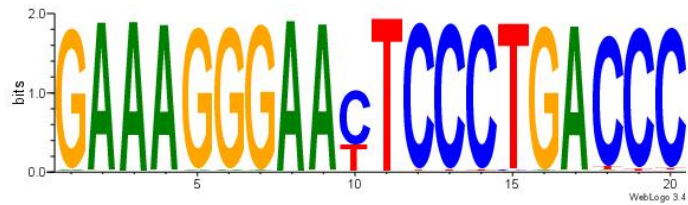
Dataset #:	1
Motif ID:	16
Motif name:	Motif 16
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	8
Number of overlap:	12
Similarity score:	0.0877995

Alignment:

```
GGGTCAGGGAGTTCCTTTC  
-----GGGTTTCACCAT-
```

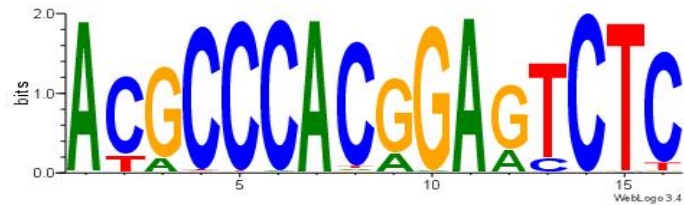
Original motif Consensus sequence: GAAAGGGA ACTCCCTGACCC

Reverse complement motif Consensus sequence:
GGGTCAGGGAGTTCCTTTC

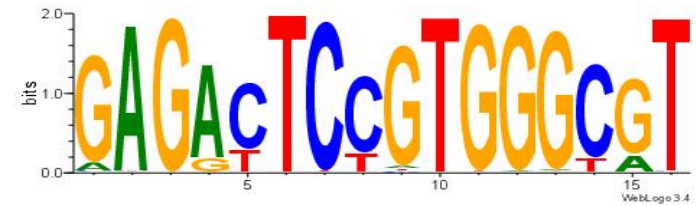


Dataset #: 1 Motif ID: 33 Motif name: Motif 33

Original motif Consensus sequence: ACGCCACGGAGTCTC



Reverse complement motif Consensus sequence: GAGACTCCGTGGGCGT



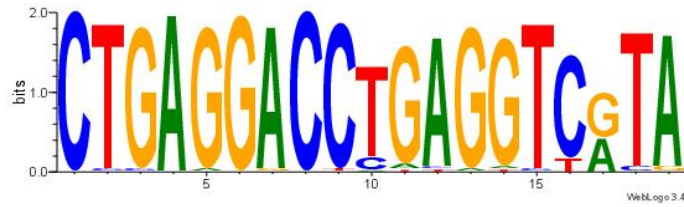
Best Matches for Motif ID 33 (Highest to Lowest)

Dataset #:	1
Motif ID:	291
Motif name:	Motif 291
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2
Number of overlap:	16
Similarity score:	0.0890595

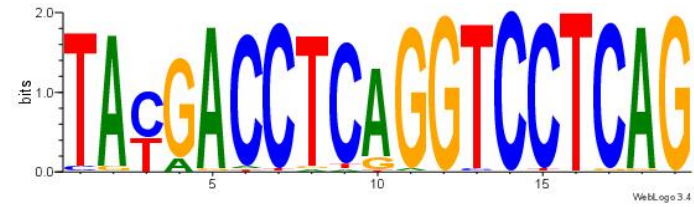
Alignment:

CTGAGGACCTGAGGTCRТА
--GAGACTCCGTGGGCGT--

Original motif Consensus sequence: CTGAGGACCTGAGGTCRТА



Reverse complement motif Consensus sequence: TAMGACCTCAGGTCCTCAG

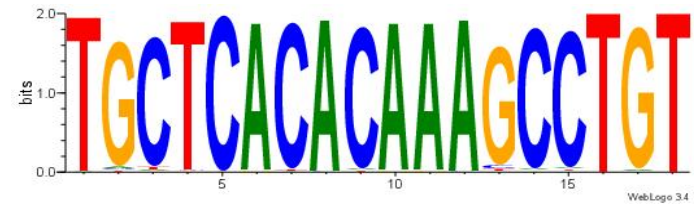
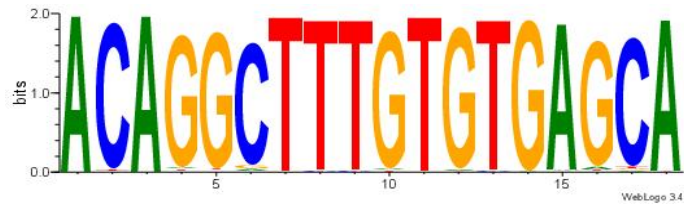


Dataset #: 1
Motif ID: 159
Motif name: Motif 159
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 2
Number of overlap: 16
Similarity score: 0.100481

Alignment:
TGCTCACACAAAGCCTGT
-ACGCCACGGAGTCTC-

Original motif Consensus sequence: ACAGGCTTTGTGTGAGCA

Reverse complement motif Consensus sequence: TGCTCACACAAAGCCTGT



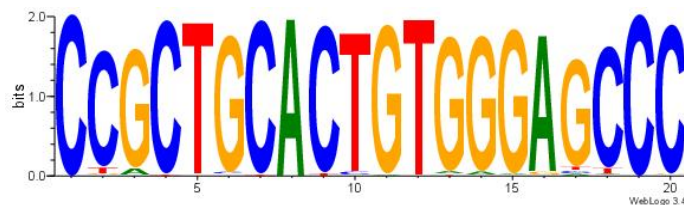
Dataset #: 1
 Motif ID: 144
 Motif name: Motif 144
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 16
 Similarity score: 0.102336

Alignment:

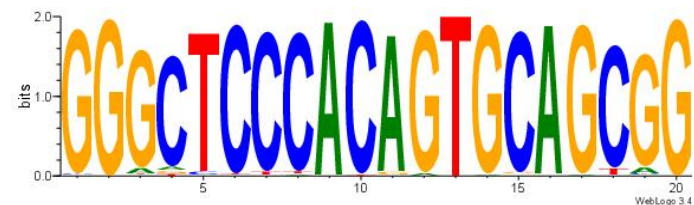
```

GGGCTCCCACAGTGCAGCGG
--ACGCCACGGAGTCTC--
  
```

Original motif Consensus sequence: CCGCTGCACTGTGGGAGCCC



Reverse complement motif Consensus sequence: GGGCTCCCACAGTGCAGCGG



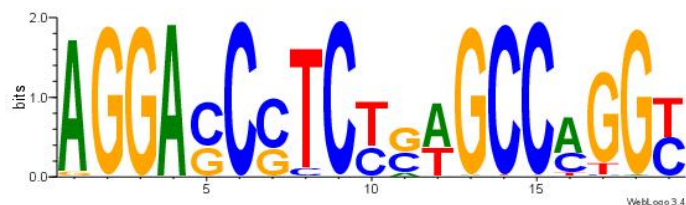
Dataset #: 1

Motif ID: 10
 Motif name: Motif 10
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 16
 Similarity score: 0.103114

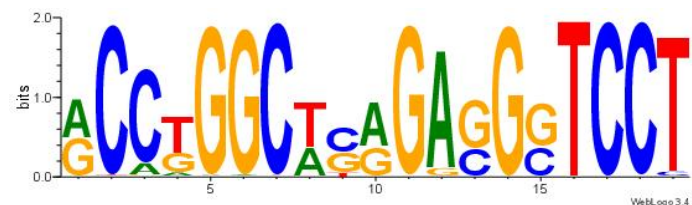
Alignment:

MCCYGGCWSMGASGSTCCT
 --ACGCCACGGAGTCTC-

Original motif Consensus sequence: AGGASCSTCYSWGCCMGY



Reverse complement motif Consensus sequence: MCCYGGCWSMGASGSTCCT



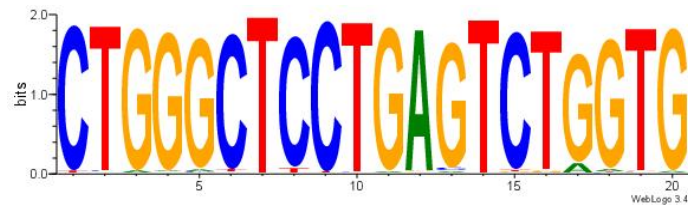
Dataset #: 1
 Motif ID: 67
 Motif name: Motif 67
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 16

Similarity score: 0.103795

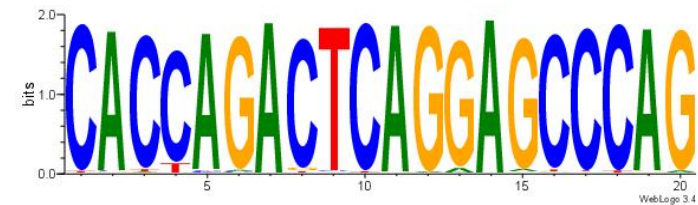
Alignment:

CACCAGACTCAGGAGCCCAG
---GAGACTCCGTGGGCGT---

Original motif Consensus sequence: CTGGGCTCCTGAGTCTGGTG



Reverse complement motif Consensus sequence: CACCAGACTCAGGAGCCCAG



Dataset #: 1 Motif ID: 34 Motif name: Motif 34

Original motif Consensus sequence: GGACGCACA



Reverse complement motif Consensus sequence: TGTGCGTCC



Best Matches for Motif ID 34 (Highest to Lowest)

Dataset #:	1
Motif ID:	314
Motif name:	Motif 314
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement

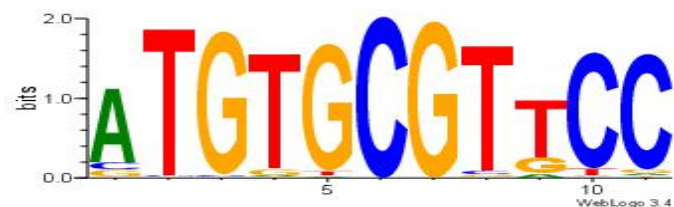
Direction: Backward
 Position number: 2
 Number of overlap: 9
 Similarity score: 0.0220227

Alignment:
 ATGTGCGTTCC
 -TGTGCGTCC-

Original motif Consensus sequence: GGAACGCACAT



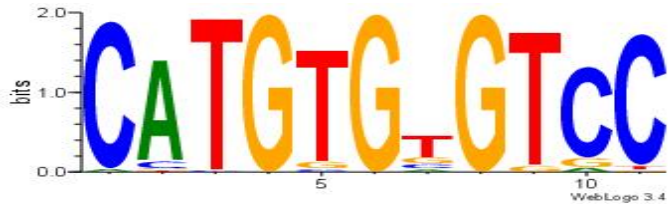
Reverse complement motif Consensus sequence: ATGTGCGTTCC



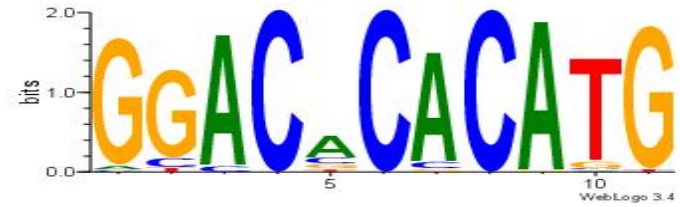
Dataset #: 1
 Motif ID: 87
 Motif name: Motif 87
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 9
 Similarity score: 0.0275308

Alignment:
 GGACACACATG
 GGACGCACA--

Original motif Consensus sequence: CATGTGTGCC



Reverse complement motif Consensus sequence: GGACACACATG

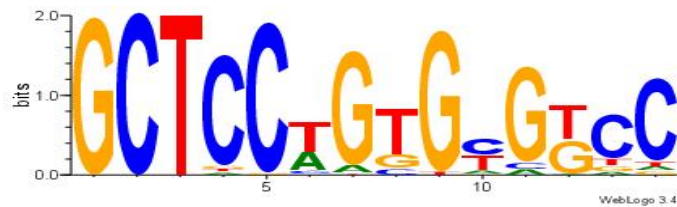


Dataset #: 1
 Motif ID: 206
 Motif name: Motif 206
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 9
 Similarity score: 0.0465084

Alignment:

GCTCCWGTGYGKCC
 -----TGTGCGTCC

Original motif Consensus sequence: GCTCCWGTGYGKCC



Reverse complement motif Consensus sequence: GGRCKCACWGGAA

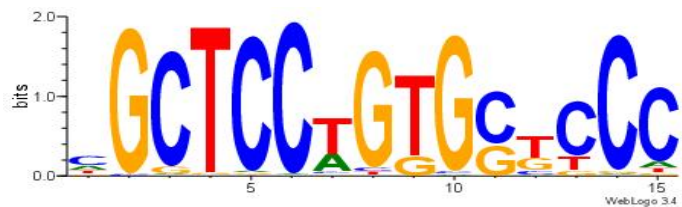


Dataset #: 1
 Motif ID: 215
 Motif name: Motif 215
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 7
 Number of overlap: 9
 Similarity score: 0.0483962

Alignment:

HGCTCCTGTGSKCCC
 -----TGTGCGTCC

Original motif Consensus sequence: HGCTCCTGTGSKCCC



Reverse complement motif Consensus sequence: GGRSCACAGGAGCD

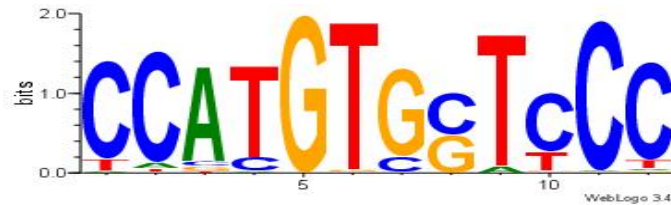


Dataset #: 1
 Motif ID: 120
 Motif name: Motif 120
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1

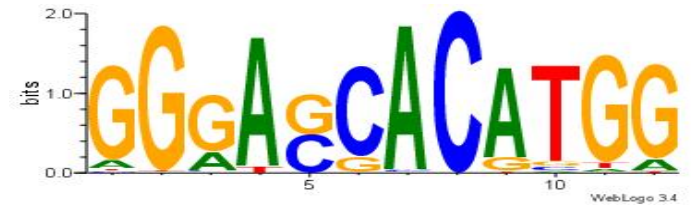
Number of overlap: 9
Similarity score: 0.0524947

Alignment:
CCATGTGSTCCC
---TGTGCGTCC

Original motif Consensus sequence: CCATGTGSTCCC

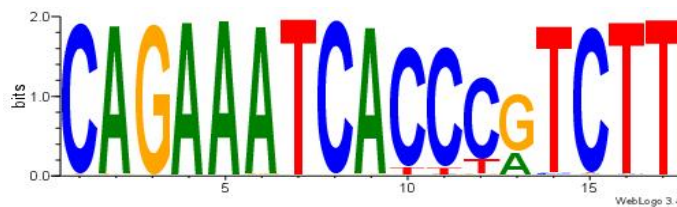


Reverse complement motif Consensus sequence: GGGASCACATGG

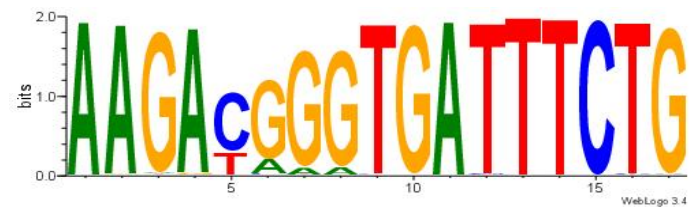


Dataset #: 1 Motif ID: 35 Motif name: Motif 35

Original motif Consensus sequence: CAGAAATCACCCGTCTT



Reverse complement motif Consensus sequence:
AAGACGGGTGATTTCTG



Best Matches for Motif ID 35 (Highest to Lowest)

Dataset #: 1
Motif ID: 85
Motif name: Motif 85
Matching format of first motif: Reverse Complement

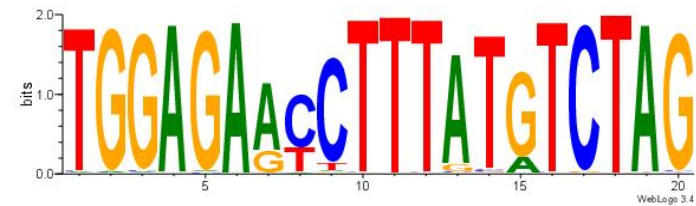
Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3
 Number of overlap: 17
 Similarity score: 0.104456

Alignment:
 TGGAGAACCTTTATGTCTAG
 --AAGACGGGTGATTTCTG--

Original motif Consensus sequence: CTAGACATAAAGGTTCTCCA



Reverse complement motif Consensus sequence: TGGAGAACCTTTATGTCTAG

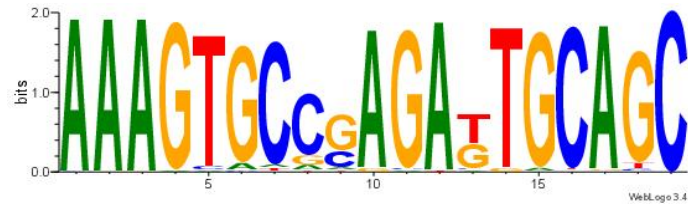


Dataset #: 1
 Motif ID: 191
 Motif name: Motif 191
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 17
 Similarity score: 0.109156

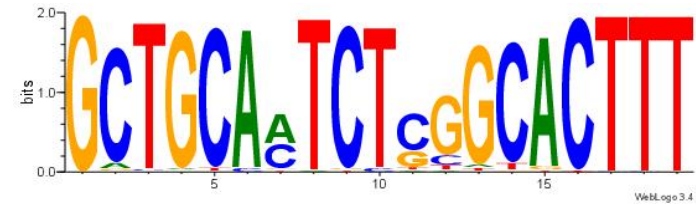
Alignment:

GCTGCARTCTCGGCACTTT
-CAGAAATCACCCGTCTT-

Original motif Consensus sequence: AAAGTGCCGAGAKTGCAGC



Reverse complement motif Consensus sequence:
GCTGCARTCTCGGCACTTT



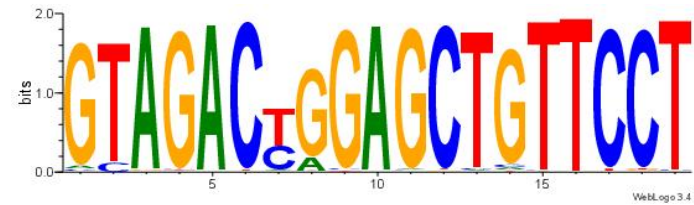
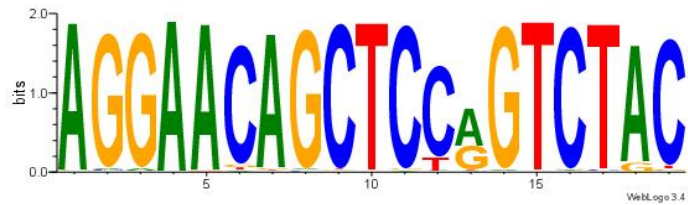
Dataset #: 1
Motif ID: 62
Motif name: Motif 62
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 2
Number of overlap: 17
Similarity score: 0.112474

Alignment:

GTAGACKGGAGCTGTTTCCT
-AAGACGGGTGATTTCTG-

Original motif Consensus sequence: AGGAACAGCTCCRGCTCTAC

Reverse complement motif Consensus sequence:
GTAGACKGGAGCTGTTTCCT

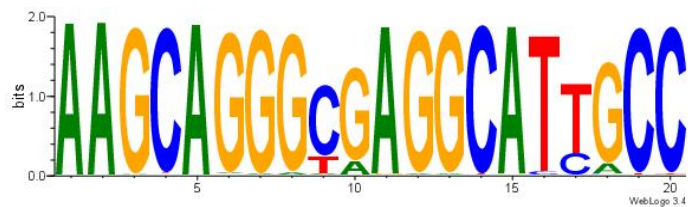


Dataset #: 1
 Motif ID: 13
 Motif name: Motif 13
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 4
 Number of overlap: 17
 Similarity score: 0.113142

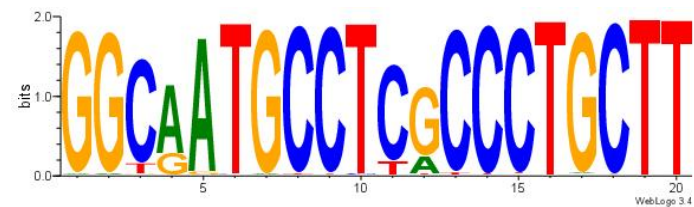
Alignment:

GGCAATGCCTCGCCCTGCTT
 CAGAAATCACCCGTCTT---

Original motif Consensus sequence: AAGCAGGGCGAGGCATTGCC



Reverse complement motif Consensus sequence: GGCAATGCCTCGCCCTGCTT



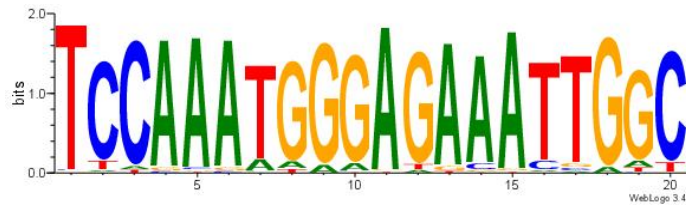
Dataset #: 1

Motif ID: 235
 Motif name: Motif 235
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 17
 Similarity score: 0.11691

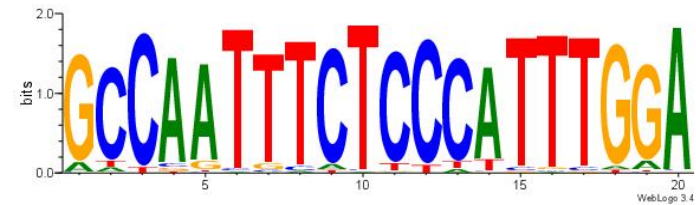
Alignment:

GCCAATTTCTCCCATTGGA
 -CAGAAATCACCCGTCTT--

Original motif Consensus sequence: TCCAATGGGAGAAATTGGC

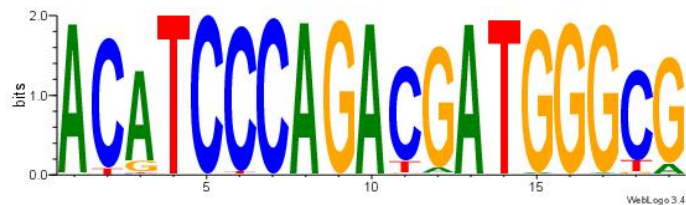


Reverse complement motif Consensus sequence: GCCAATTTCTCCCATTGGA

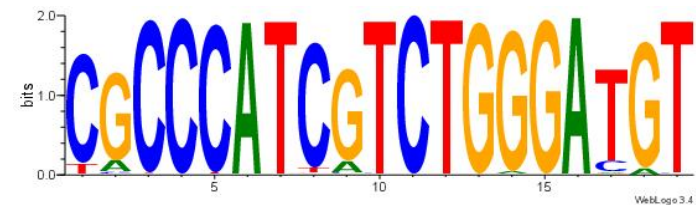


Dataset #: 1 Motif ID: 36 Motif name: Motif 36

Original motif Consensus sequence: ACATCCCAGACGATGGGCG



Reverse complement motif Consensus sequence: CGCCATCGTCTGGGATGT



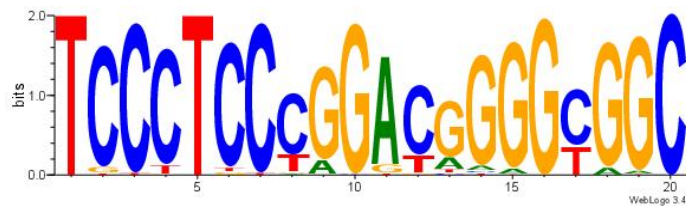
Best Matches for Motif ID 36 (Highest to Lowest)

Dataset #: 1
Motif ID: 155
Motif name: Motif 155
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 19
Similarity score: 0.102313

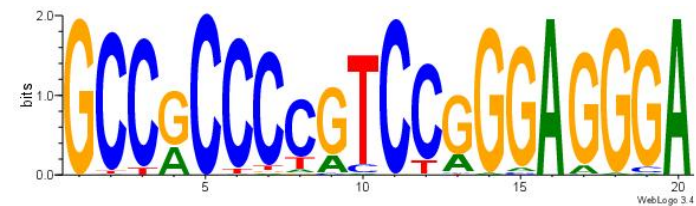
Alignment:

```
GCKCCCCGTCCGGGAGGGA  
CGCCCATCGTCTGGGATGT-
```

Original motif Consensus sequence: TCCCTCCCGGACGGGGYGGC



Reverse complement motif Consensus sequence:
GCCKCCCCGTCCGGGAGGGA



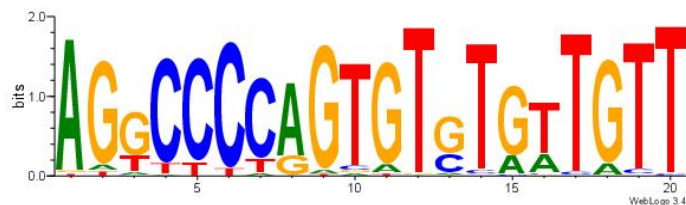
Dataset #: 1
Motif ID: 176
Motif name: Motif 176
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement

Direction: Backward
 Position number: 1
 Number of overlap: 19
 Similarity score: 0.105478

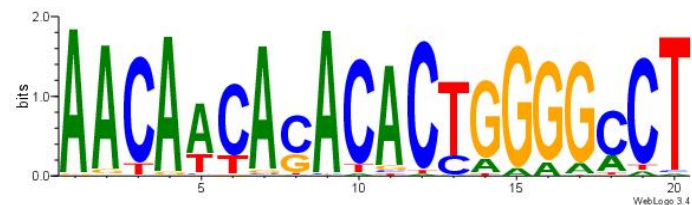
Alignment:

AACAACASACTGGGGCCT
 -ACATCCCAGACGATGGGCG

Original motif Consensus sequence: AGGCCCCAGTGTSTGTTGTT



Reverse complement motif Consensus sequence: AACAACASACTGGGGCCT

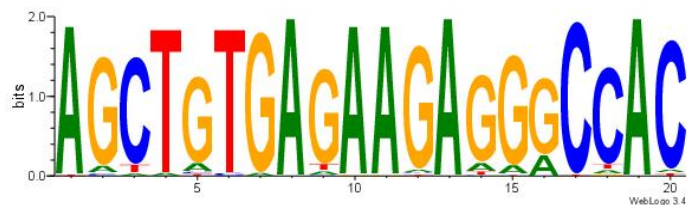


Dataset #: 1
 Motif ID: 294
 Motif name: Motif 294
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 19
 Similarity score: 0.110347

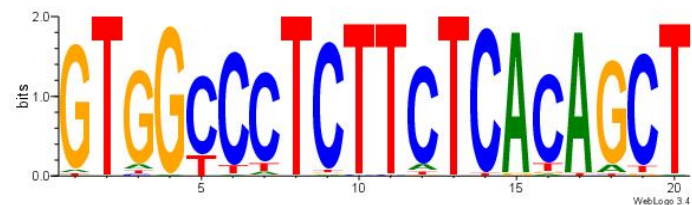
Alignment:

GTGGCCCTCTTCTCACAGCT
 -CGCCCATCGTCTGGGATGT

Original motif Consensus sequence: AGCTGTGAGAAGAGGGCCAC



Reverse complement motif Consensus sequence: GTGGCCCTCTTCTCACAGCT

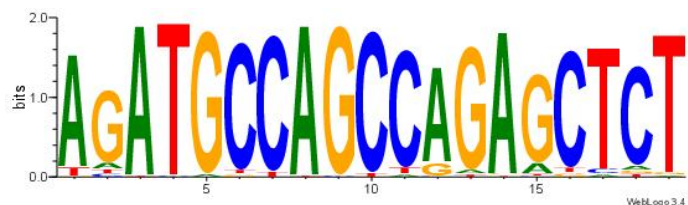


Dataset #: 1
Motif ID: 307
Motif name: Motif 307
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 19
Similarity score: 0.111784

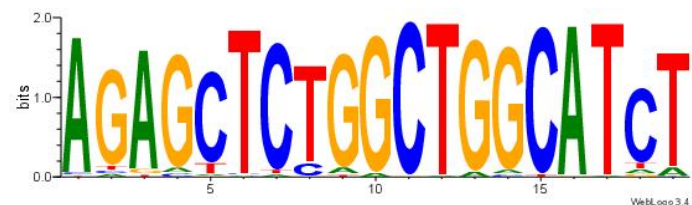
Alignment:

AGATGCCAGCCAGAGCTCT
ACATCCCAGACGATGGGCG

Original motif Consensus sequence: AGATGCCAGCCAGAGCTCT



Reverse complement motif Consensus sequence: AGAGCTCTGGCTGGCATCT

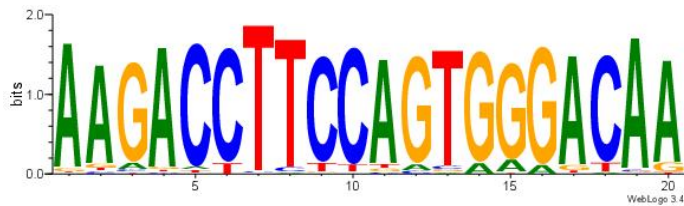


Dataset #: 1
 Motif ID: 292
 Motif name: Motif 292
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 19
 Similarity score: 0.112924

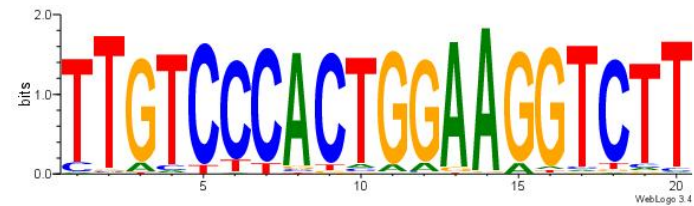
Alignment:

TTGTCCCACTGGAAGGTCTT
 ACATCCCAGACGATGGGCG-

Original motif Consensus sequence: AAGACCTTCCAGTGGGACAA



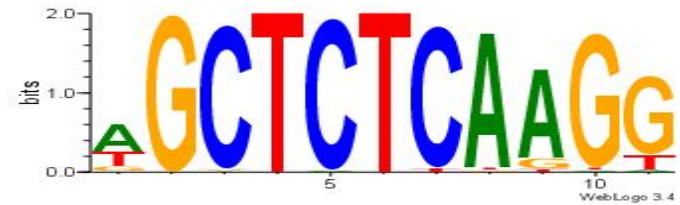
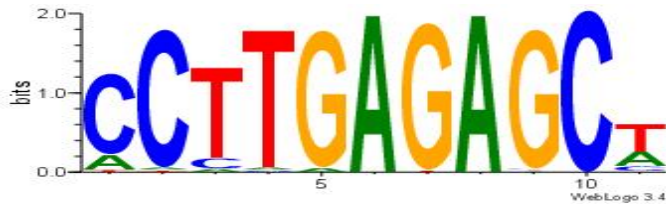
Reverse complement motif Consensus sequence: TTGTCCCACTGGAAGGTCTT



Dataset #: 1 Motif ID: 37 Motif name: Motif 37

Original motif Consensus sequence: CCTTGAGAGCW

Reverse complement motif Consensus sequence: WGCTCTCAAGG



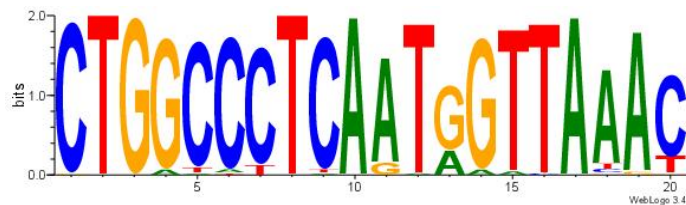
Best Matches for Motif ID 37 (Highest to Lowest)

Dataset #: 1
 Motif ID: 332
 Motif name: Motif 332
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 11
 Similarity score: 0.0617144

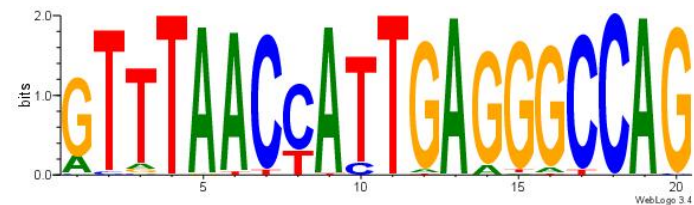
Alignment:

GTTTAACCATTGAGGGCCAG
 -----CCTTGAGAGCW--

Original motif Consensus sequence: CTGGCCCTCAATGGTTAAAC



Reverse complement motif Consensus sequence: GTTTAACCATTGAGGGCCAG

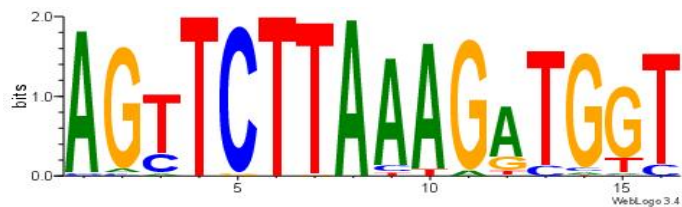


Dataset #: 1
 Motif ID: 303
 Motif name: Motif 303
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.0637615

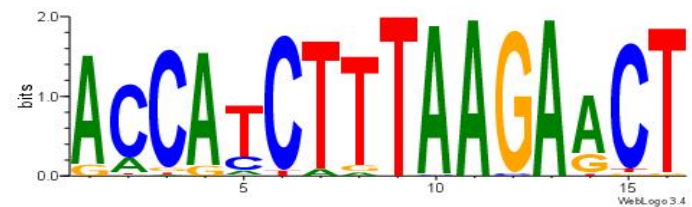
Alignment:

AGTTCTTAAAGATGGT
 WGCTCTCAAGG-----

Original motif Consensus sequence: AGTTCTTAAAGATGGT



Reverse complement motif Consensus sequence: ACCATCTTAAAGAACT



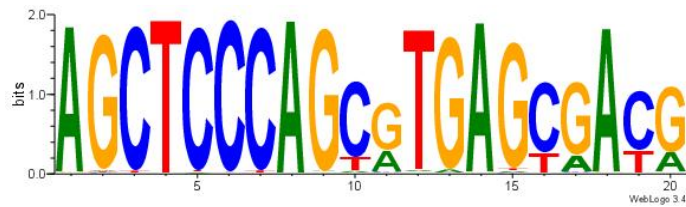
Dataset #: 1
 Motif ID: 48
 Motif name: Motif 48
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 10

Number of overlap: 11
Similarity score: 0.0663901

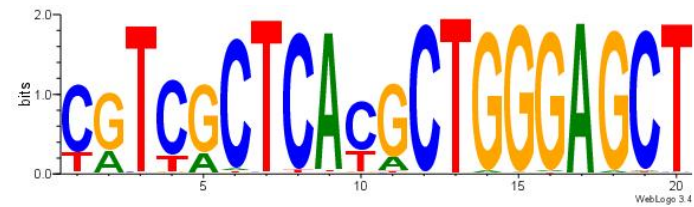
Alignment:

CGTCGCTCACGCTGGGAGCT
-----CCTTGAGAGCW

Original motif Consensus sequence: AGCTCCCAGCGTGAGCGACG



Reverse complement motif Consensus sequence:
CGTCGCTCACGCTGGGAGCT



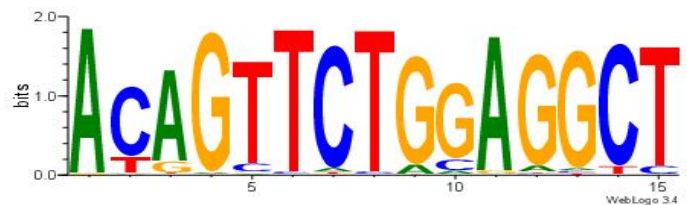
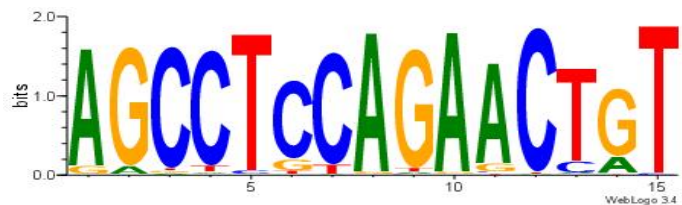
Dataset #: 1
Motif ID: 239
Motif name: Motif 239
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 3
Number of overlap: 11
Similarity score: 0.0666861

Alignment:

AGCCTCCAGAACTGT
--CCTTGAGAGCW--

Original motif Consensus sequence: AGCCTCCAGAACTGT

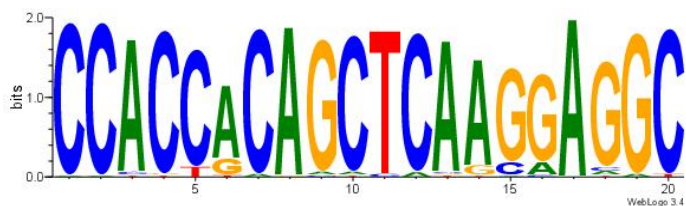
Reverse complement motif Consensus sequence: ACAGTTCTGGAGG



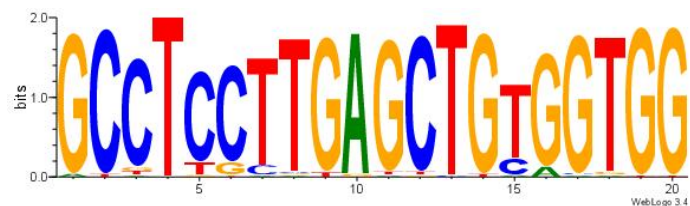
Dataset #: 1
 Motif ID: 331
 Motif name: Motif 331
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 5
 Number of overlap: 11
 Similarity score: 0.0705972

Alignment:
 GCCTCCTTGAGCTGTGGTGG
 ----CCTTGAGAGCW-----

Original motif Consensus sequence: CCACCACAGCTCAAGGAGGC

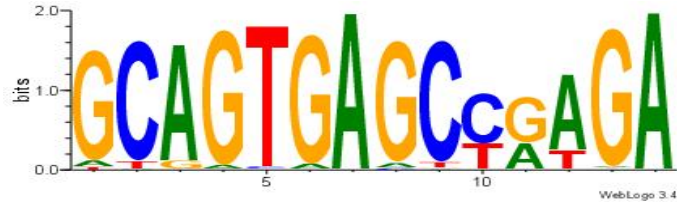


Reverse complement motif Consensus sequence: GCCTCCTTGAGCTGTGGTGG

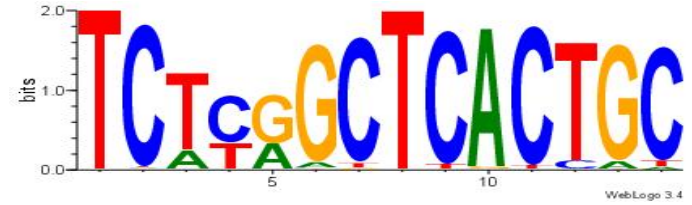


Dataset #: 1 Motif ID: 38 Motif name: Motif 38

Original motif Consensus sequence: GCAGTGAGCYRAGA



Reverse complement motif Consensus sequence: TCTMKGCTCACTG



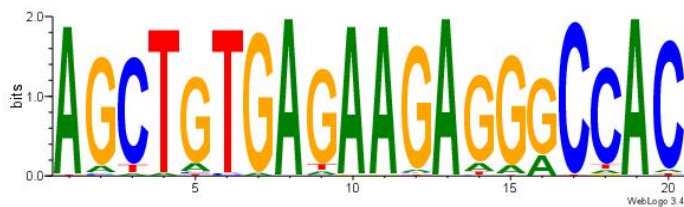
Best Matches for Motif ID 38 (Highest to Lowest)

Dataset #:	1
Motif ID:	294
Motif name:	Motif 294
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	2
Number of overlap:	14
Similarity score:	0.0688783

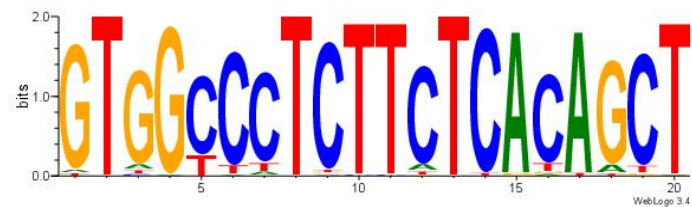
Alignment:

```
GTGGCCCTCTTCTCACAGCT
-----TCTMKGCTCACTGC-
```

Original motif Consensus sequence: AGCTGTGAGAAGAGGGCCAC



Reverse complement motif Consensus sequence: GTGGCCCTCTTCTCACAGCT

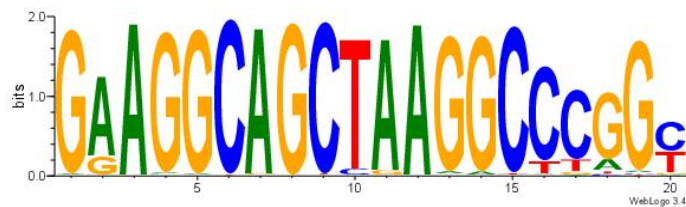


Dataset #: 1
 Motif ID: 64
 Motif name: Motif 64
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 7
 Number of overlap: 14
 Similarity score: 0.0904176

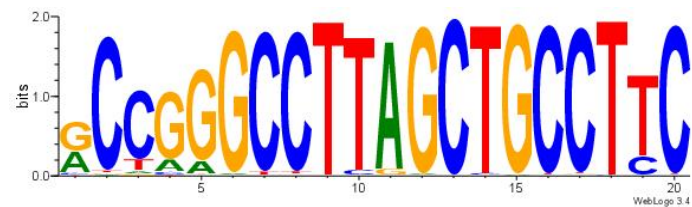
Alignment:

GAAGGCAGCTAAGGCCGGY
 GCAGTGAGCYRAGA-----

Original motif Consensus sequence: GAAGGCAGCTAAGGCCGGY



Reverse complement motif Consensus sequence: KCCGGGCTTAGCTGCCTTC



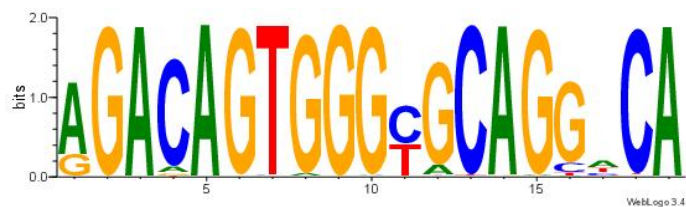
Dataset #: 1
 Motif ID: 17
 Motif name: Motif 17
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3

Number of overlap: 14
Similarity score: 0.0919739

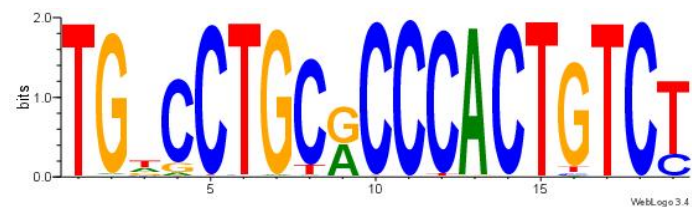
Alignment:

AGACAGTGGGYGCAGGHCA
--GCAGTGAGCYRAGA---

Original motif Consensus sequence: AGACAGTGGGYGCAGGHCA



Reverse complement motif Consensus sequence:
TGHCTGCKCCCACTGTCT

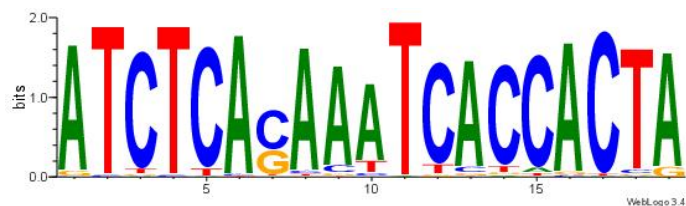


Dataset #: 1
Motif ID: 261
Motif name: Motif 261
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 3
Number of overlap: 14
Similarity score: 0.0928109

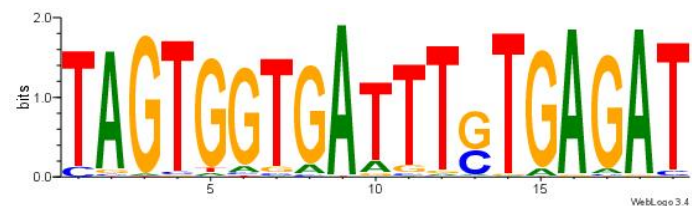
Alignment:

TAGTGGTGATTTSTGAGAT
--GCAGTGAGCYRAGA---

Original motif Consensus sequence: ATCTCASAAATCACCCTA



Reverse complement motif Consensus sequence:
TAGTGGTGAATTTGAGAT

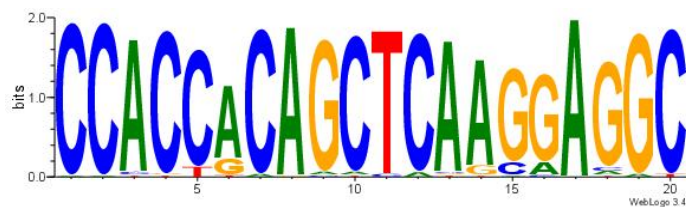


Dataset #: 1
Motif ID: 331
Motif name: Motif 331
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 4
Number of overlap: 14
Similarity score: 0.0951907

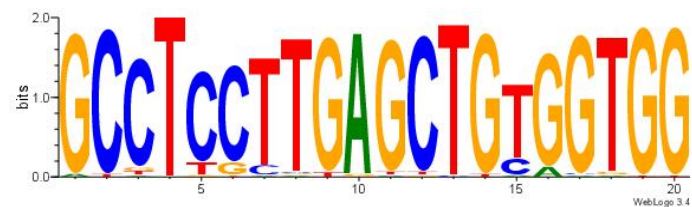
Alignment:

```
GCCTCCTTGAGCTGTGGTGG  
---GCAGTGAGCYRAGA---
```

Original motif Consensus sequence: CCACCACAGCTCAAGGAGGC

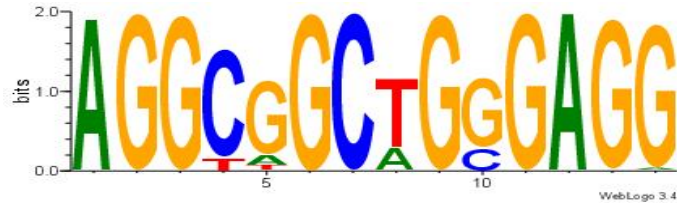


Reverse complement motif Consensus sequence:
GCCTCCTTGAGCTGTGGTGG



Dataset #: 1 Motif ID: 39 Motif name: Motif 39

Original motif Consensus sequence: AGGCGGCTGGGAGG



Reverse complement motif Consensus sequence: CCTCCCAGCCGCC



Best Matches for Motif ID 39 (Highest to Lowest)

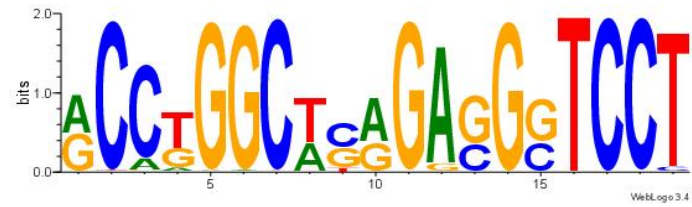
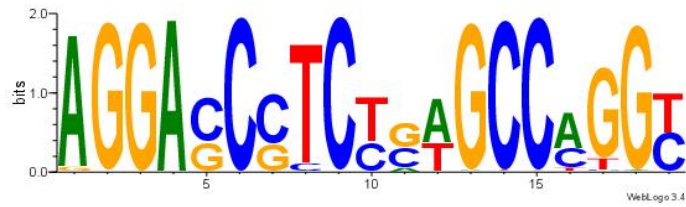
Dataset #:	1
Motif ID:	10
Motif name:	Motif 10
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	14
Similarity score:	0.0839569

Alignment:

```
AGGASCSTCYSWGCCMGGY  
CCTCCCAGCCGCCT-----
```

Original motif Consensus sequence: AGGASCSTCYSWGCCMGGY

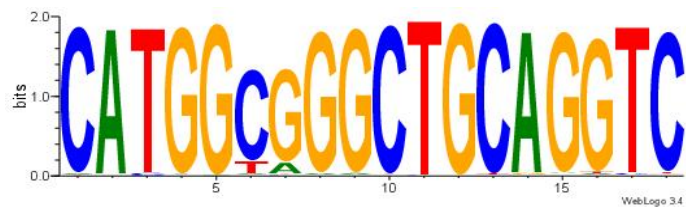
Reverse complement motif Consensus sequence:
MCCYGGCWSMGASGSTCCT



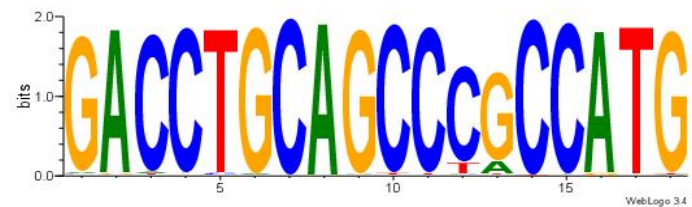
Dataset #: 1
 Motif ID: 68
 Motif name: Motif 68
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3
 Number of overlap: 14
 Similarity score: 0.0883656

Alignment:
 GACCTGCAGCCCGCCATG
 --CCTCCAGCCGCCT--

Original motif Consensus sequence: CATGGCGGGCTGCAGGTC



Reverse complement motif Consensus sequence: GACCTGCAGCCCGCCATG



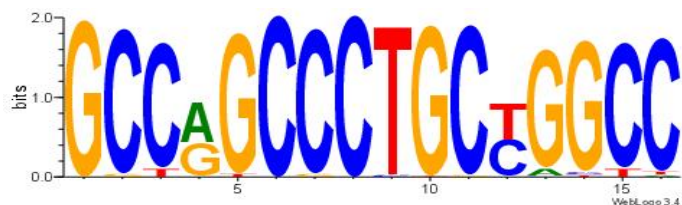
Dataset #: 1

Motif ID: 183
 Motif name: Motif 183
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 14
 Similarity score: 0.0920495

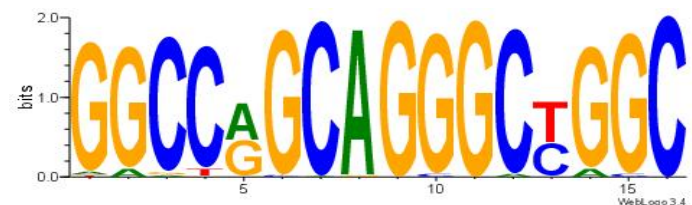
Alignment:

GCCRGCCCTGCYGGCC
 --CCTCCCAGCCGCCT

Original motif Consensus sequence: GCCRGCCCTGCYGGCC



Reverse complement motif Consensus sequence: GGCCMGCAGGGCKGGC



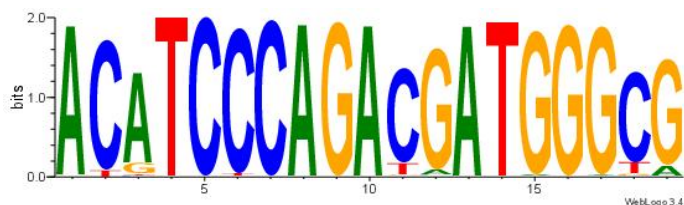
Dataset #: 1
 Motif ID: 36
 Motif name: Motif 36
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 5
 Number of overlap: 14

Similarity score: 0.0926326

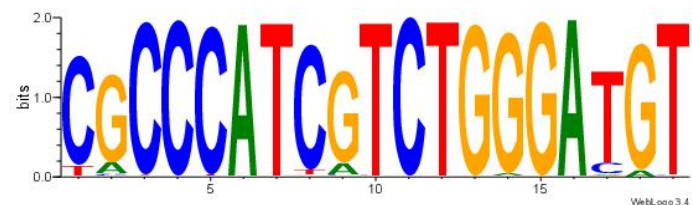
Alignment:

ACATCCCAGACGATGGGCG
----CCTCCCAGCCGCCT--

Original motif Consensus sequence: ACATCCCAGACGATGGGCG



Reverse complement motif Consensus sequence:
CGCCCATCGTCTGGGATGT



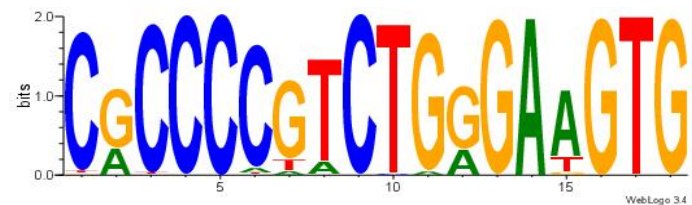
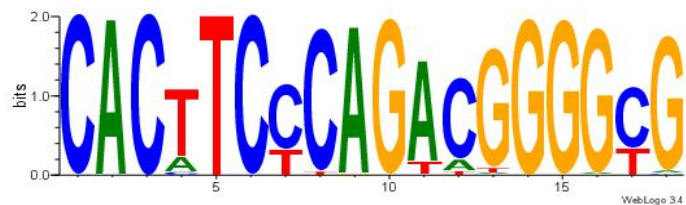
Dataset #: 1
Motif ID: 27
Motif name: Motif 27
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 3
Number of overlap: 14
Similarity score: 0.0926448

Alignment:

CGCCCGTCTGGGAAGTG
--AGGCGGCTGGGAGG--

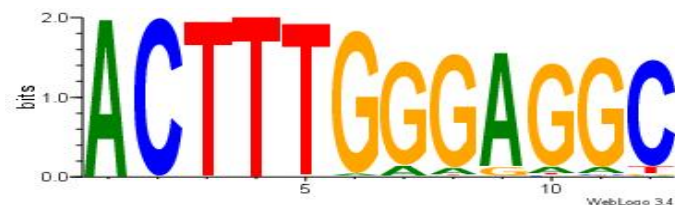
Original motif Consensus sequence: CACTTCCCAGACGGGGCG

Reverse complement motif Consensus sequence:
CGCCCGTCTGGGAAGTG

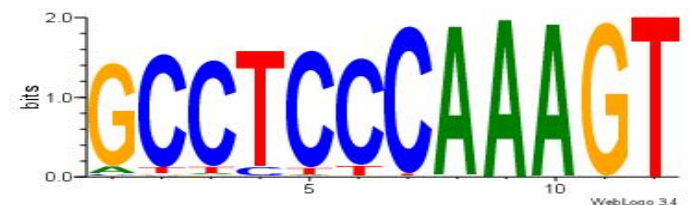


Dataset #: 1 Motif ID: 40 Motif name: Motif 40

Original motif Consensus sequence: ACTTTGGGAGGC



Reverse complement motif Consensus sequence: GCCTCCCAAAGT

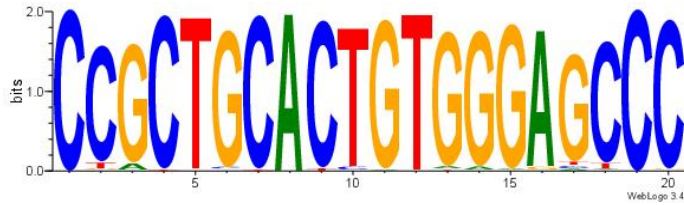


Best Matches for Motif ID 40 (Highest to Lowest)

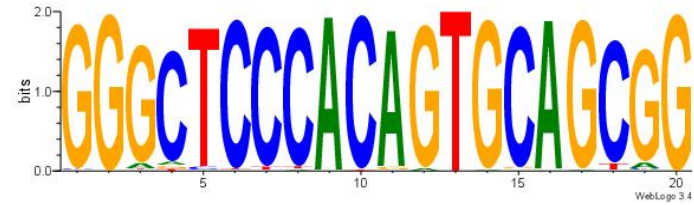
Dataset #:	1
Motif ID:	144
Motif name:	Motif 144
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	2
Number of overlap:	12
Similarity score:	0.0448889

Alignment:
GGGCTCCCACAGTGCAGCGG
-GCCTCCCAAAGT-----

Original motif Consensus sequence: CCGCTGCACTGTGGGAGCCC



Reverse complement motif Consensus sequence: GGGCTCCCACAGTGCAGCGG

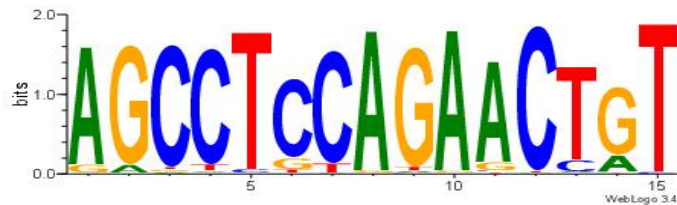


Dataset #: 1
Motif ID: 239
Motif name: Motif 239
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 3
Number of overlap: 12
Similarity score: 0.0724344

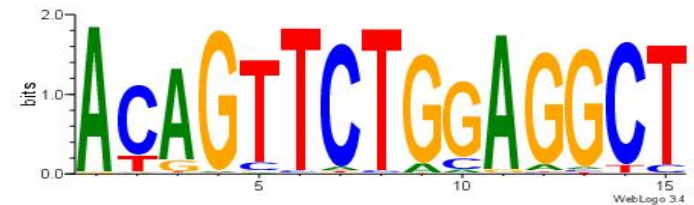
Alignment:

ACAGTTCTGGAGGCT
--ACTTTGGGAGGC--

Original motif Consensus sequence: AGCCTCCAGAACTGT



Reverse complement motif Consensus sequence: ACAGTTCTGGAGGCT

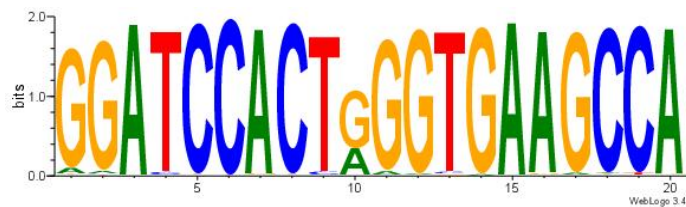


Dataset #: 1
 Motif ID: 61
 Motif name: Motif 61
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3
 Number of overlap: 12
 Similarity score: 0.0760424

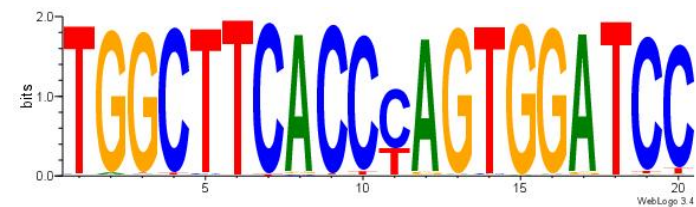
Alignment:

TGGCTTCACCCAGTGGATCC
 --GCCTCCCAAAGT-----

Original motif Consensus sequence: GGATCCACTGGGTGAAGCCA



Reverse complement motif Consensus sequence: TGGCTTCACCCAGTGGATCC



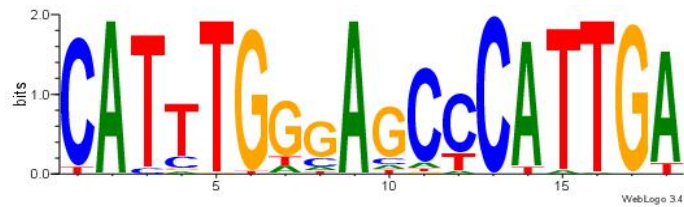
Dataset #: 1
 Motif ID: 284
 Motif name: Motif 284
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 7

Number of overlap: 12
Similarity score: 0.0785575

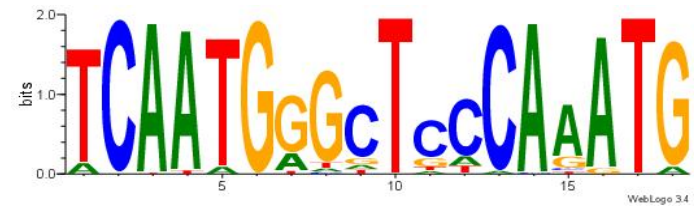
Alignment:

TCAATGGGCTCCCAAATG
-----GCCTCCCAAAGT

Original motif Consensus sequence: CATTGGGAGCCATTGA



Reverse complement motif Consensus sequence:
TCAATGGGCTCCCAAATG

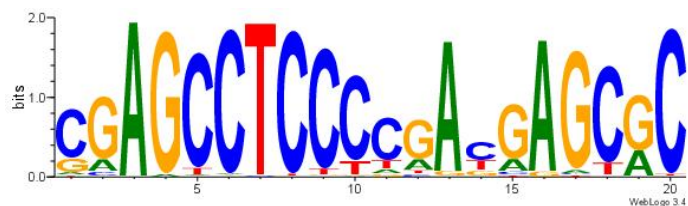


Dataset #: 1
Motif ID: 108
Motif name: Motif 108
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 6
Number of overlap: 12
Similarity score: 0.081011

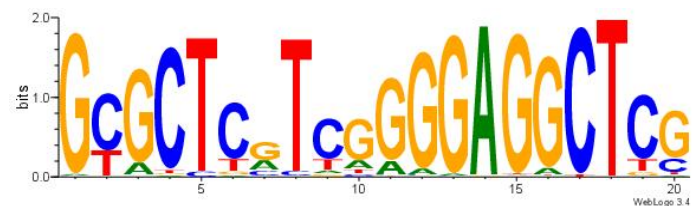
Alignment:

GCGCTCKTCGGGGAGGCTCG
-----ACTTTGGGAGGC---

Original motif Consensus sequence: CGAGCCTCCCCGAYGAGCGC

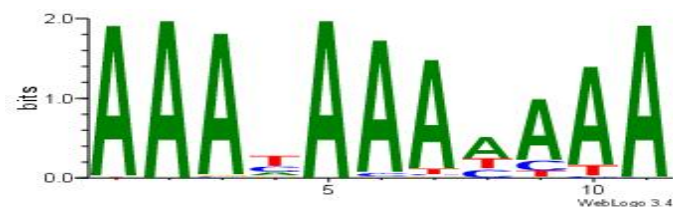


Reverse complement motif Consensus sequence: GCGCTCKTCGGGGAGGCTCG

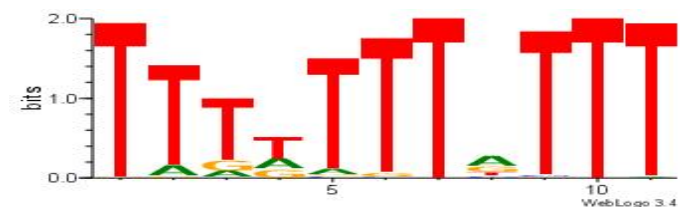


Dataset #: 1 Motif ID: 41 Motif name: Motif 41

Original motif Consensus sequence: AAAYAAAAAA



Reverse complement motif Consensus sequence: TTTTTTMTTT



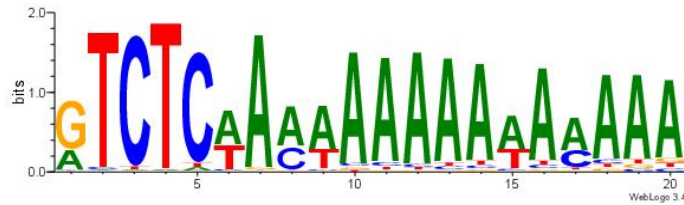
Best Matches for Motif ID 41 (Highest to Lowest)

Dataset #:	1
Motif ID:	7
Motif name:	Motif 7
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	11
Similarity score:	0.0197219

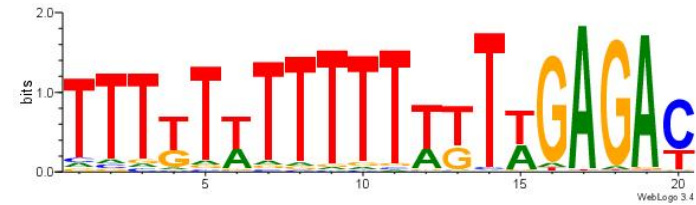
Alignment:

GTCTCWAMAAAAAWAMAAA
 -----AAAYAAAAAAA

Original motif Consensus sequence: GTCTCWAMAAAAAWAMAAA



Reverse complement motif Consensus sequence: TTTYTWTTTTTWTGAGAC

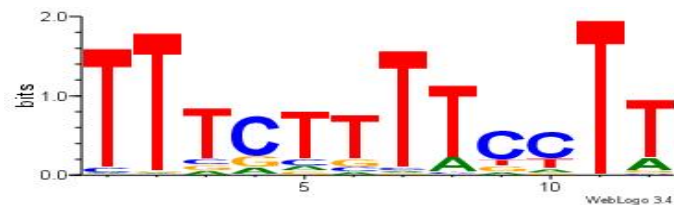


Dataset #: 1
 Motif ID: 54
 Motif name: Motif 54
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.0476983

Alignment:
 TTTCTTTTCCTT
 -TTTTTTTMTTT

Original motif Consensus sequence: AAGGAAAAGAAA

Reverse complement motif Consensus sequence: TTTCTTTTCCTT

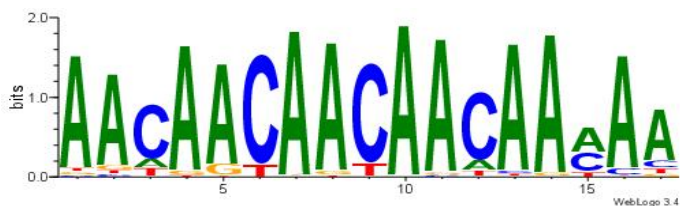


Dataset #: 1
 Motif ID: 117
 Motif name: Motif 117
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 11
 Similarity score: 0.055347

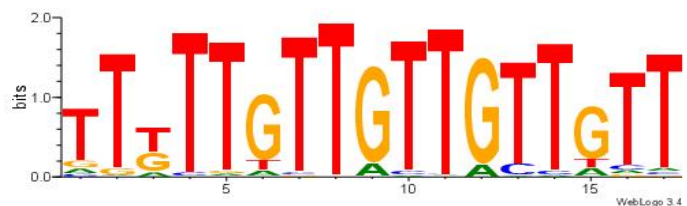
Alignment:

AACACAACAACAAMAA
 -----AAAYAAAAAA-

Original motif Consensus sequence: AACACAACAACAAMAA



Reverse complement motif Consensus sequence: TTYTTGTTGTTGTT



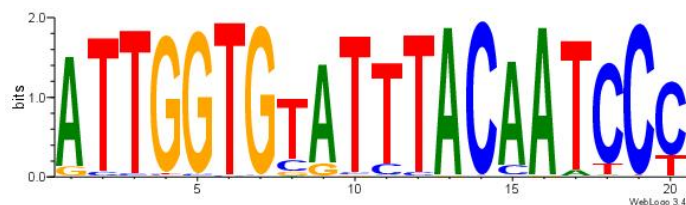
Dataset #: 1

Motif ID: 106
 Motif name: Motif 106
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 11
 Similarity score: 0.0567271

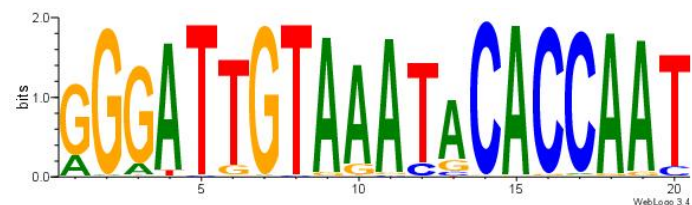
Alignment:

GGGATTGTAAATACACCAAT
 -----AAAYAAAAAAA-

Original motif Consensus sequence: ATTGGTGTATTTACAATCCC



Reverse complement motif Consensus sequence: GGGATTGTAAATACACCAAT



Dataset #: 1
 Motif ID: 328
 Motif name: Motif 328
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 6
 Number of overlap: 11

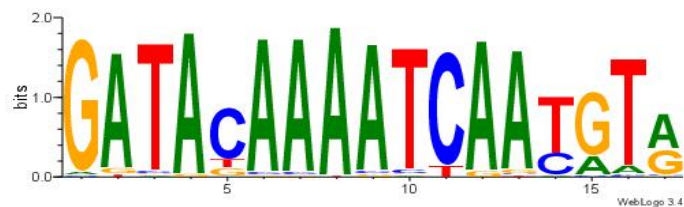
Similarity score: 0.0636192

Alignment:

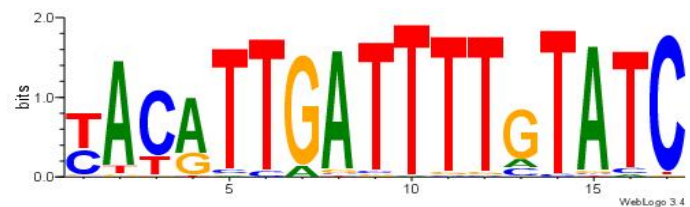
GATACAAAATCAATGTR

-AAAYAAAAAA-----

Original motif Consensus sequence: GATACAAAATCAATGTR

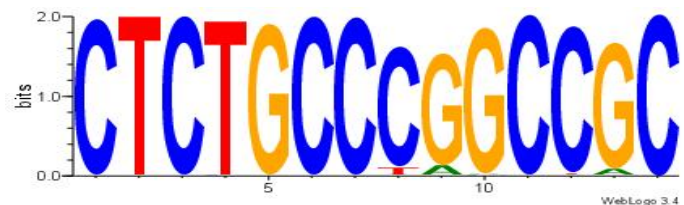


Reverse complement motif Consensus sequence: KACATTGATTTTGTATC

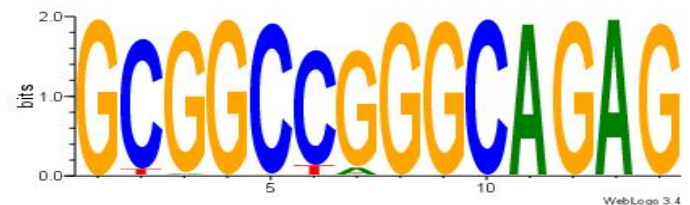


Dataset #: 1 Motif ID: 42 Motif name: Motif 42

Original motif Consensus sequence: CTCTGCCCGGCCGC



Reverse complement motif Consensus sequence: GCGGCCGGGCAGAG



Best Matches for Motif ID 42 (Highest to Lowest)

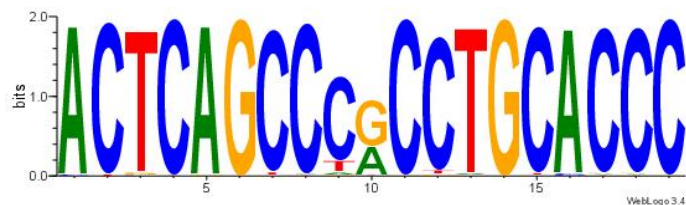
Dataset #:	1
Motif ID:	149
Motif name:	Motif 149
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement

Direction: Backward
 Position number: 2
 Number of overlap: 14
 Similarity score: 0.0584472

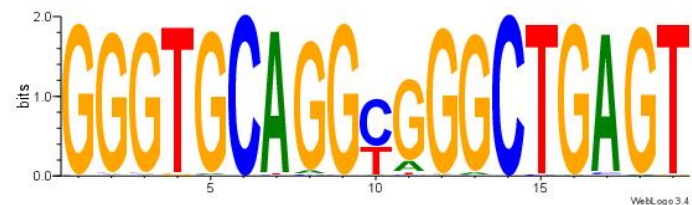
Alignment:

GGGTGCAGGMGGGCTGAGT
 ----GCGGCCGGGCAGAG--

Original motif Consensus sequence: ACTCAGCCRCCTGCACCC



Reverse complement motif Consensus sequence: GGGTGCAGGMGGGCTGAGT

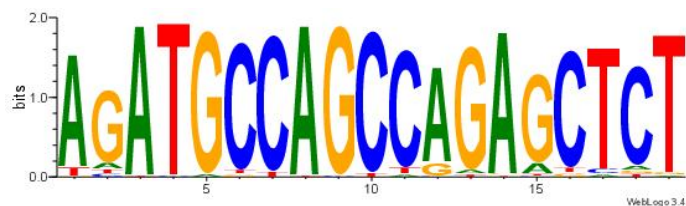


Dataset #: 1
 Motif ID: 307
 Motif name: Motif 307
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 14
 Similarity score: 0.0775689

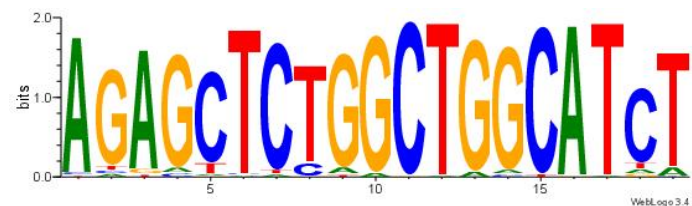
Alignment:

AGAGCTCTGGCTGGCATCT
 ----CTCTGCCCCGGCCGC--

Original motif Consensus sequence: AGATGCCAGCCAGAGCTCT



Reverse complement motif Consensus sequence: AGAGCTCTGGCTGGCATCT

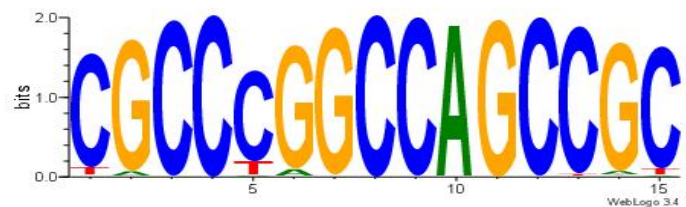


Dataset #: 1
Motif ID: 125
Motif name: Motif 125
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 14
Similarity score: 0.0841912

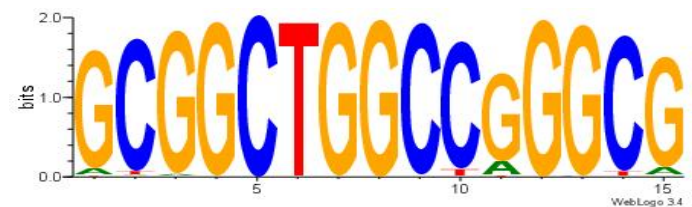
Alignment:

CGCCCGCCAGCCGC
-CTCTGCCCGCCGC

Original motif Consensus sequence: CGCCCGCCAGCCGC



Reverse complement motif Consensus sequence: GCGGCTGGCCGGCG

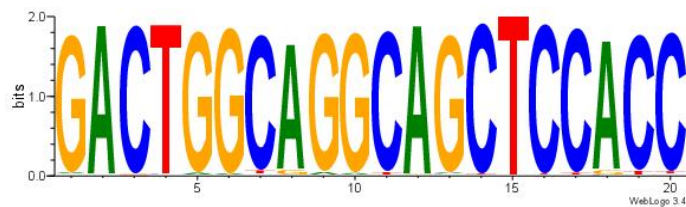


Dataset #: 1
 Motif ID: 52
 Motif name: Motif 52
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0.0856029

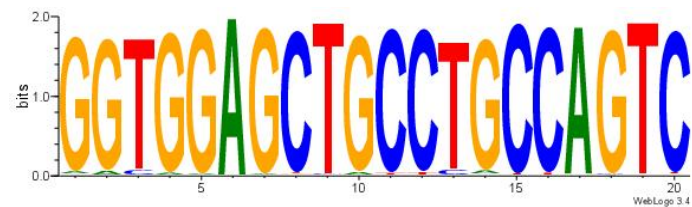
Alignment:

GGTGGAGCTGCCTGCCAGTC
 -----GCGGCCGGGCAGAG

Original motif Consensus sequence: GACTGGCAGGCAGCTCCACC



Reverse complement motif Consensus sequence: GGTGGAGCTGCCTGCCAGTC

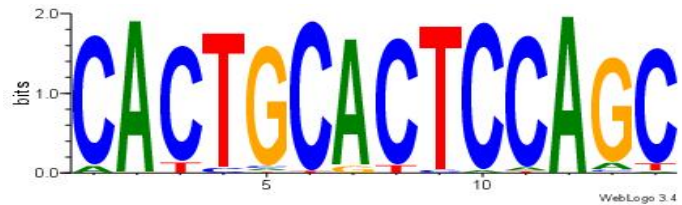


Dataset #: 1
 Motif ID: 285
 Motif name: Motif 285
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1

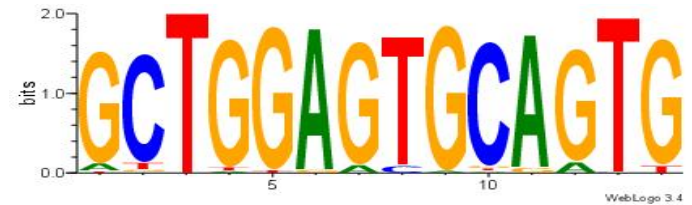
Number of overlap: 14
 Similarity score: 0.0882618

Alignment:
 GCTGGAGTGCAGTG
 GCGGCCGGGCAGAG

Original motif Consensus sequence: CACTGCACTCCAGC

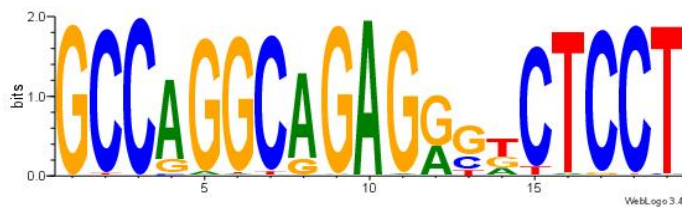


Reverse complement motif Consensus sequence: GCTGGAGTGCAGTG

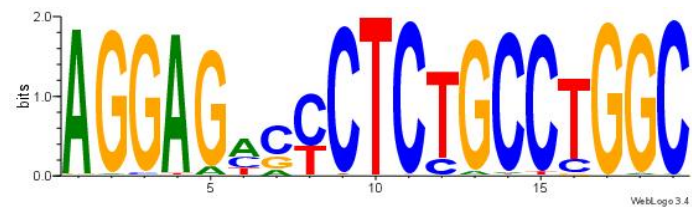


Dataset #: 1 Motif ID: 43 Motif name: Motif 43

Original motif Consensus sequence: GCCAGGCAGAGGAGGAGCTCCT



Reverse complement motif Consensus sequence: AGGAGRCMCTCTGCCTGGC



Best Matches for Motif ID 43 (Highest to Lowest)

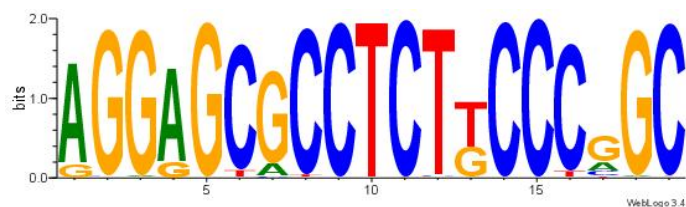
Dataset #: 1
 Motif ID: 30
 Motif name: Motif 30
 Matching format of first motif: Original Motif

Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 19
 Similarity score: 0.049578

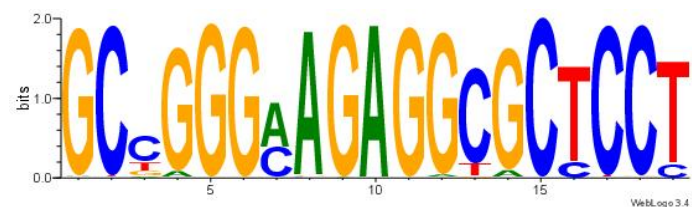
Alignment:

GCCGGGRAGAGGCGCTCCT
 GCCAGGCAGAGRKCTCCT

Original motif Consensus sequence: AGGAGCGCTCTKCCCGGC



Reverse complement motif Consensus sequence:
 GCCGGGRAGAGGCGCTCCT

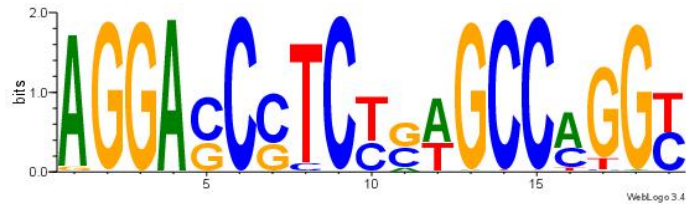


Dataset #: 1
 Motif ID: 10
 Motif name: Motif 10
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 19
 Similarity score: 0.0674635

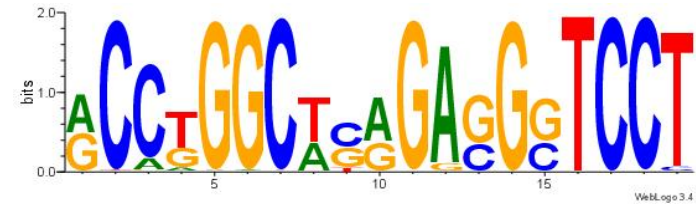
Alignment:

AGGASCSTCYSWGCCMGY
AGGAGRCMCTCTGCCTGGC

Original motif Consensus sequence: AGGASCSTCYSWGCCMGY



Reverse complement motif Consensus sequence:
MCCYGGCWSMGASGSTCCT

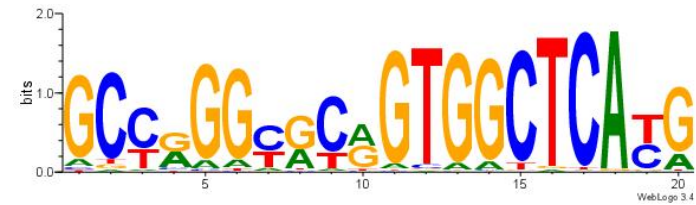
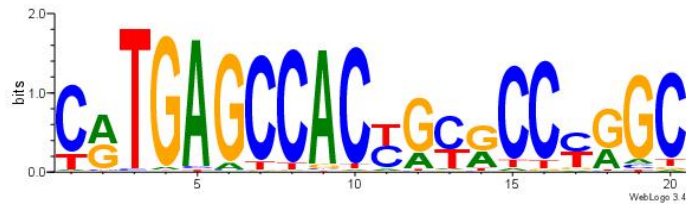


Dataset #: 1
Motif ID: 56
Motif name: Motif 56
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 19
Similarity score: 0.0870511

Alignment:
CRTGAGCCACYGYRCCYGGC
-AGGAGRCMCTCTGCCTGGC

Original motif Consensus sequence: CRTGAGCCACYGYRCCYGGC

Reverse complement motif Consensus sequence:
GCCKGGMKCMGTGGCTCAKG

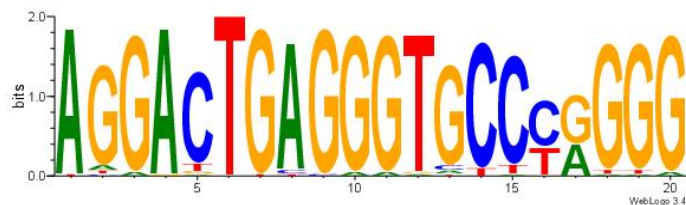


Dataset #: 1
 Motif ID: 312
 Motif name: Motif 312
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 19
 Similarity score: 0.101843

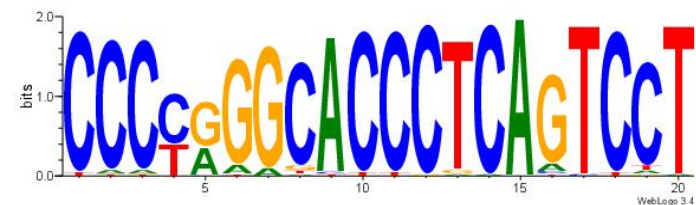
Alignment:

AGGACTGAGGGTGCCYRGGG
 AGGAGRCMCTCTGCCTGGC-

Original motif Consensus sequence: AGGACTGAGGGTGCCYRGGG



Reverse complement motif Consensus sequence: CCCMKGGCACCCTCAGTCCT



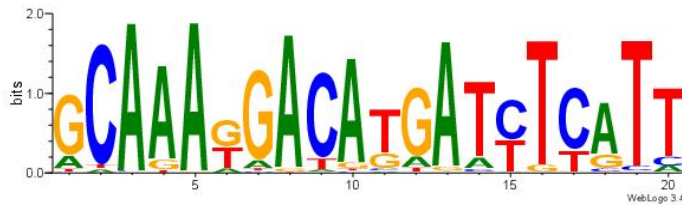
Dataset #: 1

Motif ID: 99
 Motif name: Motif 99
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 19
 Similarity score: 0.106781

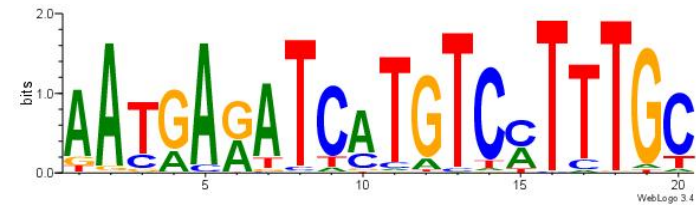
Alignment:

AATGAKATCATGTCYTTTGC
 -AGGAGRCMCTCTGCCTGGC

Original motif Consensus sequence: GCAAAGACATGATYTCATT

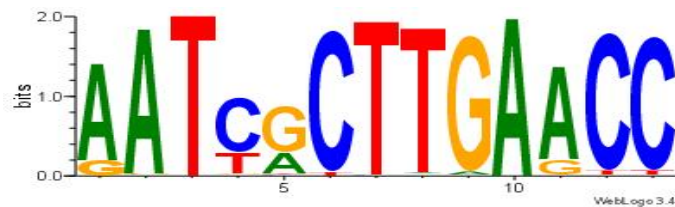


Reverse complement motif Consensus sequence: AATGAKATCATGTCYTTTGC

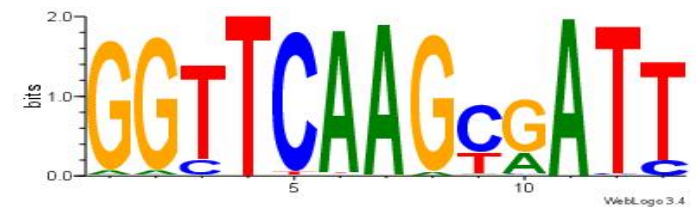


Dataset #: 1 Motif ID: 44 Motif name: Motif 44

Original motif Consensus sequence: AATCGCTTGAACC



Reverse complement motif Consensus sequence: GGTTCAAGCGATT



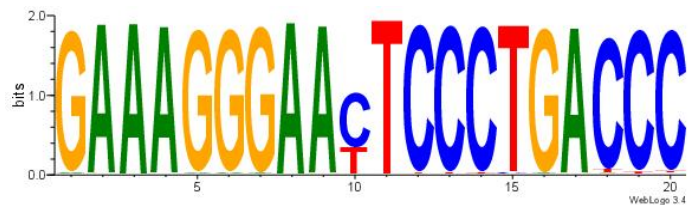
Best Matches for Motif ID 44 (Highest to Lowest)

Dataset #: 1
Motif ID: 16
Motif name: Motif 16
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 13
Similarity score: 0.0728317

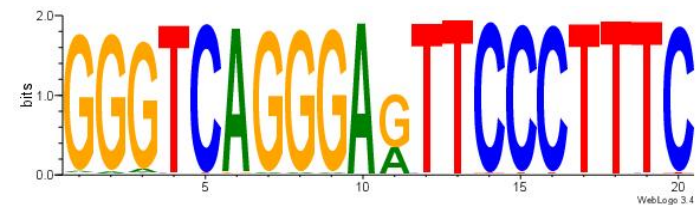
Alignment:

```
GAAAGGGA ACTCCCTGACCC  
-----AATCGCTTGAACC
```

Original motif Consensus sequence: GAAAGGGA ACTCCCTGACCC



Reverse complement motif Consensus sequence:
GGGTCAGG GAGTTC CCTTTC



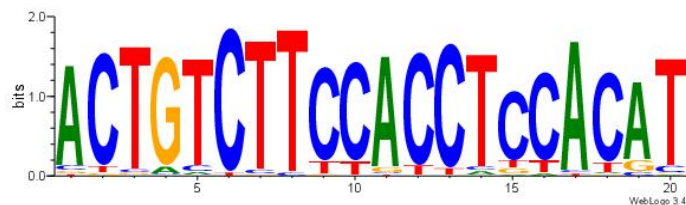
Dataset #: 1
Motif ID: 178
Motif name: Motif 178
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement

Direction: Forward
 Position number: 8
 Number of overlap: 13
 Similarity score: 0.0766097

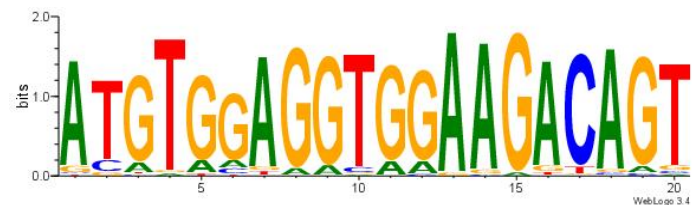
Alignment:

ATGTGGAGGTGGAAGACAGT
 -----GGTTCAAGCGATT

Original motif Consensus sequence: ACTGTCTTCCACCTCCACAT



Reverse complement motif Consensus sequence: ATGTGGAGGTGGAAGACAGT

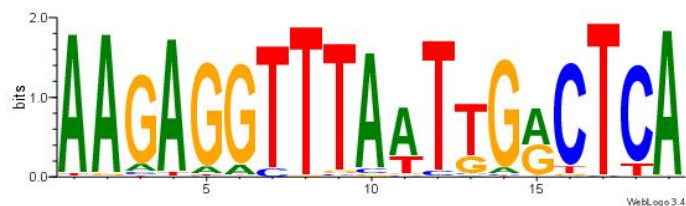


Dataset #: 1
 Motif ID: 129
 Motif name: Motif 129
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3
 Number of overlap: 13
 Similarity score: 0.0779699

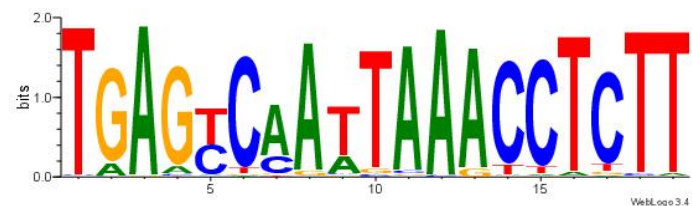
Alignment:

TGAGKCAATTAAACCTCTT
 --AATCGCTTGAACC----

Original motif Consensus sequence: AAGAGGTTTAATTGRCTCA



Reverse complement motif Consensus sequence: TGAGKCAATTAACCTCTT

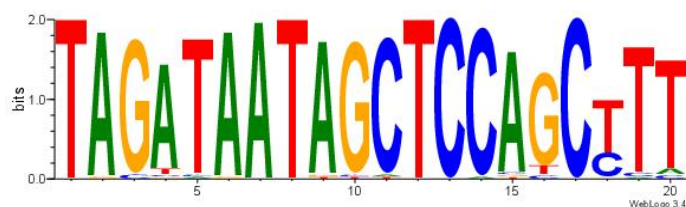


Dataset #: 1
Motif ID: 333
Motif name: Motif 333
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 6
Number of overlap: 13
Similarity score: 0.0810095

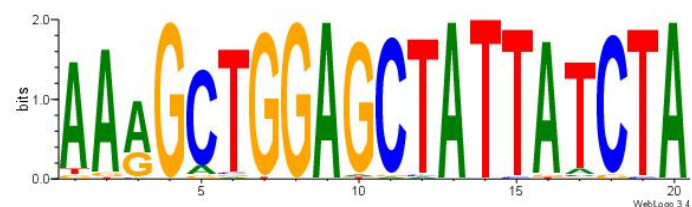
Alignment:

```
TAGATAATAGCTCCAGCTTT  
-----AATCGCTTGAACC--
```

Original motif Consensus sequence: TAGATAATAGCTCCAGCTTT



Reverse complement motif Consensus sequence: AAAGCTGGAGCTATTATCTA

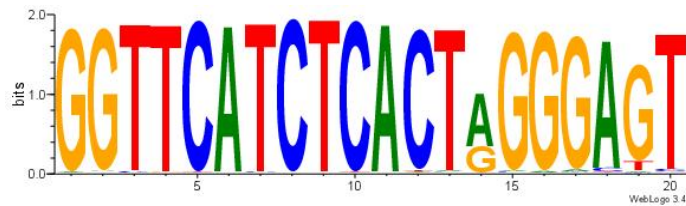


Dataset #: 1
 Motif ID: 23
 Motif name: Motif 23
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 13
 Similarity score: 0.081536

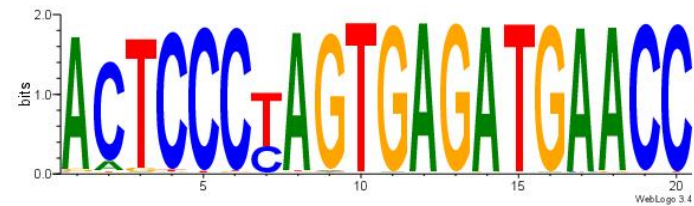
Alignment:

GGTTTCATCTCACTAGGGAGT
 -----GGTTCAAGCGATT

Original motif Consensus sequence: GGTTTCATCTCACTAGGGAGT



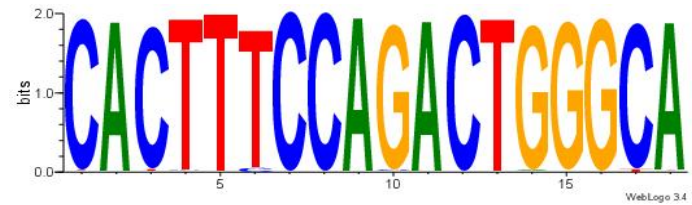
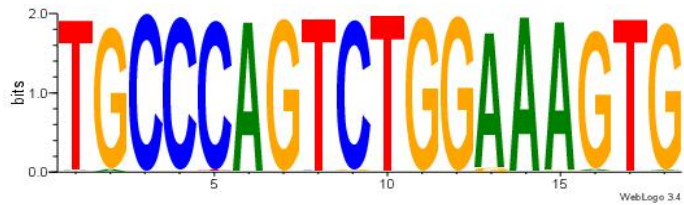
Reverse complement motif Consensus sequence: ACTCCCTAGTGAGATGAACC



Dataset #: 1 Motif ID: 45 Motif name: Motif 45

Original motif Consensus sequence: TGCCAGTCTGGAAAGTG

Reverse complement motif Consensus sequence: CACTTCCAGACTGGGCA

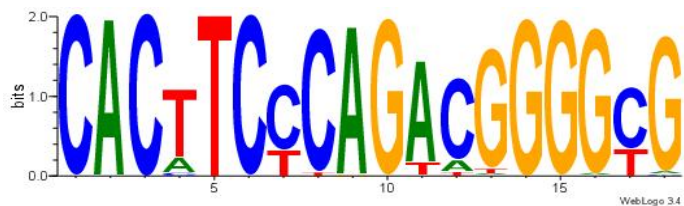


Best Matches for Motif ID 45 (Highest to Lowest)

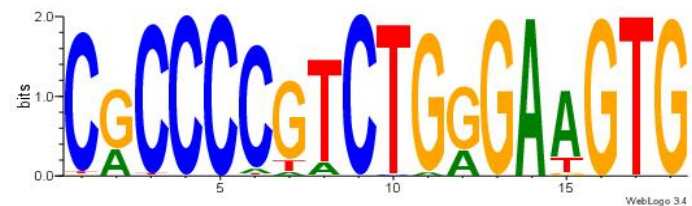
Dataset #: 1
 Motif ID: 27
 Motif name: Motif 27
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 18
 Similarity score: 0.0555298

Alignment:
 CGCCCCGTCTGGGAAGTG
 TGCCCAGTCTGGAAAGTG

Original motif Consensus sequence: CACTTCCCAGACGGGGCG



Reverse complement motif Consensus sequence: CGCCCCGTCTGGGAAGTG

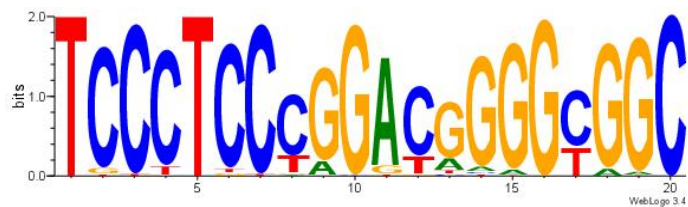


Dataset #: 1
 Motif ID: 155
 Motif name: Motif 155
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 18
 Similarity score: 0.104002

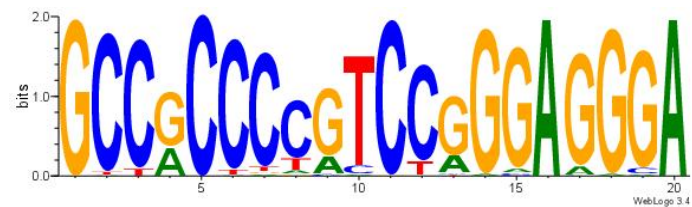
Alignment:

TCCCTCCCGGACGGGGYGGC
 CACTTTCAGACTGGGCA--

Original motif Consensus sequence: TCCCTCCCGGACGGGGYGGC



Reverse complement motif Consensus sequence: GCCKCCCCGTCCGGGAGGGA



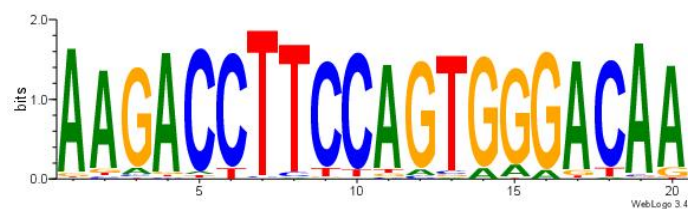
Dataset #: 1
 Motif ID: 292
 Motif name: Motif 292
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3

Number of overlap: 18
Similarity score: 0.11381

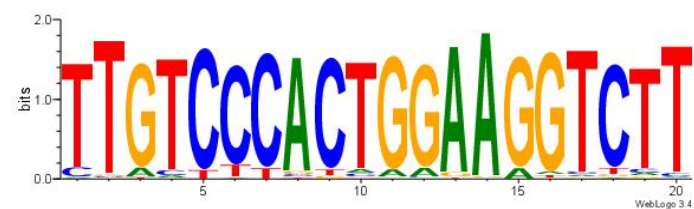
Alignment:

AAGACCTTCCAGTGGGACAA
--CACTTTCCAGACTGGGCA

Original motif Consensus sequence: AAGACCTTCCAGTGGGACAA



Reverse complement motif Consensus sequence:
TTGTCCCAGTGGAAAGGTCTT

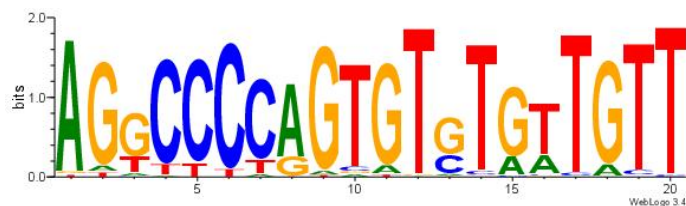


Dataset #: 1
Motif ID: 176
Motif name: Motif 176
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 18
Similarity score: 0.114247

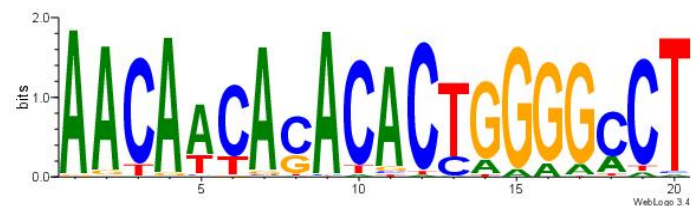
Alignment:

AGCCCCAGTGTSTGTTGTT
--TGCCCAGTCTGGAAAGTG

Original motif Consensus sequence: AGGCCCCAGTGTSTGTTGTT



Reverse complement motif Consensus sequence: AACACASACACTGGGGCCT

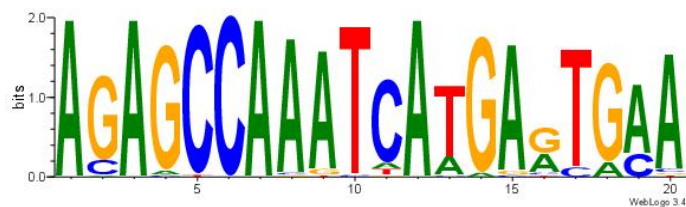


Dataset #: 1
Motif ID: 349
Motif name: Motif 349
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 3
Number of overlap: 18
Similarity score: 0.12083

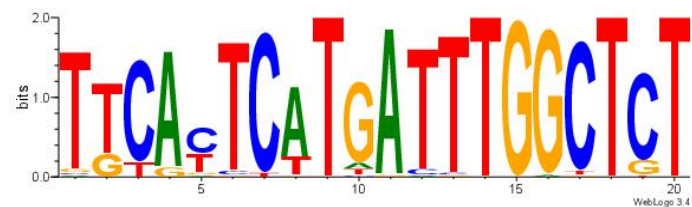
Alignment:

AGAGCCAAATCATGARTGAA
--TGCCCAGTCTGGAAAGTG

Original motif Consensus sequence: AGAGCCAAATCATGARTGAA

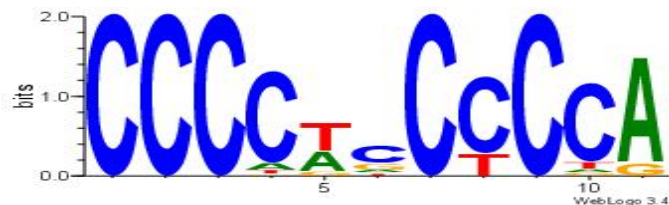


Reverse complement motif Consensus sequence: TTCAMTCATGATTTGGCTCT



Dataset #: 1 Motif ID: 46 Motif name: Motif 46

Original motif Consensus sequence: CCCCWCCCCCA



Reverse complement motif Consensus sequence: TGGGGGWGGGG



Best Matches for Motif ID 46 (Highest to Lowest)

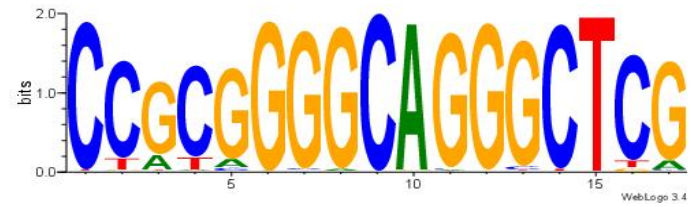
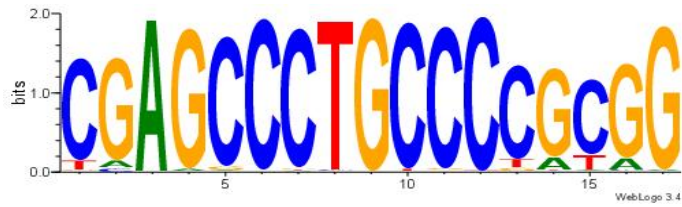
Dataset #:	1
Motif ID:	78
Motif name:	Motif 78
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	4
Number of overlap:	11
Similarity score:	0.0694266

Alignment:

```
CGAGCCCTGCCCGCGG  
---CCCCWCCCCCA---
```

Original motif Consensus sequence: CGAGCCCTGCCCGCGG

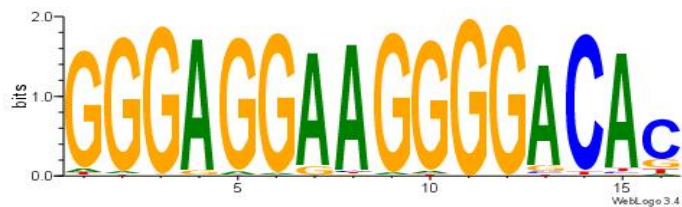
Reverse complement motif Consensus sequence:
CCGCGGGGCAGGGCTCG



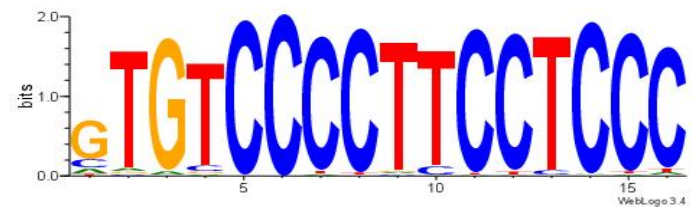
Dataset #: 1
 Motif ID: 221
 Motif name: Motif 221
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 5
 Number of overlap: 11
 Similarity score: 0.0733808

Alignment:
 GGGAGGAAGGGGACAC
 -TGGGGWGGGG----

Original motif Consensus sequence: GGGAGGAAGGGGACAC



Reverse complement motif Consensus sequence: GTGTCCCCTTCTCCC



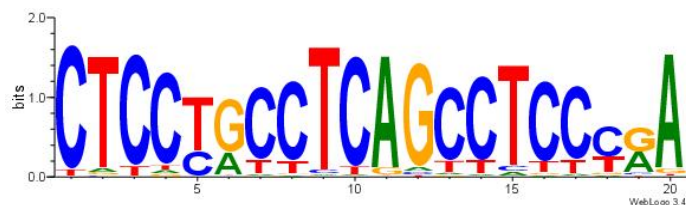
Dataset #: 1

Motif ID: 26
 Motif name: Motif 26
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.0736838

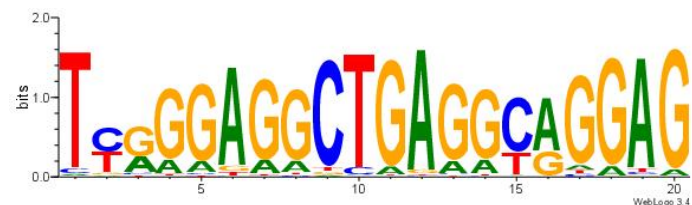
Alignment:

CTCCTGCCTCAGCCTCCCRA
 CCCCWCCCCCA-----

Original motif Consensus sequence: CTCCTGCCTCAGCCTCCCRA



Reverse complement motif Consensus sequence: TMGGGAGGCTGAGGCAGGAG



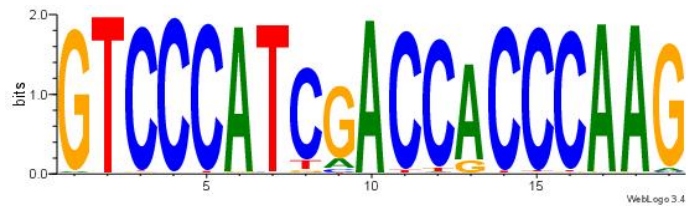
Dataset #: 1
 Motif ID: 53
 Motif name: Motif 53
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 7
 Number of overlap: 11

Similarity score: 0.0739686

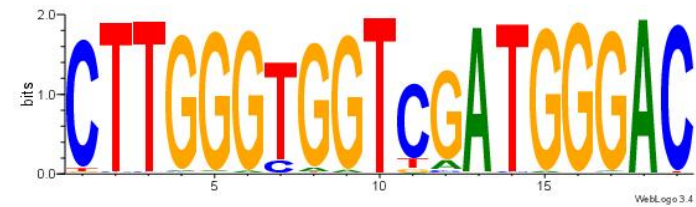
Alignment:

CTTGGGTGGTCGATGGGAC
-----TGGGGGWGGGG--

Original motif Consensus sequence: GTCCCATCGACCACCCAAG



Reverse complement motif Consensus sequence:
CTTGGGTGGTCGATGGGAC



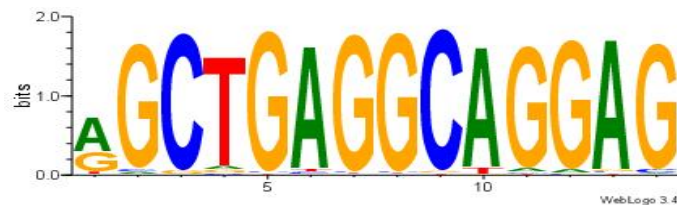
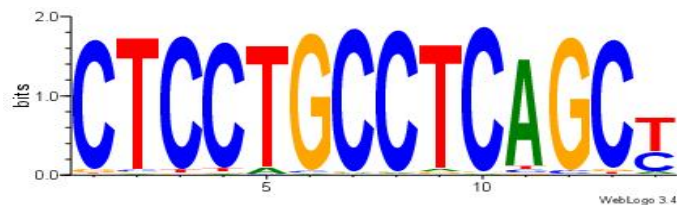
Dataset #: 1
Motif ID: 313
Motif name: Motif 313
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 11
Similarity score: 0.0768738

Alignment:

MGCTGAGGCAGGAG
---TGGGGGWGGGG

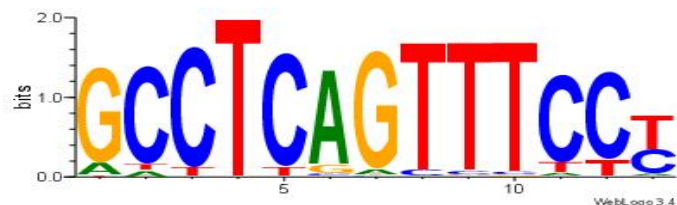
Original motif Consensus sequence: CTCCTGCCTCAGCY

Reverse complement motif Consensus sequence: MGCTGAGGCAGGAG

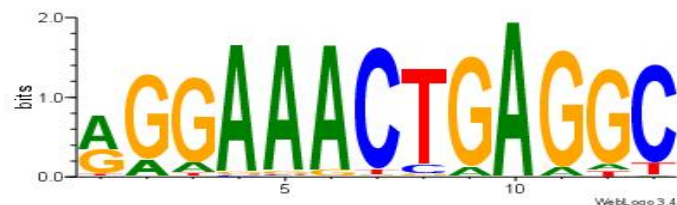


Dataset #: 1 Motif ID: 47 Motif name: Motif 47

Original motif Consensus sequence: GCCTCAGTTTCCY



Reverse complement motif Consensus sequence: MGGAACTGAGGC

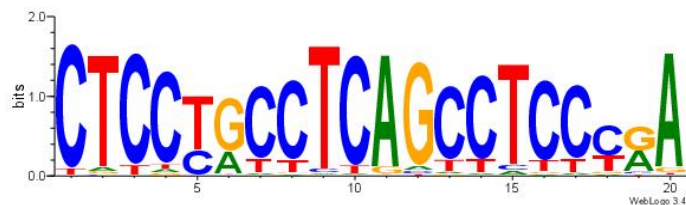


Best Matches for Motif ID 47 (Highest to Lowest)

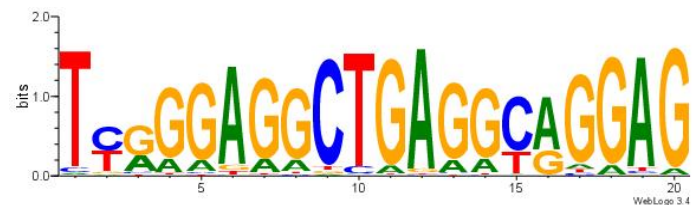
Dataset #:	1
Motif ID:	26
Motif name:	Motif 26
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	6
Number of overlap:	13
Similarity score:	0.0351242

Alignment:
 CTCCTGCCTCAGCCTCCRA
 -----GCCTCAGTTTCCY--

Original motif Consensus sequence: CTCCTGCCTCAGCCTCCRA



Reverse complement motif Consensus sequence: TMGGGAGGCTGAGGCAGGAG

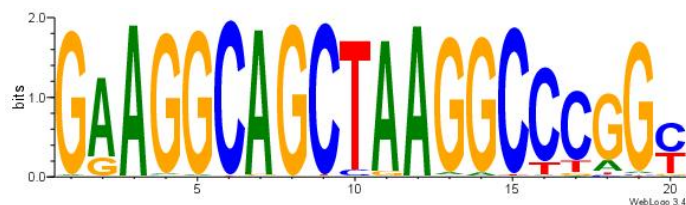


Dataset #: 1
Motif ID: 64
Motif name: Motif 64
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 3
Number of overlap: 13
Similarity score: 0.0624672

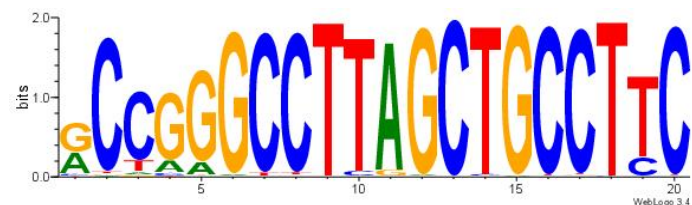
Alignment:

```
KCCGGGCCTTAGCTGCCTTC  
-----GCCTCAGTTTCCY--
```

Original motif Consensus sequence: GAAGGCAGCTAAGGCCCGGY



Reverse complement motif Consensus sequence: KCCGGGCCTTAGCTGCCTTC

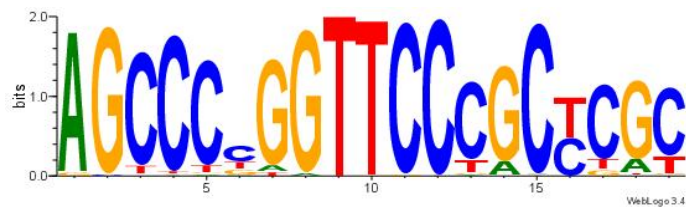


Dataset #: 1
 Motif ID: 164
 Motif name: Motif 164
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 6
 Number of overlap: 13
 Similarity score: 0.067911

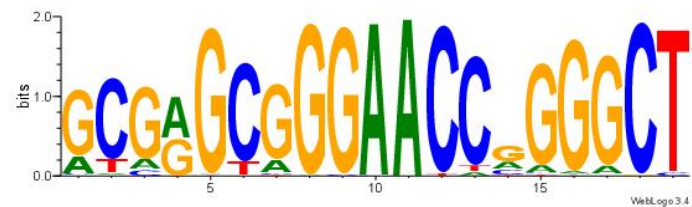
Alignment:

GCGMGCGGGAACCGGGGCT
 -----MGGAAACTGAGGC-

Original motif Consensus sequence: AGCCCCGGTTCCCGCYCGC



Reverse complement motif Consensus sequence: GCGMGCGGGAACCGGGGCT



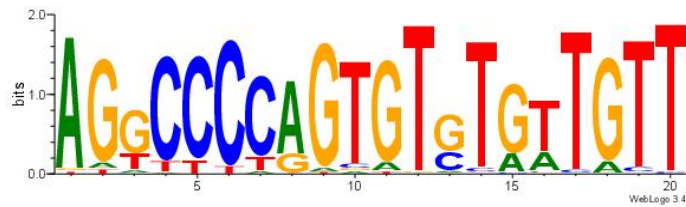
Dataset #: 1
 Motif ID: 176
 Motif name: Motif 176
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 6

Number of overlap: 13
Similarity score: 0.0734205

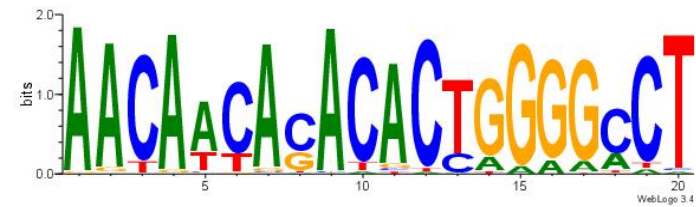
Alignment:

AACAACASACTGGGGCCT
-----MGGAAACTGAGGC--

Original motif Consensus sequence: AGGCCCCAGTGTSTGTTGTT



Reverse complement motif Consensus sequence:
AACAACASACTGGGGCCT

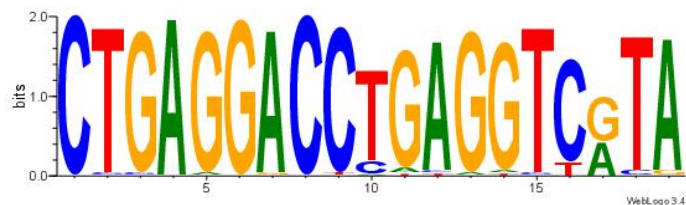


Dataset #: 1
Motif ID: 291
Motif name: Motif 291
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 5
Number of overlap: 13
Similarity score: 0.0791421

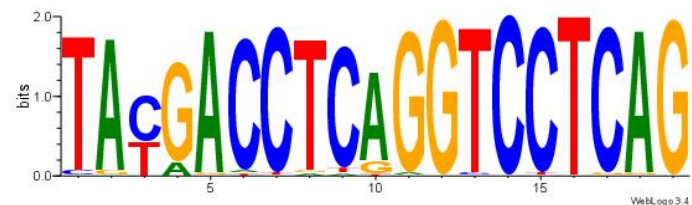
Alignment:

TAMGACCTCAGGTCCTCAG
-----GCCTCAGTTTCCY--

Original motif Consensus sequence: CTGAGGACCTGAGGTCRTA

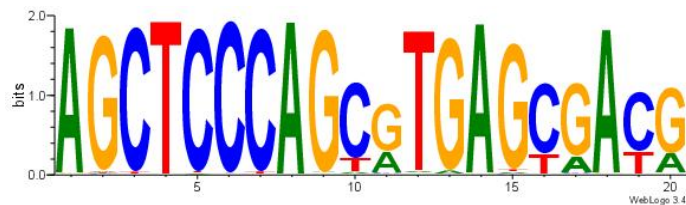


Reverse complement motif Consensus sequence: TAMGACCTCAGGTCCTCAG

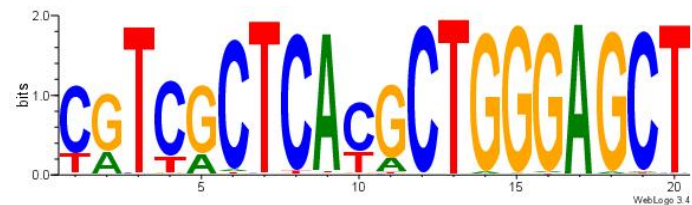


Dataset #: 1 Motif ID: 48 Motif name: Motif 48

Original motif Consensus sequence: AGCTCCCAGCGTGAGCGACG



Reverse complement motif Consensus sequence: CGTCGCTCAGCTGGGAGCT



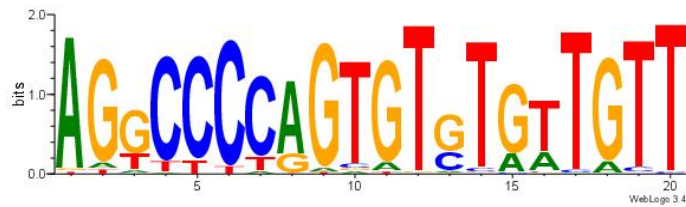
Best Matches for Motif ID 48 (Highest to Lowest)

Dataset #:	1
Motif ID:	176
Motif name:	Motif 176
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	20
Similarity score:	0.113918

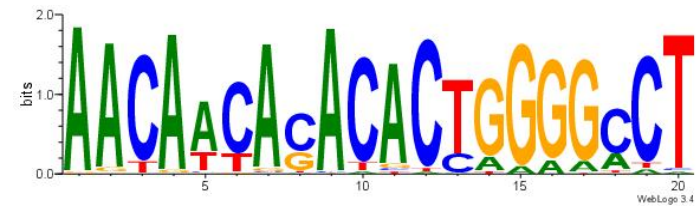
Alignment:

AGGCCCCAGTGTSTGTTGTT
AGCTCCCAGCGTGAGCGACG

Original motif Consensus sequence: AGGCCCCAGTGTSTGTTGTT



Reverse complement motif Consensus sequence:
AACAACASACACTGGGGCCT



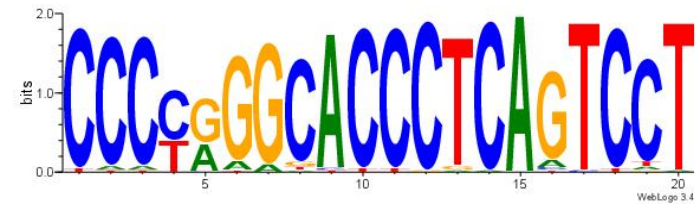
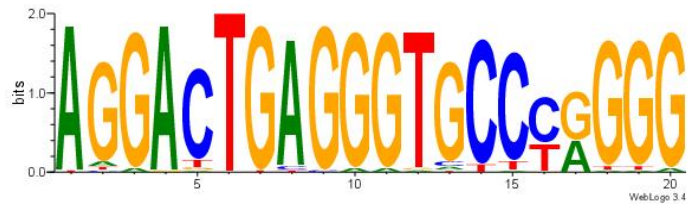
Dataset #:	1
Motif ID:	312
Motif name:	Motif 312
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	20
Similarity score:	0.121076

Alignment:

CCCMKGGCACCCTCAGTCCT
CGTCGCTCACGCTGGGAGCT

Original motif Consensus sequence: AGGACTGAGGGTGCCYRGGG

Reverse complement motif Consensus sequence:
CCCMKGGCACCCTCAGTCCT

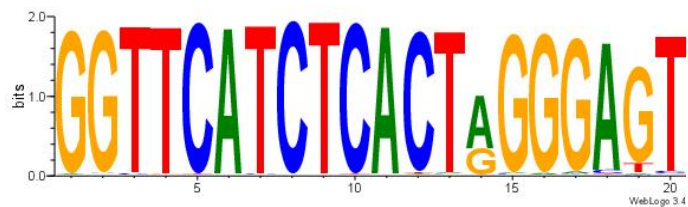


Dataset #: 1
 Motif ID: 23
 Motif name: Motif 23
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.123602

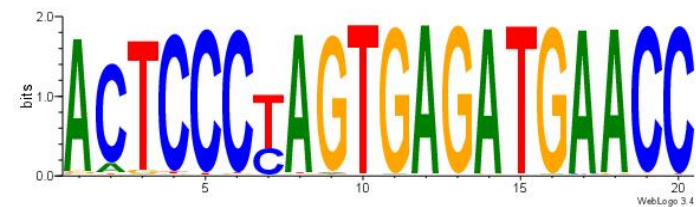
Alignment:

GGTTTCATCTCACTAGGGAGT
 CGTCGCTCACGCTGGGAGCT

Original motif Consensus sequence: GGTTTCATCTCACTAGGGAGT



Reverse complement motif Consensus sequence: ACTCCCTAGTGAGATGAACC



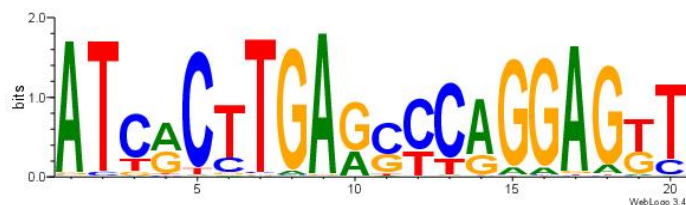
Dataset #: 1

Motif ID: 8
 Motif name: Motif 8
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.124233

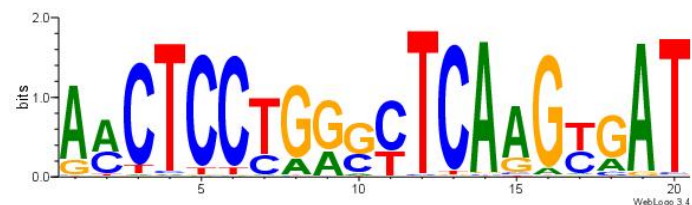
Alignment:

ARCTCCTGKSCTCAAGKGAT
 AGCTCCCAGCGTGAGCGACG

Original motif Consensus sequence: ATCRCTTGAGSYCAGGAGKT



Reverse complement motif Consensus sequence: ARCTCCTGKSCTCAAGKGAT



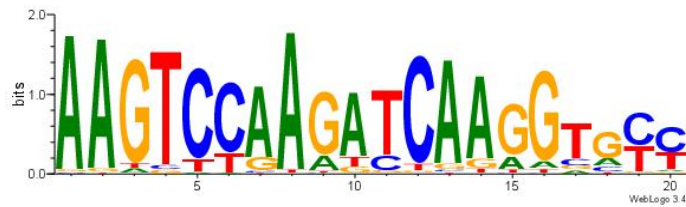
Dataset #: 1
 Motif ID: 119
 Motif name: Motif 119
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 20

Similarity score: 0.129197

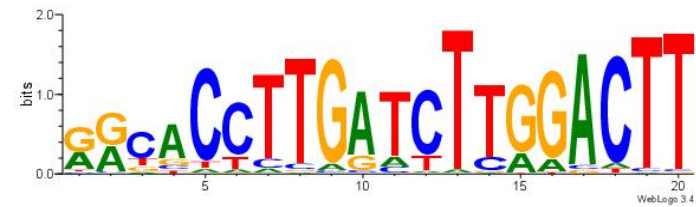
Alignment:

KKCACCTTGATCTTGGACTT
CGTCGCTCACGCTGGGAGCT

Original motif Consensus sequence: AAGTCCAAGATCAAGGTGY

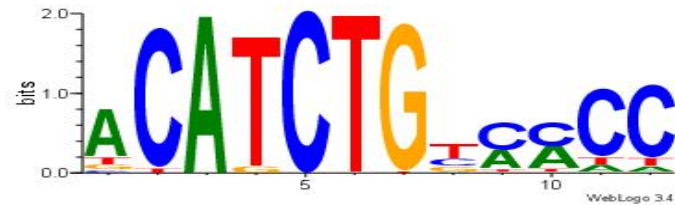


Reverse complement motif Consensus sequence: KKCACCTTGATCTTGGACTT



Dataset #: 1 Motif ID: 49 Motif name: Motif 49

Original motif Consensus sequence: ACATCTGYMMCC



Reverse complement motif Consensus sequence: GRRMCAGATGT



Best Matches for Motif ID 49 (Highest to Lowest)

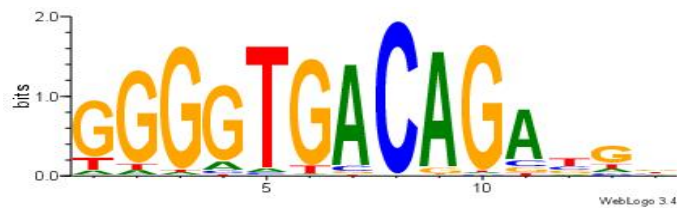
Dataset #:	1
Motif ID:	1
Motif name:	Motif 1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif

Direction: Forward
Position number: 1
Number of overlap: 12
Similarity score: 0.0495311

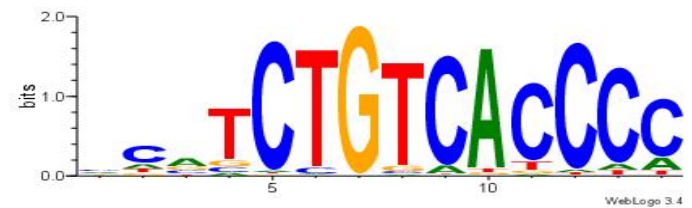
Alignment:

GGGGTGACAGABGB
GRRMCAGATGT--

Original motif Consensus sequence: GGGGTGACAGABGB



Reverse complement motif Consensus sequence: BCVTCTGTCACCC

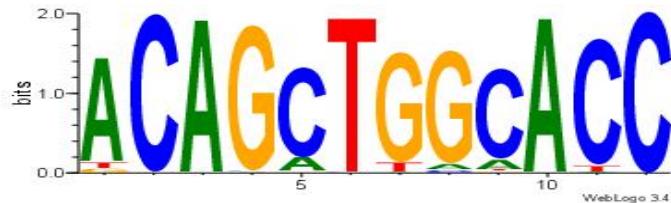


Dataset #: 1
Motif ID: 199
Motif name: Motif 199
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 12
Similarity score: 0.0505389

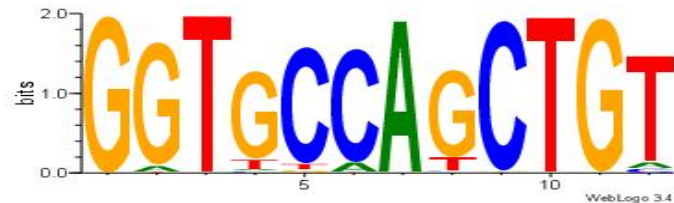
Alignment:

ACAGCTGGCACC
ACATCTGYMMCC

Original motif Consensus sequence: ACAGCTGGCACC



Reverse complement motif Consensus sequence: GGTGCCAGCTGT

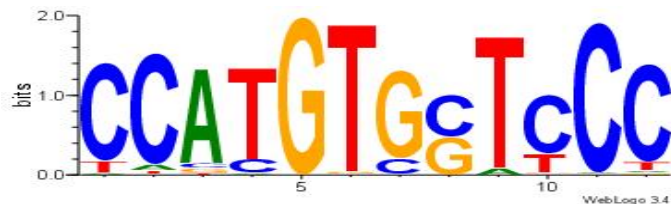


Dataset #: 1
Motif ID: 120
Motif name: Motif 120
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 12
Similarity score: 0.0662574

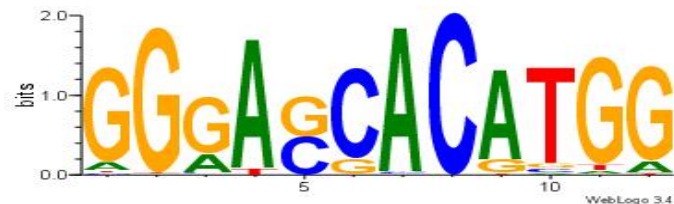
Alignment:

GGGASCACATGG
GRRMCAGATGT

Original motif Consensus sequence: CCATGTGSTCCC



Reverse complement motif Consensus sequence: GGGASCACATGG

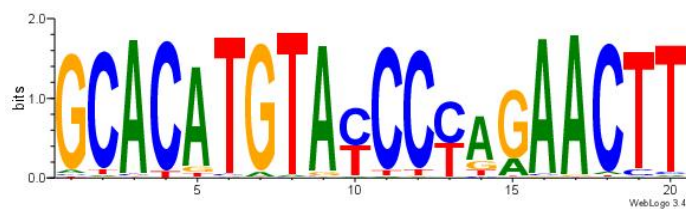


Dataset #: 1
 Motif ID: 225
 Motif name: Motif 225
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 7
 Number of overlap: 12
 Similarity score: 0.0777612

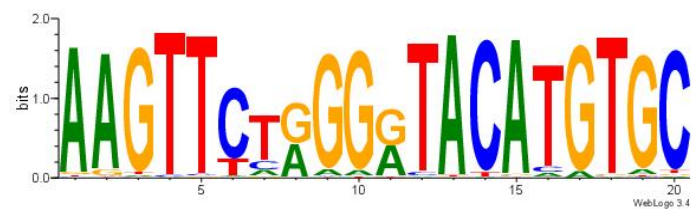
Alignment:

GCACATGTAYCCYAGAACTT
 --ACATCTGYMMCC-----

Original motif Consensus sequence: GCACATGTAYCCYAGAACTT



Reverse complement motif Consensus sequence: AAGTTCTKGGKTACATGTGC

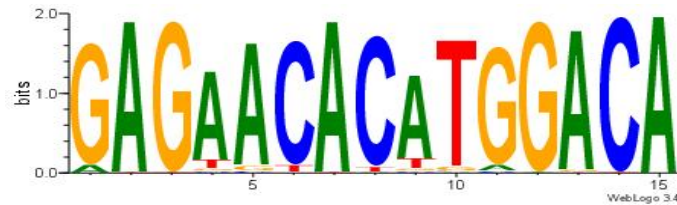


Dataset #: 1
 Motif ID: 257
 Motif name: Motif 257
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 4

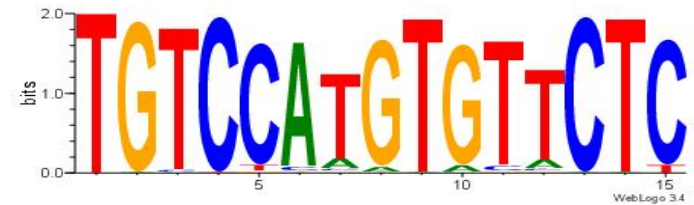
Number of overlap: 12
Similarity score: 0.0790361

Alignment:
GAGAACACATGGACA
GGRRMCAGATGT---

Original motif Consensus sequence: GAGAACACATGGACA

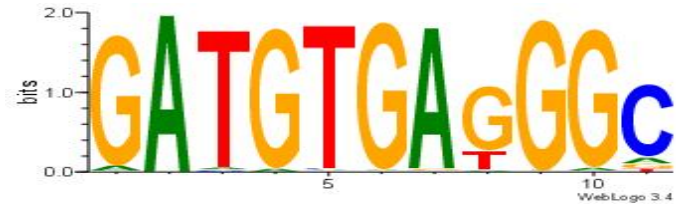


Reverse complement motif Consensus sequence: TGTCCATGTGTTCTC

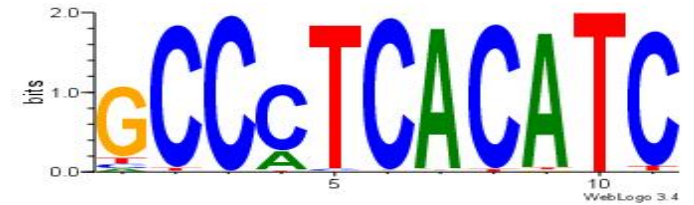


Dataset #: 1 Motif ID: 50 Motif name: Motif 50

Original motif Consensus sequence: GATGTGAGGGC



Reverse complement motif Consensus sequence: GCCCTCACATC



Best Matches for Motif ID 50 (Highest to Lowest)

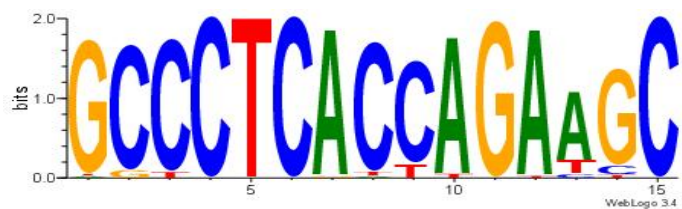
Dataset #: 1
Motif ID: 277
Motif name: Motif 277
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement

Direction: Forward
 Position number: 5
 Number of overlap: 11
 Similarity score: 0.0679708

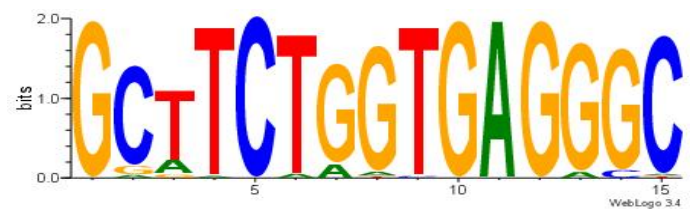
Alignment:

GCTTCTGGTGAGGGC
 ----GATGTGAGGGC

Original motif Consensus sequence: GCCCTCACCAGAAGC



Reverse complement motif Consensus sequence: GCTTCTGGTGAGGGC

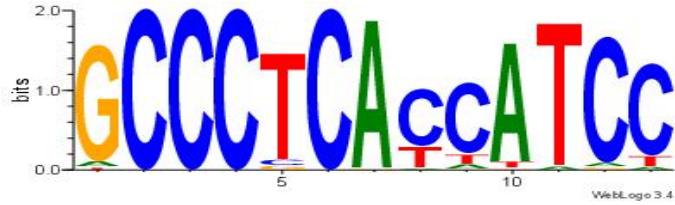


Dataset #: 1
 Motif ID: 283
 Motif name: Motif 283
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3
 Number of overlap: 11
 Similarity score: 0.0702987

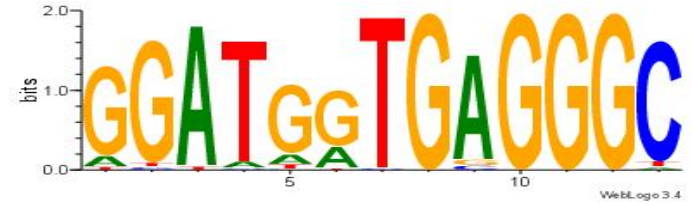
Alignment:

GGATGGTGAGGGC
 --GATGTGAGGGC

Original motif Consensus sequence: GCCCTCACCATCC



Reverse complement motif Consensus sequence: GGATGGTGAGGGG

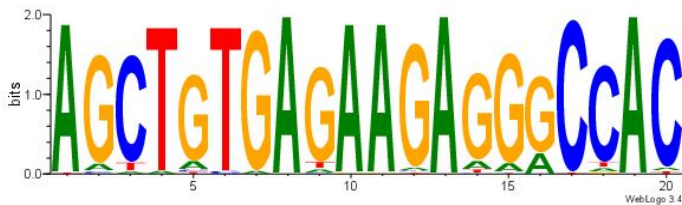


Dataset #: 1
 Motif ID: 294
 Motif name: Motif 294
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 7
 Number of overlap: 11
 Similarity score: 0.0711373

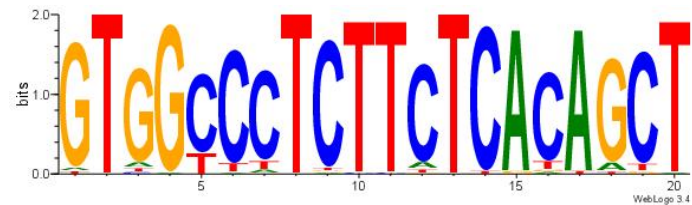
Alignment:

```
AGCTGTGAGAAGAGGGCCAC
-----GATGTGAGGGC----
```

Original motif Consensus sequence: AGCTGTGAGAAGAGGGCCAC



Reverse complement motif Consensus sequence: GTGGCCCTCTTCTCACAGCT

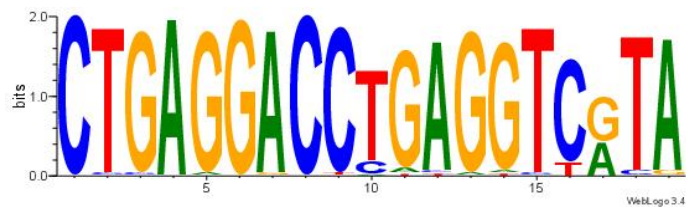


Dataset #: 1
 Motif ID: 291
 Motif name: Motif 291
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 6
 Number of overlap: 11
 Similarity score: 0.0726313

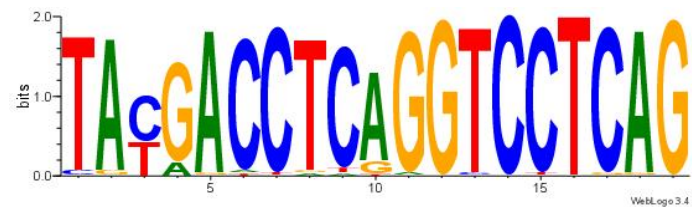
Alignment:

TAMGACCTCAGGTCCTCAG
 ---GCCCTCACATC-----

Original motif Consensus sequence: CTGAGGACCTGAGGTCRTA



Reverse complement motif Consensus sequence: TAMGACCTCAGGTCCTCAG

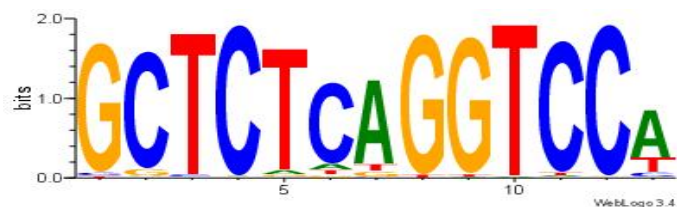


Dataset #: 1
 Motif ID: 323
 Motif name: Motif 323
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1

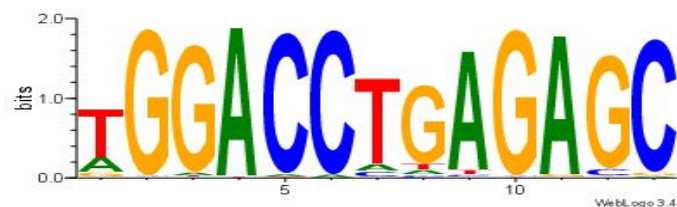
Number of overlap: 11
 Similarity score: 0.0745066

Alignment:
 TGGACCTGAGAGC
 --GATGTGAGGGC

Original motif Consensus sequence: GCTCTCAGGTCCA

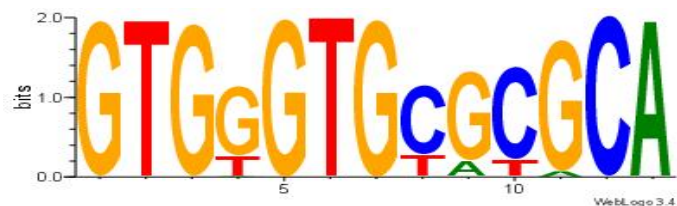


Reverse complement motif Consensus sequence: TGGACCTGAGAGC



Dataset #: 1 Motif ID: 51 Motif name: Motif 51

Original motif Consensus sequence: GTGGGTGCGCGCA



Reverse complement motif Consensus sequence: TCGCGCACCCAC



Best Matches for Motif ID 51 (Highest to Lowest)

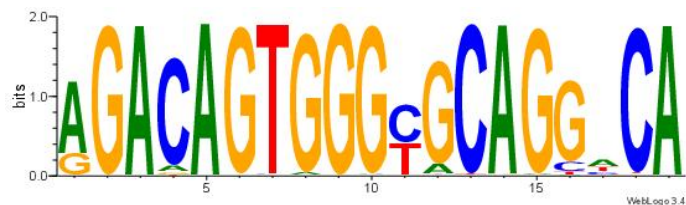
Dataset #: 1
 Motif ID: 17
 Motif name: Motif 17
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement

Direction: Forward
 Position number: 6
 Number of overlap: 13
 Similarity score: 0.0746013

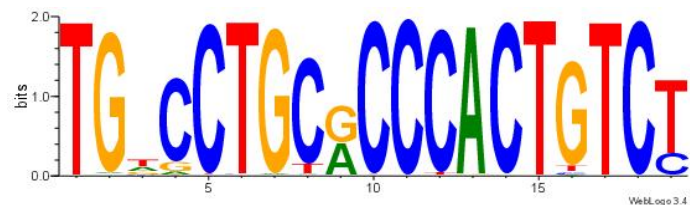
Alignment:

TGHCTGCKCCCCTGTCT
 -----TGC GCGCACCCAC--

Original motif Consensus sequence: AGACAGTGGGYGCAGGHCA



Reverse complement motif Consensus sequence: TGHCTGCKCCCCTGTCT

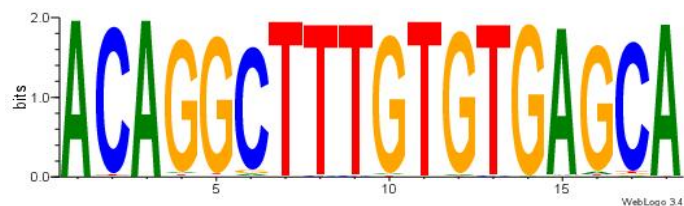


Dataset #: 1
 Motif ID: 159
 Motif name: Motif 159
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 6
 Number of overlap: 13
 Similarity score: 0.0830854

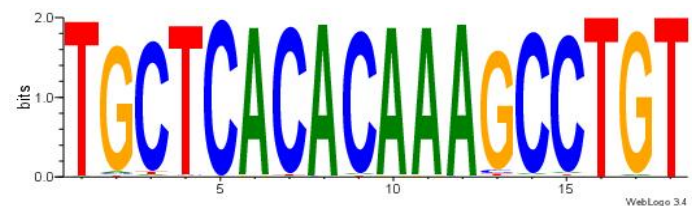
Alignment:

ACAGGCTTTGTGTGAGCA
 -----GTGGGTGCGCGCA

Original motif Consensus sequence: ACAGGCTTTGTGTGAGCA



Reverse complement motif Consensus sequence: TGCTCACACAAAGCCTGT

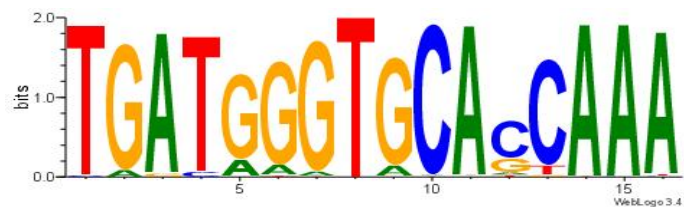


Dataset #: 1
Motif ID: 289
Motif name: Motif 289
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 3
Number of overlap: 13
Similarity score: 0.0852016

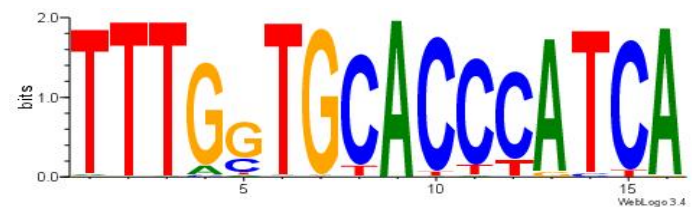
Alignment:

TGATGGGTGCACCAA
--GTGGGTGCGCGCA--

Original motif Consensus sequence: TGATGGGTGCACCAA



Reverse complement motif Consensus sequence: TTTGGTGCACCCATCA

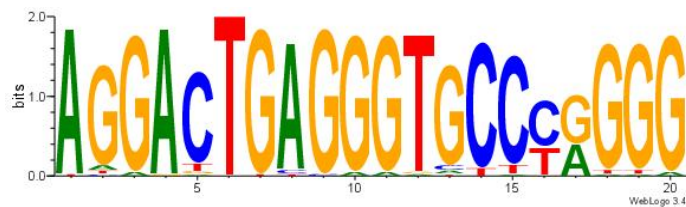


Dataset #: 1
 Motif ID: 312
 Motif name: Motif 312
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 7
 Number of overlap: 13
 Similarity score: 0.0893244

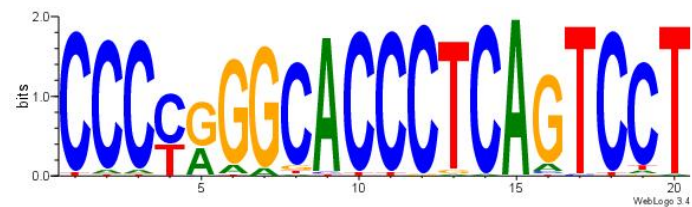
Alignment:

CCCMKGGCACCCCTCAGTCCT
 -TGC GCGCACCCAC-----

Original motif Consensus sequence: AGGACTGAGGGTGCCYRGGG



Reverse complement motif Consensus sequence: CCCMKGGCACCCCTCAGTCCT



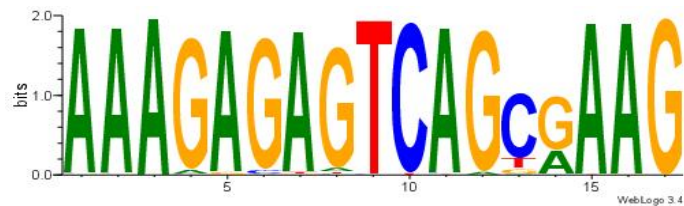
Dataset #: 1
 Motif ID: 148
 Motif name: Motif 148
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2

Number of overlap: 13
Similarity score: 0.0903644

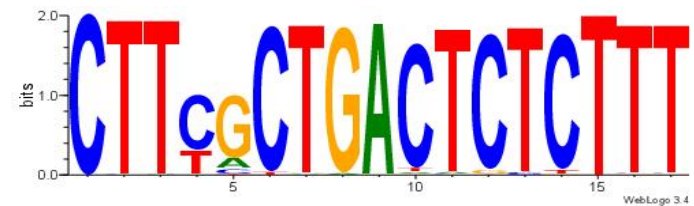
Alignment:

CTTCGCTGACTCTCTTT
-TGC GCGCACCCAC---

Original motif Consensus sequence: AAAGAGAGTCAGCGAAG

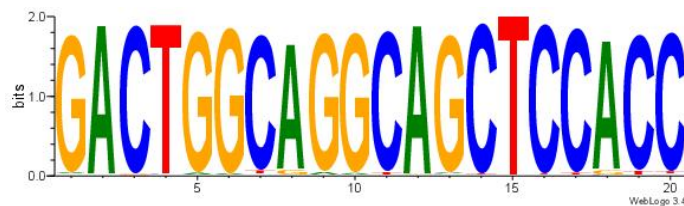


Reverse complement motif Consensus sequence:
CTTCGCTGACTCTCTTT

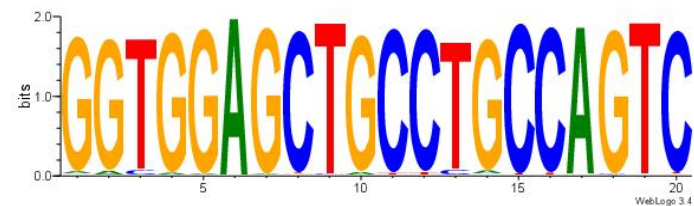


Dataset #: 1 Motif ID: 52 Motif name: Motif 52

Original motif Consensus sequence: GACTGGCAGGCAGCTCCACC



Reverse complement motif Consensus sequence:
GGTGGAGCTGCCAGTC



Best Matches for Motif ID 52 (Highest to Lowest)

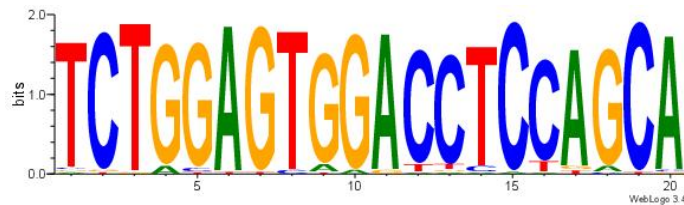
Dataset #: 1
Motif ID: 350
Motif name: Motif 350

Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	20
Similarity score:	0.108621

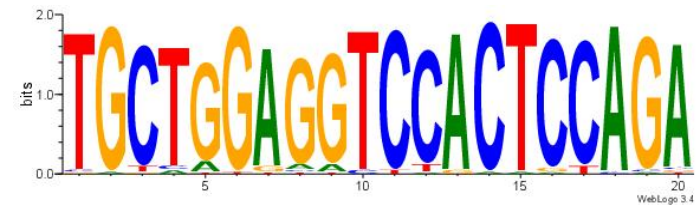
Alignment:

```
TGCTGGAGGTCCACTCCAGA
GACTGGCAGGCAGCTCCACC
```

Original motif Consensus sequence: TCTGGAGTGGACCTCCAGCA



Reverse complement motif Consensus sequence: TGCTGGAGGTCCACTCCAGA

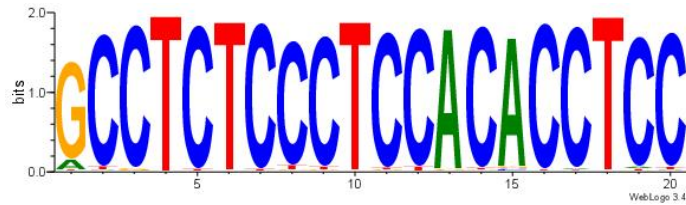


Dataset #:	1
Motif ID:	105
Motif name:	Motif 105
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	20
Similarity score:	0.118973

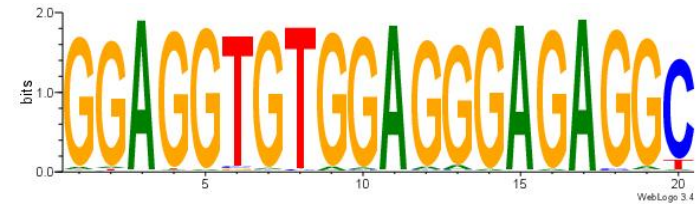
Alignment:

GGAGGTGTGGAGGGAGAGGC
GGTGGAGCTGCCTGCCAGTC

Original motif Consensus sequence: GCCTCTCCCTCCACACCTCC



Reverse complement motif Consensus sequence:
GGAGGTGTGGAGGGAGAGGC



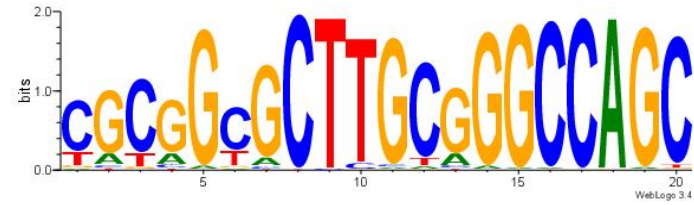
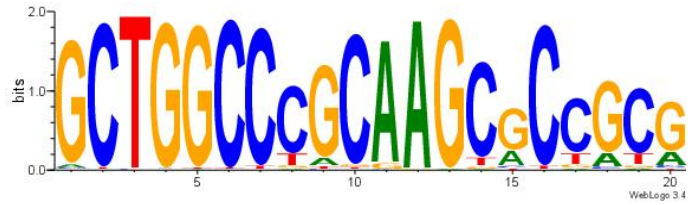
Dataset #:	1
Motif ID:	100
Motif name:	Motif 100
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	20
Similarity score:	0.11909

Alignment:

CGCGGCGCTTGCGGGCCAGC
GGTGGAGCTGCCTGCCAGTC

Original motif Consensus sequence: GCTGGCCCGCAAGCGCCGCG

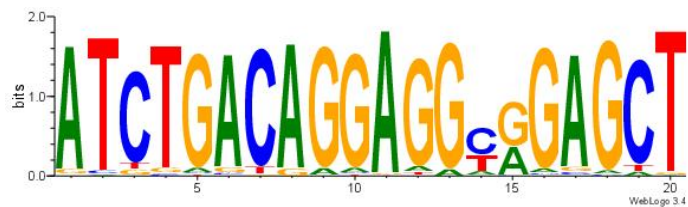
Reverse complement motif Consensus sequence:
CGCGGCGCTTGCGGGCCAGC



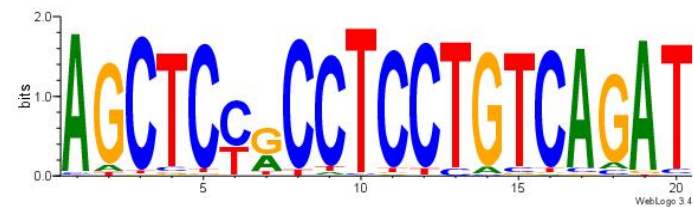
Dataset #: 1
 Motif ID: 165
 Motif name: Motif 165
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.122785

Alignment:
 AGCTCMKCCTCCTGTCAGAT
 GGTGGAGCTGCCTGCCAGTC

Original motif Consensus sequence: ATCTGACAGGAGGYRGAGCT



Reverse complement motif Consensus sequence: AGCTCMKCCTCCTGTCAGAT



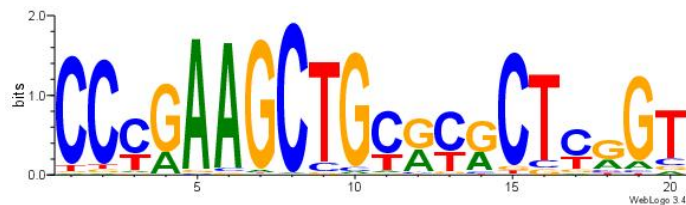
Dataset #: 1

Motif ID: 177
 Motif name: Motif 177
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.125451

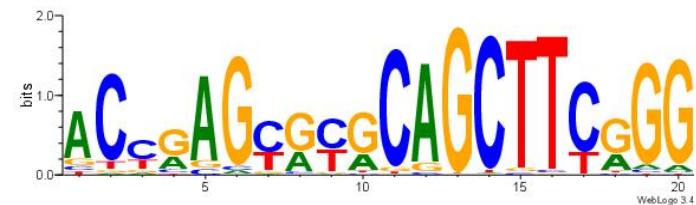
Alignment:

CCCGAAGCTGCRYRCTCGGT
 GGTGGAGCTGCCTGCCAGTC

Original motif Consensus sequence: CCCGAAGCTGCRYRCTCGGT

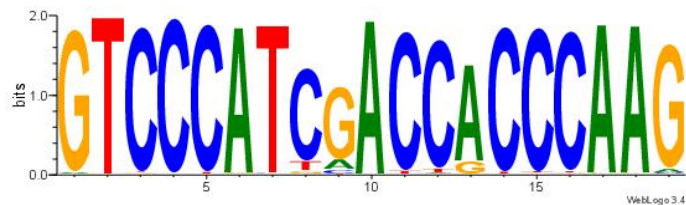


Reverse complement motif Consensus sequence: ACCGAGMKMGCAGCTTCGGG

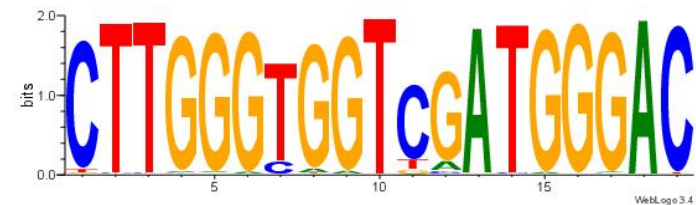


Dataset #: 1 Motif ID: 53 Motif name: Motif 53

Original motif Consensus sequence: GTCCCATCGACCACCCAAG



Reverse complement motif Consensus sequence: CTTGGGTGGTTCGATGGGAC



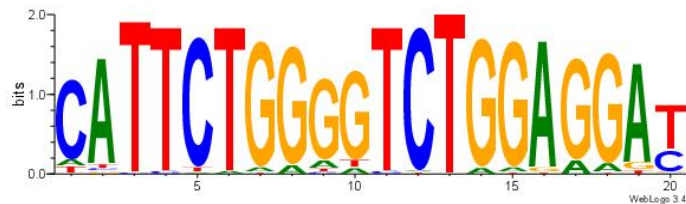
Best Matches for Motif ID 53 (Highest to Lowest)

Dataset #: 1
Motif ID: 309
Motif name: Motif 309
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 2
Number of overlap: 19
Similarity score: 0.113725

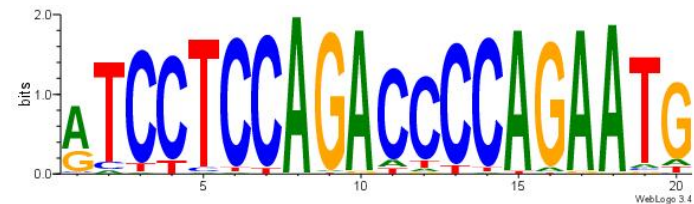
Alignment:

```
CATTCTGGGGTCTGGAGGAY  
-CTTGGGTGGTCGATGGAC
```

Original motif Consensus sequence: CATTCTGGGGTCTGGAGGAY



Reverse complement motif Consensus sequence:
MTCCTCCAGACCCCAAGAATG



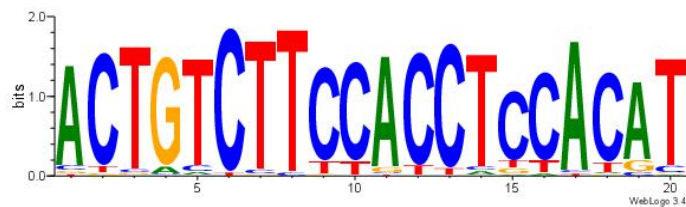
Dataset #: 1
Motif ID: 178
Motif name: Motif 178
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement

Direction: Forward
Position number: 1
Number of overlap: 19
Similarity score: 0.118023

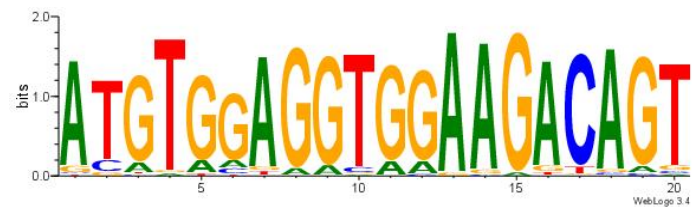
Alignment:

ATGTGGAGGTGGAAGACAGT
CTTGGGTGGTCGATGGGAC-

Original motif Consensus sequence: ACTGTCTTCCACCTCCACAT



Reverse complement motif Consensus sequence: ATGTGGAGGTGGAAGACAGT

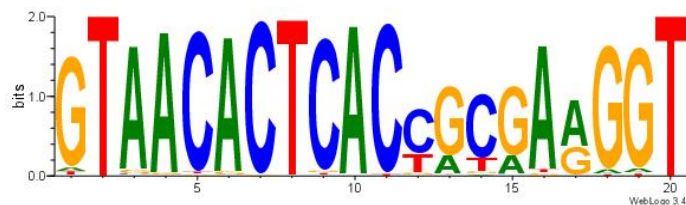


Dataset #: 1
Motif ID: 201
Motif name: Motif 201
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 19
Similarity score: 0.119118

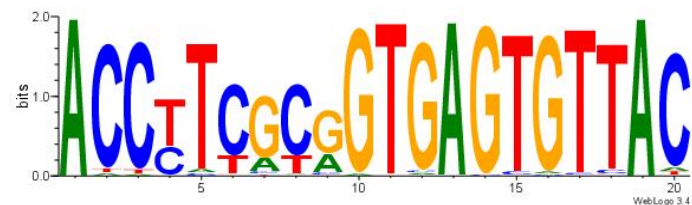
Alignment:

GTAACACTCACCGCGARGGT
GTCCCATCGACCACCCAAG-

Original motif Consensus sequence: GTAACACTCACCGCGARGGT



Reverse complement motif Consensus sequence: ACCKTCGCGGTGAGTGTTAC

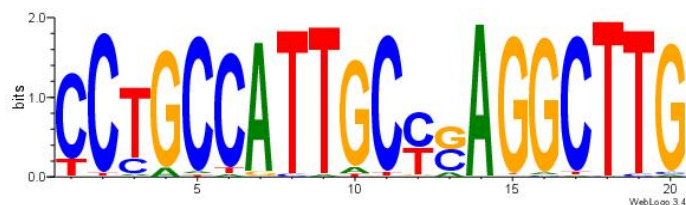


Dataset #: 1
Motif ID: 196
Motif name: Motif 196
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 19
Similarity score: 0.119924

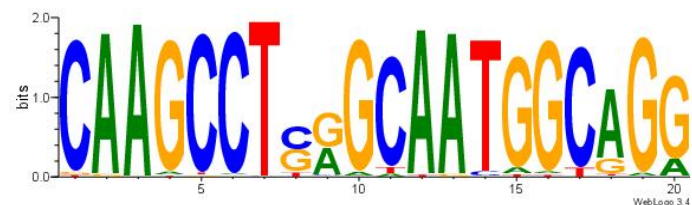
Alignment:

CCTGCCATTGCYSAGGCTTG
-GTCCCATCGACCACCCAAG

Original motif Consensus sequence: CCTGCCATTGCYSAGGCTTG



Reverse complement motif Consensus sequence: CAAGCCTSKGCAATGGCAGG

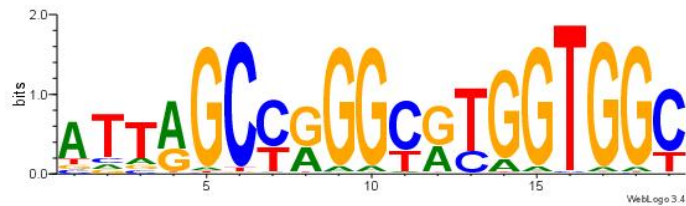


Dataset #: 1
 Motif ID: 2
 Motif name: Motif 2
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 19
 Similarity score: 0.127526

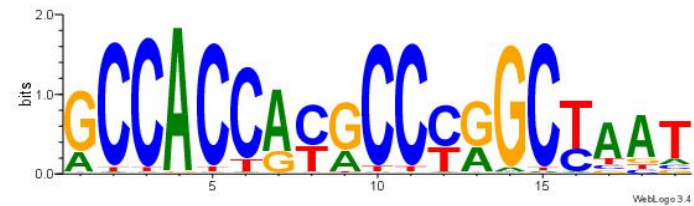
Alignment:

GCCACCAMGCCMKGCTAAT
 GTCCCATCGACCACCCAAG

Original motif Consensus sequence: ATTAGCYRGGCRTGGTGGC



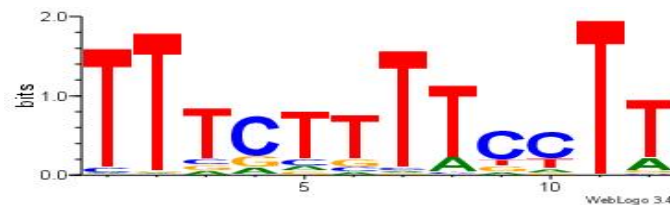
Reverse complement motif Consensus sequence: GCCACCAMGCCMKGCTAAT



Dataset #: 1 Motif ID: 54 Motif name: Motif 54

Original motif Consensus sequence: AAGGAAAAGAAA

Reverse complement motif Consensus sequence: TTTCTTTTCCTT



Best Matches for Motif ID 54 (Highest to Lowest)

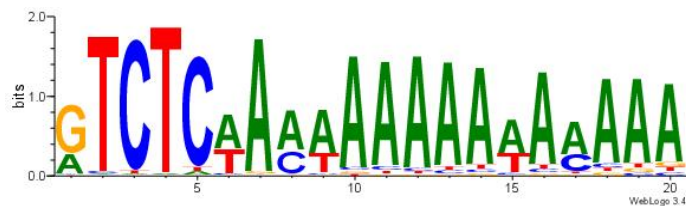
Dataset #: 1
 Motif ID: 7
 Motif name: Motif 7
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 12
 Similarity score: 0.0346455

Alignment:

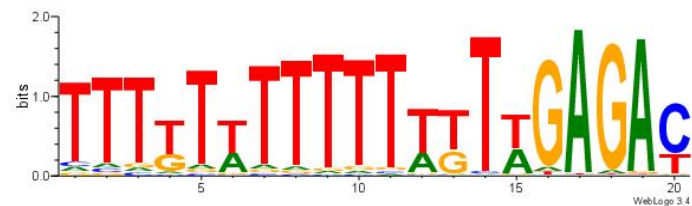
```

GTCTCWAMAAAAAAWAMAAA
-----AAGGAAAAGAAA
  
```

Original motif Consensus sequence: GTCTCWAMAAAAAAWAMAAA



Reverse complement motif Consensus sequence: TTTTWTCTTTTGGAGAC

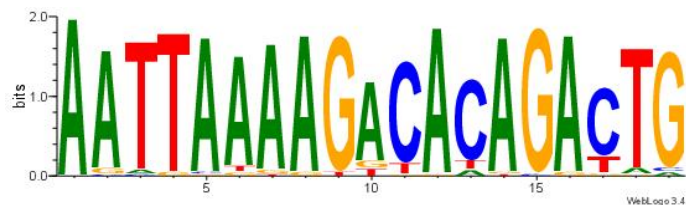


Dataset #: 1
 Motif ID: 356
 Motif name: Motif 356
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 12
 Similarity score: 0.0458962

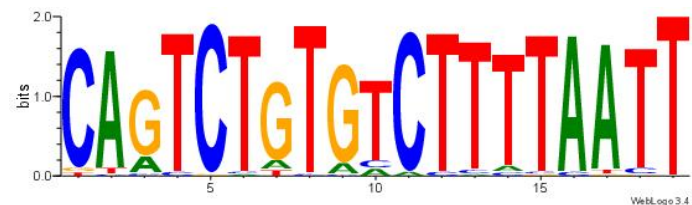
Alignment:

CAGTCTGTGTCTTTTAATT
 -----TTTCTTTTCCTT

Original motif Consensus sequence: AATTAAAGACACAGACTG



Reverse complement motif Consensus sequence: CAGTCTGTGTCTTTTAATT

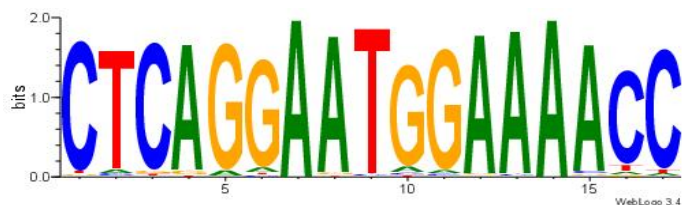


Dataset #: 1
 Motif ID: 214
 Motif name: Motif 214
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 4

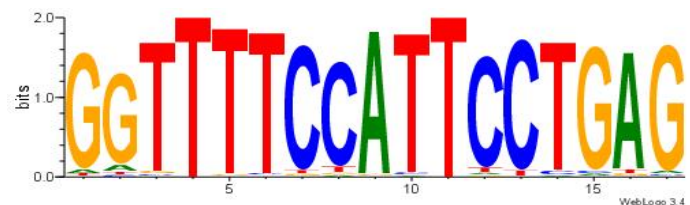
Number of overlap: 12
Similarity score: 0.0516933

Alignment:
CTCAGGAATGGAAAACC
--AAGGAAAAGAAA---

Original motif Consensus sequence: CTCAGGAATGGAAAACC



Reverse complement motif Consensus sequence:
GGTTTTCCATTCCCTGAG

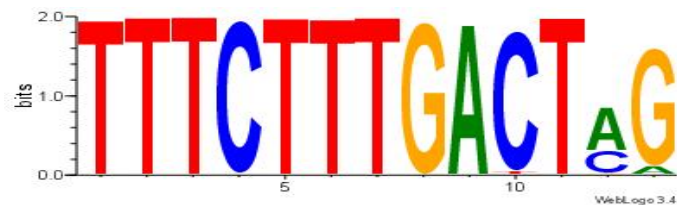
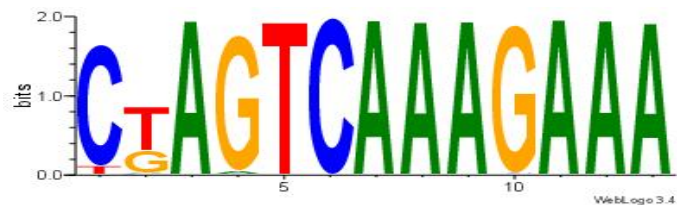


Dataset #: 1
Motif ID: 24
Motif name: Motif 24
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 12
Similarity score: 0.052923

Alignment:
TTTCTTTGACTRG
TTTCTTTTCCTT-

Original motif Consensus sequence: CKAGTCAAAGAAA

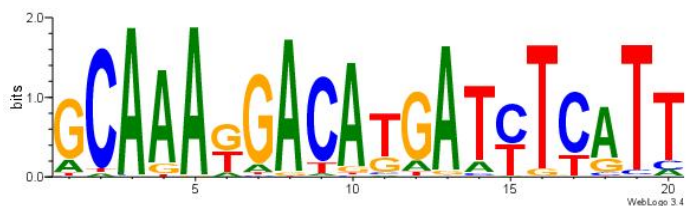
Reverse complement motif Consensus sequence: TTTCTTTGACTRG



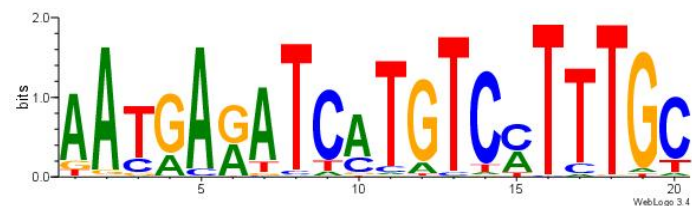
Dataset #: 1
 Motif ID: 99
 Motif name: Motif 99
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 6
 Number of overlap: 12
 Similarity score: 0.0590252

Alignment:
 AATGAKATCATGTCYTTTGC
 -----TTTCTTTTCCTT---

Original motif Consensus sequence: GCAAAGACATGATYTCATT

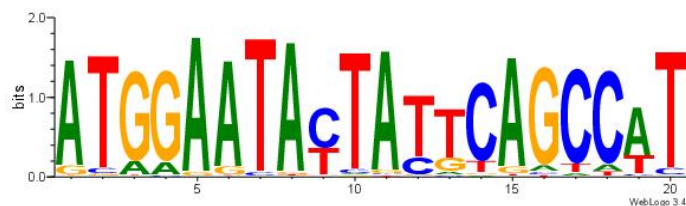


Reverse complement motif Consensus sequence: AATGAKATCATGTCYTTTGC

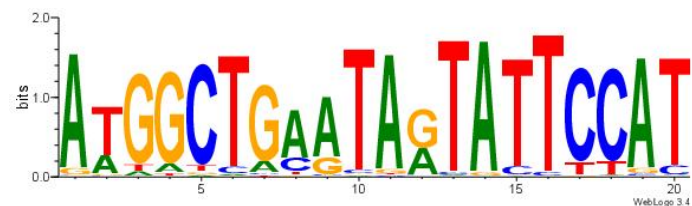


Dataset #: 1 Motif ID: 55 Motif name: Motif 55

Original motif Consensus sequence: ATGGAATAYTATTCAGCCAT



Reverse complement motif Consensus sequence: ATGGCTGAATAKTATTCCAT



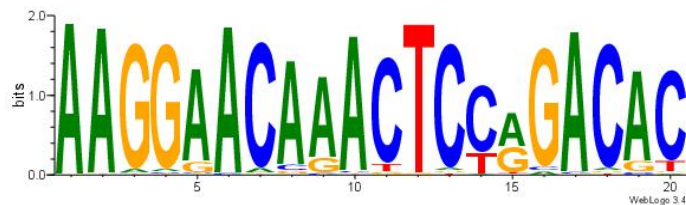
Best Matches for Motif ID 55 (Highest to Lowest)

Dataset #:	1
Motif ID:	234
Motif name:	Motif 234
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	20
Similarity score:	0.0832183

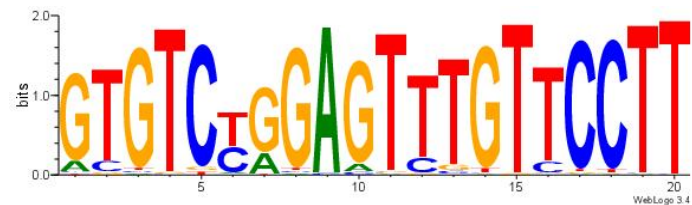
Alignment:

```
GTGTCKGGAGTTTGTTCCTT  
ATGGCTGAATAKTATTCCAT
```

Original motif Consensus sequence: AAGGAACAACTCCRGACAC



Reverse complement motif Consensus sequence: GTGTCKGGAGTTTGTTCCTT

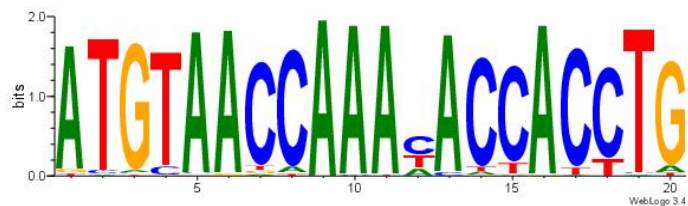


Dataset #: 1
 Motif ID: 336
 Motif name: Motif 336
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.102251

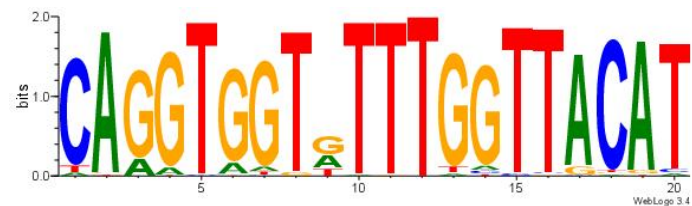
Alignment:

CAGGTGGTKTTTGGTTACAT
 ATGGCTGAATAKTATTCCAT

Original motif Consensus sequence: ATGTAACCAAAYACCACCTG



Reverse complement motif Consensus sequence: CAGGTGGTKTTTGGTTACAT



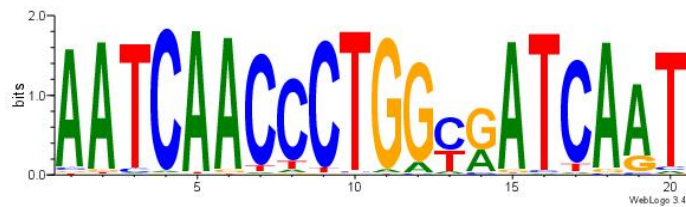
Dataset #: 1
 Motif ID: 170
 Motif name: Motif 170
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward

Position number: 1
Number of overlap: 20
Similarity score: 0.109578

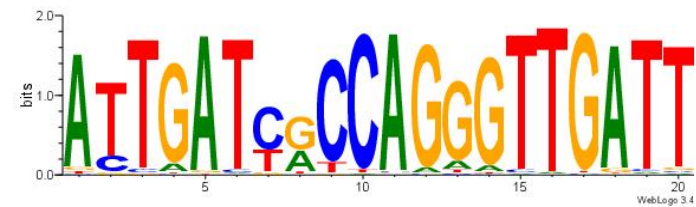
Alignment:

ATTGATMKCCAGGGTTGATT
ATGGCTGAATAKTATTCCAT

Original motif Consensus sequence: AATCAACCCTGGYRATCAAT



Reverse complement motif Consensus sequence: ATTGATMKCCAGGGTTGATT

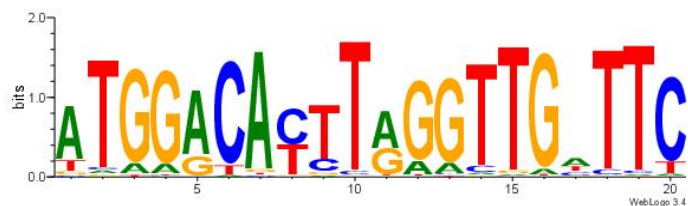


Dataset #: 1
Motif ID: 58
Motif name: Motif 58
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 20
Similarity score: 0.110655

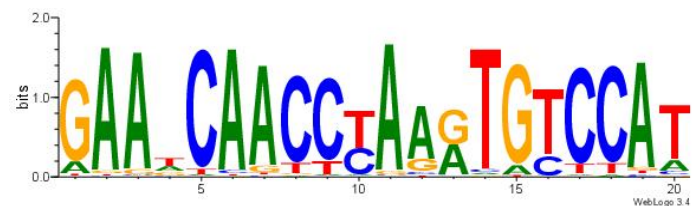
Alignment:

ATGGACAYTTRGGTTGHTTC
ATGGAATAYTATTCAGCCAT

Original motif Consensus sequence: ATGGACAYTTRGGTTGHTTC



Reverse complement motif Consensus sequence: GAAHCAACCKAAKTGTCCAT

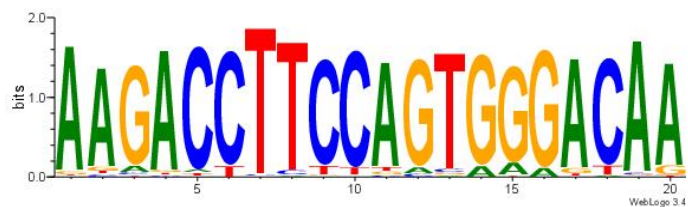


Dataset #: 1
Motif ID: 292
Motif name: Motif 292
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 20
Similarity score: 0.116225

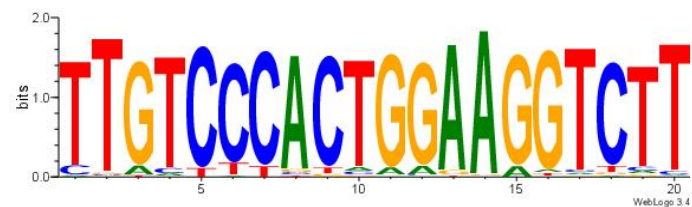
Alignment:

TTGTCCCCTGGAAGGTCTT
ATGGCTGAATAKTATTCCAT

Original motif Consensus sequence: AAGACCTTCCAGTGGGACAA

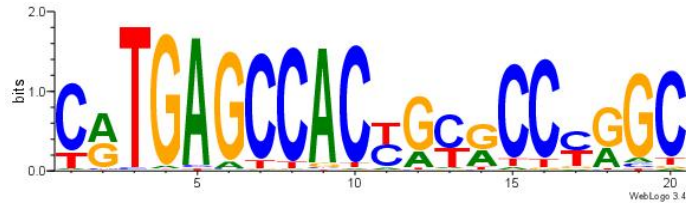


Reverse complement motif Consensus sequence: TTGTCCCCTGGAAGGTCTT

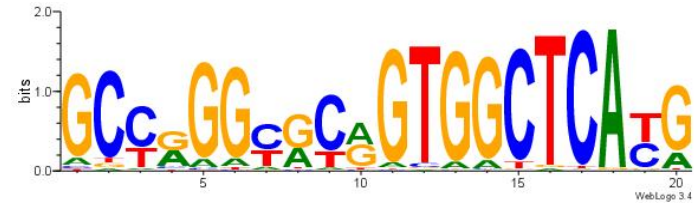


Dataset #: 1 Motif ID: 56 Motif name: Motif 56

Original motif Consensus sequence: CRTGAGCCACYGYRCCYGGC



Reverse complement motif Consensus sequence: GCCKGGMKCMGTGGCTCAKG



Best Matches for Motif ID 56 (Highest to Lowest)

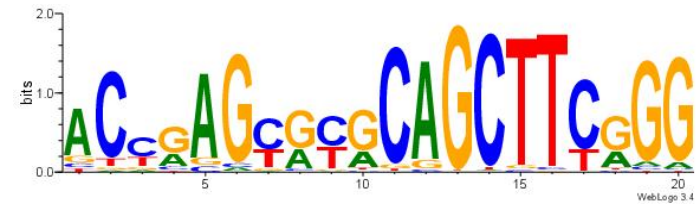
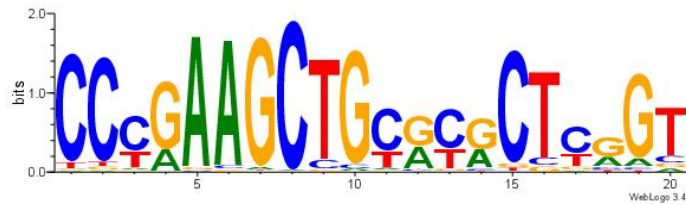
Dataset #:	1
Motif ID:	177
Motif name:	Motif 177
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	20
Similarity score:	0.0865863

Alignment:

```
CCCGAAGCTGCRYRCTCGGT  
CRTGAGCCACYGYRCCYGGC
```

Original motif Consensus sequence: CCCGAAGCTGCRYRCTCGGT

Reverse complement motif Consensus sequence: ACCGAGMKMGCAGCTTCGGG

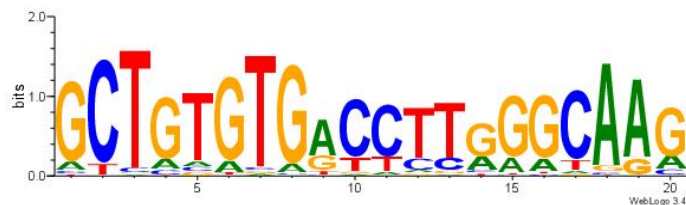


Dataset #: 1
 Motif ID: 112
 Motif name: Motif 112
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.103187

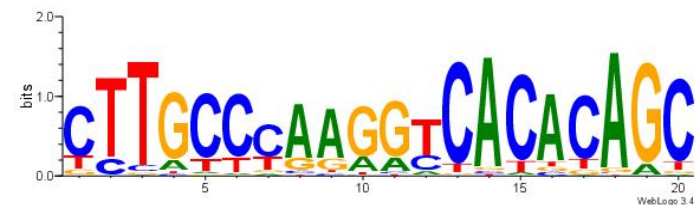
Alignment:

CTTGCCCAAGGTCACACAGC
 CRTGAGCCACYGYRCCYGGC

Original motif Consensus sequence: GCTGTGTGACCTTGGGCAAG



Reverse complement motif Consensus sequence: CTTGCCCAAGGTCACACAGC



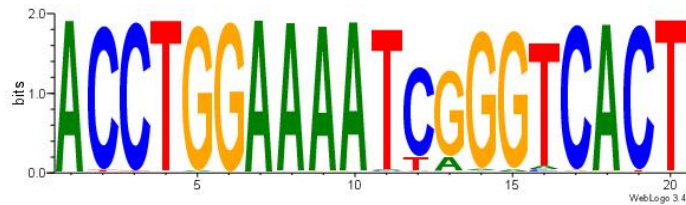
Dataset #: 1

Motif ID: 14
 Motif name: Motif 14
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.10735

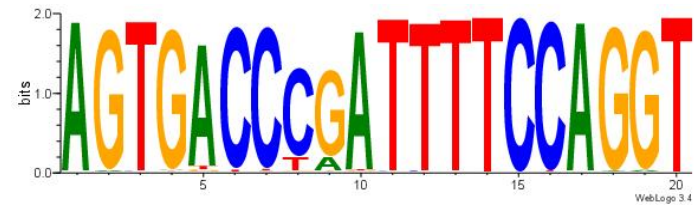
Alignment:

AGTGACCCGATTTTCCAGGT
 CRTGAGCCACYGYRCCYGGC

Original motif Consensus sequence: ACCTGGAAAATCGGGTCACT



Reverse complement motif Consensus sequence: AGTGACCCGATTTTCCAGGT



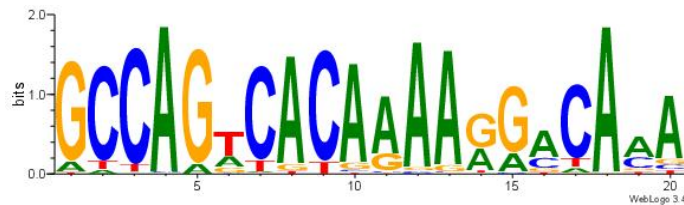
Dataset #: 1
 Motif ID: 145
 Motif name: Motif 145
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 20

Similarity score: 0.113075

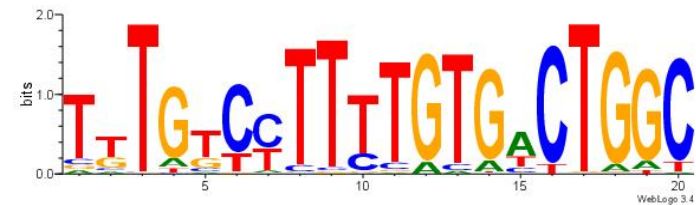
Alignment:

TYTGTCMTTTTGTGACTGGC
CRTGAGCCACYGYRCCYGGC

Original motif Consensus sequence: GCCAGTCACAAAARGACAMA



Reverse complement motif Consensus sequence: TYTGTCMTTTTGTGACTGGC



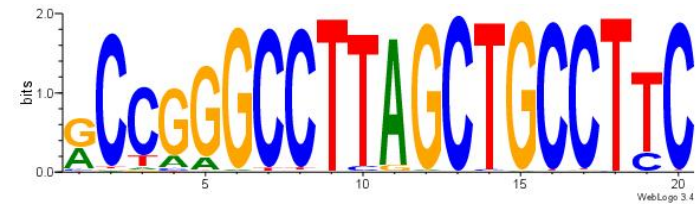
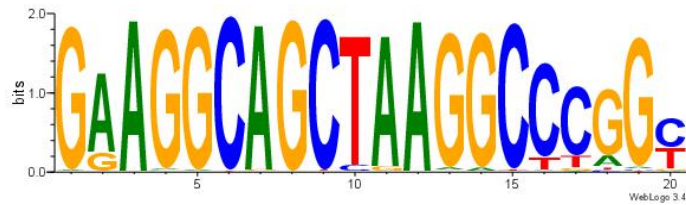
Dataset #: 1
Motif ID: 64
Motif name: Motif 64
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 20
Similarity score: 0.117573

Alignment:

GAAGGCAGCTAAGGCCCGGY
GCCKGGMKCMGTGGCTCAKG

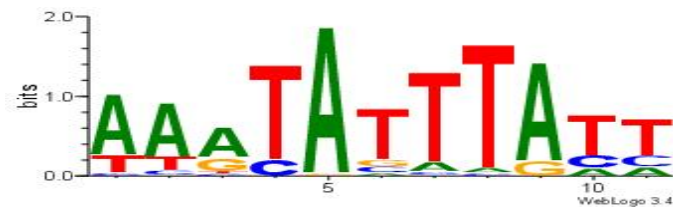
Original motif Consensus sequence: GAAGGCAGCTAAGGCCCGGY

Reverse complement motif Consensus sequence: KCCGGGCCTTAGCTGCCTTC

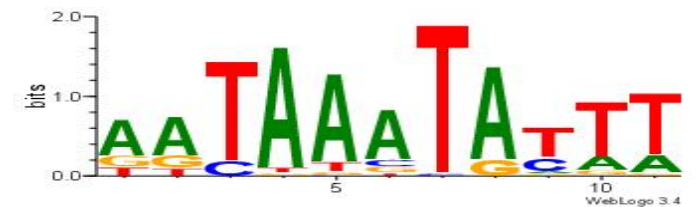


Dataset #: 1 Motif ID: 57 Motif name: Motif 57

Original motif Consensus sequence: AAATATTTATT



Reverse complement motif Consensus sequence: AATAAATATTT

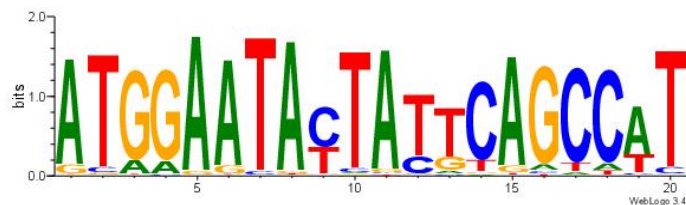


Best Matches for Motif ID 57 (Highest to Lowest)

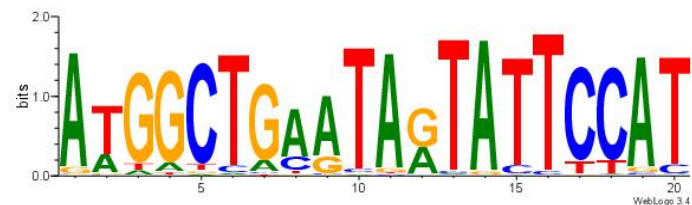
Dataset #:	1
Motif ID:	55
Motif name:	Motif 55
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	4
Number of overlap:	11
Similarity score:	0.0640425

Alignment:
 ATGGCTGAATAKTATTCCAT
 ---AATAAATATTT-----

Original motif Consensus sequence: ATGGAATAYTATTCAGCCAT



Reverse complement motif Consensus sequence: ATGGCTGAATAKTATTCCAT

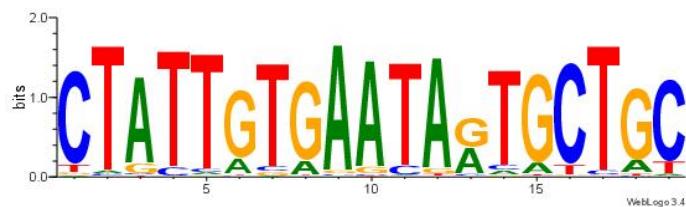


Dataset #: 1
Motif ID: 70
Motif name: Motif 70
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 5
Number of overlap: 11
Similarity score: 0.0653502

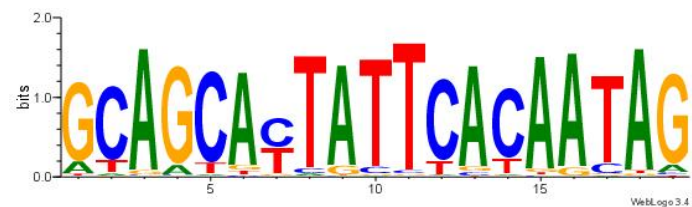
Alignment:

GCAGCAMTATTCACAATAG
----AAATATTTATT----

Original motif Consensus sequence: CTATTGTGAATARTGCTGC



Reverse complement motif Consensus sequence: GCAGCAMTATTCACAATAG

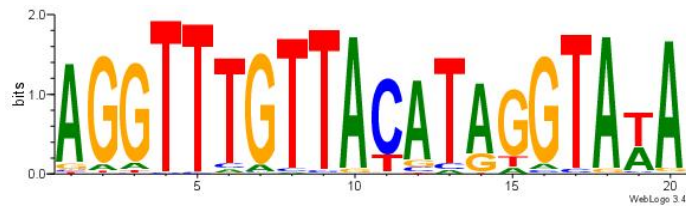


Dataset #: 1
 Motif ID: 137
 Motif name: Motif 137
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 10
 Number of overlap: 11
 Similarity score: 0.0659605

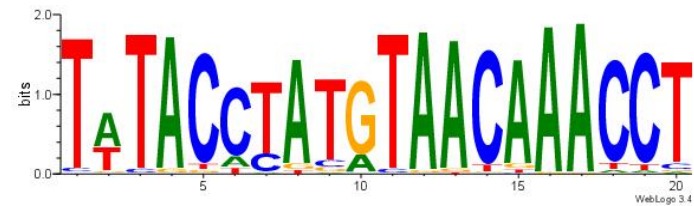
Alignment:

AGGTTTGTTACATAGGTAWA
 -----AAATATTTATT

Original motif Consensus sequence: AGGTTTGTTACATAGGTAWA



Reverse complement motif Consensus sequence: TWTACCTATGTAACAAACCT



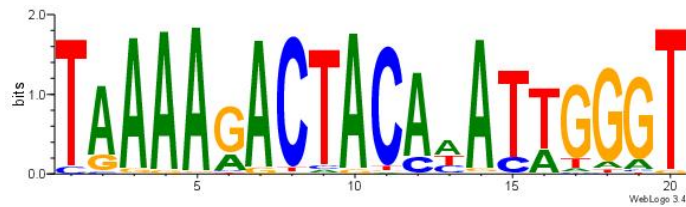
Dataset #: 1
 Motif ID: 195
 Motif name: Motif 195
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 4

Number of overlap: 11
Similarity score: 0.0663702

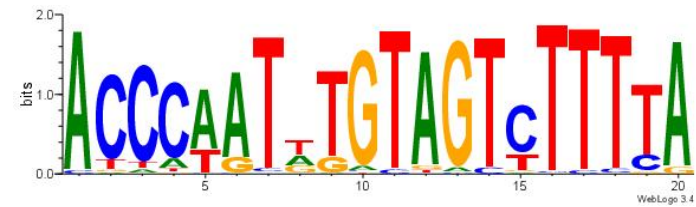
Alignment:

TAAAAGACTACAWATTGGGT
-----AATAAATATTT---

Original motif Consensus sequence: TAAAAGACTACAWATTGGGT



Reverse complement motif Consensus sequence:
ACCCAATWTGTAGTCTTTTA

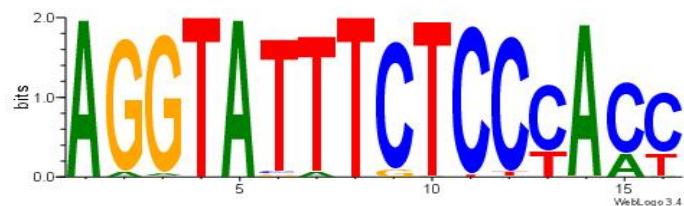


Dataset #: 1
Motif ID: 168
Motif name: Motif 168
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 6
Number of overlap: 11
Similarity score: 0.066951

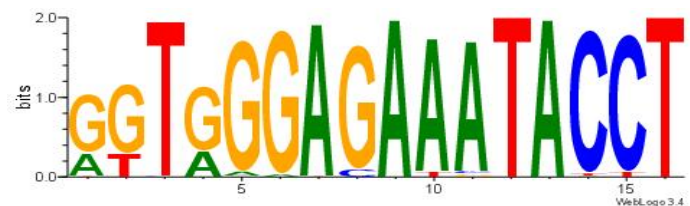
Alignment:

AGGTATTTCTCCCACC
AAATATTTATT-----

Original motif Consensus sequence: AGGTATTCTCCACC

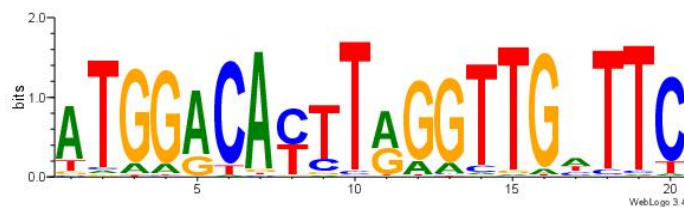


Reverse complement motif Consensus sequence: GGTGGGAGAAATACCT

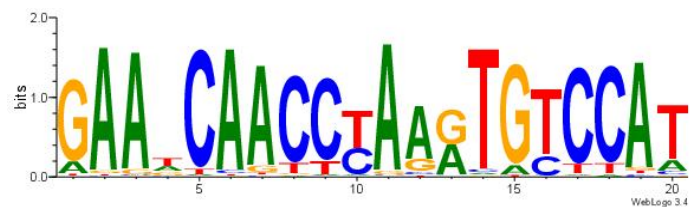


Dataset #: 1 Motif ID: 58 Motif name: Motif 58

Original motif Consensus sequence: ATGGACAYTTRGGTTGHTTC



Reverse complement motif Consensus sequence: GAAHCAACCKAAKTGTCCAT



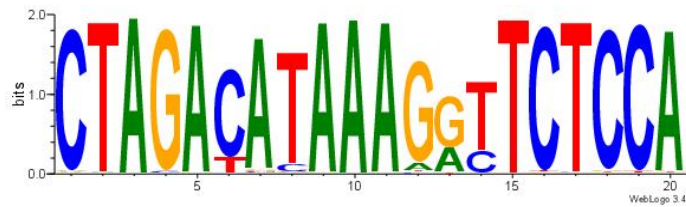
Best Matches for Motif ID 58 (Highest to Lowest)

Dataset #:	1
Motif ID:	85
Motif name:	Motif 85
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	20
Similarity score:	0.107048

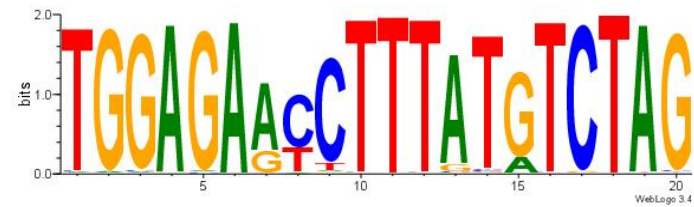
Alignment:

CTAGACATAAAGGTTCTCCA
ATGGACAYTTRGGTTGHTTC

Original motif Consensus sequence: CTAGACATAAAGGTTCTCCA



Reverse complement motif Consensus sequence:
TGGAGAACCTTTATGTCTAG



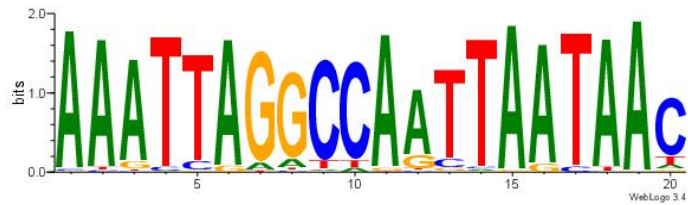
Dataset #:	1
Motif ID:	308
Motif name:	Motif 308
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	20
Similarity score:	0.10886

Alignment:

GTTATTAATTGGCCTAATTT
ATGGACAYTTRGGTTGHTTC

Original motif Consensus sequence: AAATTAGGCCAATTAATAAC

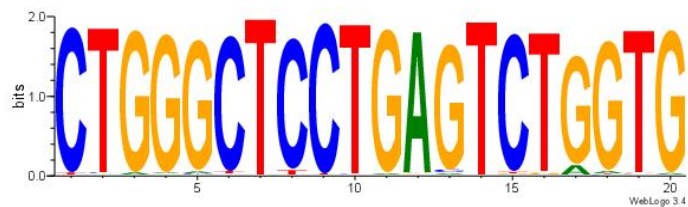
Reverse complement motif Consensus sequence:
GTTATTAATTGGCCTAATTT



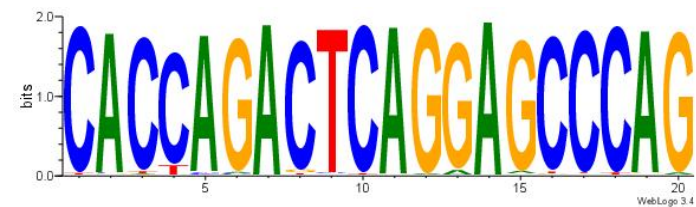
Dataset #: 1
 Motif ID: 67
 Motif name: Motif 67
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.111911

Alignment:
 CTGGGCTCCTGAGTCTGGTG
 ATGGACAYTTRGGTTGHTTC

Original motif Consensus sequence: CTGGGCTCCTGAGTCTGGTG



Reverse complement motif Consensus sequence: CACCAGACTCAGGAGCCCAG



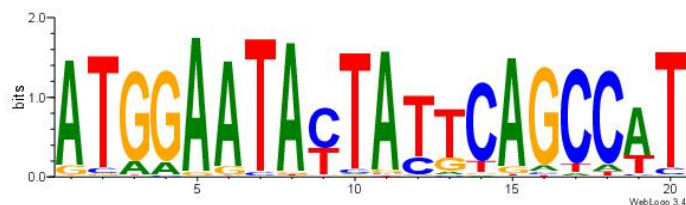
Dataset #: 1

Motif ID: 55
 Motif name: Motif 55
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.111988

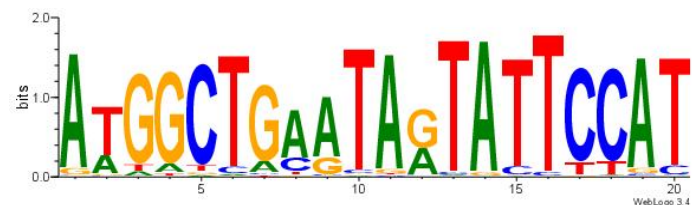
Alignment:

ATGGAATAYTATTCAGCCAT
 ATGGACAYTTRGGTTGHTTC

Original motif Consensus sequence: ATGGAATAYTATTCAGCCAT



Reverse complement motif Consensus sequence: ATGGCTGAATAKTATTCCAT



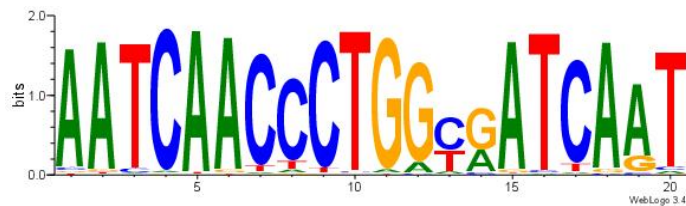
Dataset #: 1
 Motif ID: 170
 Motif name: Motif 170
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 20

Similarity score: 0.112726

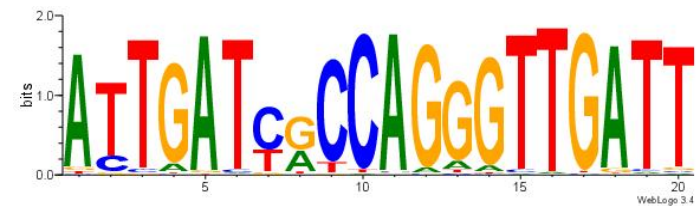
Alignment:

ATTGATMKCCAGGGTTGATT
ATGGACAYTTRGGTTGHTTC

Original motif Consensus sequence: AATCAACCCTGGYRATCAAT

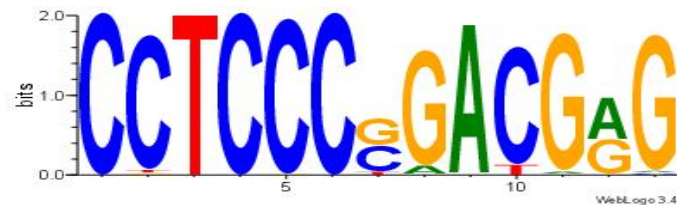


Reverse complement motif Consensus sequence: ATTGATMKCCAGGGTTGATT

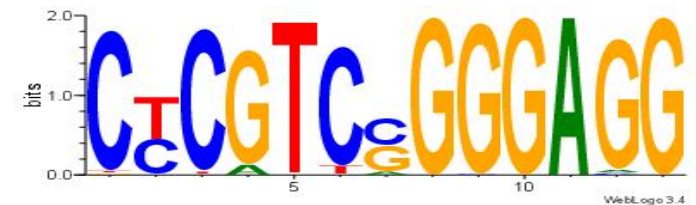


Dataset #: 1 Motif ID: 59 Motif name: Motif 59

Original motif Consensus sequence: CCTCCSGACGRG



Reverse complement motif Consensus sequence: CKCGTCSGGAGG



Best Matches for Motif ID 59 (Highest to Lowest)

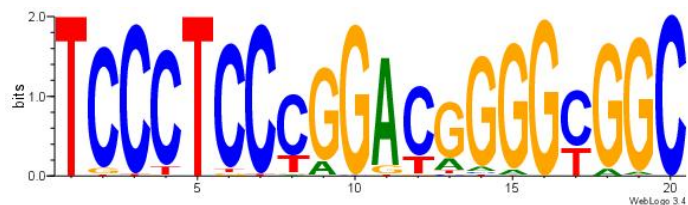
Dataset #:	1
Motif ID:	155
Motif name:	Motif 155
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif

Direction: Forward
 Position number: 3
 Number of overlap: 13
 Similarity score: 0.0335165

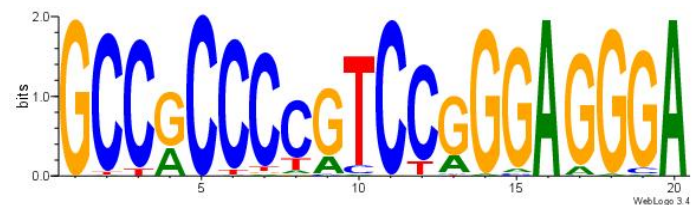
Alignment:

TCCCTCCCGGACGGGGYGGC
 --CCTCCCSGACGRG-----

Original motif Consensus sequence: TCCCTCCCGGACGGGGYGGC



Reverse complement motif Consensus sequence: GCCKCCCCGTCCGGGAGGGA

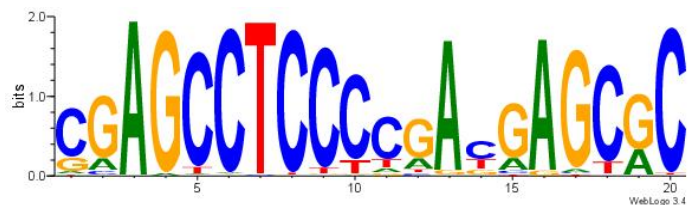


Dataset #: 1
 Motif ID: 108
 Motif name: Motif 108
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 4
 Number of overlap: 13
 Similarity score: 0.0365108

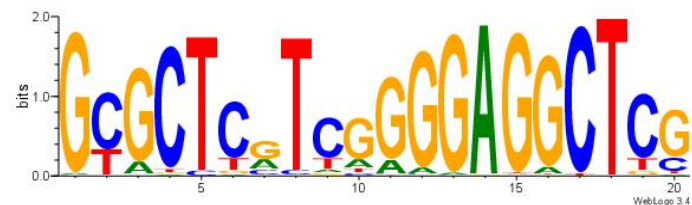
Alignment:

GCGCTCKTCGGGGAGGCTCG
 ---CKCGTCSGGGAGG----

Original motif Consensus sequence: CGAGCCTCCCCGAYGAGCGC



Reverse complement motif Consensus sequence: GCGCTCKTCGGGGAGGCTCG

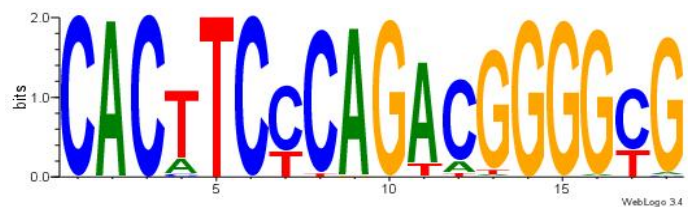


Dataset #: 1
Motif ID: 27
Motif name: Motif 27
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 3
Number of overlap: 13
Similarity score: 0.0569667

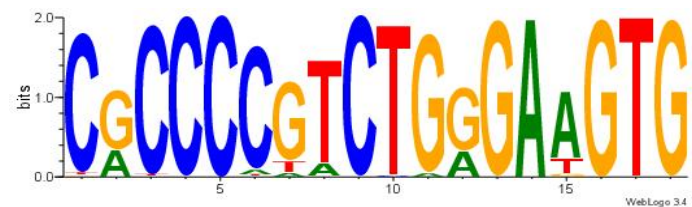
Alignment:

CACTTCCCAGACGGGGCG
--CCTCCCSGACGRG---

Original motif Consensus sequence: CACTTCCCAGACGGGGCG



Reverse complement motif Consensus sequence: CGCCCCGTCTGGGAAGTG

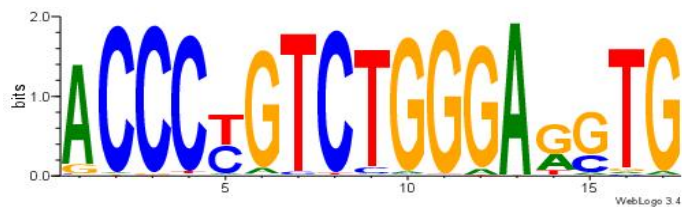


Dataset #: 1
 Motif ID: 95
 Motif name: Motif 95
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 13
 Similarity score: 0.0606018

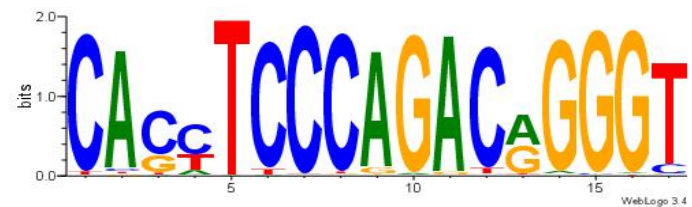
Alignment:

ACCCYGTCTGGGAGGTG
 --CKCGTCSGGGAGG--

Original motif Consensus sequence: ACCCYGTCTGGGAGGTG



Reverse complement motif Consensus sequence: CACCTCCCAGACMGGGT



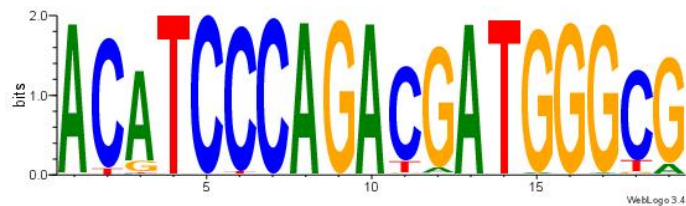
Dataset #: 1
 Motif ID: 36
 Motif name: Motif 36
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 6

Number of overlap: 13
Similarity score: 0.0628382

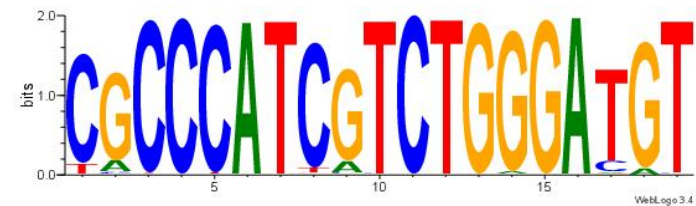
Alignment:

CGCCCATCGTCTGGGATGT
-----CKCGTCSGGGAGG-

Original motif Consensus sequence: ACATCCCAGACGATGGGCG

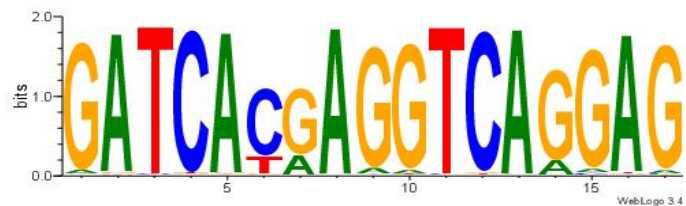


Reverse complement motif Consensus sequence:
CGCCCATCGTCTGGGATGT

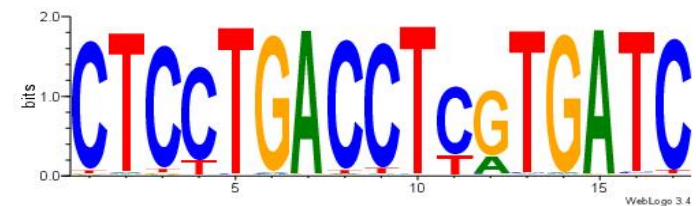


Dataset #: 1 Motif ID: 60 Motif name: Motif 60

Original motif Consensus sequence: GATCAGAGGTCAGGAG



Reverse complement motif Consensus sequence:
CTCCTGACCTCGTGATC



Best Matches for Motif ID 60 (Highest to Lowest)

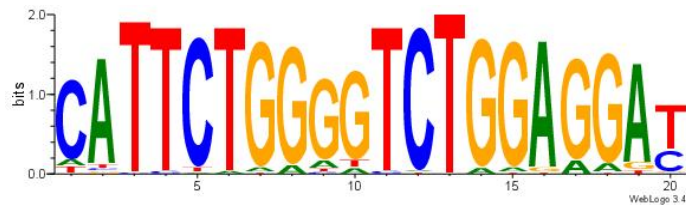
Dataset #: 1
Motif ID: 309
Motif name: Motif 309

Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	4
Number of overlap:	17
Similarity score:	0.08025

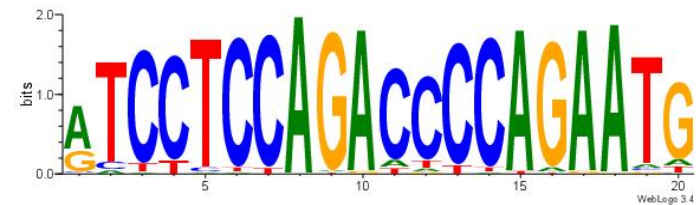
Alignment:

```
CATTCTGGGGTCTGGAGGAY
GATCACGAGGTCAGGAG---
```

Original motif Consensus sequence: CATTCTGGGGTCTGGAGGAY



Reverse complement motif Consensus sequence: MTCCTCCAGACCCAGAAATG

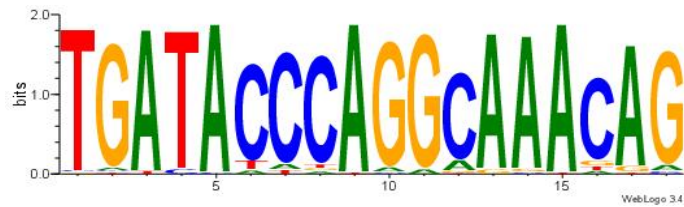


Dataset #:	1
Motif ID:	290
Motif name:	Motif 290
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	2
Number of overlap:	17
Similarity score:	0.0894593

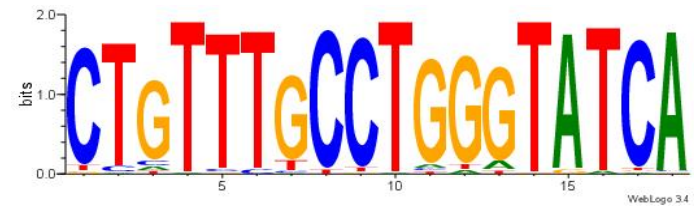
Alignment:

CTGTTTGCCTGGGTATCA
CTCCTGACCTCGTGATC-

Original motif Consensus sequence: TGATACCCAGGCAAACAG



Reverse complement motif Consensus sequence:
CTGTTTGCCTGGGTATCA



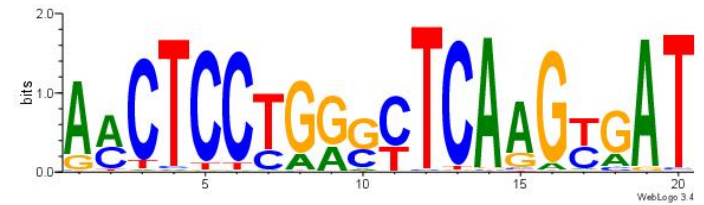
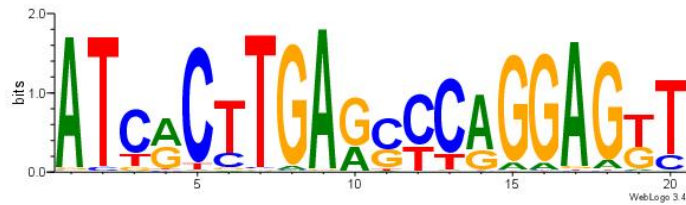
Dataset #: 1
Motif ID: 8
Motif name: Motif 8
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 3
Number of overlap: 17
Similarity score: 0.0913916

Alignment:

ATCRCTTGAGSYCAGGAGKT
-GATCACGAGGTCAGGAG--

Original motif Consensus sequence: ATCRCTTGAGSYCAGGAGKT

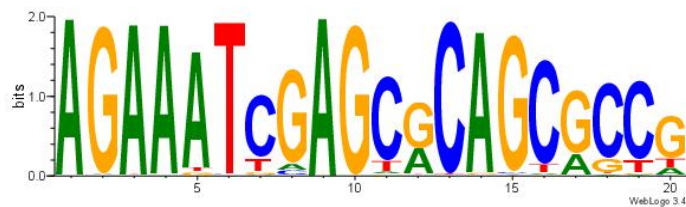
Reverse complement motif Consensus sequence:
ARCTCCTGKSCTCAAGKGAT



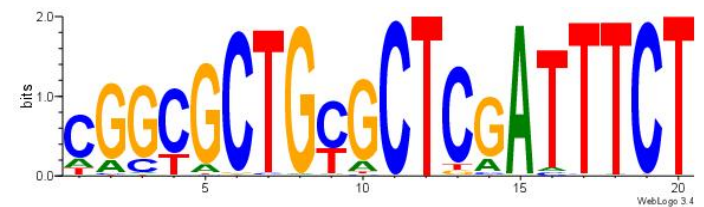
Dataset #: 1
 Motif ID: 65
 Motif name: Motif 65
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3
 Number of overlap: 17
 Similarity score: 0.101368

Alignment:
 CGGCGCTGMGCTCGATTCT
 --CTCCTGACCTCGTGATC--

Original motif Consensus sequence: AGAAATCGAGCRCAGCGCCG



Reverse complement motif Consensus sequence: CGGCGCTGMGCTCGATTCT



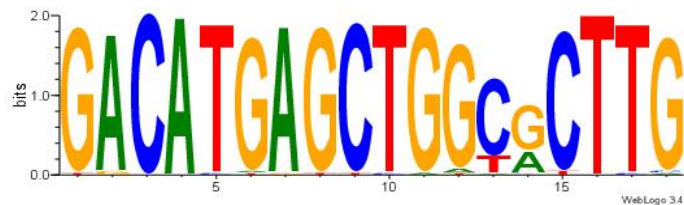
Dataset #: 1

Motif ID: 306
 Motif name: Motif 306
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 17
 Similarity score: 0.1095

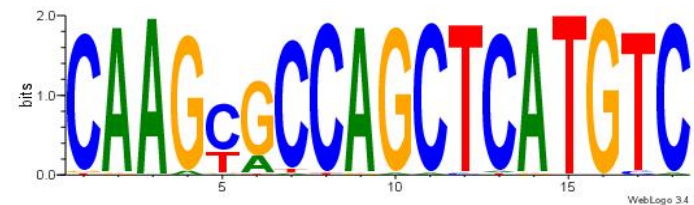
Alignment:

GACATGAGCTGGCGCTTG
 CTCCTGACCTCGTGATC-

Original motif Consensus sequence: GACATGAGCTGGCGCTTG

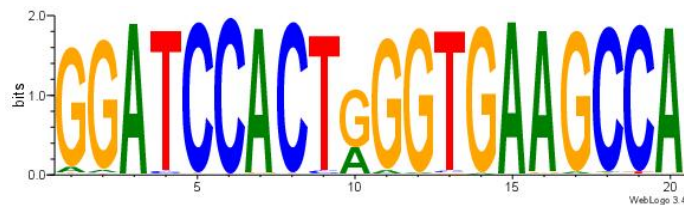


Reverse complement motif Consensus sequence: CAAGCGCCAGCTCATGTC

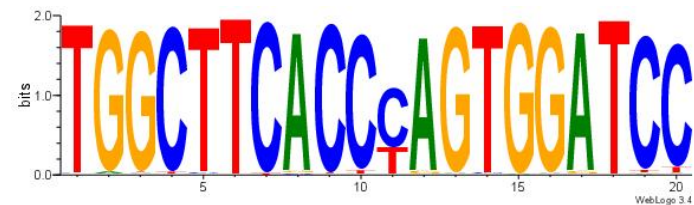


Dataset #: 1 Motif ID: 61 Motif name: Motif 61

Original motif Consensus sequence: GGATCCACTGGGTGAAGCCA



Reverse complement motif Consensus sequence: TGGCTTCAACCAGTGGATCC



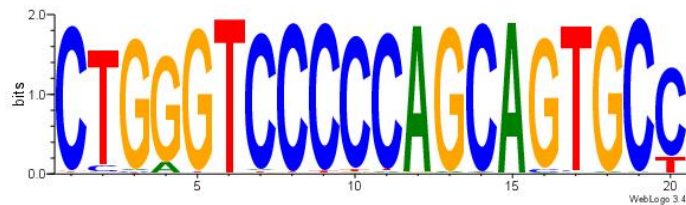
Best Matches for Motif ID 61 (Highest to Lowest)

Dataset #: 1
Motif ID: 84
Motif name: Motif 84
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 20
Similarity score: 0.110456

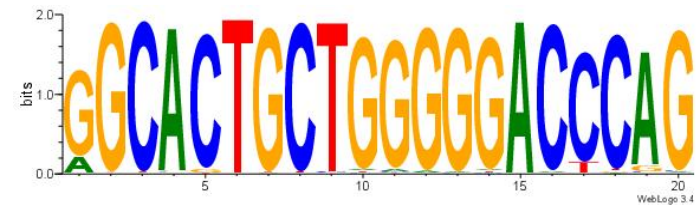
Alignment:

```
GGCACTGCTGGGGGACCCAG  
GGATCCACTGGGTGAAGCCA
```

Original motif Consensus sequence: CTGGGTCCCCCAGCAGTGCC



Reverse complement motif Consensus sequence: GGCACTGCTGGGGGACCCAG



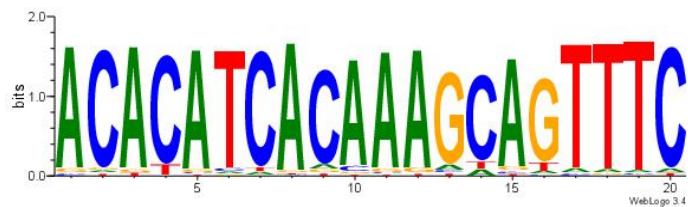
Dataset #: 1
Motif ID: 202
Motif name: Motif 202
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif

Direction: Backward
Position number: 1
Number of overlap: 20
Similarity score: 0.116364

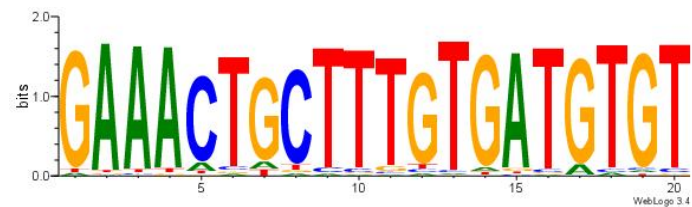
Alignment:

ACACATCACAAAGCAGTTTC
TGGCTTCACCCAGTGGATCC

Original motif Consensus sequence: ACACATCACAAAGCAGTTTC



Reverse complement motif Consensus sequence: GAAACTGCTTTGTGATGTGT

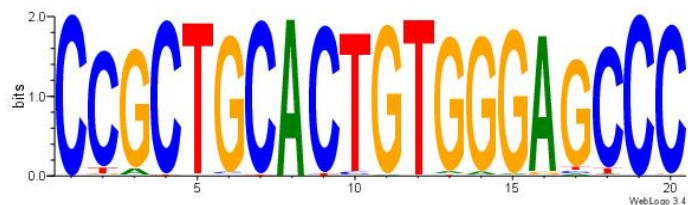


Dataset #: 1
Motif ID: 144
Motif name: Motif 144
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 20
Similarity score: 0.117839

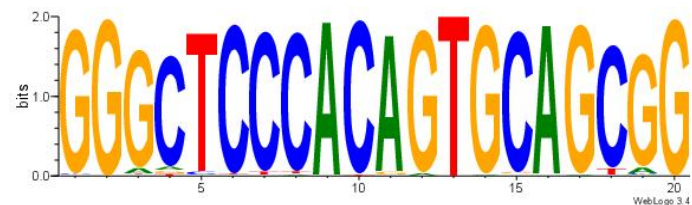
Alignment:

CCGCTGCACTGTGGGAGCCC
TGGCTTCACCCAGTGGATCC

Original motif Consensus sequence: CCGCTGCACTGTGGGAGCCC



Reverse complement motif Consensus sequence: GGGCTCCCACAGTGCAGCGG

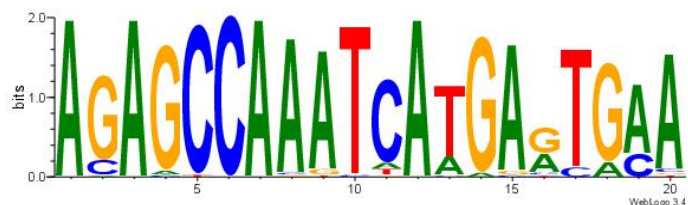


Dataset #: 1
Motif ID: 349
Motif name: Motif 349
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 20
Similarity score: 0.125399

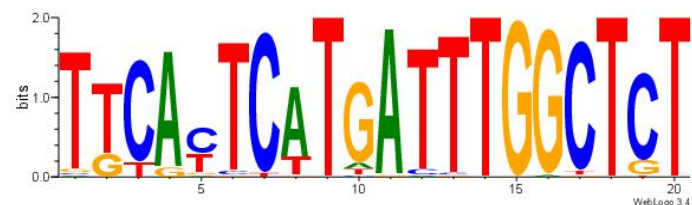
Alignment:

AGAGCCAAATCATGARTGAA
GGATCCACTGGGTGAAGCCA

Original motif Consensus sequence: AGAGCCAAATCATGARTGAA



Reverse complement motif Consensus sequence: TTCAMTCATGATTTGGCTCT

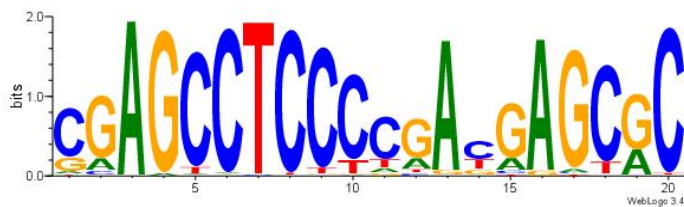


Dataset #: 1
 Motif ID: 108
 Motif name: Motif 108
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.128668

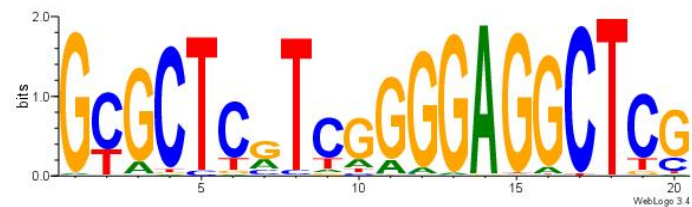
Alignment:

CGAGCCTCCCCGAYGAGCGC
 GGATCCACTGGGTGAAGCCA

Original motif Consensus sequence: CGAGCCTCCCCGAYGAGCGC



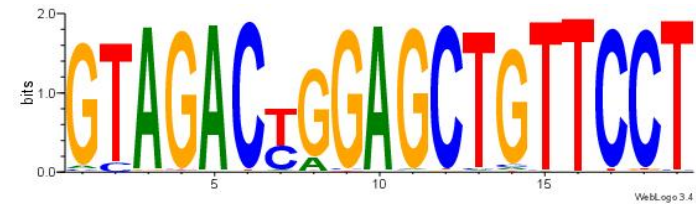
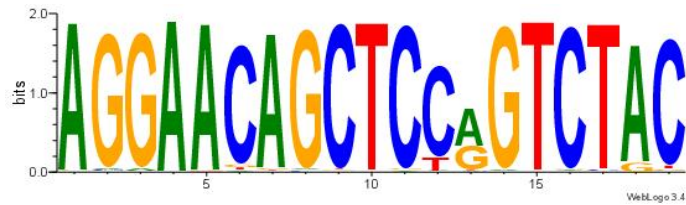
Reverse complement motif Consensus sequence: GCGCTCKTCGGGGAGGCTCG



Dataset #: 1 Motif ID: 62 Motif name: Motif 62

Original motif Consensus sequence: AGGAACAGCTCCRGCTAC

Reverse complement motif Consensus sequence: GTAGACKGGAGCTGTTCT

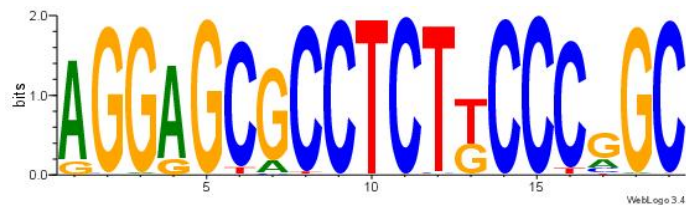


Best Matches for Motif ID 62 (Highest to Lowest)

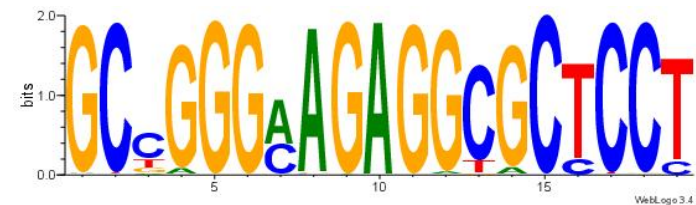
Dataset #: 1
 Motif ID: 30
 Motif name: Motif 30
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 19
 Similarity score: 0.108892

Alignment:
 AGGAGCGCCTCTKCCCGGC
 AGGAACAGCTCCRGTCTAC

Original motif Consensus sequence: AGGAGCGCCTCTKCCCGGC



Reverse complement motif Consensus sequence: GCCGGGRAGAGGCGCTCT

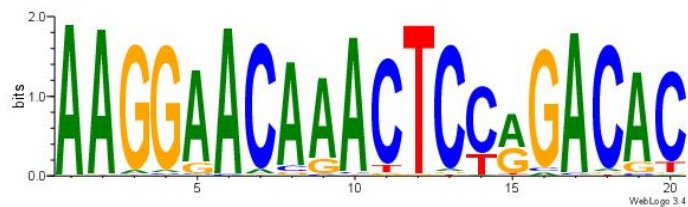


Dataset #: 1
 Motif ID: 234
 Motif name: Motif 234
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 19
 Similarity score: 0.110299

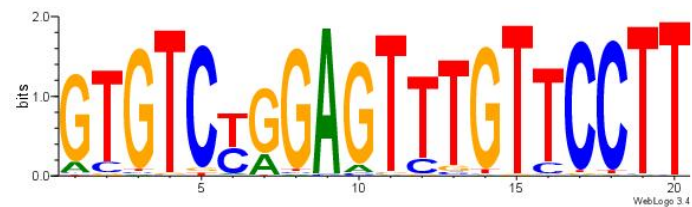
Alignment:

AAGGAACAAACTCCRGACAC
 -AGGAACAGCTCCRGCTCTAC

Original motif Consensus sequence: AAGGAACAAACTCCRGACAC



Reverse complement motif Consensus sequence: GTGTCGGAGTTTGTTCCTT



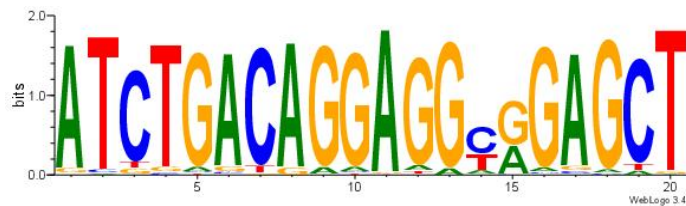
Dataset #: 1
 Motif ID: 165
 Motif name: Motif 165
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1

Number of overlap: 19
Similarity score: 0.116495

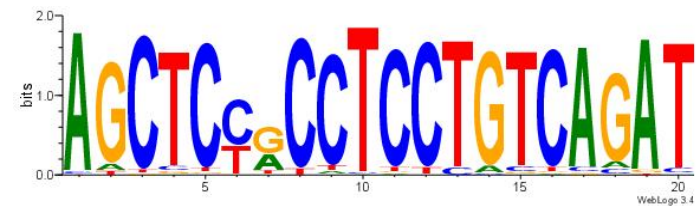
Alignment:

ATCTGACAGGAGGYRGAGCT
-GTAGACKGGAGCTGTTTCCT

Original motif Consensus sequence: ATCTGACAGGAGGYRGAGCT



Reverse complement motif Consensus sequence:
AGCTCMKCCTCCTGTCAGAT

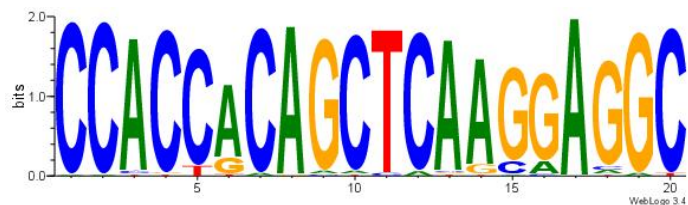


Dataset #: 1
Motif ID: 331
Motif name: Motif 331
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 19
Similarity score: 0.118299

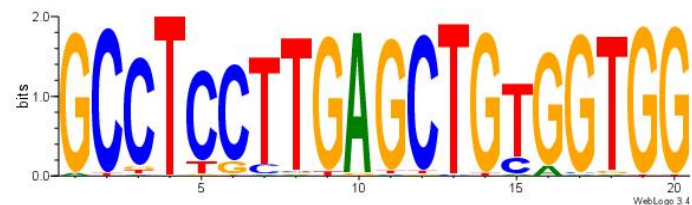
Alignment:

GCCTCCTTGAGCTGTGGTGG
GTAGACKGGAGCTGTTTCCT-

Original motif Consensus sequence: CCACCACAGCTCAAGGAGGC



Reverse complement motif Consensus sequence: GCCTCCTTGAGCTGTGGTGG

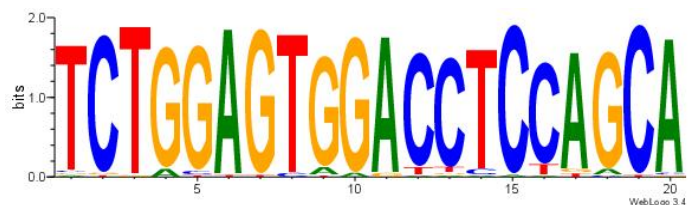


Dataset #: 1
Motif ID: 350
Motif name: Motif 350
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 2
Number of overlap: 19
Similarity score: 0.120152

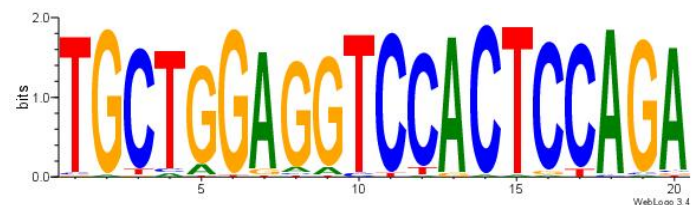
Alignment:

TCTGGAGTGGACCTCCAGCA
-GTAGACKGGAGCTGTTTCCT

Original motif Consensus sequence: TCTGGAGTGGACCTCCAGCA

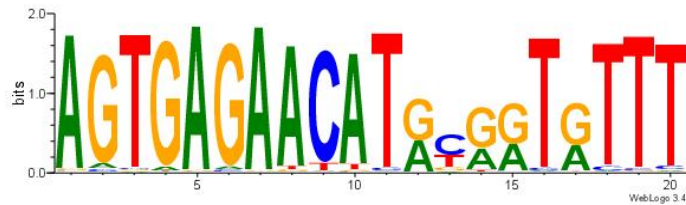


Reverse complement motif Consensus sequence: TGCTGGAGTCCACTCCAGA

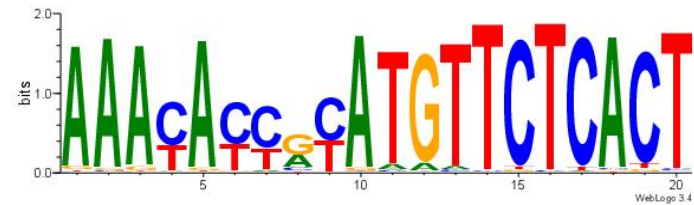


Dataset #: 1 Motif ID: 63 Motif name: Motif 63

Original motif Consensus sequence: AGTGAGAACATRYRRTTTT



Reverse complement motif Consensus sequence: AAAMAMMKMATGTTCTCACT



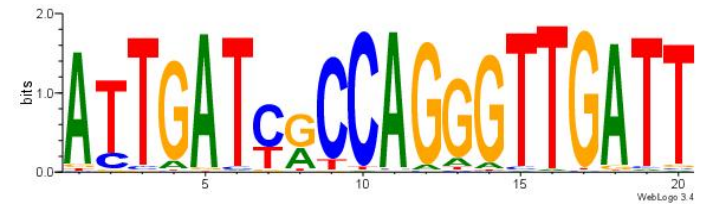
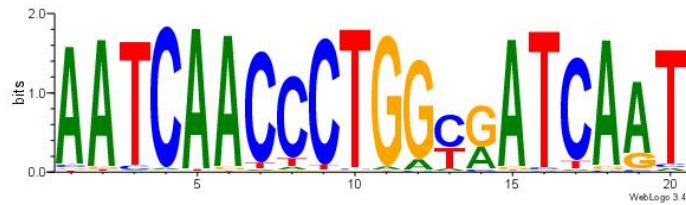
Best Matches for Motif ID 63 (Highest to Lowest)

Dataset #:	1
Motif ID:	170
Motif name:	Motif 170
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	20
Similarity score:	0.10502

Alignment:
AATCAACCCTGGYRATCAAT
AAAMAMMKMATGTTCTCACT

Original motif Consensus sequence: AATCAACCCTGGYRATCAAT

Reverse complement motif Consensus sequence: ATTGATMKCCAGGGTTGATT

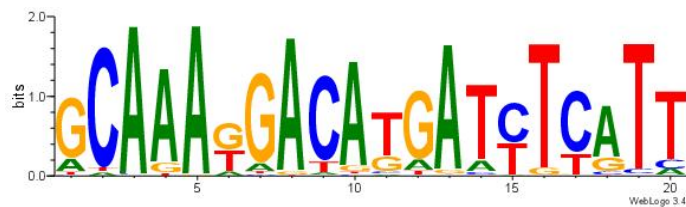


Dataset #: 1
 Motif ID: 99
 Motif name: Motif 99
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.106569

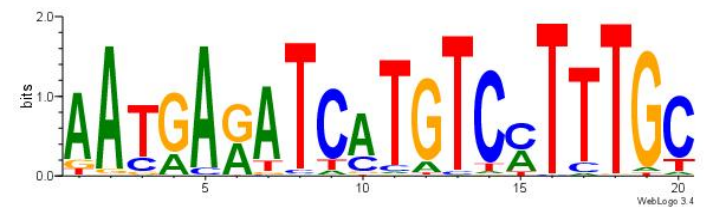
Alignment:

GCAAAGACATGATYTCATT
 AAAMAMMKMATGTTCTCACT

Original motif Consensus sequence: GCAAAGACATGATYTCATT



Reverse complement motif Consensus sequence: AATGAKATCATGTCYTTTGC



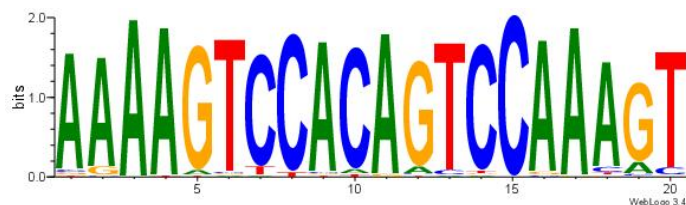
Dataset #: 1

Motif ID: 171
 Motif name: Motif 171
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.121267

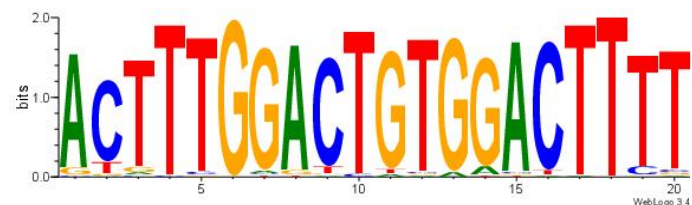
Alignment:

AAAAGTCCACAGTCCAAAGT
 AAAMAMMKMATGTTCTCACT

Original motif Consensus sequence: AAAAGTCCACAGTCCAAAGT



Reverse complement motif Consensus sequence: ACTTTGGACTGTGGACTTTT



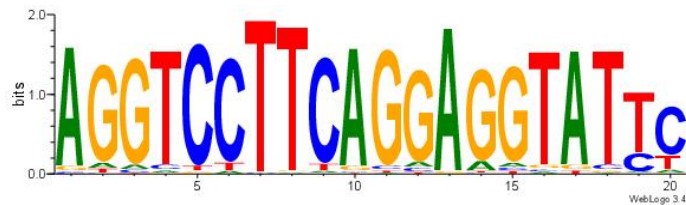
Dataset #: 1
 Motif ID: 179
 Motif name: Motif 179
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 20

Similarity score: 0.121353

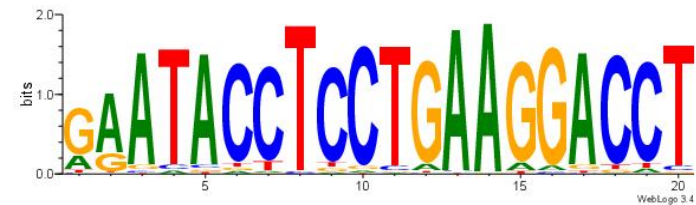
Alignment:

AGGTCCTTCAGGAGGTATTC
AGTGAGAACATRYRRTRTTT

Original motif Consensus sequence: AGGTCCTTCAGGAGGTATTC



Reverse complement motif Consensus sequence:
GAATACCTCCTGAAGGACCT



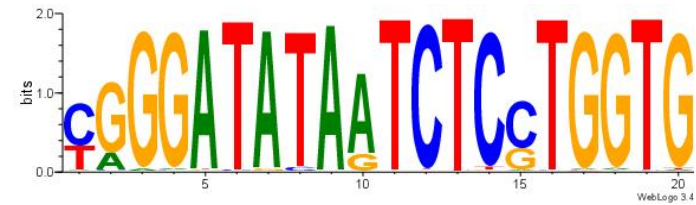
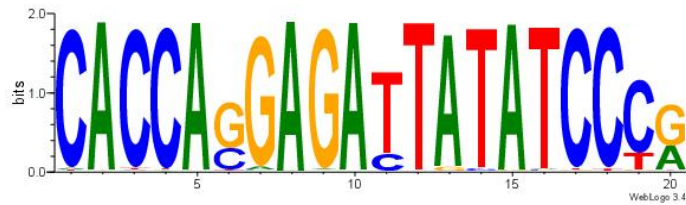
Dataset #: 1
Motif ID: 19
Motif name: Motif 19
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 20
Similarity score: 0.123743

Alignment:

CACCAGGAGATTATATCCCR
AAAMAMMKMATGTTCTCACT

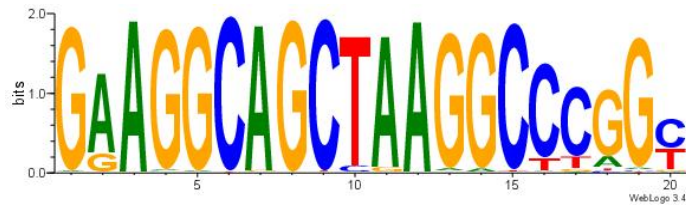
Original motif Consensus sequence: CACCAGGAGATTATATCCCR

Reverse complement motif Consensus sequence:
MGGATATAATCTCCTGGTG

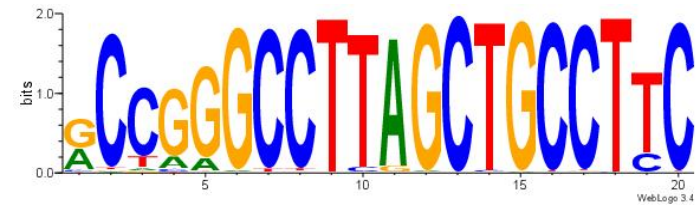


Dataset #: 1 Motif ID: 64 Motif name: Motif 64

Original motif Consensus sequence: GAAGGCAGCTAAGGCCCGGY



Reverse complement motif Consensus sequence: KCCGGGCCTTAGCTGCCTTC



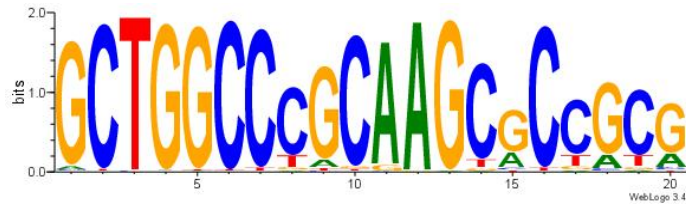
Best Matches for Motif ID 64 (Highest to Lowest)

Dataset #:	1
Motif ID:	100
Motif name:	Motif 100
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	20
Similarity score:	0.088142

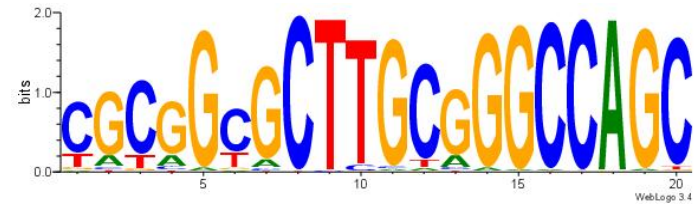
Alignment:

CGCGGCGCTTGCGGGCCAGC
KCCGGGCCTTAGCTGCCTTC

Original motif Consensus sequence: GCTGGCCCGCAAGCGCCGCG



Reverse complement motif Consensus sequence:
CGCGGCGCTTGCGGGCCAGC



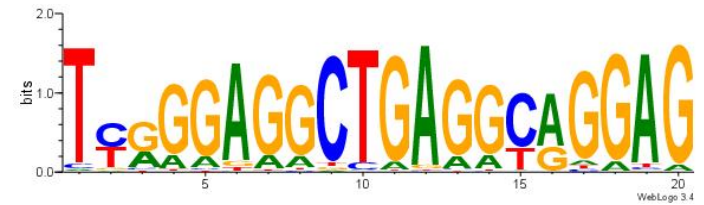
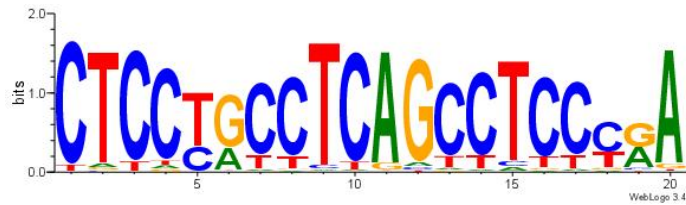
Dataset #: 1
Motif ID: 26
Motif name: Motif 26
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 20
Similarity score: 0.0936635

Alignment:

CTCCTGCCTCAGCCTCCRA
KCCGGGCCTTAGCTGCCTTC

Original motif Consensus sequence: CTCCTGCCTCAGCCTCCRA

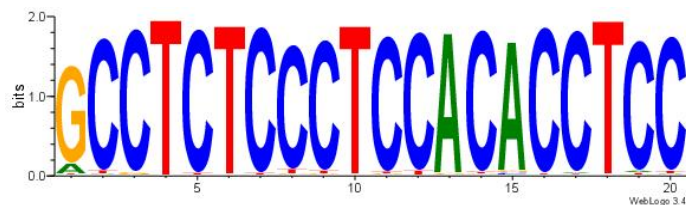
Reverse complement motif Consensus sequence:
TMGGGAGGCTGAGGCAGGAG



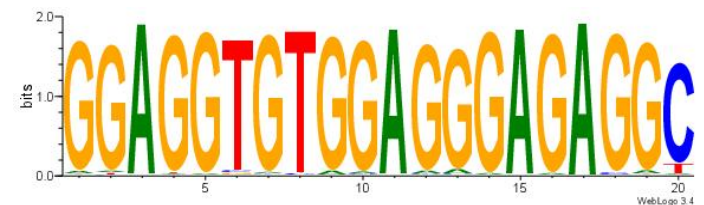
Dataset #: 1
 Motif ID: 105
 Motif name: Motif 105
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.0969655

Alignment:
 GGAGGTGTGGAGGGAGAGGC
 GAAGGCAGCTAAGGCCCGY

Original motif Consensus sequence: GCCTCTCCCTCCACACCTCC



Reverse complement motif Consensus sequence: GGAGGTGTGGAGGGAGAGGC



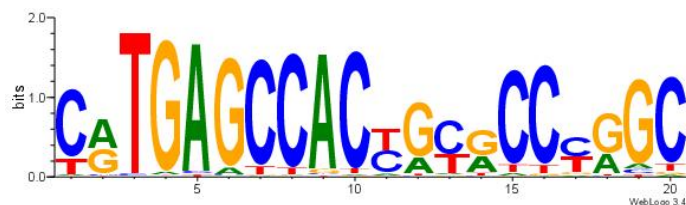
Dataset #: 1

Motif ID: 56
 Motif name: Motif 56
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.100994

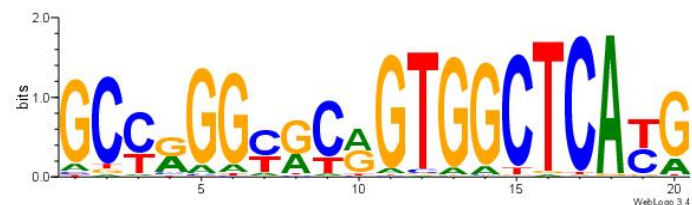
Alignment:

CRTGAGCCACYGYRCCYGGC
 KCCGGGCCTTAGCTGCCTTC

Original motif Consensus sequence: CRTGAGCCACYGYRCCYGGC



Reverse complement motif Consensus sequence: GCKGGMKCMGTGGCTCAKG



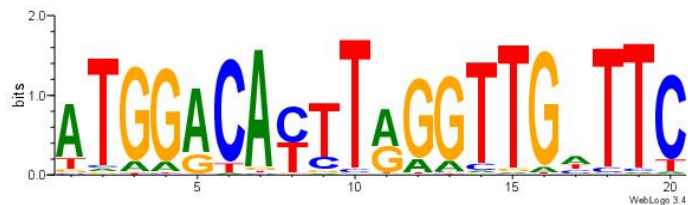
Dataset #: 1
 Motif ID: 58
 Motif name: Motif 58
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 20

Similarity score: 0.102861

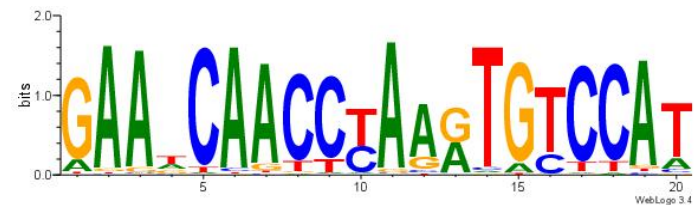
Alignment:

GAAHCAACCKAAKTGTCCAT
GAAGGCAGCTAAGGCCCGY

Original motif Consensus sequence: ATGGACAYTTRGGTTGHTTC

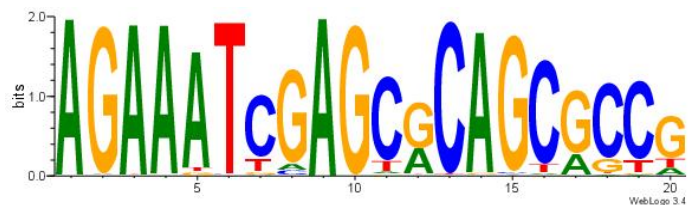


Reverse complement motif Consensus sequence: GAAHCAACCKAAKTGTCCAT

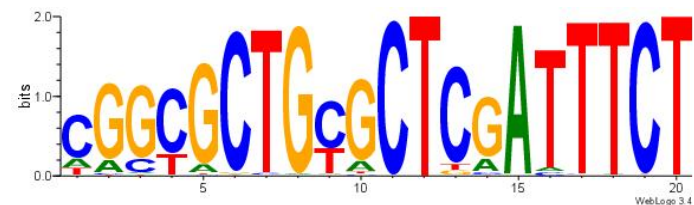


Dataset #: 1 Motif ID: 65 Motif name: Motif 65

Original motif Consensus sequence: AGAAATCGAGCRCAGCGCCG



Reverse complement motif Consensus sequence: CGGCGCTGMGCTCGATTTCT



Best Matches for Motif ID 65 (Highest to Lowest)

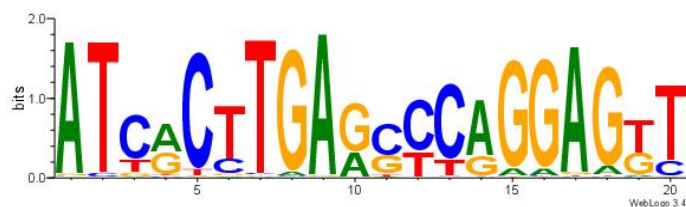
Dataset #:	1
Motif ID:	8
Motif name:	Motif 8
Matching format of first motif:	Reverse Complement

Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.126973

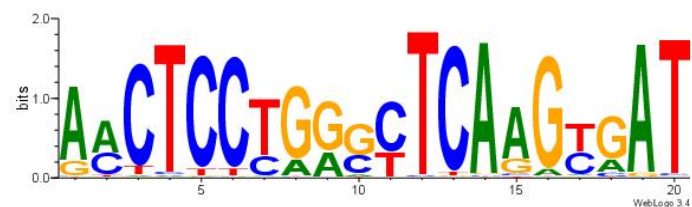
Alignment:

ARCTCCTGKSCTCAAGKGAT
 CGGCGCTGMGCTCGATTTCT

Original motif Consensus sequence: ATCRCTTGAGSYCAGGAGKT



Reverse complement motif Consensus sequence:
 ARCTCCTGKSCTCAAGKGAT

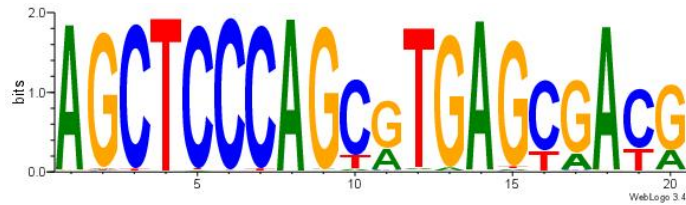


Dataset #: 1
 Motif ID: 48
 Motif name: Motif 48
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.134703

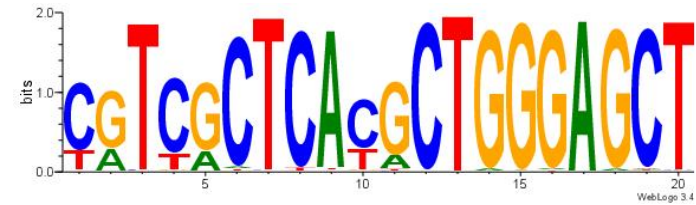
Alignment:

CGTCGCTCACGCTGGGAGCT
CGGCGCTGMGCTCGATTTCT

Original motif Consensus sequence: AGCTCCCAGCGTGAGCGACG



Reverse complement motif Consensus sequence:
CGTCGCTCACGCTGGGAGCT

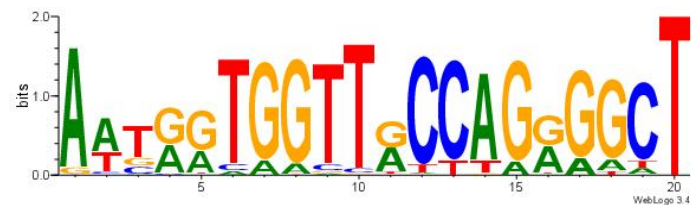
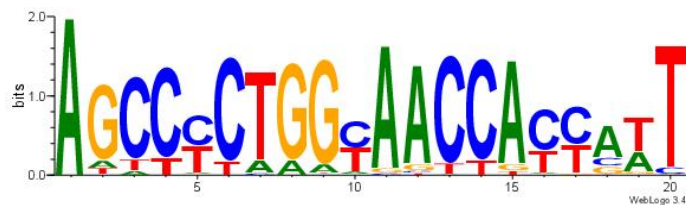


Dataset #: 1
Motif ID: 139
Motif name: Motif 139
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 20
Similarity score: 0.135709

Alignment:
AGCCYCTGGYAACCAYYAWT
CGGCGCTGMGCTCGATTTCT

Original motif Consensus sequence: AGCCYCTGGYAACCAYYAWT

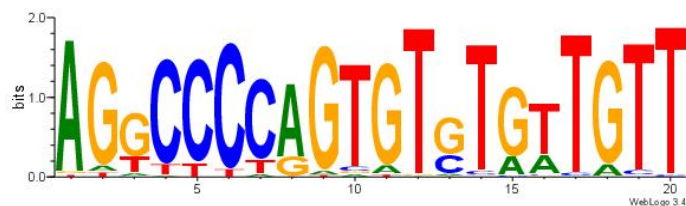
Reverse complement motif Consensus sequence:
AWTKKTGGTTKCCAGKGGCT



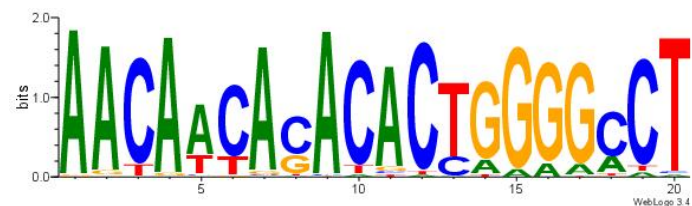
Dataset #: 1
 Motif ID: 176
 Motif name: Motif 176
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.135953

Alignment:
 AGCCCCAGTGTSTGTTGTT
 CGGCGCTGMGCTCGATTTCT

Original motif Consensus sequence: AGCCCCAGTGTSTGTTGTT



Reverse complement motif Consensus sequence: AACACASACTGGGGCCT



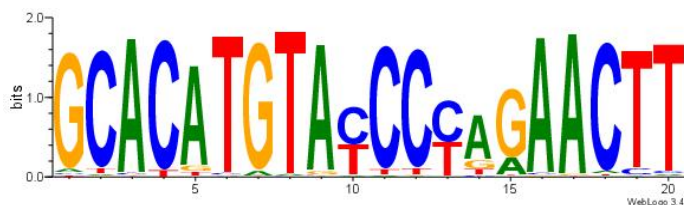
Dataset #: 1

Motif ID: 225
 Motif name: Motif 225
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.137378

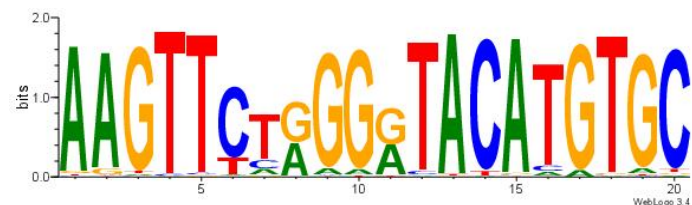
Alignment:

GCACATGTAYCCYAGAACTT
 AGAAATCGAGCRCAGCGCCG

Original motif Consensus sequence: GCACATGTAYCCYAGAACTT

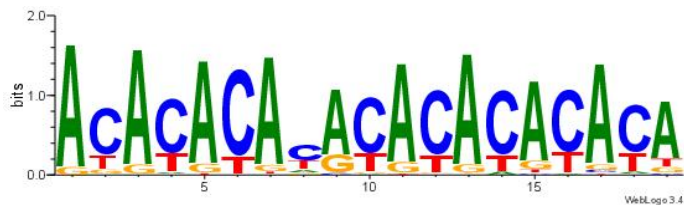


Reverse complement motif Consensus sequence: AAGTTCTKGGKTACATGTGC

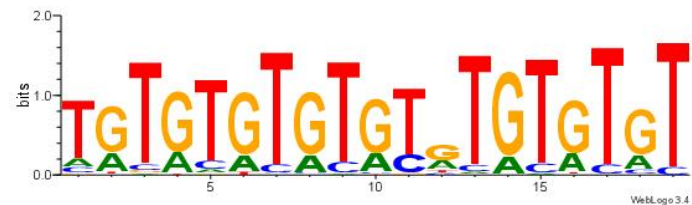


Dataset #: 1 Motif ID: 66 Motif name: Motif 66

Original motif Consensus sequence: ACACACAYACACACACACA



Reverse complement motif Consensus sequence: TGTGTGTGKTGTGTGT



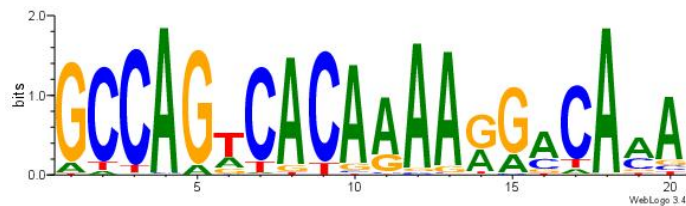
Best Matches for Motif ID 66 (Highest to Lowest)

Dataset #: 1
Motif ID: 145
Motif name: Motif 145
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 19
Similarity score: 0.0762936

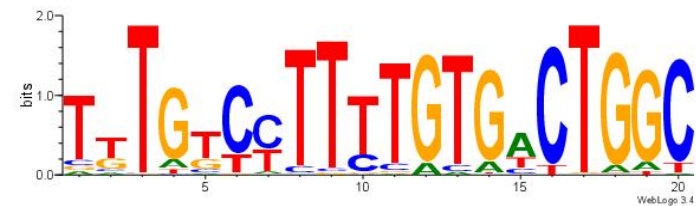
Alignment:

```
TYTGTCMTTTTGTGACTGGC  
TGTGTGTGTGTKTGTGTGT-
```

Original motif Consensus sequence: GCCAGTCACAAAARGACAMA



Reverse complement motif Consensus sequence: TYTGTCMTTTTGTGACTGGC



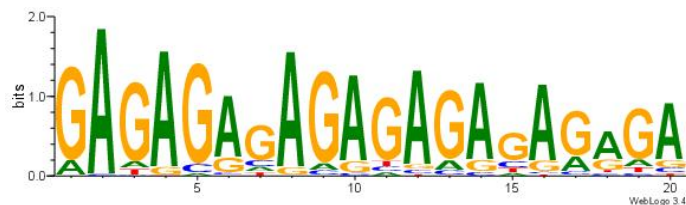
Dataset #: 1
Motif ID: 109
Motif name: Motif 109
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif

Direction: Backward
 Position number: 1
 Number of overlap: 19
 Similarity score: 0.084962

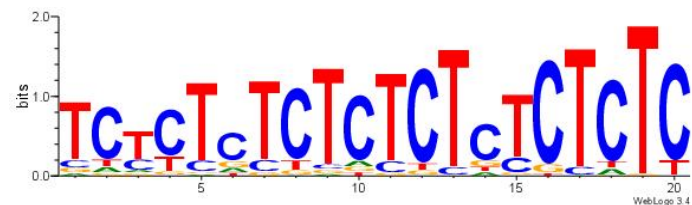
Alignment:

GAGAGAGAGAGAGAGAGAGA
 -ACACACAYACACACACACA

Original motif Consensus sequence: GAGAGAGAGAGAGAGAGA



Reverse complement motif Consensus sequence: TCTCTCTCTCTCTCTCTC

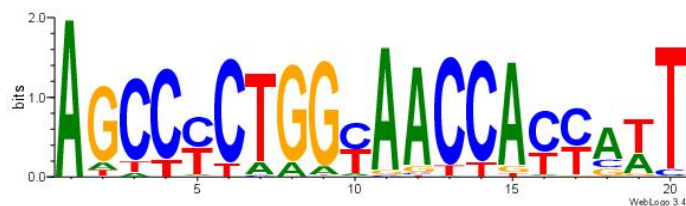


Dataset #: 1
 Motif ID: 139
 Motif name: Motif 139
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 19
 Similarity score: 0.0883926

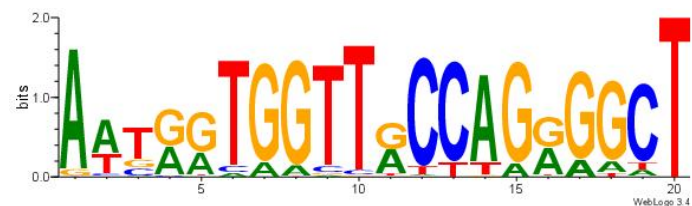
Alignment:

AWTKKTGGTTKCCAGKGGCT
 -TGTGTGTGTGKTGTGTGT

Original motif Consensus sequence: AGCCYCTGGYAACCAYYAWT



Reverse complement motif Consensus sequence: AWTKKTGGTTKCCAGKGGCT

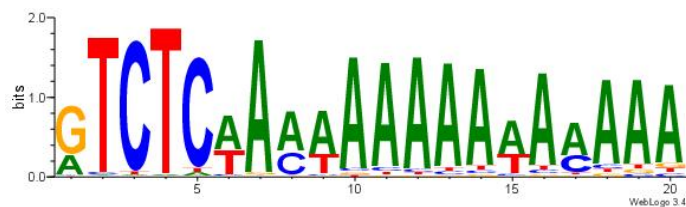


Dataset #: 1
Motif ID: 7
Motif name: Motif 7
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 2
Number of overlap: 19
Similarity score: 0.0886505

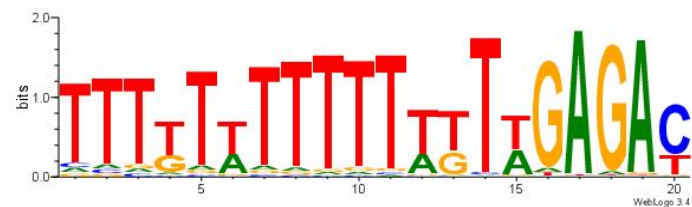
Alignment:

TTTYTWTTTTTTTYTWGAGAC
TGTGTGTGTGTKGTGTGT-

Original motif Consensus sequence: GTCTWAMAAAAAWAMAAA



Reverse complement motif Consensus sequence: TTTYTWTTTTTTTYTWGAGAC

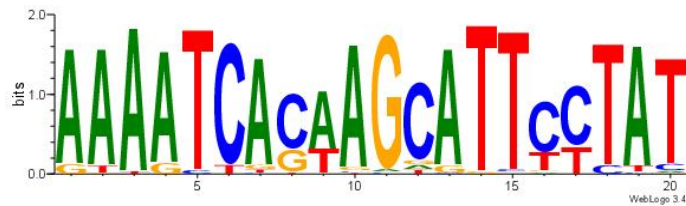


Dataset #: 1
 Motif ID: 254
 Motif name: Motif 254
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 19
 Similarity score: 0.0911508

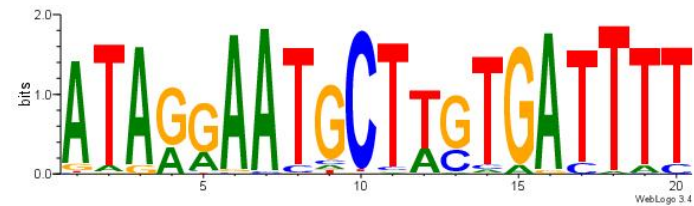
Alignment:

ATAGGAATGCTTGTGATTTT
 -TGTGTGTGTGKTGTGTGT

Original motif Consensus sequence: AAAATCACAGCATTCTAT



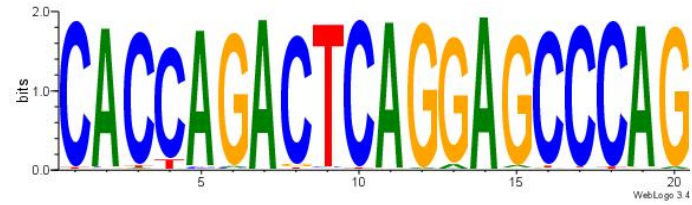
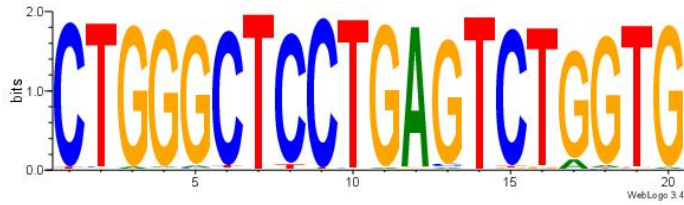
Reverse complement motif Consensus sequence: ATAGGAATGCTTGTGATTTT



Dataset #: 1 Motif ID: 67 Motif name: Motif 67

Original motif Consensus sequence: CTGGGCTCCTGAGTCTGGTG

Reverse complement motif Consensus sequence: CACCAGACTCAGGAGCCCAG

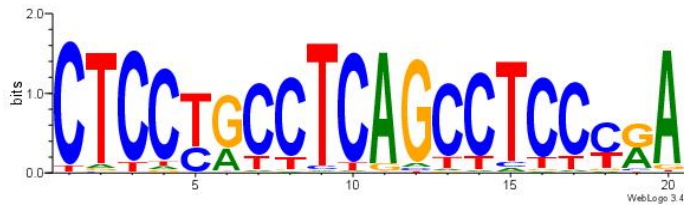


Best Matches for Motif ID 67 (Highest to Lowest)

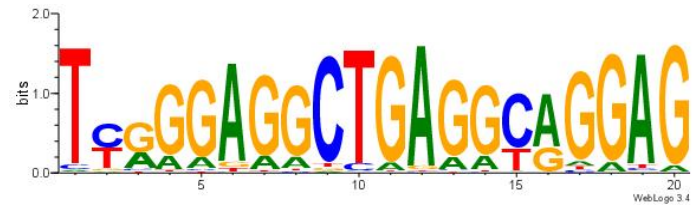
Dataset #: 1
 Motif ID: 26
 Motif name: Motif 26
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.10051

Alignment:
 TMGGGAGGCTGAGGCAGGAG
 CTGGGCTCCTGAGTCTGGTG

Original motif Consensus sequence: CTCTGCCTCAGCCTCCRA



Reverse complement motif Consensus sequence: TMGGGAGGCTGAGGCAGGAG

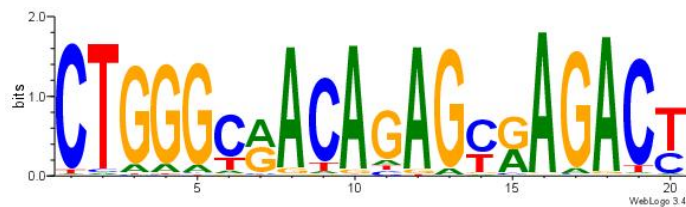


Dataset #: 1
 Motif ID: 29
 Motif name: Motif 29
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.107414

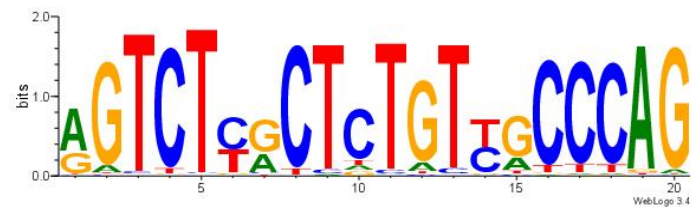
Alignment:

CTGGGCRACAGAGYRAGACY
 CTGGGCTCCTGAGTCTGGTG

Original motif Consensus sequence: CTGGGCRACAGAGYRAGACY



Reverse complement motif Consensus sequence: MGTCTMKCTCTGKGCCAG



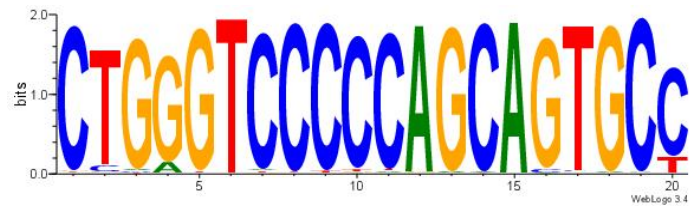
Dataset #: 1
 Motif ID: 84
 Motif name: Motif 84
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1

Number of overlap: 20
Similarity score: 0.116021

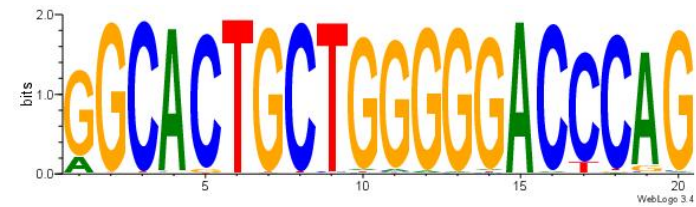
Alignment:

GGCACTGCTGGGGGACCCAG
CACCAGACTCAGGAGCCCAG

Original motif Consensus sequence: CTGGGTCCCCCAGCAGTGCC



Reverse complement motif Consensus sequence: GGCACTGCTGGGGGACCCAG

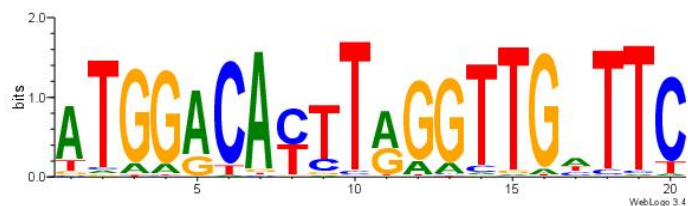


Dataset #: 1
Motif ID: 58
Motif name: Motif 58
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 20
Similarity score: 0.123442

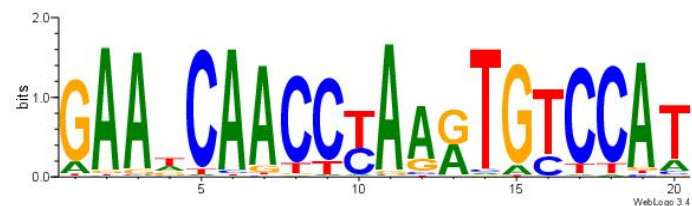
Alignment:

ATGGACAYTTRGGTTGHTTC
CTGGGCTCCTGAGTCTGGTG

Original motif Consensus sequence: ATGGACAYTTRGGTTGHTTC



Reverse complement motif Consensus sequence: GAAHCAACCKAAKTGTCCAT

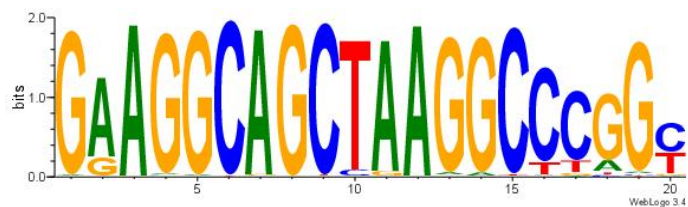


Dataset #: 1
Motif ID: 64
Motif name: Motif 64
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 20
Similarity score: 0.126703

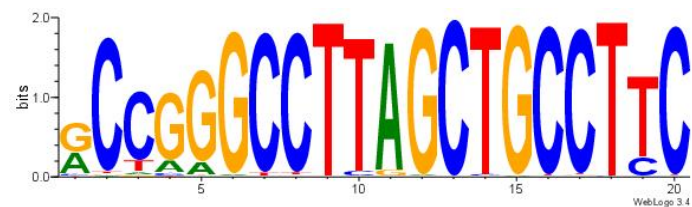
Alignment:

GAAGGCAGCTAAGGCCGGY
CTGGGCTCCTGAGTCTGGTG

Original motif Consensus sequence: GAAGGCAGCTAAGGCCGGY

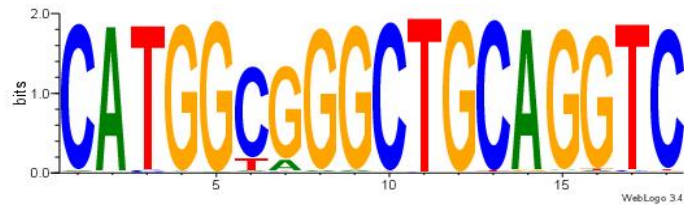


Reverse complement motif Consensus sequence: KCCGGGCTTAGCTGCCCTC

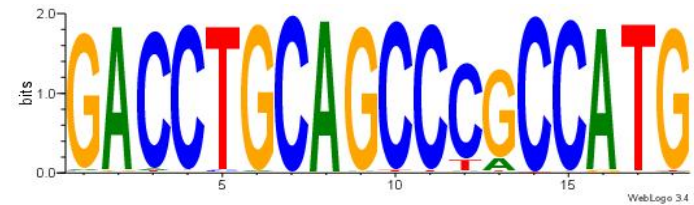


Dataset #: 1 Motif ID: 68 Motif name: Motif 68

Original motif Consensus sequence: CATGGCGGGCTGCAGGTC



Reverse complement motif Consensus sequence: GACCTGCAGCCCGCCATG



Best Matches for Motif ID 68 (Highest to Lowest)

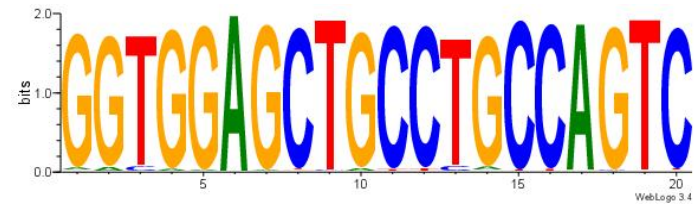
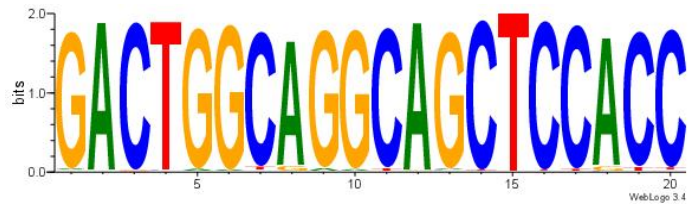
Dataset #:	1
Motif ID:	52
Motif name:	Motif 52
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	18
Similarity score:	0.102941

Alignment:

```
GACTGGCAGGCAGCTCCACC  
-CATGGCGGGCTGCAGGTC-
```

Original motif Consensus sequence: GACTGGCAGGCAGCTCCACC

Reverse complement motif Consensus sequence: GGTGGAGCTGCCTGCCAGTC

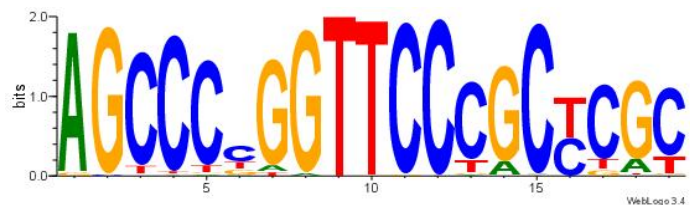


Dataset #: 1
 Motif ID: 164
 Motif name: Motif 164
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 18
 Similarity score: 0.111785

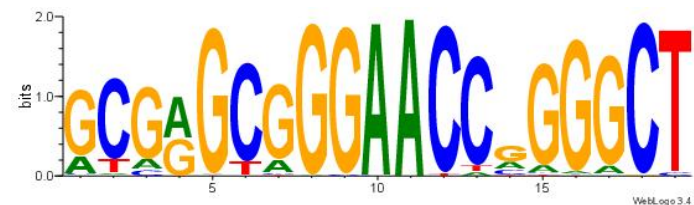
Alignment:

AGCCCCGGTTCCCGCYCGC
 -GACCTGCAGCCCGCCATG

Original motif Consensus sequence: AGCCCCGGTTCCCGCYCGC



Reverse complement motif Consensus sequence: GCGMCGGGAACCGGGCT



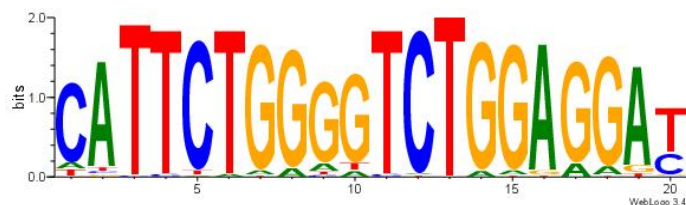
Dataset #: 1

Motif ID: 309
 Motif name: Motif 309
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 18
 Similarity score: 0.116332

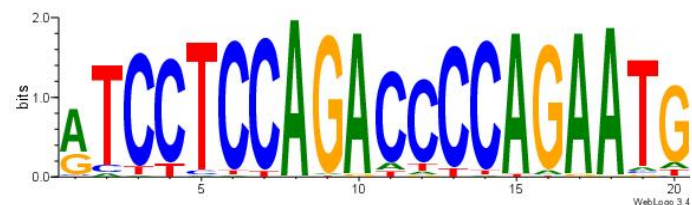
Alignment:

CATTCTGGGGTCTGGAGGAY
 --CATGGCGGGCTGCAGGTC

Original motif Consensus sequence: CATTCTGGGGTCTGGAGGAY



Reverse complement motif Consensus sequence: MTCCTCCAGACCCCAGAATG



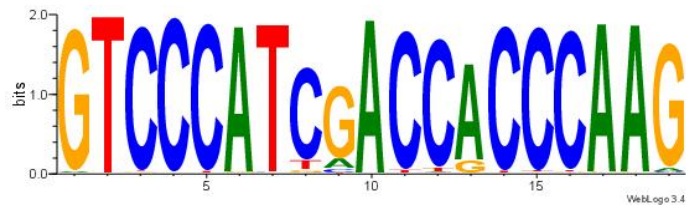
Dataset #: 1
 Motif ID: 53
 Motif name: Motif 53
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 18

Similarity score: 0.116432

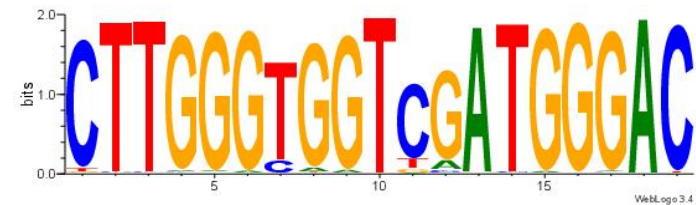
Alignment:

CTTGGGTGGTCGATGGGAC
-CATGGCGGGCTGCAGGTC

Original motif Consensus sequence: GTCCCATCGACCACCCAAG



Reverse complement motif Consensus sequence:
CTTGGGTGGTCGATGGGAC



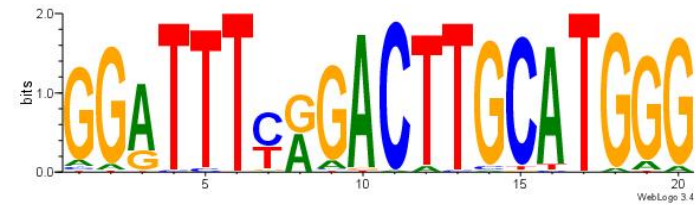
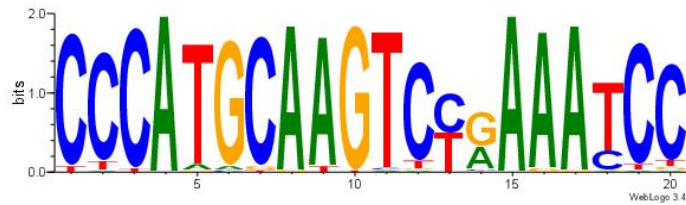
Dataset #: 1
Motif ID: 310
Motif name: Motif 310
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 3
Number of overlap: 18
Similarity score: 0.116568

Alignment:

CCCATGCAAGTCYRAAATCC
--CATGGCGGGCTGCAGGTC

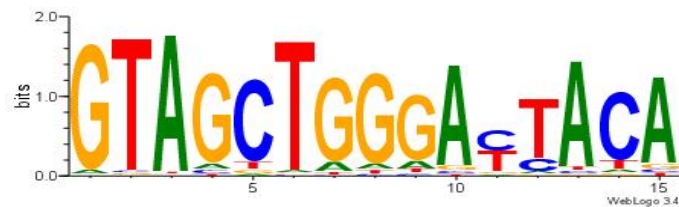
Original motif Consensus sequence: CCCATGCAAGTCYRAAATCC

Reverse complement motif Consensus sequence:
GGATTTMKGACTTGCATGGG

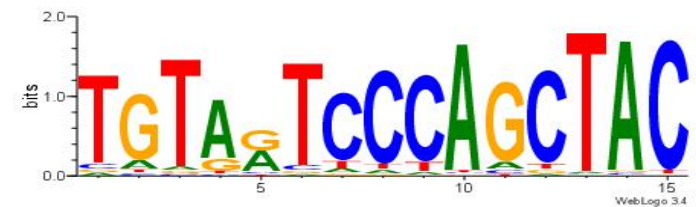


Dataset #: 1 Motif ID: 69 Motif name: Motif 69

Original motif Consensus sequence: GTAGCTGGGAYTACA



Reverse complement motif Consensus sequence: TGTAKTCCCAGCTA

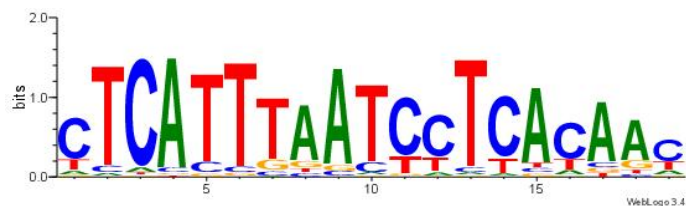


Best Matches for Motif ID 69 (Highest to Lowest)

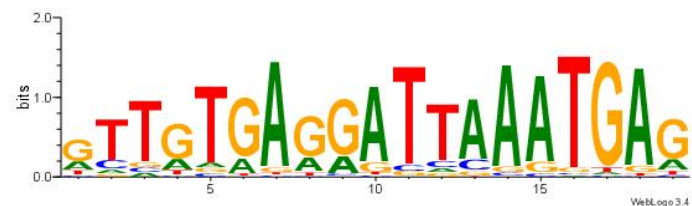
Dataset #:	1
Motif ID:	102
Motif name:	Motif 102
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	15
Similarity score:	0.0936422

Alignment:
 GTTGTGAGGATTAAATGAG
 GTAGCTGGGAYTACA-----

Original motif Consensus sequence: CTCATTTAATCCTCACAAC



Reverse complement motif Consensus sequence: GTTGTGAGGATTAATGAG

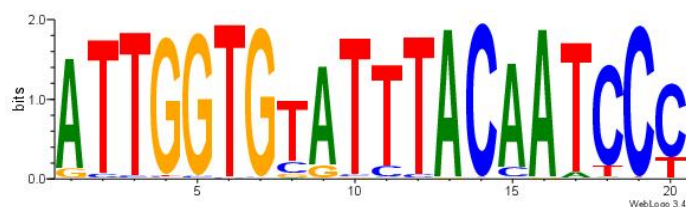


Dataset #: 1
Motif ID: 106
Motif name: Motif 106
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 6
Number of overlap: 15
Similarity score: 0.0994445

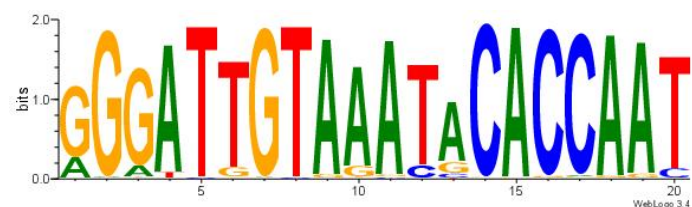
Alignment:

ATTGGTGTATTTACAATCCC
GTAGCTGGGAYTACA-----

Original motif Consensus sequence: ATTGGTGTATTTACAATCCC



Reverse complement motif Consensus sequence: GGGATTGTAAATACACCAAT

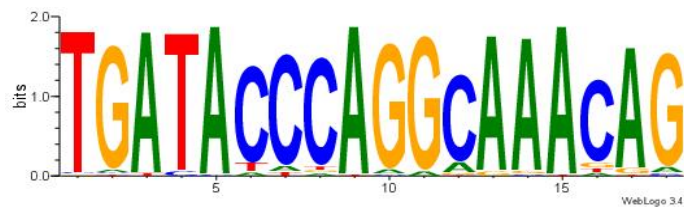


Dataset #: 1
 Motif ID: 290
 Motif name: Motif 290
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 15
 Similarity score: 0.0999355

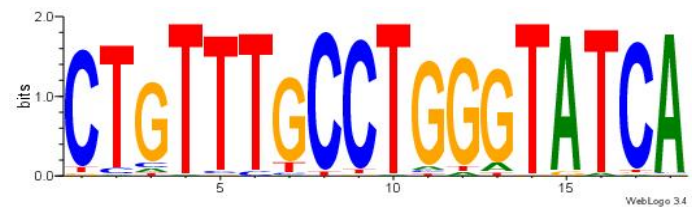
Alignment:

CTGTTTGCCTGGGTATCA
 -TGTAKTCCCAGCTAC--

Original motif Consensus sequence: TGATACCCAGGCAAACAG



Reverse complement motif Consensus sequence: CTGTTTGCCTGGGTATCA



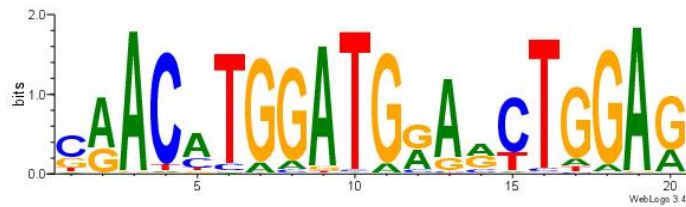
Dataset #: 1
 Motif ID: 104
 Motif name: Motif 104
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2

Number of overlap: 15
Similarity score: 0.102257

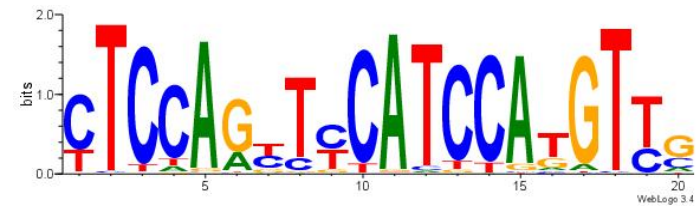
Alignment:

CAACATGGATGRARCTGGAG
----GTAGCTGGGAYTACA-

Original motif Consensus sequence: CAACATGGATGRARCTGGAG



Reverse complement motif Consensus sequence:
CTCCAGKTMCATCCATGTTG

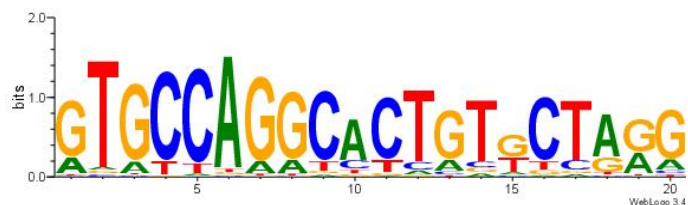


Dataset #: 1
Motif ID: 76
Motif name: Motif 76
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 6
Number of overlap: 15
Similarity score: 0.102692

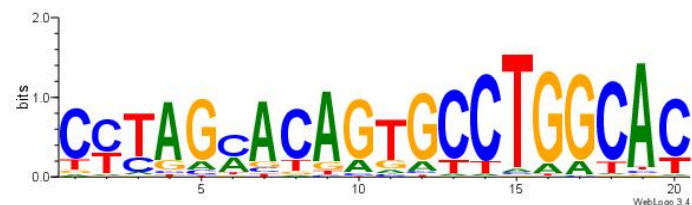
Alignment:

GTGCCAGGCACTGTKCTARG
GTAGCTGGGAYTACA-----

Original motif Consensus sequence: GTGCCAGGCACTGKCTARG

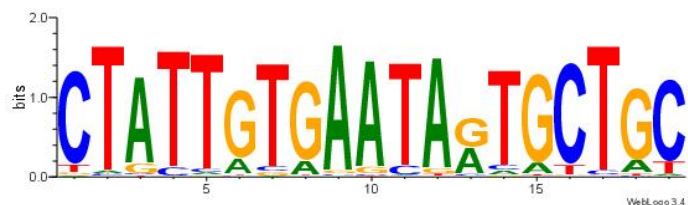


Reverse complement motif Consensus sequence: CMTAGYACAGTGCCTGGCAC

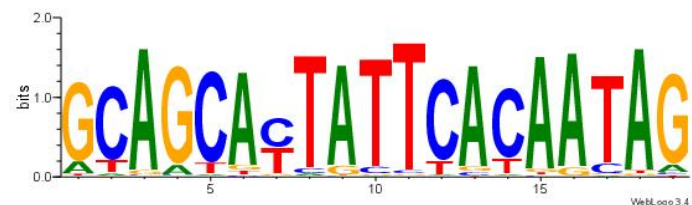


Dataset #: 1 Motif ID: 70 Motif name: Motif 70

Original motif Consensus sequence: CTATTGTGAATARTGCTGC



Reverse complement motif Consensus sequence: GCAGCAMTATTCACAATAG



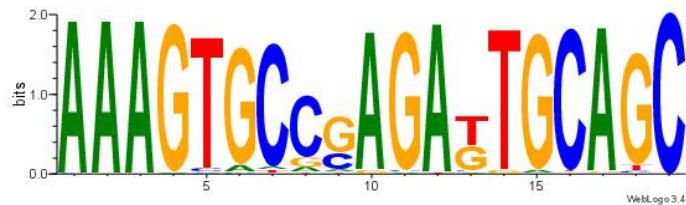
Best Matches for Motif ID 70 (Highest to Lowest)

Dataset #:	1
Motif ID:	191
Motif name:	Motif 191
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	19
Similarity score:	0.0948966

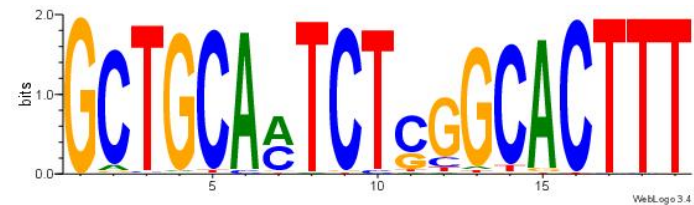
Alignment:

GCTGCARTCTCGGCACTTT
GCAGCAMTATTCACAATAG

Original motif Consensus sequence: AAAGTGCCGAGAKTGCAGC



Reverse complement motif Consensus sequence:
GCTGCARTCTCGGCACTTT



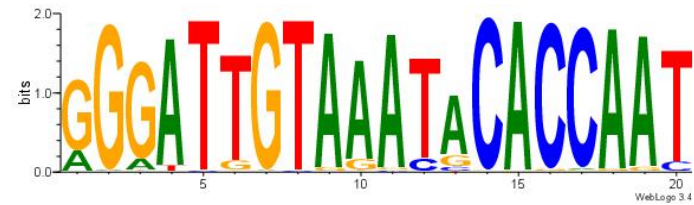
Dataset #:	1
Motif ID:	106
Motif name:	Motif 106
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	19
Similarity score:	0.100944

Alignment:

GGGATTGTAAATACACCAAT
-CTATTGTGAATARTGCTGC

Original motif Consensus sequence: ATTGGTGTATTTACAATCCC

Reverse complement motif Consensus sequence:
GGGATTGTAAATACACCAAT

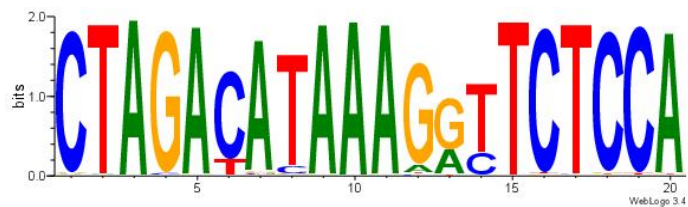


Dataset #: 1
 Motif ID: 85
 Motif name: Motif 85
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 19
 Similarity score: 0.102726

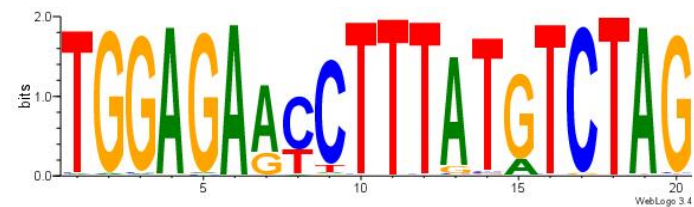
Alignment:

TGGAGAACCTTTATGTCTAG
 -GCAGCAMTATTCACAATAG

Original motif Consensus sequence: CTAGACATAAAGGTTCTCCA



Reverse complement motif Consensus sequence: TGGAGAACCTTTATGTCTAG



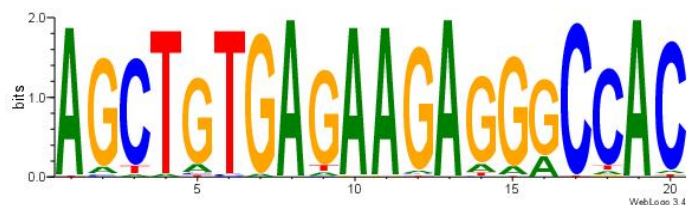
Dataset #: 1

Motif ID: 294
 Motif name: Motif 294
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 19
 Similarity score: 0.10487

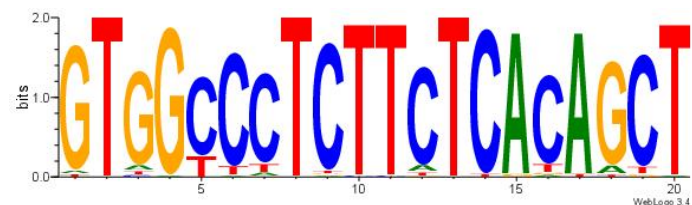
Alignment:

GTGGCCCTCTTCTCACAGCT
 GCAGCMTATTTCACAATAG-

Original motif Consensus sequence: AGCTGTGAGAAGAGGGCCAC



Reverse complement motif Consensus sequence: GTGGCCCTCTTCTCACAGCT



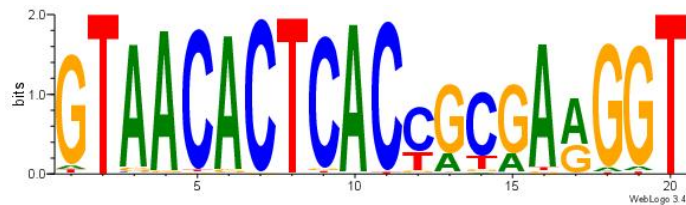
Dataset #: 1
 Motif ID: 201
 Motif name: Motif 201
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 19

Similarity score: 0.105823

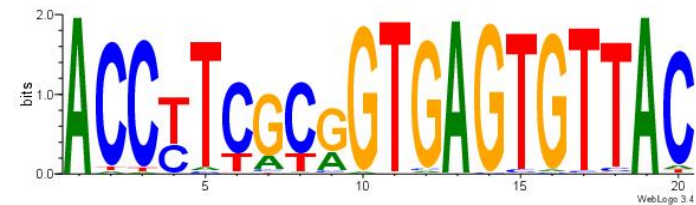
Alignment:

GTAACACTCACCGCGARGGT
GCAGCMTATTACAATAG-

Original motif Consensus sequence: GTAACACTCACCGCGARGGT

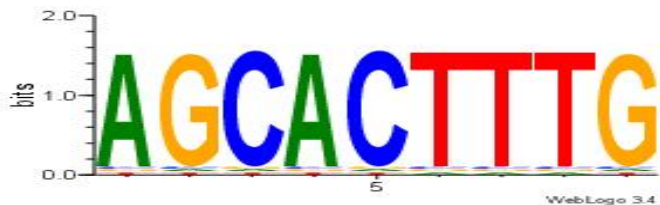


Reverse complement motif Consensus sequence: ACCKTCGCGGTGAGTGTTAC

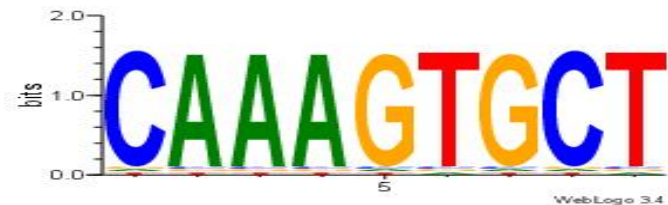


Dataset #: 1 Motif ID: 71 Motif name: Motif 71

Original motif Consensus sequence: AGCACTTTG



Reverse complement motif Consensus sequence: CAAAGTGCT



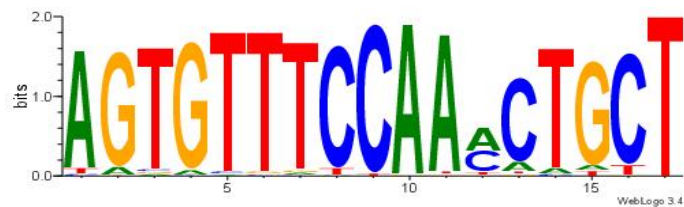
Best Matches for Motif ID 71 (Highest to Lowest)

Dataset #:	1
Motif ID:	304
Motif name:	Motif 304
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement

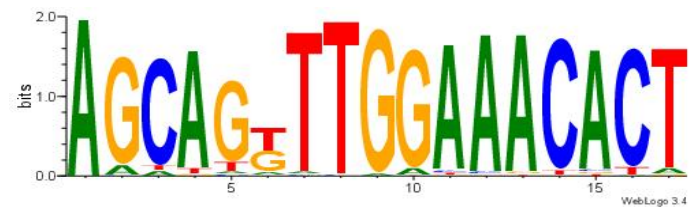
Direction: Forward
Position number: 1
Number of overlap: 9
Similarity score: 0.039262

Alignment:
AGCAGYTTGGAAACACT
AGCACTTTG-----

Original motif Consensus sequence: AGTGTTTCCAAMCTGCT



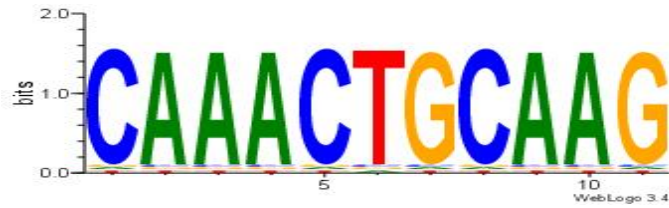
Reverse complement motif Consensus sequence: AGCAGYTTGGAAACACT



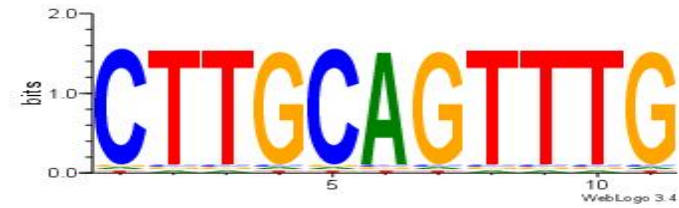
Dataset #: 1
Motif ID: 73
Motif name: Motif 73
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 9
Similarity score: 0.0420544

Alignment:
CAAAGTCAAG
CAAAGTCT--

Original motif Consensus sequence: CAAACTGCAAG



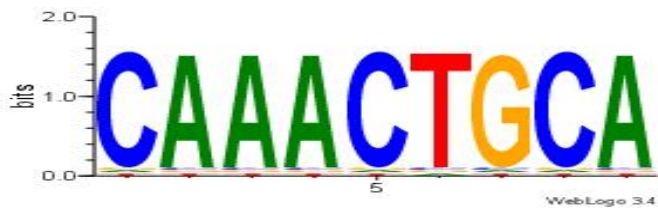
Reverse complement motif Consensus sequence: CTTGCAGTTTG



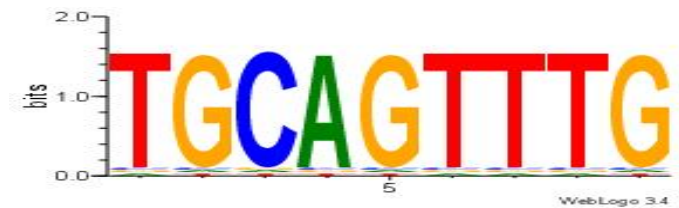
Dataset #: 1
Motif ID: 134
Motif name: Motif 134
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 9
Similarity score: 0.0420544

Alignment:
CAAAGTGCA
CAAAGTGCT

Original motif Consensus sequence: CAAACTGCA



Reverse complement motif Consensus sequence: TGCAGTTTG



Dataset #: 1
Motif ID: 123
Motif name: Motif 123
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 3
Number of overlap: 9
Similarity score: 0.0420544

Alignment:

CTCAGACTGCT
--CAAAGTGCT

Original motif Consensus sequence: AGCAGTCTGAG



Reverse complement motif Consensus sequence: CTCAGACTGCT



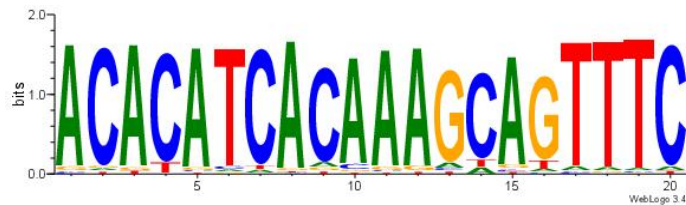
Dataset #: 1
Motif ID: 202
Motif name: Motif 202
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 9

Similarity score: 0.0501263

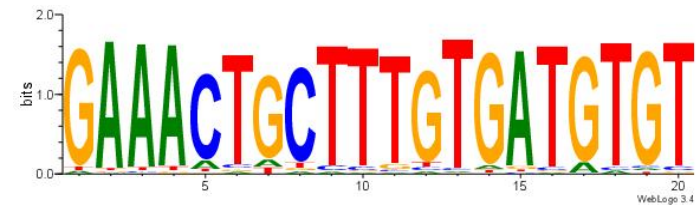
Alignment:

GAAACTGCTTTGTGATGTGT
CAAAGTGCT-----

Original motif Consensus sequence: ACACATCACAAGCAGTTTC

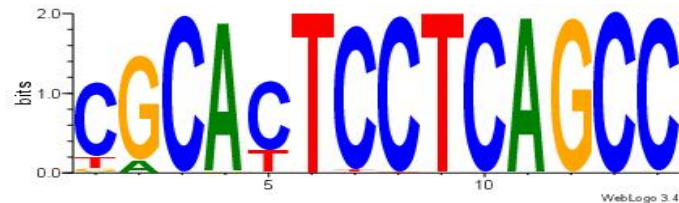


Reverse complement motif Consensus sequence: GAAACTGCTTTGTGATGTGT

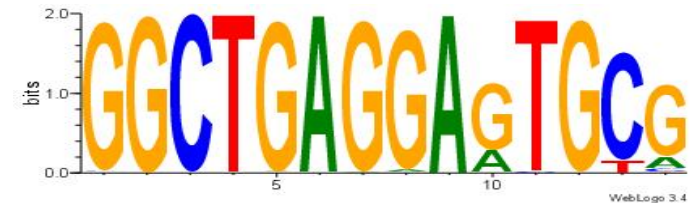


Dataset #: 1 Motif ID: 72 Motif name: Motif 72

Original motif Consensus sequence: CGCACTCCTCAGCC



Reverse complement motif Consensus sequence: GGCTGAGGAGTGC



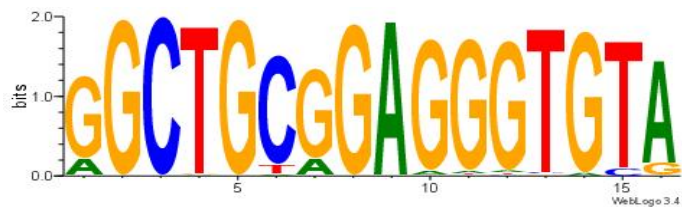
Best Matches for Motif ID 72 (Highest to Lowest)

Dataset #:	1
Motif ID:	89
Motif name:	Motif 89
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement

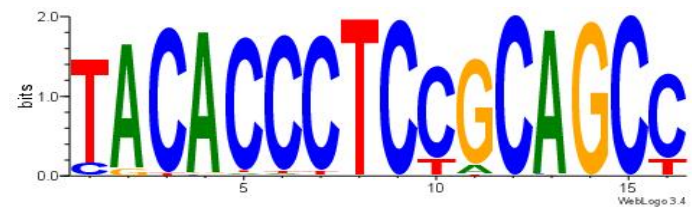
Direction: Backward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0.0631515

Alignment:
 TACACCCTCCGCAGCC
 --CGCACTCCTCAGCC

Original motif Consensus sequence: GGCTGCGGAGGGTGTA



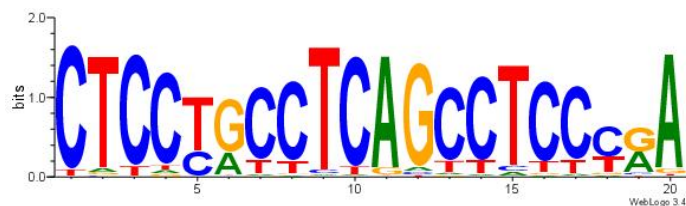
Reverse complement motif Consensus sequence: TACACCCTCCGCAGCC



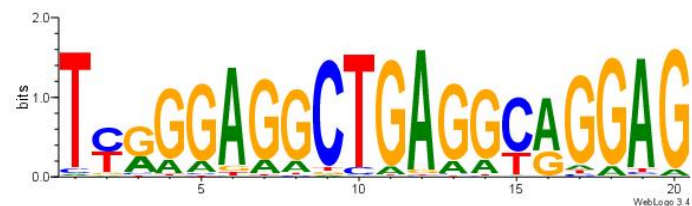
Dataset #: 1
 Motif ID: 26
 Motif name: Motif 26
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0.0793425

Alignment:
 CTCCTGCCTCAGCCTCCRA
 CGCACTCCTCAGCC-----

Original motif Consensus sequence: CTCCTGCCTCAGCCTCCCRA



Reverse complement motif Consensus sequence: TMGGGAGGCTGAGGCAGGAG

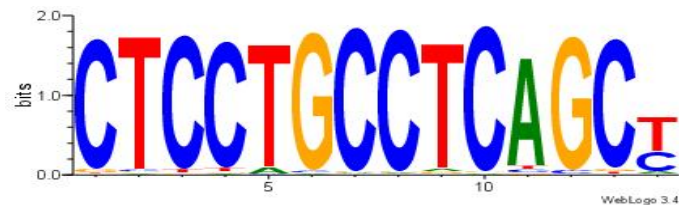


Dataset #: 1
Motif ID: 313
Motif name: Motif 313
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 14
Similarity score: 0.0845425

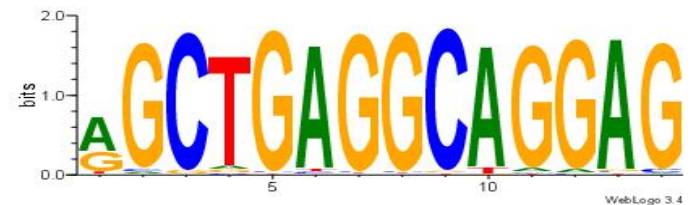
Alignment:

CTCCTGCCTCAGCY
CGCACTCCTCAGCC

Original motif Consensus sequence: CTCCTGCCTCAGCY



Reverse complement motif Consensus sequence: MGCTGAGGCAGGAG

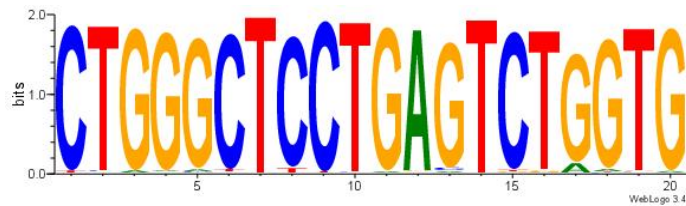


Dataset #: 1
 Motif ID: 67
 Motif name: Motif 67
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 6
 Number of overlap: 14
 Similarity score: 0.0925295

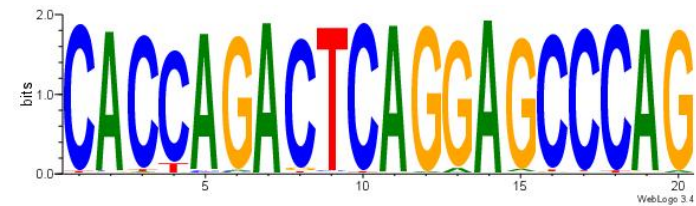
Alignment:

CTGGGCTCCTGAGTCTGGTG
 -CGCACTCCTCAGCC-----

Original motif Consensus sequence: CTGGGCTCCTGAGTCTGGTG



Reverse complement motif Consensus sequence: CACCAGACTCAGGAGCCCAG



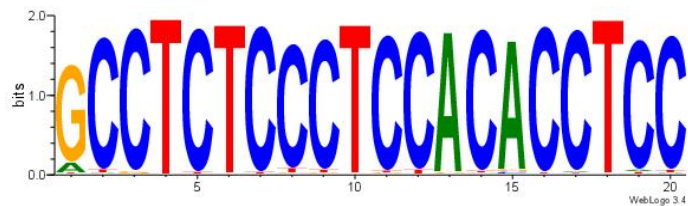
Dataset #: 1
 Motif ID: 105
 Motif name: Motif 105
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 5

Number of overlap: 14
Similarity score: 0.0943803

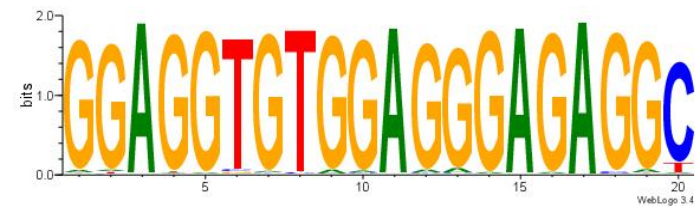
Alignment:

GGAGGTGTGGAGGGAGAGGC
--GGCTGAGGAGTGCG----

Original motif Consensus sequence: GCCTCTCCCTCCACACCTCC

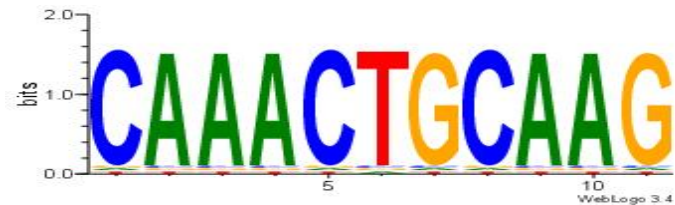


Reverse complement motif Consensus sequence:
GGAGGTGTGGAGGGAGAGGC

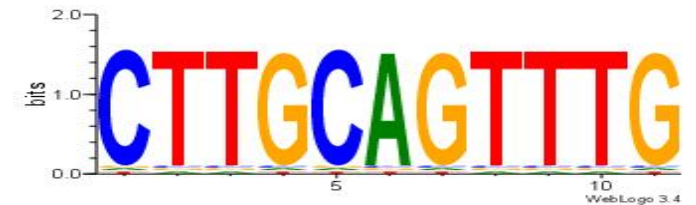


Dataset #: 1 Motif ID: 73 Motif name: Motif 73

Original motif Consensus sequence: CAAACTGCAAG



Reverse complement motif Consensus sequence: CTTGCAGTTTG



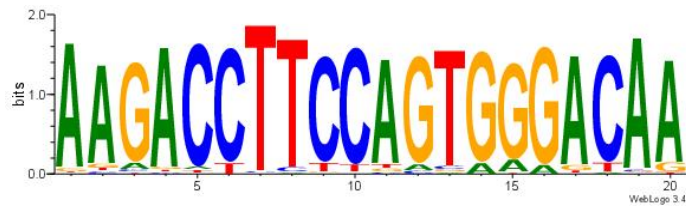
Best Matches for Motif ID 73 (Highest to Lowest)

Dataset #: 1
Motif ID: 292
Motif name: Motif 292
Matching format of first motif: Original Motif

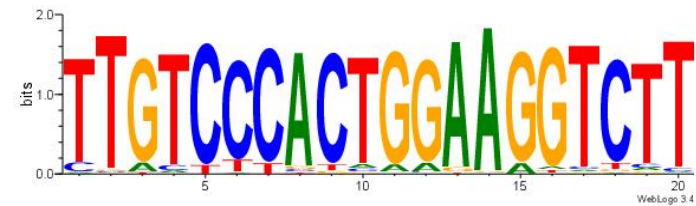
Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 6
 Number of overlap: 11
 Similarity score: 0.0679381

Alignment:
 TTGTCCCCTGGAAGGTCTT
 ----CAAAGTCAAG-----

Original motif Consensus sequence: AAGACCTCCAGTGGGACAA



Reverse complement motif Consensus sequence: TTGTCCCCTGGAAGGTCTT

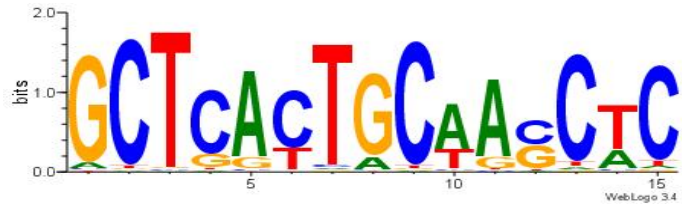


Dataset #: 1
 Motif ID: 6
 Motif name: Motif 6
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 11
 Similarity score: 0.0730245

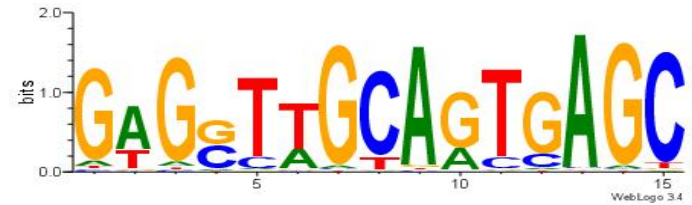
Alignment:

GAGSTTGCAGTGAGC
 ---CTTGCAGTTTG-

Original motif Consensus sequence: GCTCACTGCAASCTC



Reverse complement motif Consensus sequence: GAGSTTGCAGTGA



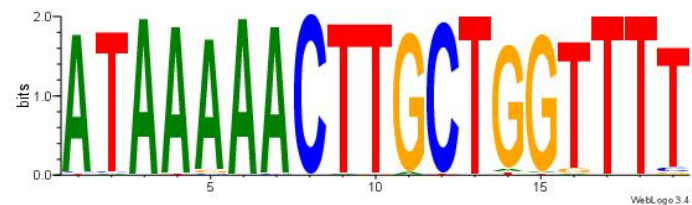
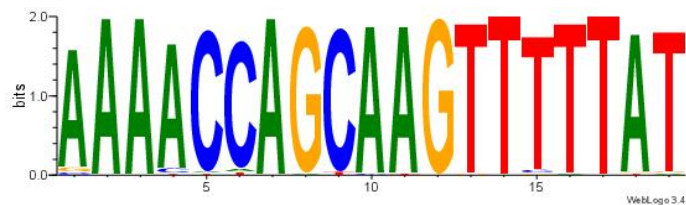
Dataset #: 1
 Motif ID: 330
 Motif name: Motif 330
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 11
 Similarity score: 0.0750068

Alignment:

ATAAAAACCTTGCTGGTTTT
 -----CTTGCAGTTTG-

Original motif Consensus sequence: AAAACCAGCAAGTTTTTAT

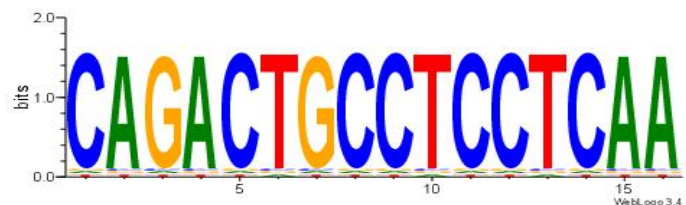
Reverse complement motif Consensus sequence:
 ATAAAACCTTGCTGGTTTT



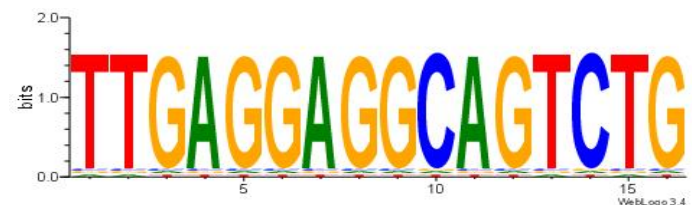
Dataset #: 1
 Motif ID: 245
 Motif name: Motif 245
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.0826446

Alignment:
 TTGAGGAGGCAGTCTG
 -----CTTGCAGTTTG

Original motif Consensus sequence: CAGACTGCCTCCTCAA



Reverse complement motif Consensus sequence: TTGAGGAGGCAGTCTG



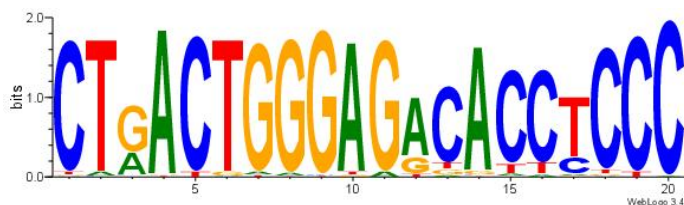
Dataset #: 1

Motif ID: 293
 Motif name: Motif 293
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 10
 Number of overlap: 11
 Similarity score: 0.0847484

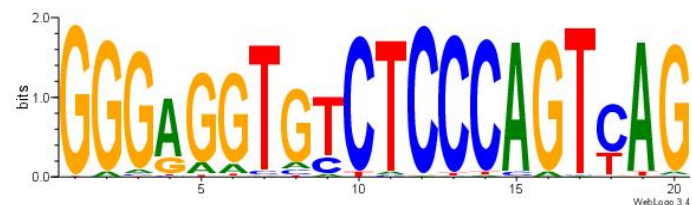
Alignment:

CTGACTGGGAGACACCTCCC
 CAAACTGCAAG-----

Original motif Consensus sequence: CTGACTGGGAGACACCTCCC

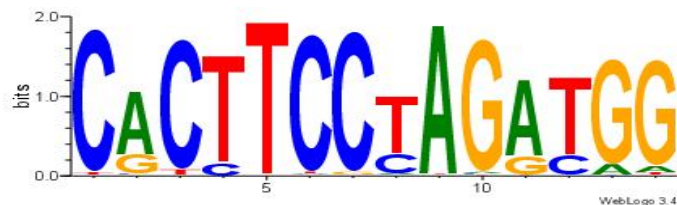


Reverse complement motif Consensus sequence: GGGAGGTGTCTCCAGTCAG

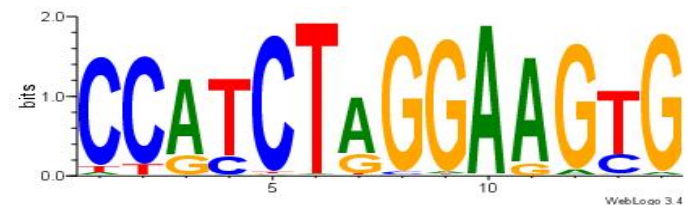


Dataset #: 1 Motif ID: 74 Motif name: Motif 74

Original motif Consensus sequence: CACTTCC TAGATGG



Reverse complement motif Consensus sequence: CCATCTAGGAAGT



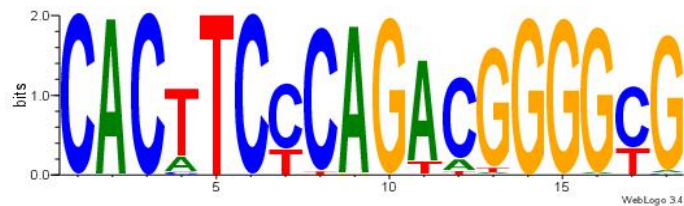
Best Matches for Motif ID 74 (Highest to Lowest)

Dataset #: 1
 Motif ID: 27
 Motif name: Motif 27
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0.0286091

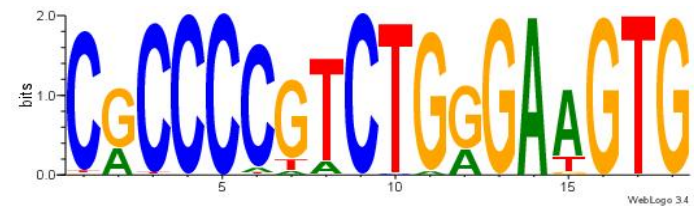
Alignment:

CACTTCCCAGACGGGGCG
 CACTTCTAGATGG-----

Original motif Consensus sequence: CACTTCCCAGACGGGGCG



Reverse complement motif Consensus sequence: CGCCCCGTCTGGGAAGTG

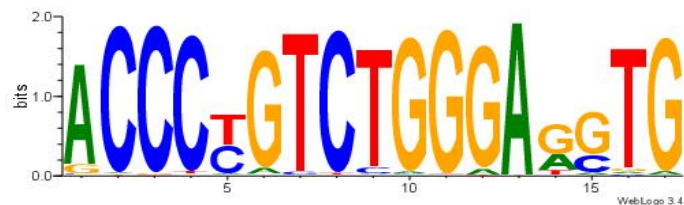


Dataset #: 1
 Motif ID: 95
 Motif name: Motif 95
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif

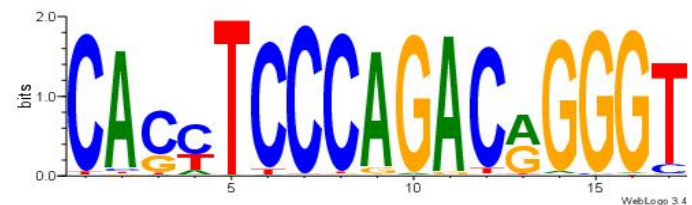
Direction: Backward
Position number: 1
Number of overlap: 14
Similarity score: 0.0523125

Alignment:
ACCCYGTCTGGGAGGTG
---CCATCTAGGAAGTG

Original motif Consensus sequence: ACCCYGTCTGGGAGGTG



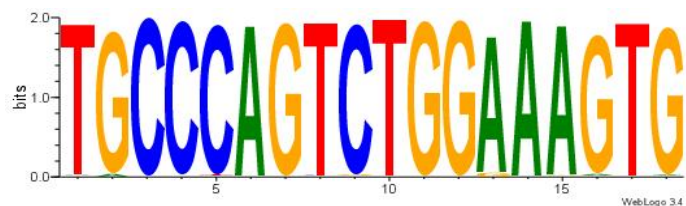
Reverse complement motif Consensus sequence: CACCTCCCAGACMGGGT



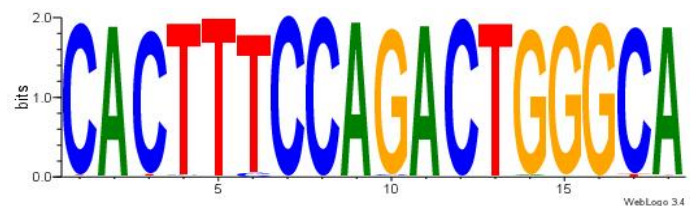
Dataset #: 1
Motif ID: 45
Motif name: Motif 45
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 14
Similarity score: 0.0563676

Alignment:
TGCCCAGTCTGGAAAGTG
CCATCTAGGAAGTG----

Original motif Consensus sequence: TGCCCAGTCTGGAAAGTG



Reverse complement motif Consensus sequence: CACTTCCAGACTGGGCA

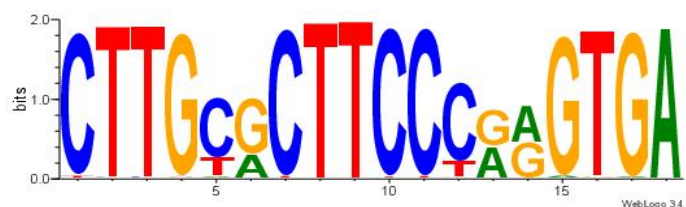


Dataset #: 1
Motif ID: 15
Motif name: Motif 15
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 14
Similarity score: 0.0605408

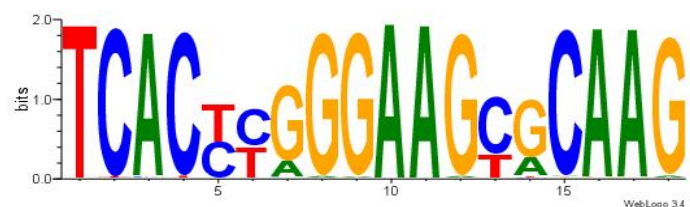
Alignment:

```
CTTGCGCTTCCCRRGTGA  
----CACTTCCCTAGATGG
```

Original motif Consensus sequence: CTTGCGCTTCCCRRGTGA



Reverse complement motif Consensus sequence: TCACKMGGGAAGCGCAAG

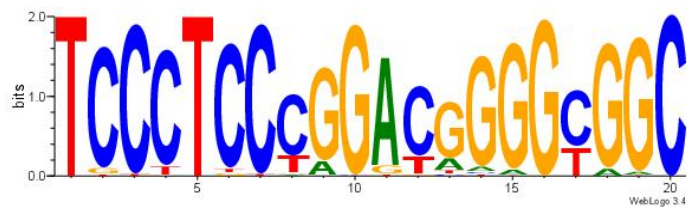


Dataset #: 1
 Motif ID: 155
 Motif name: Motif 155
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 6
 Number of overlap: 14
 Similarity score: 0.0688109

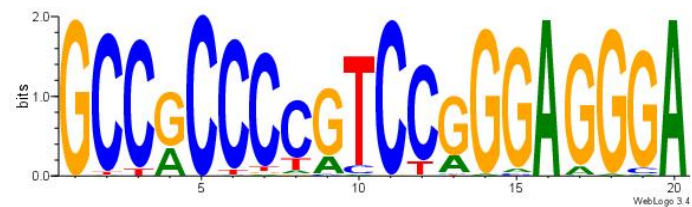
Alignment:

TCCCTCCCGGACGGGGYGGC
 -CCATCTAGGAAGTG-----

Original motif Consensus sequence: TCCCTCCCGGACGGGGYGGC



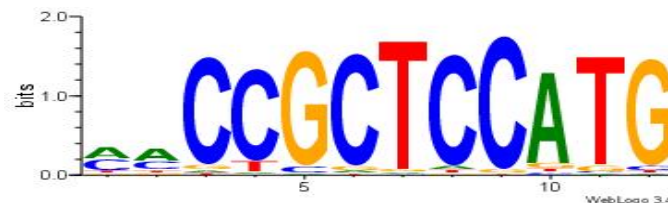
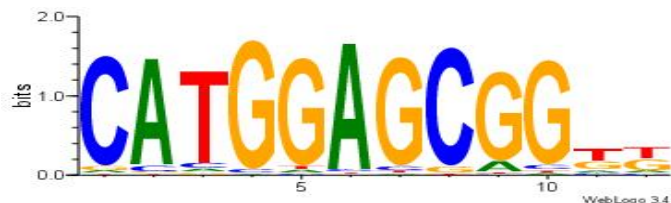
Reverse complement motif Consensus sequence: GCCCCCCGTCCGGGAGGGA



Dataset #: 1 Motif ID: 75 Motif name: Motif 75

Original motif Consensus sequence: CATGGAGCGGKK

Reverse complement motif Consensus sequence: RRCCGCTCCATG



Best Matches for Motif ID 75 (Highest to Lowest)

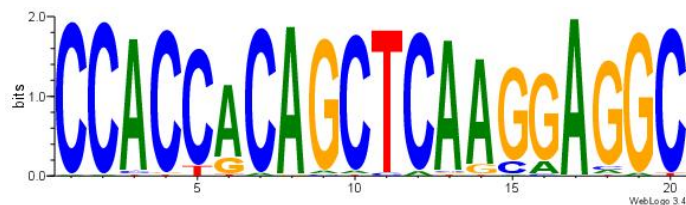
Dataset #: 1
 Motif ID: 331
 Motif name: Motif 331
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 5
 Number of overlap: 12
 Similarity score: 0.0720918

Alignment:

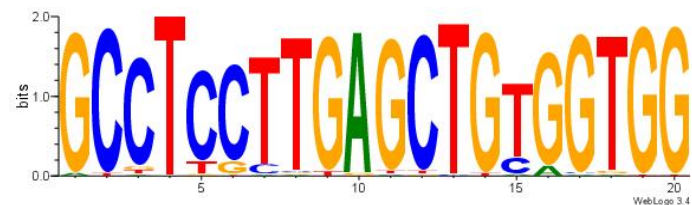
```

GCCTCCTTGAGCTGTGGTGG
----CATGGAGCGGKK----
  
```

Original motif Consensus sequence: CCACCACAGCTCAAGGAGGC



Reverse complement motif Consensus sequence: GCCTCCTTGAGCTGTGGTGG

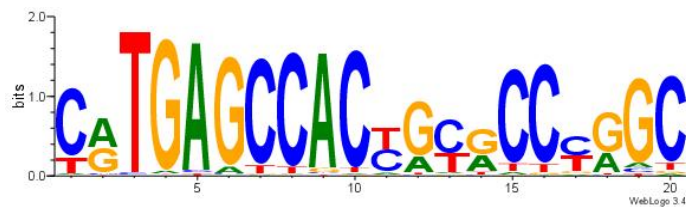


Dataset #: 1
 Motif ID: 56
 Motif name: Motif 56
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 12
 Similarity score: 0.0764369

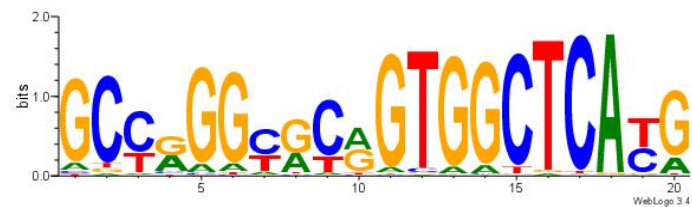
Alignment:

CRTGAGCCACYGYRCCYGGC
 -RRCCGCTCCATG-----

Original motif Consensus sequence: CRTGAGCCACYGYRCCYGGC



Reverse complement motif Consensus sequence: GCCKGGMKCMGTGGCTCAKG



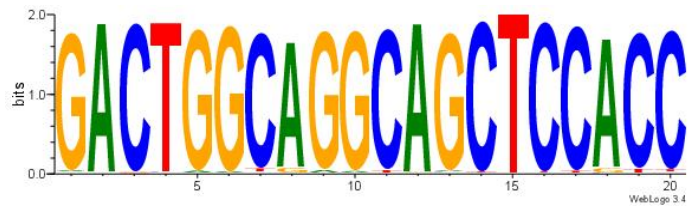
Dataset #: 1
 Motif ID: 52
 Motif name: Motif 52
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1

Number of overlap: 12
Similarity score: 0.0782422

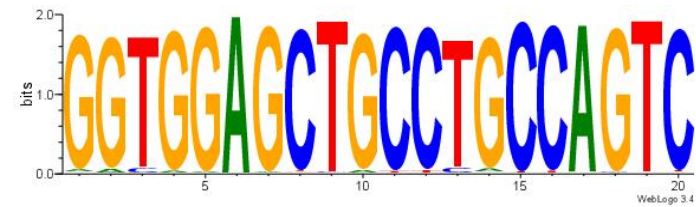
Alignment:

GGTGGAGCTGCCTGCCAGTC
-----CATGGAGCGGKK

Original motif Consensus sequence: GACTGGCAGGCAGCTCCACC



Reverse complement motif Consensus sequence:
GGTGGAGCTGCCTGCCAGTC

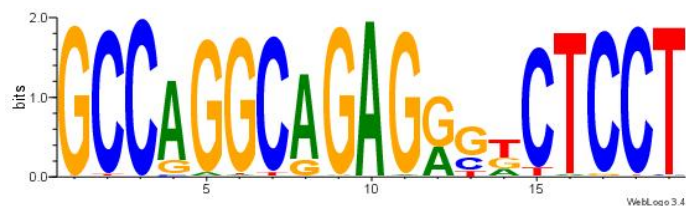


Dataset #: 1
Motif ID: 43
Motif name: Motif 43
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 3
Number of overlap: 12
Similarity score: 0.0795317

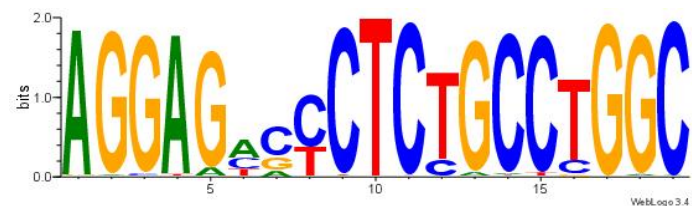
Alignment:

GCCAGGCAGAGRGKCTCCT
--CATGGAGCGGKK-----

Original motif Consensus sequence: GCCAGGCAGAGRGKCTCCT



Reverse complement motif Consensus sequence: AGGAGRCMCTCTGCCTGGC

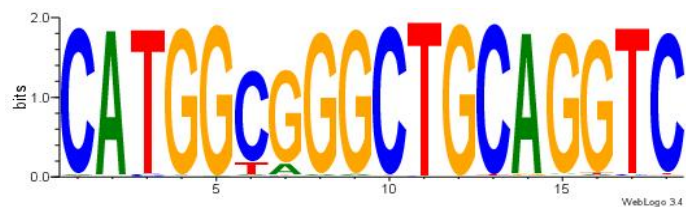


Dataset #: 1
Motif ID: 68
Motif name: Motif 68
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 12
Similarity score: 0.0797618

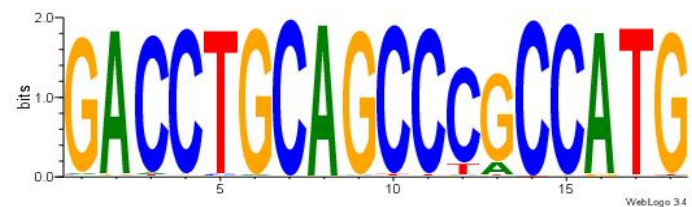
Alignment:

CATGGCGGGCTGCAGGTC
CATGGAGCGGKK-----

Original motif Consensus sequence: CATGGCGGGCTGCAGGTC

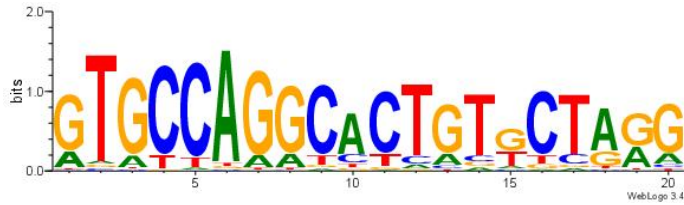


Reverse complement motif Consensus sequence: GACCTGCAGCCCGCCATG

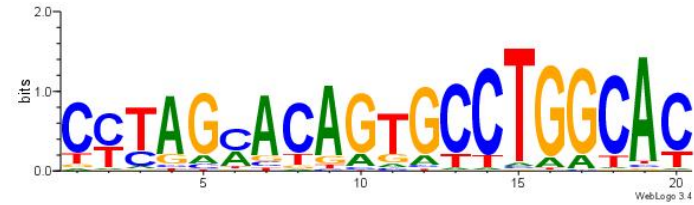


Dataset #: 1 Motif ID: 76 Motif name: Motif 76

Original motif Consensus sequence: GTGCCAGGCACTGKCTARG



Reverse complement motif Consensus sequence: CMTAGYACAGTGCCTGGCAC



Best Matches for Motif ID 76 (Highest to Lowest)

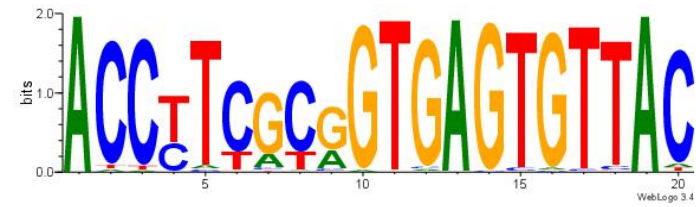
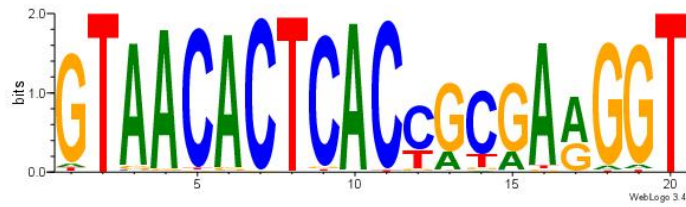
Dataset #:	1
Motif ID:	201
Motif name:	Motif 201
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	20
Similarity score:	0.101723

Alignment:

```
GTAACACTCACCGCGARGGT  
GTGCCAGGCACTGKCTARG
```

Original motif Consensus sequence: GTAACACTCACCGCGARGGT

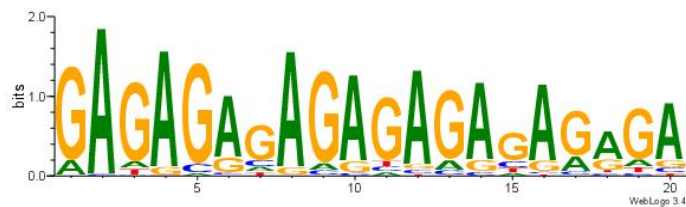
Reverse complement motif Consensus sequence:
ACCKTCGCGGTGAGTGTTAC



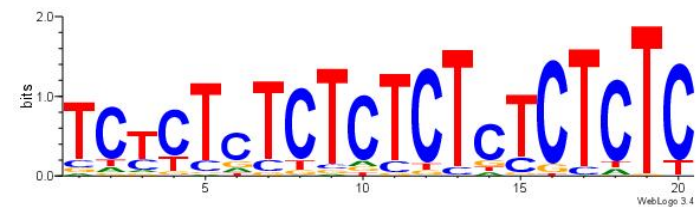
Dataset #: 1
 Motif ID: 109
 Motif name: Motif 109
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.102379

Alignment:
 TCTCTCTCTCTCTCTCTC
 CMTAGYACAGTGCCTGGCAC

Original motif Consensus sequence: GAGAGAGAGAGAGAGAGA



Reverse complement motif Consensus sequence: TCTCTCTCTCTCTCTC



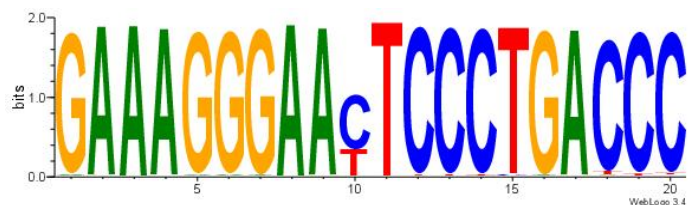
Dataset #: 1

Motif ID: 16
 Motif name: Motif 16
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.103246

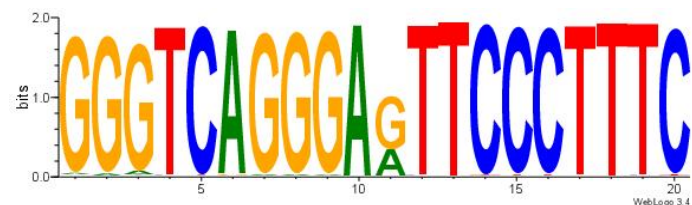
Alignment:

GGGTCAGGGAGTTC CCTTTC
 GTGCCAGGCACTG TKCTARG

Original motif Consensus sequence: GAAAGGGA ACTCCCTGACCC



Reverse complement motif Consensus sequence: GGGTCAGGGAGTTC CCTTTC



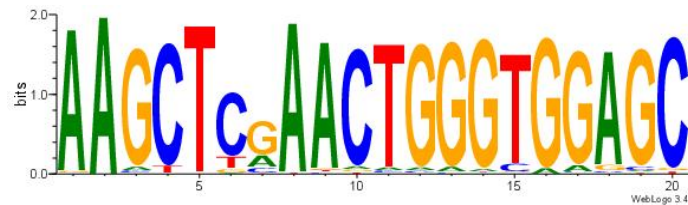
Dataset #: 1
 Motif ID: 321
 Motif name: Motif 321
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 20

Similarity score: 0.110477

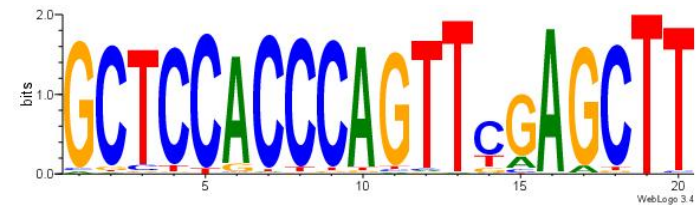
Alignment:

AAGCTCGAACTGGGTGGAGC
CMTAGYACAGTGCCTGGCAC

Original motif Consensus sequence: AAGCTCGAACTGGGTGGAGC



Reverse complement motif Consensus sequence:
GCTCCACCCAGTTCGAGCTT



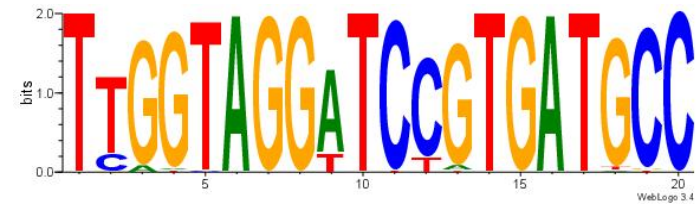
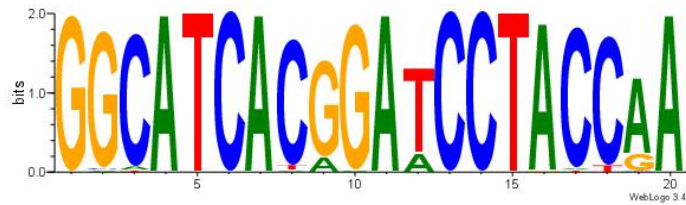
Dataset #: 1
Motif ID: 311
Motif name: Motif 311
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 20
Similarity score: 0.110507

Alignment:

GGCATCACGGATCCTACCAA
CMTAGYACAGTGCCTGGCAC

Original motif Consensus sequence: GGCATCACGGATCCTACCAA

Reverse complement motif Consensus sequence:
TTGGTAGGATCCGTGATGCC

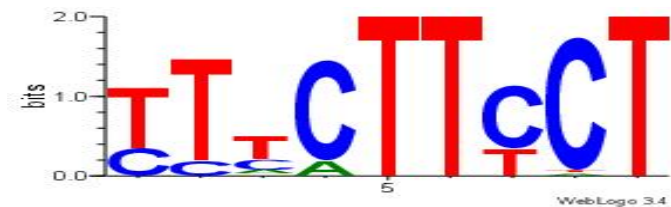


Dataset #: 1 Motif ID: 77 Motif name: Motif 77

Original motif Consensus sequence: AGGAAGAA



Reverse complement motif Consensus sequence: TTTCTTCCT



Best Matches for Motif ID 77 (Highest to Lowest)

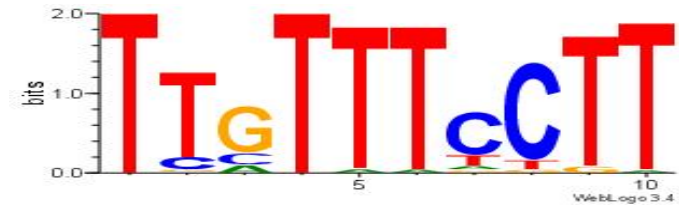
Dataset #:	1
Motif ID:	173
Motif name:	Motif 173
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	9
Similarity score:	0.0441796

Alignment:
 TTGTTTCCTT
 TTTCTTCCT-

Original motif Consensus sequence: AAGGAAACAA



Reverse complement motif Consensus sequence: TTGTTTCCTT

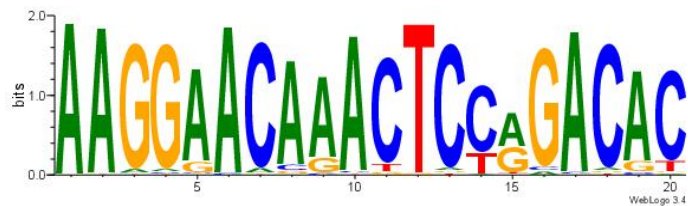


Dataset #: 1
Motif ID: 234
Motif name: Motif 234
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 2
Number of overlap: 9
Similarity score: 0.0447051

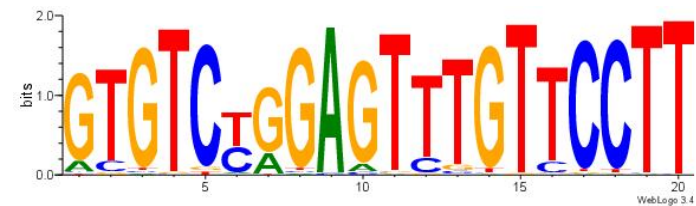
Alignment:

AAGGAACAAACTCCRGACAC
-AGGAAGAAA-----

Original motif Consensus sequence: AAGGAACAAACTCCRGACAC



Reverse complement motif Consensus sequence: GTGTCGGAGTTTGTTCCTT

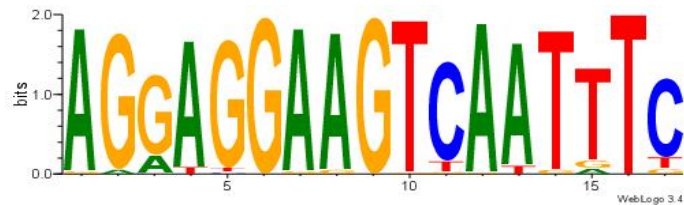


Dataset #: 1
 Motif ID: 327
 Motif name: Motif 327
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 4
 Number of overlap: 9
 Similarity score: 0.0555228

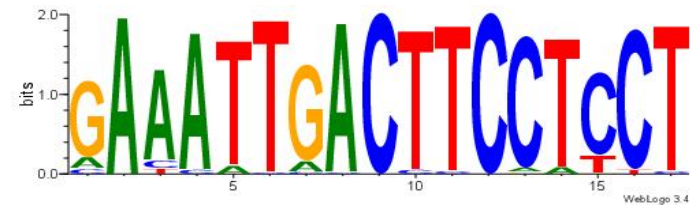
Alignment:

GAAATTGACTTCCTCCT
 -----TTTCTTCCT----

Original motif Consensus sequence: AGGAGGAAGTCAATTC



Reverse complement motif Consensus sequence: GAAATTGACTTCCTCCT

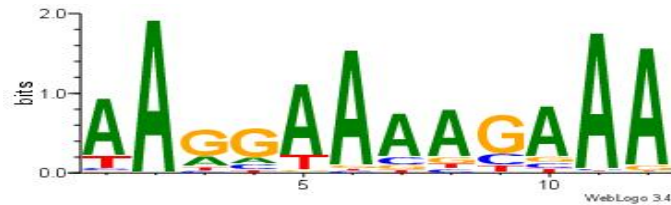


Dataset #: 1
 Motif ID: 54
 Motif name: Motif 54
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3

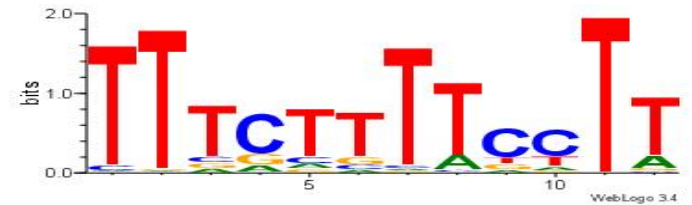
Number of overlap: 9
Similarity score: 0.0606671

Alignment:
TTTCTTTTCCTT
--TTTCTTCCT-

Original motif Consensus sequence: AAGGAAAAGAAA



Reverse complement motif Consensus sequence: TTTCTTTTCCTT

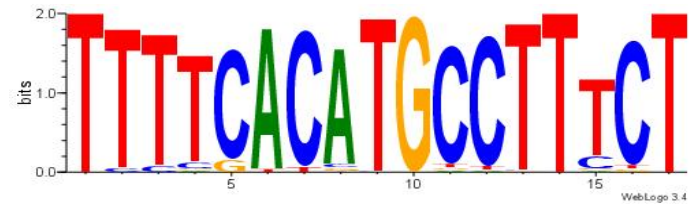
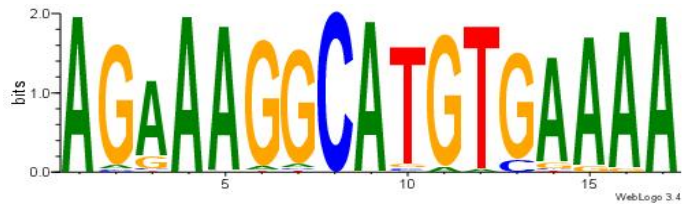


Dataset #: 1
Motif ID: 230
Motif name: Motif 230
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 9
Number of overlap: 9
Similarity score: 0.0607922

Alignment:
AGAAAGGCATGTGAAAA
AGGAAGAAA-----

Original motif Consensus sequence: AGAAAGGCATGTGAAAA

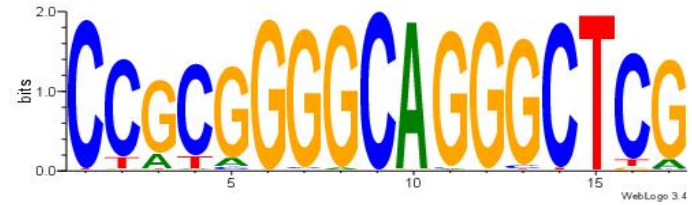
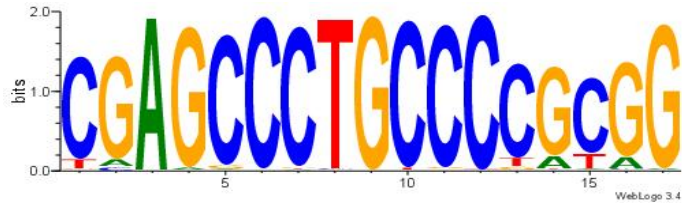
Reverse complement motif Consensus sequence:
TTTTCACATGCCTTTCT



Dataset #: 1 Motif ID: 78 Motif name: Motif 78

Original motif Consensus sequence: CGAGCCCTGCCCGCGG

Reverse complement motif Consensus sequence: CCGCGGGGCAGGGCTCG



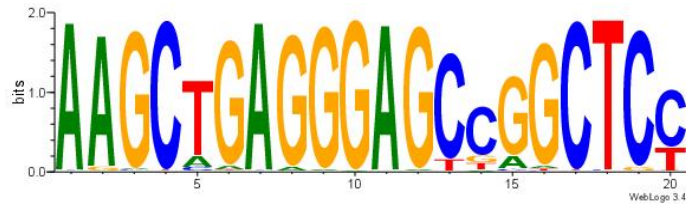
Best Matches for Motif ID 78 (Highest to Lowest)

Dataset #:	1
Motif ID:	96
Motif name:	Motif 96
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	17
Similarity score:	0.0803184

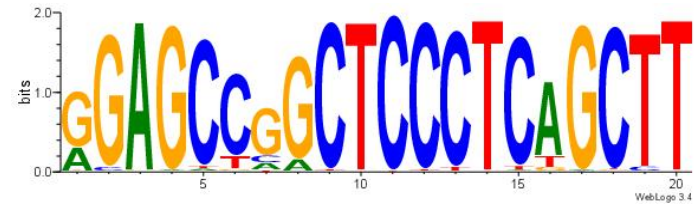
Alignment:

AAGCTGAGGGAGCCGGCTCC
---CCGCGGGGCAGGGCTCG

Original motif Consensus sequence: AAGCTGAGGGAGCCGGCTCC



Reverse complement motif Consensus sequence:
GGAGCCGGCTCCCTCAGCTT

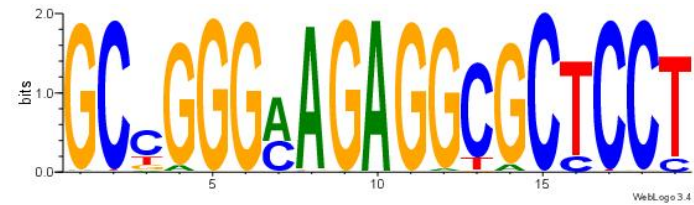
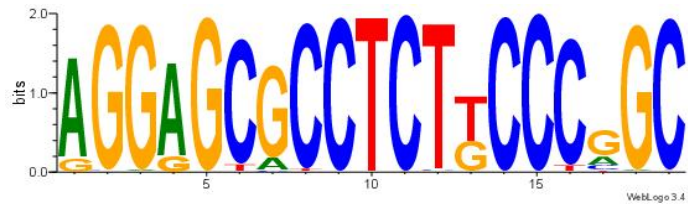


Dataset #: 1
Motif ID: 30
Motif name: Motif 30
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 2
Number of overlap: 17
Similarity score: 0.0851642

Alignment:
GCCGGGRAGAGGCGCTCCT
-CCGCGGGGCAGGGCTCG-

Original motif Consensus sequence: AGGAGCGCCTCTKCCCGGC

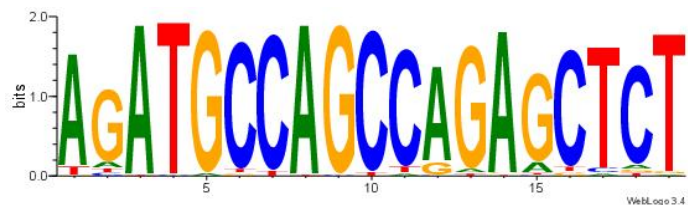
Reverse complement motif Consensus sequence:
GCCGGGRAGAGGCGCTCCT



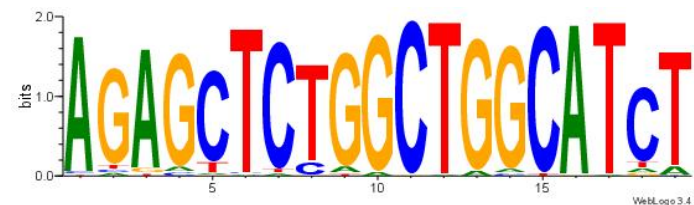
Dataset #: 1
 Motif ID: 307
 Motif name: Motif 307
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 17
 Similarity score: 0.0879196

Alignment:
 AGAGCTCTGGCTGGCATCT
 CGAGCCCTGCCCGCGG--

Original motif Consensus sequence: AGATGCCAGCCAGAGCTCT



Reverse complement motif Consensus sequence: AGAGCTCTGGCTGGCATCT



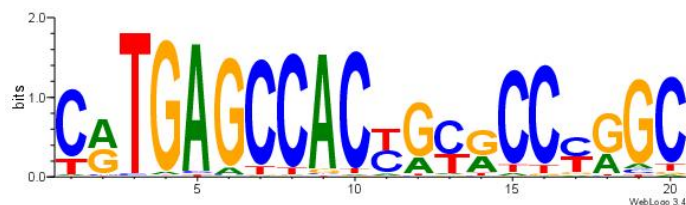
Dataset #: 1

Motif ID: 56
 Motif name: Motif 56
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 17
 Similarity score: 0.0902181

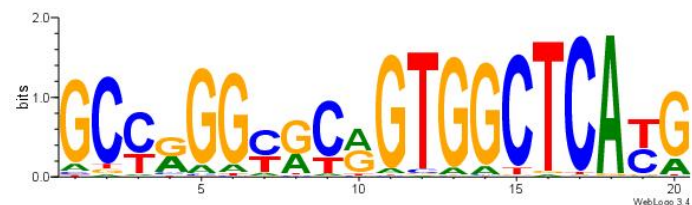
Alignment:

GCCKGGMKCMGTGGCTCAKG
 -CCGCGGGGCAGGGCTCG--

Original motif Consensus sequence: CRTGAGCCACYGYRCCYGGC



Reverse complement motif Consensus sequence: GCCKGGMKCMGTGGCTCAKG



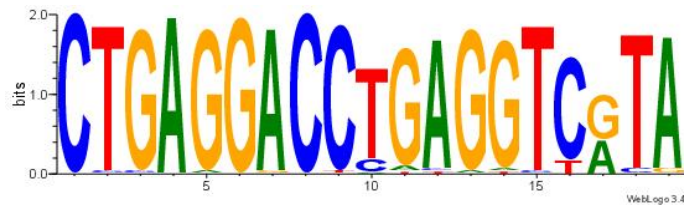
Dataset #: 1
 Motif ID: 291
 Motif name: Motif 291
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3
 Number of overlap: 17

Similarity score: 0.0910467

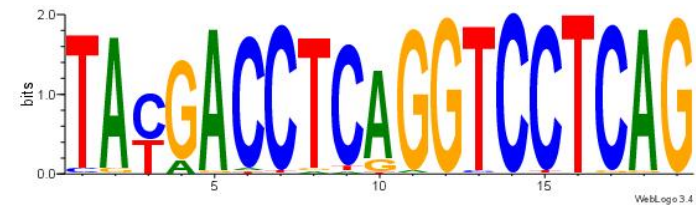
Alignment:

TAMGACCTCAGGTCCTCAG
--CGAGCCCTGCCCCGCGG

Original motif Consensus sequence: CTGAGGACCTGAGGTCGTA

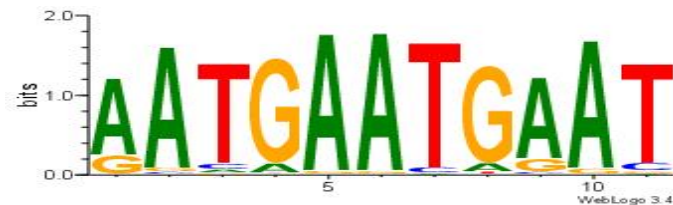


Reverse complement motif Consensus sequence: TAMGACCTCAGGTCCTCAG

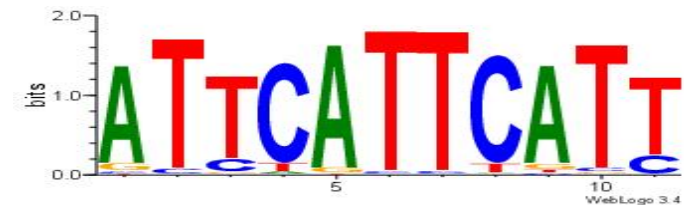


Dataset #: 1 Motif ID: 79 Motif name: Motif 79

Original motif Consensus sequence: AATGAATGAAT



Reverse complement motif Consensus sequence: ATTCATTCATT



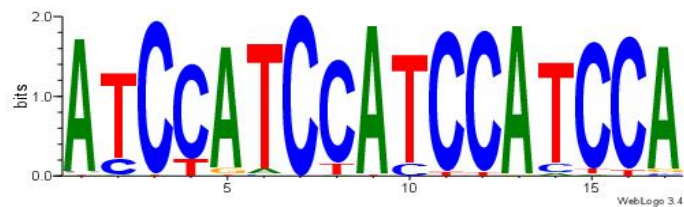
Best Matches for Motif ID 79 (Highest to Lowest)

Dataset #:	1
Motif ID:	341
Motif name:	Motif 341
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement

Direction: Forward
Position number: 3
Number of overlap: 11
Similarity score: 0.0536965

Alignment:
TGGATGGATGGATGGAT
--AATGAATGAAT-----

Original motif Consensus sequence: ATCCATCCATCCATCCA



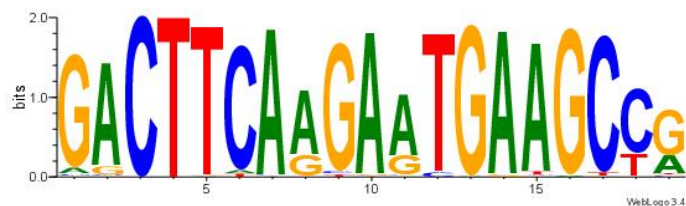
Reverse complement motif Consensus sequence: TGGATGGATGGATGGAT



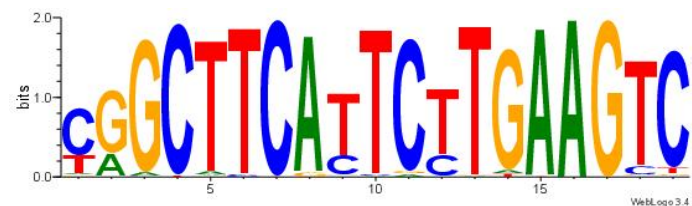
Dataset #: 1
Motif ID: 211
Motif name: Motif 211
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 4
Number of overlap: 11
Similarity score: 0.0549499

Alignment:
CGGCTTCATTCTTGAAGTC
---ATTCATTCATT-----

Original motif Consensus sequence: GACTTCAAGAATGAAGCCG



Reverse complement motif Consensus sequence: CGGCTTCATTCTGAAGTC

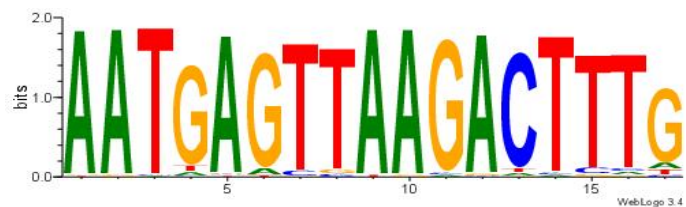


Dataset #: 1
Motif ID: 224
Motif name: Motif 224
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 7
Number of overlap: 11
Similarity score: 0.0557571

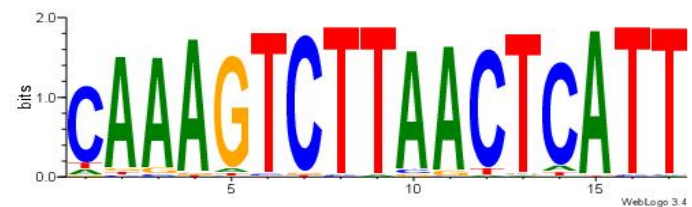
Alignment:

```
CAAAGTCTTAACTCATT  
-----ATTCATTCATT
```

Original motif Consensus sequence: AATGAGTTAAGACTTTG



Reverse complement motif Consensus sequence: CAAAGTCTTAACTCATT

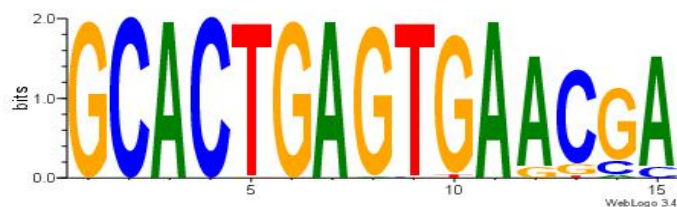


Dataset #: 1
 Motif ID: 241
 Motif name: Motif 241
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 11
 Similarity score: 0.0618186

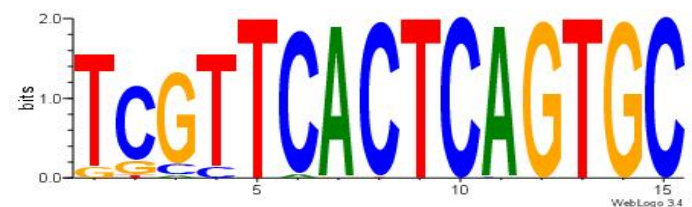
Alignment:

GCACTGAGTGAACGA
 --AATGAATGAAT--

Original motif Consensus sequence: GCACTGAGTGAACGA



Reverse complement motif Consensus sequence: TCGTTCAGTGC



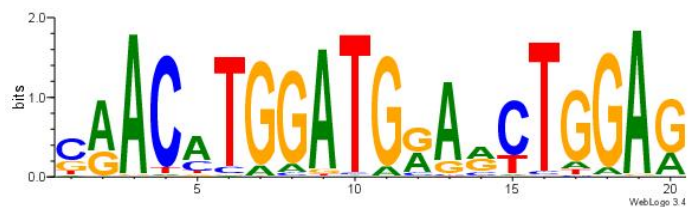
Dataset #: 1
 Motif ID: 104
 Motif name: Motif 104
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 7
 Number of overlap: 11

Similarity score: 0.0646429

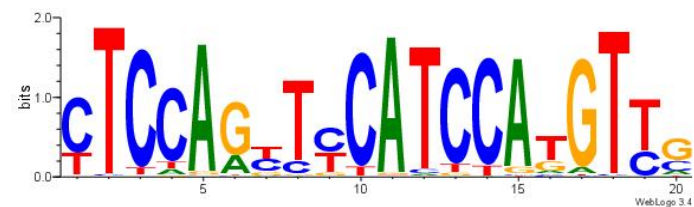
Alignment:

```
CAACATGGATGRARCTGGAG  
---AATGAATGAAT-----
```

Original motif Consensus sequence: CAACATGGATGRARCTGGAG

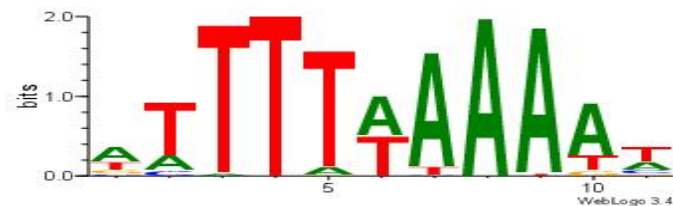


Reverse complement motif Consensus sequence: CTCCAGKTMCATCCATGTTG

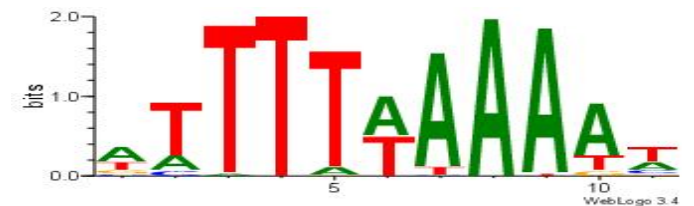


Dataset #: 1 Motif ID: 80 Motif name: Motif 80

Original motif Consensus sequence: WTTTTWAAA AW



Reverse complement motif Consensus sequence: WTTTTWAAA AW



Best Matches for Motif ID 80 (Highest to Lowest)

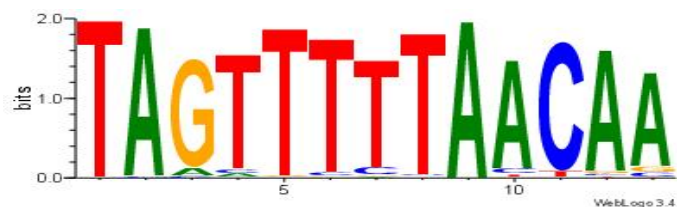
Dataset #:	1
Motif ID:	319
Motif name:	Motif 319
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif

Direction: Backward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.0536456

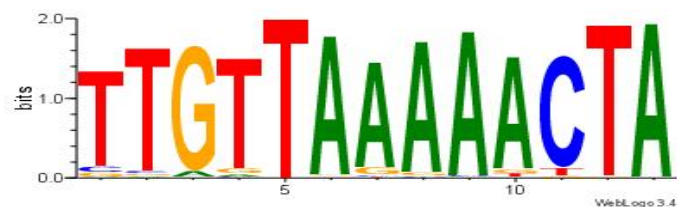
Alignment:

TAGTTTTTAACAA
 --WTTTTWAAAAW

Original motif Consensus sequence: TAGTTTTTAACAA



Reverse complement motif Consensus sequence: TTGTTAAAACTA

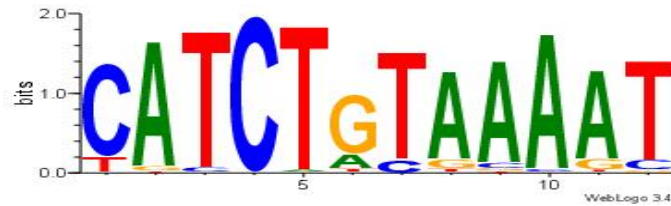


Dataset #: 1
 Motif ID: 81
 Motif name: Motif 81
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 11
 Similarity score: 0.0558466

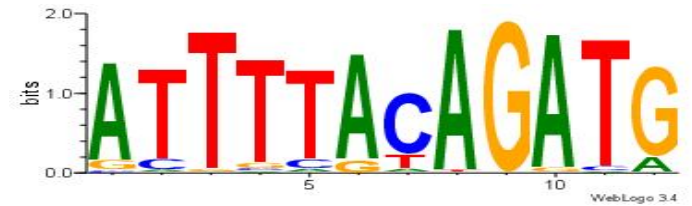
Alignment:

ATTTTACAGATG
 WTTTTWAAAAW-

Original motif Consensus sequence: CATCTGTAAAAT



Reverse complement motif Consensus sequence: ATTTTACAGATG

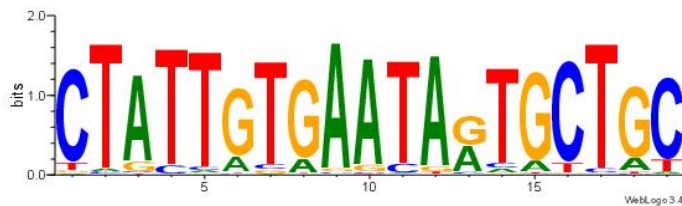


Dataset #: 1
Motif ID: 70
Motif name: Motif 70
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 3
Number of overlap: 11
Similarity score: 0.0629985

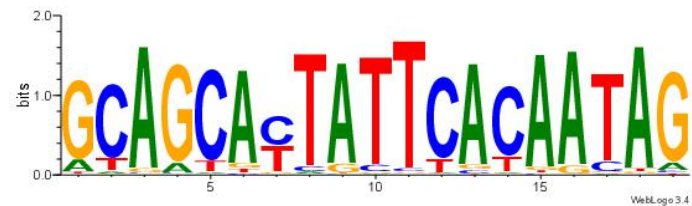
Alignment:

```
GCAGCAMTATTCACAATAG  
-----WTTTTWAAAAW--
```

Original motif Consensus sequence: CTATTGTGAATARTGCTGC



Reverse complement motif Consensus sequence:
GCAGCAMTATTCACAATAG

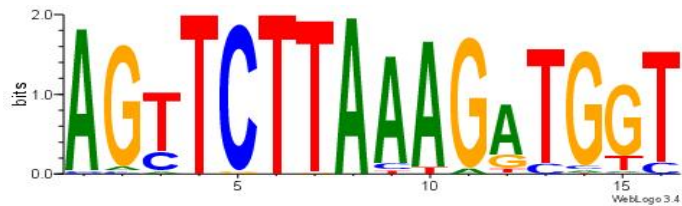


Dataset #: 1
 Motif ID: 303
 Motif name: Motif 303
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 4
 Number of overlap: 11
 Similarity score: 0.0640096

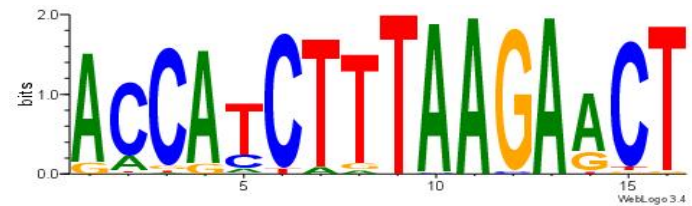
Alignment:

AGTTCTTAAAGATGGT
 --WTTTTWAAAAW---

Original motif Consensus sequence: AGTTCTTAAAGATGGT



Reverse complement motif Consensus sequence: ACCATCTTAAAGAACT



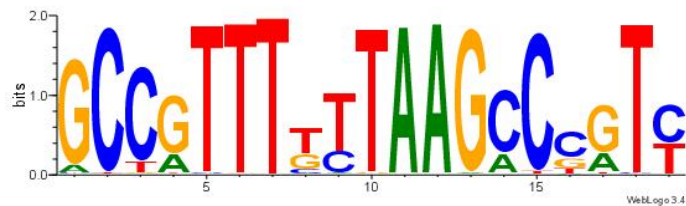
Dataset #: 1
 Motif ID: 21
 Motif name: Motif 21
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4

Number of overlap: 11
 Similarity score: 0.0694174

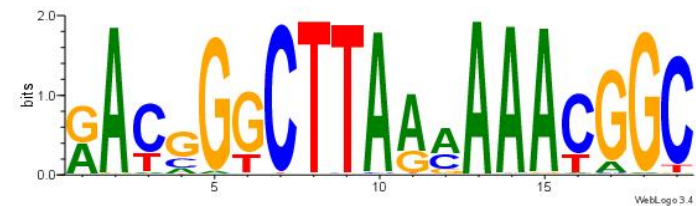
Alignment:

GCCGTTTKTTAAGCCCGTY
 ---WTTTWWAAA---

Original motif Consensus sequence: GCCGTTTKTTAAGCCCGTY

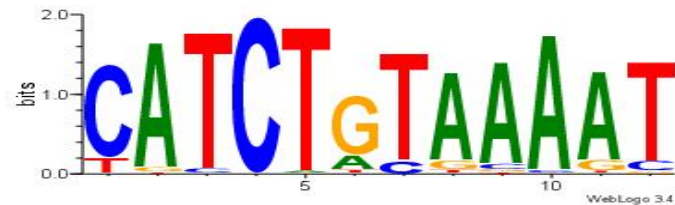


Reverse complement motif Consensus sequence:
 KACGGGCTTAARAAACGGC

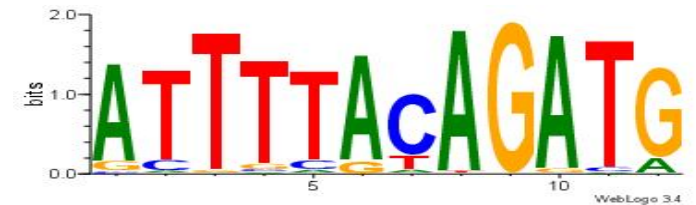


Dataset #: 1 Motif ID: 81 Motif name: Motif 81

Original motif Consensus sequence: CATCTGTAAAAT



Reverse complement motif Consensus sequence: ATTTTACAGATG



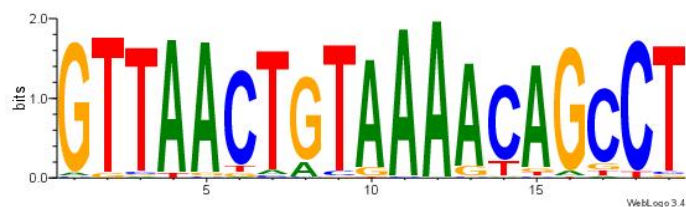
Best Matches for Motif ID 81 (Highest to Lowest)

Dataset #: 1
 Motif ID: 233
 Motif name: Motif 233
 Matching format of first motif: Original Motif

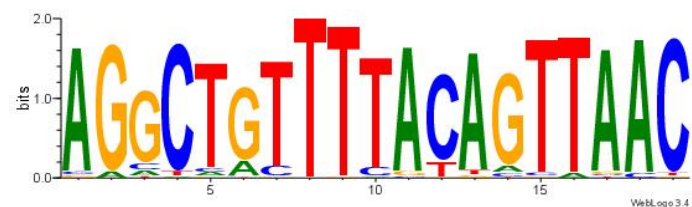
Matching format of second motif: Original Motif
Direction: Forward
Position number: 3
Number of overlap: 12
Similarity score: 0.0547757

Alignment:
GTAACTGTAAAACAGCCT
--CATCTGTAAAAT-----

Original motif Consensus sequence: GTAACTGTAAAACAGCCT



Reverse complement motif Consensus sequence:
AGGCTGTTTACAGTTAAC

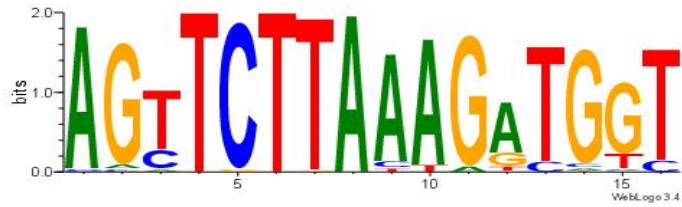


Dataset #: 1
Motif ID: 303
Motif name: Motif 303
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 3
Number of overlap: 12
Similarity score: 0.0658845

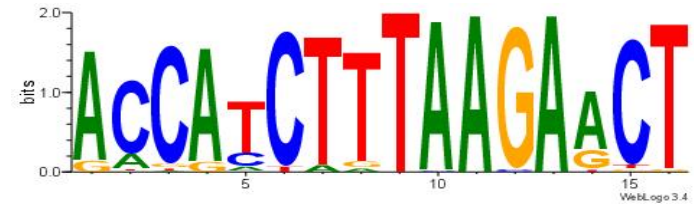
Alignment:

AGTTCTTAAAGATGGT
--ATTTTACAGATG--

Original motif Consensus sequence: AGTTCTTAAAGATGGT



Reverse complement motif Consensus sequence:
ACCATCTTTAAGAACT

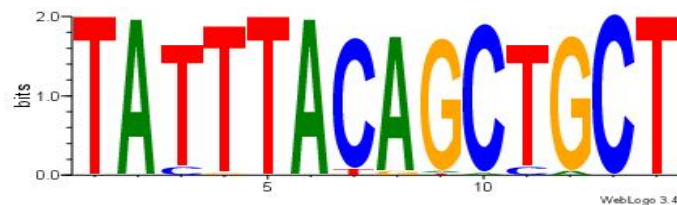
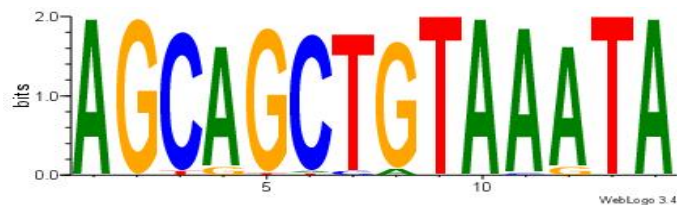


Dataset #:	1
Motif ID:	325
Motif name:	Motif 325
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	12
Similarity score:	0.068248

Alignment:
TATTTACAGCTGCT
ATTTTACAGATG--

Original motif Consensus sequence: AGCAGCTGTAATA

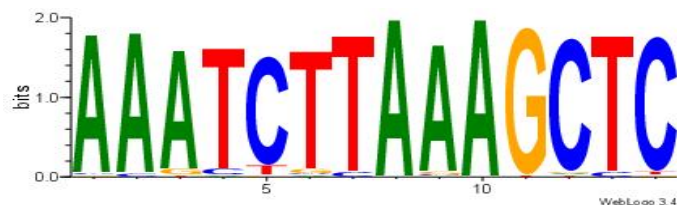
Reverse complement motif Consensus sequence: TATTTACAGCTGCT



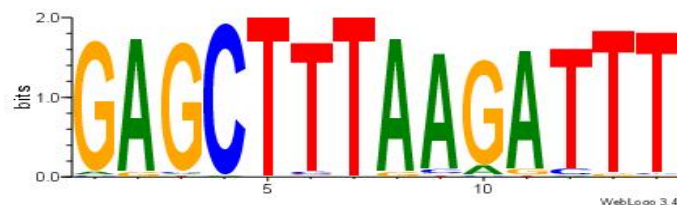
Dataset #: 1
 Motif ID: 346
 Motif name: Motif 346
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 12
 Similarity score: 0.0776147

Alignment:
 AAATCTTAAAGCTC
 --ATTTTACAGATG

Original motif Consensus sequence: AAATCTTAAAGCTC



Reverse complement motif Consensus sequence: GAGCTTTAAGATTT



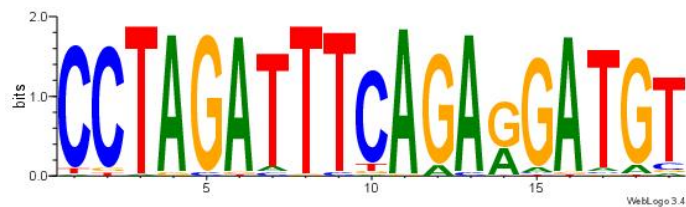
Dataset #: 1
 Motif ID: 280

Motif name: Motif 280
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 5
 Number of overlap: 12
 Similarity score: 0.0783249

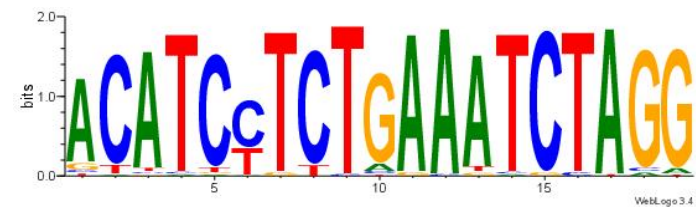
Alignment:

ACATCMTCTGAAATCTAGG
 ----CATCTGTAAAAT----

Original motif Consensus sequence: CCTAGATTTcAGAGgGATGT

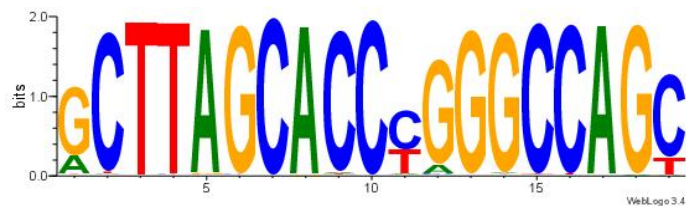


Reverse complement motif Consensus sequence: ACATCMTCTGAAATCTAGG

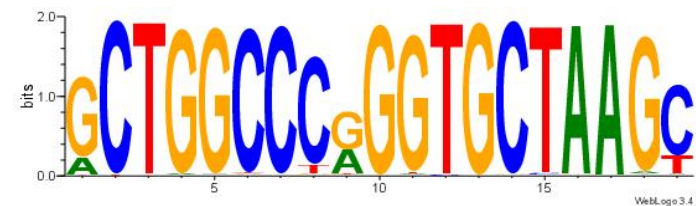


Dataset #: 1 Motif ID: 82 Motif name: Motif 82

Original motif Consensus sequence: GCTTAGCACCCcGGGCCAGc



Reverse complement motif Consensus sequence: GCTGGCCCKGGTGCTAAGC



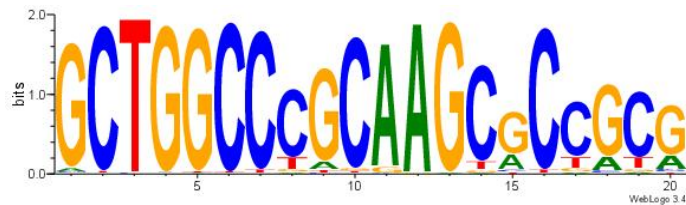
Best Matches for Motif ID 82 (Highest to Lowest)

Dataset #: 1
Motif ID: 100
Motif name: Motif 100
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 19
Similarity score: 0.0733424

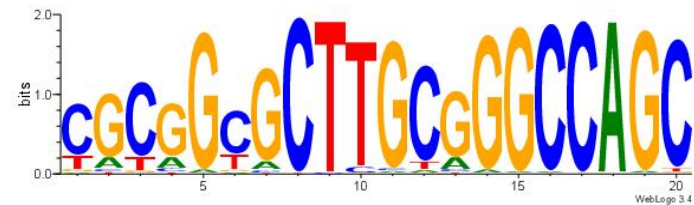
Alignment:

```
CGCGGCGCTTGCGGGCCAGC  
-GCTTAGCACCYGGGCCAGC
```

Original motif Consensus sequence: GCTGGCCCGCAAGCGCCGCG



Reverse complement motif Consensus sequence: CGCGGCGCTTGCGGGCCAGC



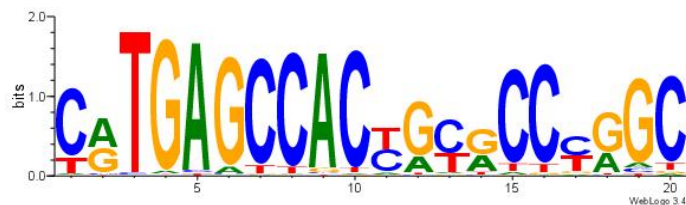
Dataset #: 1
Motif ID: 56
Motif name: Motif 56
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement

Direction: Backward
 Position number: 1
 Number of overlap: 19
 Similarity score: 0.104947

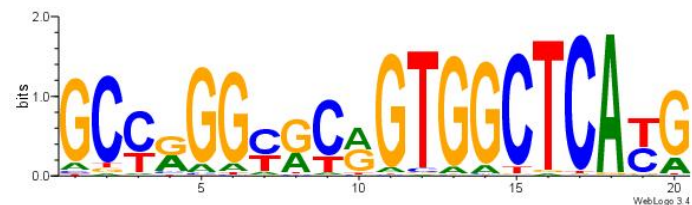
Alignment:

GCCKGGMKCMGTGGCTCAKG
 -GCTGGCCCKGGTGCTAAGC

Original motif Consensus sequence: CRTGAGCCACYGYRCCYGGC



Reverse complement motif Consensus sequence: GCCKGGMKCMGTGGCTCAKG

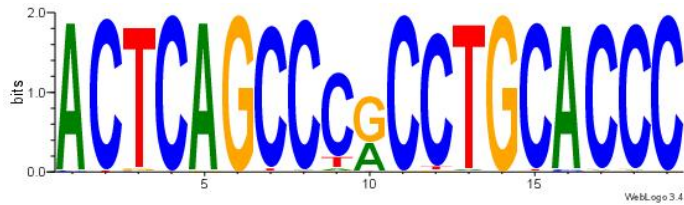


Dataset #: 1
 Motif ID: 149
 Motif name: Motif 149
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 19
 Similarity score: 0.10979

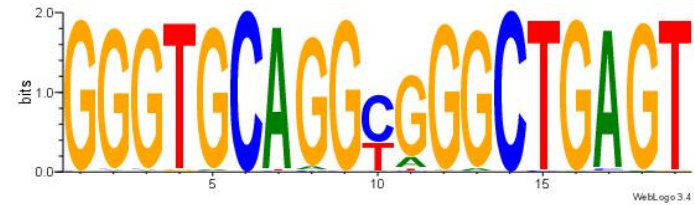
Alignment:

ACTCAGCCRCCTGCACCC
 GCTTAGCACCYGGGCCAGC

Original motif Consensus sequence: ACTCAGCCRCCTGCACCC



Reverse complement motif Consensus sequence: GGGTGCAGMGGGCTGAGT

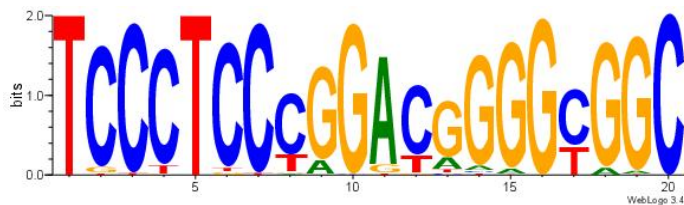


Dataset #: 1
Motif ID: 155
Motif name: Motif 155
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 2
Number of overlap: 19
Similarity score: 0.114535

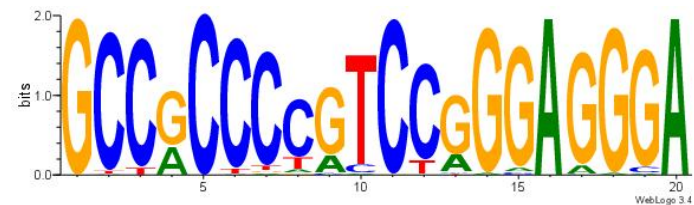
Alignment:

TCCCTCCCGGACGGGGYGGC
-GCTTAGCACCYGGGCCAGC

Original motif Consensus sequence: TCCCTCCCGGACGGGGYGGC



Reverse complement motif Consensus sequence: GCCKCCCCGTCCGGGAGGGA

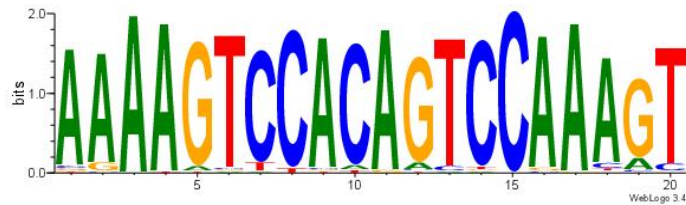


Dataset #: 1
 Motif ID: 171
 Motif name: Motif 171
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 19
 Similarity score: 0.115408

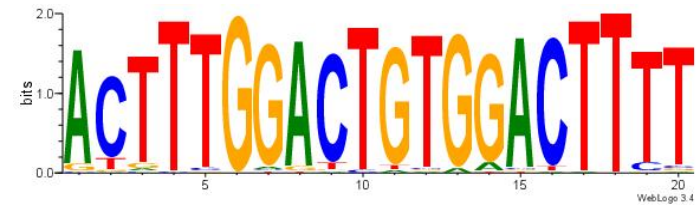
Alignment:

ACTTTGGACTGTGGACTTTT
 GCTTAGCACCYGGGCCAGC-

Original motif Consensus sequence: AAAAGTCCACAGTCCAAAGT



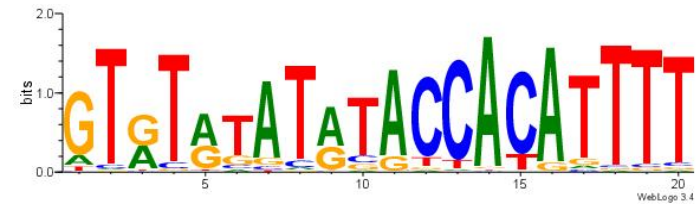
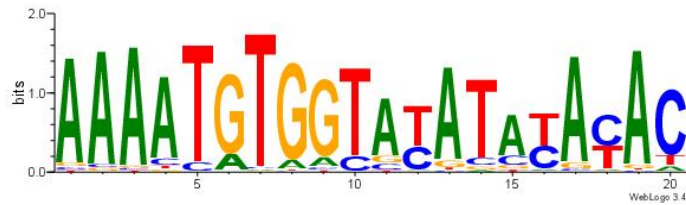
Reverse complement motif Consensus sequence: ACTTTGGACTGTGGACTTTT



Dataset #: 1 Motif ID: 83 Motif name: Motif 83

Original motif Consensus sequence: AAAATGTGGTAYATAYAYAC

Reverse complement motif Consensus sequence: GTKTMTATMTACCACATTTT

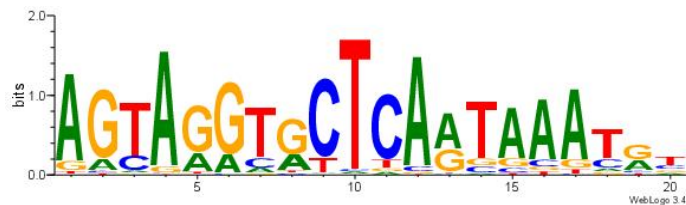


Best Matches for Motif ID 83 (Highest to Lowest)

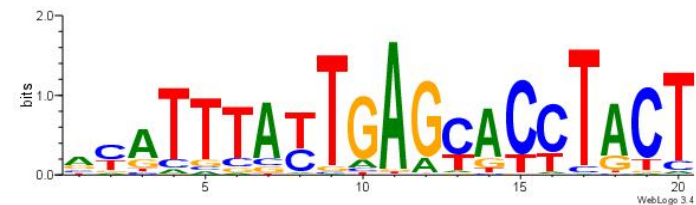
Dataset #: 1
 Motif ID: 86
 Motif name: Motif 86
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.100064

Alignment:
 AGTAGGTGCTCARTAAATRB
 AAAATGTGGTAYATAYAYAC

Original motif Consensus sequence: AGTAGGTGCTCARTAAATRB



Reverse complement motif Consensus sequence: VMATTTAKTGAGCACCTACT

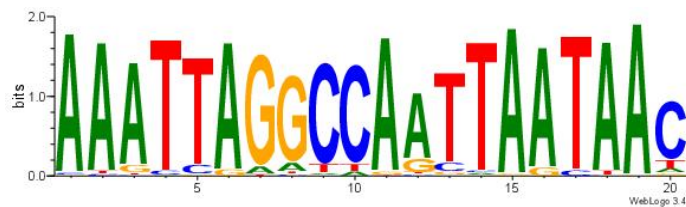


Dataset #: 1
 Motif ID: 308
 Motif name: Motif 308
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.110604

Alignment:

GTTATTAATTGGCCTAATTT
 GTKTMTATMTACCACATTTT

Original motif Consensus sequence: AAATTAGGCCAATTAATAAC



Reverse complement motif Consensus sequence: GTTATTAATTGGCCTAATTT



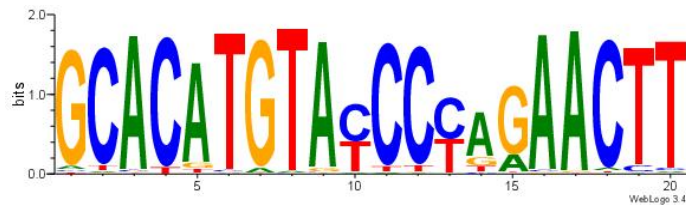
Dataset #: 1
 Motif ID: 225
 Motif name: Motif 225
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1

Number of overlap: 20
Similarity score: 0.110608

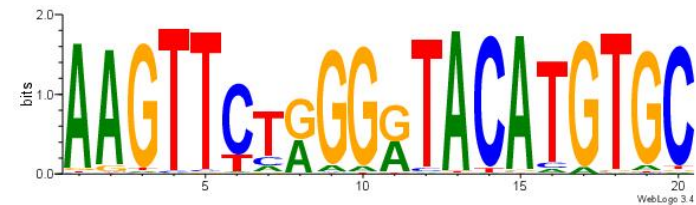
Alignment:

GCACATGTAYCCYAGAACTT
GTKTMTATMTACCACATTTT

Original motif Consensus sequence: GCACATGTAYCCYAGAACTT



Reverse complement motif Consensus sequence:
AAGTTCTKGGKTACATGTGC

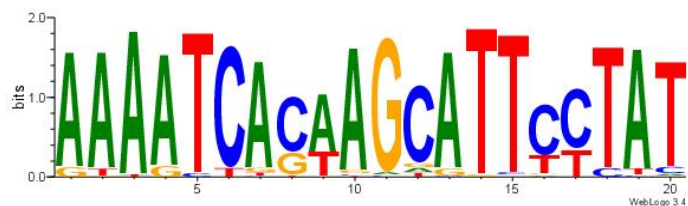


Dataset #: 1
Motif ID: 254
Motif name: Motif 254
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 20
Similarity score: 0.111201

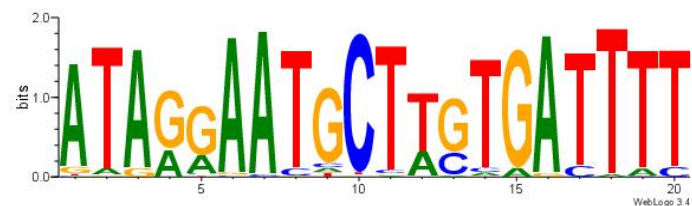
Alignment:

AAAATCACAAGCATTCTAT
AAAATGTGGTAYATAYAYAC

Original motif Consensus sequence: AAAATCACAAGCATTCTAT



Reverse complement motif Consensus sequence: ATAGGAATGCTTGTGATTTT

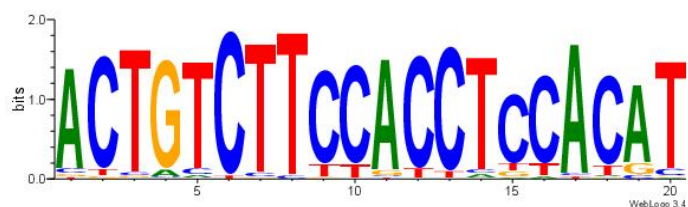


Dataset #: 1
Motif ID: 178
Motif name: Motif 178
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 20
Similarity score: 0.120185

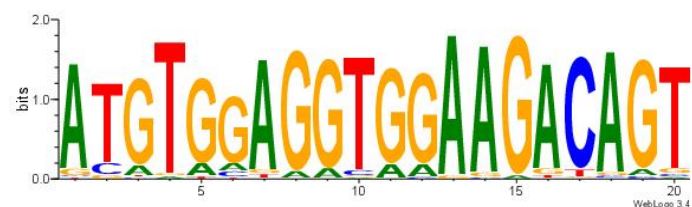
Alignment:

ACTGTCTTCCACCTCCACAT
AAAATGTGGTAYATAYAYAC

Original motif Consensus sequence: ACTGTCTTCCACCTCCACAT

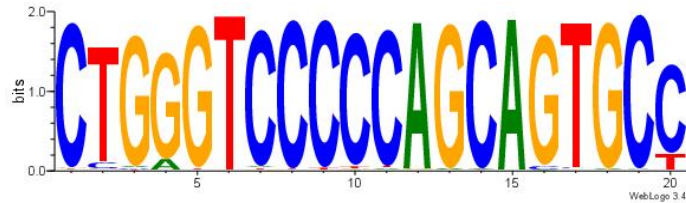


Reverse complement motif Consensus sequence: ATGTGGAGGTGGAAGACAGT

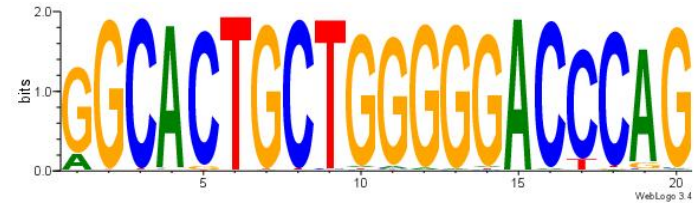


Dataset #: 1 Motif ID: 84 Motif name: Motif 84

Original motif Consensus sequence: CTGGGTCCCCCAGCAGTGCC



Reverse complement motif Consensus sequence: GGCAGTCTGGGGGACCCAG



Best Matches for Motif ID 84 (Highest to Lowest)

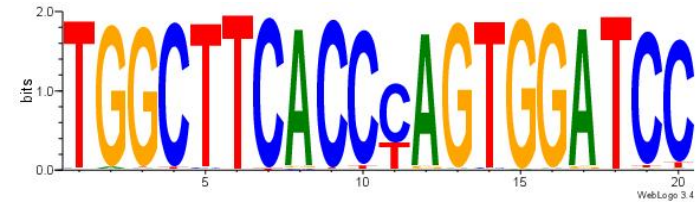
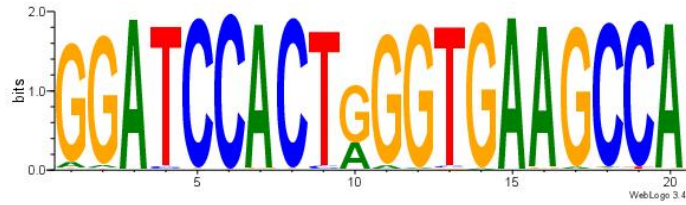
Dataset #:	1
Motif ID:	61
Motif name:	Motif 61
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	20
Similarity score:	0.106094

Alignment:

```
TGGCTTCACCCAGTGGATCC  
CTGGGTCCCCCAGCAGTGCC
```

Original motif Consensus sequence: GGATCCACTGGGTGAAGCCA

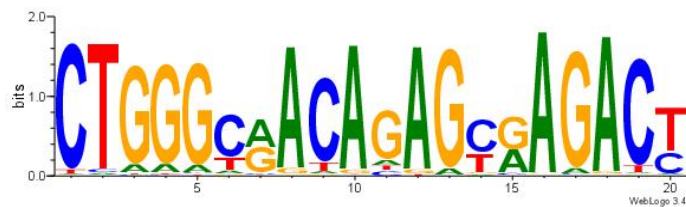
Reverse complement motif Consensus sequence:
TGGCTTCACCCAGTGGATCC



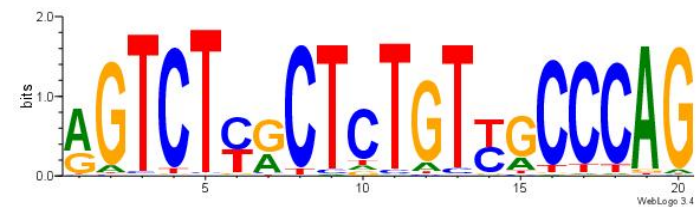
Dataset #: 1
 Motif ID: 29
 Motif name: Motif 29
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.107291

Alignment:
 CTGGGCRACAGAGYRAGACY
 CTGGGTCCCCCAGCAGTGCC

Original motif Consensus sequence: CTGGGCRACAGAGYRAGACY



Reverse complement motif Consensus sequence: MGTCTMKCTCTGKGGCCAG



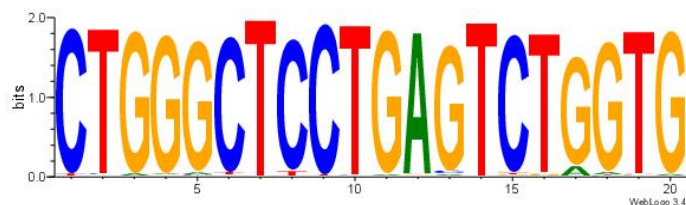
Dataset #: 1

Motif ID: 67
 Motif name: Motif 67
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.113605

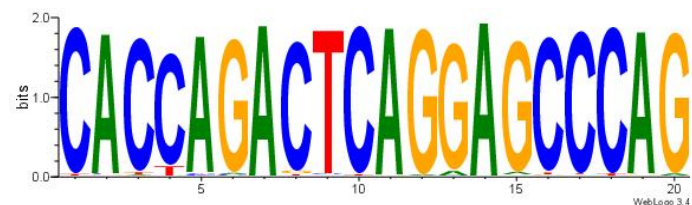
Alignment:

CACCAGACTCAGGAGCCCAG
 GGCCTGCTGGGGGACCCAG

Original motif Consensus sequence: CTGGGCTCCTGAGTCTGGTG



Reverse complement motif Consensus sequence: CACCAGACTCAGGAGCCCAG



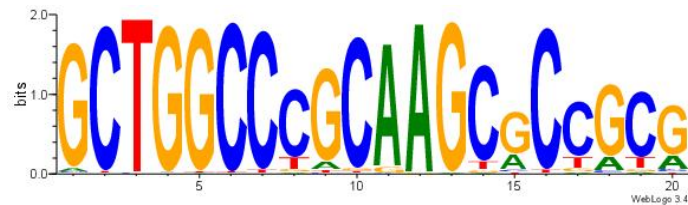
Dataset #: 1
 Motif ID: 100
 Motif name: Motif 100
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 20

Similarity score: 0.113686

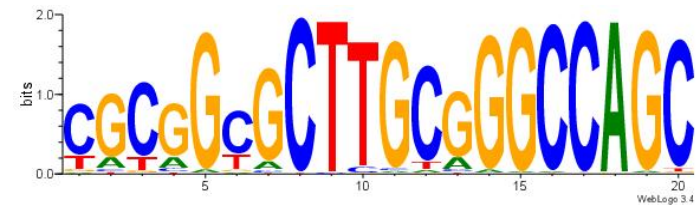
Alignment:

GCTGGCCCGCAAGCGCCGCG
CTGGGTCCCCCAGCAGTGCC

Original motif Consensus sequence: GCTGGCCCGCAAGCGCCGCG



Reverse complement motif Consensus sequence:
CGCGGCGCTTGCGGGCCAGC



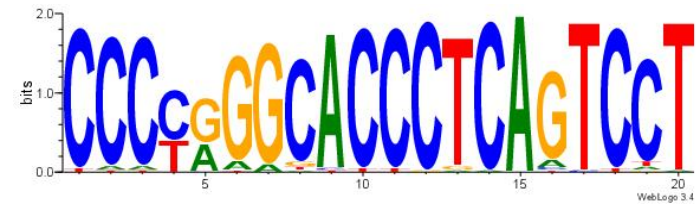
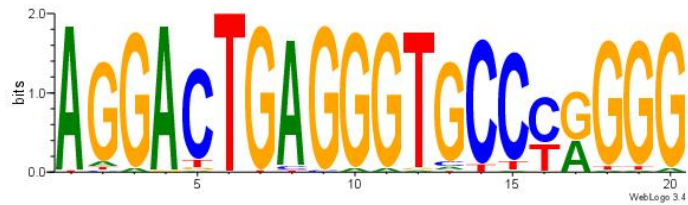
Dataset #: 1
Motif ID: 312
Motif name: Motif 312
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 20
Similarity score: 0.115597

Alignment:

CCCMKGGCACCCTCAGTCCT
CTGGGTCCCCCAGCAGTGCC

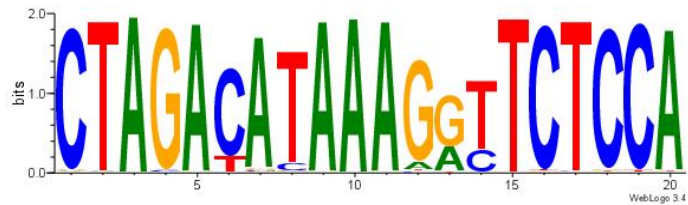
Original motif Consensus sequence: AGGACTGAGGGTGCCYRGGG

Reverse complement motif Consensus sequence:
CCCMKGGCACCCTCAGTCCT

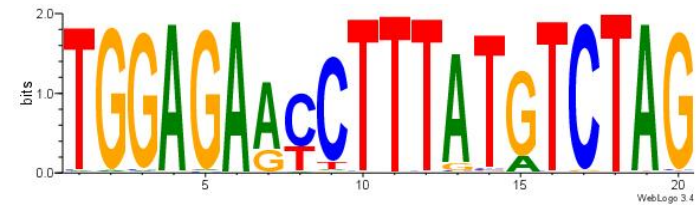


Dataset #: 1 Motif ID: 85 Motif name: Motif 85

Original motif Consensus sequence: CTAGACATAAAGGTTCTCCA



Reverse complement motif Consensus sequence: TGGAGAACCTTTATGTCTAG



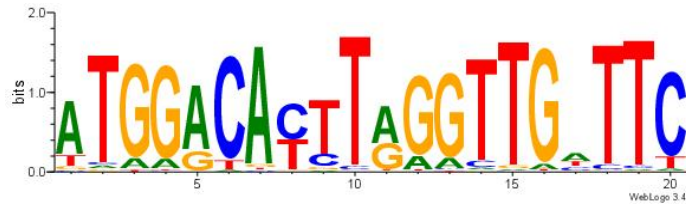
Best Matches for Motif ID 85 (Highest to Lowest)

Dataset #:	1
Motif ID:	58
Motif name:	Motif 58
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	20
Similarity score:	0.122722

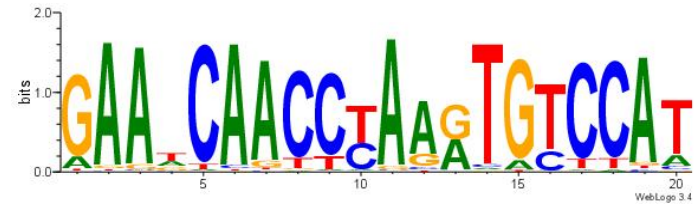
Alignment:

ATGGACAYTTRGGTTGHTTC
CTAGACATAAAGGTTCTCCA

Original motif Consensus sequence: ATGGACAYTTRGGTTGHTTC



Reverse complement motif Consensus sequence:
GAAHCAACCKAAKTGTCCAT



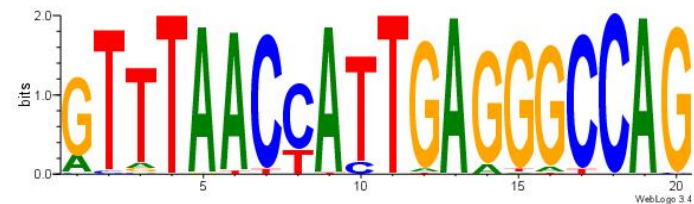
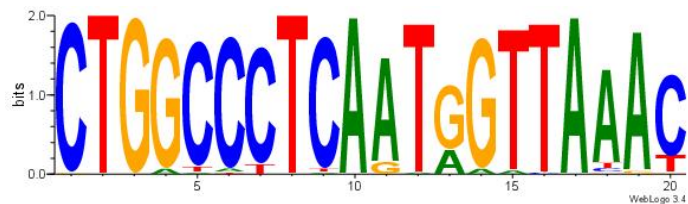
Dataset #: 1
Motif ID: 332
Motif name: Motif 332
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 20
Similarity score: 0.127727

Alignment:

GTTTAACCATTGAGGGCCAG
TGGAGAACCTTTATGTCTAG

Original motif Consensus sequence: CTGGCCCTCAATGGTTAAAC

Reverse complement motif Consensus sequence:
GTTTAACCATTGAGGGCCAG

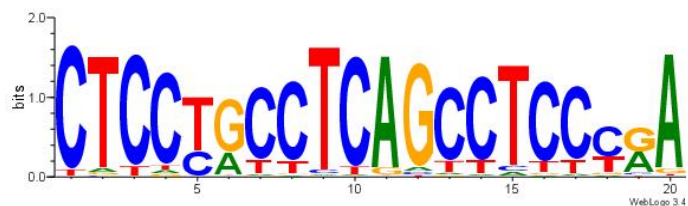


Dataset #: 1
 Motif ID: 26
 Motif name: Motif 26
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.1415

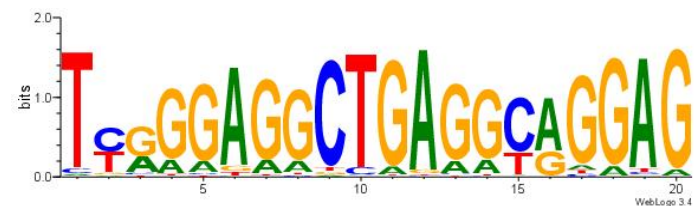
Alignment:

CTCCTGCCTCAGCCTCCRA
 CTAGACATAAAGGTTCTCCA

Original motif Consensus sequence: CTCCTGCCTCAGCCTCCRA



Reverse complement motif Consensus sequence: TMGGGAGGCTGAGGCAGGAG



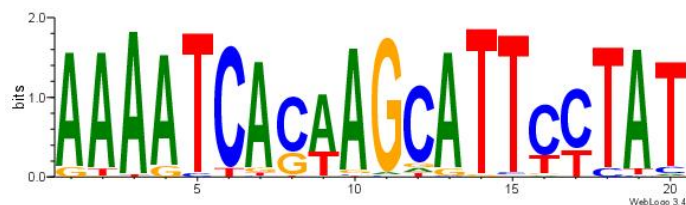
Dataset #: 1

Motif ID: 254
 Motif name: Motif 254
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.141611

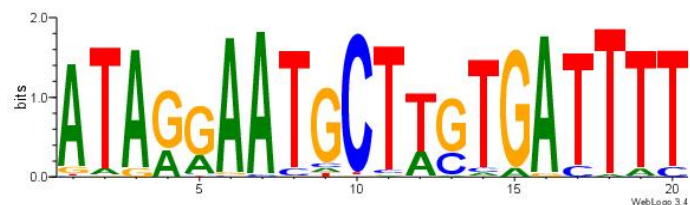
Alignment:

AAAATCACAAGCATTCTAT
 CTAGACATAAAGGTTCTCCA

Original motif Consensus sequence: AAAATCACAAGCATTCTAT



Reverse complement motif Consensus sequence: ATAGGAATGCTTGTGATTTT



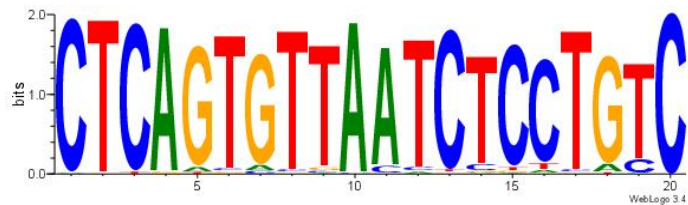
Dataset #: 1
 Motif ID: 262
 Motif name: Motif 262
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 20

Similarity score: 0.142355

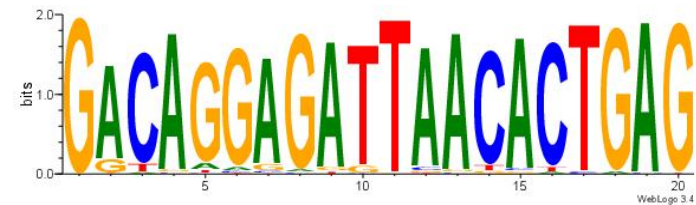
Alignment:

CTCAGTGTTAATCTCCTGTC
CTAGACATAAAGGTTCTCCA

Original motif Consensus sequence: CTCAGTGTTAATCTCCTGTC

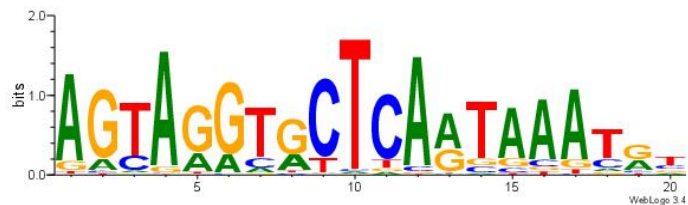


Reverse complement motif Consensus sequence: GACAGGAGATTAACACTGAG

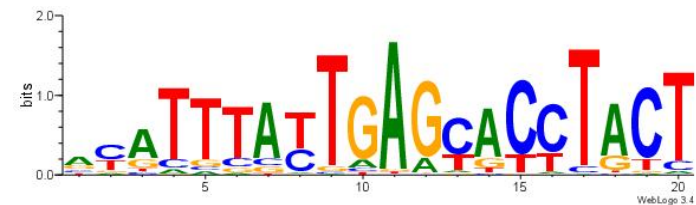


Dataset #: 1 Motif ID: 86 Motif name: Motif 86

Original motif Consensus sequence: AGTAGGTGCTCARTAAATRB



Reverse complement motif Consensus sequence: VMATTTAKTGAGCACCTACT



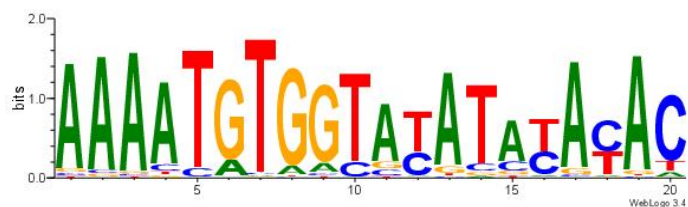
Best Matches for Motif ID 86 (Highest to Lowest)

Dataset #:	1
Motif ID:	83
Motif name:	Motif 83
Matching format of first motif:	Original Motif

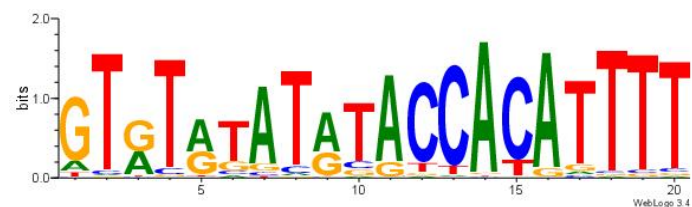
Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.0711295

Alignment:
 AAAATGTGGTAYATAYAYAC
 AGTAGGTGCTCARTAAATRB

Original motif Consensus sequence: AAAATGTGGTAYATAYAYAC



Reverse complement motif Consensus sequence: GTKTMTATMTACCACATTTT

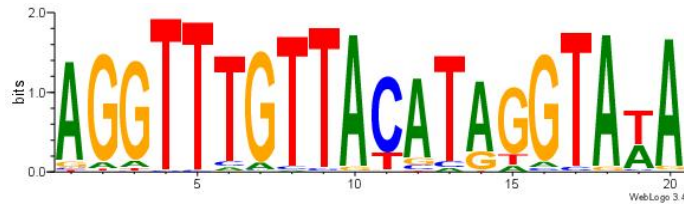


Dataset #: 1
 Motif ID: 137
 Motif name: Motif 137
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.0944134

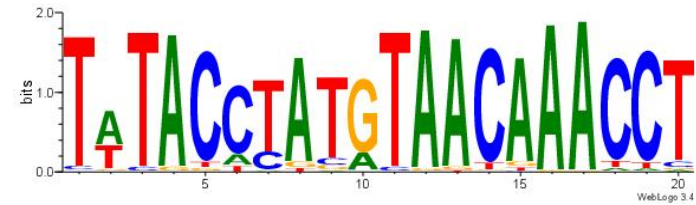
Alignment:

TWTACCTATGTAACAAACCT
AGTAGGTGCTCARTAAATRB

Original motif Consensus sequence: AGGTTTGTACATAGGTAWA



Reverse complement motif Consensus sequence:
TWTACCTATGTAACAAACCT

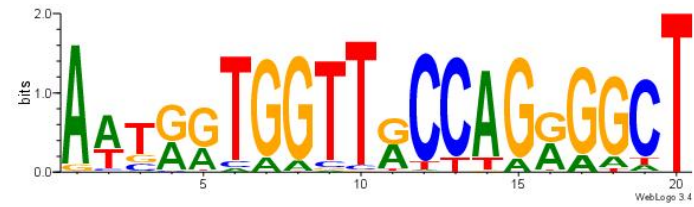
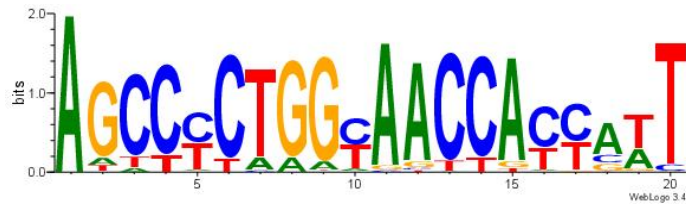


Dataset #: 1
Motif ID: 139
Motif name: Motif 139
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 20
Similarity score: 0.097593

Alignment:
AWTKKTGGTTKCCAGKGGCT
VMATTTAKTGAGCACCTACT

Original motif Consensus sequence: AGCCYCTGGYAACCAYYAWT

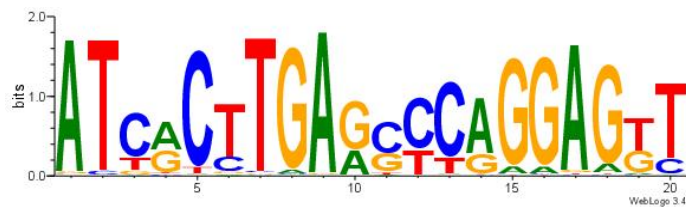
Reverse complement motif Consensus sequence:
AWTKKTGGTTKCCAGKGGCT



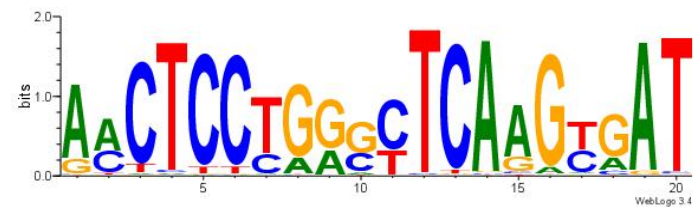
Dataset #: 1
 Motif ID: 8
 Motif name: Motif 8
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.0992318

Alignment:
 ARCTCCTGKSCTCAAGKGAT
 VMATTTAKTGAGCACCTACT

Original motif Consensus sequence: ATCRCTTGAGSYCAGGAGKT



Reverse complement motif Consensus sequence: ARCTCCTGKSCTCAAGKGAT



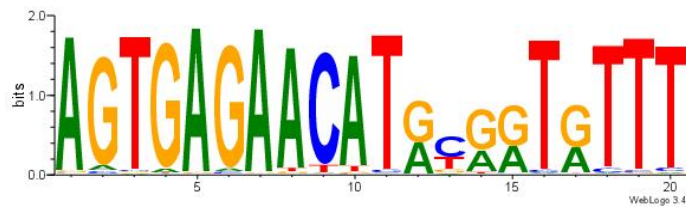
Dataset #: 1

Motif ID: 63
 Motif name: Motif 63
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.100826

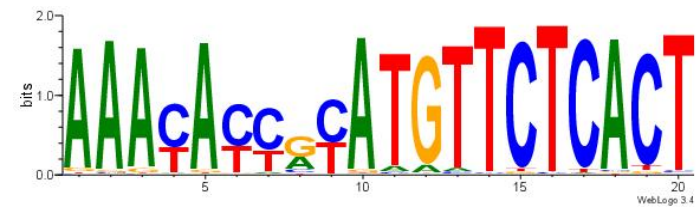
Alignment:

AGTGAGAACATRYRRTRTTT
 AGTAGGTGCTCARTAAATRB

Original motif Consensus sequence: AGTGAGAACATRYRRTRTTT

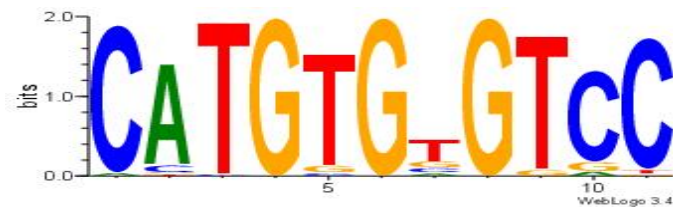


Reverse complement motif Consensus sequence: AAAMAMMKMATGTTCTCACT

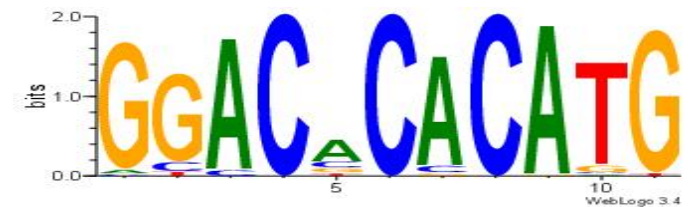


Dataset #: 1 Motif ID: 87 Motif name: Motif 87

Original motif Consensus sequence: CATGTGTG_GTcC



Reverse complement motif Consensus sequence: GGACACACATG



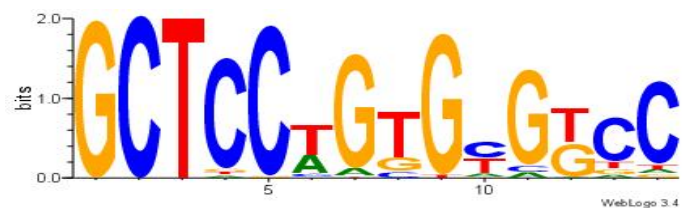
Best Matches for Motif ID 87 (Highest to Lowest)

Dataset #: 1
Motif ID: 206
Motif name: Motif 206
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 11
Similarity score: 0.0574969

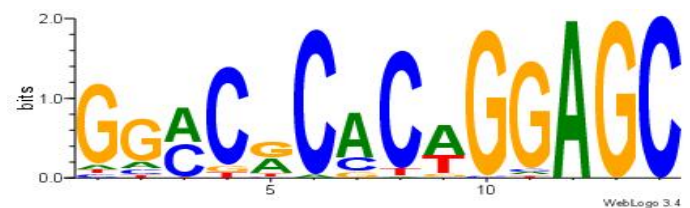
Alignment:

```
GCTCCWGTGYGKCC  
---CATGTGTGTCC
```

Original motif Consensus sequence: GCTCCWGTGYGKCC



Reverse complement motif Consensus sequence: GGRCKCACWGGAA

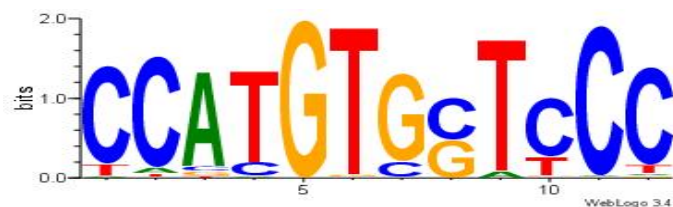


Dataset #: 1
Motif ID: 120
Motif name: Motif 120
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif

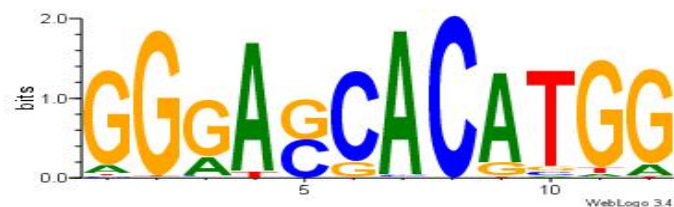
Direction: Forward
Position number: 2
Number of overlap: 11
Similarity score: 0.062082

Alignment:
CCATGTGSTCCC
-CATGTGTGTCC

Original motif Consensus sequence: CCATGTGSTCCC



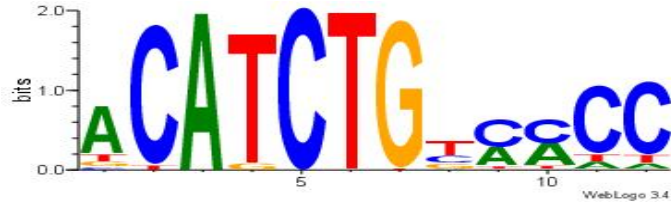
Reverse complement motif Consensus sequence: GGGASCACATGG



Dataset #: 1
Motif ID: 49
Motif name: Motif 49
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 2
Number of overlap: 11
Similarity score: 0.0650944

Alignment:
GRRMCAGATGT
GGACACACATG-

Original motif Consensus sequence: ACATCTGYMMCC



Reverse complement motif Consensus sequence: GGRRMCAGATGT

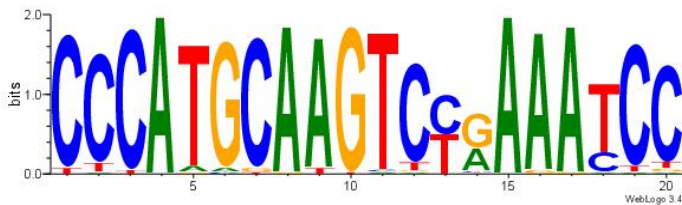


Dataset #: 1
Motif ID: 310
Motif name: Motif 310
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 3
Number of overlap: 11
Similarity score: 0.0757271

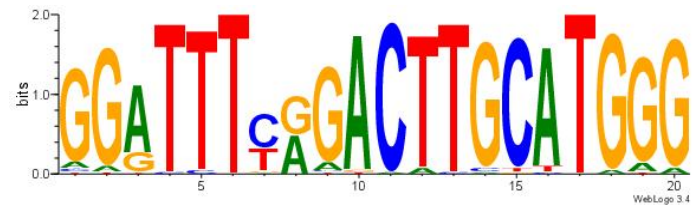
Alignment:

```
CCCATGCAAGTCYRAAATCC  
--CATGTGTGTCC-----
```

Original motif Consensus sequence: CCCATGCAAGTCYRAAATCC



Reverse complement motif Consensus sequence: GGATTTMKGACTTGCATGGG

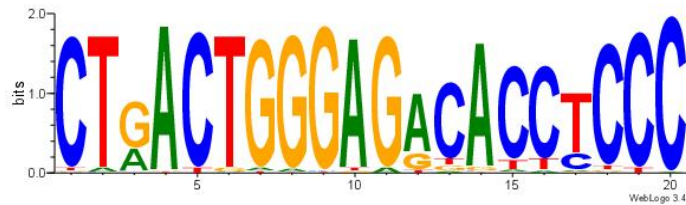


Dataset #: 1
 Motif ID: 293
 Motif name: Motif 293
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 8
 Number of overlap: 11
 Similarity score: 0.076468

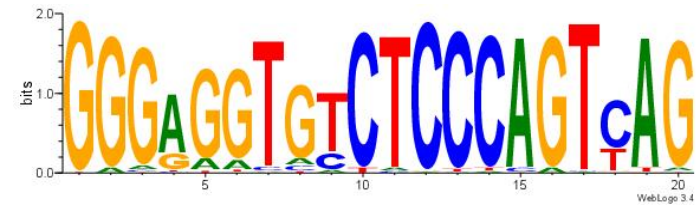
Alignment:

GGGAGGTGTCTCCCAGTCAG
 --CATGTGTGTCC-----

Original motif Consensus sequence: CTGACTGGGAGACACCTCCC



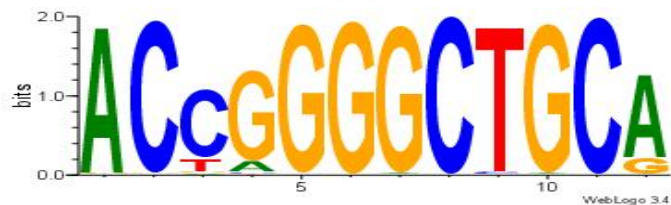
Reverse complement motif Consensus sequence: GGGAGGTGTCTCCCAGTCAG



Dataset #: 1 Motif ID: 88 Motif name: Motif 88

Original motif Consensus sequence: ACCGGGGCTGCA

Reverse complement motif Consensus sequence: TGCAGCCCCGGT

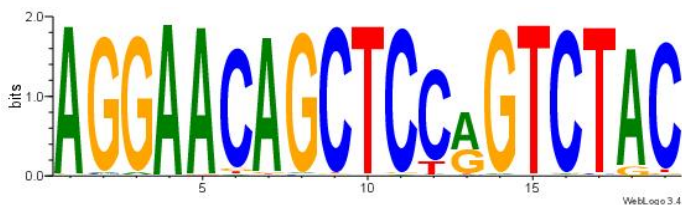


Best Matches for Motif ID 88 (Highest to Lowest)

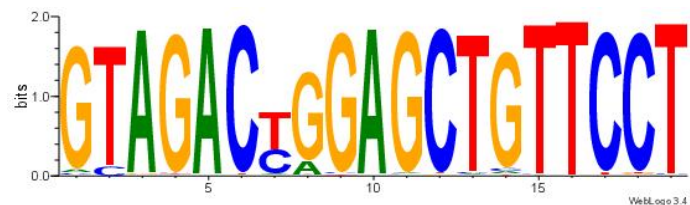
Dataset #: 1
 Motif ID: 62
 Motif name: Motif 62
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 4
 Number of overlap: 12
 Similarity score: 0.0744827

Alignment:
 GTAGACKGGAGCTGTTTCCT
 ---ACCGGGCTGCA----

Original motif Consensus sequence: AGGAACAGCTCCcGTCTAC



Reverse complement motif Consensus sequence: GTAGACKGGAGCTGTTTCCT

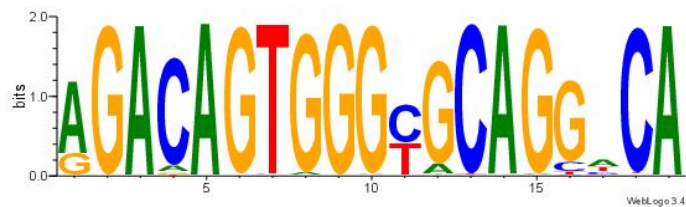


Dataset #: 1
 Motif ID: 17
 Motif name: Motif 17
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 12
 Similarity score: 0.0782839

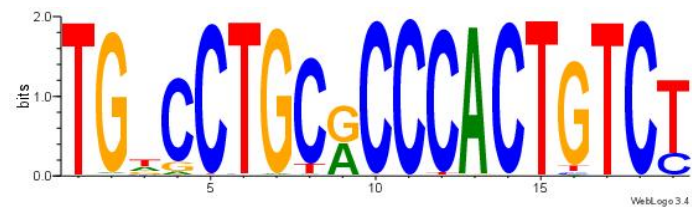
Alignment:

AGACAGTGGGYGCAGGHCA
 --ACCGGGGCTGCA-----

Original motif Consensus sequence: AGACAGTGGGYGCAGGHCA



Reverse complement motif Consensus sequence: TGHCCTGKCCCCACTGTCT



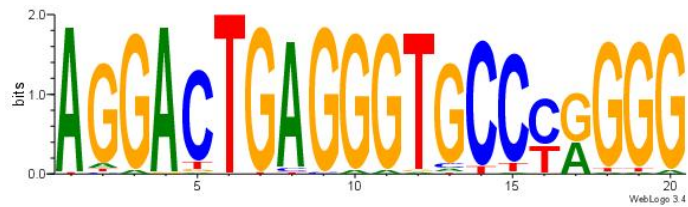
Dataset #: 1
 Motif ID: 312
 Motif name: Motif 312
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 4

Number of overlap: 12
Similarity score: 0.0814191

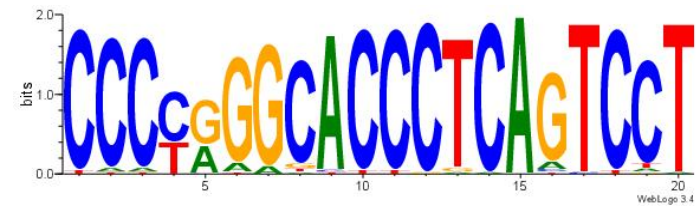
Alignment:

CCCMKGGCACCCCTCAGTCCT
-----TGCAGCCCCGGT---

Original motif Consensus sequence: AGGACTGAGGGTGCCYRGGG



Reverse complement motif Consensus sequence:
CCCMKGGCACCCCTCAGTCCT

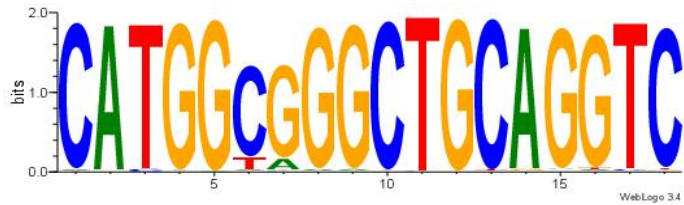


Dataset #: 1
Motif ID: 68
Motif name: Motif 68
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 5
Number of overlap: 12
Similarity score: 0.0835295

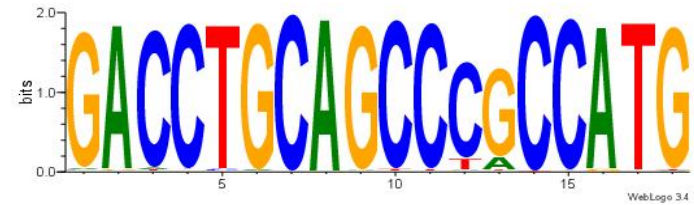
Alignment:

GACCTGCAGCCCCGCCATG
-----TGCAGCCCCGGT---

Original motif Consensus sequence: CATGGCGGGCTGCAGGTC



Reverse complement motif Consensus sequence: GACCTGCAGCCCGCCATG

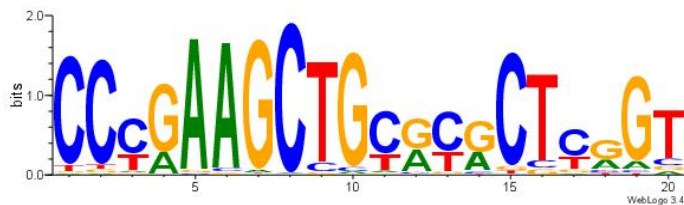


Dataset #: 1
Motif ID: 177
Motif name: Motif 177
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 12
Similarity score: 0.0835511

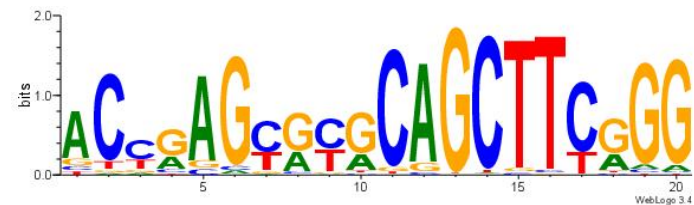
Alignment:

CCCGAAGCTGCRYRCTCGGT
ACCGGGGCTGCA-----

Original motif Consensus sequence: CCCGAAGCTGCRYRCTCGGT

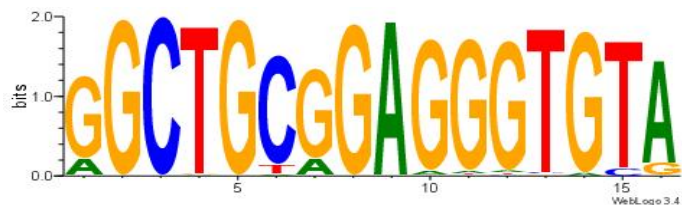


Reverse complement motif Consensus sequence: ACCGAGMKMGCAGCTTCGGG

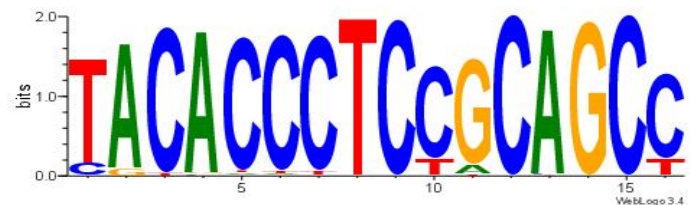


Dataset #: 1 Motif ID: 89 Motif name: Motif 89

Original motif Consensus sequence: GGCTGCGAGGGTGTA



Reverse complement motif Consensus sequence: TACACCCTCCGAGCC



Best Matches for Motif ID 89 (Highest to Lowest)

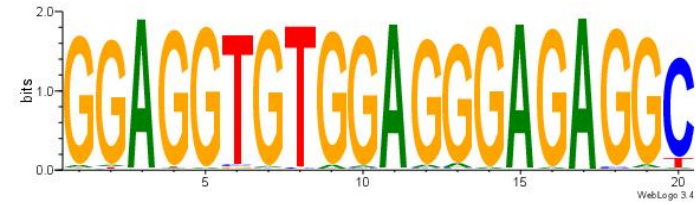
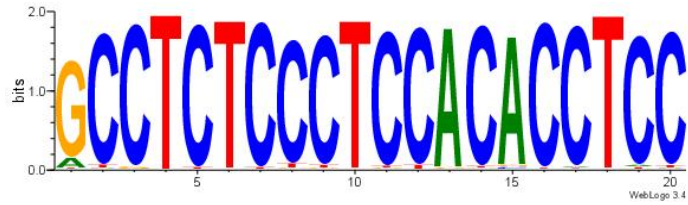
Dataset #:	1
Motif ID:	105
Motif name:	Motif 105
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	3
Number of overlap:	16
Similarity score:	0.0814615

Alignment:

```
GGAGGTGTGGAGGGAGAGGC  
--GGCTGCGAGGGTGTA--
```

Original motif Consensus sequence: GCCTCTCCCTCCACACCTCC

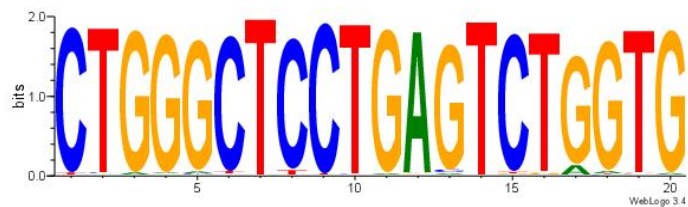
Reverse complement motif Consensus sequence: GGAGGTGTGGAGGGAGAGGC



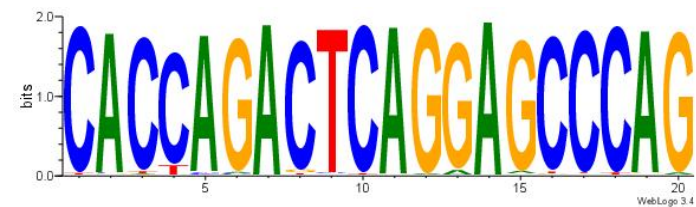
Dataset #: 1
 Motif ID: 67
 Motif name: Motif 67
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 4
 Number of overlap: 16
 Similarity score: 0.0835227

Alignment:
 CACCAGACTCAGGAGCCCAG
 -TACACCCTCCGCAGCC---

Original motif Consensus sequence: CTGGGCTCCTGAGTCTGGTG



Reverse complement motif Consensus sequence: CACCAGACTCAGGAGCCCAG



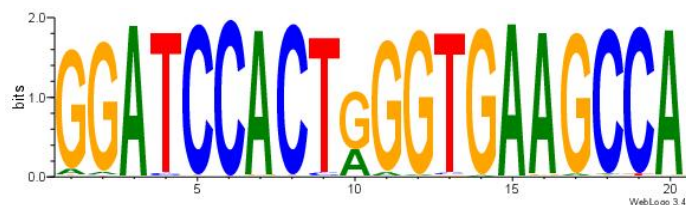
Dataset #: 1

Motif ID: 61
 Motif name: Motif 61
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 5
 Number of overlap: 16
 Similarity score: 0.089486

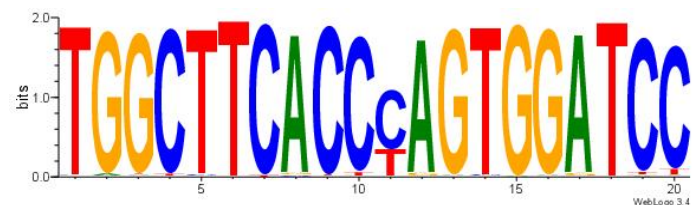
Alignment:

GGATCCACTGGGTGAAGCCA
 GGCTGCGGAGGGTGTA----

Original motif Consensus sequence: GGATCCACTGGGTGAAGCCA



Reverse complement motif Consensus sequence: TGGCTTCACCCAGTGGATCC



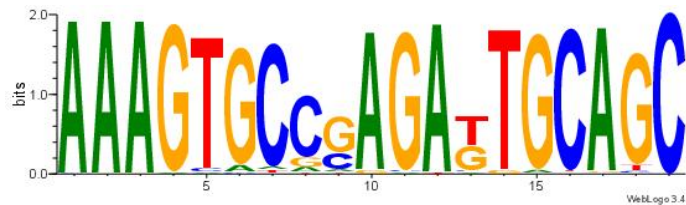
Dataset #: 1
 Motif ID: 191
 Motif name: Motif 191
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 16

Similarity score: 0.0927728

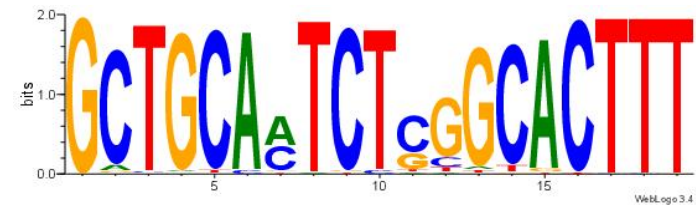
Alignment:

AAAGTGCCGAGAKTGCAGC
-GGCTGCGGAGGGTGTA--

Original motif Consensus sequence: AAAGTGCCGAGAKTGCAGC



Reverse complement motif Consensus sequence:
GCTGCARTCTCGGCACTTT



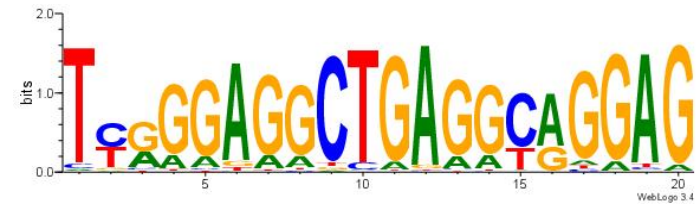
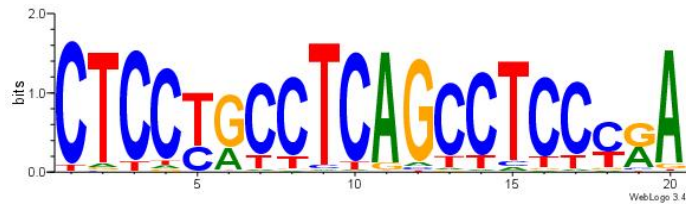
Dataset #: 1
Motif ID: 26
Motif name: Motif 26
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2
Number of overlap: 16
Similarity score: 0.0932417

Alignment:

CTCCTGCCTCAGCCTCCCRA
---TACACCCTCCGCAGCC-

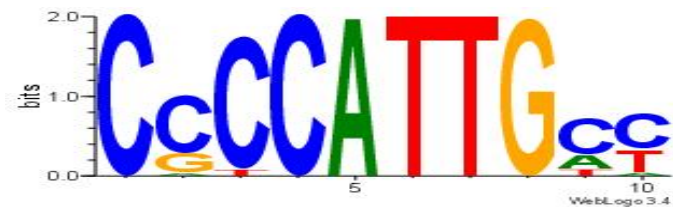
Original motif Consensus sequence: CTCCTGCCTCAGCCTCCCRA

Reverse complement motif Consensus sequence:
TMGGGAGGCTGAGGCAGGAG

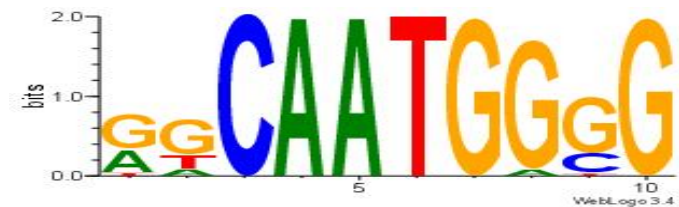


Dataset #: 1 Motif ID: 90 Motif name: Motif 90

Original motif Consensus sequence: CCCATTGCY



Reverse complement motif Consensus sequence: KGCAATGGGG

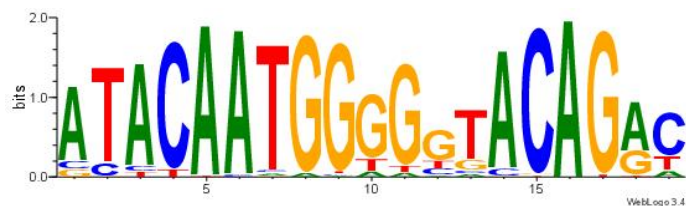


Best Matches for Motif ID 90 (Highest to Lowest)

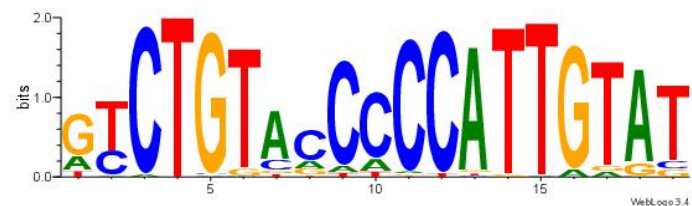
Dataset #:	1
Motif ID:	193
Motif name:	Motif 193
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	9
Number of overlap:	10
Similarity score:	0.0254376

Alignment:
 ATACAATGGGGGTACAGRC
 -KGCAATGGGG-----

Original motif Consensus sequence: ATACAATGGGGTACAGRC



Reverse complement motif Consensus sequence: GKCTGTACCCCCATTGTAT

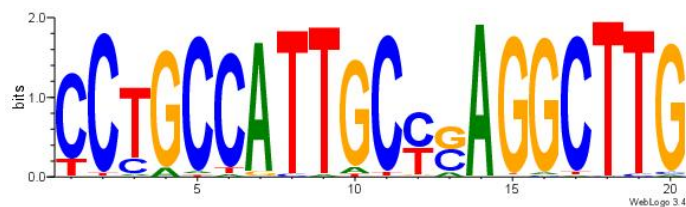


Dataset #: 1
Motif ID: 196
Motif name: Motif 196
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 9
Number of overlap: 10
Similarity score: 0.0348826

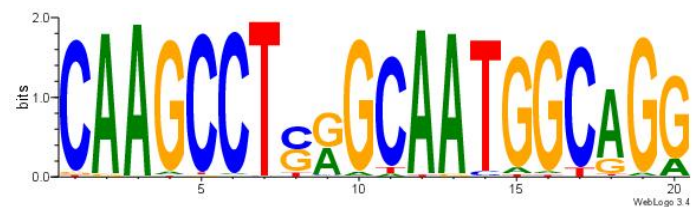
Alignment:

```
CCTGCCATTGCYSAGGCTTG  
--CCCCATTGCY-----
```

Original motif Consensus sequence: CCTGCCATTGCYSAGGCTTG



Reverse complement motif Consensus sequence: CAAGCCTSKGCAATGGCAGG

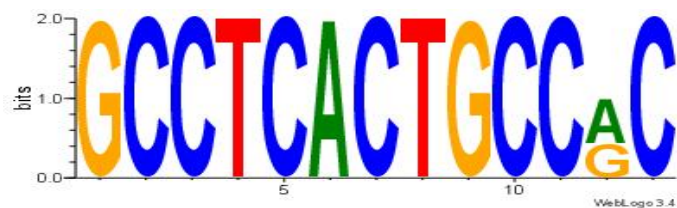


Dataset #: 1
 Motif ID: 247
 Motif name: Motif 247
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 10
 Similarity score: 0.0547148

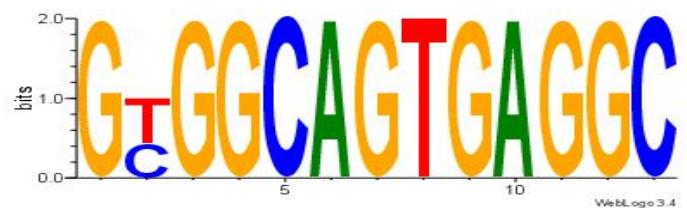
Alignment:

GCCTCACTGCCRC
 -CCCCATTGCY--

Original motif Consensus sequence: GCCTCACTGCCRC



Reverse complement motif Consensus sequence: GKGGCAGTGAGGC



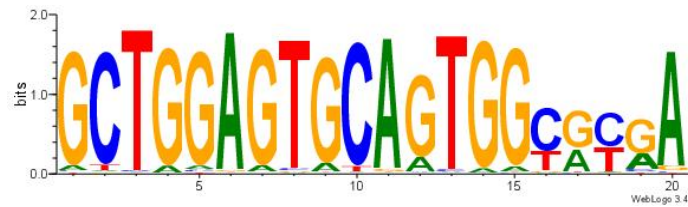
Dataset #: 1
 Motif ID: 3
 Motif name: Motif 3
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 4
 Number of overlap: 10

Similarity score: 0.0556877

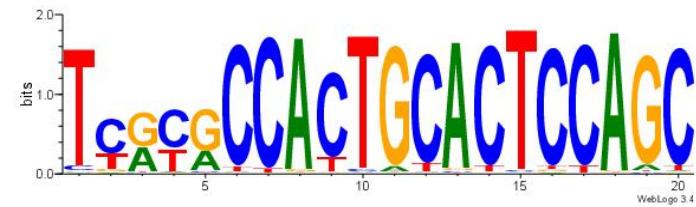
Alignment:

TCKMGCCACTGCACTCCAGC
-----CCCCATTGCY----

Original motif Consensus sequence: GCTGGAGTGCAGTGGCRYGA



Reverse complement motif Consensus sequence:
TCKMGCCACTGCACTCCAGC



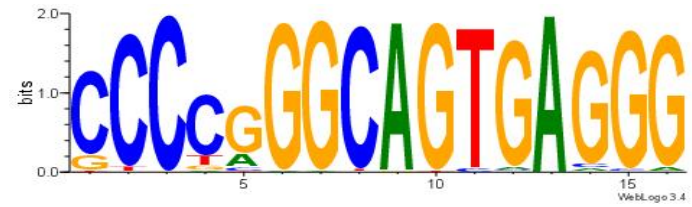
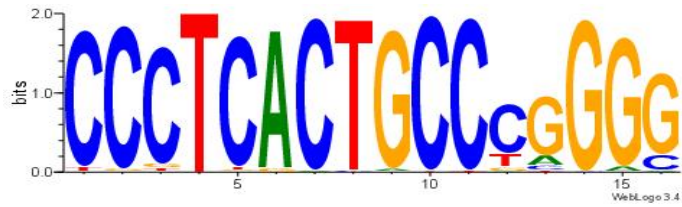
Dataset #: 1
Motif ID: 136
Motif name: Motif 136
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 6
Number of overlap: 10
Similarity score: 0.0564416

Alignment:

CCCTCACTGCCCGGGG
-CCCCATTGCY-----

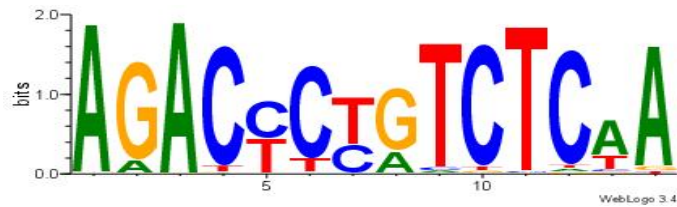
Original motif Consensus sequence: CCCTCACTGCCCGGGG

Reverse complement motif Consensus sequence:
CCCCGGGCAGTGAGGG

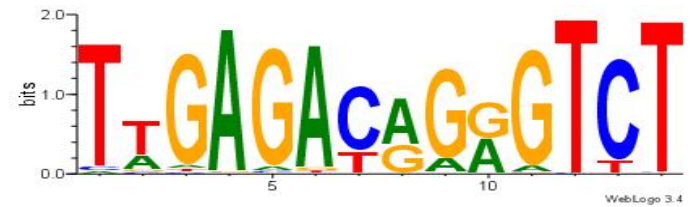


Dataset #: 1 Motif ID: 91 Motif name: Motif 91

Original motif Consensus sequence: AGACYCYGTCTCAA



Reverse complement motif Consensus sequence: TTGAGACMGKGTCT

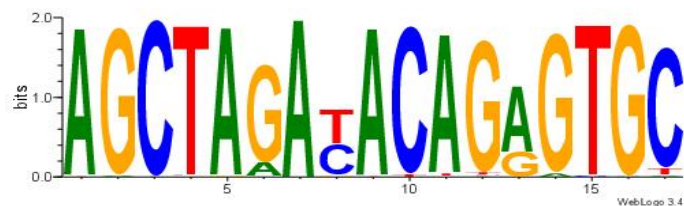


Best Matches for Motif ID 91 (Highest to Lowest)

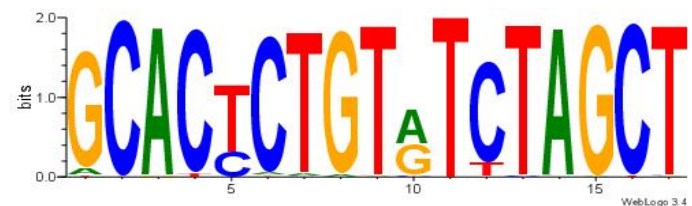
Dataset #:	1
Motif ID:	175
Motif name:	Motif 175
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	4
Number of overlap:	14
Similarity score:	0.0743241

Alignment:
 GCACTCTGTMCTAGCT
 AGACYCYGTCTCAA---

Original motif Consensus sequence: AGCTAGAYACAGAGTGC



Reverse complement motif Consensus sequence: GCACTCTGTMCTAGCT

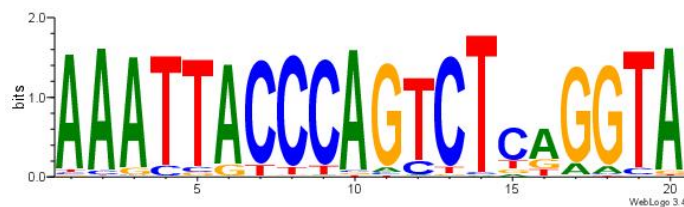


Dataset #: 1
Motif ID: 160
Motif name: Motif 160
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 4
Number of overlap: 14
Similarity score: 0.0811922

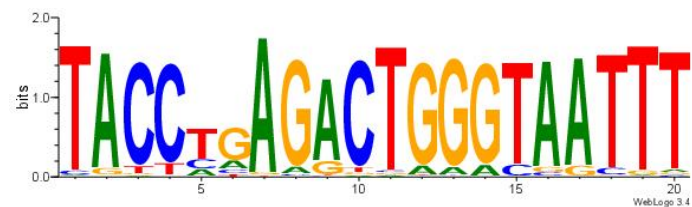
Alignment:

TACCTGAGACTGGGTAATTT
---TTGAGACMGKGTCT---

Original motif Consensus sequence: AAATTACCCAGTCTCAGGTA



Reverse complement motif Consensus sequence: TACCTGAGACTGGGTAATTT

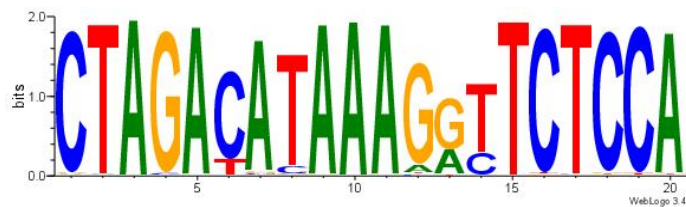


Dataset #: 1
 Motif ID: 85
 Motif name: Motif 85
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0.0815627

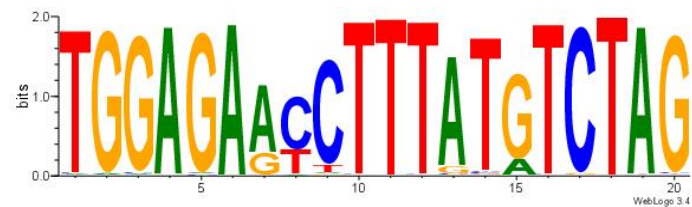
Alignment:

TGGAGAACCTTTATGTCTAG
 TTGAGACMGKGTCT-----

Original motif Consensus sequence: CTAGACATAAAGGTTCTCCA



Reverse complement motif Consensus sequence: TGGAGAACCTTTATGTCTAG



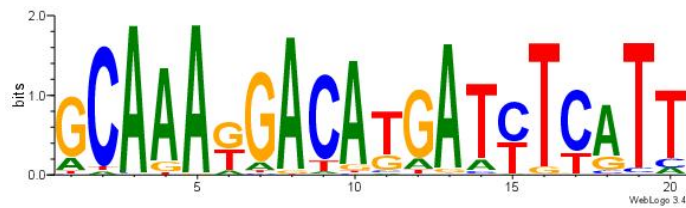
Dataset #: 1
 Motif ID: 99
 Motif name: Motif 99
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 6

Number of overlap: 14
Similarity score: 0.0862654

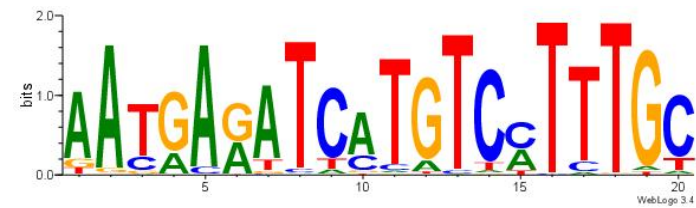
Alignment:

AATGAKATCATGTCYTTTGC
-TTGAGACMGKTCT-----

Original motif Consensus sequence: GCAAAGACATGATYTCATT



Reverse complement motif Consensus sequence:
AATGAKATCATGTCYTTTGC

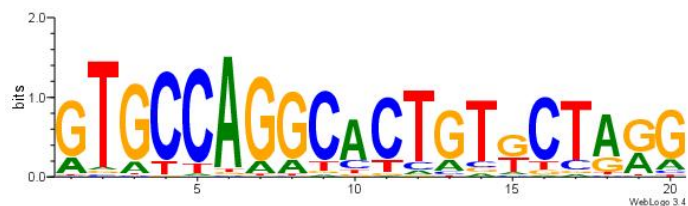


Dataset #: 1
Motif ID: 76
Motif name: Motif 76
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 6
Number of overlap: 14
Similarity score: 0.0925706

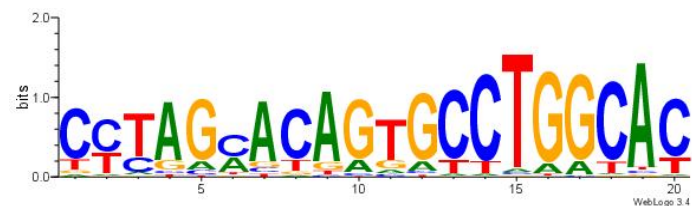
Alignment:

GTGCCAGGCACTGTKCTARG
-----AGACYCYGTCTCAA-

Original motif Consensus sequence: GTGCCAGGCACTGKCTARG

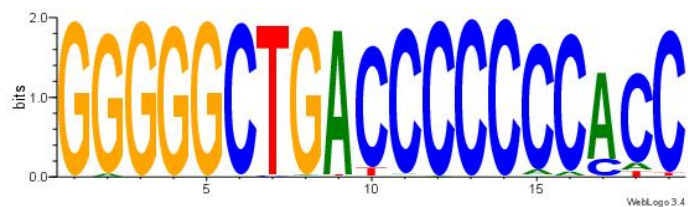


Reverse complement motif Consensus sequence: CMTAGYACAGTGCCTGGCAC

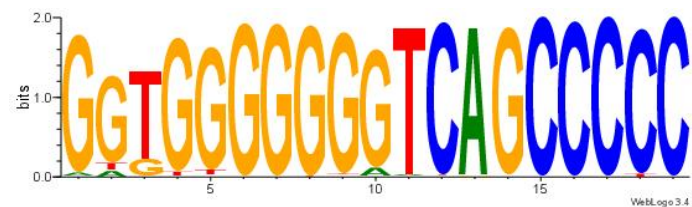


Dataset #: 1 Motif ID: 92 Motif name: Motif 92

Original motif Consensus sequence: GGGGGCTGACCCCCCACC



Reverse complement motif Consensus sequence: GGTGGGGGGTTCAGCCCCC



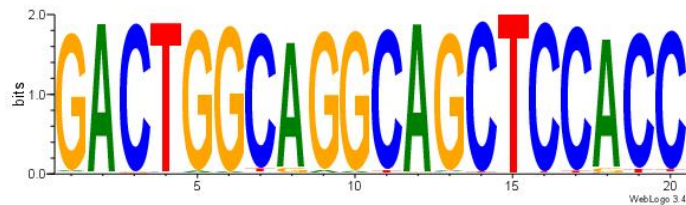
Best Matches for Motif ID 92 (Highest to Lowest)

Dataset #:	1
Motif ID:	52
Motif name:	Motif 52
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	19
Similarity score:	0.100201

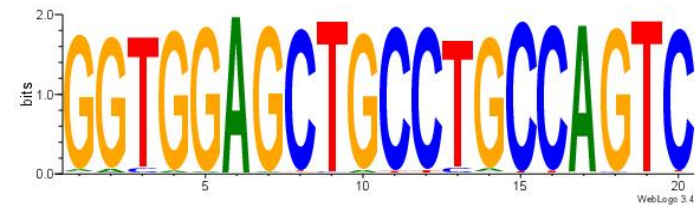
Alignment:

GACTGGCAGGCAGCTCCACC
-GGGGGCTGACCCCCCACC

Original motif Consensus sequence: GACTGGCAGGCAGCTCCACC



Reverse complement motif Consensus sequence:
GGTGGAGCTGCCTGCCAGTC



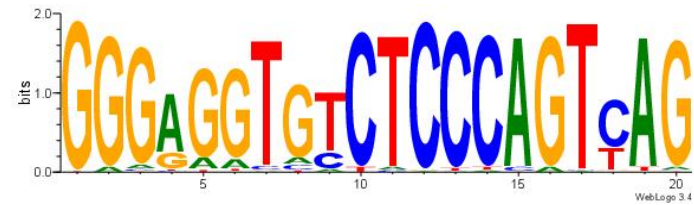
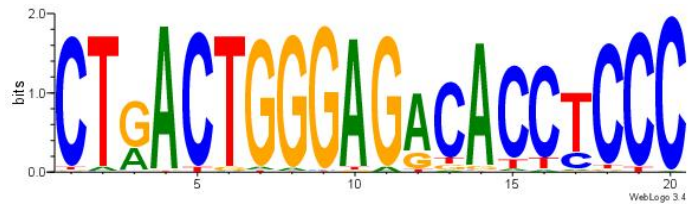
Dataset #:	1
Motif ID:	293
Motif name:	Motif 293
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	19
Similarity score:	0.10109

Alignment:

CTGACTGGGAGACACCTCCC
-GGTGGGGGGGTCAGCCCC

Original motif Consensus sequence: CTGACTGGGAGACACCTCCC

Reverse complement motif Consensus sequence:
GGGAGGTGTCTCCAGTCAG

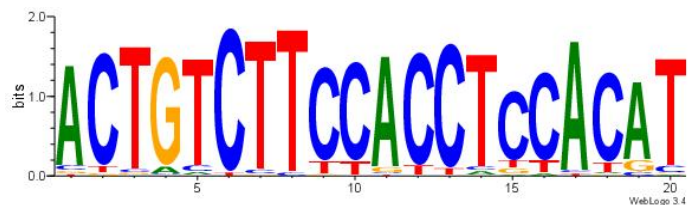


Dataset #: 1
 Motif ID: 178
 Motif name: Motif 178
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 19
 Similarity score: 0.111897

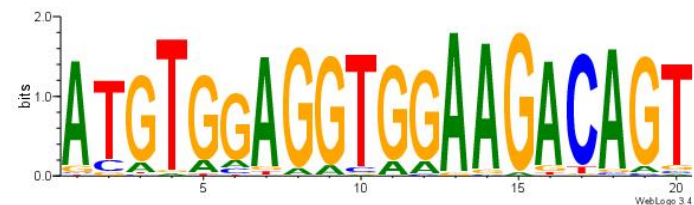
Alignment:

ATGTGGAGGTGGAAGACAGT
 -GGTGGGGGGGTCAGCCCCC

Original motif Consensus sequence: ACTGTCTTCCACCTCCACAT



Reverse complement motif Consensus sequence: ATGTGGAGGTGGAAGACAGT



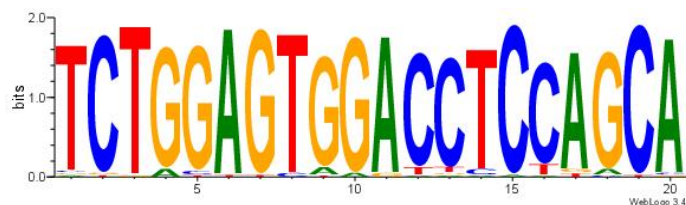
Dataset #: 1

Motif ID: 350
 Motif name: Motif 350
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 19
 Similarity score: 0.111901

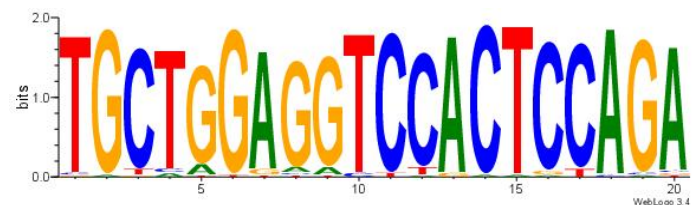
Alignment:

TGCTGGAGGTCCACTCCAGA
 -GGGGGCTGACCCCCCACC

Original motif Consensus sequence: TCTGGAGTGGACCTCCAGCA



Reverse complement motif Consensus sequence: TGCTGGAGGTCCACTCCAGA



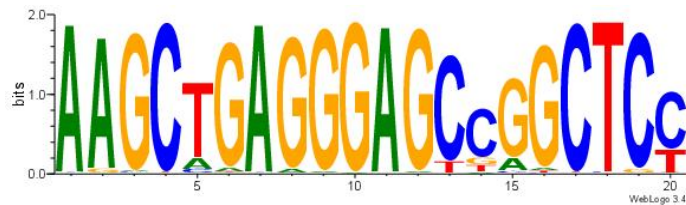
Dataset #: 1
 Motif ID: 96
 Motif name: Motif 96
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 19

Similarity score: 0.113858

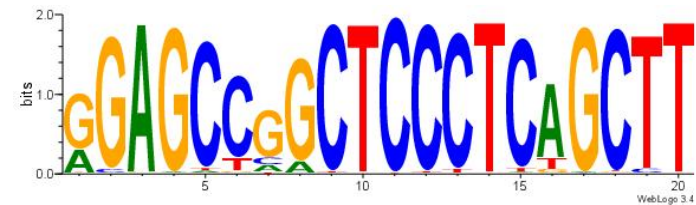
Alignment:

GGAGCCGGCTCCCTCAGCTT
GGGGGCTGACCCCCCACC-

Original motif Consensus sequence: AAGCTGAGGGAGCCGGCTCC



Reverse complement motif Consensus sequence: GGAGCCGGCTCCCTCAGCTT



Dataset #: 1 Motif ID: 93 Motif name: Motif 93

Original motif Consensus sequence: CCATGTGCGG



Reverse complement motif Consensus sequence: CCGCACATGG



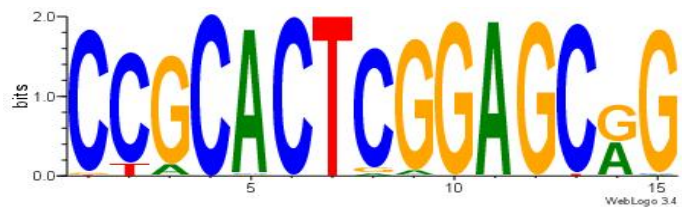
Best Matches for Motif ID 93 (Highest to Lowest)

Dataset #:	1
Motif ID:	128
Motif name:	Motif 128
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement

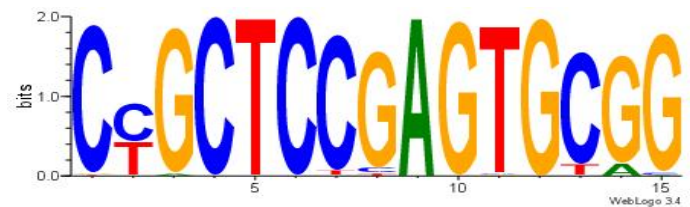
Direction: Backward
Position number: 1
Number of overlap: 10
Similarity score: 0.0496914

Alignment:
CMGCTCCGAGTGCGG
-----CCATGTGCGG

Original motif Consensus sequence: CCGCACTCGGAGCRG



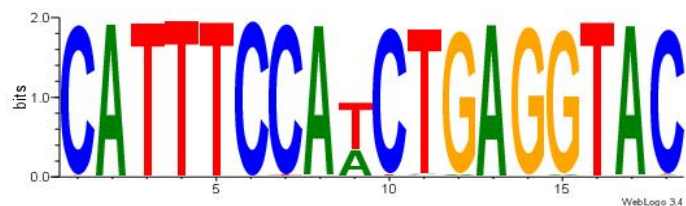
Reverse complement motif Consensus sequence: CMGCTCCGAGTGCGG



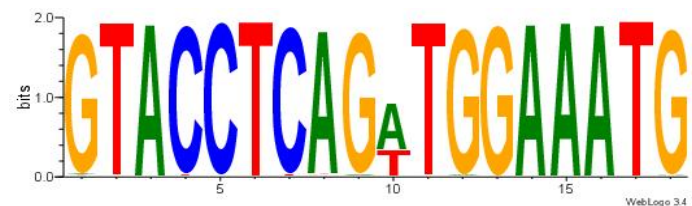
Dataset #: 1
Motif ID: 25
Motif name: Motif 25
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 6
Number of overlap: 10
Similarity score: 0.0540497

Alignment:
GTACCTCAGWTGGAAATG
---CCGCACATGG-----

Original motif Consensus sequence: CATTCCA WCTGAGGTAC



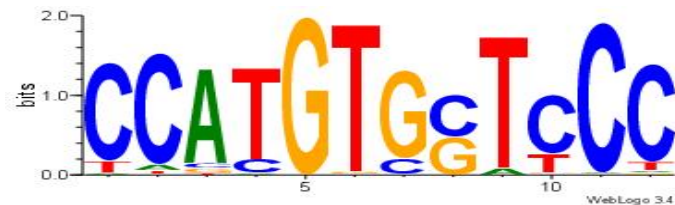
Reverse complement motif Consensus sequence: GTACCTCAGW TGGAAATG



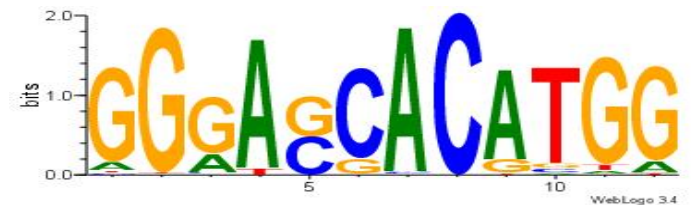
Dataset #: 1
Motif ID: 120
Motif name: Motif 120
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 3
Number of overlap: 10
Similarity score: 0.0552113

Alignment:
CCATGTGSTCCC
CCATGTGCGG--

Original motif Consensus sequence: CCATGTG *Gc* T *c* CC



Reverse complement motif Consensus sequence: GGGASCACATGG

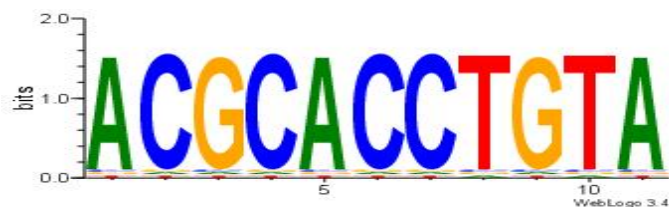


Dataset #: 1
Motif ID: 324
Motif name: Motif 324
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 2
Number of overlap: 10
Similarity score: 0.0568222

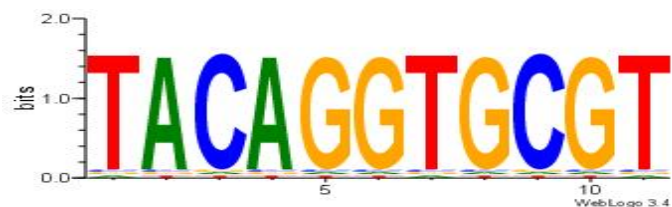
Alignment:

TACAGGTGCGT
-CCATGTGCGG

Original motif Consensus sequence: ACGCACCTGTA



Reverse complement motif Consensus sequence: TACAGGTGCGT



Dataset #: 1
Motif ID: 257
Motif name: Motif 257
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 3
Number of overlap: 10

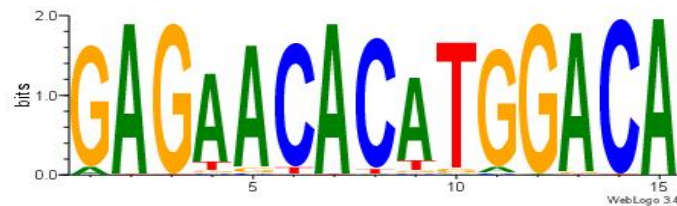
Similarity score: 0.0665322

Alignment:

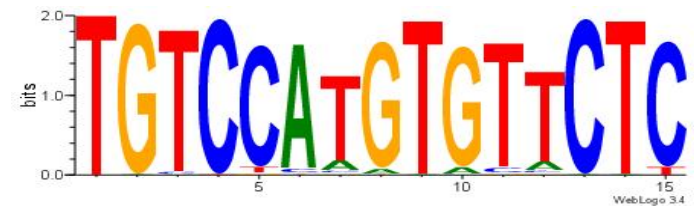
GAGAACACATGGACA

--CCGCACATGG---

Original motif Consensus sequence: GAGAACACATGGACA

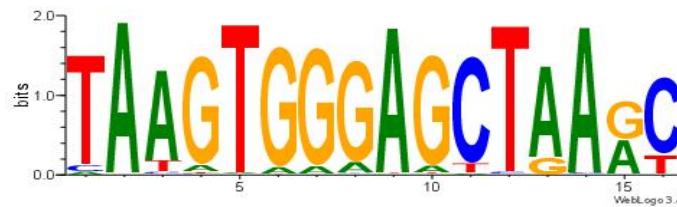


Reverse complement motif Consensus sequence: TGTCCATGTGTTCTC

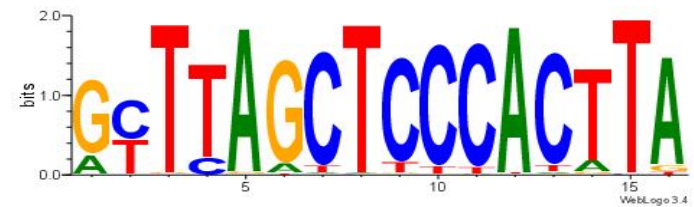


Dataset #: 1 Motif ID: 94 Motif name: Motif 94

Original motif Consensus sequence: TAAGTGGGAGCTAA GC



Reverse complement motif Consensus sequence: GMTTAGCTCCCACTTA



Best Matches for Motif ID 94 (Highest to Lowest)

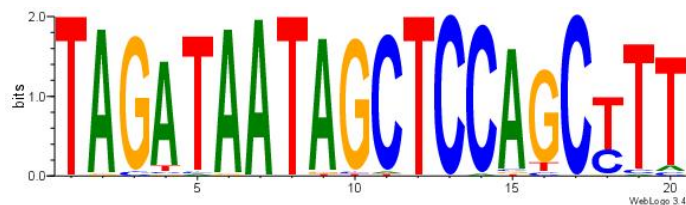
Dataset #:	1
Motif ID:	333
Motif name:	Motif 333
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif

Direction: Backward
 Position number: 1
 Number of overlap: 16
 Similarity score: 0.062587

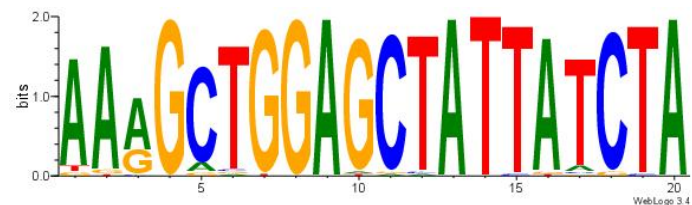
Alignment:

TAGATAATAGCTCCAGCTTT
 ----GMTTAGCTCCCACTTA

Original motif Consensus sequence: TAGATAATAGCTCCAGCTTT



Reverse complement motif Consensus sequence: AAAGCTGGAGCTATTATCTA

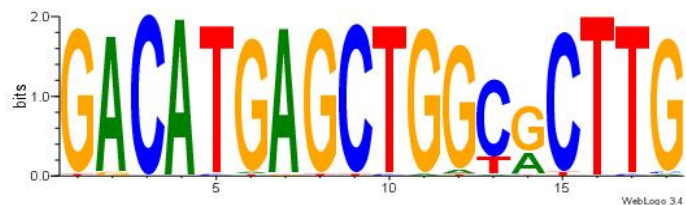


Dataset #: 1
 Motif ID: 306
 Motif name: Motif 306
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 16
 Similarity score: 0.0700236

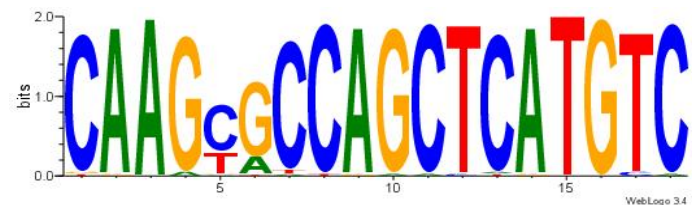
Alignment:

GACATGAGCTGGCGCTTG
 --GMTTAGCTCCCACTTA

Original motif Consensus sequence: GACATGAGCTGGCGCTTG



Reverse complement motif Consensus sequence: CAAGCGCCAGCTCATGTC

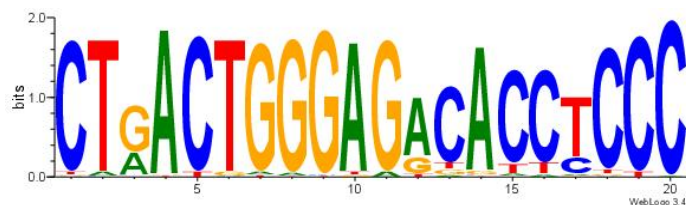


Dataset #: 1
Motif ID: 293
Motif name: Motif 293
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 2
Number of overlap: 16
Similarity score: 0.0707484

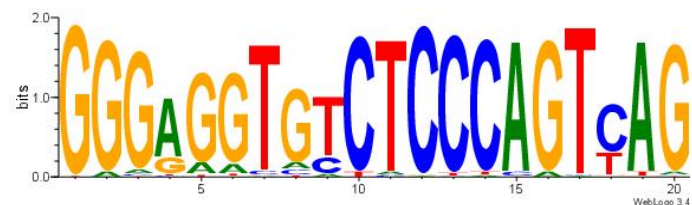
Alignment:

CTGACTGGGAGACACCTCCC
-TAAGTGGGAGCTAARC---

Original motif Consensus sequence: CTGACTGGGAGACACCTCCC



Reverse complement motif Consensus sequence: GGGAGGTGTCTCCCAGTCAG

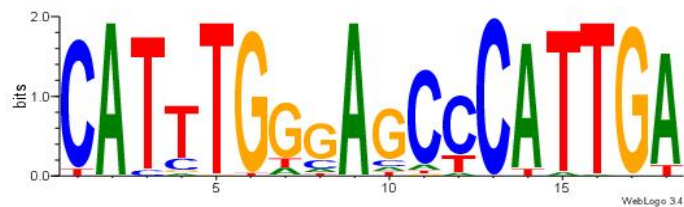


Dataset #: 1
 Motif ID: 284
 Motif name: Motif 284
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3
 Number of overlap: 16
 Similarity score: 0.0721808

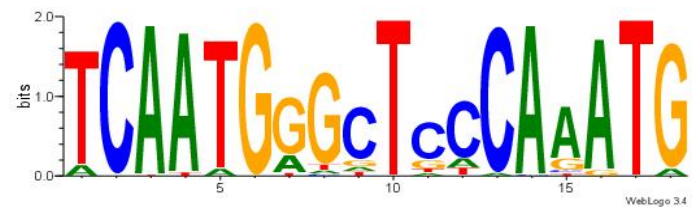
Alignment:

TCAATGGGCTCCCAAATG
 --GMTTAGCTCCCCTTA

Original motif Consensus sequence: CATTGGGAGCCATTGA



Reverse complement motif Consensus sequence: TCAATGGGCTCCCAAATG



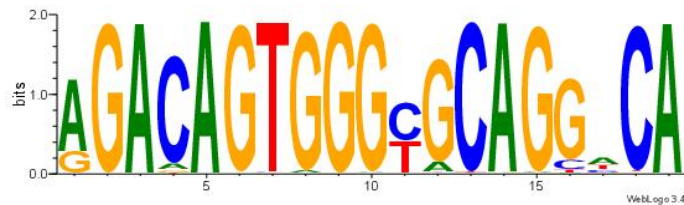
Dataset #: 1
 Motif ID: 17
 Motif name: Motif 17
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3

Number of overlap: 16
Similarity score: 0.0724147

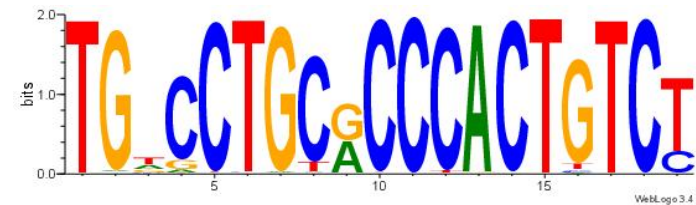
Alignment:

TGHCCTGCKCCCCTGTCT
-GMTTAGCTCCCCTTA--

Original motif Consensus sequence: AGACAGTGGGCGCAGGCA

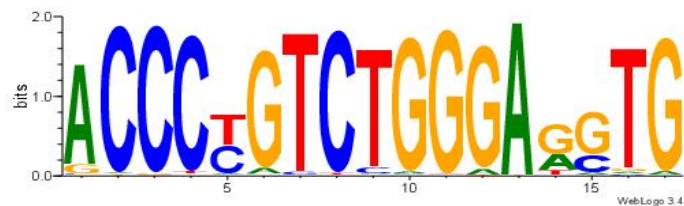


Reverse complement motif Consensus sequence:
TGHCCTGCKCCCCTGTCT

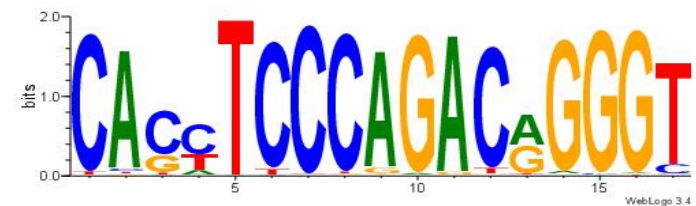


Dataset #: 1 Motif ID: 95 Motif name: Motif 95

Original motif Consensus sequence: ACCYGTCTGGGAGGTG



Reverse complement motif Consensus sequence:
CACCTCCAGACMGGGT



Best Matches for Motif ID 95 (Highest to Lowest)

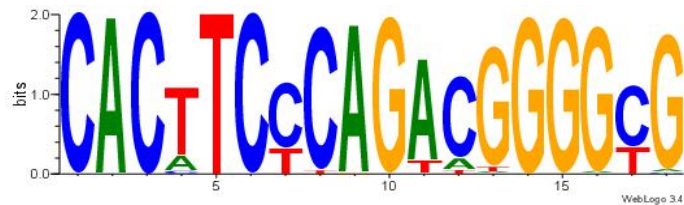
Dataset #: 1
Motif ID: 27
Motif name: Motif 27

Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	17
Similarity score:	0.0376618

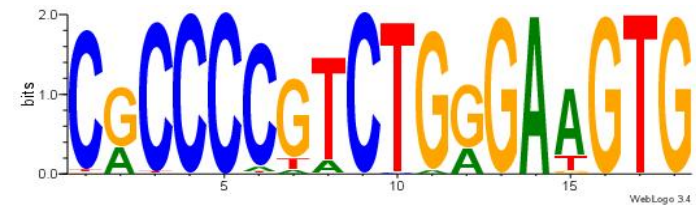
Alignment:

```
CACTTCCCAGACGGGGCG
-CACCTCCCAGACMGGGT
```

Original motif Consensus sequence: CACTTCCCAGACGGGGCG



Reverse complement motif Consensus sequence: CGCCCCGTCTGGGAAGTG

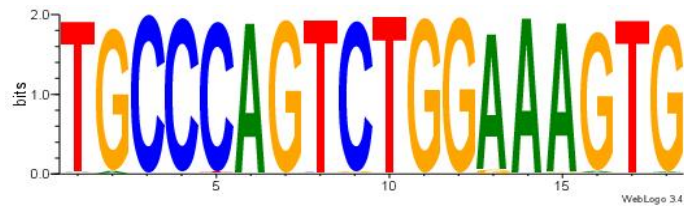


Dataset #:	1
Motif ID:	45
Motif name:	Motif 45
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	17
Similarity score:	0.0519023

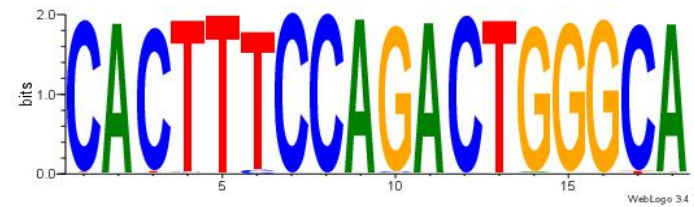
Alignment:

TGCCCAGTCTGGAAAGTG
-ACCCYGTCTGGGAGGTG

Original motif Consensus sequence: TGCCCAGTCTGGAAAGTG



Reverse complement motif Consensus sequence:
CACTTTCAGACTGGGCA



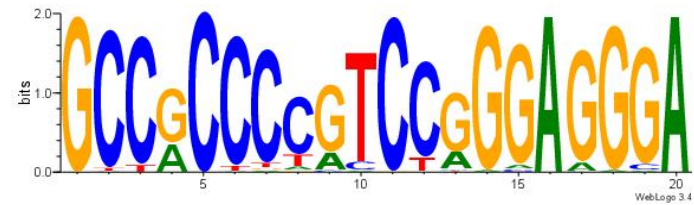
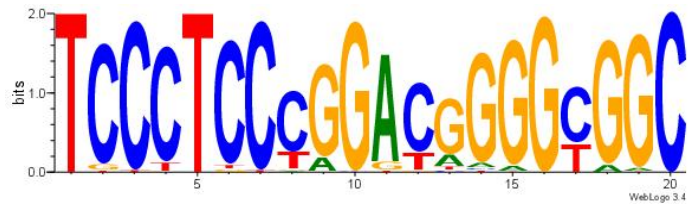
Dataset #:	1
Motif ID:	155
Motif name:	Motif 155
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	4
Number of overlap:	17
Similarity score:	0.0726859

Alignment:

GCCKCCCCGTCCGGGAGGGA
---ACCCYGTCTGGGAGGTG

Original motif Consensus sequence: TCCCTCCCGGACGGGGYGGC

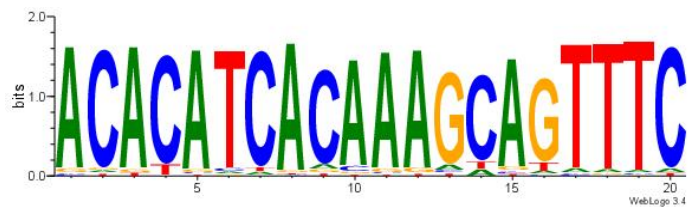
Reverse complement motif Consensus sequence:
GCCKCCCCGTCCGGGAGGGA



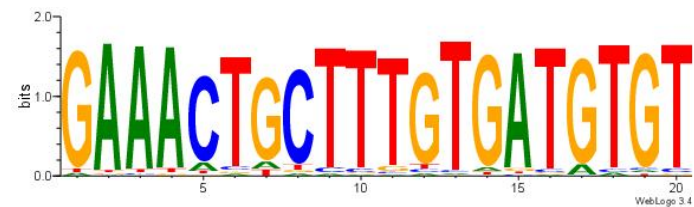
Dataset #: 1
 Motif ID: 202
 Motif name: Motif 202
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 17
 Similarity score: 0.0892583

Alignment:
 ACACATCACAAAGCAGTTTC
 -CACCTCCAGACMGGGT--

Original motif Consensus sequence: ACACATCACAAAGCAGTTTC



Reverse complement motif Consensus sequence: GAAACTGCTTTGTGATGTGT



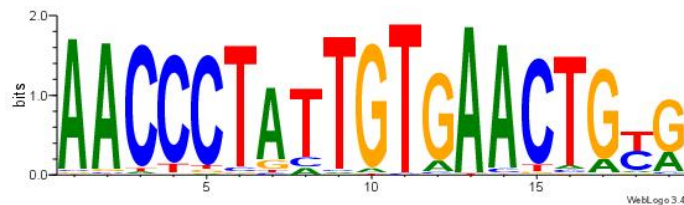
Dataset #: 1

Motif ID: 242
 Motif name: Motif 242
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 17
 Similarity score: 0.0946365

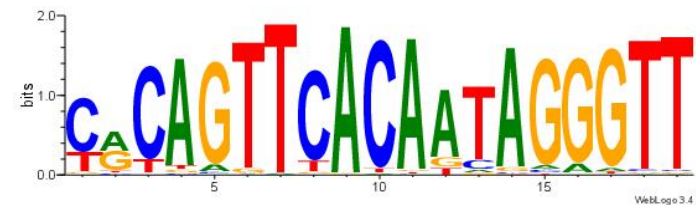
Alignment:

AACCTATTGTGAACTGYG
 ACCCYGTCTGGGAGGTG--

Original motif Consensus sequence: AACCTATTGTGAACTGYG

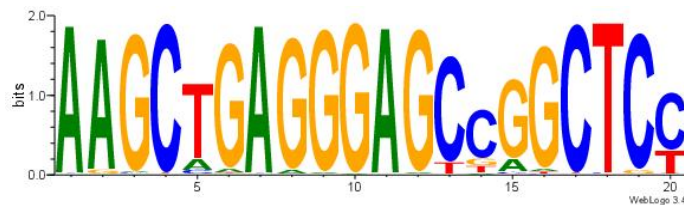


Reverse complement motif Consensus sequence: CMCAGTTCACAATAGGGTT

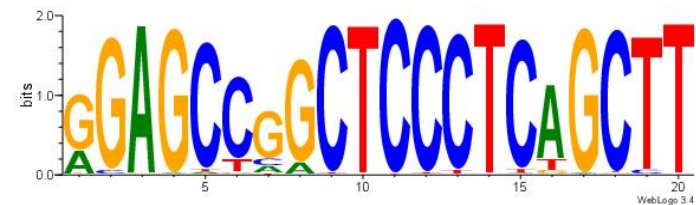


Dataset #: 1 Motif ID: 96 Motif name: Motif 96

Original motif Consensus sequence: AAGCTGAGGGAGCCGGCTCC



Reverse complement motif Consensus sequence: GGAGCCGGCTCCCTCAGCTT



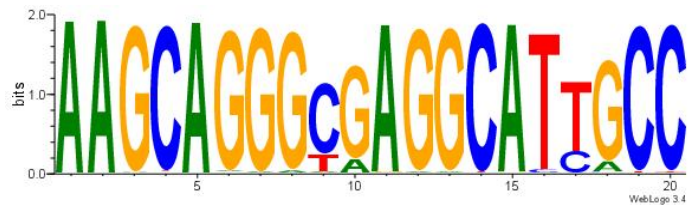
Best Matches for Motif ID 96 (Highest to Lowest)

Dataset #: 1
Motif ID: 13
Motif name: Motif 13
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 20
Similarity score: 0.0900694

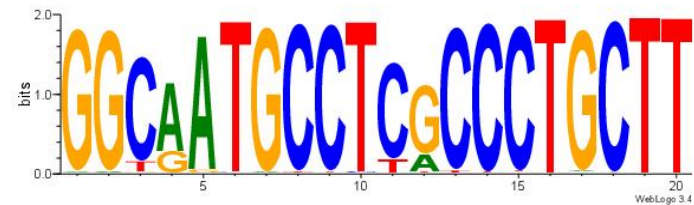
Alignment:

```
AAGCAGGGCGAGGCATTGCC  
AAGCTGAGGGAGCCGGCTCC
```

Original motif Consensus sequence: AAGCAGGGCGAGGCATTGCC



Reverse complement motif Consensus sequence:
GGCAATGCCTCGCCCTGCTT



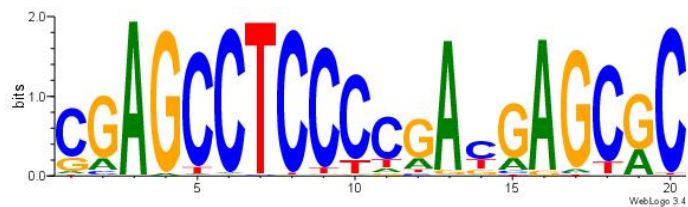
Dataset #: 1
Motif ID: 108
Motif name: Motif 108
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif

Direction: Forward
Position number: 1
Number of overlap: 20
Similarity score: 0.11205

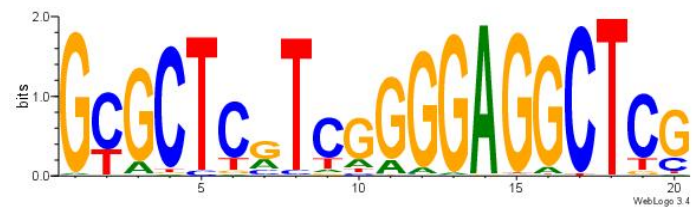
Alignment:

CGAGCCTCCCCGAYGAGCGC
GGAGCCGGCTCCCTCAGCTT

Original motif Consensus sequence: CGAGCCTCCCCGAYGAGCGC



Reverse complement motif Consensus sequence: GCGCTCKTCGGGGAGGCTCG

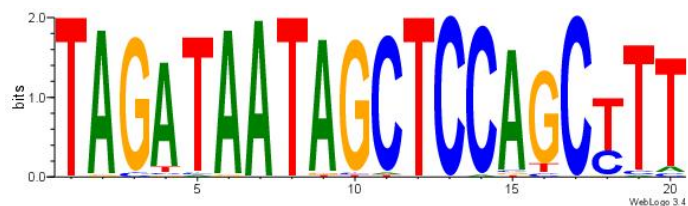


Dataset #: 1
Motif ID: 333
Motif name: Motif 333
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 20
Similarity score: 0.116847

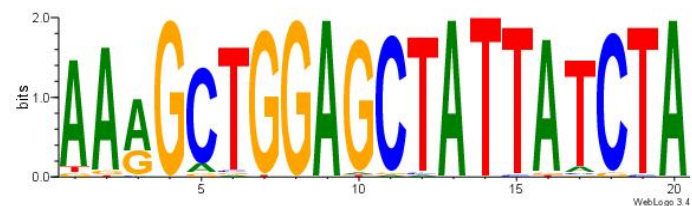
Alignment:

TAGATAATAGCTCCAGCTTT
AAGCTGAGGGAGCCGGCTCC

Original motif Consensus sequence: TAGATAATAGCTCCAGCTTT



Reverse complement motif Consensus sequence: AAAGCTGGAGCTATTATCTA

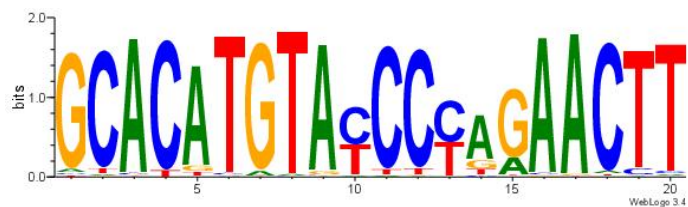


Dataset #: 1
Motif ID: 225
Motif name: Motif 225
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 20
Similarity score: 0.118204

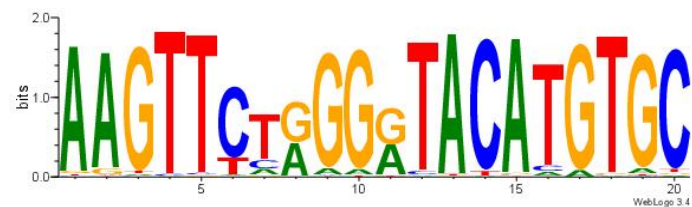
Alignment:

GCACATGTAYCCYAGAACTT
GGAGCCGGCTCCCTCAGCTT

Original motif Consensus sequence: GCACATGTAYCCYAGAACTT



Reverse complement motif Consensus sequence: AAGTTCTKGGKTACATGTGC

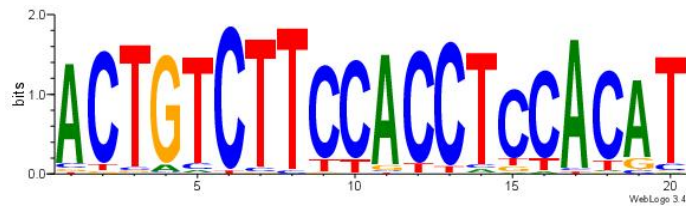


Dataset #: 1
 Motif ID: 178
 Motif name: Motif 178
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.125147

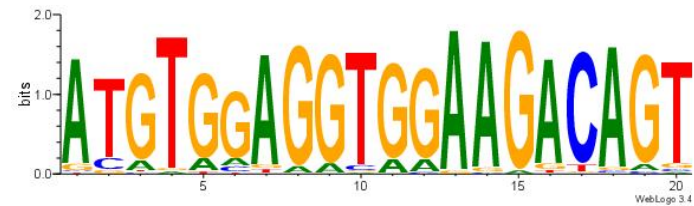
Alignment:

ACTGTCTTCCACCTCCACAT
 GGAGCCGGCTCCCTCAGCTT

Original motif Consensus sequence: ACTGTCTTCCACCTCCACAT



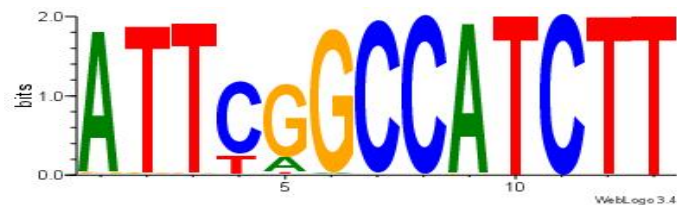
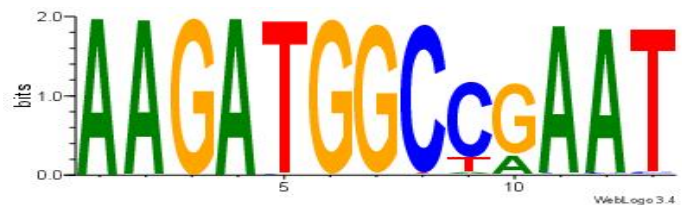
Reverse complement motif Consensus sequence: ATGTGGAGGTGGAAGACAGT



Dataset #: 1 Motif ID: 97 Motif name: Motif 97

Original motif Consensus sequence: AAGATGGCCGAAT

Reverse complement motif Consensus sequence: ATTCGGCCATCTT

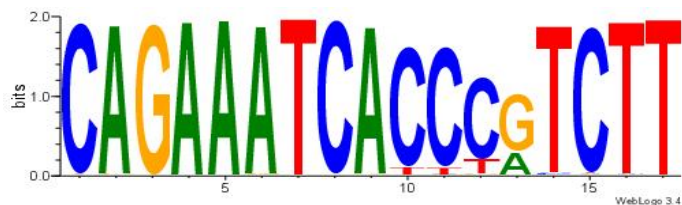


Best Matches for Motif ID 97 (Highest to Lowest)

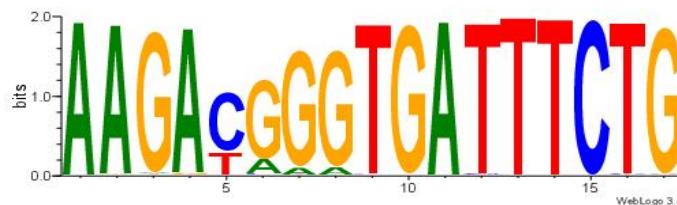
Dataset #: 1
 Motif ID: 35
 Motif name: Motif 35
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 13
 Similarity score: 0.0664224

Alignment:
 AAGACGGGTGATTTCTG
 ----AAGATGGCCGAAT

Original motif Consensus sequence: CAGAAATCACCCGTTCTT



Reverse complement motif Consensus sequence: AAGACGGGTGATTTCTG

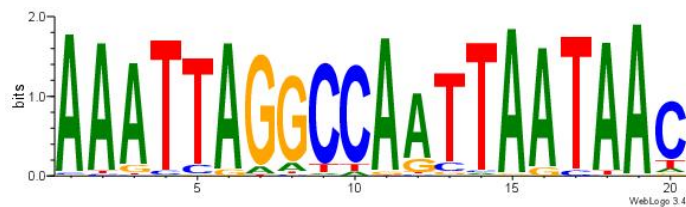


Dataset #: 1
 Motif ID: 308
 Motif name: Motif 308
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 6
 Number of overlap: 13
 Similarity score: 0.0712075

Alignment:

AAATTAGGCCAATTAATAAC
 --ATTCGGCCATCTT-----

Original motif Consensus sequence: AAATTAGGCCAATTAATAAC



Reverse complement motif Consensus sequence: GTTATTAATTGGCCTAATTT



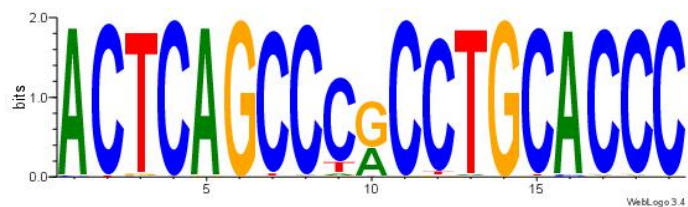
Dataset #: 1
 Motif ID: 149
 Motif name: Motif 149
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 7

Number of overlap: 13
Similarity score: 0.0758335

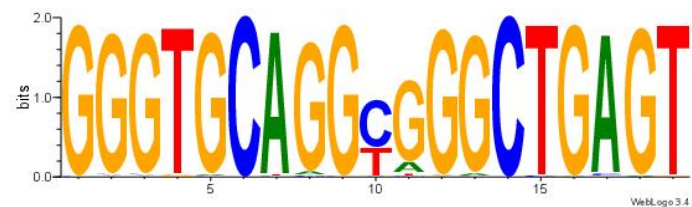
Alignment:

GGGTGCAGGMGGGCTGAGT
-----AAGATGGCCGAAT

Original motif Consensus sequence: ACTCAGCCRCCTGCACCC



Reverse complement motif Consensus sequence:
GGGTGCAGGMGGGCTGAGT

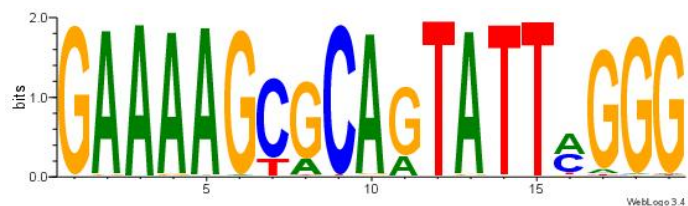


Dataset #: 1
Motif ID: 18
Motif name: Motif 18
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 6
Number of overlap: 13
Similarity score: 0.0829089

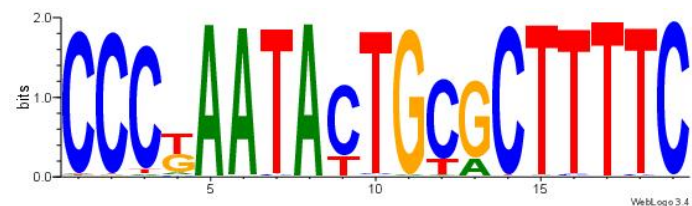
Alignment:

CCCYAATACTGCGCTTTTC
-----ATTCGGCCATCTT-

Original motif Consensus sequence: GAAAAGCGCAGTATTMGGG



Reverse complement motif Consensus sequence: CCCYAATACTGCGCTTTTC

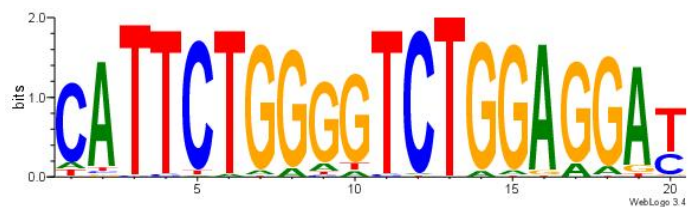


Dataset #: 1
Motif ID: 309
Motif name: Motif 309
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 2
Number of overlap: 13
Similarity score: 0.0840391

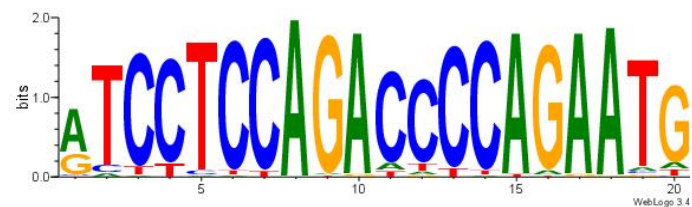
Alignment:

```
CATTCTGGGGTCTGGAGGAY  
-ATTCCGCCATCTT-----
```

Original motif Consensus sequence: CATTCTGGGGTCTGGAGGAY

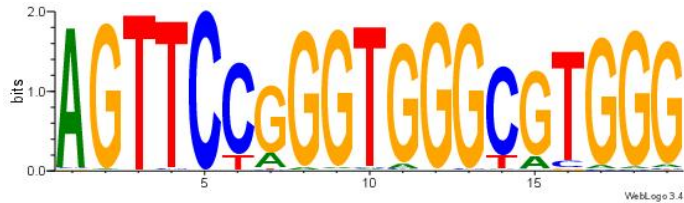


Reverse complement motif Consensus sequence: MTCCTCCAGACCCAGAAATG

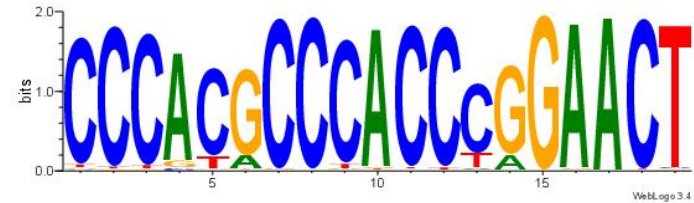


Dataset #: 1 Motif ID: 98 Motif name: Motif 98

Original motif Consensus sequence: AGTTCCGGTGGGCGTGGG



Reverse complement motif Consensus sequence: CCCACGCCACCCGGAAC



Best Matches for Motif ID 98 (Highest to Lowest)

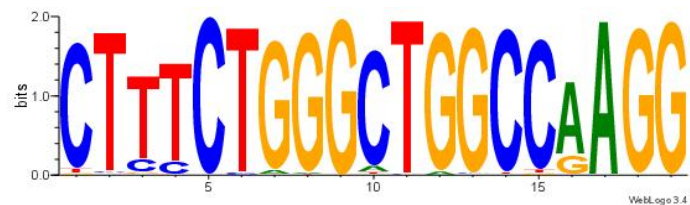
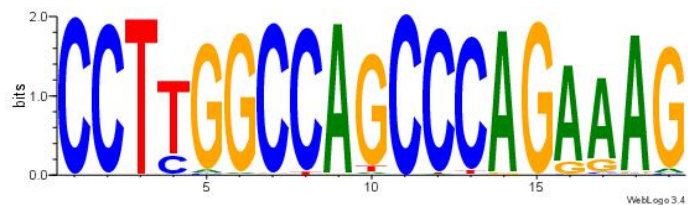
Dataset #:	1
Motif ID:	122
Motif name:	Motif 122
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	19
Similarity score:	0.0965972

Alignment:

```
CTTTCTGGGCTGGCCAAGG  
AGTTCCGGGTGGGCGTGGG
```

Original motif Consensus sequence: CCTTGCCAGCCCAGAAAG

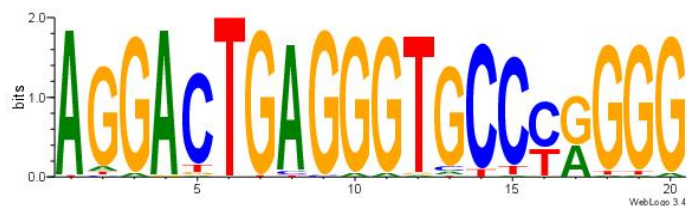
Reverse complement motif Consensus sequence:
CTTTCTGGGCTGGCCAAGG



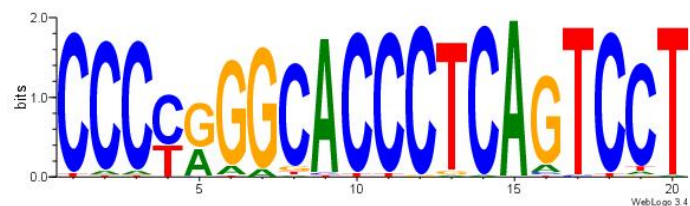
Dataset #: 1
 Motif ID: 312
 Motif name: Motif 312
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 19
 Similarity score: 0.0978875

Alignment:
 AGGACTGAGGGTGCCYRGGG
 AGTTCCGGGTGGCGTGGG-

Original motif Consensus sequence: AGGACTGAGGGTGCCYRGGG



Reverse complement motif Consensus sequence: CCCMKGGCACCCTCAGTCCT



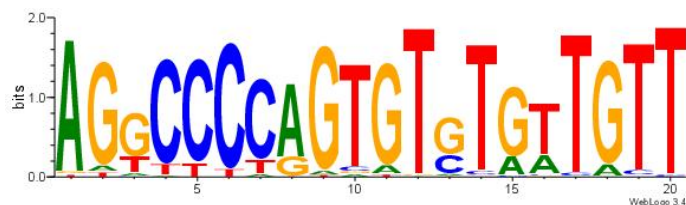
Dataset #: 1

Motif ID: 176
 Motif name: Motif 176
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 19
 Similarity score: 0.0980426

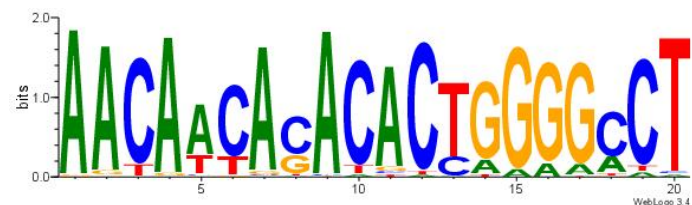
Alignment:

AGGCCCCAGTGTSTGTTGTT
 AGTTCCGGGTGGGCGTGGG-

Original motif Consensus sequence: AGGCCCCAGTGTSTGTTGTT



Reverse complement motif Consensus sequence: AACACASACACTGGGGCCT



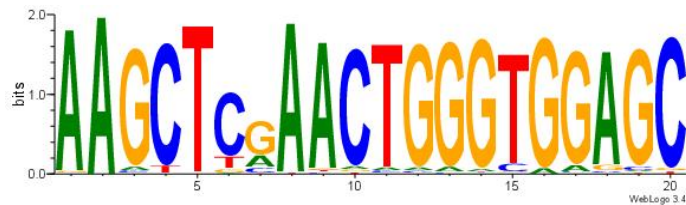
Dataset #: 1
 Motif ID: 321
 Motif name: Motif 321
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 19

Similarity score: 0.102363

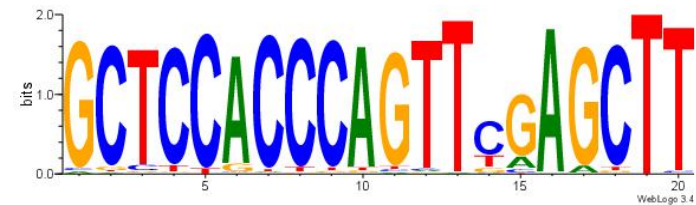
Alignment:

AAGCTCGAACTGGGTGGAGC
-AGTTCCGGGTGGGCGTGGG

Original motif Consensus sequence: AAGCTCGAACTGGGTGGAGC



Reverse complement motif Consensus sequence:
GCTCCACCCAGTTCGAGCTT



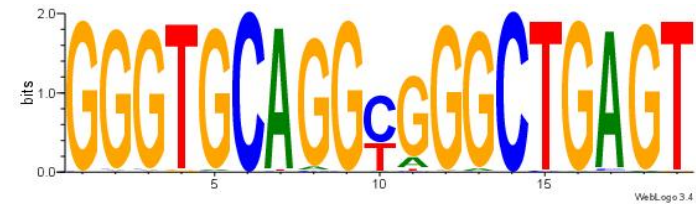
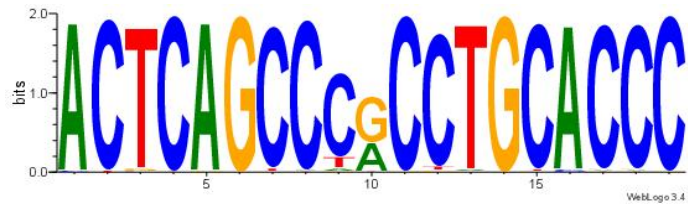
Dataset #: 1
Motif ID: 149
Motif name: Motif 149
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 19
Similarity score: 0.103971

Alignment:

ACTCAGCCRCCTGCACCC
CCCACGCCACCCGGAACT

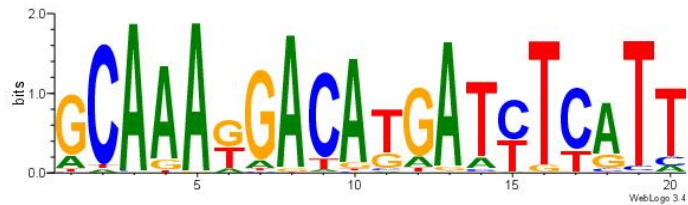
Original motif Consensus sequence: ACTCAGCCRCCTGCACCC

Reverse complement motif Consensus sequence:
GGGTGCAGGMGGGCTGAGT

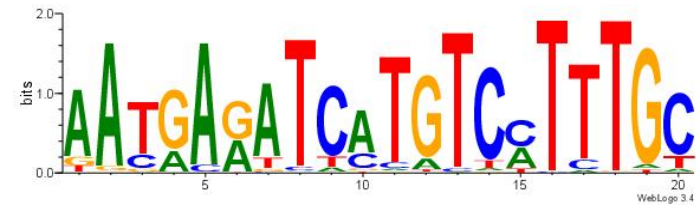


Dataset #: 1 Motif ID: 99 Motif name: Motif 99

Original motif Consensus sequence: GCAAAGACATGATYTCATT



Reverse complement motif Consensus sequence: AATGAKATCATGTCYTTTGC



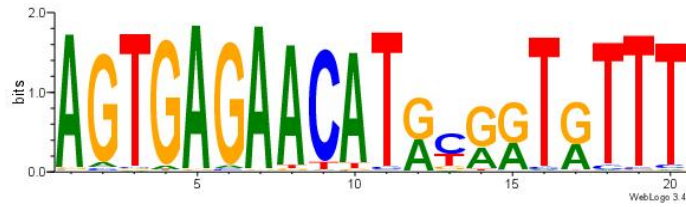
Best Matches for Motif ID 99 (Highest to Lowest)

Dataset #:	1
Motif ID:	63
Motif name:	Motif 63
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	20
Similarity score:	0.0793398

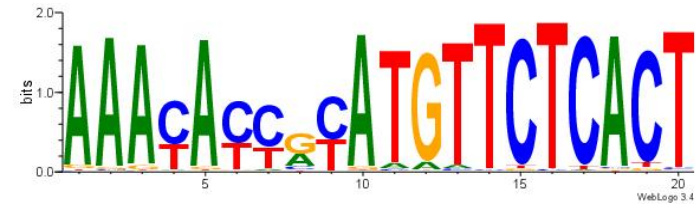
Alignment:

AGTGAGAACATRYRRTRTTT
AATGAKATCATGTCYTTTGC

Original motif Consensus sequence: AGTGAGAACATRYRRTRTTT



Reverse complement motif Consensus sequence:
AAAMAMMKMATGTTCTCACT

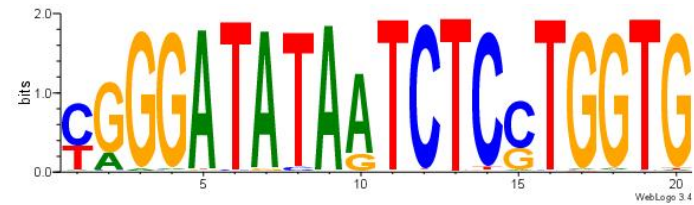
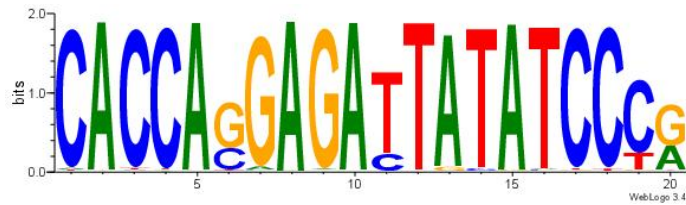


Dataset #: 1
Motif ID: 19
Motif name: Motif 19
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 20
Similarity score: 0.0873595

Alignment:
MGGGATATAATCTCCTGGTG
AATGAKATCATGTCYTTTGC

Original motif Consensus sequence: CACCAGGAGATTATATCCCR

Reverse complement motif Consensus sequence:
MGGGATATAATCTCCTGGTG

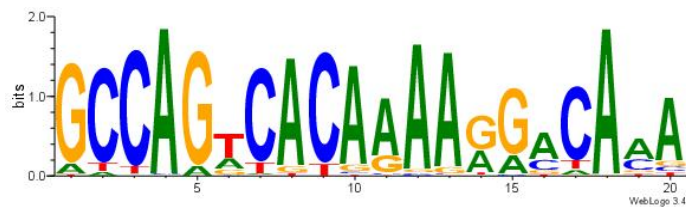


Dataset #: 1
 Motif ID: 145
 Motif name: Motif 145
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.0892295

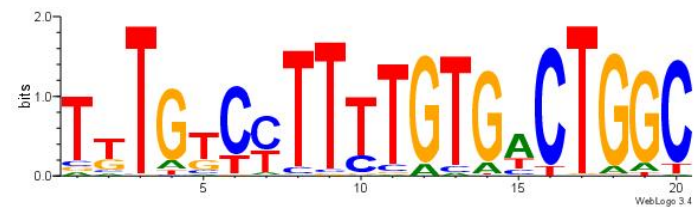
Alignment:

GCCAGTCACAAAARGACAMA
 GCAAAGACATGATYTCATT

Original motif Consensus sequence: GCCAGTCACAAAARGACAMA



Reverse complement motif Consensus sequence: TYTGCMTTTTGTGACTGGC



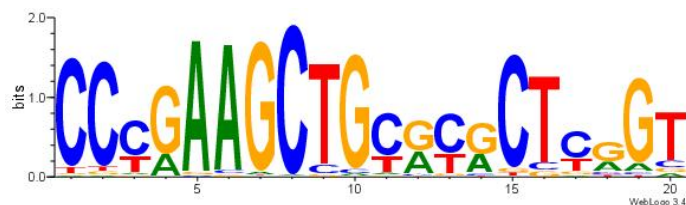
Dataset #: 1

Motif ID: 177
 Motif name: Motif 177
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.0978439

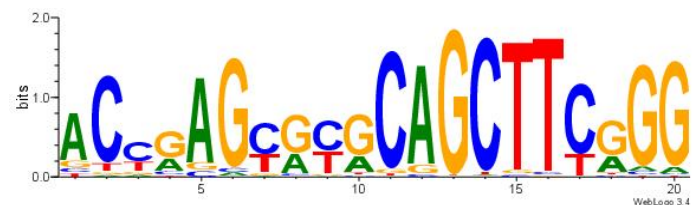
Alignment:

ACCGAGMKMGCAGCTTCGGG
 AATGAKATCATGTCYTTTGC

Original motif Consensus sequence: CCCGAAGCTGCRYRCTCGGT



Reverse complement motif Consensus sequence: ACCGAGMKMGCAGCTTCGGG



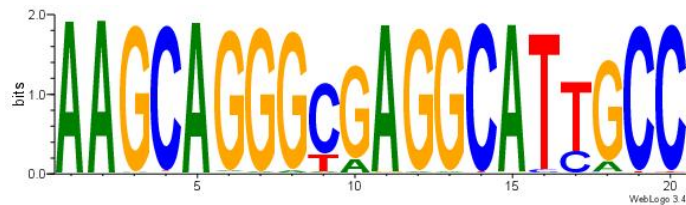
Dataset #: 1
 Motif ID: 13
 Motif name: Motif 13
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 20

Similarity score: 0.0984998

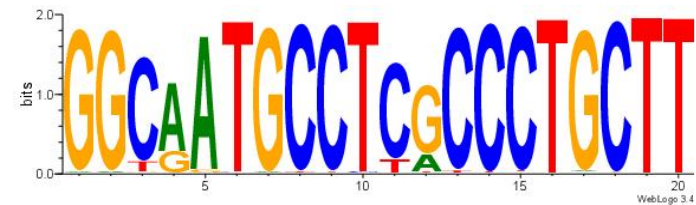
Alignment:

GGCAATGCCTCGCCCTGCTT
GCAAAGKACATGATYTCATT

Original motif Consensus sequence: AAGCAGGGCGAGGCATTGCC

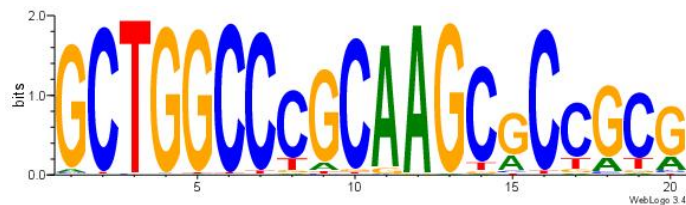


Reverse complement motif Consensus sequence: GGCAATGCCTCGCCCTGCTT

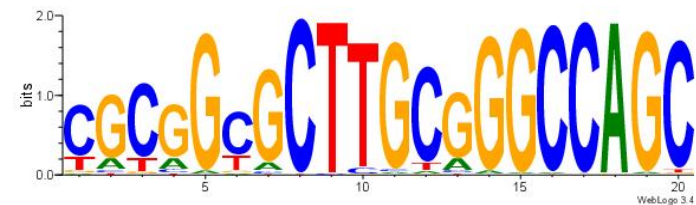


Dataset #: 1 Motif ID: 100 Motif name: Motif 100

Original motif Consensus sequence: GCTGGCCCGCAAGCCGCG



Reverse complement motif Consensus sequence: CGCGGCGCTTGC GGCCAGC



Best Matches for Motif ID 100 (Highest to Lowest)

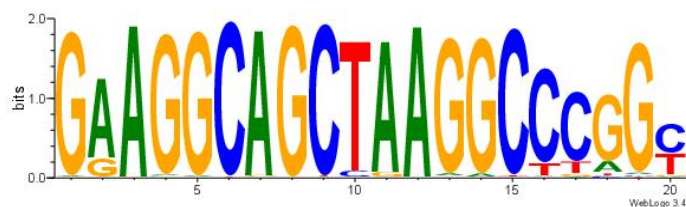
Dataset #: 1
Motif ID: 64
Motif name: Motif 64
Matching format of first motif: Reverse Complement

Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.109117

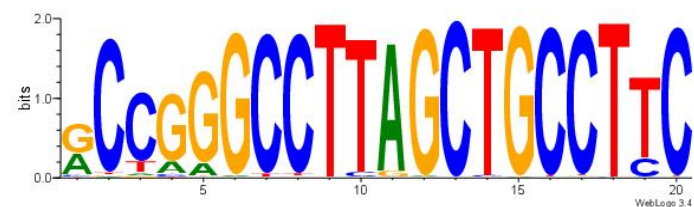
Alignment:

KCCGGGCCTTAGCTGCCTTC
 CGCGGCCTTGCGGGCCAGC

Original motif Consensus sequence: GAAGGCAGCTAAGGCCGG



Reverse complement motif Consensus sequence: KCCGGGCCTTAGCTGCCTTC

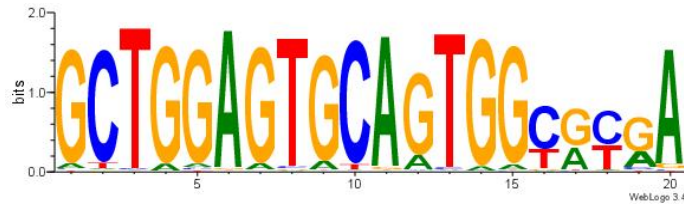


Dataset #: 1
 Motif ID: 3
 Motif name: Motif 3
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.111065

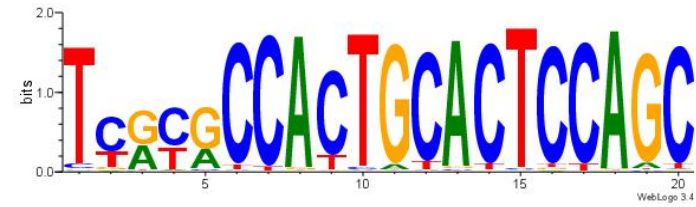
Alignment:

GCTGGAGTGCAGTGGCRYGA
GCTGGCCC GCAAGCGCCGCG

Original motif Consensus sequence: GCTGGAGTGCAGTGGCRYGA



Reverse complement motif Consensus sequence:
TCKMGCCACTGCACTCCAGC

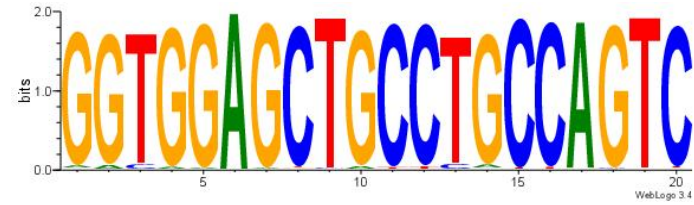
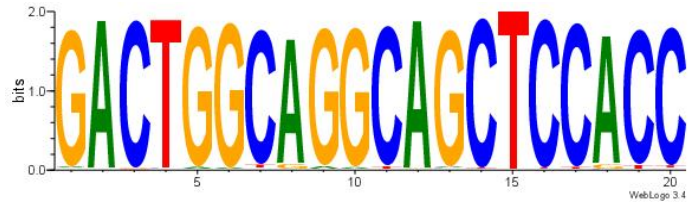


Dataset #: 1
Motif ID: 52
Motif name: Motif 52
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 20
Similarity score: 0.112704

Alignment:
GGTGGAGCTGCCTGCCAGTC
CGCGGCGCTTGCGGGCCAGC

Original motif Consensus sequence: GACTGGCAGGCAGCTCCACC

Reverse complement motif Consensus sequence:
GGTGGAGCTGCCTGCCAGTC

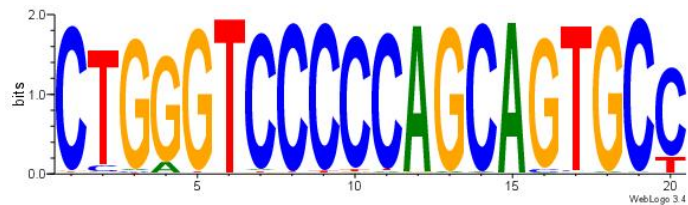


Dataset #: 1
 Motif ID: 84
 Motif name: Motif 84
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.114051

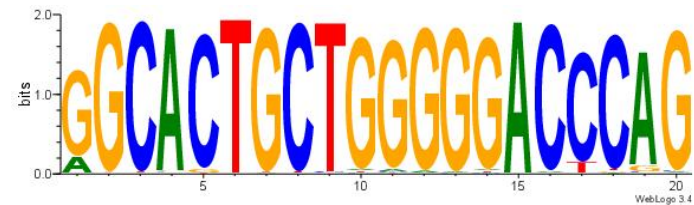
Alignment:

CTGGGTCCCCCAGCAGTGCC
 GCTGGCCCGCAAGCGCCGCG

Original motif Consensus sequence: CTGGGTCCCCCAGCAGTGCC



Reverse complement motif Consensus sequence: GGCAGTCTGGGGGACCCAG



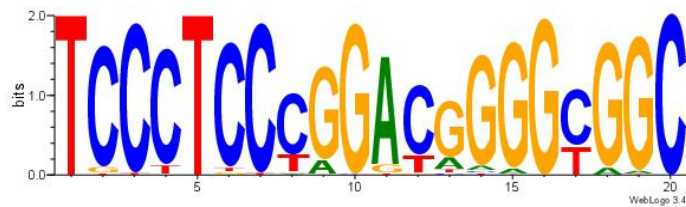
Dataset #: 1

Motif ID: 155
 Motif name: Motif 155
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.12131

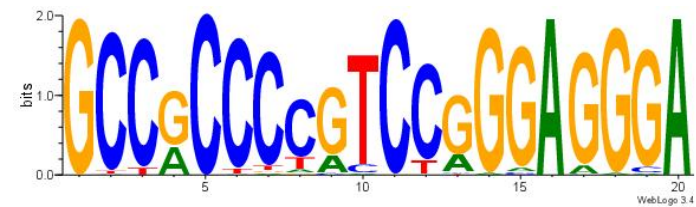
Alignment:

GCCKCCCCGTCCGGGAGGGA
 CGCGGCGCTTGCGGGCCAGC

Original motif Consensus sequence: TCCCTCCCGACGGGGYGGC

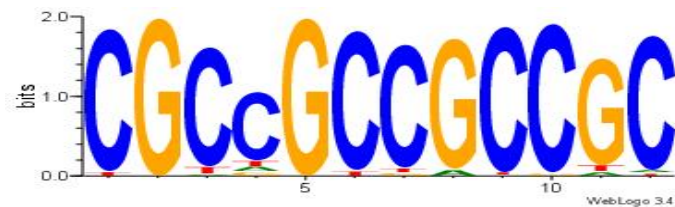


Reverse complement motif Consensus sequence: GCCKCCCCGTCCGGGAGGGA

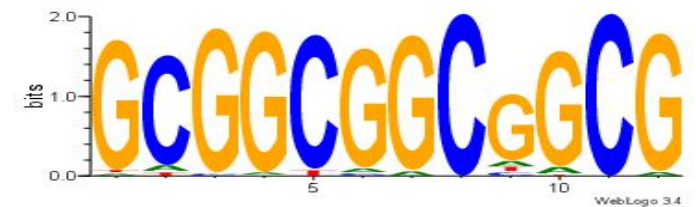


Dataset #: 1 Motif ID: 101 Motif name: Motif 101

Original motif Consensus sequence: CGCCGCCCGC



Reverse complement motif Consensus sequence: GCGGCGGCGGCG



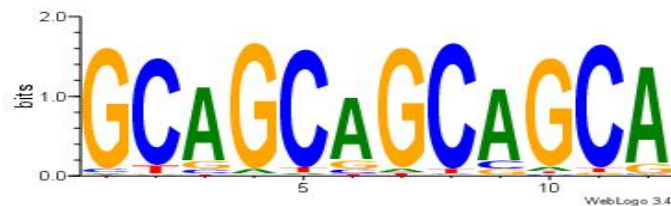
Best Matches for Motif ID 101 (Highest to Lowest)

Dataset #: 1
Motif ID: 266
Motif name: Motif 266
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 12
Similarity score: 0.0686683

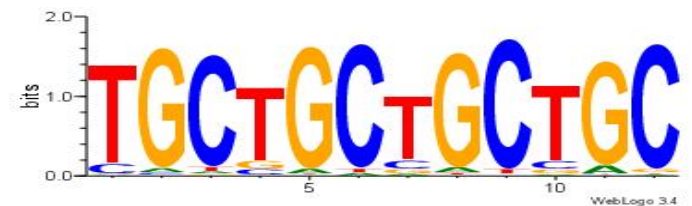
Alignment:

GCAGCAGCAGCA
GCGGCGGCGGCG

Original motif Consensus sequence: GCAGCAGCAGCA



Reverse complement motif Consensus sequence: TGCTGCTGCTGC



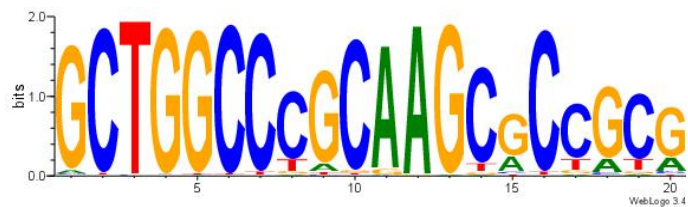
Dataset #: 1
Motif ID: 100
Motif name: Motif 100
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif

Direction: Backward
 Position number: 2
 Number of overlap: 12
 Similarity score: 0.0752454

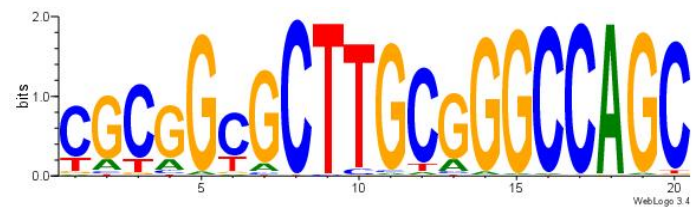
Alignment:

GCTGGCCCGCAAGCGCCGCG
 -----CGCCGCCGCCGC--

Original motif Consensus sequence: GCTGGCCCGCAAGCGCCGCG



Reverse complement motif Consensus sequence: CGCGGCGCTTGC GGGCCAGC

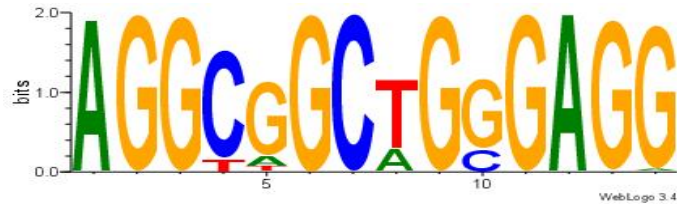


Dataset #: 1
 Motif ID: 39
 Motif name: Motif 39
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 12
 Similarity score: 0.0783129

Alignment:

AGGCGGCTGGGAGG
 GCGGCGGCGGCG--

Original motif Consensus sequence: AGGCGGCTGGGAGG



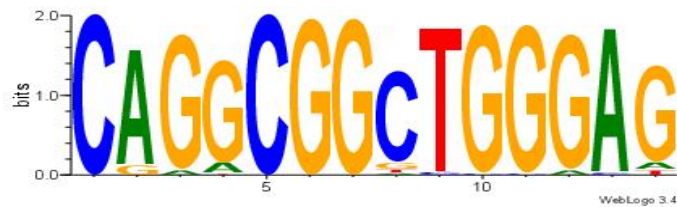
Reverse complement motif Consensus sequence: CCTCCAGCCGCC



Dataset #: 1
Motif ID: 286
Motif name: Motif 286
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 3
Number of overlap: 12
Similarity score: 0.078982

Alignment:
CTCCCAGCCGCTG
--CGCCGCCGCCG

Original motif Consensus sequence: CAGGCGGCTGGGAG



Reverse complement motif Consensus sequence: CTCCCAGCCGCC

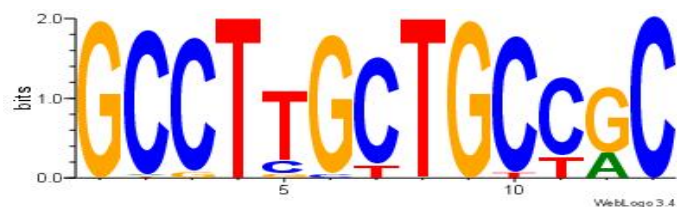


Dataset #: 1
 Motif ID: 229
 Motif name: Motif 229
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 12
 Similarity score: 0.0792901

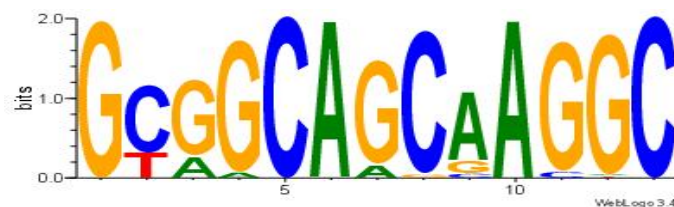
Alignment:

GCCTTGCTGCCGC
 -CGCCGCCGCCGC

Original motif Consensus sequence: GCCTTGCTGCCGC



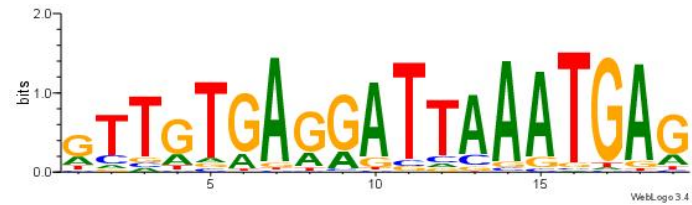
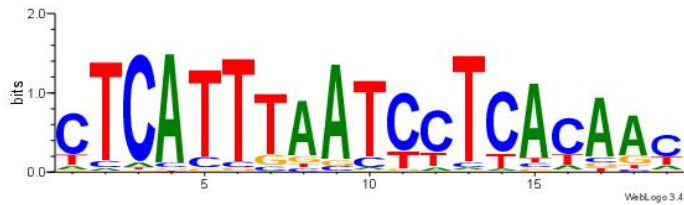
Reverse complement motif Consensus sequence: GCGGCAGCAAGGC



Dataset #: 1 Motif ID: 102 Motif name: Motif 102

Original motif Consensus sequence: CTCATTTAATCCTCACAAC

Reverse complement motif Consensus sequence:
GTTGTGAGGATTAATGAG

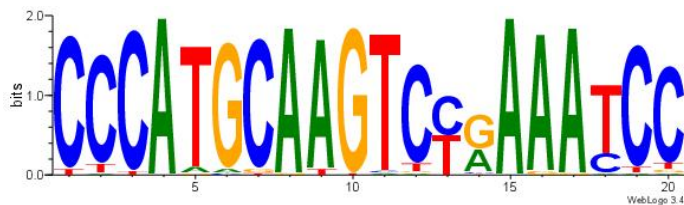


Best Matches for Motif ID 102 (Highest to Lowest)

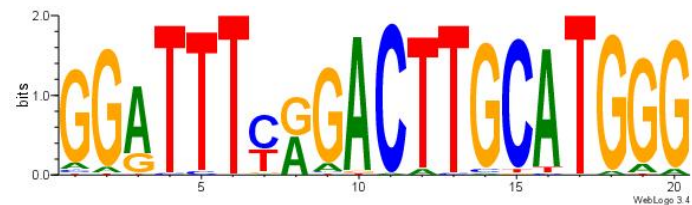
Dataset #: 1
 Motif ID: 310
 Motif name: Motif 310
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 19
 Similarity score: 0.0961125

Alignment:
 CCCATGCAAGTCYRAAATCC
 CTCATTTAATCCTCACAAC-

Original motif Consensus sequence: CCCATGCAAGTCYRAAATCC



Reverse complement motif Consensus sequence: GGATTTMKGACTTGCA TGGG

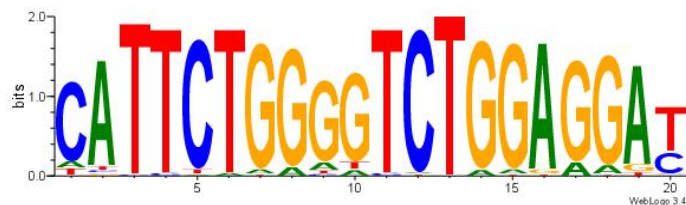


Dataset #: 1
 Motif ID: 309
 Motif name: Motif 309
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 19
 Similarity score: 0.0968109

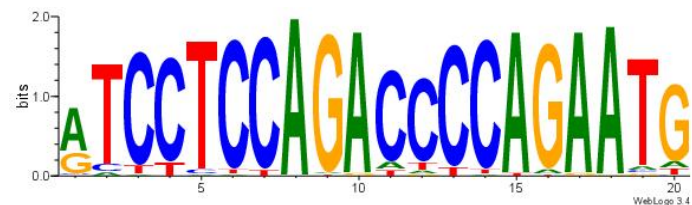
Alignment:

MTCCTCCAGACCCCAGAATG
 CTCATTTAATCCTCACAAC-

Original motif Consensus sequence: CATTCTGGGGTCTGGAGGAY



Reverse complement motif Consensus sequence: MTCCTCCAGACCCCAGAATG



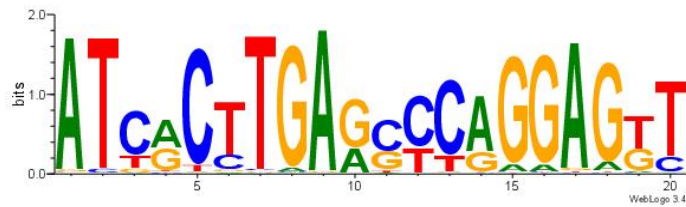
Dataset #: 1
 Motif ID: 8
 Motif name: Motif 8
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1

Number of overlap: 19
Similarity score: 0.0987666

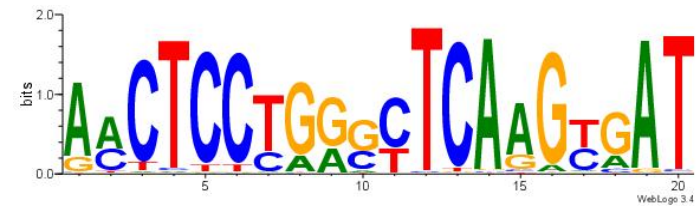
Alignment:

ARCTCCTGKSCTCAAGKGAT
-GTTGTGAGGATTAAATGAG

Original motif Consensus sequence: ATCRCTTGAGSYCAGGAGKT



Reverse complement motif Consensus sequence:
ARCTCCTGKSCTCAAGKGAT

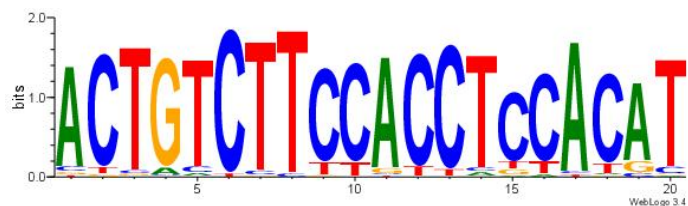


Dataset #: 1
Motif ID: 178
Motif name: Motif 178
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 19
Similarity score: 0.101876

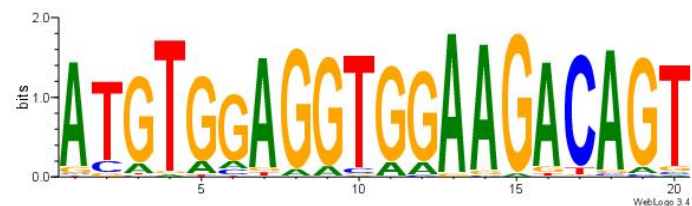
Alignment:

ATGTGGAGGTGGAAGACAGT
GTTGTGAGGATTAAATGAG-

Original motif Consensus sequence: ACTGTCTTCCACCTCCACAT



Reverse complement motif Consensus sequence: ATGTGGAGGTGGAAGACAGT

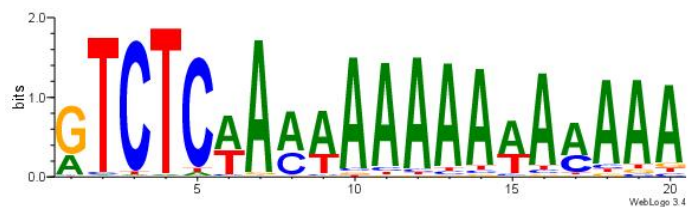


Dataset #: 1
Motif ID: 7
Motif name: Motif 7
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 2
Number of overlap: 19
Similarity score: 0.101917

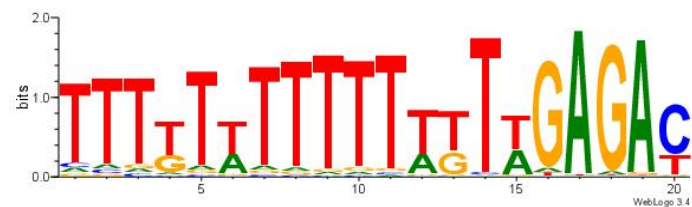
Alignment:

GTCTCWAMAAAAAWAMAAA
-GTTGTGAGGATTAAATGAG

Original motif Consensus sequence: GTCTCWAMAAAAAWAMAAA

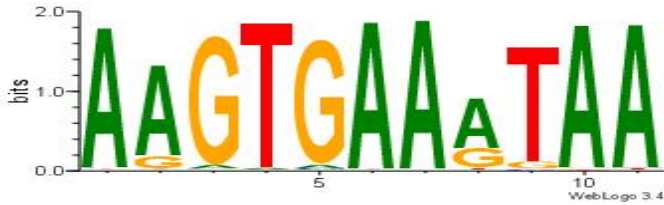


Reverse complement motif Consensus sequence: TTTYTWTTTTTYTWGAGAC

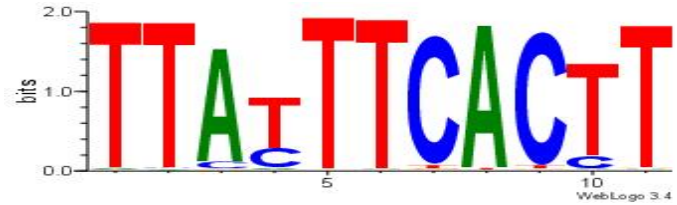


Dataset #: 1 Motif ID: 103 Motif name: Motif 103

Original motif Consensus sequence: AAGTGAAATAA



Reverse complement motif Consensus sequence: TTATTTCACTT



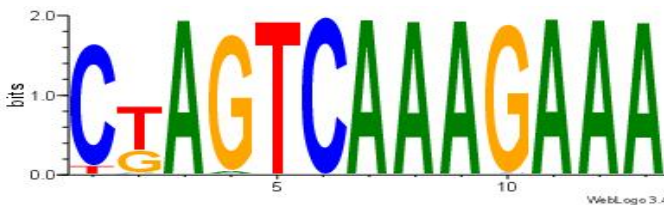
Best Matches for Motif ID 103 (Highest to Lowest)

Dataset #:	1
Motif ID:	24
Motif name:	Motif 24
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	11
Similarity score:	0.0659798

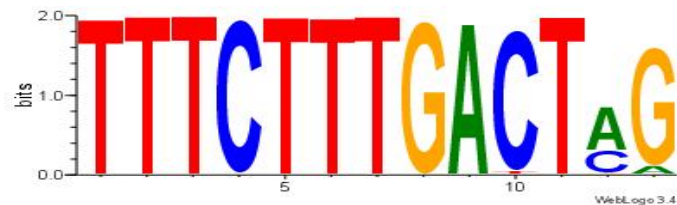
Alignment:

CKAGTCAAAGAAA
 -AAGTGAAATAA-

Original motif Consensus sequence: CKAGTCAAAGAAA



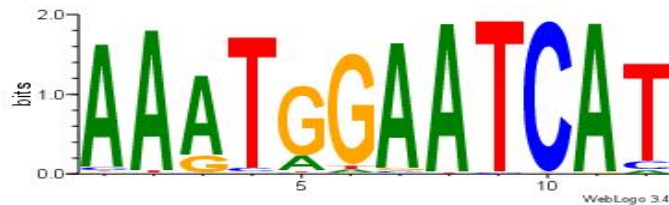
Reverse complement motif Consensus sequence: TTTCTTTGACTRG



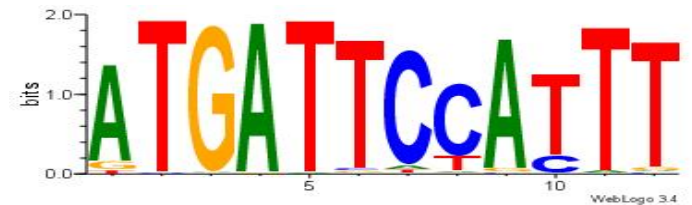
Dataset #: 1
 Motif ID: 281
 Motif name: Motif 281
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.068219

Alignment:
 AAATGGAATCAT
 AAGTCAAATAA-

Original motif Consensus sequence: AAATGGAATCAT



Reverse complement motif Consensus sequence: ATGATTCCATTT



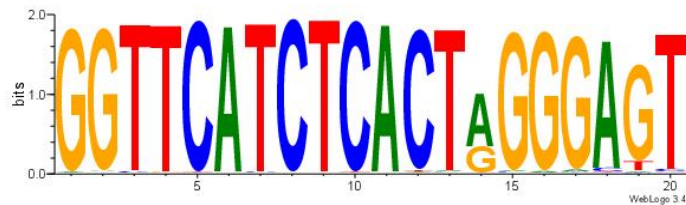
Dataset #: 1
 Motif ID: 23
 Motif name: Motif 23
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 7

Number of overlap: 11
Similarity score: 0.069022

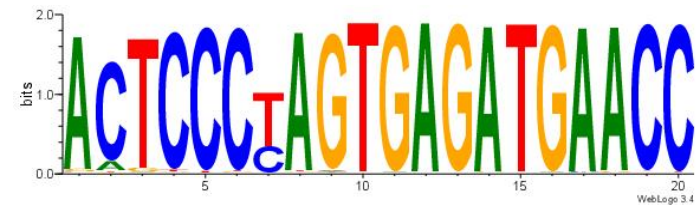
Alignment:

GGTTCATCTCACTAGGGAGT
-----TTATTTCACTT---

Original motif Consensus sequence: GGTTCATCTCACTAGGGAGT



Reverse complement motif Consensus sequence:
ACTCCCTAGTGAGATGAACC

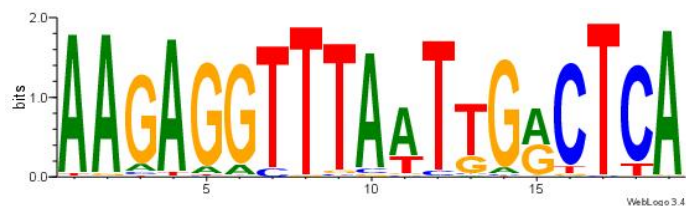


Dataset #: 1
Motif ID: 129
Motif name: Motif 129
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2
Number of overlap: 11
Similarity score: 0.0694615

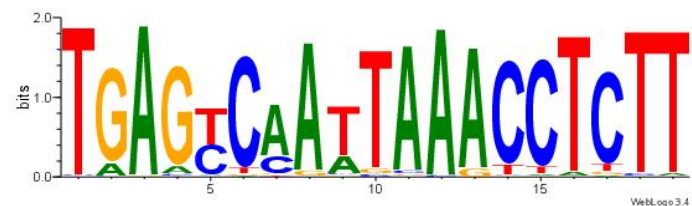
Alignment:

AAGAGGTTTAATTGRCTCA
-----TTATTTCACTT---

Original motif Consensus sequence: AAGAGGTTTAATTGRCTCA



Reverse complement motif Consensus sequence: TGAGKCAATTAACCTCTT

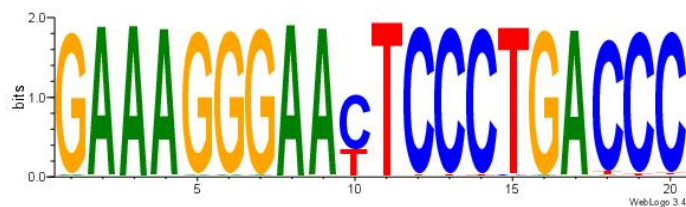


Dataset #: 1
Motif ID: 16
Motif name: Motif 16
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 3
Number of overlap: 11
Similarity score: 0.0711874

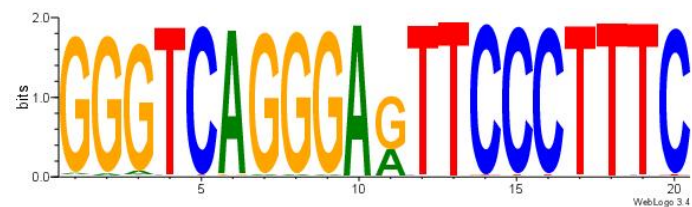
Alignment:

```
GGGTCAGGGAGTTCCTTTC  
-----TTATTTCACTT--
```

Original motif Consensus sequence: GAAAGGGAAGTCCCTGACCC

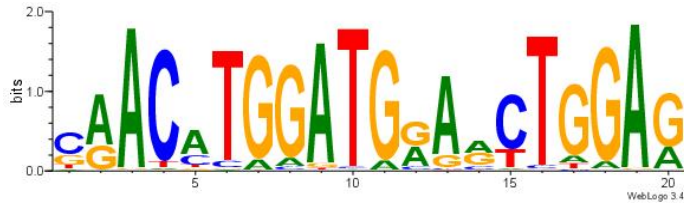


Reverse complement motif Consensus sequence: GGGTCAGGGAGTTCCTTTC

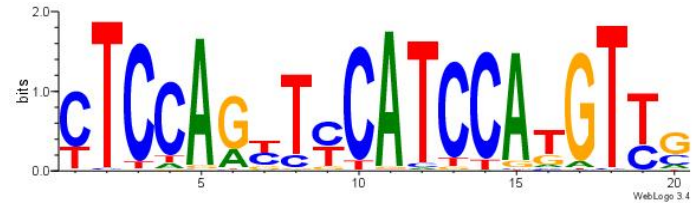


Dataset #: 1 Motif ID: 104 Motif name: Motif 104

Original motif Consensus sequence: CAACATGGATGRARCTGGAG



Reverse complement motif Consensus sequence: CTCCAGKTMCATCCATGTTG



Best Matches for Motif ID 104 (Highest to Lowest)

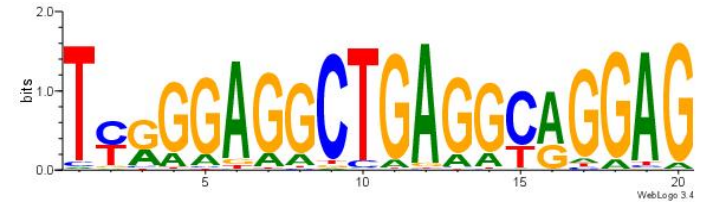
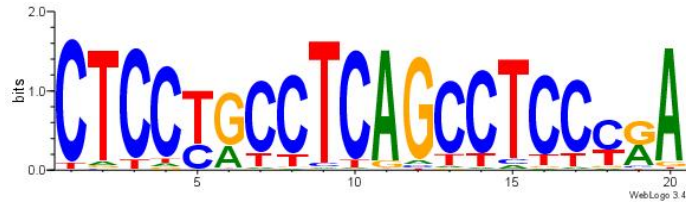
Dataset #:	1
Motif ID:	26
Motif name:	Motif 26
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	20
Similarity score:	0.0969491

Alignment:

```
CTCCTGCCTCAGCCTCCCRA
CTCCAGKTMCATCCATGTTG
```

Original motif Consensus sequence: CTCCTGCCTCAGCCTCCCRA

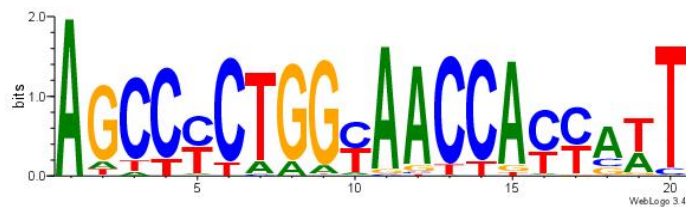
Reverse complement motif Consensus sequence: TMGGGAGGCTGAGGCAGGAG



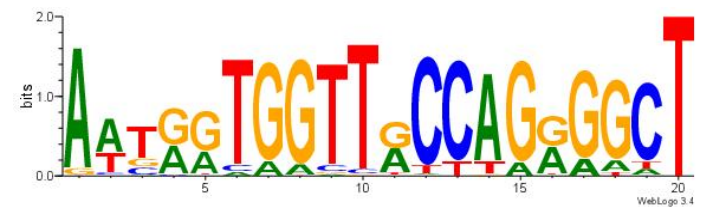
Dataset #: 1
 Motif ID: 139
 Motif name: Motif 139
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.111535

Alignment:
 AGCCYCTGGYAACCAYYAWT
 CTCCAGKTMCATCCATGTTG

Original motif Consensus sequence: AGCCYCTGGYAACCAYYAWT



Reverse complement motif Consensus sequence: AWTKKTGGTTKCCAGKGGCT



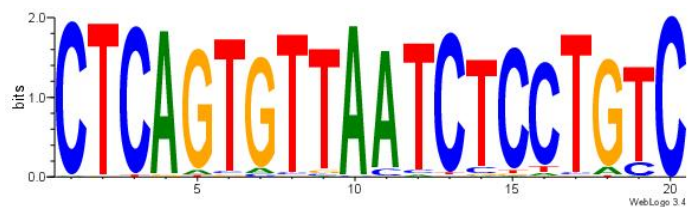
Dataset #: 1

Motif ID: 262
Motif name: Motif 262
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 20
Similarity score: 0.113078

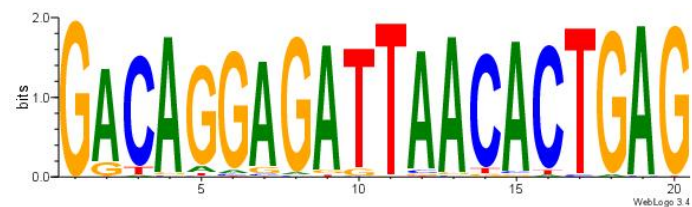
Alignment:

CTCAGTGTTAATCTCCTGTC
CTCCAGKTMCATCCATGTTG

Original motif Consensus sequence: CTCAGTGTTAATCTCCTGTC



Reverse complement motif Consensus sequence:
GACAGGAGATTAACACTGAG



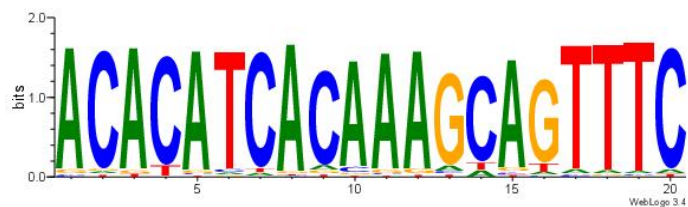
Dataset #: 1
Motif ID: 202
Motif name: Motif 202
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 20

Similarity score: 0.113748

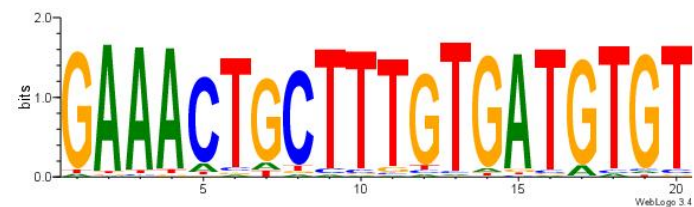
Alignment:

ACACATCACAAAGCAGTTTC
CTCCAGKTMCATCCATGTTG

Original motif Consensus sequence: ACACATCACAAAGCAGTTTC



Reverse complement motif Consensus sequence:
GAAACTGCTTTGTGATGTGT



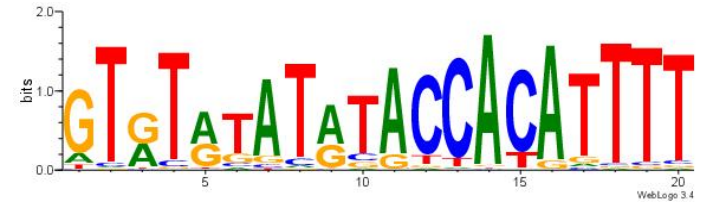
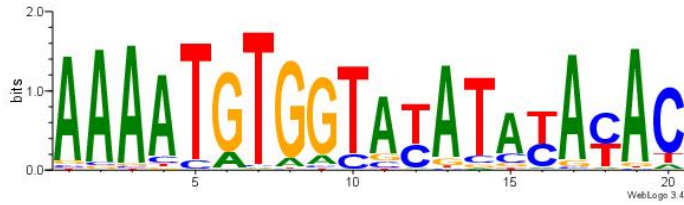
Dataset #: 1
Motif ID: 83
Motif name: Motif 83
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 20
Similarity score: 0.117001

Alignment:

GTKTMTATMTACCACATTTT
CTCCAGKTMCATCCATGTTG

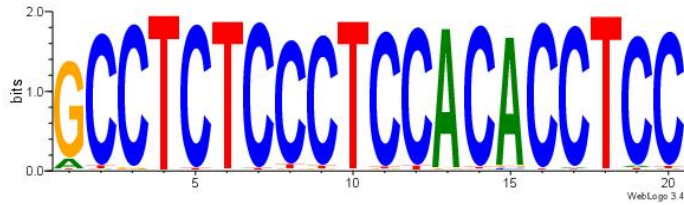
Original motif Consensus sequence: AAAATGTGGTAYATAYAYAC

Reverse complement motif Consensus sequence:
GTKTMTATMTACCACATTTT

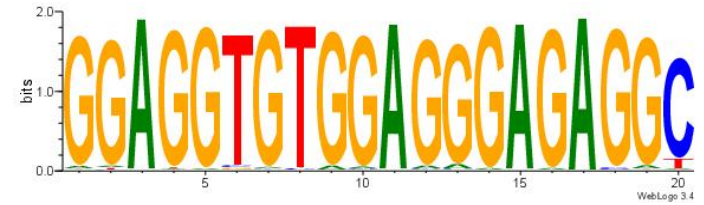


Dataset #: 1 Motif ID: 105 Motif name: Motif 105

Original motif Consensus sequence: GCCTCTCCCTCCACACCTCC



Reverse complement motif Consensus sequence: GGAGGTGTGGAGGGAGAGGC



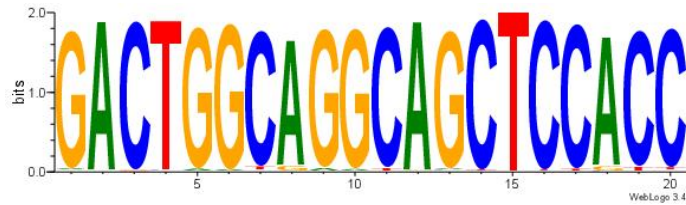
Best Matches for Motif ID 105 (Highest to Lowest)

Dataset #:	1
Motif ID:	52
Motif name:	Motif 52
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	20
Similarity score:	0.118803

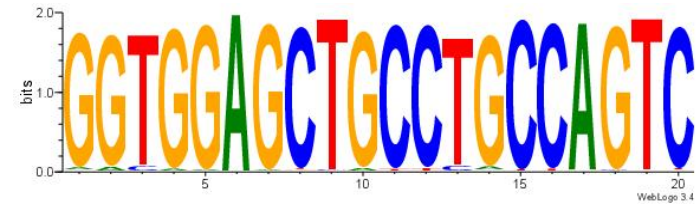
Alignment:

GGTGGAGCTGCCTGCCAGTC
GGAGGTGTGGAGGGAGAGGC

Original motif Consensus sequence: GACTGGCAGGCAGCTCCACC



Reverse complement motif Consensus sequence:
GGTGGAGCTGCCTGCCAGTC



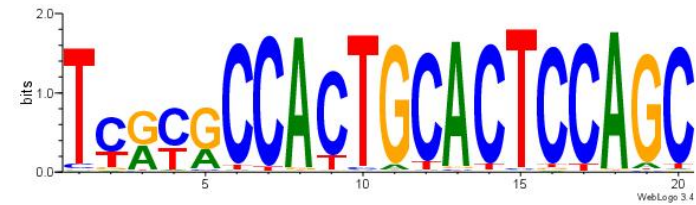
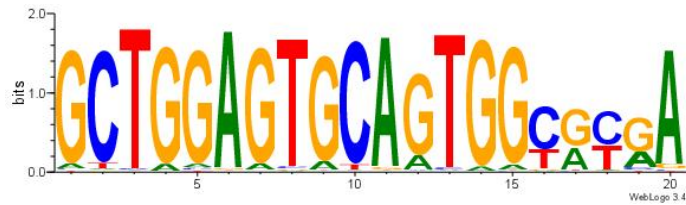
Dataset #:	1
Motif ID:	3
Motif name:	Motif 3
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	20
Similarity score:	0.11947

Alignment:

TCKMGCCACTGCACTCCAGC
GCCTCTCCCTCCACACCTCC

Original motif Consensus sequence: GCTGGAGTGCAGTGGCRYGA

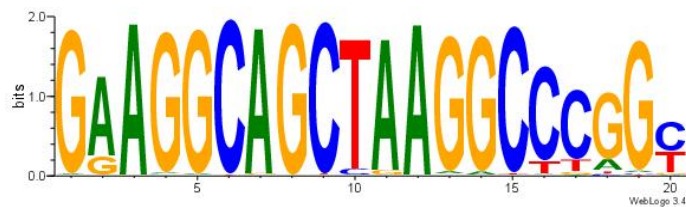
Reverse complement motif Consensus sequence:
TCKMGCCACTGCACTCCAGC



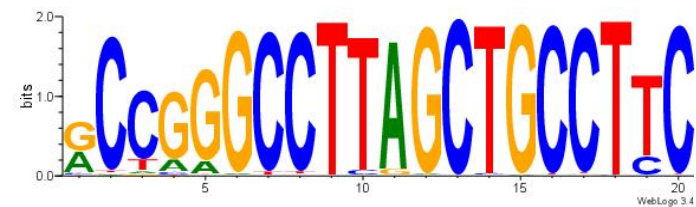
Dataset #: 1
 Motif ID: 64
 Motif name: Motif 64
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.124156

Alignment:
 KCCGGGCCTTAGCTGCCTTC
 GCCTCTCCCTCCACACCTCC

Original motif Consensus sequence: GAAGGCAGCTAAGGCCcCGG



Reverse complement motif Consensus sequence: KCCGGGCCTTAGCTGCCTTC



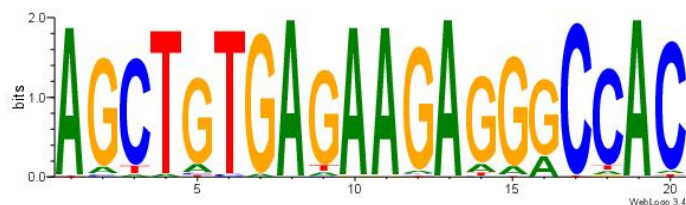
Dataset #: 1

Motif ID: 294
 Motif name: Motif 294
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.124772

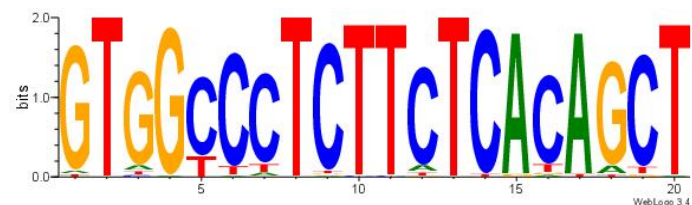
Alignment:

GTGGCCCTCTTCTCACAGCT
 GCCTCTCCCTCCACACCTCC

Original motif Consensus sequence: AGCTGTGAGAAGAGGGCCAC



Reverse complement motif Consensus sequence: GTGGCCCTCTTCTCACAGCT



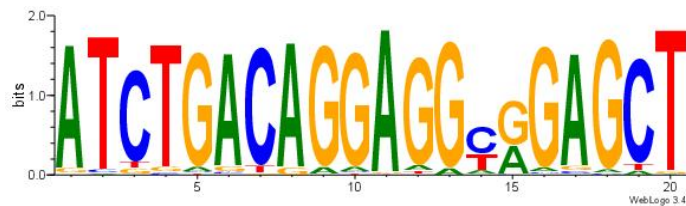
Dataset #: 1
 Motif ID: 165
 Motif name: Motif 165
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 20

Similarity score: 0.127369

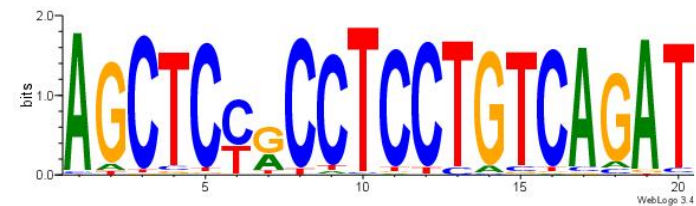
Alignment:

ATCTGACAGGAGGYRGAGCT
GGAGGTGTGGAGGGAGAGGC

Original motif Consensus sequence: ATCTGACAGGAGGYRGAGCT

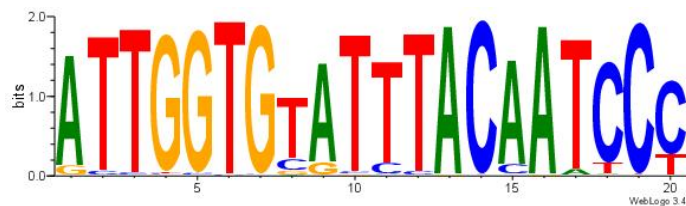


Reverse complement motif Consensus sequence:
AGCTCMKCCTCCTGTCAGAT

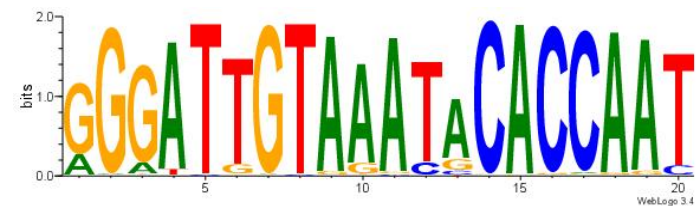


Dataset #: 1 Motif ID: 106 Motif name: Motif 106

Original motif Consensus sequence: ATTGGTGTATTACAATCCC



Reverse complement motif Consensus sequence:
GGGATTGTAAATACACCAAT



Best Matches for Motif ID 106 (Highest to Lowest)

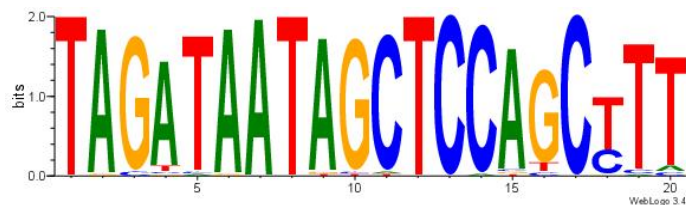
Dataset #: 1
Motif ID: 333
Motif name: Motif 333
Matching format of first motif: Reverse Complement

Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	20
Similarity score:	0.112321

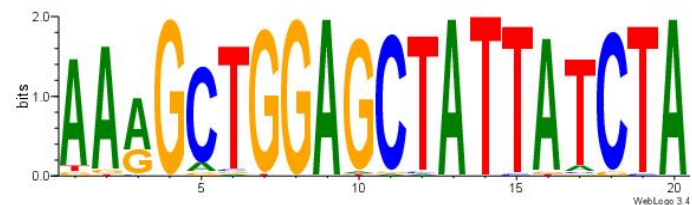
Alignment:

```
TAGATAATAGCTCCAGCTTT
GGGATTGTAAATACACCAAT
```

Original motif Consensus sequence: TAGATAATAGCTCCAGCTTT



Reverse complement motif Consensus sequence: AAAGCTGGAGCTATTATCTA

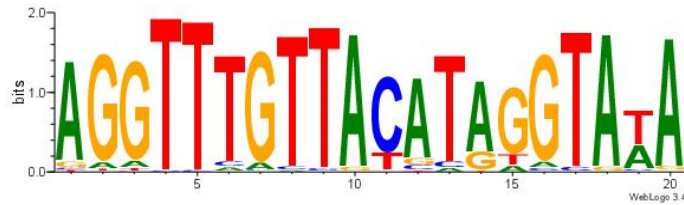


Dataset #:	1
Motif ID:	137
Motif name:	Motif 137
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	20
Similarity score:	0.123702

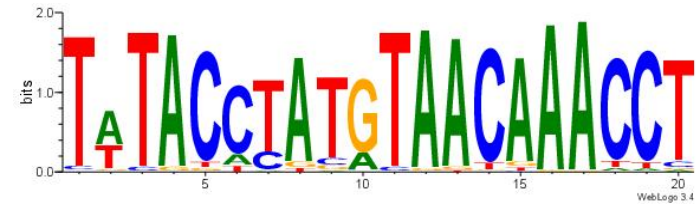
Alignment:

TWTACCTATGTAACAAACCT
ATTGGTGTATTTACAATCCC

Original motif Consensus sequence: AGGTTTGTTACATAGGTAWA



Reverse complement motif Consensus sequence:
TWTACCTATGTAACAAACCT

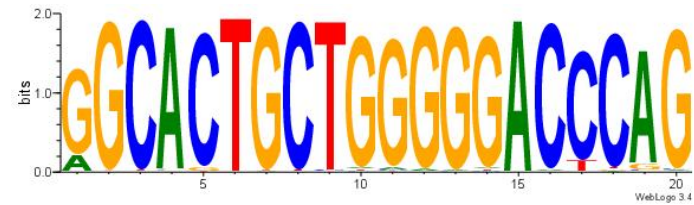
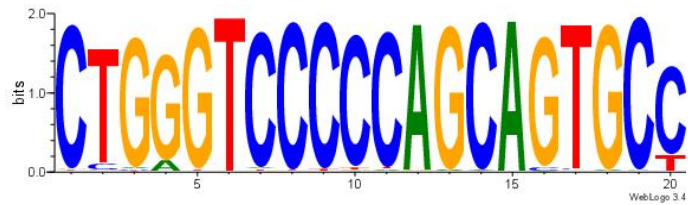


Dataset #: 1
Motif ID: 84
Motif name: Motif 84
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 20
Similarity score: 0.124374

Alignment:
CTGGGTCCCCCAGCAGTGCC
ATTGGTGTATTTACAATCCC

Original motif Consensus sequence: CTGGGTCCCCCAGCAGTGCC

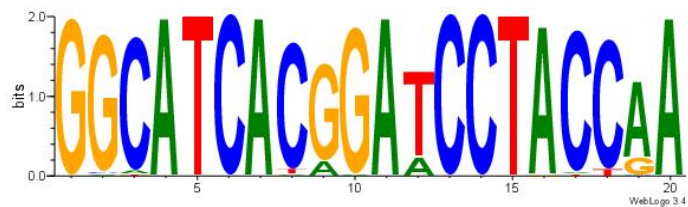
Reverse complement motif Consensus sequence:
GGCACTGCTGGGGGACCCAG



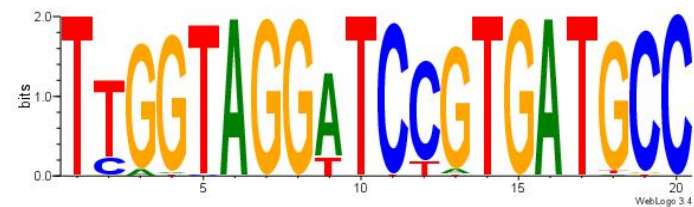
Dataset #: 1
 Motif ID: 311
 Motif name: Motif 311
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.128647

Alignment:
 GGCATCACGGATCCTACCAA
 GGGATTGTAAATACACCAAT

Original motif Consensus sequence: GGCATCACGGATCCTACCAA



Reverse complement motif Consensus sequence: TTGGTAGGATCCGTGATGCC



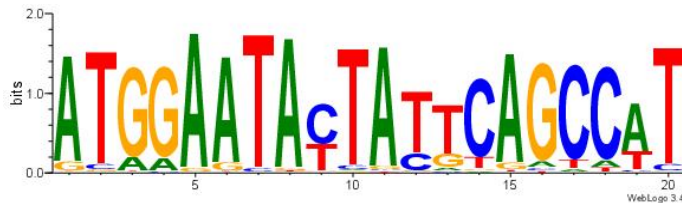
Dataset #: 1

Motif ID: 55
 Motif name: Motif 55
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.134342

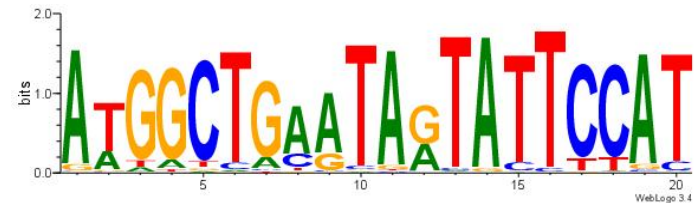
Alignment:

ATGGCTGAATAKTATTCCAT
 GGGATTGTAAATACACCAAT

Original motif Consensus sequence: ATGGAATAYTATTCAGCCAT

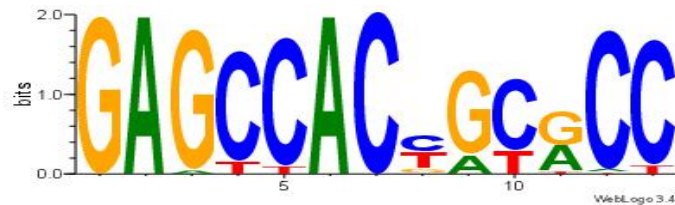


Reverse complement motif Consensus sequence: ATGGCTGAATAKTATTCCAT



Dataset #: 1 Motif ID: 107 Motif name: Motif 107

Original motif Consensus sequence: GAGCCACYGCRCC



Reverse complement motif Consensus sequence: GGMGCKGTGGCTC



Best Matches for Motif ID 107 (Highest to Lowest)

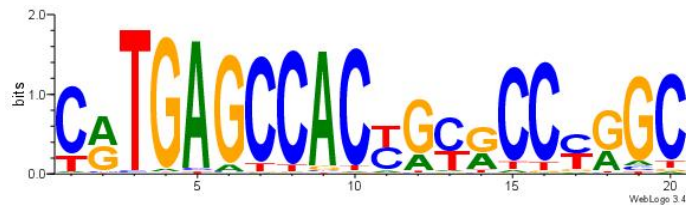
Dataset #: 1
 Motif ID: 56
 Motif name: Motif 56
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 5
 Number of overlap: 13
 Similarity score: 0.00724402

Alignment:

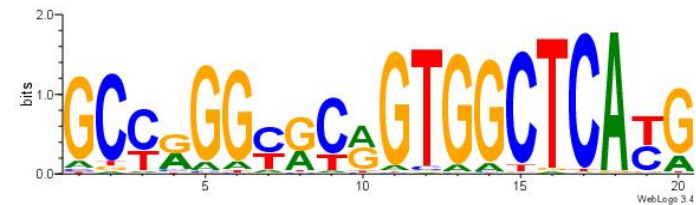
```

CRTGAGCCACYGYRCCYGGC
---GAGCCACYGCRCC----
  
```

Original motif Consensus sequence: CRTGAGCCACYGYRCCYGGC



Reverse complement motif Consensus sequence: GCCKGGMKCMGTGGCTCAKG



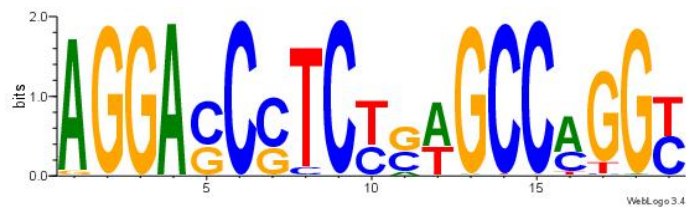
Dataset #: 1
 Motif ID: 10
 Motif name: Motif 10
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif

Direction: Forward
 Position number: 3
 Number of overlap: 13
 Similarity score: 0.0668268

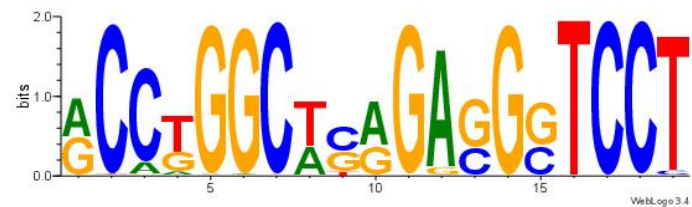
Alignment:

AGGASCSTCYSWGCCMGY
 --GAGCCACYGCRCC----

Original motif Consensus sequence: AGGASCSTCYSWGCCMGY



Reverse complement motif Consensus sequence: MCCYGGCWSMGASGSTCCT

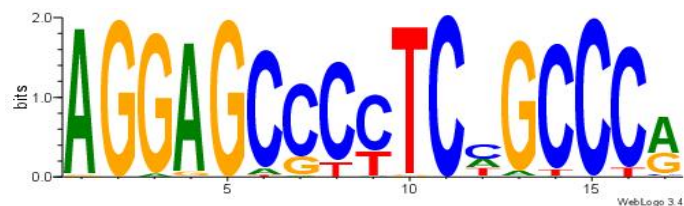


Dataset #: 1
 Motif ID: 111
 Motif name: Motif 111
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 13
 Similarity score: 0.070263

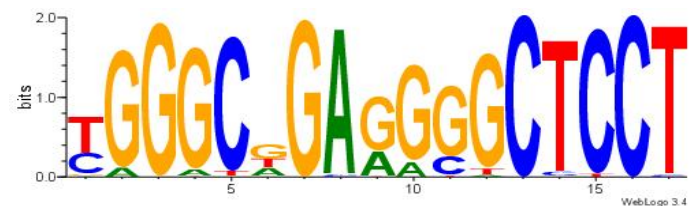
Alignment:

AGGAGCCCCTCHGCCCR
 --GAGCCACYGCRCC--

Original motif Consensus sequence: AGGAGCCCCTCHGCCCR



Reverse complement motif Consensus sequence: KGGGCDGAGGGGCTCCT

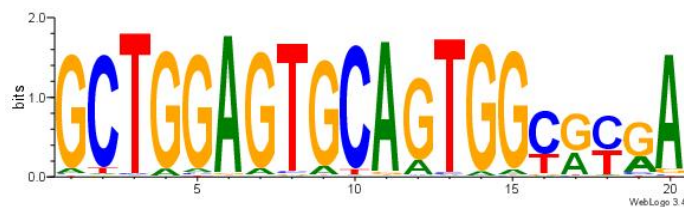


Dataset #: 1
Motif ID: 3
Motif name: Motif 3
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 3
Number of overlap: 13
Similarity score: 0.0734949

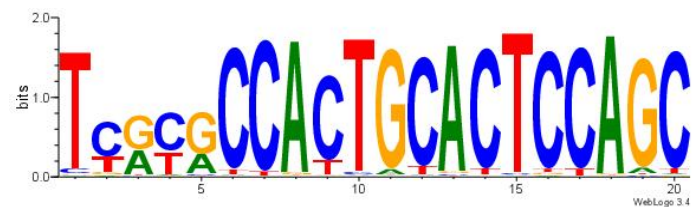
Alignment:

```
GCTGGAGTGCAGTGGCRYGA  
--GGMGCKGTGGCTC-----
```

Original motif Consensus sequence: GCTGGAGTGCAGTGGCRYGA



Reverse complement motif Consensus sequence: TCKMGCCACTGCACTCCAGC

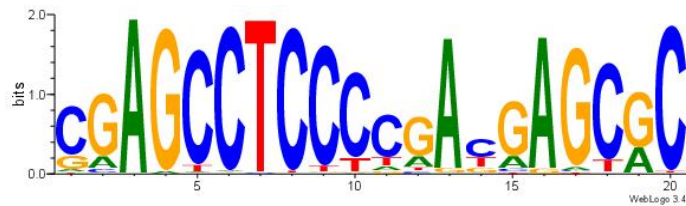


Dataset #: 1
 Motif ID: 108
 Motif name: Motif 108
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 13
 Similarity score: 0.0783677

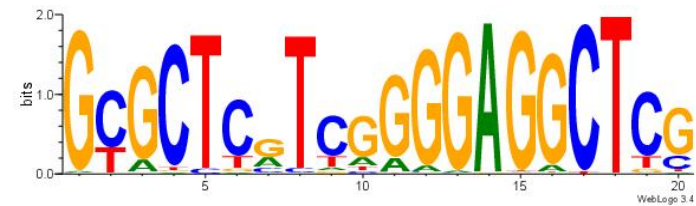
Alignment:

GCGCTCKTCGGGGAGGCTCG
 -----GGMGCKGTGGCTC-

Original motif Consensus sequence: CGAGCCTCCCCGAYGAGCGC



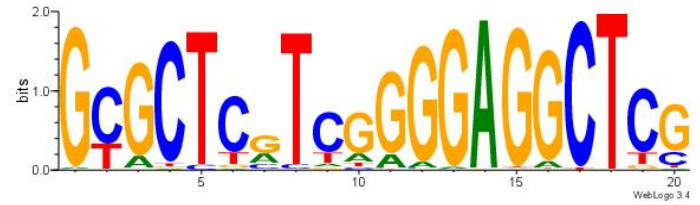
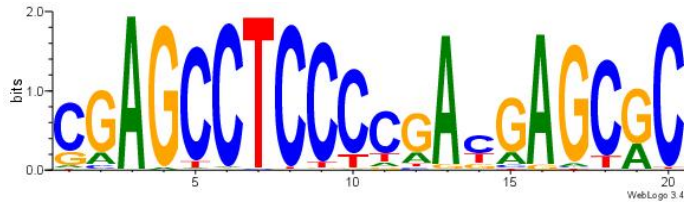
Reverse complement motif Consensus sequence: GCGCTCKTCGGGGAGGCTCG



Dataset #: 1 Motif ID: 108 Motif name: Motif 108

Original motif Consensus sequence: CGAGCCTCCCCGAYGAGCGC

Reverse complement motif Consensus sequence: GCGCTCKTCGGGGAGGCTCG

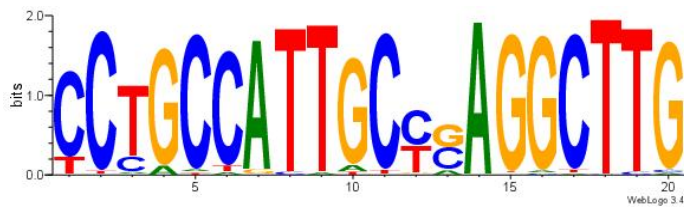


Best Matches for Motif ID 108 (Highest to Lowest)

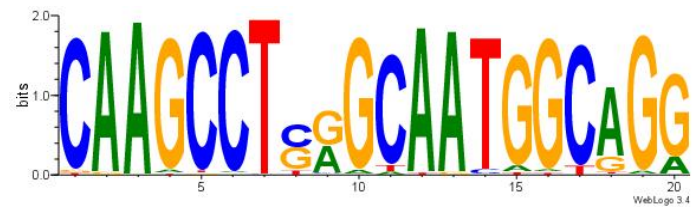
Dataset #: 1
 Motif ID: 196
 Motif name: Motif 196
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.0943206

Alignment:
 CAAGCCTSKGCAATGGCAGG
 CGAGCCTCCCCGAYGAGCGC

Original motif Consensus sequence: CCTGCCATTGCYSAGGCTTG



Reverse complement motif Consensus sequence: CAAGCCTSKGCAATGGCAGG

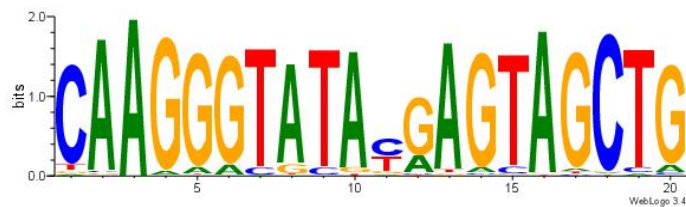


Dataset #: 1
 Motif ID: 194
 Motif name: Motif 194
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.095821

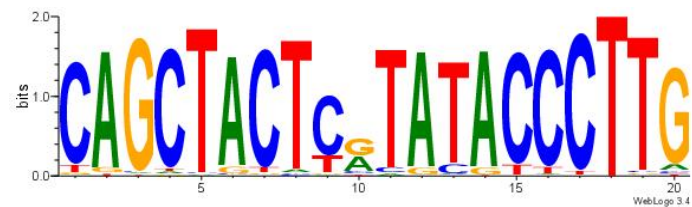
Alignment:

CAGCTACTCKTATACCCTTG
 GCGCTCKTCGGGGAGGCTCG

Original motif Consensus sequence: CAAGGGTATAYGAGTAGCTG



Reverse complement motif Consensus sequence: CAGCTACTCKTATACCCTTG



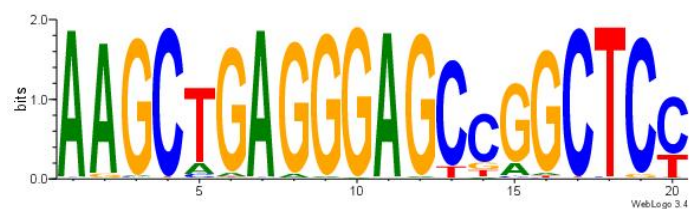
Dataset #: 1
 Motif ID: 96
 Motif name: Motif 96
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1

Number of overlap: 20
Similarity score: 0.100601

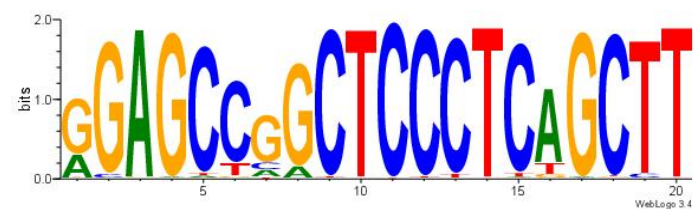
Alignment:

AAGCTGAGGGAGCCGGCTCC
GCGCTCKTCGGGGAGGCTCG

Original motif Consensus sequence: AAGCTGAGGGAGCCGGCTCC



Reverse complement motif Consensus sequence: GGAGCCGGCTCCCTCAGCTT

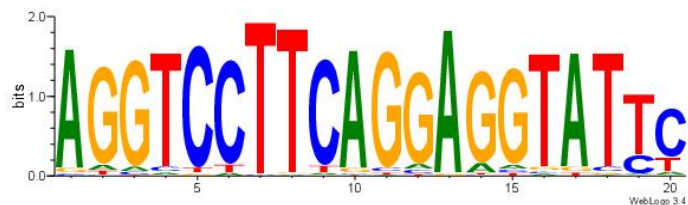


Dataset #: 1
Motif ID: 179
Motif name: Motif 179
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 20
Similarity score: 0.107842

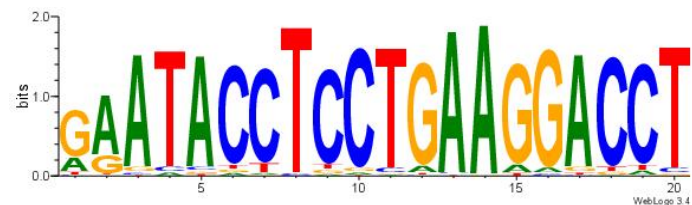
Alignment:

GAATACCTCCTGAAGGACCT
GCGCTCKTCGGGGAGGCTCG

Original motif Consensus sequence: AGGTCCTCAGGAGGTATTC



Reverse complement motif Consensus sequence: GAATACCTCCTGAAGGACCT

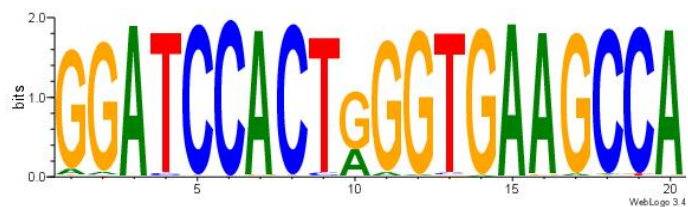


Dataset #: 1
Motif ID: 61
Motif name: Motif 61
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 20
Similarity score: 0.112636

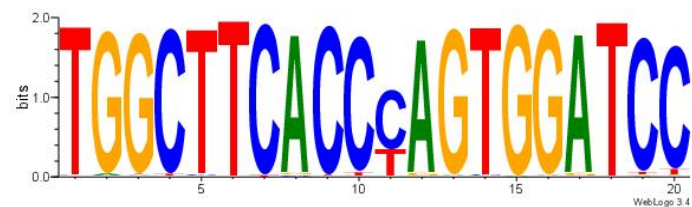
Alignment:

GGATCCACTGGGTGAAGCCA
CGAGCCTCCCCGAYGAGCGC

Original motif Consensus sequence: GGATCCACTGGGTGAAGCCA

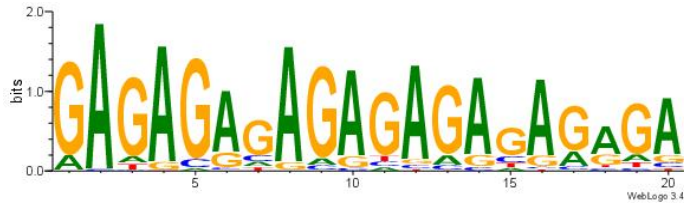


Reverse complement motif Consensus sequence: TGGCTTCACCAGTGGATCC

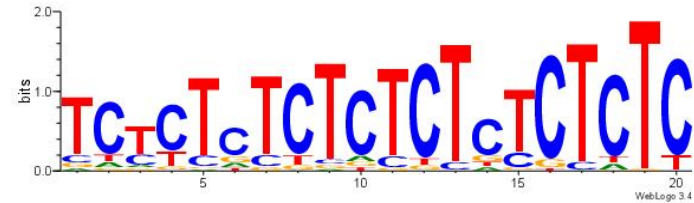


Dataset #: 1 Motif ID: 109 Motif name: Motif 109

Original motif Consensus sequence: GAGAGAGAGAGAGAGAGA



Reverse complement motif Consensus sequence: TCTCTCTCTCTCTCTCTC



Best Matches for Motif ID 109 (Highest to Lowest)

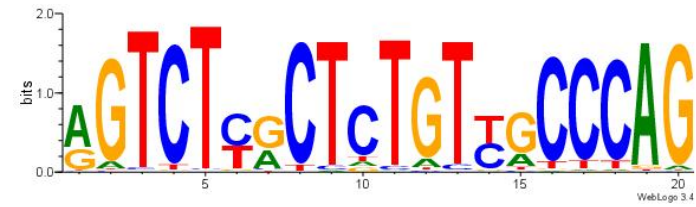
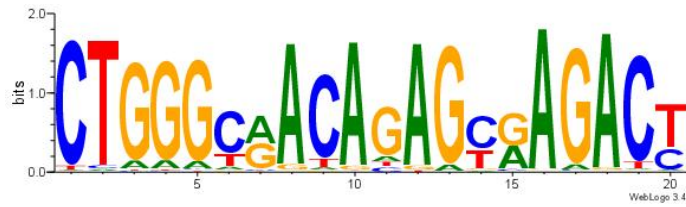
Dataset #:	1
Motif ID:	29
Motif name:	Motif 29
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	20
Similarity score:	0.0851551

Alignment:

```
MGTCMKCTCTGTKGCCAG
TCTCTCTCTCTCTCTCTC
```

Original motif Consensus sequence: CTGGGCRACAGAGYRAGACY

Reverse complement motif Consensus sequence: MGTCMKCTCTGTKGCCAG

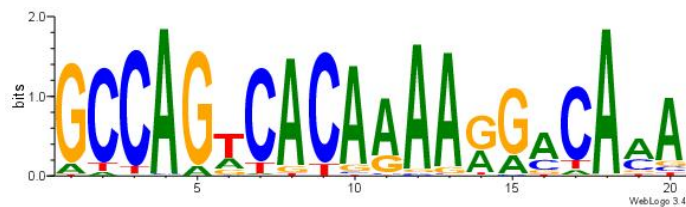


Dataset #: 1
 Motif ID: 145
 Motif name: Motif 145
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.0867304

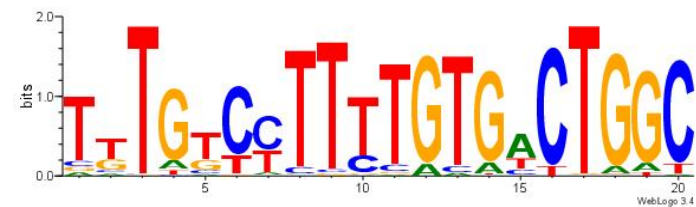
Alignment:

GCCAGTCACAAAARGACAMA
 GAGAGAGAGAGAGAGAGAGA

Original motif Consensus sequence: GCCAGTCACAAAARGACAMA



Reverse complement motif Consensus sequence: TYTGTCTTTGTGACTGGC



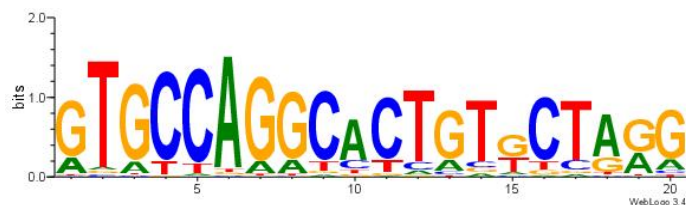
Dataset #: 1

Motif ID: 76
 Motif name: Motif 76
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.105417

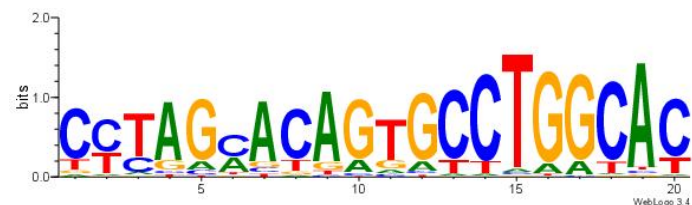
Alignment:

CMTAGYACAGTGCCTGGCAC
 TCTCTCTCTCTCTCTCTCTC

Original motif Consensus sequence: GTGCCAGGCACTGKCTARG



Reverse complement motif Consensus sequence: CMTAGYACAGTGCCTGGCAC



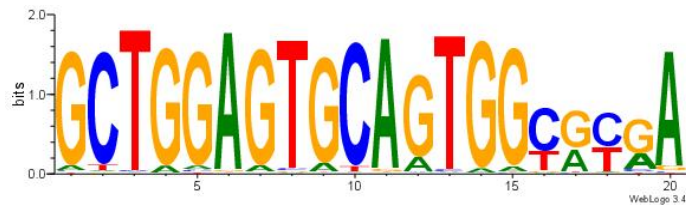
Dataset #: 1
 Motif ID: 3
 Motif name: Motif 3
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 20

Similarity score: 0.10584

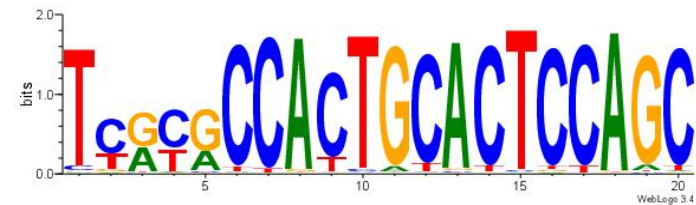
Alignment:

TCKMGCCACTGCACTCCAGC
TCTCTCTCTCTCTCTCTCTC

Original motif Consensus sequence: GCTGGAGTGCAGTGGCRYGA



Reverse complement motif Consensus sequence:
TCKMGCCACTGCACTCCAGC



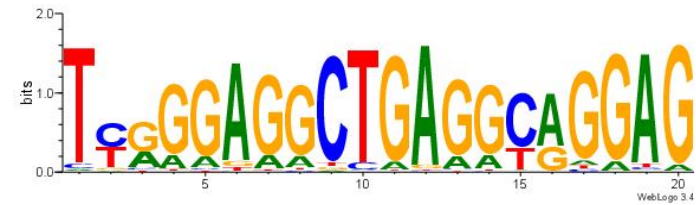
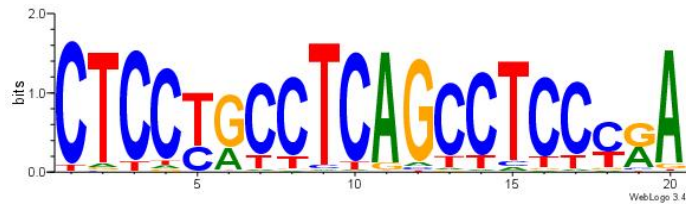
Dataset #: 1
Motif ID: 26
Motif name: Motif 26
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 20
Similarity score: 0.107291

Alignment:

CTCCTGCCTCAGCCTCCCRA
TCTCTCTCTCTCTCTCTCTC

Original motif Consensus sequence: CTCCTGCCTCAGCCTCCCRA

Reverse complement motif Consensus sequence:
TMGGGAGGCTGAGGCAGGAG



Dataset #: 1 Motif ID: 110 Motif name: Motif 110

Original motif Consensus sequence: ATGGGGTGCCA



Reverse complement motif Consensus sequence: TGGCACCCCAT

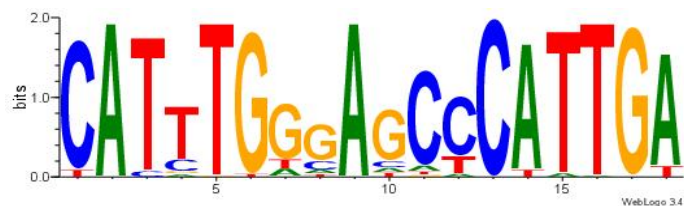


Best Matches for Motif ID 110 (Highest to Lowest)

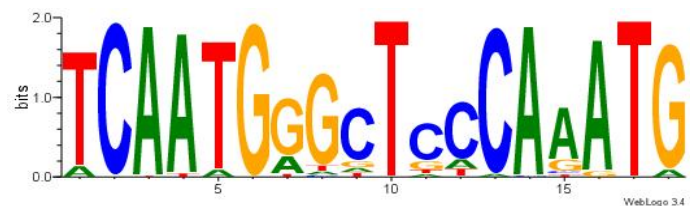
Dataset #:	1
Motif ID:	284
Motif name:	Motif 284
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	5
Number of overlap:	11
Similarity score:	0.0371465

Alignment:
 CATTGGGAGCCCATTGA
 ----TGGCACCCCAT----

Original motif Consensus sequence: CATTGGGAGCCATTGA



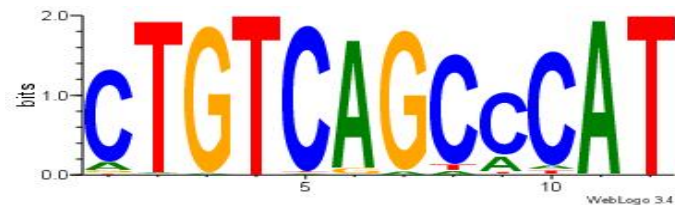
Reverse complement motif Consensus sequence: TCAATGGGCTCCCAAATG



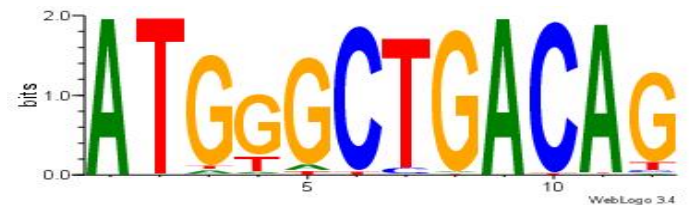
Dataset #: 1
Motif ID: 209
Motif name: Motif 209
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 11
Similarity score: 0.0451831

Alignment:
CTGTCAGCCCAT
-TGGCACCCCAT

Original motif Consensus sequence: CTGTCAGCCCAT



Reverse complement motif Consensus sequence: ATGGGCTGACAG

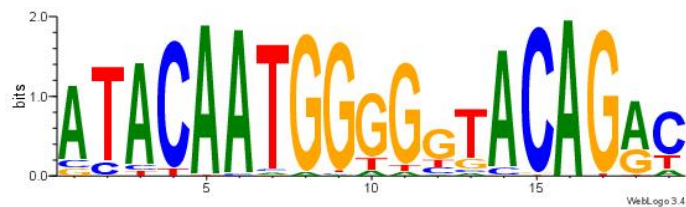


Dataset #: 1
 Motif ID: 193
 Motif name: Motif 193
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 6
 Number of overlap: 11
 Similarity score: 0.0571751

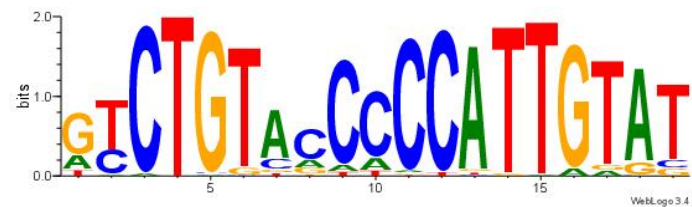
Alignment:

ATACAATGGGGGTACAGRC
 -----ATGGGGTGCCA---

Original motif Consensus sequence: ATACAATGGGGGTACAGRC



Reverse complement motif Consensus sequence: GKCTGTACCCCATTTGTAT



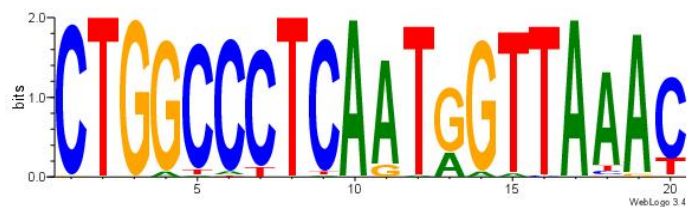
Dataset #: 1
 Motif ID: 332
 Motif name: Motif 332
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 9

Number of overlap: 11
Similarity score: 0.0710968

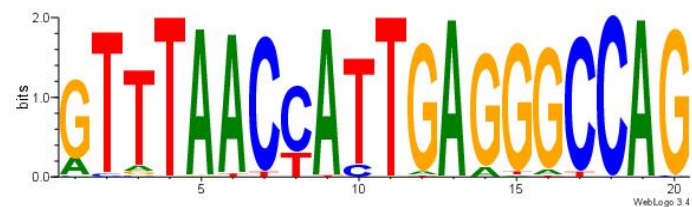
Alignment:

CTGGCCCTCAATGGTTAAAC
-TGGCACCCCAT-----

Original motif Consensus sequence: CTGGCCCTCAATGGTTAAAC



Reverse complement motif Consensus sequence:
GTTTAACCATTGAGGGCCAG

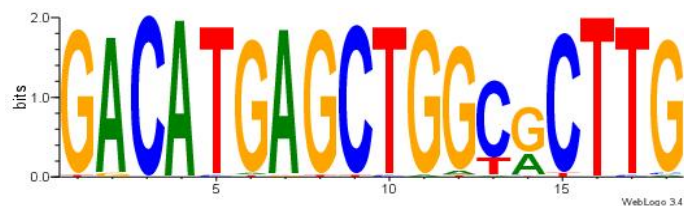


Dataset #: 1
Motif ID: 306
Motif name: Motif 306
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 4
Number of overlap: 11
Similarity score: 0.07764

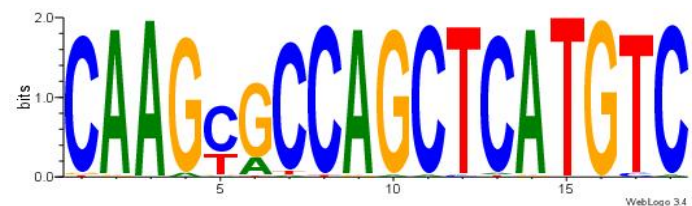
Alignment:

GACATGAGCTGGCGCTTG
---ATGGGGTGCCA----

Original motif Consensus sequence: GACATGAGCTGGCGCTTG

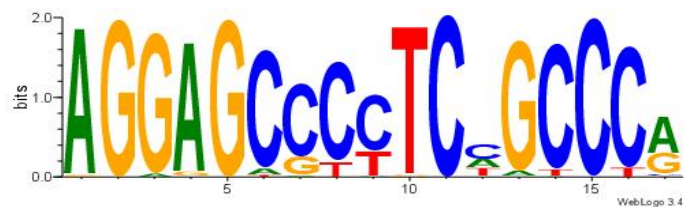


Reverse complement motif Consensus sequence: CAAGCGCCAGCTCATGTC

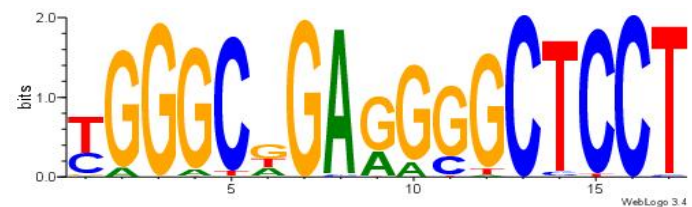


Dataset #: 1 Motif ID: 111 Motif name: Motif 111

Original motif Consensus sequence: AGGAGCCCCTCHGCCCR



Reverse complement motif Consensus sequence: KGGGCDGAGGGGCTCCT



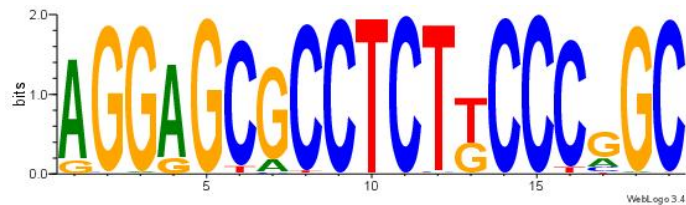
Best Matches for Motif ID 111 (Highest to Lowest)

Dataset #:	1
Motif ID:	30
Motif name:	Motif 30
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	17
Similarity score:	0.0374525

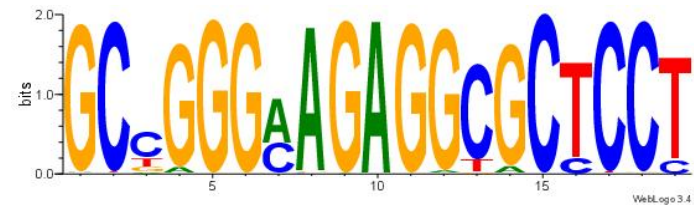
Alignment:

AGGAGCGCCTCTKCCCGGC
AGGAGCCCCTCHGCCCR--

Original motif Consensus sequence: AGGAGCGCCTCTKCCCGGC



Reverse complement motif Consensus sequence:
GCCGGGRAGAGGCGCTCCT



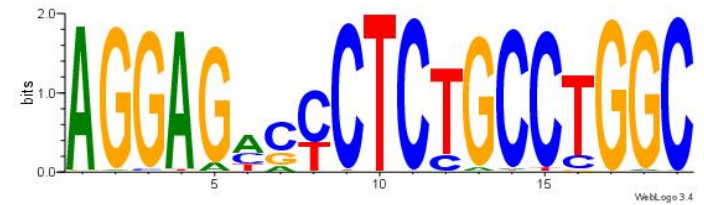
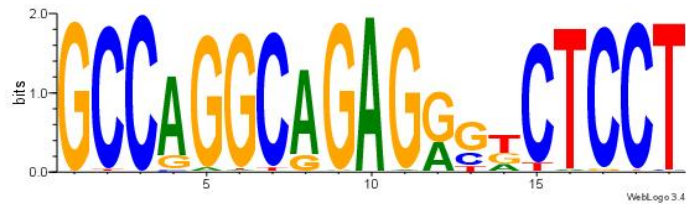
Dataset #:	1
Motif ID:	43
Motif name:	Motif 43
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	3
Number of overlap:	17
Similarity score:	0.0498697

Alignment:

AGGAGRCMCTCTGCCTGGC
--AGGAGCCCCTCHGCCCR

Original motif Consensus sequence: GCCAGGCAGAGRGKCTCCT

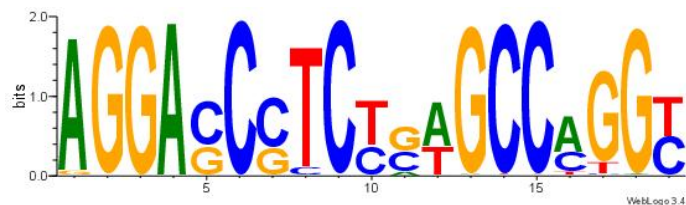
Reverse complement motif Consensus sequence:
AGGAGRCMCTCTGCCTGGC



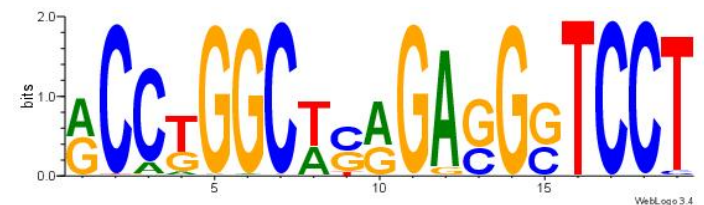
Dataset #: 1
 Motif ID: 10
 Motif name: Motif 10
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 17
 Similarity score: 0.0589885

Alignment:
 AGGASCSTCYSWGCCMGGY
 AGGAGCCCCTCHGCCCR--

Original motif Consensus sequence: AGGASCSTCYSWGCCMGGY



Reverse complement motif Consensus sequence: MCCYGGCWSMGASGSTCCT



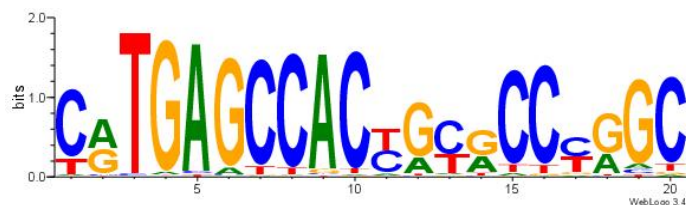
Dataset #: 1

Motif ID: 56
 Motif name: Motif 56
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 17
 Similarity score: 0.0794456

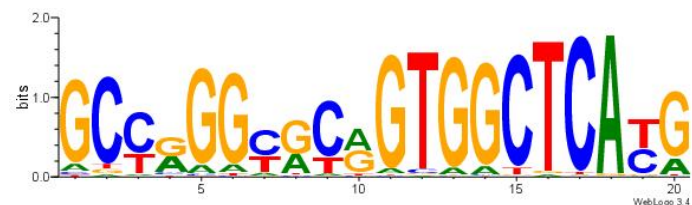
Alignment:

CRTGAGCCACYGYRCCYGGC
 -AGGAGCCCCTCHGCCCR--

Original motif Consensus sequence: CRTGAGCCACYGYRCCYGGC



Reverse complement motif Consensus sequence: GCKGGMKCMGTGGCTCAKG



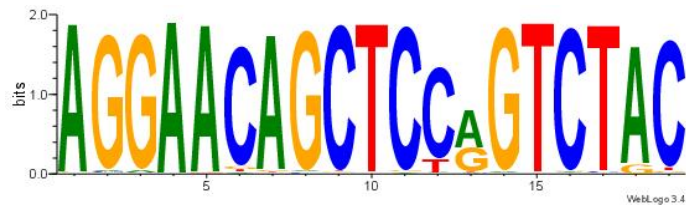
Dataset #: 1
 Motif ID: 62
 Motif name: Motif 62
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 17

Similarity score: 0.0976585

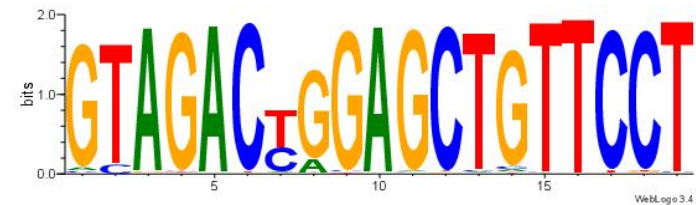
Alignment:

AGGAACAGCTCCRGCTCTAC
AGGAGCCCCTCHGCCCR--

Original motif Consensus sequence: AGGAACAGCTCCRGCTCTAC

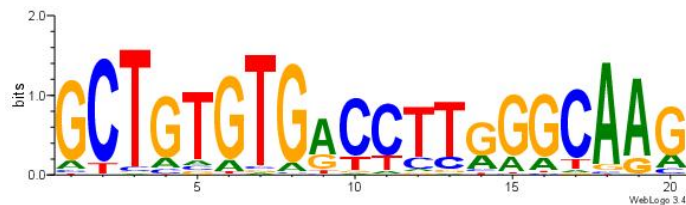


Reverse complement motif Consensus sequence: GTAGACKGGAGCTGTTCCCT

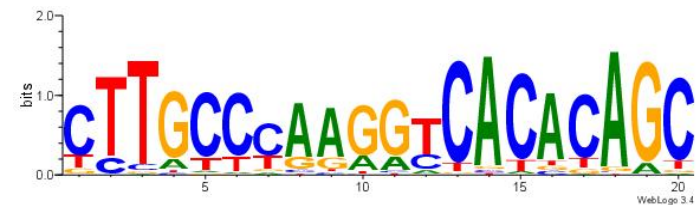


Dataset #: 1 Motif ID: 112 Motif name: Motif 112

Original motif Consensus sequence: GCTGTGTGACCTTGGGCAAG



Reverse complement motif Consensus sequence: CTTGCCAAGGTCACACAGC



Best Matches for Motif ID 112 (Highest to Lowest)

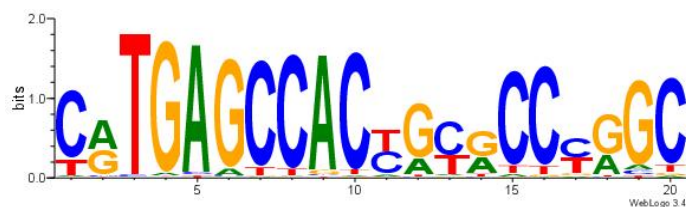
Dataset #:	1
Motif ID:	56
Motif name:	Motif 56
Matching format of first motif:	Original Motif

Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.100531

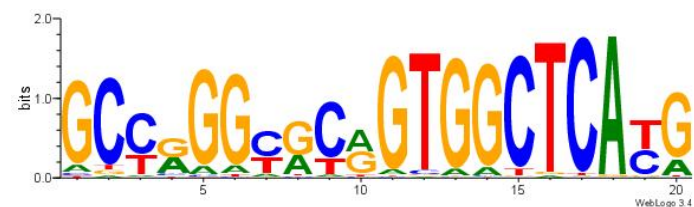
Alignment:

GCKKGGMKCMGTGGCTCAKG
 GCTGTGTGACCTTGGGCAAG

Original motif Consensus sequence: CRTGAGCCACYGYRCCYGGC



Reverse complement motif Consensus sequence: GCKKGGMKCMGTGGCTCAKG

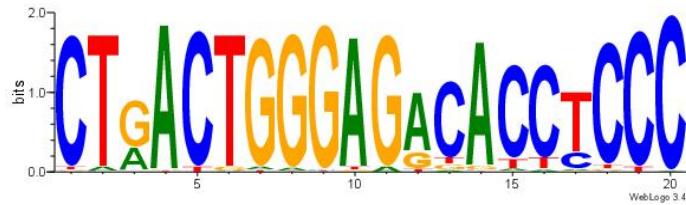


Dataset #: 1
 Motif ID: 293
 Motif name: Motif 293
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.117214

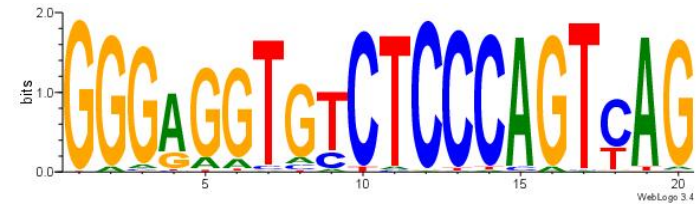
Alignment:

GGGAGGTGTCTCCCAGTCAG
GCTGTGTGACCTTGGGCAAG

Original motif Consensus sequence: CTGACTGGGAGACACCTCCC



Reverse complement motif Consensus sequence:
GGGAGGTGTCTCCCAGTCAG



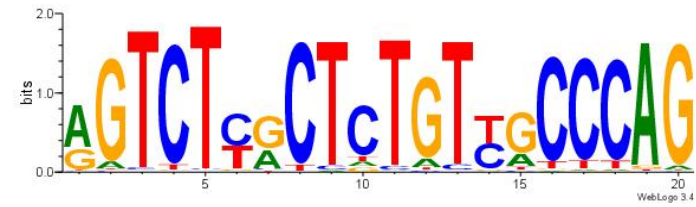
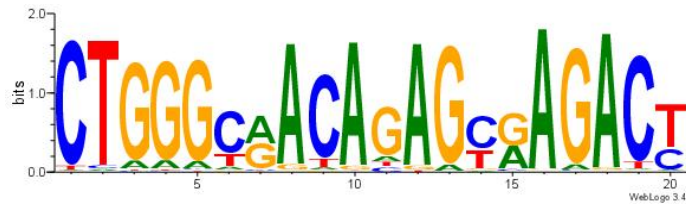
Dataset #: 1
Motif ID: 29
Motif name: Motif 29
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 20
Similarity score: 0.117422

Alignment:

CTGGGCRACAGAGYRAGACY
CTTGCCCAAGGTCACACAGC

Original motif Consensus sequence: CTGGGCRACAGAGYRAGACY

Reverse complement motif Consensus sequence:
MGCTMKCTCTGKGGCCAG

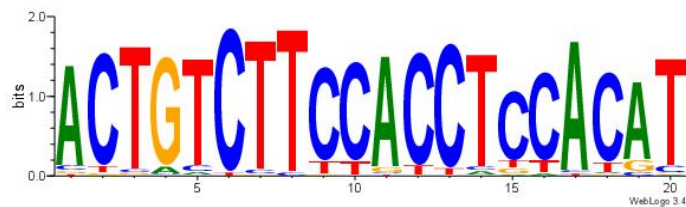


Dataset #: 1
 Motif ID: 178
 Motif name: Motif 178
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.121986

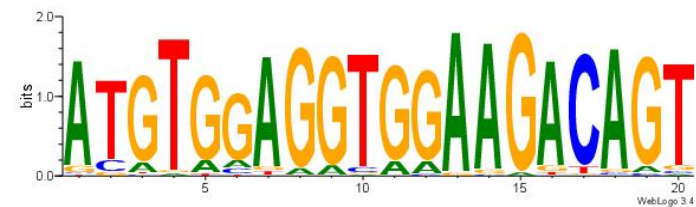
Alignment:

ATGTGGAGGTGGAAGACAGT
 CTTGCCCAAGGTCACACAGC

Original motif Consensus sequence: ACTGTCTTCCACCTCCACAT



Reverse complement motif Consensus sequence: ATGTGGAGGTGGAAGACAGT



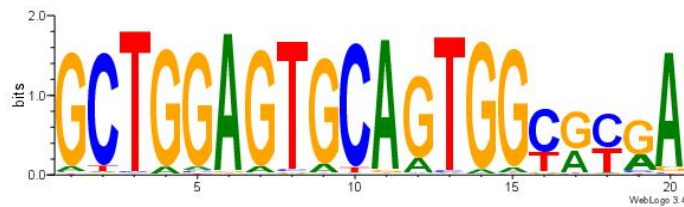
Dataset #: 1

Motif ID: 3
 Motif name: Motif 3
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.122256

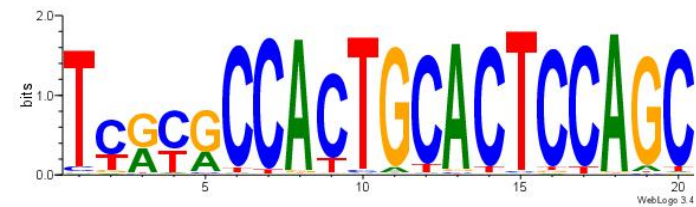
Alignment:

TCKMGCCACTGCACTCCAGC
 CTTGCCCAAGGTCACACAGC

Original motif Consensus sequence: GCTGGAGTGCAGTGGCRYGA

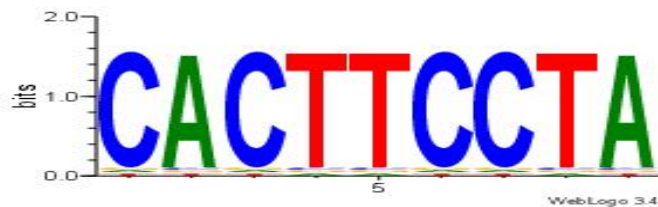


Reverse complement motif Consensus sequence: TCKMGCCACTGCACTCCAGC

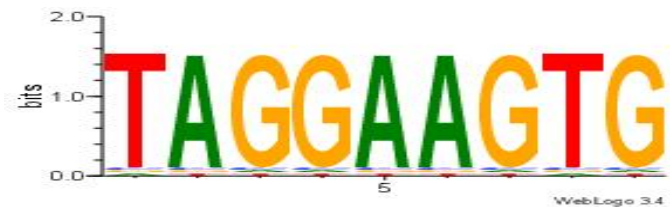


Dataset #: 1 Motif ID: 113 Motif name: Motif 113

Original motif Consensus sequence: CACTTCCTA



Reverse complement motif Consensus sequence: TAGGAAGTG



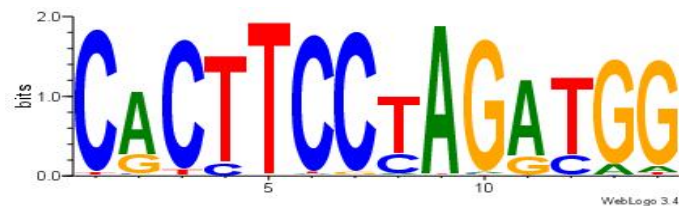
Best Matches for Motif ID 113 (Highest to Lowest)

Dataset #: 1
Motif ID: 74
Motif name: Motif 74
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 9
Similarity score: 0.0147795

Alignment:

```
CCATCTAGGAAGTG  
-----TAGGAAGTG
```

Original motif Consensus sequence: CACTTCCTAGATGG



Reverse complement motif Consensus sequence: CCATCTAGGAAGT

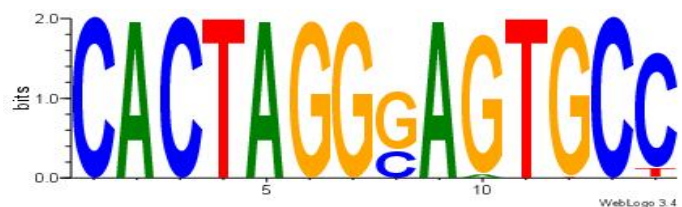


Dataset #: 1
Motif ID: 153
Motif name: Motif 153
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement

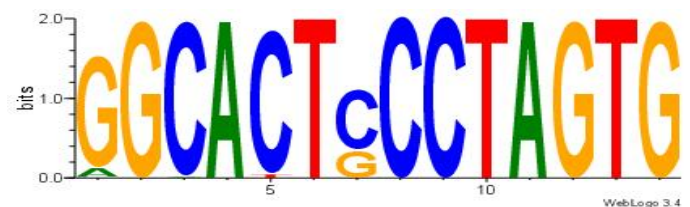
Direction: Forward
Position number: 3
Number of overlap: 9
Similarity score: 0.0332374

Alignment:
GGCACTCCCTAGTG
--CACTTCCTA---

Original motif Consensus sequence: CACTAGGGAGTGCC



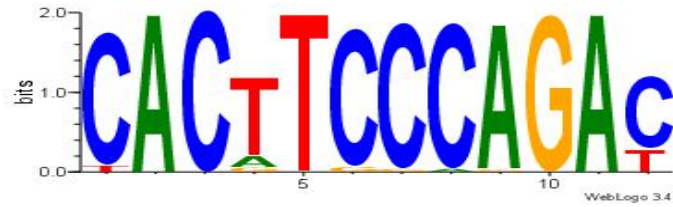
Reverse complement motif Consensus sequence: GGCACTCCCTAGTG



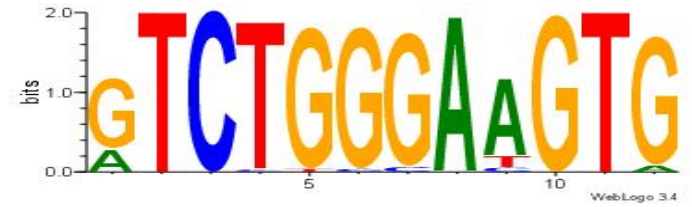
Dataset #: 1
Motif ID: 156
Motif name: Motif 156
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 4
Number of overlap: 9
Similarity score: 0.0333368

Alignment:
GTCTGGGAAGTG
---TAGGAAGTG

Original motif Consensus sequence: CACTTCCCAGAC



Reverse complement motif Consensus sequence: GTCTGGGAAGTG

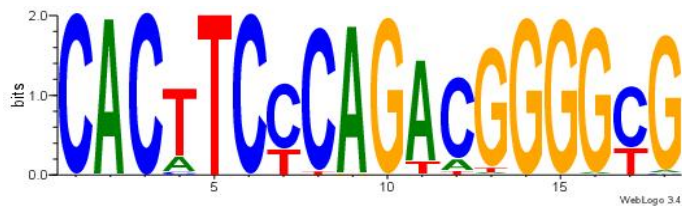


Dataset #: 1
Motif ID: 27
Motif name: Motif 27
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 9
Similarity score: 0.0419916

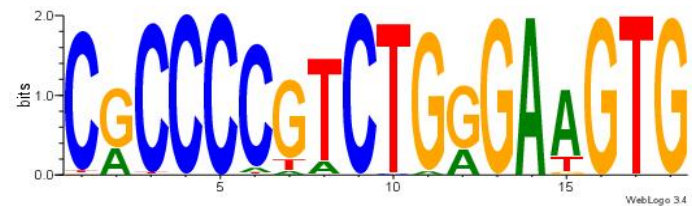
Alignment:

CACTTCCCAGACGGGGCG
CACTTCCTA-----

Original motif Consensus sequence: CACTTCCCAGACGGGGCG



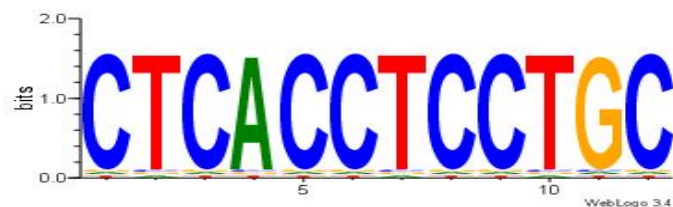
Reverse complement motif Consensus sequence: CGCCCCGTCTGGGAAGTG



Dataset #: 1
 Motif ID: 339
 Motif name: Motif 339
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 9
 Similarity score: 0.0431985

Alignment:
 GCAGGAGGTGAG
 -TAGGAAGTG--

Original motif Consensus sequence: CTCACCTCCTGC

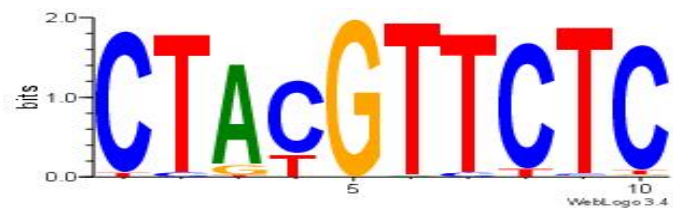


Reverse complement motif Consensus sequence: GCAGGAGGTGAG



Dataset #: 1 Motif ID: 114 Motif name: Motif 114

Original motif Consensus sequence: CTACGTTCTC



Reverse complement motif Consensus sequence: GAGAACGTAG



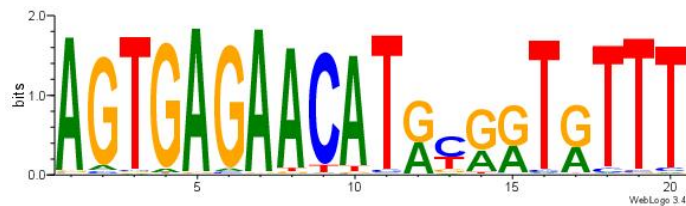
Best Matches for Motif ID 114 (Highest to Lowest)

Dataset #: 1
Motif ID: 63
Motif name: Motif 63
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 4
Number of overlap: 10
Similarity score: 0.0559267

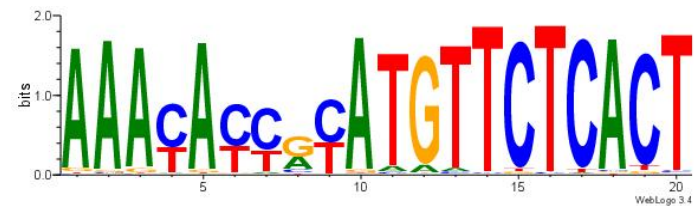
Alignment:

```
AAAMAMMKMATGTTCTCACT  
---CTACGTTCTC-----
```

Original motif Consensus sequence: AGTGAGAACATRYRRTTTT



Reverse complement motif Consensus sequence:
AAAMAMMKMATGTTCTCACT



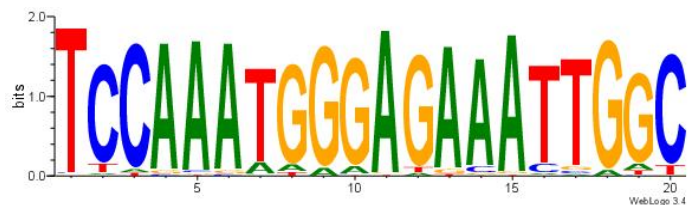
Dataset #: 1
Motif ID: 235
Motif name: Motif 235
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif

Direction: Backward
 Position number: 2
 Number of overlap: 10
 Similarity score: 0.0641267

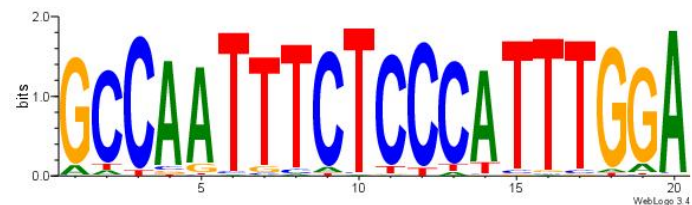
Alignment:

TCCAAATGGGAGAAATTGGC
 -----GAGAACGTAG--

Original motif Consensus sequence: TCCAAATGGGAGAAATTGGC



Reverse complement motif Consensus sequence: GCCAATTTCTCCCATTTGGA

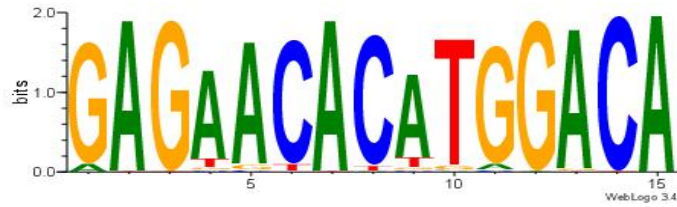


Dataset #: 1
 Motif ID: 257
 Motif name: Motif 257
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 6
 Number of overlap: 10
 Similarity score: 0.064949

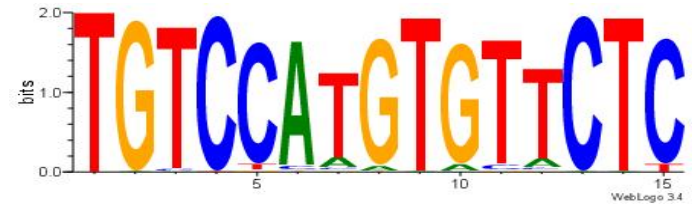
Alignment:

TGTCCATGTGTTCTC
 -----CTACGTTCTC

Original motif Consensus sequence: GAGAACACATGGACA



Reverse complement motif Consensus sequence: TGTCCATGTGTTCTC

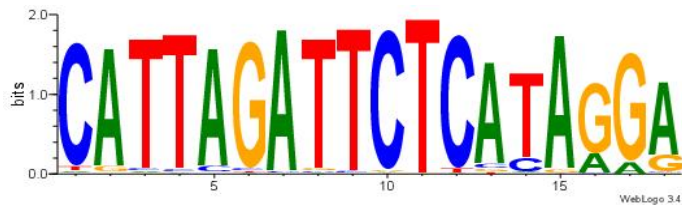


Dataset #: 1
Motif ID: 154
Motif name: Motif 154
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 7
Number of overlap: 10
Similarity score: 0.0660371

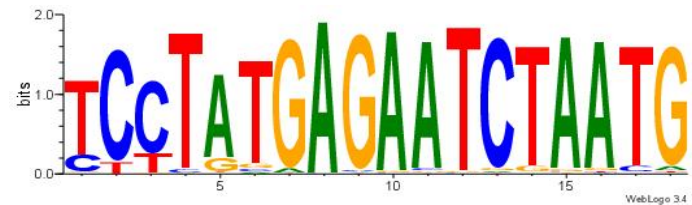
Alignment:

CATTAGATTCTCATAGGA
--CTACGTTCTC-----

Original motif Consensus sequence: CATTAGATTCTCATAGGA



Reverse complement motif Consensus sequence: TCCTATGAGAATCTAATG

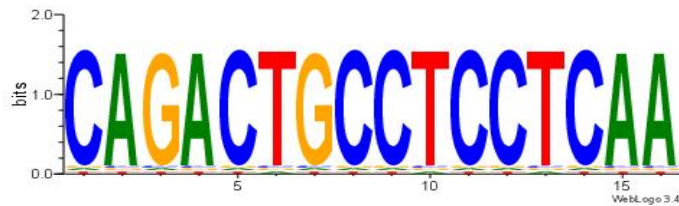


Dataset #: 1
 Motif ID: 245
 Motif name: Motif 245
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 5
 Number of overlap: 10
 Similarity score: 0.0692709

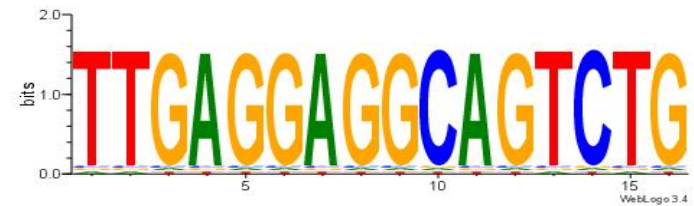
Alignment:

CAGACTGCCTCCTCAA
 ----CTACGTTCTC--

Original motif Consensus sequence: CAGACTGCCTCCTCAA



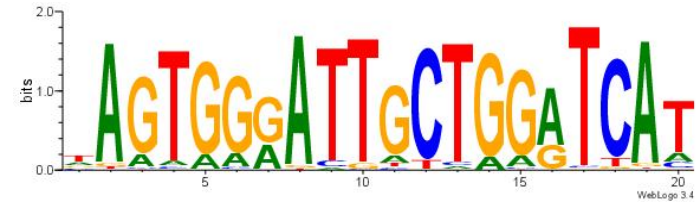
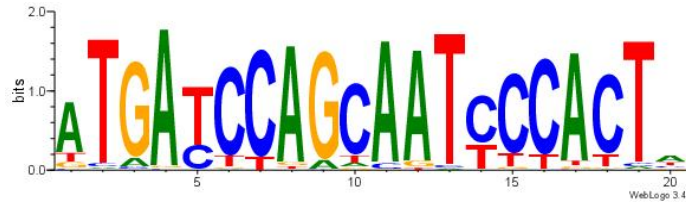
Reverse complement motif Consensus sequence: TTGAGGAGGCAGTCTG



Dataset #: 1 Motif ID: 115 Motif name: Motif 115

Original motif Consensus sequence: ATGATCCAGCAATYCCACTH

Reverse complement motif Consensus sequence: HAGTGGKATTGCTGGATCAT

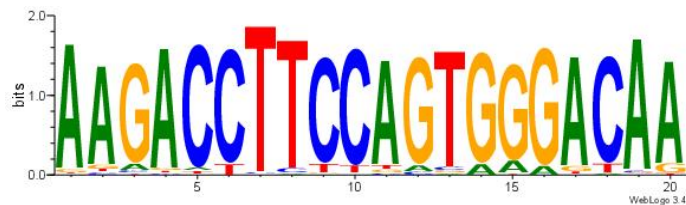


Best Matches for Motif ID 115 (Highest to Lowest)

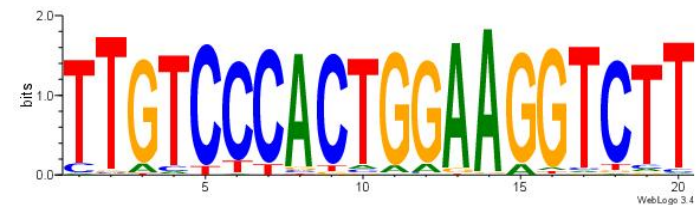
Dataset #: 1
 Motif ID: 292
 Motif name: Motif 292
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.106467

Alignment:
 AAGACCTTCCAGTGGGACAA
 ATGATCCAGCAATYCCACTH

Original motif Consensus sequence: AAGACCTTCCAGTGGGACAA



Reverse complement motif Consensus sequence: TTGTTCCACTGGAAAGGTCTT

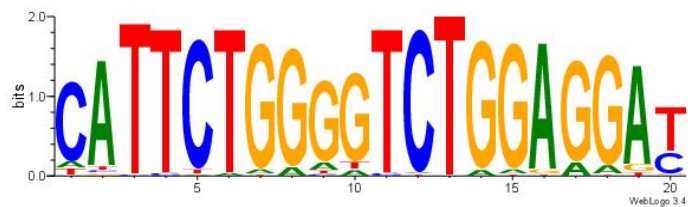


Dataset #: 1
 Motif ID: 309
 Motif name: Motif 309
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.108003

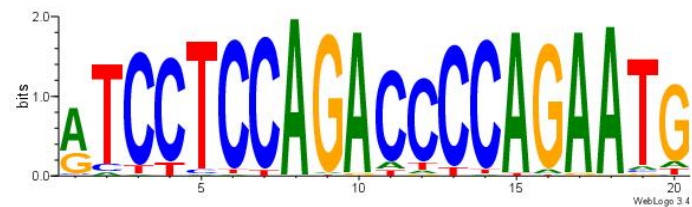
Alignment:

CATTCTGGGGTCTGGAGGAY
 HAGTGGKATTGCTGGATCAT

Original motif Consensus sequence: CATTCTGGGGTCTGGAGGAY



Reverse complement motif Consensus sequence: MTCCTCCAGACCCAGAAATG



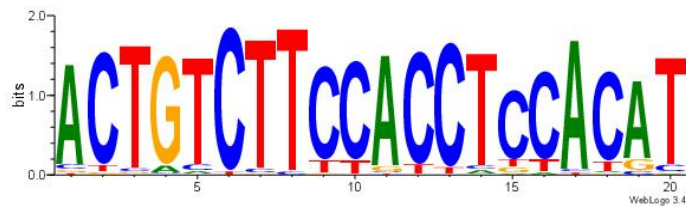
Dataset #: 1
 Motif ID: 178
 Motif name: Motif 178
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1

Number of overlap: 20
Similarity score: 0.110049

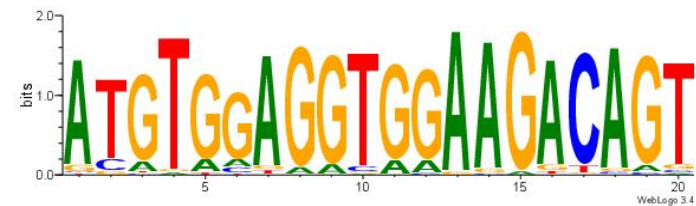
Alignment:

ACTGTCTTCCACCTCCACAT
ATGATCCAGCAATYCCACTH

Original motif Consensus sequence: ACTGTCTTCCACCTCCACAT



Reverse complement motif Consensus sequence:
ATGTGGAGGTGGAAGACAGT

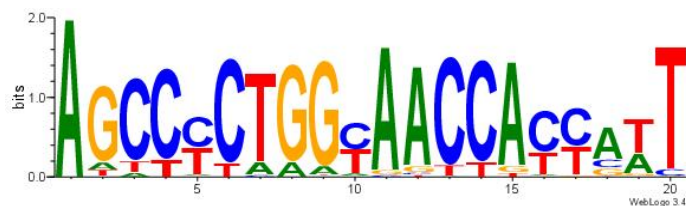


Dataset #: 1
Motif ID: 139
Motif name: Motif 139
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 20
Similarity score: 0.110453

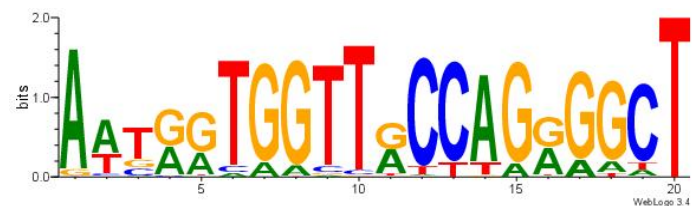
Alignment:

AGCCYCTGGYAACCAYYAWT
ATGATCCAGCAATYCCACTH

Original motif Consensus sequence: AGCCYCTGGYAACCAYYAWT



Reverse complement motif Consensus sequence: AWTKKTGGTTKCCAGKGGCT

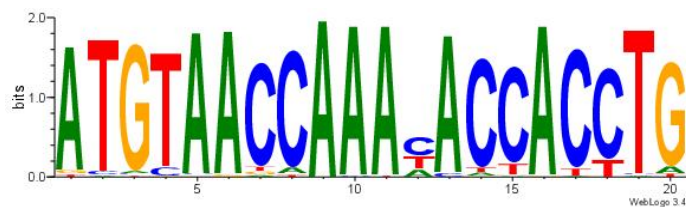


Dataset #: 1
Motif ID: 336
Motif name: Motif 336
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 20
Similarity score: 0.110612

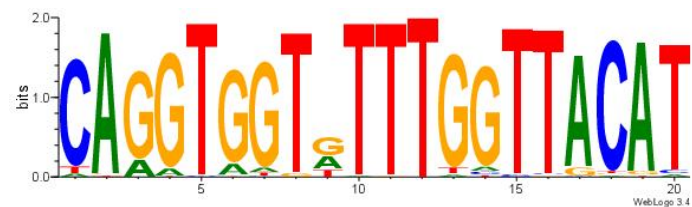
Alignment:

CAGGTGGTKTTTGGTTACAT
HAGTGGKATTGCTGGATCAT

Original motif Consensus sequence: ATGTAACCAAAYACCACCTG

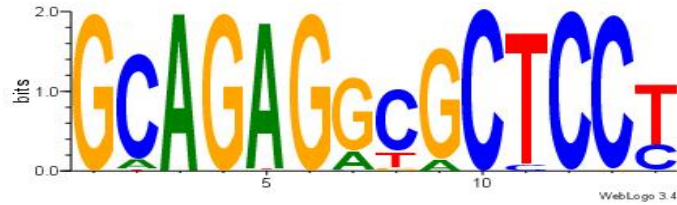


Reverse complement motif Consensus sequence: CAGGTGGTKTTTGGTTACAT

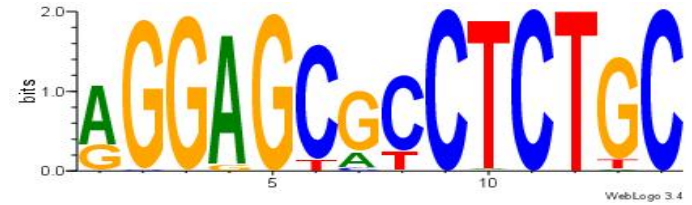


Dataset #: 1 Motif ID: 116 Motif name: Motif 116

Original motif Consensus sequence: GCAGAGGCGCTCCT



Reverse complement motif Consensus sequence: AGGAGCGCCTCTG



Best Matches for Motif ID 116 (Highest to Lowest)

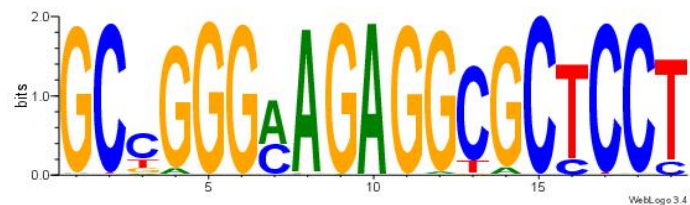
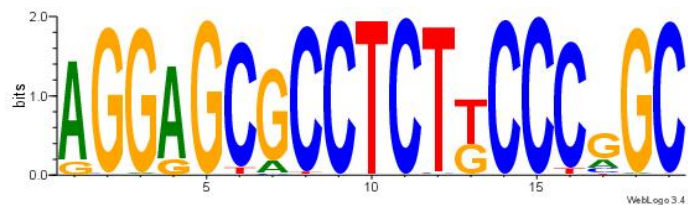
Dataset #:	1
Motif ID:	30
Motif name:	Motif 30
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	6
Number of overlap:	14
Similarity score:	0.023579

Alignment:

```
GCCGGGRAGAGGCGCTCCT
GCAGAGGCGCTCCT-----
```

Original motif Consensus sequence: AGGAGCGCCTCTKCCCGGC

Reverse complement motif Consensus sequence: GCCGGGRAGAGGCGCTCCT



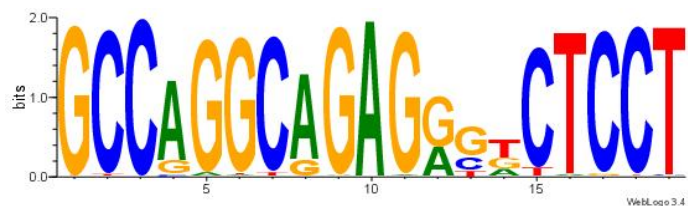
Dataset #: 1
 Motif ID: 43
 Motif name: Motif 43
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 6
 Number of overlap: 14
 Similarity score: 0.0315071

Alignment:

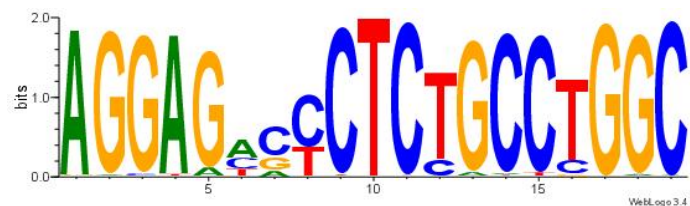
```

GCCAGGCAGAGRGKCTCCT
-----GCAGAGGCGCTCCT
  
```

Original motif Consensus sequence: GCCAGGCAGAGRGKCTCCT



Reverse complement motif Consensus sequence: AGGAGRCMCTCTGCCTGGC



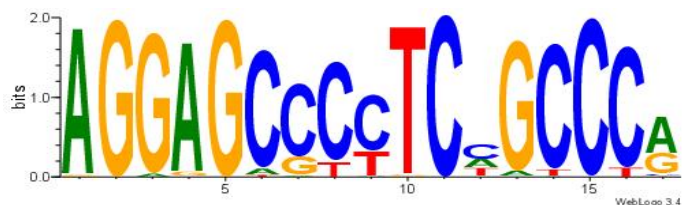
Dataset #: 1

Motif ID: 111
 Motif name: Motif 111
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0.0401354

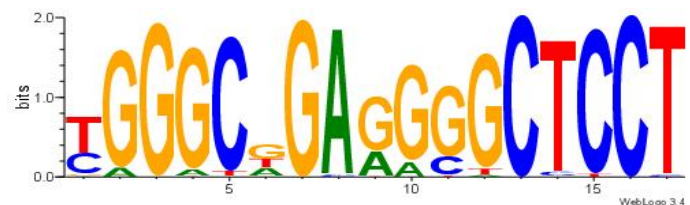
Alignment:

AGGAGCCCCTCHGCCCCR
 ---AGGAGCGCCTCTGC

Original motif Consensus sequence: AGGAGCCCCTCHGCCCCR



Reverse complement motif Consensus sequence: KGGGCDGAGGGGCTCCT



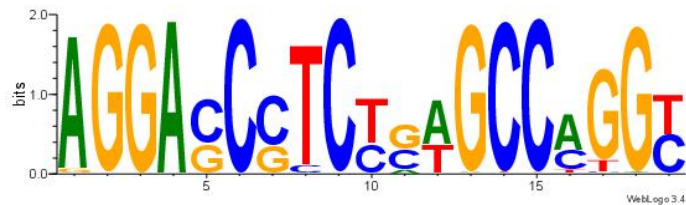
Dataset #: 1
 Motif ID: 10
 Motif name: Motif 10
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 14

Similarity score: 0.068644

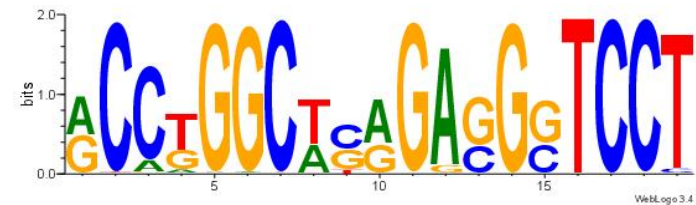
Alignment:

AGGASCSTCYSWGCCMGY
-----AGGAGCGCCTCTGC

Original motif Consensus sequence: AGGASCSTCYSWGCCMGY



Reverse complement motif Consensus sequence:
MCCYGGCWSMGASGSTCCT



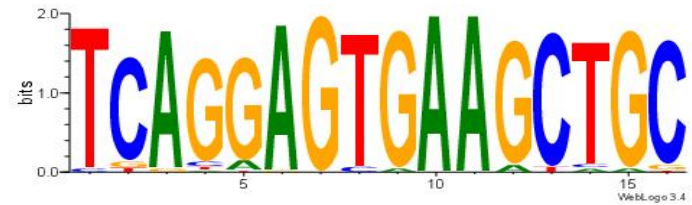
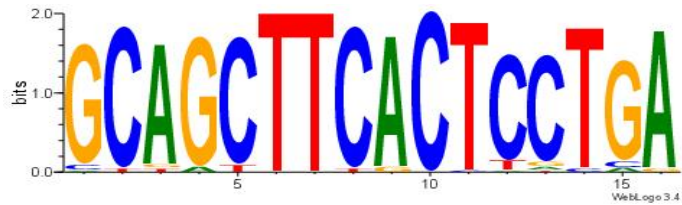
Dataset #: 1
Motif ID: 246
Motif name: Motif 246
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 14
Similarity score: 0.0780562

Alignment:

TCAGGAGTGAAGCTGC
--AGGAGCGCCTCTGC

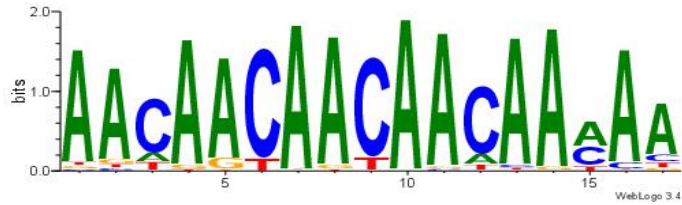
Original motif Consensus sequence: GCAGCTTCACTCCTGA

Reverse complement motif Consensus sequence:
TCAGGAGTGAAGCTGC

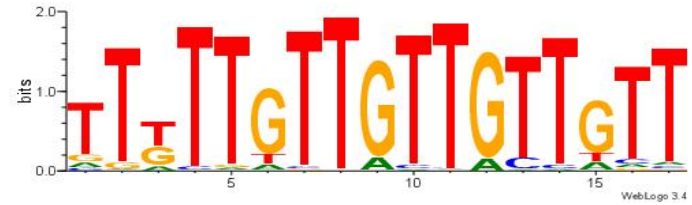


Dataset #: 1 Motif ID: 117 Motif name: Motif 117

Original motif Consensus sequence: AACACAACAACAAMAA



Reverse complement motif Consensus sequence: TTYTTGTTGTTGTT



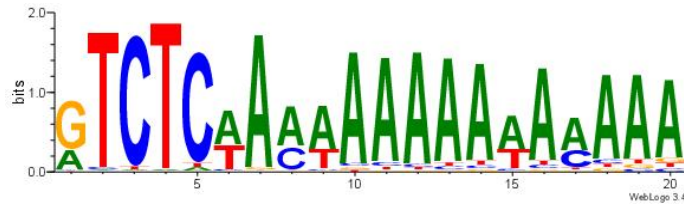
Best Matches for Motif ID 117 (Highest to Lowest)

Dataset #:	1
Motif ID:	7
Motif name:	Motif 7
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	3
Number of overlap:	17
Similarity score:	0.0705339

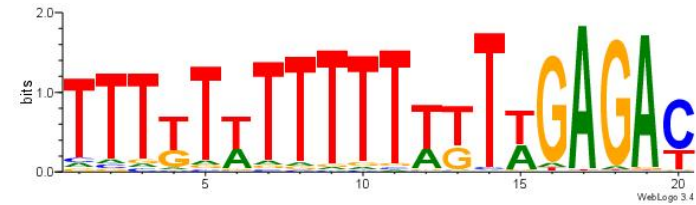
Alignment:

GTCTCWAMAAAAAWAMAAA
 --AACAACAACAACAAMAA-

Original motif Consensus sequence: GTCTCWAMAAAAAWAMAAA



Reverse complement motif Consensus sequence:
 TTTYTWTTTTTWTGAGAC

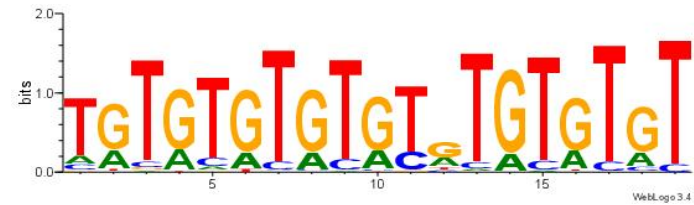
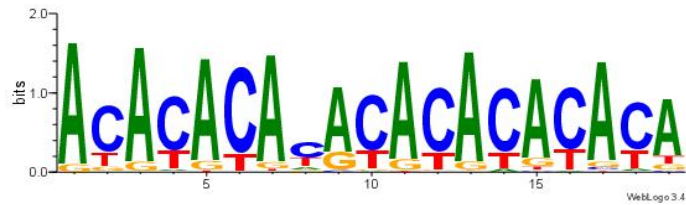


Dataset #: 1
 Motif ID: 66
 Motif name: Motif 66
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3
 Number of overlap: 17
 Similarity score: 0.0820961

Alignment:
 TGTGTGTGTGKTGTGTGT
 --TTYTTGTTGTTGTTGTT

Original motif Consensus sequence: ACACACAYACACACACA

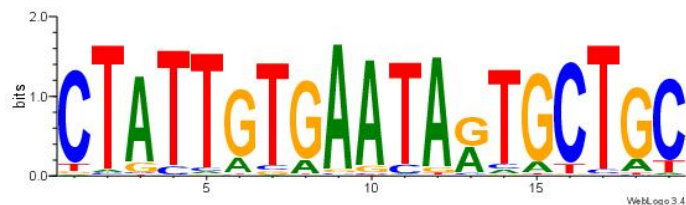
Reverse complement motif Consensus sequence:
 TGTGTGTGTGKTGTGTGT



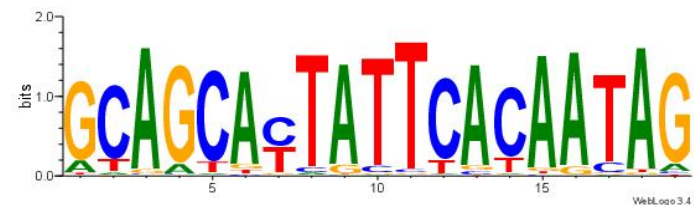
Dataset #: 1
 Motif ID: 70
 Motif name: Motif 70
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 17
 Similarity score: 0.0864402

Alignment:
 CTATTGTGAATARTGCTGC
 --TTYTTGTTGTTGTTGTT

Original motif Consensus sequence: CTATTGTGAATARTGCTGC



Reverse complement motif Consensus sequence: GCAGCMTATTCACAATAG



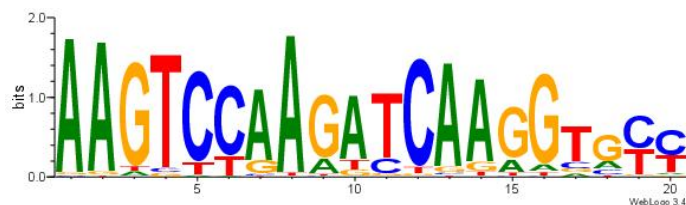
Dataset #: 1

Motif ID: 119
 Motif name: Motif 119
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 17
 Similarity score: 0.0907831

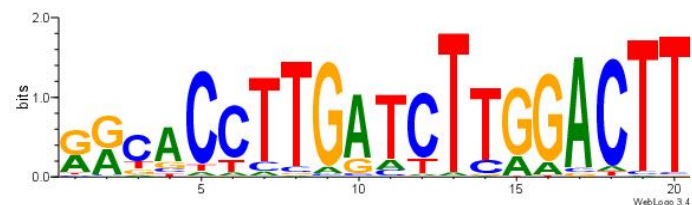
Alignment:

KKCACCTTGATCTTGGACTT
 ---TTYTTGTTGTTGTTGTT

Original motif Consensus sequence: AAGTCCAAGATCAAGGTGY



Reverse complement motif Consensus sequence: KKCACCTTGATCTTGGACTT



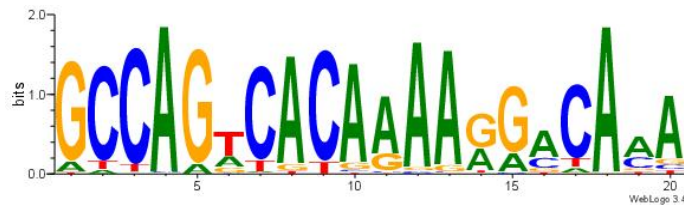
Dataset #: 1
 Motif ID: 145
 Motif name: Motif 145
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 17

Similarity score: 0.0925617

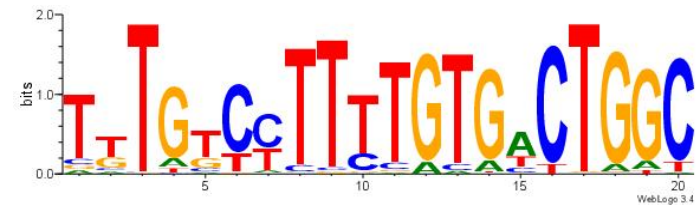
Alignment:

```
TYTGTCMTTTTGTGACTGGC  
TTYTTGTTGTTGTTGTT---
```

Original motif Consensus sequence: GCCAGTCACAAAARGACAMA

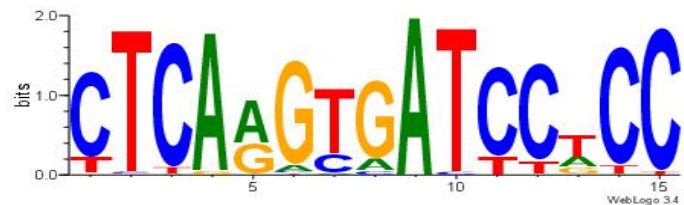


Reverse complement motif Consensus sequence: TYTGTCMTTTTGTGACTGGC



Dataset #: 1 Motif ID: 118 Motif name: Motif 118

Original motif Consensus sequence: CTCARGTGATCCTCC



Reverse complement motif Consensus sequence: GGAGGATCACTGAG



Best Matches for Motif ID 118 (Highest to Lowest)

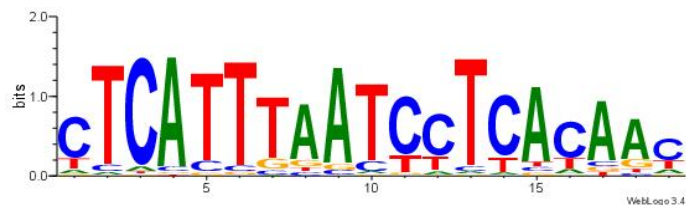
Dataset #:	1
Motif ID:	102
Motif name:	Motif 102
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif

Direction: Backward
Position number: 5
Number of overlap: 15
Similarity score: 0.0724382

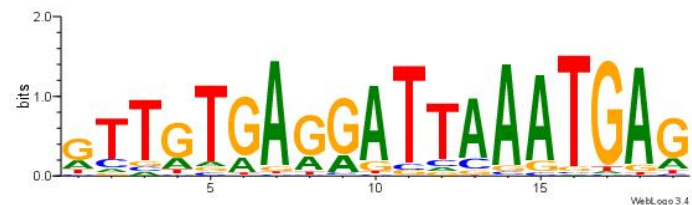
Alignment:

CTCATTTAATCCTCACAAC
CTCARGTGATCCTCC----

Original motif Consensus sequence: CTCATTTAATCCTCACAAC



Reverse complement motif Consensus sequence: GTTGTGAGGATTAATGAG

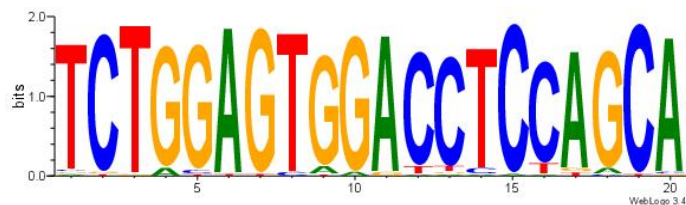


Dataset #: 1
Motif ID: 350
Motif name: Motif 350
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 5
Number of overlap: 15
Similarity score: 0.0817171

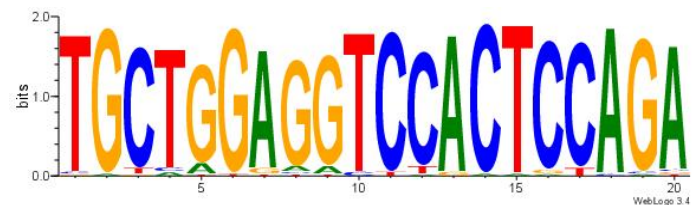
Alignment:

TCTGGAGTGGACCTCCAGCA
-CTCARGTGATCCTCC----

Original motif Consensus sequence: TCTGGAGTGGACCTCCAGCA



Reverse complement motif Consensus sequence: TGCTGGAGGTCCACTCCAGA

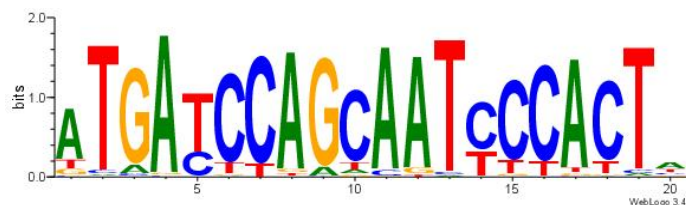


Dataset #: 1
Motif ID: 115
Motif name: Motif 115
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 3
Number of overlap: 15
Similarity score: 0.0933094

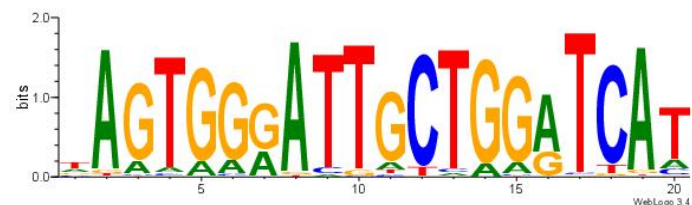
Alignment:

```
HAGTGGKATTGCTGGATCAT  
--GGAGGATCACKTGAG---
```

Original motif Consensus sequence: ATGATCCAGCAATYCCACTH



Reverse complement motif Consensus sequence: HAGTGGKATTGCTGGATCAT

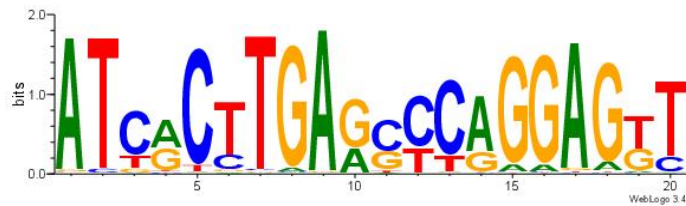


Dataset #: 1
 Motif ID: 8
 Motif name: Motif 8
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 15
 Similarity score: 0.0976823

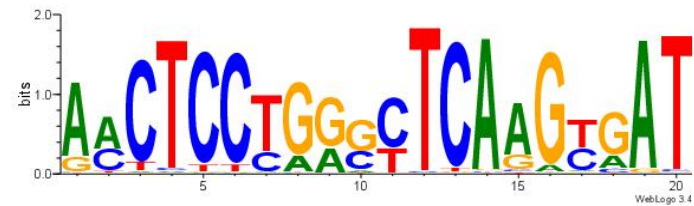
Alignment:

ARCTCCTGKSCTCAAGKGAT
 -----GGAGGATCACKTGAG

Original motif Consensus sequence: ATCRCTTGAGSYCAGGAGKT



Reverse complement motif Consensus sequence: ARCTCCTGKSCTCAAGKGAT



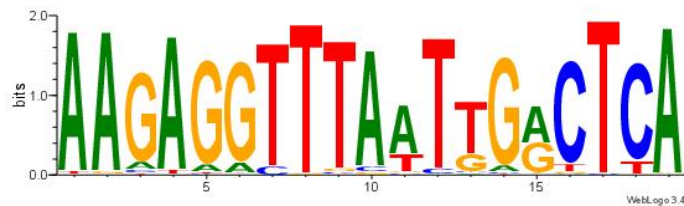
Dataset #: 1
 Motif ID: 129
 Motif name: Motif 129
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2

Number of overlap: 15
 Similarity score: 0.0995502

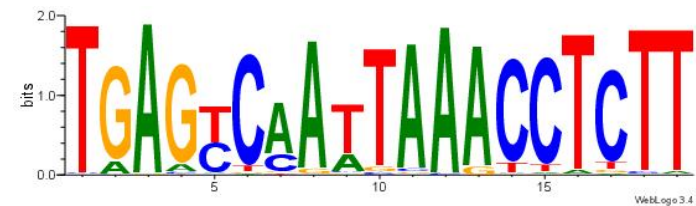
Alignment:

TGAGKCAATTAAACCTCTT
 ---CTCARGTGATCCTCC-

Original motif Consensus sequence: AAGAGGTTTAATTGRCTCA

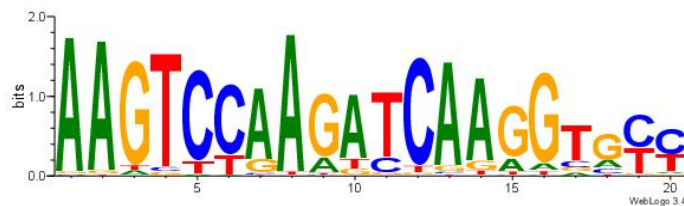


Reverse complement motif Consensus sequence:
 TGAGKCAATTAAACCTCTT

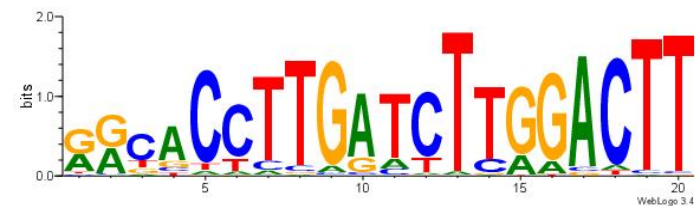


Dataset #: 1 Motif ID: 119 Motif name: Motif 119

Original motif Consensus sequence: AAGTCCAAGATCAAGGTGY



Reverse complement motif Consensus sequence:
 KKCACCTTGATCTTGGACTT



Best Matches for Motif ID 119 (Highest to Lowest)

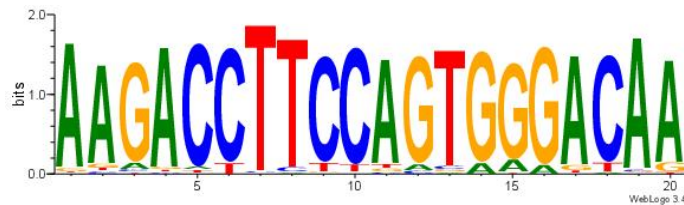
Dataset #: 1
 Motif ID: 292
 Motif name: Motif 292

Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	20
Similarity score:	0.103662

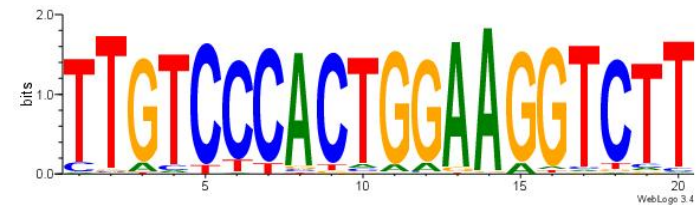
Alignment:

```
TTGTCCCACTGGAAGGTCTT
AAGTCCAAGATCAAGGTGY
```

Original motif Consensus sequence: AAGACCTCCAGTGGGACAA



Reverse complement motif Consensus sequence: TTGTCCCACTGGAAGGTCTT

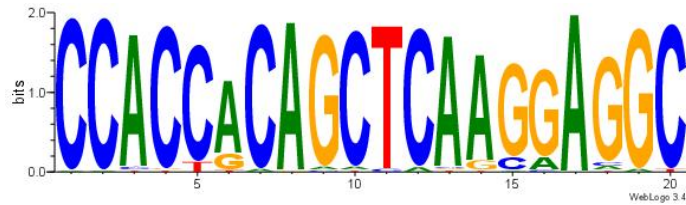


Dataset #:	1
Motif ID:	331
Motif name:	Motif 331
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	20
Similarity score:	0.107278

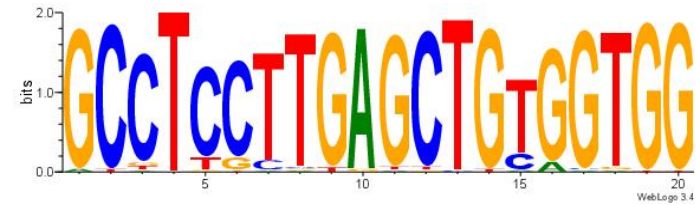
Alignment:

GCCTCCTTGAGCTGTGGTGG
KKCACCTTGATCTTGGACTT

Original motif Consensus sequence: CCACCACAGCTCAAGGAGGC



Reverse complement motif Consensus sequence:
GCCTCCTTGAGCTGTGGTGG



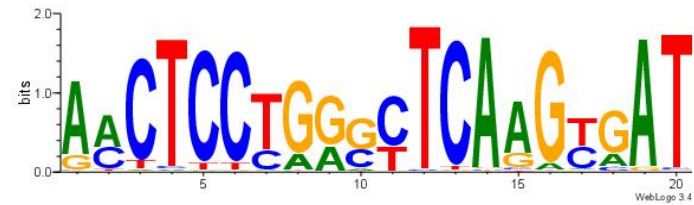
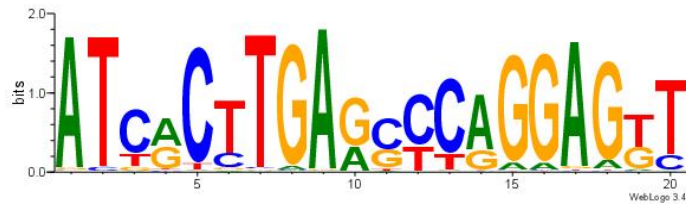
Dataset #:	1
Motif ID:	8
Motif name:	Motif 8
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	20
Similarity score:	0.111713

Alignment:

ARCTCCTGKSCTCAAGKGAT
AAGTCCAAGATCAAGGTGY

Original motif Consensus sequence: ATCRCTTGAGSYCAGGAGKT

Reverse complement motif Consensus sequence:
ARCTCCTGKSCTCAAGKGAT

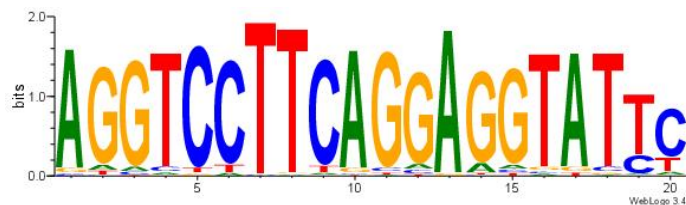


Dataset #: 1
 Motif ID: 179
 Motif name: Motif 179
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.11466

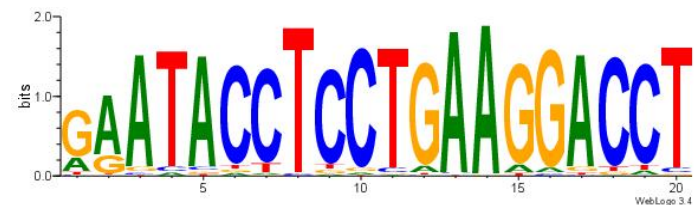
Alignment:

AGGTCCTTCAGGAGGTATTC
 AAGTCCAAGATCAAGGTGY

Original motif Consensus sequence: AGGTCCTTCAGGAGGTATTC



Reverse complement motif Consensus sequence: GAATACCTCTGAAGGACCT



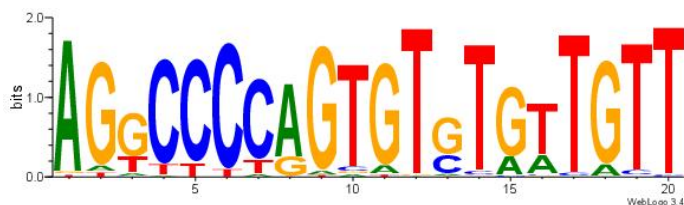
Dataset #: 1

Motif ID: 176
 Motif name: Motif 176
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.118674

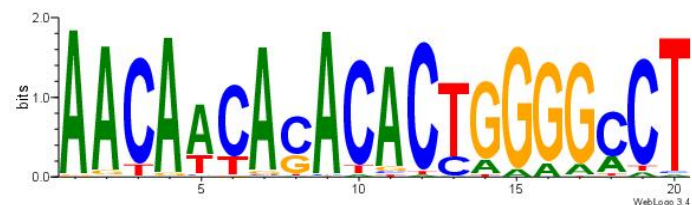
Alignment:

AGGCCCCAGTGTSTGTTGTT
 AAGTCCAAGATCAAGGTGY

Original motif Consensus sequence: AGGCCCCAGTGTSTGTTGTT

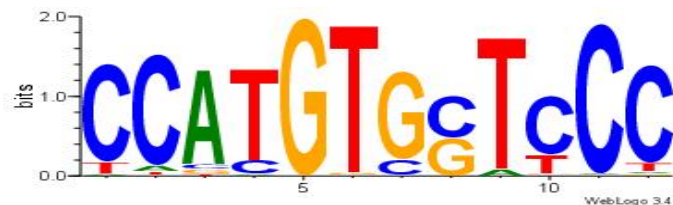


Reverse complement motif Consensus sequence: AACACASACACTGGGGCCT

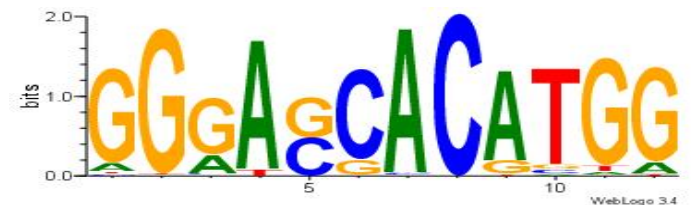


Dataset #: 1 Motif ID: 120 Motif name: Motif 120

Original motif Consensus sequence: CCATGTGcTcCc



Reverse complement motif Consensus sequence: GGGASCACATGG



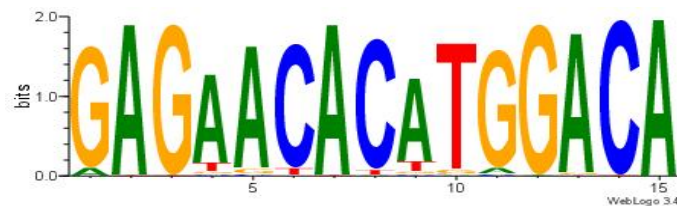
Best Matches for Motif ID 120 (Highest to Lowest)

Dataset #: 1
Motif ID: 257
Motif name: Motif 257
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 12
Similarity score: 0.0458809

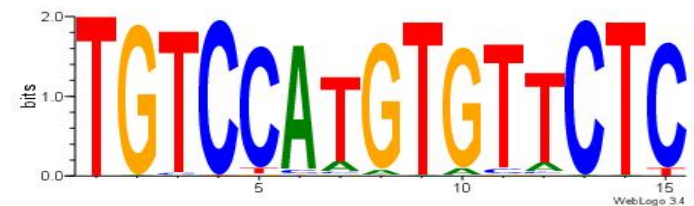
Alignment:

```
GAGAACACATGGACA  
GGGASCACATGG---
```

Original motif Consensus sequence: GAGAACACATGGACA



Reverse complement motif Consensus sequence: TGTCCATGTGTTCTC



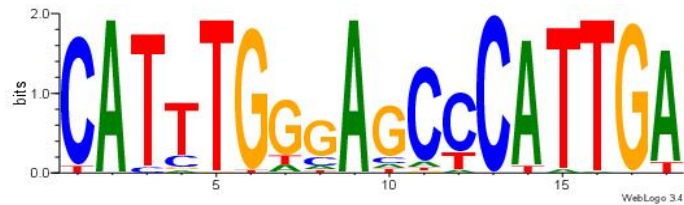
Dataset #: 1
Motif ID: 284
Motif name: Motif 284
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement

Direction: Backward
 Position number: 6
 Number of overlap: 12
 Similarity score: 0.0509107

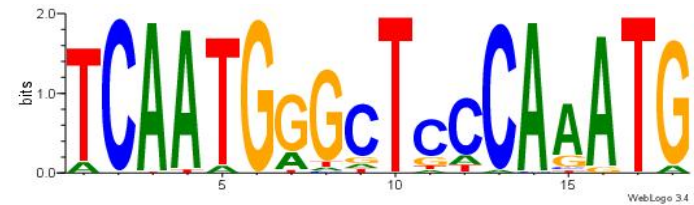
Alignment:

TCAATGGGCTCCCAAATG
 -CCATGTGSTCC-----

Original motif Consensus sequence: CATTGGGAGCCATTGA



Reverse complement motif Consensus sequence: TCAATGGGCTCCCAAATG

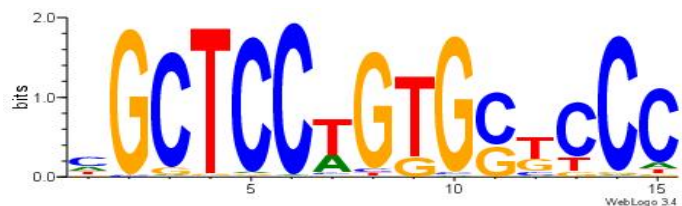


Dataset #: 1
 Motif ID: 215
 Motif name: Motif 215
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 12
 Similarity score: 0.0529225

Alignment:

HGCTCCTGTGSKCCC
 ---CCATGTGSTCCC

Original motif Consensus sequence: HGCTCCTGTGSKCCC



Reverse complement motif Consensus sequence: GGRSCACAGGAGCD

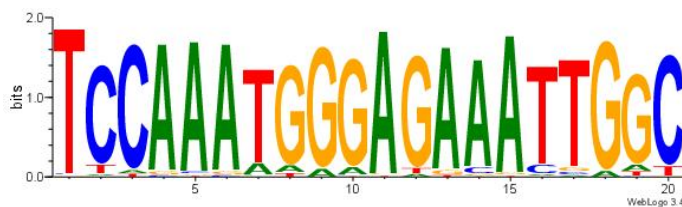


Dataset #: 1
Motif ID: 235
Motif name: Motif 235
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 2
Number of overlap: 12
Similarity score: 0.0661093

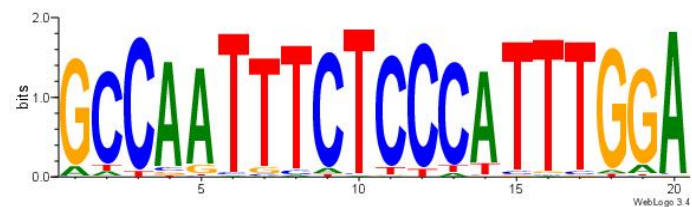
Alignment:

```
GCCAATTTCTCCCATTTGGA  
-CCATGTGSTCCC-----
```

Original motif Consensus sequence: TCCAATGGGAGAAATTGGC



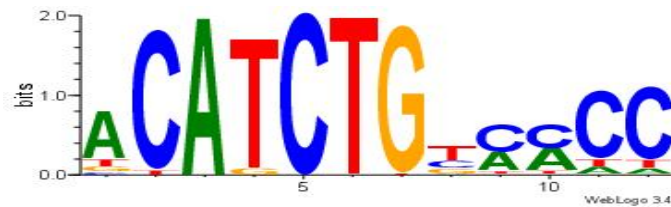
Reverse complement motif Consensus sequence: GCCAATTTCTCCCATTTGGA



Dataset #: 1
 Motif ID: 49
 Motif name: Motif 49
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 12
 Similarity score: 0.0699992

Alignment:
 GRRMCAGATGT
 GGGASCACATGG

Original motif Consensus sequence: ACATCTGYMMCC



Reverse complement motif Consensus sequence: GRRMCAGATGT

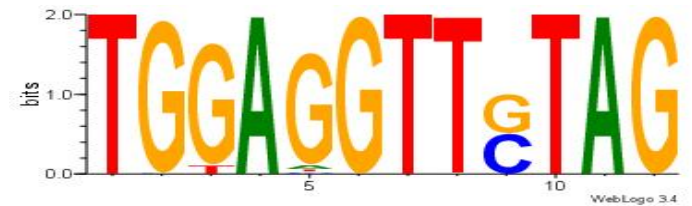


Dataset #: 1 Motif ID: 121 Motif name: Motif 121

Original motif Consensus sequence: CTASAACCTCCA



Reverse complement motif Consensus sequence: TGGAGGTTSTAG



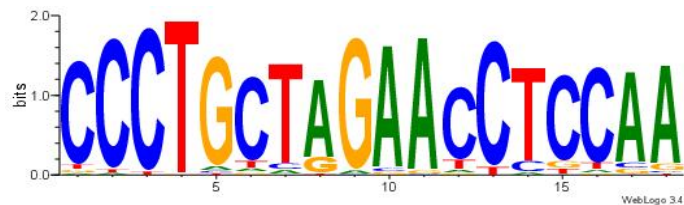
Best Matches for Motif ID 121 (Highest to Lowest)

Dataset #: 1
Motif ID: 299
Motif name: Motif 299
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 6
Number of overlap: 12
Similarity score: 0.0292892

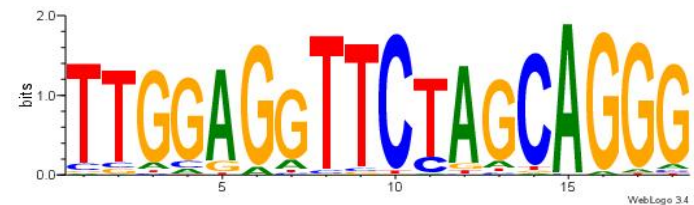
Alignment:

```
CCCTGCTAGAACCTCCAA  
-----CTASAACCTCCA-
```

Original motif Consensus sequence: CCCTGCTAGAACCTCCAA



Reverse complement motif Consensus sequence:
TTGGAGGTTCTAGCAGGG

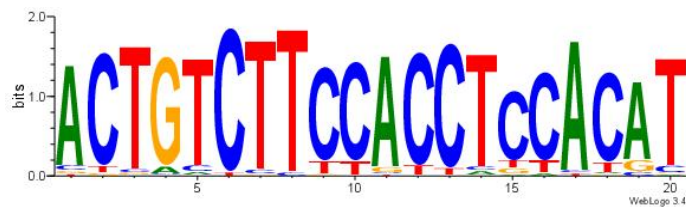


Dataset #: 1
Motif ID: 178
Motif name: Motif 178
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement

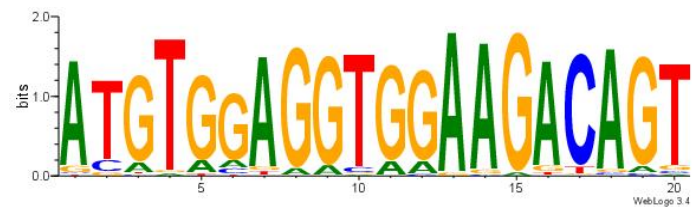
Direction: Forward
Position number: 4
Number of overlap: 12
Similarity score: 0.0571056

Alignment:
ATGTGGAGGTGGAAGACAGT
---TGGAGGTTSTAG-----

Original motif Consensus sequence: ACTGTCTTCCACCTCCACAT



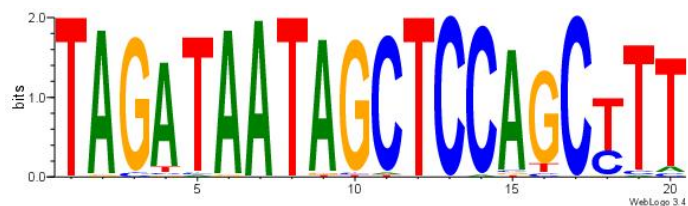
Reverse complement motif Consensus sequence: ATGTGGAGGTGGAAGACAGT



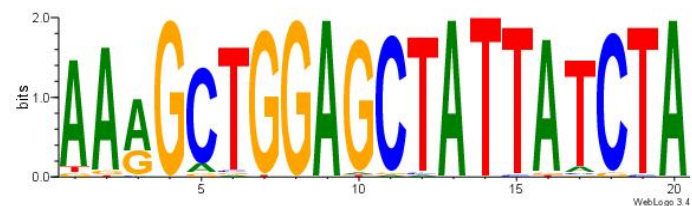
Dataset #: 1
Motif ID: 333
Motif name: Motif 333
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 6
Number of overlap: 12
Similarity score: 0.0815825

Alignment:
AAAGCTGGAGCTATTATCTA
-----TGGAGGTTSTAG---

Original motif Consensus sequence: TAGATAATAGCTCCAGCTTT



Reverse complement motif Consensus sequence: AAAGCTGGAGCTATTATCTA

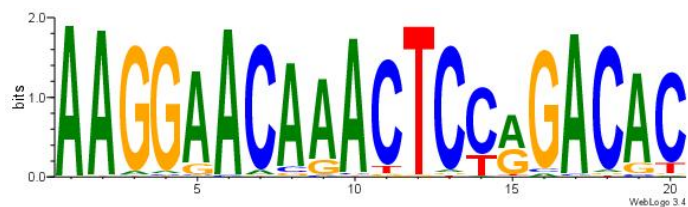


Dataset #: 1
Motif ID: 234
Motif name: Motif 234
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 4
Number of overlap: 12
Similarity score: 0.0881505

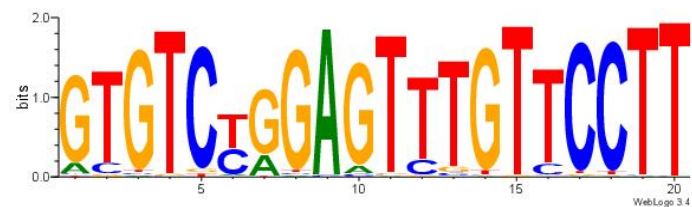
Alignment:

```
AAGGAACAAACTCCRGACAC  
---CTASAACCTCCA-----
```

Original motif Consensus sequence: AAGGAACAAACTCCRGACAC



Reverse complement motif Consensus sequence: GTGTCGGAGTTTGTTCCTT

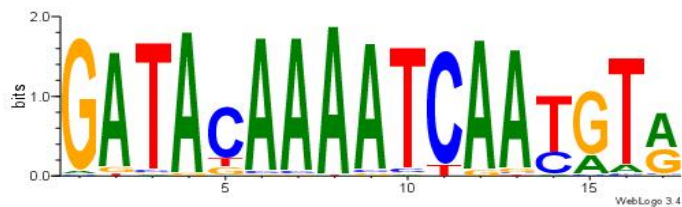


Dataset #: 1
 Motif ID: 328
 Motif name: Motif 328
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 12
 Similarity score: 0.0886401

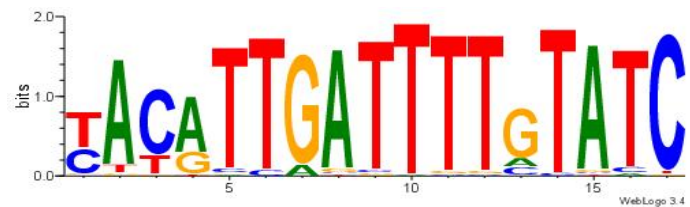
Alignment:

KACATTGATTTTGTATC
 ----TGGAGGTTSTAG-

Original motif Consensus sequence: GATACAAAATCAATGTR



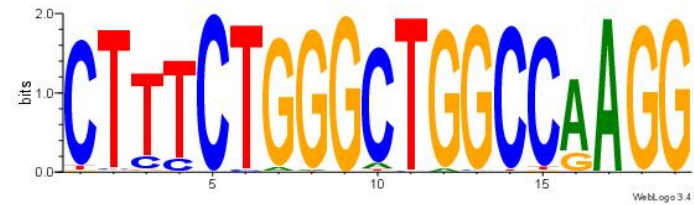
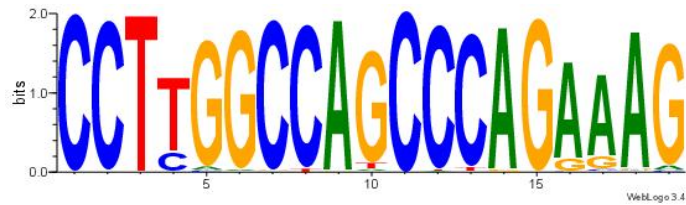
Reverse complement motif Consensus sequence: KACATTGATTTTGTATC



Dataset #: 1 Motif ID: 122 Motif name: Motif 122

Original motif Consensus sequence: CCTTGGCCAGCCCAGAAAG

Reverse complement motif Consensus sequence: CTTTCTGGGCTGGCCAAGG

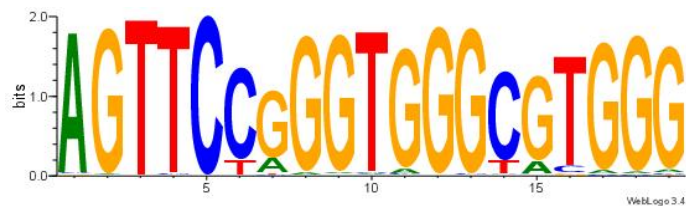


Best Matches for Motif ID 122 (Highest to Lowest)

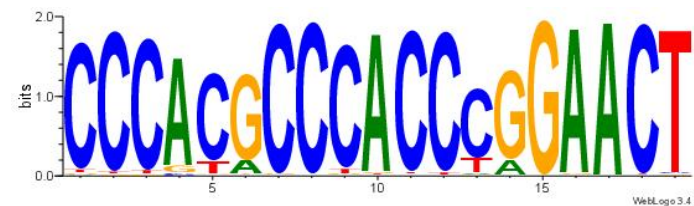
Dataset #: 1
 Motif ID: 98
 Motif name: Motif 98
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 19
 Similarity score: 0.0950931

Alignment:
 CCCACGCCACCCGGA
 CCTTGGCCAGCCCAGAAAG

Original motif Consensus sequence: AGTTCCGGTGGGCGTGGG



Reverse complement motif Consensus sequence: CCCACGCCACCCGGA

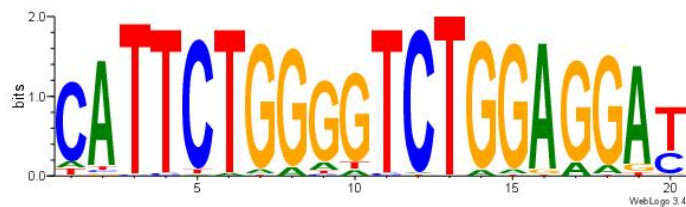


Dataset #: 1
 Motif ID: 309
 Motif name: Motif 309
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 19
 Similarity score: 0.0996139

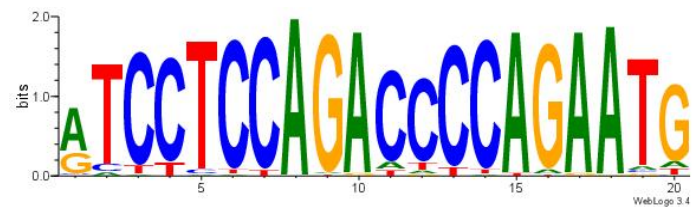
Alignment:

CATTCTGGGGTCTGGAGGAY
 CTTTCTGGGCTGGCCAAGG-

Original motif Consensus sequence: CATTCTGGGGTCTGGAGGAY



Reverse complement motif Consensus sequence: MTCCTCCAGACCCCAAGT



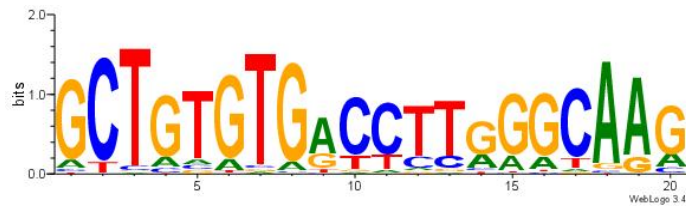
Dataset #: 1
 Motif ID: 112
 Motif name: Motif 112
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1

Number of overlap: 19
Similarity score: 0.110655

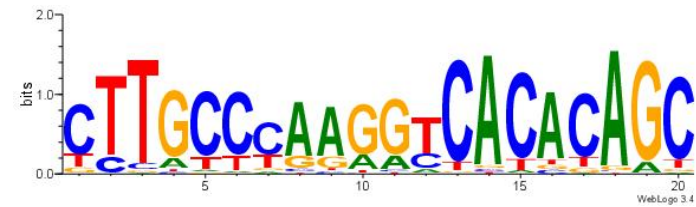
Alignment:

CTTGCCCAAGGTCACACAGC
-CCTTGGCCAGCCCAGAAAG

Original motif Consensus sequence: GCTGTGTGACCTTGGGCAAG



Reverse complement motif Consensus sequence:
CTTGCCCAAGGTCACACAGC

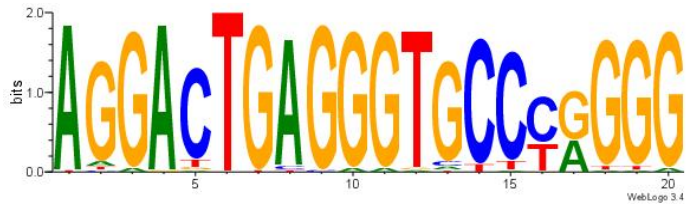


Dataset #: 1
Motif ID: 312
Motif name: Motif 312
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 19
Similarity score: 0.111917

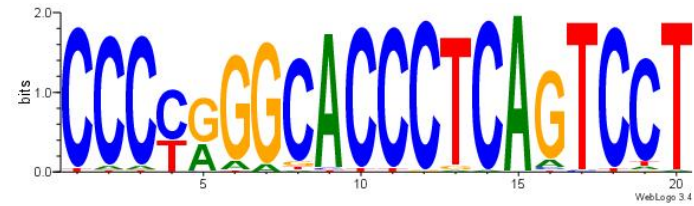
Alignment:

AGGACTGAGGGTGCCYRGGG
CTTTCTGGGCTGGCCAAGG-

Original motif Consensus sequence: AGGACTGAGGGTGCCYRGGG



Reverse complement motif Consensus sequence: CCCMKGGCACCCCTCAGTCCT

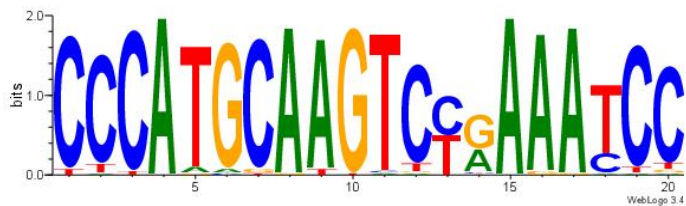


Dataset #: 1
Motif ID: 310
Motif name: Motif 310
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2
Number of overlap: 19
Similarity score: 0.1122

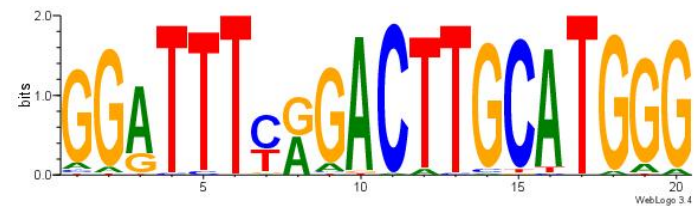
Alignment:

CCCATGCAAGTCYRAAATCC
CCTTGGCCAGCCCAGAAAG-

Original motif Consensus sequence: CCCATGCAAGTCYRAAATCC



Reverse complement motif Consensus sequence: GGATTTMKGACTTGCATGGG



Dataset #: 1 Motif ID: 123 Motif name: Motif 123

Original motif Consensus sequence: AGCAGTCTGAG



Reverse complement motif Consensus sequence: CTCAGACTGCT



Best Matches for Motif ID 123 (Highest to Lowest)

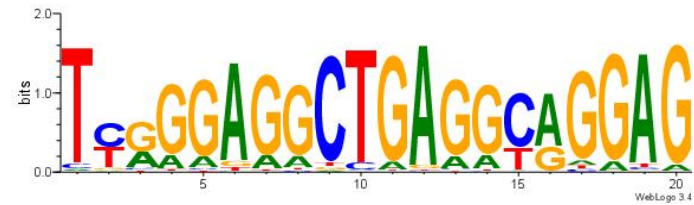
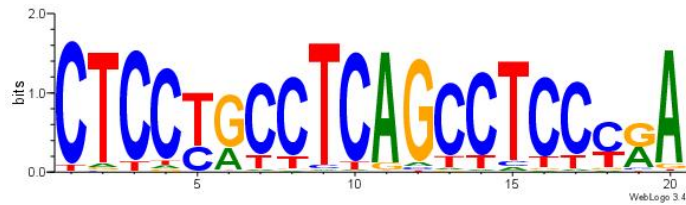
Dataset #:	1
Motif ID:	26
Motif name:	Motif 26
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	8
Number of overlap:	11
Similarity score:	0.0598949

Alignment:

```
TMGGGAGGCTGAGGCAGGAG
-----AGCAGTCTGAG--
```

Original motif Consensus sequence: CTCCTGCCTCAGCCTCCRA

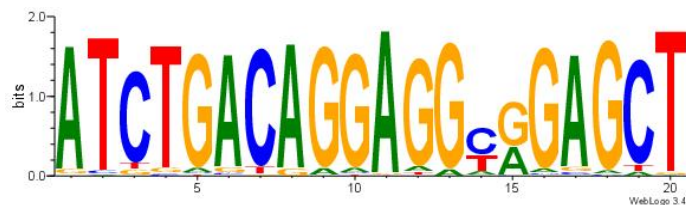
Reverse complement motif Consensus sequence:
TMGGGAGGCTGAGGCAGGAG



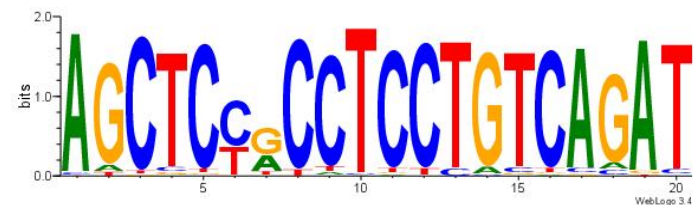
Dataset #: 1
 Motif ID: 165
 Motif name: Motif 165
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 8
 Number of overlap: 11
 Similarity score: 0.0609349

Alignment:
 AGCTCMKCCTCCTGTCAGAT
 --CTCAGACTGCT-----

Original motif Consensus sequence: ATCTGACAGGAGGYRGAGCT



Reverse complement motif Consensus sequence: AGCTCMKCCTCCTGTCAGAT



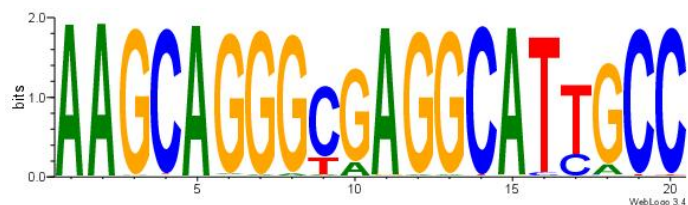
Dataset #: 1

Motif ID: 13
 Motif name: Motif 13
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 9
 Number of overlap: 11
 Similarity score: 0.0631275

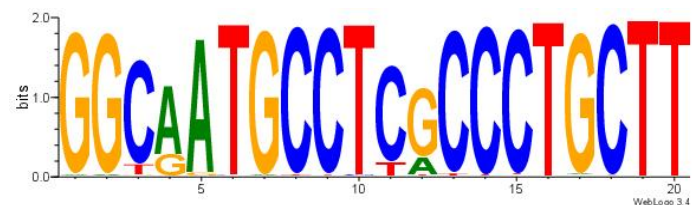
Alignment:

AAGCAGGGCGAGGCATTGCC
 -AGCAGTCTGAG-----

Original motif Consensus sequence: AAGCAGGGCGAGGCATTGCC



Reverse complement motif Consensus sequence: GGCAATGCCTCGCCCTGCTT



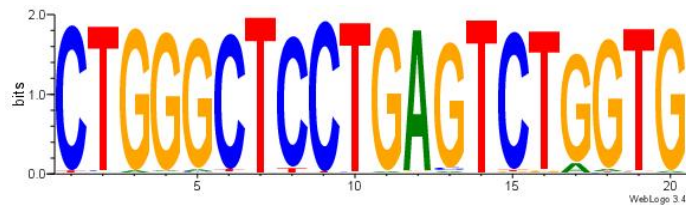
Dataset #: 1
 Motif ID: 67
 Motif name: Motif 67
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 11

Similarity score: 0.0649018

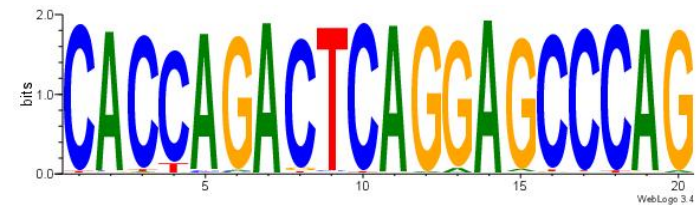
Alignment:

CACCAGACTCAGGAGCCCAG
-----AGCAGTCTGAG-

Original motif Consensus sequence: CTGGGCTCCTGAGTCTGGTG



Reverse complement motif Consensus sequence:
CACCAGACTCAGGAGCCCAG



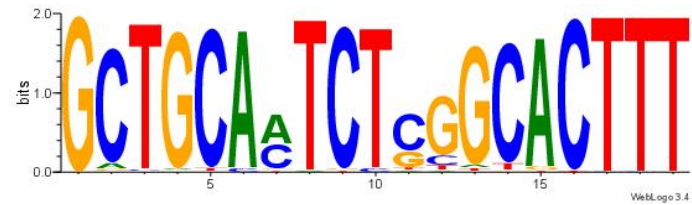
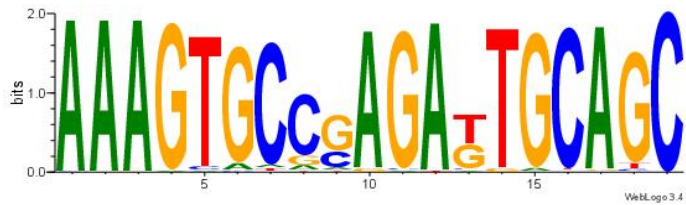
Dataset #: 1
Motif ID: 191
Motif name: Motif 191
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 3
Number of overlap: 11
Similarity score: 0.0650683

Alignment:

GCTGCARTCTCGGCACTTT
--AGCAGTCTGAG-----

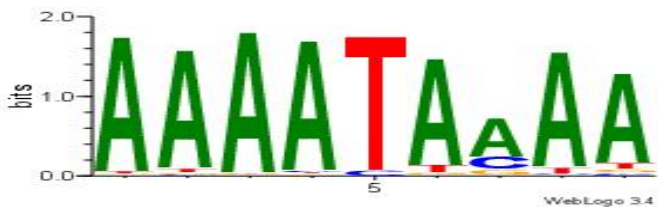
Original motif Consensus sequence: AAAGTGCCGAGAKTGCAGC

Reverse complement motif Consensus sequence:
GCTGCARTCTCGGCACTTT

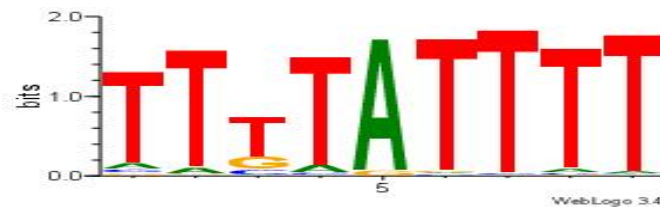


Dataset #: 1 Motif ID: 124 Motif name: Motif 124

Original motif Consensus sequence: AAAATAAAA



Reverse complement motif Consensus sequence: TTTATTTTT

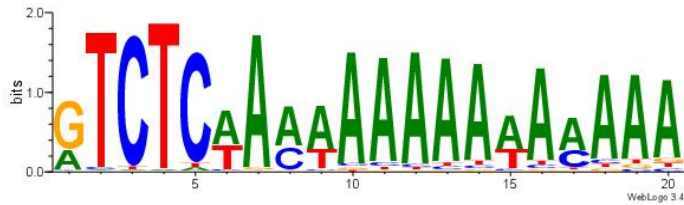


Best Matches for Motif ID 124 (Highest to Lowest)

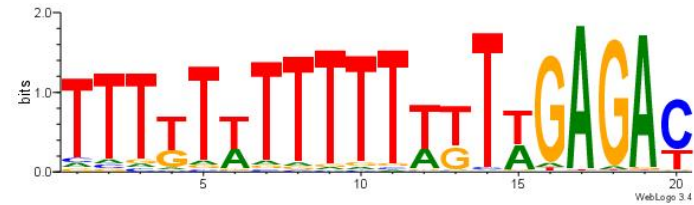
Dataset #:	1
Motif ID:	7
Motif name:	Motif 7
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2
Number of overlap:	9
Similarity score:	0.021153

Alignment:
 GTCTCWAMAAAAAAWAMAAA
 -----AAAATAAAA-

Original motif Consensus sequence: GTCTCWAMAAAAAWAMAAA



Reverse complement motif Consensus sequence: TTTYTWTTTTTYYTWGAGAC

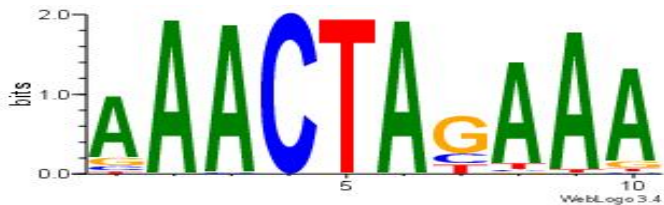


Dataset #: 1
Motif ID: 337
Motif name: Motif 337
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 9
Similarity score: 0.0464816

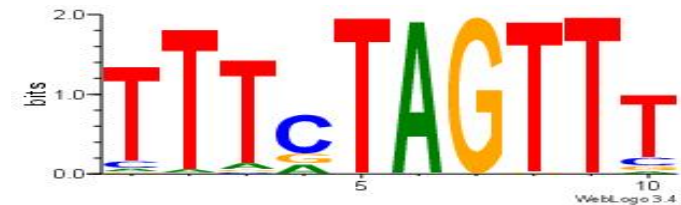
Alignment:

TTTCTAGTTT
-TTTTATTTT

Original motif Consensus sequence: AACTAGAAA



Reverse complement motif Consensus sequence: TTTCTAGTTT

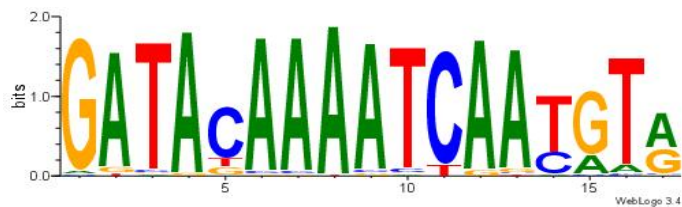


Dataset #: 1
 Motif ID: 328
 Motif name: Motif 328
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 6
 Number of overlap: 9
 Similarity score: 0.0522862

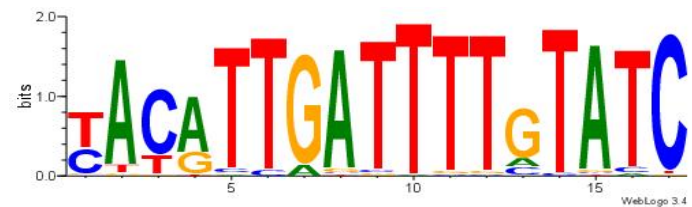
Alignment:

KACATTGATTTTGTATC
 ---TTTTATTTT-----

Original motif Consensus sequence: GATACAAAATCAATGTR



Reverse complement motif Consensus sequence: KACATTGATTTTGTATC

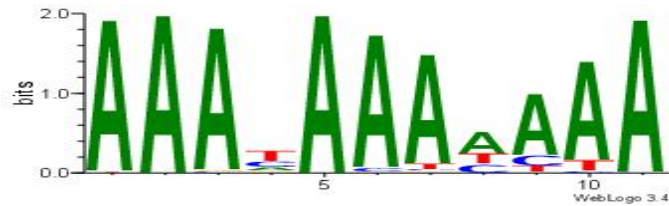


Dataset #: 1
 Motif ID: 41
 Motif name: Motif 41
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2

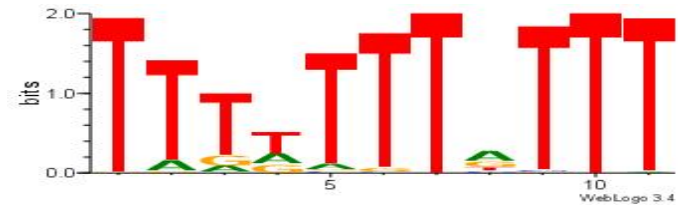
Number of overlap: 9
 Similarity score: 0.0560355

Alignment:
 AAAYAAAAAA
 -AAAATAAAA-

Original motif Consensus sequence: AAAYAAAAAA



Reverse complement motif Consensus sequence: TTTTTTMTTT

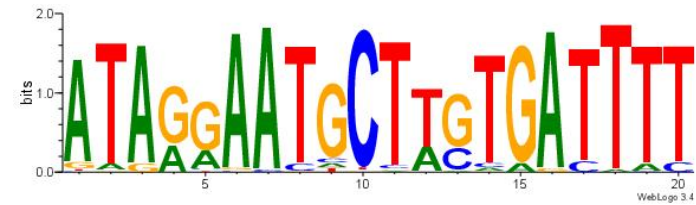
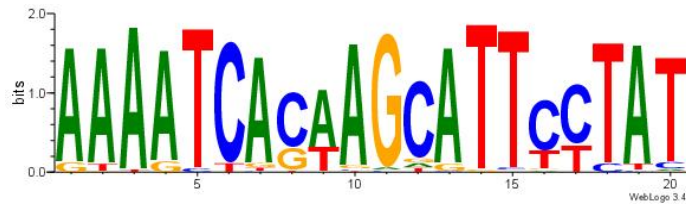


Dataset #: 1
 Motif ID: 254
 Motif name: Motif 254
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 9
 Similarity score: 0.0620817

Alignment:
 ATAGGAATGCTTGTGATTTT
 -----TTTTATTTT

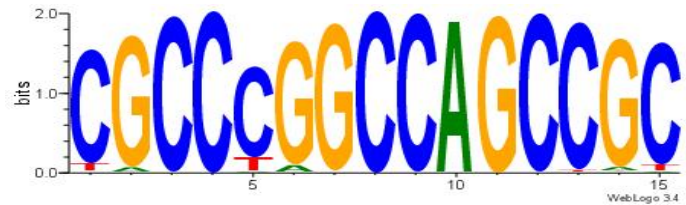
Original motif Consensus sequence: AAAATCACAAGCATTCTAT

Reverse complement motif Consensus sequence:
 ATAGGAATGCTTGTGATTTT

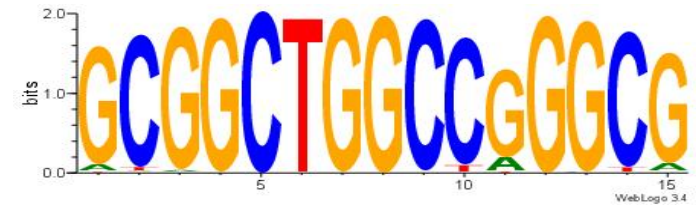


Dataset #: 1 Motif ID: 125 Motif name: Motif 125

Original motif Consensus sequence: CGCCGGCCAGCCGC



Reverse complement motif Consensus sequence: GCGGCTGGCCGGCG



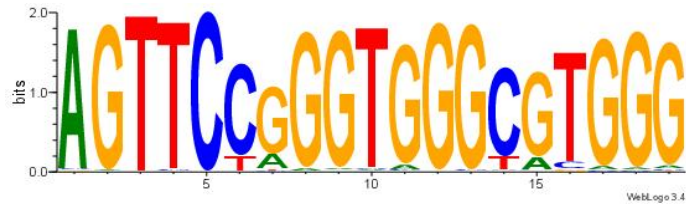
Best Matches for Motif ID 125 (Highest to Lowest)

Dataset #:	1
Motif ID:	98
Motif name:	Motif 98
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	5
Number of overlap:	15
Similarity score:	0.0866862

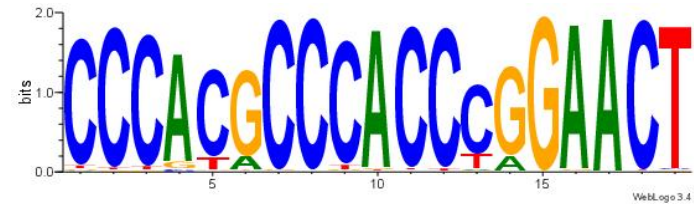
Alignment:

AGTTCCGGGTGGGCGTGGG
GCGGCTGGCCGGGCG----

Original motif Consensus sequence: AGTTCCGGGTGGGCGTGGG



Reverse complement motif Consensus sequence:
CCCACGCCACCCGGAAC

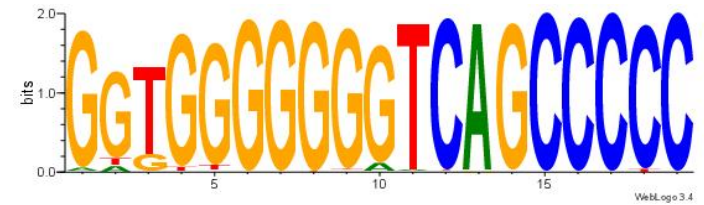
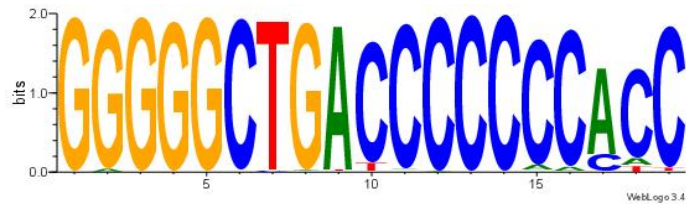


Dataset #: 1
Motif ID: 92
Motif name: Motif 92
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 4
Number of overlap: 15
Similarity score: 0.0950761

Alignment:
GGTGGGGGGGTCAGCCCC
-CGCCGGCCAGCCGC---

Original motif Consensus sequence: GGGGCTGACCCCCACC

Reverse complement motif Consensus sequence:
GGTGGGGGGGTCAGCCCC



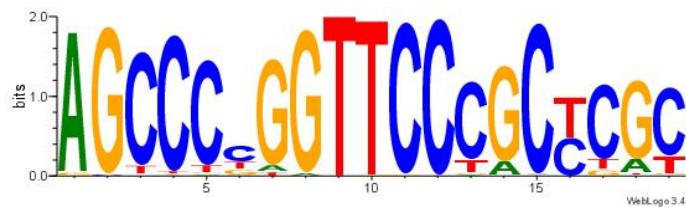
Dataset #: 1
 Motif ID: 164
 Motif name: Motif 164
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 15
 Similarity score: 0.0965381

Alignment:

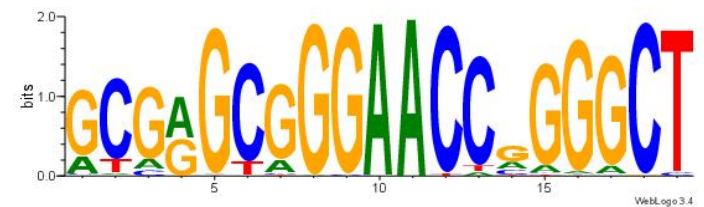
```

GCGMCGGGAACCGGGCT
----GCGGCTGGCCGGCG
  
```

Original motif Consensus sequence: AGCCCGTTCCCGCYCGC



Reverse complement motif Consensus sequence: GCGMCGGGAACCGGGCT



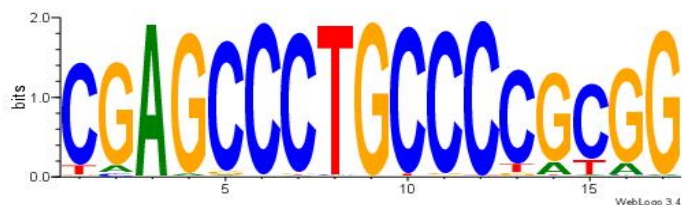
Dataset #: 1

Motif ID: 78
 Motif name: Motif 78
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 15
 Similarity score: 0.0972915

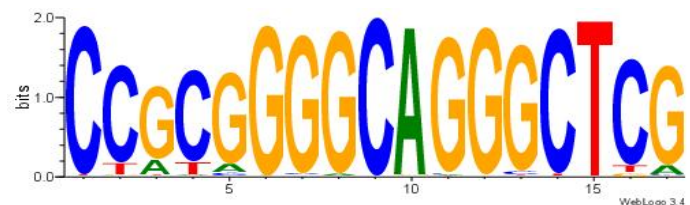
Alignment:

CCGCGGGGCAGGGCTCG
 GCGGCTGGCCGGGCG--

Original motif Consensus sequence: CGAGCCCTGCCCGCGG



Reverse complement motif Consensus sequence: CCGCGGGGCAGGGCTCG



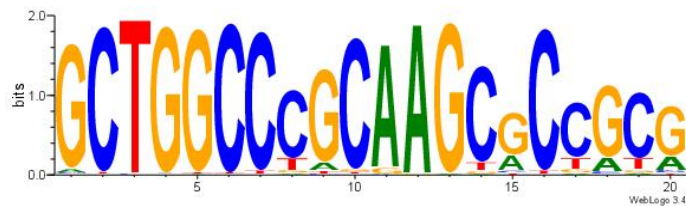
Dataset #: 1
 Motif ID: 100
 Motif name: Motif 100
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 15

Similarity score: 0.098833

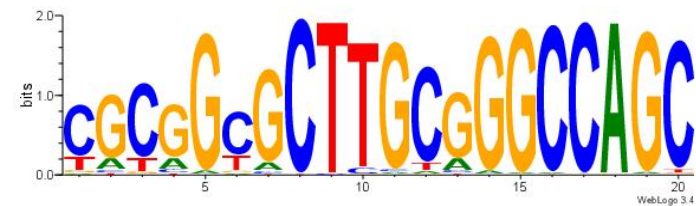
Alignment:

GCTGGCCCGCAAGCGCCGCG
--CGCCCCGGCCAGCCGC---

Original motif Consensus sequence: GCTGGCCCGCAAGCGCCGCG

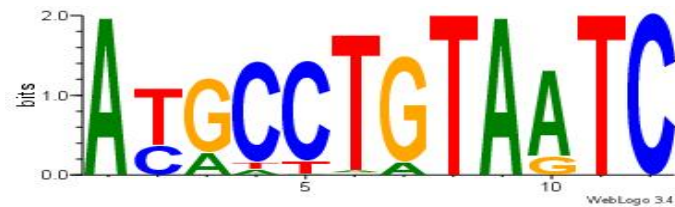


Reverse complement motif Consensus sequence: CGCGGCGCTTGCGGGCCAGC

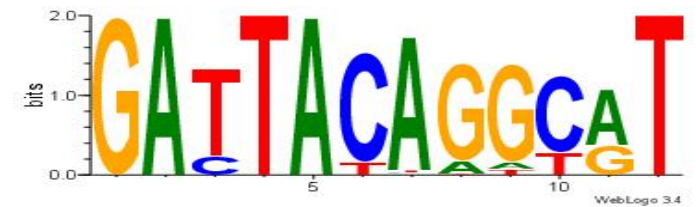


Dataset #: 1 Motif ID: 126 Motif name: Motif 126

Original motif Consensus sequence: AYGCTGTAATC



Reverse complement motif Consensus sequence: GATTACAGGCMT



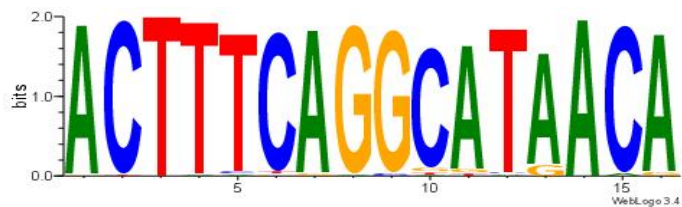
Best Matches for Motif ID 126 (Highest to Lowest)

Dataset #:	1
Motif ID:	278
Motif name:	Motif 278
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif

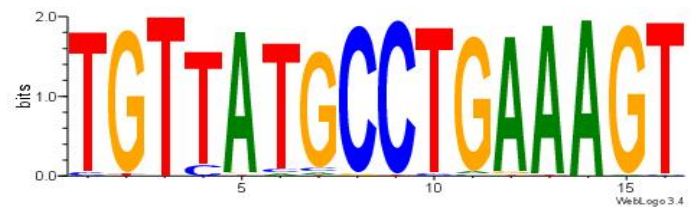
Direction: Forward
Position number: 1
Number of overlap: 12
Similarity score: 0.0669992

Alignment:
ACTTTCAGGCATAACA
GATTACAGGCMT-----

Original motif Consensus sequence: ACTTTCAGGCATAACA



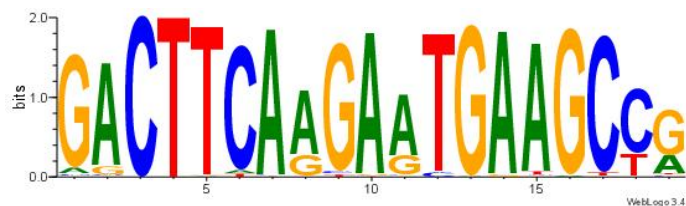
Reverse complement motif Consensus sequence: TGTTATGCCTGAAAGT



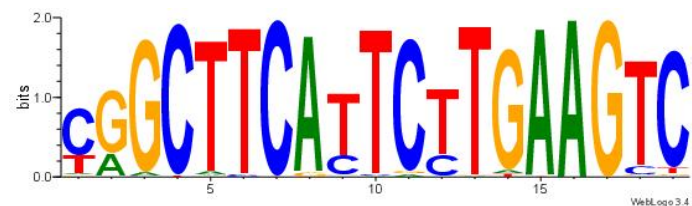
Dataset #: 1
Motif ID: 211
Motif name: Motif 211
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 12
Similarity score: 0.0695709

Alignment:
GACTTCAAGAATGAAGCCG
GATTACAGGCMT-----

Original motif Consensus sequence: GACTTCAAGAATGAAGCCG



Reverse complement motif Consensus sequence: CGGCTTCATTCTGAAGTC

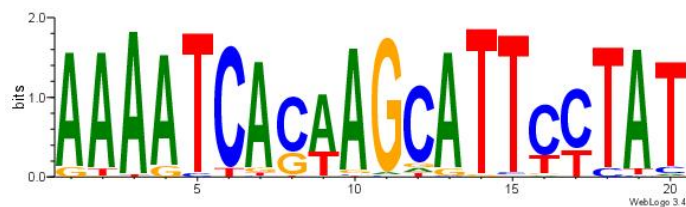


Dataset #: 1
Motif ID: 254
Motif name: Motif 254
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 3
Number of overlap: 12
Similarity score: 0.0736473

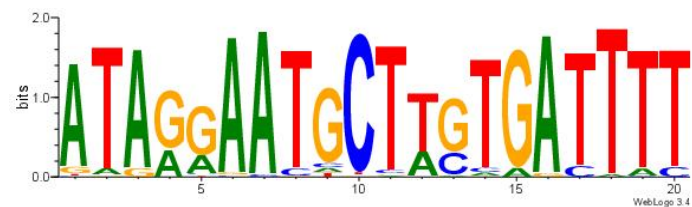
Alignment:

```
ATAGGAATGCTTGTGATTTT  
-----AYGCCTGTAATC--
```

Original motif Consensus sequence: AAAATCACAAGCATTCTAT



Reverse complement motif Consensus sequence: ATAGGAATGCTTGTGATTTT



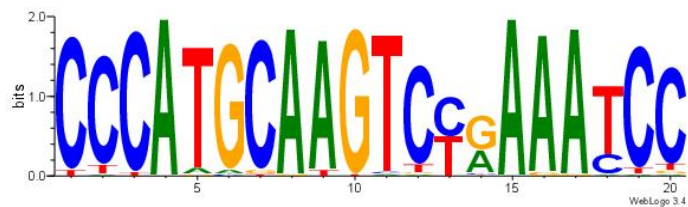
Dataset #: 1
 Motif ID: 310
 Motif name: Motif 310
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 8
 Number of overlap: 12
 Similarity score: 0.0740911

Alignment:

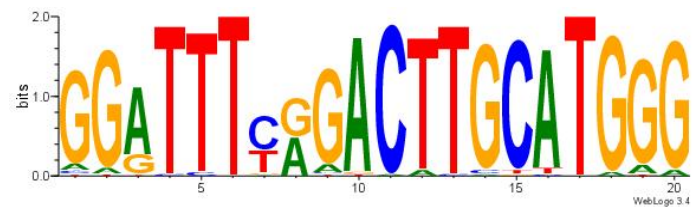
```

CCCATGCAAGTCYRAAATCC
-----AYGCCTGTAATC-
  
```

Original motif Consensus sequence: CCCATGCAAGTCYRAAATCC



Reverse complement motif Consensus sequence: GGATTTMKGACTTGCATGGG

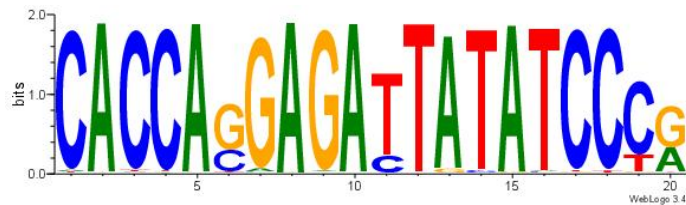


Dataset #: 1
 Motif ID: 19
 Motif name: Motif 19
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1

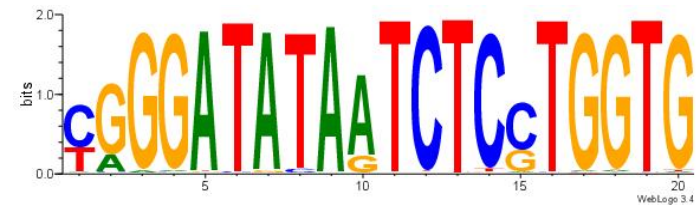
Number of overlap: 12
 Similarity score: 0.0813954

Alignment:
 CACCAGGAGATTATATCCCR
 GATTACAGGCMT-----

Original motif Consensus sequence: CACCAGGAGATTATATCCCR

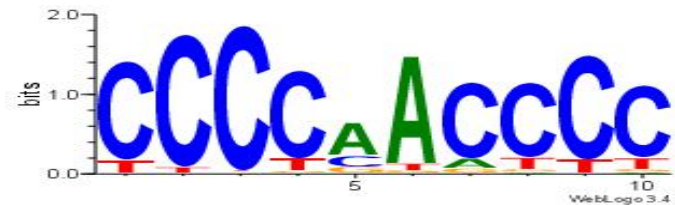


Reverse complement motif Consensus sequence:
 MGGGATATAATCTCCTGGTG

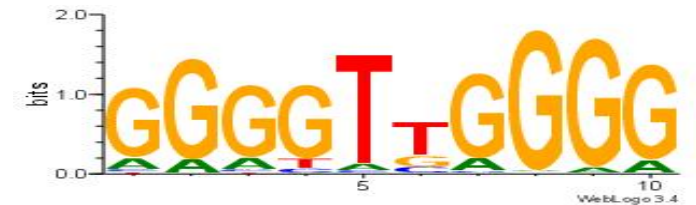


Dataset #: 1 Motif ID: 127 Motif name: Motif 127

Original motif Consensus sequence: CCCAACCCC



Reverse complement motif Consensus sequence: GGGTTGGGG



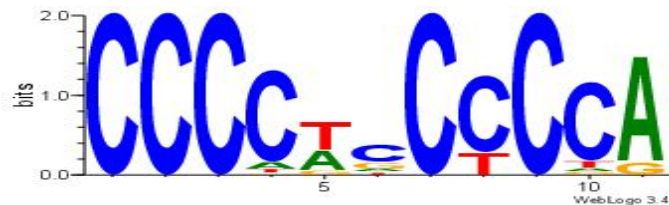
Best Matches for Motif ID 127 (Highest to Lowest)

Dataset #: 1
 Motif ID: 46
 Motif name: Motif 46
 Matching format of first motif: Original Motif

Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 10
 Similarity score: 0.0369517

Alignment:
 CCCCWCCCCCA
 CCCCAACCCC-

Original motif Consensus sequence: CCCCWCCCCCA



Reverse complement motif Consensus sequence: TGGGGWGGGG

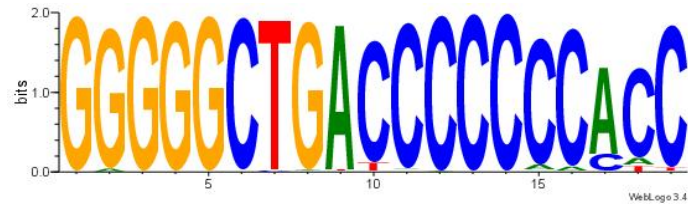


Dataset #: 1
 Motif ID: 92
 Motif name: Motif 92
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 10
 Similarity score: 0.0650488

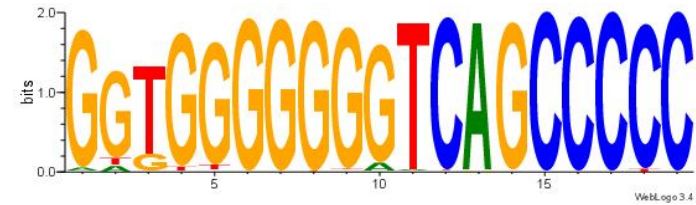
Alignment:

GGGGGCTGACCCCCCACC
 -----CCCCAACCCC

Original motif Consensus sequence: GGGGGCTGACCCCCCACC



Reverse complement motif Consensus sequence:
 GGTGGGGGGGTCAGCCCCC

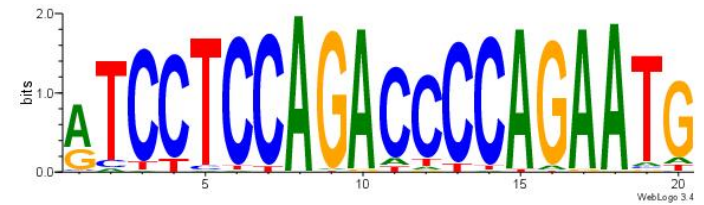
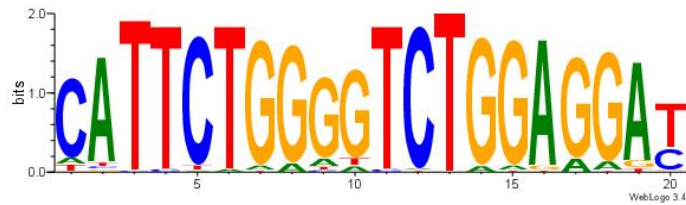


Dataset #:	1
Motif ID:	309
Motif name:	Motif 309
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	5
Number of overlap:	10
Similarity score:	0.0661693

Alignment:
 CATTCTGGGGTCTGGAGGAY
 -----GGGGTTGGGG-----

Original motif Consensus sequence: CATTCTGGGGTCTGGAGGAY

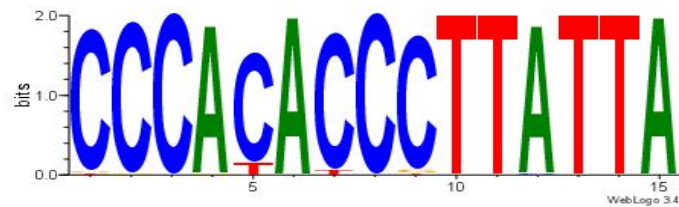
Reverse complement motif Consensus sequence:
 MTCCTCCAGACCCCAGAATG



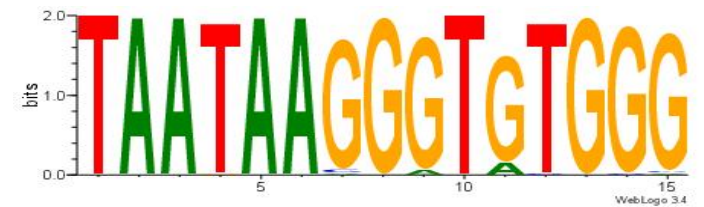
Dataset #: 1
 Motif ID: 259
 Motif name: Motif 259
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 6
 Number of overlap: 10
 Similarity score: 0.0688836

Alignment:
 TAATAAGGGTGTGGG
 -----GGGGTTGGGG

Original motif Consensus sequence: CCCACACCCTTATTA



Reverse complement motif Consensus sequence: TAATAAGGGTGTGGG



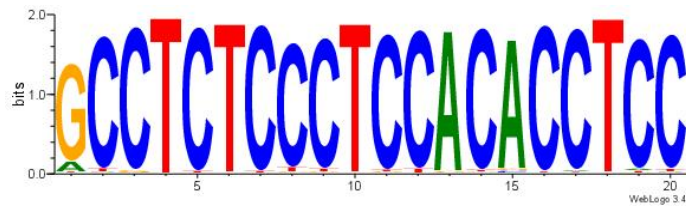
Dataset #: 1
 Motif ID: 105

Motif name: Motif 105
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 8
 Number of overlap: 10
 Similarity score: 0.0693706

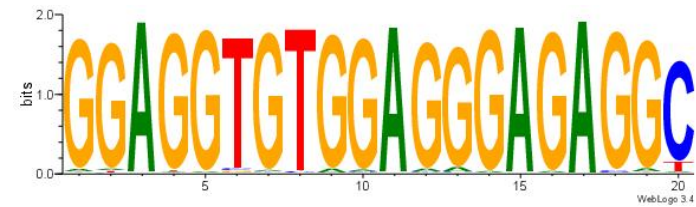
Alignment:

GGAGGTGTGGAGGGAGAGGC
 ---GGGGTTGGGG-----

Original motif Consensus sequence: GCCTCTCCCTCCACACCTCC

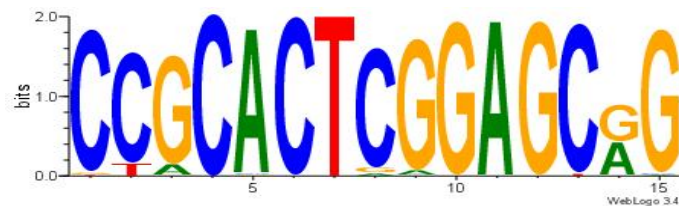


Reverse complement motif Consensus sequence: GGAGGTGTGGAGGGAGAGGC

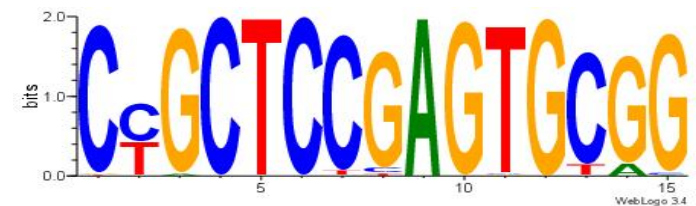


Dataset #: 1 Motif ID: 128 Motif name: Motif 128

Original motif Consensus sequence: CCGACTCGGAGCRG



Reverse complement motif Consensus sequence: CMGCTCCGAGTGC GG



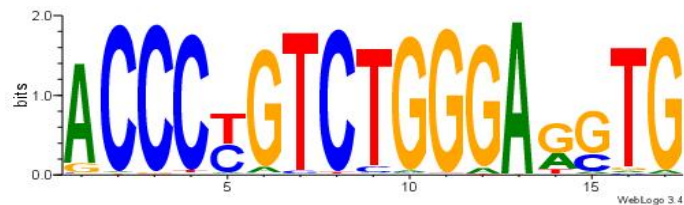
Best Matches for Motif ID 128 (Highest to Lowest)

Dataset #: 1
Motif ID: 95
Motif name: Motif 95
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 15
Similarity score: 0.0771871

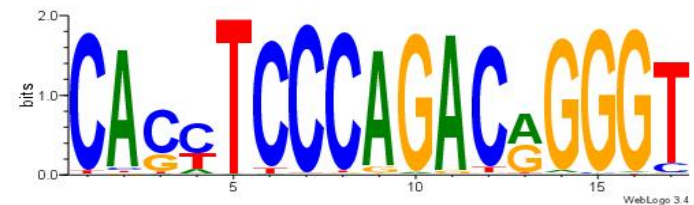
Alignment:

```
CACCTCCCAGACMGGGT  
CMGCTCCGAGTGCGG--
```

Original motif Consensus sequence: ACCYGTCTGGGAGGTG



Reverse complement motif Consensus sequence:
CACCTCCCAGACMGGGT



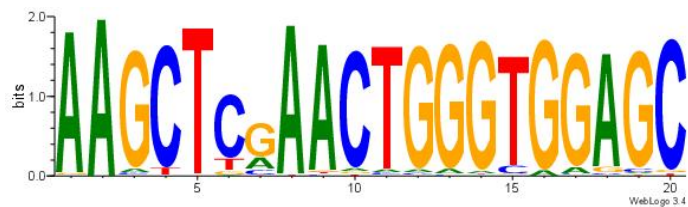
Dataset #: 1
Motif ID: 321
Motif name: Motif 321
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif

Direction: Backward
Position number: 2
Number of overlap: 15
Similarity score: 0.0895427

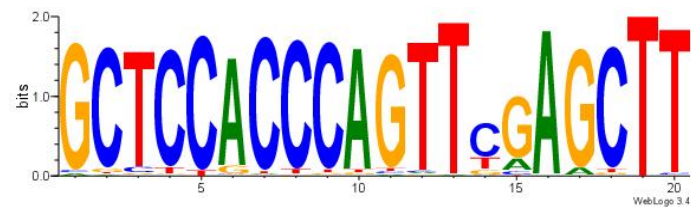
Alignment:

AAGCTCGAACTGGGTGGAGC
----CCGCACTCGGAGCRG--

Original motif Consensus sequence: AAGCTCGAACTGGGTGGAGC



Reverse complement motif Consensus sequence: GCTCCACCCAGTTCGAGCTT

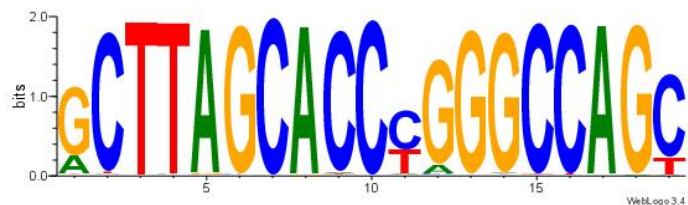


Dataset #: 1
Motif ID: 82
Motif name: Motif 82
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 4
Number of overlap: 15
Similarity score: 0.090819

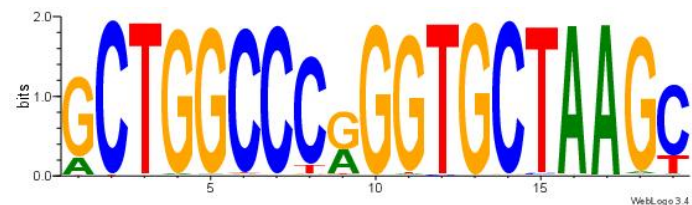
Alignment:

GCTTAGCACCYGGGCCAGC
---CCGCACTCGGAGCRG--

Original motif Consensus sequence: GCTTAGCACCCGGGCCAGC



Reverse complement motif Consensus sequence:
GCTGGCCCKGGTGCTAAGC

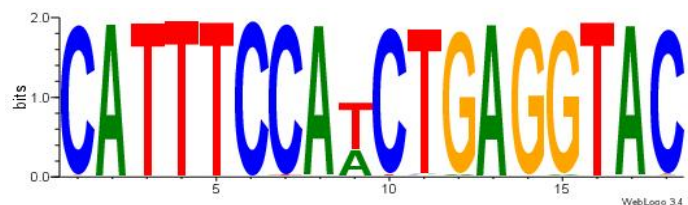


Dataset #: 1
Motif ID: 25
Motif name: Motif 25
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 15
Similarity score: 0.0937468

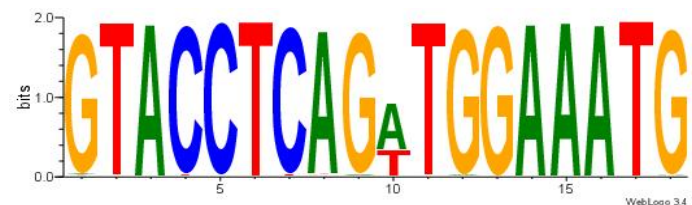
Alignment:

GTACCTCAGWTGGAAATG
CCGCACTCGGAGCRG---

Original motif Consensus sequence: CATTTCCTGAGGTAC



Reverse complement motif Consensus sequence:
GTACCTCAGWTGGAAATG

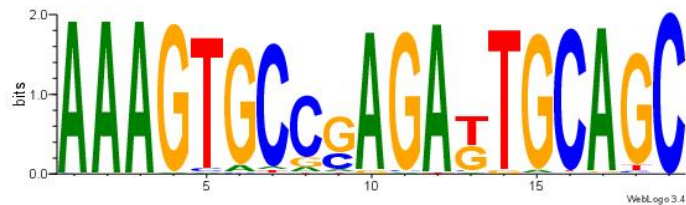


Dataset #: 1
 Motif ID: 191
 Motif name: Motif 191
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 15
 Similarity score: 0.0954398

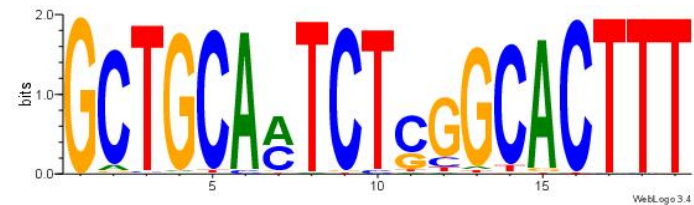
Alignment:

GCTGCARTCTCGGCACTTT
 -CCGCACTCGGAGCRG---

Original motif Consensus sequence: AAAGTGCCGAGAKTGCAGC



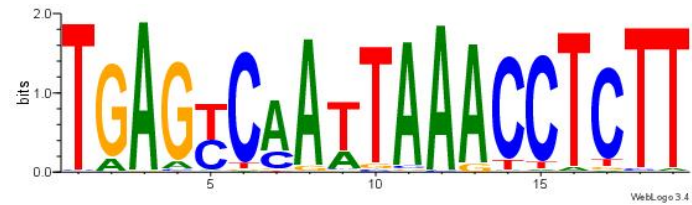
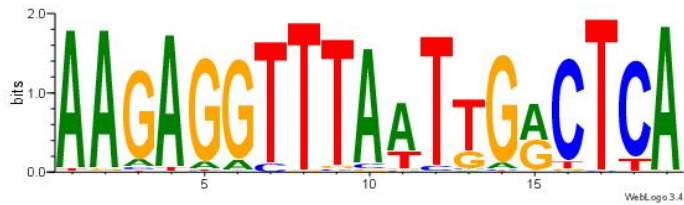
Reverse complement motif Consensus sequence: GCTGCARTCTCGGCACTTT



Dataset #: 1 Motif ID: 129 Motif name: Motif 129

Original motif Consensus sequence: AAGAGGTTTAATTGRCTCA

Reverse complement motif Consensus sequence: TGAGKCAATTAAACCTCTT

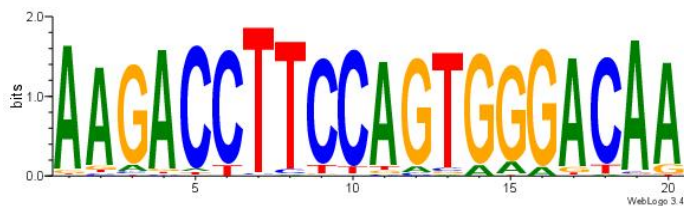


Best Matches for Motif ID 129 (Highest to Lowest)

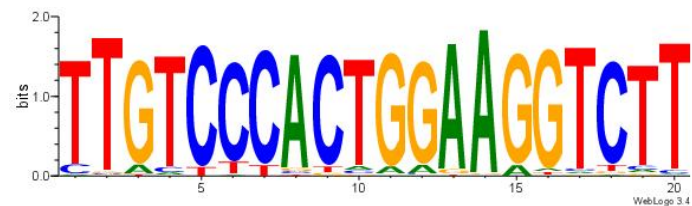
Dataset #: 1
 Motif ID: 292
 Motif name: Motif 292
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 19
 Similarity score: 0.093225

Alignment:
 AAGACCTTCCAGTGGGACAA
 AAGAGGTTTAATTGRCTCA-

Original motif Consensus sequence: AAGACCTTCCAGTGGGACAA



Reverse complement motif Consensus sequence: TTGTTCCCACTGGAAAGGTCTT

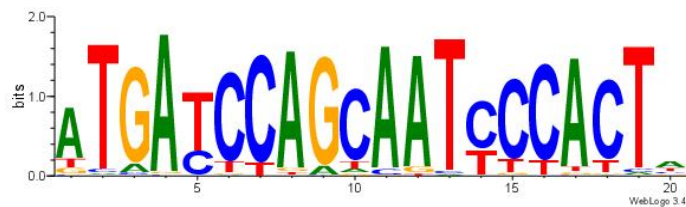


Dataset #: 1
 Motif ID: 115
 Motif name: Motif 115
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 19
 Similarity score: 0.0969481

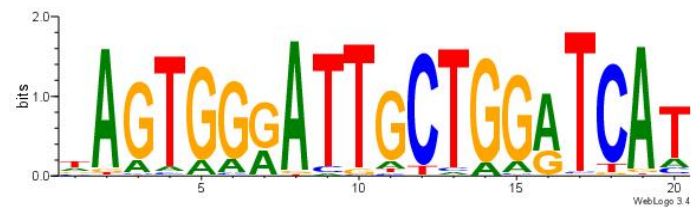
Alignment:

ATGATCCAGCAATYCCACTH
 TGAGKCAATTAAACCTCTT-

Original motif Consensus sequence: ATGATCCAGCAATYCCACTH



Reverse complement motif Consensus sequence: HAGTGGKATTGCTGGATCAT



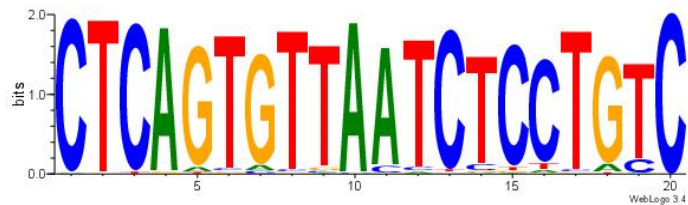
Dataset #: 1
 Motif ID: 262
 Motif name: Motif 262
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2

Number of overlap: 19
Similarity score: 0.110541

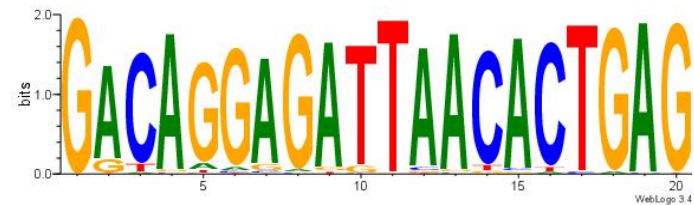
Alignment:

GACAGGAGATTAACACTGAG
-TGAGKCAATTAACCTCTT

Original motif Consensus sequence: CTCAGTGTTAATCTCCTGTC



Reverse complement motif Consensus sequence:
GACAGGAGATTAACACTGAG

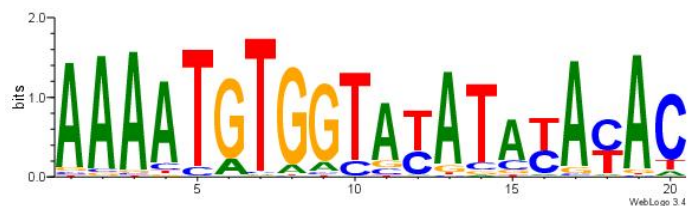


Dataset #: 1
Motif ID: 83
Motif name: Motif 83
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2
Number of overlap: 19
Similarity score: 0.114822

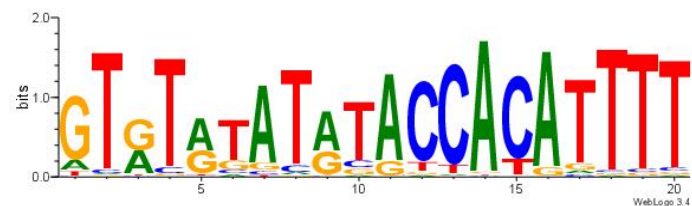
Alignment:

AAAATGTGGTAYATAYAYAC
AAGAGGTTTAATTGRCTCA-

Original motif Consensus sequence: AAAATGTGGTAYATAYAYAC



Reverse complement motif Consensus sequence: GTKTMTATMTACCACATTTT

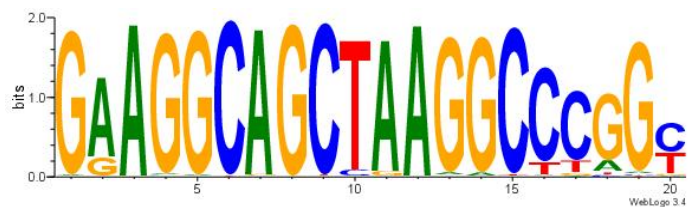


Dataset #: 1
Motif ID: 64
Motif name: Motif 64
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 19
Similarity score: 0.116601

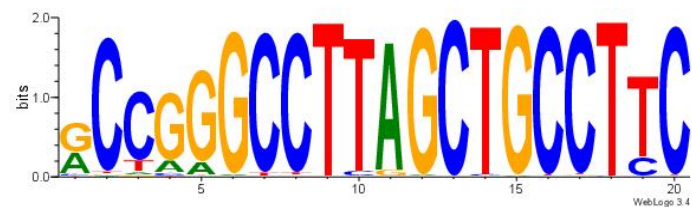
Alignment:

KCCGGGCCTTAGCTGCCTTC
AAGAGGTTTAATTGRCTCA-

Original motif Consensus sequence: GAAGGCAGCTAAGGCCCGGY

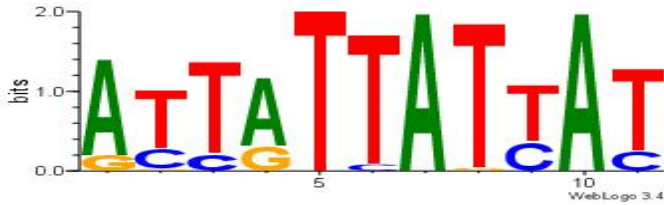


Reverse complement motif Consensus sequence: KCCGGGCCTTAGCTGCCTTC

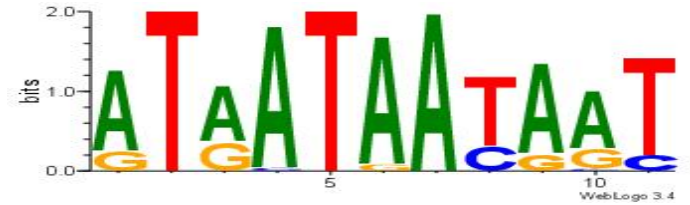


Dataset #: 1 Motif ID: 130 Motif name: Motif 130

Original motif Consensus sequence: ATTATTATYAT



Reverse complement motif Consensus sequence: ATMATAATAAT



Best Matches for Motif ID 130 (Highest to Lowest)

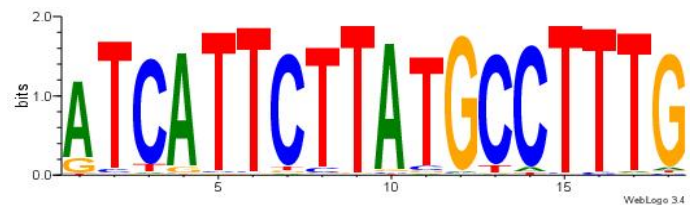
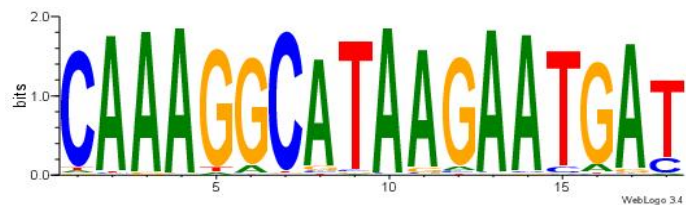
Dataset #:	1
Motif ID:	190
Motif name:	Motif 190
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	11
Similarity score:	0.0362259

Alignment:

```
ATCATTCTTATGCCTTTG
ATTATTATYAT-----
```

Original motif Consensus sequence: CAAAGGCATAAGAATGAT

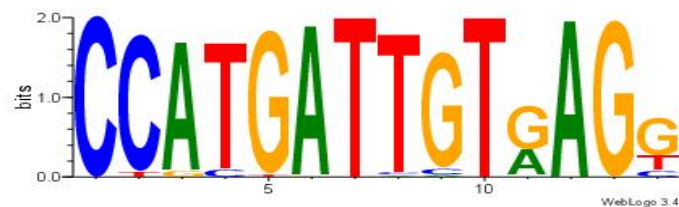
Reverse complement motif Consensus sequence: ATCATTCTTATGCCTTTG



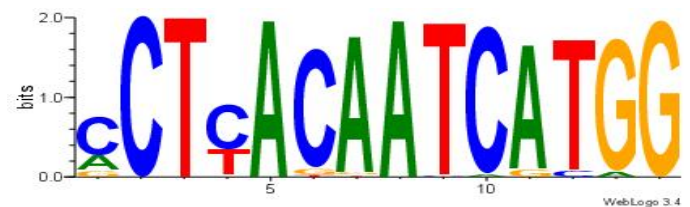
Dataset #: 1
 Motif ID: 270
 Motif name: Motif 270
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 11
 Similarity score: 0.0458076

Alignment:
 CCTMACAATCATGG
 -ATMATAATAAT--

Original motif Consensus sequence: CCATGATTGTRAGG



Reverse complement motif Consensus sequence: CCTMACAATCATGG



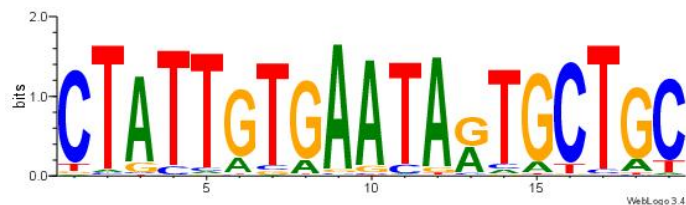
Dataset #: 1
 Motif ID: 70

Motif name: Motif 70
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 7
 Number of overlap: 11
 Similarity score: 0.0543851

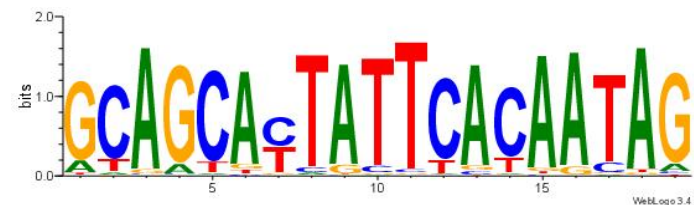
Alignment:

GCAGCAMTATTCAATAG
 -----ATMATAATAAT--

Original motif Consensus sequence: CTATTGTGAATARTGCTGC



Reverse complement motif Consensus sequence: GCAGCAMTATTCAATAG

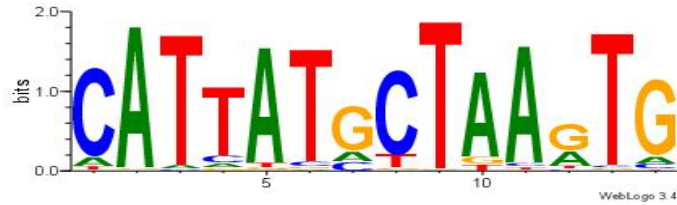


Dataset #: 1
 Motif ID: 287
 Motif name: Motif 287
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 11
 Similarity score: 0.0550832

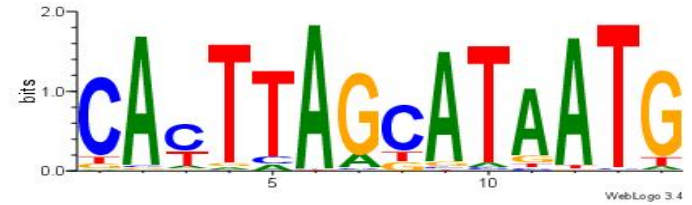
Alignment:

CAMTTAGCATAATG
--ATMATAATAAT--

Original motif Consensus sequence: CATTATGCTAARTG



Reverse complement motif Consensus sequence: CAMTTAGCATAATG



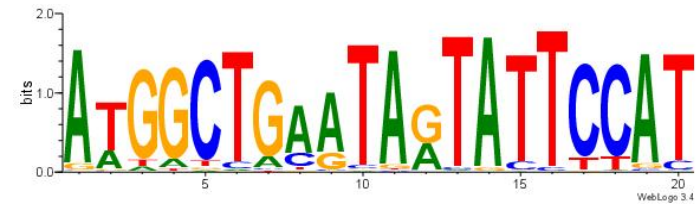
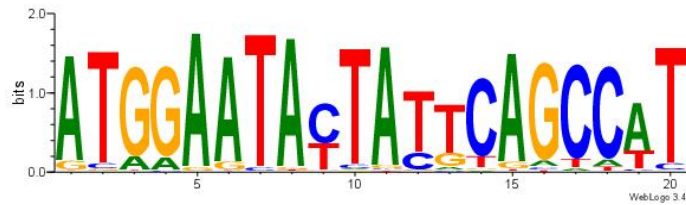
Dataset #: 1
Motif ID: 55
Motif name: Motif 55
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 8
Number of overlap: 11
Similarity score: 0.0576294

Alignment:

ATGGAATAYTATTCAGCCAT
-----ATMATAATAAT--

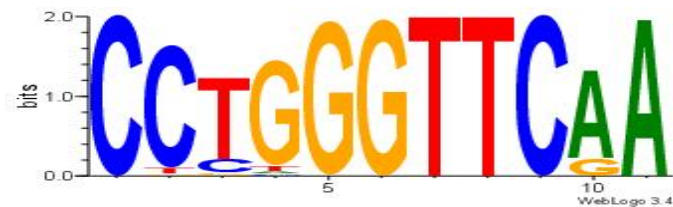
Original motif Consensus sequence: ATGGAATAYTATTCAGCCAT

Reverse complement motif Consensus sequence:
ATGGCTGAATAKTATTCCAT



Dataset #: 1 Motif ID: 131 Motif name: Motif 131

Original motif Consensus sequence: CCTGGGTTCAA



Reverse complement motif Consensus sequence: TTGAACCCAGG

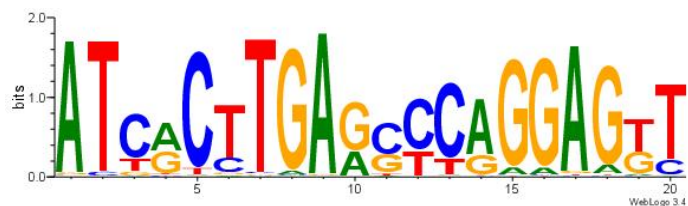


Best Matches for Motif ID 131 (Highest to Lowest)

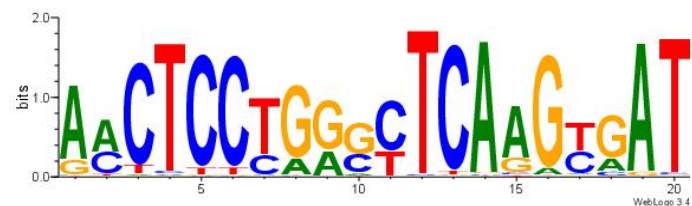
Dataset #:	1
Motif ID:	8
Motif name:	Motif 8
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	6
Number of overlap:	11
Similarity score:	0.044498

Alignment:
 ARCTCCTGKSCTCAAGKGAT
 -----CCTGGGTTCAA-----

Original motif Consensus sequence: ATCRCTTGAGSYCAGGAGKT



Reverse complement motif Consensus sequence: ARCTCCTGKSCTCAAGKGAT

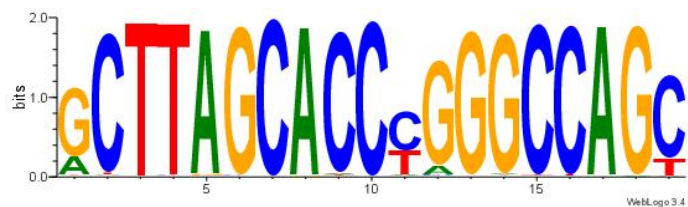


Dataset #: 1
Motif ID: 82
Motif name: Motif 82
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 6
Number of overlap: 11
Similarity score: 0.0639634

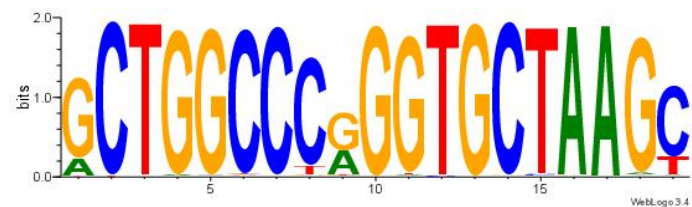
Alignment:

GCTTAGCACCYGGGCCAGC
-----TTGAACCCAGG----

Original motif Consensus sequence: GCTTAGCACCYGGGCCAGC



Reverse complement motif Consensus sequence: GCTGGCCCKGGTGCTAAGC

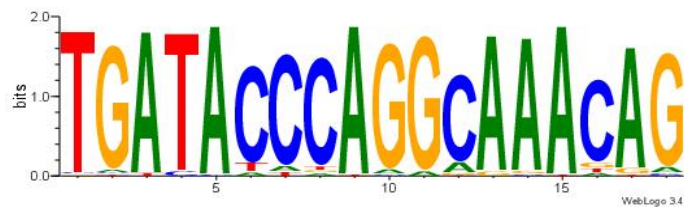


Dataset #: 1
 Motif ID: 290
 Motif name: Motif 290
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.0646962

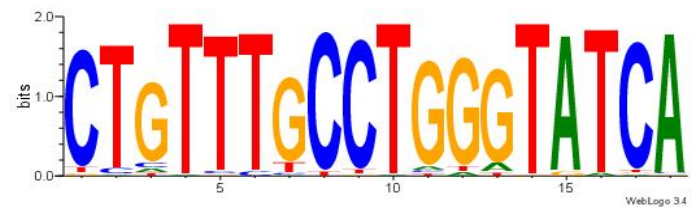
Alignment:

TGATACCCAGGCAAACAG
 TTGAACCCAGG-----

Original motif Consensus sequence: TGATACCCAGGCAAACAG



Reverse complement motif Consensus sequence: CTGTTTGCCTGGGTATCA

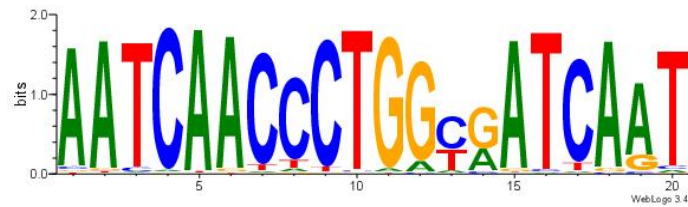


Dataset #: 1
 Motif ID: 170
 Motif name: Motif 170
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 9

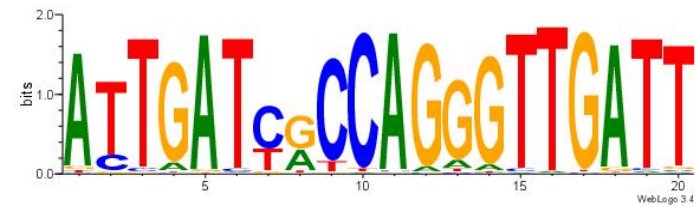
Number of overlap: 11
Similarity score: 0.0706085

Alignment:
ATTGATMKCCAGGGTTGATT
-----CCTGGGTTCAA-

Original motif Consensus sequence: AATCAACCCTGGYRATCAAT



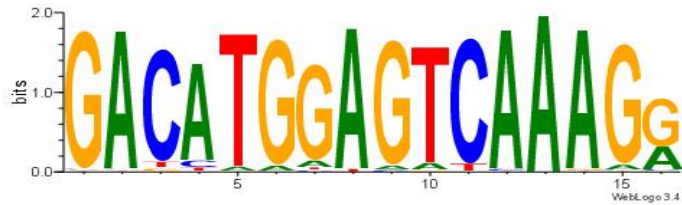
Reverse complement motif Consensus sequence:
ATTGATMKCCAGGGTTGATT



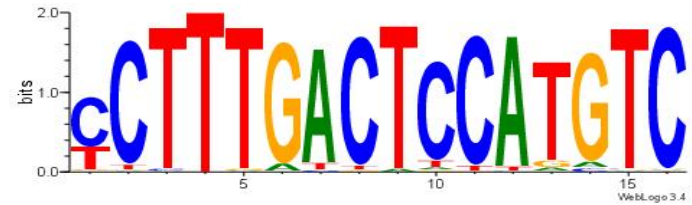
Dataset #: 1
Motif ID: 326
Motif name: Motif 326
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 3
Number of overlap: 11
Similarity score: 0.0708014

Alignment:
GACATGGAGTCAAAGG
--CCTGGGTTCAA---

Original motif Consensus sequence: GACATGGAGTCAAAGG

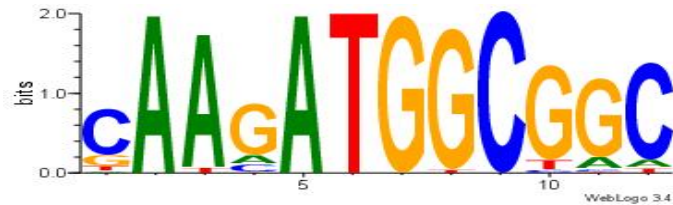


Reverse complement motif Consensus sequence: CCTTTGACTCCATGTC

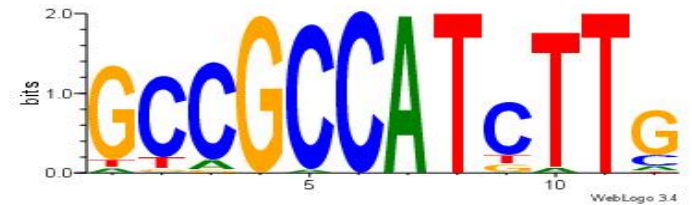


Dataset #: 1 Motif ID: 132 Motif name: Motif 132

Original motif Consensus sequence: CAAGATGGCGGC



Reverse complement motif Consensus sequence: GCCGCCATCTTG



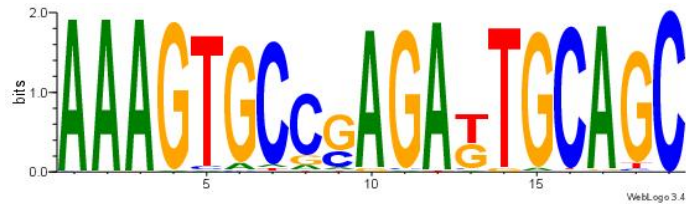
Best Matches for Motif ID 132 (Highest to Lowest)

Dataset #:	1
Motif ID:	191
Motif name:	Motif 191
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	8
Number of overlap:	12
Similarity score:	0.0630794

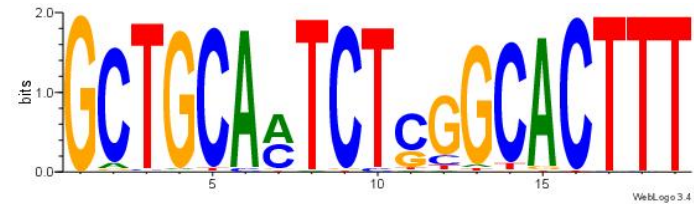
Alignment:

GCTGCARTCTCGGCACTTT
GCCGCCATCTTG-----

Original motif Consensus sequence: AAAGTGCCGAGAKTGCAGC



Reverse complement motif Consensus sequence:
GCTGCARTCTCGGCACTTT



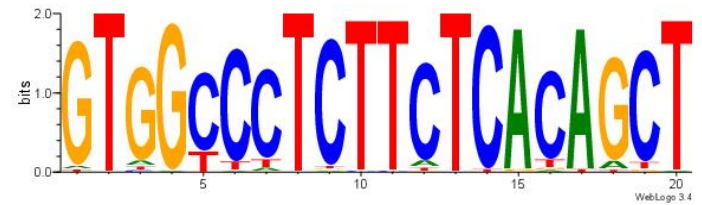
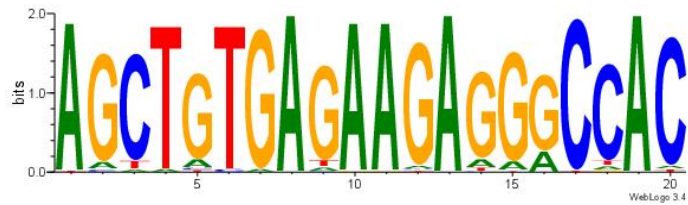
Dataset #: 1
Motif ID: 294
Motif name: Motif 294
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 9
Number of overlap: 12
Similarity score: 0.0641012

Alignment:

AGCTGTGAGAAGAGGGCCAC
-----CAAGATGGCGGC

Original motif Consensus sequence: AGCTGTGAGAAGAGGGCCAC

Reverse complement motif Consensus sequence:
GTGGCCCTCTTCTCACAGCT



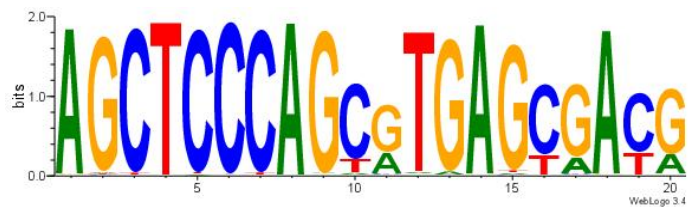
Dataset #: 1
 Motif ID: 48
 Motif name: Motif 48
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 8
 Number of overlap: 12
 Similarity score: 0.0710877

Alignment:

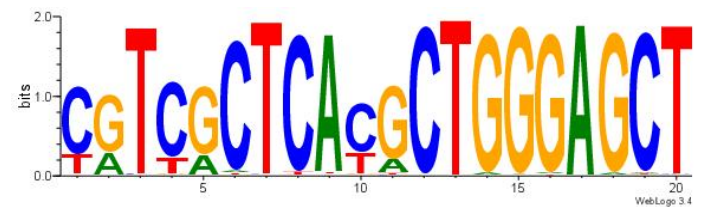
```

AGCTCCCAGCGTGAGCGACG
-----GCCGCCATCTTG-
  
```

Original motif Consensus sequence: AGCTCCCAGCGTGAGCGACG



Reverse complement motif Consensus sequence: CGTCGCTCAGCTGGGAGCT



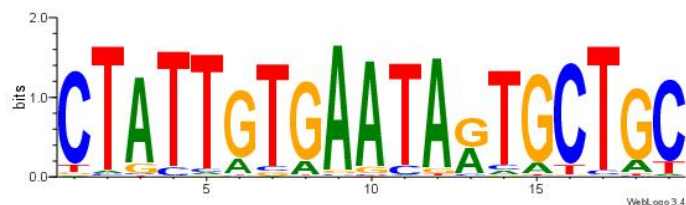
Dataset #: 1

Motif ID: 70
 Motif name: Motif 70
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 8
 Number of overlap: 12
 Similarity score: 0.0731765

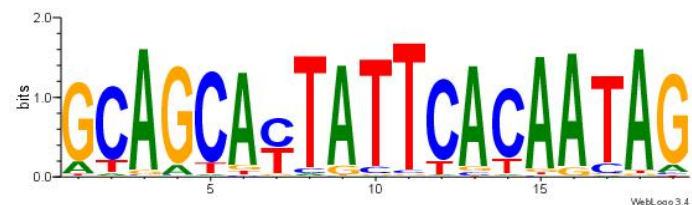
Alignment:

GCAGCAMTATTCACAATAG
 GCCGCCATCTTG-----

Original motif Consensus sequence: CTATTGTGAATARTGCTGC



Reverse complement motif Consensus sequence: GCAGCAMTATTCACAATAG



Dataset #: 1
 Motif ID: 222
 Motif name: Motif 222
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 12

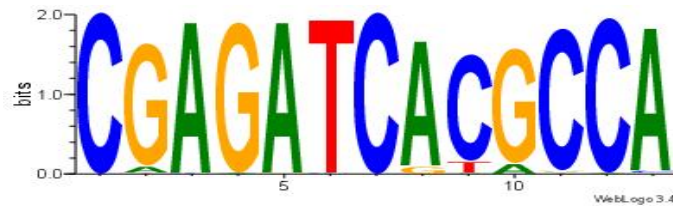
Similarity score: 0.0777048

Alignment:

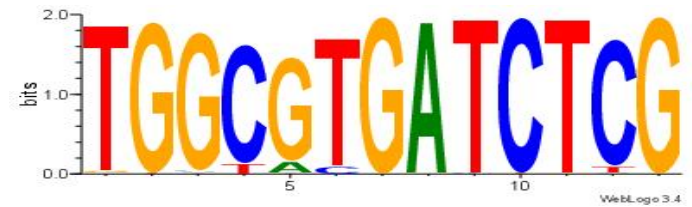
CGAGATCACGCCA

CAAGATGGCGGC-

Original motif Consensus sequence: CGAGATCACGCCA

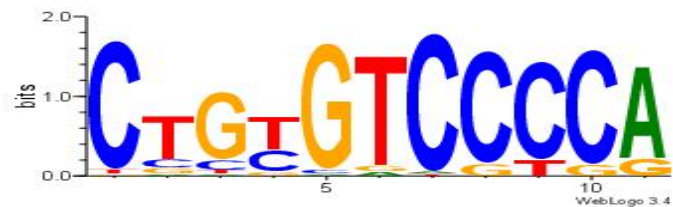


Reverse complement motif Consensus sequence: TGGCGTGATCTCG



Dataset #: 1 Motif ID: 133 Motif name: Motif 133

Original motif Consensus sequence: CTGYGTCCCA



Reverse complement motif Consensus sequence: TGGGGACMCAG



Best Matches for Motif ID 133 (Highest to Lowest)

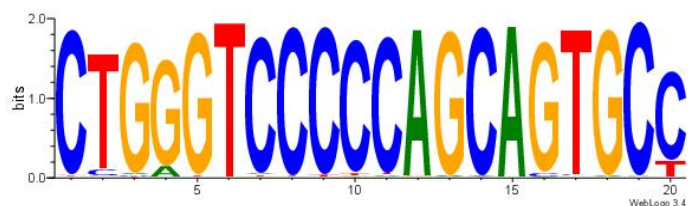
Dataset #:	1
Motif ID:	84
Motif name:	Motif 84
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward

Position number: 1
Number of overlap: 11
Similarity score: 0.0319466

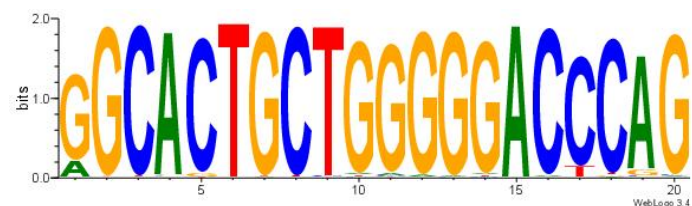
Alignment:

GGCACTGCTGGGGGACCCAG
-----TGGGGACMCAG

Original motif Consensus sequence: CTGGGTCCCCCAGCAGTGCC



Reverse complement motif Consensus sequence: GGCACTGCTGGGGGACCCAG

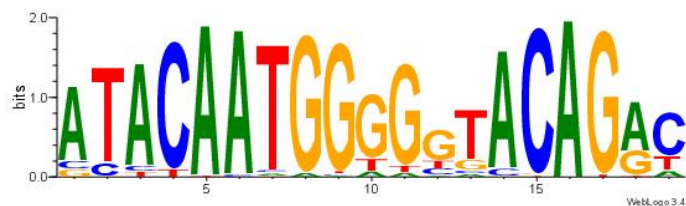


Dataset #: 1
Motif ID: 193
Motif name: Motif 193
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 3
Number of overlap: 11
Similarity score: 0.0508347

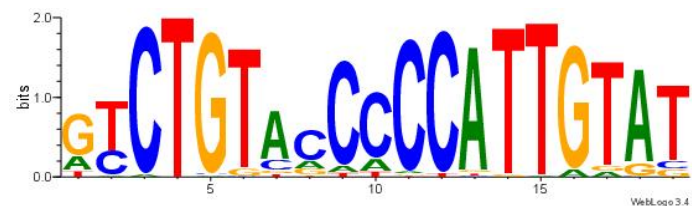
Alignment:

GKCTGTACCCCCATTGTAT
--CTGYGTCCCCA-----

Original motif Consensus sequence: ATACAATGGGGTACAGRC



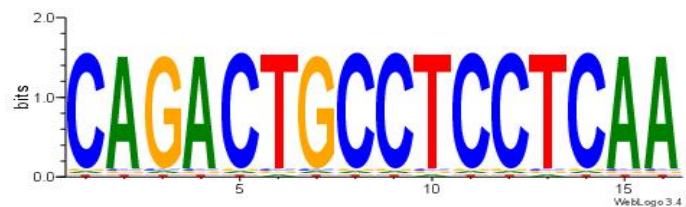
Reverse complement motif Consensus sequence: GKCTGTACCCCATTTGTAT



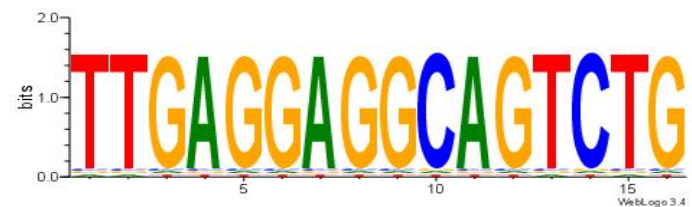
Dataset #: 1
Motif ID: 245
Motif name: Motif 245
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2
Number of overlap: 11
Similarity score: 0.0518197

Alignment:
CAGACTGCCTCCTCAA
----CTGYGTCCCA--

Original motif Consensus sequence: CAGACTGCCTCCTCAA



Reverse complement motif Consensus sequence: TTGAGGAGGCAGTCTG

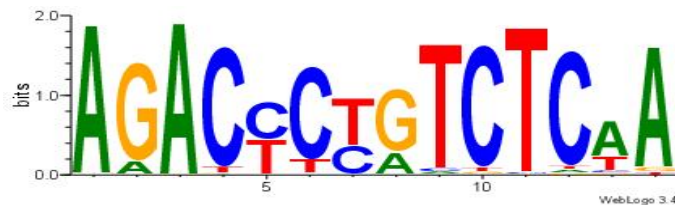


Dataset #: 1
 Motif ID: 91
 Motif name: Motif 91
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.0670325

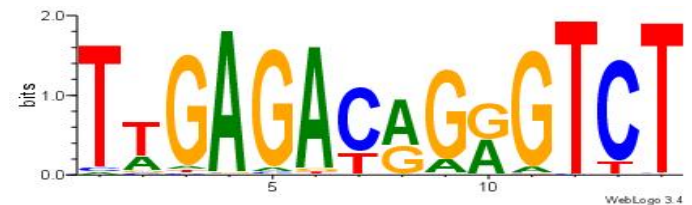
Alignment:

AGACYCYGTCTCAA
 ---CTGYGTCCCCA

Original motif Consensus sequence: AGACYCYGTCTCAA



Reverse complement motif Consensus sequence: TTGAGACMGKGTCT



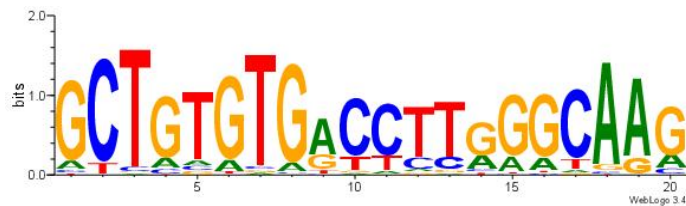
Dataset #: 1
 Motif ID: 112
 Motif name: Motif 112
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 11

Similarity score: 0.0690455

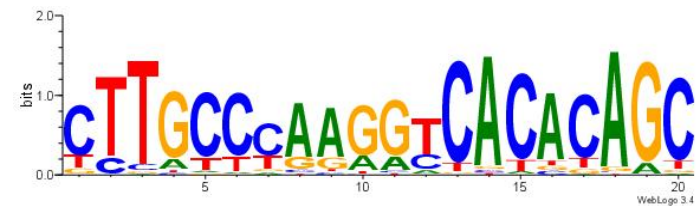
Alignment:

```
CTTGCCCAAGGTCACACAGC  
-----TGGGGACMCAG--
```

Original motif Consensus sequence: GCTGTGTGACCTTGGGCAAG

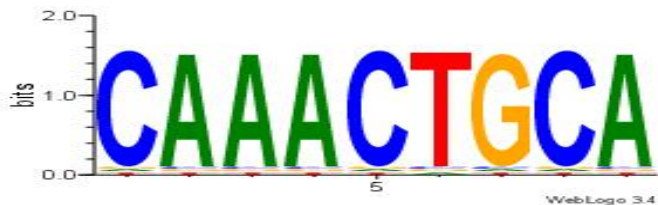


Reverse complement motif Consensus sequence: CTTGCCCAAGGTCACACAGC

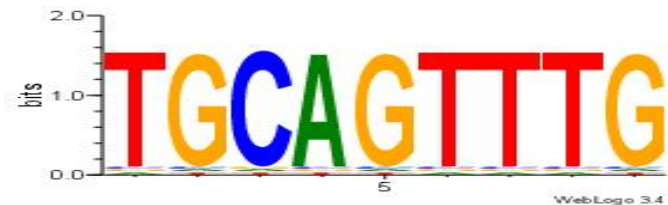


Dataset #: 1 Motif ID: 134 Motif name: Motif 134

Original motif Consensus sequence: CAAACTGCA



Reverse complement motif Consensus sequence: TGCAGTTTG



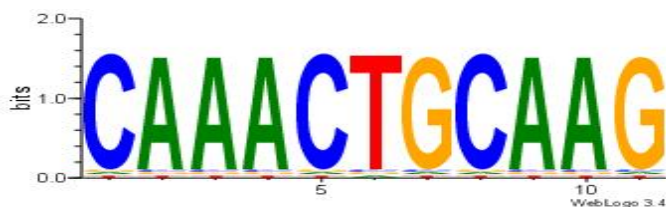
Best Matches for Motif ID 134 (Highest to Lowest)

Dataset #:	1
Motif ID:	73
Motif name:	Motif 73
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif

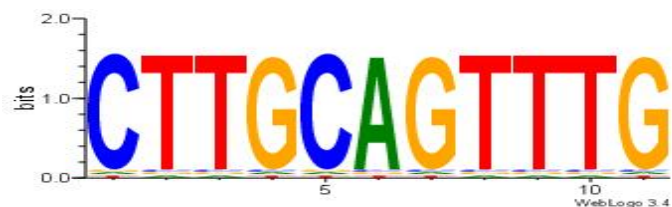
Direction: Backward
Position number: 3
Number of overlap: 9
Similarity score: 0

Alignment:
CAAAGTCAAG
CAAAGTCA--

Original motif Consensus sequence: CAAAGTCAAG



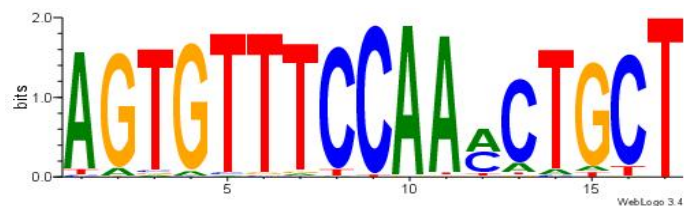
Reverse complement motif Consensus sequence: CTTGCAAGTTG



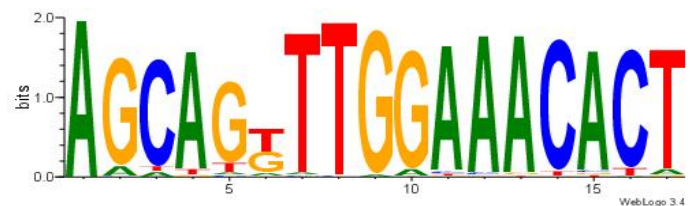
Dataset #: 1
Motif ID: 304
Motif name: Motif 304
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 9
Similarity score: 0.0499634

Alignment:
AGTGTTC AAMCTGCT
-----CAAAGTCA

Original motif Consensus sequence: AGTGTTTCCAAMCTGCT



Reverse complement motif Consensus sequence: AGCAGYTTGGAAACACT

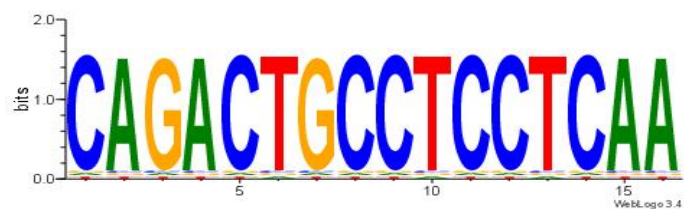


Dataset #: 1
Motif ID: 245
Motif name: Motif 245
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 9
Similarity score: 0.050505

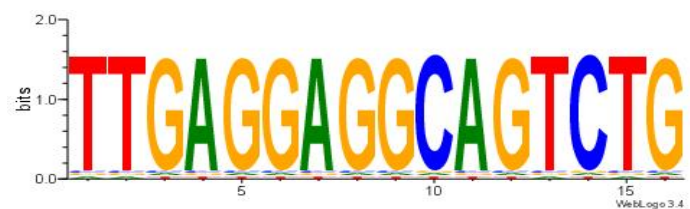
Alignment:

```
TTGAGGAGGCAGTCTG  
-----TGCAGTTTG
```

Original motif Consensus sequence: CAGACTGCCTCCTCAA



Reverse complement motif Consensus sequence: TTGAGGAGGCAGTCTG



Dataset #: 1
Motif ID: 123
Motif name: Motif 123
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 3
Number of overlap: 9
Similarity score: 0.050505

Alignment:

CTCAGACTGCT
CAAAC TGCA--

Original motif Consensus sequence: AGCAGTCTGAG



Reverse complement motif Consensus sequence: CTCAGACTGCT



Dataset #: 1
Motif ID: 71
Motif name: Motif 71
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 9

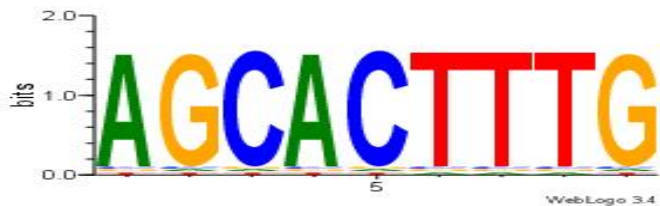
Similarity score: 0.050505

Alignment:

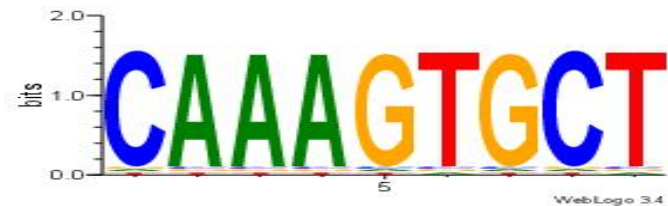
CAAAGTGCT

CAAAC TGCA

Original motif Consensus sequence: AGCACTTTG

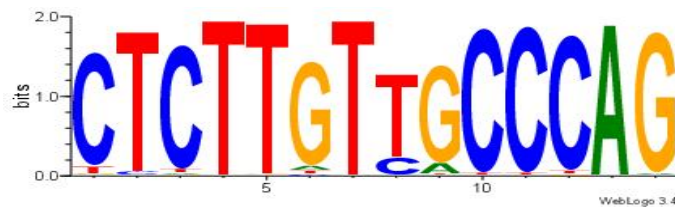


Reverse complement motif Consensus sequence: CAAAGTGCT

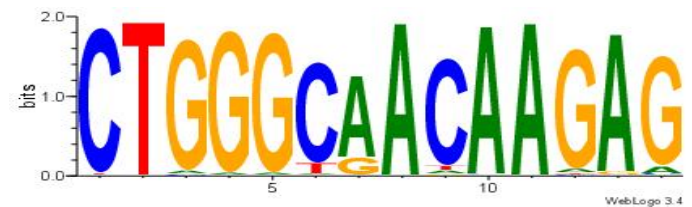


Dataset #: 1 Motif ID: 135 Motif name: Motif 135

Original motif Consensus sequence: CTCTTGTTGCCAG



Reverse complement motif Consensus sequence: CTGGGCAACAAGAG



Best Matches for Motif ID 135 (Highest to Lowest)

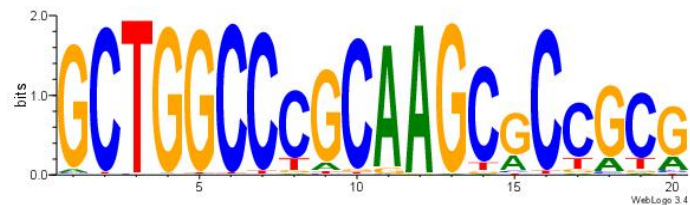
Dataset #:	1
Motif ID:	100
Motif name:	Motif 100
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward

Position number: 2
Number of overlap: 14
Similarity score: 0.0668647

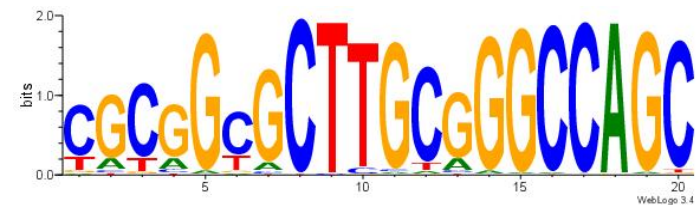
Alignment:

GCTGGCCCGCAAGCGCCGCG
-----CTGGGCAACAAGAG--

Original motif Consensus sequence: GCTGGCCCGCAAGCGCCGCG



Reverse complement motif Consensus sequence: CGCGGCGCTTGCGGGCCAGC

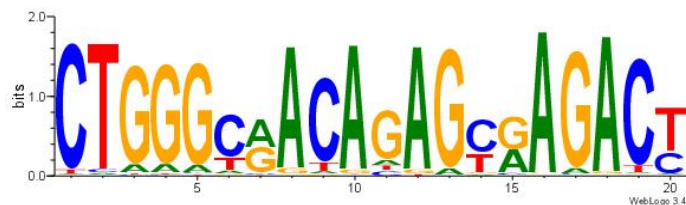


Dataset #: 1
Motif ID: 29
Motif name: Motif 29
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 7
Number of overlap: 14
Similarity score: 0.0777944

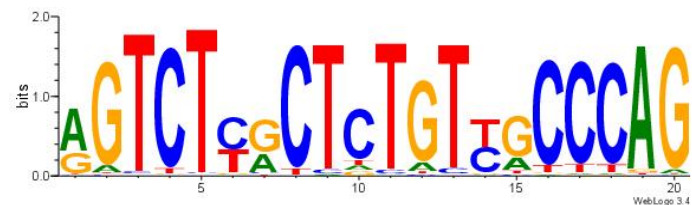
Alignment:

MGTCTMKCTCTGTKGCCAG
CTCTTGTTGCCAG-----

Original motif Consensus sequence: CTGGGCRACAGAGYRAGACY



Reverse complement motif Consensus sequence: MGTCTMKCTCTGTGKCCCAG

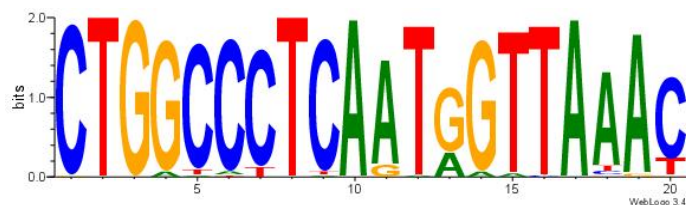


Dataset #: 1
Motif ID: 332
Motif name: Motif 332
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 14
Similarity score: 0.078748

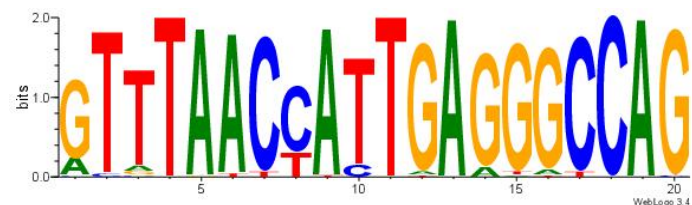
Alignment:

CTGGCCCTCAATGGTTAAAC
CTGGGCAACAAGAG-----

Original motif Consensus sequence: CTGGCCCTCAATGGTTAAAC



Reverse complement motif Consensus sequence: GTTTAACATTGAGGGCCAG

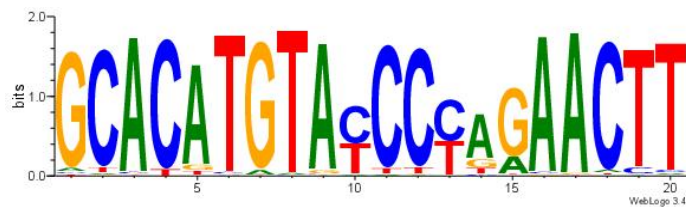


Dataset #: 1
 Motif ID: 225
 Motif name: Motif 225
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 6
 Number of overlap: 14
 Similarity score: 0.0800399

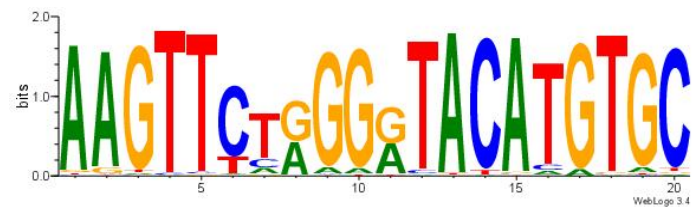
Alignment:

AAGTTCTKGGKTACATGTGC
 -----CTGGGCAACAAGAG-

Original motif Consensus sequence: GCACATGTAYCCYAGAACTT



Reverse complement motif Consensus sequence: AAGTTCTKGGKTACATGTGC

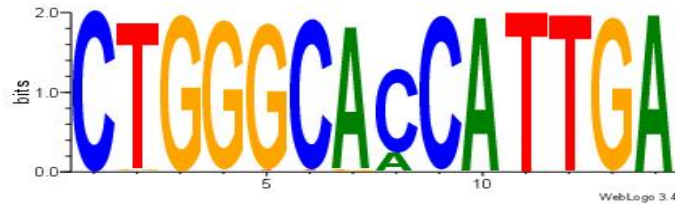


Dataset #: 1
 Motif ID: 147
 Motif name: Motif 147
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1

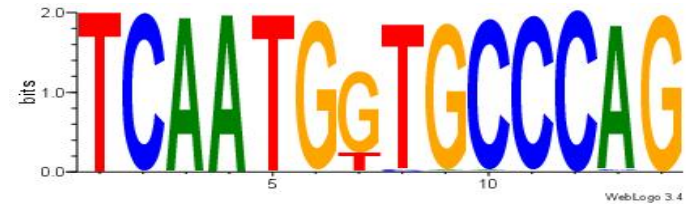
Number of overlap: 14
Similarity score: 0.0850974

Alignment:
CTGGGCACCATTGA
CTGGGCAACAAGAG

Original motif Consensus sequence: CTGGGCACCATTGA

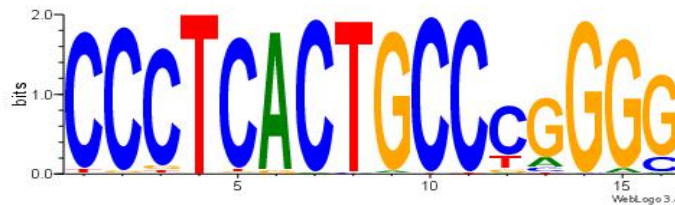


Reverse complement motif Consensus sequence: TCAATGGTGCCCA

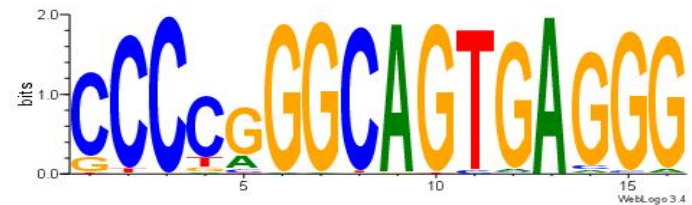


Dataset #: 1 Motif ID: 136 Motif name: Motif 136

Original motif Consensus sequence: CCCTACTGCCGGGG



Reverse complement motif Consensus sequence: CCGGGCAGTGAGGG



Best Matches for Motif ID 136 (Highest to Lowest)

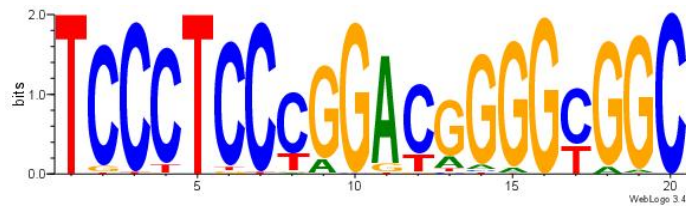
Dataset #: 1
Motif ID: 155
Motif name: Motif 155
Matching format of first motif: Reverse Complement

Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 4
 Number of overlap: 16
 Similarity score: 0.0741545

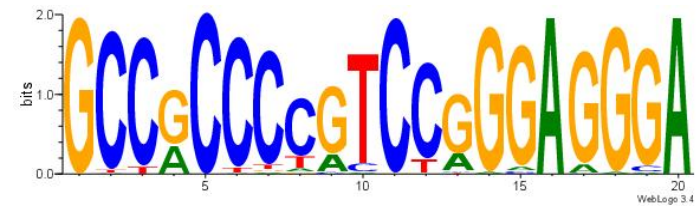
Alignment:

GCKCCCCGTCCGGGAGGGA
 ---CCCCGGGCAGTGAGGG-

Original motif Consensus sequence: TCCCTCCCGGACGGGGYGGC



Reverse complement motif Consensus sequence: GCKCCCCGTCCGGGAGGGA

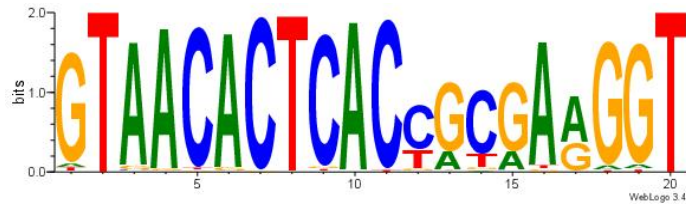


Dataset #: 1
 Motif ID: 201
 Motif name: Motif 201
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 16
 Similarity score: 0.0805996

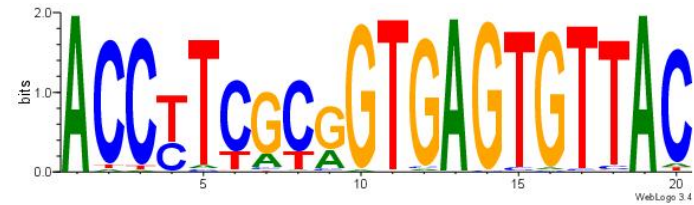
Alignment:

GTAACACTCACCGCGARGGT
----CCCTCACTGCCCCGGG

Original motif Consensus sequence: GTAACACTCACCGCGARGGT



Reverse complement motif Consensus sequence:
ACCKTCGCGGTGAGTGTTAC

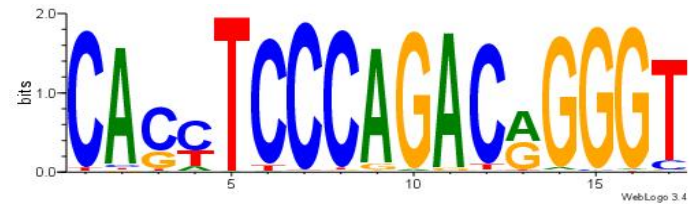
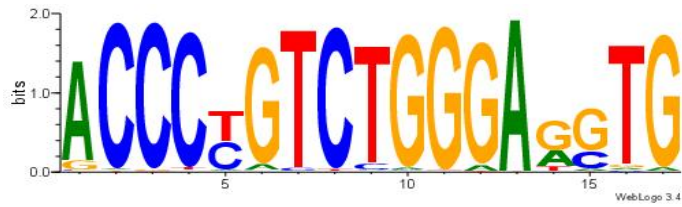


Dataset #: 1
Motif ID: 95
Motif name: Motif 95
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 16
Similarity score: 0.090189

Alignment:
ACCCYGTCTGGGAGGTG
-CCCCGGCAGTGAGGG

Original motif Consensus sequence: ACCCYGTCTGGGAGGTG

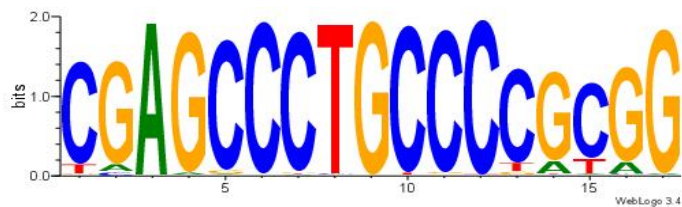
Reverse complement motif Consensus sequence:
CACCTCCCAGACMGGGT



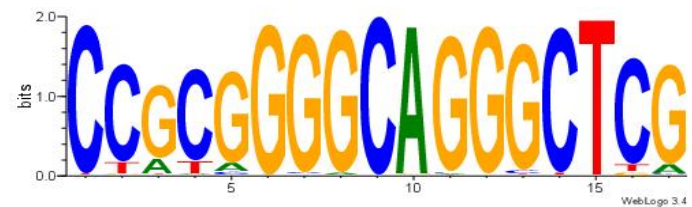
Dataset #: 1
 Motif ID: 78
 Motif name: Motif 78
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 16
 Similarity score: 0.0920974

Alignment:
 CCGCGGGGCAGGGCTCG
 -CCCCGGGCAGTGAGGG

Original motif Consensus sequence: CGAGCCCTGCCCGCGG



Reverse complement motif Consensus sequence: CCGCGGGGCAGGGCTCG



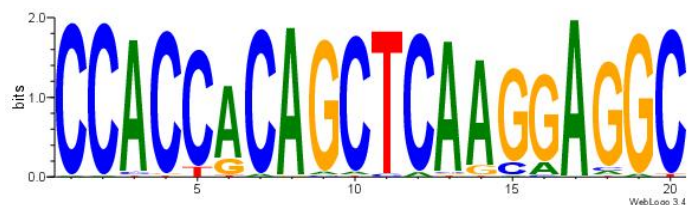
Dataset #: 1

Motif ID: 331
 Motif name: Motif 331
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 5
 Number of overlap: 16
 Similarity score: 0.0934462

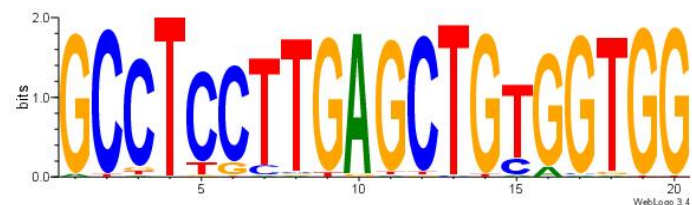
Alignment:

CCACCACAGCTCAAGGAGGC
 CCCTCACTGCCCGGGG-----

Original motif Consensus sequence: CCACCACAGCTCAAGGAGGC

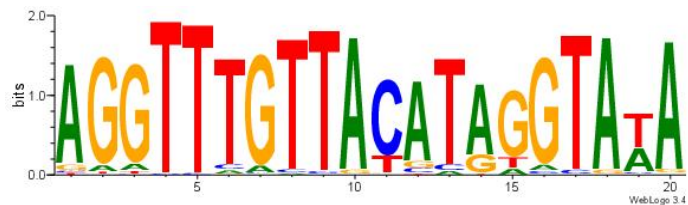


Reverse complement motif Consensus sequence: GCCTCCTTGAGCTGTGGTGG

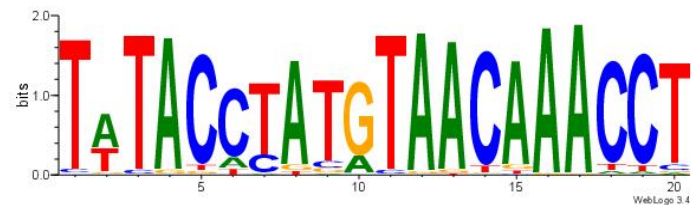


Dataset #: 1 Motif ID: 137 Motif name: Motif 137

Original motif Consensus sequence: AGGTTTGTTACATAGGTAWA



Reverse complement motif Consensus sequence: TWTACCTATGTAACAAACCT



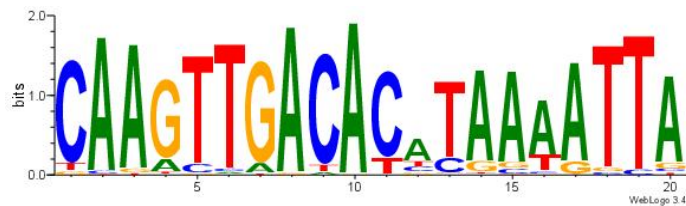
Best Matches for Motif ID 137 (Highest to Lowest)

Dataset #: 1
Motif ID: 357
Motif name: Motif 357
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 20
Similarity score: 0.114314

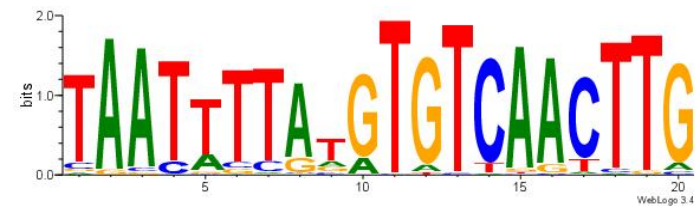
Alignment:

```
TAATTTTATGTGTCAACTTG  
TWTACCTATGTAACAAACCT
```

Original motif Consensus sequence: CAAGTTGACACATAAAATTA



Reverse complement motif Consensus sequence:
TAATTTTATGTGTCAACTTG



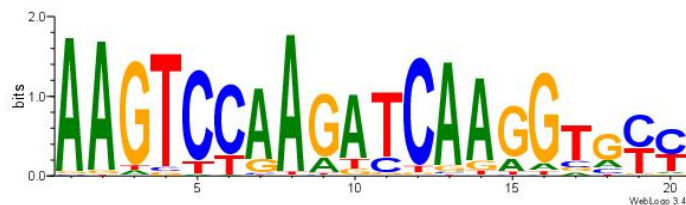
Dataset #: 1
Motif ID: 119
Motif name: Motif 119
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif

Direction: Backward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.118814

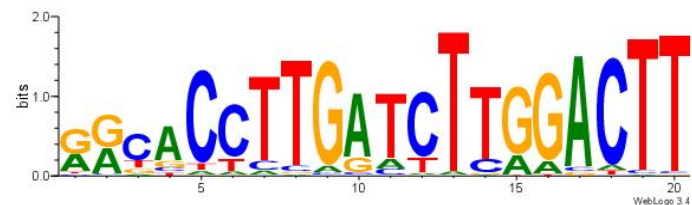
Alignment:

AAGTCCAAGATCAAGGTGY
 AGGTTTGTACATAGGTAWA

Original motif Consensus sequence: AAGTCCAAGATCAAGGTGY



Reverse complement motif Consensus sequence: KKCACCTTGATCTGGACTT

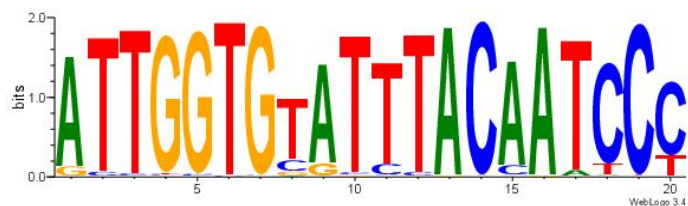


Dataset #: 1
 Motif ID: 106
 Motif name: Motif 106
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.120138

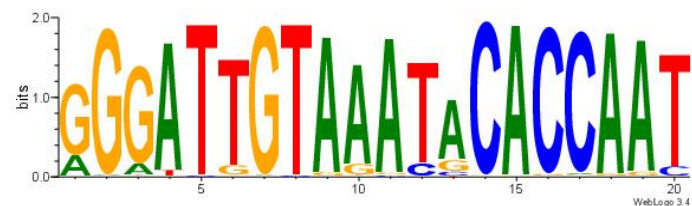
Alignment:

GGGATTGTAATAACCAAT
 AGGTTTGTACATAGGTAWA

Original motif Consensus sequence: ATTGGTGTATTACAATCCC



Reverse complement motif Consensus sequence: GGGATTGTAAATACACCAAT

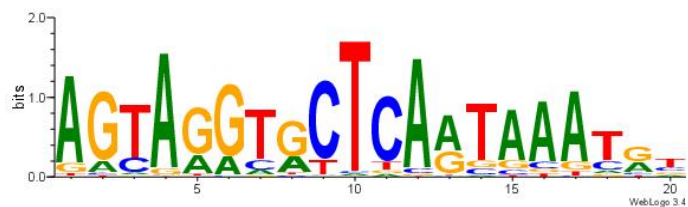


Dataset #: 1
Motif ID: 86
Motif name: Motif 86
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 20
Similarity score: 0.120421

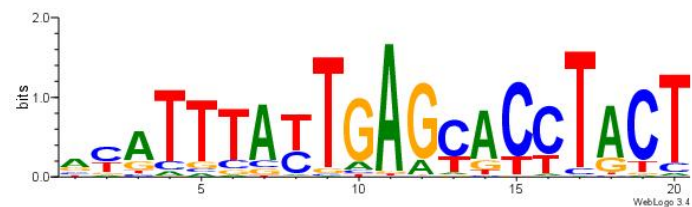
Alignment:

VMATTTAKTGAGCACCTACT
AGGTTTGTTACATAGGTAWA

Original motif Consensus sequence: AGTAGGTGCTCARTAAATRB



Reverse complement motif Consensus sequence: VMATTTAKTGAGCACCTACT

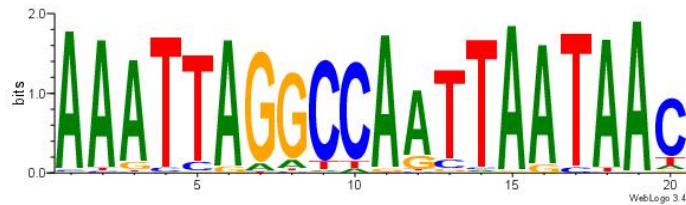


Dataset #: 1
 Motif ID: 308
 Motif name: Motif 308
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.122062

Alignment:

GTTATTAATTGGCCTAATTT
 TWTACCTATGTAACAAACCT

Original motif Consensus sequence: AAATTAGGCCAATTAATAAC



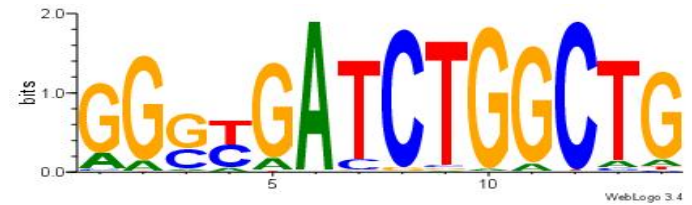
Reverse complement motif Consensus sequence: GTTATTAATTGGCCTAATTT



Dataset #: 1 Motif ID: 138 Motif name: Motif 138

Original motif Consensus sequence: CAGCCAGATCRSCC

Reverse complement motif Consensus sequence: GSKGATCTGGCT

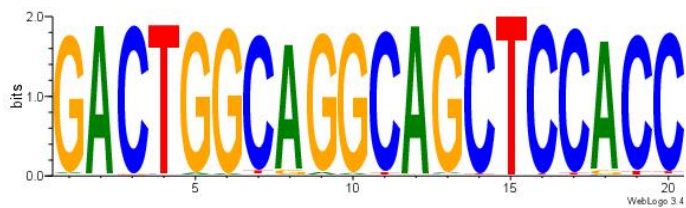


Best Matches for Motif ID 138 (Highest to Lowest)

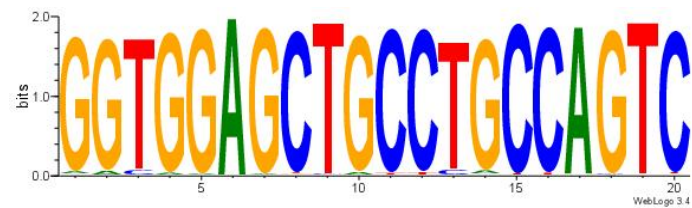
Dataset #: 1
 Motif ID: 52
 Motif name: Motif 52
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 7
 Number of overlap: 14
 Similarity score: 0.0576267

Alignment:
 GGTGGAGCTGCCAGTC
 GSKGATCTGGCTG-----

Original motif Consensus sequence: GACTGGCAGGCAGCTCCACC



Reverse complement motif Consensus sequence: GGTGGAGCTGCCAGTC

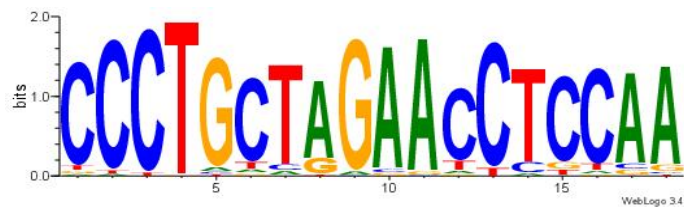


Dataset #: 1
 Motif ID: 299
 Motif name: Motif 299
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 14
 Similarity score: 0.0761753

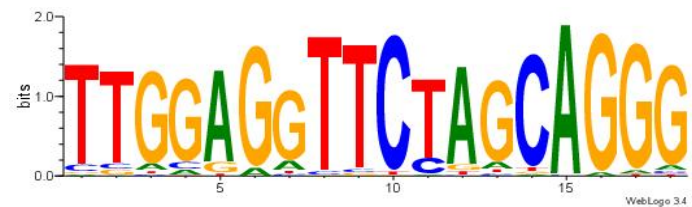
Alignment:

TTGGAGGTTCTAGCAGGG
 --GSKGATCTGGCTG--

Original motif Consensus sequence: CCCTGCTAGAACCTCCAA



Reverse complement motif Consensus sequence: TTGGAGGTTCTAGCAGGG



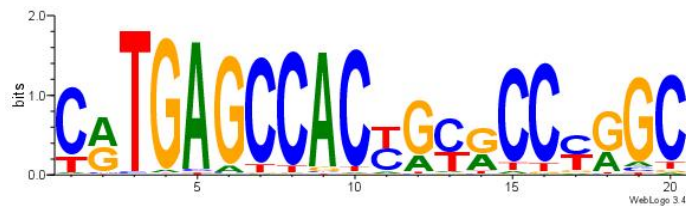
Dataset #: 1
 Motif ID: 56
 Motif name: Motif 56
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4

Number of overlap: 14
Similarity score: 0.0779469

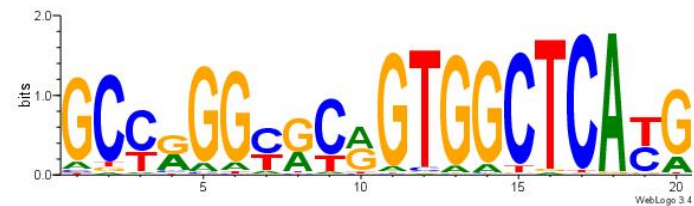
Alignment:

CRTGAGCCACYGYRCCYGGC
---CAGCCAGATCRSCC---

Original motif Consensus sequence: CRTGAGCCACYGYRCCYGGC



Reverse complement motif Consensus sequence:
GCCCKGGMKCMGTGGCTCAKG

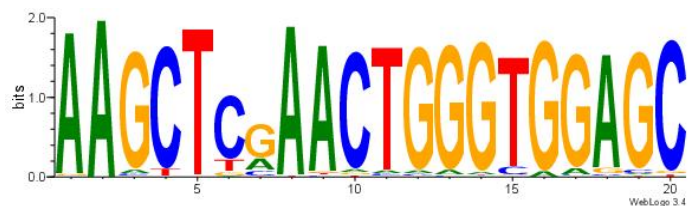


Dataset #: 1
Motif ID: 321
Motif name: Motif 321
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 3
Number of overlap: 14
Similarity score: 0.0788168

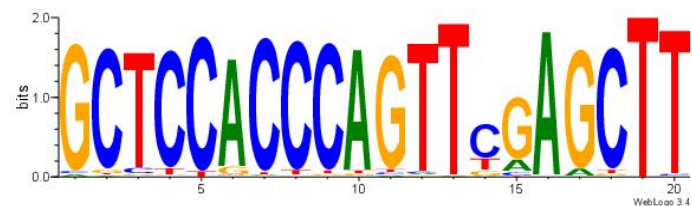
Alignment:

GCTCCACCCAGTTCGAGCTT
----CAGCCAGATCRSCC--

Original motif Consensus sequence: AAGCTCGAACTGGGTGGAGC



Reverse complement motif Consensus sequence: GCTCCACCCAGTTCGAGCTT

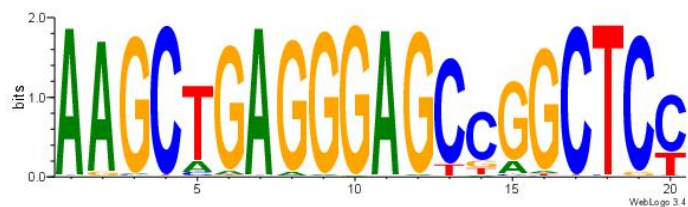


Dataset #: 1
Motif ID: 96
Motif name: Motif 96
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 2
Number of overlap: 14
Similarity score: 0.081782

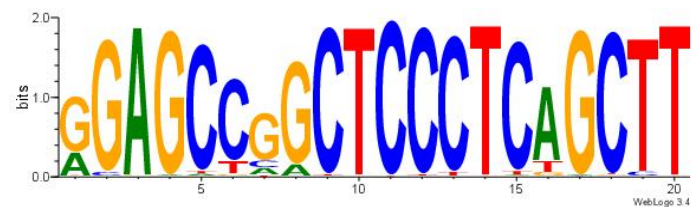
Alignment:

```
GGAGCCGGCTCCCTCAGCTT  
-----CAGCCAGATCRSCC-
```

Original motif Consensus sequence: AAGCTGAGGGAGCCGGCTCC

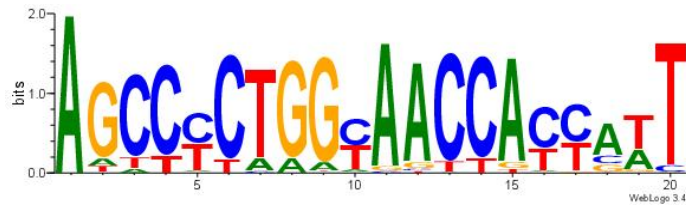


Reverse complement motif Consensus sequence: GGAGCCGGCTCCCTCAGCTT

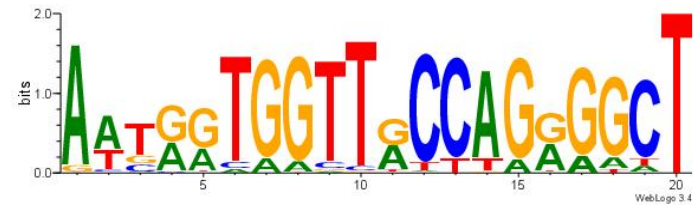


Dataset #: 1 Motif ID: 139 Motif name: Motif 139

Original motif Consensus sequence: AGCCYCTGGYAACCAYYAWT



Reverse complement motif Consensus sequence: AWTKKTGGTTKCCAGKGGCT



Best Matches for Motif ID 139 (Highest to Lowest)

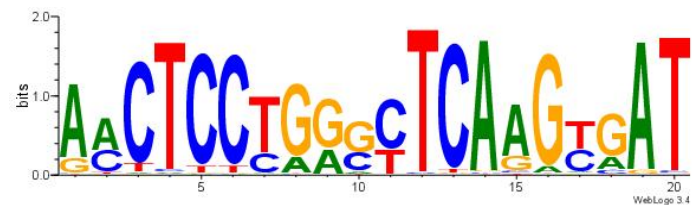
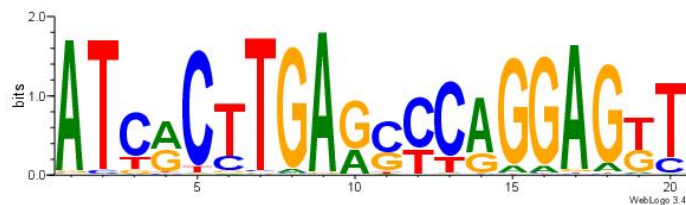
Dataset #:	1
Motif ID:	8
Motif name:	Motif 8
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	20
Similarity score:	0.087556

Alignment:

```
ATCRCTTGAGSYCAGGAGKT
AWTKKTGGTTKCCAGKGGCT
```

Original motif Consensus sequence: ATCRCTTGAGSYCAGGAGKT

Reverse complement motif Consensus sequence: ARCTCCTGKSCTCAAGKGAT

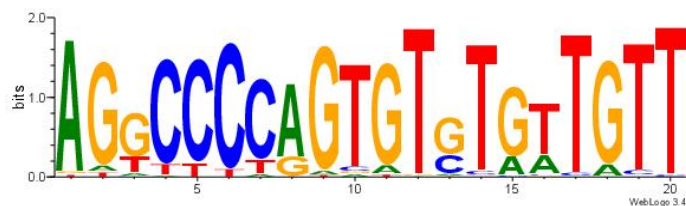


Dataset #: 1
 Motif ID: 176
 Motif name: Motif 176
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.0947311

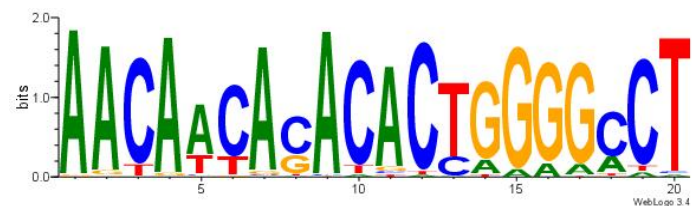
Alignment:

AGGCCCCAGTGTSTGTTGTT
 AGCCYCTGGYAACCAYYAWT

Original motif Consensus sequence: AGGCCCCAGTGTSTGTTGTT



Reverse complement motif Consensus sequence: AACACASACACTGGGGCCT



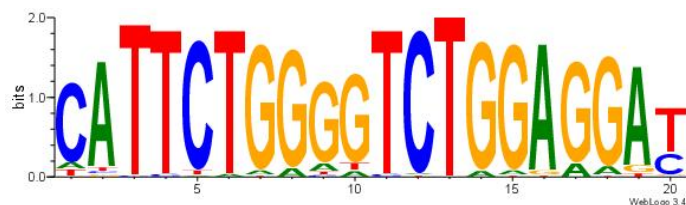
Dataset #: 1

Motif ID: 309
 Motif name: Motif 309
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.099271

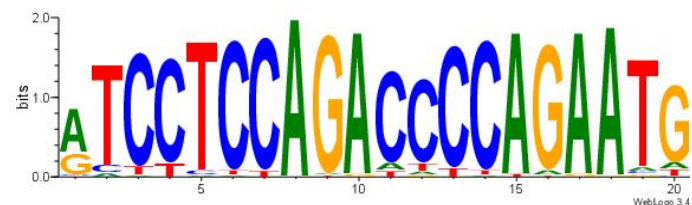
Alignment:

CATTCTGGGGTCTGGAGGAY
 AWTKKTGGTTKCCAGKGGCT

Original motif Consensus sequence: CATTCTGGGGTCTGGAGGAY



Reverse complement motif Consensus sequence: MTCCTCCAGACCCCAGAATG



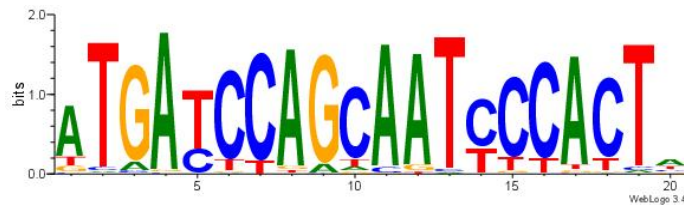
Dataset #: 1
 Motif ID: 115
 Motif name: Motif 115
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 20

Similarity score: 0.103788

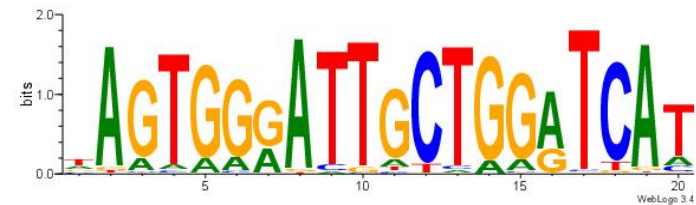
Alignment:

ATGATCCAGCAATYCCACTH
AGCCYCTGGYAACCAYYAWT

Original motif Consensus sequence: ATGATCCAGCAATYCCACTH



Reverse complement motif Consensus sequence:
HAGTGGKATTGCTGGATCAT



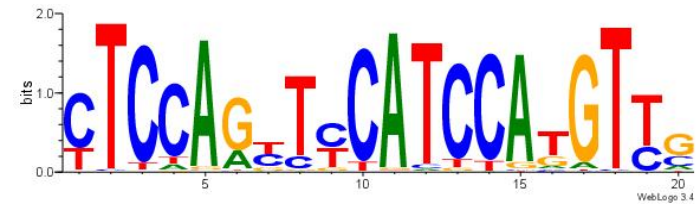
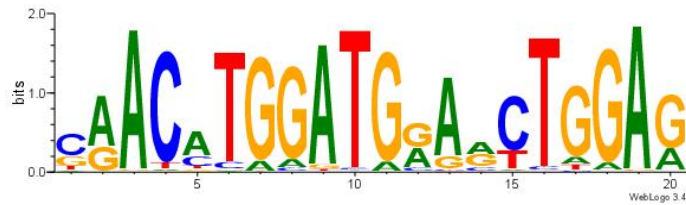
Dataset #: 1
Motif ID: 104
Motif name: Motif 104
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 20
Similarity score: 0.108741

Alignment:

CAACATGGATGRARCTGGAG
AWTKKTGGTTKCCAGKGGCT

Original motif Consensus sequence: CAACATGGATGRARCTGGAG

Reverse complement motif Consensus sequence:
CTCCAGKTCATCCATGTTG

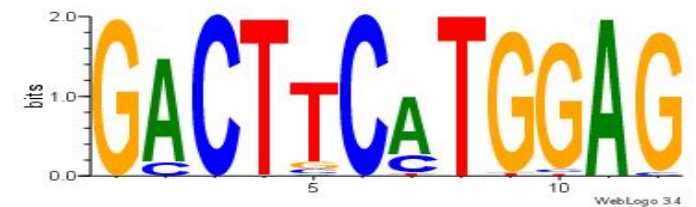


Dataset #: 1 Motif ID: 140 Motif name: Motif 140

Original motif Consensus sequence: CTCCATGAAGTC



Reverse complement motif Consensus sequence: GACTTCATGGAG



Best Matches for Motif ID 140 (Highest to Lowest)

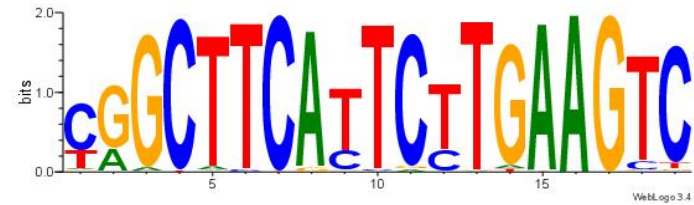
Dataset #:	1
Motif ID:	211
Motif name:	Motif 211
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	8
Number of overlap:	12
Similarity score:	0.0741011

Alignment:
GACTTCAAGAATGAAGCCG
GACTTCATGGAG-----

Original motif Consensus sequence: GACTTCAAGAATGAAGCCG



Reverse complement motif Consensus sequence: CGGCTTCATTCTGAAGTC

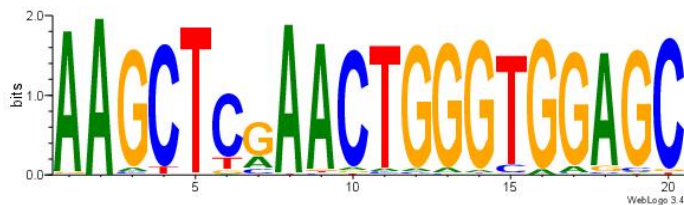


Dataset #: 1
Motif ID: 321
Motif name: Motif 321
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 8
Number of overlap: 12
Similarity score: 0.0805058

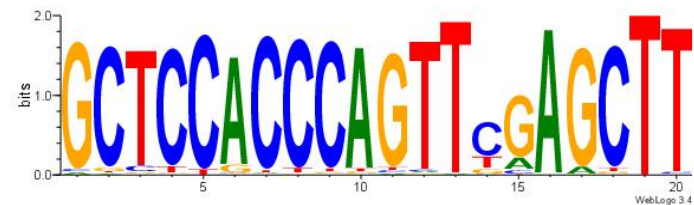
Alignment:

```
AAGCTCGAACTGGGTGGAGC  
-----GACTTCATGGAG--
```

Original motif Consensus sequence: AAGCTCGAACTGGGTGGAGC



Reverse complement motif Consensus sequence: GCTCCACCCAGTTCTGAGCTT

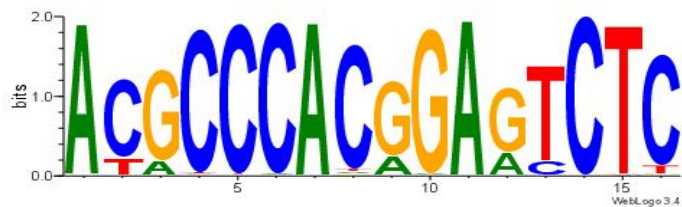


Dataset #: 1
 Motif ID: 33
 Motif name: Motif 33
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 12
 Similarity score: 0.0841075

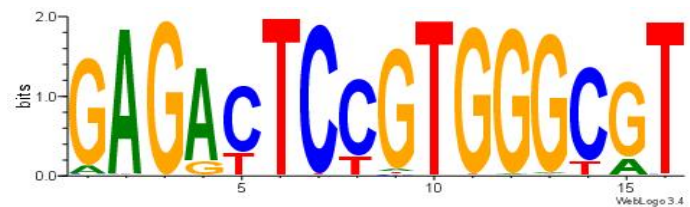
Alignment:

GAGACTCCGTGGGCGT
 --GACTTCATGGAG--

Original motif Consensus sequence: ACGCCACGGAGTCTC



Reverse complement motif Consensus sequence: GAGACTCCGTGGGCGT



Dataset #: 1
 Motif ID: 163
 Motif name: Motif 163
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2

Number of overlap: 12
Similarity score: 0.0844469

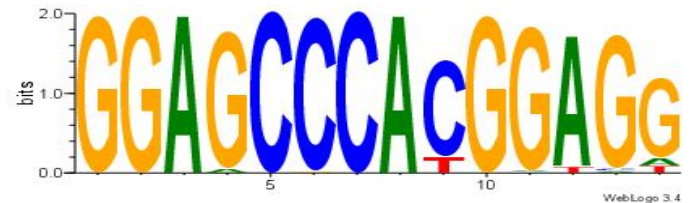
Alignment:

CCTCCGTGGGCTCC
-CTCCATGAAGTC-

Original motif Consensus sequence: CCTCCGTGGGCTCC



Reverse complement motif Consensus sequence: GGAGCCCACGGAG



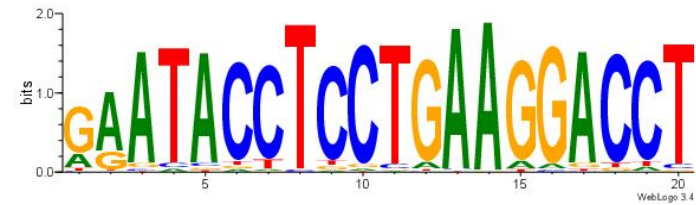
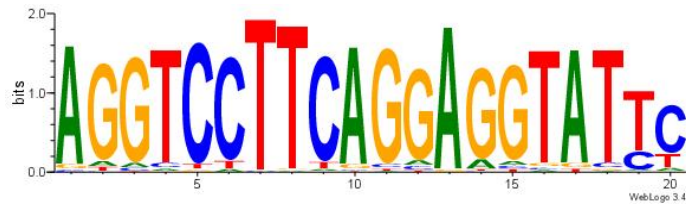
Dataset #: 1
Motif ID: 179
Motif name: Motif 179
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 6
Number of overlap: 12
Similarity score: 0.0846544

Alignment:

AGGTCCTCAGGAGGTATTC
-----CTCCATGAAGTC---

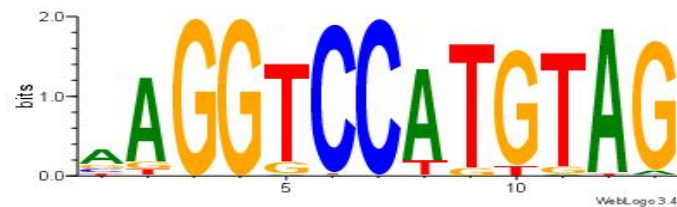
Original motif Consensus sequence: AGGTCCTCAGGAGGTATTC

Reverse complement motif Consensus sequence:
GAATACCTCCTGAAGGACCT

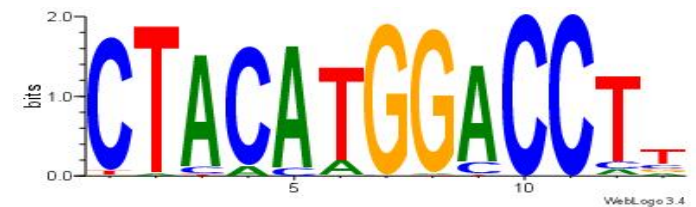


Dataset #: 1 Motif ID: 141 Motif name: Motif 141

Original motif Consensus sequence: AAGGTCCATGTAG



Reverse complement motif Consensus sequence: CTACATGGACCT

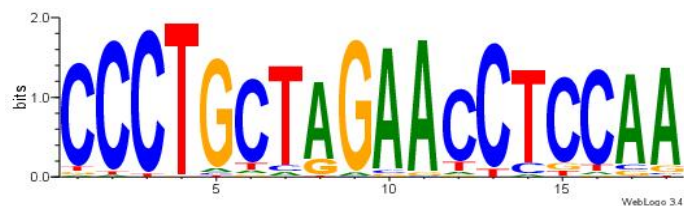


Best Matches for Motif ID 141 (Highest to Lowest)

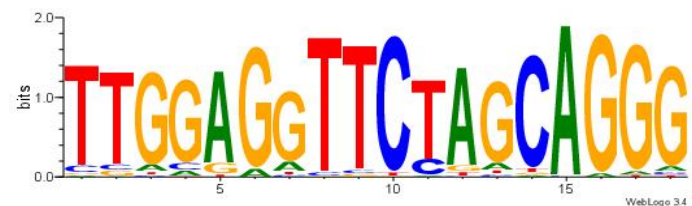
Dataset #:	1
Motif ID:	299
Motif name:	Motif 299
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	4
Number of overlap:	13
Similarity score:	0.0879979

Alignment:
 CCCTGCTAGAACCTCCA
 --CTACATGGACCTT---

Original motif Consensus sequence: CCCTGCTAGAACCTCCAA



Reverse complement motif Consensus sequence: TTGGAGTTCTAGCAGGG

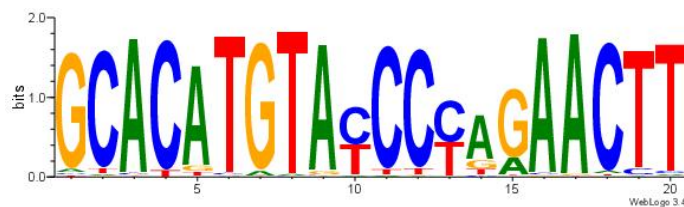


Dataset #: 1
Motif ID: 225
Motif name: Motif 225
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 8
Number of overlap: 13
Similarity score: 0.0909434

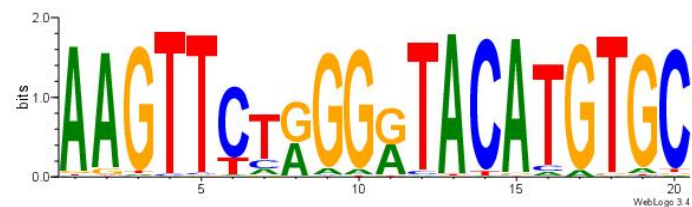
Alignment:

GCACATGTAYCCYAGAACTT
CTACATGGACCTT-----

Original motif Consensus sequence: GCACATGTAYCCYAGAACTT



Reverse complement motif Consensus sequence: AAGTTCTKGGKTACATGTGC

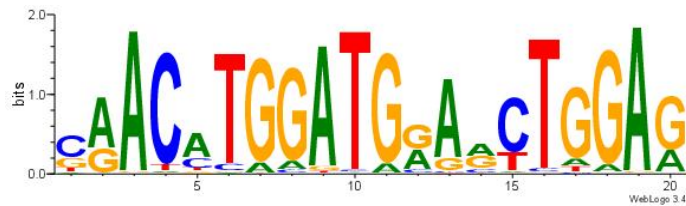


Dataset #: 1
 Motif ID: 104
 Motif name: Motif 104
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 4
 Number of overlap: 13
 Similarity score: 0.0949678

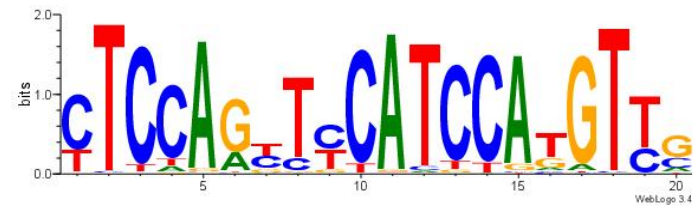
Alignment:

CTCCAGKTMCATCCATGTTG
 ----AAGGTCCATGTAG----

Original motif Consensus sequence: CAACATGGATGRARCTGGAG



Reverse complement motif Consensus sequence: CTCCAGKTMCATCCATGTTG



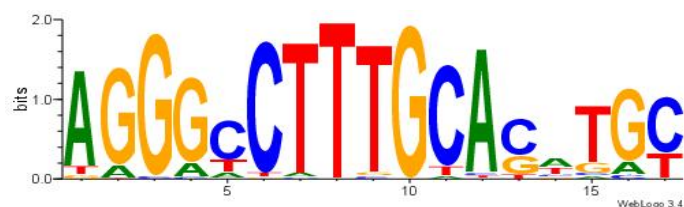
Dataset #: 1
 Motif ID: 322
 Motif name: Motif 322
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1

Number of overlap: 13
Similarity score: 0.101755

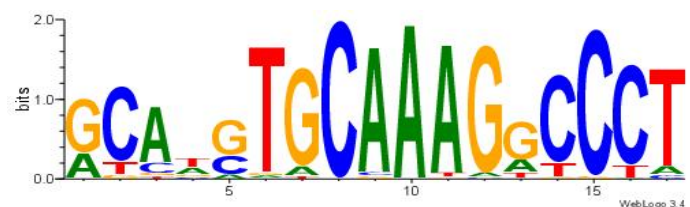
Alignment:

AGGGCCTTTGCASWTGC
AAGGTCCATGTAG----

Original motif Consensus sequence: AGGGCCTTTGCASWTGC



Reverse complement motif Consensus sequence: GCAWSTGCAAAGGCCCT

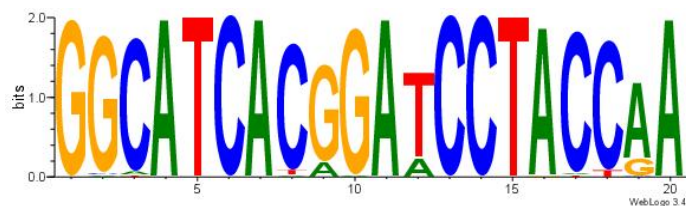


Dataset #: 1
Motif ID: 311
Motif name: Motif 311
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 3
Number of overlap: 13
Similarity score: 0.102169

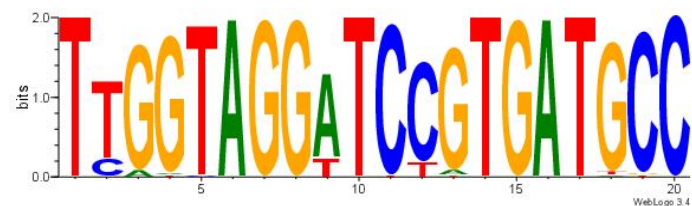
Alignment:

TTGGTAGGATCCGTGATGCC
-----AAGGTCCATGTAG--

Original motif Consensus sequence: GGCATCACGGATCCTACCAA



Reverse complement motif Consensus sequence: TTGGTAGGATCCGTGATGCC



Dataset #: 1 Motif ID: 142 Motif name: Motif 142

Original motif Consensus sequence: CAGATGTC



Reverse complement motif Consensus sequence: GACATCTG



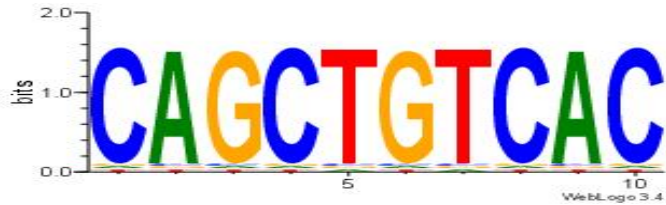
Best Matches for Motif ID 142 (Highest to Lowest)

Dataset #:	1
Motif ID:	272
Motif name:	Motif 272
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	3
Number of overlap:	8
Similarity score:	0.0284091

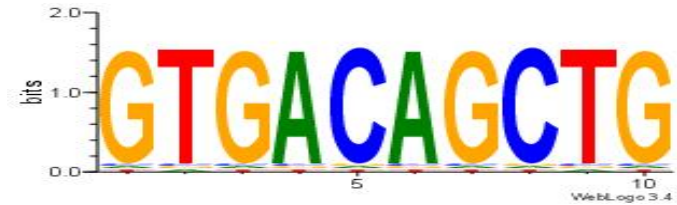
Alignment:

CAGCTGTCAC
CAGATGTC--

Original motif Consensus sequence: CAGCTGTCAC



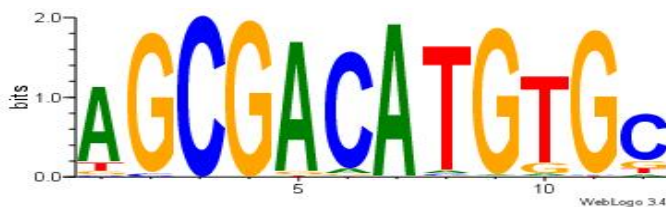
Reverse complement motif Consensus sequence: GTGACAGCTG



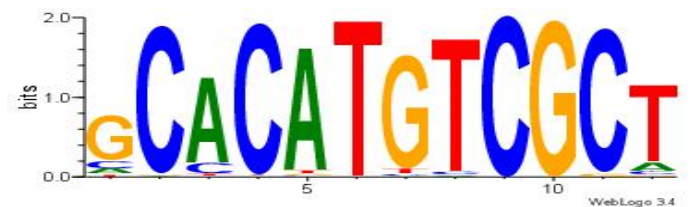
Dataset #: 1
Motif ID: 269
Motif name: Motif 269
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 2
Number of overlap: 8
Similarity score: 0.0407488

Alignment:
GCACATGTCGCT
-CAGATGTC---

Original motif Consensus sequence: AGCGACATGTGc



Reverse complement motif Consensus sequence: GCACATGTCGCT

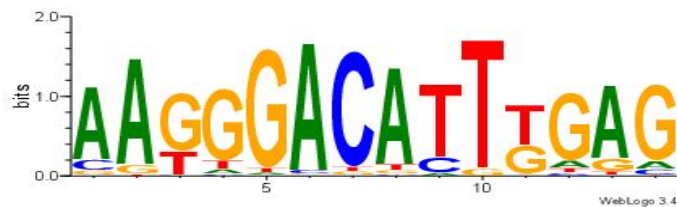


Dataset #: 1
Motif ID: 166
Motif name: Motif 166
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 5
Number of overlap: 8
Similarity score: 0.0533279

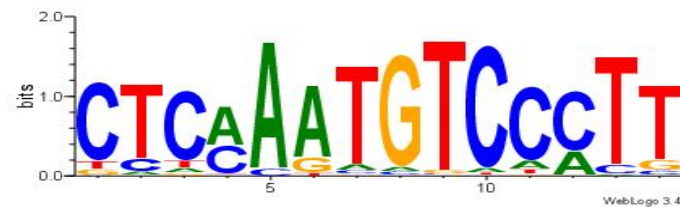
Alignment:

CTCRAATGTC CCTT
--CAGATGTC-----

Original motif Consensus sequence: AAGGGACATTKGAG



Reverse complement motif Consensus sequence: CTCRAATGTC CCTT



Dataset #: 1
Motif ID: 216
Motif name: Motif 216
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1

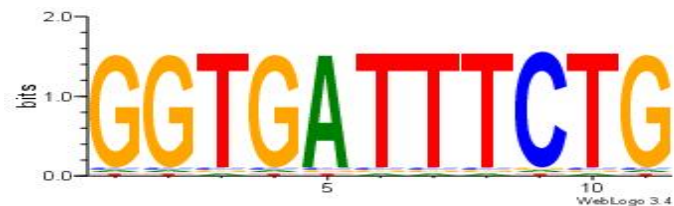
Number of overlap: 8
Similarity score: 0.0568181

Alignment:
GGTGATTTCTG
---GACATCTG

Original motif Consensus sequence: CAGAAATCACC



Reverse complement motif Consensus sequence: GGTGATTTCTG

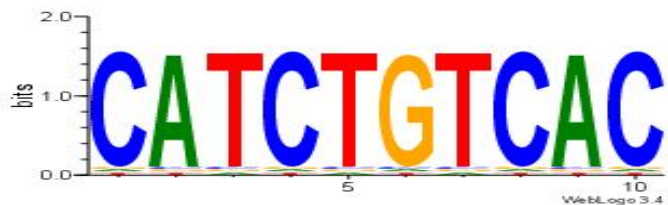


Dataset #: 1
Motif ID: 334
Motif name: Motif 334
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 8
Similarity score: 0.0568181

Alignment:
CATCTGTCAC
CAGATGTC--

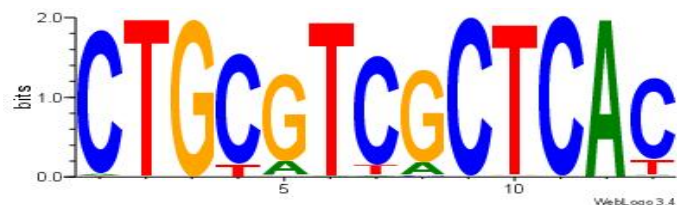
Original motif Consensus sequence: CATCTGTCAC

Reverse complement motif Consensus sequence: GTGACAGATG

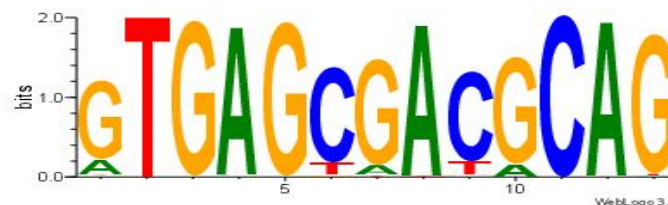


Dataset #: 1 Motif ID: 143 Motif name: Motif 143

Original motif Consensus sequence: CTGCGTCGCTCAC



Reverse complement motif Consensus sequence: GTGAGCGACGCA



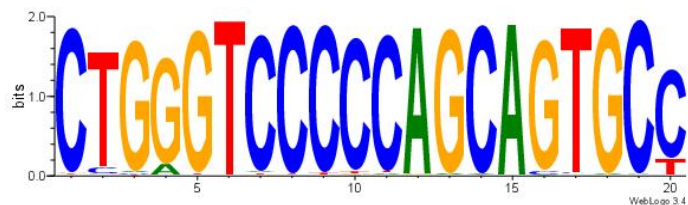
Best Matches for Motif ID 143 (Highest to Lowest)

Dataset #:	1
Motif ID:	84
Motif name:	Motif 84
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	8
Number of overlap:	13
Similarity score:	0.0703083

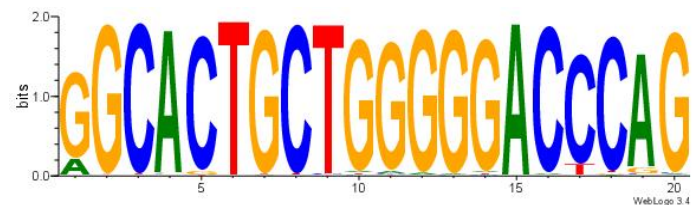
Alignment:

```
CTGGGTCCCCCAGCAGTGCC
CTGCGTCGCTCAC-----
```

Original motif Consensus sequence: CTGGGTCCCCCAGCAGTGCC



Reverse complement motif Consensus sequence: GGCAGTCTGGGGGACCCAG

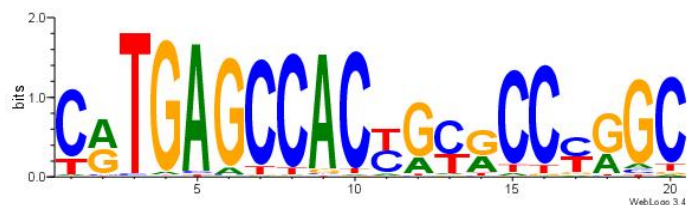


Dataset #: 1
Motif ID: 56
Motif name: Motif 56
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 7
Number of overlap: 13
Similarity score: 0.0789125

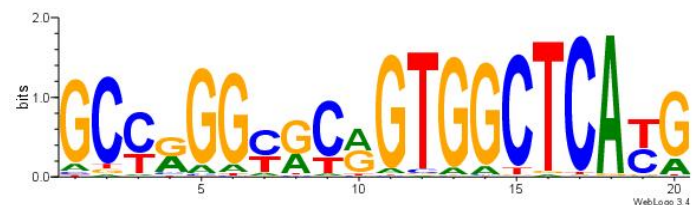
Alignment:

```
CRTGAGCCACYGYRCCYGGC  
-----GTGAGCGACGCAG-
```

Original motif Consensus sequence: CRTGAGCCACYGYRCCYGGC



Reverse complement motif Consensus sequence: GCKGGMKCMGTGGCTCAKG

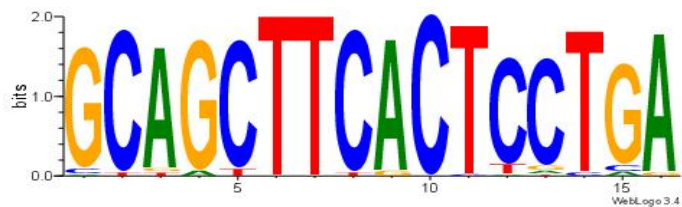


Dataset #: 1
 Motif ID: 246
 Motif name: Motif 246
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 13
 Similarity score: 0.0814278

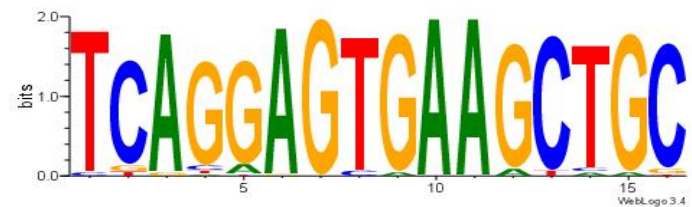
Alignment:

GCAGCTTCACTCCTGA
 -CTGCGTCGCTCAC--

Original motif Consensus sequence: GCAGCTTCACTCCTGA



Reverse complement motif Consensus sequence: TCAGGAGTGAAGCTGC



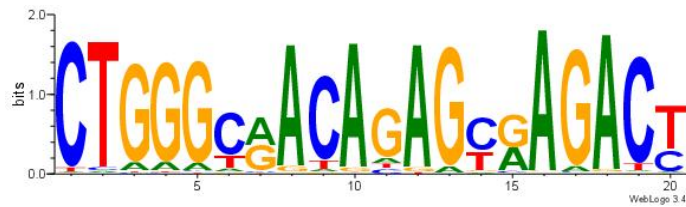
Dataset #: 1
 Motif ID: 29
 Motif name: Motif 29
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 8

Number of overlap: 13
Similarity score: 0.0830321

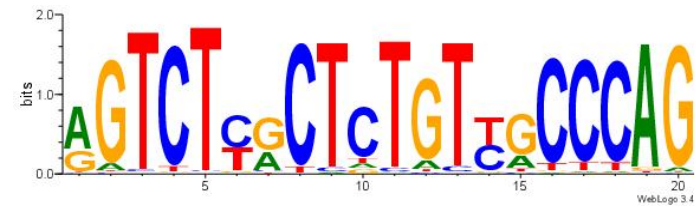
Alignment:

MGTCTMKCTCTGTKGCCCAG
CTGCGTCGCTCAC-----

Original motif Consensus sequence: CTGGGCRACAGAGYRAGACY



Reverse complement motif Consensus sequence:
MGTCTMKCTCTGTKGCCCAG



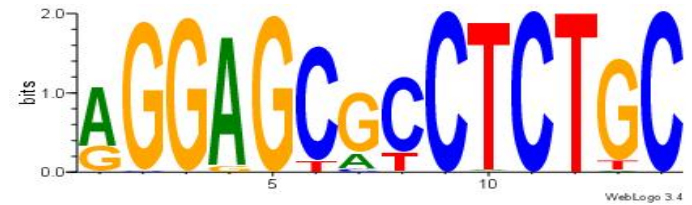
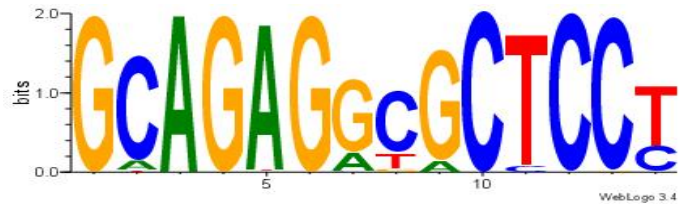
Dataset #: 1
Motif ID: 116
Motif name: Motif 116
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 2
Number of overlap: 13
Similarity score: 0.0837431

Alignment:

GCAGAGGCGCTCCT
-CTGCGTCGCTCAC

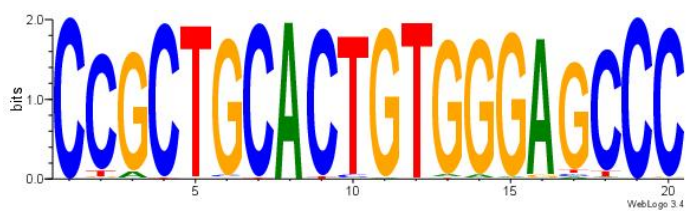
Original motif Consensus sequence: GCAGAGGCGCTCCT

Reverse complement motif Consensus sequence: AGGAGCGCCTCTG

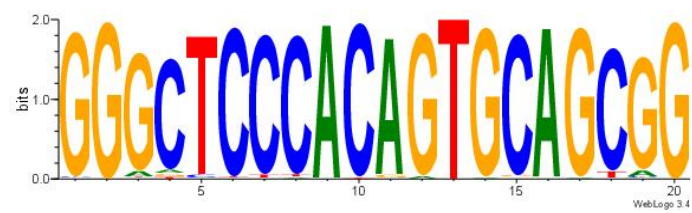


Dataset #: 1 Motif ID: 144 Motif name: Motif 144

Original motif Consensus sequence: CCGCTGCACTGTGGGAGCCC



Reverse complement motif Consensus sequence: GGGCTCCCACAGTGCAGCGG



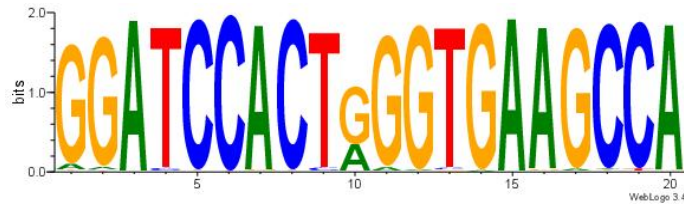
Best Matches for Motif ID 144 (Highest to Lowest)

Dataset #:	1
Motif ID:	61
Motif name:	Motif 61
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	20
Similarity score:	0.120211

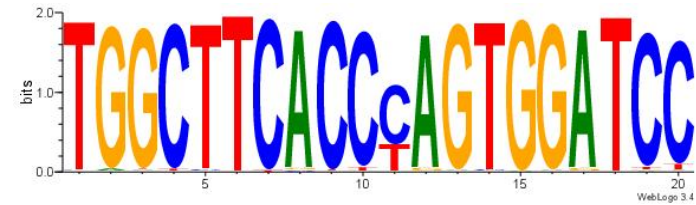
Alignment:

GGATCCACTGGGTGAAGCCA
GGGCTCCCACAGTGCAGCGG

Original motif Consensus sequence: GGATCCACTGGGTGAAGCCA



Reverse complement motif Consensus sequence:
TGGCTTCAACCAGTGGATCC

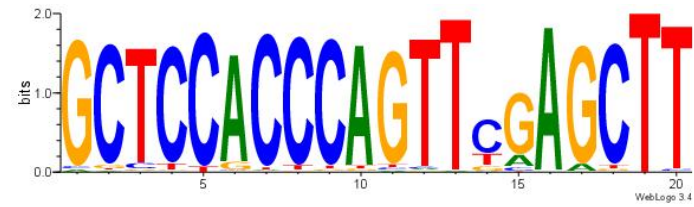
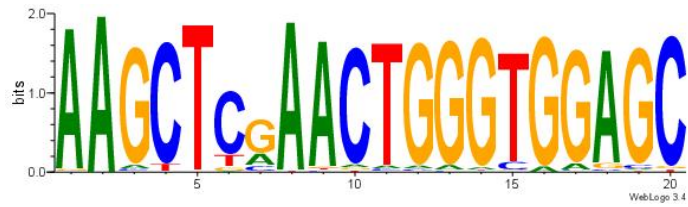


Dataset #: 1
Motif ID: 321
Motif name: Motif 321
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 20
Similarity score: 0.121341

Alignment:
AAGCTCGAACTGGGTGGAGC
GGGCTCCCACAGTGCAGCGG

Original motif Consensus sequence: AAGCTCGAACTGGGTGGAGC

Reverse complement motif Consensus sequence:
GCTCCACCCAGTTCGAGCTT

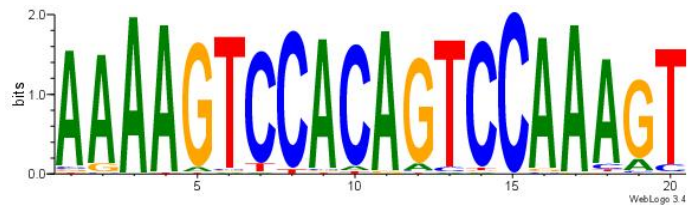


Dataset #: 1
 Motif ID: 171
 Motif name: Motif 171
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.121783

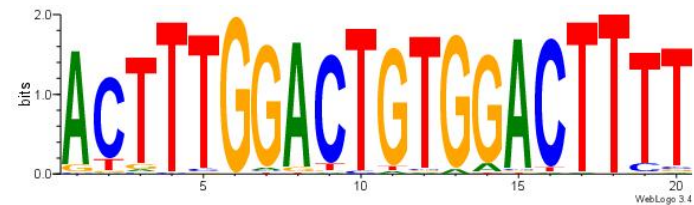
Alignment:

AAAAGTCCACAGTCCAAAGT
 GGGCTCCACAGTGCAGCGG

Original motif Consensus sequence: AAAAGTCCACAGTCCAAAGT



Reverse complement motif Consensus sequence: ACTTTGGACTGTGGACTTTT



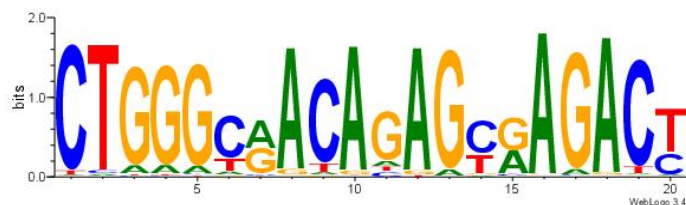
Dataset #: 1

Motif ID: 29
 Motif name: Motif 29
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.123294

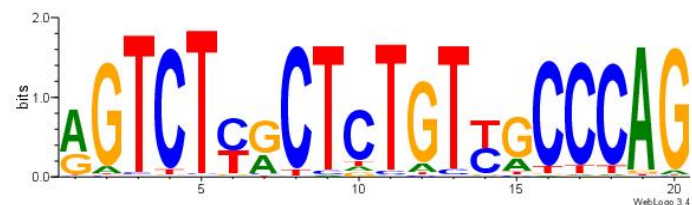
Alignment:

MGTCTMKCTCTGTKGCCCAG
 GGGCTCCACAGTGCAGCGG

Original motif Consensus sequence: CTGGGCRACAGAGYRAGACY



Reverse complement motif Consensus sequence: MGTCTMKCTCTGTKGCCCAG



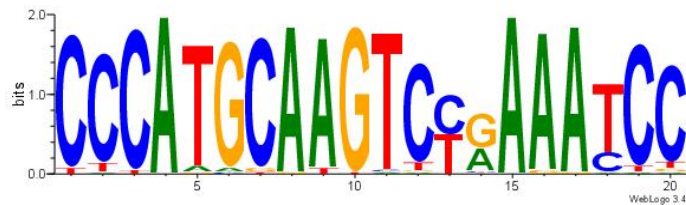
Dataset #: 1
 Motif ID: 310
 Motif name: Motif 310
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 20

Similarity score: 0.123788

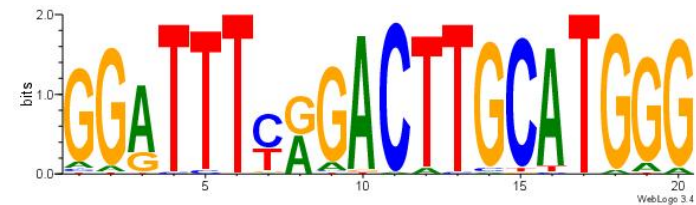
Alignment:

CCCATGCAAGTCYRAAATCC
CCGCTGCACTGTGGGAGCCC

Original motif Consensus sequence: CCCATGCAAGTCYRAAATCC

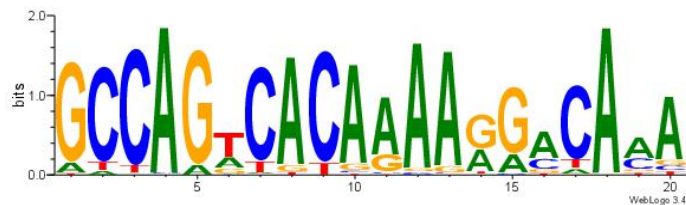


Reverse complement motif Consensus sequence: GGATTTMKGACTTGCATGGG

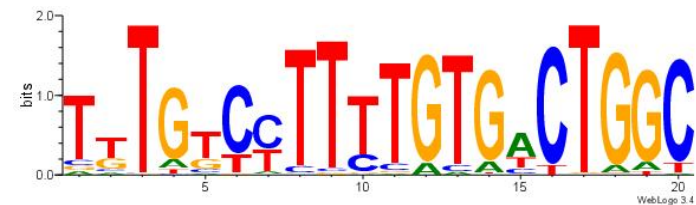


Dataset #: 1 Motif ID: 145 Motif name: Motif 145

Original motif Consensus sequence: GCCAGTCACAAAARGACAMA



Reverse complement motif Consensus sequence: TYTGCMTTTTGTGACTGGC



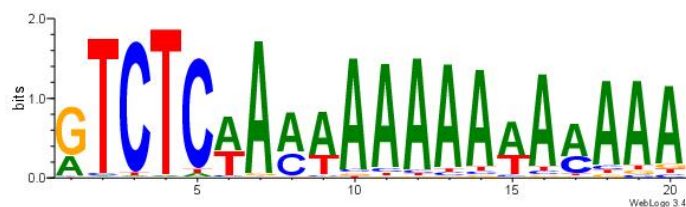
Best Matches for Motif ID 145 (Highest to Lowest)

Dataset #:	1
Motif ID:	7
Motif name:	Motif 7
Matching format of first motif:	Original Motif

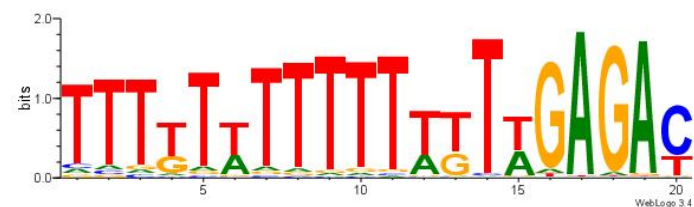
Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.0929275

Alignment:
 GTCTCWAMAAAAAWAMAAA
 GCCAGTCACAAAARGACAMA

Original motif Consensus sequence: GTCTCWAMAAAAAWAMAAA



Reverse complement motif Consensus sequence: TTTYTWTTTTTWTGAGAC

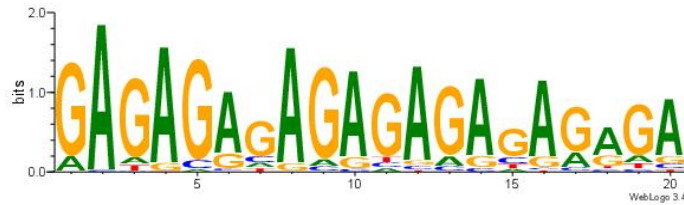


Dataset #: 1
 Motif ID: 109
 Motif name: Motif 109
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.0984643

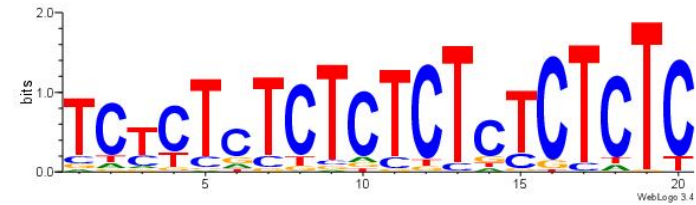
Alignment:

GAGAGAGAGAGAGAGAGA
GCCAGTCACAAAARGACAMA

Original motif Consensus sequence: GAGAGAGAGAGAGAGAGA



Reverse complement motif Consensus sequence:
TCTCTCTCTCTCTCTCTC



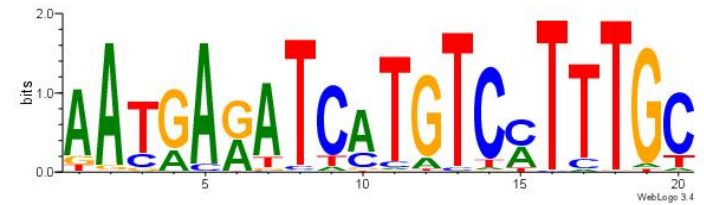
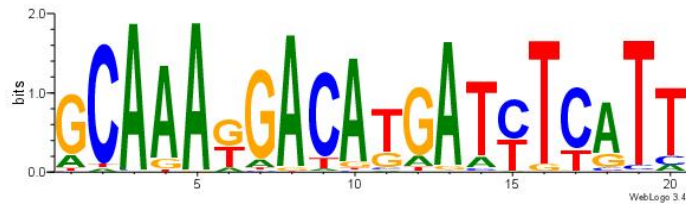
Dataset #: 1
Motif ID: 99
Motif name: Motif 99
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 20
Similarity score: 0.110928

Alignment:

GCAAAGACATGATYTCATT
GCCAGTCACAAAARGACAMA

Original motif Consensus sequence: GCAAAGACATGATYTCATT

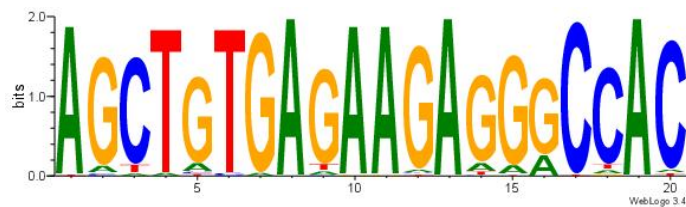
Reverse complement motif Consensus sequence:
AATGAKATCATGTCYTTTGC



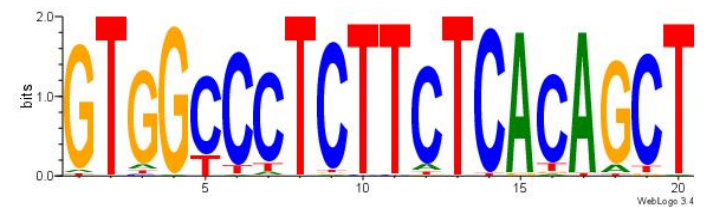
Dataset #: 1
 Motif ID: 294
 Motif name: Motif 294
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.114037

Alignment:
 AGCTGTGAGAAGAGGGCCAC
 GCCAGTCACAAAARGACAMA

Original motif Consensus sequence: AGCTGTGAGAAGAGGGCCAC



Reverse complement motif Consensus sequence:
 GTGGCCCTCTTCTCACAGCT



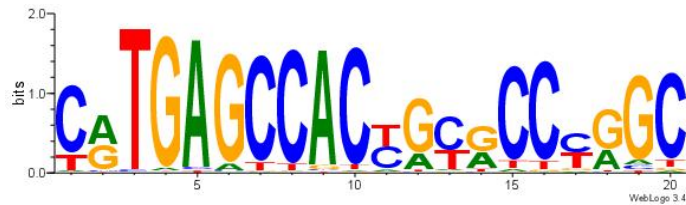
Dataset #: 1

Motif ID: 56
 Motif name: Motif 56
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.115384

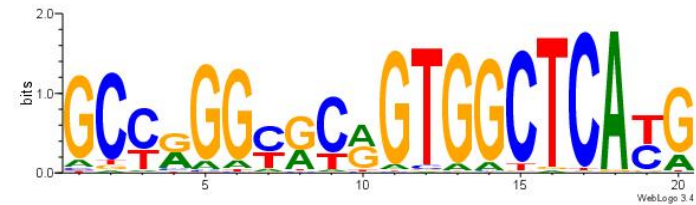
Alignment:

GCCKGGMKCMGTGGCTCAKG
 GCCAGTCACAAAARGACAMA

Original motif Consensus sequence: CRTGAGCCACYGYRCCYGGC



Reverse complement motif Consensus sequence: GCCKGGMKCMGTGGCTCAKG

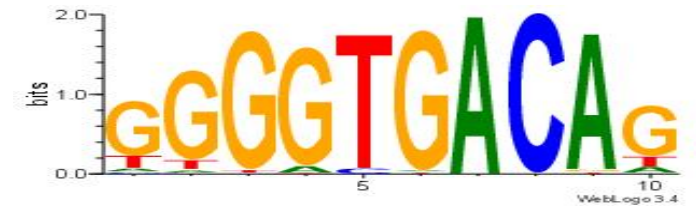


Dataset #: 1 Motif ID: 146 Motif name: Motif 146

Original motif Consensus sequence: CTGTCACCCC



Reverse complement motif Consensus sequence: GGGGTGACAG



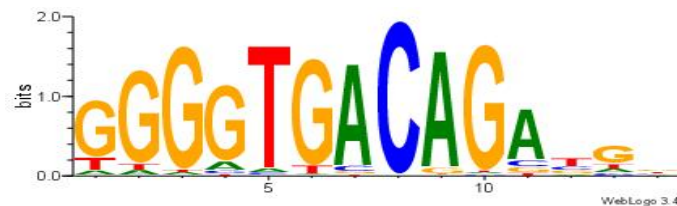
Best Matches for Motif ID 146 (Highest to Lowest)

Dataset #: 1
Motif ID: 1
Motif name: Motif 1
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 10
Similarity score: 0.00304976

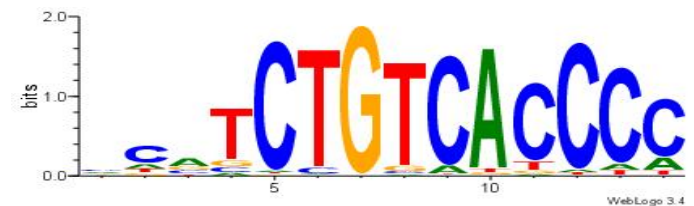
Alignment:

```
GGGGTGACAGABGB  
----GGGGTGACAG
```

Original motif Consensus sequence: GGGGTGACAGABGB



Reverse complement motif Consensus sequence: BCVTCTGTCACCC



Dataset #: 1
Motif ID: 209
Motif name: Motif 209
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif

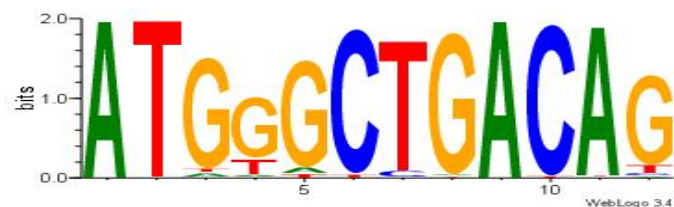
Direction: Forward
 Position number: 1
 Number of overlap: 10
 Similarity score: 0.021009

Alignment:
 CTGTCAGCCCAT
 CTGTCACCCC--

Original motif Consensus sequence: CTGTCAGCCCAT



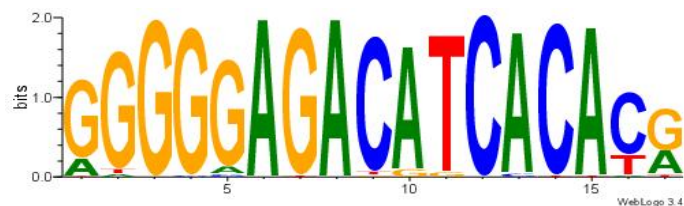
Reverse complement motif Consensus sequence: ATGGGCTGACAG



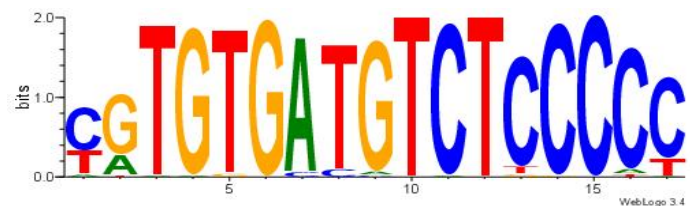
Dataset #: 1
 Motif ID: 279
 Motif name: Motif 279
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 7
 Number of overlap: 10
 Similarity score: 0.0415588

Alignment:
 MGTGTGATGTCTCCCCC
 -----CTGTCACCCC-

Original motif Consensus sequence: GGGGGAGACATCACACR



Reverse complement motif Consensus sequence: MGTGTGATGTCTCCCC

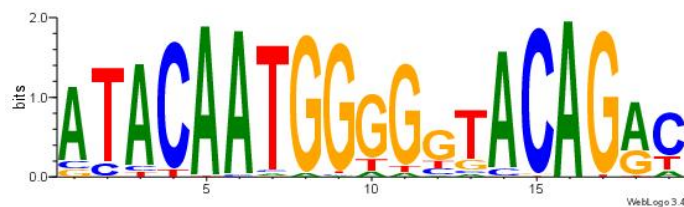


Dataset #: 1
Motif ID: 193
Motif name: Motif 193
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 3
Number of overlap: 10
Similarity score: 0.0448872

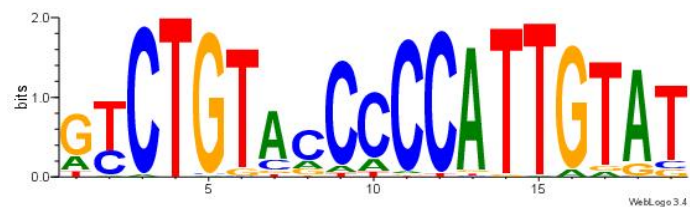
Alignment:

```
ATACAATGGGGGTACAGRC  
-----GGGGTGACAG--
```

Original motif Consensus sequence: ATACAATGGGGGTACAGRC



Reverse complement motif Consensus sequence: GKCTGTACCCCATTTGTAT

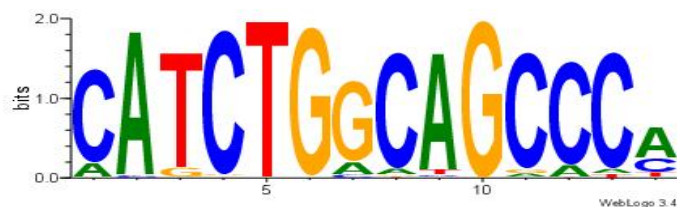


Dataset #: 1
 Motif ID: 205
 Motif name: Motif 205
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 10
 Similarity score: 0.0451314

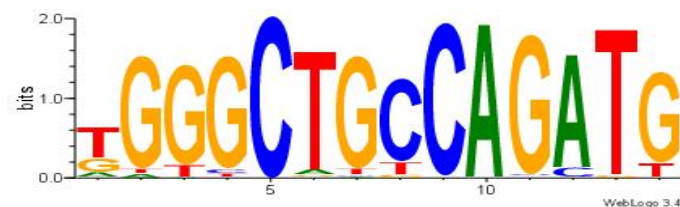
Alignment:

TGGGCTGCCAGATG
 -GGGGTGACAG---

Original motif Consensus sequence: CATCTGGCAGCCCA

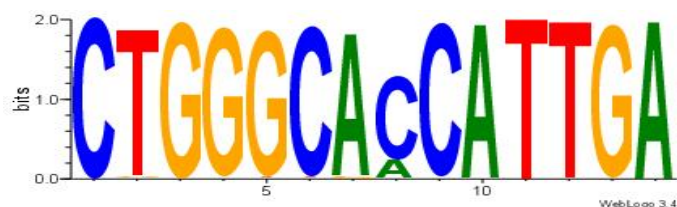


Reverse complement motif Consensus sequence: TGGGCTGCCAGATG

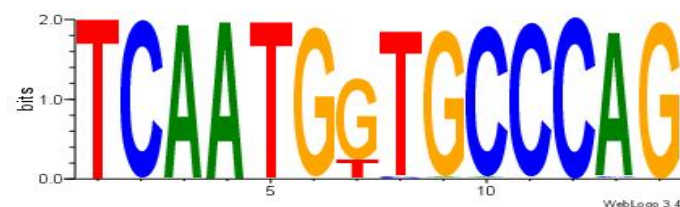


Dataset #: 1 Motif ID: 147 Motif name: Motif 147

Original motif Consensus sequence: CTGGGCACCATTGA



Reverse complement motif Consensus sequence: TCAATGGTGCCCAAG



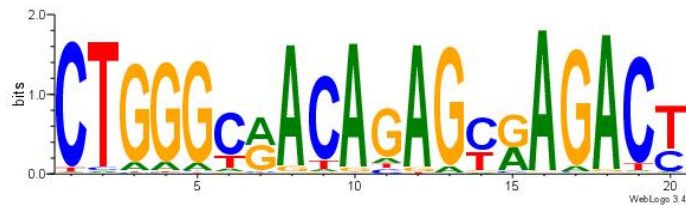
Best Matches for Motif ID 147 (Highest to Lowest)

Dataset #: 1
Motif ID: 29
Motif name: Motif 29
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 7
Number of overlap: 14
Similarity score: 0.0836978

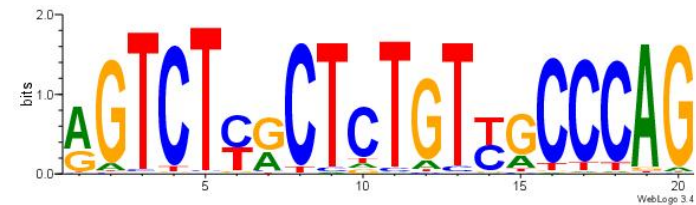
Alignment:

```
MGTCCTMKCTCTGTKGCCAG  
-----TCAATGGTGCCAG
```

Original motif Consensus sequence: CTGGGCRACAGAGYRAGACY



Reverse complement motif Consensus sequence: MGTCCTMKCTCTGTKGCCAG



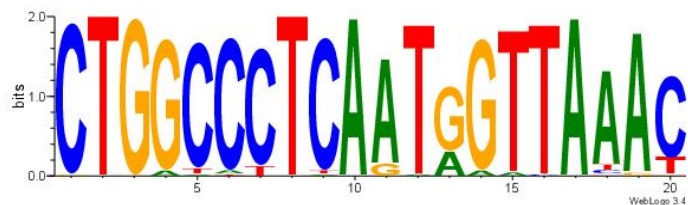
Dataset #: 1
Motif ID: 332
Motif name: Motif 332
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement

Direction: Backward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0.088413

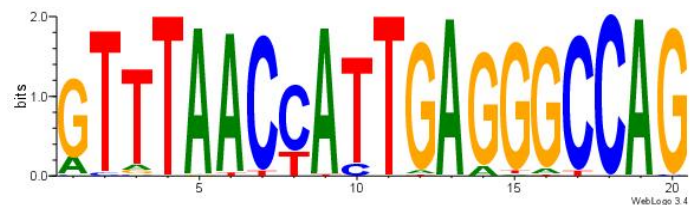
Alignment:

GTTTAACCATTTGAGGGCCAG
 -----TCAATGGTGCCCAG

Original motif Consensus sequence: CTGGCCCTCAATGGTTAAAC



Reverse complement motif Consensus sequence: GTTTAACCATTTGAGGGCCAG

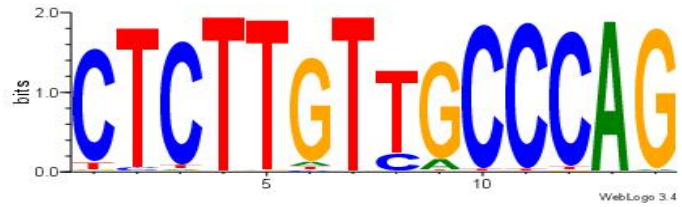


Dataset #: 1
 Motif ID: 135
 Motif name: Motif 135
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0.0903886

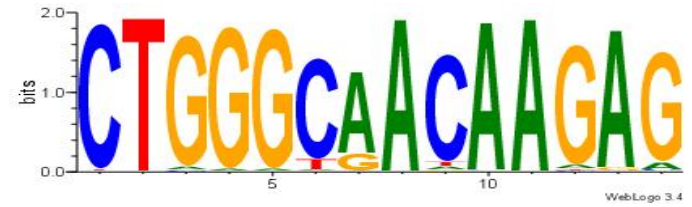
Alignment:

CTCTTGTGCCCAG
 TCAATGGTGCCCAG

Original motif Consensus sequence: CTCTTGTTGCCAG



Reverse complement motif Consensus sequence: CTGGGCAACAAGAG

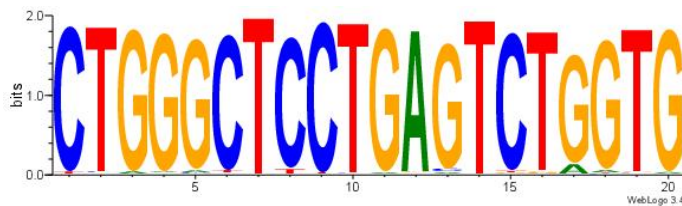


Dataset #: 1
 Motif ID: 67
 Motif name: Motif 67
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0.0918241

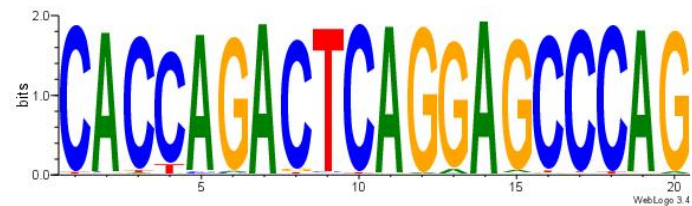
Alignment:

```
CACCAGACTCAGGAGCCCAG
-----TCAATGGTGCCCAG
```

Original motif Consensus sequence: CTGGGCTCCTGAGTCTGGTG



Reverse complement motif Consensus sequence: CACCAGACTCAGGAGCCCAG

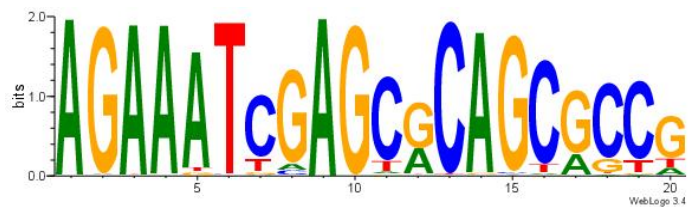


Dataset #: 1
 Motif ID: 65
 Motif name: Motif 65
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 14
 Similarity score: 0.0919503

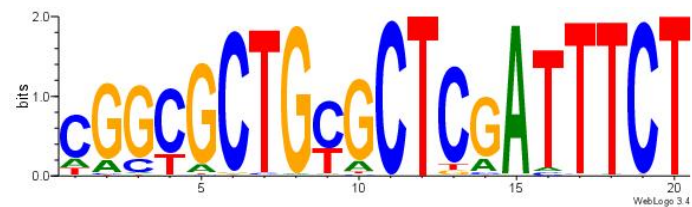
Alignment:

AGAAATCGAGCRCAGCGCCG
 -----TCAATGGTGCCCAG--

Original motif Consensus sequence: AGAAATCGAGCRCAGCGCCG



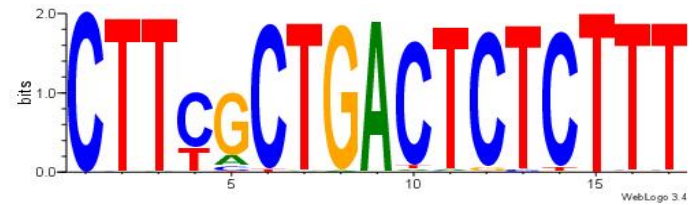
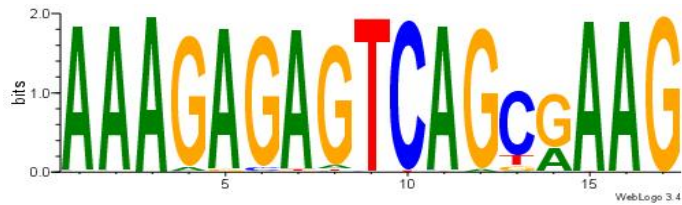
Reverse complement motif Consensus sequence: CGGCGCTGMGCTCGATTCT



Dataset #: 1 Motif ID: 148 Motif name: Motif 148

Original motif Consensus sequence: AAAGAGATCAGCGAAG

Reverse complement motif Consensus sequence: CTTGCTGACTCTCTT

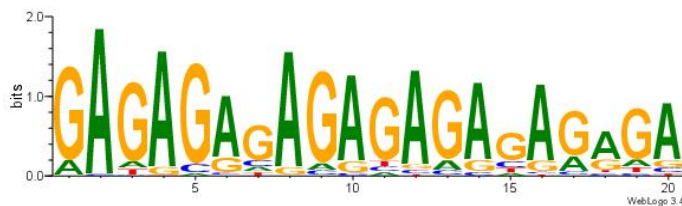


Best Matches for Motif ID 148 (Highest to Lowest)

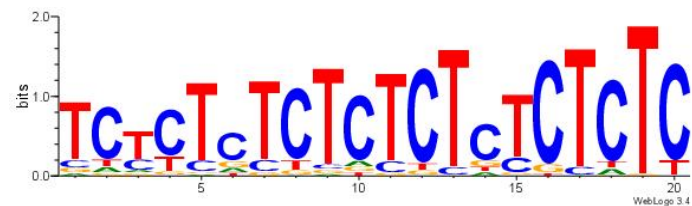
Dataset #: 1
 Motif ID: 109
 Motif name: Motif 109
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 17
 Similarity score: 0.0787922

Alignment:
 GAGAGAGAGAGAGAGAGAGA
 -AAAGAGAGTCAGCGAAG--

Original motif Consensus sequence: GAGAGAGAGAGAGAGAGA



Reverse complement motif Consensus sequence: TCTCTCTCTCTCTCTCTC

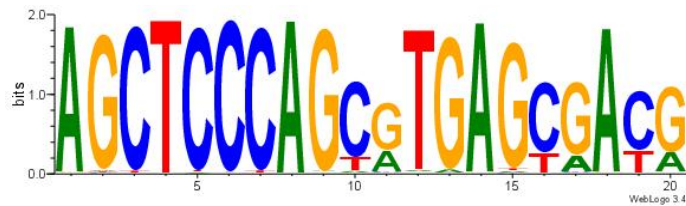


Dataset #: 1
 Motif ID: 48
 Motif name: Motif 48
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 4
 Number of overlap: 17
 Similarity score: 0.0890404

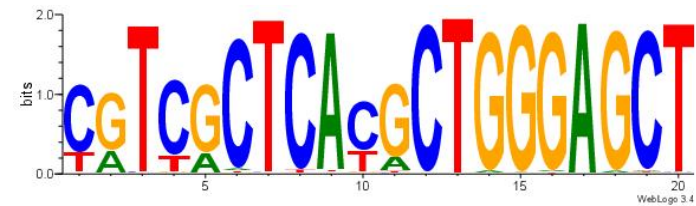
Alignment:

CGTCGCTCACGCTGGGAGCT
 CTTCGCTGACTCTCTTT---

Original motif Consensus sequence: AGCTCCCAGCGTGAGCGACG



Reverse complement motif Consensus sequence: CGTCGCTCACGCTGGGAGCT



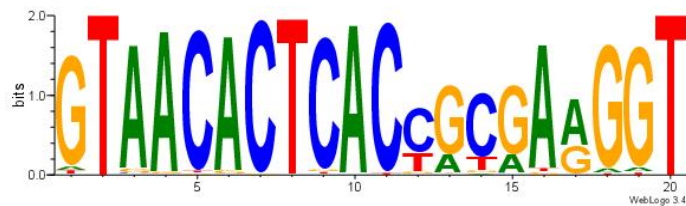
Dataset #: 1
 Motif ID: 201
 Motif name: Motif 201
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2

Number of overlap: 17
Similarity score: 0.0907364

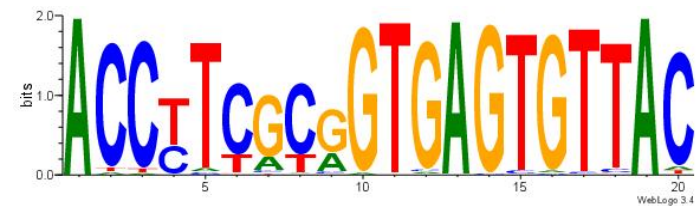
Alignment:

ACCKTCGCGGTGAGTGTTAC
--CTTCGCTGACTCTCTTT--

Original motif Consensus sequence: GTAACACTCACCGCGARGGT



Reverse complement motif Consensus sequence:
ACCKTCGCGGTGAGTGTTAC

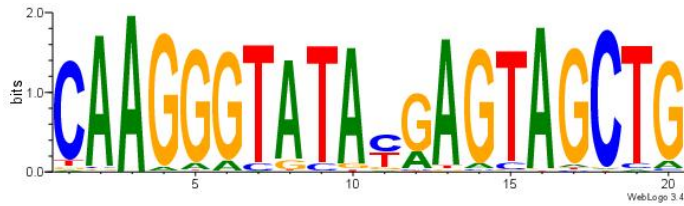


Dataset #: 1
Motif ID: 194
Motif name: Motif 194
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 17
Similarity score: 0.0975057

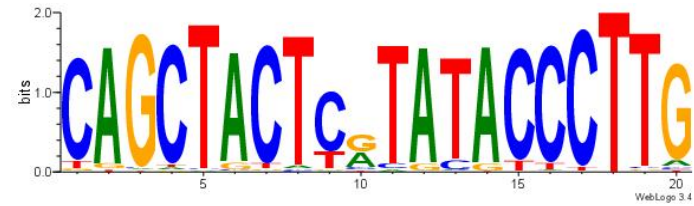
Alignment:

CAGCTACTCKTATACCCTTG
---CTTCGCTGACTCTCTTT

Original motif Consensus sequence: CAAGGGTATAYGAGTAGCTG



Reverse complement motif Consensus sequence: CAGCTACTCKTATACCCTTG

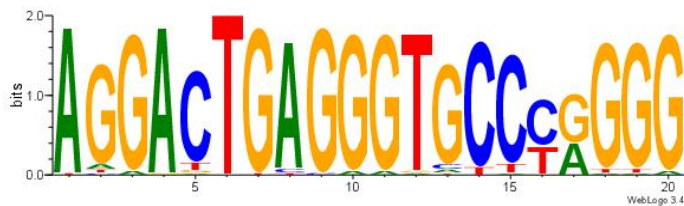


Dataset #: 1
Motif ID: 312
Motif name: Motif 312
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 17
Similarity score: 0.1019

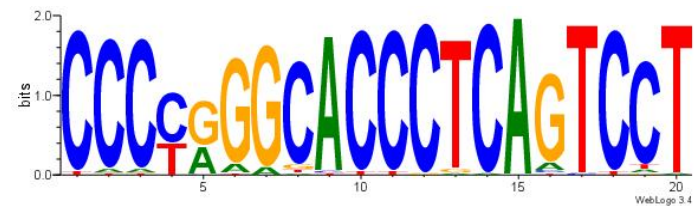
Alignment:

CCCMKGGCACCCTCAGTCCT
CTTCGCTGACTCTCTTT---

Original motif Consensus sequence: AGGACTGAGGGTGCCCGGG

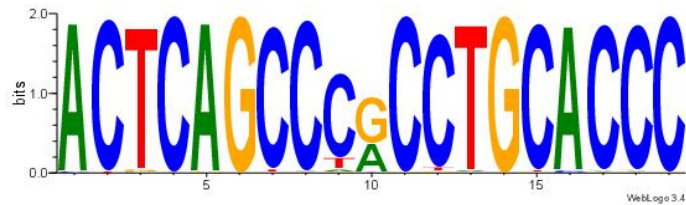


Reverse complement motif Consensus sequence: CCCMKGGCACCCTCAGTCCT

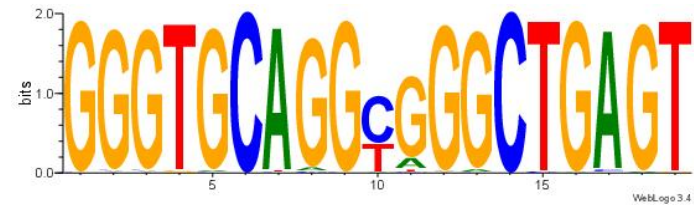


Dataset #: 1 Motif ID: 149 Motif name: Motif 149

Original motif Consensus sequence: ACTCAGCCRCCTGCACCC



Reverse complement motif Consensus sequence: GGGTGCAGGMGGCTGAGT



Best Matches for Motif ID 149 (Highest to Lowest)

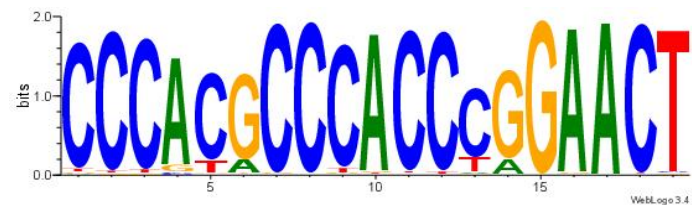
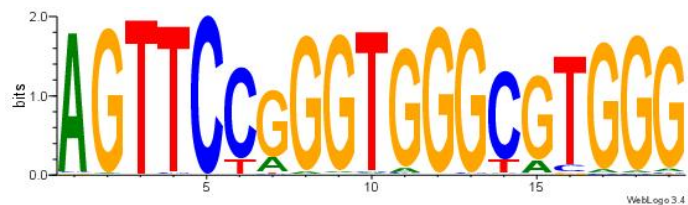
Dataset #:	1
Motif ID:	98
Motif name:	Motif 98
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	19
Similarity score:	0.107094

Alignment:

```
AGTTCCGGGTGGGCGTGGG  
GGGTGCAGGMGGCTGAGT
```

Original motif Consensus sequence: AGTTCCGGGTGGGCGTGGG

Reverse complement motif Consensus sequence: CCCACGCCACCCGGAAC

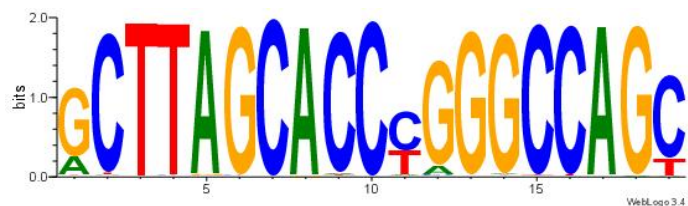


Dataset #: 1
 Motif ID: 82
 Motif name: Motif 82
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 19
 Similarity score: 0.11583

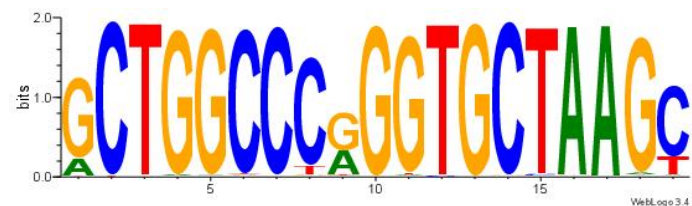
Alignment:

GCTTAGCACCYGGGCCAGC
 ACTCAGCCRCCTGCACCC

Original motif Consensus sequence: GCTTAGCACCYGGGCCAGC



Reverse complement motif Consensus sequence: GCTGGCCCKGGTGCTAAGC



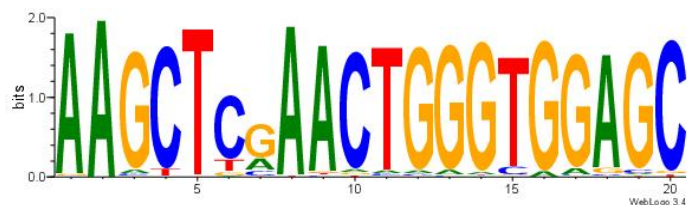
Dataset #: 1

Motif ID: 321
 Motif name: Motif 321
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 19
 Similarity score: 0.118514

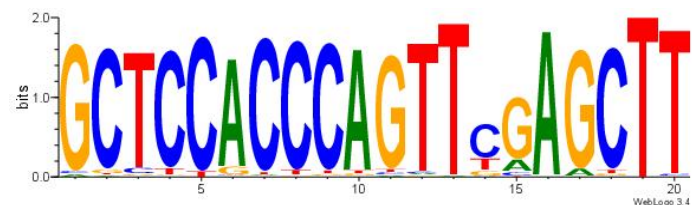
Alignment:

GCTCCACCCAGTTCGAGCTT
 ACTCAGCCCRCTGCACCC-

Original motif Consensus sequence: AAGCTCGAACTGGGTGGAGC



Reverse complement motif Consensus sequence: GCTCCACCCAGTTCGAGCTT



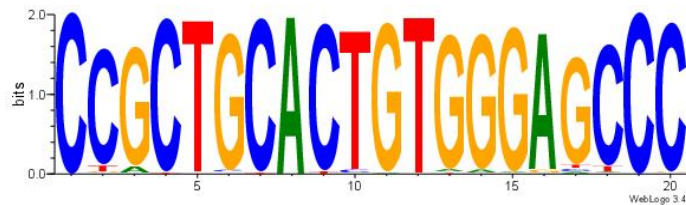
Dataset #: 1
 Motif ID: 144
 Motif name: Motif 144
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 19

Similarity score: 0.119864

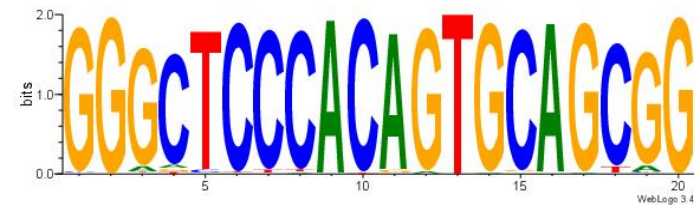
Alignment:

GGGCTCCCACAGTGCAGCGG
-GGGTGCAGGMGGGCTGAGT

Original motif Consensus sequence: CCGCTGCACTGTGGGAGCCC



Reverse complement motif Consensus sequence:
GGGCTCCCACAGTGCAGCGG



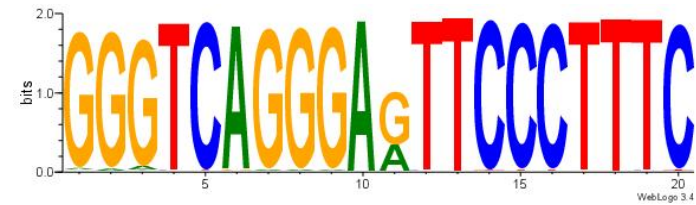
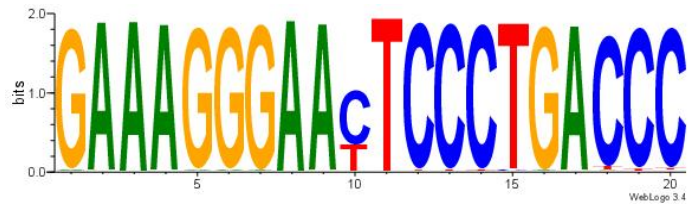
Dataset #: 1
Motif ID: 16
Motif name: Motif 16
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 19
Similarity score: 0.120923

Alignment:

GGGTCAGGGAGTTCCTTTC
GGGTGCAGGMGGGCTGAGT-

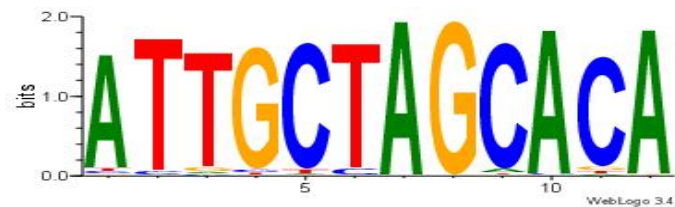
Original motif Consensus sequence: GAAAGGGA ACTCCCTGACCC

Reverse complement motif Consensus sequence:
GGGTCAGGGAGTTCCTTTC

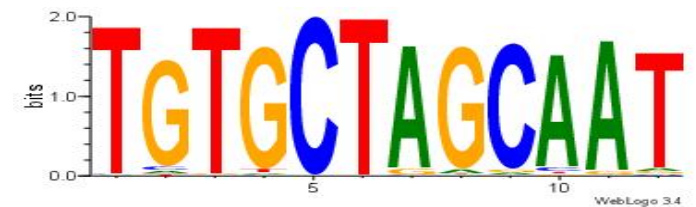


Dataset #: 1 Motif ID: 150 Motif name: Motif 150

Original motif Consensus sequence: ATTGCTAGCACA



Reverse complement motif Consensus sequence: TGTGCTAGCAAT

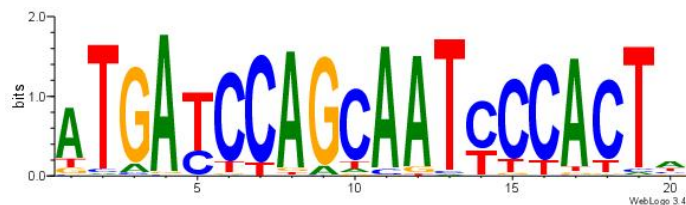


Best Matches for Motif ID 150 (Highest to Lowest)

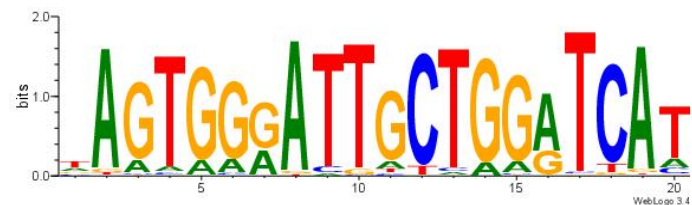
Dataset #:	1
Motif ID:	115
Motif name:	Motif 115
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2
Number of overlap:	12
Similarity score:	0.0632108

Alignment:
 ATGATCCAGCAATYCCACTH
 -----TGTGCTAGCAAT-

Original motif Consensus sequence: ATGATCCAGCAATYCCACTH



Reverse complement motif Consensus sequence: HAGTGGKATTGCTGGATCAT

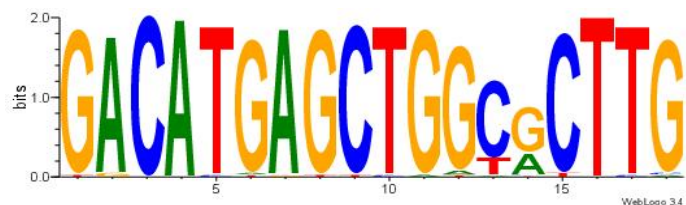


Dataset #: 1
Motif ID: 306
Motif name: Motif 306
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 3
Number of overlap: 12
Similarity score: 0.0772146

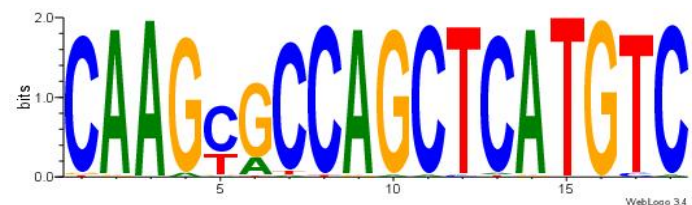
Alignment:

GACATGAGCTGGCGCTTG
----TGTGCTAGCAAT--

Original motif Consensus sequence: GACATGAGCTGGCGCTTG



Reverse complement motif Consensus sequence: CAAGCGCCAGCTCATGTC

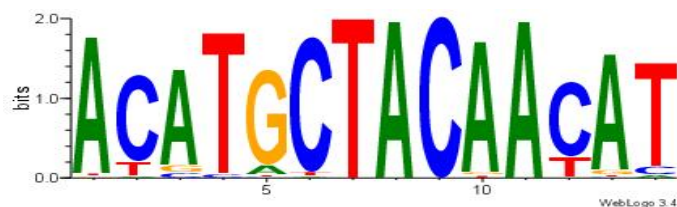


Dataset #: 1
 Motif ID: 317
 Motif name: Motif 317
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 12
 Similarity score: 0.0823231

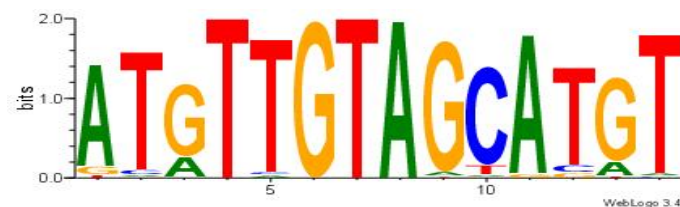
Alignment:

ATGTTGTAGCATGT
 -TGTGCTAGCAAT-

Original motif Consensus sequence: ACATGCTACAACAT



Reverse complement motif Consensus sequence: ATGTTGTAGCATGT



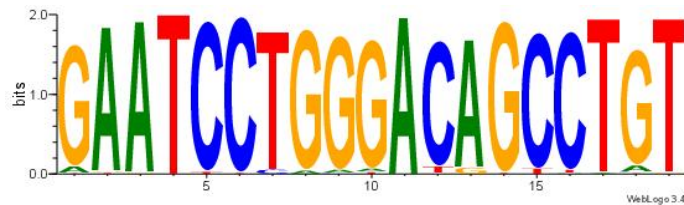
Dataset #: 1
 Motif ID: 192
 Motif name: Motif 192
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 7
 Number of overlap: 12

Similarity score: 0.0825726

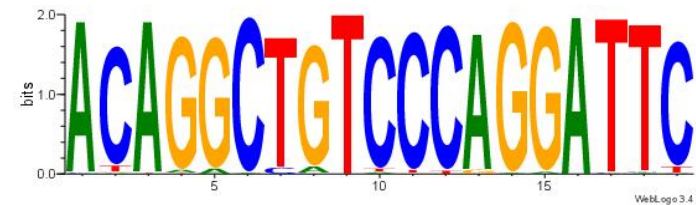
Alignment:

GAATCCTGGGACAGCCTGT
-ATTGCTAGCACA-----

Original motif Consensus sequence: GAATCCTGGGACAGCCTGT



Reverse complement motif Consensus sequence:
ACAGGCTGTCCCAGGATTC



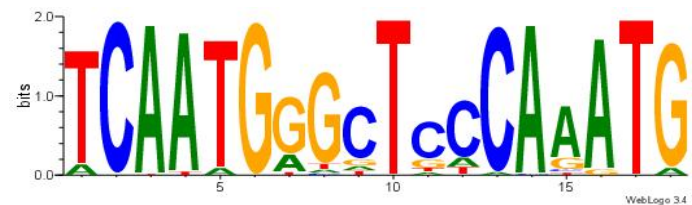
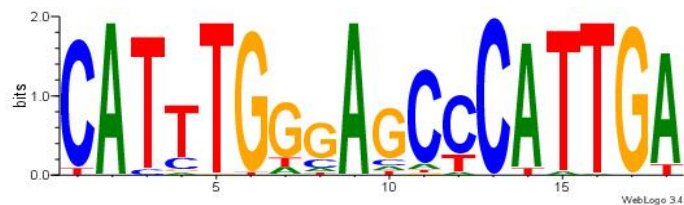
Dataset #: 1
Motif ID: 284
Motif name: Motif 284
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 5
Number of overlap: 12
Similarity score: 0.0836196

Alignment:

TCAATGGGCTCCCAAATG
----TGTGCTAGCAAT--

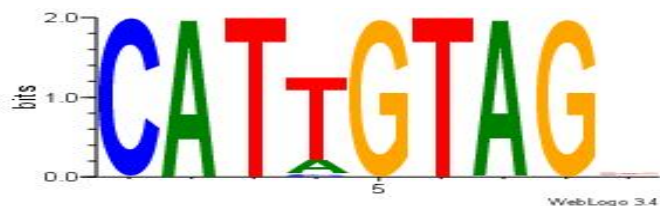
Original motif Consensus sequence: CATTGGGAGCCCATTGA

Reverse complement motif Consensus sequence:
TCAATGGGCTCCCAAATG

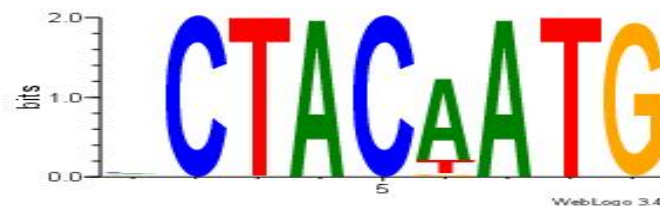


Dataset #: 1 Motif ID: 151 Motif name: Motif 151

Original motif Consensus sequence: CATTGTAGB



Reverse complement motif Consensus sequence: BCTACAATG



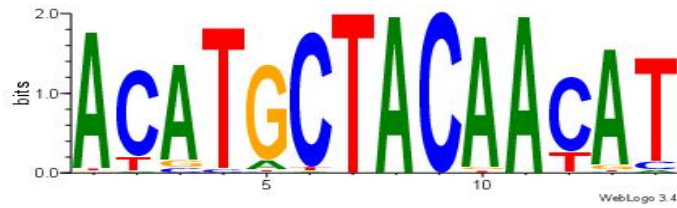
Best Matches for Motif ID 151 (Highest to Lowest)

Dataset #:	1
Motif ID:	317
Motif name:	Motif 317
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	5
Number of overlap:	9
Similarity score:	0.0584909

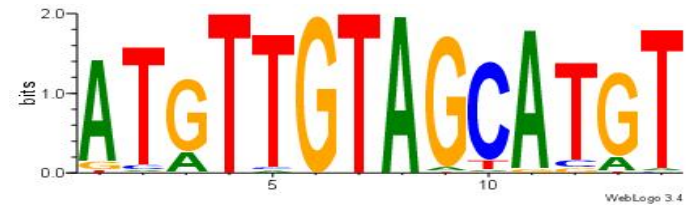
Alignment:

```
ACATGCTACAACAT
----BCTACAATG--
```

Original motif Consensus sequence: ACATGCTACAACAT



Reverse complement motif Consensus sequence: ATGTTGTAGCATG

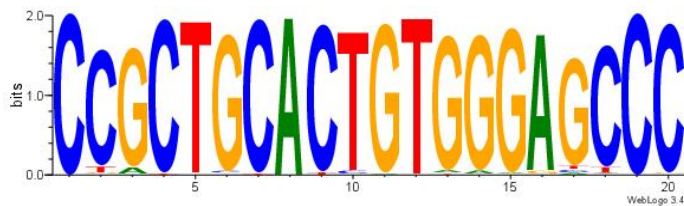


Dataset #: 1
Motif ID: 144
Motif name: Motif 144
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 7
Number of overlap: 9
Similarity score: 0.0645319

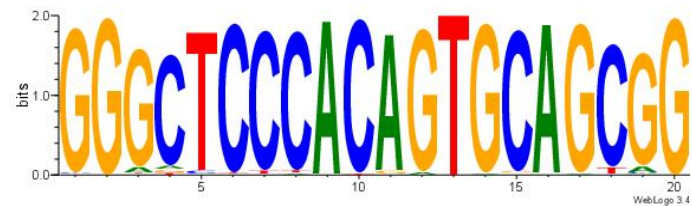
Alignment:

```
CCGCTGCACTGTGGGAGCCC  
-----CATTGTAGB-----
```

Original motif Consensus sequence: CCGCTGCACTGTGGGAGCCC



Reverse complement motif Consensus sequence: GGGCTCCCACAGTGCAGCGG

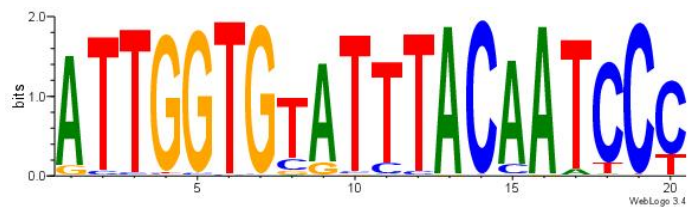


Dataset #: 1
 Motif ID: 106
 Motif name: Motif 106
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 10
 Number of overlap: 9
 Similarity score: 0.0647318

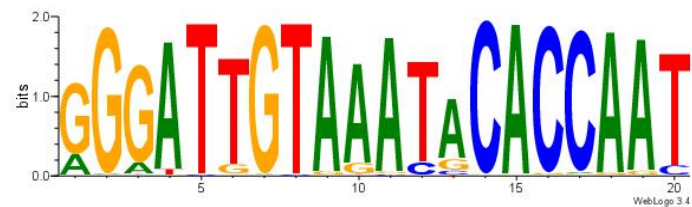
Alignment:

GGGATTGTAAATACACCAAT
 -----CATTGTAGB--

Original motif Consensus sequence: ATTGGTGTATTACAATCCC



Reverse complement motif Consensus sequence: GGGATTGTAAATACACCAAT



Dataset #: 1
 Motif ID: 344
 Motif name: Motif 344
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1

Number of overlap: 9
Similarity score: 0.0674469

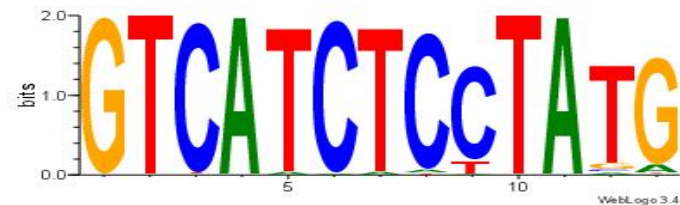
Alignment:

GTCATCTCCTATG
----BCTACAATG

Original motif Consensus sequence: CATAGGAGATGAC



Reverse complement motif Consensus sequence: GTCATCTCCTATG



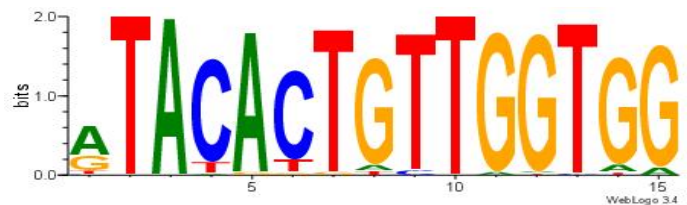
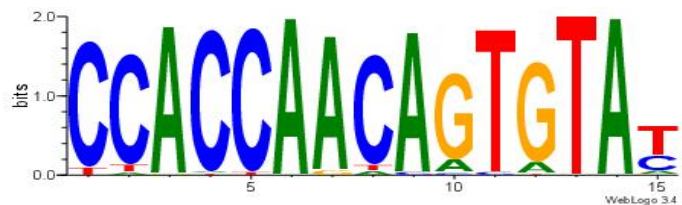
Dataset #: 1
Motif ID: 258
Motif name: Motif 258
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 4
Number of overlap: 9
Similarity score: 0.0683218

Alignment:

CCACCAACAGTGTA
---BCTACAATG---

Original motif Consensus sequence: CCACCAACAGTGTA

Reverse complement motif Consensus sequence: MTACACTGTTGGT

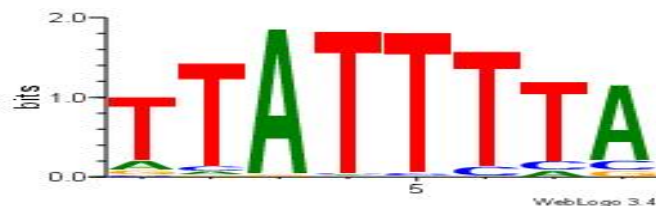


Dataset #: 1 Motif ID: 152 Motif name: Motif 152

Original motif Consensus sequence: TAAAATAA



Reverse complement motif Consensus sequence: TTATTTTA

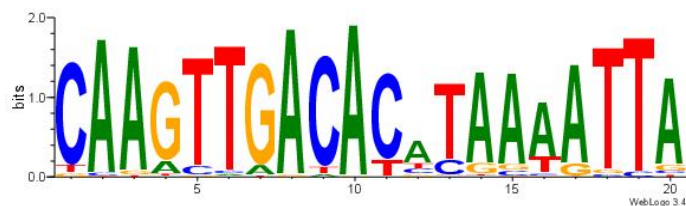


Best Matches for Motif ID 152 (Highest to Lowest)

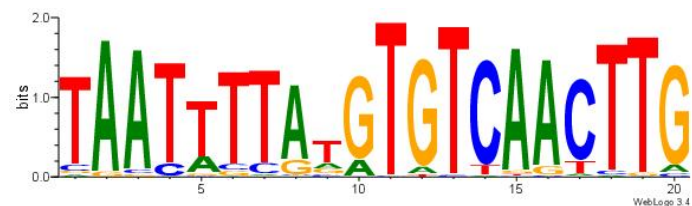
Dataset #:	1
Motif ID:	357
Motif name:	Motif 357
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	8
Similarity score:	0.0340112

Alignment:
 TAATTTTATGTGCAACTTG
 TTATTTTA-----

Original motif Consensus sequence: CAAGTTGACACATAAAATTA



Reverse complement motif Consensus sequence: TAATTTTATGTGTCAACTTG

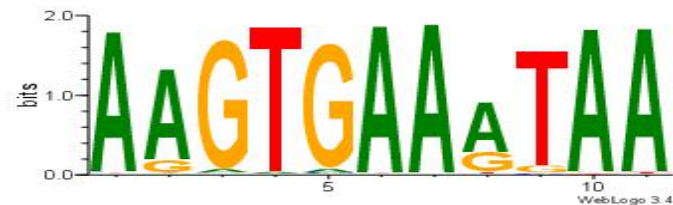


Dataset #: 1
Motif ID: 103
Motif name: Motif 103
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 8
Similarity score: 0.0363851

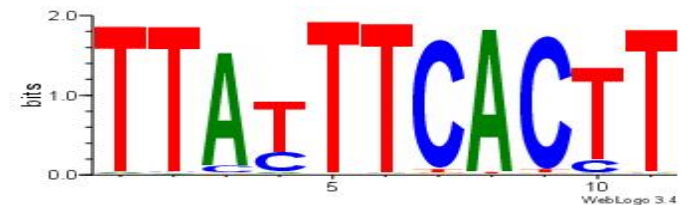
Alignment:

AAGTGAAATAA
---TAAAATAA

Original motif Consensus sequence: AAGTGAAATAA



Reverse complement motif Consensus sequence: TTATTTCACTT

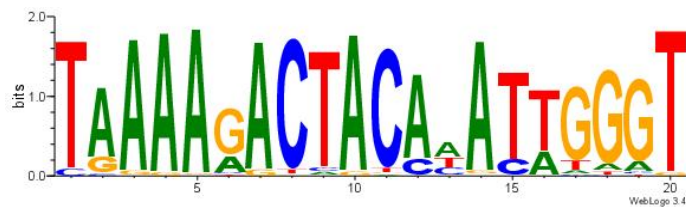


Dataset #: 1
 Motif ID: 195
 Motif name: Motif 195
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 13
 Number of overlap: 8
 Similarity score: 0.044499

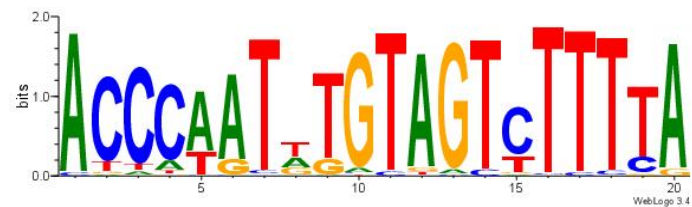
Alignment:

ACCCAATWTGTAGTCTTTTA
 -----TTATTTTA

Original motif Consensus sequence: TAAAAGACTACAWATTGGGT



Reverse complement motif Consensus sequence: ACCCAATWTGTAGTCTTTTA



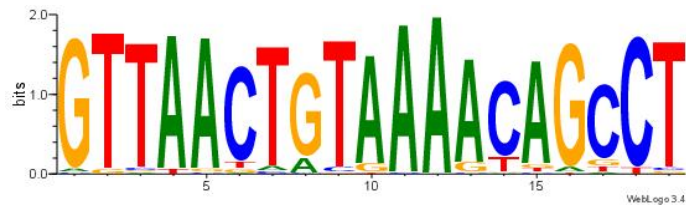
Dataset #: 1
 Motif ID: 233
 Motif name: Motif 233
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 9

Number of overlap: 8
Similarity score: 0.0489303

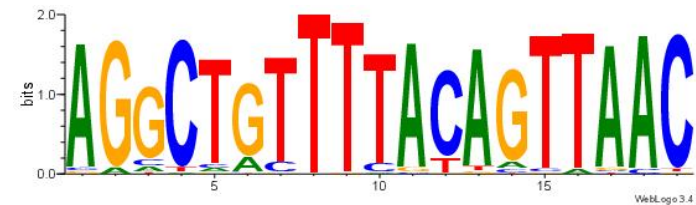
Alignment:

GTAACTGTAAAACAGCCT
-----TAAAATAA----

Original motif Consensus sequence: GTAACTGTAAAACAGCCT



Reverse complement motif Consensus sequence:
AGGCTGTTTTACAGTTAAC

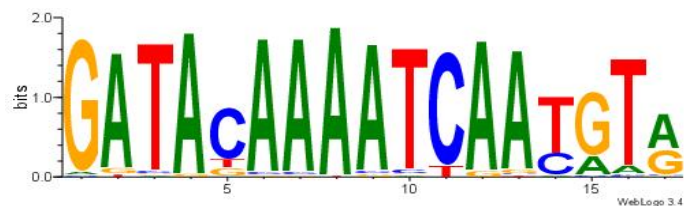


Dataset #: 1
Motif ID: 328
Motif name: Motif 328
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 5
Number of overlap: 8
Similarity score: 0.0492169

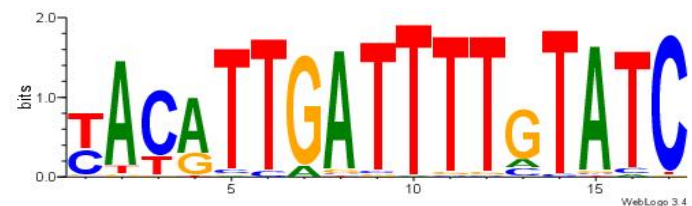
Alignment:

GATACAAAATCAATGTR
----TAAAATAA-----

Original motif Consensus sequence: GATACAAAATCAATGTR

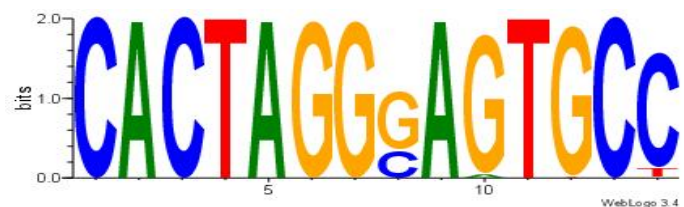


Reverse complement motif Consensus sequence: KACATTGATTTTGTATC

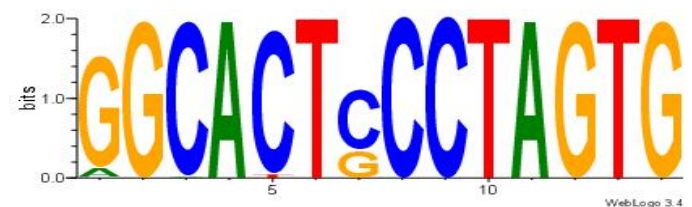


Dataset #: 1 Motif ID: 153 Motif name: Motif 153

Original motif Consensus sequence: CACTAGGGAGTGCC



Reverse complement motif Consensus sequence: GGCACTCCCTAGT



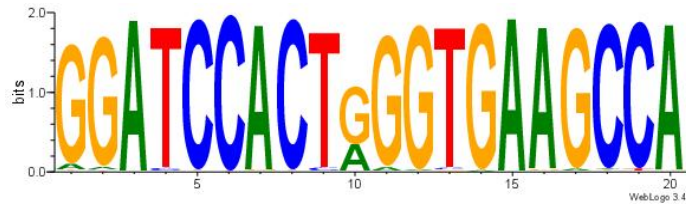
Best Matches for Motif ID 153 (Highest to Lowest)

Dataset #:	1
Motif ID:	61
Motif name:	Motif 61
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2
Number of overlap:	14
Similarity score:	0.0824482

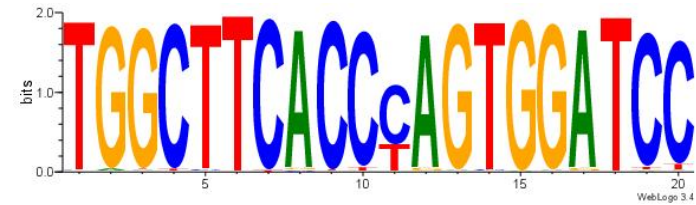
Alignment:

GGATCCACTGGGTGAAGCCA
-----CACTAGGGAGTGCC-

Original motif Consensus sequence: GGATCCACTGGGTGAAGCCA



Reverse complement motif Consensus sequence:
TGGCTTCACCCAGTGGATCC

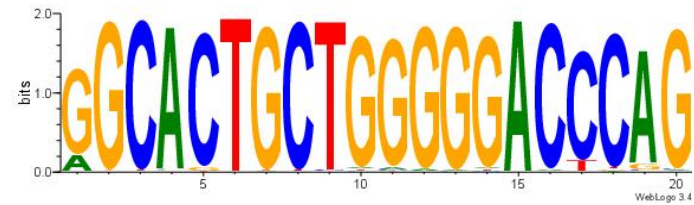
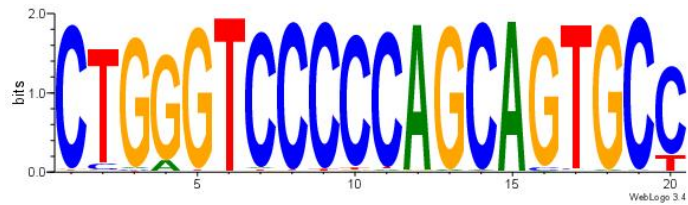


Dataset #: 1
Motif ID: 84
Motif name: Motif 84
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 14
Similarity score: 0.082834

Alignment:
CTGGGTCCCCCAGCAGTGCC
-----CACTAGGGAGTGCC

Original motif Consensus sequence: CTGGGTCCCCCAGCAGTGCC

Reverse complement motif Consensus sequence:
GGCACTGCTGGGGGACCCAG



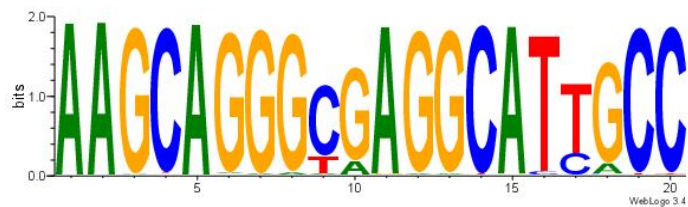
Dataset #: 1
 Motif ID: 13
 Motif name: Motif 13
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 7
 Number of overlap: 14
 Similarity score: 0.0887847

Alignment:

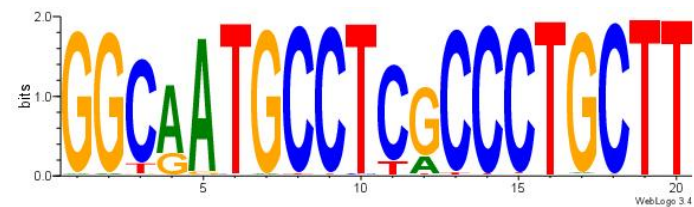
```

GGCAATGCCTCGCCCTGCTT
GGCACTCCCTAGTG-----
  
```

Original motif Consensus sequence: AAGCAGGGCGAGGCATTGCC



Reverse complement motif Consensus sequence: GGCAATGCCTCGCCCTGCTT



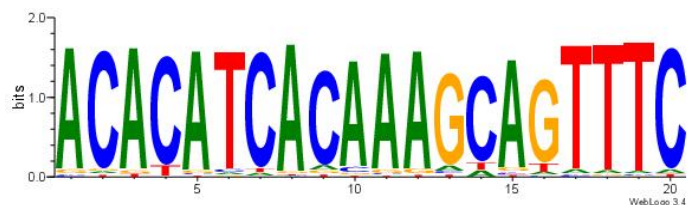
Dataset #: 1

Motif ID: 202
 Motif name: Motif 202
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0.0903253

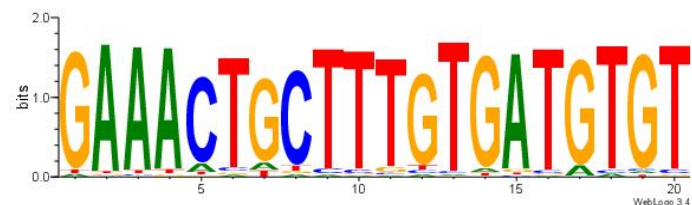
Alignment:

ACACATCACAAGCAGTTTC
 -----CACTAGGGAGTGCC

Original motif Consensus sequence: ACACATCACAAGCAGTTTC



Reverse complement motif Consensus sequence: GAAACTGCTTTGTGATGTGT



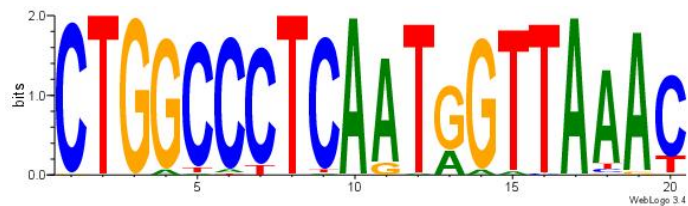
Dataset #: 1
 Motif ID: 332
 Motif name: Motif 332
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 14

Similarity score: 0.0915329

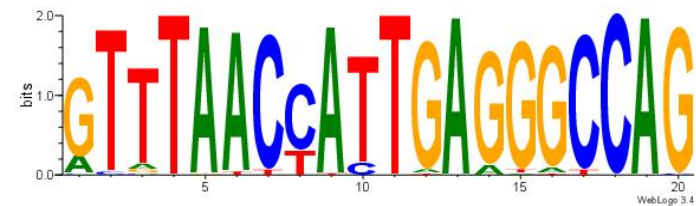
Alignment:

CTGGCCCTCAATGGTTAAAC
--GGCACTCCCTAGTG----

Original motif Consensus sequence: CTGGCCCTCAATGGTTAAAC

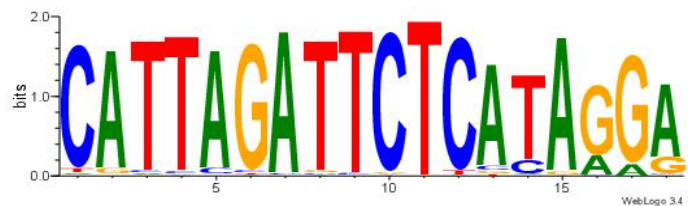


Reverse complement motif Consensus sequence: GTTTAACCATTGAGGGCCAG

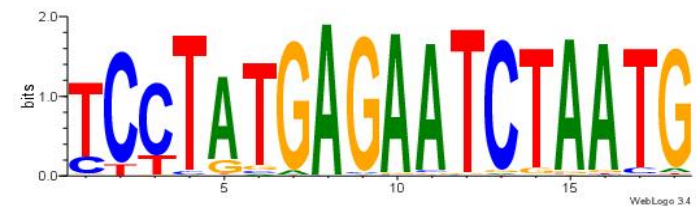


Dataset #: 1 Motif ID: 154 Motif name: Motif 154

Original motif Consensus sequence: CATTAGATTCTCATAGGA



Reverse complement motif Consensus sequence: TCCTATGAGAATCTAATG



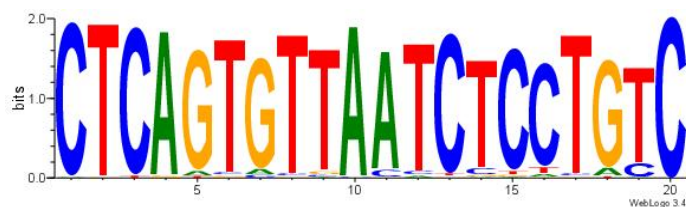
Best Matches for Motif ID 154 (Highest to Lowest)

Dataset #:	1
Motif ID:	262
Motif name:	Motif 262
Matching format of first motif:	Original Motif

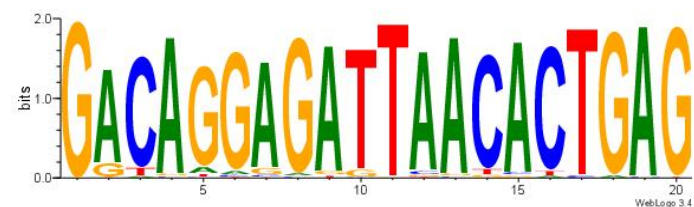
Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 18
 Similarity score: 0.100102

Alignment:
 GACAGGAGATTAACACTGAG
 --CATTAGATTCTCATAGGA

Original motif Consensus sequence: CTCAGTGTTAATCTCCTGTC



Reverse complement motif Consensus sequence:
 GACAGGAGATTAACACTGAG

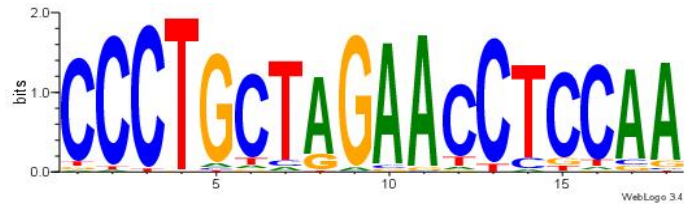


Dataset #: 1
 Motif ID: 299
 Motif name: Motif 299
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 18
 Similarity score: 0.111266

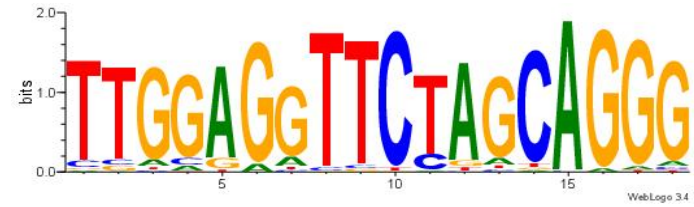
Alignment:

TTGGAGGTTCTAGCAGGG
CATTAGATTCTCATAGGA

Original motif Consensus sequence: CCCTGCTAGAACCTCCAA



Reverse complement motif Consensus sequence:
TTGGAGGTTCTAGCAGGG

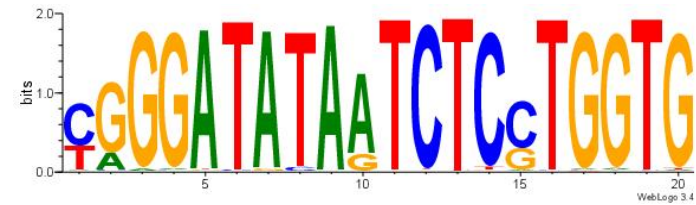
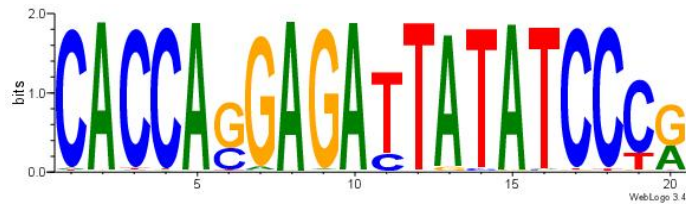


Dataset #: 1
Motif ID: 19
Motif name: Motif 19
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 18
Similarity score: 0.114558

Alignment:
CACCAGGAGATTATATCCCR
--TCCTATGAGAATCTAATG

Original motif Consensus sequence: CACCAGGAGATTATATCCCR

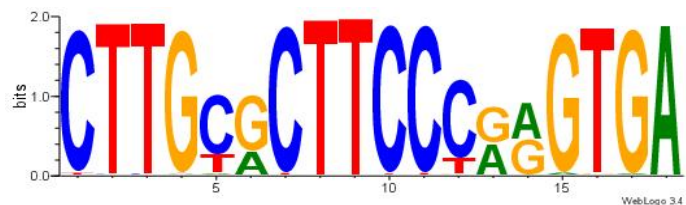
Reverse complement motif Consensus sequence:
MGGATATAATCTCTGGTG



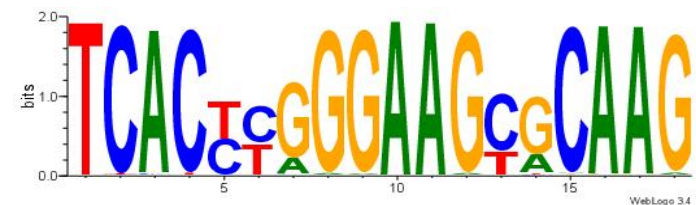
Dataset #: 1
 Motif ID: 15
 Motif name: Motif 15
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 18
 Similarity score: 0.116802

Alignment:
 CTTGCGCTTCCCRRGTGA
 CATTAGATTCTCATAGGA

Original motif Consensus sequence: CTTGCGCTTCCCRRGTGA



Reverse complement motif Consensus sequence: TCACKMGGGAAGCGCAAG



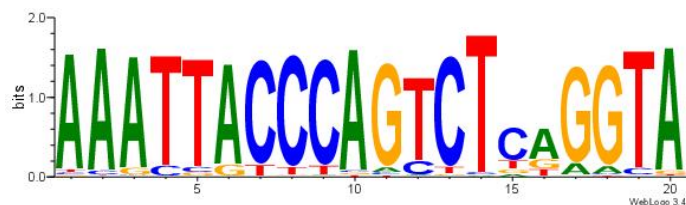
Dataset #: 1

Motif ID: 160
 Motif name: Motif 160
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 18
 Similarity score: 0.117572

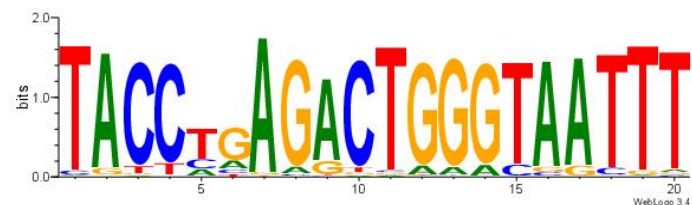
Alignment:

AAATTACCCAGTCTCAGGTA
 -CATTAGATTCTCATAGGA-

Original motif Consensus sequence: AAATTACCCAGTCTCAGGTA

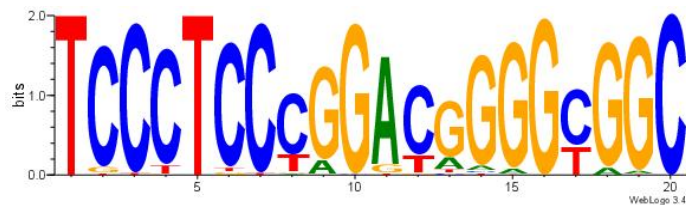


Reverse complement motif Consensus sequence: TACCTGAGACTGGGTAATTT

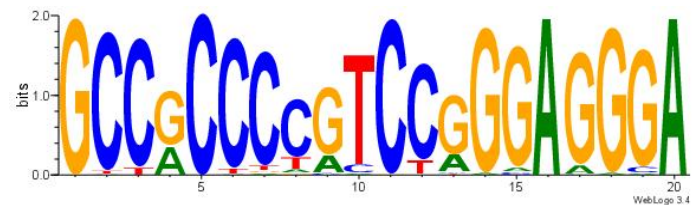


Dataset #: 1 Motif ID: 155 Motif name: Motif 155

Original motif Consensus sequence: TCCCTCCCGACGGGGYGGC



Reverse complement motif Consensus sequence: GCCCCCCGTCCGGGAGGGGA



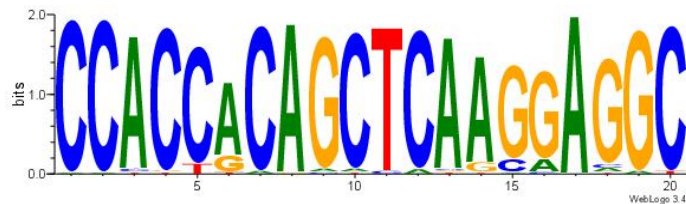
Best Matches for Motif ID 155 (Highest to Lowest)

Dataset #: 1
Motif ID: 331
Motif name: Motif 331
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 20
Similarity score: 0.112683

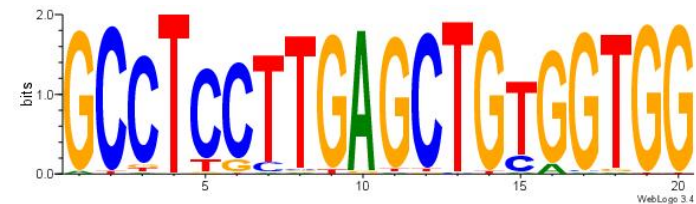
Alignment:

```
GCCTCCTTGAGCTGTGGTGG  
GCCKCCCCGTCCGGGAGGGA
```

Original motif Consensus sequence: CCACCACAGCTCAAGGAGGC



Reverse complement motif Consensus sequence: GCCTCCTTGAGCTGTGGTGG



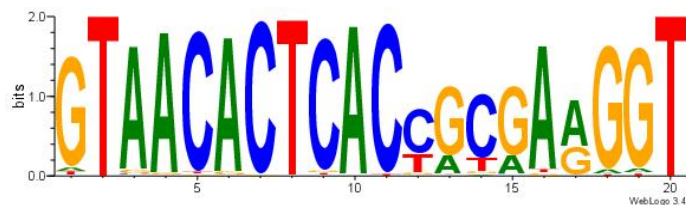
Dataset #: 1
Motif ID: 201
Motif name: Motif 201
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement

Direction: Backward
Position number: 1
Number of overlap: 20
Similarity score: 0.117283

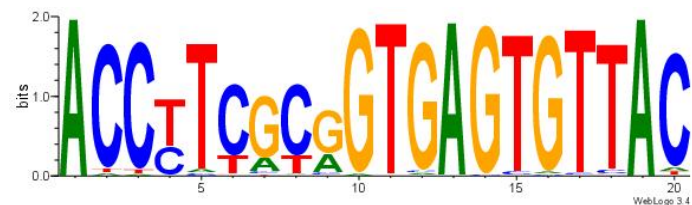
Alignment:

ACCKTCGCGGTGAGTGTTAC
TCCCTCCCGGACGGGGYGGC

Original motif Consensus sequence: GTAACACTCACCGCGARGGT



Reverse complement motif Consensus sequence: ACCKTCGCGGTGAGTGTTAC

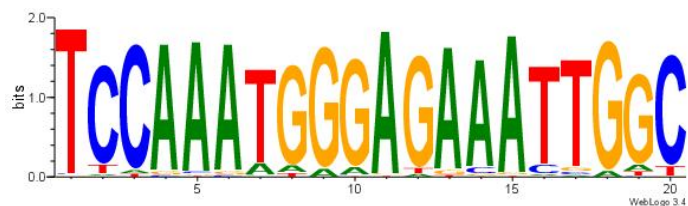


Dataset #: 1
Motif ID: 235
Motif name: Motif 235
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 20
Similarity score: 0.121478

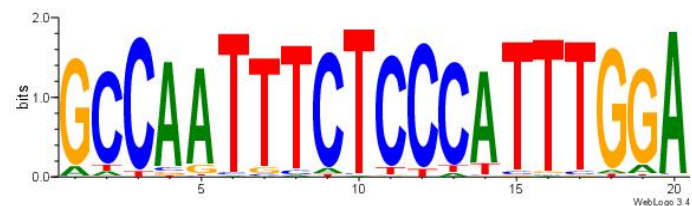
Alignment:

TCCAAATGGGAGAAATTGGC
TCCCTCCCGGACGGGGYGGC

Original motif Consensus sequence: TCCAATGGGAGAAATTGGC



Reverse complement motif Consensus sequence: GCCAATTTCTCCCATTTGGA

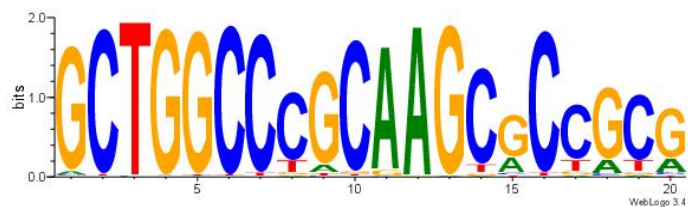


Dataset #: 1
Motif ID: 100
Motif name: Motif 100
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 20
Similarity score: 0.122155

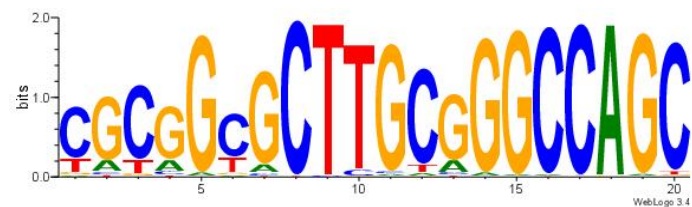
Alignment:

CGCGGCGCTTGCGGGCCAGC
GCKCCCCGTCCGGGAGGGA

Original motif Consensus sequence: GCTGGCCCGCAAGCCGCG



Reverse complement motif Consensus sequence: CGCGGCGCTTGCGGGCCAGC

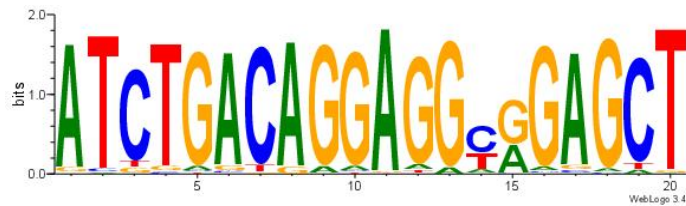


Dataset #: 1
 Motif ID: 165
 Motif name: Motif 165
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.125857

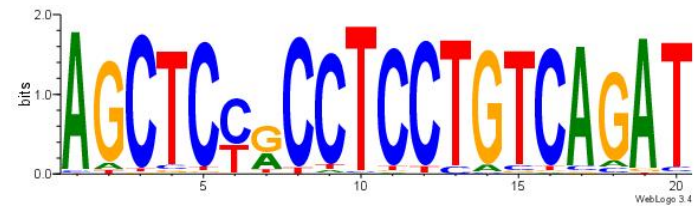
Alignment:

AGCTCMKCCTCCTGTCAGAT
 GCCKCCCCGTCCGGGAGGGA

Original motif Consensus sequence: ATCTGACAGGAGGYRGAGCT



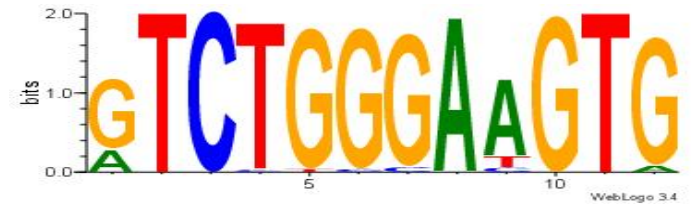
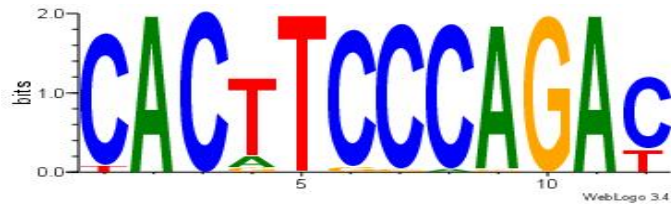
Reverse complement motif Consensus sequence: AGCTCMKCCTCCTGTCAGAT



Dataset #: 1 Motif ID: 156 Motif name: Motif 156

Original motif Consensus sequence: CACTTCCCAGAC

Reverse complement motif Consensus sequence: GTCTGGGAAGTG

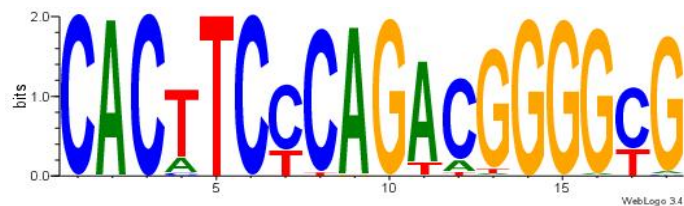


Best Matches for Motif ID 156 (Highest to Lowest)

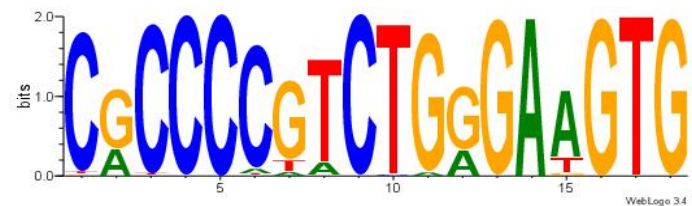
Dataset #: 1
 Motif ID: 27
 Motif name: Motif 27
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 7
 Number of overlap: 12
 Similarity score: 0.00564821

Alignment:
 CACTTCCCAGACGGGGCG
 CACTTCCCAGAC-----

Original motif Consensus sequence: CACTTCCCAGACGGGGCG



Reverse complement motif Consensus sequence: CGCCCCGTCTGGGAAGTG

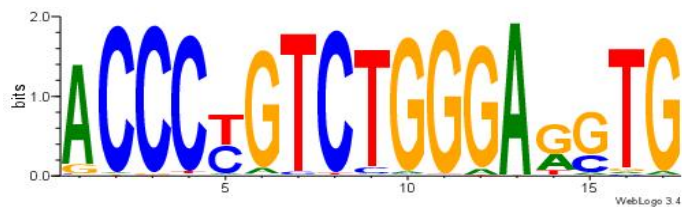


Dataset #: 1
 Motif ID: 95
 Motif name: Motif 95
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 6
 Number of overlap: 12
 Similarity score: 0.0183065

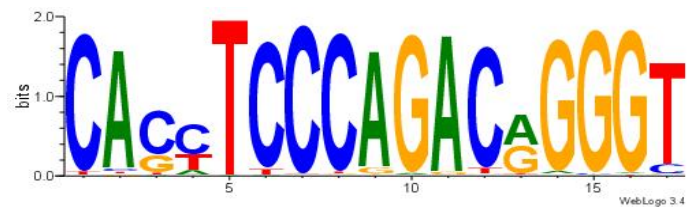
Alignment:

CACCTCCCAGACMGGGT
 -----CACTTCCCAGAC

Original motif Consensus sequence: ACCCYGTCTGGGAGGTG



Reverse complement motif Consensus sequence: CACCTCCCAGACMGGGT



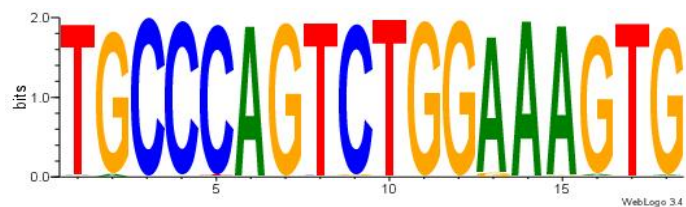
Dataset #: 1
 Motif ID: 45
 Motif name: Motif 45
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1

Number of overlap: 12
Similarity score: 0.0205412

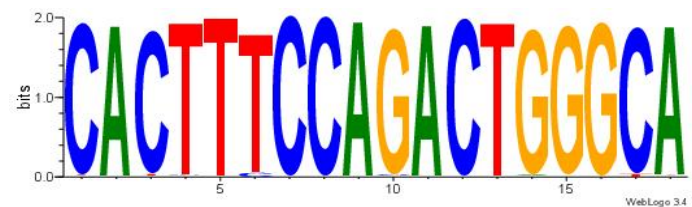
Alignment:

TGCCCAGTCTGGAAAGTG
GTCTGGGAAGTG-----

Original motif Consensus sequence: TGCCCAGTCTGGAAAGTG



Reverse complement motif Consensus sequence:
CACTTCCAGACTGGGCA



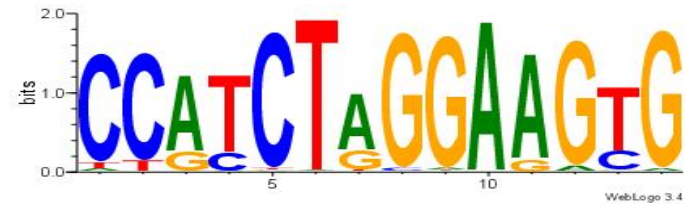
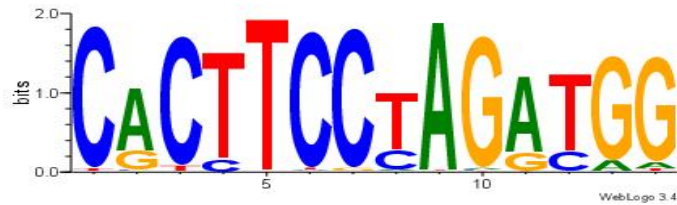
Dataset #: 1
Motif ID: 74
Motif name: Motif 74
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 3
Number of overlap: 12
Similarity score: 0.0315299

Alignment:

CACTTCCCTAGATGG
CACTTCCAGAC--

Original motif Consensus sequence: CACTTCCCTAGATGG

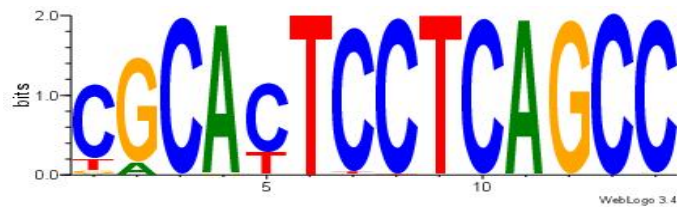
Reverse complement motif Consensus sequence: CCATCTAGGAAGT



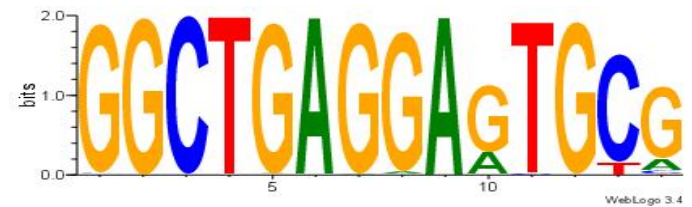
Dataset #: 1
 Motif ID: 72
 Motif name: Motif 72
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 12
 Similarity score: 0.0670258

Alignment:
 CGCACTCCTCAGCC
 --CACTTCCCAGAC

Original motif Consensus sequence: CGCACTCCTCAGCC

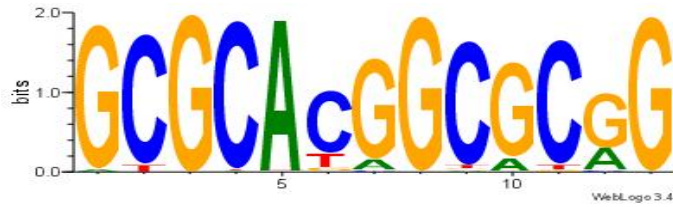


Reverse complement motif Consensus sequence: GGCTGAGGAGTGC

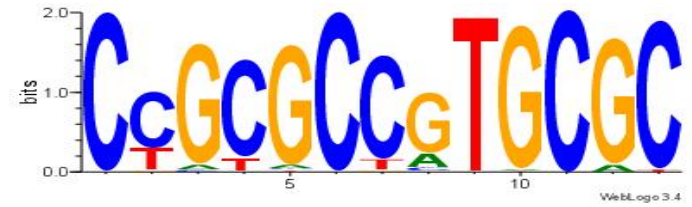


Dataset #: 1 Motif ID: 157 Motif name: Motif 157

Original motif Consensus sequence: GCGCACGGCGCGG



Reverse complement motif Consensus sequence: CCGCGCCGTGCGG



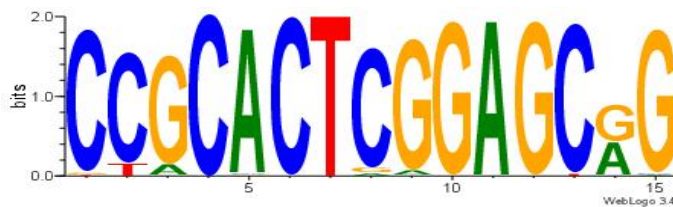
Best Matches for Motif ID 157 (Highest to Lowest)

Dataset #:	1
Motif ID:	128
Motif name:	Motif 128
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	13
Similarity score:	0.056845

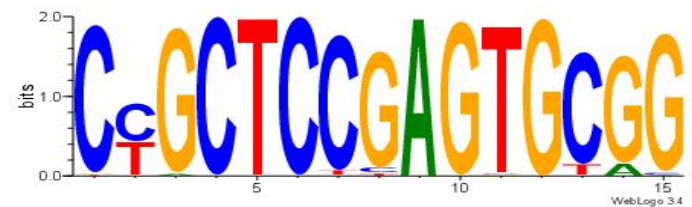
Alignment:

```
CMGCTCCGAGTGCGG  
CCGCGCCGTGCGC--
```

Original motif Consensus sequence: CCGCACTCGGAGCRG



Reverse complement motif Consensus sequence:
CMGCTCCGAGTGCGG

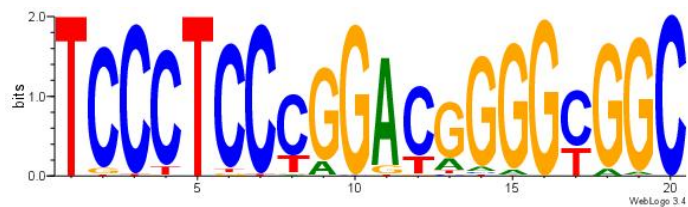


Dataset #: 1
 Motif ID: 155
 Motif name: Motif 155
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 13
 Similarity score: 0.0678809

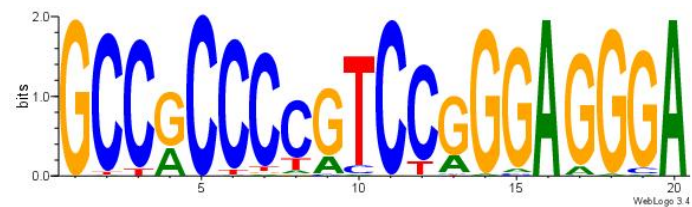
Alignment:

GCCKCCCCGTCCGGGAGGGA
 -CCGCGCCGTGCGC-----

Original motif Consensus sequence: TCCCTCCCGGACGGGGYGGC



Reverse complement motif Consensus sequence: GCCKCCCCGTCCGGGAGGGA



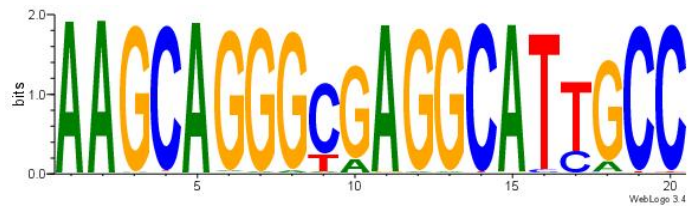
Dataset #: 1
 Motif ID: 13
 Motif name: Motif 13
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 8

Number of overlap: 13
Similarity score: 0.0702925

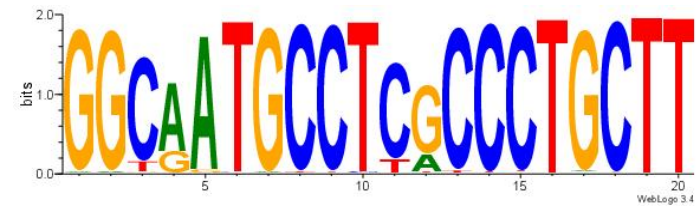
Alignment:

GGCAATGCCTCGCCCTGCTT
-----CCGCGCCGTGCGC

Original motif Consensus sequence: AAGCAGGGCGAGGCATTGCC



Reverse complement motif Consensus sequence:
GGCAATGCCTCGCCCTGCTT

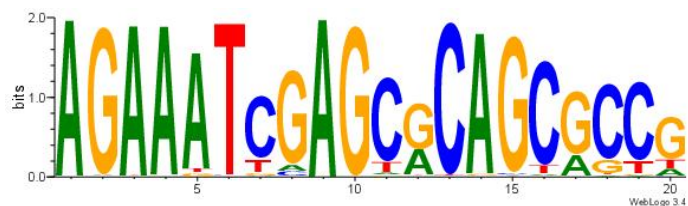


Dataset #: 1
Motif ID: 65
Motif name: Motif 65
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 13
Similarity score: 0.0726491

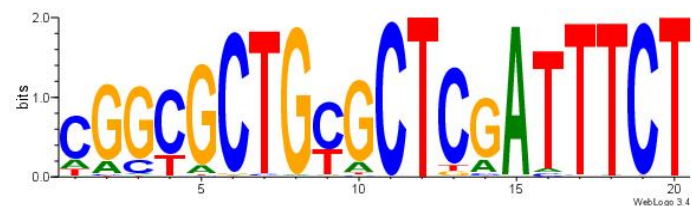
Alignment:

AGAAATCGAGCRCAGCGCCG
-----GCGCACGGCGCGG

Original motif Consensus sequence: AGAAATCGAGCRCAGCGCCG



Reverse complement motif Consensus sequence: CGGCGCTGMGCTCGATTCT

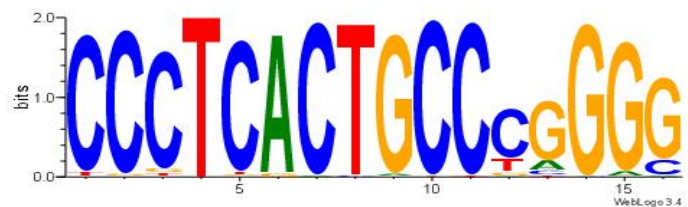


Dataset #: 1
Motif ID: 136
Motif name: Motif 136
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 2
Number of overlap: 13
Similarity score: 0.0740305

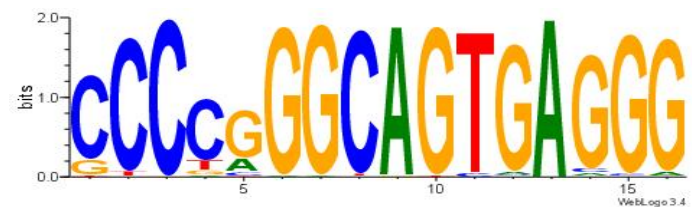
Alignment:

CCCCGGGCAGTGAGGG
--CCGCGCCGTGCGC--

Original motif Consensus sequence: CCCTACTGCCGGGG

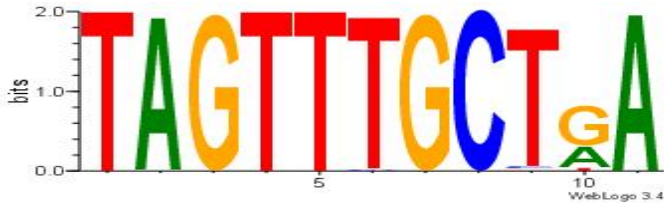


Reverse complement motif Consensus sequence: CCCC GG CAGT GAGGG



Dataset #: 1 Motif ID: 158 Motif name: Motif 158

Original motif Consensus sequence: TAGTTTGCTGA



Reverse complement motif Consensus sequence: TCAGCAAACCTA



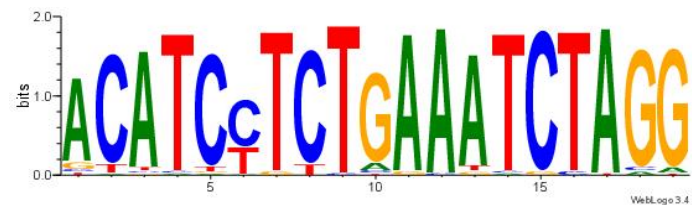
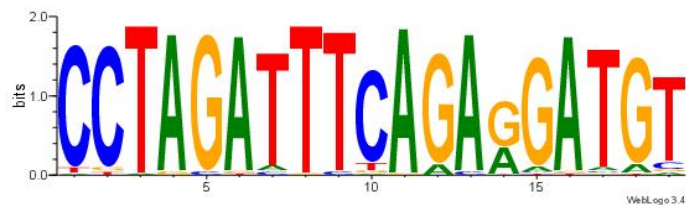
Best Matches for Motif ID 158 (Highest to Lowest)

Dataset #:	1
Motif ID:	280
Motif name:	Motif 280
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	7
Number of overlap:	11
Similarity score:	0.0721214

Alignment:
ACATCMTCTGAAATCTAGG
-----TCAGCAAACCTA--

Original motif Consensus sequence: CCTAGATTTTCAGARGATGT

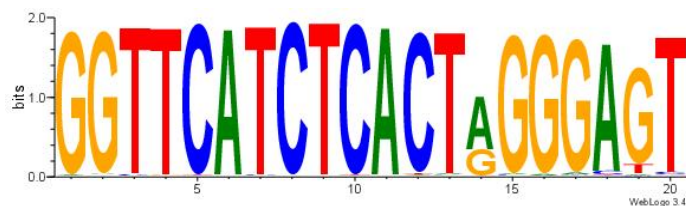
Reverse complement motif Consensus sequence:
ACATCMTCTGAAATCTAGG



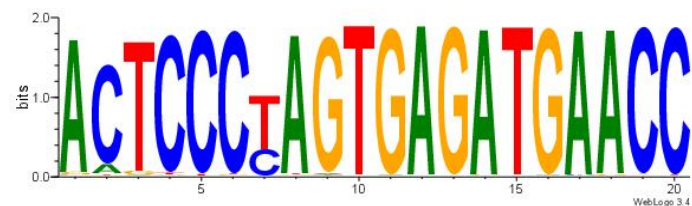
Dataset #: 1
 Motif ID: 23
 Motif name: Motif 23
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 4
 Number of overlap: 11
 Similarity score: 0.077411

Alignment:
 GGTTTCATCTCACTAGGGAGT
 -----TCAGCAAATA----

Original motif Consensus sequence: GGTTTCATCTCACTAGGGAGT



Reverse complement motif Consensus sequence: ACTCCCTAGTGAGATGAACC



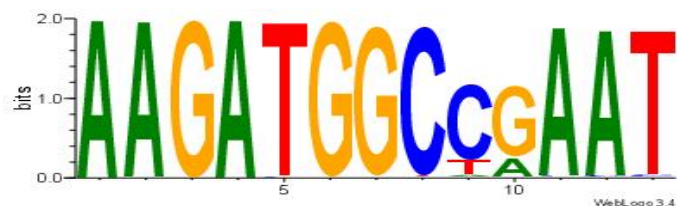
Dataset #: 1

Motif ID: 97
 Motif name: Motif 97
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.0826841

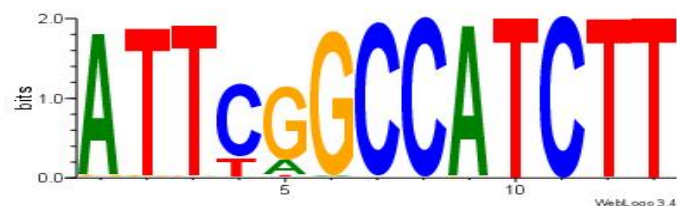
Alignment:

AAGATGGCCGAAT
 TAGTTTGCTGA--

Original motif Consensus sequence: AAGATGGCCGAAT



Reverse complement motif Consensus sequence: ATTCGGCCATCTT

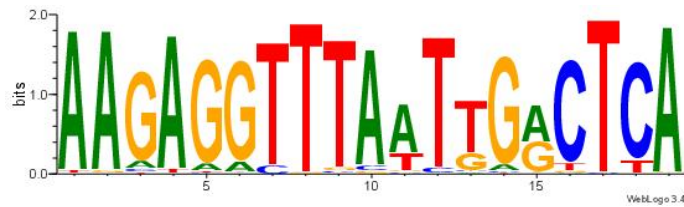


Dataset #: 1
 Motif ID: 129
 Motif name: Motif 129
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 9
 Number of overlap: 11
 Similarity score: 0.0832491

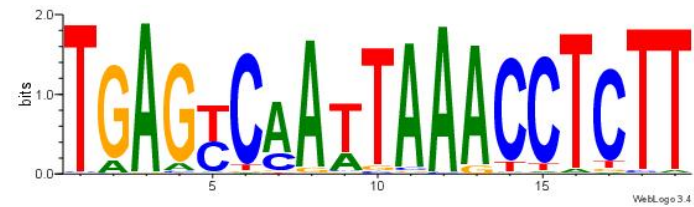
Alignment:

AAGAGGTTTAATTGRCTCA
-----TAGTTTGCTGA

Original motif Consensus sequence: AAGAGGTTTAATTGRCTCA



Reverse complement motif Consensus sequence:
TGAGKCAATTAACCTCTT



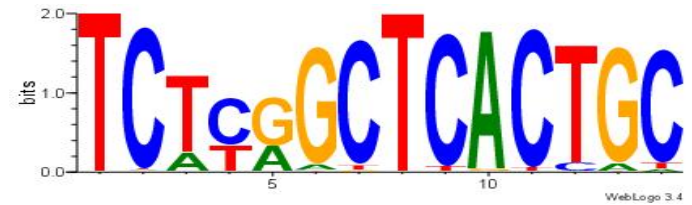
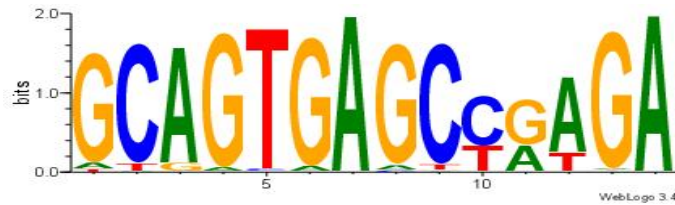
Dataset #:	1
Motif ID:	38
Motif name:	Motif 38
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	11
Similarity score:	0.0844969

Alignment:

GCAGTGAGCYRAGA
-TAGTTTGCTGA--

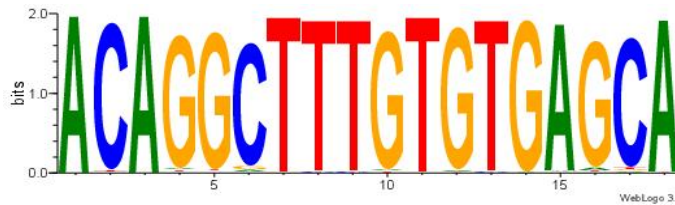
Original motif Consensus sequence: GCAGTGAGCYRAGA

Reverse complement motif Consensus sequence: TCTMKGCTCACTG

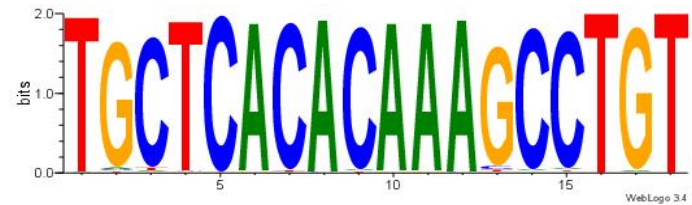


Dataset #: 1 Motif ID: 159 Motif name: Motif 159

Original motif Consensus sequence: ACAGGCTTTGTGTGAGCA



Reverse complement motif Consensus sequence: TGCTCACAAAGCCTGT



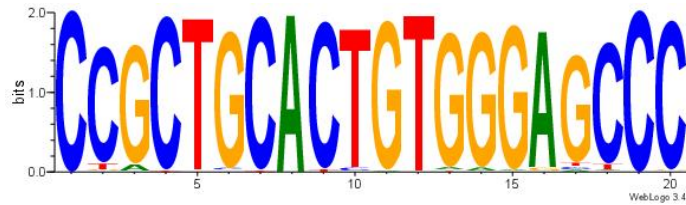
Best Matches for Motif ID 159 (Highest to Lowest)

Dataset #:	1
Motif ID:	144
Motif name:	Motif 144
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	2
Number of overlap:	18
Similarity score:	0.104283

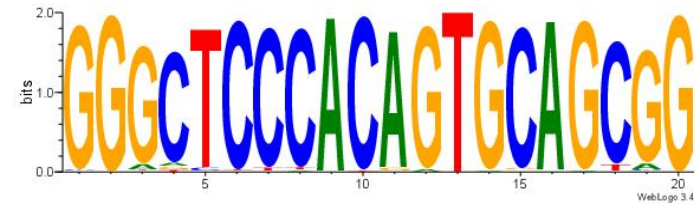
Alignment:

GGGCTCCACAGTGCAGCGG
-TGCTCACACAAAGCCTGT-

Original motif Consensus sequence: CCGCTGCACTGTGGGAGCCC



Reverse complement motif Consensus sequence:
GGGCTCCACAGTGCAGCGG



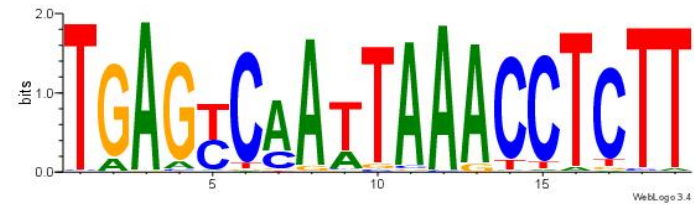
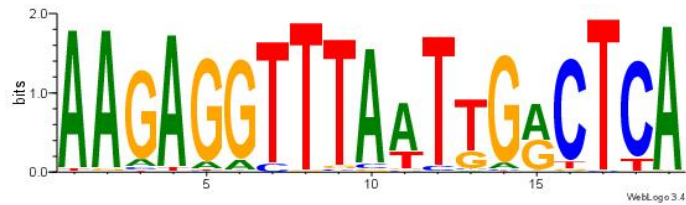
Dataset #:	1
Motif ID:	129
Motif name:	Motif 129
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	18
Similarity score:	0.109531

Alignment:

AAGAGGTTTAATTGRCTCA
-ACAGGCTTTGTGTGAGCA

Original motif Consensus sequence: AAGAGGTTTAATTGRCTCA

Reverse complement motif Consensus sequence:
TGAGKCAATTAACCTCTT

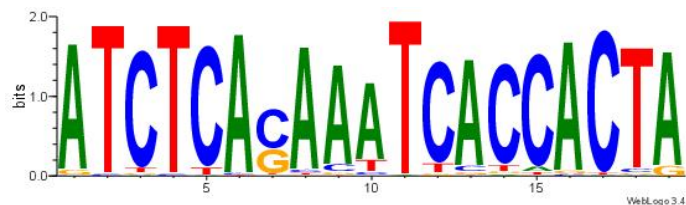


Dataset #: 1
 Motif ID: 261
 Motif name: Motif 261
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 18
 Similarity score: 0.111806

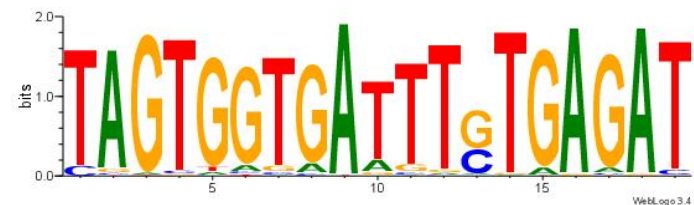
Alignment:

TAGTGGTGATTTSTGAGAT
 -ACAGGCTTTGTGTGAGCA

Original motif Consensus sequence: ATCTCASAAATCACCCTA



Reverse complement motif Consensus sequence: TAGTGGTGATTTSTGAGAT



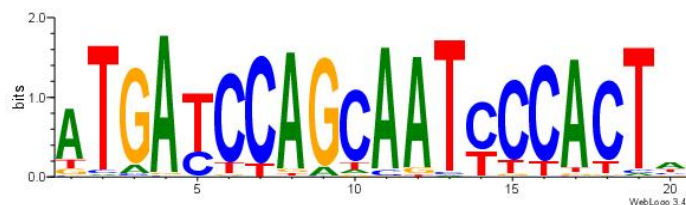
Dataset #: 1

Motif ID: 115
 Motif name: Motif 115
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 18
 Similarity score: 0.114641

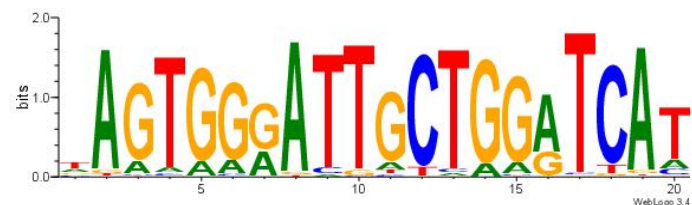
Alignment:

ATGATCCAGCAATYCCACTH
 -TGCTCACACAAAGCCTGT-

Original motif Consensus sequence: ATGATCCAGCAATYCCACTH



Reverse complement motif Consensus sequence: HAGTGGKATTGCTGGATCAT



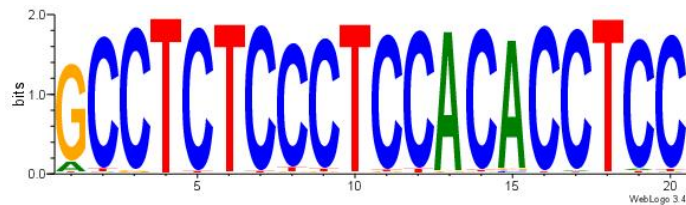
Dataset #: 1
 Motif ID: 105
 Motif name: Motif 105
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 18

Similarity score: 0.115994

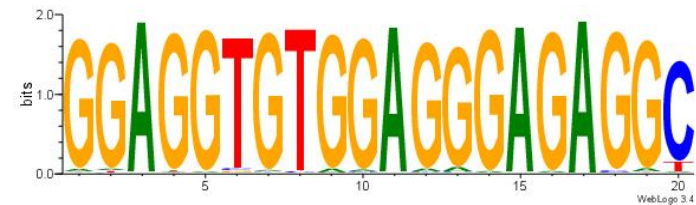
Alignment:

GCCTCTCCCTCCACACCTCC
TGCTCACACAAAGCCTGT--

Original motif Consensus sequence: GCCTCTCCCTCCACACCTCC

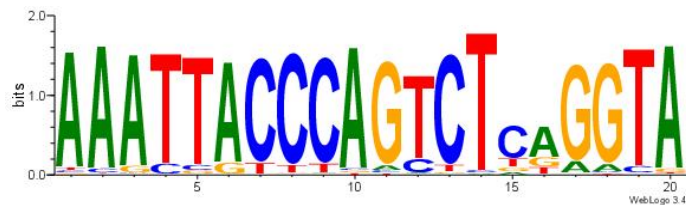


Reverse complement motif Consensus sequence: GGAGGTGTGGAGGGAGAGGC

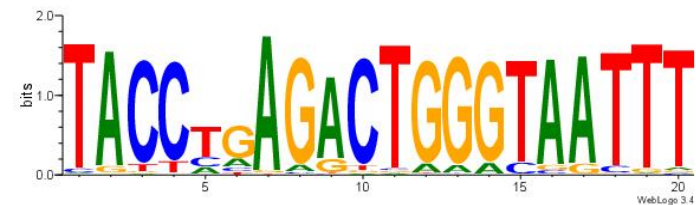


Dataset #: 1 Motif ID: 160 Motif name: Motif 160

Original motif Consensus sequence: AAATTACCCAGTCTCAAGGTA



Reverse complement motif Consensus sequence: TACCTGAGACTGGGTAATTT



Best Matches for Motif ID 160 (Highest to Lowest)

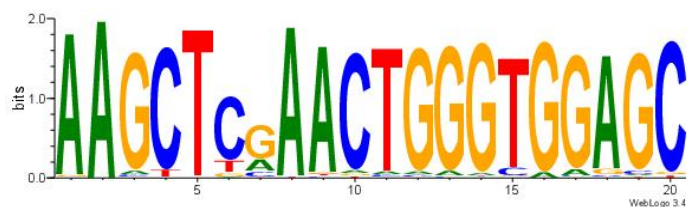
Dataset #: 1
Motif ID: 321
Motif name: Motif 321
Matching format of first motif: Reverse Complement

Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	20
Similarity score:	0.115677

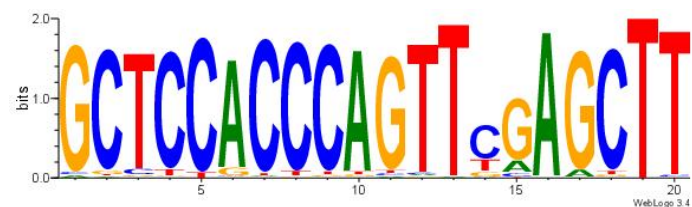
Alignment:

```
AAGCTCGAACTGGGTGGAGC
TACCTGAGACTGGGTAATTT
```

Original motif Consensus sequence: AAGCTCGAACTGGGTGGAGC



Reverse complement motif Consensus sequence: GCTCCACCCAGTTGAGCTT

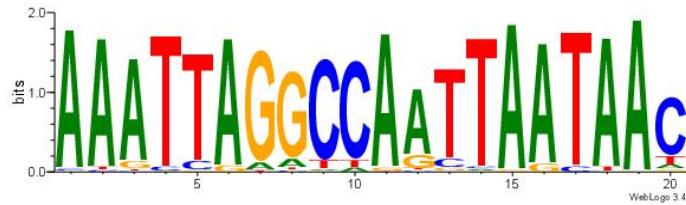


Dataset #:	1
Motif ID:	308
Motif name:	Motif 308
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	20
Similarity score:	0.123051

Alignment:

GTTATTAATTGGCCTAATTT
TACCTGAGACTGGGTAATTT

Original motif Consensus sequence: AAATTAGGCCAATTAATAAC



Reverse complement motif Consensus sequence:
GTTATTAATTGGCCTAATTT



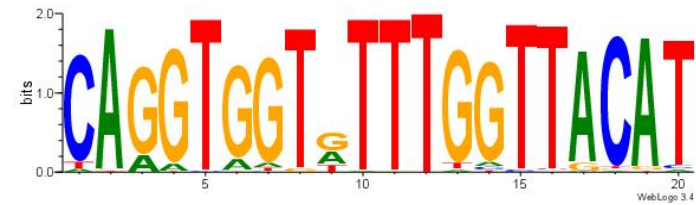
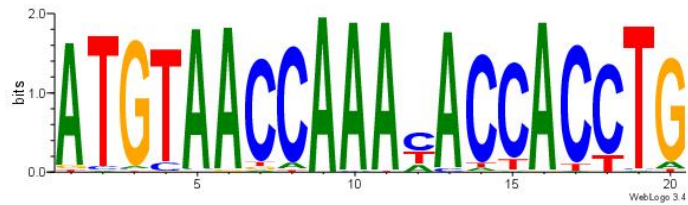
Dataset #: 1
Motif ID: 336
Motif name: Motif 336
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 20
Similarity score: 0.12689

Alignment:

ATGTAACCAAAYACCACCTG
AAATTACCCAGTCTCAGGTA

Original motif Consensus sequence: ATGTAACCAAAYACCACCTG

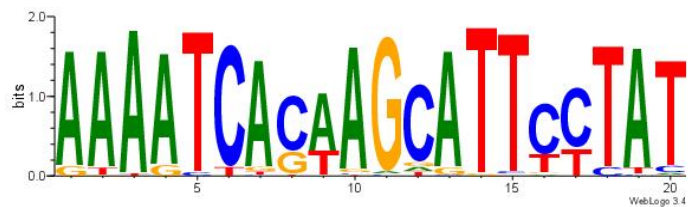
Reverse complement motif Consensus sequence:
CAGGTGGTKTTTGGTTACAT



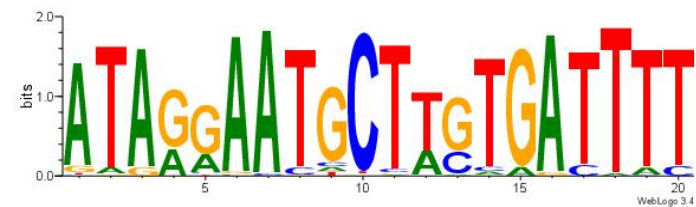
Dataset #: 1
 Motif ID: 254
 Motif name: Motif 254
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.129148

Alignment:
 ATAGGAATGCTTGTGATTTT
 TACCTGAGACTGGGTAATTT

Original motif Consensus sequence: AAAATCACAAGCATTCTAT



Reverse complement motif Consensus sequence: ATAGGAATGCTTGTGATTTT



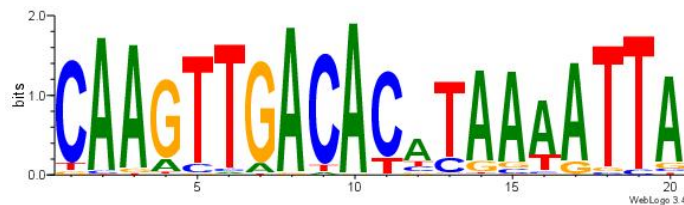
Dataset #: 1

Motif ID: 357
 Motif name: Motif 357
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.129326

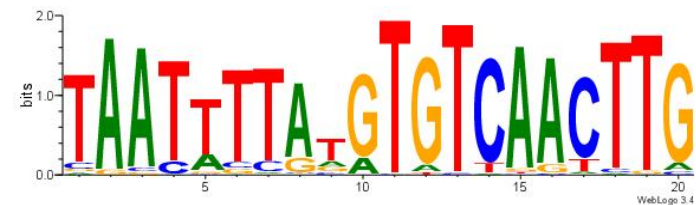
Alignment:

TAATTTTATGTGTCAACTTG
 TACCTGAGACTGGGTAATTT

Original motif Consensus sequence: CAAGTTGACACATAAAATTA

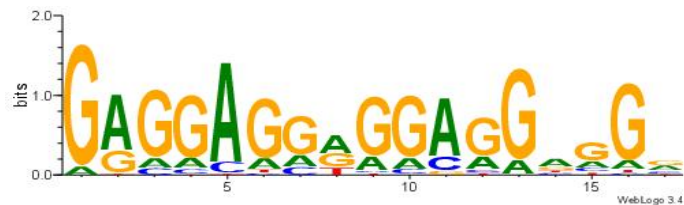


Reverse complement motif Consensus sequence: TAATTTTATGTGTCAACTTG

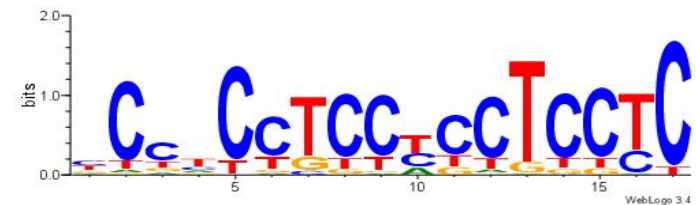


Dataset #: 1 Motif ID: 161 Motif name: Motif 161

Original motif Consensus sequence: GAGGAGGRGGAGGDGGV



Reverse complement motif Consensus sequence: VCCDCCTCCKCCTCCTC



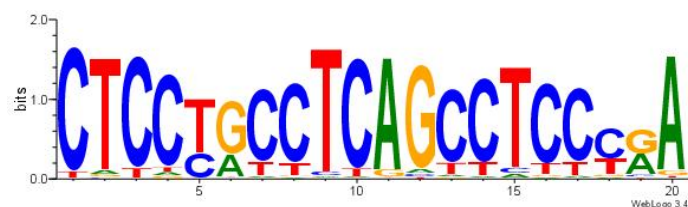
Best Matches for Motif ID 161 (Highest to Lowest)

Dataset #: 1
Motif ID: 26
Motif name: Motif 26
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 2
Number of overlap: 17
Similarity score: 0.0527497

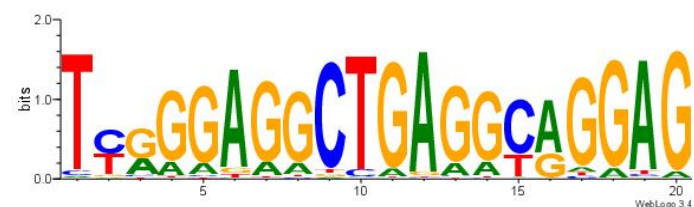
Alignment:

TMGGGAGGCTGAGGCAGGAG
--GAGGAGGRGGAGGDGGV--

Original motif Consensus sequence: CTCCTGCCTCAGCCTCCCRA



Reverse complement motif Consensus sequence: TMGGGAGGCTGAGGCAGGAG



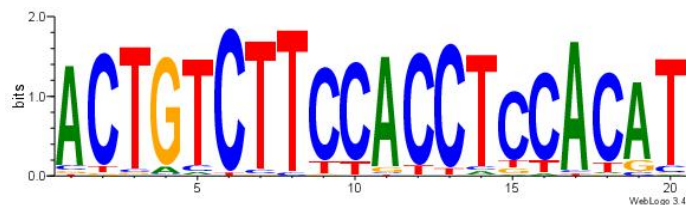
Dataset #: 1
Motif ID: 178
Motif name: Motif 178
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement

Direction: Backward
Position number: 2
Number of overlap: 17
Similarity score: 0.0591495

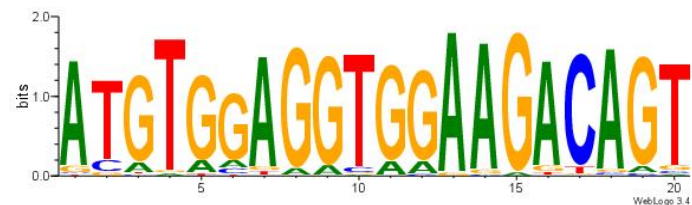
Alignment:

ATGTGGAGGTGGAAGACAGT
--GAGGAGGRGGAGGDGGV--

Original motif Consensus sequence: ACTGTCTTCCACCTCCACAT



Reverse complement motif Consensus sequence: ATGTGGAGGTGGAAGACAGT

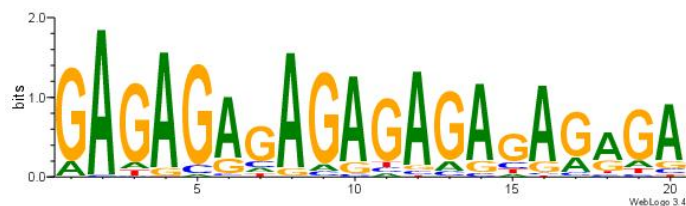


Dataset #: 1
Motif ID: 109
Motif name: Motif 109
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 4
Number of overlap: 17
Similarity score: 0.062256

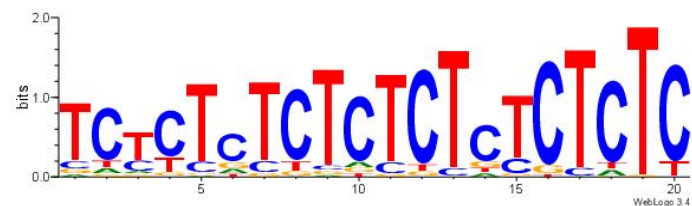
Alignment:

GAGAGAGAGAGAGAGAGA
---GAGGAGGRGGAGGDGGV

Original motif Consensus sequence: GAGAGAGAGAGAGAGAGA



Reverse complement motif Consensus sequence: TCTCTCTCTCTCTCTCTC

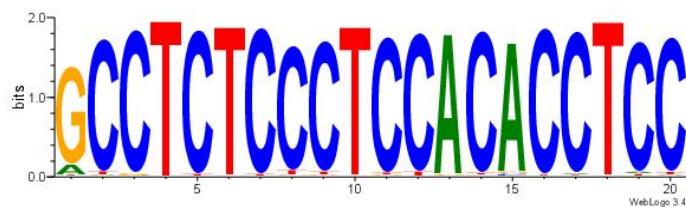


Dataset #: 1
Motif ID: 105
Motif name: Motif 105
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 4
Number of overlap: 17
Similarity score: 0.0741592

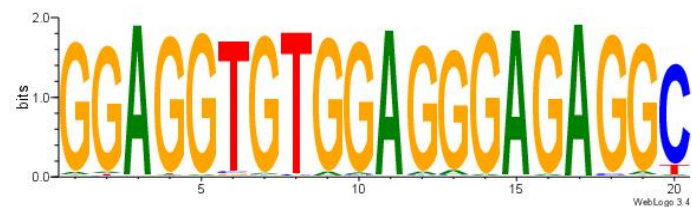
Alignment:

```
GCCTCTCCCTCCACACCTCC  
---VCCDCCTCCKCCTCCTC
```

Original motif Consensus sequence: GCCTCTCCCTCCACACCTCC



Reverse complement motif Consensus sequence: GGAGGTGTGGAGGGAGAGGC

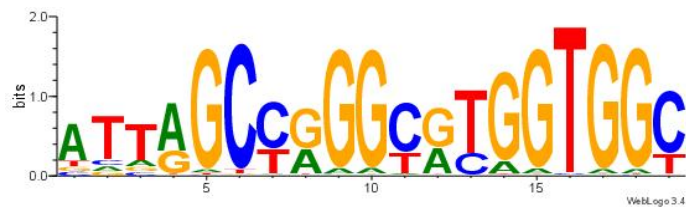


Dataset #: 1
 Motif ID: 2
 Motif name: Motif 2
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 17
 Similarity score: 0.080042

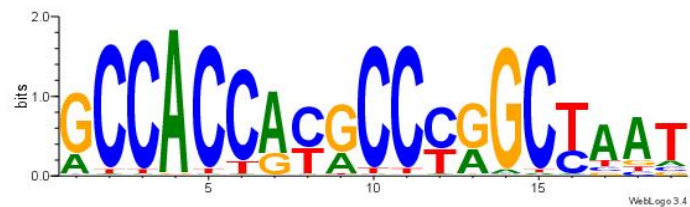
Alignment:

ATTAGCYRGGCRTGGTGGC
 --GAGGAGGRGGAGGDGGV

Original motif Consensus sequence: ATTAGCYRGGCRTGGTGGC



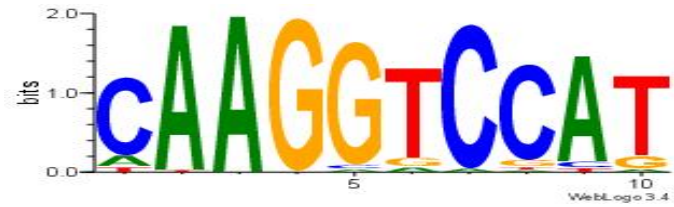
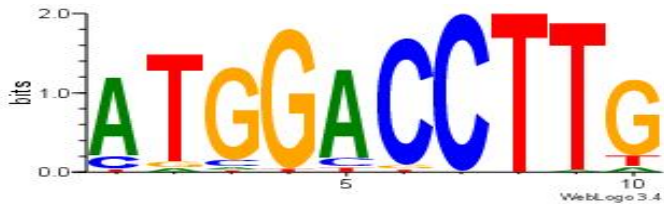
Reverse complement motif Consensus sequence: GCCACCMGCCMKGCTAAT



Dataset #: 1 Motif ID: 162 Motif name: Motif 162

Original motif Consensus sequence: ATGGACCTTG

Reverse complement motif Consensus sequence: CAAGGTCCAT



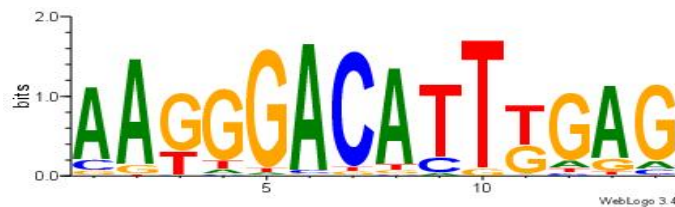
Best Matches for Motif ID 162 (Highest to Lowest)

Dataset #: 1
 Motif ID: 166
 Motif name: Motif 166
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 10
 Similarity score: 0.0562526

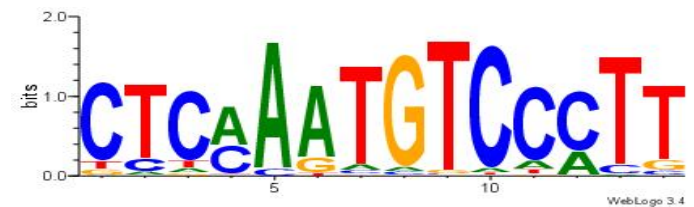
Alignment:

AAGGGACATTKGAG
 -ATGGACCTTG---

Original motif Consensus sequence: AAGGGACATTKGAG



Reverse complement motif Consensus sequence: CTCRAATGTCCCT



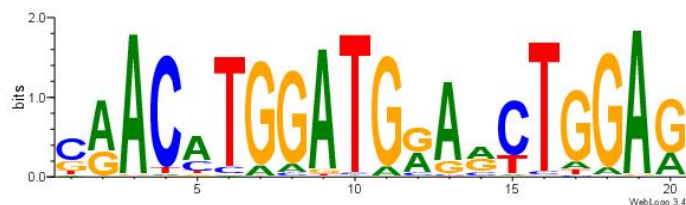
Dataset #: 1

Motif ID: 104
 Motif name: Motif 104
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 9
 Number of overlap: 10
 Similarity score: 0.0574028

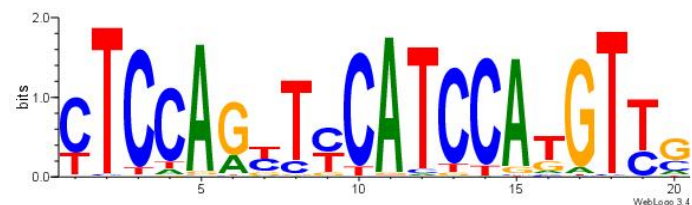
Alignment:

CTCCAGKTMCATCCATGTTG
 --CAAGGTCCAT-----

Original motif Consensus sequence: CAACATGGATGRARCTGGAG



Reverse complement motif Consensus sequence: CTCCAGKTMCATCCATGTTG



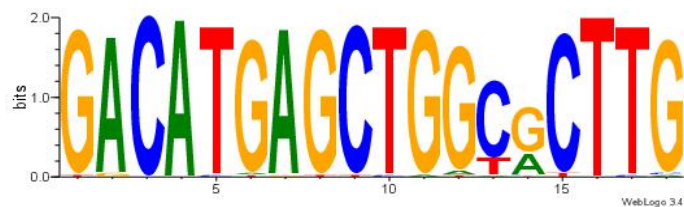
Dataset #: 1
 Motif ID: 306
 Motif name: Motif 306
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 10

Similarity score: 0.0633278

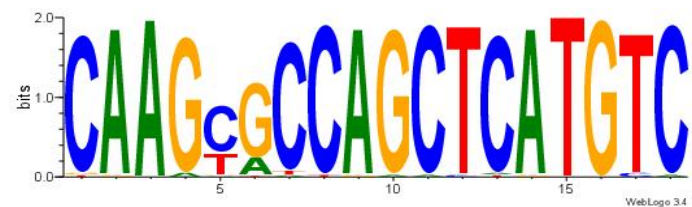
Alignment:

GACATGAGCTGGCGCTTG
-----ATGGACCTTG

Original motif Consensus sequence: GACATGAGCTGGCGCTTG



Reverse complement motif Consensus sequence:
CAAGCGCCAGCTCATGTC



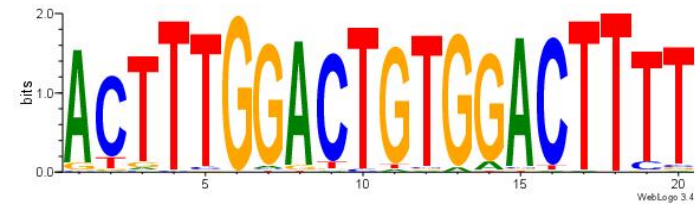
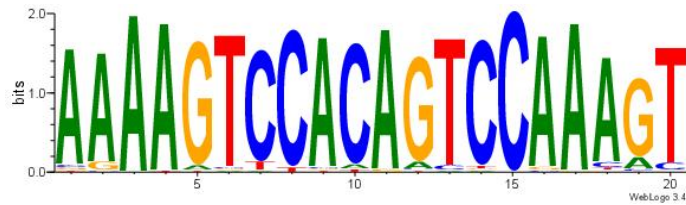
Dataset #: 1
Motif ID: 171
Motif name: Motif 171
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 10
Similarity score: 0.0659068

Alignment:

AAAAGTCCACAGTCCAAAGT
CAAGGTCCAT-----

Original motif Consensus sequence: AAAAGTCCACAGTCCAAAGT

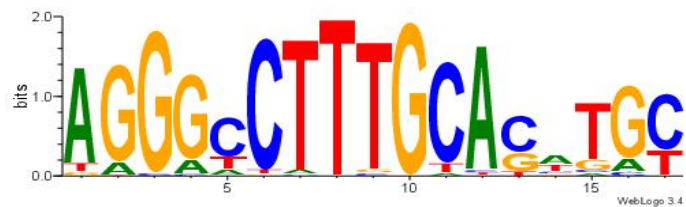
Reverse complement motif Consensus sequence:
ACTTTGGACTGTGGACTTTT



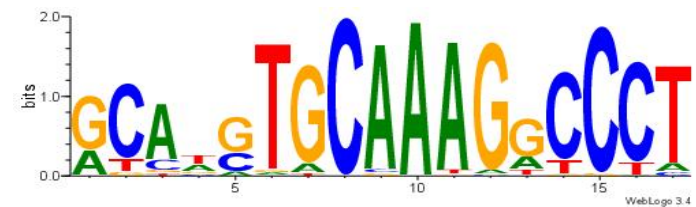
Dataset #: 1
 Motif ID: 322
 Motif name: Motif 322
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 8
 Number of overlap: 10
 Similarity score: 0.0673833

Alignment:
 GCAWSTGCAAAGGCCCT
 -----CAAGGTCCAT

Original motif Consensus sequence: AGGGCCTTGCASWTGC



Reverse complement motif Consensus sequence: GCAWSTGCAAAGGCCCT

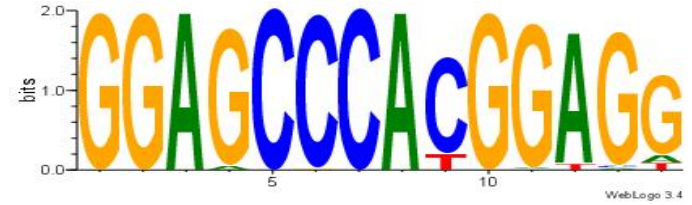


Dataset #: 1 Motif ID: 163 Motif name: Motif 163

Original motif Consensus sequence: CCTCCGTGGGCTCC



Reverse complement motif Consensus sequence: GGAGCCCACGGAGG



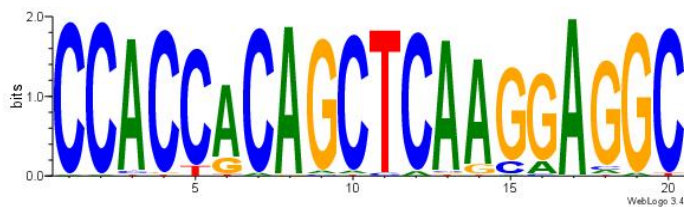
Best Matches for Motif ID 163 (Highest to Lowest)

Dataset #:	1
Motif ID:	331
Motif name:	Motif 331
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2
Number of overlap:	14
Similarity score:	0.0750229

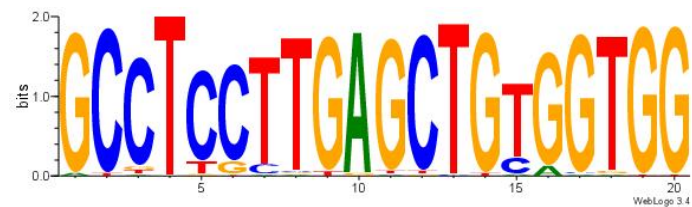
Alignment:

```
CCACCACAGCTCAAGGAGGC
-----GGAGCCCACGGAGG-
```

Original motif Consensus sequence: CCACCACAGCTCAAGGAGGC



Reverse complement motif Consensus sequence: GCCTCCTTGAGCTGTGGTGG

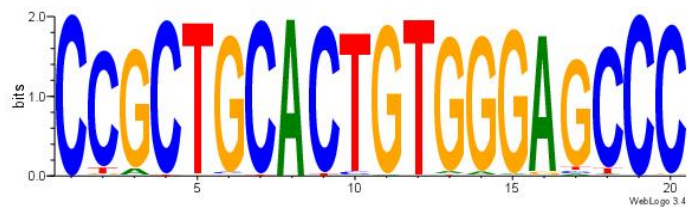


Dataset #: 1
 Motif ID: 144
 Motif name: Motif 144
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 14
 Similarity score: 0.0899923

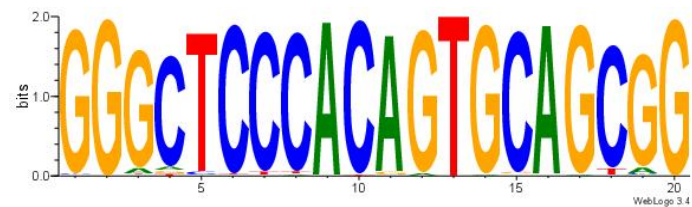
Alignment:

GGGCTCCCACAGTGCAGCGG
 -GGAGCCCACGGAGG-----

Original motif Consensus sequence: CCGCTGCACTGTGGGAGCCC



Reverse complement motif Consensus sequence: GGGCTCCCACAGTGCAGCGG



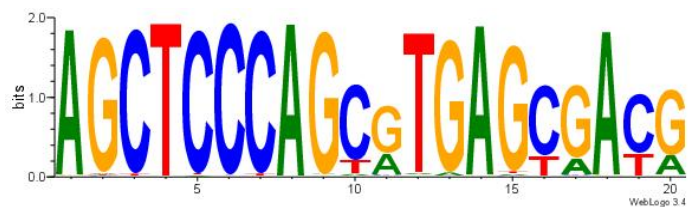
Dataset #: 1
 Motif ID: 48
 Motif name: Motif 48
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 6

Number of overlap: 14
Similarity score: 0.102654

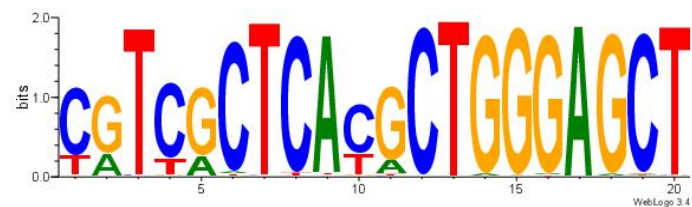
Alignment:

CGTCGCTCACGCTGGGAGCT
-GGAGCCCACGGAGG-----

Original motif Consensus sequence: AGCTCCCAGCGTGAGCGACG



Reverse complement motif Consensus sequence:
CGTCGCTCACGCTGGGAGCT

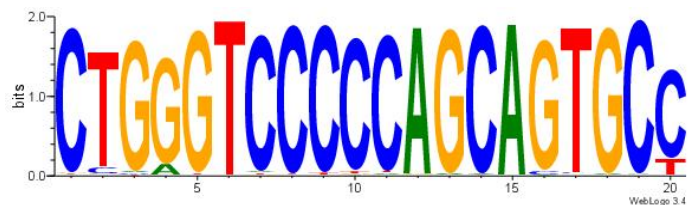


Dataset #: 1
Motif ID: 84
Motif name: Motif 84
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 4
Number of overlap: 14
Similarity score: 0.104798

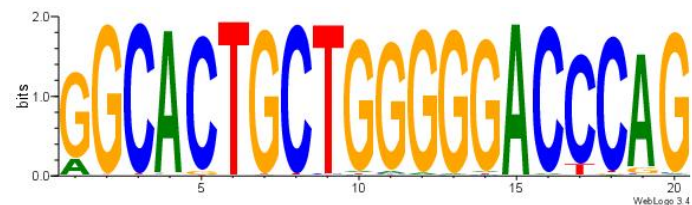
Alignment:

GGCACTGCTGGGGGACCCAG
---CCTCCGTGGGCTCC---

Original motif Consensus sequence: CTGGGTCCCCCAGCAGTGCC



Reverse complement motif Consensus sequence: GGCAGTCTGGGGGACCCAG

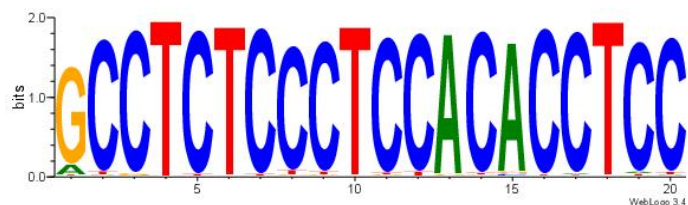


Dataset #: 1
Motif ID: 105
Motif name: Motif 105
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 4
Number of overlap: 14
Similarity score: 0.105867

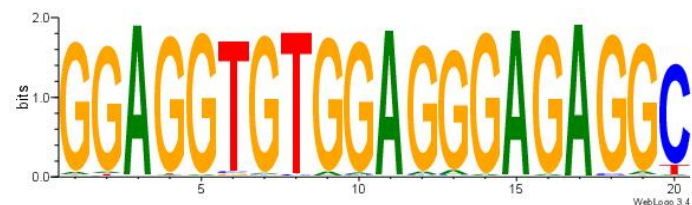
Alignment:

```
GCCTCTCCCTCCACACCTCC  
---CCTCCGTGGGCTCC---
```

Original motif Consensus sequence: GCCTCTCCCTCCACACCTCC

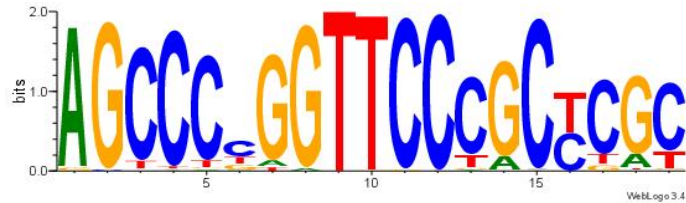


Reverse complement motif Consensus sequence: GGAGGTGTGGAGGGAGAGGC

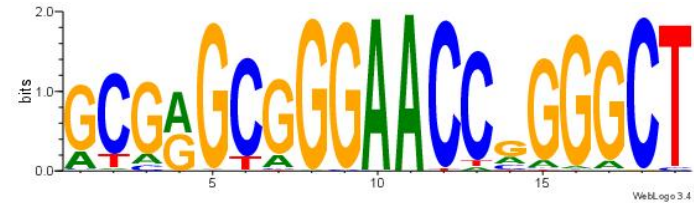


Dataset #: 1 Motif ID: 164 Motif name: Motif 164

Original motif Consensus sequence: AGCCCCGGTCCCGCYCGC



Reverse complement motif Consensus sequence: GCGMGCGGGAACCGGGGCT



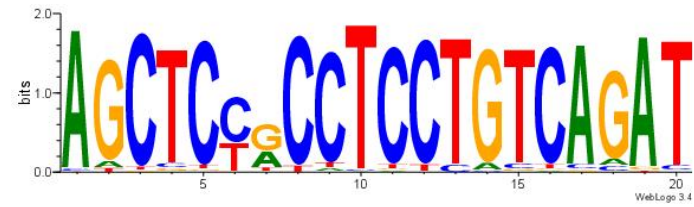
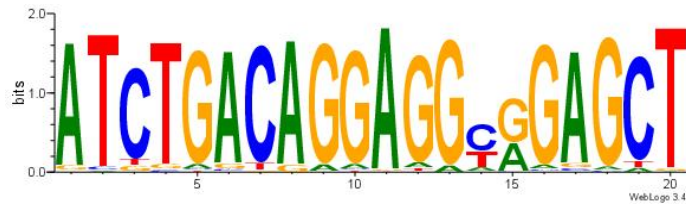
Best Matches for Motif ID 164 (Highest to Lowest)

Dataset #:	1
Motif ID:	165
Motif name:	Motif 165
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	2
Number of overlap:	19
Similarity score:	0.102596

Alignment:
 AGCTCMKCCTCCTGTCAGAT
 AGCCCCGGTCCCGCYCGC-

Original motif Consensus sequence: ATCTGACAGGAGGYRGAGCT

Reverse complement motif Consensus sequence:
 AGCTCMKCCTCCTGTCAGAT



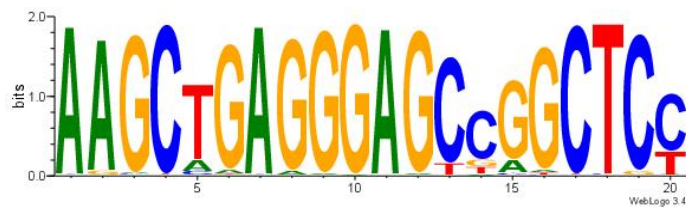
Dataset #: 1
 Motif ID: 96
 Motif name: Motif 96
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 19
 Similarity score: 0.111018

Alignment:

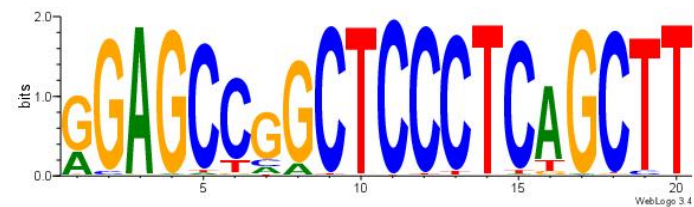
```

GGAGCCGGCTCCCTCAGCTT
-AGCCCCGGTTCCCGCYCGC
  
```

Original motif Consensus sequence: AAGCTGAGGGAGCCGGCTCC



Reverse complement motif Consensus sequence: GGAGCCGGCTCCCTCAGCTT



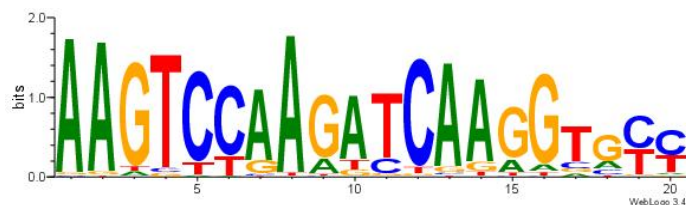
Dataset #: 1

Motif ID: 119
 Motif name: Motif 119
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 19
 Similarity score: 0.112548

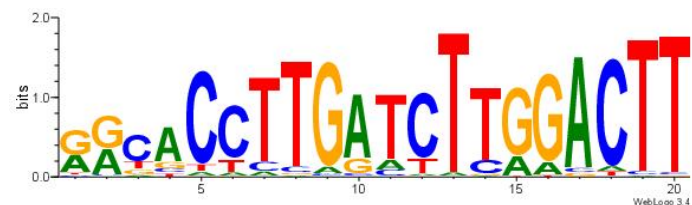
Alignment:

KKCACCTTGATCTTGGACTT
 GCGMGCGGGAACCGGGGCT-

Original motif Consensus sequence: AAGTCCAAGATCAAGGTGY



Reverse complement motif Consensus sequence: KKCACCTTGATCTTGGACTT



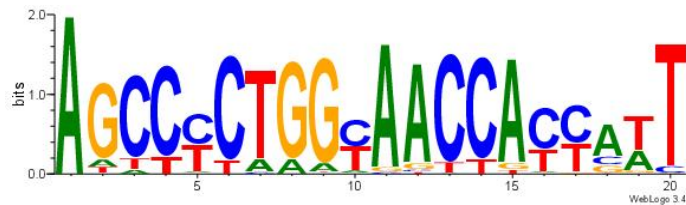
Dataset #: 1
 Motif ID: 139
 Motif name: Motif 139
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 19

Similarity score: 0.112947

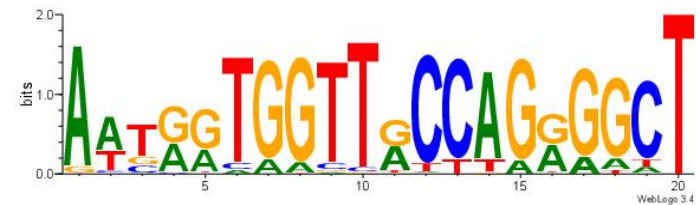
Alignment:

AGCCYCTGGYAACCAYYAWT
GCGMGCGGGAACCGGGGCT-

Original motif Consensus sequence: AGCCYCTGGYAACCAYYAWT



Reverse complement motif Consensus sequence:
AWTKKTGGTTKCCAGKGGCT



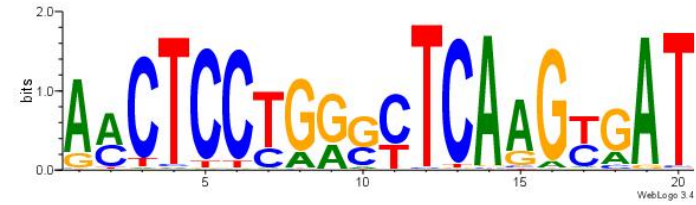
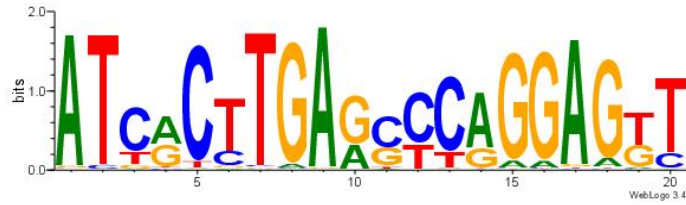
Dataset #: 1
Motif ID: 8
Motif name: Motif 8
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 2
Number of overlap: 19
Similarity score: 0.119454

Alignment:

ARCTCCTGKSCTCAAGKGAT
-GCGMGCGGGAACCGGGGCT

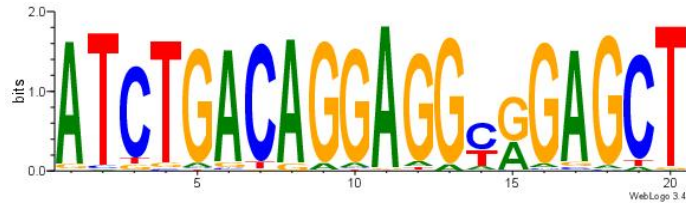
Original motif Consensus sequence: ATCRCTTGAGSYCAGGAGKT

Reverse complement motif Consensus sequence:
ARCTCCTGKSCTCAAGKGAT

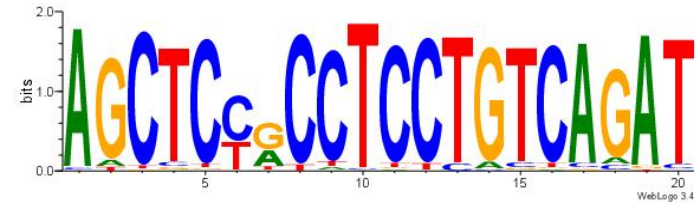


Dataset #: 1 Motif ID: 165 Motif name: Motif 165

Original motif Consensus sequence: ATCTGACAGGAGGYRGAGCT



Reverse complement motif Consensus sequence: AGCTCMKCCTCCTGTCAGAT



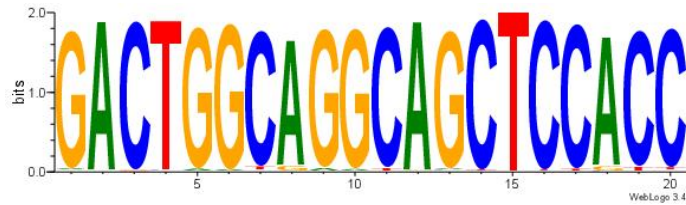
Best Matches for Motif ID 165 (Highest to Lowest)

Dataset #:	1
Motif ID:	52
Motif name:	Motif 52
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	20
Similarity score:	0.118513

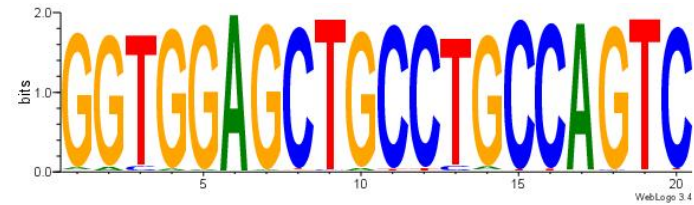
Alignment:

GGTGGAGCTGCCTGCCAGTC
AGCTCMKCCTCCTGTCAGAT

Original motif Consensus sequence: GACTGGCAGGCAGCTCCACC



Reverse complement motif Consensus sequence:
GGTGGAGCTGCCTGCCAGTC

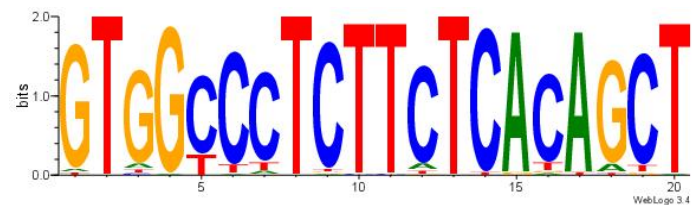
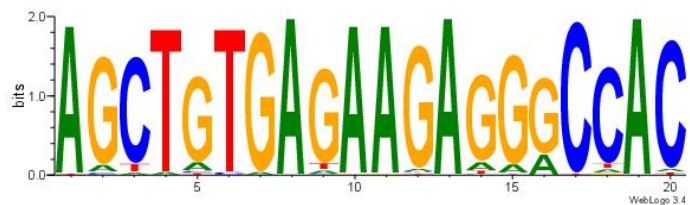


Dataset #: 1
Motif ID: 294
Motif name: Motif 294
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 20
Similarity score: 0.1205

Alignment:
GTGGCCCTCTTCTCACAGCT
AGCTCMKCCTCCTGTCAGAT

Original motif Consensus sequence: AGCTGTGAGAAGAGGGCCAC

Reverse complement motif Consensus sequence:
GTGGCCCTCTTCTCACAGCT

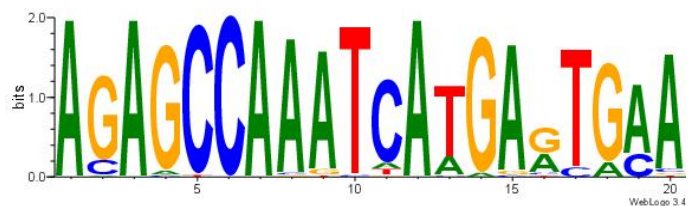


Dataset #: 1
 Motif ID: 349
 Motif name: Motif 349
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.123054

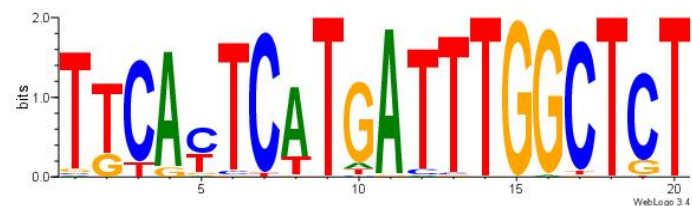
Alignment:

TTCAMTCATGATTTGGCTCT
 ATCTGACAGGAGGYRGAGCT

Original motif Consensus sequence: AGAGCCAAATCATGARTGAA



Reverse complement motif Consensus sequence: TTCAMTCATGATTTGGCTCT



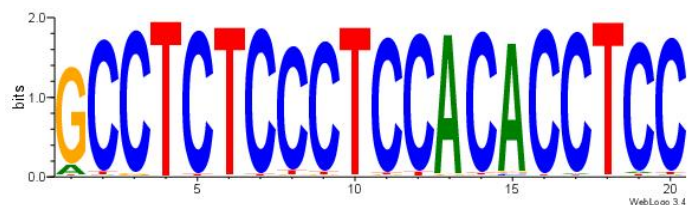
Dataset #: 1

Motif ID: 105
 Motif name: Motif 105
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.123269

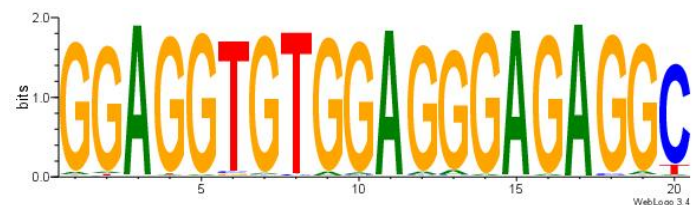
Alignment:

GCCTCTCCCTCCACACCTCC
 AGCTCMKCCTCCTGTCAGAT

Original motif Consensus sequence: GCCTCTCCCTCCACACCTCC



Reverse complement motif Consensus sequence: GGAGGTGTGGAGGGAGAGGC



Dataset #: 1
 Motif ID: 8
 Motif name: Motif 8
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 20

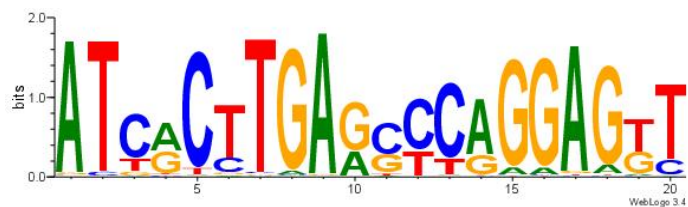
Similarity score: 0.12362

Alignment:

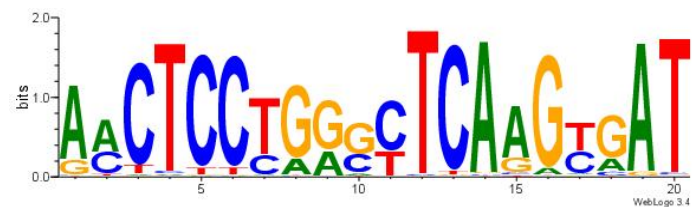
ARCTCCTGKSCTCAAGKGAT

AGCTCMKCCTCCTGTCAGAT

Original motif Consensus sequence: ATCRCTTGAGSYCAGGAGKT

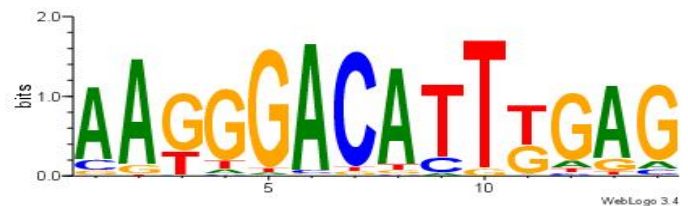


Reverse complement motif Consensus sequence: ARCTCCTGKSCTCAAGKGAT

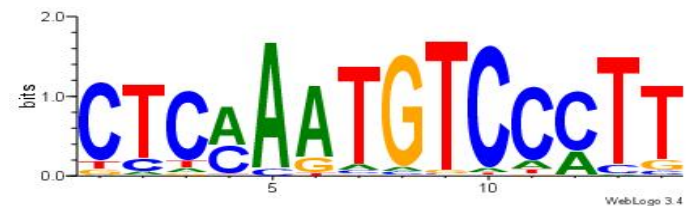


Dataset #: 1 Motif ID: 166 Motif name: Motif 166

Original motif Consensus sequence: AAGGGACATTKGAG



Reverse complement motif Consensus sequence: CTCRAATGTCCTT



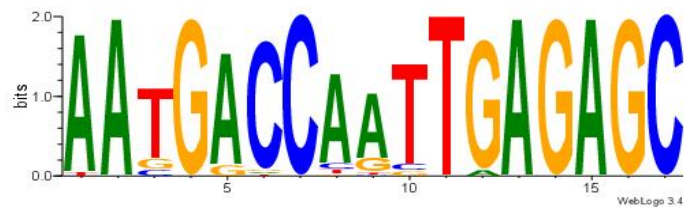
Best Matches for Motif ID 166 (Highest to Lowest)

Dataset #:	1
Motif ID:	305
Motif name:	Motif 305
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif

Direction: Backward
 Position number: 4
 Number of overlap: 14
 Similarity score: 0.0470693

Alignment:
 AATGACCAATTGAGAGC
 AAGGGACATTKGAG---

Original motif Consensus sequence: AATGACCAATTGAGAGC



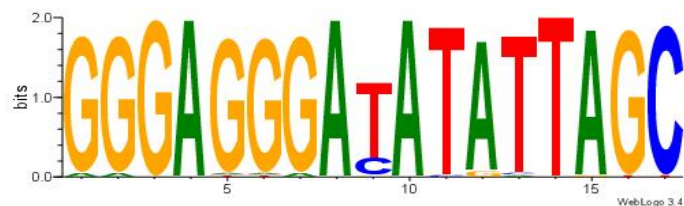
Reverse complement motif Consensus sequence: GCTCTCAATTGGTCATT



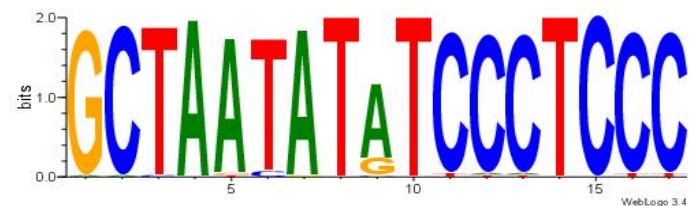
Dataset #: 1
 Motif ID: 329
 Motif name: Motif 329
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 14
 Similarity score: 0.0535951

Alignment:
 GGGAGGGATATATTAGC
 --AAGGGACATTKGAG-

Original motif Consensus sequence: GGGAGGGATATATTAGC



Reverse complement motif Consensus sequence: GCTAATATATCCCTCCC

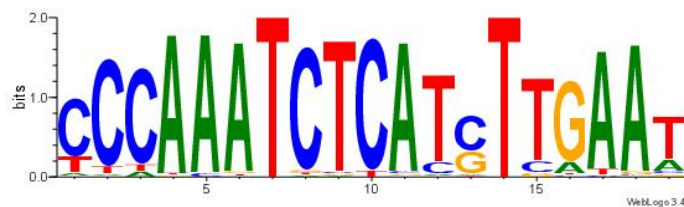


Dataset #: 1
Motif ID: 227
Motif name: Motif 227
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 14
Similarity score: 0.0576035

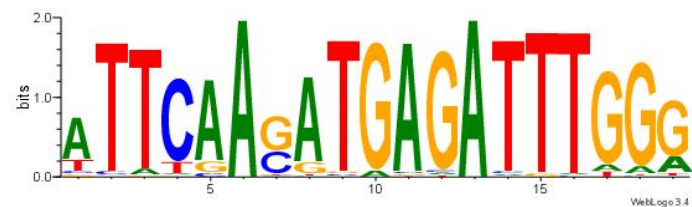
Alignment:

CCCAAATCTCATSTTGAAT
CTCRAATGTCCCTT-----

Original motif Consensus sequence: CCCAAATCTCATSTTGAAT



Reverse complement motif Consensus sequence: ATTC AATGAGATTTGGG

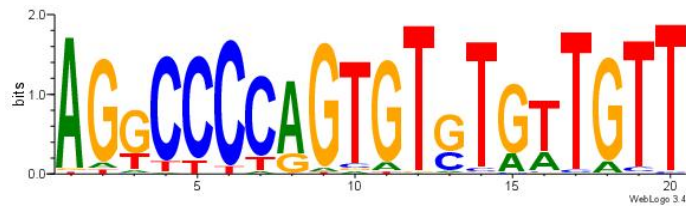


Dataset #: 1
 Motif ID: 176
 Motif name: Motif 176
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 4
 Number of overlap: 14
 Similarity score: 0.0589344

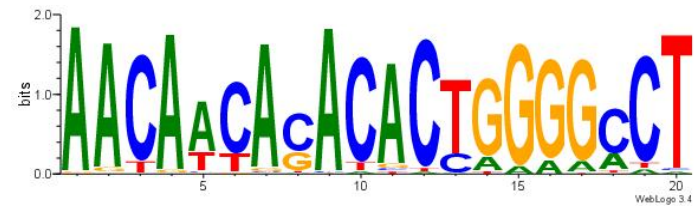
Alignment:

AAC AACASACTGGGGCCT
 ---AAGGGACATTKGAG---

Original motif Consensus sequence: AGGCCCCAGTGTSTGTTGTT



Reverse complement motif Consensus sequence: AAC AACASACTGGGGCCT

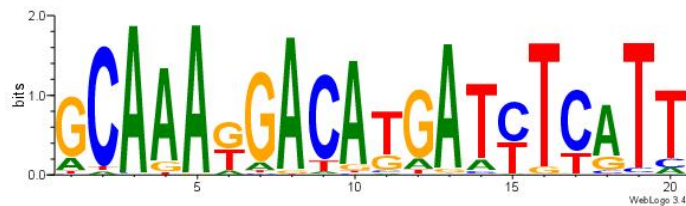


Dataset #: 1
 Motif ID: 99
 Motif name: Motif 99
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3

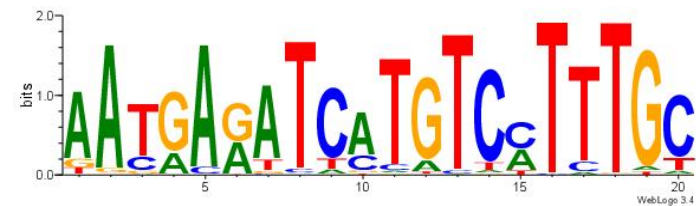
Number of overlap: 14
 Similarity score: 0.0601117

Alignment:
 AATGAKATCATGTCYTTTGC
 ----CTCRAATGTCCTT--

Original motif Consensus sequence: GCAAAGACATGATYTCATT

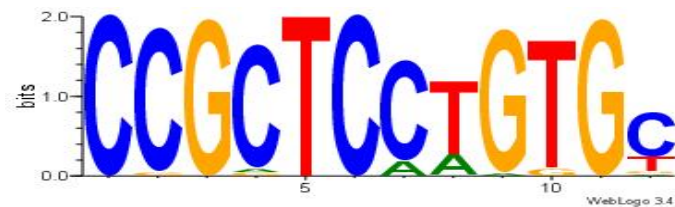


Reverse complement motif Consensus sequence: AATGAKATCATGTCYTTTGC

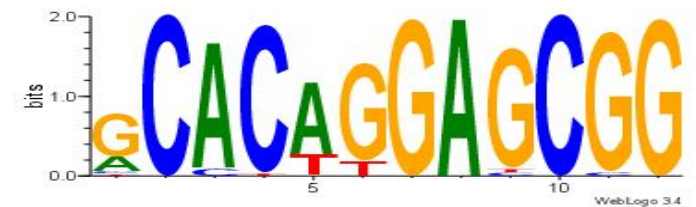


Dataset #: 1 Motif ID: 167 Motif name: Motif 167

Original motif Consensus sequence: CCGCTCCTGTGC



Reverse complement motif Consensus sequence: GCACAGGAGCGG



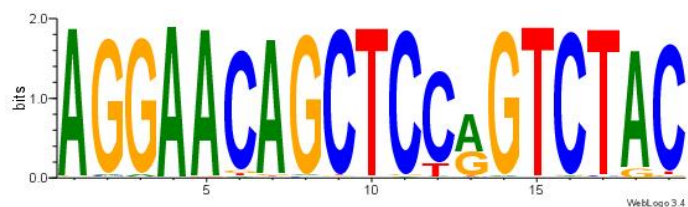
Best Matches for Motif ID 167 (Highest to Lowest)

Dataset #: 1
 Motif ID: 62
 Motif name: Motif 62
 Matching format of first motif: Original Motif

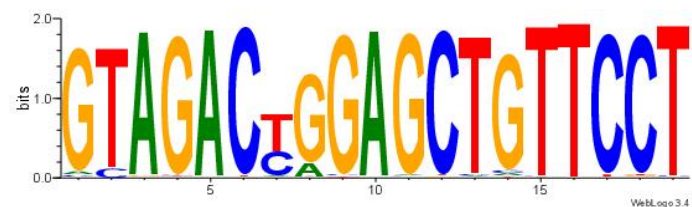
Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 12
 Similarity score: 0.0721943

Alignment:
 AGGAACAGCTCCRGCTCTAC
 -----CCGCTCCTGTGC--

Original motif Consensus sequence: AGGAACAGCTCCRGCTCTAC



Reverse complement motif Consensus sequence:
 GTAGACKGGAGCTGTTCCCT

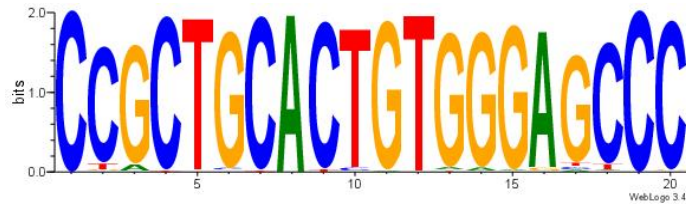


Dataset #: 1
 Motif ID: 144
 Motif name: Motif 144
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 12
 Similarity score: 0.0736876

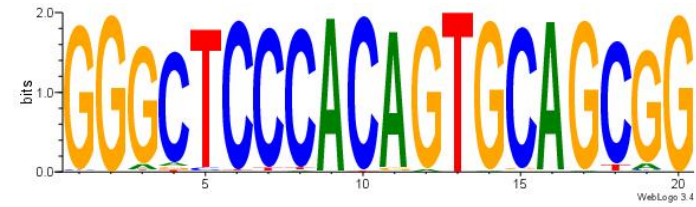
Alignment:

CCGCTGCACTGTGGGAGCCC
CCGCTCCTGTGC-----

Original motif Consensus sequence: CCGCTGCACTGTGGGAGCCC



Reverse complement motif Consensus sequence:
GGGCTCCCACAGTGCAGCGG



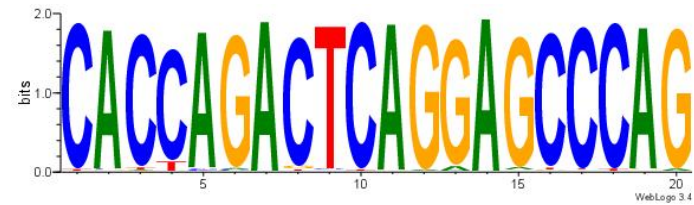
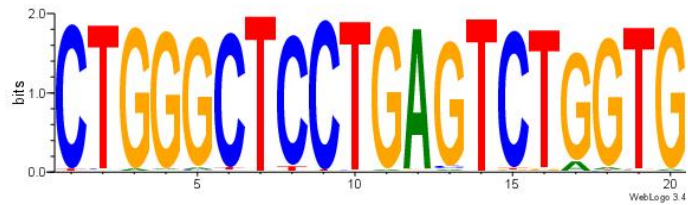
Dataset #: 1
Motif ID: 67
Motif name: Motif 67
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 7
Number of overlap: 12
Similarity score: 0.0807459

Alignment:

CTGGGCTCCTGAGTCTGGTG
--CCGCTCCTGTGC-----

Original motif Consensus sequence: CTGGGCTCCTGAGTCTGGTG

Reverse complement motif Consensus sequence:
CACCAGACTCAGGAGCCCAG



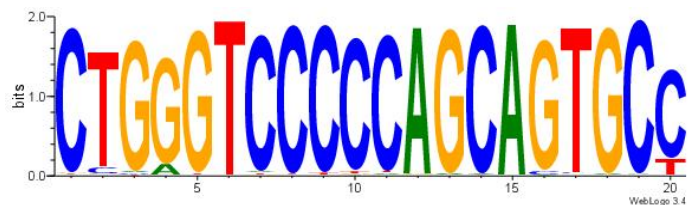
Dataset #: 1
 Motif ID: 84
 Motif name: Motif 84
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 8
 Number of overlap: 12
 Similarity score: 0.082955

Alignment:

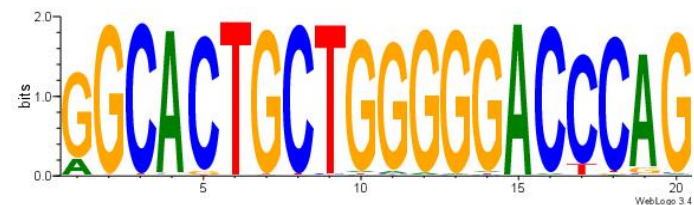
```

CTGGGTCCCCCAGCAGTGCC
-----CCGCTCCTGTGC-
  
```

Original motif Consensus sequence: CTGGGTCCCCCAGCAGTGCC



Reverse complement motif Consensus sequence: GGCAGTCTGGGGGACCCAG



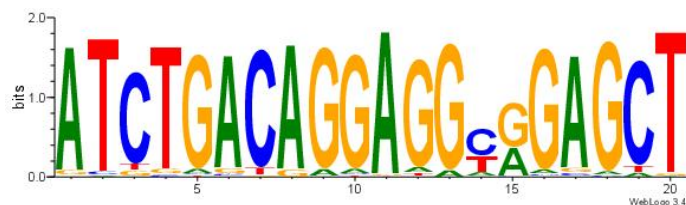
Dataset #: 1

Motif ID: 165
 Motif name: Motif 165
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 4
 Number of overlap: 12
 Similarity score: 0.0877385

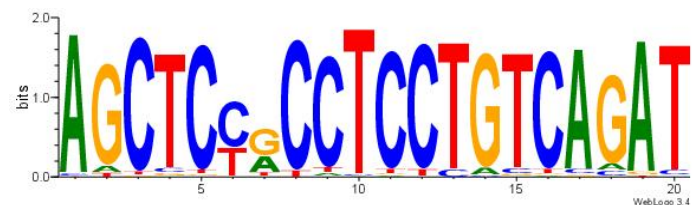
Alignment:

AGCTCMKCCTCCTGTCAGAT
 ---CCGCTCCTGTGC-----

Original motif Consensus sequence: ATCTGACAGGAGGYRGAGCT

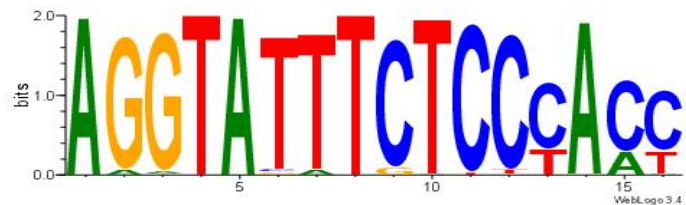


Reverse complement motif Consensus sequence: AGCTCMKCCTCCTGTCAGAT

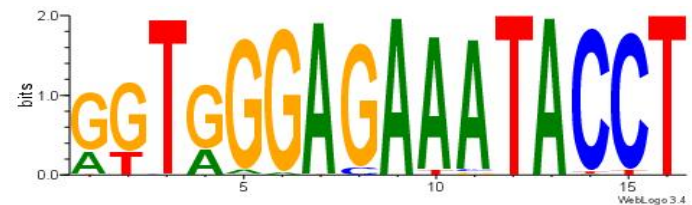


Dataset #: 1 Motif ID: 168 Motif name: Motif 168

Original motif Consensus sequence: AGGTATTTCTCCCACC



Reverse complement motif Consensus sequence: GGTGGGAGAAATACCT



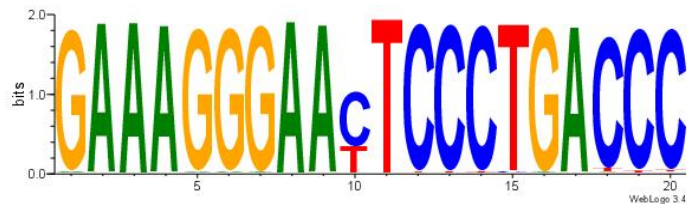
Best Matches for Motif ID 168 (Highest to Lowest)

Dataset #: 1
Motif ID: 16
Motif name: Motif 16
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 4
Number of overlap: 16
Similarity score: 0.0930663

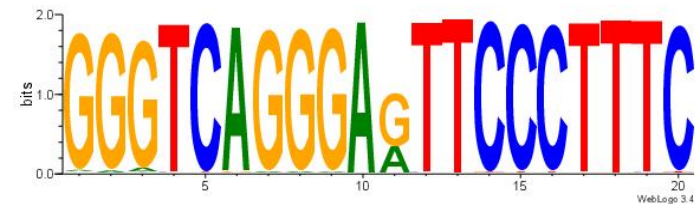
Alignment:

```
GAAAGGGA ACTCCCTGACCC  
---AGGTATTTCTCCCACC---
```

Original motif Consensus sequence: GAAAGGGA ACTCCCTGACCC



Reverse complement motif Consensus sequence:
GGGTCAGGGAG TTCCCTTTC



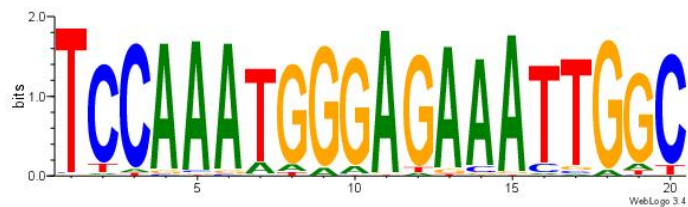
Dataset #: 1
Motif ID: 235
Motif name: Motif 235
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif

Direction: Forward
Position number: 5
Number of overlap: 16
Similarity score: 0.0952107

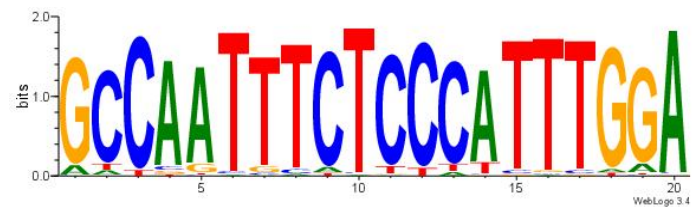
Alignment:

TCCAAATGGGAGAAATTGGC
----GGTGGGAGAAATACCT

Original motif Consensus sequence: TCCAAATGGGAGAAATTGGC



Reverse complement motif Consensus sequence: GCCAATTTCTCCCATTGGGA

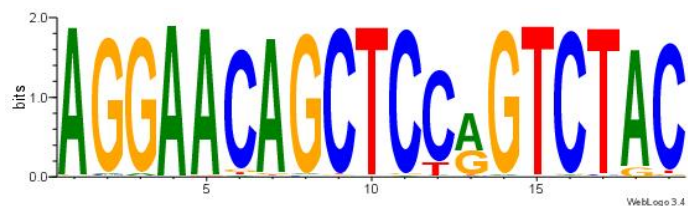


Dataset #: 1
Motif ID: 62
Motif name: Motif 62
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 4
Number of overlap: 16
Similarity score: 0.0971787

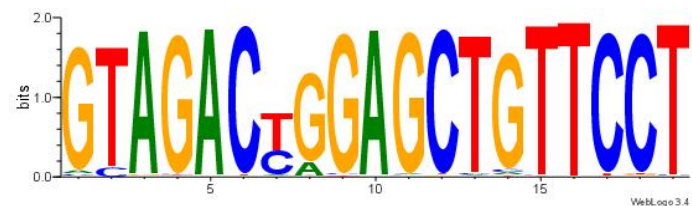
Alignment:

GTAGACKGGAGCTGTTTCCT
---GGTGGGAGAAATACCT

Original motif Consensus sequence: AGGAACAGCTCC_cAGTCTAC



Reverse complement motif Consensus sequence: GTAGACKGGAGCTGTTCCCT

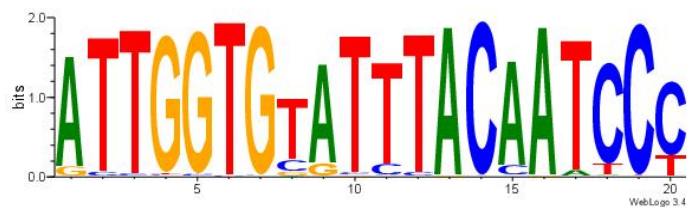


Dataset #: 1
Motif ID: 106
Motif name: Motif 106
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 3
Number of overlap: 16
Similarity score: 0.10263

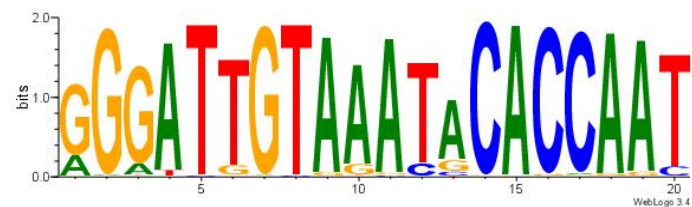
Alignment:

```
GGGATTGTAAATACACCAAT  
--GGTGGGAGAAATACCT--
```

Original motif Consensus sequence: ATTGGTGTATTACAATCC_c



Reverse complement motif Consensus sequence: GGGATTGTAAATACACCAAT

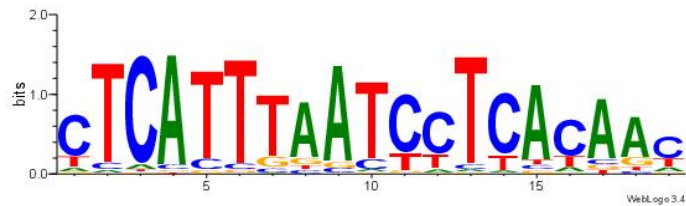


Dataset #: 1
 Motif ID: 102
 Motif name: Motif 102
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 16
 Similarity score: 0.104426

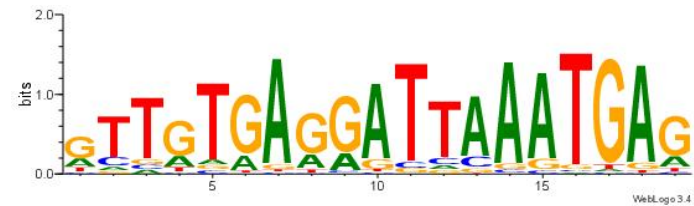
Alignment:

CTCATTTAATCCTCACAAC
 ---AGGTATTTCTCCCACC

Original motif Consensus sequence: CTCATTTAATCCTCACAAC



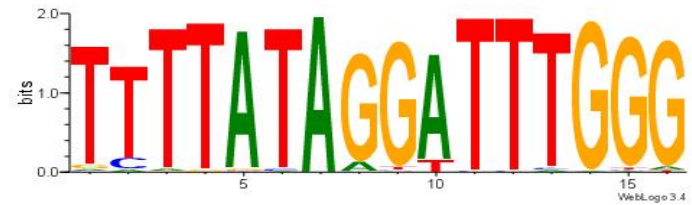
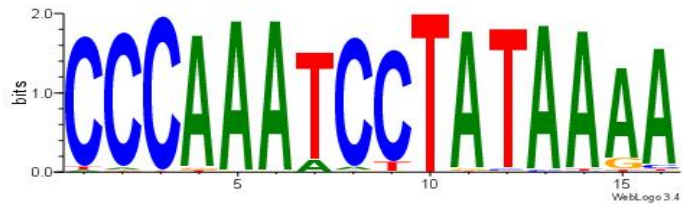
Reverse complement motif Consensus sequence: GTTGTGAGGATTAATGAG



Dataset #: 1 Motif ID: 169 Motif name: Motif 169

Original motif Consensus sequence: CCCAATCCTATAAAA

Reverse complement motif Consensus sequence: TTTTATAGGATTTGGG



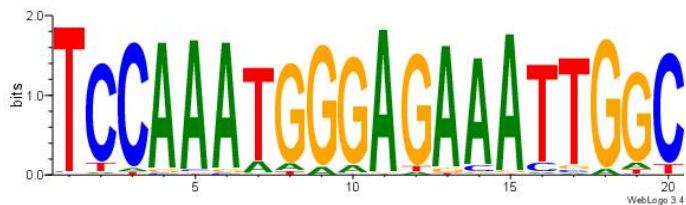
Best Matches for Motif ID 169 (Highest to Lowest)

Dataset #: 1
 Motif ID: 235
 Motif name: Motif 235
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 16
 Similarity score: 0.0869109

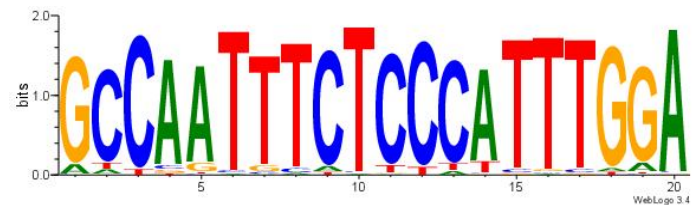
Alignment:

GCCAATTTCTCCCATTTGGA
 ----TTTTATAGGATTTGGG

Original motif Consensus sequence: TCCAATGGGAGAAATTGGC



Reverse complement motif Consensus sequence:
 GCCAATTTCTCCCATTTGGA

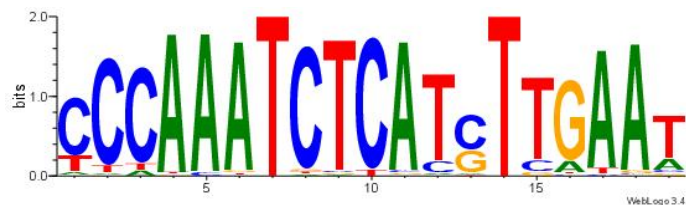


Dataset #: 1
 Motif ID: 227
 Motif name: Motif 227
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 16
 Similarity score: 0.0879004

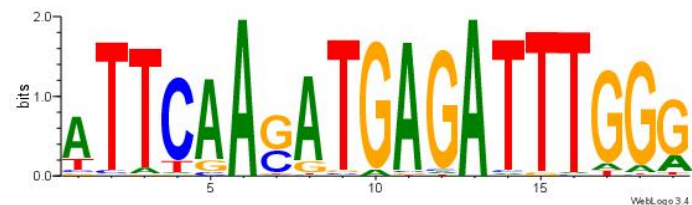
Alignment:

CCCAAATCTCATSTTGAAT
 CCCAAATCCTATAAAA---

Original motif Consensus sequence: CCCAAATCTCATSTTGAAT



Reverse complement motif Consensus sequence: ATTCAASATGAGATTTGGG



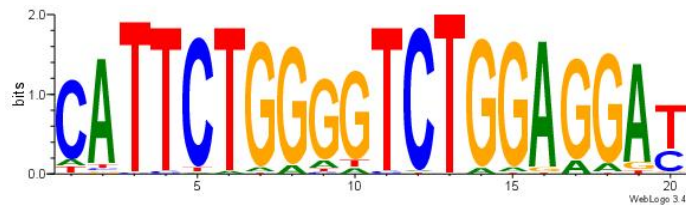
Dataset #: 1
 Motif ID: 309
 Motif name: Motif 309
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1

Number of overlap: 16
Similarity score: 0.0971624

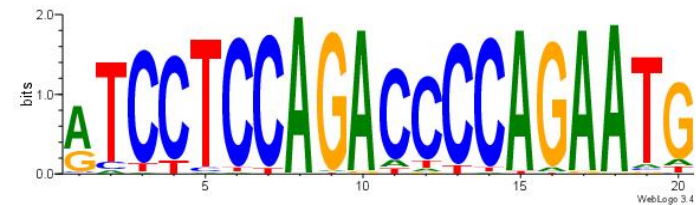
Alignment:

CATTCTGGGGTCTGGAGGAY
TTTTATAGGATTTGGG----

Original motif Consensus sequence: CATTCTGGGGTCTGGAGGAY



Reverse complement motif Consensus sequence:
MTCCTCCAGACCCCAGAATG

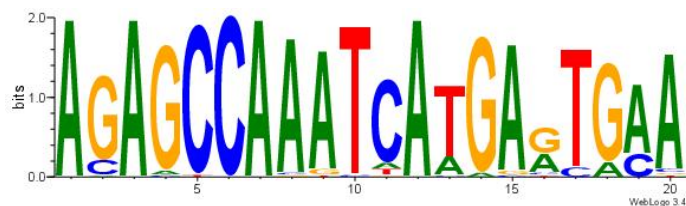


Dataset #: 1
Motif ID: 349
Motif name: Motif 349
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 4
Number of overlap: 16
Similarity score: 0.0994535

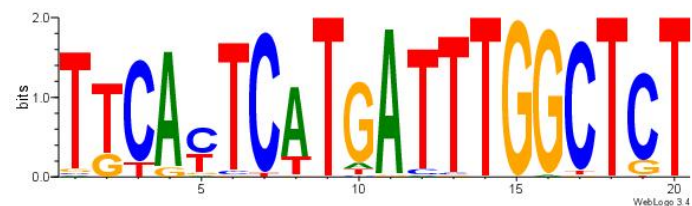
Alignment:

AGAGCCAAATCATGARTGAA
---CCCAAATCCTATAAAA-

Original motif Consensus sequence: AGAGCCAAATCATGARTGAA



Reverse complement motif Consensus sequence: TTCAMTCATGATTTGGCTCT

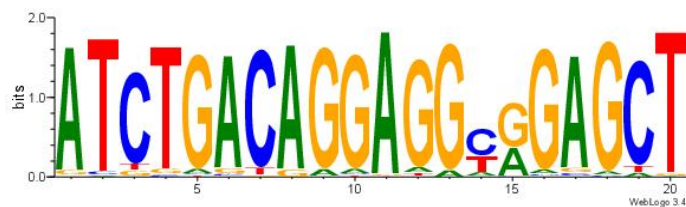


Dataset #: 1
Motif ID: 165
Motif name: Motif 165
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 2
Number of overlap: 16
Similarity score: 0.100749

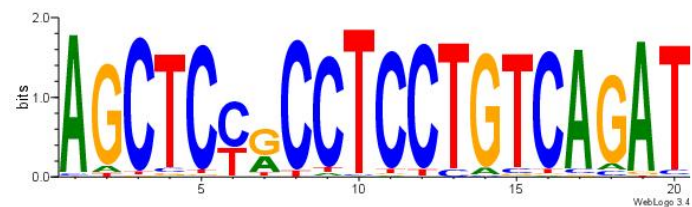
Alignment:

AGCTCMKCCTCCTGTCAGAT
-CCCAAATCCTATAAAA---

Original motif Consensus sequence: ATCTGACAGGAGGYRGAGCT

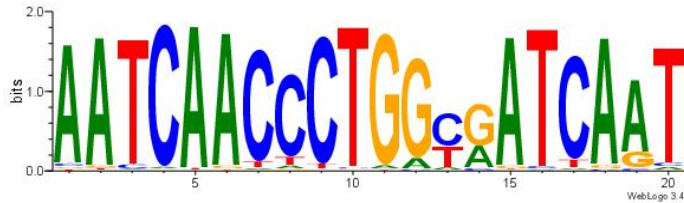


Reverse complement motif Consensus sequence: AGCTCMKCCTCCTGTCAGAT

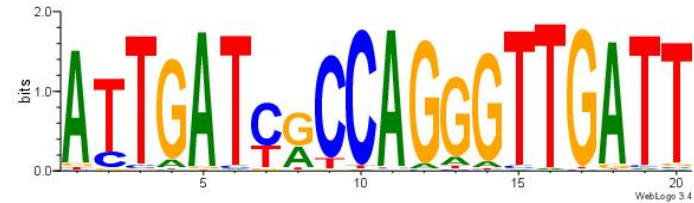


Dataset #: 1 Motif ID: 170 Motif name: Motif 170

Original motif Consensus sequence: AATCAACCCTGGYRATCAAT



Reverse complement motif Consensus sequence: ATTGATMKCCAGGGTTGATT



Best Matches for Motif ID 170 (Highest to Lowest)

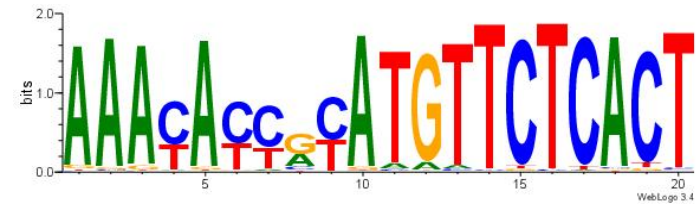
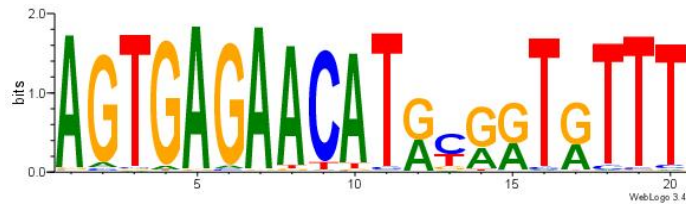
Dataset #:	1
Motif ID:	63
Motif name:	Motif 63
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	20
Similarity score:	0.0971686

Alignment:

```
AGTGAGAACATRYRRTRTTT
ATTGATMKCCAGGGTTGATT
```

Original motif Consensus sequence: AGTGAGAACATRYRRTRTTT

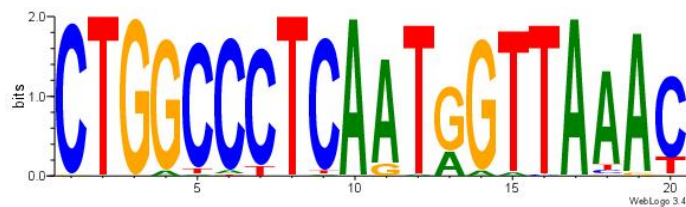
Reverse complement motif Consensus sequence: AAAMAMMKMATGTTCTCACT



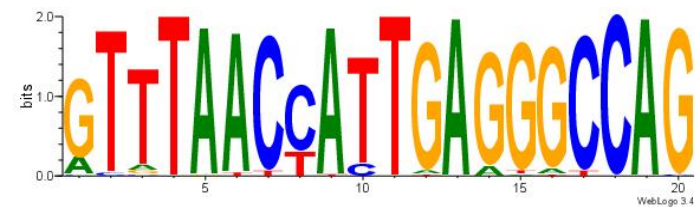
Dataset #: 1
 Motif ID: 332
 Motif name: Motif 332
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.114396

Alignment:
 CTGGCCCTCAATGGTTAAAC
 ATTGATMKCCAGGGTTGATT

Original motif Consensus sequence: CTGGCCCTCAATGGTTAAAC



Reverse complement motif Consensus sequence: GTTTAACCATTGAGGGCCAG



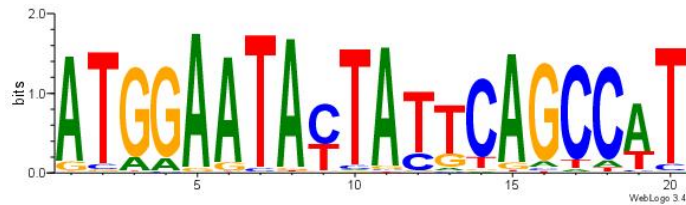
Dataset #: 1

Motif ID: 55
 Motif name: Motif 55
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.115985

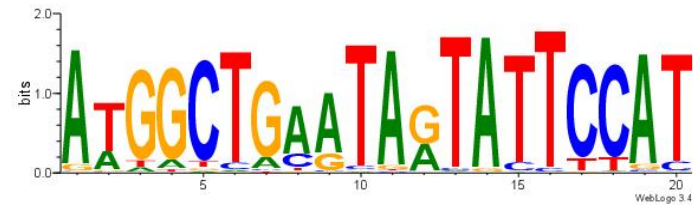
Alignment:

ATGGCTGAATAKTATTCCAT
 ATTGATMKCCAGGGTTGATT

Original motif Consensus sequence: ATGGAATAYTATTCAGCCAT



Reverse complement motif Consensus sequence: ATGGCTGAATAKTATTCCAT



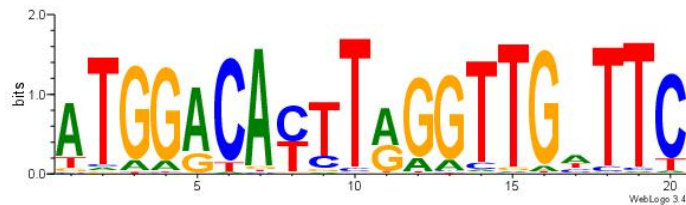
Dataset #: 1
 Motif ID: 58
 Motif name: Motif 58
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 20

Similarity score: 0.117799

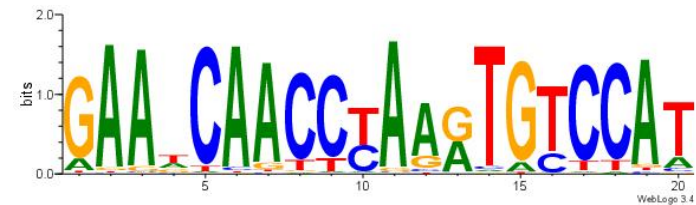
Alignment:

GAAHCAACCKAAKTGTCCAT
AATCAACCCTGGYRATCAAT

Original motif Consensus sequence: ATGGACAYTTRGGTTGHTTC



Reverse complement motif Consensus sequence:
GAAHCAACCKAAKTGTCCAT



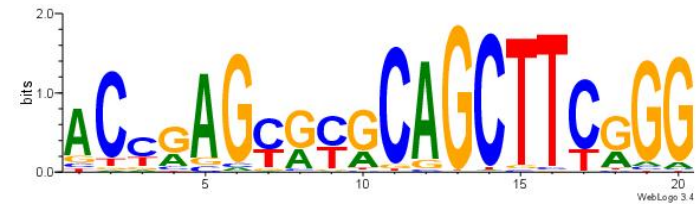
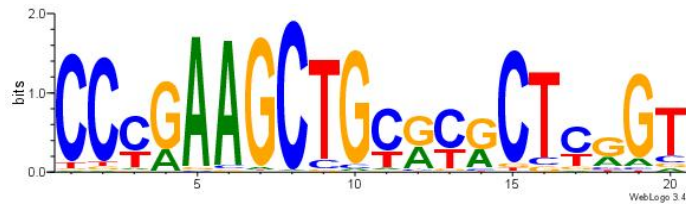
Dataset #: 1
Motif ID: 177
Motif name: Motif 177
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 20
Similarity score: 0.120018

Alignment:

CCCGAAGCTGCRYRCTCGGT
AATCAACCCTGGYRATCAAT

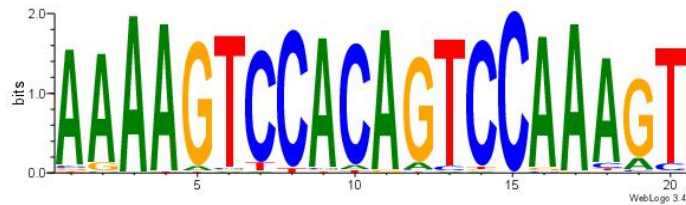
Original motif Consensus sequence: CCCGAAGCTGCRYRCTCGGT

Reverse complement motif Consensus sequence:
ACCGAGMKMGCAGCTTCGGG

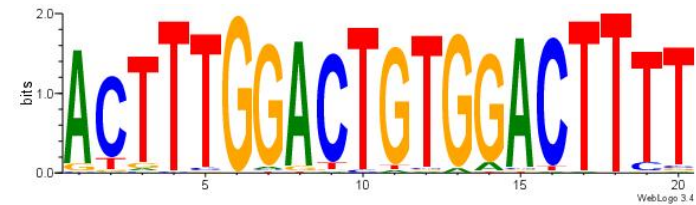


Dataset #: 1 Motif ID: 171 Motif name: Motif 171

Original motif Consensus sequence: AAAAGTCCACAGTCCAAAGT



Reverse complement motif Consensus sequence: ACTTTGGACTGTGGACTTTT



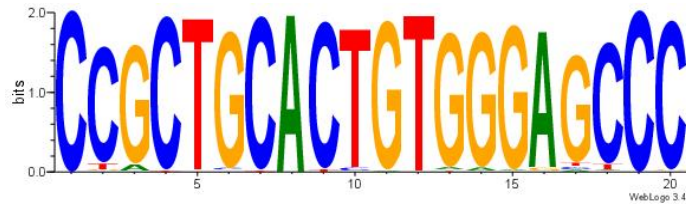
Best Matches for Motif ID 171 (Highest to Lowest)

Dataset #:	1
Motif ID:	144
Motif name:	Motif 144
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	20
Similarity score:	0.11926

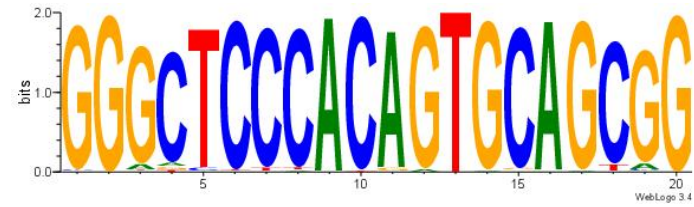
Alignment:

CCGCTGCACTGTGGGAGCCC
ACTTTGGACTGTGGACTTTT

Original motif Consensus sequence: CCGCTGCACTGTGGGAGCCC



Reverse complement motif Consensus sequence:
GGGCTCCCACAGTGCAGCGG



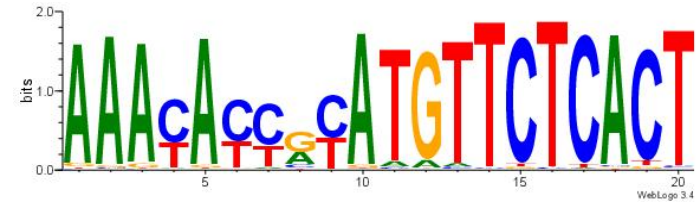
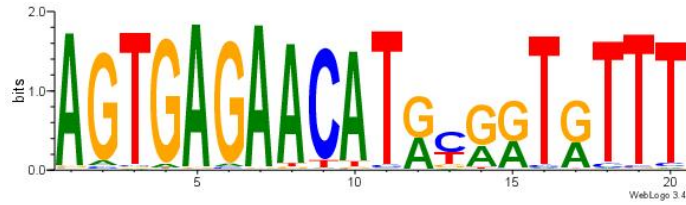
Dataset #: 1
Motif ID: 63
Motif name: Motif 63
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 20
Similarity score: 0.121669

Alignment:

AGTGAGAACATRYRRTRTTT
ACTTTGGACTGTGGACTTTT

Original motif Consensus sequence: AGTGAGAACATRYRRTRTTT

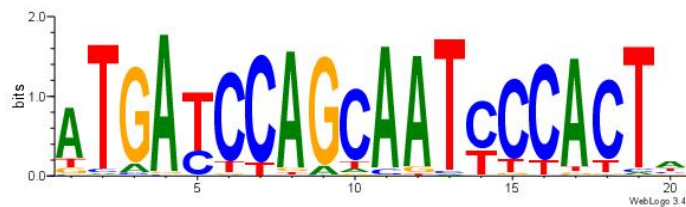
Reverse complement motif Consensus sequence:
AAAMAMMKMATGTTCTCACT



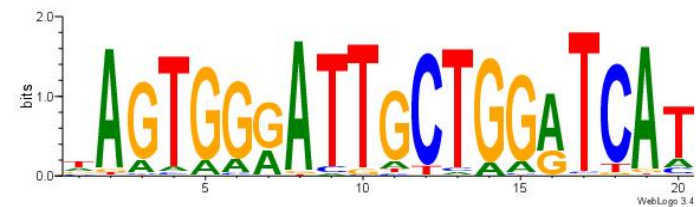
Dataset #: 1
 Motif ID: 115
 Motif name: Motif 115
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.124783

Alignment:
 HAGTGGKATTGCTGGATCAT
 ACTTTGGACTGTGGACTTTT

Original motif Consensus sequence: ATGATCCAGCAATYCCACTH



Reverse complement motif Consensus sequence: HAGTGGKATTGCTGGATCAT



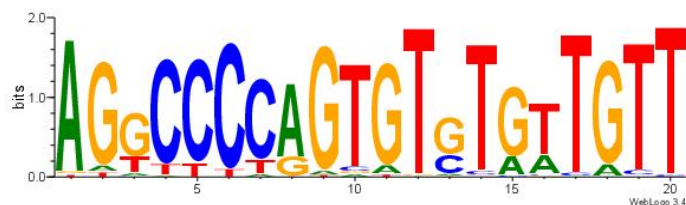
Dataset #: 1

Motif ID: 176
 Motif name: Motif 176
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.127032

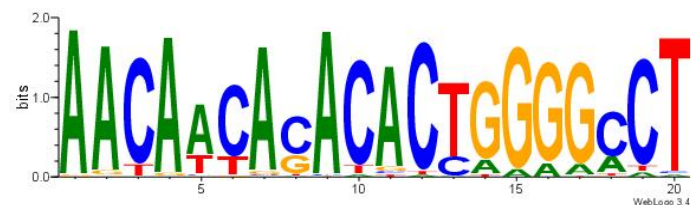
Alignment:

AGGCCCCAGTGTSTGTTGTT
 ACTTTGGACTGTGGACTTTT

Original motif Consensus sequence: AGGCCCCAGTGTSTGTTGTT



Reverse complement motif Consensus sequence: AACACASACACTGGGGCCT



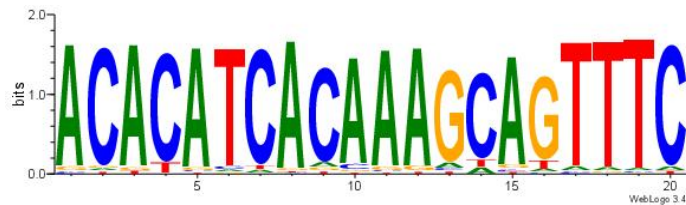
Dataset #: 1
 Motif ID: 202
 Motif name: Motif 202
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 20

Similarity score: 0.127973

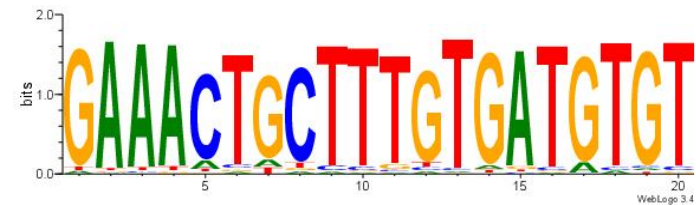
Alignment:

ACACATCACAAAGCAGTTTC
ACTTTGGACTGTGGACTTTT

Original motif Consensus sequence: ACACATCACAAAGCAGTTTC

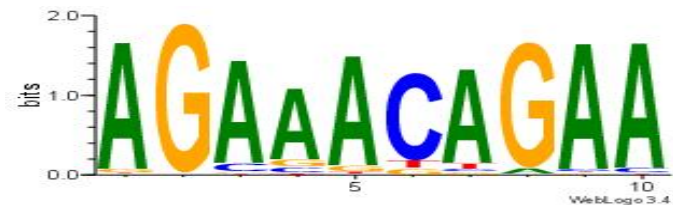


Reverse complement motif Consensus sequence: GAAACTGCTTTGTGATGTGT

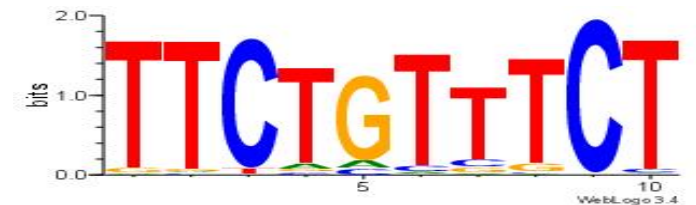


Dataset #: 1 Motif ID: 172 Motif name: Motif 172

Original motif Consensus sequence: AGAAACAGAA



Reverse complement motif Consensus sequence: TTCTGTTTCT



Best Matches for Motif ID 172 (Highest to Lowest)

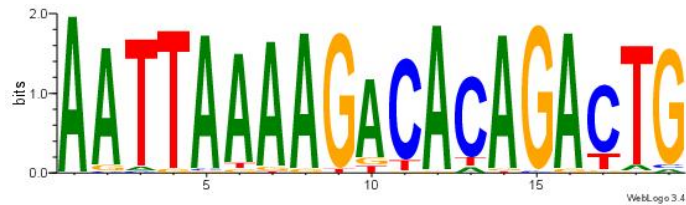
Dataset #:	1
Motif ID:	356
Motif name:	Motif 356
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement

Direction: Backward
 Position number: 8
 Number of overlap: 10
 Similarity score: 0.0394673

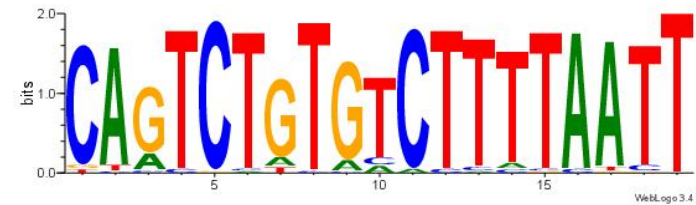
Alignment:

CAGTCTGTGTCTTTTAATT
 --TTCTGTTTCT-----

Original motif Consensus sequence: AATTAAGACAGACTG



Reverse complement motif Consensus sequence: CAGTCTGTGTCTTTTAATT

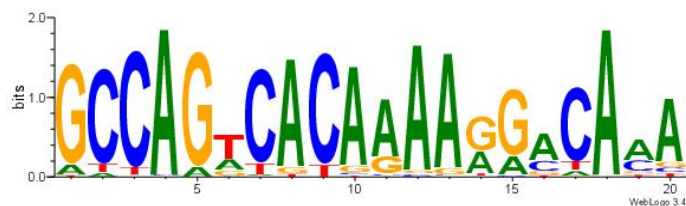


Dataset #: 1
 Motif ID: 145
 Motif name: Motif 145
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 8
 Number of overlap: 10
 Similarity score: 0.0541669

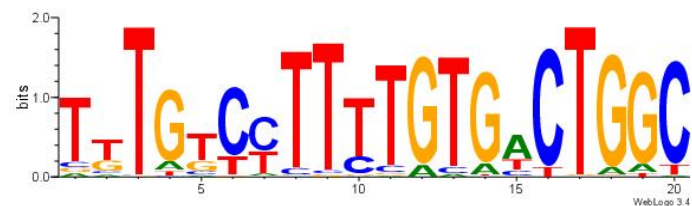
Alignment:

GCCAGTCACAAAARGACAMA
 ---AGAAACAGAA-----

Original motif Consensus sequence: GCCAGTCACAAAARGACAMA



Reverse complement motif Consensus sequence: TYTGTCMTTTTGTGACTGGC

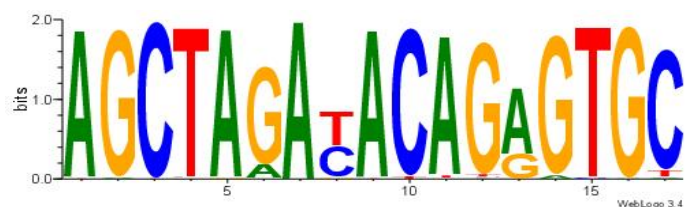


Dataset #: 1
Motif ID: 175
Motif name: Motif 175
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 5
Number of overlap: 10
Similarity score: 0.0544219

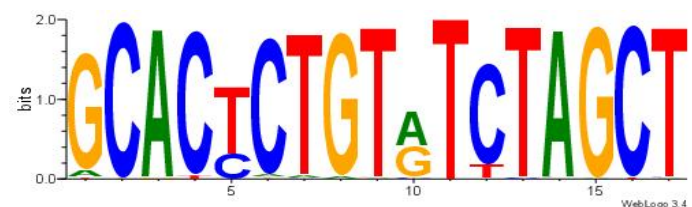
Alignment:

GCACTCTGTMTCTAGCT
---TTCTGTTTCT----

Original motif Consensus sequence: AGCTAGAYACAGAGTGC



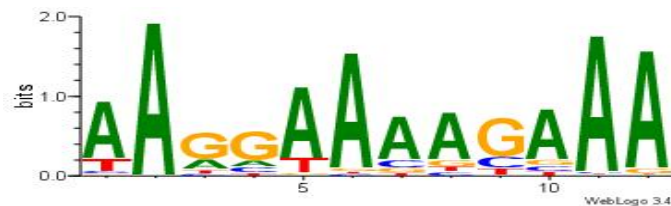
Reverse complement motif Consensus sequence: GCACTCTGTMTCTAGCT



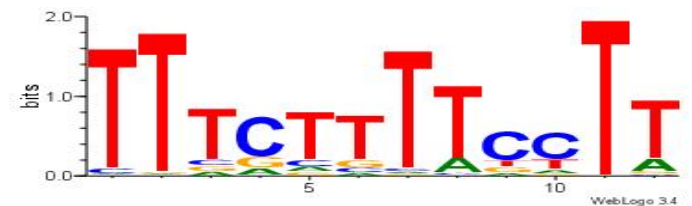
Dataset #: 1
 Motif ID: 54
 Motif name: Motif 54
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 10
 Similarity score: 0.0568571

Alignment:
 AAGGAAAAGAAA
 -AGAAACAGAA-

Original motif Consensus sequence: AAGGAAAAGAAA



Reverse complement motif Consensus sequence: TTTCTTTTCCTT



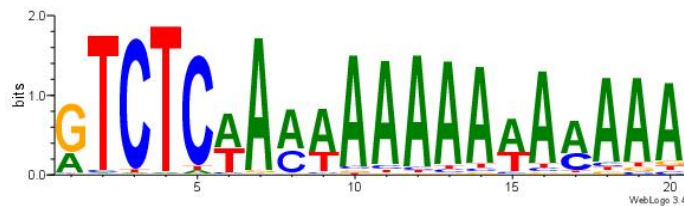
Dataset #: 1
 Motif ID: 7
 Motif name: Motif 7
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 10

Similarity score: 0.0594764

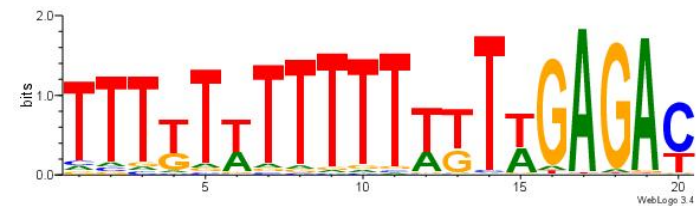
Alignment:

TTYTWTWTWTWTWTWTWGAGAC
-TTCTGTTTCT-----

Original motif Consensus sequence: GTCTCWAMAAAAAAWAMAAA



Reverse complement motif Consensus sequence: TTYTWTWTWTWTWTWGAGAC

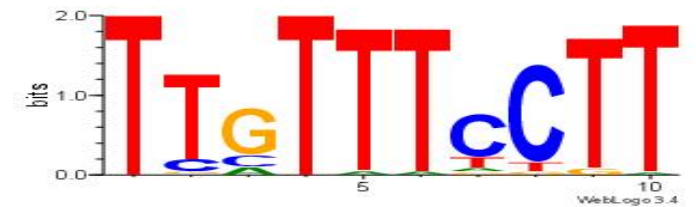


Dataset #: 1 Motif ID: 173 Motif name: Motif 173

Original motif Consensus sequence: AAGGAAACAA



Reverse complement motif Consensus sequence: TTGTTTCCTT



Best Matches for Motif ID 173 (Highest to Lowest)

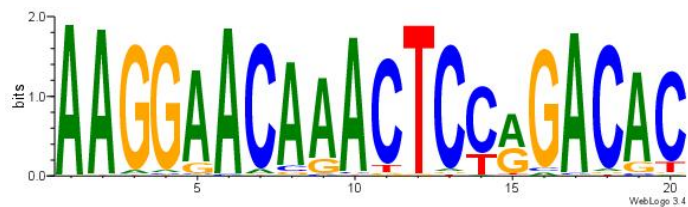
Dataset #:	1
Motif ID:	234
Motif name:	Motif 234
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement

Direction: Forward
Position number: 11
Number of overlap: 10
Similarity score: 0.043227

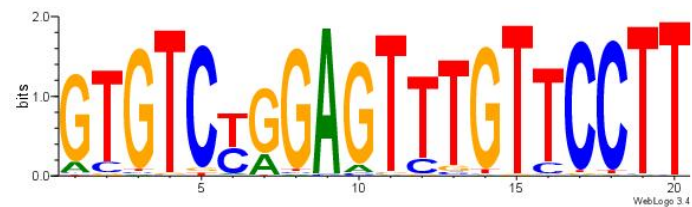
Alignment:

```
GTGTCKGGAGTTTGTTTCCTT  
-----TTGTTTCCTT
```

Original motif Consensus sequence: AAGGAACAACTCCRGACAC



Reverse complement motif Consensus sequence: GTGTCKGGAGTTTGTTTCCTT

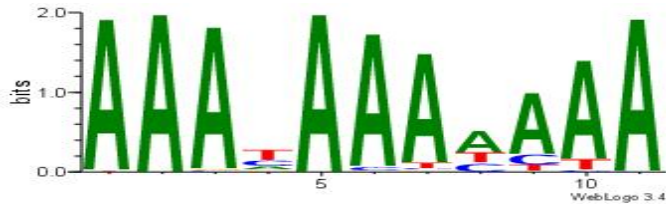


Dataset #: 1
Motif ID: 41
Motif name: Motif 41
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 2
Number of overlap: 10
Similarity score: 0.0491703

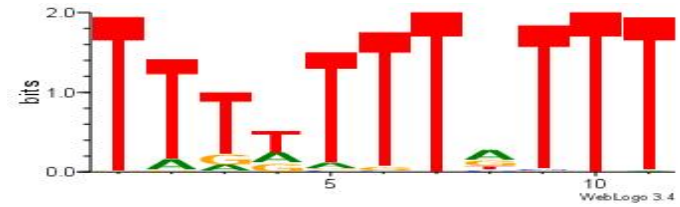
Alignment:

```
TTTTTTTMTTT  
-TTGTTTCCTT
```


Original motif Consensus sequence: AAAYAAAAAA



Reverse complement motif Consensus sequence: TTTTTTMTTT



Dataset #: 1
Motif ID: 54
Motif name: Motif 54
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 3
Number of overlap: 10
Similarity score: 0.0529937

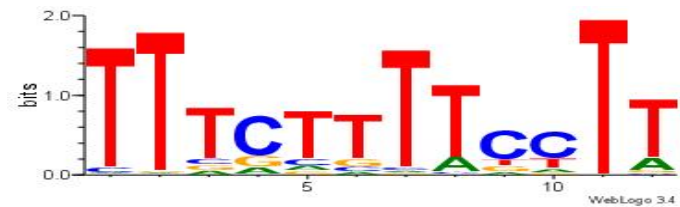
Alignment:

```
TTTCTTTCCTT  
--TTGTTTCCTT
```

Original motif Consensus sequence: AAGGAAAAGAAA



Reverse complement motif Consensus sequence: TTTCTTTCCTT

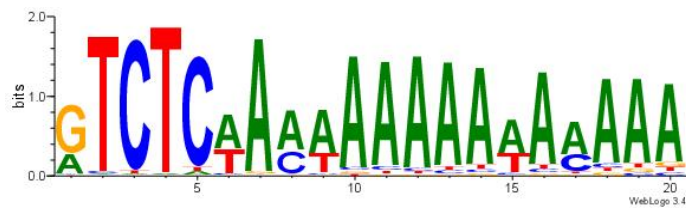


Dataset #: 1
 Motif ID: 7
 Motif name: Motif 7
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 10
 Number of overlap: 10
 Similarity score: 0.0605263

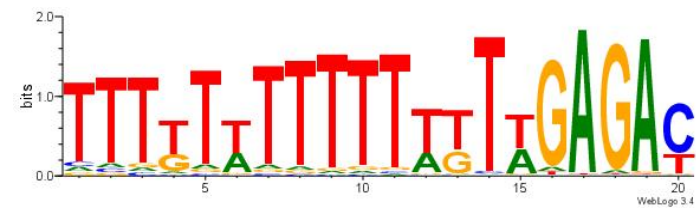
Alignment:

GTCTCWAMAAAAAWAMAAA
 -----AAGGAAACAA-

Original motif Consensus sequence: GTCTCWAMAAAAAWAMAAA



Reverse complement motif Consensus sequence: TTTYTWTTTTTWTGAGAC

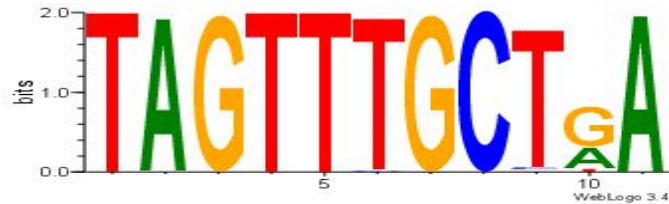


Dataset #: 1
 Motif ID: 158
 Motif name: Motif 158
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1

Number of overlap: 10
Similarity score: 0.0611844

Alignment:
TAGTTTGCTGA
-TTGTTTCCTT

Original motif Consensus sequence: TAGTTTGCTGA



Reverse complement motif Consensus sequence: TCAGCAAACCTA

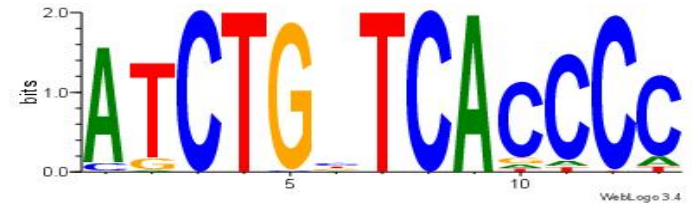


Dataset #: 1 Motif ID: 174 Motif name: Motif 174

Original motif Consensus sequence: GGGGTGACAGAT



Reverse complement motif Consensus sequence: ATCTGTCACCC



Best Matches for Motif ID 174 (Highest to Lowest)

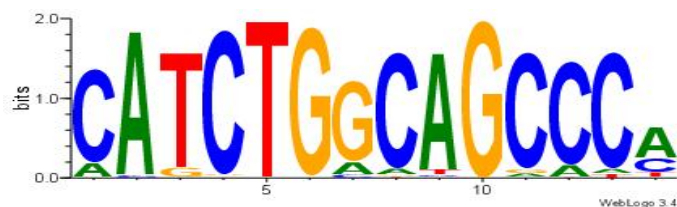
Dataset #: 1
Motif ID: 205
Motif name: Motif 205
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif

Direction: Forward
Position number: 2
Number of overlap: 13
Similarity score: 0.0735305

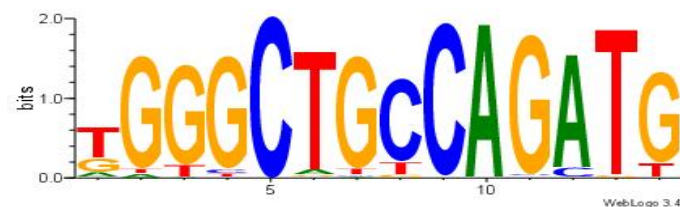
Alignment:

CATCTGGCAGCCCA
-ATCTGVTCACCCC

Original motif Consensus sequence: CATCTGGCAGCCCA



Reverse complement motif Consensus sequence: TGGGCTGCCAGATG

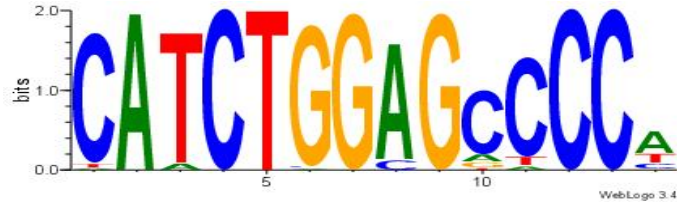


Dataset #: 1
Motif ID: 320
Motif name: Motif 320
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 13
Similarity score: 0.0766821

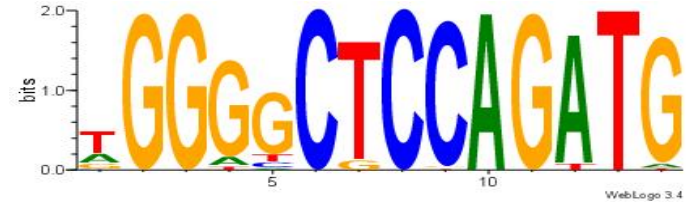
Alignment:

CATCTGGAGCCCA
-ATCTGVTCACCCC

Original motif Consensus sequence: CATCTGGAGCCCCA



Reverse complement motif Consensus sequence: TGGGGCTCCAGATG

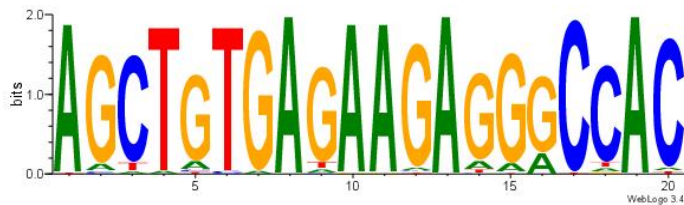


Dataset #: 1
 Motif ID: 294
 Motif name: Motif 294
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 7
 Number of overlap: 13
 Similarity score: 0.0767655

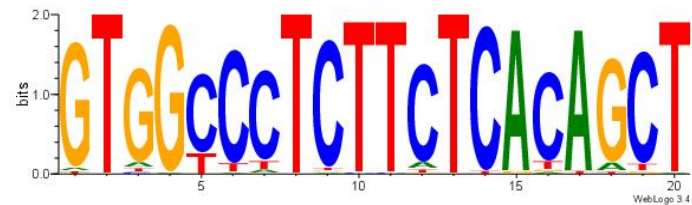
Alignment:

```
AGCTGTGAGAAGAGGGCCAC
-GGGTGAVCAGAT-----
```

Original motif Consensus sequence: AGCTGTGAGAAGAGGGCCAC



Reverse complement motif Consensus sequence: GTGGCCCTCTTCTCACAGCT



Dataset #: 1
 Motif ID: 38
 Motif name: Motif 38
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 13
 Similarity score: 0.0827379

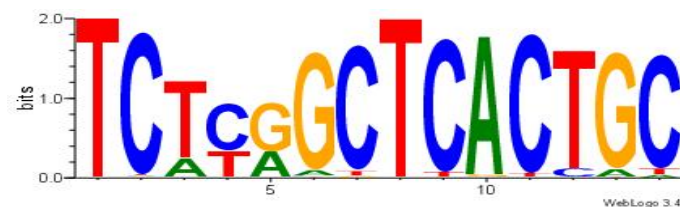
Alignment:

TCTMKGCTCACTGC
 -ATCTGVTCACCCC

Original motif Consensus sequence: GCAGTGAGCYRAGA



Reverse complement motif Consensus sequence: TCTMKGCTCACTGC



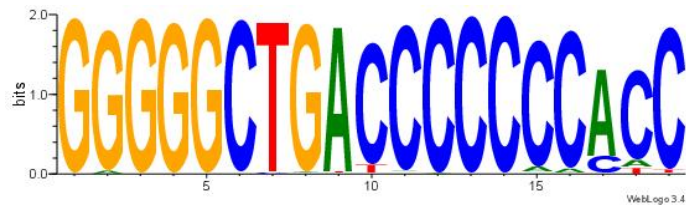
Dataset #: 1
 Motif ID: 92
 Motif name: Motif 92
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 4
 Number of overlap: 13

Similarity score: 0.083141

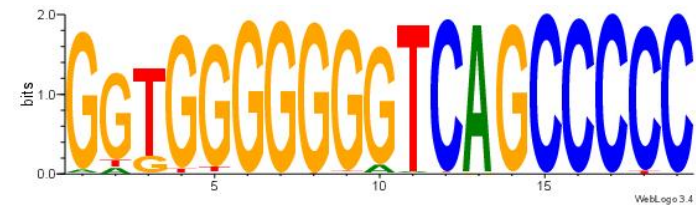
Alignment:

GGTGGGGGGGTCAGCCCC
---GGGGTGAVCAGAT---

Original motif Consensus sequence: GGGGGCTGACCCCCCACC

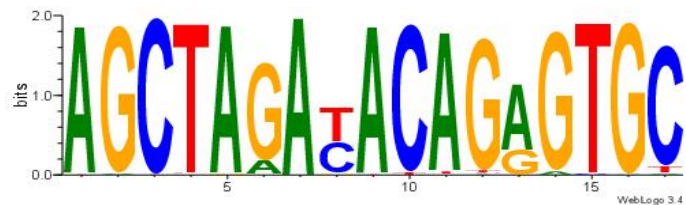


Reverse complement motif Consensus sequence: GGTGGGGGGGTCAGCCCC

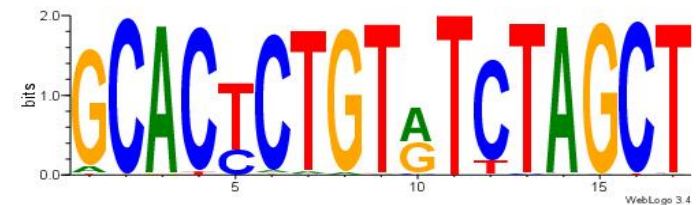


Dataset #: 1 Motif ID: 175 Motif name: Motif 175

Original motif Consensus sequence: AGCTAGAYACAGAGTGC



Reverse complement motif Consensus sequence: GCACTCTGMTCTAGCT



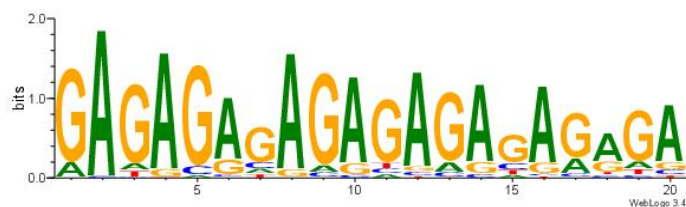
Best Matches for Motif ID 175 (Highest to Lowest)

Dataset #:	1
Motif ID:	109
Motif name:	Motif 109
Matching format of first motif:	Reverse Complement

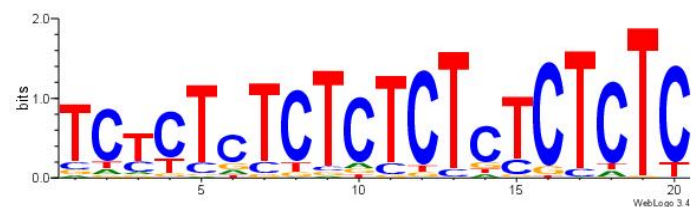
Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 17
 Similarity score: 0.0923803

Alignment:
 TCTCTCTCTCTCTCTCTCTC
 GCACTCTGTMTCTAGCT---

Original motif Consensus sequence: GAGAGAGAGAGAGAGAGA



Reverse complement motif Consensus sequence: TCTCTCTCTCTCTCTCTC

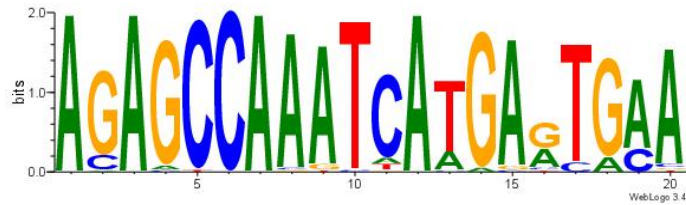


Dataset #: 1
 Motif ID: 349
 Motif name: Motif 349
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 17
 Similarity score: 0.0970004

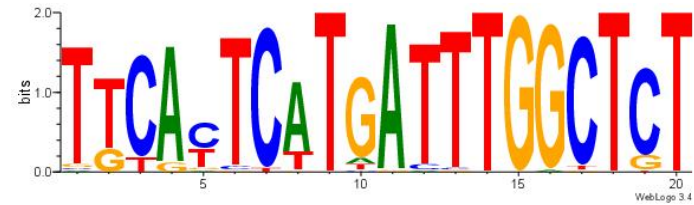
Alignment:

AGAGCCAAATCATGARTGAA
--AGCTAGAYACAGAGTGC--

Original motif Consensus sequence: AGAGCCAAATCATGARTGAA



Reverse complement motif Consensus sequence:
TTCAMTCATGATTTGGCTCT

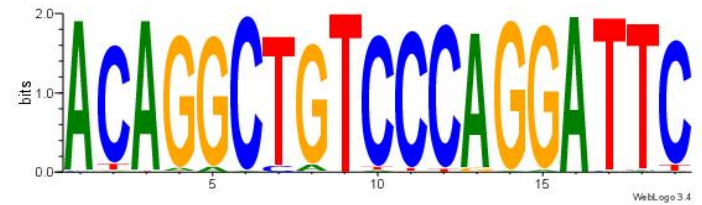
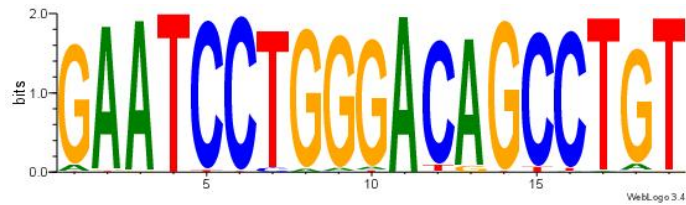


Dataset #: 1
Motif ID: 192
Motif name: Motif 192
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 3
Number of overlap: 17
Similarity score: 0.106953

Alignment:
ACAGGCTGTCCCAGGATTC
GCACTCTGTMTCTAGCT--

Original motif Consensus sequence: GAATCCTGGGACAGCCTGT

Reverse complement motif Consensus sequence:
ACAGGCTGTCCCAGGATTC



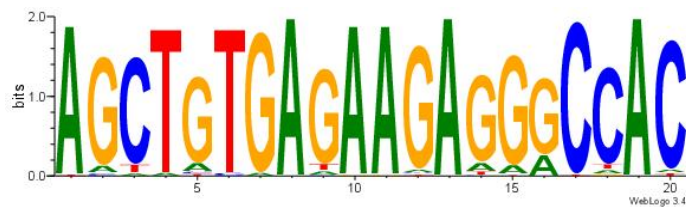
Dataset #: 1
 Motif ID: 294
 Motif name: Motif 294
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 17
 Similarity score: 0.107528

Alignment:

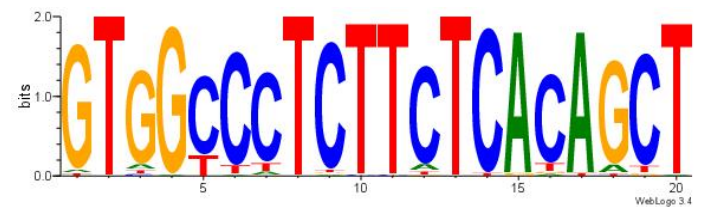
```

GTGGCCCTCTTCTCACAGCT
---GCACTCTGTMTCTAGCT
  
```

Original motif Consensus sequence: AGCTGTGAGAAGAGGGCCAC



Reverse complement motif Consensus sequence: GTGGCCCTCTTCTCACAGCT



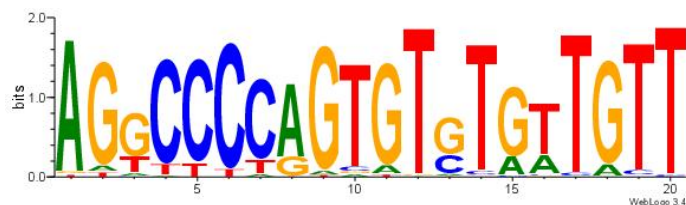
Dataset #: 1

Motif ID: 176
 Motif name: Motif 176
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 17
 Similarity score: 0.112575

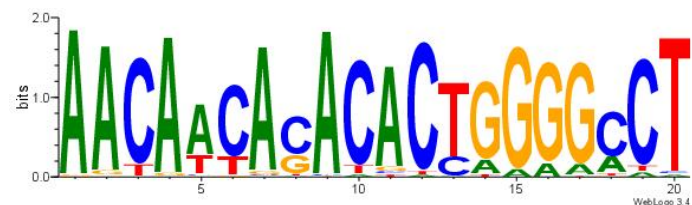
Alignment:

AACAAASACTGGGGCCT
 AGCTAGAYACAGAGTGC---

Original motif Consensus sequence: AGGCCCCAGTGTSTGTTGTT

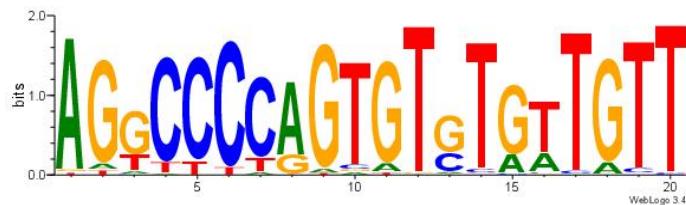


Reverse complement motif Consensus sequence: AACAAASACTGGGGCCT

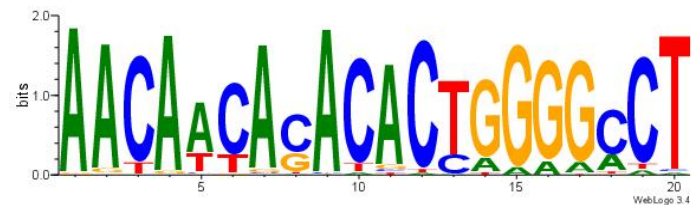


Dataset #: 1 Motif ID: 176 Motif name: Motif 176

Original motif Consensus sequence: AGGCCCCAGTGTSTGTTGTT



Reverse complement motif Consensus sequence: AACAAASACTGGGGCCT



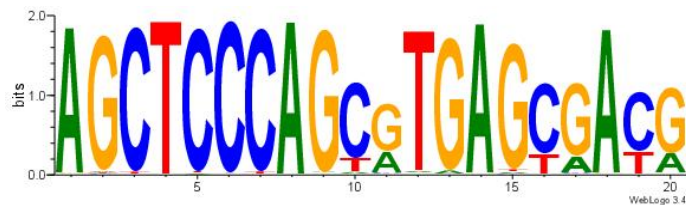
Best Matches for Motif ID 176 (Highest to Lowest)

Dataset #: 1
Motif ID: 48
Motif name: Motif 48
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 20
Similarity score: 0.100522

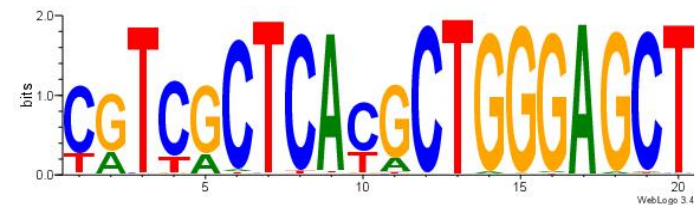
Alignment:

```
AGCTCCCAGCGTGAGCGACG  
AGGCCCCAGTGTSTGTTGTT
```

Original motif Consensus sequence: AGCTCCCAGCGTGAGCGACG



Reverse complement motif Consensus sequence:
CGTCGCTCACGCTGGGAGCT



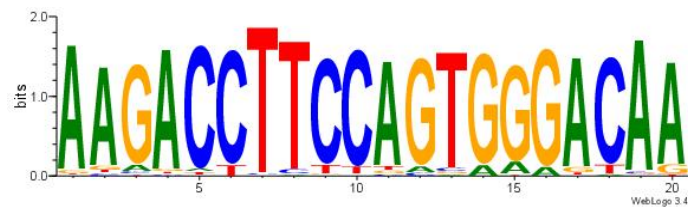
Dataset #: 1
Motif ID: 292
Motif name: Motif 292
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement

Direction: Forward
Position number: 1
Number of overlap: 20
Similarity score: 0.103197

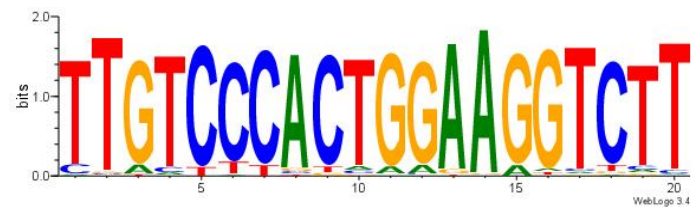
Alignment:

TTGTCCCACTGGAAGGTCTT
AGGCCCCAGTGTSTGTTGTT

Original motif Consensus sequence: AAGACCTCCAGTGGGACAA



Reverse complement motif Consensus sequence: TTGTCCCACTGGAAGGTCTT

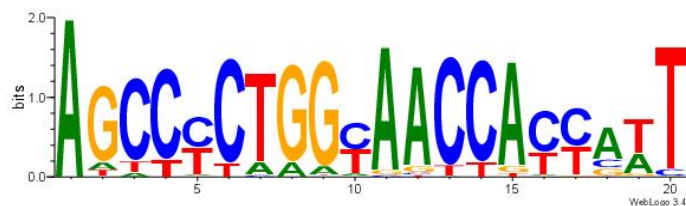


Dataset #: 1
Motif ID: 139
Motif name: Motif 139
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 20
Similarity score: 0.106256

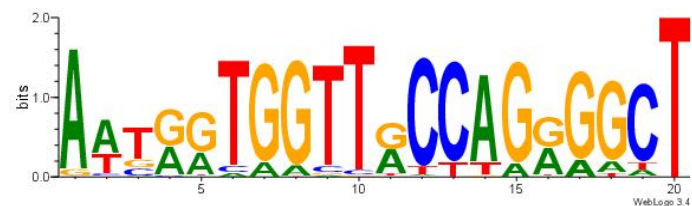
Alignment:

AGCCYCTGGYAACCAYYAWT
AGGCCCCAGTGTSTGTTGTT

Original motif Consensus sequence: AGCCYCTGGYAACCAYYAWT



Reverse complement motif Consensus sequence: AWTKKTGGTTKCCAGKGGCT

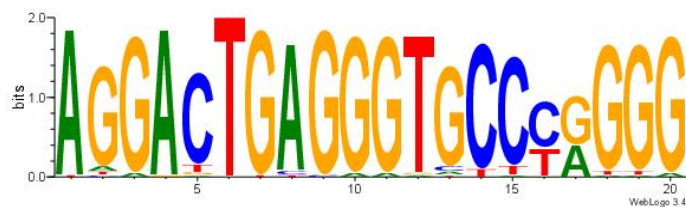


Dataset #: 1
Motif ID: 312
Motif name: Motif 312
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 20
Similarity score: 0.108547

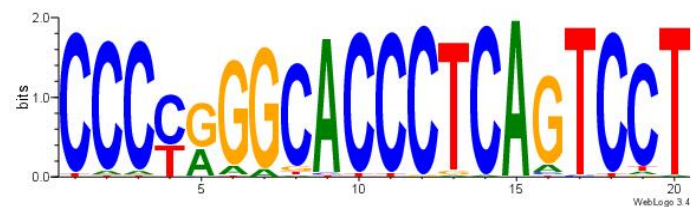
Alignment:

CCCMKGGCACCCCTCAGTCCT
AACACASACACTGGGGCCT

Original motif Consensus sequence: AGGACTGAGGGTGCCYRGGG



Reverse complement motif Consensus sequence: CCCMKGGCACCCCTCAGTCCT

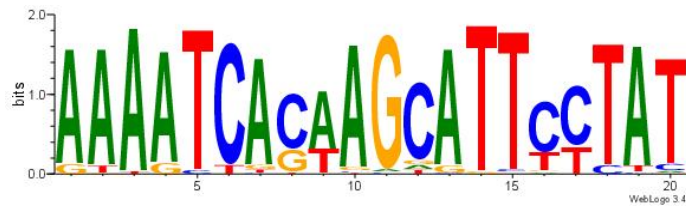


Dataset #: 1
 Motif ID: 254
 Motif name: Motif 254
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.115174

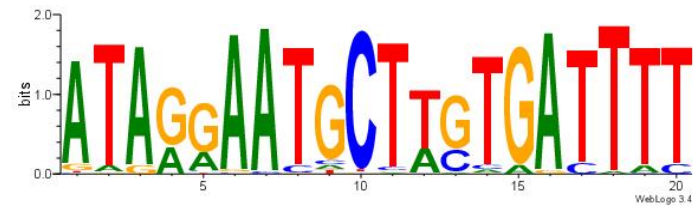
Alignment:

AAAATCACAAGCATTCTAT
 AACACASACTGGGGCCT

Original motif Consensus sequence: AAAATCACAAGCATTCTAT



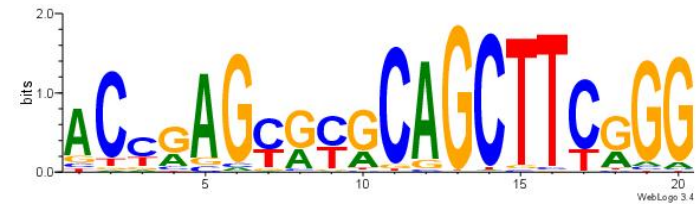
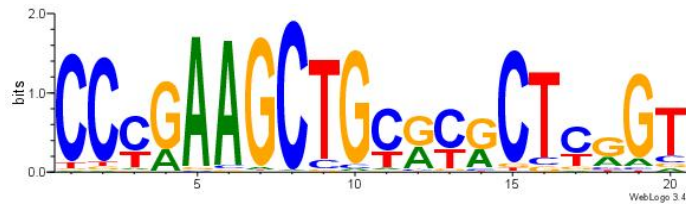
Reverse complement motif Consensus sequence: ATAGGAATGCTTGATTTT



Dataset #: 1 Motif ID: 177 Motif name: Motif 177

Original motif Consensus sequence: CCCGAAGCTGCRYRCTCGGT

Reverse complement motif Consensus sequence: ACCGAGMKMGCAGCTTCGGG



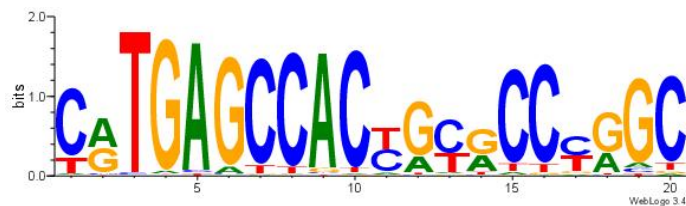
Best Matches for Motif ID 177 (Highest to Lowest)

Dataset #: 1
 Motif ID: 56
 Motif name: Motif 56
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.0760829

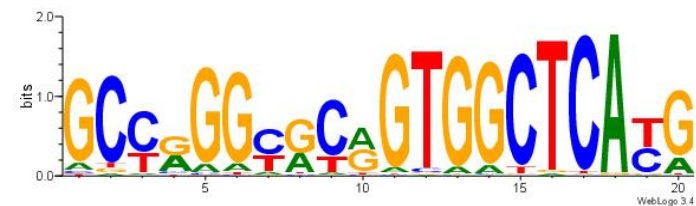
Alignment:

CRTGAGCCACYGYRCCYGGC
 CCCGAAGCTGCRYRCTCGGT

Original motif Consensus sequence: CRTGAGCCACYGYRCCYGGC



Reverse complement motif Consensus sequence: GCCKGGMKCMGTGGCTCAKG

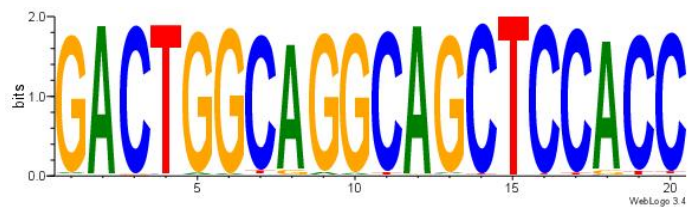


Dataset #: 1
Motif ID: 52
Motif name: Motif 52
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 20
Similarity score: 0.104166

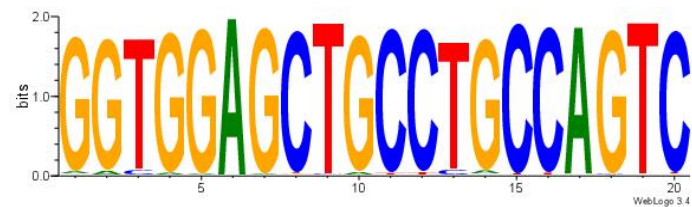
Alignment:

GACTGGCAGGCAGCTCCACC
ACCGAGMKMGCAGCTTCGGG

Original motif Consensus sequence: GACTGGCAGGCAGCTCCACC



Reverse complement motif Consensus sequence: GGTGGAGCTGCCTGCCAGTC



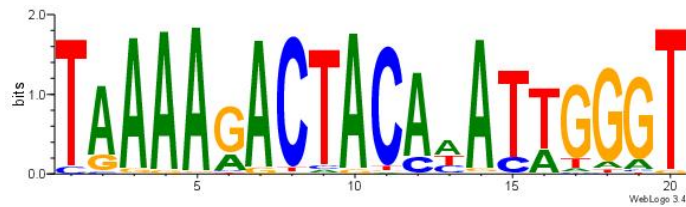
Dataset #: 1
Motif ID: 195
Motif name: Motif 195
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1

Number of overlap: 20
Similarity score: 0.104438

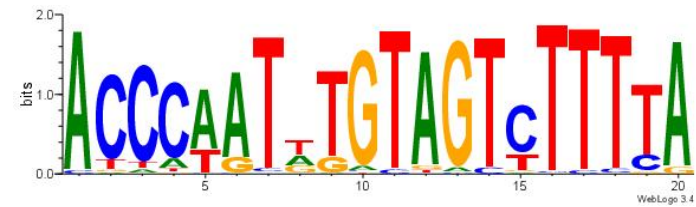
Alignment:

TAAAAGACTACAWATTGGGT
CCCGAAGCTGCRYRCTCGGT

Original motif Consensus sequence: TAAAAGACTACAWATTGGGT



Reverse complement motif Consensus sequence:
ACCCAATWTGTAGTCTTTTA

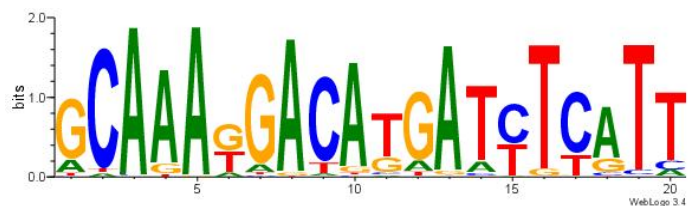


Dataset #: 1
Motif ID: 99
Motif name: Motif 99
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 20
Similarity score: 0.106729

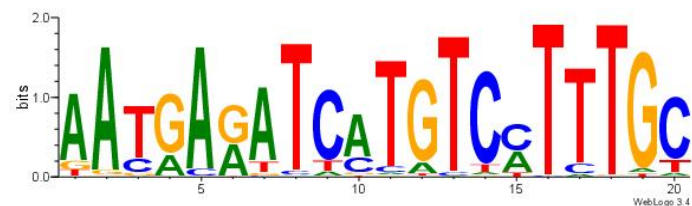
Alignment:

AATGAKATCATGTCYTTTGC
ACCGAGMKMGCAGCTTCGGG

Original motif Consensus sequence: GCAAAGACATGATYTCATT



Reverse complement motif Consensus sequence: AATGAKATCATGTCTTTGC

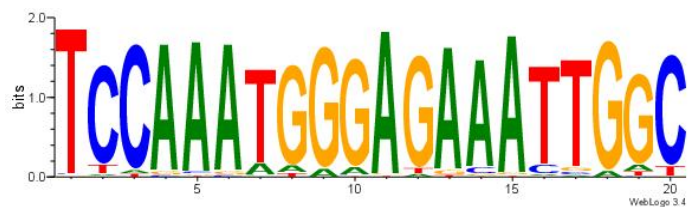


Dataset #: 1
Motif ID: 235
Motif name: Motif 235
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 20
Similarity score: 0.107691

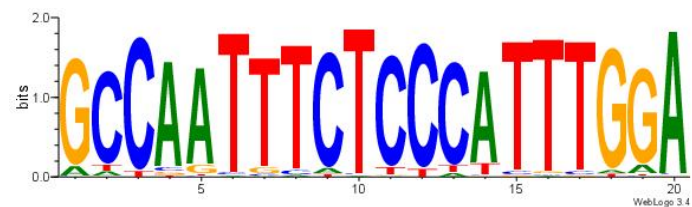
Alignment:

TCCAAATGGGAGAAATTGGC
CCCGAAGCTGCRYRCTCGGT

Original motif Consensus sequence: TCCAAATGGGAGAAATTGGC

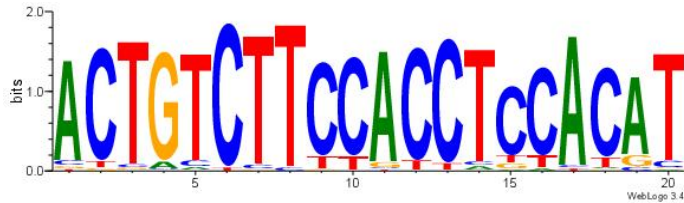


Reverse complement motif Consensus sequence: GCCAATTTCTCCCATTTGGA

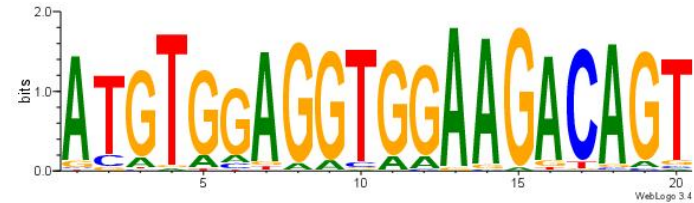


Dataset #: 1 Motif ID: 178 Motif name: Motif 178

Original motif Consensus sequence: ACTGTCTTCCACCTCCACAT



Reverse complement motif Consensus sequence: ATGTGGAGGTGGAAGACAGT



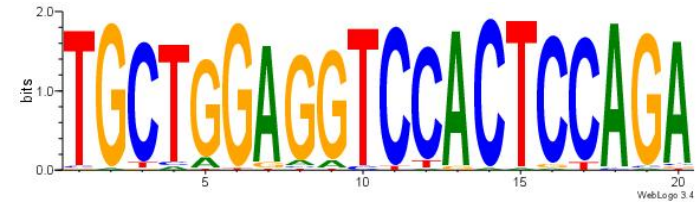
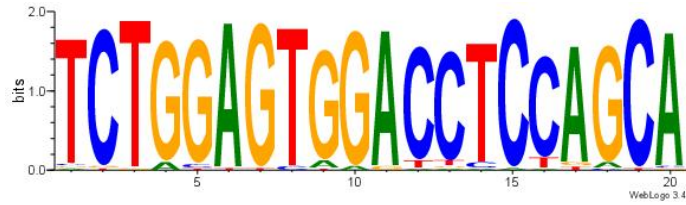
Best Matches for Motif ID 178 (Highest to Lowest)

Dataset #:	1
Motif ID:	350
Motif name:	Motif 350
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	20
Similarity score:	0.101056

Alignment:
TGCTGGAGGTCCACTCCAGA
ATGTGGAGGTGGAAGACAGT

Original motif Consensus sequence: TCTGGAGTGGACCTCCAGCA

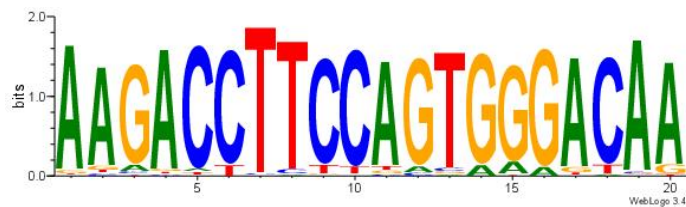
Reverse complement motif Consensus sequence: TGCTGGAGGTCCACTCCAGA



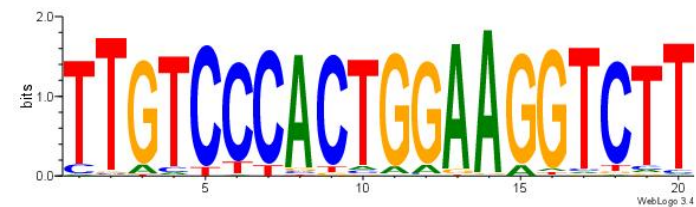
Dataset #: 1
 Motif ID: 292
 Motif name: Motif 292
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.111286

Alignment:
 TTGTCCCACTGGAAGGTCTT
 ATGTGGAGGTGGAAGACAGT

Original motif Consensus sequence: AAGACCTTCCAGTGGGACAA



Reverse complement motif Consensus sequence: TTGTCCCACTGGAAGGTCTT



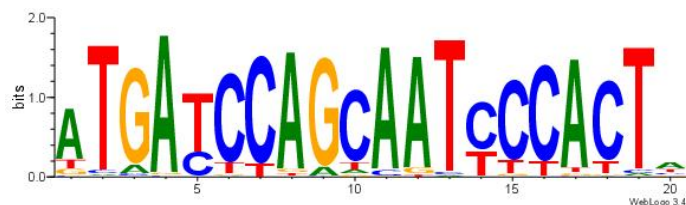
Dataset #: 1

Motif ID: 115
 Motif name: Motif 115
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.119924

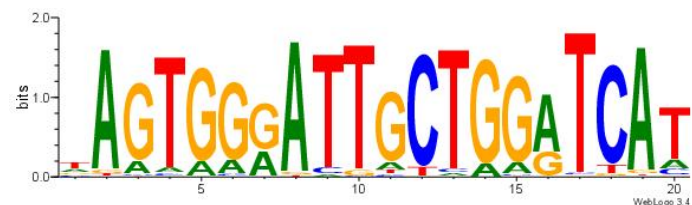
Alignment:

ATGATCCAGCAATYCCACTH
 ACTGTCTTCCACCTCCACAT

Original motif Consensus sequence: ATGATCCAGCAATYCCACTH



Reverse complement motif Consensus sequence: HAGTGGKATTGCTGGATCAT



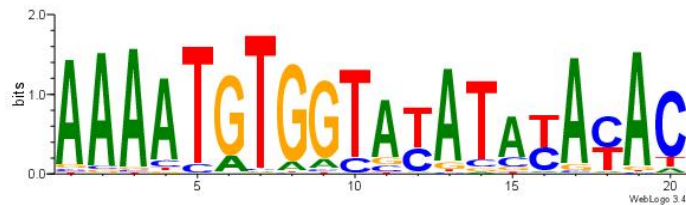
Dataset #: 1
 Motif ID: 83
 Motif name: Motif 83
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 20

Similarity score: 0.121173

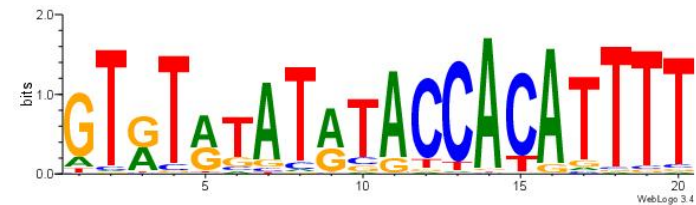
Alignment:

AAAATGTGGTAYATAYAYAC
ACTGTCTTCCACCTCCACAT

Original motif Consensus sequence: AAAATGTGGTAYATAYAYAC



Reverse complement motif Consensus sequence:
GTKTMTATMTACCACATTTT



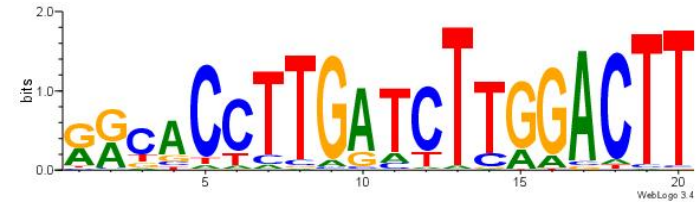
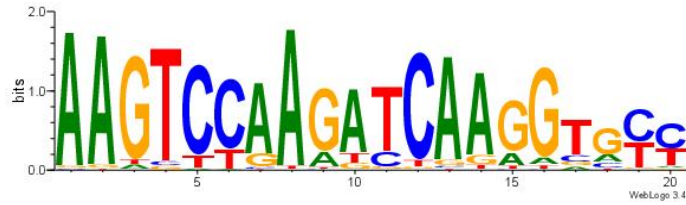
Dataset #: 1
Motif ID: 119
Motif name: Motif 119
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 20
Similarity score: 0.125588

Alignment:

KKCACCTTGATCTTGGACTT
ACTGTCTTCCACCTCCACAT

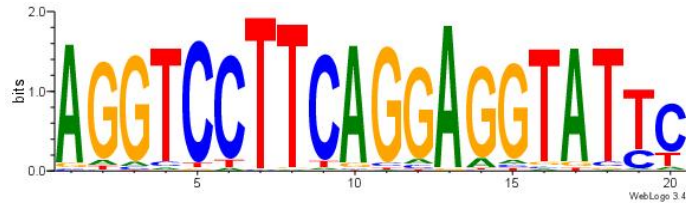
Original motif Consensus sequence: AAGTCCAAGATCAAGGTGY

Reverse complement motif Consensus sequence:
KKCACCTTGATCTTGGACTT

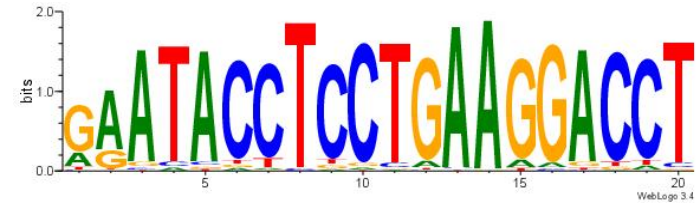


Dataset #: 1 Motif ID: 179 Motif name: Motif 179

Original motif Consensus sequence: AGGTCCTTCAGGAGGTATTC



Reverse complement motif Consensus sequence: GAATACCTCTGAAGGACCT



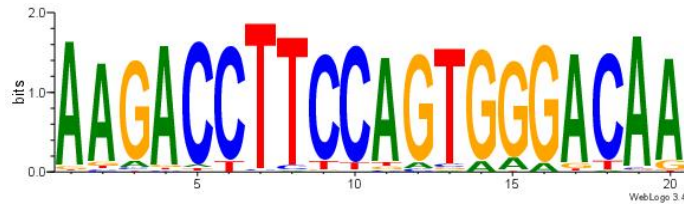
Best Matches for Motif ID 179 (Highest to Lowest)

Dataset #:	1
Motif ID:	292
Motif name:	Motif 292
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	20
Similarity score:	0.0979569

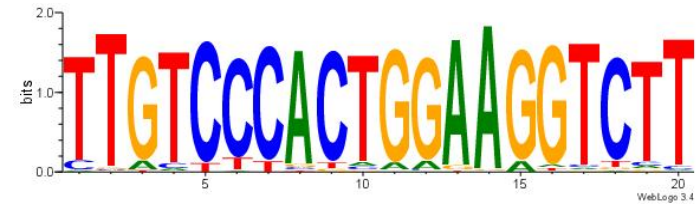
Alignment:

TTGTCCCCTGGAAGGTCTT
GAATACCTCCTGAAGGACCT

Original motif Consensus sequence: AAGACCTCCAGTGGGACAA



Reverse complement motif Consensus sequence:
TTGTCCCCTGGAAGGTCTT



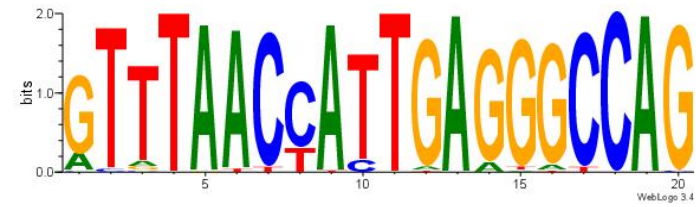
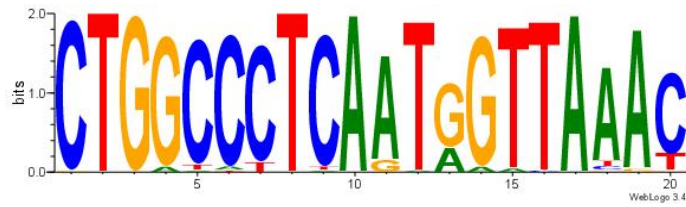
Dataset #: 1
Motif ID: 332
Motif name: Motif 332
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 20
Similarity score: 0.114535

Alignment:

CTGGCCCTCAATGGTTAAAC
AGGTCCTTCAGGAGGTATTC

Original motif Consensus sequence: CTGGCCCTCAATGGTTAAAC

Reverse complement motif Consensus sequence:
GTTTAAACCATTGAGGGCCAG

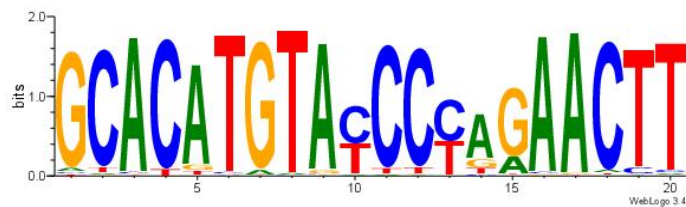


Dataset #: 1
 Motif ID: 225
 Motif name: Motif 225
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.12063

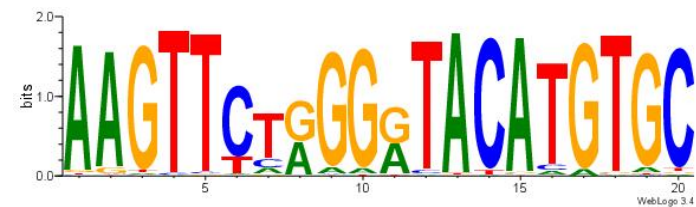
Alignment:

AAGTTCTKGGKTACATGTGC
 AGGTCCTTCAGGAGGTATTC

Original motif Consensus sequence: GCACATGTAYCCYAGAACTT



Reverse complement motif Consensus sequence: AAGTTCTKGGKTACATGTGC



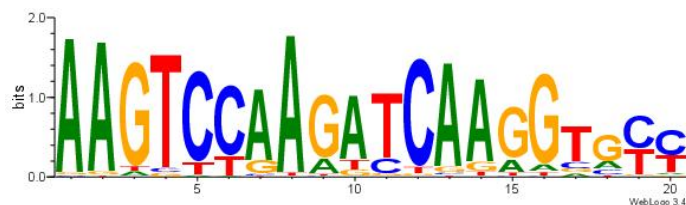
Dataset #: 1

Motif ID: 119
 Motif name: Motif 119
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.120895

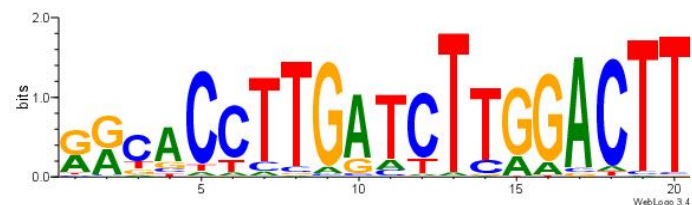
Alignment:

AAGTCCAAGATCAAGGTGY
 AGGTCCTTCAGGAGGTATTC

Original motif Consensus sequence: AAGTCCAAGATCAAGGTGY



Reverse complement motif Consensus sequence: KKCACCTTGATCTGGACTT



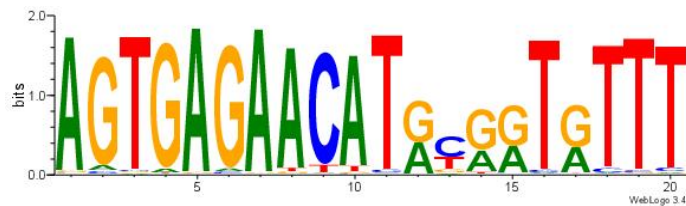
Dataset #: 1
 Motif ID: 63
 Motif name: Motif 63
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 20

Similarity score: 0.122039

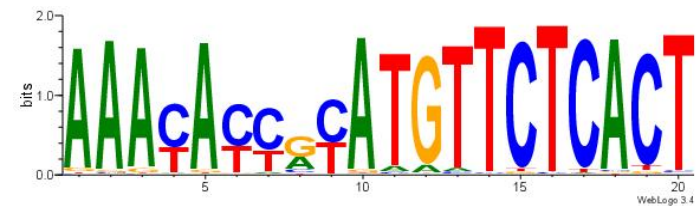
Alignment:

AGTGAGAACATRYRRTRTTT
AGGTCCTTCAGGAGGTATTC

Original motif Consensus sequence: AGTGAGAACATRYRRTRTTT



Reverse complement motif Consensus sequence: AAAMAMMKMATGTTCTCACT



Dataset #: 1 Motif ID: 180 Motif name: Motif 180

Original motif Consensus sequence: TGCGCATGCGCA



Reverse complement motif Consensus sequence: TGCGCATGCGCA



Best Matches for Motif ID 180 (Highest to Lowest)

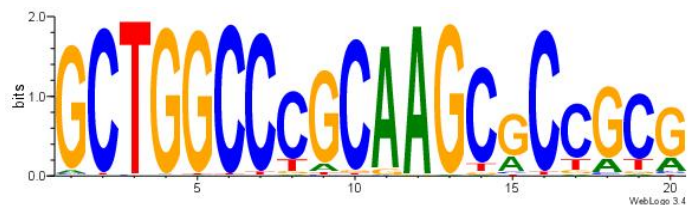
Dataset #:	1
Motif ID:	100
Motif name:	Motif 100
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif

Direction: Forward
Position number: 4
Number of overlap: 12
Similarity score: 0.0728388

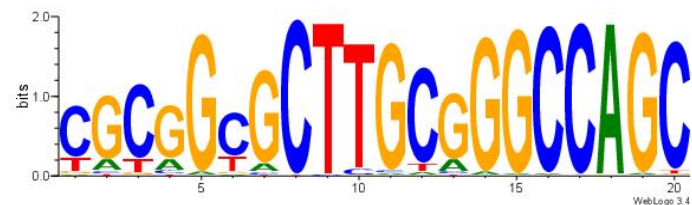
Alignment:

```
GCTGGCCCGCAAGCGCCGCG  
---TGCGCATGCGCA-----
```

Original motif Consensus sequence: GCTGGCCCGCAAGCGCCGCG



Reverse complement motif Consensus sequence: CGCGGCGCTTGC GGGCCAGC

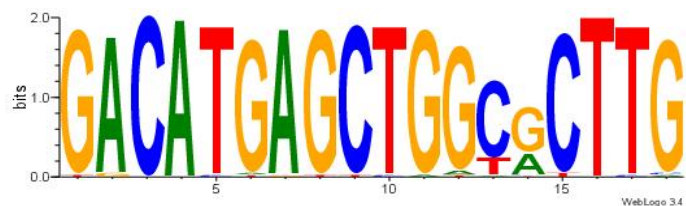


Dataset #: 1
Motif ID: 306
Motif name: Motif 306
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 5
Number of overlap: 12
Similarity score: 0.0731846

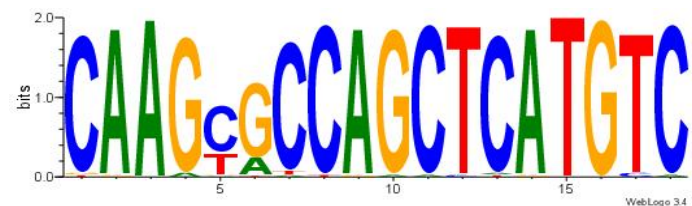
Alignment:

```
GACATGAGCTGGCGCTTG  
----TGCGCATGCGCA--
```

Original motif Consensus sequence: GACATGAGCTGGCGCTTG



Reverse complement motif Consensus sequence: CAAGCGCCAGCTCATGTC

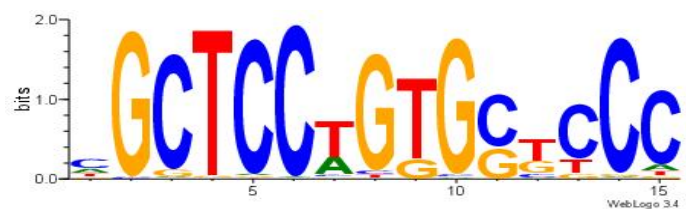


Dataset #: 1
Motif ID: 215
Motif name: Motif 215
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 4
Number of overlap: 12
Similarity score: 0.0736063

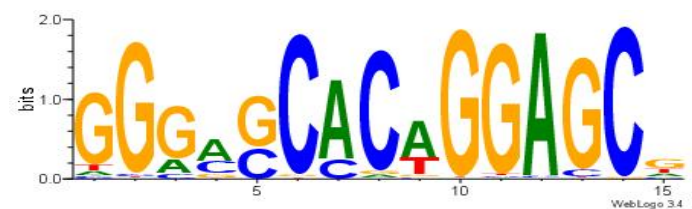
Alignment:

GGRSCACAGGAGCD
---TGCGCATGCGCA

Original motif Consensus sequence: HGCTCCTGTGSKCCC



Reverse complement motif Consensus sequence: GGRSCACAGGAGCD

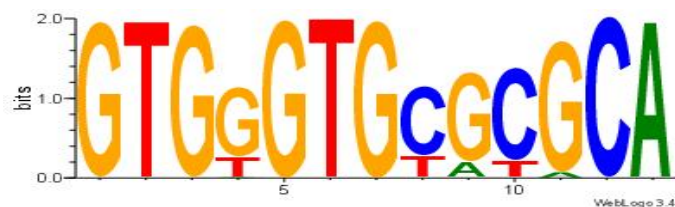


Dataset #: 1
 Motif ID: 51
 Motif name: Motif 51
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 12
 Similarity score: 0.0741066

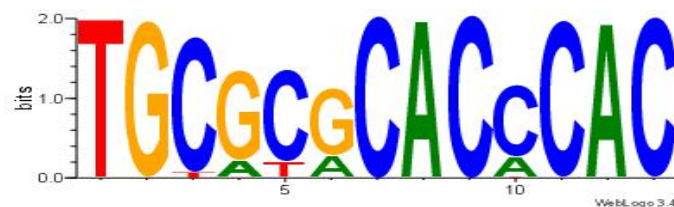
Alignment:

TGC GCGCACCCAC
 -TGC GCATGCGCA

Original motif Consensus sequence: GTGGGTGCGCGCA



Reverse complement motif Consensus sequence: TGCGCGCACCCAC



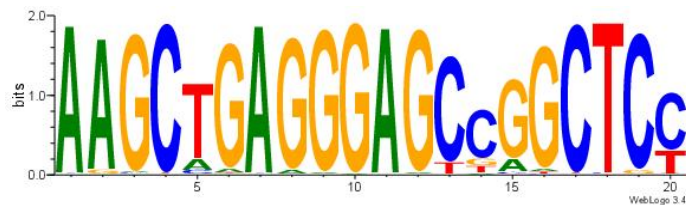
Dataset #: 1
 Motif ID: 96
 Motif name: Motif 96
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 9
 Number of overlap: 12

Similarity score: 0.0850468

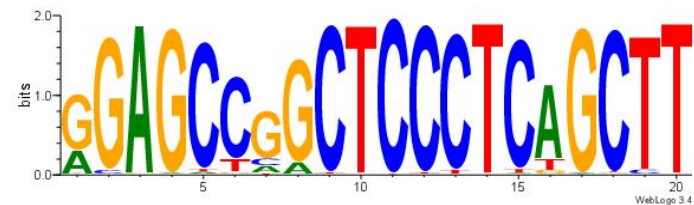
Alignment:

GGAGCCGGCTCCCTCAGCTT
TGCGCATGCGCA-----

Original motif Consensus sequence: AAGCTGAGGGAGCCGGCTCC

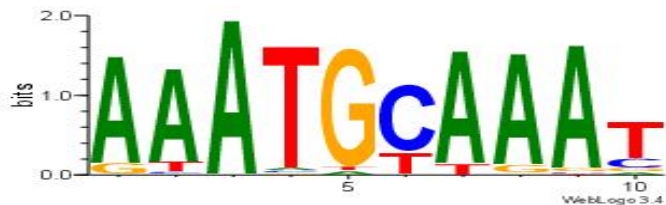


Reverse complement motif Consensus sequence: GGAGCCGGCTCCCTCAGCTT

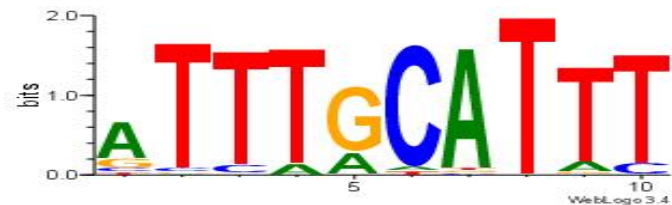


Dataset #: 1 Motif ID: 181 Motif name: Motif 181

Original motif Consensus sequence: AAATGCAAAT



Reverse complement motif Consensus sequence: ATTTGCATTT



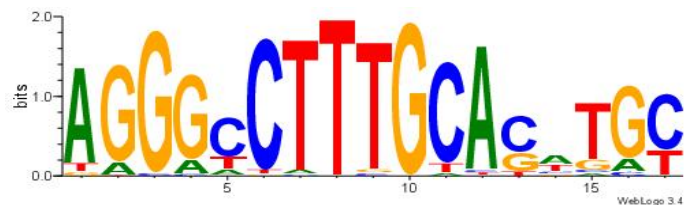
Best Matches for Motif ID 181 (Highest to Lowest)

Dataset #:	1
Motif ID:	322
Motif name:	Motif 322
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif

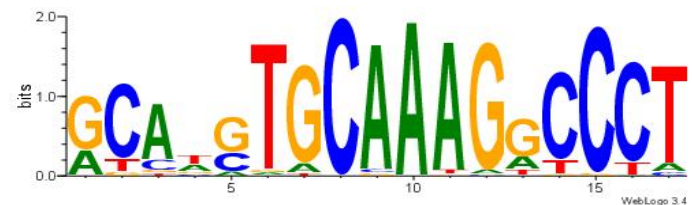
Direction: Forward
 Position number: 6
 Number of overlap: 10
 Similarity score: 0.0560732

Alignment:
 AGGGCCTTTGCASWTGC
 -----ATTTGCATTT--

Original motif Consensus sequence: AGGGCCTTTGCASWTGC



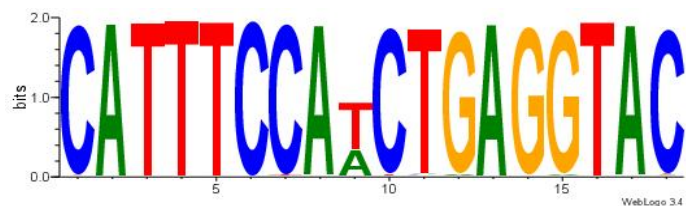
Reverse complement motif Consensus sequence: GCAWSTGCAAAGGCCCT



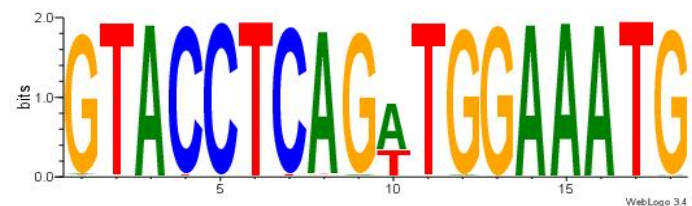
Dataset #: 1
 Motif ID: 25
 Motif name: Motif 25
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 10
 Similarity score: 0.0591841

Alignment:
 GTACCTCAGWTGGAAATG
 -AAATGCAAAT-----

Original motif Consensus sequence: CATTCCAWCTGAGGTAC



Reverse complement motif Consensus sequence: GTACCTCAGWTGGAAATG

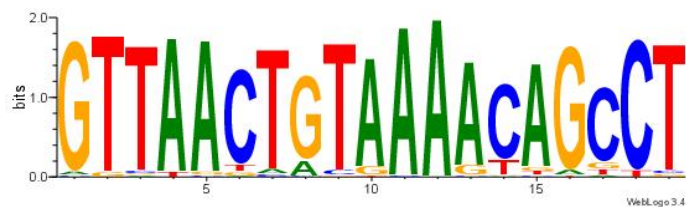


Dataset #: 1
Motif ID: 233
Motif name: Motif 233
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 4
Number of overlap: 10
Similarity score: 0.0615448

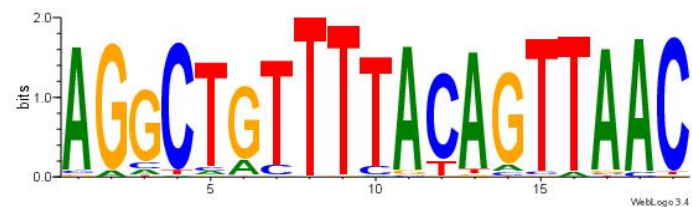
Alignment:

GTAACTGTAAAACAGCCT
---AAATGCAAAT-----

Original motif Consensus sequence: GTAACTGTAAAACAGcCT



Reverse complement motif Consensus sequence: AGGCTGTTTTACAGTTAAC



Dataset #: 1
 Motif ID: 214
 Motif name: Motif 214
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 6
 Number of overlap: 10
 Similarity score: 0.0631714

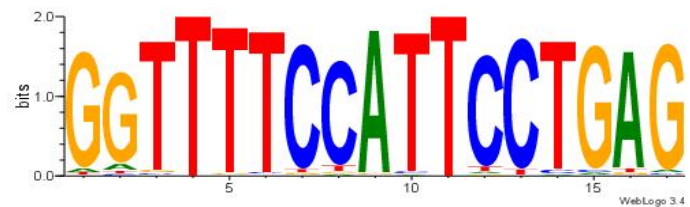
Alignment:

CTCAGGAATGGAAAACC
 -----AAATGCAAAT--

Original motif Consensus sequence: CTCAGGAATGGAAAACC



Reverse complement motif Consensus sequence: GGTTTCCATTCCCTGAG



Dataset #: 1
 Motif ID: 106
 Motif name: Motif 106
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 9

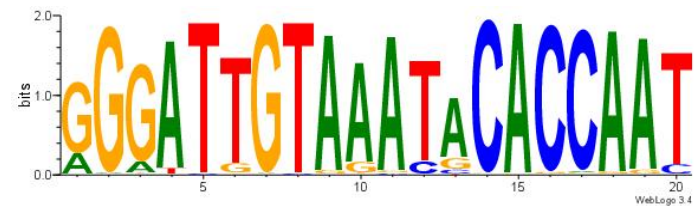
Number of overlap: 10
 Similarity score: 0.0657257

Alignment:
 ATTGGTGTATTTACAATCCC
 --ATTGCATTT-----

Original motif Consensus sequence: ATTGGTGTATTTACAATCCC



Reverse complement motif Consensus sequence: GGGATTGTAAATACACCAAT

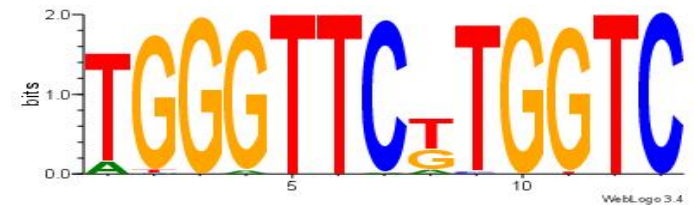


Dataset #: 1 Motif ID: 182 Motif name: Motif 182

Original motif Consensus sequence: GACCAMGAACCCA



Reverse complement motif Consensus sequence: TGGGTTTCYTGGTC



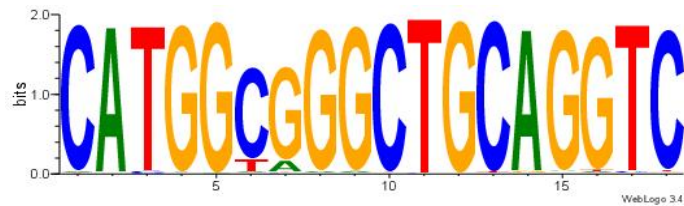
Best Matches for Motif ID 182 (Highest to Lowest)

Dataset #: 1
 Motif ID: 68
 Motif name: Motif 68
 Matching format of first motif: Original Motif

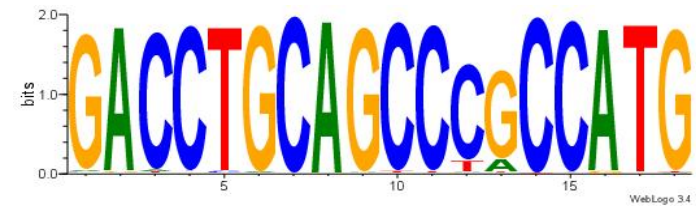
Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 13
 Similarity score: 0.0852314

Alignment:
 GACCTGCAGCCCGCCATG
 -----GACCAMGAACCCA

Original motif Consensus sequence: CATGGCGGGCTGCAGGTC



Reverse complement motif Consensus sequence: GACCTGCAGCCCGCCATG

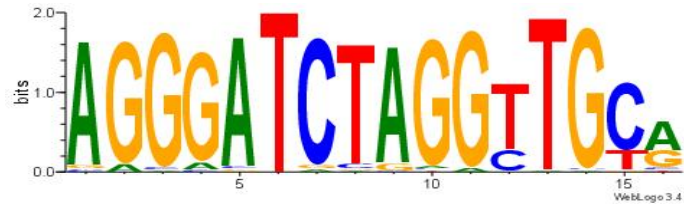


Dataset #: 1
 Motif ID: 271
 Motif name: Motif 271
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 13
 Similarity score: 0.0870886

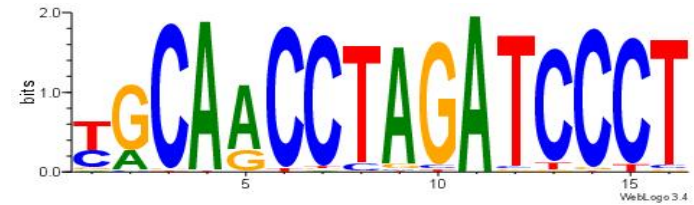
Alignment:

KGCAACCTAGATCCCT
---GACCAMGAACCCA

Original motif Consensus sequence: AGGGATCTAGGTTGCR



Reverse complement motif Consensus sequence:
KGCAACCTAGATCCCT

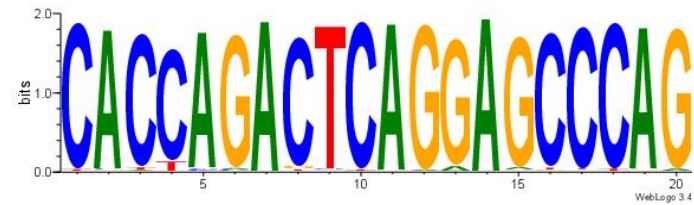
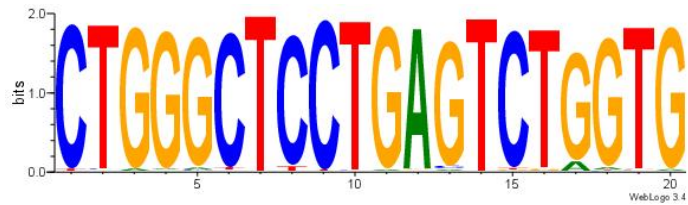


Dataset #: 1
Motif ID: 67
Motif name: Motif 67
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 2
Number of overlap: 13
Similarity score: 0.0874714

Alignment:
CACCAGACTCAGGAGCCCAG
-GACCAMGAACCCA-----

Original motif Consensus sequence: CTGGGCTCCTGAGTCTGGTG

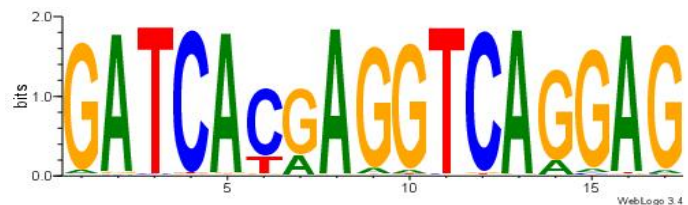
Reverse complement motif Consensus sequence:
CACCAGACTCAGGAGCCCAG



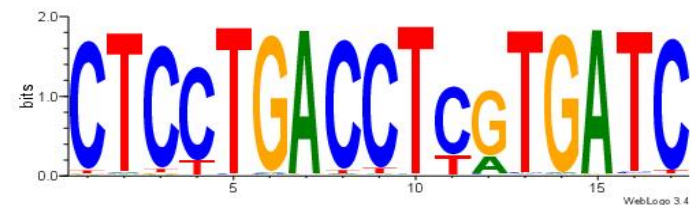
Dataset #: 1
 Motif ID: 60
 Motif name: Motif 60
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 13
 Similarity score: 0.0899738

Alignment:
 GATCACGAGGTCAGGAG
 GACCAMGAACCCA-----

Original motif Consensus sequence: GATCACGAGGTCAGGAG



Reverse complement motif Consensus sequence: CTCCTGACCTCGTGATC



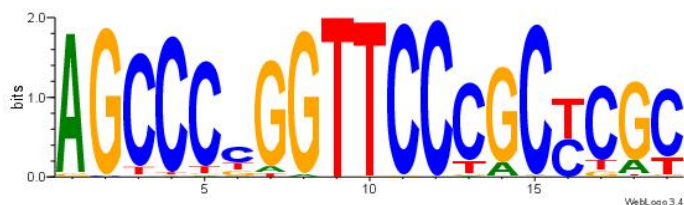
Dataset #: 1

Motif ID: 164
 Motif name: Motif 164
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 13
 Similarity score: 0.0928807

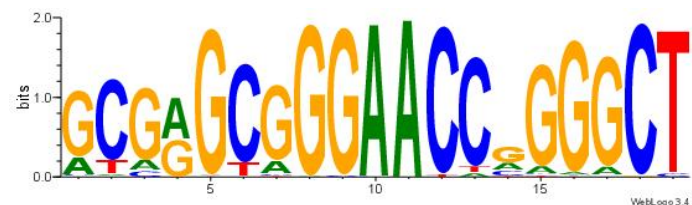
Alignment:

GCGMGCGGGAACCGGGGCT
 ----GACCAMGAACCCA--

Original motif Consensus sequence: AGCCCCGGTCCCGCYCGC

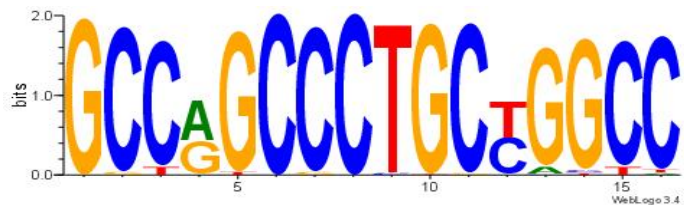


Reverse complement motif Consensus sequence: GCGMGCGGGAACCGGGGCT

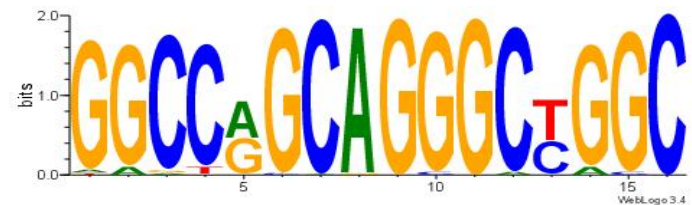


Dataset #: 1 Motif ID: 183 Motif name: Motif 183

Original motif Consensus sequence: GCCRGCCTGCYGGCC



Reverse complement motif Consensus sequence: GGCCMGCAGGGCKGGC



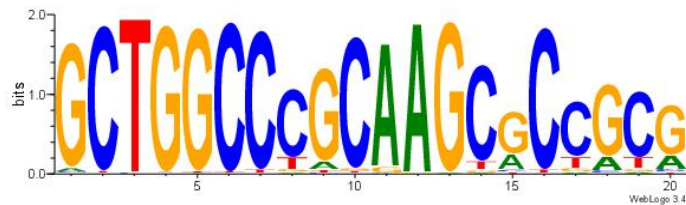
Best Matches for Motif ID 183 (Highest to Lowest)

Dataset #: 1
Motif ID: 100
Motif name: Motif 100
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 4
Number of overlap: 16
Similarity score: 0.0673082

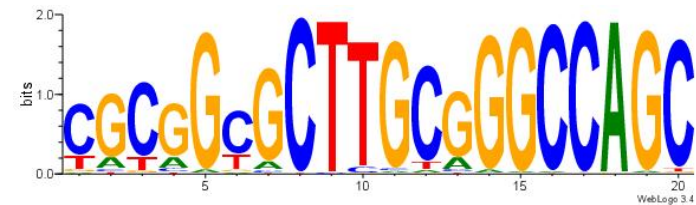
Alignment:

```
GCTGGCCCGCAAGCGCCGCG  
-GGCCMGCAGGGCKGGC---
```

Original motif Consensus sequence: GCTGGCCCGCAAGCGCCGCG



Reverse complement motif Consensus sequence: CGCGGCGCTTGCGGGCCAGC



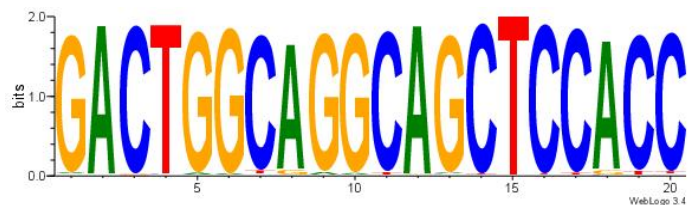
Dataset #: 1
Motif ID: 52
Motif name: Motif 52
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif

Direction: Forward
Position number: 1
Number of overlap: 16
Similarity score: 0.0703996

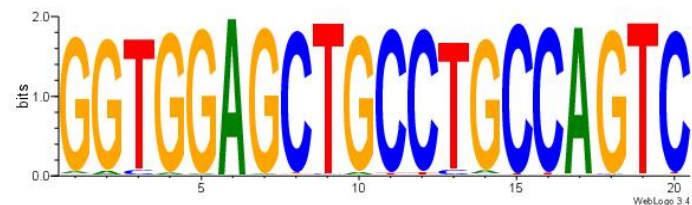
Alignment:

GACTGGCAGGCAGCTCCACC
GGCCMGCAGGGCKGGC----

Original motif Consensus sequence: GACTGGCAGGCAGCTCCACC



Reverse complement motif Consensus sequence: GGTGGAGCTGCCTGCCAGTC

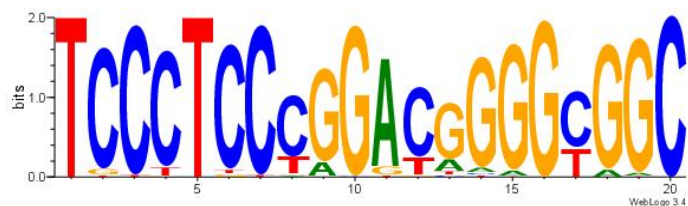


Dataset #: 1
Motif ID: 155
Motif name: Motif 155
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 16
Similarity score: 0.0746523

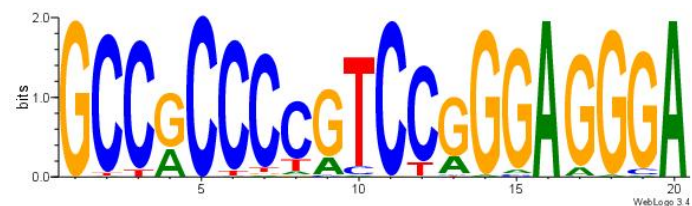
Alignment:

TCCCTCCCGGACGGGGYGGC
GGCCMGCAGGGCKGGC----

Original motif Consensus sequence: TCCCTCCCGACGGGGYGGC



Reverse complement motif Consensus sequence: GCCKCCCCGTCCGGGAGGGA

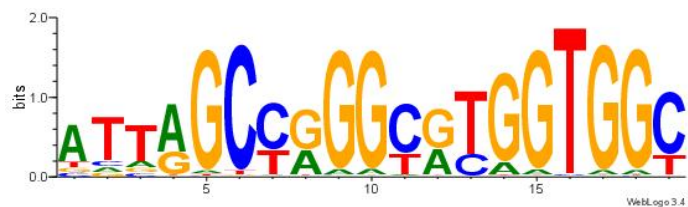


Dataset #: 1
Motif ID: 2
Motif name: Motif 2
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 4
Number of overlap: 16
Similarity score: 0.079611

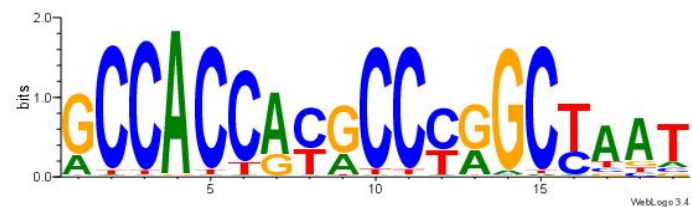
Alignment:

ATTAGCYRGGC RTGGTGGC
GGCCMGCAGGGCKGGC---

Original motif Consensus sequence: ATTAGCYRGGC RTGGTGGC



Reverse complement motif Consensus sequence: GCCACCAMGCCMKGCTAAT

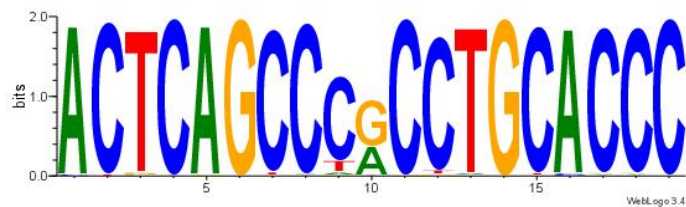


Dataset #: 1
 Motif ID: 149
 Motif name: Motif 149
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3
 Number of overlap: 16
 Similarity score: 0.081514

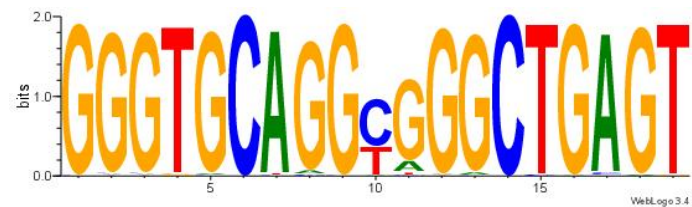
Alignment:

GGGTGCAGGMGGGCTGAGT
 --GGCCMGCAGGGCKGGC--

Original motif Consensus sequence: ACTCAGCCRCCTGCACCC



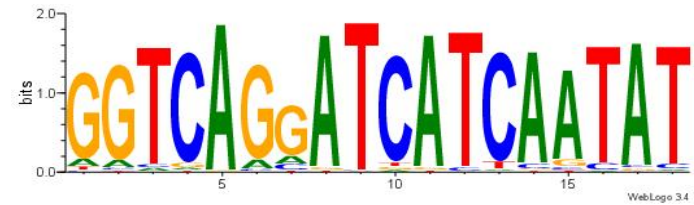
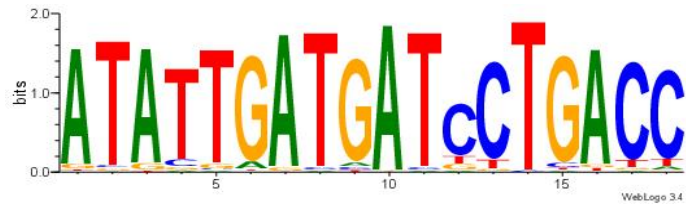
Reverse complement motif Consensus sequence: GGGTGCAGGMGGGCTGAGT



Dataset #: 1 Motif ID: 184 Motif name: Motif 184

Original motif Consensus sequence: ATATTGATGATCCTGACC

Reverse complement motif Consensus sequence: GGTCAGGATCATCAATAT



Best Matches for Motif ID 184 (Highest to Lowest)

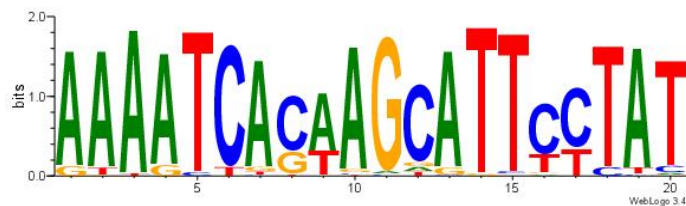
Dataset #: 1
 Motif ID: 254
 Motif name: Motif 254
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 18
 Similarity score: 0.08828

Alignment:

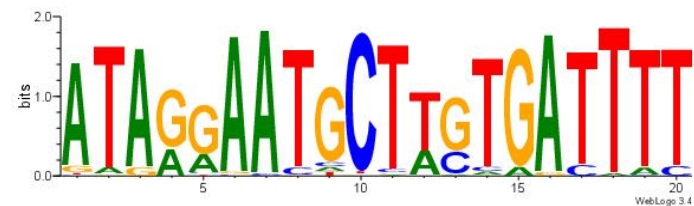
```

ATAGGAATGCTTGTGATTTT
ATATTGATGATCCTGACC--
  
```

Original motif Consensus sequence: AAAATCACAAAGCATTcCTAT



Reverse complement motif Consensus sequence: ATAGGAATGCTTGTGATTTT

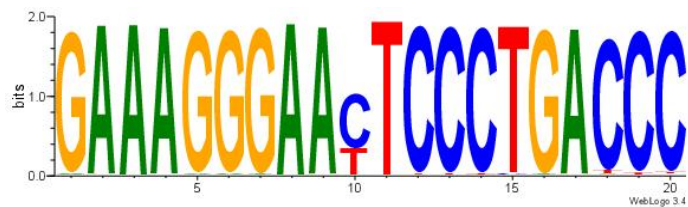


Dataset #: 1
 Motif ID: 16
 Motif name: Motif 16
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 18
 Similarity score: 0.0954042

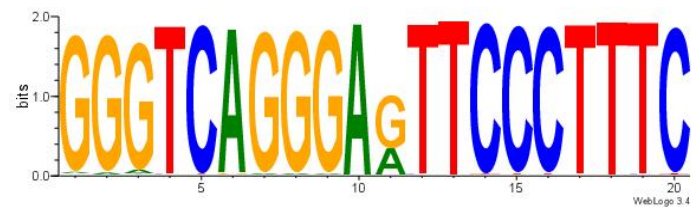
Alignment:

GAAAGGGA ACTCCCTGACCC
 -ATATTGATGATCCTGACC-

Original motif Consensus sequence: GAAAGGGA ACTCCCTGACCC



Reverse complement motif Consensus sequence: GGGTCAGG GAGTTCCCTTTC



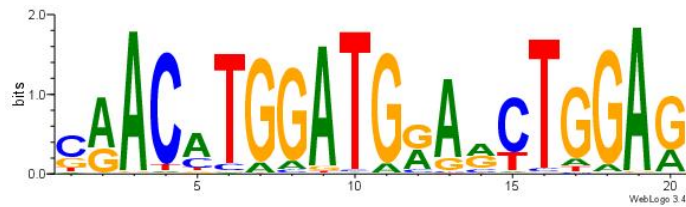
Dataset #: 1
 Motif ID: 104
 Motif name: Motif 104
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1

Number of overlap: 18
Similarity score: 0.0972719

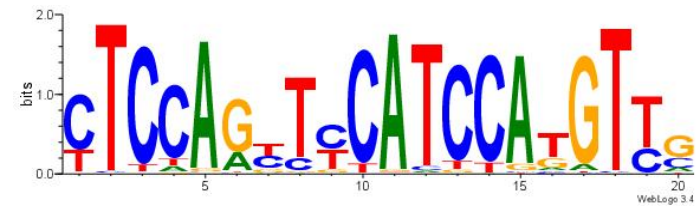
Alignment:

CAACATGGATGRARCTGGAG
--ATATTGATGATCCTGACC

Original motif Consensus sequence: CAACATGGATGRARCTGGAG



Reverse complement motif Consensus sequence:
CTCCAGKTMCATCCATGTTG

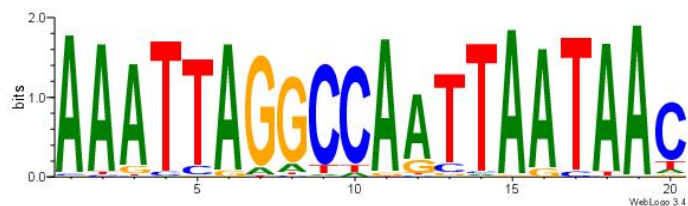


Dataset #: 1
Motif ID: 308
Motif name: Motif 308
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 2
Number of overlap: 18
Similarity score: 0.104578

Alignment:

GTTATTAATTGGCCTAATTT
-ATATTGATGATCCTGACC-

Original motif Consensus sequence: AAATTAGGCCAATTAATAAC



Reverse complement motif Consensus sequence: GTTATTAATTGGCCTAATTT

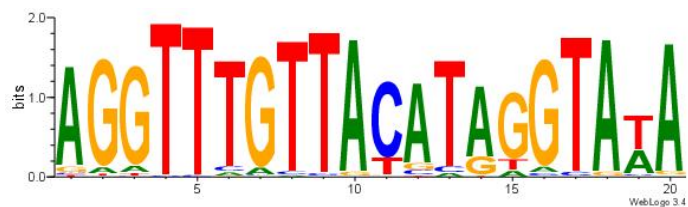


Dataset #: 1
Motif ID: 137
Motif name: Motif 137
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 2
Number of overlap: 18
Similarity score: 0.106783

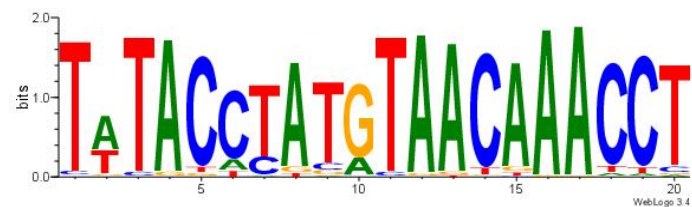
Alignment:

AGGTTTGTTACATAGGTAWA
-GGTCAGGATCATCAATAT-

Original motif Consensus sequence: AGGTTTGTTACATAGGTAWA



Reverse complement motif Consensus sequence: TWTACCTATGTAACAAACCT

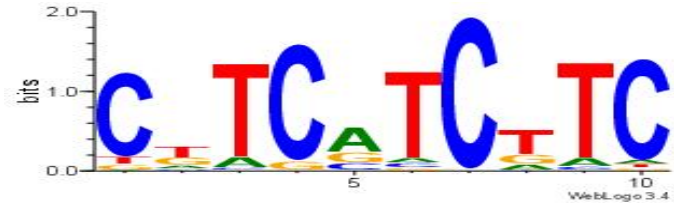


Dataset #: 1 Motif ID: 185 Motif name: Motif 185

Original motif Consensus sequence: GAAGATGAMG



Reverse complement motif Consensus sequence: CYTCATCTTC



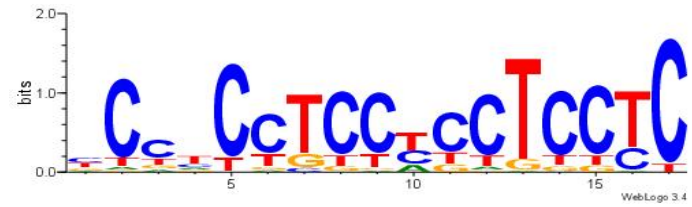
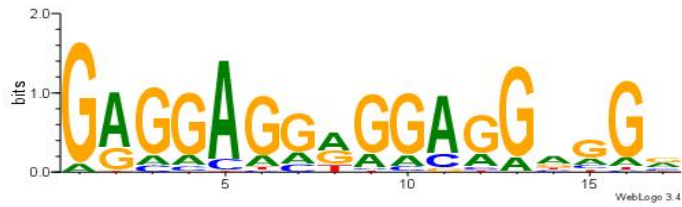
Best Matches for Motif ID 185 (Highest to Lowest)

Dataset #:	1
Motif ID:	161
Motif name:	Motif 161
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	4
Number of overlap:	10
Similarity score:	0.038579

Alignment:
VCCDCCTCCKCCTCCTC
----CYTCATCTTC----

Original motif Consensus sequence: GAGGAGGRGGAGGDGGV

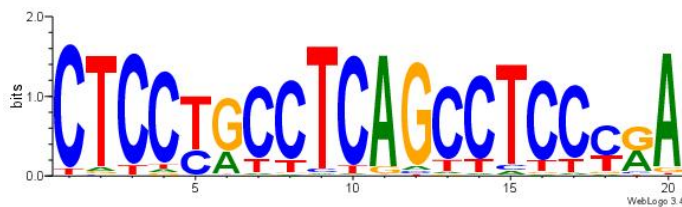
Reverse complement motif Consensus sequence:
VCCDCCTCCKCCTCCTC



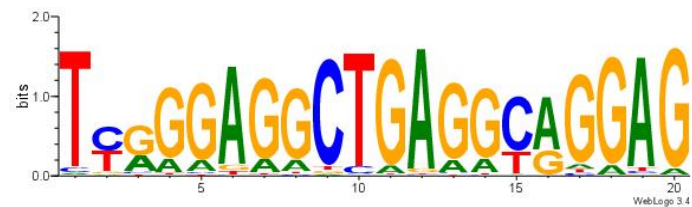
Dataset #: 1
 Motif ID: 26
 Motif name: Motif 26
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 7
 Number of overlap: 10
 Similarity score: 0.0396628

Alignment:
 TMGGGAGGCTGAGGCAGGAG
 -----GAAGATGAMG-----

Original motif Consensus sequence: CTCCTGCCTCAGCCTCCRA



Reverse complement motif Consensus sequence: TMGGGAGGCTGAGGCAGGAG



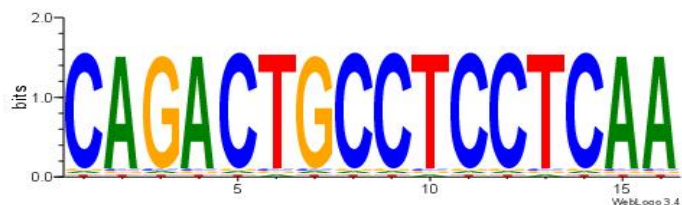
Dataset #: 1

Motif ID: 245
Motif name: Motif 245
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 3
Number of overlap: 10
Similarity score: 0.0437873

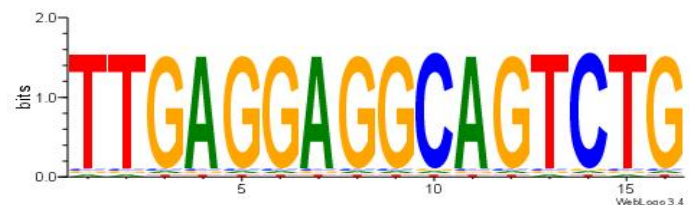
Alignment:

CAGACTGCCTCCTCAA
----CYTCATCTTC--

Original motif Consensus sequence: CAGACTGCCTCCTCAA



Reverse complement motif Consensus sequence: TTGAGGAGGCAGTCTG



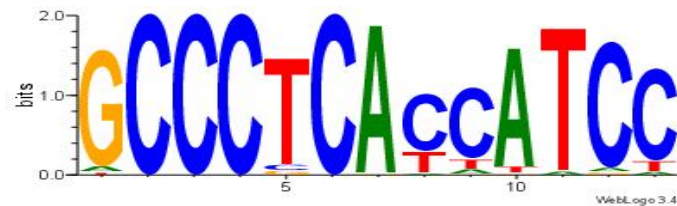
Dataset #: 1
Motif ID: 283
Motif name: Motif 283
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2
Number of overlap: 10

Similarity score: 0.0453186

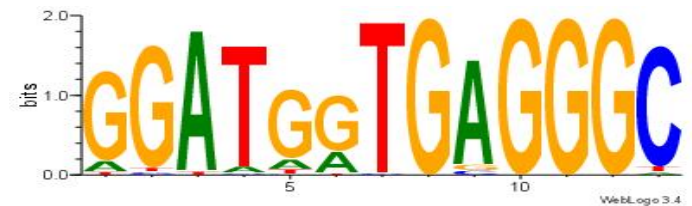
Alignment:

GCCCTCACCATCC
--CYTCATCTTC--

Original motif Consensus sequence: GCCCTCACCATCC



Reverse complement motif Consensus sequence: GGATGGTGAGGG



Dataset #:	1
Motif ID:	5
Motif name:	Motif 5
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	10
Similarity score:	0.0464636

Alignment:

GGAGGCKGAGG
GAAGATGAMG--

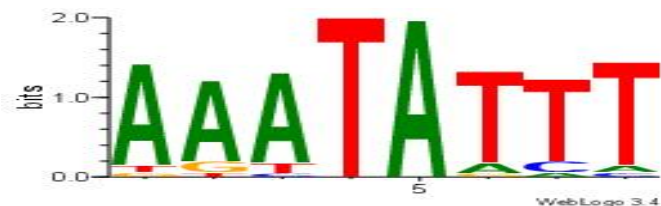
Original motif Consensus sequence: CCTCRGCCTCC

Reverse complement motif Consensus sequence: GGAGGCKGAGG

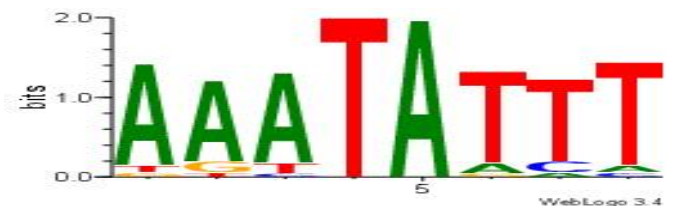


Dataset #: 1 Motif ID: 186 Motif name: Motif 186

Original motif Consensus sequence: AAATATTT



Reverse complement motif Consensus sequence: AAATATTT

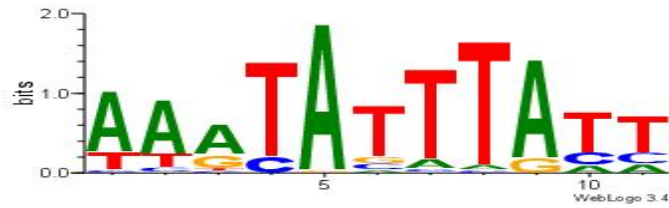


Best Matches for Motif ID 186 (Highest to Lowest)

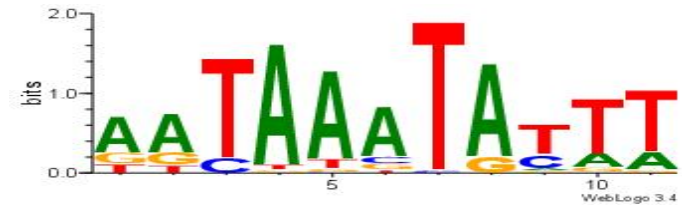
Dataset #:	1
Motif ID:	57
Motif name:	Motif 57
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	8
Similarity score:	0.0174942

Alignment:
AATAAATATTT
AAATATTT---

Original motif Consensus sequence: AAATATTTATT



Reverse complement motif Consensus sequence: AATAAATATTT

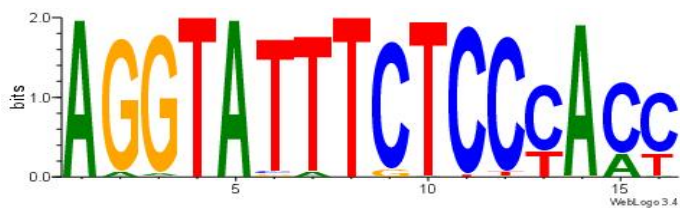


Dataset #: 1
 Motif ID: 168
 Motif name: Motif 168
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 8
 Similarity score: 0.0532506

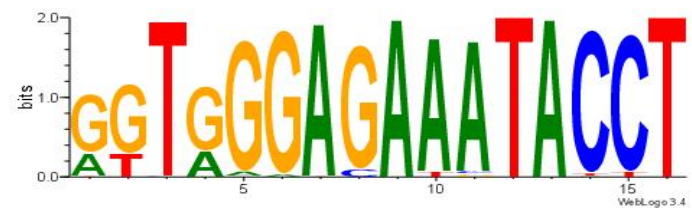
Alignment:

```
AGGTATTTCTCCCACC
-----AAATATTT
```

Original motif Consensus sequence: AGGTATTTCTCCCACC



Reverse complement motif Consensus sequence: GGTGGGAGAAATACCT

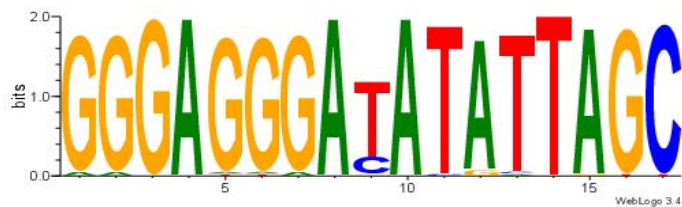


Dataset #: 1
 Motif ID: 329
 Motif name: Motif 329
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 8
 Number of overlap: 8
 Similarity score: 0.055379

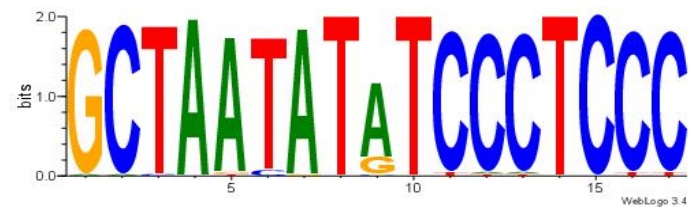
Alignment:

GCTAATATATCCCTCCC
 --AAATATTT-----

Original motif Consensus sequence: GGGAGGGATATATTAGC



Reverse complement motif Consensus sequence: GCTAATATATCCCTCCC

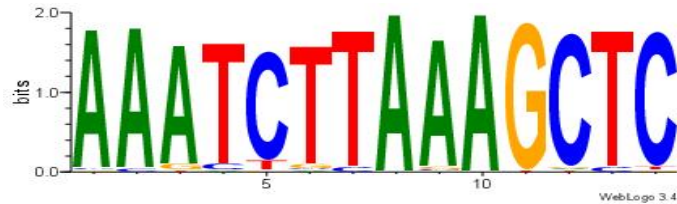


Dataset #: 1
 Motif ID: 346
 Motif name: Motif 346
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 7

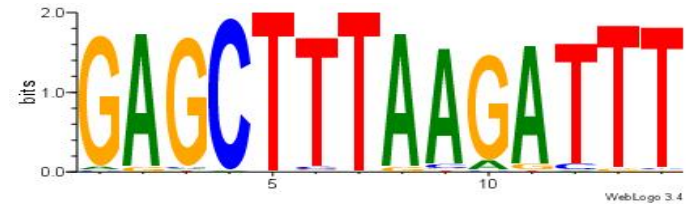
Number of overlap: 8
Similarity score: 0.060748

Alignment:
GAGCTTTAAGATTT
-----AAATATTT

Original motif Consensus sequence: AAATCTTAAAGCTC



Reverse complement motif Consensus sequence: GAGCTTTAAGATTT

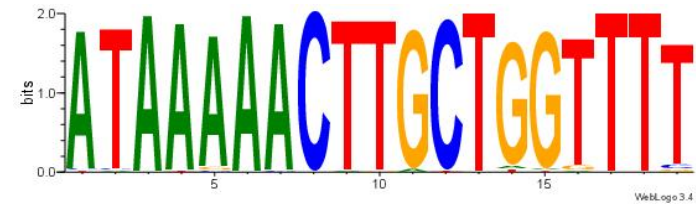
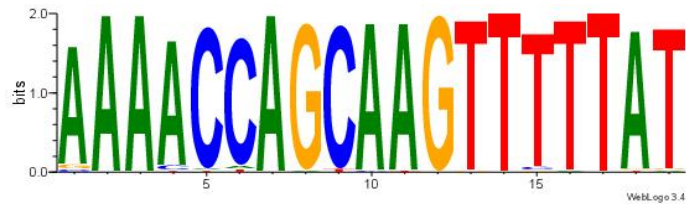


Dataset #: 1
Motif ID: 330
Motif name: Motif 330
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 3
Number of overlap: 8
Similarity score: 0.0630537

Alignment:
AAAACCAGCAAGTTTTTAT
-----AAATATTT--

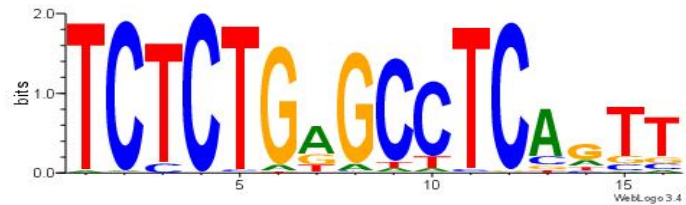
Original motif Consensus sequence: AAAACCAGCAAGTTTTTAT

Reverse complement motif Consensus sequence:
ATAAAAAGTCTGCTGTTTT

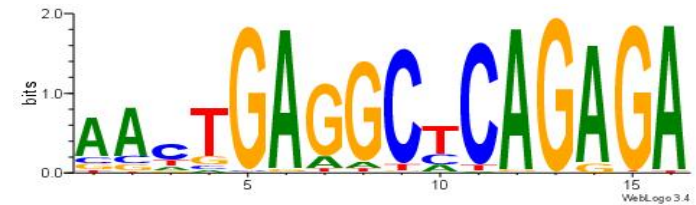


Dataset #: 1 Motif ID: 187 Motif name: Motif 187

Original motif Consensus sequence: TCTCTGAGCCTCAGTT



Reverse complement motif Consensus sequence: AACTGAGGCTCAGAGA



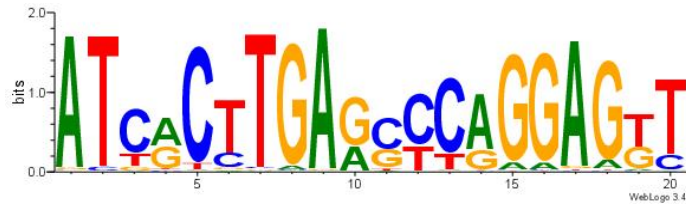
Best Matches for Motif ID 187 (Highest to Lowest)

Dataset #:	1
Motif ID:	8
Motif name:	Motif 8
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	4
Number of overlap:	16
Similarity score:	0.0912831

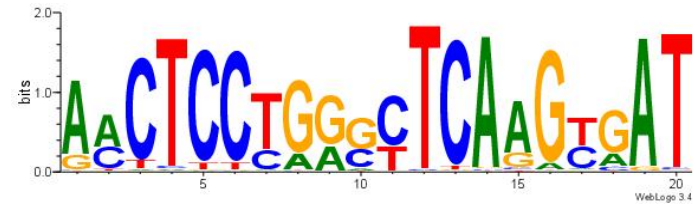
Alignment:

ATCRCTTGAGSYCAGGAGKT
-AACTGAGGCTCAGAGA---

Original motif Consensus sequence: ATCRCTTGAGSYCAGGAGKT



Reverse complement motif Consensus sequence:
ARCTCCTGKSCTCAAGKGAT

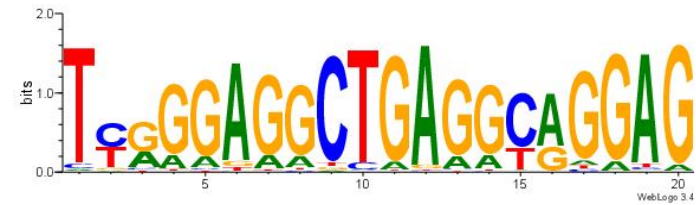
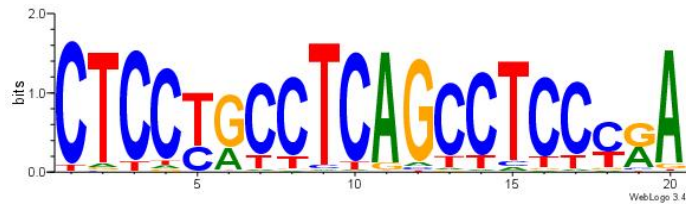


Dataset #:	1
Motif ID:	26
Motif name:	Motif 26
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	16
Similarity score:	0.0936416

Alignment:
TMGGGAGGCTGAGGCAGGAG
AACTGAGGCTCAGAGA----

Original motif Consensus sequence: CTCCTGCCTCAGCCTCCRA

Reverse complement motif Consensus sequence:
TMGGGAGGCTGAGGCAGGAG

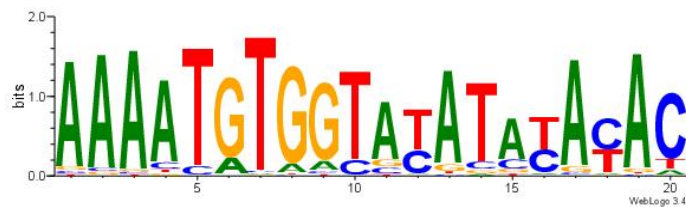


Dataset #: 1
 Motif ID: 83
 Motif name: Motif 83
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 16
 Similarity score: 0.097136

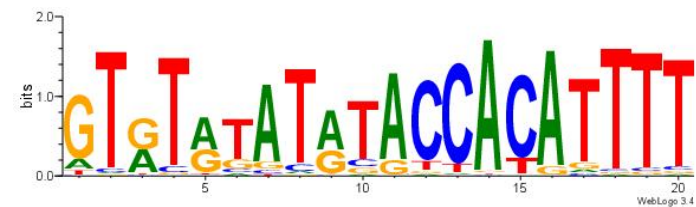
Alignment:

GTKTMTATMTACCACATTTT
 -TCTCTGAGCCTCAGTT---

Original motif Consensus sequence: AAAATGTGGTAYATAYAYAC



Reverse complement motif Consensus sequence: GTKTMTATMTACCACATTTT



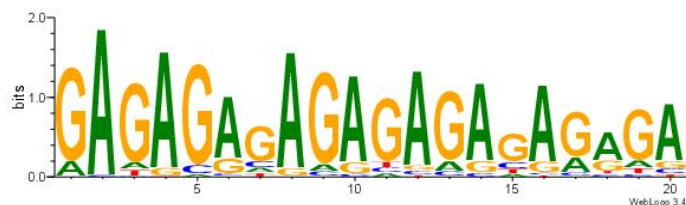
Dataset #: 1

Motif ID: 109
 Motif name: Motif 109
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 5
 Number of overlap: 16
 Similarity score: 0.0973627

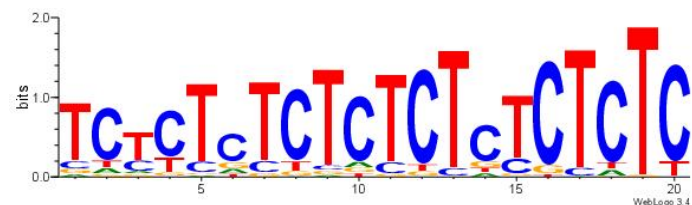
Alignment:

GAGAGAGAGAGAGAGAGAGA
 AACTGAGGCTCAGAGA-----

Original motif Consensus sequence: GAGAGAGAGAGAGAGAGA



Reverse complement motif Consensus sequence: TCTCTCTCTCTCTCTCTC



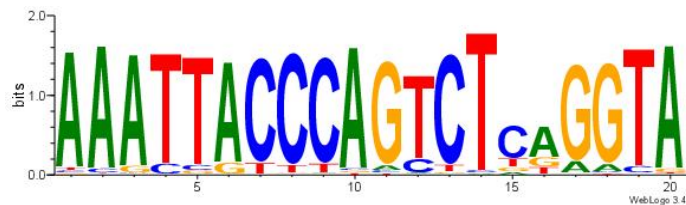
Dataset #: 1
 Motif ID: 160
 Motif name: Motif 160
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 5
 Number of overlap: 16

Similarity score: 0.09885

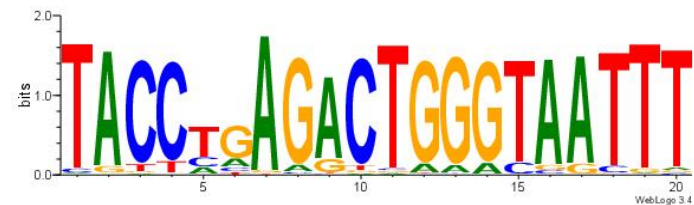
Alignment:

AAATTACCCAGTCTCAGGTA
AACTGAGGCTCAGAGA----

Original motif Consensus sequence: AAATTACCCAGTCTCAGGTA



Reverse complement motif Consensus sequence: TACCTGAGACTGGGTAATTT

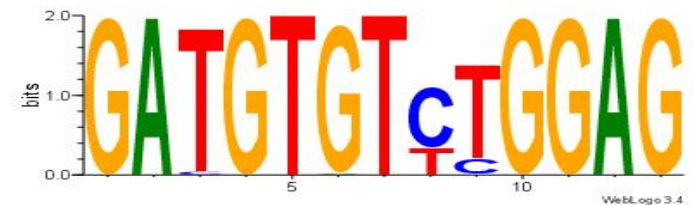


Dataset #: 1 Motif ID: 188 Motif name: Motif 188

Original motif Consensus sequence: CTCCAGACACATC



Reverse complement motif Consensus sequence: GATGTGTCTGGAG



Best Matches for Motif ID 188 (Highest to Lowest)

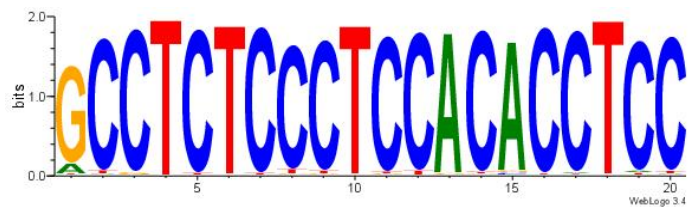
Dataset #:	1
Motif ID:	105
Motif name:	Motif 105
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement

Direction: Forward
Position number: 4
Number of overlap: 13
Similarity score: 0.0694148

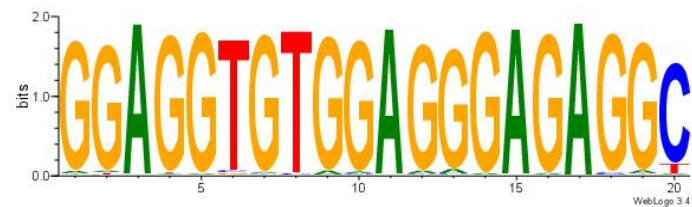
Alignment:

GGAGGTGTGGAGGGAGAGGC
---GATGTGTCTGGAG----

Original motif Consensus sequence: GCCTCTCCCTCCACACCTCC



Reverse complement motif Consensus sequence: GGAGGTGTGGAGGGAGAGGC

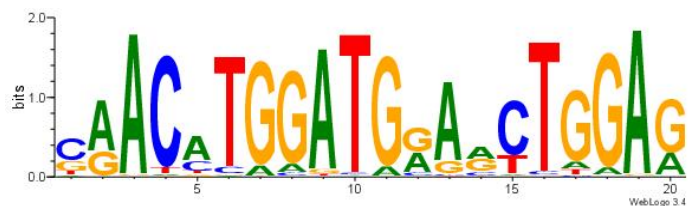


Dataset #: 1
Motif ID: 104
Motif name: Motif 104
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 8
Number of overlap: 13
Similarity score: 0.0708894

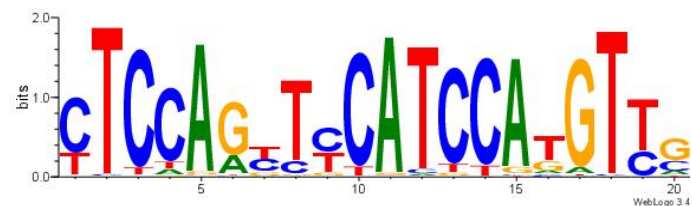
Alignment:

CAACATGGATGRARCTGGAG
GATGTGTCTGGAG-----

Original motif Consensus sequence: CAACATGGATGRARCTGGAG



Reverse complement motif Consensus sequence: CTCAGKTMCATCCATGTTG

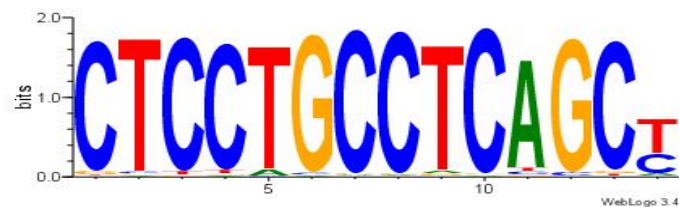


Dataset #: 1
Motif ID: 313
Motif name: Motif 313
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 13
Similarity score: 0.0851305

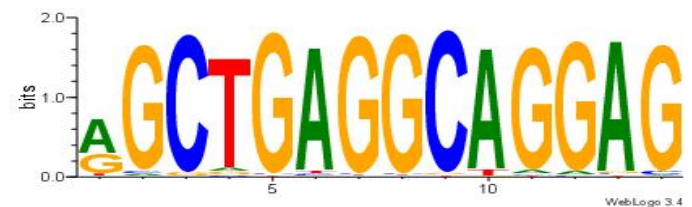
Alignment:

CTCCTGCCTCAGCY
CTCCAGACACATC-

Original motif Consensus sequence: CTCCTGCCTCAGCY



Reverse complement motif Consensus sequence: MGCTGAGGCAGGAG

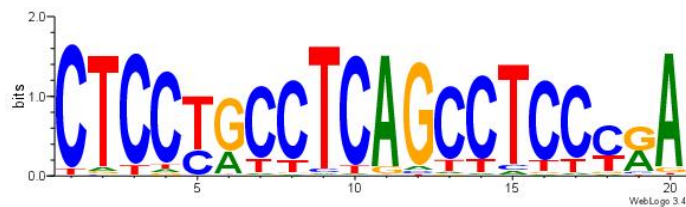


Dataset #: 1
 Motif ID: 26
 Motif name: Motif 26
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 8
 Number of overlap: 13
 Similarity score: 0.0869612

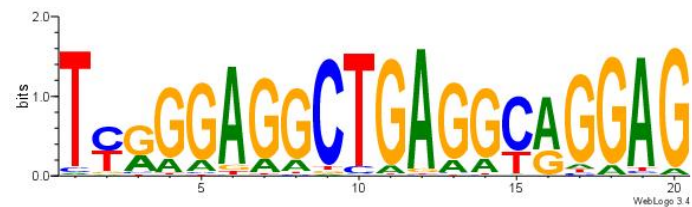
Alignment:

TMGGGAGGCTGAGGCAGGAG
 -----GATGTGTCTGGAG

Original motif Consensus sequence: CTCCTGCCTCAGCCTCCRA



Reverse complement motif Consensus sequence: TMGGGAGGCTGAGGCAGGAG



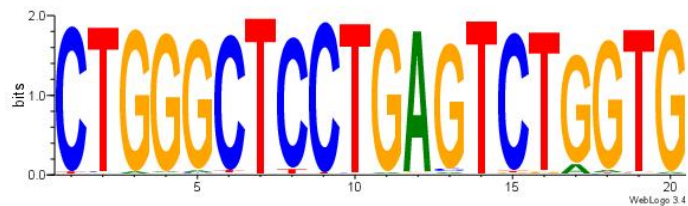
Dataset #: 1
 Motif ID: 67
 Motif name: Motif 67
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 8

Number of overlap: 13
Similarity score: 0.0873184

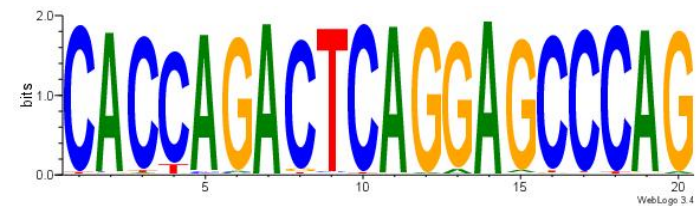
Alignment:

CTGGGCTCCTGAGTCTGGTG
GATGTGTCTGGAG-----

Original motif Consensus sequence: CTGGGCTCCTGAGTCTGGTG

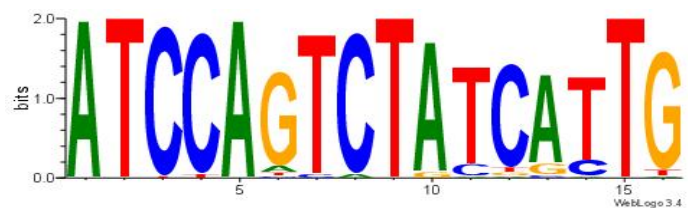


Reverse complement motif Consensus sequence:
CACCAGACTCAGGAGCCCAG

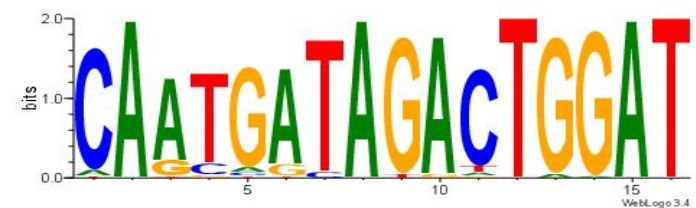


Dataset #: 1 Motif ID: 189 Motif name: Motif 189

Original motif Consensus sequence: ATCCAGTCTATCATTG



Reverse complement motif Consensus sequence:
CAATGATAGACTGGAT



Best Matches for Motif ID 189 (Highest to Lowest)

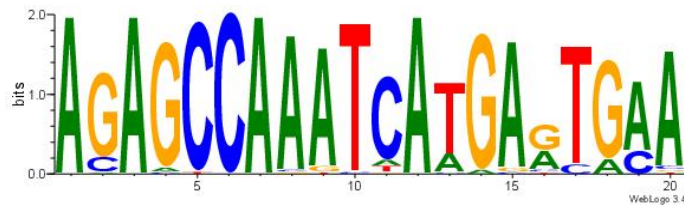
Dataset #: 1
Motif ID: 349
Motif name: Motif 349

Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3
 Number of overlap: 16
 Similarity score: 0.0977739

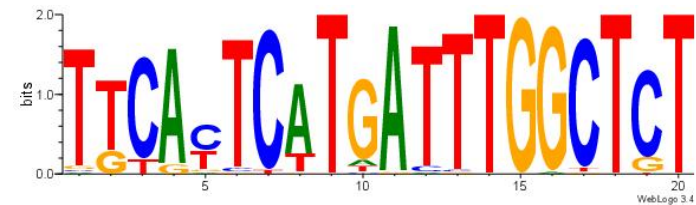
Alignment:

TTCAMTCATGATTTGGCTCT
 --CAATGATAGACTGGAT--

Original motif Consensus sequence: AGAGCCAAATCATGARTGAA



Reverse complement motif Consensus sequence: TTCAMTCATGATTTGGCTCT

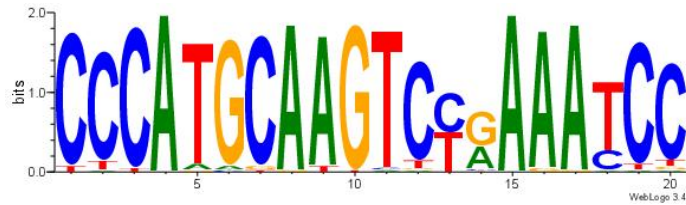


Dataset #: 1
 Motif ID: 310
 Motif name: Motif 310
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 16
 Similarity score: 0.106334

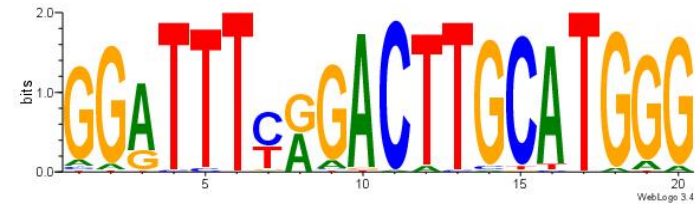
Alignment:

CCCATGCAAGTCYRAAATCC
-CAATGATAGACTGGAT---

Original motif Consensus sequence: CCCATGCAAGTCYRAAATCC



Reverse complement motif Consensus sequence:
GGATTTMKGACTTGCATGGG



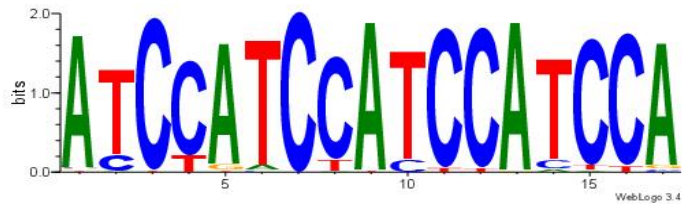
Dataset #: 1
Motif ID: 341
Motif name: Motif 341
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 16
Similarity score: 0.108161

Alignment:

ATCCATCCATCCATCCA
ATCCAGTCTATCATTG-

Original motif Consensus sequence: ATCCATCCATCCATCCA

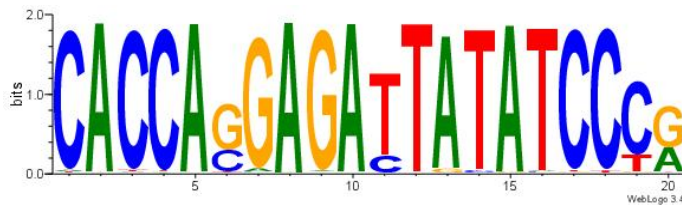
Reverse complement motif Consensus sequence:
TGGATGGATGGATGGAT



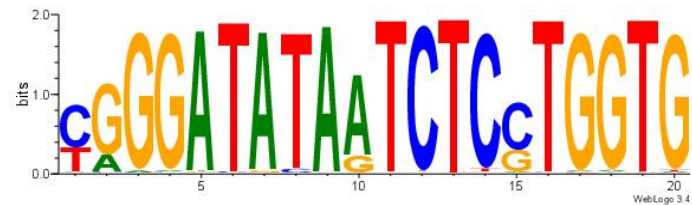
Dataset #: 1
 Motif ID: 19
 Motif name: Motif 19
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 16
 Similarity score: 0.108907

Alignment:
 MGGGATATAATCTCCTGGTG
 ATCCAGTCTATCATTG----

Original motif Consensus sequence: CACCAGGAGATTATATCCCR



Reverse complement motif Consensus sequence: MGGGATATAATCTCCTGGTG



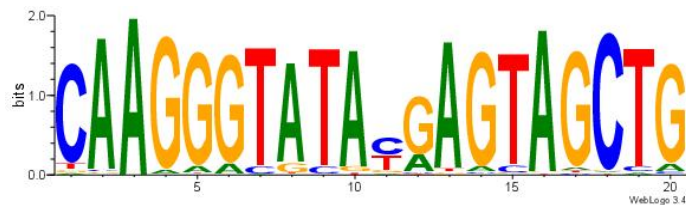
Dataset #: 1

Motif ID: 194
 Motif name: Motif 194
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 5
 Number of overlap: 16
 Similarity score: 0.10982

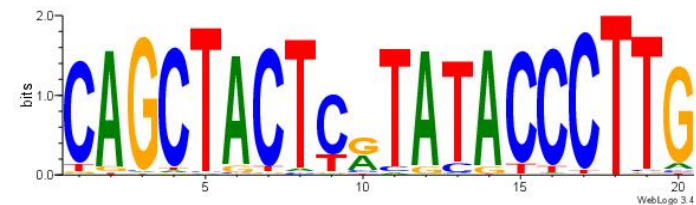
Alignment:

CAGCTACTCKTATACCCTTG
 ----ATCCAGTCTATCATTG

Original motif Consensus sequence: CAAGGGTATAYGAGTAGCTG

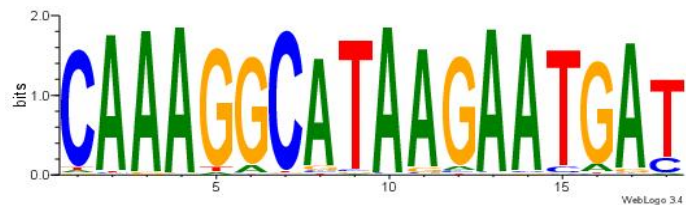


Reverse complement motif Consensus sequence: CAGCTACTCKTATACCCTTG

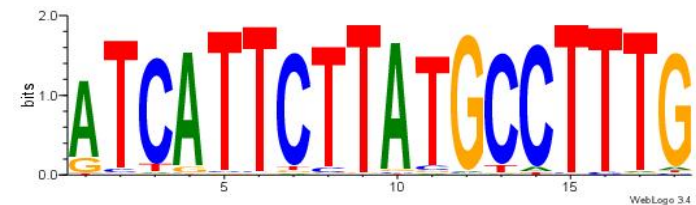


Dataset #: 1 Motif ID: 190 Motif name: Motif 190

Original motif Consensus sequence: CAAAGGCATAAGAATGAT



Reverse complement motif Consensus sequence: ATCATTCTTATGCCTTTG



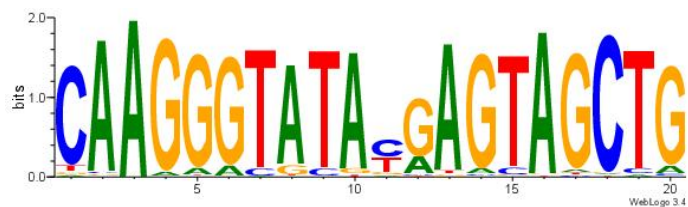
Best Matches for Motif ID 190 (Highest to Lowest)

Dataset #: 1
Motif ID: 194
Motif name: Motif 194
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 3
Number of overlap: 18
Similarity score: 0.0879984

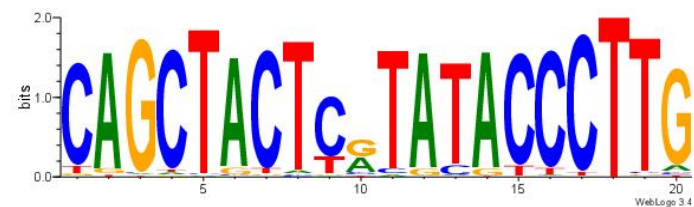
Alignment:

```
CAAGGGTATAYGAGTAGCTG  
CAAAGGCATAAGAATGAT--
```

Original motif Consensus sequence: CAAGGGTATAYGAGTAGCTG



Reverse complement motif Consensus sequence:
CAGCTACTCKTATACCCTTG



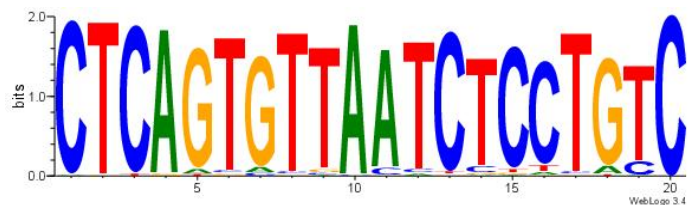
Dataset #: 1
Motif ID: 262
Motif name: Motif 262
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif

Direction: Backward
Position number: 3
Number of overlap: 18
Similarity score: 0.101423

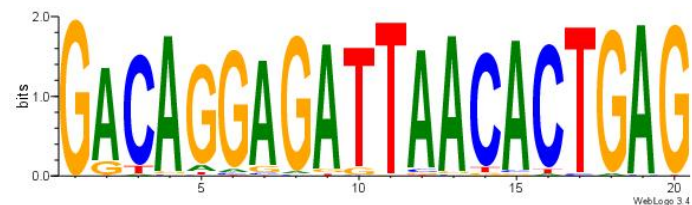
Alignment:

CTCAGTGTTAATCTCCTGTC
ATCATTCTTATGCCTTTG--

Original motif Consensus sequence: CTCAGTGTTAATCTCCTGTC



Reverse complement motif Consensus sequence: GACAGGAGATTAACACTGAG

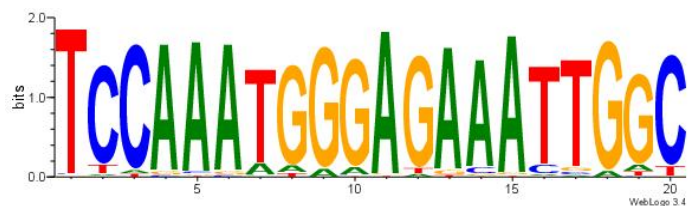


Dataset #: 1
Motif ID: 235
Motif name: Motif 235
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 18
Similarity score: 0.110461

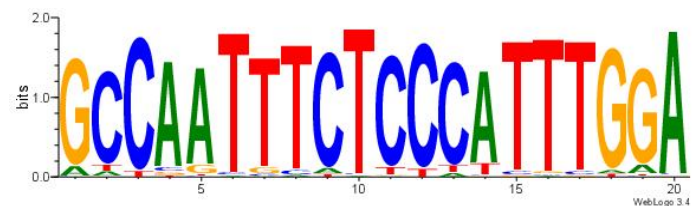
Alignment:

TCCAAATGGGAGAAATTGGC
--CAAAGGCATAAGAATGAT

Original motif Consensus sequence: TCCAATGGGAGAAATTGGC



Reverse complement motif Consensus sequence: GCCAATTTCTCCCATTTGGA

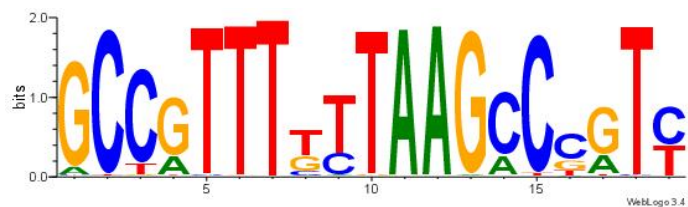


Dataset #: 1
Motif ID: 21
Motif name: Motif 21
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 18
Similarity score: 0.111473

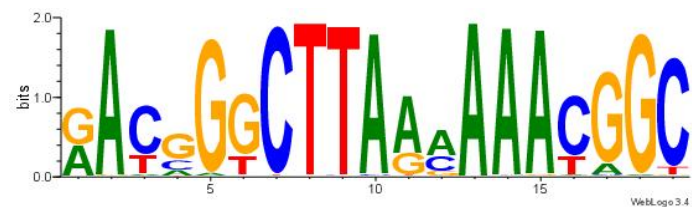
Alignment:

GCCGTTTKTTAAGCCCGTY
ATCATTCTTATGCCTTTG-

Original motif Consensus sequence: GCCGTTTKTTAAGCCCGTY



Reverse complement motif Consensus sequence: KACGGGCTTAARAAACGGC

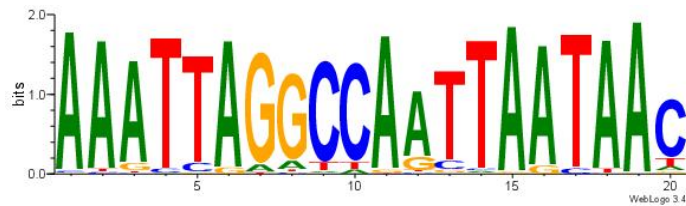


Dataset #: 1
 Motif ID: 308
 Motif name: Motif 308
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 18
 Similarity score: 0.114401

Alignment:

AAATTAGGCCAATTAATAAC
 --CAAAGGCATAAGAATGAT

Original motif Consensus sequence: AAATTAGGCCAATTAATAAC



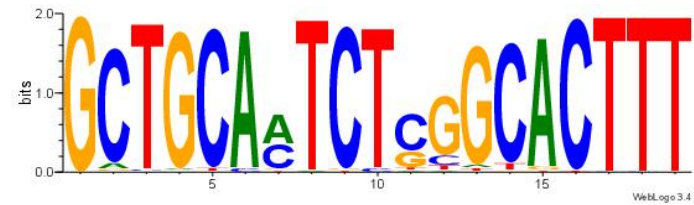
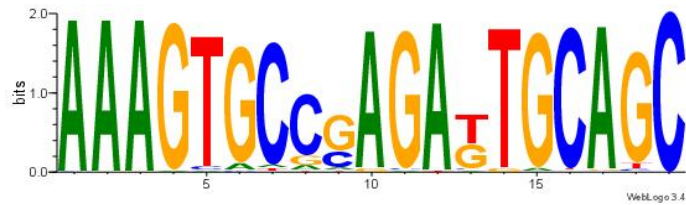
Reverse complement motif Consensus sequence: GTTATTAATTGGCCTAATTT



Dataset #: 1 Motif ID: 191 Motif name: Motif 191

Original motif Consensus sequence: AAAGTGCCGAGAKTGCAGC

Reverse complement motif Consensus sequence: GCTGCARTCTCGGCACTTT

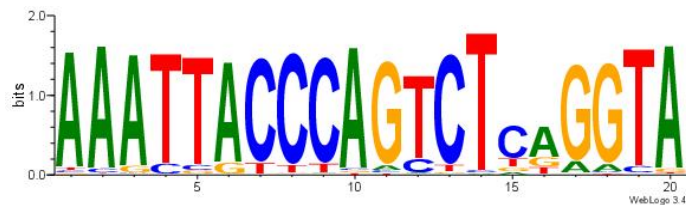


Best Matches for Motif ID 191 (Highest to Lowest)

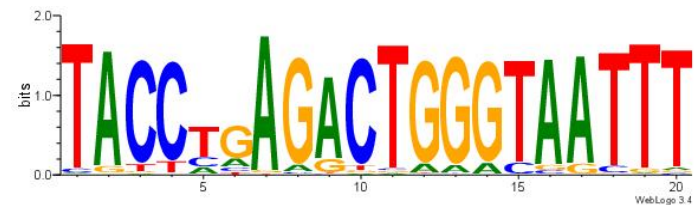
Dataset #: 1
 Motif ID: 160
 Motif name: Motif 160
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 19
 Similarity score: 0.105699

Alignment:
 TACCTGAGACTGGGTAATTT
 -GCTGCARTCTCGGCACTTT

Original motif Consensus sequence: AAATTACCCAGTCTCAAGGTA



Reverse complement motif Consensus sequence: TACCTGAGACTGGGTAATTT

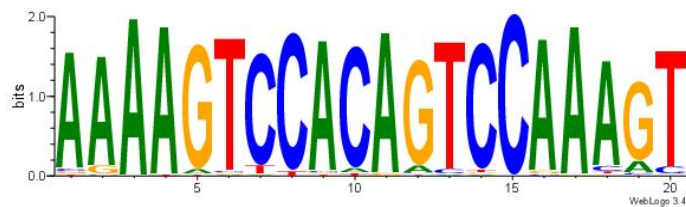


Dataset #: 1
 Motif ID: 171
 Motif name: Motif 171
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 19
 Similarity score: 0.106747

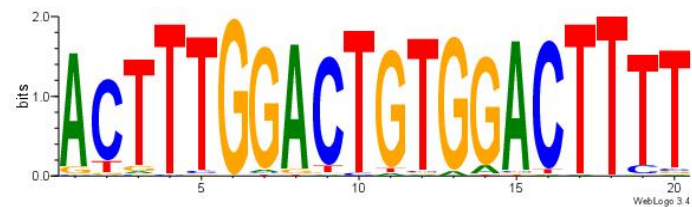
Alignment:

ACTTTGGACTGTGGACTTTT
 GCTGCARTCTCGGCACTTT-

Original motif Consensus sequence: AAAAGTCCACAGTCCAAAGT



Reverse complement motif Consensus sequence: ACTTTGGACTGTGGACTTTT



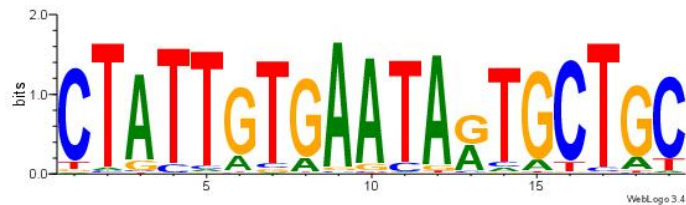
Dataset #: 1
 Motif ID: 70
 Motif name: Motif 70
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1

Number of overlap: 19
Similarity score: 0.111752

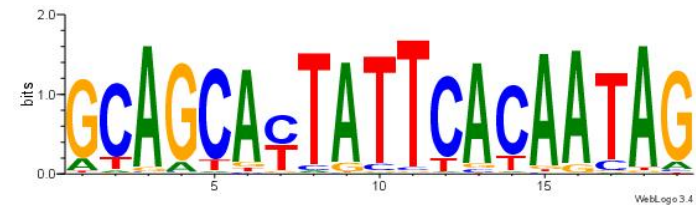
Alignment:

GCAGCAMTATTACAATAG
GCTGCARTCTCGGCACTTT

Original motif Consensus sequence: CTATTGTGAATARTGCTGC



Reverse complement motif Consensus sequence:
GCAGCAMTATTACAATAG

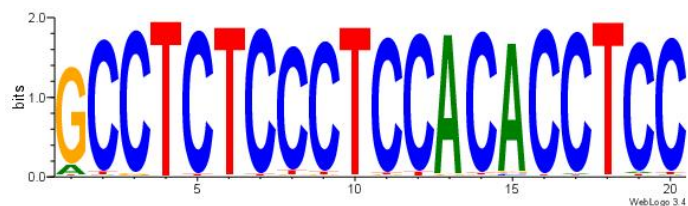


Dataset #: 1
Motif ID: 105
Motif name: Motif 105
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 19
Similarity score: 0.11316

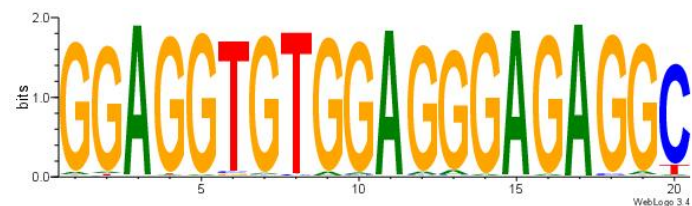
Alignment:

GCCTCTCCCTCCACACCTCC
-GCTGCARTCTCGGCACTTT

Original motif Consensus sequence: GCCTCTCCCTCCACACCTCC



Reverse complement motif Consensus sequence: GGAGGTGTGGAGGGAGAGGC

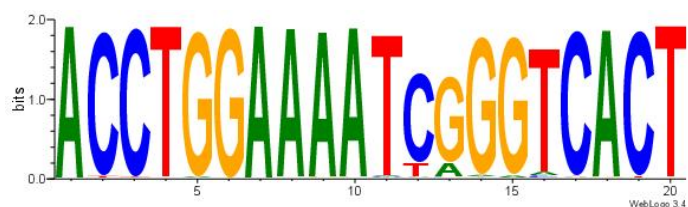


Dataset #: 1
Motif ID: 14
Motif name: Motif 14
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 2
Number of overlap: 19
Similarity score: 0.114153

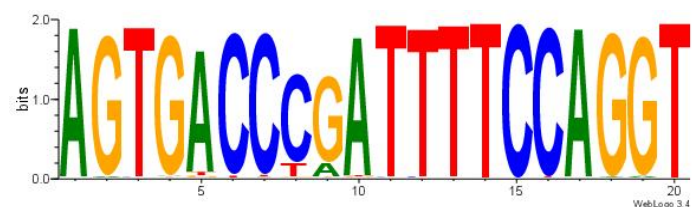
Alignment:

AGTGACCCGATTTTCCAGGT
-AAAGTGCCGAGAKTGCAGC

Original motif Consensus sequence: ACCTGGAAAATCGGGTCACT

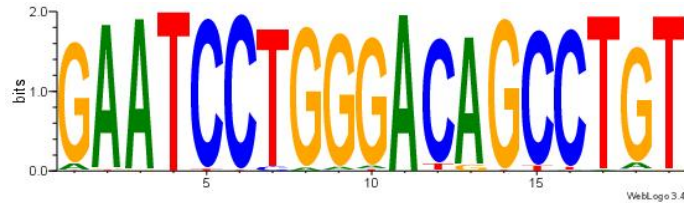


Reverse complement motif Consensus sequence: AGTGACCCGATTTTCCAGGT

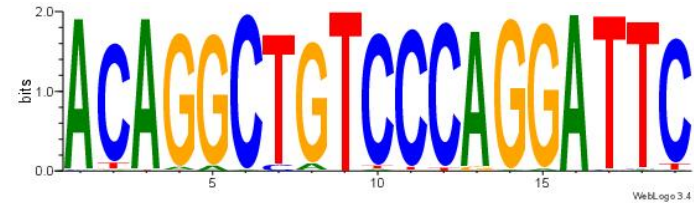


Dataset #: 1 Motif ID: 192 Motif name: Motif 192

Original motif Consensus sequence: GAATCCTGGGACAGCCTGT



Reverse complement motif Consensus sequence:
ACAGGCTGTCCCAGGATTC



Best Matches for Motif ID 192 (Highest to Lowest)

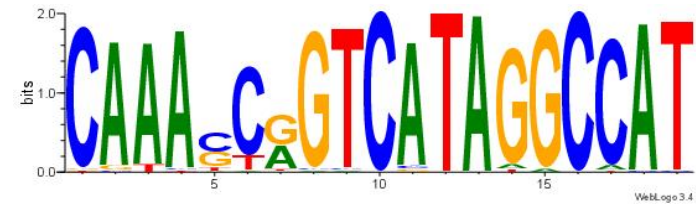
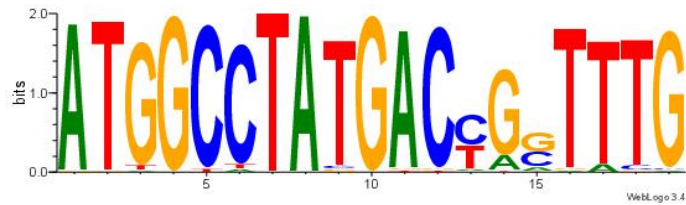
Dataset #:	1
Motif ID:	348
Motif name:	Motif 348
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	19
Similarity score:	0.111729

Alignment:

```
CAAASCKGTCATAGGCCAT  
GAATCCTGGGACAGCCTGT
```

Original motif Consensus sequence: ATGGCCTATGACYGSTTTG

Reverse complement motif Consensus sequence:
CAAASCKGTCATAGGCCAT

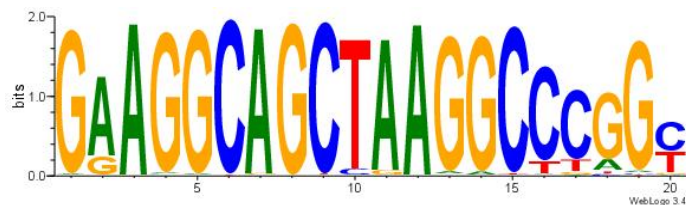


Dataset #: 1
 Motif ID: 64
 Motif name: Motif 64
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 19
 Similarity score: 0.111948

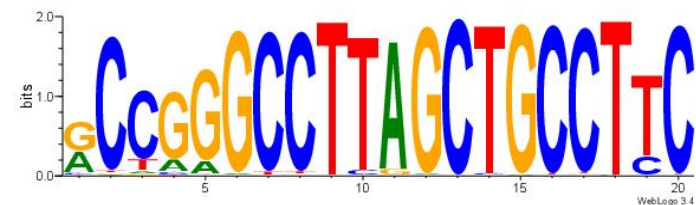
Alignment:

GAAGGCAGCTAAGGCCGGY
 GAATCCTGGGACAGCCTGT-

Original motif Consensus sequence: GAAGGCAGCTAAGGCCGGY



Reverse complement motif Consensus sequence: KCCGGGCCCTTAGCTGCCTTC



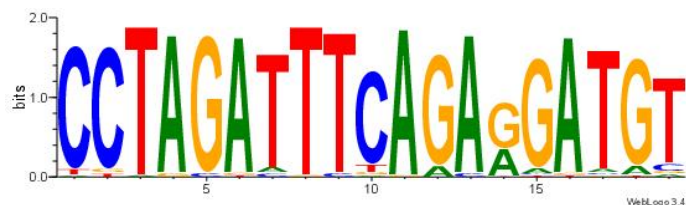
Dataset #: 1

Motif ID: 280
 Motif name: Motif 280
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 19
 Similarity score: 0.113733

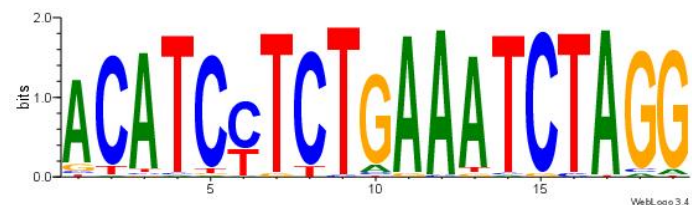
Alignment:

CCTAGATTTcAGARGATGT
 ACAGGCTGTCCCAGGATTC

Original motif Consensus sequence: CCTAGATTTcAGARGATGT



Reverse complement motif Consensus sequence: ACATCMTCTGAAATCTAGG



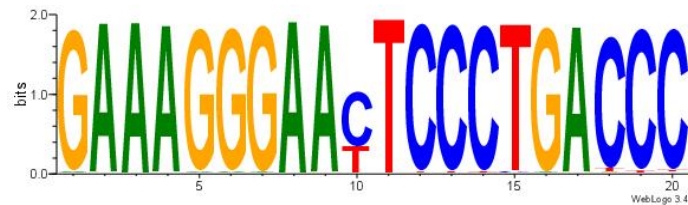
Dataset #: 1
 Motif ID: 16
 Motif name: Motif 16
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 19

Similarity score: 0.116458

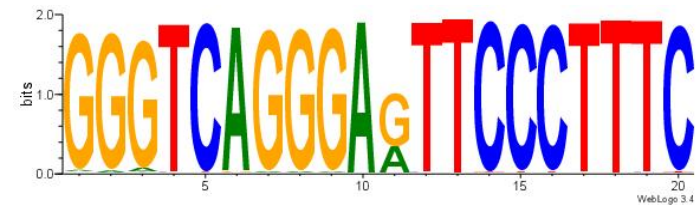
Alignment:

GGGTCAGGGAGTTC CCTTTC
-GAATCCTGGGACAGCCTGT

Original motif Consensus sequence: GAAAGGGA ACTCCCTGACCC



Reverse complement motif Consensus sequence:
GGGTCAGGGAGTTC CCTTTC



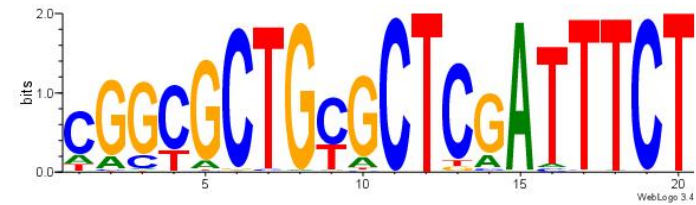
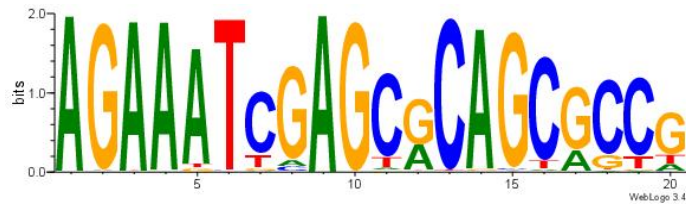
Dataset #: 1
Motif ID: 65
Motif name: Motif 65
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 19
Similarity score: 0.11685

Alignment:

AGAAATCGAGCRCAGCGCCG
-GAATCCTGGGACAGCCTGT

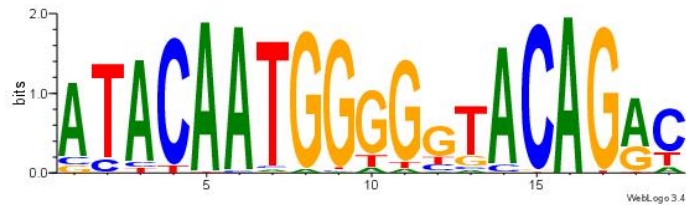
Original motif Consensus sequence: AGAAATCGAGCRCAGCGCCG

Reverse complement motif Consensus sequence:
CGGCGCTGMGCTCGATTCT

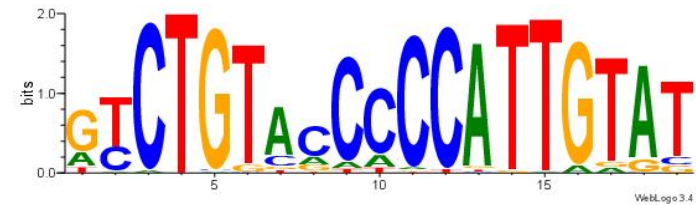


Dataset #: 1 Motif ID: 193 Motif name: Motif 193

Original motif Consensus sequence: ATACAATGGGGTACAGRC



Reverse complement motif Consensus sequence: GKCTGTACCCCATTTGTAT



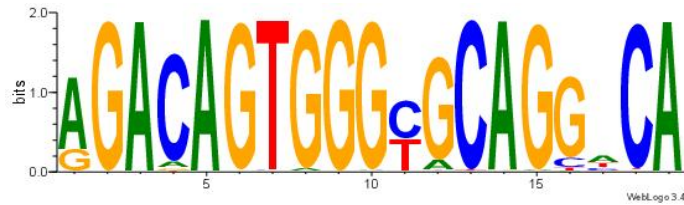
Best Matches for Motif ID 193 (Highest to Lowest)

Dataset #:	1
Motif ID:	17
Motif name:	Motif 17
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	19
Similarity score:	0.0903363

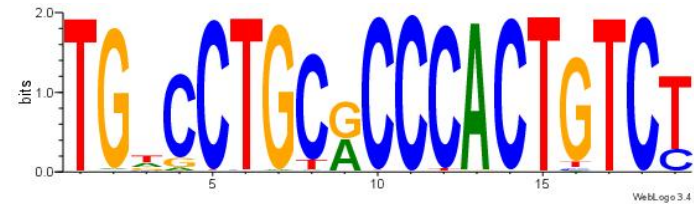
Alignment:

TGHCCTGCKCCCCTGTCT
GKCTGTACCCCATTGTAT

Original motif Consensus sequence: AGACAGTGGGCGCAGGCA



Reverse complement motif Consensus sequence:
TGHCCTGCKCCCCTGTCT



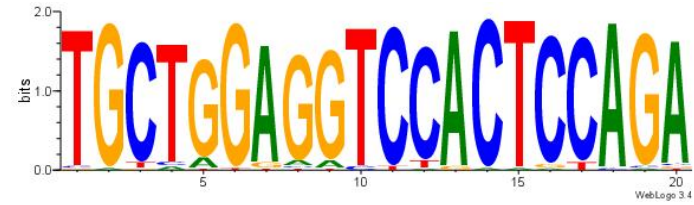
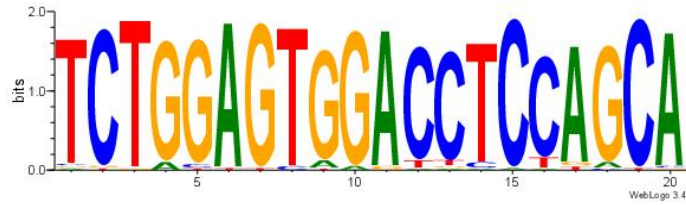
Dataset #: 1
Motif ID: 350
Motif name: Motif 350
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 19
Similarity score: 0.0979844

Alignment:

TGCTGGAGGTCCACTCCAGA
GKCTGTACCCCATTGTAT-

Original motif Consensus sequence: TCTGGAGTGGACCTCCAGCA

Reverse complement motif Consensus sequence:
TGCTGGAGGTCCACTCCAGA

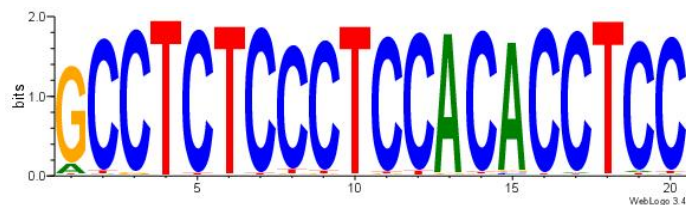


Dataset #: 1
 Motif ID: 105
 Motif name: Motif 105
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 19
 Similarity score: 0.105978

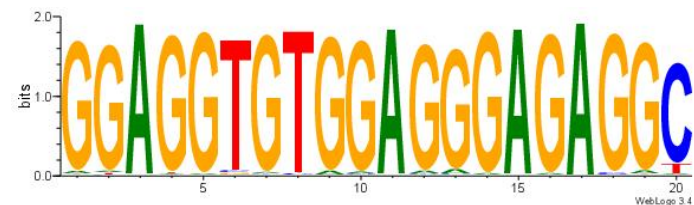
Alignment:

GCCTCTCCCTCCACACCTCC
 -GKCTGTACCCCATTTGTAT

Original motif Consensus sequence: GCCTCTCCCTCCACACCTCC



Reverse complement motif Consensus sequence: GGAGGTGTGGAGGGAGAGGC



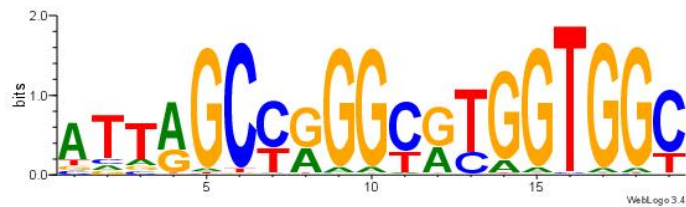
Dataset #: 1

Motif ID: 2
 Motif name: Motif 2
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 19
 Similarity score: 0.109522

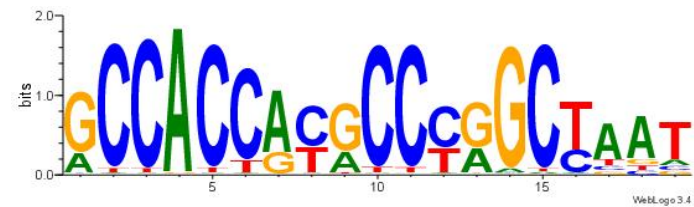
Alignment:

ATTAGCYRGGC RTGGTGGC
 ATACAATGGGGGTACAGRC

Original motif Consensus sequence: ATTAGCYRGGC RTGGTGGC



Reverse complement motif Consensus sequence: GCCACCAcGcCGGC TAAcT



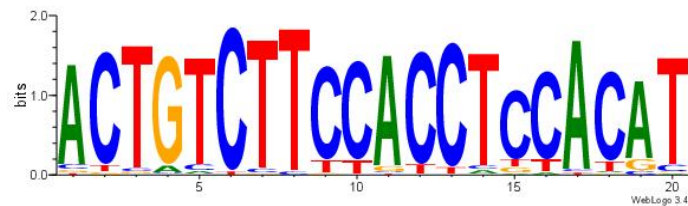
Dataset #: 1
 Motif ID: 178
 Motif name: Motif 178
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 19

Similarity score: 0.110084

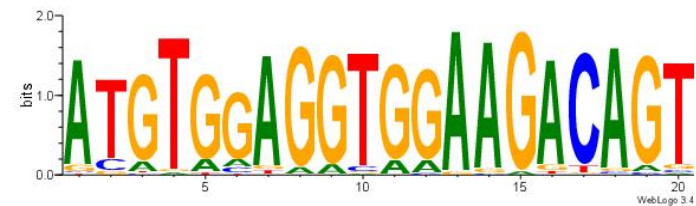
Alignment:

ATGTGGAGGTGGAAGACAGT
-ATACAATGGGGGTACAGRC

Original motif Consensus sequence: ACTGTCTTCCACCTCCACAT

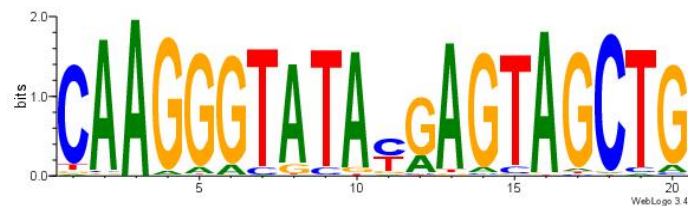


Reverse complement motif Consensus sequence:
ATGTGGAGGTGGAAGACAGT

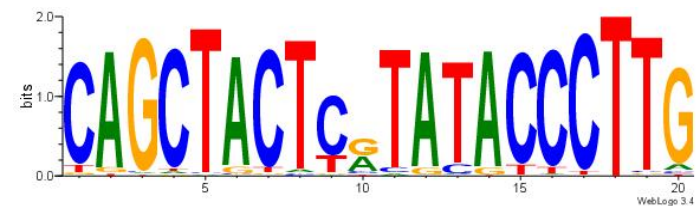


Dataset #: 1 Motif ID: 194 Motif name: Motif 194

Original motif Consensus sequence: CAAGGGTATAYGAGTAGCTG



Reverse complement motif Consensus sequence:
CAGCTACTCKTATACCCTTG



Best Matches for Motif ID 194 (Highest to Lowest)

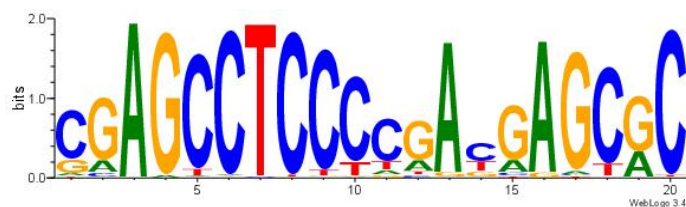
Dataset #:	1
Motif ID:	108
Motif name:	Motif 108
Matching format of first motif:	Reverse Complement

Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.111361

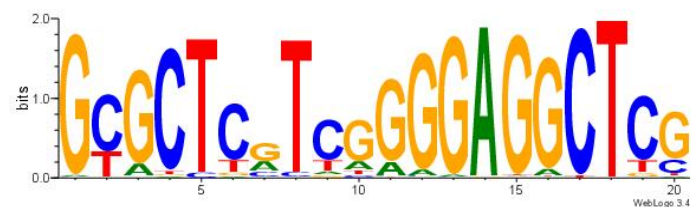
Alignment:

GCGCTCKTCGGGGAGGCTCG
 CAGCTACTCKTATACCCTTG

Original motif Consensus sequence: CGAGCCTCCCCGAYGAGCGC



Reverse complement motif Consensus sequence:
 GCGCTCKTCGGGGAGGCTCG

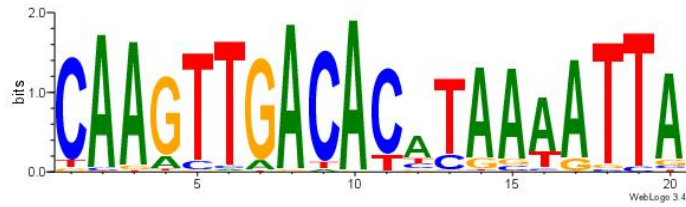


Dataset #: 1
 Motif ID: 357
 Motif name: Motif 357
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.126829

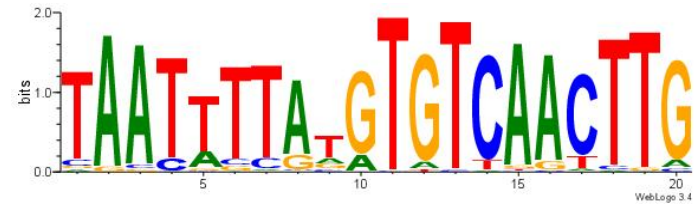
Alignment:

CAAGTTGACACATAAAATTA
CAAGGGTATAYGAGTAGCTG

Original motif Consensus sequence: CAAGTTGACACATAAAATTA



Reverse complement motif Consensus sequence:
TAATTTTATGTGTCAACTTG



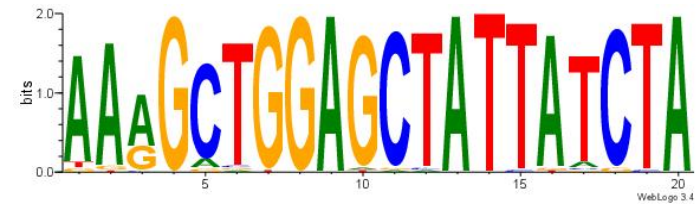
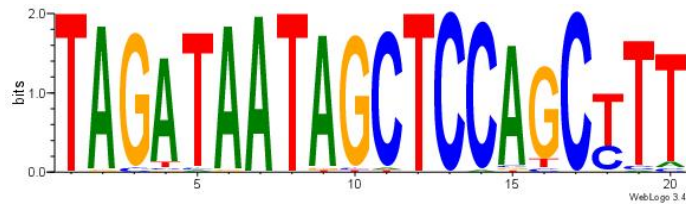
Dataset #:	1
Motif ID:	333
Motif name:	Motif 333
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	20
Similarity score:	0.13392

Alignment:

TAGATAATAGCTCCAGCTTT
CAGCTACTCKTATACCCTTG

Original motif Consensus sequence: TAGATAATAGCTCCAGCTTT

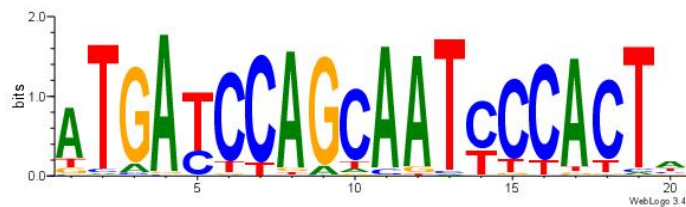
Reverse complement motif Consensus sequence:
AAAGCTGGAGCTATTATCTA



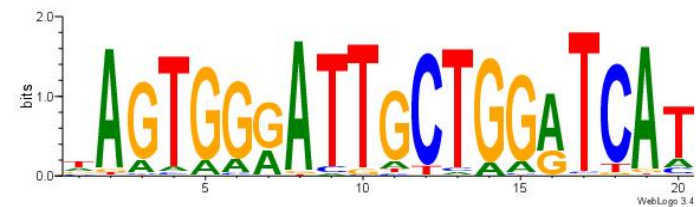
Dataset #: 1
 Motif ID: 115
 Motif name: Motif 115
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.134335

Alignment:
 ATGATCCAGCAATYCCACTH
 CAGCTACTCKTATACCCTTG

Original motif Consensus sequence: ATGATCCAGCAATYCCACTH



Reverse complement motif Consensus sequence: HAGTGGKATTGCTGGATCAT



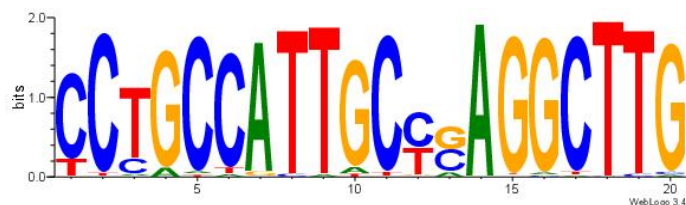
Dataset #: 1

Motif ID: 196
 Motif name: Motif 196
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.134728

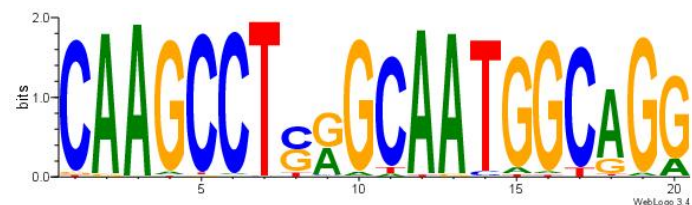
Alignment:

CAAGCCTSKGCAATGGCAGG
 CAAGGGTATAYGAGTAGCTG

Original motif Consensus sequence: CCTGCCATTGCYSAGGCTTG

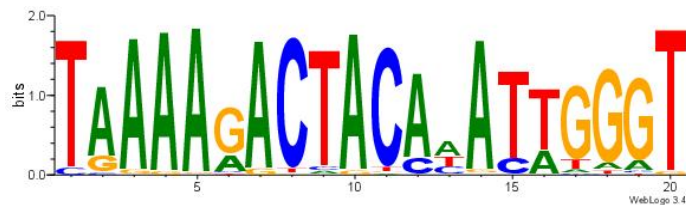


Reverse complement motif Consensus sequence: CAAGCCTSKGCAATGGCAGG

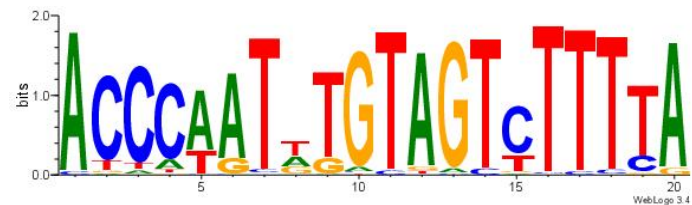


Dataset #: 1 Motif ID: 195 Motif name: Motif 195

Original motif Consensus sequence: TAAAAGACTACAWATTGGGT



Reverse complement motif Consensus sequence: ACCCAATWTGTAGTCTTTTA



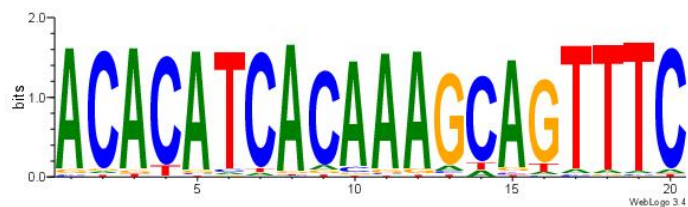
Best Matches for Motif ID 195 (Highest to Lowest)

Dataset #: 1
Motif ID: 202
Motif name: Motif 202
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 20
Similarity score: 0.113069

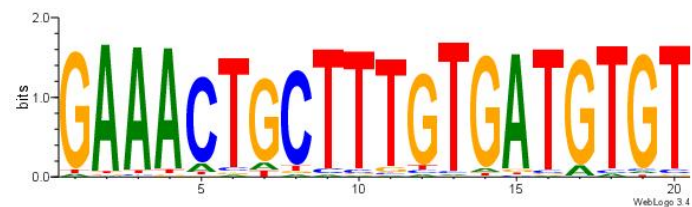
Alignment:

ACACATCACAAAGCAGTTTC
ACCCAATWTGTAGTCTTTTA

Original motif Consensus sequence: ACACATCACAAAGCAGTTTC



Reverse complement motif Consensus sequence: GAAACTGCTTTGTGATGTGT



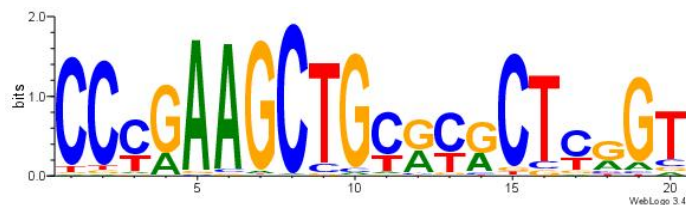
Dataset #: 1
Motif ID: 177
Motif name: Motif 177
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif

Direction: Forward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.113969

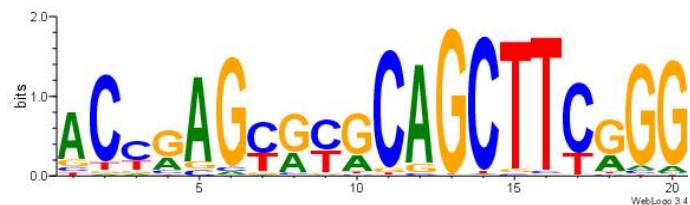
Alignment:

CCCGAAGCTGCRYRCTCGGT
 TAAAAGACTACAWATTGGGT

Original motif Consensus sequence: CCCGAAGCTGCRYRCTCGGT



Reverse complement motif Consensus sequence: ACCGAGMKMGCAGCTTCGGG

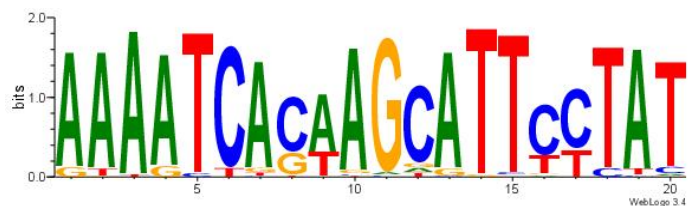


Dataset #: 1
 Motif ID: 254
 Motif name: Motif 254
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.122348

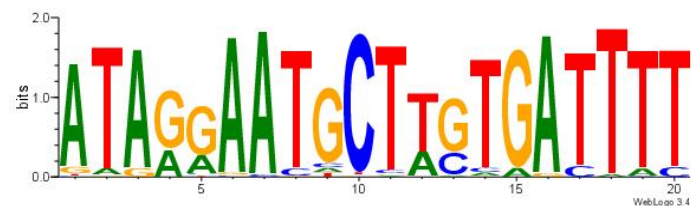
Alignment:

AAAATCACAAGCATTCTAT
 TAAAAGACTACAWATTGGGT

Original motif Consensus sequence: AAAATCACAAGCATTCTAT



Reverse complement motif Consensus sequence: ATAGGAATGCTTGTGATTTT

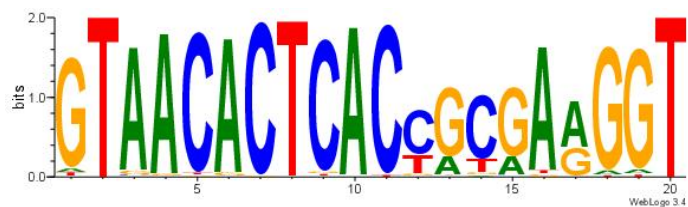


Dataset #: 1
Motif ID: 201
Motif name: Motif 201
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 20
Similarity score: 0.123108

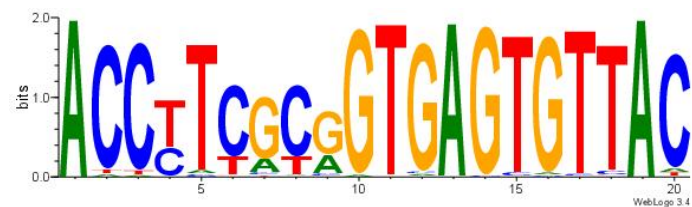
Alignment:

ACCKTCGCGGTGAGTGTTAC
ACCCAATWTGTAGTCTTTTA

Original motif Consensus sequence: GTAACACTCACCGCGARGGT



Reverse complement motif Consensus sequence: ACCKTCGCGGTGAGTGTTAC

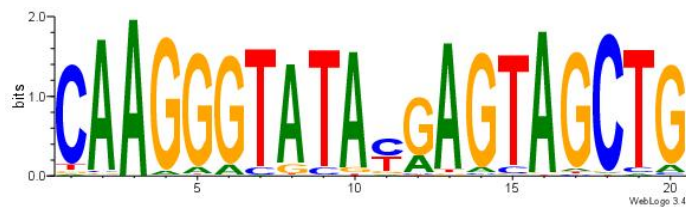


Dataset #: 1
 Motif ID: 194
 Motif name: Motif 194
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.128438

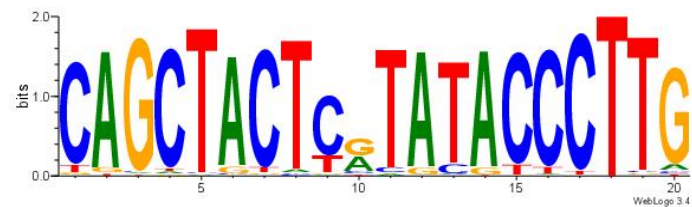
Alignment:

CAAGGGTATAYGAGTAGCTG
 TAAAAGACTACAWATTGGGT

Original motif Consensus sequence: CAAGGGTATAYGAGTAGCTG



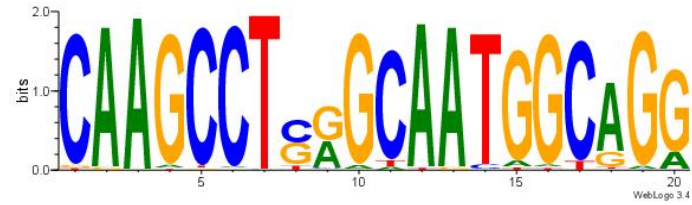
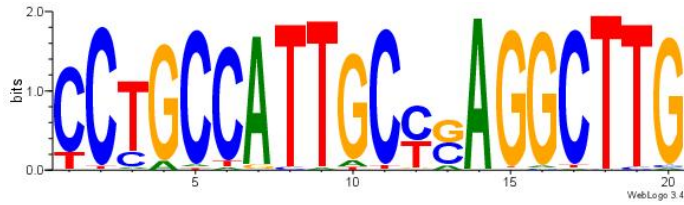
Reverse complement motif Consensus sequence: CAGCTACTCKTATACCCTTG



Dataset #: 1 Motif ID: 196 Motif name: Motif 196

Original motif Consensus sequence: CCTGCCATTGCYSAGGCTTG

Reverse complement motif Consensus sequence: CAAGCCTSKGCAATGGCAGG

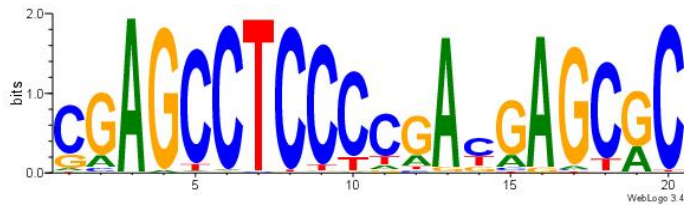


Best Matches for Motif ID 196 (Highest to Lowest)

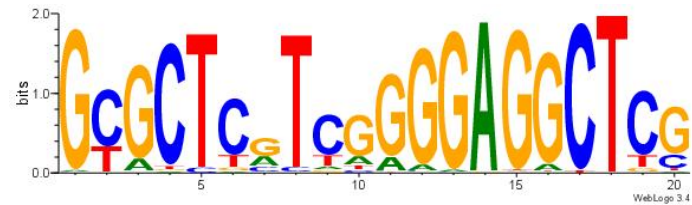
Dataset #: 1
 Motif ID: 108
 Motif name: Motif 108
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.113175

Alignment:
 GCGCTCKTCGGGGAGGCTCG
 CCTGCCATTGCYSAGGCTTG

Original motif Consensus sequence: CGAGCCTCCCCGAYGAGCGC



Reverse complement motif Consensus sequence: GCGCTCKTCGGGGAGGCTCG

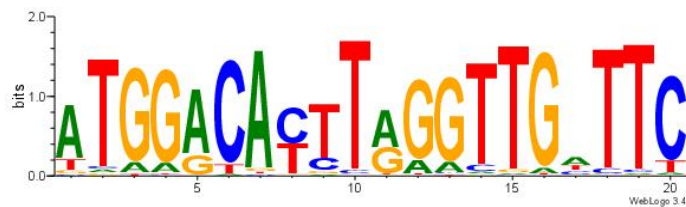


Dataset #: 1
 Motif ID: 58
 Motif name: Motif 58
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.135677

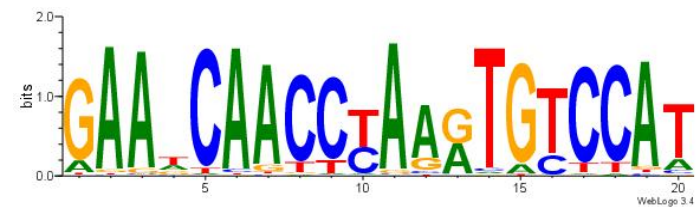
Alignment:

GAAHCAACCKAAKTGTCCAT
 CAAGCCTSKGCAATGGCAGG

Original motif Consensus sequence: ATGGACAYTTRGGTTGHTTC



Reverse complement motif Consensus sequence: GAAHCAACCKAAKTGTCCAT



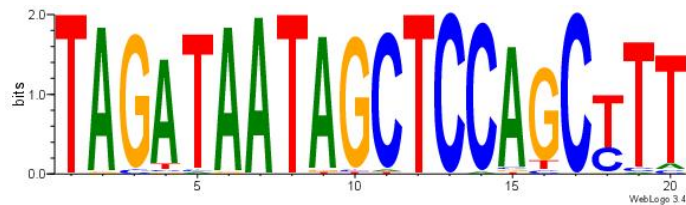
Dataset #: 1
 Motif ID: 333
 Motif name: Motif 333
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1

Number of overlap: 20
Similarity score: 0.136179

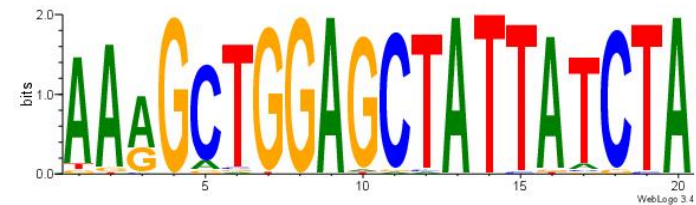
Alignment:

TAGATAATAGCTCCAGCTTT
CCTGCCATTGCYSAGGCTTG

Original motif Consensus sequence: TAGATAATAGCTCCAGCTTT



Reverse complement motif Consensus sequence: AAAGCTGGAGCTATTATCTA

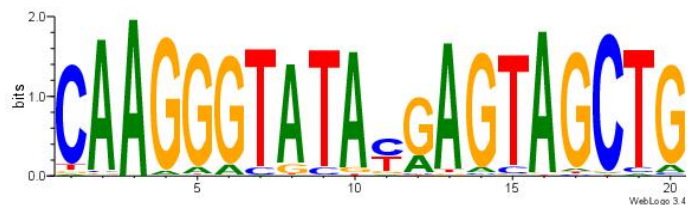


Dataset #: 1
Motif ID: 194
Motif name: Motif 194
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 20
Similarity score: 0.138043

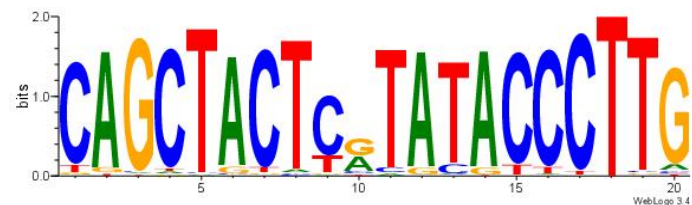
Alignment:

CAGCTACTCKTATACCCTTG
CCTGCCATTGCYSAGGCTTG

Original motif Consensus sequence: CAAGGGTATAYGAGTAGCTG



Reverse complement motif Consensus sequence: CAGCTACTCKTATACCCTTG

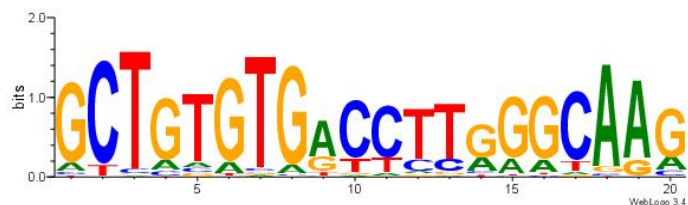


Dataset #: 1
Motif ID: 112
Motif name: Motif 112
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 20
Similarity score: 0.139891

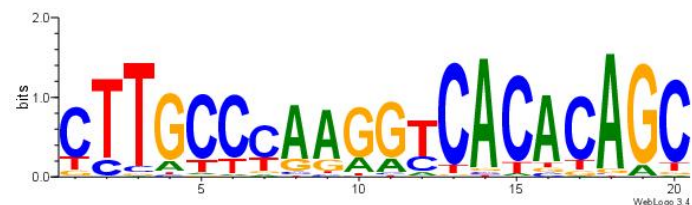
Alignment:

GCTGTGTGACCTTGGGCAAG
CAAGCCTSKGCAATGGCAGG

Original motif Consensus sequence: GCTGTGTGACCTTGGGCAAG

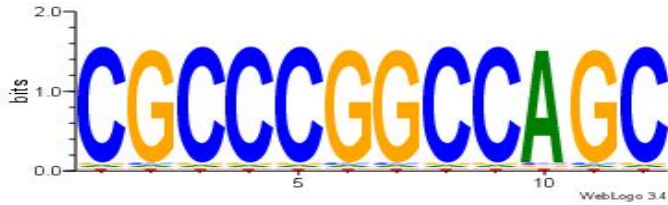


Reverse complement motif Consensus sequence: CTTGCCCAAGGTCACACAGC

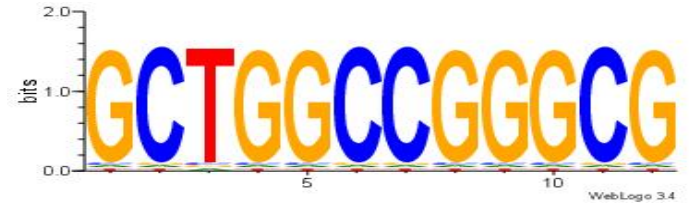


Dataset #: 1 Motif ID: 197 Motif name: Motif 197

Original motif Consensus sequence: CGCCCGGCCAGC



Reverse complement motif Consensus sequence: GCTGGCCGGGCG



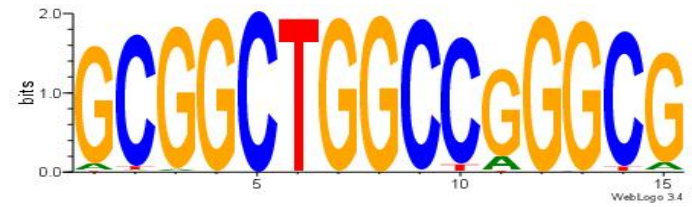
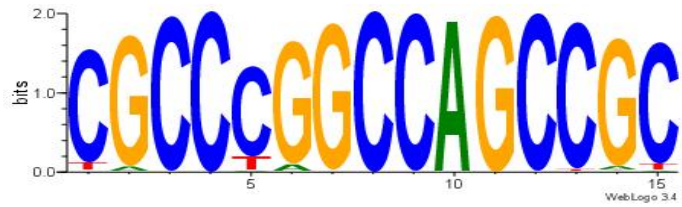
Best Matches for Motif ID 197 (Highest to Lowest)

Dataset #:	1
Motif ID:	125
Motif name:	Motif 125
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	12
Similarity score:	0.0154405

Alignment:
GCGGCTGGCCGGGCG
---GCTGGCCGGGCG

Original motif Consensus sequence: CGCCCGGCCAGCCGC

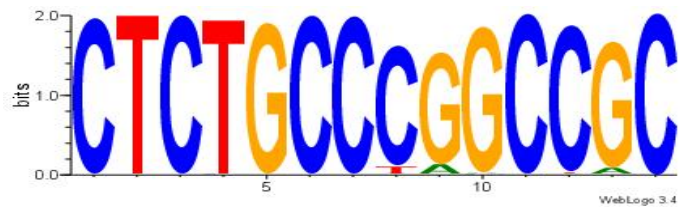
Reverse complement motif Consensus sequence:
GCGGCTGGCCGGGCG



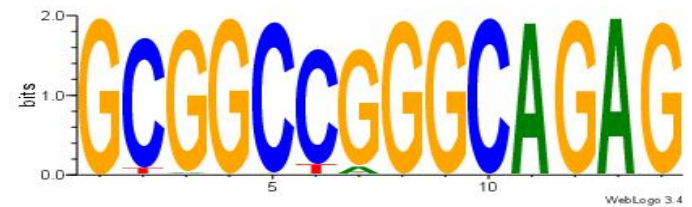
Dataset #: 1
 Motif ID: 42
 Motif name: Motif 42
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 12
 Similarity score: 0.0710698

Alignment:
 CTCTGCCCGGCCGC
 -GCTGGCCGGGCG-

Original motif Consensus sequence: CTCTGCCCGGCCGC



Reverse complement motif Consensus sequence: GCGGGCCGGGCG



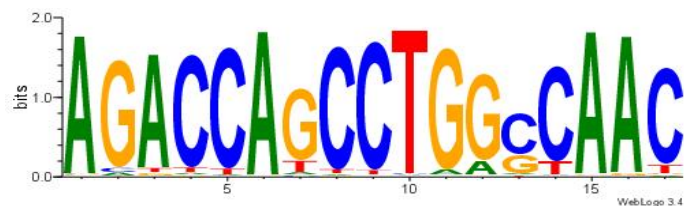
Dataset #: 1
 Motif ID: 12

Motif name: Motif 12
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 12
 Similarity score: 0.076685

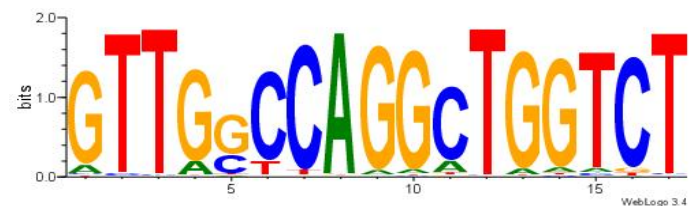
Alignment:

GTTGGCCAGGCTGGTCT
 GCTGGCCGGGCG-----

Original motif Consensus sequence: AGACCAGCCTGGCCAAC



Reverse complement motif Consensus sequence: GTTGGCCAGGCTGGTCT

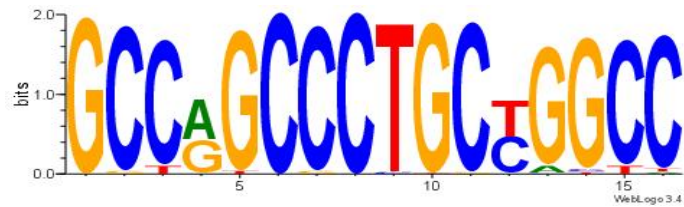


Dataset #: 1
 Motif ID: 183
 Motif name: Motif 183
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 12
 Similarity score: 0.0771111

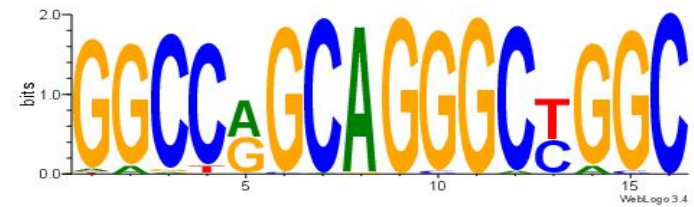
Alignment:

GCCRGCCCTGCYGGCC
---CGCCCGGCCAGC-

Original motif Consensus sequence: GCCRGCCCTGCYGGCC



Reverse complement motif Consensus sequence:
GGCCMGCAGGGCKGGC



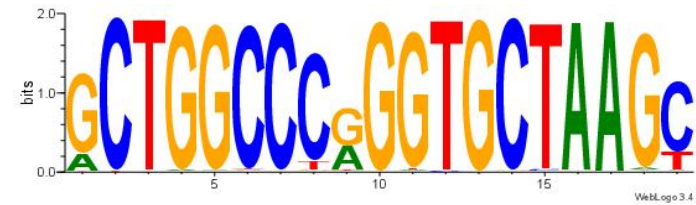
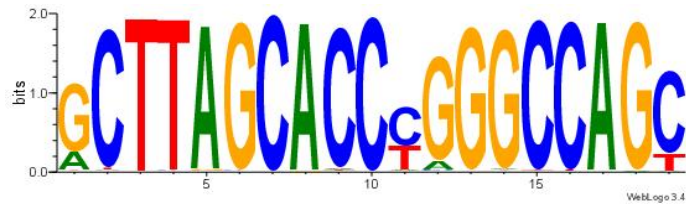
Dataset #: 1
Motif ID: 82
Motif name: Motif 82
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 8
Number of overlap: 12
Similarity score: 0.0775994

Alignment:

GCTTAGCACCYGGGCCAGC
-----CGCCCGGCCAGC

Original motif Consensus sequence: GCTTAGCACCYGGGCCAGC

Reverse complement motif Consensus sequence:
GCTGGCCCKGGTGCTAAGC

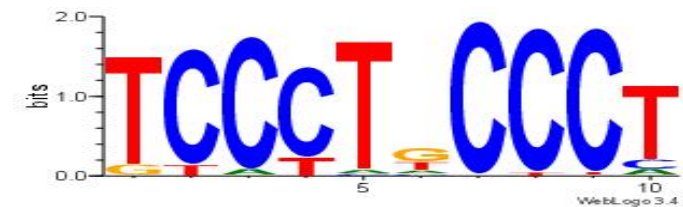


Dataset #: 1 Motif ID: 198 Motif name: Motif 198

Original motif Consensus sequence: AGGGMAGGGA



Reverse complement motif Consensus sequence: TCCCTRCCCT

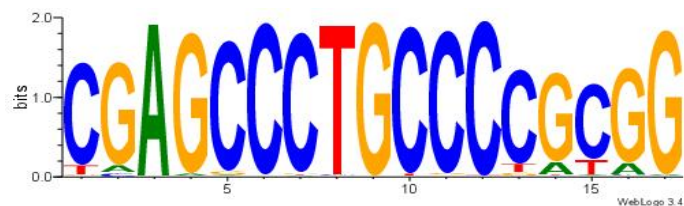


Best Matches for Motif ID 198 (Highest to Lowest)

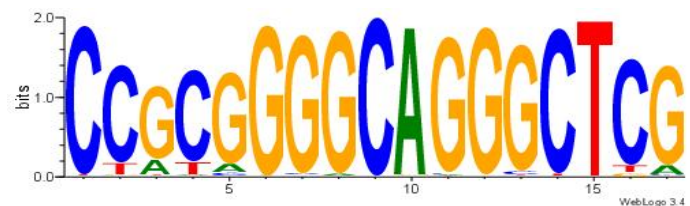
Dataset #:	1
Motif ID:	78
Motif name:	Motif 78
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	5
Number of overlap:	10
Similarity score:	0.0499279

Alignment:
 CGAGCCCTGCCCGCGG
 ----TCCCTRCCCT----

Original motif Consensus sequence: CGAGCCCTGCCCGCGG



Reverse complement motif Consensus sequence: CCGCGGGGCAGGGCTCG

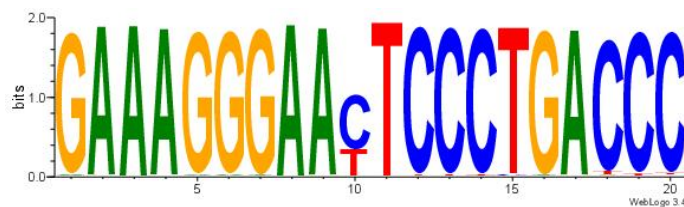


Dataset #: 1
Motif ID: 16
Motif name: Motif 16
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 10
Similarity score: 0.0554968

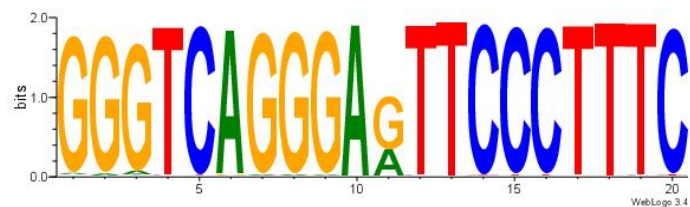
Alignment:

```
GAAAGGGA ACTCCCTGACCC  
TCCCTRCCCT-----
```

Original motif Consensus sequence: GAAAGGGA ACTCCCTGACCC



Reverse complement motif Consensus sequence: GGGTCAGGGAG TTCCCTTTC

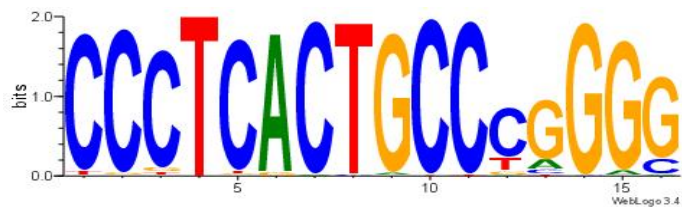


Dataset #: 1
 Motif ID: 136
 Motif name: Motif 136
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 10
 Similarity score: 0.0566967

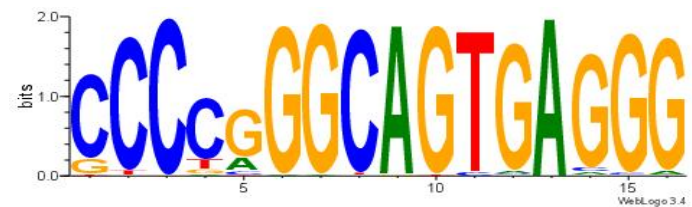
Alignment:

CCCTCACTGCCCGGGG
 ---TCCCTRCCCT---

Original motif Consensus sequence: CCCTCACTGCCCGGGG



Reverse complement motif Consensus sequence: CCCCggGCAGTGAGGGG

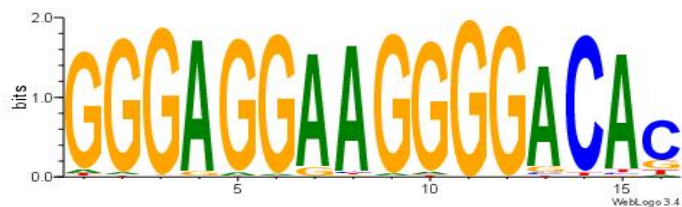


Dataset #: 1
 Motif ID: 221
 Motif name: Motif 221
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4

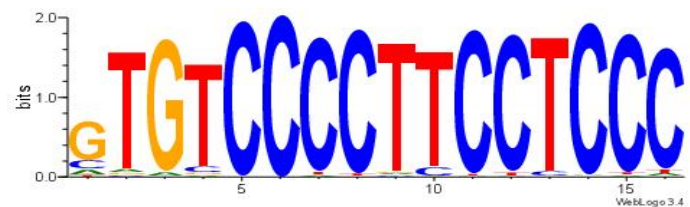
Number of overlap: 10
Similarity score: 0.0612344

Alignment:
GGGAGGAAGGGGACAC
---AGGGMAGGGA---

Original motif Consensus sequence: GGGAGGAAGGGGACAC



Reverse complement motif Consensus sequence:
GTGTCCCCTTCCTCCC

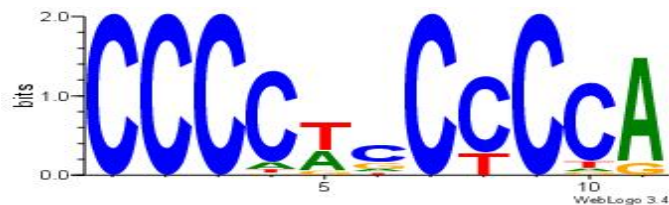


Dataset #: 1
Motif ID: 46
Motif name: Motif 46
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 10
Similarity score: 0.0645706

Alignment:
TGGGGGWGGGG
AGGGMAGGGA-

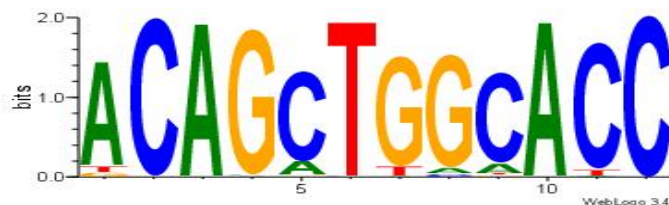
Original motif Consensus sequence: CCCWCCCCCA

Reverse complement motif Consensus sequence: TGGGGGWGGGG

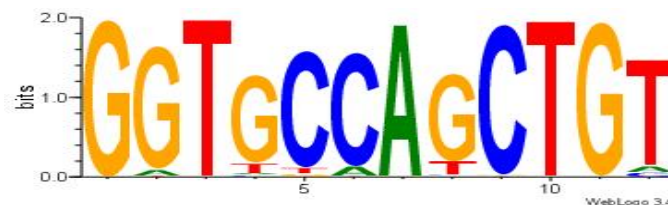


Dataset #: 1 Motif ID: 199 Motif name: Motif 199

Original motif Consensus sequence: ACAGCTGGCACC



Reverse complement motif Consensus sequence: GGTGCCAGCTGT

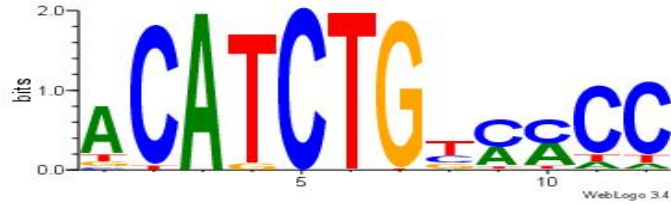


Best Matches for Motif ID 199 (Highest to Lowest)

Dataset #:	1
Motif ID:	49
Motif name:	Motif 49
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	12
Similarity score:	0.0585218

Alignment:
ACATCTGYMMCC
ACAGCTGGCACC

Original motif Consensus sequence: ACATCTGYMMCC



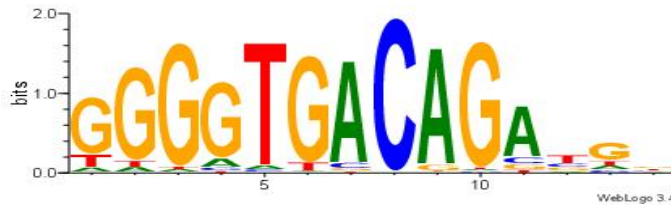
Reverse complement motif Consensus sequence: GGRRMCAGATGT



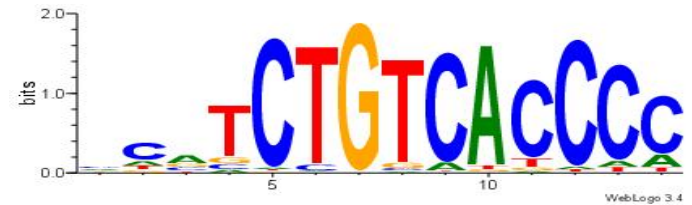
Dataset #: 1
 Motif ID: 1
 Motif name: Motif 1
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 12
 Similarity score: 0.0698583

Alignment:
 BCVTCTGTCACCCC
 --ACAGCTGGCACC

Original motif Consensus sequence: GGGGTGACAGABGB



Reverse complement motif Consensus sequence: BCVTCTGTCACCCC

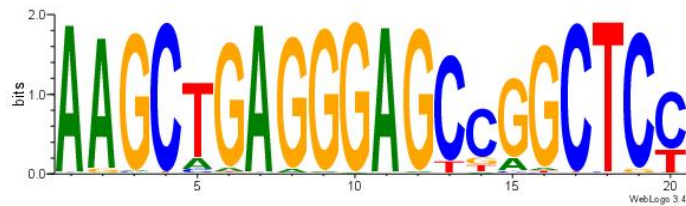


Dataset #: 1
 Motif ID: 96
 Motif name: Motif 96
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 12
 Similarity score: 0.0749537

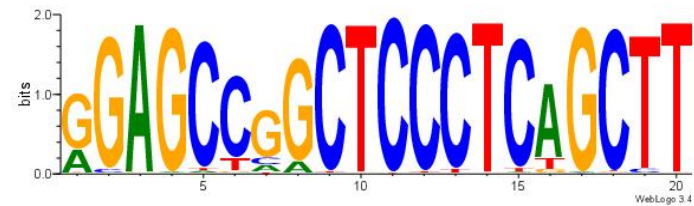
Alignment:

GGAGCCGGCTCCCTCAGCTT
 -----ACAGCTGGCACC

Original motif Consensus sequence: AAGCTGAGGGAGCCGGCTCC



Reverse complement motif Consensus sequence: GGAGCCGGCTCCCTCAGCTT



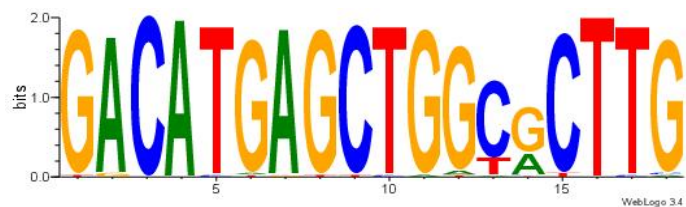
Dataset #: 1
 Motif ID: 306
 Motif name: Motif 306
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3

Number of overlap: 12
Similarity score: 0.0751946

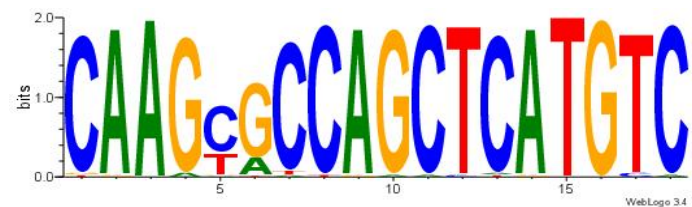
Alignment:

GACATGAGCTGGCGCTTG
----ACAGCTGGCACC--

Original motif Consensus sequence: GACATGAGCTGGCGCTTG



Reverse complement motif Consensus sequence: CAAGCGCCAGCTCATGTC

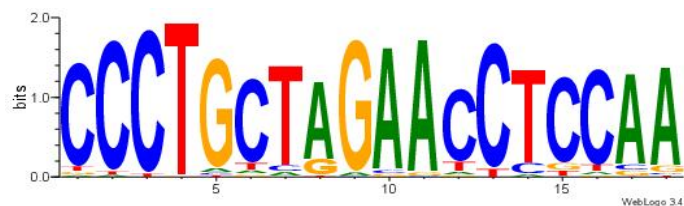


Dataset #: 1
Motif ID: 299
Motif name: Motif 299
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 6
Number of overlap: 12
Similarity score: 0.075898

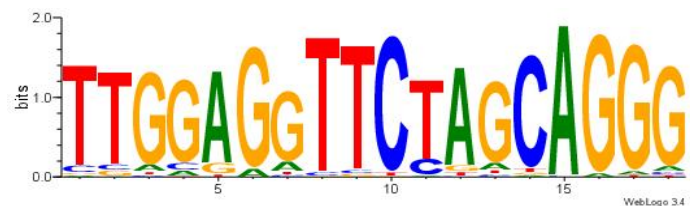
Alignment:

CCCTGCTAGAACCTCCAA
-ACAGCTGGCACC-----

Original motif Consensus sequence: CCCTGCTAGAACCTCCAA

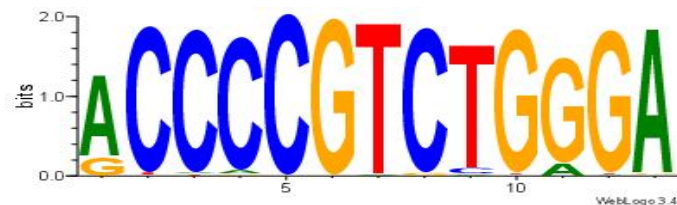


Reverse complement motif Consensus sequence: TTGGAGTTCTAGCAGGG



Dataset #: 1 Motif ID: 200 Motif name: Motif 200

Original motif Consensus sequence: ACCCGTCTGGGA



Reverse complement motif Consensus sequence: TCCAGACGGGGT



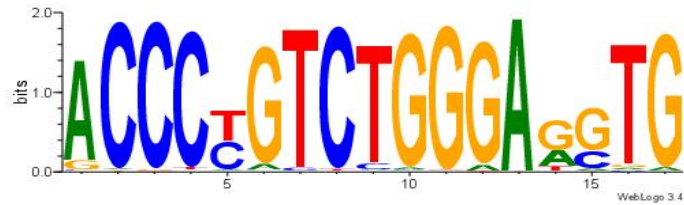
Best Matches for Motif ID 200 (Highest to Lowest)

Dataset #:	1
Motif ID:	95
Motif name:	Motif 95
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	5
Number of overlap:	13
Similarity score:	0.0106929

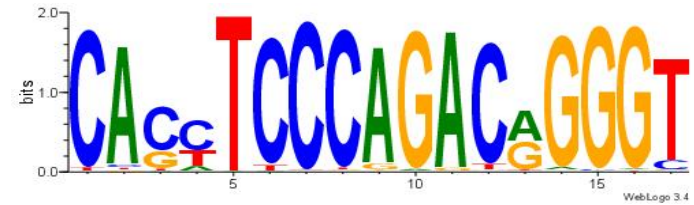
Alignment:

ACCCYGTCTGGGAGGTG
ACCCCGTCTGGGA-----

Original motif Consensus sequence: ACCCYGTCTGGGAGGTG



Reverse complement motif Consensus sequence: CACCTCCCAGACMGGGT

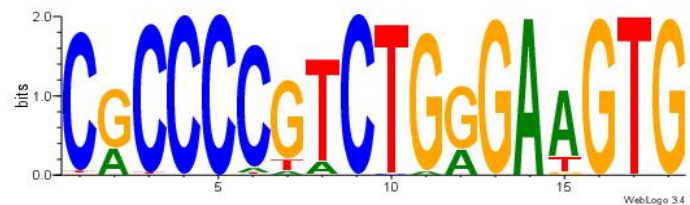
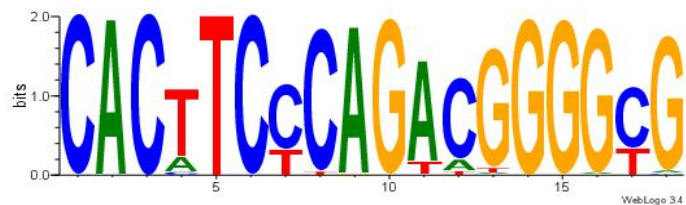


Dataset #: 1
Motif ID: 27
Motif name: Motif 27
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 5
Number of overlap: 13
Similarity score: 0.0207173

Alignment:
CGCCCCGTCTGGGAAGTG
-----ACCCCGTCTGGGA-

Original motif Consensus sequence: CACTTCCCAGACGGGGCG

Reverse complement motif Consensus sequence: CGCCCCGTCTGGGAAGTG

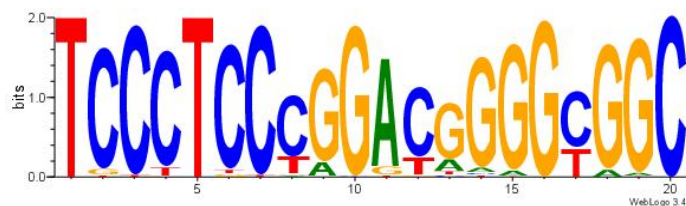


Dataset #: 1
 Motif ID: 155
 Motif name: Motif 155
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 4
 Number of overlap: 13
 Similarity score: 0.040436

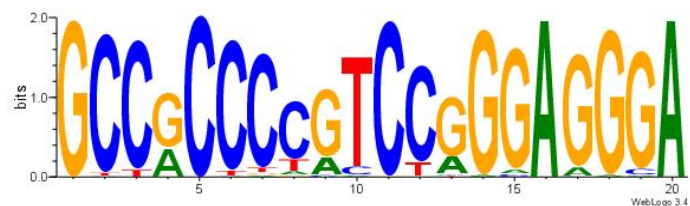
Alignment:

GCCKCCCCGTCCGGGAGGGA
 ----ACCCCGTCTGGGA----

Original motif Consensus sequence: TCCCTCCCGGACGGGGYGGC



Reverse complement motif Consensus sequence: GCCKCCCCGTCCGGGAGGGA



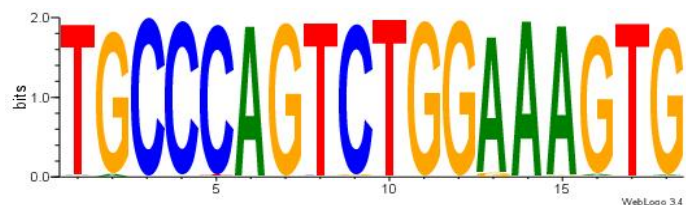
Dataset #: 1

Motif ID: 45
 Motif name: Motif 45
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 5
 Number of overlap: 13
 Similarity score: 0.0497149

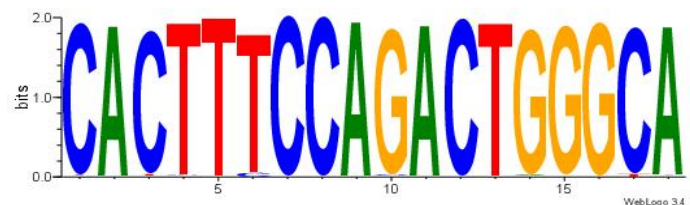
Alignment:

TGCCCAGTCTGGAAAGTG
 -ACCCCGTCTGGGA-----

Original motif Consensus sequence: TGCCCAGTCTGGAAAGTG



Reverse complement motif Consensus sequence: CACTTTCAGACTGGGCA



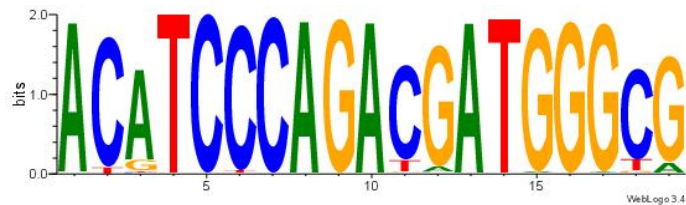
Dataset #: 1
 Motif ID: 36
 Motif name: Motif 36
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 4
 Number of overlap: 13

Similarity score: 0.0528184

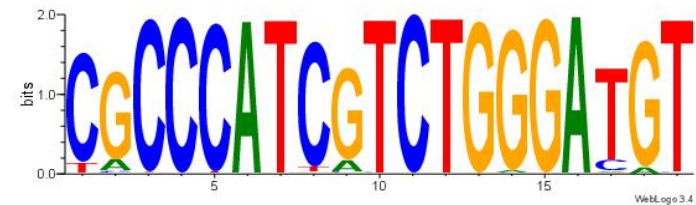
Alignment:

CGCCCATCGTCTGGGATGT
---ACCCCGTCTGGGA---

Original motif Consensus sequence: ACATCCCAGACGATGGGCG

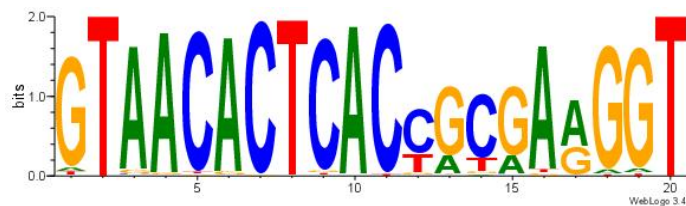


Reverse complement motif Consensus sequence:
CGCCCATCGTCTGGGATGT

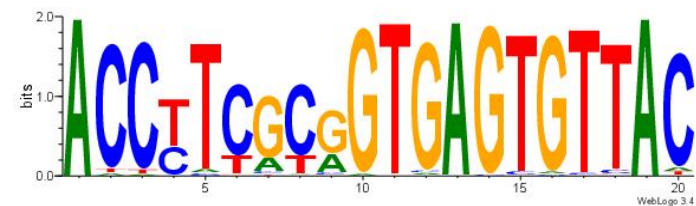


Dataset #: 1 Motif ID: 201 Motif name: Motif 201

Original motif Consensus sequence: GTAACACTCACC GCGARGGT



Reverse complement motif Consensus sequence:
ACCKTCGCGGTGAGTGTTAC



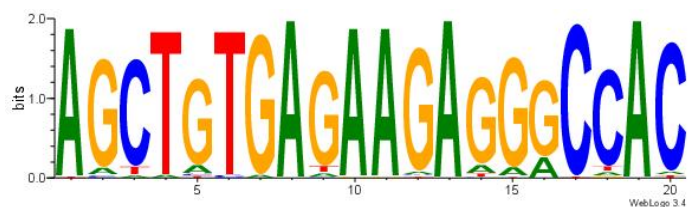
Best Matches for Motif ID 201 (Highest to Lowest)

Dataset #: 1
Motif ID: 294
Motif name: Motif 294
Matching format of first motif: Original Motif

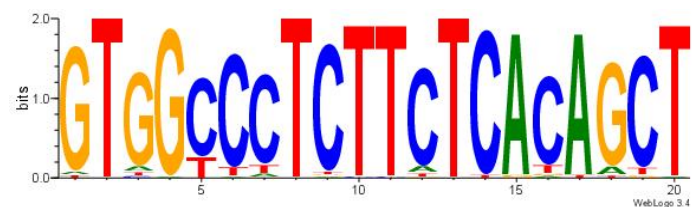
Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.11338

Alignment:
 GTGGCCCTCTTCTCACAGCT
 GTAACACTCACCGCGARGGT

Original motif Consensus sequence: AGCTGTGAGAAGAGGGCCAC



Reverse complement motif Consensus sequence:
 GTGGCCCTCTTCTCACAGCT

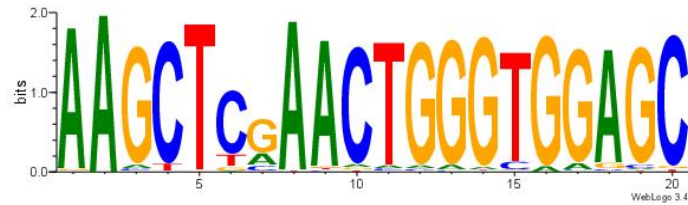


Dataset #: 1
 Motif ID: 321
 Motif name: Motif 321
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.114848

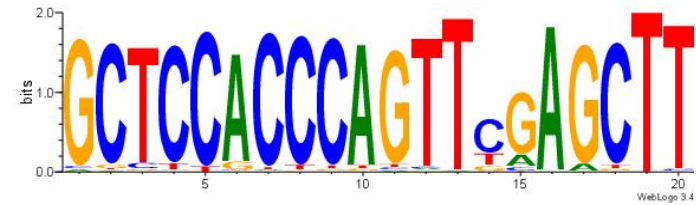
Alignment:

GCTCCACCCAGTTCGAGCTT
GTAACACTCACCGCGARGGT

Original motif Consensus sequence: AAGCTCGAACTGGGTGGAGC



Reverse complement motif Consensus sequence:
GCTCCACCCAGTTCGAGCTT

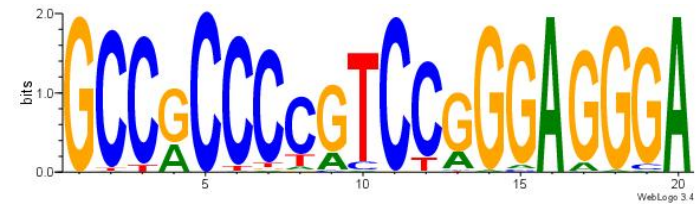
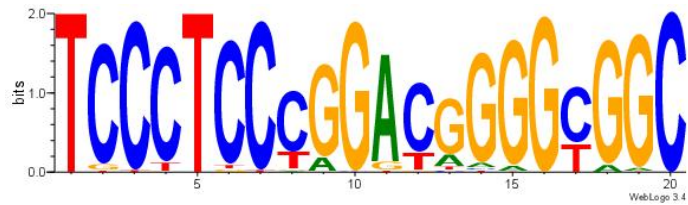


Dataset #: 1
Motif ID: 155
Motif name: Motif 155
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 20
Similarity score: 0.120361

Alignment:
GCCKCCCCGTCCGGGAGGGA
GTAACACTCACCGCGARGGT

Original motif Consensus sequence: TCCCTCCCGGACGGGGYGGC

Reverse complement motif Consensus sequence:
GCCKCCCCGTCCGGGAGGGA

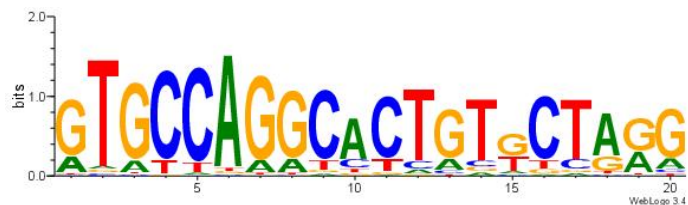


Dataset #: 1
 Motif ID: 76
 Motif name: Motif 76
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.122505

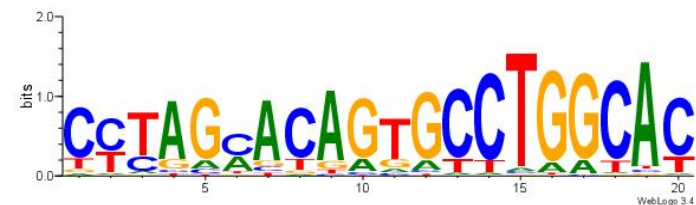
Alignment:

GTGCCAGGCACTGKCTARG
 GTAACACTCACCGCGARGGT

Original motif Consensus sequence: GTGCCAGGCACTGKCTARG



Reverse complement motif Consensus sequence: CMTAGYACAGTGCCTGGCAC



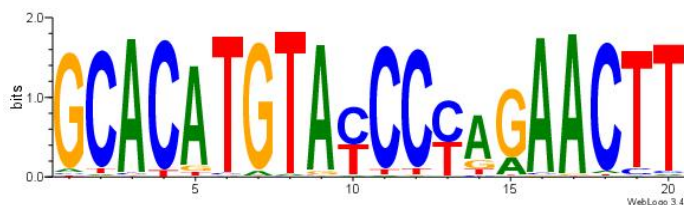
Dataset #: 1

Motif ID: 225
 Motif name: Motif 225
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.125295

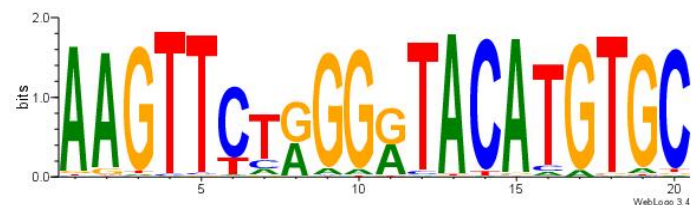
Alignment:

AAGTTCTKGGKTACATGTGC
 ACCKTCGCGGTGAGTGTTAC

Original motif Consensus sequence: GCACATGTAYCCYAGAACTT

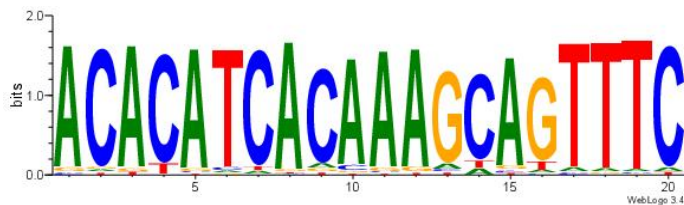


Reverse complement motif Consensus sequence: AAGTTCTKGGKTACATGTGC

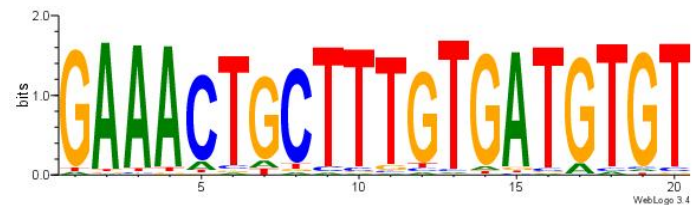


Dataset #: 1 Motif ID: 202 Motif name: Motif 202

Original motif Consensus sequence: ACACATCACAAAGCAGTTTC



Reverse complement motif Consensus sequence: GAAACTGCTTTTGATGTGT



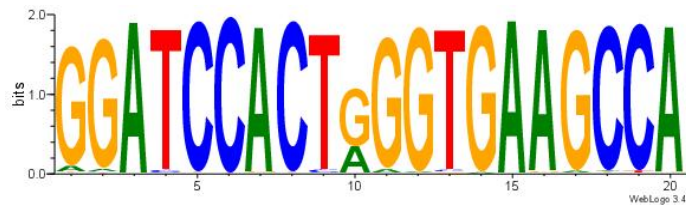
Best Matches for Motif ID 202 (Highest to Lowest)

Dataset #: 1
Motif ID: 61
Motif name: Motif 61
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 20
Similarity score: 0.117486

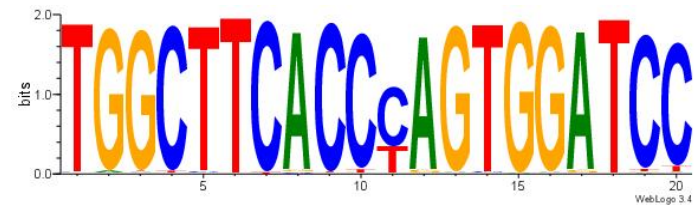
Alignment:

GGATCCACTGGGTGAAGCCA
GAAACTGCTTTGTGATGTGT

Original motif Consensus sequence: GGATCCACTGGGTGAAGCCA



Reverse complement motif Consensus sequence:
TGGCTTCACCCAGTGGATCC



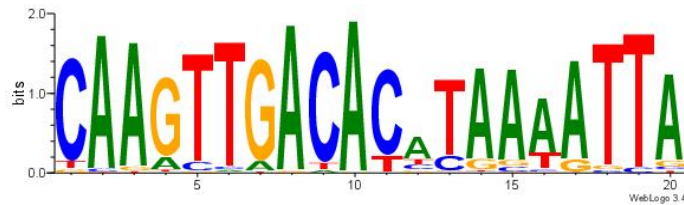
Dataset #: 1
Motif ID: 357
Motif name: Motif 357
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement

Direction: Forward
Position number: 1
Number of overlap: 20
Similarity score: 0.1227

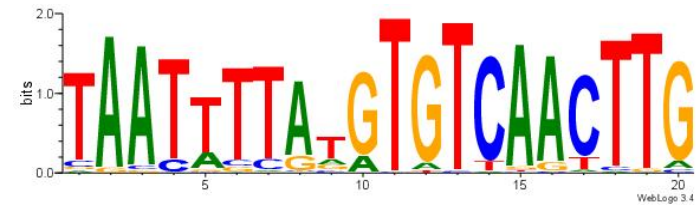
Alignment:

TAATTTTATGTGTCAACTTG
GAAACTGCTTTGTGATGTGT

Original motif Consensus sequence: CAAGTTGACACATAAAATTA



Reverse complement motif Consensus sequence: TAATTTTATGTGTCAACTTG

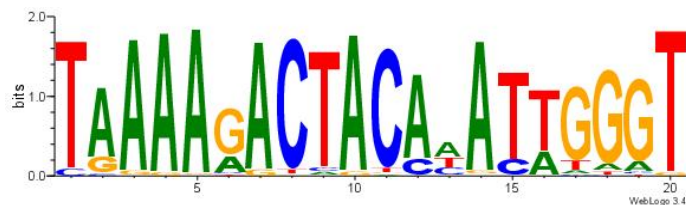


Dataset #: 1
Motif ID: 195
Motif name: Motif 195
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 20
Similarity score: 0.123556

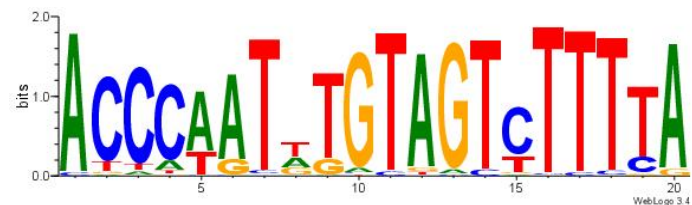
Alignment:

TAAAAGACTACAWATTGGGT
GAAACTGCTTTGTGATGTGT

Original motif Consensus sequence: TAAAAGACTACAWATTGGGT



Reverse complement motif Consensus sequence: ACCCAATWTGTAGTCTTTTA

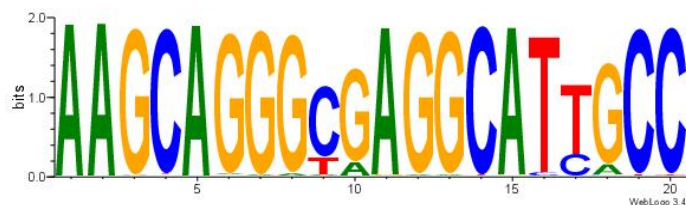


Dataset #: 1
Motif ID: 13
Motif name: Motif 13
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 20
Similarity score: 0.123649

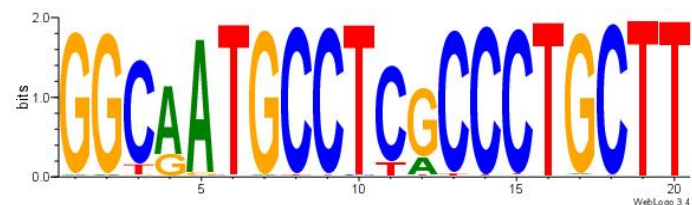
Alignment:

AAGCAGGGCGAGGCATTGCC
ACACATCACAAAGCAGTTTC

Original motif Consensus sequence: AAGCAGGGCGAGGCATTGCC



Reverse complement motif Consensus sequence: GGCAATGCCTCGCCCTGCTT

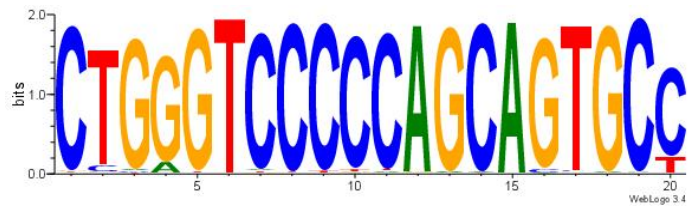


Dataset #: 1
 Motif ID: 84
 Motif name: Motif 84
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.123761

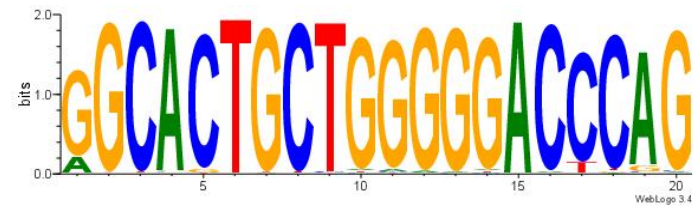
Alignment:

CTGGGTCCCCCAGCAGTGCC
 ACACATCACAAAGCAGTTTC

Original motif Consensus sequence: CTGGGTCCCCCAGCAGTGCC



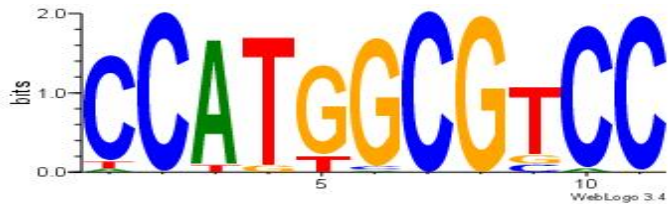
Reverse complement motif Consensus sequence: GGCAGTCTGGGGGACCCAG



Dataset #: 1 Motif ID: 203 Motif name: Motif 203

Original motif Consensus sequence: CCATGGCGTCC

Reverse complement motif Consensus sequence: GGACGCCATGG

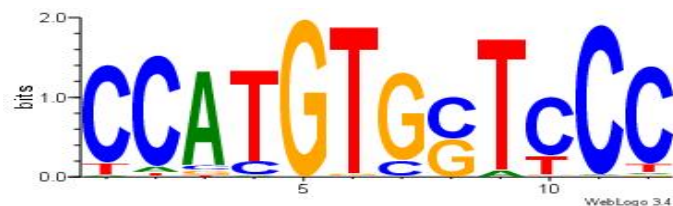


Best Matches for Motif ID 203 (Highest to Lowest)

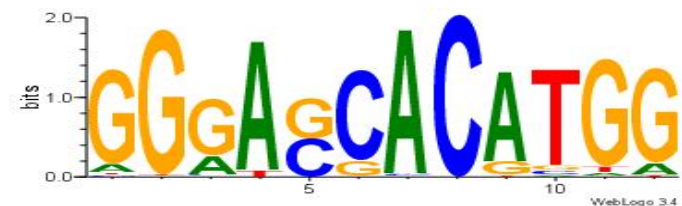
Dataset #: 1
 Motif ID: 120
 Motif name: Motif 120
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.0640975

Alignment:
 GGGASCACATGG
 -GGACGCCATGG

Original motif Consensus sequence: CCATGTGSTCCC



Reverse complement motif Consensus sequence: GGGASCACATGG



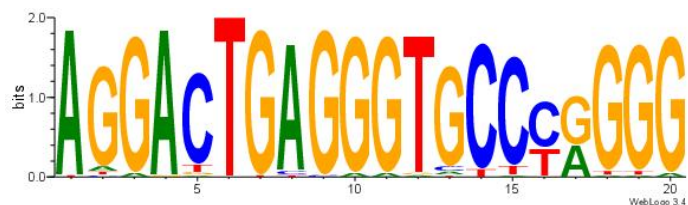
Dataset #: 1

Motif ID: 312
 Motif name: Motif 312
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 9
 Number of overlap: 11
 Similarity score: 0.0662761

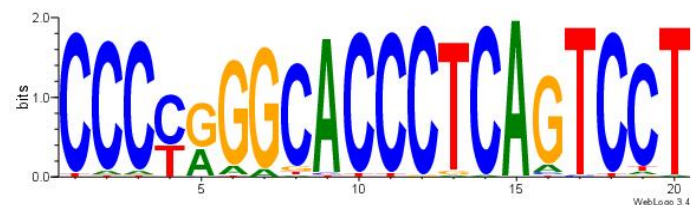
Alignment:

CCCMKGGCACCCCTCAGTCCT
 -CCATGGCGTCC-----

Original motif Consensus sequence: AGGACTGAGGGTGCCYRGGG



Reverse complement motif Consensus sequence: CCCMKGGCACCCCTCAGTCCT



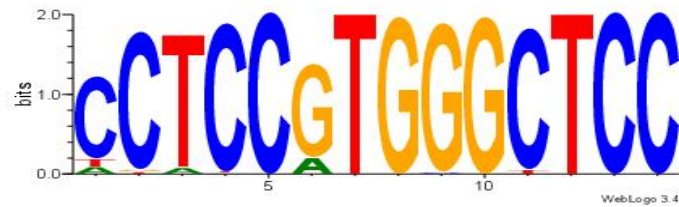
Dataset #: 1
 Motif ID: 163
 Motif name: Motif 163
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 11

Similarity score: 0.066425

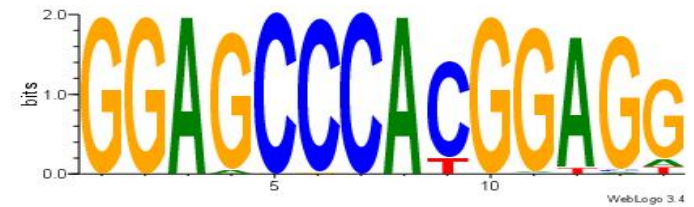
Alignment:

CCTCCGTGGGCTCC
---CCATGGCGTCC

Original motif Consensus sequence: CCTCCGTGGGCTCC



Reverse complement motif Consensus sequence: GGAGCCACGGAG



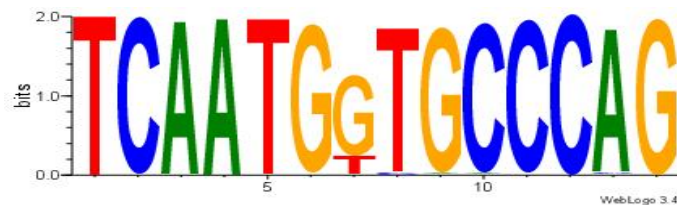
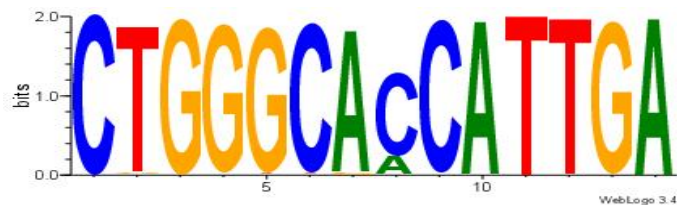
Dataset #: 1
Motif ID: 147
Motif name: Motif 147
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 3
Number of overlap: 11
Similarity score: 0.0668759

Alignment:

TCAATGGTGCCCAG
--CCATGGCGTCC--

Original motif Consensus sequence: CTGGCACCATTGA

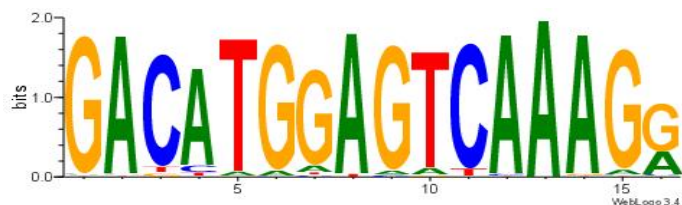
Reverse complement motif Consensus sequence: TCAATGGTGCCCAG



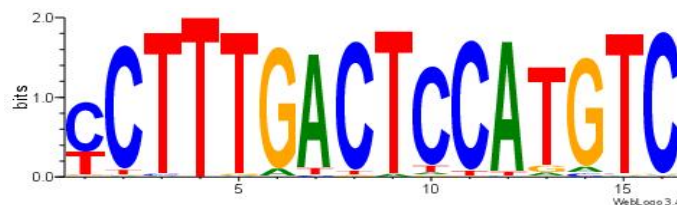
Dataset #: 1
 Motif ID: 326
 Motif name: Motif 326
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 11
 Similarity score: 0.071383

Alignment:
 CCTTTGACTCCATGTC
 ----GGACGCCATGG-

Original motif Consensus sequence: GACATGGAGTCAAAGG



Reverse complement motif Consensus sequence: CCTTTGACTCCATGTC

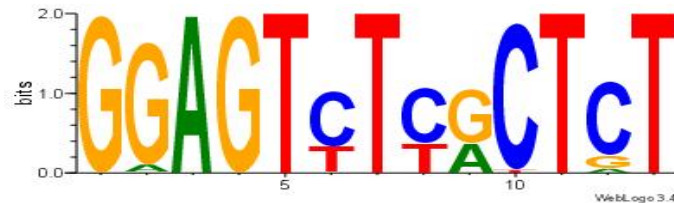


Dataset #: 1 Motif ID: 204 Motif name: Motif 204

Original motif Consensus sequence: AGAGYRAGACTCC



Reverse complement motif Consensus sequence: GGAGTCTMKCTCT



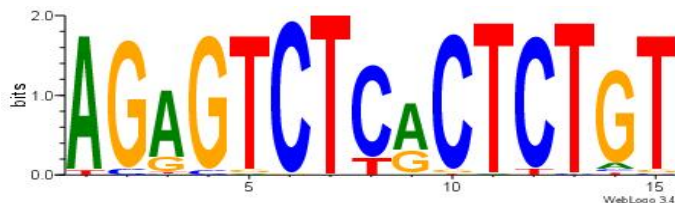
Best Matches for Motif ID 204 (Highest to Lowest)

Dataset #:	1
Motif ID:	253
Motif name:	Motif 253
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	3
Number of overlap:	13
Similarity score:	0.0513045

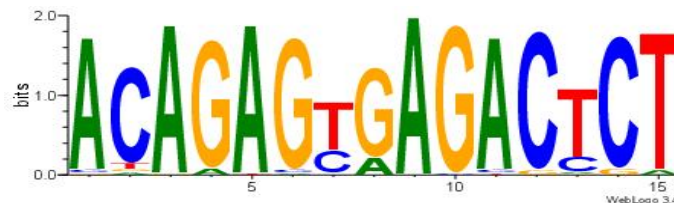
Alignment:

```
ACAGAGTGAGACTCT
--AGAGYRAGACTCC
```

Original motif Consensus sequence: AGAGTCTCACTCTGT



Reverse complement motif Consensus sequence: ACAGAGTGAGACTCT

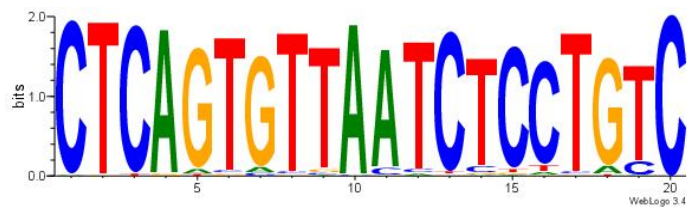


Dataset #: 1
 Motif ID: 262
 Motif name: Motif 262
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 13
 Similarity score: 0.0874128

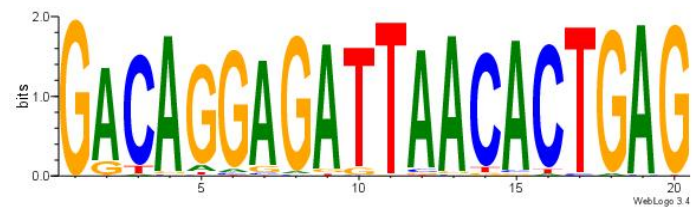
Alignment:

CTCAGTGTTAATCTCCTGTC
 ---AGAGYRAGACTCC----

Original motif Consensus sequence: CTCAGTGTTAATCTCCTGTC



Reverse complement motif Consensus sequence: GACAGGAGATTAACACTGAG



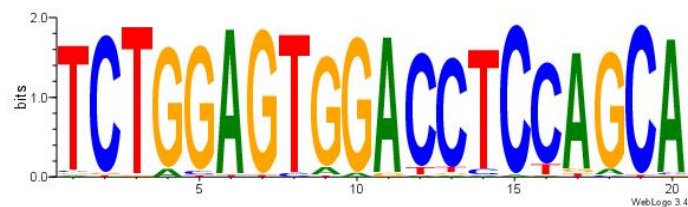
Dataset #: 1
 Motif ID: 350
 Motif name: Motif 350
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4

Number of overlap: 13
Similarity score: 0.0904804

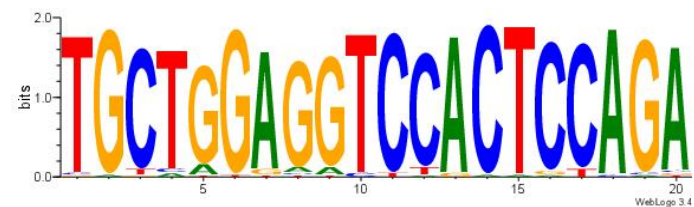
Alignment:

TCTGGAGTGGACCTCCAGCA
---GGAGTCTMKCTCT----

Original motif Consensus sequence: TCTGGAGTGGACCTCCAGCA



Reverse complement motif Consensus sequence:
TGCTGGAGGTCCACTCCAGA

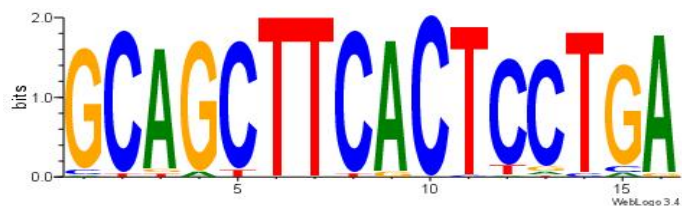


Dataset #: 1
Motif ID: 246
Motif name: Motif 246
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 13
Similarity score: 0.091609

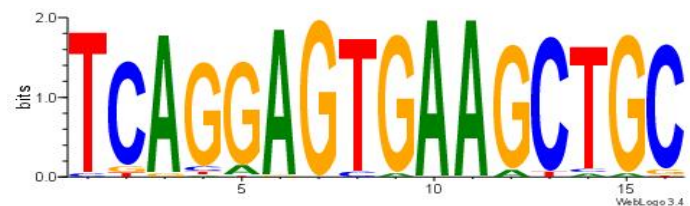
Alignment:

TCAGGAGTGAAGCTGC
---AGAGYRAGACTCC

Original motif Consensus sequence: GCAGCTTCACTCCCTGA



Reverse complement motif Consensus sequence: TCAGGAGTGAAGCTGC

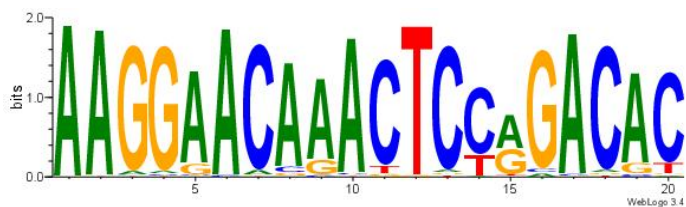


Dataset #: 1
Motif ID: 234
Motif name: Motif 234
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 7
Number of overlap: 13
Similarity score: 0.093082

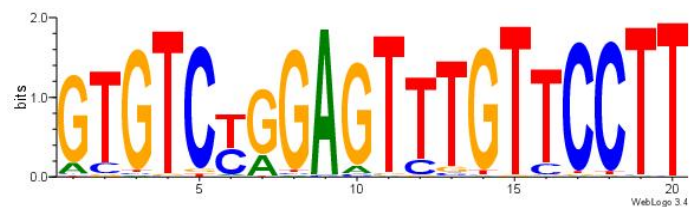
Alignment:

AAGGAACAACTCCRGACAC
-AGAGYRAGACTCC-----

Original motif Consensus sequence: AAGGAACAACTCCGACAC

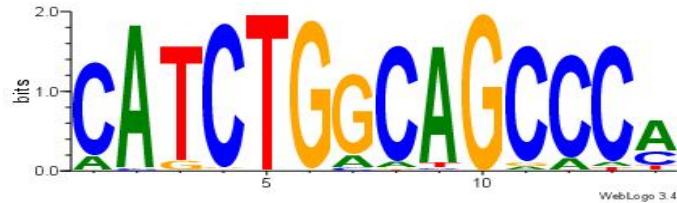


Reverse complement motif Consensus sequence: GTGTCGGAGTTTGTTCCTT

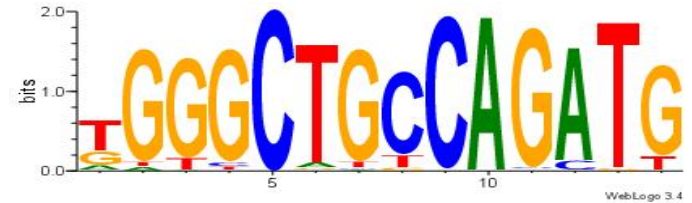


Dataset #: 1 Motif ID: 205 Motif name: Motif 205

Original motif Consensus sequence: CATCTGGCAGCCCA



Reverse complement motif Consensus sequence: TGGGCTGCCAGAT



Best Matches for Motif ID 205 (Highest to Lowest)

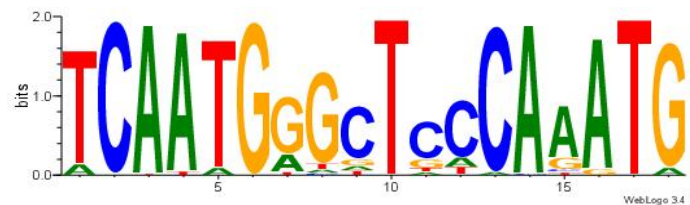
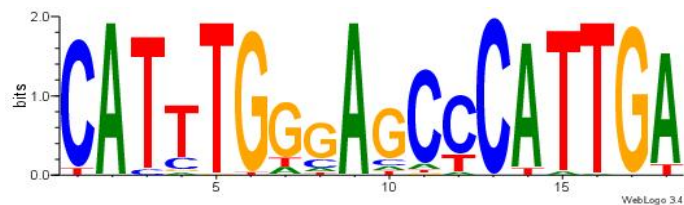
Dataset #:	1
Motif ID:	284
Motif name:	Motif 284
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	5
Number of overlap:	14
Similarity score:	0.036398

Alignment:

```
CATTTGGGAGCCCATTGA
CATCTGGCAGCCCA-----
```

Original motif Consensus sequence: CATTTGGGAGCCCATTGA

Reverse complement motif Consensus sequence: TCAATGGGCTCCCAAATG

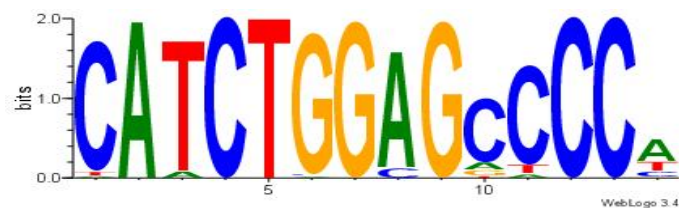


Dataset #: 1
 Motif ID: 320
 Motif name: Motif 320
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0.0491079

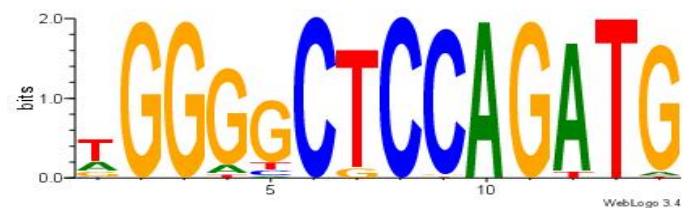
Alignment:

CATCTGGAGCCCCA
 CATCTGGCAGCCCCA

Original motif Consensus sequence: CATCTGGAGCCCCA



Reverse complement motif Consensus sequence: TGGGGCTCCAGATG



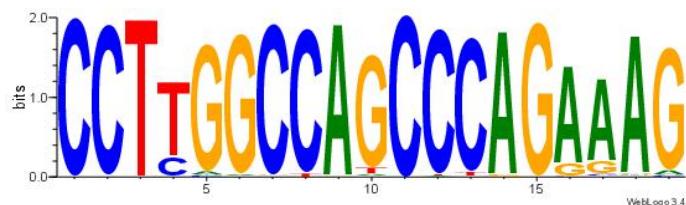
Dataset #: 1
 Motif ID: 122

Motif name: Motif 122
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 6
 Number of overlap: 14
 Similarity score: 0.0681372

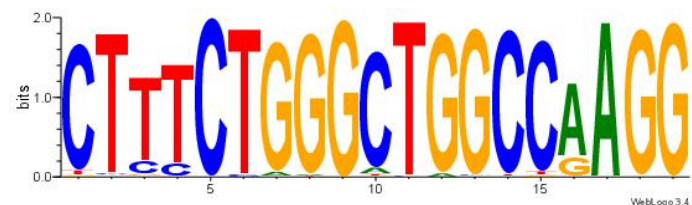
Alignment:

CCTTGGCCAGCCCAGAAAG
 CATCTGGCAGCCCA-----

Original motif Consensus sequence: CCTTGGCCAGCCCAGAAAG



Reverse complement motif Consensus sequence: CTTTCTGGGCTGGCCAAGG

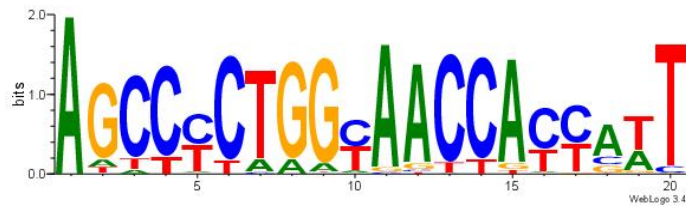


Dataset #: 1
 Motif ID: 139
 Motif name: Motif 139
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 5
 Number of overlap: 14
 Similarity score: 0.0781052

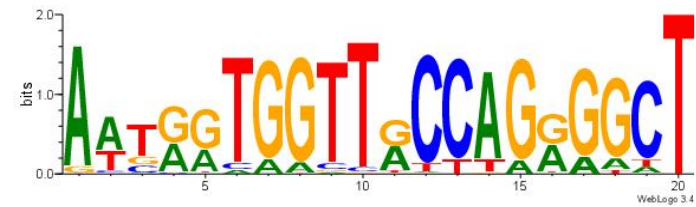
Alignment:

AGCCYCTGGYAACCAYYAWT
--CATCTGGCAGCCCA-----

Original motif Consensus sequence: AGCCYCTGGYAACCAYYAWT



Reverse complement motif Consensus sequence:
AWTKKTGGTTKCCAGKGGCT



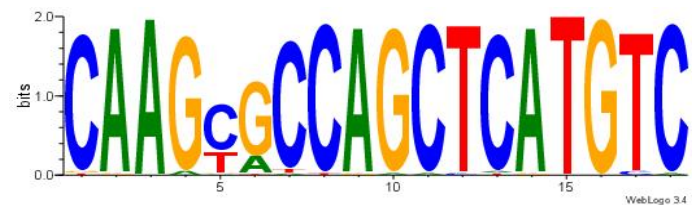
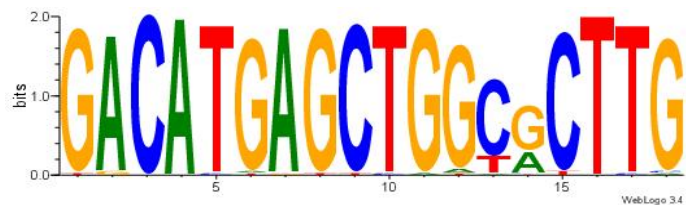
Dataset #: 1
Motif ID: 306
Motif name: Motif 306
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 14
Similarity score: 0.0803617

Alignment:

GACATGAGCTGGCGCTTG
----TGGGCTGCCAGATG

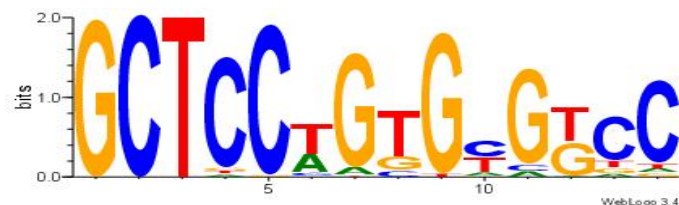
Original motif Consensus sequence: GACATGAGCTGGCGCTTG

Reverse complement motif Consensus sequence:
CAAGCGCCAGCTCATGTC

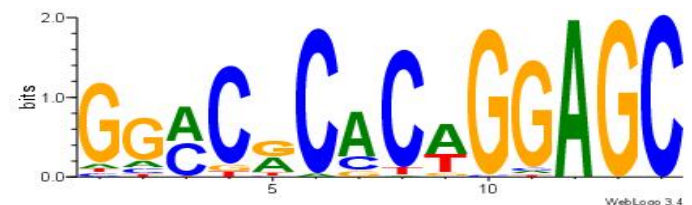


Dataset #: 1 Motif ID: 206 Motif name: Motif 206

Original motif Consensus sequence: GCTCCWGTGYGKCC



Reverse complement motif Consensus sequence: GGRCKCACWGGAGC

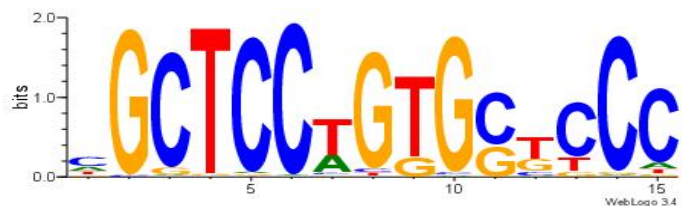


Best Matches for Motif ID 206 (Highest to Lowest)

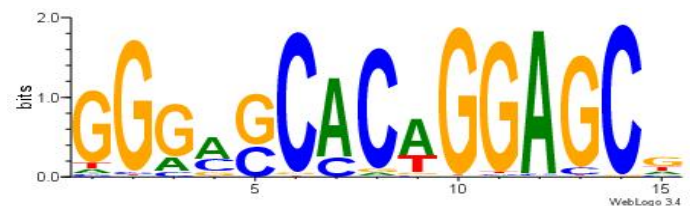
Dataset #:	1
Motif ID:	215
Motif name:	Motif 215
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	2
Number of overlap:	14
Similarity score:	0.038263

Alignment:
GGGRSCACAGGAGCD
GGRCKCACWGGAGC-

Original motif Consensus sequence: HGCTCCTGTGSKCCC



Reverse complement motif Consensus sequence: GGRSCACAGGAGCD

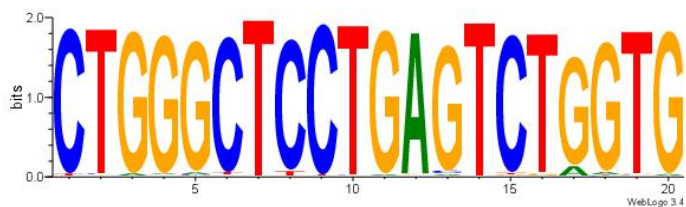


Dataset #: 1
Motif ID: 67
Motif name: Motif 67
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 3
Number of overlap: 14
Similarity score: 0.0894523

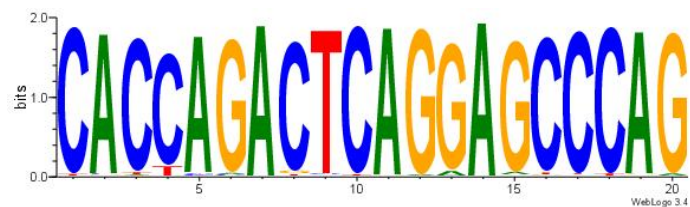
Alignment:

```
CTGGGCTCCTGAGTCTGGTG  
----GCTCCWGTGYGKCC--
```

Original motif Consensus sequence: CTGGGCTCCTGAGTCTGGTG



Reverse complement motif Consensus sequence: CACCAGACTCAGGAGCCCAG

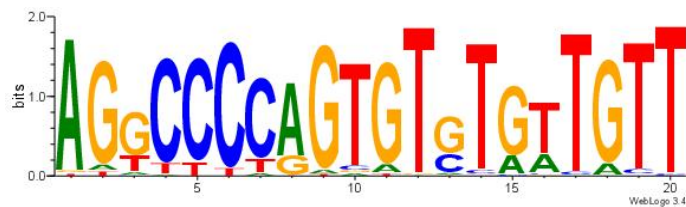


Dataset #: 1
 Motif ID: 176
 Motif name: Motif 176
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 14
 Similarity score: 0.0920579

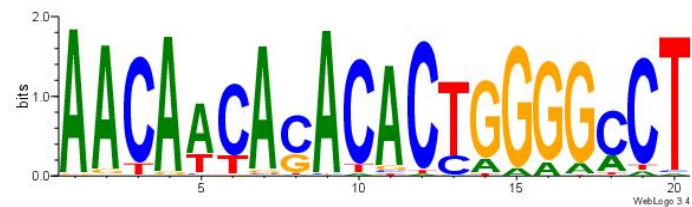
Alignment:

AGGCCCCAGTGTSTGTTGTT
 --GCTCCWGTGYGKCC----

Original motif Consensus sequence: AGGCCCCAGTGTSTGTTGTT



Reverse complement motif Consensus sequence: AACACASACACTGGGGCCT



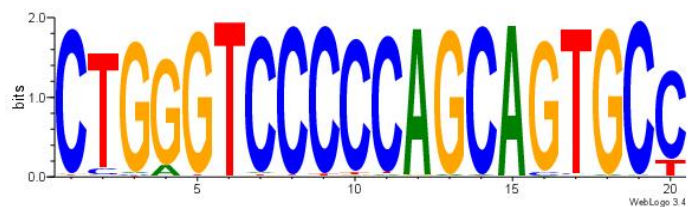
Dataset #: 1
 Motif ID: 84
 Motif name: Motif 84
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 4

Number of overlap: 14
Similarity score: 0.0936498

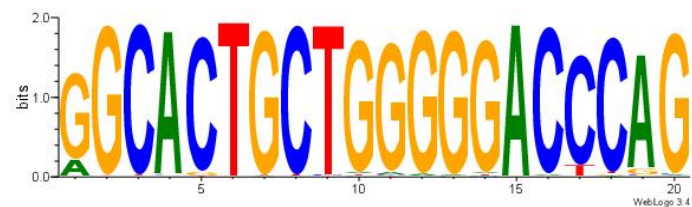
Alignment:

CTGGGTCCCCCAGCAGTGCC
---GGRCKCACWGGAGC---

Original motif Consensus sequence: CTGGGTCCCCCAGCAGTGCC



Reverse complement motif Consensus sequence: GGCAGTCTGGGGGACCCAG

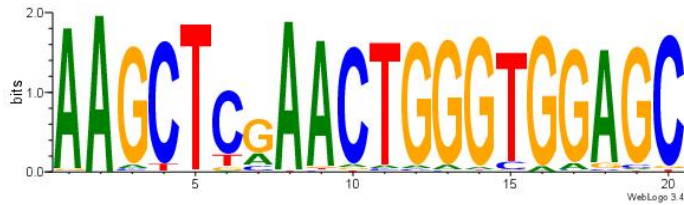


Dataset #: 1
Motif ID: 321
Motif name: Motif 321
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 7
Number of overlap: 14
Similarity score: 0.095951

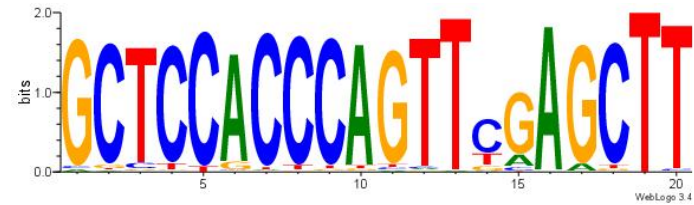
Alignment:

AAGCTCGAACTGGGTGGAGC
-----GGRCKCACWGGAGC

Original motif Consensus sequence: AAGCTCGAACTGGGTGGAGC

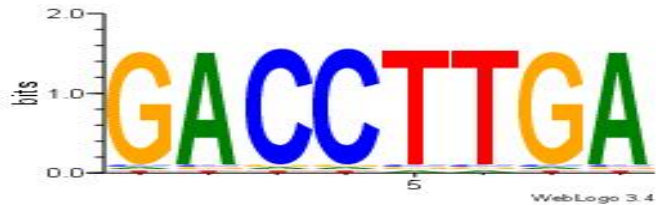


Reverse complement motif Consensus sequence: GCTCCACCCAGTTCGAGCTT



Dataset #: 1 Motif ID: 207 Motif name: Motif 207

Original motif Consensus sequence: GACCTTGA



Reverse complement motif Consensus sequence: TCAAGGTC



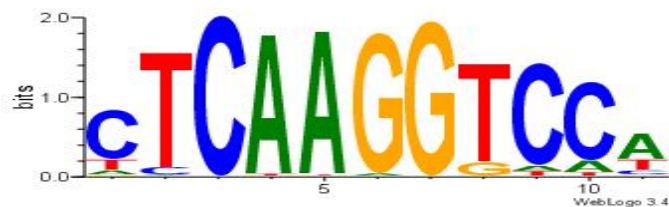
Best Matches for Motif ID 207 (Highest to Lowest)

Dataset #:	1
Motif ID:	11
Motif name:	Motif 11
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	2
Number of overlap:	8
Similarity score:	0.0145765

Alignment:

TGGACCTTGAG
-GACCTTGA--

Original motif Consensus sequence: CTCAAGGTCCA



Reverse complement motif Consensus sequence: TGGACCTTGAG

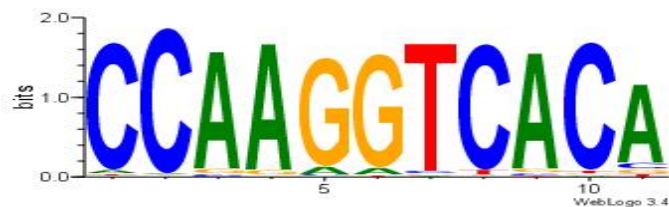


Dataset #: 1
Motif ID: 264
Motif name: Motif 264
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 8
Similarity score: 0.0364604

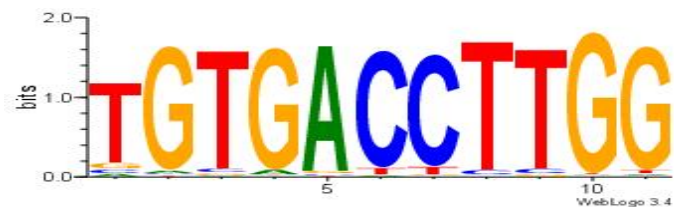
Alignment:

TGTGACCTTGG
---GACCTTGA

Original motif Consensus sequence: CCAAGGTCACA



Reverse complement motif Consensus sequence: TGTGACCTTGG

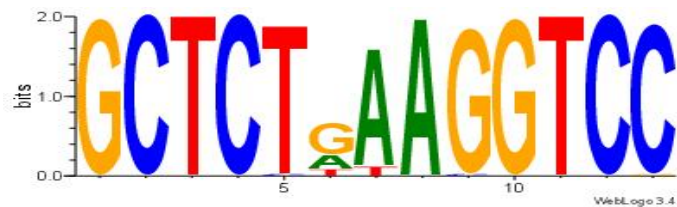


Dataset #: 1
 Motif ID: 362
 Motif name: Motif 362
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 8
 Similarity score: 0.0423228

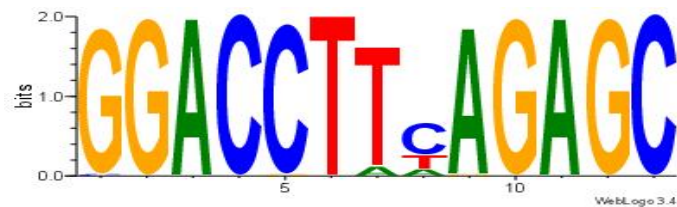
Alignment:

GCTCTGAAGGTCC
 ----TCAAGGTC-

Original motif Consensus sequence: GCTCTGAAGGTCC



Reverse complement motif Consensus sequence: GGACCTTCAGAGC



Dataset #: 1
 Motif ID: 302
 Motif name: Motif 302
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 5

Number of overlap: 8
Similarity score: 0.0468349

Alignment:
GCTCTCAGGGTC
----TCAAGGTC

Original motif Consensus sequence: GACCCTGAGAGC



Reverse complement motif Consensus sequence: GCTCTCAGGGTC

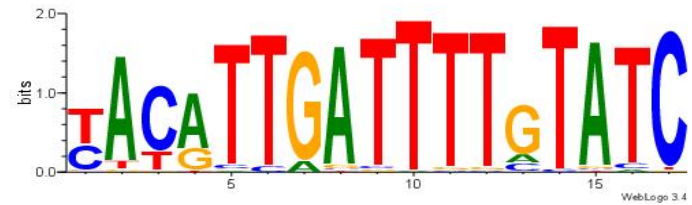
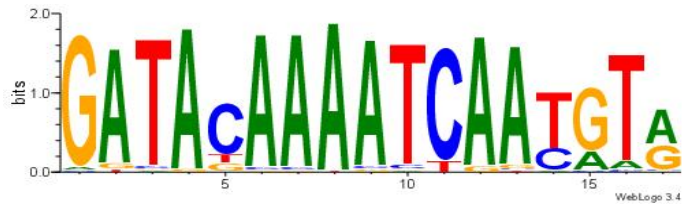


Dataset #: 1
Motif ID: 328
Motif name: Motif 328
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 10
Number of overlap: 8
Similarity score: 0.0507846

Alignment:
KACATTGATTTTGTATC
GACCTTGA-----

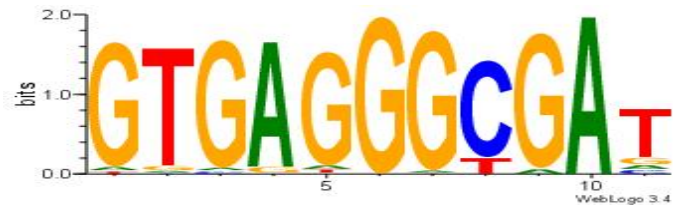
Original motif Consensus sequence: GATACAAAATCAATGTR

Reverse complement motif Consensus sequence:
KACATTGATTTTGTATC

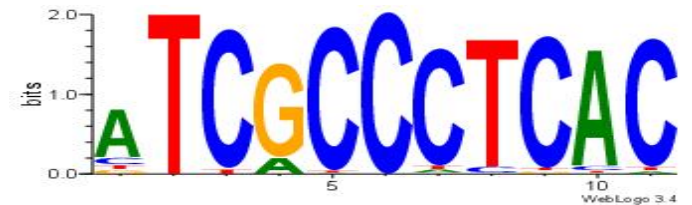


Dataset #: 1 Motif ID: 208 Motif name: Motif 208

Original motif Consensus sequence: GTGAGGGCGAT



Reverse complement motif Consensus sequence: ATCGCCCTCAC

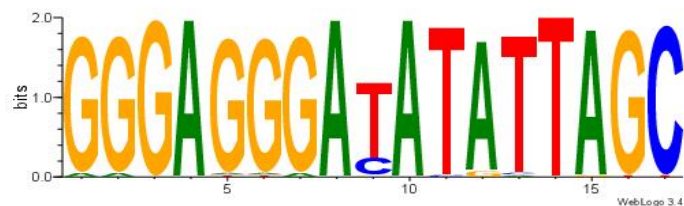


Best Matches for Motif ID 208 (Highest to Lowest)

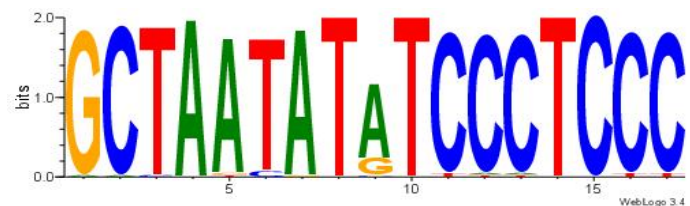
Dataset #:	1
Motif ID:	329
Motif name:	Motif 329
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	7
Number of overlap:	11
Similarity score:	0.0622115

Alignment:
GCTAATATATCCCTCCC
-----ATCGCCCTCAC

Original motif Consensus sequence: GGGAGGGATATATTAGC



Reverse complement motif Consensus sequence: GCTAATATATCCCTCCC

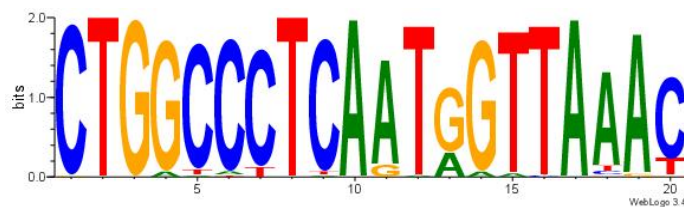


Dataset #: 1
Motif ID: 332
Motif name: Motif 332
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 10
Number of overlap: 11
Similarity score: 0.0654927

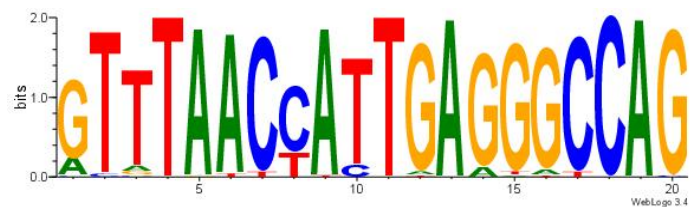
Alignment:

GTTTAACCATTGAGGGCCAG
-----GTGAGGGCGAT

Original motif Consensus sequence: CTGGCCCTCAATGGTTAAAC



Reverse complement motif Consensus sequence: GTTTAACCATTGAGGGCCAG

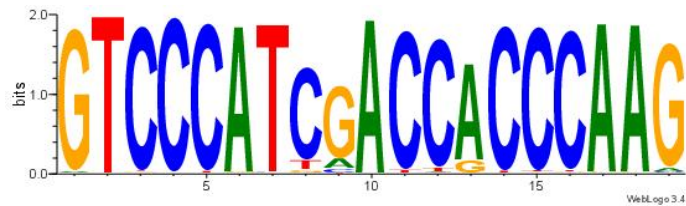


Dataset #: 1
 Motif ID: 53
 Motif name: Motif 53
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 6
 Number of overlap: 11
 Similarity score: 0.0735725

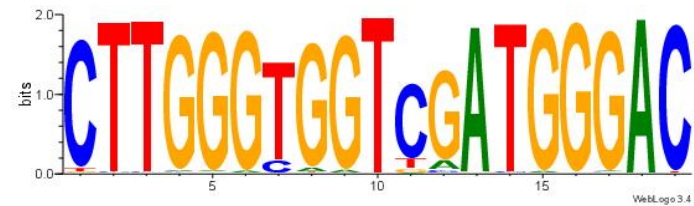
Alignment:

GTCCCATCGACCACCCAAG
 ---ATCGCCCTCAC-----

Original motif Consensus sequence: GTCCCATCGACCACCCAAG



Reverse complement motif Consensus sequence: CTTGGGTGGTGGTGGAC



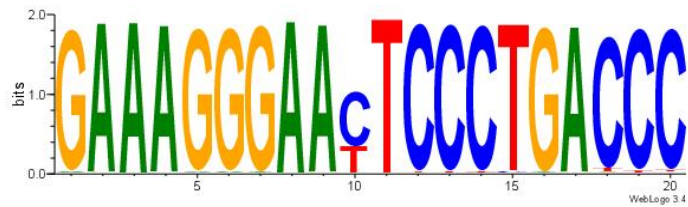
Dataset #: 1
 Motif ID: 16
 Motif name: Motif 16
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 8

Number of overlap: 11
Similarity score: 0.0751839

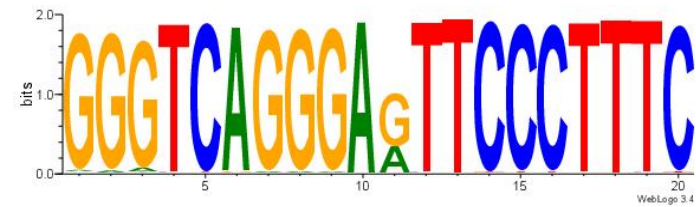
Alignment:

GGGTCAGGGAGTTC CCTTTC
-----GTGAGGGCGAT--

Original motif Consensus sequence: GAAAGGGA ACTCCCTGACCC



Reverse complement motif Consensus sequence:
GGGTCAGGGAGTTC CCTTTC

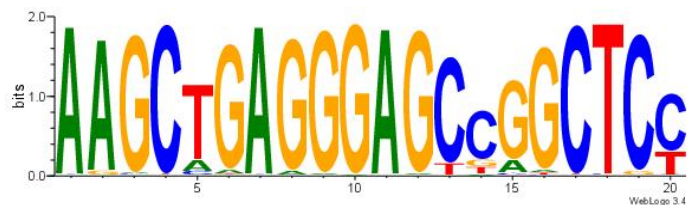


Dataset #: 1
Motif ID: 96
Motif name: Motif 96
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 7
Number of overlap: 11
Similarity score: 0.0788665

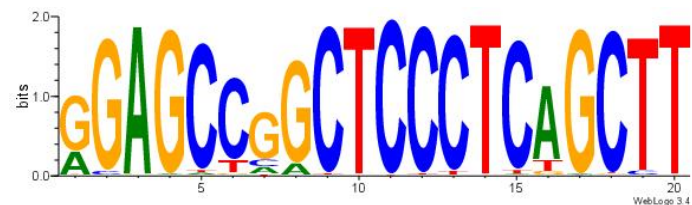
Alignment:

GGAGCCGGCTCCCTCAGCTT
-----ATCGCCCTCAC---

Original motif Consensus sequence: AAGCTGAGGGAGCCGGCTCC

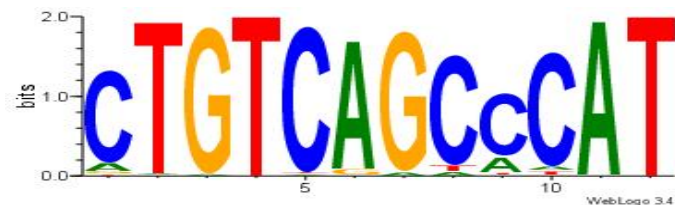


Reverse complement motif Consensus sequence: GGAGCCGGCTCCCTCAGCTT

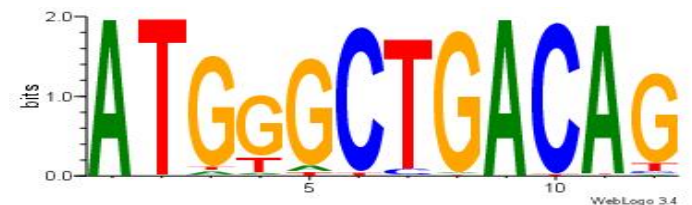


Dataset #: 1 Motif ID: 209 Motif name: Motif 209

Original motif Consensus sequence: CTGTCAGCCCAT



Reverse complement motif Consensus sequence: ATGGGCTGACAG



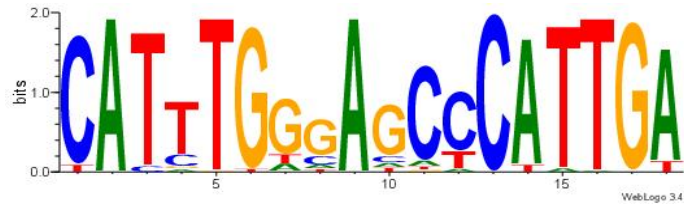
Best Matches for Motif ID 209 (Highest to Lowest)

Dataset #:	1
Motif ID:	284
Motif name:	Motif 284
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	4
Number of overlap:	12
Similarity score:	0.0568336

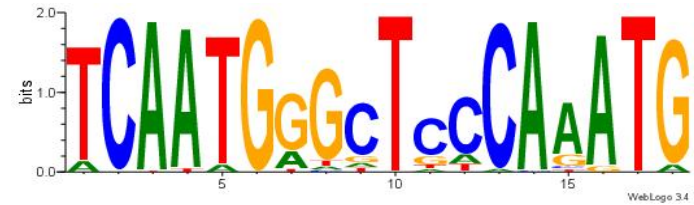
Alignment:

CATTTGGGAGCCCATTGA
 ---CTGTCAGCCCAT---

Original motif Consensus sequence: CATTTGGGAGCCCATTGA



Reverse complement motif Consensus sequence:
 TCAATGGGCTCCCAAATG

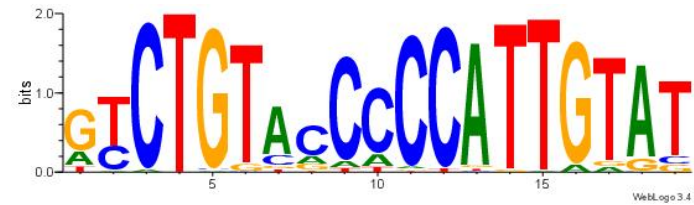
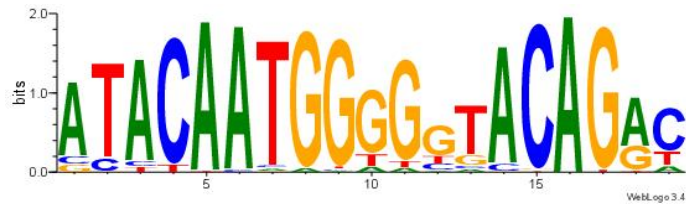


Dataset #: 1
 Motif ID: 193
 Motif name: Motif 193
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 6
 Number of overlap: 12
 Similarity score: 0.0594073

Alignment:
 GKCTGTACCCCATTTGTAT
 -----CTGTCAGCCCAT--

Original motif Consensus sequence: ATACAATGGGGGTACAGRC

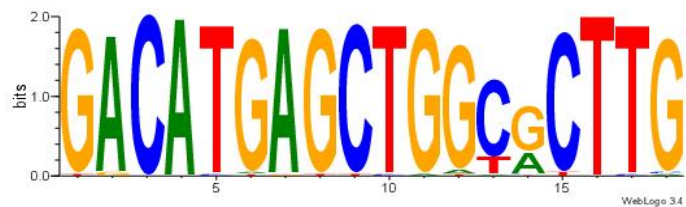
Reverse complement motif Consensus sequence:
 GKCTGTACCCCATTTGTAT



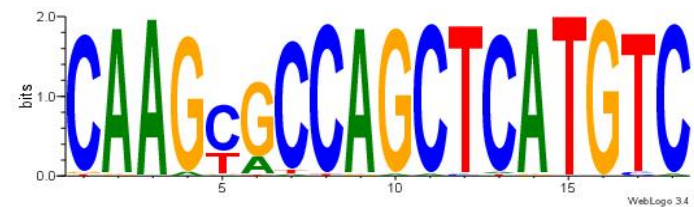
Dataset #: 1
 Motif ID: 306
 Motif name: Motif 306
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 12
 Similarity score: 0.0708524

Alignment:
 GACATGAGCTGGCGCTTG
 ---ATGGGCTGACAG---

Original motif Consensus sequence: GACATGAGCTGGCGCTTG



Reverse complement motif Consensus sequence: CAAGCGCCAGCTCATGTC



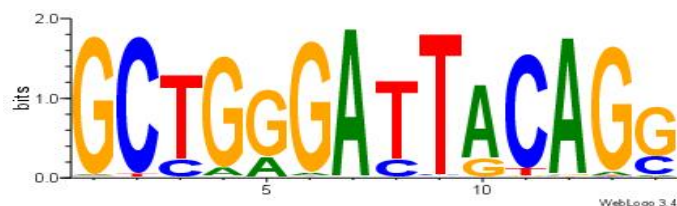
Dataset #: 1

Motif ID: 4
 Motif name: Motif 4
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 12
 Similarity score: 0.071408

Alignment:

GCTGGGATTACAGG
 -ATGGGCTGACAG-

Original motif Consensus sequence: GCTGGGATTACAGG



Reverse complement motif Consensus sequence: CCTGTAATCCCAG

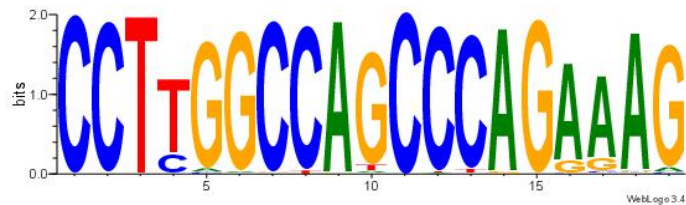


Dataset #: 1
 Motif ID: 122
 Motif name: Motif 122
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 5
 Number of overlap: 12
 Similarity score: 0.0804186

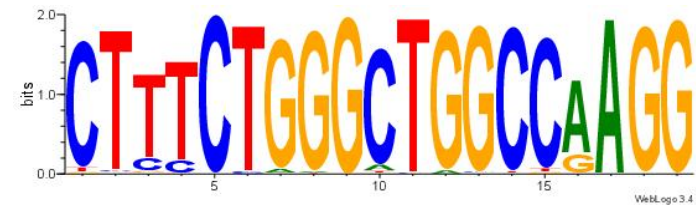
Alignment:

```
CCTTGGCCAGCCCAGAAAG  
---CTGTCAGCCCAT-----
```

Original motif Consensus sequence: CCTTGGCCAGCCCAGAAAG



Reverse complement motif Consensus sequence: CTTTCTGGGCTGGCCAAGG

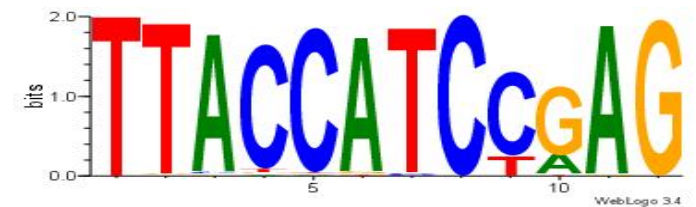


Dataset #: 1 Motif ID: 210 Motif name: Motif 210

Original motif Consensus sequence: CTCGGATGGTAA



Reverse complement motif Consensus sequence: TTACCATCCGAG



Best Matches for Motif ID 210 (Highest to Lowest)

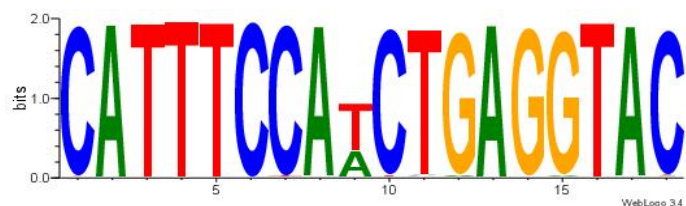
Dataset #:	1
Motif ID:	25
Motif name:	Motif 25
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward

Position number: 3
Number of overlap: 12
Similarity score: 0.0447432

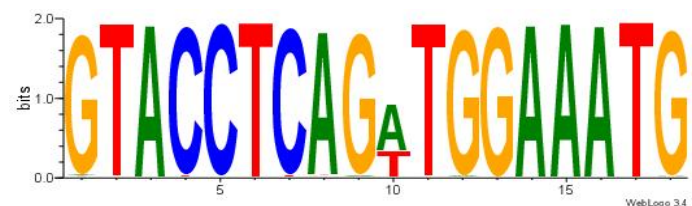
Alignment:

CATTTCCAWCTGAGGTAC
----TTACCATCCGAG--

Original motif Consensus sequence: CATTTCCAWCTGAGGTAC



Reverse complement motif Consensus sequence: GTACCTCAGWTGGAAATG

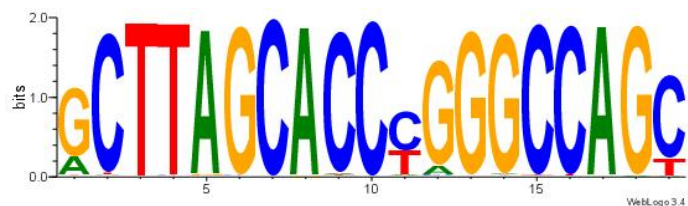


Dataset #: 1
Motif ID: 82
Motif name: Motif 82
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 3
Number of overlap: 12
Similarity score: 0.0679752

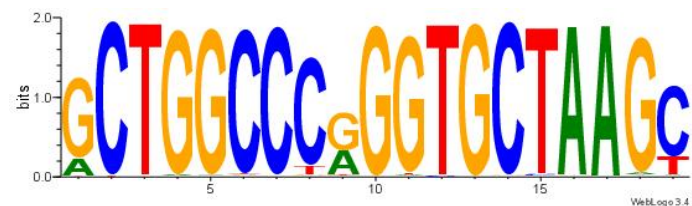
Alignment:

GCTTAGCACCYGGGCCAGC
-----TTACCATCCGAG--

Original motif Consensus sequence: GCTTAGCACCCGGGCCAGC



Reverse complement motif Consensus sequence:
GCTGGCCCKGGTGCTAAGC

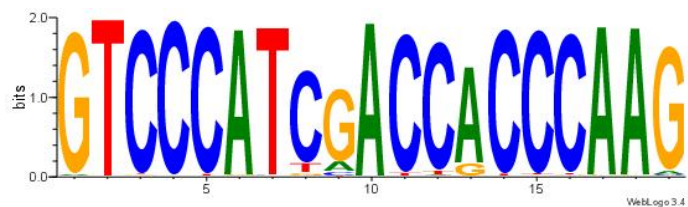


Dataset #: 1
Motif ID: 53
Motif name: Motif 53
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 8
Number of overlap: 12
Similarity score: 0.078255

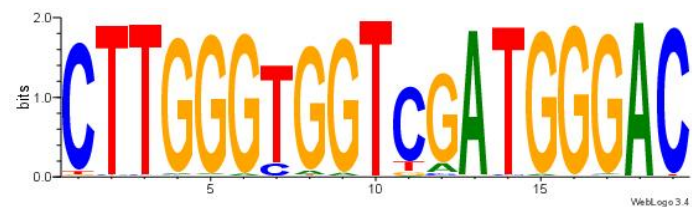
Alignment:

GTCCCATCGACCACCCAAG
TTACCATCCGAG-----

Original motif Consensus sequence: GTCCCATCGACCACCCAAG



Reverse complement motif Consensus sequence:
CTTGGGTGGTTCGATGGGAC



Dataset #: 1
 Motif ID: 214
 Motif name: Motif 214
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 12
 Similarity score: 0.0812199

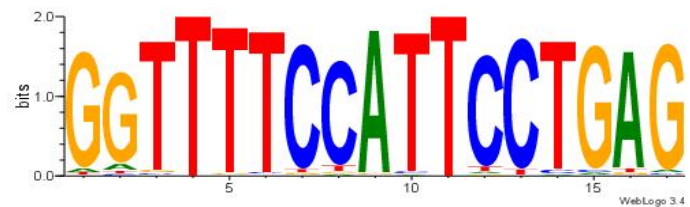
Alignment:

CTCAGGAATGGAAAACC
 --CTCGGATGGTAA---

Original motif Consensus sequence: CTCAGGAATGGAAAACC



Reverse complement motif Consensus sequence: GGTTTCCATTcCTGAG

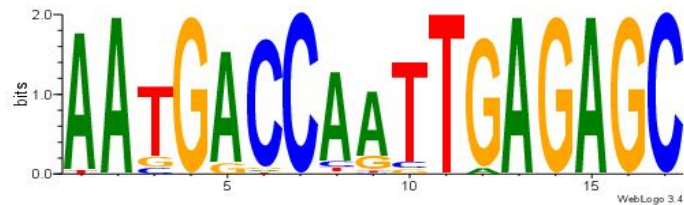


Dataset #: 1
 Motif ID: 305
 Motif name: Motif 305
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3

Number of overlap: 12
Similarity score: 0.0825424

Alignment:
GCTCTCAATTGGTCATT
---CTCGGATGGTAA--

Original motif Consensus sequence: AATGACCAATTGAGAGC

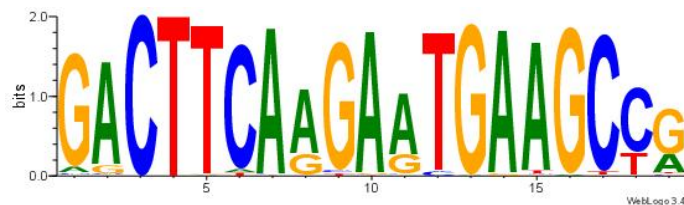


Reverse complement motif Consensus sequence:
GCTCTCAATTGGTCATT

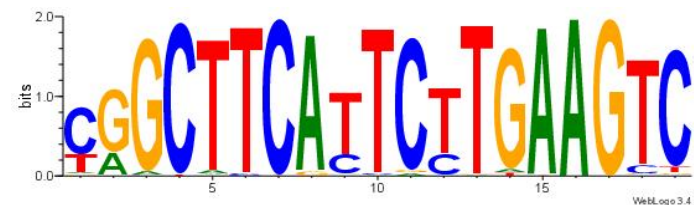


Dataset #: 1 Motif ID: 211 Motif name: Motif 211

Original motif Consensus sequence: GACTTCAAGAATGAAGCCG



Reverse complement motif Consensus sequence:
CGGCTTCATTCTTGAAGTC



Best Matches for Motif ID 211 (Highest to Lowest)

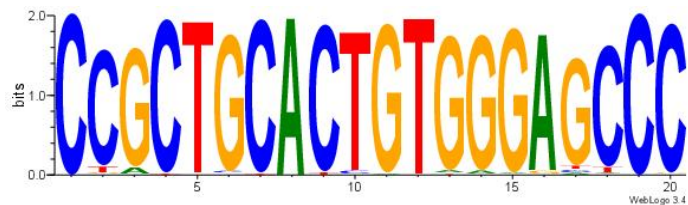
Dataset #: 1
Motif ID: 144
Motif name: Motif 144

Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	19
Similarity score:	0.0872886

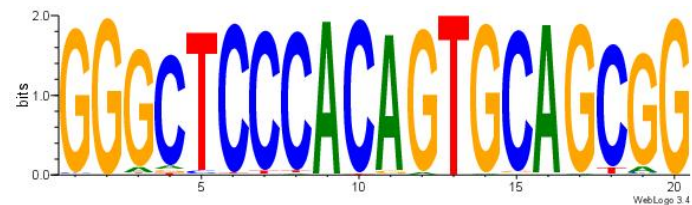
Alignment:

```
CCGCTGCACTGTGGGAGCCC
-CGGCTTCATTCTTGAAGTC
```

Original motif Consensus sequence: CCGCTGCACTGTGGGAGCCC



Reverse complement motif Consensus sequence: GGGCTCCCACAGTGCAGCGG

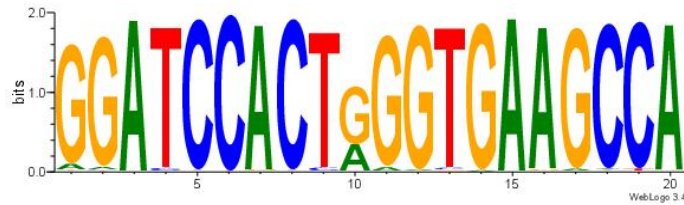


Dataset #:	1
Motif ID:	61
Motif name:	Motif 61
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	19
Similarity score:	0.109235

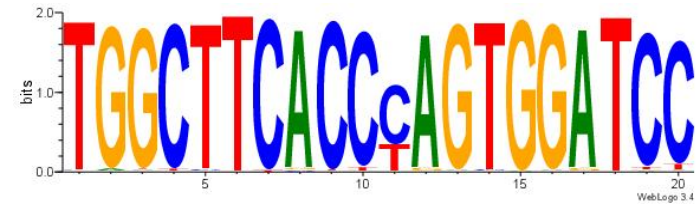
Alignment:

GGATCCACTGGGTGAAGCCA
-GACTTCAAGAATGAAGCCG

Original motif Consensus sequence: GGATCCACTGGGTGAAGCCA



Reverse complement motif Consensus sequence:
TGGCTTCACCCAGTGGATCC



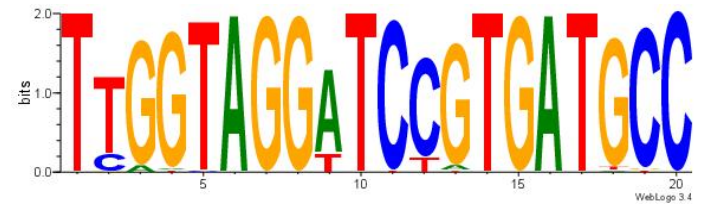
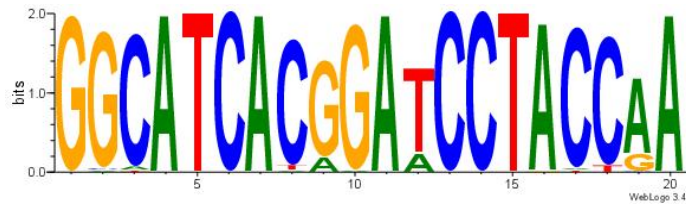
Dataset #: 1
Motif ID: 311
Motif name: Motif 311
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 19
Similarity score: 0.112192

Alignment:

GGCATCACGGATCCTACCAA
GACTTCAAGAATGAAGCCG-

Original motif Consensus sequence: GGCATCACGGATCCTACCAA

Reverse complement motif Consensus sequence:
TTGGTAGGATCCGTGATGCC

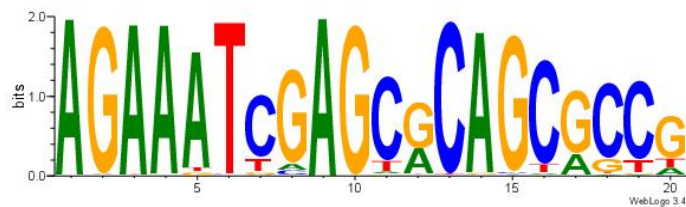


Dataset #: 1
 Motif ID: 65
 Motif name: Motif 65
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 19
 Similarity score: 0.113323

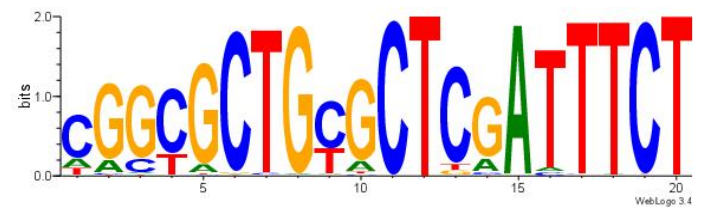
Alignment:

AGAAATCGAGCRCAGCGCCG
 -GACTTCAAGAATGAAGCCG

Original motif Consensus sequence: AGAAATCGAGCRCAGCGCCG



Reverse complement motif Consensus sequence: CGGCGCTGMGCTCGATTCT



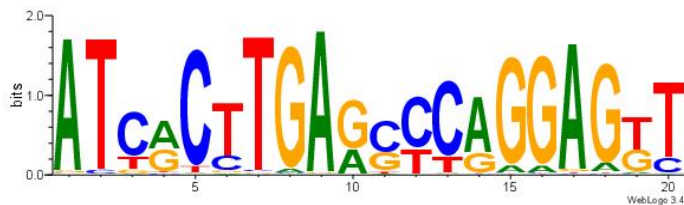
Dataset #: 1

Motif ID: 8
 Motif name: Motif 8
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 19
 Similarity score: 0.114911

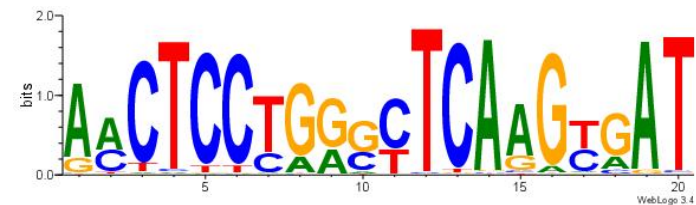
Alignment:

ARCTCCTGKSCTCAAGKGAT
 -GACTTCAAGAATGAAGCCG

Original motif Consensus sequence: ATCRCTTGAGSYCAGGAGKT

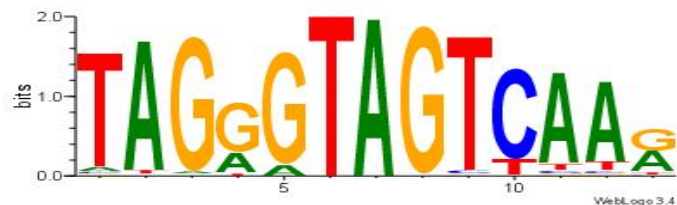


Reverse complement motif Consensus sequence: ARCTCCTGKSCTCAAGKGAT

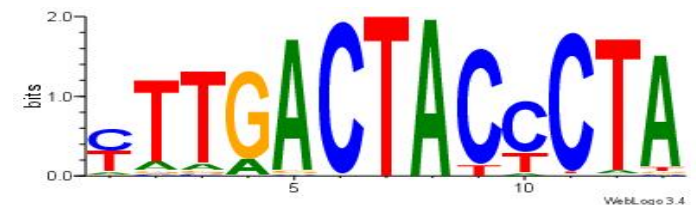


Dataset #: 1 Motif ID: 212 Motif name: Motif 212

Original motif Consensus sequence: TAGGGTAGTCAAR



Reverse complement motif Consensus sequence: MTTGACTACCCTA



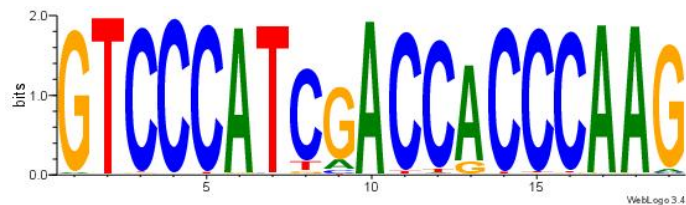
Best Matches for Motif ID 212 (Highest to Lowest)

Dataset #: 1
Motif ID: 53
Motif name: Motif 53
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 6
Number of overlap: 13
Similarity score: 0.0571978

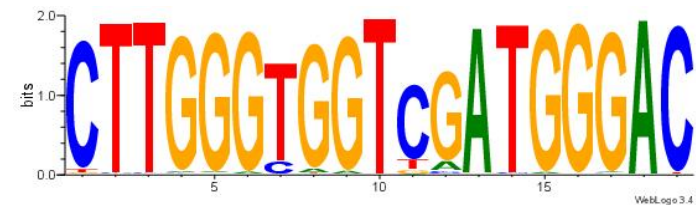
Alignment:

```
CTTGGGTGGTCGATGGGAC  
-----TAGGGTAGTCAAR-
```

Original motif Consensus sequence: GTCCCATCGACCACCCAAG



Reverse complement motif Consensus sequence:
CTTGGGTGGTCGATGGGAC

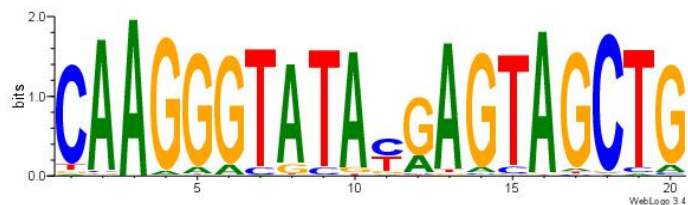


Dataset #: 1
Motif ID: 194
Motif name: Motif 194
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif

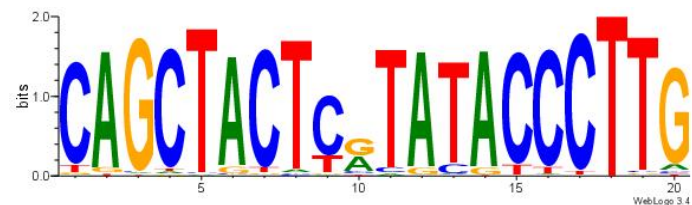
Direction: Forward
Position number: 2
Number of overlap: 13
Similarity score: 0.0722477

Alignment:
CAAGGGTATAYGAGTAGCTG
-TAGGGTAGTCAAR-----

Original motif Consensus sequence: CAAGGGTATAYGAGTAGCTG



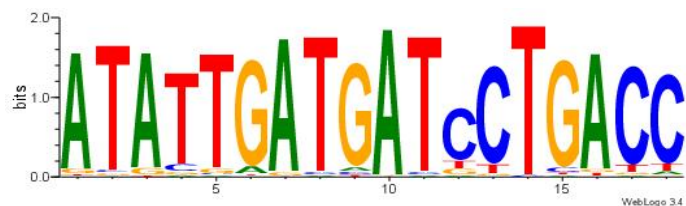
Reverse complement motif Consensus sequence: CAGCTACTCKTATACCCTTG



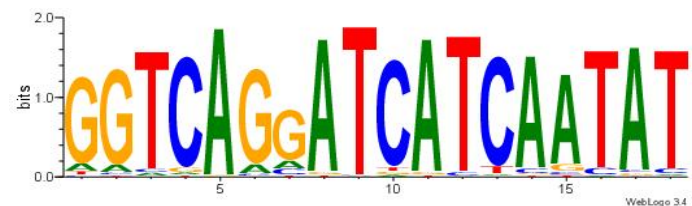
Dataset #: 1
Motif ID: 184
Motif name: Motif 184
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 3
Number of overlap: 13
Similarity score: 0.0728242

Alignment:
GGTCAGGATCATCAATAT
--TAGGGTAGTCAAR---

Original motif Consensus sequence: ATATTGATGATCCTGACC



Reverse complement motif Consensus sequence: GGTCAGGATCATCAATAT

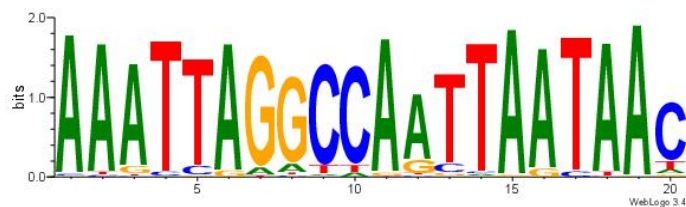


Dataset #: 1
Motif ID: 308
Motif name: Motif 308
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 4
Number of overlap: 13
Similarity score: 0.0736225

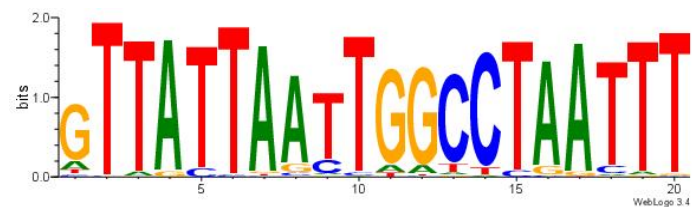
Alignment:

```
GTTATTAATTGGCCTAATTT  
---MTTGACTACCCTA-----
```

Original motif Consensus sequence: AAATTAGGCCAATTAATAAC



Reverse complement motif Consensus sequence: GTTATTAATTGGCCTAATTT

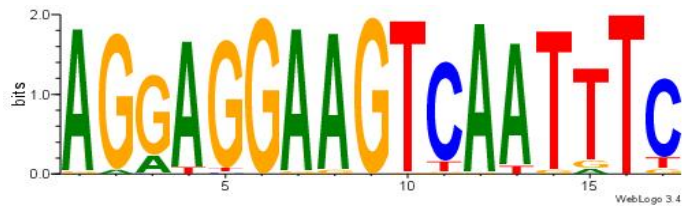


Dataset #: 1
 Motif ID: 327
 Motif name: Motif 327
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 4
 Number of overlap: 13
 Similarity score: 0.0737666

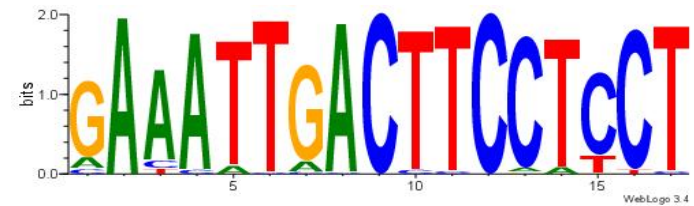
Alignment:

GAAATTGACTTCCTCCT
 ---MTTGACTACCCTA-

Original motif Consensus sequence: AGGAGGAAGTCAATTC



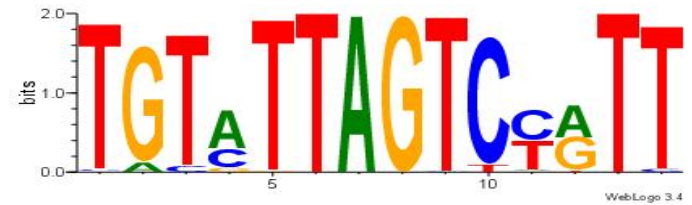
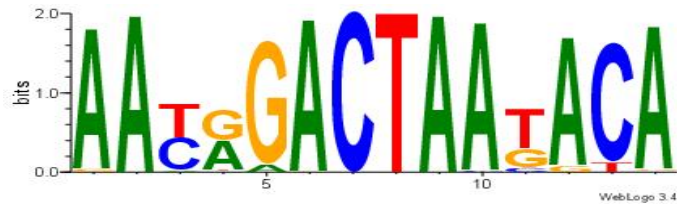
Reverse complement motif Consensus sequence: GAAATTGACTTCCTCCT



Dataset #: 1 Motif ID: 213 Motif name: Motif 213

Original motif Consensus sequence: AAYRGACTAATACA

Reverse complement motif Consensus sequence: TGTATTAGTCMMT

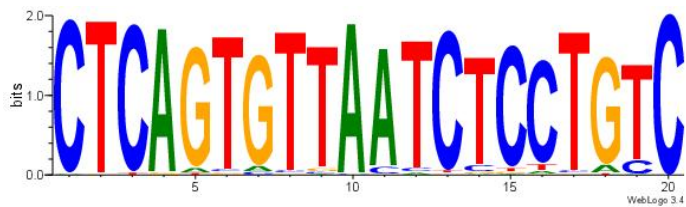


Best Matches for Motif ID 213 (Highest to Lowest)

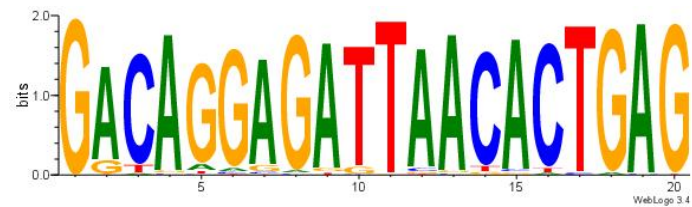
Dataset #: 1
 Motif ID: 262
 Motif name: Motif 262
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 4
 Number of overlap: 14
 Similarity score: 0.0676805

Alignment:
 CTCAGTGTTAATCTCCTGTC
 ---TGTATTAGTCMMTT---

Original motif Consensus sequence: CTCAGTGTTAATCTCCTGTC



Reverse complement motif Consensus sequence:
 GACAGGAGATTAACACTGAG



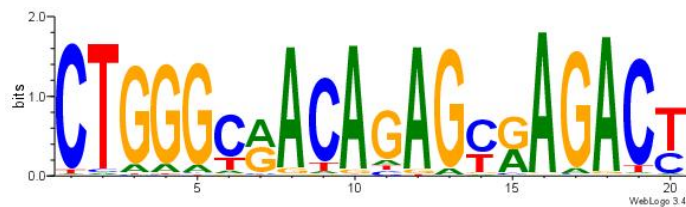
Dataset #: 1
 Motif ID: 29
 Motif name: Motif 29
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 7
 Number of overlap: 14
 Similarity score: 0.0742206

Alignment:

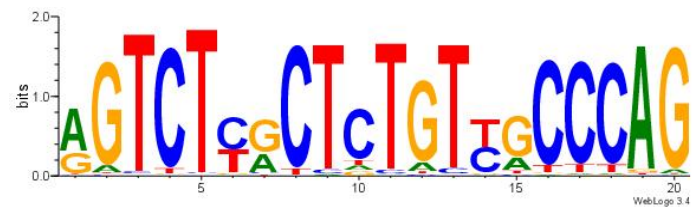
```

CTGGGCRACAGAGYRAGACY
-----AAYRGACTAATACA
  
```

Original motif Consensus sequence: CTGGGCRACAGAGYRAGACY



Reverse complement motif Consensus sequence: MGTCTMKCTCTGKGCCAG



Dataset #: 1
 Motif ID: 224
 Motif name: Motif 224
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1

Number of overlap: 14
Similarity score: 0.0749712

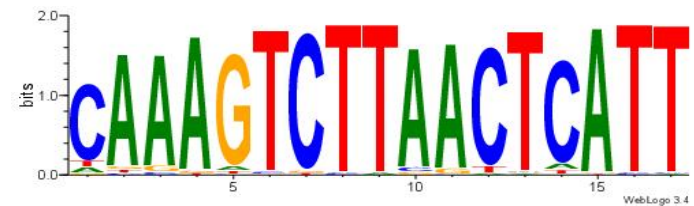
Alignment:

AATGAGTTAAGACTTTG
AAYRGACTAATACA---

Original motif Consensus sequence: AATGAGTTAAGACTTTG



Reverse complement motif Consensus sequence:
CAAAGTCTTAACTCATT

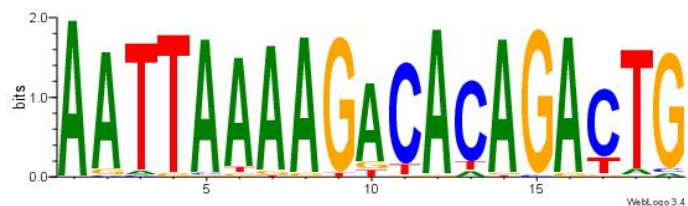


Dataset #: 1
Motif ID: 356
Motif name: Motif 356
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 5
Number of overlap: 14
Similarity score: 0.0750949

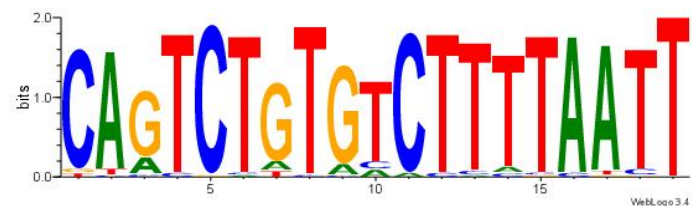
Alignment:

AATTAAAAGACACAGACTG
-----AAYRGACTAATACA-

Original motif Consensus sequence: AATTAAGACACAGACTG



Reverse complement motif Consensus sequence: CAGTCTGTCTTTTAATT

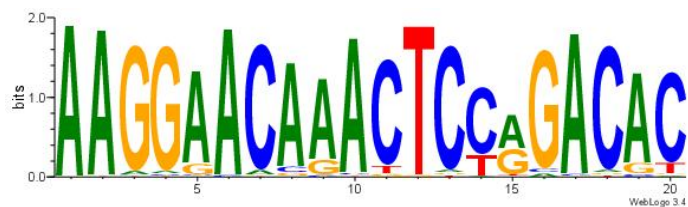


Dataset #: 1
Motif ID: 234
Motif name: Motif 234
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 7
Number of overlap: 14
Similarity score: 0.0758743

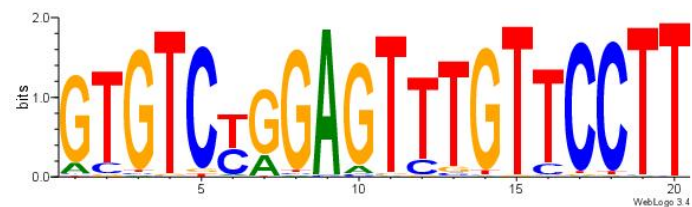
Alignment:

```
GTGTCKGGAGTTTGTTCCTT  
-----TGTATTAGTCMMTT
```

Original motif Consensus sequence: AAGGAACAACTCCGACAC

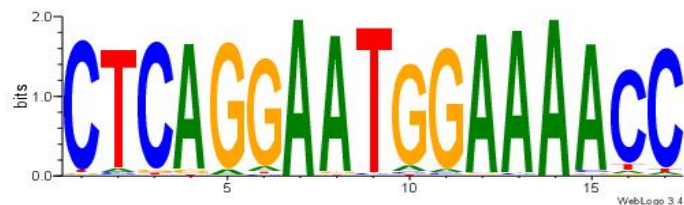


Reverse complement motif Consensus sequence: GTGTCKGGAGTTTGTTCCTT

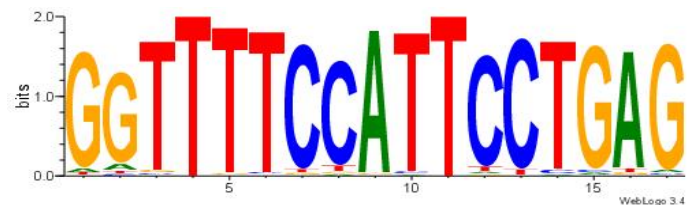


Dataset #: 1 Motif ID: 214 Motif name: Motif 214

Original motif Consensus sequence: CTCAGGAATGGAAAACC



Reverse complement motif Consensus sequence: GGTTTCCATTCCCTGAG



Best Matches for Motif ID 214 (Highest to Lowest)

Dataset #:	1
Motif ID:	7
Motif name:	Motif 7
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	2
Number of overlap:	17
Similarity score:	0.10823

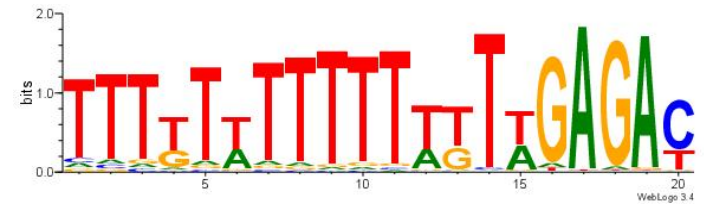
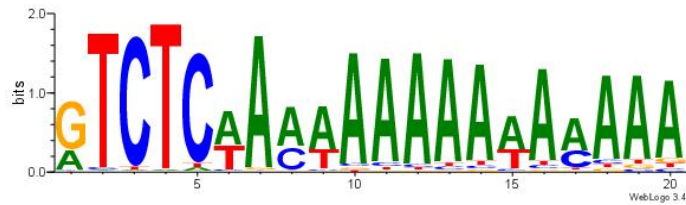
Alignment:

```

TTTTTWTTTTTTTTWTGAGAC
-GGTTTCCATTCCCTGAG--
    
```

Original motif Consensus sequence: GTCTWAMAAAAAWAMAAA

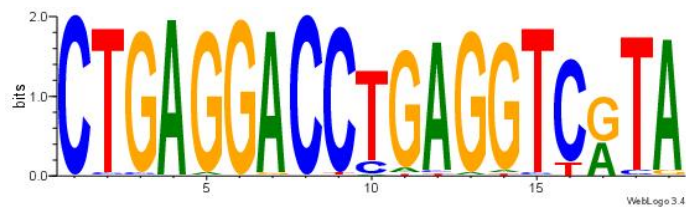
Reverse complement motif Consensus sequence: TTTYTWTTTTTTTTWTGAGAC



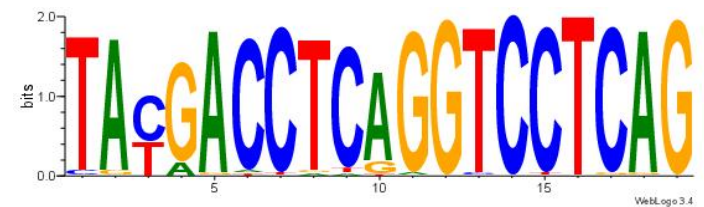
Dataset #: 1
 Motif ID: 291
 Motif name: Motif 291
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3
 Number of overlap: 17
 Similarity score: 0.109842

Alignment:
 TAMGACCTCAGGTCCTCAG
 --GGTTTTCCATTCCTGAG

Original motif Consensus sequence: CTGAGGACCTGAGGTCRTA



Reverse complement motif Consensus sequence: TAMGACCTCAGGTCCTCAG



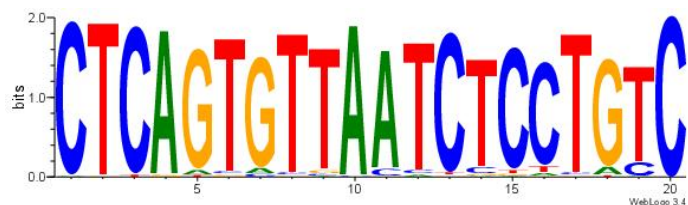
Dataset #: 1

Motif ID: 262
 Motif name: Motif 262
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 17
 Similarity score: 0.110599

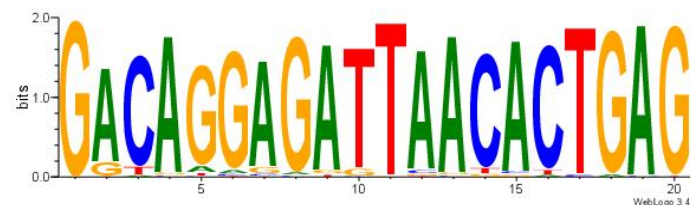
Alignment:

CTCAGTGTTAATCTCCTGTC
 ---GGTTTTCCATTCCTGAG

Original motif Consensus sequence: CTCAGTGTTAATCTCCTGTC



Reverse complement motif Consensus sequence: GACAGGAGATTAACACTGAG



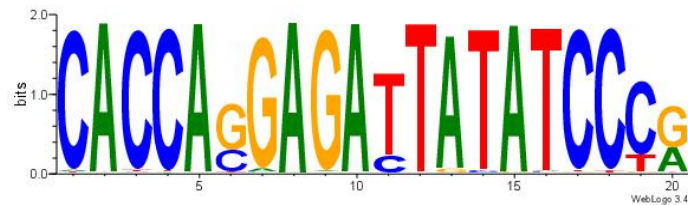
Dataset #: 1
 Motif ID: 19
 Motif name: Motif 19
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 17

Similarity score: 0.112077

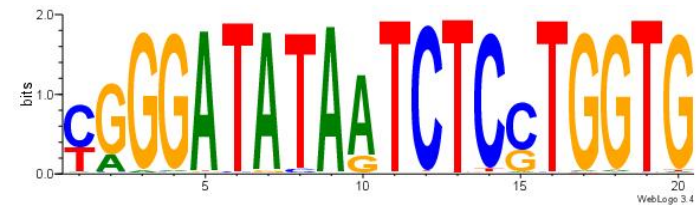
Alignment:

```
MGGGATATAATCTCCTGGTG  
--GGTTTTCCATTCCTGAG--
```

Original motif Consensus sequence: CACCAGGAGATTATATCCCR



Reverse complement motif Consensus sequence:
MGGGATATAATCTCCTGGTG



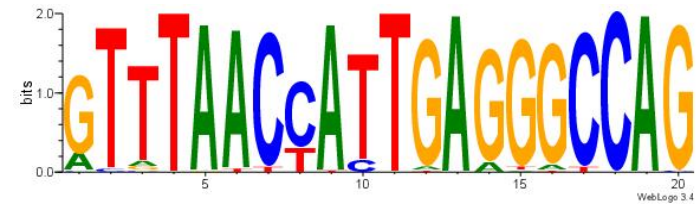
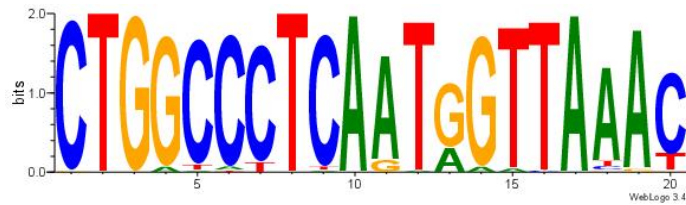
Dataset #: 1
Motif ID: 332
Motif name: Motif 332
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 17
Similarity score: 0.112221

Alignment:

```
GTTTAACCATTGAGGGCCAG  
GGTTTTCCATTCCTGAG---
```

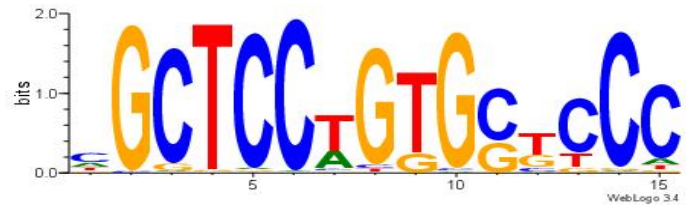
Original motif Consensus sequence: CTGGCCCTCAATGGTTAAAC

Reverse complement motif Consensus sequence:
GTTTAACCATTGAGGGCCAG



Dataset #: 1 Motif ID: 215 Motif name: Motif 215

Original motif Consensus sequence: HGCTCCTGTGSKCCC



Reverse complement motif Consensus sequence: GGRSCACAGGAGCD



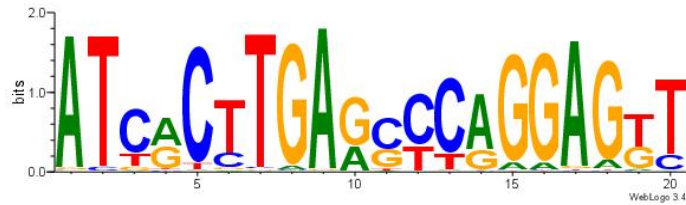
Best Matches for Motif ID 215 (Highest to Lowest)

Dataset #:	1
Motif ID:	8
Motif name:	Motif 8
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	6
Number of overlap:	15
Similarity score:	0.0619315

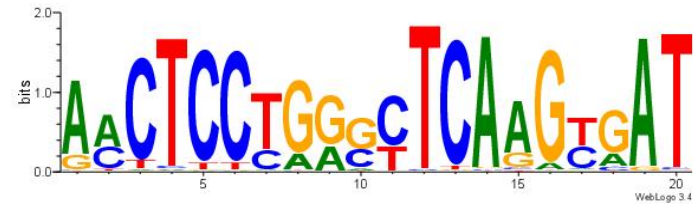
Alignment:

ATCRCTTGAGSYCAGGAGKT
 GGGRSCACAGGAGCD-----

Original motif Consensus sequence: ATCRCTTGAGSYCAGGAGKT



Reverse complement motif Consensus sequence:
 ARCTCCTGKSCTCAAGKGAT

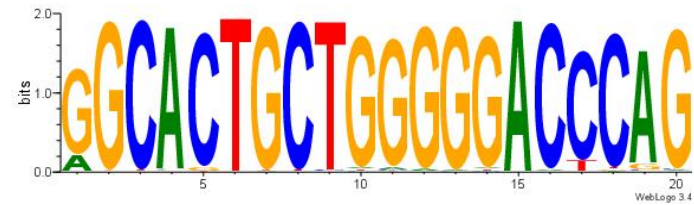
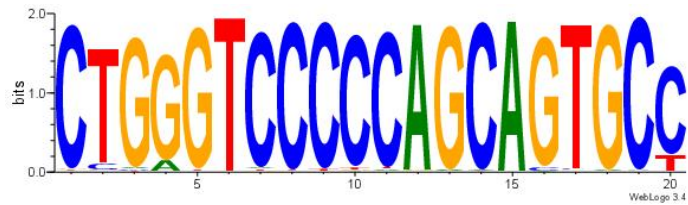


Dataset #:	1
Motif ID:	84
Motif name:	Motif 84
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	4
Number of overlap:	15
Similarity score:	0.0736896

Alignment:
 CTGGGTCCCCCAGCAGTGCC
 --GGGRSCACAGGAGCD---

Original motif Consensus sequence: CTGGGTCCCCCAGCAGTGCC

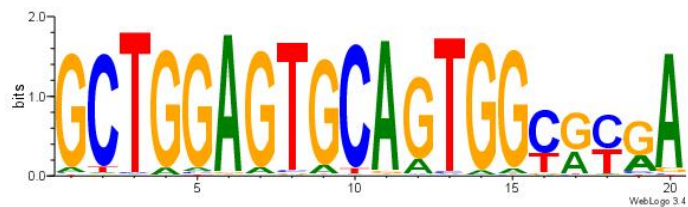
Reverse complement motif Consensus sequence:
 GGCAGTCTGGGGGACCCAG



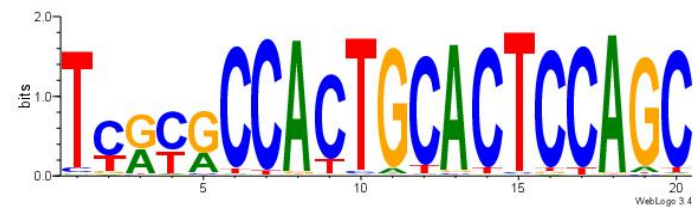
Dataset #: 1
 Motif ID: 3
 Motif name: Motif 3
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 15
 Similarity score: 0.0753884

Alignment:
 GCTGGAGTGCAGTGGCRYGA
 -GGRSCACAGGAGCD----

Original motif Consensus sequence: GCTGGAGTGCAGTGGCRYGA



Reverse complement motif Consensus sequence: TCKMGCCACTGCACTCCAGC



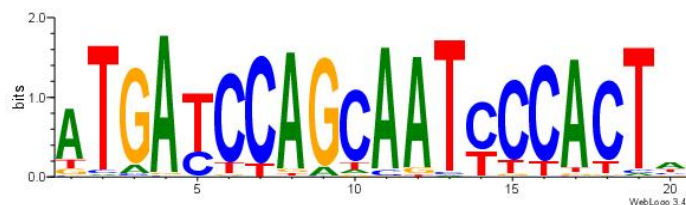
Dataset #: 1

Motif ID: 115
 Motif name: Motif 115
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 5
 Number of overlap: 15
 Similarity score: 0.0800012

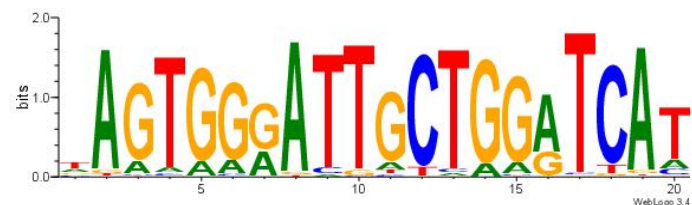
Alignment:

HAGTGGKATTGCTGGATCAT
 ----GGGRSCACAGGAGCD-

Original motif Consensus sequence: ATGATCCAGCAATYCCACTH



Reverse complement motif Consensus sequence: HAGTGGKATTGCTGGATCAT



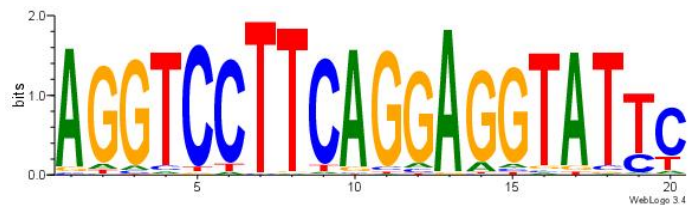
Dataset #: 1
 Motif ID: 179
 Motif name: Motif 179
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 5
 Number of overlap: 15

Similarity score: 0.0803784

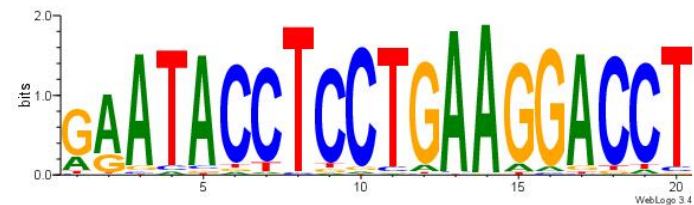
Alignment:

AGGTCCTTCAGGAGGTATTC
----GGGRSCACAGGAGCD--

Original motif Consensus sequence: AGGTCCTTCAGGAGGTATTC



Reverse complement motif Consensus sequence: GAATACCTCTGAAGGACCT

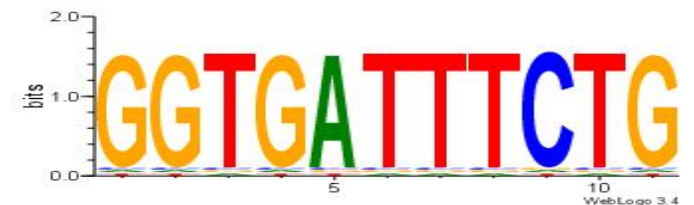


Dataset #: 1 Motif ID: 216 Motif name: Motif 216

Original motif Consensus sequence: CAGAAATCACC



Reverse complement motif Consensus sequence: GGTGATTTCTG



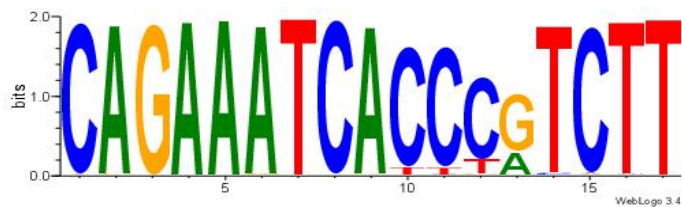
Best Matches for Motif ID 216 (Highest to Lowest)

Dataset #:	1
Motif ID:	35
Motif name:	Motif 35
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif

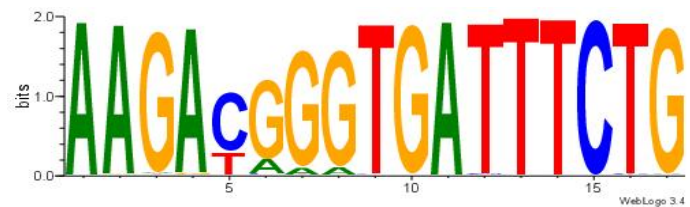
Direction: Backward
 Position number: 7
 Number of overlap: 11
 Similarity score: 0.0137887

Alignment:
 CAGAAATCACCCGTCTT
 CAGAAATCACC-----

Original motif Consensus sequence: CAGAAATCACCCGTCTT



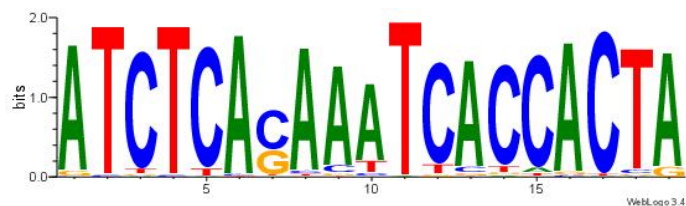
Reverse complement motif Consensus sequence: AAGACGGGTGATTTCTG



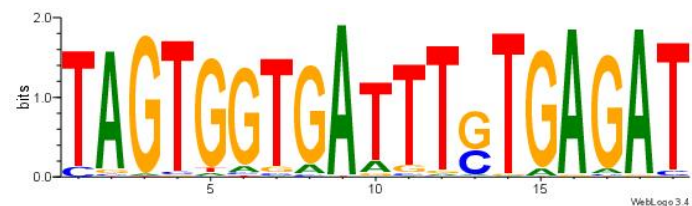
Dataset #: 1
 Motif ID: 261
 Motif name: Motif 261
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 5
 Number of overlap: 11
 Similarity score: 0.0239476

Alignment:
 TAGTGGTGATTTSTGAGAT
 ----GGTGATTTCTG----

Original motif Consensus sequence: ATCTCASAAATCACCCTA



Reverse complement motif Consensus sequence: TAGTGGTGA TTT GAGAT

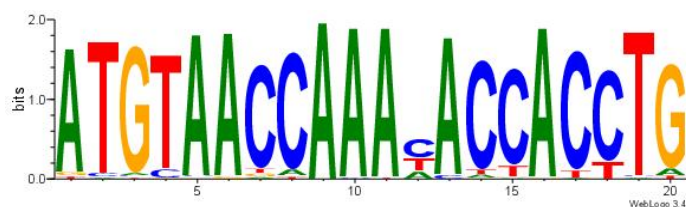


Dataset #: 1
Motif ID: 336
Motif name: Motif 336
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 3
Number of overlap: 11
Similarity score: 0.0684419

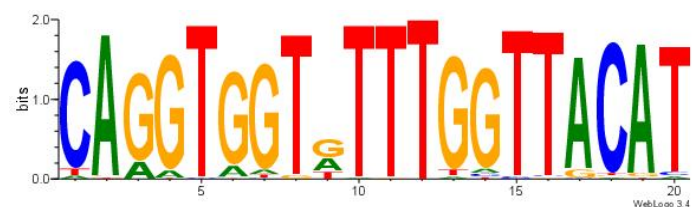
Alignment:

```
CAGGTGGTKTTTGGTTACAT  
--GGTGATTTCTG-----
```

Original motif Consensus sequence: ATGTAACCAAAYACCACCTG



Reverse complement motif Consensus sequence: CAGGTGGTKTTTGGTTACAT

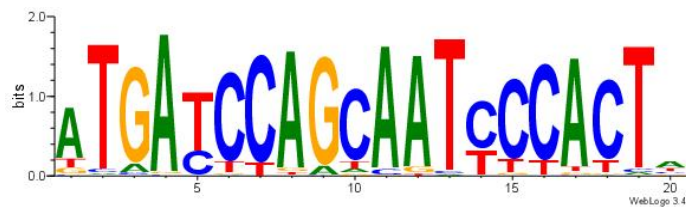


Dataset #: 1
 Motif ID: 115
 Motif name: Motif 115
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 7
 Number of overlap: 11
 Similarity score: 0.0740976

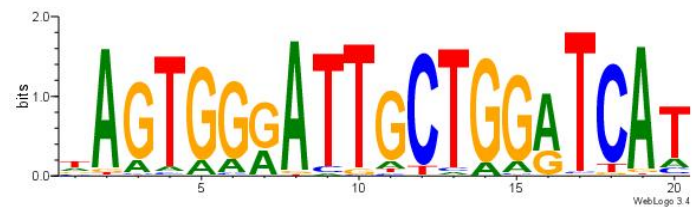
Alignment:

HAGTGGKATTGCTGGATCAT
 ---GGTGATTTCTG-----

Original motif Consensus sequence: ATGATCCAGCAATYCCACTH



Reverse complement motif Consensus sequence: HAGTGGKATTGCTGGATCAT

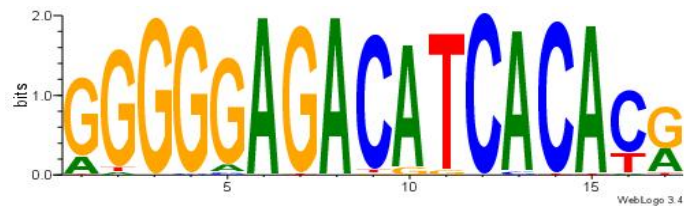


Dataset #: 1
 Motif ID: 279
 Motif name: Motif 279
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3

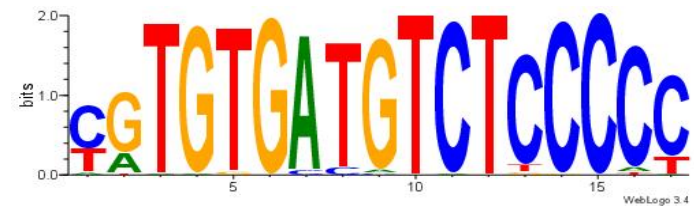
Number of overlap: 11
 Similarity score: 0.0743914

Alignment:
 MGTGTGATGTCTCCCC
 --GGTGATTTCTG----

Original motif Consensus sequence: GGGGGAGACATCACACR

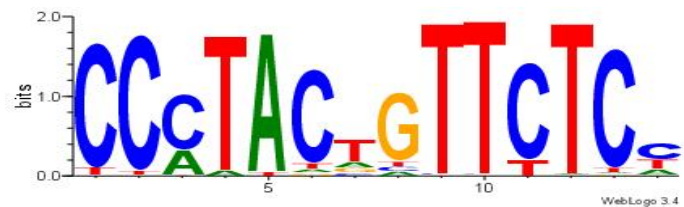


Reverse complement motif Consensus sequence: MGTGTGATGTCTCCCC



Dataset #: 1 Motif ID: 217 Motif name: Motif 217

Original motif Consensus sequence: CCCTACTGTTCTCY



Reverse complement motif Consensus sequence: KGAGAACAGTAGG



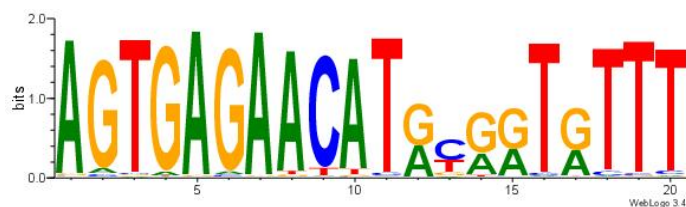
Best Matches for Motif ID 217 (Highest to Lowest)

Dataset #: 1
 Motif ID: 63
 Motif name: Motif 63
 Matching format of first motif: Reverse Complement

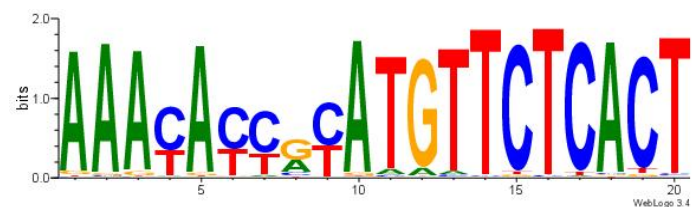
Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 5
 Number of overlap: 14
 Similarity score: 0.0624984

Alignment:
 AGTGAGAACATRYRRTRTTT
 ----KGAGAACAGTAGGG--

Original motif Consensus sequence: AGTGAGAACATRYRRTRTTT



Reverse complement motif Consensus sequence:
 AAAMAMMKMATGTTCTCACT

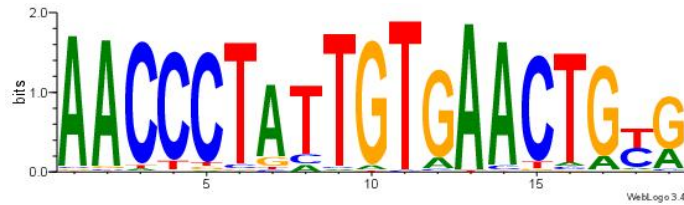


Dataset #: 1
 Motif ID: 242
 Motif name: Motif 242
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 4
 Number of overlap: 14
 Similarity score: 0.070491

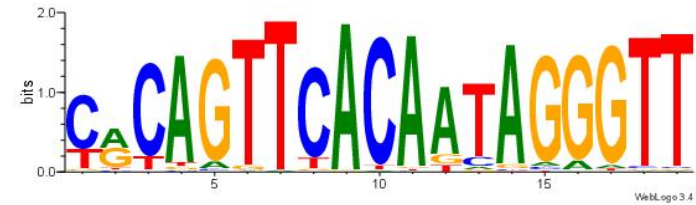
Alignment:

CMCAGTTCACAATAGGGTT
---KGAGAACAGTAGGG---

Original motif Consensus sequence: AACCTATTGTGAACTGYG



Reverse complement motif Consensus sequence:
CMCAGTTCACAATAGGGTT

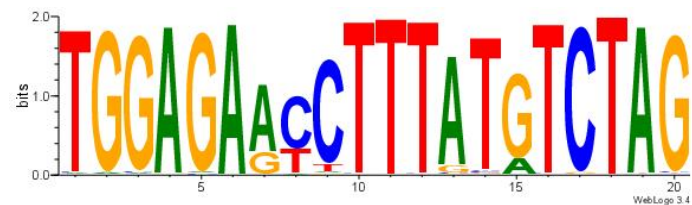


Dataset #: 1
Motif ID: 85
Motif name: Motif 85
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 2
Number of overlap: 14
Similarity score: 0.073742

Alignment:
TGGAGAACCTTTATGTCTAG
-KGAGAACAGTAGGG-----

Original motif Consensus sequence: CTAGACATAAAGGTTCTCCA

Reverse complement motif Consensus sequence:
TGGAGAACCTTTATGTCTAG

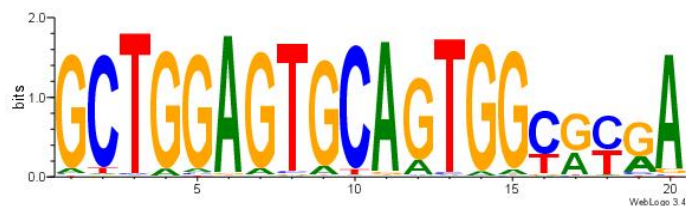


Dataset #: 1
 Motif ID: 3
 Motif name: Motif 3
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 4
 Number of overlap: 14
 Similarity score: 0.0746812

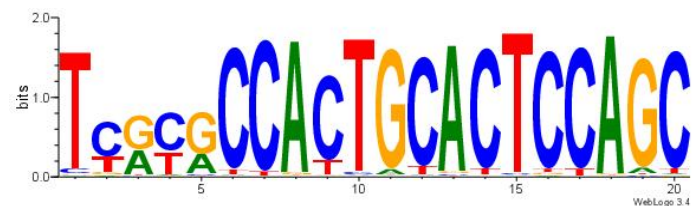
Alignment:

TCKMGCCACTGCACTCCAGC
 ---CCCTACTGTTCTCY---

Original motif Consensus sequence: GCTGGAGTGCAGTGGCRYGA



Reverse complement motif Consensus sequence: TCKMGCCACTGCACTCCAGC



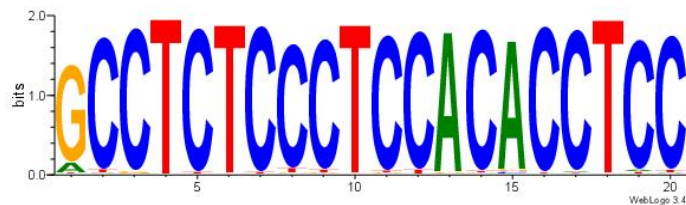
Dataset #: 1

Motif ID: 105
 Motif name: Motif 105
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0.0768892

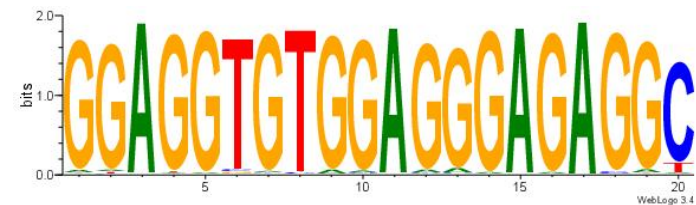
Alignment:

GCCTCTCCCTCCACACCTCC
 -----CCCTACTGTTCTCY

Original motif Consensus sequence: GCCTCTCCCTCCACACCTCC

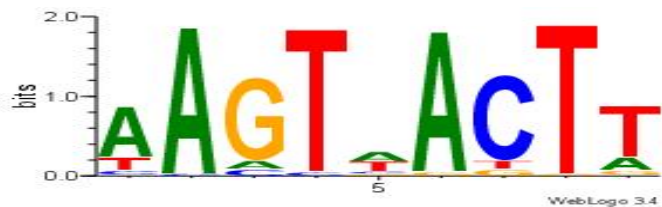


Reverse complement motif Consensus sequence: GGAGGTGTGGAGGGAGAGGC

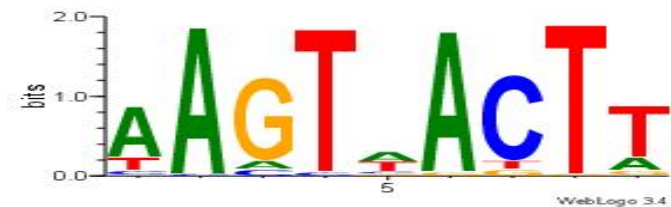


Dataset #: 1 Motif ID: 218 Motif name: Motif 218

Original motif Consensus sequence: AAGTWACTT



Reverse complement motif Consensus sequence: AAGTWACTT



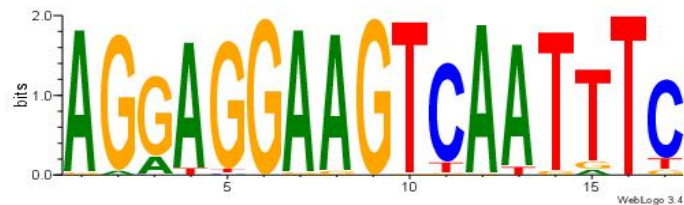
Best Matches for Motif ID 218 (Highest to Lowest)

Dataset #: 1
Motif ID: 327
Motif name: Motif 327
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 7
Number of overlap: 9
Similarity score: 0.0387296

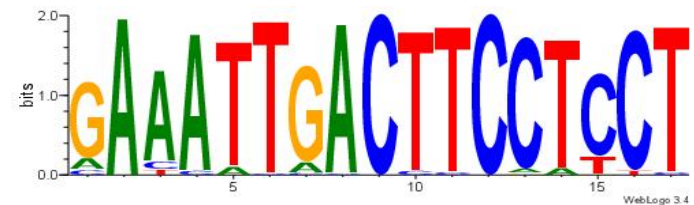
Alignment:

```
GAAATTGACTTCCTCCT  
--AAGTWACTT-----
```

Original motif Consensus sequence: AGGAGGAAGTCAATTC



Reverse complement motif Consensus sequence:
GAAATTGACTTCCTCCT

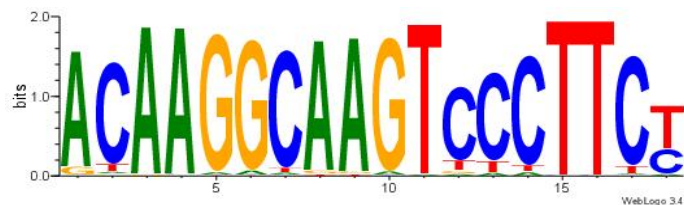


Dataset #: 1
Motif ID: 231
Motif name: Motif 231
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement

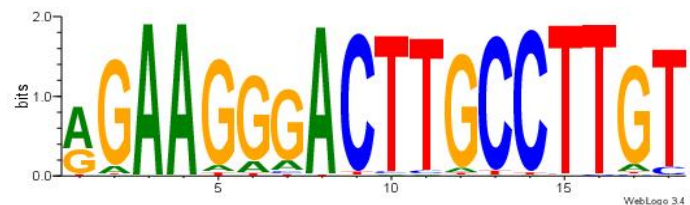
Direction: Backward
 Position number: 8
 Number of overlap: 9
 Similarity score: 0.0394637

Alignment:
 MGAAGGGACTTGCCTTGT
 --AAGTWACTT-----

Original motif Consensus sequence: ACAAGGCAAGTCCCTTCY



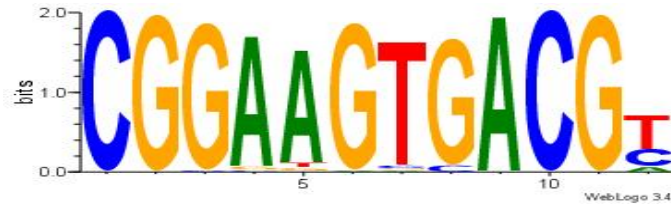
Reverse complement motif Consensus sequence: MGAAGGGACTTGCCTTGT



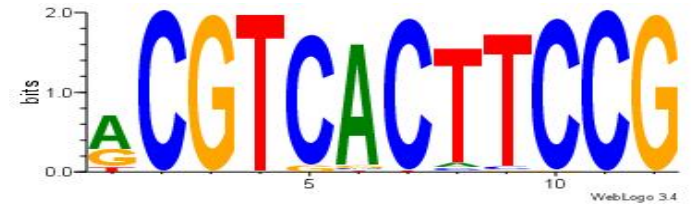
Dataset #: 1
 Motif ID: 316
 Motif name: Motif 316
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 9
 Similarity score: 0.0489965

Alignment:
 ACGTCACTTCCG
 AAGTWACTT---

Original motif Consensus sequence: CGGAAGTGACGT



Reverse complement motif Consensus sequence: ACGTCACTTCCG

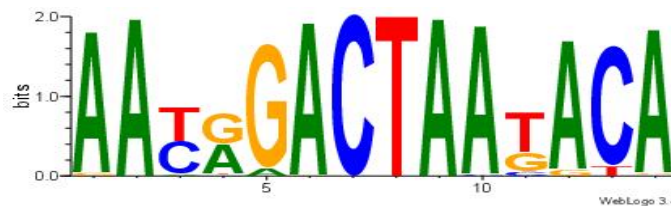


Dataset #: 1
Motif ID: 213
Motif name: Motif 213
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 6
Number of overlap: 9
Similarity score: 0.0574127

Alignment:

TGTATTAGTCMMTT
-----AAGTWACTT

Original motif Consensus sequence: AAYRGACTAATACA



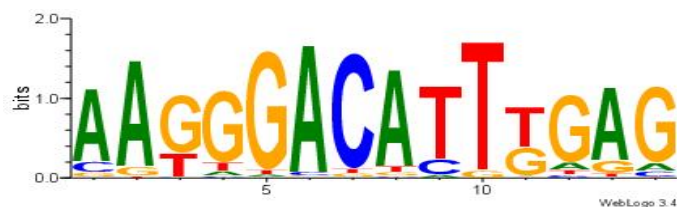
Reverse complement motif Consensus sequence: TGTATTAGTCMMTT



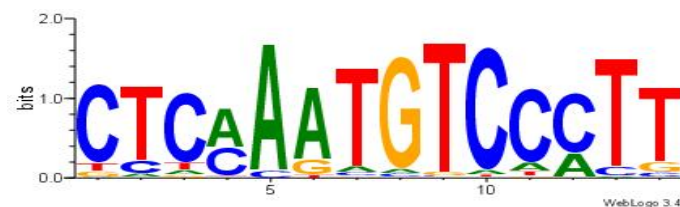
Dataset #: 1
 Motif ID: 166
 Motif name: Motif 166
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 9
 Similarity score: 0.0685527

Alignment:
 CTCRAATGTCCCTT
 AAGTWACTT-----

Original motif Consensus sequence: AAGGGACATTKGAG



Reverse complement motif Consensus sequence: CTCRAATGTCCCTT

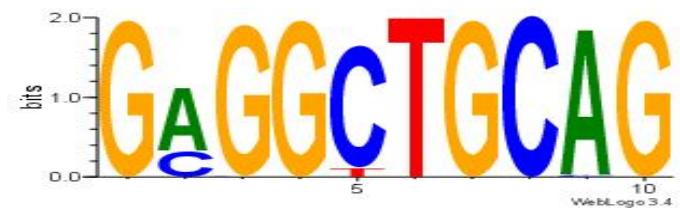


Dataset #: 1 Motif ID: 219 Motif name: Motif 219

Original motif Consensus sequence: CTGCAGCCTC



Reverse complement motif Consensus sequence: GAGGCTGCAG



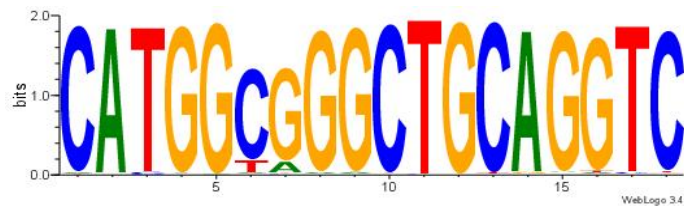
Best Matches for Motif ID 219 (Highest to Lowest)

Dataset #: 1
Motif ID: 68
Motif name: Motif 68
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 4
Number of overlap: 10
Similarity score: 0.0362773

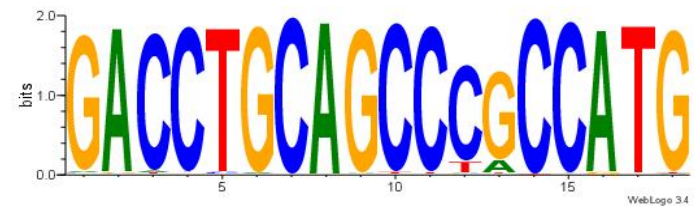
Alignment:

```
GACCTGCAGCCCGCCATG  
-----CTGCAGCCTC----
```

Original motif Consensus sequence: CATGGCGGGCTGCAGGTC



Reverse complement motif Consensus sequence:
GACCTGCAGCCCGCCATG

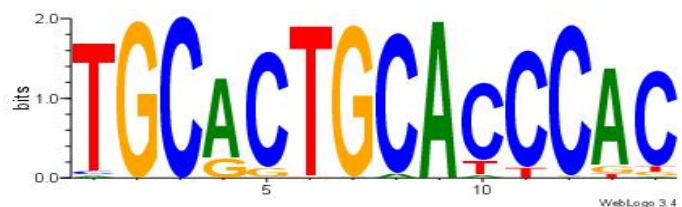


Dataset #: 1
Motif ID: 220
Motif name: Motif 220
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement

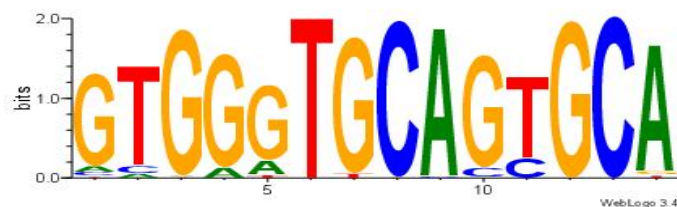
Direction: Forward
 Position number: 1
 Number of overlap: 10
 Similarity score: 0.0471481

Alignment:
 GTGGGTGCAGTGCA
 GAGGCTGCAG-----

Original motif Consensus sequence: TGCACTGCACCCAC



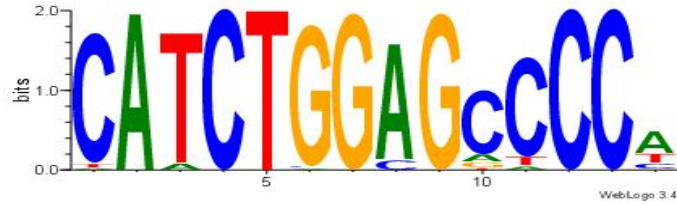
Reverse complement motif Consensus sequence: GTGGGTGCAGTGC



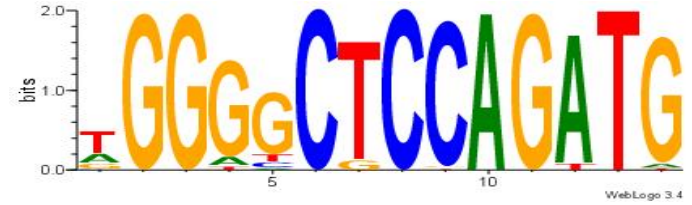
Dataset #: 1
 Motif ID: 320
 Motif name: Motif 320
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 4
 Number of overlap: 10
 Similarity score: 0.0475708

Alignment:
 TGGGGCTCCAGATG
 -GAGGCTGCAG---

Original motif Consensus sequence: CATCTGGAGCCCCA



Reverse complement motif Consensus sequence: TGGGGCTCCAGATG

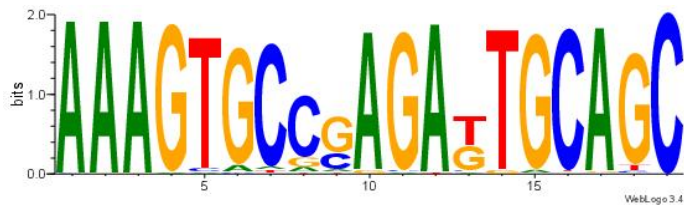


Dataset #: 1
 Motif ID: 191
 Motif name: Motif 191
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 10
 Similarity score: 0.049186

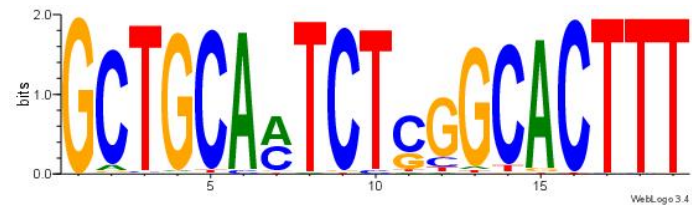
Alignment:

```
AAAGTGCCGAGAKTGCAGC
-GAGGCTGCAG-----
```

Original motif Consensus sequence: AAAGTGCCGAGAKTGCAGC



Reverse complement motif Consensus sequence: GCTGCARTCTCGGCACTTT

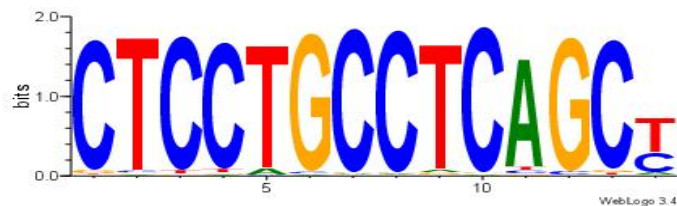


Dataset #: 1
 Motif ID: 313
 Motif name: Motif 313
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 5
 Number of overlap: 10
 Similarity score: 0.0535162

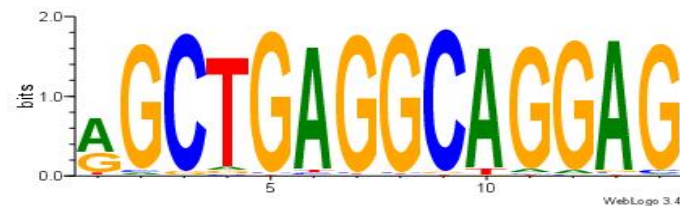
Alignment:

CTCCTGCCTCAGCY
 CTGCAGCCTC-----

Original motif Consensus sequence: CTCCTGCCTCAGCY

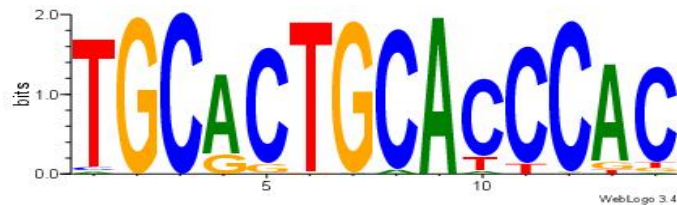


Reverse complement motif Consensus sequence: MGCTGAGGCAGG

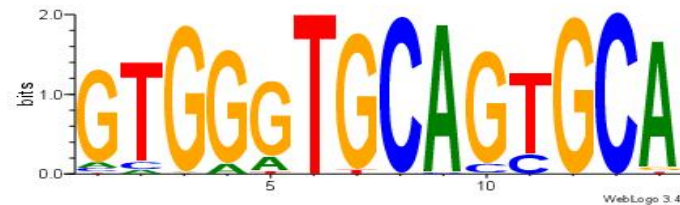


Dataset #: 1 Motif ID: 220 Motif name: Motif 220

Original motif Consensus sequence: TGCACTGCACCCAC



Reverse complement motif Consensus sequence: GTGGGTGCAGTGC



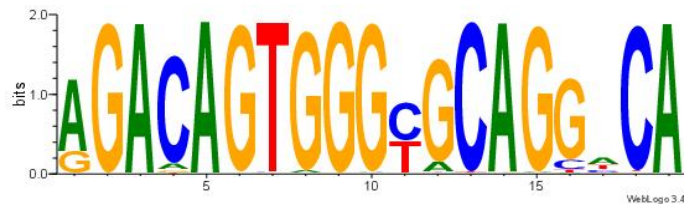
Best Matches for Motif ID 220 (Highest to Lowest)

Dataset #: 1
Motif ID: 17
Motif name: Motif 17
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 14
Similarity score: 0.0478061

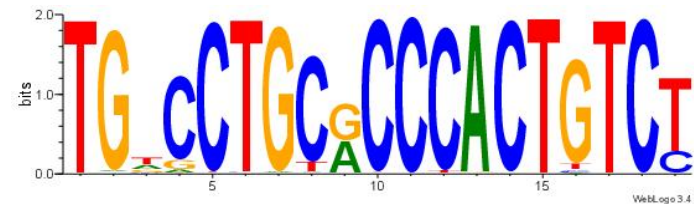
Alignment:

```
TGHCCTGCKCCCCTGTCT  
-----TGCCTGCACCCAC
```

Original motif Consensus sequence: AGACAGTGGGCGCAGGCA



Reverse complement motif Consensus sequence:
TGHCCTGCKCCCCTGTCT

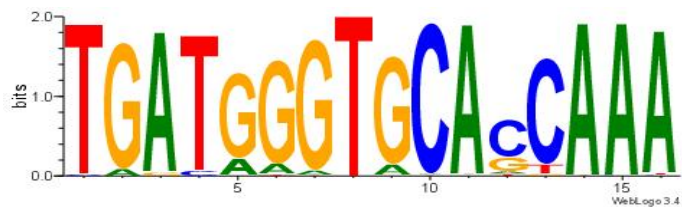


Dataset #: 1
Motif ID: 289
Motif name: Motif 289
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement

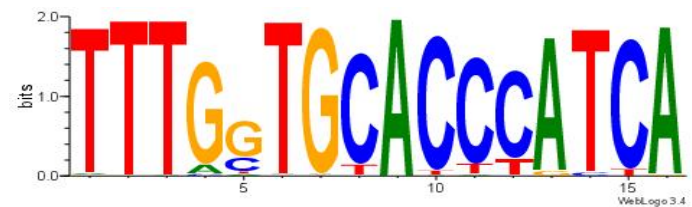
Direction: Backward
 Position number: 3
 Number of overlap: 14
 Similarity score: 0.0840846

Alignment:
 TTTGGTGCACCCATCA
 TGCACTGCACCCAC--

Original motif Consensus sequence: TGATGGGTGCACAAA



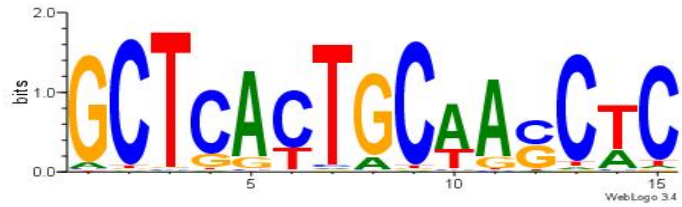
Reverse complement motif Consensus sequence: TTTGGTGCACCCATCA



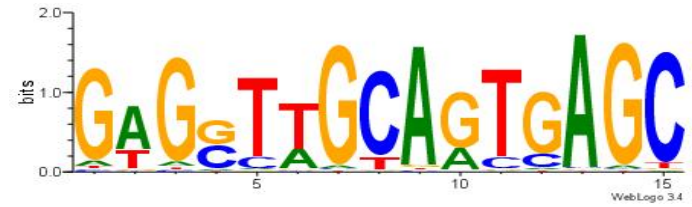
Dataset #: 1
 Motif ID: 6
 Motif name: Motif 6
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 14
 Similarity score: 0.0843879

Alignment:
 GAGSTTGCAGTGAGC
 GTGGGTGCAGTGCA-

Original motif Consensus sequence: GCTCACTGCAASCTC



Reverse complement motif Consensus sequence: GAGSTTGCAGTGA

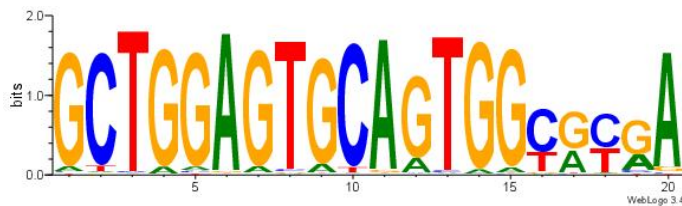


Dataset #: 1
Motif ID: 3
Motif name: Motif 3
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 5
Number of overlap: 14
Similarity score: 0.0884996

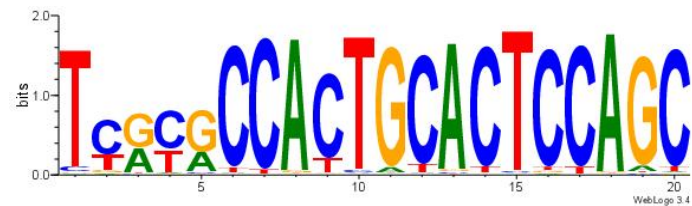
Alignment:

```
GCTGGAGTGCAGTGGCRYGA  
----GTGGGTGCAGTGCA--
```

Original motif Consensus sequence: GCTGGAGTGCAGTGGCRYGA



Reverse complement motif Consensus sequence: TCKMGCCACTGCACTCCAGC

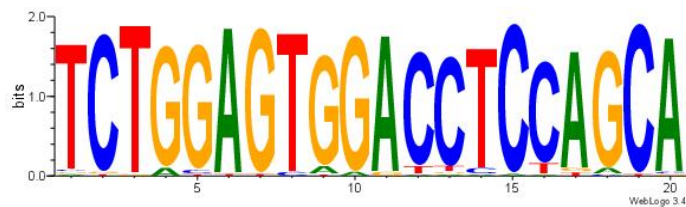


Dataset #: 1
 Motif ID: 350
 Motif name: Motif 350
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 14
 Similarity score: 0.0914277

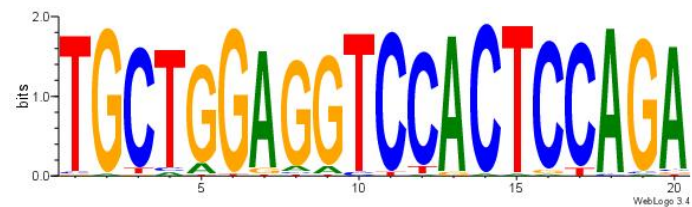
Alignment:

TGCTGGAGGTCCACTCCAGA
 ----GTGGGTGCAGTGCA--

Original motif Consensus sequence: TCTGGAGTGGACCTCCAGCA



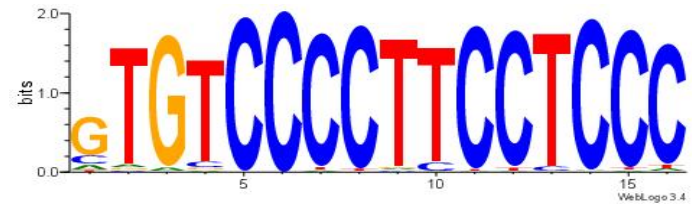
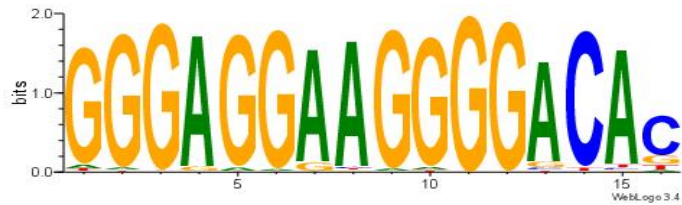
Reverse complement motif Consensus sequence: TGCTGGAGGTCCACTCCAGA



Dataset #: 1 Motif ID: 221 Motif name: Motif 221

Original motif Consensus sequence: GGGAGGAAGGGGACAC

Reverse complement motif Consensus sequence: GTGTCCCCTTCTCCC

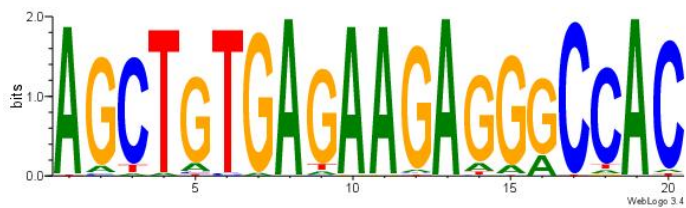


Best Matches for Motif ID 221 (Highest to Lowest)

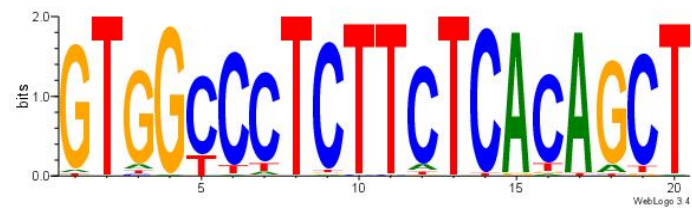
Dataset #: 1
 Motif ID: 294
 Motif name: Motif 294
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 5
 Number of overlap: 16
 Similarity score: 0.0830942

Alignment:
 GTGGCCCTCTTCTCACAGCT
 GTGTCCCCTTCCCTCCC-----

Original motif Consensus sequence: AGCTGTGAGAAGAGGGCCAC



Reverse complement motif Consensus sequence: GTGGCCCTCTTCTCACAGCT

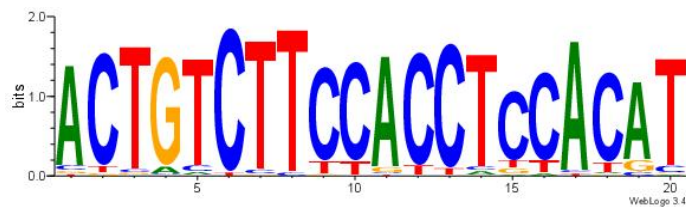


Dataset #: 1
 Motif ID: 178
 Motif name: Motif 178
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 4
 Number of overlap: 16
 Similarity score: 0.0878739

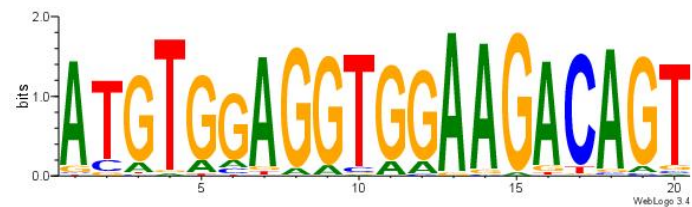
Alignment:

ATGTGGAGGTGGAAGACAGT
 -GGGAGGAAGGGGACAC---

Original motif Consensus sequence: ACTGTCTTCCACCTCCACAT



Reverse complement motif Consensus sequence: ATGTGGAGGTGGAAGACAGT



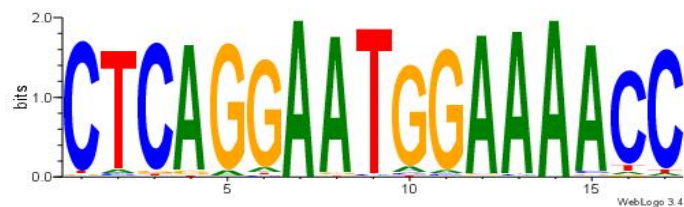
Dataset #: 1
 Motif ID: 214
 Motif name: Motif 214
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1

Number of overlap: 16
Similarity score: 0.0907477

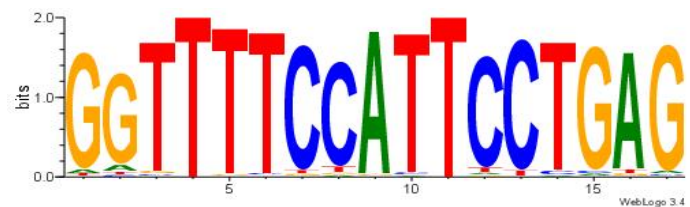
Alignment:

GGTTTTCCATTCTGAG
-GTGTCCCCTTCCTCCC

Original motif Consensus sequence: CTCAGGAATGGAAAACC



Reverse complement motif Consensus sequence: GGTTTTCCATTCTGAG

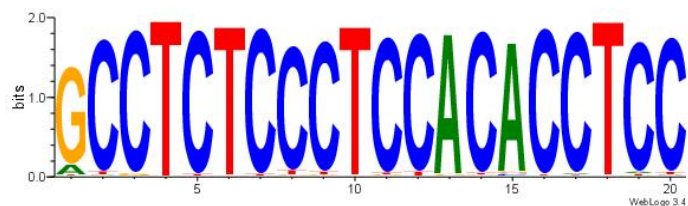


Dataset #: 1
Motif ID: 105
Motif name: Motif 105
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 16
Similarity score: 0.090827

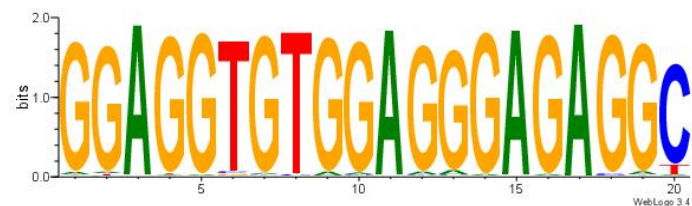
Alignment:

GGAGGTGTGGAGGGAGAGGC
GGGAGGAAGGGGACAC----

Original motif Consensus sequence: GCCTCTCCCTCCACACCTCC



Reverse complement motif Consensus sequence: GGAGGTGTGGAGGGAGAGGC

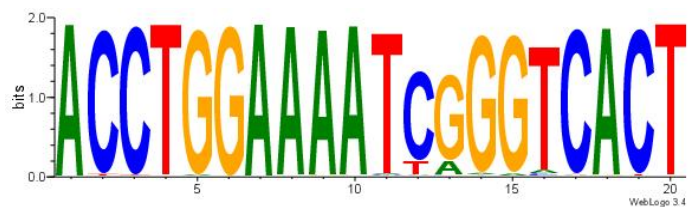


Dataset #: 1
Motif ID: 14
Motif name: Motif 14
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 4
Number of overlap: 16
Similarity score: 0.0917203

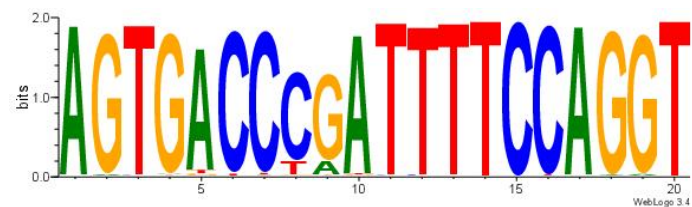
Alignment:

ACCTGGAAAATCGGGTCACT
---GGGAGGAAGGGGACAC-

Original motif Consensus sequence: ACCTGGAAAATCGGGTCACT

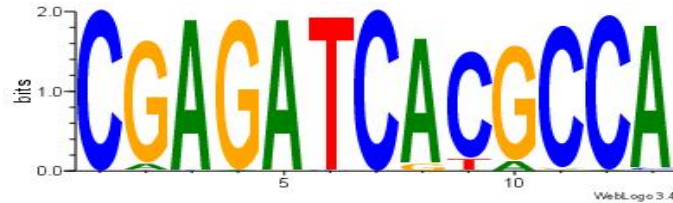


Reverse complement motif Consensus sequence: AGTGACCCGATTTTCCAGGT

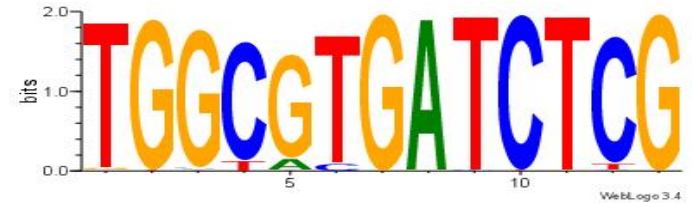


Dataset #: 1 Motif ID: 222 Motif name: Motif 222

Original motif Consensus sequence: CGAGATCACGCCA



Reverse complement motif Consensus sequence: TGGCGTGATCTCG



Best Matches for Motif ID 222 (Highest to Lowest)

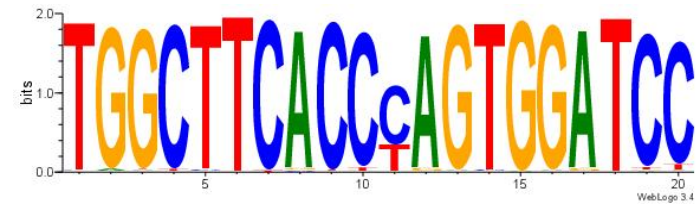
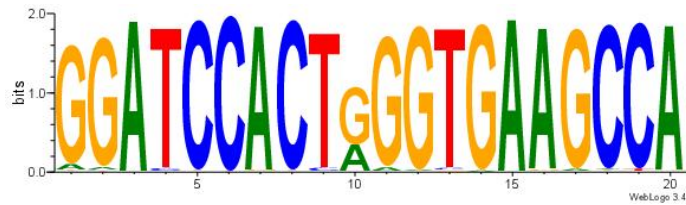
Dataset #:	1
Motif ID:	61
Motif name:	Motif 61
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	8
Number of overlap:	13
Similarity score:	0.0800547

Alignment:

```
GGATCCACTGGGTGAAGCCA  
-----CGAGATCACGCCA
```

Original motif Consensus sequence: GGATCCACTGGGTGAAGCCA

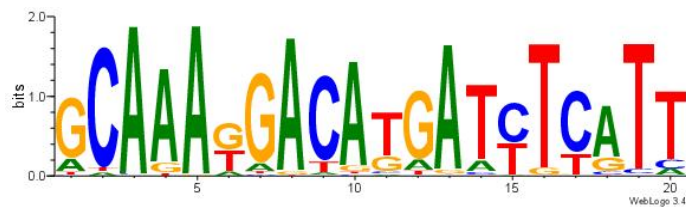
Reverse complement motif Consensus sequence:
TGGCTTCACCCAGTGGATCC



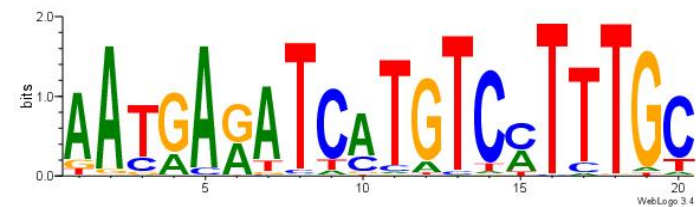
Dataset #: 1
 Motif ID: 99
 Motif name: Motif 99
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 13
 Similarity score: 0.0816199

Alignment:
 AATGAKATCATGTCYTTTGC
 -----CGAGATCACGCCA--

Original motif Consensus sequence: GCAAAGACATGATYTCATT



Reverse complement motif Consensus sequence: AATGAKATCATGTCYTTTGC



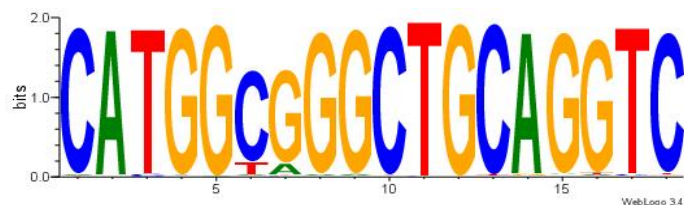
Dataset #: 1

Motif ID: 68
 Motif name: Motif 68
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3
 Number of overlap: 13
 Similarity score: 0.0858328

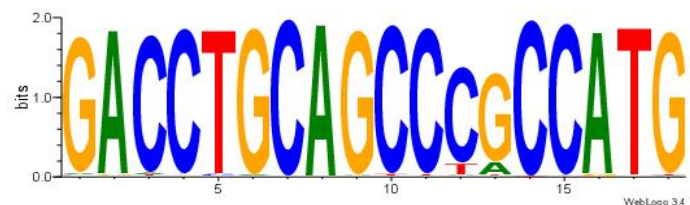
Alignment:

GACCTGCAGCCCGCCATG
 --CGAGATCACGCCA---

Original motif Consensus sequence: CATGGCGGGCTGCAGGTC



Reverse complement motif Consensus sequence: GACCTGCAGCCCGCCATG



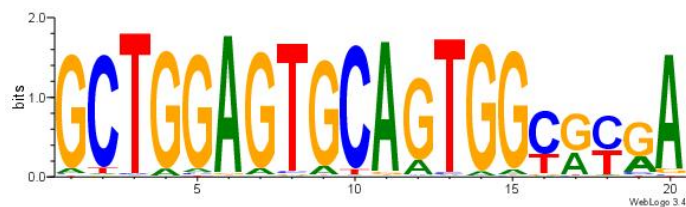
Dataset #: 1
 Motif ID: 3
 Motif name: Motif 3
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 6
 Number of overlap: 13

Similarity score: 0.0874221

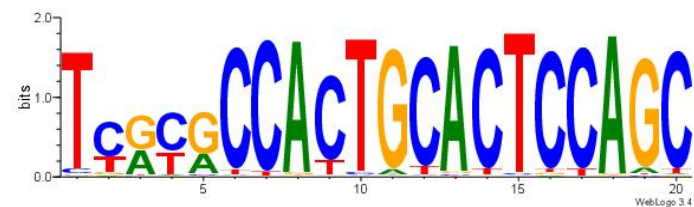
Alignment:

TCKMGCCACTGCACTCCAGC
--CGAGATCACGCCA-----

Original motif Consensus sequence: GCTGGAGTGCAGTGGCRYGA



Reverse complement motif Consensus sequence:
TCKMGCCACTGCACTCCAGC



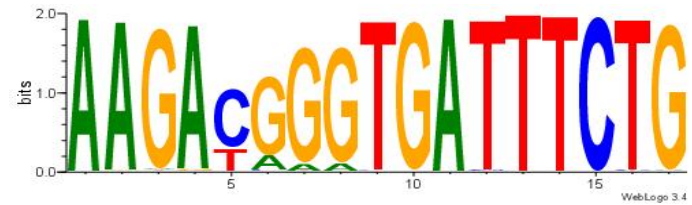
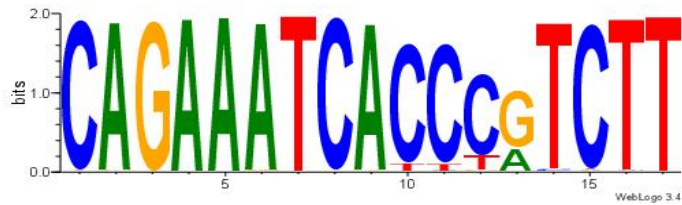
Dataset #: 1
Motif ID: 35
Motif name: Motif 35
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 4
Number of overlap: 13
Similarity score: 0.0876684

Alignment:

AAGACGGGTGATTTCTG
---TGGCGTGATCTCG-

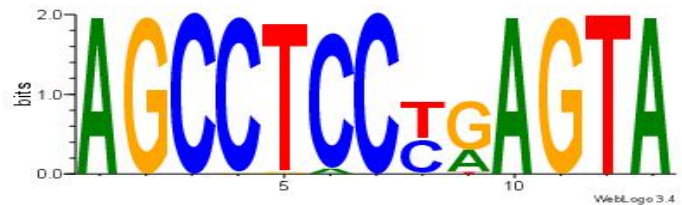
Original motif Consensus sequence: CAGAAATCACCCGTCTT

Reverse complement motif Consensus sequence:
AAGACGGGTGATTTCTG

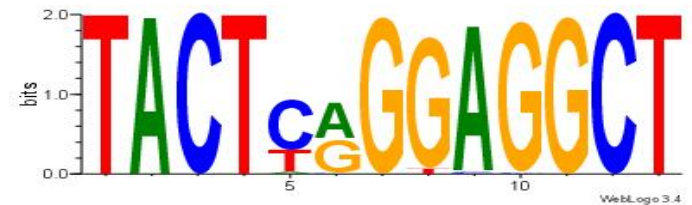


Dataset #: 1 Motif ID: 223 Motif name: Motif 223

Original motif Consensus sequence: AGCCTCCYGAGTA



Reverse complement motif Consensus sequence: TACTCMGGAGGCT

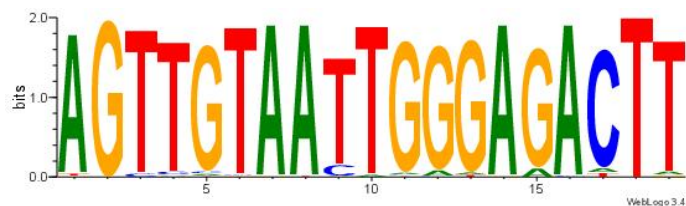


Best Matches for Motif ID 223 (Highest to Lowest)

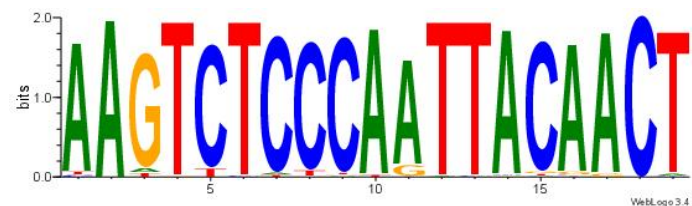
Dataset #:	1
Motif ID:	232
Motif name:	Motif 232
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	2
Number of overlap:	13
Similarity score:	0.0672113

Alignment:
AAGTCTCCCAATTACA ACT
-AGCCTCCYGAGTA-----

Original motif Consensus sequence: AGTTGTAATTGGGAGACTT



Reverse complement motif Consensus sequence: AAGTCTCCCAATTACAAC

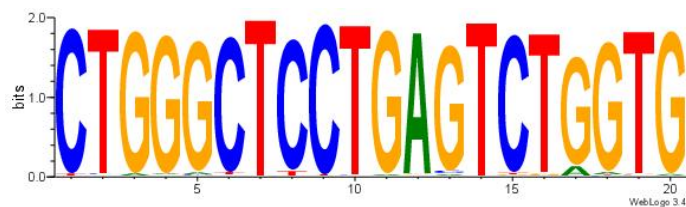


Dataset #: 1
Motif ID: 67
Motif name: Motif 67
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 6
Number of overlap: 13
Similarity score: 0.075298

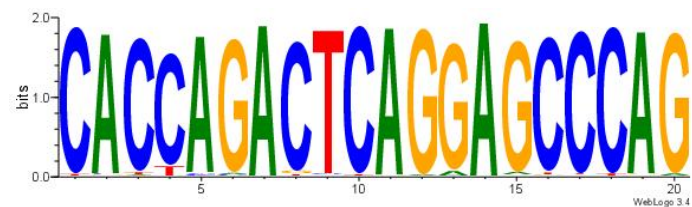
Alignment:

```
CTGGGCTCCTGAGTCTGGTG  
--AGCCTCCYGAGTA-----
```

Original motif Consensus sequence: CTGGGCTCCTGAGTCTGGTG



Reverse complement motif Consensus sequence: CACCAGACTCAGGAGCCCAG

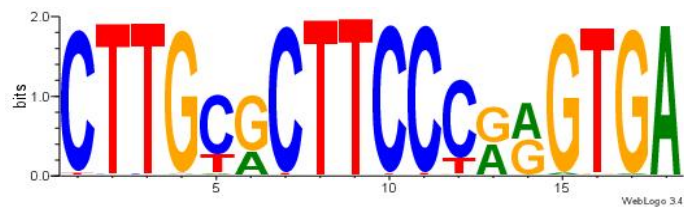


Dataset #: 1
 Motif ID: 15
 Motif name: Motif 15
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 5
 Number of overlap: 13
 Similarity score: 0.0838744

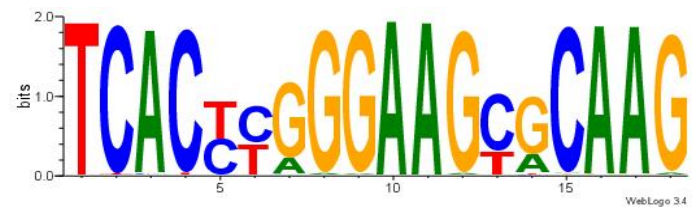
Alignment:

CTTGCGCTTCCCRRGTGA
 ----AGCCTCCYGAGTA-

Original motif Consensus sequence: CTTGCGCTTCCCRRGTGA



Reverse complement motif Consensus sequence: TCACKMGGGAAGCGCAAG

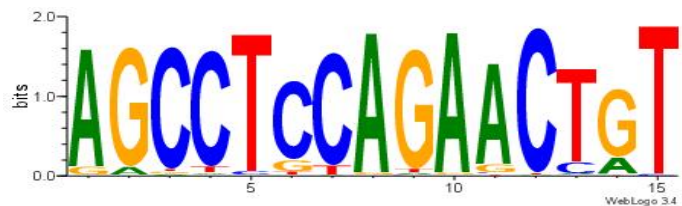


Dataset #: 1
 Motif ID: 239
 Motif name: Motif 239
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3

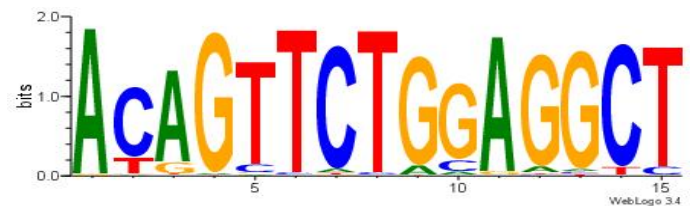
Number of overlap: 13
Similarity score: 0.0898433

Alignment:
AGCCTCCAGAACTGT
AGCCTCCYGAGTA--

Original motif Consensus sequence: AGCCTCCAGAACTGT



Reverse complement motif Consensus sequence: ACAGTTCTGGAGG

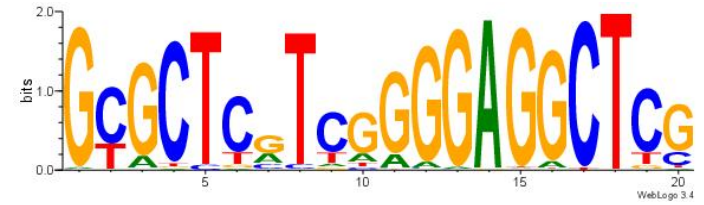
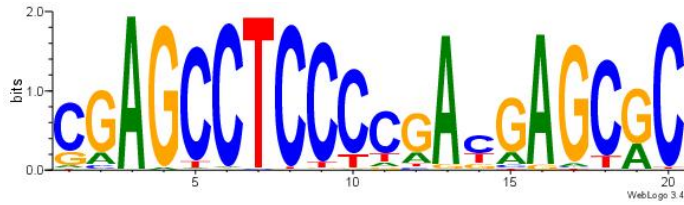


Dataset #: 1
Motif ID: 108
Motif name: Motif 108
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 3
Number of overlap: 13
Similarity score: 0.0907206

Alignment:
CGAGCCTCCCCGAYGAGCGC
--AGCCTCCYGAGTA-----

Original motif Consensus sequence: CGAGCCTCCCCGAYGAGCGC

Reverse complement motif Consensus sequence:
GCGCTCKTCGGGGAGGCTCG

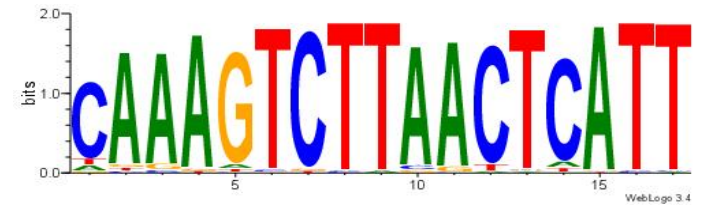


Dataset #: 1 Motif ID: 224 Motif name: Motif 224

Original motif Consensus sequence: AATGAGTTAAGACTTTG



Reverse complement motif Consensus sequence: CAAAGTCTTAACTCATT



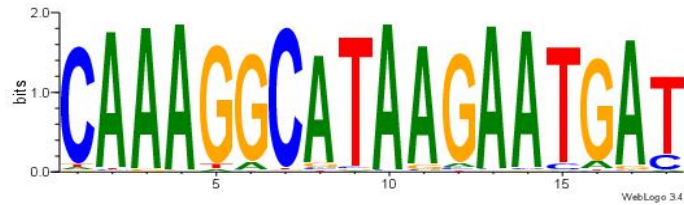
Best Matches for Motif ID 224 (Highest to Lowest)

Dataset #:	1
Motif ID:	190
Motif name:	Motif 190
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	17
Similarity score:	0.10346

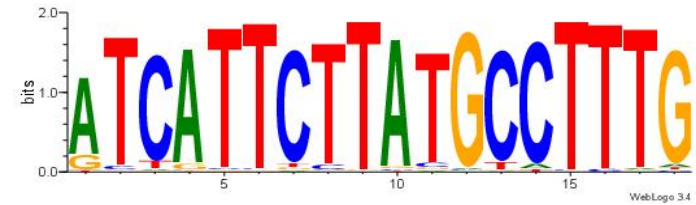
Alignment:

ATCATTCTTATGCCTTTG
CAAAGTCTTAACTCATT-

Original motif Consensus sequence: CAAAGGCATAAGAATGAT



Reverse complement motif Consensus sequence:
ATCATTCTTATGCCTTTG

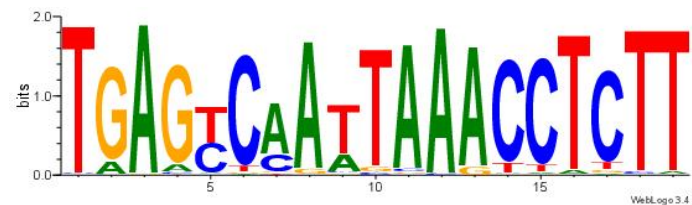
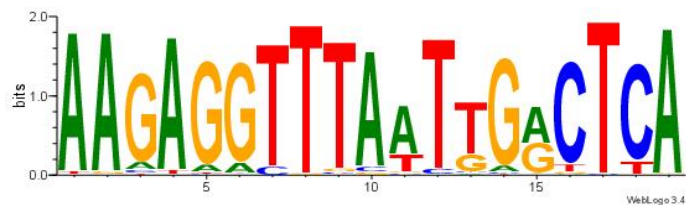


Dataset #: 1
Motif ID: 129
Motif name: Motif 129
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 17
Similarity score: 0.103511

Alignment:
TGAGKCAATTAAACCTCTT
AATGAGTTAAGACTTTG--

Original motif Consensus sequence: AAGAGTTTAATTGRCTCA

Reverse complement motif Consensus sequence:
TGAGKCAATTAAACCTCTT



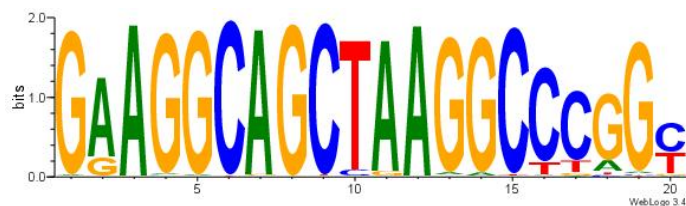
Dataset #: 1
 Motif ID: 64
 Motif name: Motif 64
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 17
 Similarity score: 0.105466

Alignment:

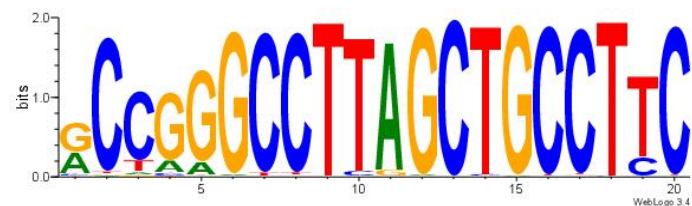
```

GAAGGCAGCTAAGGCCGGY
--AATGAGTTAAGACTTTG-
  
```

Original motif Consensus sequence: GAAGGCAGCTAAGGCCGGY



Reverse complement motif Consensus sequence: KCCGGGCCCTTAGCTGCCCTC



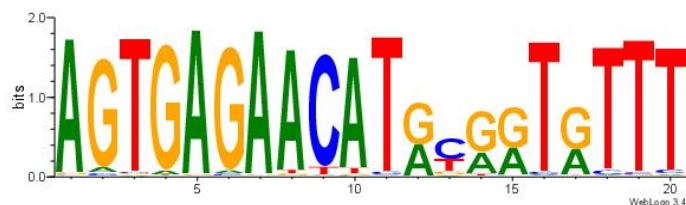
Dataset #: 1

Motif ID: 63
 Motif name: Motif 63
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 4
 Number of overlap: 17
 Similarity score: 0.107183

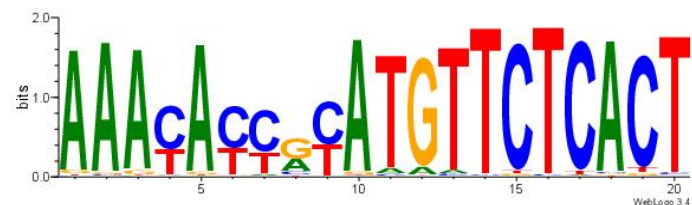
Alignment:

AAAMAMMKMATGTTCTCACT
 ---CAAAGTCTTAACTCATT

Original motif Consensus sequence: AGTGAGAACATRYRRTTTT



Reverse complement motif Consensus sequence: AAAMAMMKMATGTTCTCACT



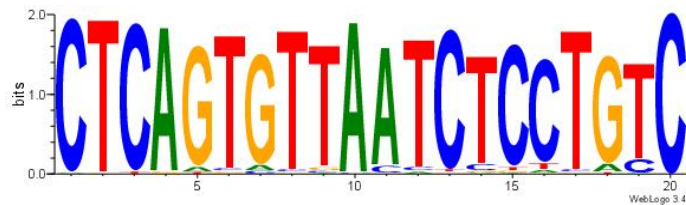
Dataset #: 1
 Motif ID: 262
 Motif name: Motif 262
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 17

Similarity score: 0.107753

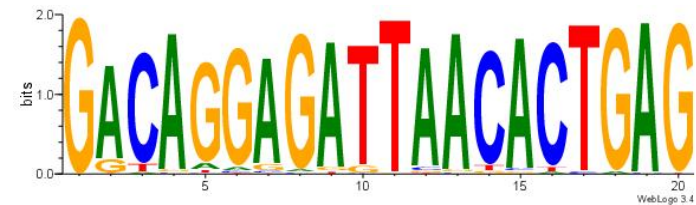
Alignment:

CTCAGTGTTAATCTCCTGTC
CAAAGTCTTAACTCATT---

Original motif Consensus sequence: CTCAGTGTTAATCTCCTGTC

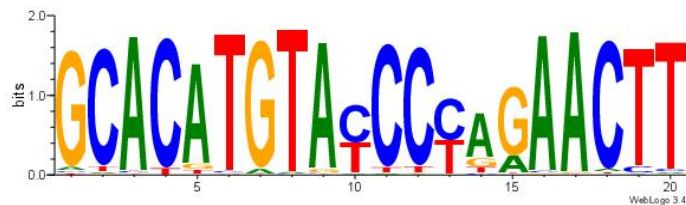


Reverse complement motif Consensus sequence: GACAGGAGATTAACACTGAG

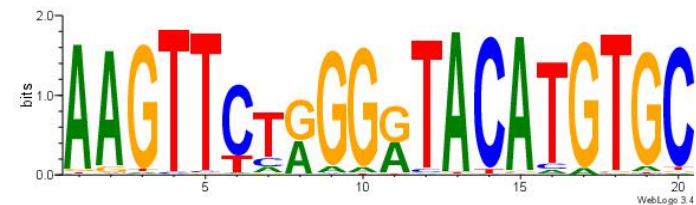


Dataset #: 1 Motif ID: 225 Motif name: Motif 225

Original motif Consensus sequence: GCACATGTAYCCYAGAACTT



Reverse complement motif Consensus sequence: AAGTTCTKGGKTACATGTGC



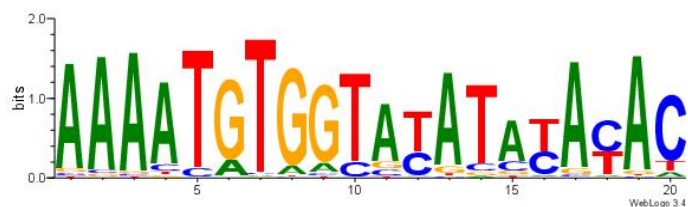
Best Matches for Motif ID 225 (Highest to Lowest)

Dataset #:	1
Motif ID:	83
Motif name:	Motif 83
Matching format of first motif:	Reverse Complement

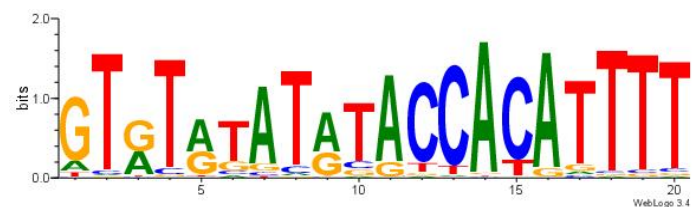
Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.113312

Alignment:
 AAAATGTGGTAYATAYAYAC
 AAGTTCTKGGKTACATGTGC

Original motif Consensus sequence: AAAATGTGGTAYATAYAYAC



Reverse complement motif Consensus sequence: GTKTMTATMTACCACATTTT

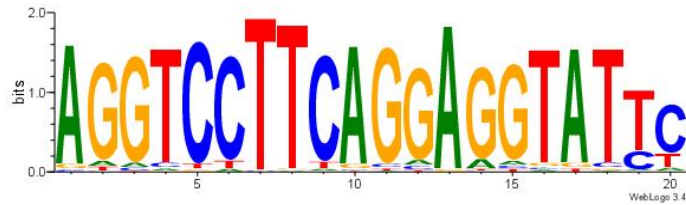


Dataset #: 1
 Motif ID: 179
 Motif name: Motif 179
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.118212

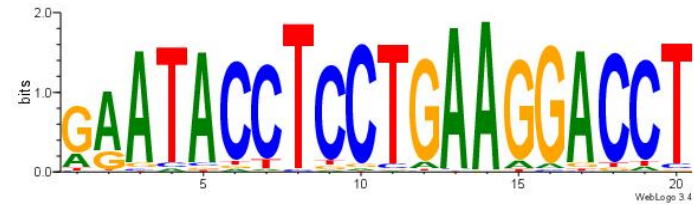
Alignment:

GAATACCTCCTGAAGGACCT
GCACATGTAYCCYAGAACTT

Original motif Consensus sequence: AGGTCCTTCAGGAGGTATTC



Reverse complement motif Consensus sequence:
GAATACCTCCTGAAGGACCT



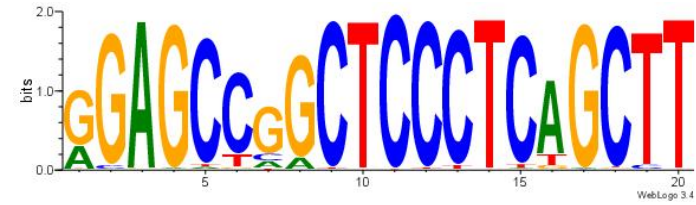
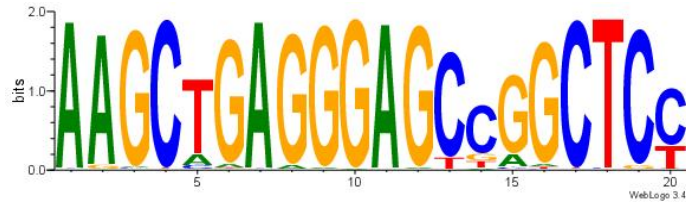
Dataset #:	1
Motif ID:	96
Motif name:	Motif 96
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	20
Similarity score:	0.120502

Alignment:

AAGCTGAGGGAGCCGGCTCC
AAGTTCTKGGKTACATGTGC

Original motif Consensus sequence: AAGCTGAGGGAGCCGGCTCC

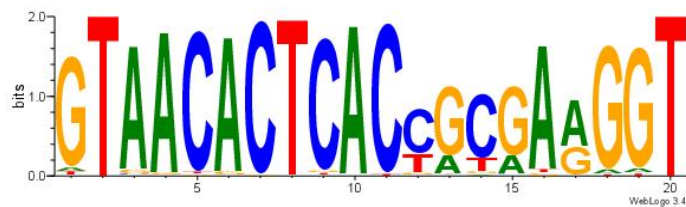
Reverse complement motif Consensus sequence:
GGAGCCGGCTCCCTCAGCTT



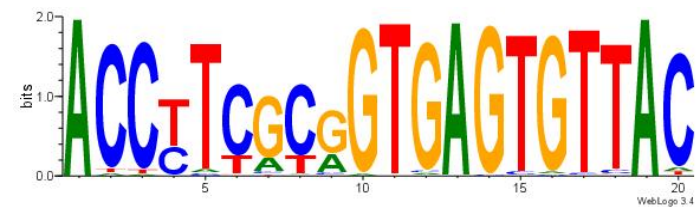
Dataset #: 1
 Motif ID: 201
 Motif name: Motif 201
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.123085

Alignment:
 ACCKTCGCGGTGAGTGTTAC
 AAGTTCTKGGKTACATGTGC

Original motif Consensus sequence: GTAACACTCACCgCGARGGT



Reverse complement motif Consensus sequence: ACCKTCGCGGTGAGTGTTAC



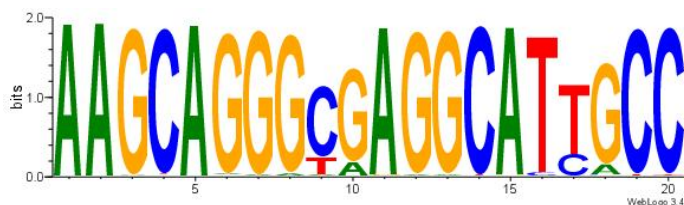
Dataset #: 1

Motif ID: 13
 Motif name: Motif 13
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.125642

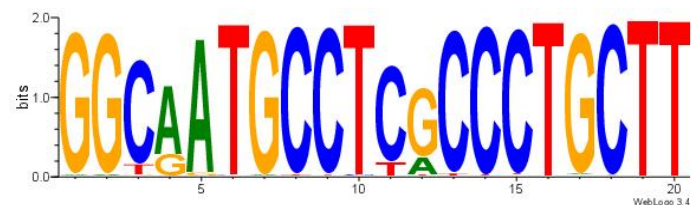
Alignment:

AAGCAGGGCGAGGCATTGCC
 AAGTTCTKGGKTACATGTGC

Original motif Consensus sequence: AAGCAGGGCGAGGCATTGCC

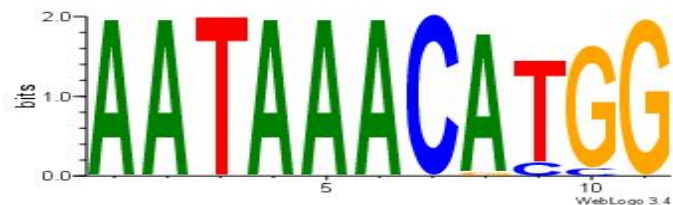


Reverse complement motif Consensus sequence: GGCAATGCCTCGCCCTGCTT

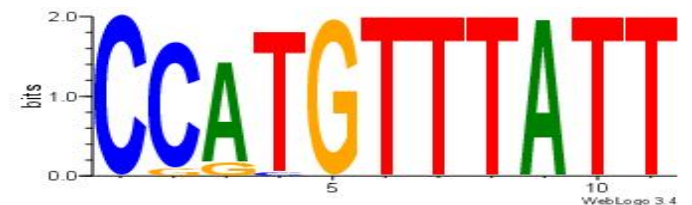


Dataset #: 1 Motif ID: 226 Motif name: Motif 226

Original motif Consensus sequence: AATAACATGG



Reverse complement motif Consensus sequence: CCATGTTTATT



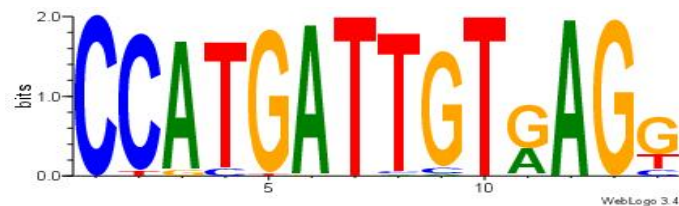
Best Matches for Motif ID 226 (Highest to Lowest)

Dataset #: 1
Motif ID: 270
Motif name: Motif 270
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 11
Similarity score: 0.0612696

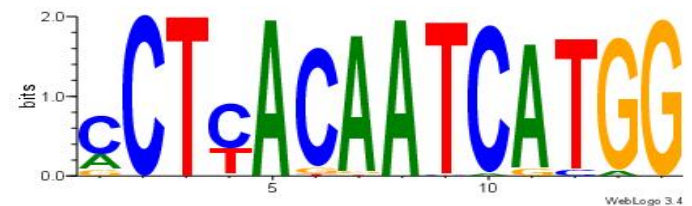
Alignment:

```
CCTMACAATCATGG  
---AATAACATGG
```

Original motif Consensus sequence: CCATGATTGTRAGG



Reverse complement motif Consensus sequence: CCTMACAATCATGG



Dataset #: 1
Motif ID: 252
Motif name: Motif 252
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement

Direction: Forward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.0671681

Alignment:
 CCMKGCTAATT
 CCATGTTTATT

Original motif Consensus sequence: AATTAGCYRGG



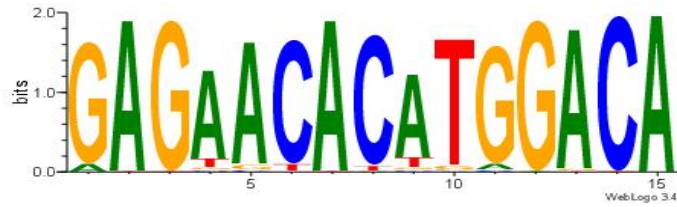
Reverse complement motif Consensus sequence: CCMKGCTAATT



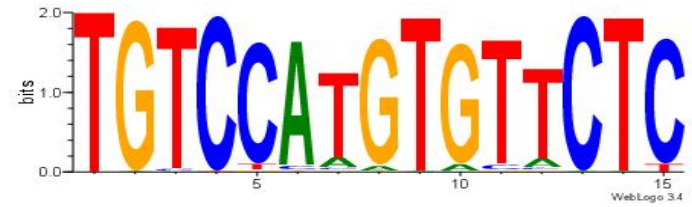
Dataset #: 1
 Motif ID: 257
 Motif name: Motif 257
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 11
 Similarity score: 0.0686983

Alignment:
 TGTCCATGTGTTCTC
 ---CCATGTTTATT-

Original motif Consensus sequence: GAGAACACATGGACA



Reverse complement motif Consensus sequence: TGCCATGTGTTCTC

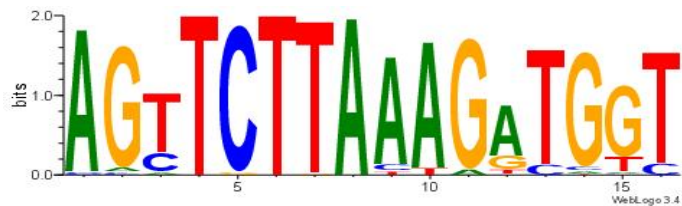


Dataset #: 1
Motif ID: 303
Motif name: Motif 303
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2
Number of overlap: 11
Similarity score: 0.0776401

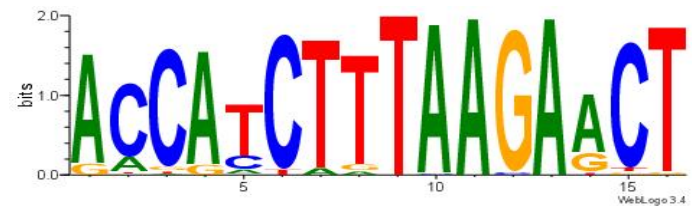
Alignment:

AGTTCTTAAAGATGGT
----AATAACATGG--

Original motif Consensus sequence: AGTTCTTAAAGATGGT



Reverse complement motif Consensus sequence: ACCATCTTAAAGAACT

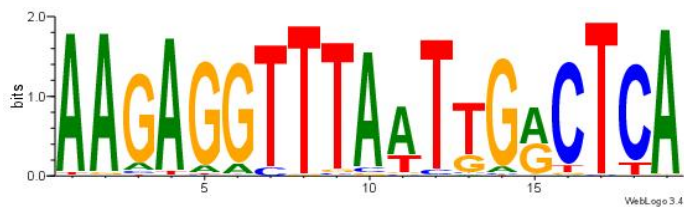


Dataset #: 1
 Motif ID: 129
 Motif name: Motif 129
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 8
 Number of overlap: 11
 Similarity score: 0.0862085

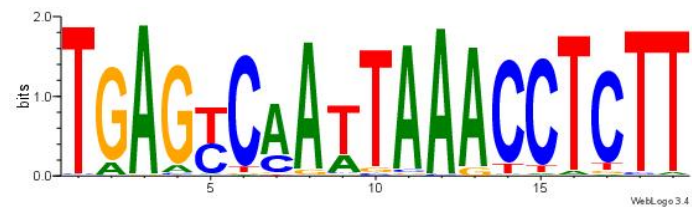
Alignment:

AAGAGGTTTAATTGRCTCA
 -----CCATGTTTATT-

Original motif Consensus sequence: AAGAGGTTTAATTGRCTCA



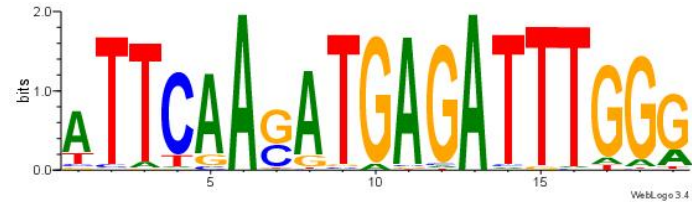
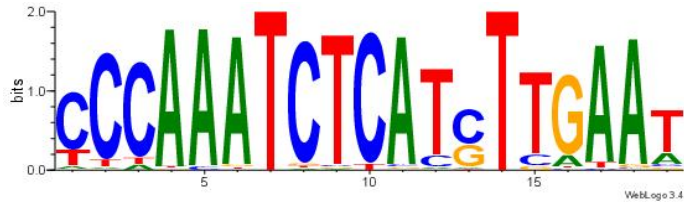
Reverse complement motif Consensus sequence: TGAGKCAATTAACCTCTT



Dataset #: 1 Motif ID: 227 Motif name: Motif 227

Original motif Consensus sequence: CCCAATCTCATSTTGAAT

Reverse complement motif Consensus sequence: ATCAASATGAGATTTGGG

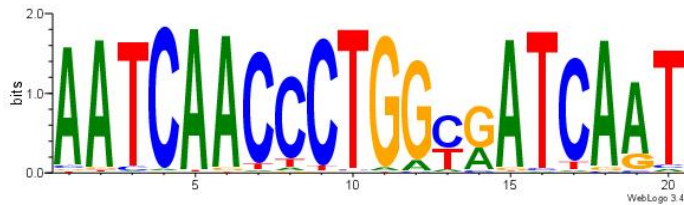


Best Matches for Motif ID 227 (Highest to Lowest)

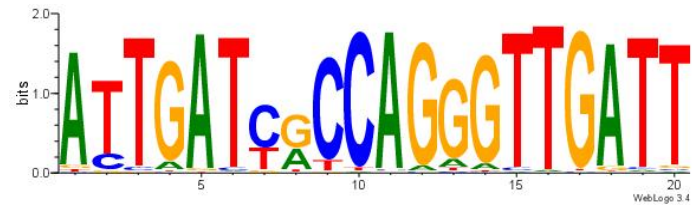
Dataset #: 1
 Motif ID: 170
 Motif name: Motif 170
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 19
 Similarity score: 0.103606

Alignment:
 AATCAACCCTGGYRATCAAT
 -CCCAAATCTCATSTTGAAT

Original motif Consensus sequence: AATCAACCCTGGYRATCAAT



Reverse complement motif Consensus sequence: ATTGATMKCCAGGGTTGATT

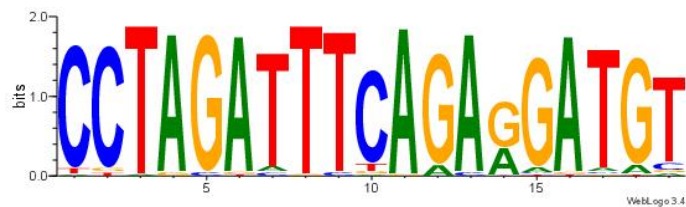


Dataset #: 1
 Motif ID: 280
 Motif name: Motif 280
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 19
 Similarity score: 0.107017

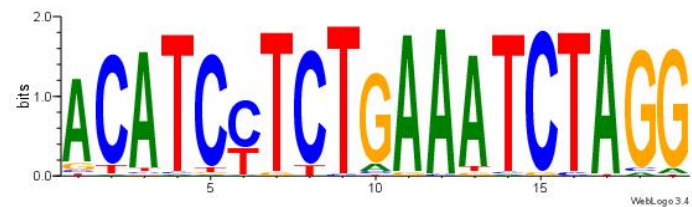
Alignment:

ACATCMTCTGAAATCTAGG
 ATTCAASATGAGATTTGGG

Original motif Consensus sequence: CCTAGATTTcAGAGGATGT



Reverse complement motif Consensus sequence: ACATCMTCTGAAATCTAGG



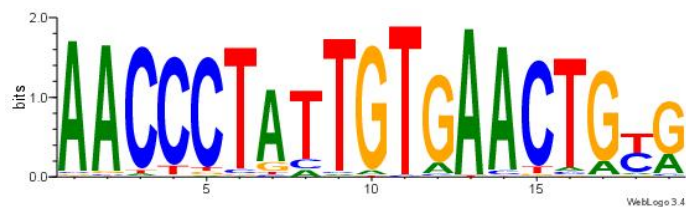
Dataset #: 1
 Motif ID: 242
 Motif name: Motif 242
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1

Number of overlap: 19
Similarity score: 0.108656

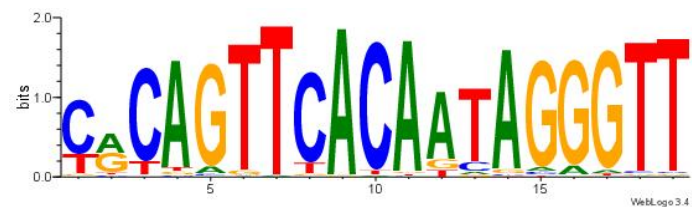
Alignment:

CMCAGTTCACAATAGGGTT
CCCAAATCTCATSTTGAAT

Original motif Consensus sequence: AACCTATTGTGAACTGYG



Reverse complement motif Consensus sequence:
CMCAGTTCACAATAGGGTT

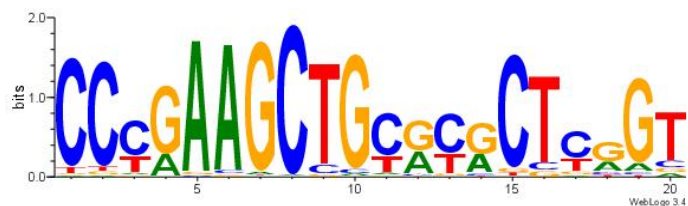


Dataset #: 1
Motif ID: 177
Motif name: Motif 177
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 19
Similarity score: 0.10976

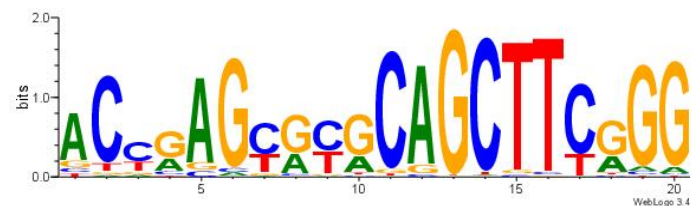
Alignment:

ACCGAGMKMGCAGCTTCGGG
-ATTCAASATGAGATTTGGG

Original motif Consensus sequence: CCCGAAGCTGCRYRCTCGGT



Reverse complement motif Consensus sequence: ACCGAGMKMGCAGCTTCGGG

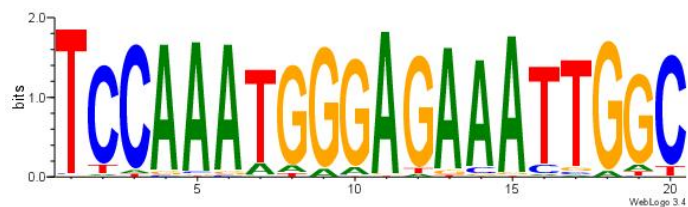


Dataset #: 1
Motif ID: 235
Motif name: Motif 235
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2
Number of overlap: 19
Similarity score: 0.110263

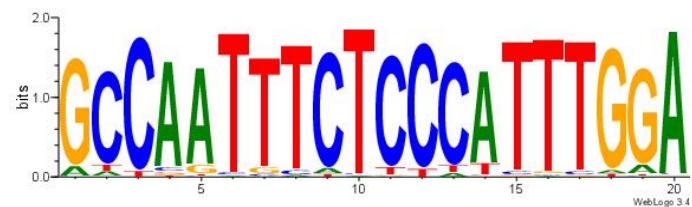
Alignment:

TCCAAATGGGAGAAATTGGC
ATTCAASATGAGATTTGGG-

Original motif Consensus sequence: TCCAAATGGGAGAAATTGGC

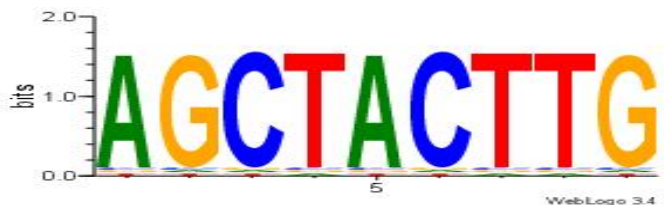


Reverse complement motif Consensus sequence: GCCAATTTCTCCCATTTGGA



Dataset #: 1 Motif ID: 228 Motif name: Motif 228

Original motif Consensus sequence: AGCTACTTG



Reverse complement motif Consensus sequence: CAAGTAGCT



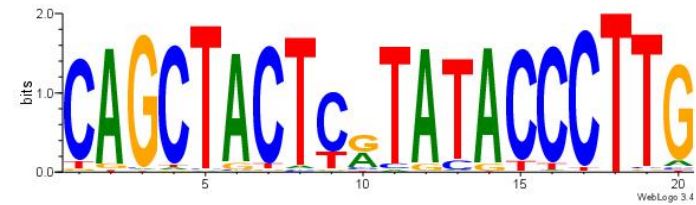
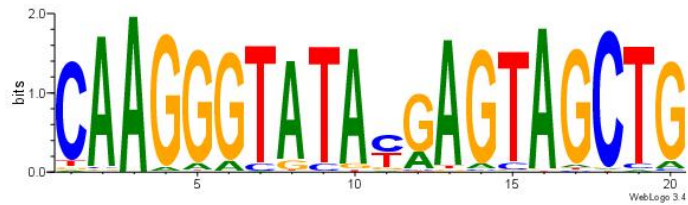
Best Matches for Motif ID 228 (Highest to Lowest)

Dataset #:	1
Motif ID:	194
Motif name:	Motif 194
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	11
Number of overlap:	9
Similarity score:	0.0385506

Alignment:
CAGCTACTCKTATACCCTTG
-----AGCTACTTG-

Original motif Consensus sequence: CAAGGGTATAYGAGTAGCTG

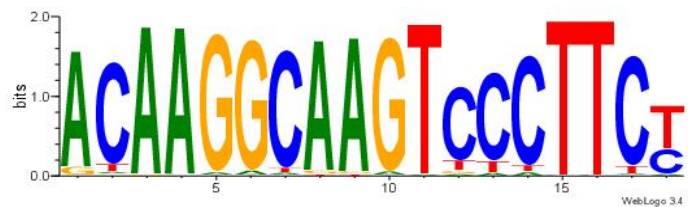
Reverse complement motif Consensus sequence:
CAGCTACTCKTATACCCTTG



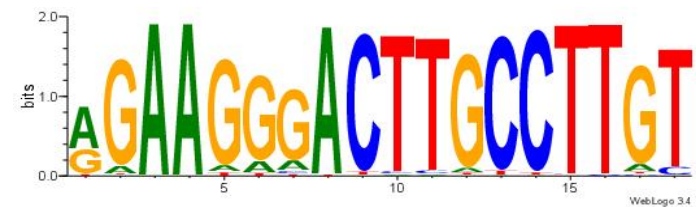
Dataset #: 1
 Motif ID: 231
 Motif name: Motif 231
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 4
 Number of overlap: 9
 Similarity score: 0.0563554

Alignment:
 MGAAGGGACTTGCCTTGT
 ---AGCTACTTG-----

Original motif Consensus sequence: ACAAGGCAAGTCCCTTCY



Reverse complement motif Consensus sequence: MGAAGGGACTTGCCTTGT



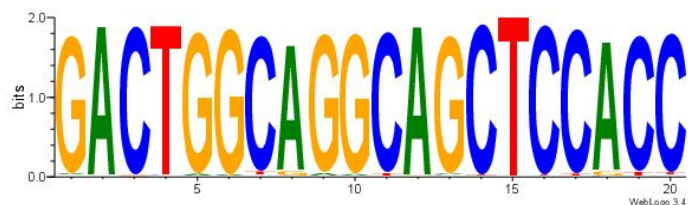
Dataset #: 1

Motif ID: 52
 Motif name: Motif 52
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 7
 Number of overlap: 9
 Similarity score: 0.0620324

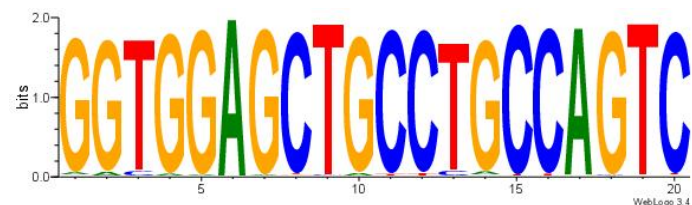
Alignment:

GGTGGAGCTGCCTGCCAGTC
 -----AGCTACTTG-----

Original motif Consensus sequence: GACTGGCAGGCAGCTCCACC



Reverse complement motif Consensus sequence: GGTGGAGCTGCCTGCCAGTC

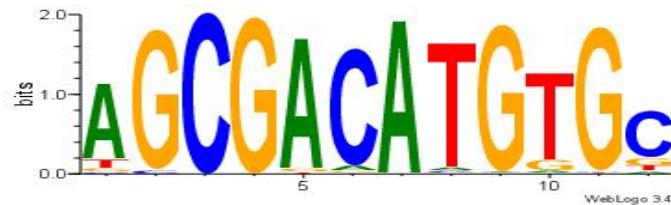


Dataset #: 1
 Motif ID: 269
 Motif name: Motif 269
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 4
 Number of overlap: 9

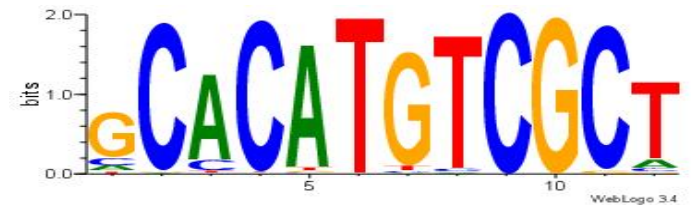
Similarity score: 0.0633451

Alignment:
AGCGACATGTGC
AGCTACTTG---

Original motif Consensus sequence: AGCGACATGTGC



Reverse complement motif Consensus sequence: GCACATGTCGCT

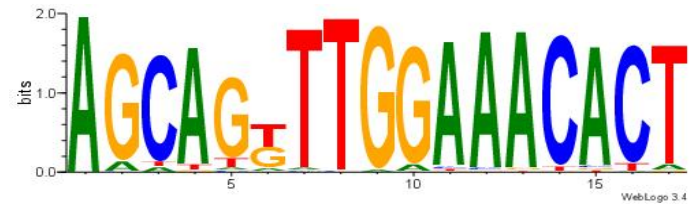
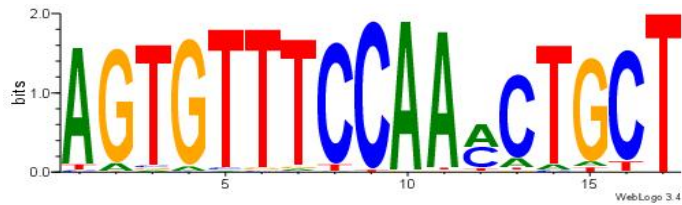


Dataset #: 1
Motif ID: 304
Motif name: Motif 304
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 9
Number of overlap: 9
Similarity score: 0.0713836

Alignment:
AGCAGYTTGGAAACACT
AGCTACTTG-----

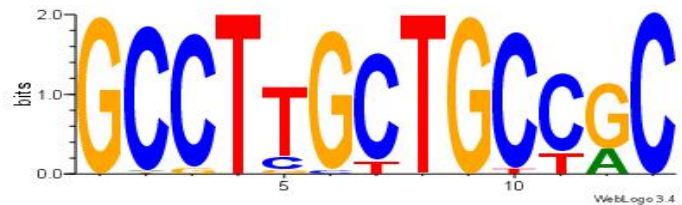
Original motif Consensus sequence: AGTGTTCCTCAAMCTGCT

Reverse complement motif Consensus sequence:
AGCAGYTTGGAAACACT

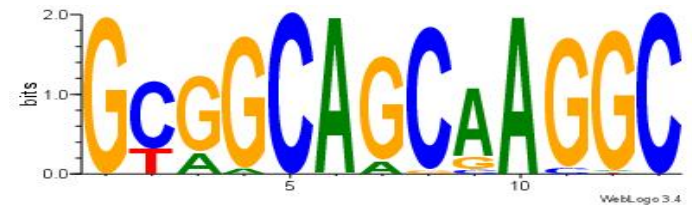


Dataset #: 1 Motif ID: 229 Motif name: Motif 229

Original motif Consensus sequence: GCCTTGCTGCCGC



Reverse complement motif Consensus sequence: GCGGCAGCAAGGC

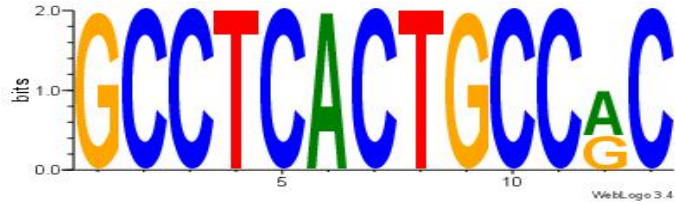


Best Matches for Motif ID 229 (Highest to Lowest)

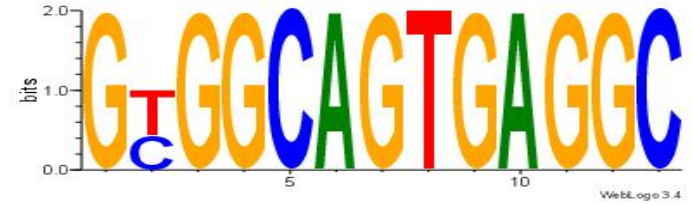
Dataset #:	1
Motif ID:	247
Motif name:	Motif 247
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	13
Similarity score:	0.0380597

Alignment:
 GCCTCACTGCCRC
 GCCTTGCTGCCGC

Original motif Consensus sequence: GCCTCACTGCCRC



Reverse complement motif Consensus sequence: GKGGCAGTGAGG

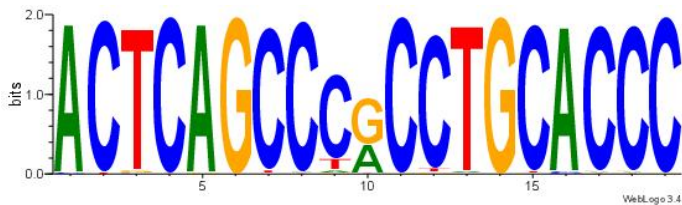


Dataset #: 1
Motif ID: 149
Motif name: Motif 149
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 6
Number of overlap: 13
Similarity score: 0.0728792

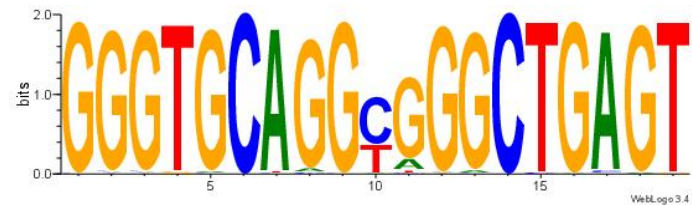
Alignment:

```
GGGTGCAGGMGGGCTGAGT  
-GCGGCAGCAAGGC-----
```

Original motif Consensus sequence: ACTCAGCCRCCTGCACCC



Reverse complement motif Consensus sequence: GGGTGCAGGMGGGCTGAGT

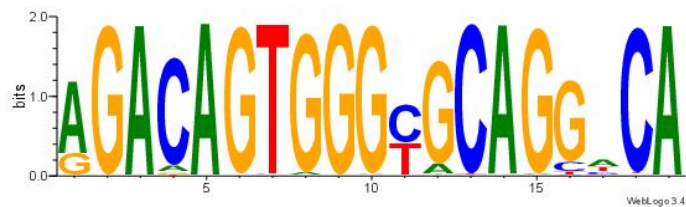


Dataset #: 1
 Motif ID: 17
 Motif name: Motif 17
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 6
 Number of overlap: 13
 Similarity score: 0.0799361

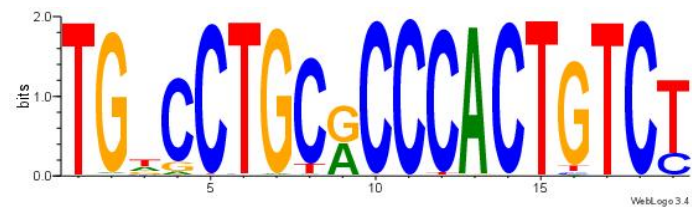
Alignment:

AGACAGTGGGYGCAGGHCA
 -GCGGCAGCAAGGC-----

Original motif Consensus sequence: AGACAGTGGGYGCAGGHCA



Reverse complement motif Consensus sequence: TGHCCTGCKCCCACTGTCT



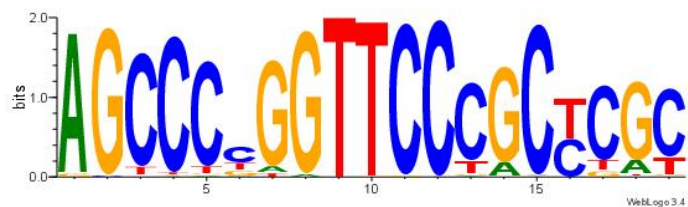
Dataset #: 1
 Motif ID: 164
 Motif name: Motif 164
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 5

Number of overlap: 13
Similarity score: 0.0833059

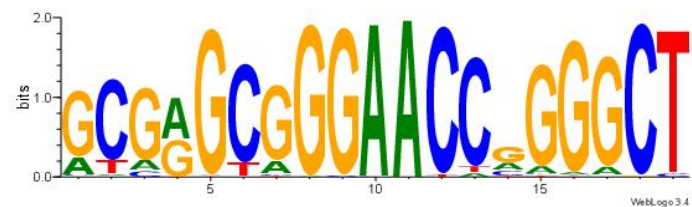
Alignment:

AGCCCCGGTTCCCGCYCGC
--GCCTTGCTGCCGC-----

Original motif Consensus sequence: AGCCCCGGTTCCCGCYCGC



Reverse complement motif Consensus sequence:
GCGMGCGGGAACCGGGGCT

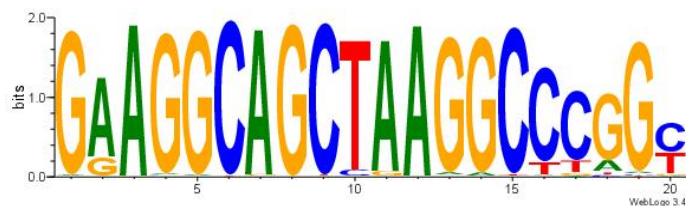


Dataset #: 1
Motif ID: 64
Motif name: Motif 64
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 2
Number of overlap: 13
Similarity score: 0.0835602

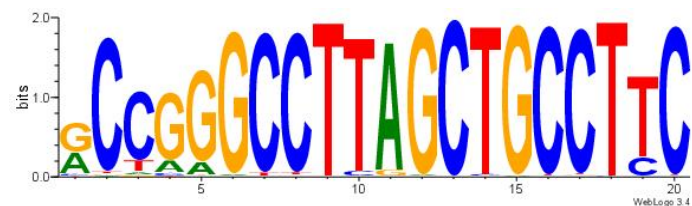
Alignment:

KCCGGGCCTTAGCTGCCTTC
-GCCTTGCTGCCGC-----

Original motif Consensus sequence: GAAGGCAGCTAAGGCCGGY

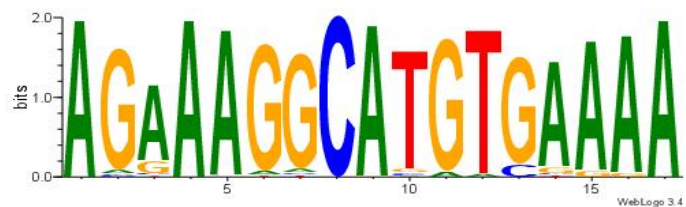


Reverse complement motif Consensus sequence: KCCGGGCCTTAGCTGCCTTC

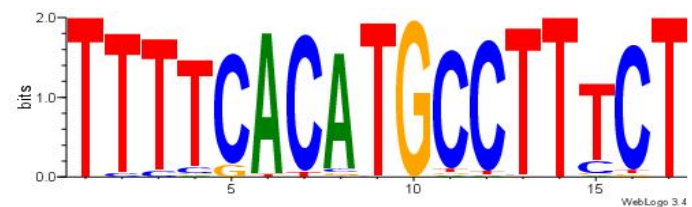


Dataset #: 1 Motif ID: 230 Motif name: Motif 230

Original motif Consensus sequence: AGAAAGGCATGTGAAAA



Reverse complement motif Consensus sequence: TTTTCACATGCCTTCT



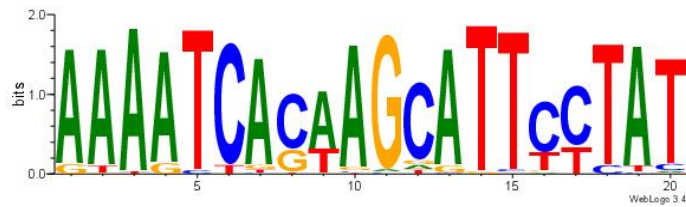
Best Matches for Motif ID 230 (Highest to Lowest)

Dataset #:	1
Motif ID:	254
Motif name:	Motif 254
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	17
Similarity score:	0.093628

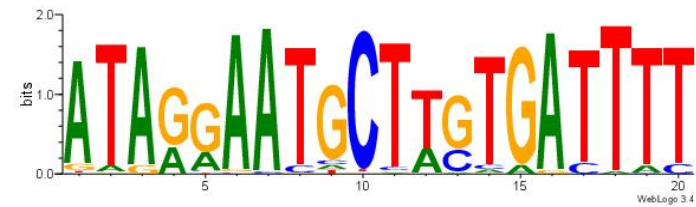
Alignment:

AAAATCACAAGCATTCTAT
-TTTTACATGCCTTTCT--

Original motif Consensus sequence: AAAATCACAAGCATTCTAT



Reverse complement motif Consensus sequence:
ATAGGAATGCTTGTGATTTT



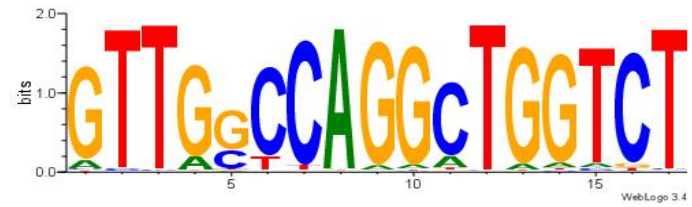
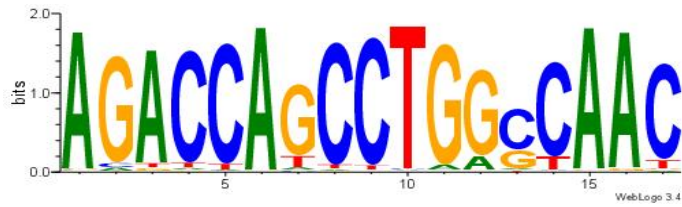
Dataset #: 1
Motif ID: 12
Motif name: Motif 12
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 17
Similarity score: 0.102426

Alignment:

GTTGGCCAGGCTGGTCT
TTTTACATGCCTTTCT

Original motif Consensus sequence: AGACCAGCCTGGCCAAC

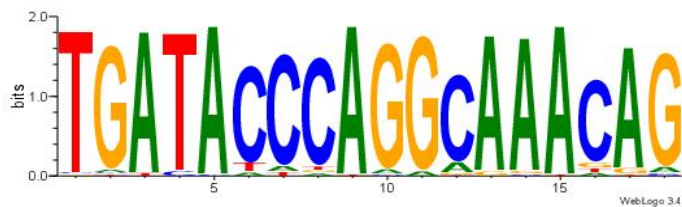
Reverse complement motif Consensus sequence:
GTTGGCCAGGCTGGTCT



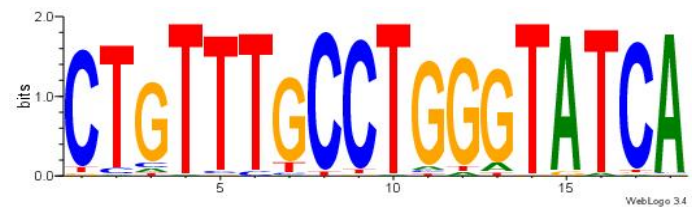
Dataset #: 1
 Motif ID: 290
 Motif name: Motif 290
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 17
 Similarity score: 0.110581

Alignment:
 CTGTTTGCCTGGGTATCA
 -TTTTACATGCCTTTCT

Original motif Consensus sequence: TGATACCCAGGCAAACAG



Reverse complement motif Consensus sequence: CTGTTTGCCTGGGTATCA



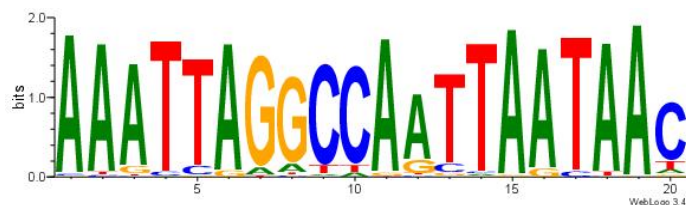
Dataset #: 1

Motif ID: 308
 Motif name: Motif 308
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 17
 Similarity score: 0.11099

Alignment:

GTTATTAATTGGCCTAATTT
 -TTTTCACATGCCTTTCT--

Original motif Consensus sequence: AAATTAGGCCAATTAATAAC



Reverse complement motif Consensus sequence: GTTATTAATTGGCCTAATTT



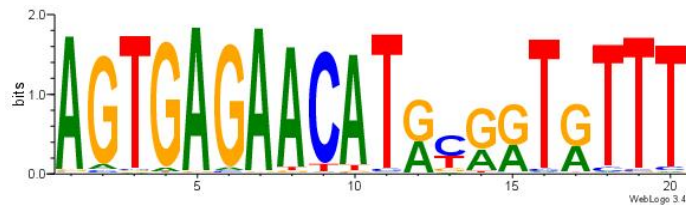
Dataset #: 1
 Motif ID: 63
 Motif name: Motif 63
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 17

Similarity score: 0.111345

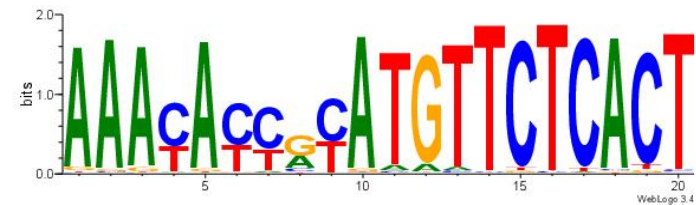
Alignment:

```
AGTGAGAACATRYRRTRTTT  
-TTTTACATGCCTTTCT--
```

Original motif Consensus sequence: AGTGAGAACATRYRRTRTTT

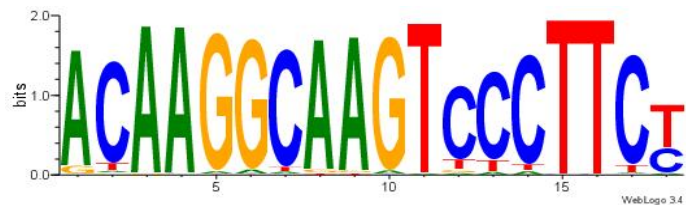


Reverse complement motif Consensus sequence: AAAMAMMKMATGTTCTCACT

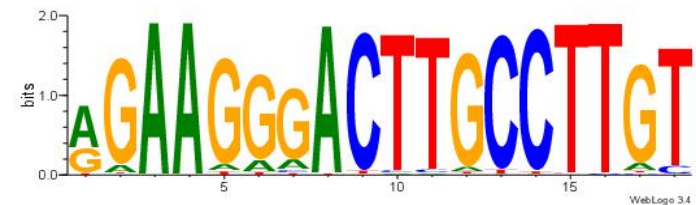


Dataset #: 1 Motif ID: 231 Motif name: Motif 231

Original motif Consensus sequence: ACAAGGCAAGTcccTTC



Reverse complement motif Consensus sequence: MGAAGGACTTGCCTTGT



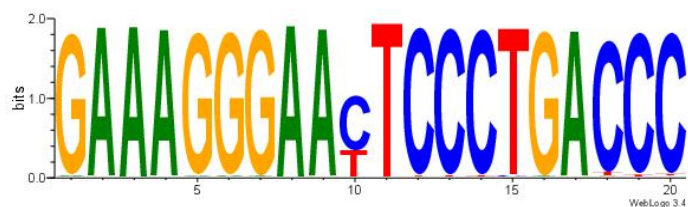
Best Matches for Motif ID 231 (Highest to Lowest)

Dataset #:	1
Motif ID:	16
Motif name:	Motif 16
Matching format of first motif:	Original Motif

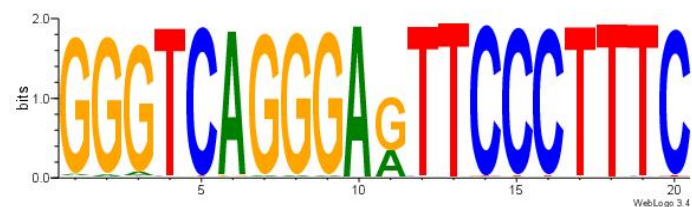
Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 18
 Similarity score: 0.0860131

Alignment:
 GAAAGGGA ACTCCCTGACCC
 ACAAGGCAAGTCCCTTCY--

Original motif Consensus sequence: GAAAGGGA ACTCCCTGACCC



Reverse complement motif Consensus sequence:
 GGGTCAGG GAGTCCCTTTC

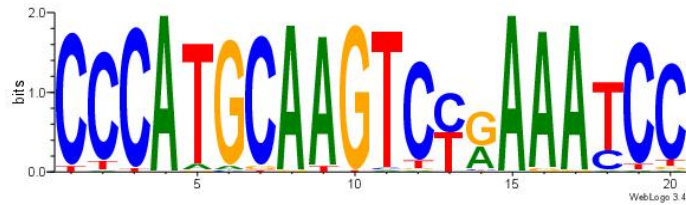


Dataset #: 1
 Motif ID: 310
 Motif name: Motif 310
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 18
 Similarity score: 0.0932717

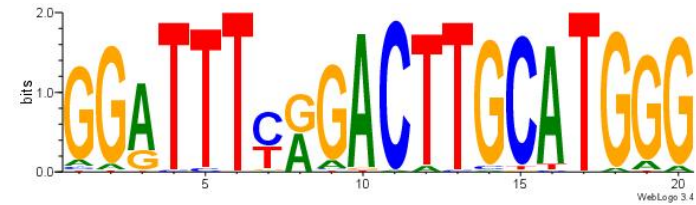
Alignment:

GGATTTMKGACTTGCATGGG
--MGAAGGGACTTGCCTTGT

Original motif Consensus sequence: CCCATGCAAGTCYRAAATCC



Reverse complement motif Consensus sequence:
GGATTTMKGACTTGCATGGG

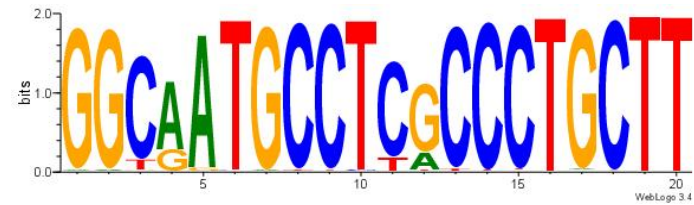
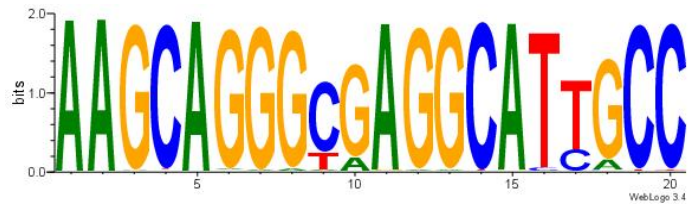


Dataset #: 1
Motif ID: 13
Motif name: Motif 13
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2
Number of overlap: 18
Similarity score: 0.0987599

Alignment:
AAGCAGGGCGAGGCATTGCC
-MGAAGGGACTTGCCTTGT-

Original motif Consensus sequence: AAGCAGGGCGAGGCATTGCC

Reverse complement motif Consensus sequence:
GGCAATGCCTCGCCCTGCTT



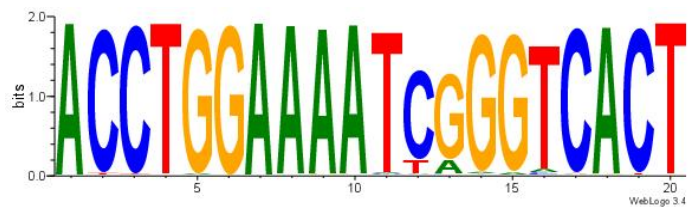
Dataset #: 1
 Motif ID: 14
 Motif name: Motif 14
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 18
 Similarity score: 0.103588

Alignment:

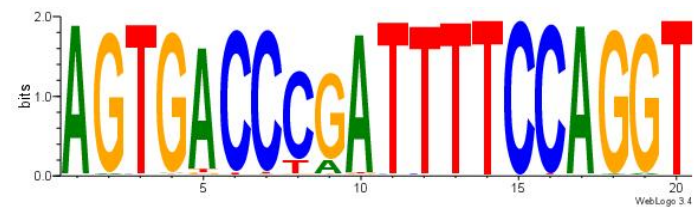
```

AGTGACCCGATTTTCCAGGT
--MGAAGGGACTTGCCTTGT
  
```

Original motif Consensus sequence: ACCTGGAAAATcGGGTCACT



Reverse complement motif Consensus sequence: AGTGACCCGATTTTCCAGGT



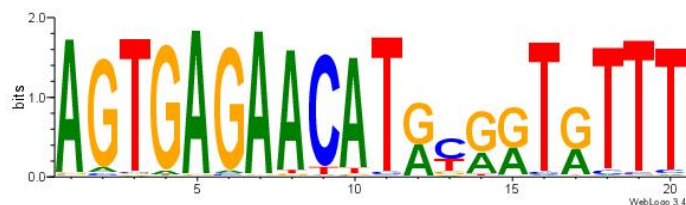
Dataset #: 1

Motif ID: 63
 Motif name: Motif 63
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 18
 Similarity score: 0.103835

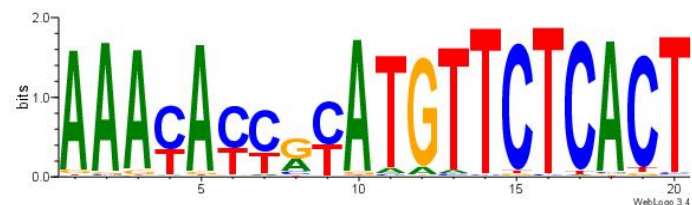
Alignment:

AGTGAGAACATRYRRTRTTT
 --MGAAGGGACTTGCCTTGT

Original motif Consensus sequence: AGTGAGAACATRYRRTRTTT

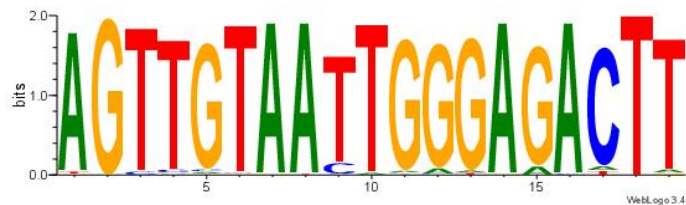


Reverse complement motif Consensus sequence: AAAMAMMKMATGTTCTCACT

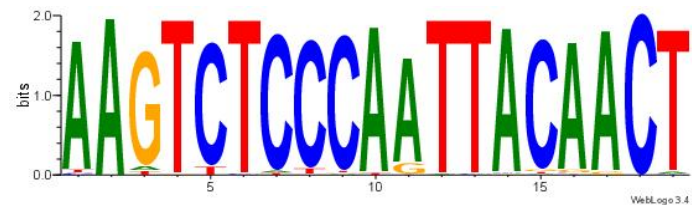


Dataset #: 1 Motif ID: 232 Motif name: Motif 232

Original motif Consensus sequence: AGTTGTAATTGGGAGACTT



Reverse complement motif Consensus sequence: AAGTCTCCAATTACAAC



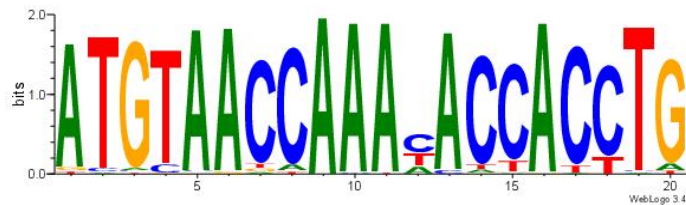
Best Matches for Motif ID 232 (Highest to Lowest)

Dataset #: 1
Motif ID: 336
Motif name: Motif 336
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 19
Similarity score: 0.0998938

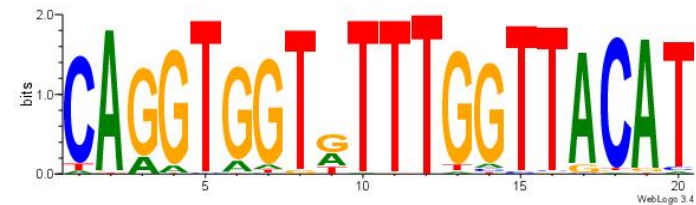
Alignment:

ATGTAACCAAAYACCACCTG
AAGTCTCCAATTACAAC T-

Original motif Consensus sequence: ATGTAACCAAAYACCACCTG



Reverse complement motif Consensus sequence:
CAGGTGGTKTTTGGTTACAT



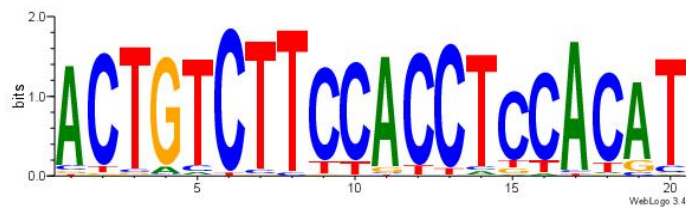
Dataset #: 1
Motif ID: 178
Motif name: Motif 178
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif

Direction: Forward
Position number: 1
Number of overlap: 19
Similarity score: 0.102119

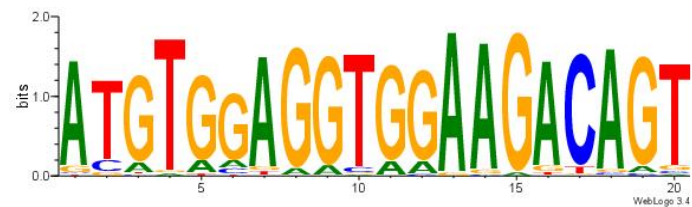
Alignment:

ACTGTCTTCCACCTCCACAT
AAGTCTCCCAATTACAAC-

Original motif Consensus sequence: ACTGTCTTCCACCTCCACAT



Reverse complement motif Consensus sequence: ATGTGGAGGTGGAAGACAGT

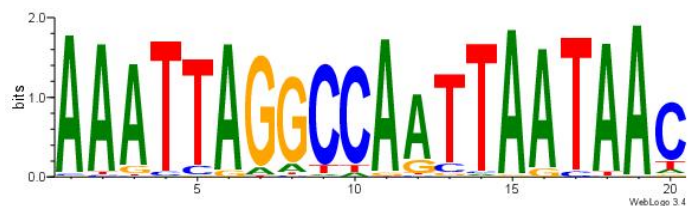


Dataset #: 1
Motif ID: 308
Motif name: Motif 308
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 19
Similarity score: 0.103158

Alignment:

GTTATTAATTGGCCTAATTT
AGTTGTAATTGGGAGACTT-

Original motif Consensus sequence: AAATTAGGCCAATTAATAAC



Reverse complement motif Consensus sequence: GTTATTAATTGGCCTAATTT

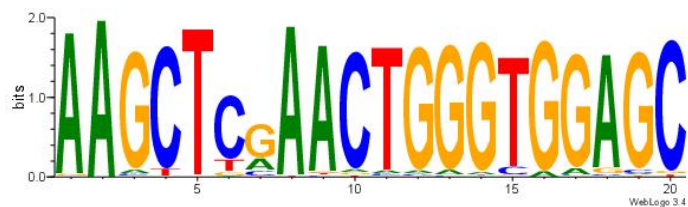


Dataset #: 1
Motif ID: 321
Motif name: Motif 321
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 2
Number of overlap: 19
Similarity score: 0.107769

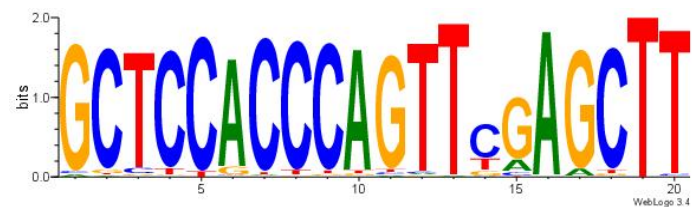
Alignment:

GCTCCACCCAGTTCGAGCTT
AAGTCTCCAATTACAAC-

Original motif Consensus sequence: AAGCTCGAACTGGGTGGAGC



Reverse complement motif Consensus sequence: GCTCCACCCAGTTCGAGCTT

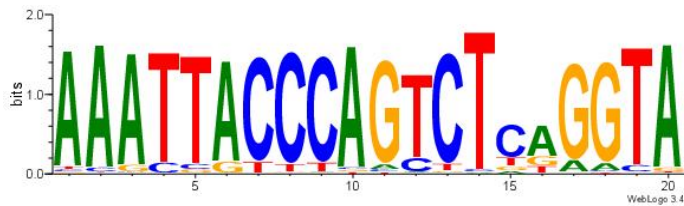


Dataset #: 1
 Motif ID: 160
 Motif name: Motif 160
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 19
 Similarity score: 0.109016

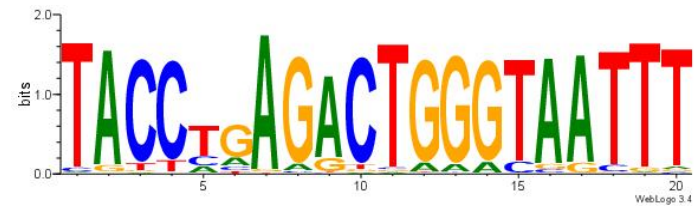
Alignment:

TACCTGAGACTGGGTAATTT
 AGTTGTAATTGGGAGACTT-

Original motif Consensus sequence: AAATTACCCAGTCTCAGGTA



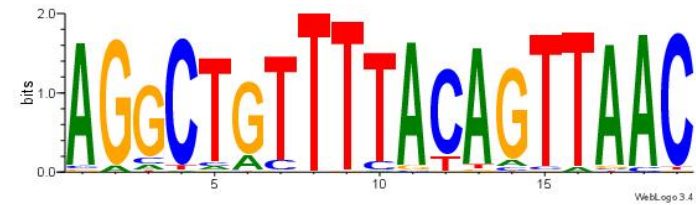
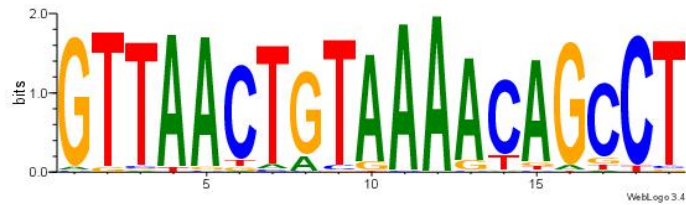
Reverse complement motif Consensus sequence: TACCTGAGACTGGGTAATTT



Dataset #: 1 Motif ID: 233 Motif name: Motif 233

Original motif Consensus sequence: GTTAACTGTA AACAGCCT

Reverse complement motif Consensus sequence: AGGCTGTTTTACAGTTAAC

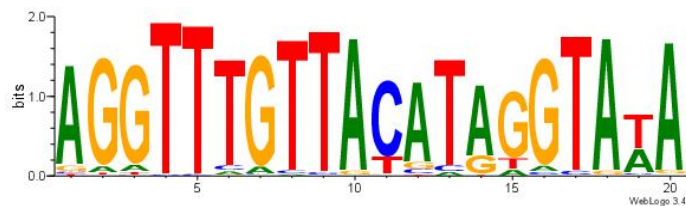


Best Matches for Motif ID 233 (Highest to Lowest)

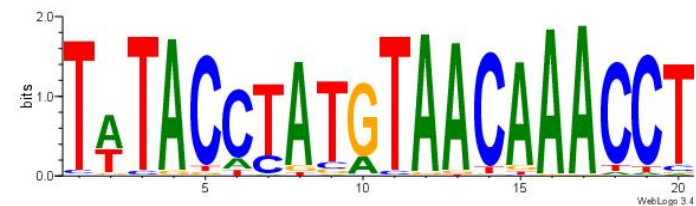
Dataset #: 1
 Motif ID: 137
 Motif name: Motif 137
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 19
 Similarity score: 0.105595

Alignment:
 TWTACCTATGTAACAAACCT
 -GTTAACTGTAAAAACAGCCT

Original motif Consensus sequence: AGGTTTGTACATAGGTAWA



Reverse complement motif Consensus sequence: TWTACCTATGTAACAAACCT

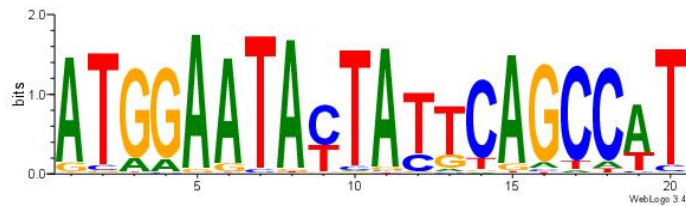


Dataset #: 1
 Motif ID: 55
 Motif name: Motif 55
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 19
 Similarity score: 0.106073

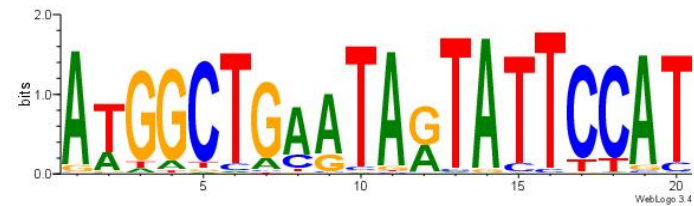
Alignment:

ATGGAATAYTATTCAGCCAT
 GTTAACTGTAAAACAGCCT-

Original motif Consensus sequence: ATGGAATAYTATTCAGCCAT



Reverse complement motif Consensus sequence: ATGGCTGAATAKTATTCCAT



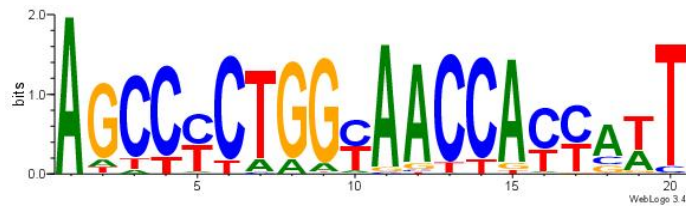
Dataset #: 1
 Motif ID: 139
 Motif name: Motif 139
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1

Number of overlap: 19
Similarity score: 0.109762

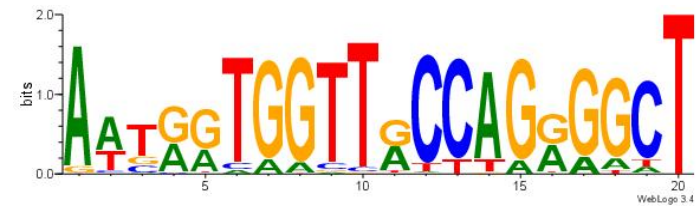
Alignment:

AWTKKTGGTTKCCAGKGGCT
-AGGCTGTTTTACAGTTAAC

Original motif Consensus sequence: AGCCYCTGGYAACCAYYAWT



Reverse complement motif Consensus sequence:
AWTKKTGGTTKCCAGKGGCT

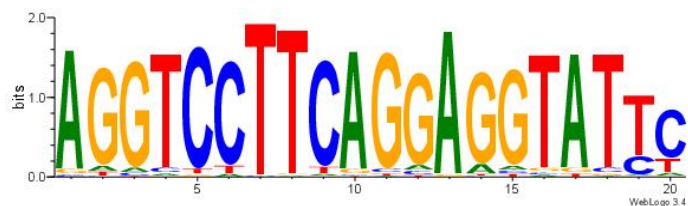


Dataset #: 1
Motif ID: 179
Motif name: Motif 179
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 2
Number of overlap: 19
Similarity score: 0.115112

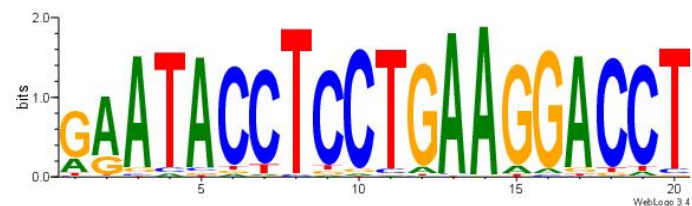
Alignment:

GAATACCTCCTGAAGGACCT
GTAACTGTAAAACAGCCT-

Original motif Consensus sequence: AGGTCCTCAGGAGGTATTC



Reverse complement motif Consensus sequence: GAATACCTCCTGAAGGACCT

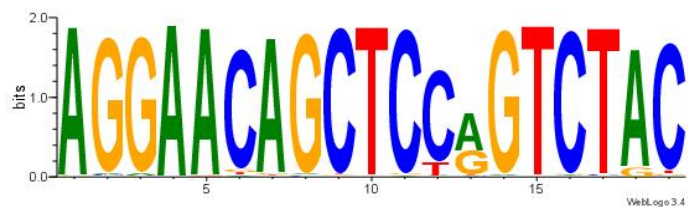


Dataset #: 1
Motif ID: 62
Motif name: Motif 62
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 19
Similarity score: 0.116079

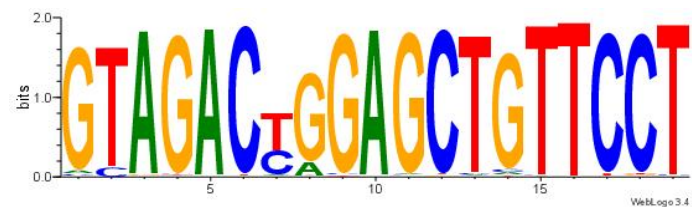
Alignment:

GTAGACKGGAGCTGTTTCCT
GTTAACTGTAAAACAGCCT

Original motif Consensus sequence: AGGAACAGCTCCcAGTCTAC

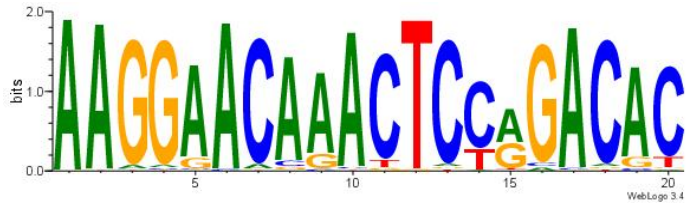


Reverse complement motif Consensus sequence: GTAGACKGGAGCTGTTTCCT

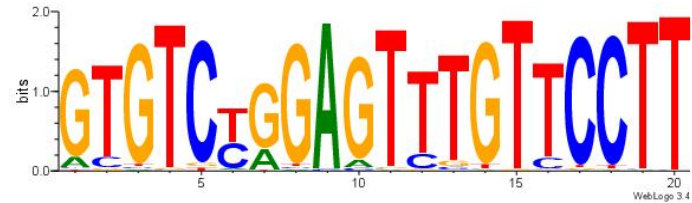


Dataset #: 1 Motif ID: 234 Motif name: Motif 234

Original motif Consensus sequence: AAGGAACAACTCCRGACAC



Reverse complement motif Consensus sequence: GTGTCKGGAGTTTGTTTCCTT



Best Matches for Motif ID 234 (Highest to Lowest)

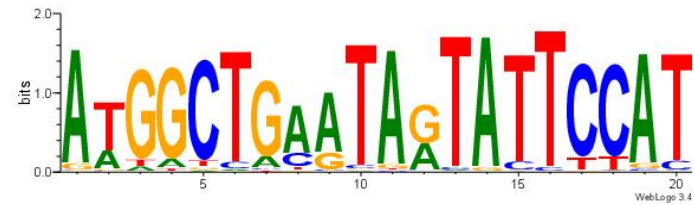
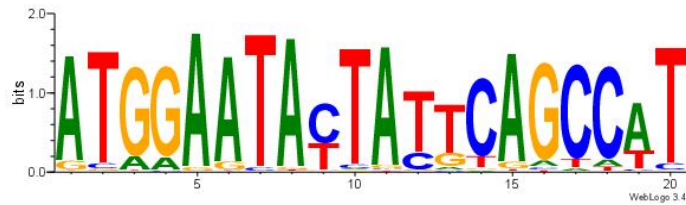
Dataset #:	1
Motif ID:	55
Motif name:	Motif 55
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	20
Similarity score:	0.0933537

Alignment:

```
ATGGCTGAATAKTATTCCAT
GTGTCKGGAGTTTGTTTCCTT
```

Original motif Consensus sequence: ATGGAATAYTATTCAGCCAT

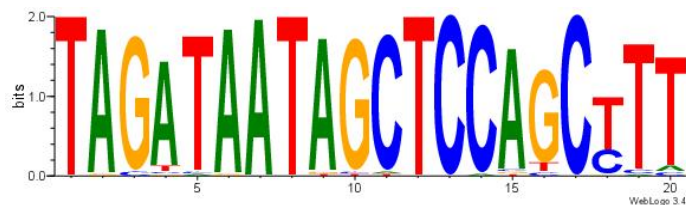
Reverse complement motif Consensus sequence: ATGGCTGAATAKTATTCCAT



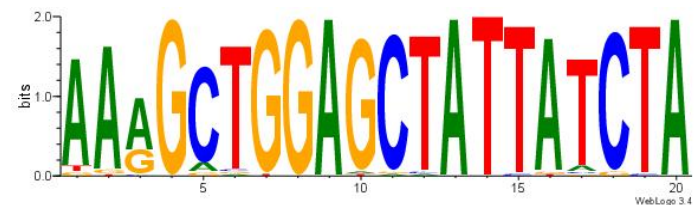
Dataset #: 1
 Motif ID: 333
 Motif name: Motif 333
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.117565

Alignment:
 TAGATAATAGCTCCAGCTTT
 AAGGAACAAACTCCRGACAC

Original motif Consensus sequence: TAGATAATAGCTCCAGCTTT



Reverse complement motif Consensus sequence: AAAGCTGGAGCTATTATCTA



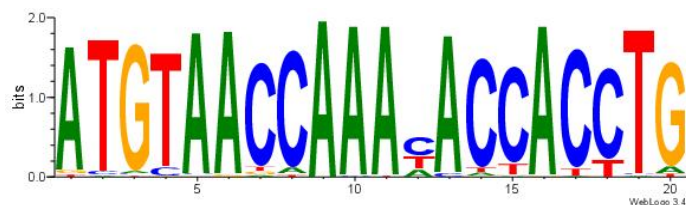
Dataset #: 1

Motif ID: 336
 Motif name: Motif 336
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.120219

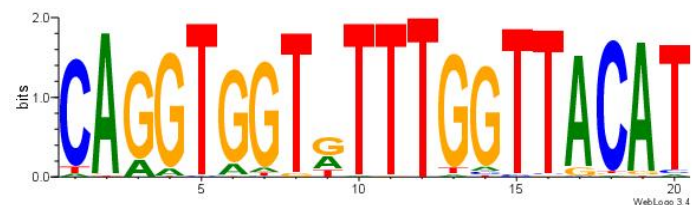
Alignment:

CAGGTGGTKTTTGGTTACAT
 GTGTCKGGAGTTTGTTCCTT

Original motif Consensus sequence: ATGTAACCAAAYACCACCTG



Reverse complement motif Consensus sequence: CAGGTGGTKTTTGGTTACAT



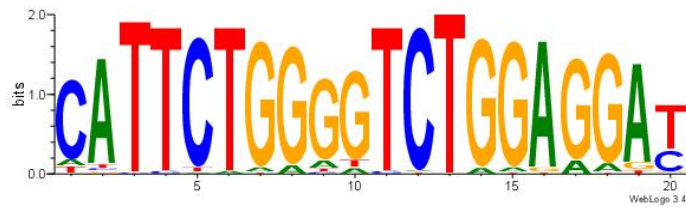
Dataset #: 1
 Motif ID: 309
 Motif name: Motif 309
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 20

Similarity score: 0.120596

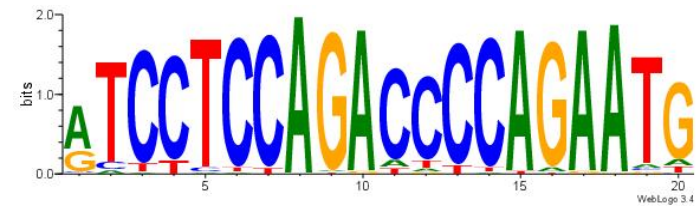
Alignment:

MTCCTCCAGACCCCAGAATG
AAGGAACAAACTCCRGACAC

Original motif Consensus sequence: CATTCTGGGGTCTGGAGGAY



Reverse complement motif Consensus sequence:
MTCCTCCAGACCCCAGAATG



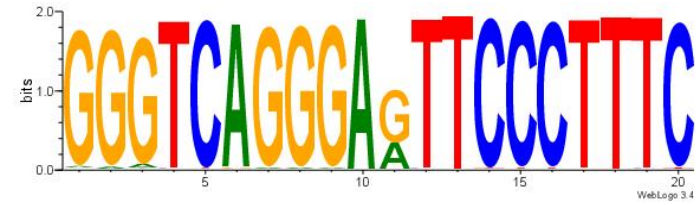
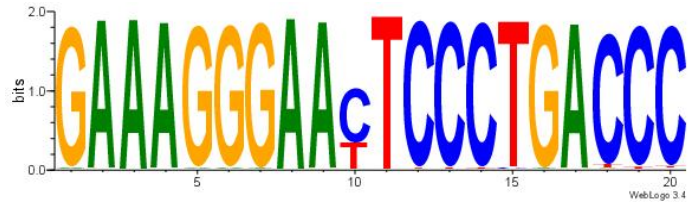
Dataset #: 1
Motif ID: 16
Motif name: Motif 16
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 20
Similarity score: 0.126322

Alignment:

GGGTCAGGGAGTTCCTTTC
GTGTCKGGAGTTGTTTCCTT

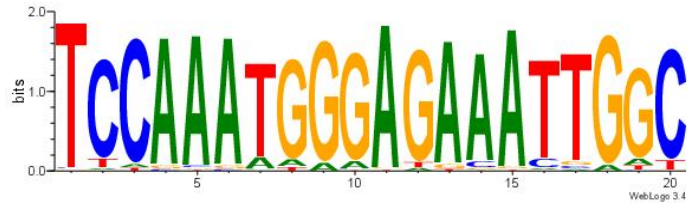
Original motif Consensus sequence: GAAAGGGA ACTCCCTGACCC

Reverse complement motif Consensus sequence:
GGGTCAGGGAGTTCCTTTC

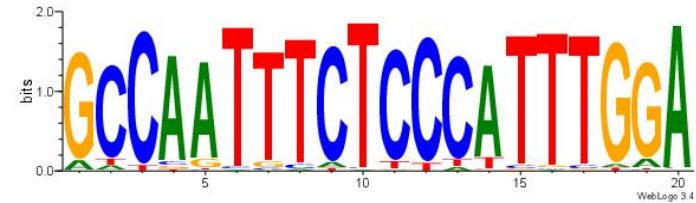


Dataset #: 1 Motif ID: 235 Motif name: Motif 235

Original motif Consensus sequence: TCCAATGGGAGAAATTGGC



Reverse complement motif Consensus sequence: GCCAATTTCTCCCATTTGGA



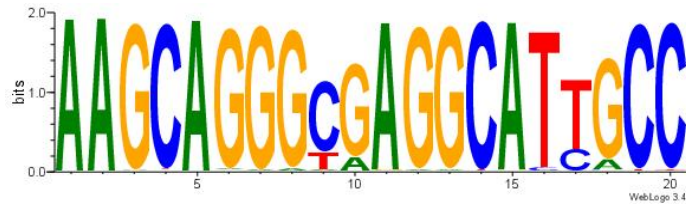
Best Matches for Motif ID 235 (Highest to Lowest)

Dataset #:	1
Motif ID:	13
Motif name:	Motif 13
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	20
Similarity score:	0.119043

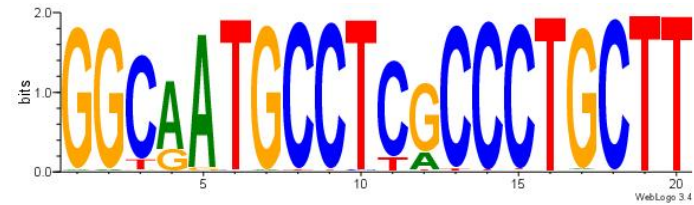
Alignment:

AAGCAGGGCGAGGCATTGCC
TCCAAATGGGAGAAATTGGC

Original motif Consensus sequence: AAGCAGGGCGAGGCATTGCC



Reverse complement motif Consensus sequence:
GGCAATGCCTCGCCCTGCTT



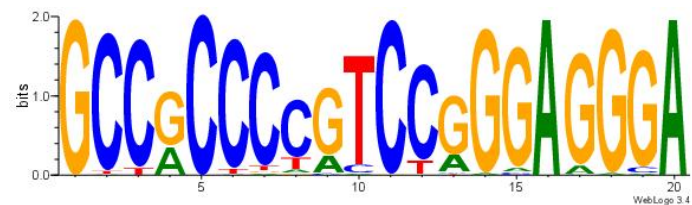
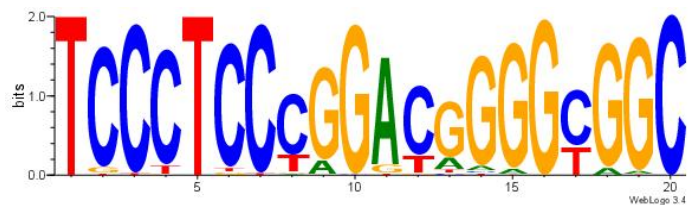
Dataset #: 1
Motif ID: 155
Motif name: Motif 155
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 20
Similarity score: 0.121347

Alignment:

TCCCTCCCGGACGGGGYGGC
TCCAAATGGGAGAAATTGGC

Original motif Consensus sequence: TCCCTCCCGGACGGGGYGGC

Reverse complement motif Consensus sequence:
GCCKCCCCGTCCGGGAGGGA

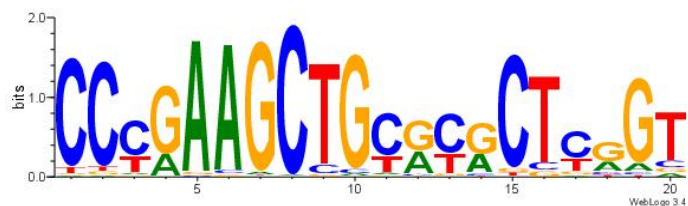


Dataset #: 1
 Motif ID: 177
 Motif name: Motif 177
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.123305

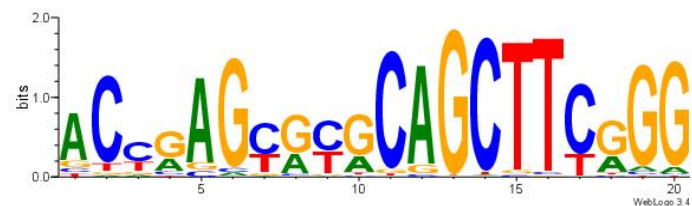
Alignment:

CCCGAAGCTGCRYRCTCGGT
 TCCAAATGGGAGAAATTGGC

Original motif Consensus sequence: CCCGAAGCTGCRYRCTCGGT



Reverse complement motif Consensus sequence: ACCGAGMKMGCAGCTTCGGG



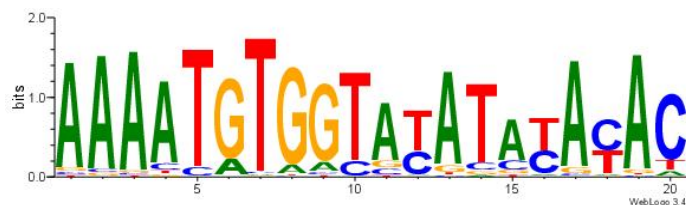
Dataset #: 1

Motif ID: 83
 Motif name: Motif 83
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.126931

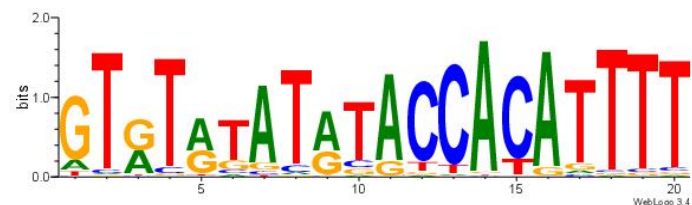
Alignment:

GTKTMTATMTACCACATTTT
 GCCAATTTCTCCATTTGGA

Original motif Consensus sequence: AAAATGTGGTAYATAYAYAC



Reverse complement motif Consensus sequence: GTKTMTATMTACCACATTTT



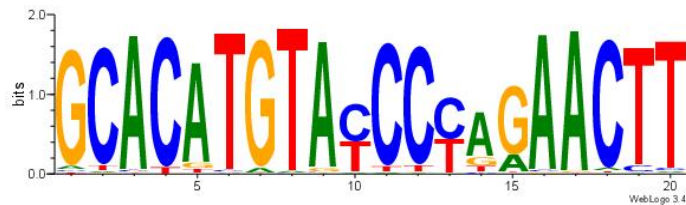
Dataset #: 1
 Motif ID: 225
 Motif name: Motif 225
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 20

Similarity score: 0.127095

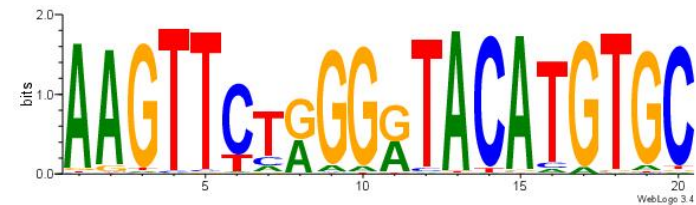
Alignment:

AAGTTCTKGGKTACATGTGC
TCCAAATGGGAGAAATTGGC

Original motif Consensus sequence: GCACATGTAYCCYAGAACTT



Reverse complement motif Consensus sequence: AAGTTCTKGGKTACATGTGC



Dataset #: 1 Motif ID: 236 Motif name: Motif 236

Original motif Consensus sequence: ATCTGAGGTACCG



Reverse complement motif Consensus sequence: CGGTACCTCAGAT



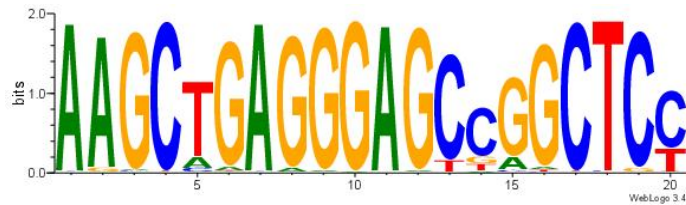
Best Matches for Motif ID 236 (Highest to Lowest)

Dataset #:	1
Motif ID:	96
Motif name:	Motif 96
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement

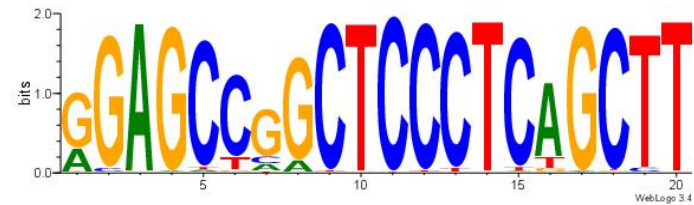
Direction: Forward
 Position number: 7
 Number of overlap: 13
 Similarity score: 0.072129

Alignment:
 GGAGCCGGCTCCCTCAGCTT
 -----CGGTACCTCAGAT-

Original motif Consensus sequence: AAGCTGAGGGAGCCGGCTCC



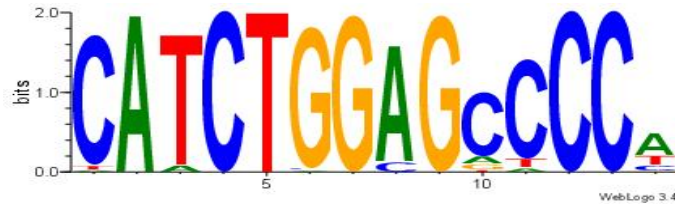
Reverse complement motif Consensus sequence: GGAGCCGGCTCCCTCAGCTT



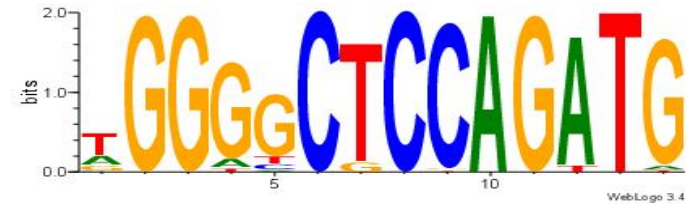
Dataset #: 1
 Motif ID: 320
 Motif name: Motif 320
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 13
 Similarity score: 0.0813404

Alignment:
 TGGGGCTCCAGATG
 CGGTACCTCAGAT-

Original motif Consensus sequence: CATCTGGAGCCCCA



Reverse complement motif Consensus sequence: TGGGGCTCCAGATG

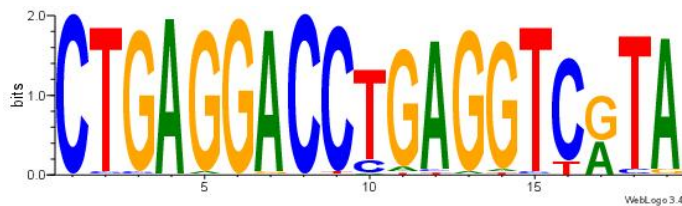


Dataset #: 1
Motif ID: 291
Motif name: Motif 291
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 13
Similarity score: 0.0882611

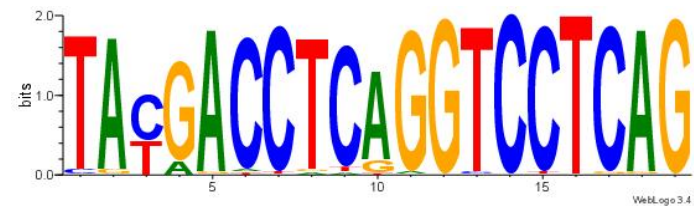
Alignment:

```
CTGAGGACCTGAGGTCRTA  
-----ATCTGAGGTACCG
```

Original motif Consensus sequence: CTGAGGACCTGAGGTCRTA



Reverse complement motif Consensus sequence: TAMGACCTCAGGTCCTCAG

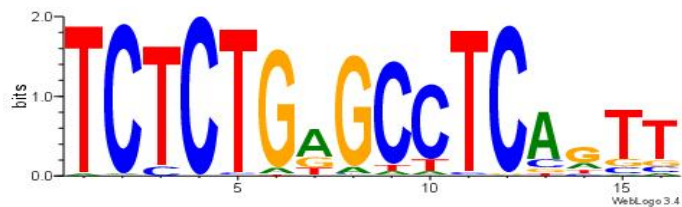


Dataset #: 1
 Motif ID: 187
 Motif name: Motif 187
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 4
 Number of overlap: 13
 Similarity score: 0.0890438

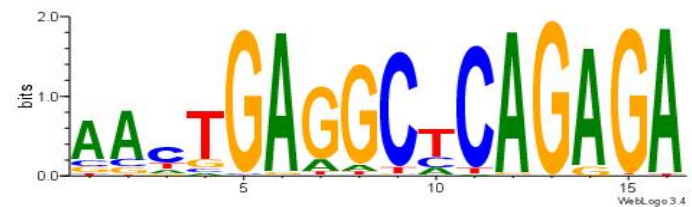
Alignment:

AACTGAGGCTCAGAGA
 ---ATCTGAGGTACCG

Original motif Consensus sequence: TCTCTGAGCCTCAGTT



Reverse complement motif Consensus sequence: AACTGAGGCTCAGAGA



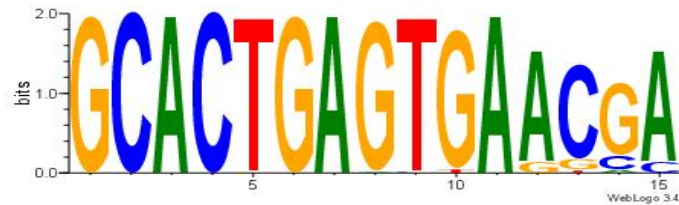
Dataset #: 1
 Motif ID: 241
 Motif name: Motif 241
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2

Number of overlap: 13
Similarity score: 0.089076

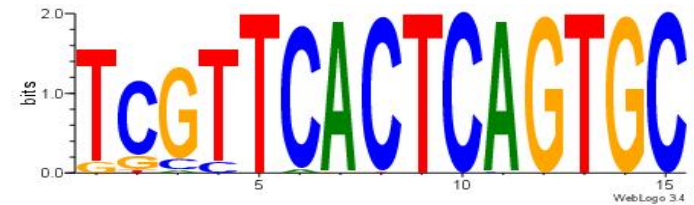
Alignment:

TCGTTCACTCAGTGC
-CGGTACCTCAGAT-

Original motif Consensus sequence: GCACTGAGTGAACGA

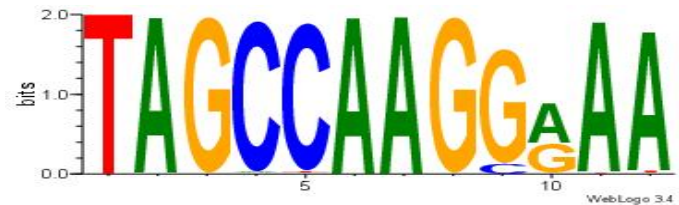


Reverse complement motif Consensus sequence: TCGTTCACTCAGTGC

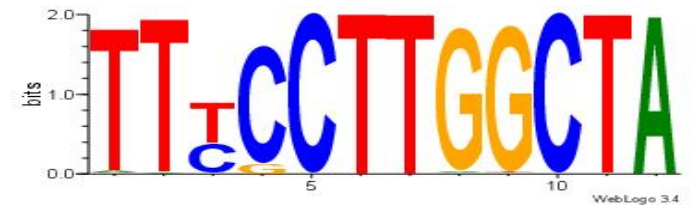


Dataset #: 1 Motif ID: 237 Motif name: Motif 237

Original motif Consensus sequence: TAGCCAAGGAA



Reverse complement motif Consensus sequence: TTKCCTTGGCTA



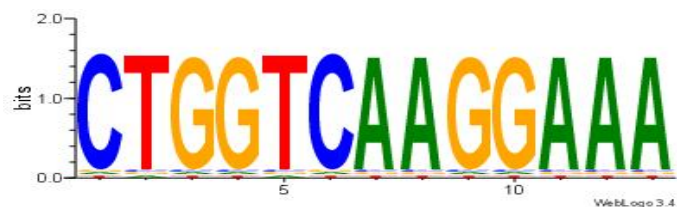
Best Matches for Motif ID 237 (Highest to Lowest)

Dataset #: 1
Motif ID: 274
Motif name: Motif 274
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif

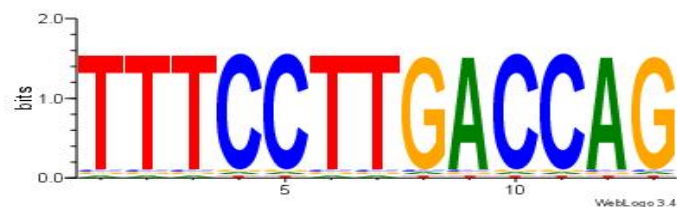
Direction: Forward
Position number: 2
Number of overlap: 12
Similarity score: 0.056906

Alignment:
CTGGTCAAGGAAA
-TAGCCAAGGRAA

Original motif Consensus sequence: CTGGTCAAGGAAA



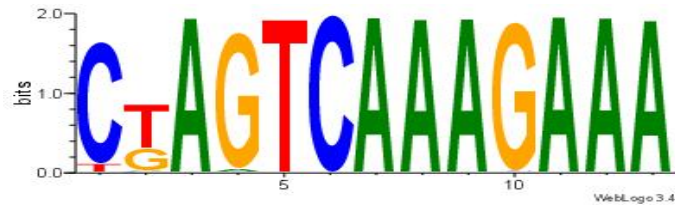
Reverse complement motif Consensus sequence: TTTCTTGACCAG



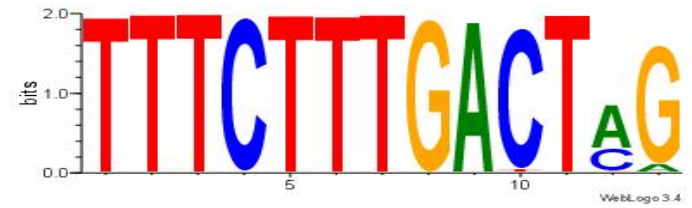
Dataset #: 1
Motif ID: 24
Motif name: Motif 24
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 12
Similarity score: 0.0581846

Alignment:
TTTCTTGACTRG
TTKCCTTGGCTA-

Original motif Consensus sequence: CKAGTCAAAGAAA



Reverse complement motif Consensus sequence: TTTCTTTGACTRG

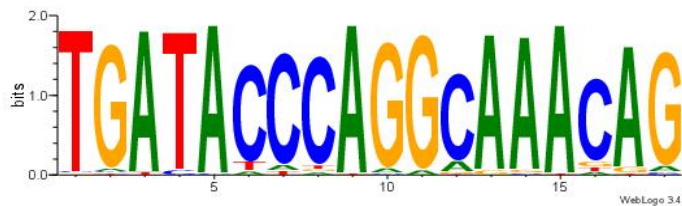


Dataset #: 1
Motif ID: 290
Motif name: Motif 290
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 4
Number of overlap: 12
Similarity score: 0.0704633

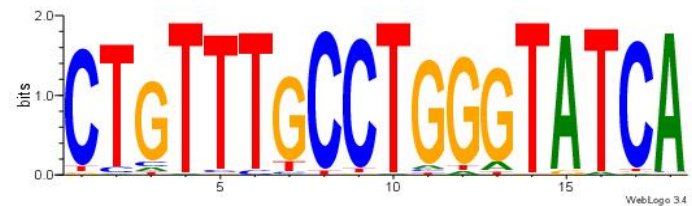
Alignment:

TGATACCCAGGCAAACAG
---TAGCCAAGGRAA---

Original motif Consensus sequence: TGATACCCAGGCAAACAG



Reverse complement motif Consensus sequence: CTGTTTGCCTGGGTATCA

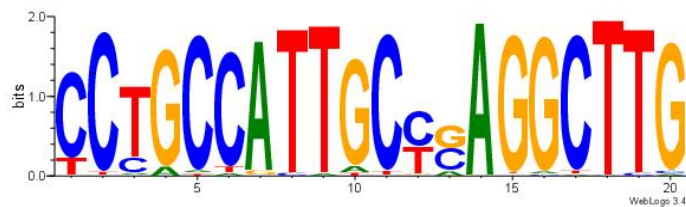


Dataset #: 1
 Motif ID: 196
 Motif name: Motif 196
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 12
 Similarity score: 0.0840989

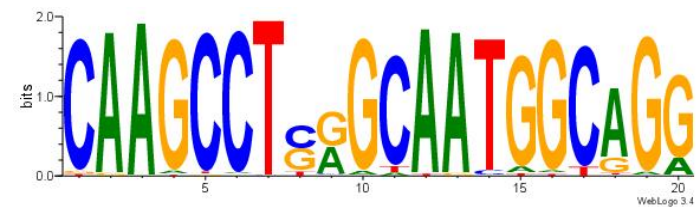
Alignment:

CAAGCCTSKGCAATGGCAGG
 -----TAGCCAAGGRAA-

Original motif Consensus sequence: CCTGCCATTGCYSAGGCTTG



Reverse complement motif Consensus sequence: CAAGCCTSKGCAATGGCAGG



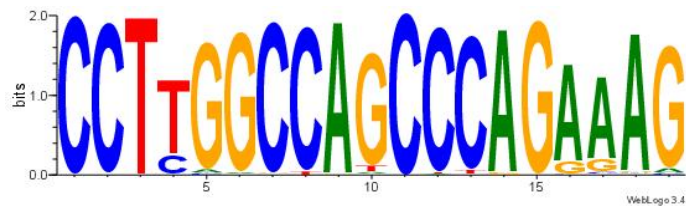
Dataset #: 1
 Motif ID: 122
 Motif name: Motif 122
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1

Number of overlap: 12
Similarity score: 0.0852018

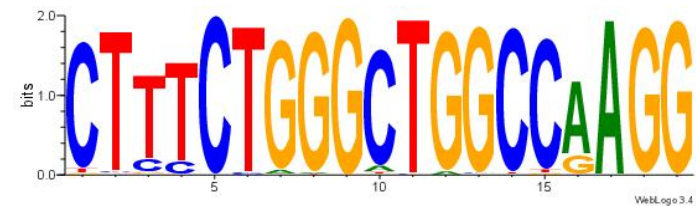
Alignment:

CCTTGGCCAGCCCAGAAAG
-----TAGCCAAGGRAA

Original motif Consensus sequence: CCTTGGCCAGCCCAGAAAG

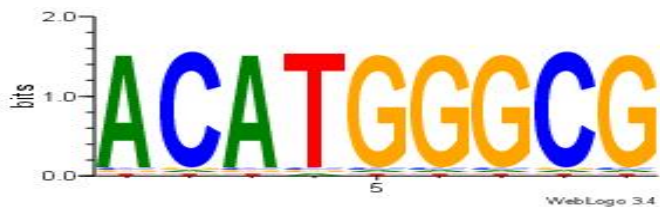


Reverse complement motif Consensus sequence:
CTTTCTGGGCTGGCCAAGG

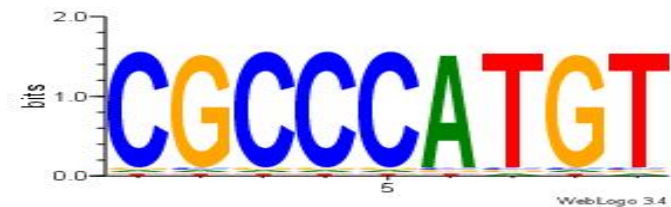


Dataset #: 1 Motif ID: 238 Motif name: Motif 238

Original motif Consensus sequence: ACATGGGCG



Reverse complement motif Consensus sequence: CGCCCATGT



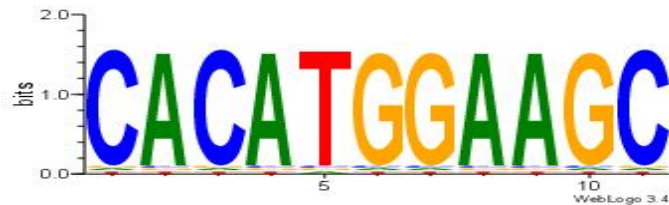
Best Matches for Motif ID 238 (Highest to Lowest)

Dataset #: 1
Motif ID: 353
Motif name: Motif 353
Matching format of first motif: Original Motif

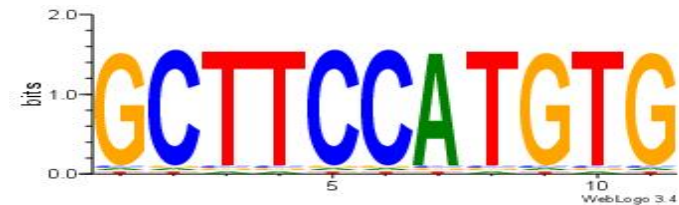
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2
Number of overlap: 9
Similarity score: 0.0421539

Alignment:
CACATGGAAGC
-ACATGGGCG-

Original motif Consensus sequence: CACATGGAAGC



Reverse complement motif Consensus sequence: GCTTCCATGTG

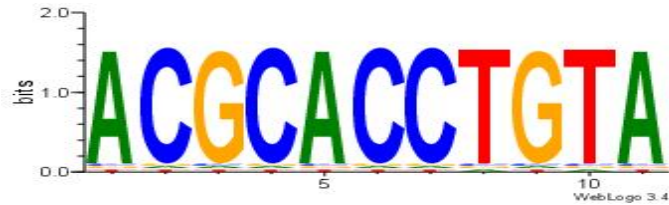


Dataset #: 1
Motif ID: 324
Motif name: Motif 324
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 2
Number of overlap: 9
Similarity score: 0.0421539

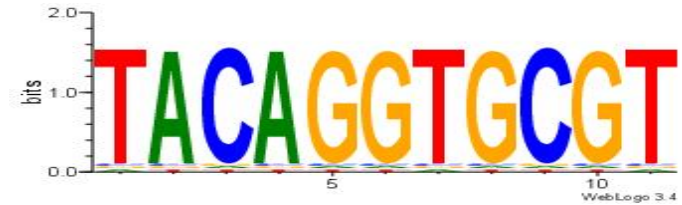
Alignment:

TACAGGTGCGT
-ACATGGGCG-

Original motif Consensus sequence: ACGCACCTGTA



Reverse complement motif Consensus sequence: TACAGGTGCGT



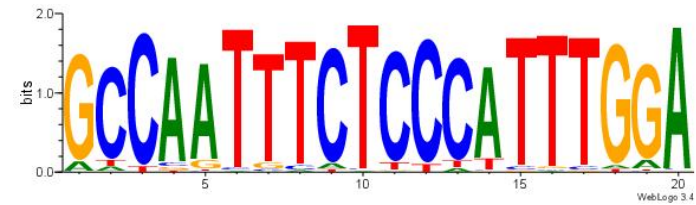
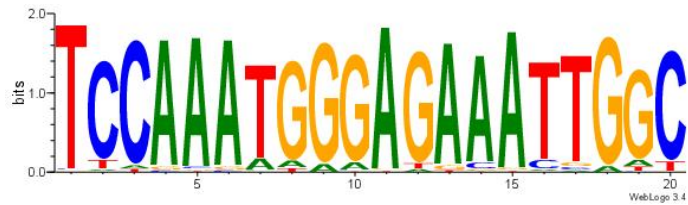
Dataset #: 1
Motif ID: 235
Motif name: Motif 235
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 9
Number of overlap: 9
Similarity score: 0.0532025

Alignment:

TCCAAATGGGAGAAATTGGC
---ACATGGGCG-----

Original motif Consensus sequence: TCCAAATGGGAGAAATTGGC

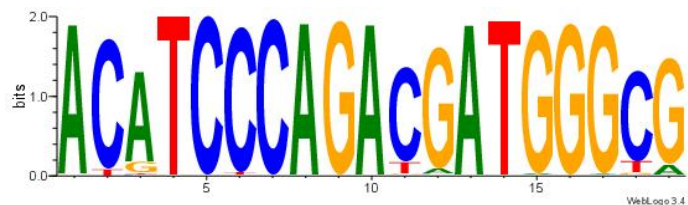
Reverse complement motif Consensus sequence:
GCCAATTTCTCCCATTTGGA



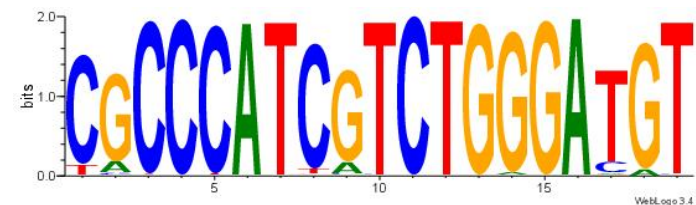
Dataset #: 1
 Motif ID: 36
 Motif name: Motif 36
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 11
 Number of overlap: 9
 Similarity score: 0.0536448

Alignment:
 CGCCCATCGTCTGGGATGT
 CGCCCATGT-----

Original motif Consensus sequence: ACATCCCAGACGATGGGCG



Reverse complement motif Consensus sequence: CGCCCATCGTCTGGGATGT

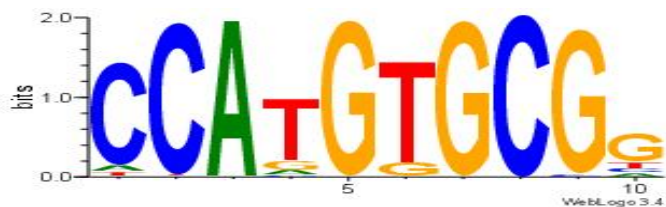


Dataset #: 1

Motif ID: 93
 Motif name: Motif 93
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 9
 Similarity score: 0.0544118

Alignment:
 CCATGTGCGG
 ACATGGGCG-

Original motif Consensus sequence: CCATGTGCGG

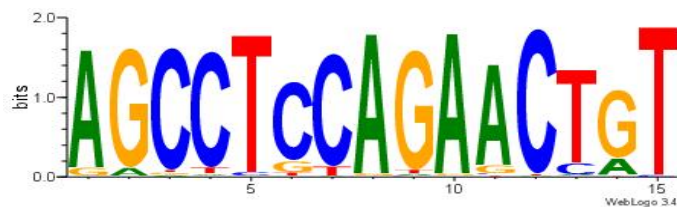


Reverse complement motif Consensus sequence: CCGCACATGG

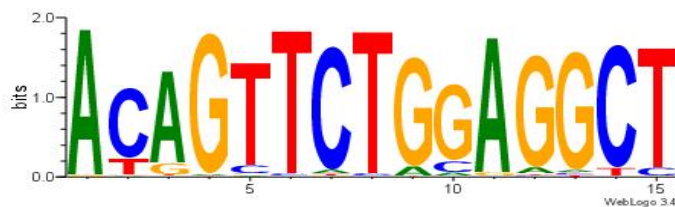


Dataset #: 1 Motif ID: 239 Motif name: Motif 239

Original motif Consensus sequence: AGCCTCCAGAACTGT



Reverse complement motif Consensus sequence: ACAGTTCTGGAGG



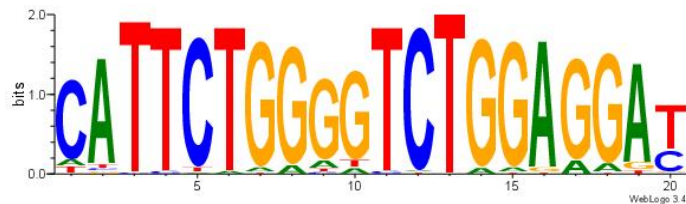
Best Matches for Motif ID 239 (Highest to Lowest)

Dataset #: 1
Motif ID: 309
Motif name: Motif 309
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 6
Number of overlap: 15
Similarity score: 0.0847179

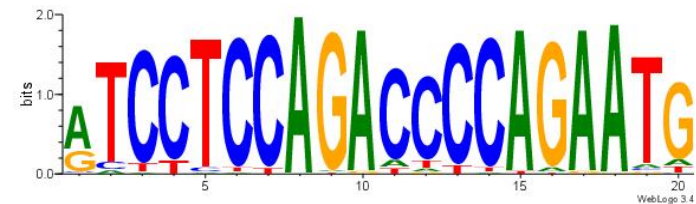
Alignment:

```
MTCCTCCAGACCCCAGAATG  
AGCCTCCAGAACTGT-----
```

Original motif Consensus sequence: CATTCTGGGGTCTGGAGGAY



Reverse complement motif Consensus sequence:
MTCCTCCAGACCCCAGAATG



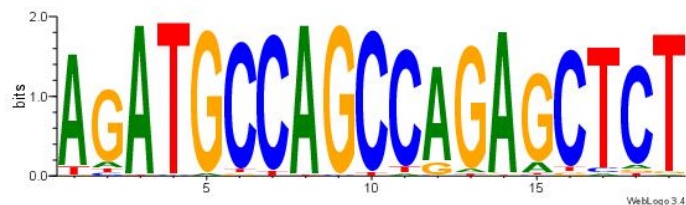
Dataset #: 1
Motif ID: 307
Motif name: Motif 307
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif

Direction: Backward
Position number: 1
Number of overlap: 15
Similarity score: 0.0931523

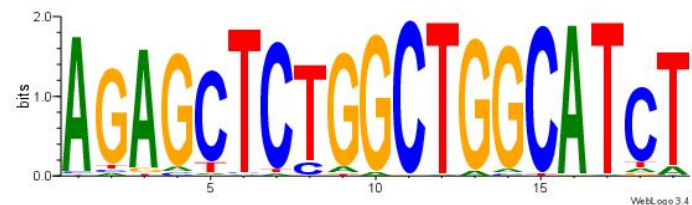
Alignment:

AGATGCCAGCCAGAGCTCT
----AGCCTCCAGAACTGT

Original motif Consensus sequence: AGATGCCAGCCAGAGCTCT



Reverse complement motif Consensus sequence: AGAGCTCTGGCTGGCATCT

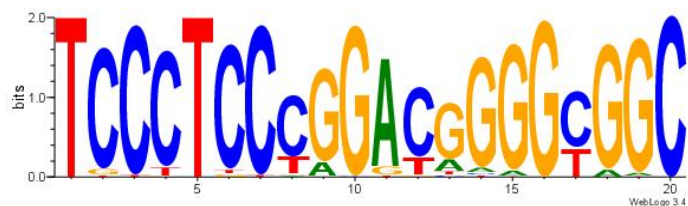


Dataset #: 1
Motif ID: 155
Motif name: Motif 155
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 6
Number of overlap: 15
Similarity score: 0.0940799

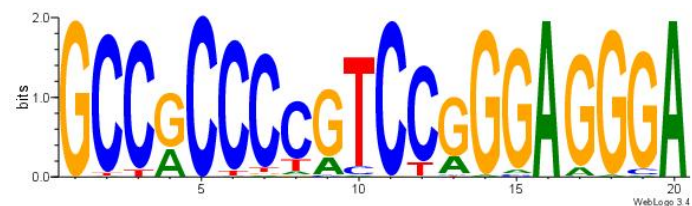
Alignment:

GCCKCCCCGTCCGGGAGGGA
-----ACAGTTCTGGAGGCT

Original motif Consensus sequence: TCCCTCCCGACGGGGYGGC



Reverse complement motif Consensus sequence: GCCKCCCCGTCCGGGAGGGA

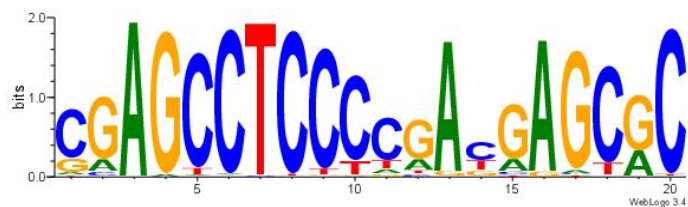


Dataset #: 1
Motif ID: 108
Motif name: Motif 108
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 3
Number of overlap: 15
Similarity score: 0.0951379

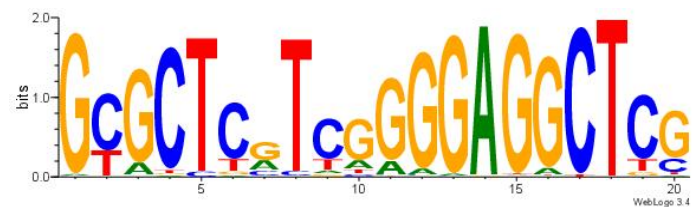
Alignment:

```
GCGCTCKTCGGGGAGGCTCG  
---ACAGTTCTGGAGGCT--
```

Original motif Consensus sequence: CGAGCCTCCCCGAYGAGCGC



Reverse complement motif Consensus sequence: GCGCTCKTCGGGGAGGCTCG

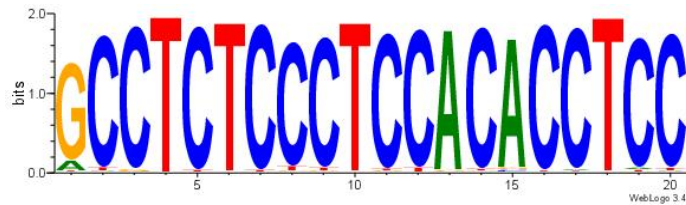


Dataset #: 1
 Motif ID: 105
 Motif name: Motif 105
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 6
 Number of overlap: 15
 Similarity score: 0.0954906

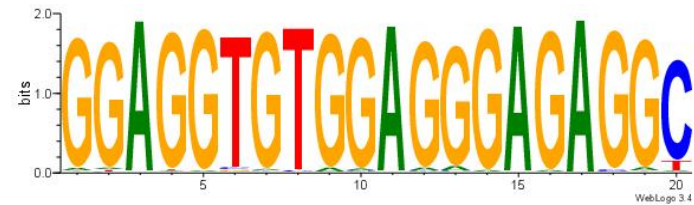
Alignment:

GGAGGTGTGGAGGGAGAGGC
 ACAGTTCTGGAGGCT-----

Original motif Consensus sequence: GCCTCTCCCTCCACACCTCC



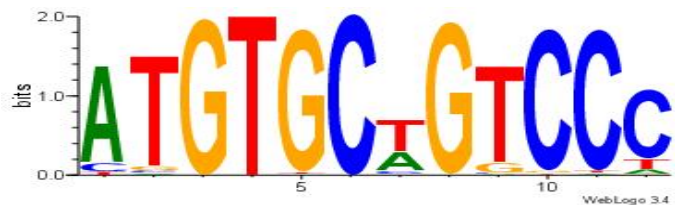
Reverse complement motif Consensus sequence: GGAGGTGTGGAGGGAGAGGC



Dataset #: 1 Motif ID: 240 Motif name: Motif 240

Original motif Consensus sequence: ATGTGCWGTCCC

Reverse complement motif Consensus sequence: GGGACWGCACAT



Best Matches for Motif ID 240 (Highest to Lowest)

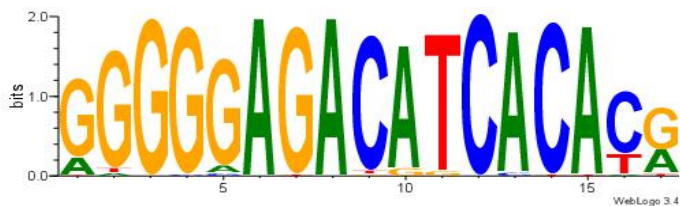
Dataset #: 1
 Motif ID: 279
 Motif name: Motif 279
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 5
 Number of overlap: 12
 Similarity score: 0.0578868

Alignment:

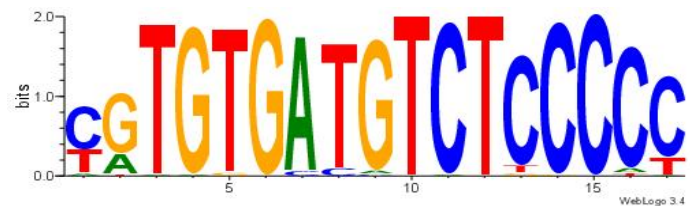
```

GGGGGAGACATCACACR
----GGGACWGCACAT-
  
```

Original motif Consensus sequence: GGGGGAGACATCACACR



Reverse complement motif Consensus sequence: MGTGTGATGTCTCCCC

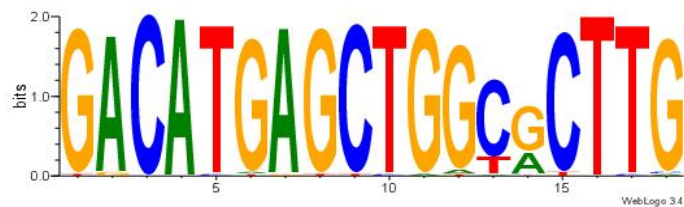


Dataset #: 1
 Motif ID: 306
 Motif name: Motif 306
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 4
 Number of overlap: 12
 Similarity score: 0.0660844

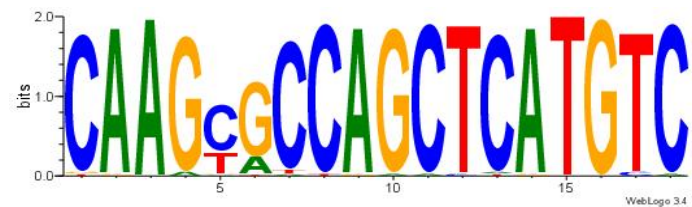
Alignment:

GACATGAGCTGGCGCTTG
 ---ATGTGCWGTCCC---

Original motif Consensus sequence: GACATGAGCTGGCGCTTG



Reverse complement motif Consensus sequence: CAAGCGCCAGCTCATGTC



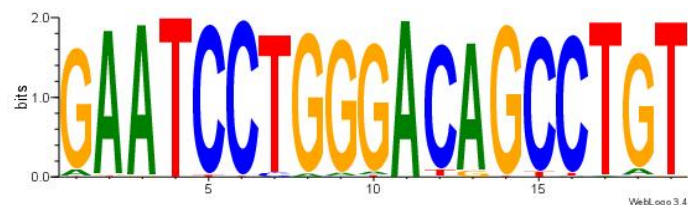
Dataset #: 1
 Motif ID: 192
 Motif name: Motif 192
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 8

Number of overlap: 12
Similarity score: 0.0665252

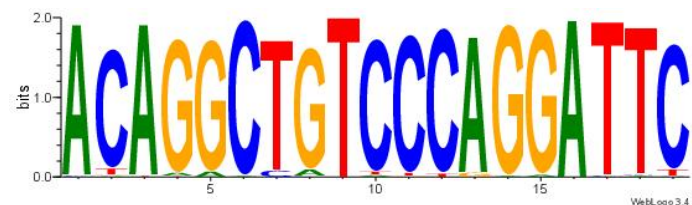
Alignment:

ACAGGCTGTCCCAGGATTC
-----ATGTGCWGTCCC

Original motif Consensus sequence: GAATCCTGGGACAGCCTGT



Reverse complement motif Consensus sequence:
ACAGGCTGTCCCAGGATTC



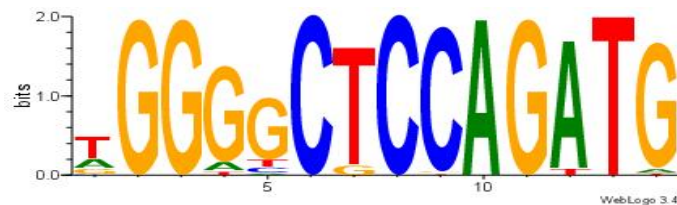
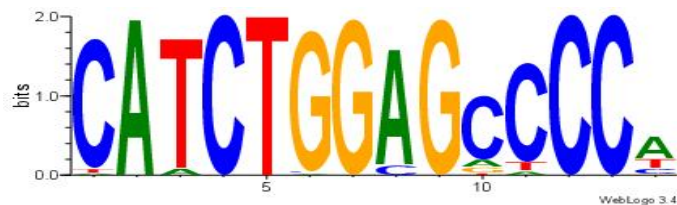
Dataset #: 1
Motif ID: 320
Motif name: Motif 320
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 2
Number of overlap: 12
Similarity score: 0.0676775

Alignment:

TGGGGCTCCAGATG
-GGGACWGCACAT-

Original motif Consensus sequence: CATCTGGAGCCCCA

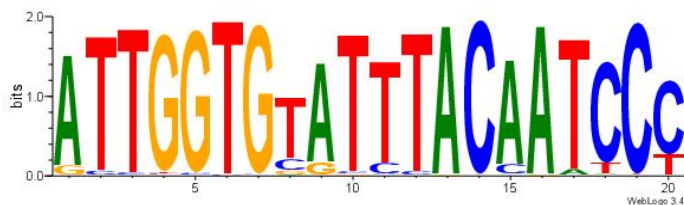
Reverse complement motif Consensus sequence: TGGGGCTCCAGATG



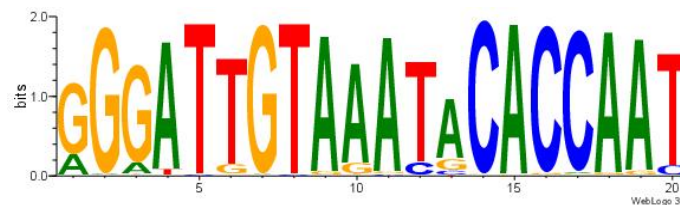
Dataset #: 1
 Motif ID: 106
 Motif name: Motif 106
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 12
 Similarity score: 0.069616

Alignment:
 GGGATTGTAAATACACCAAT
 GGGACWGCACAT-----

Original motif Consensus sequence: ATTGGTGTATTTACAATCCC

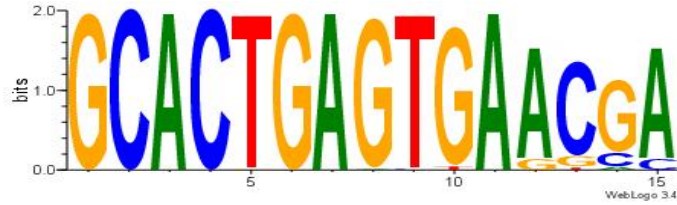


Reverse complement motif Consensus sequence: GGGATTGTAAATACACCAAT

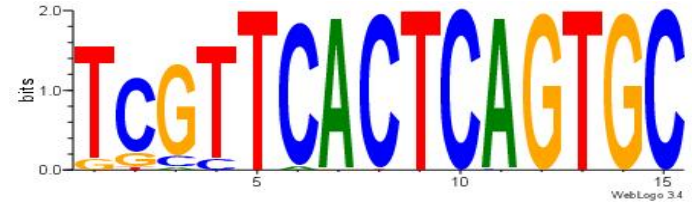


Dataset #: 1 Motif ID: 241 Motif name: Motif 241

Original motif Consensus sequence: GCACTGAGTGAACGA



Reverse complement motif Consensus sequence: TCGTTCAGTGC



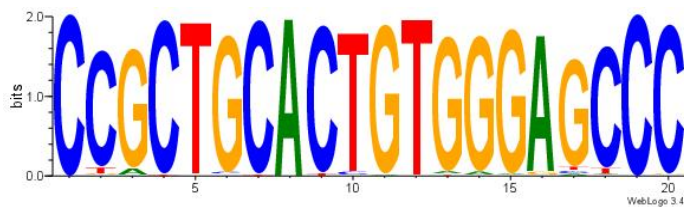
Best Matches for Motif ID 241 (Highest to Lowest)

Dataset #:	1
Motif ID:	144
Motif name:	Motif 144
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	6
Number of overlap:	15
Similarity score:	0.0442756

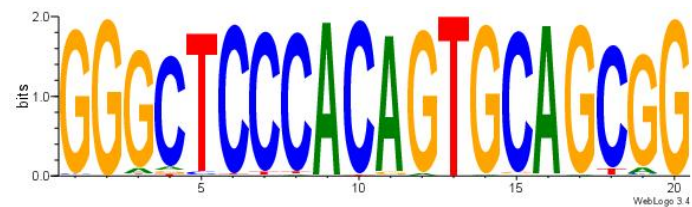
Alignment:

```
CCGCTGCACTGTGGGAGCCC  
-----GCACTGAGTGAACGA
```

Original motif Consensus sequence: CCGCTGCACTGTGGGAGCCC



Reverse complement motif Consensus sequence: GGGTCCCACAGTGCAGCGG

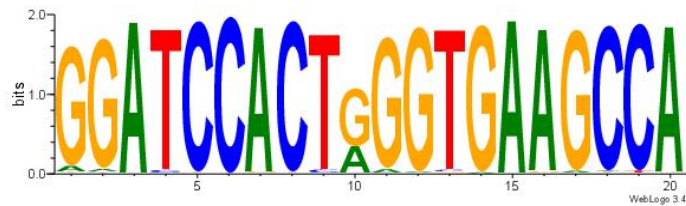


Dataset #: 1
 Motif ID: 61
 Motif name: Motif 61
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 5
 Number of overlap: 15
 Similarity score: 0.0478162

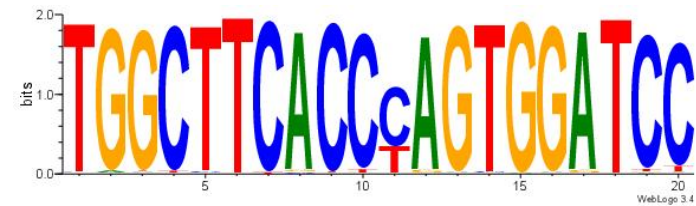
Alignment:

GGATCCACTGGGTGAAGCCA
 ----GCACTGAGTGAACGA-

Original motif Consensus sequence: GGATCCACTGGGTGAAGCCA



Reverse complement motif Consensus sequence: TGGCTTCACCCAGTGGATCC



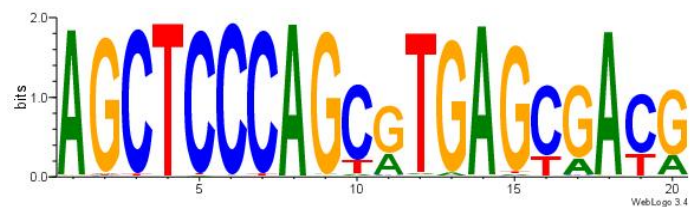
Dataset #: 1
 Motif ID: 48
 Motif name: Motif 48
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3

Number of overlap: 15
Similarity score: 0.0574241

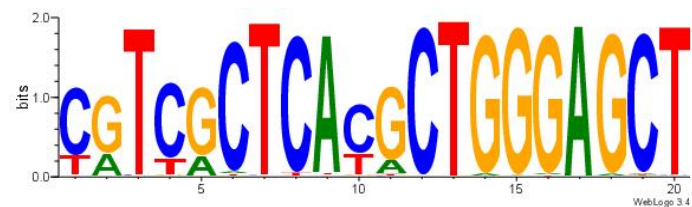
Alignment:

CGTCGCTCACGCTGGGAGCT
--TCGTTCACTCAGTGC---

Original motif Consensus sequence: AGCTCCCAGCGTGAGCGACG



Reverse complement motif Consensus sequence:
CGTCGCTCACGCTGGGAGCT

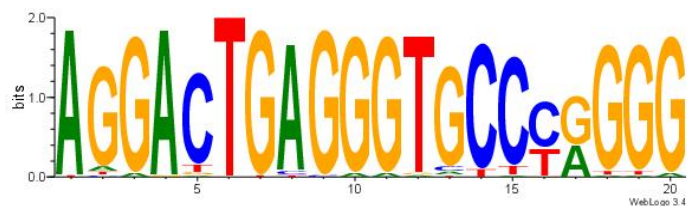


Dataset #: 1
Motif ID: 312
Motif name: Motif 312
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 2
Number of overlap: 15
Similarity score: 0.0588064

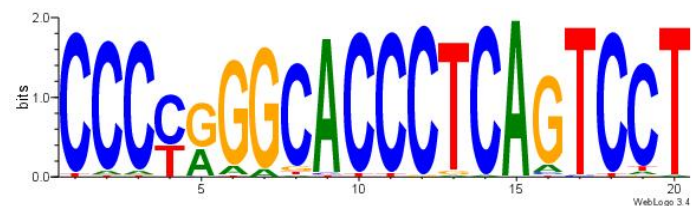
Alignment:

CCCMKGGCACCTCAGTCCT
----TCGTTCACTCAGTGC--

Original motif Consensus sequence: AGGACTGAGGGTGCCYRGGG



Reverse complement motif Consensus sequence: CCCMKGGCACCCTCAGTCCT

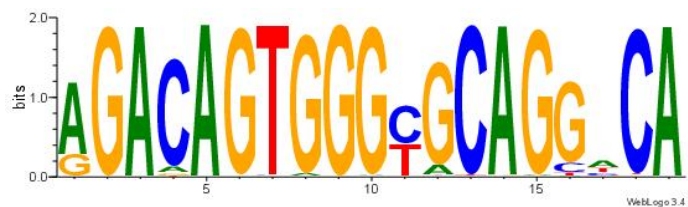


Dataset #: 1
Motif ID: 17
Motif name: Motif 17
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 3
Number of overlap: 15
Similarity score: 0.0672559

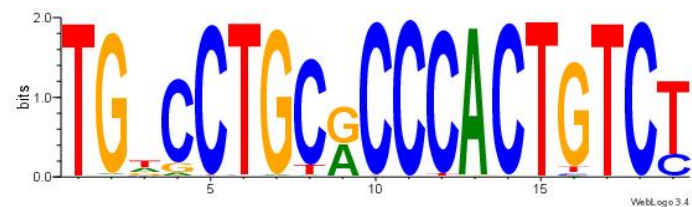
Alignment:

AGACAGTGGGYGCAGGHCA
--GCACTGAGTGAACGA--

Original motif Consensus sequence: AGACAGTGGGYGCAGGHCA

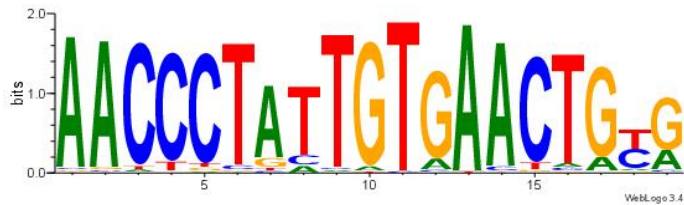


Reverse complement motif Consensus sequence: TGHCTGCKCCCACTGTCT

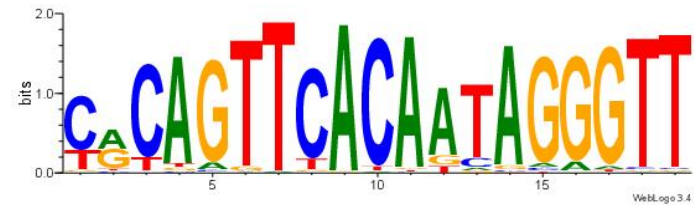


Dataset #: 1 Motif ID: 242 Motif name: Motif 242

Original motif Consensus sequence: AACCTATTGTGAACTGYG



Reverse complement motif Consensus sequence: CMCAGTTCACAATAGGGTT



Best Matches for Motif ID 242 (Highest to Lowest)

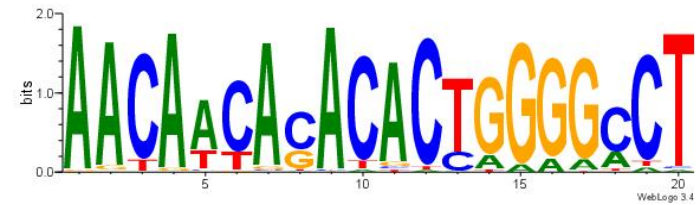
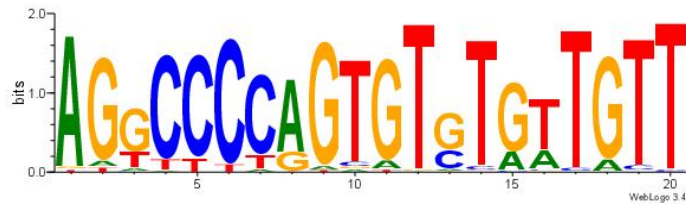
Dataset #:	1
Motif ID:	176
Motif name:	Motif 176
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	2
Number of overlap:	19
Similarity score:	0.0985886

Alignment:

```
AACAACASACTGGGGCCT
CMCAGTTCACAATAGGGTT-
```

Original motif Consensus sequence: AGGCCCCAGTGTSTGTTGTT

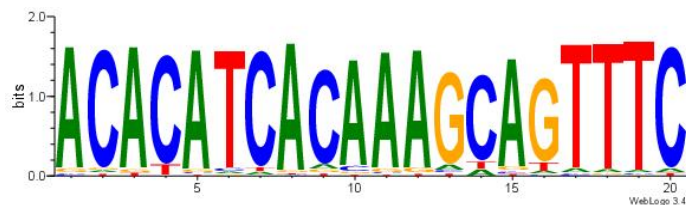
Reverse complement motif Consensus sequence: AACAACASACTGGGGCCT



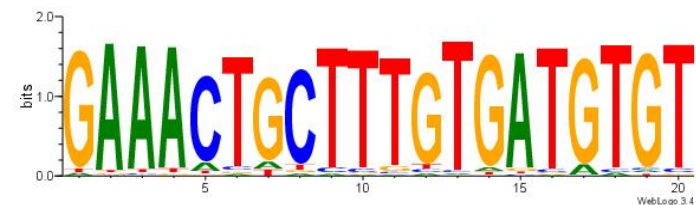
Dataset #: 1
 Motif ID: 202
 Motif name: Motif 202
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 19
 Similarity score: 0.11357

Alignment:
 ACACATCACAAAGCAGTTTC
 CMCAGTTCACAATAGGGTT-

Original motif Consensus sequence: ACACATCACAAAGCAGTTTC



Reverse complement motif Consensus sequence: GAAACTGCTTTGTGATGTGT



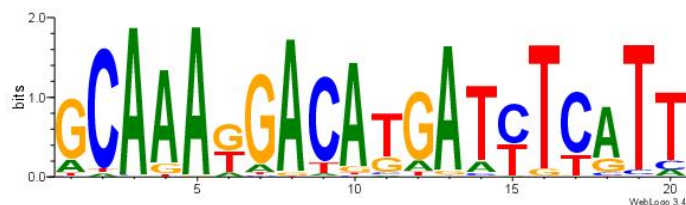
Dataset #: 1

Motif ID: 99
 Motif name: Motif 99
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 19
 Similarity score: 0.115902

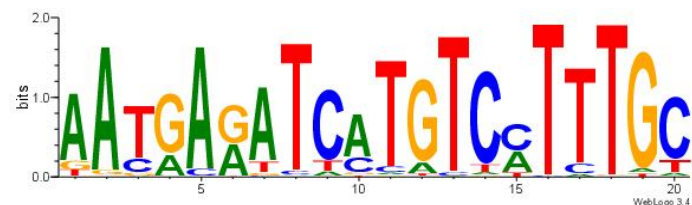
Alignment:

GCAAAGACATGATYTCATT
 CMCAGTTCACAATAGGGTT-

Original motif Consensus sequence: GCAAAGACATGATYTCATT



Reverse complement motif Consensus sequence: AATGAKATCATGTCYTTTGC



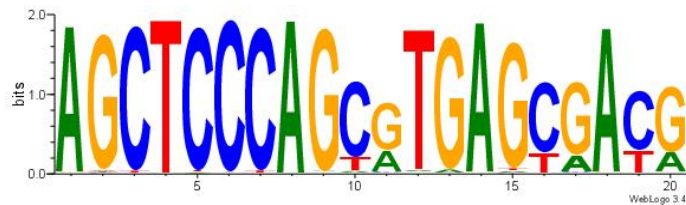
Dataset #: 1
 Motif ID: 48
 Motif name: Motif 48
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 19

Similarity score: 0.116379

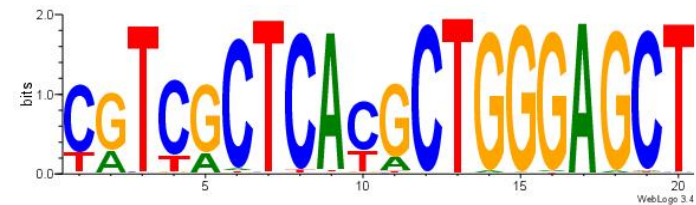
Alignment:

AGCTCCCAGCGTGAGCGACG
-AACCCCTATTGTGAACTGYG

Original motif Consensus sequence: AGCTCCCAGCGTGAGCGACG



Reverse complement motif Consensus sequence:
CGTCGCTCACGCTGGGAGCT



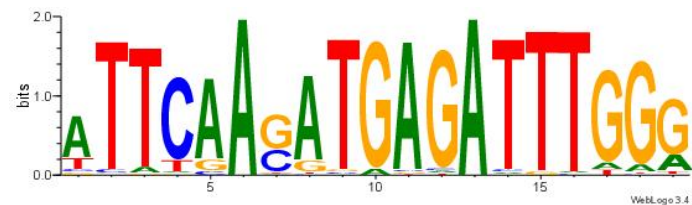
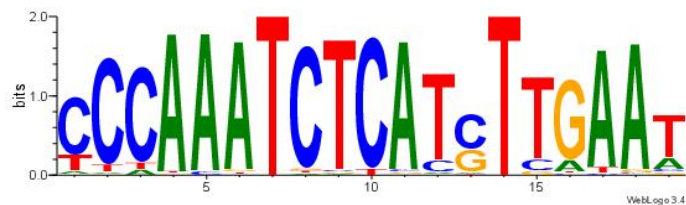
Dataset #: 1
Motif ID: 227
Motif name: Motif 227
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 19
Similarity score: 0.11749

Alignment:

ATTCAASATGAGATTTGGG
AACCCCTATTGTGAACTGYG

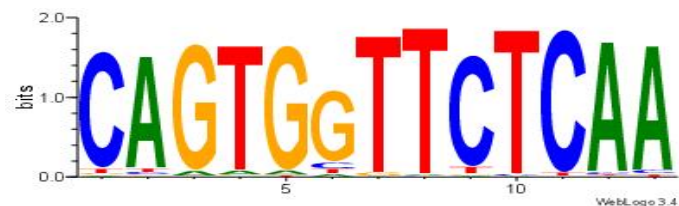
Original motif Consensus sequence: CCCAAATCTCATSTTGAAT

Reverse complement motif Consensus sequence:
ATTCAASATGAGATTTGGG



Dataset #: 1 Motif ID: 243 Motif name: Motif 243

Original motif Consensus sequence: CAGTGGTTCTCAA



Reverse complement motif Consensus sequence: TTGAGAACCACTG



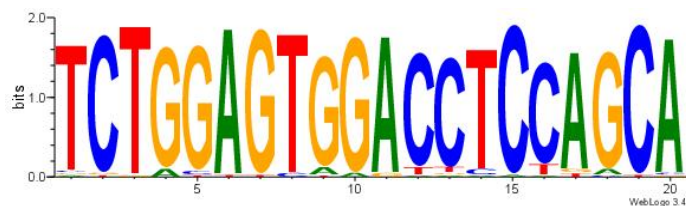
Best Matches for Motif ID 243 (Highest to Lowest)

Dataset #:	1
Motif ID:	350
Motif name:	Motif 350
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	5
Number of overlap:	13
Similarity score:	0.0720775

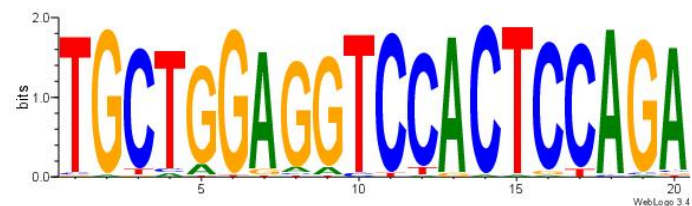
Alignment:

```
TGCTGGAGGTCCACTCCAGA
---TTGAGAACCACTG----
```

Original motif Consensus sequence: TCTGGAGTGGACCTCCAGCA



Reverse complement motif Consensus sequence: TGCTGGAGGTCCACTCCAGA

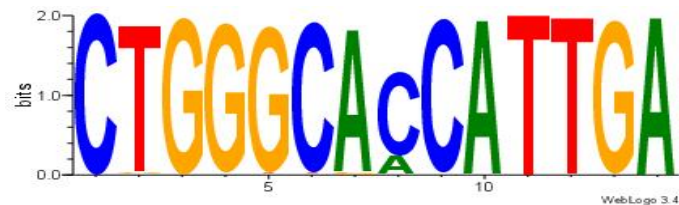


Dataset #: 1
Motif ID: 147
Motif name: Motif 147
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 13
Similarity score: 0.0768151

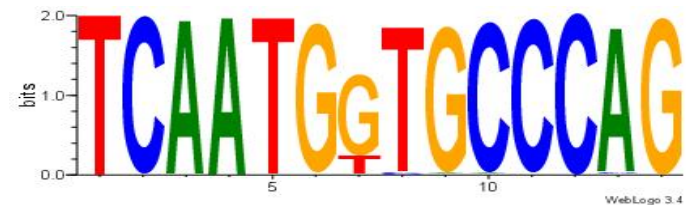
Alignment:

CTGGGCACCATTGA
-TTGAGAACCACTG

Original motif Consensus sequence: CTGGGCACCATTGA



Reverse complement motif Consensus sequence: TCAATGGTGCCCAAG

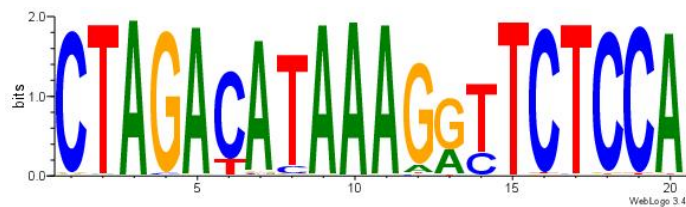


Dataset #: 1
 Motif ID: 85
 Motif name: Motif 85
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 8
 Number of overlap: 13
 Similarity score: 0.0785125

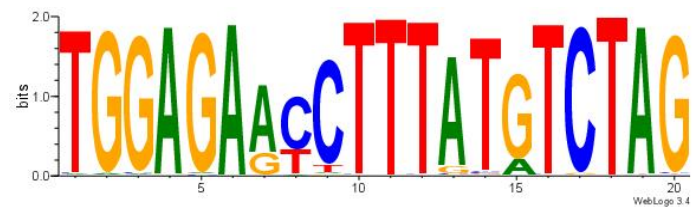
Alignment:

CTAGACATAAAGGTTCTCCA
 -----CAGTGGTTCTCAA

Original motif Consensus sequence: CTAGACATAAAGGTTCTCCA



Reverse complement motif Consensus sequence: TGGAGAACCTTTATGTCTAG



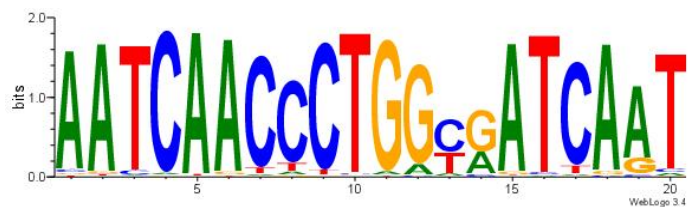
Dataset #: 1
 Motif ID: 170
 Motif name: Motif 170
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2

Number of overlap: 13
Similarity score: 0.0831649

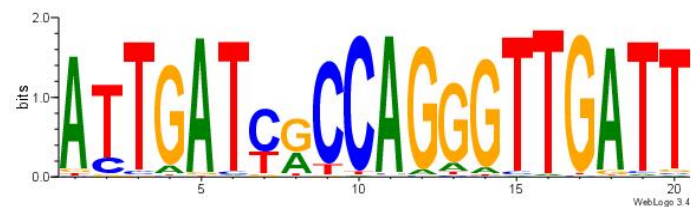
Alignment:

ATTGATMKCCAGGGTTGATT
-TTGAGAACCACTG-----

Original motif Consensus sequence: AATCAACCCTGGYRATCAAT



Reverse complement motif Consensus sequence:
ATTGATMKCCAGGGTTGATT

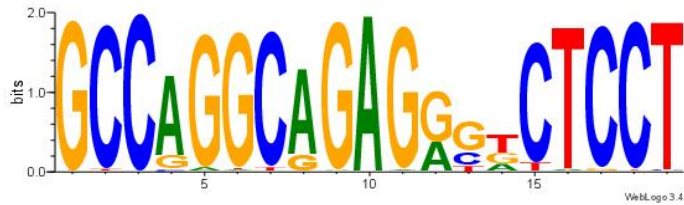


Dataset #: 1
Motif ID: 43
Motif name: Motif 43
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 13
Similarity score: 0.0849124

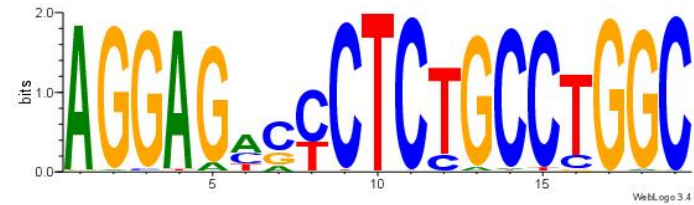
Alignment:

GCCAGGCAGAGRGKCTCCT
-----CAGTGGTTCTCAA

Original motif Consensus sequence: GCCAGGCAGAGRGKCTCCT

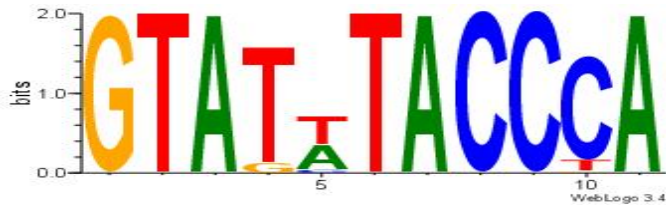


Reverse complement motif Consensus sequence: AGGAGRCMCTCTGCCTGGC



Dataset #: 1 Motif ID: 244 Motif name: Motif 244

Original motif Consensus sequence: GTATWTACCCA



Reverse complement motif Consensus sequence: TGGGTAWATAC



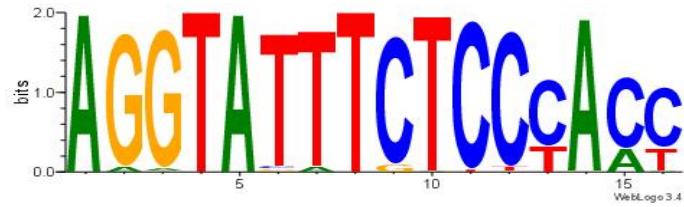
Best Matches for Motif ID 244 (Highest to Lowest)

Dataset #:	1
Motif ID:	168
Motif name:	Motif 168
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	3
Number of overlap:	11
Similarity score:	0.0692202

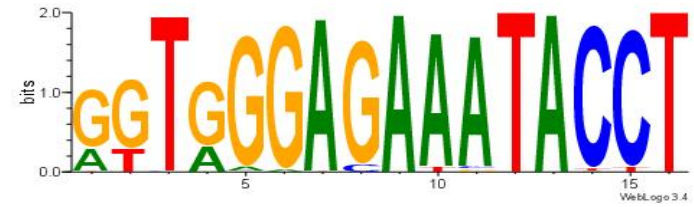
Alignment:

GGTGGGAGAAATACCT
---TGGGTAWATAC--

Original motif Consensus sequence: AGGTATTTCTCCCACC



Reverse complement motif Consensus sequence:
GGTGGGAGAAATACCT

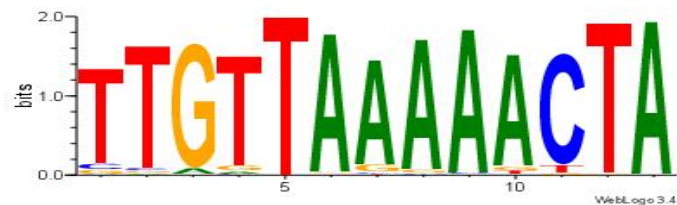
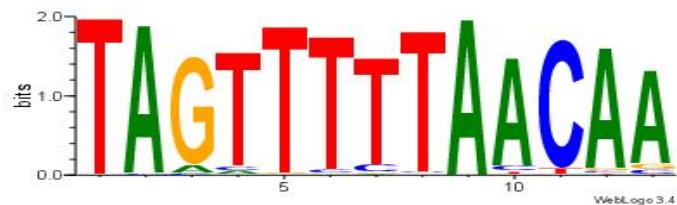


Dataset #: 1
Motif ID: 319
Motif name: Motif 319
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 11
Similarity score: 0.0769317

Alignment:
TTGTTAAAACTA
TGGGTAWATAC--

Original motif Consensus sequence: TAGTTTTTAACAA

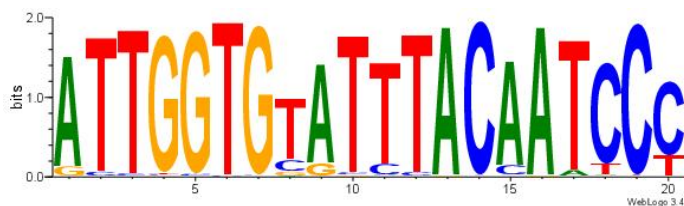
Reverse complement motif Consensus sequence: TTGTTAAAACTA



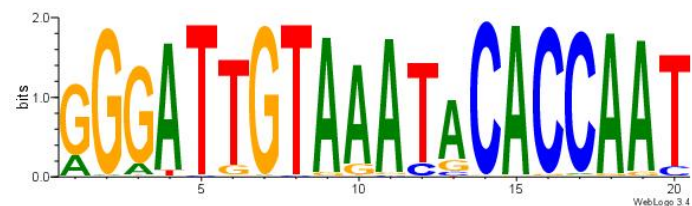
Dataset #: 1
 Motif ID: 106
 Motif name: Motif 106
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 4
 Number of overlap: 11
 Similarity score: 0.077946

Alignment:
 GGGATTGTAAATACACCAAT
 ---TGGGTAWATAC-----

Original motif Consensus sequence: ATTGGTGTATTTACAATCCC



Reverse complement motif Consensus sequence: GGGATTGTAAATACACCAAT



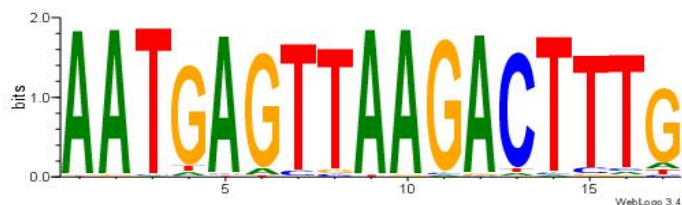
Dataset #: 1

Motif ID: 224
Motif name: Motif 224
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 5
Number of overlap: 11
Similarity score: 0.0793596

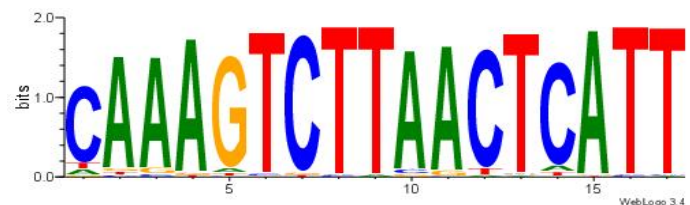
Alignment:

AATGAGTTAAGACTTTG
----TGGGTAWATAC--

Original motif Consensus sequence: AATGAGTTAAGACTTTG



Reverse complement motif Consensus sequence: CAAAGTCTTAACTCATT



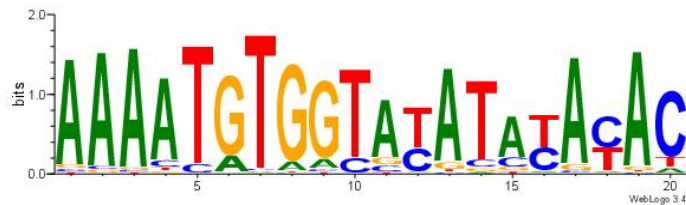
Dataset #: 1
Motif ID: 83
Motif name: Motif 83
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 9
Number of overlap: 11

Similarity score: 0.0804324

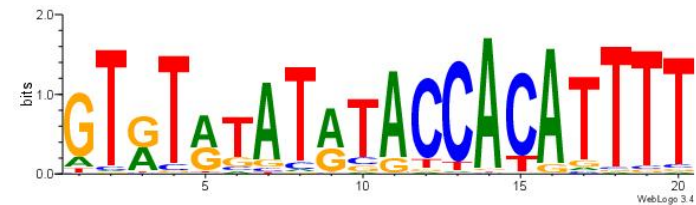
Alignment:

```
AAAATGTGGTAYATAYAYAC  
-----GTATWTACCCA-
```

Original motif Consensus sequence: AAAATGTGGTAYATAYAYAC

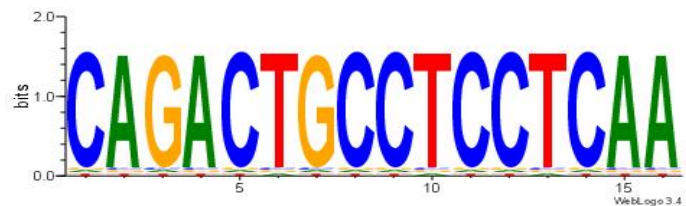


Reverse complement motif Consensus sequence: GTKTMTATMTACCACATTTT

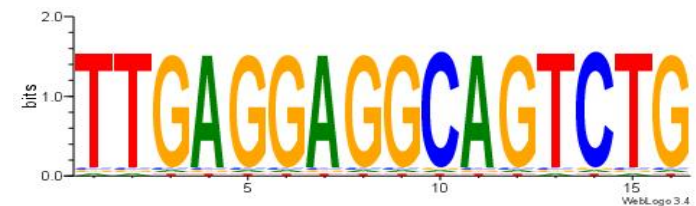


Dataset #: 1 Motif ID: 245 Motif name: Motif 245

Original motif Consensus sequence: CAGACTGCCTCCTCAA



Reverse complement motif Consensus sequence: TTGAGGAGGCAGTCTG



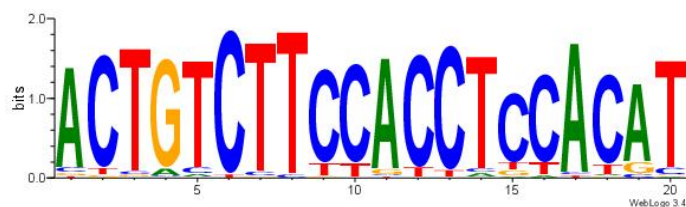
Best Matches for Motif ID 245 (Highest to Lowest)

Dataset #:	1
Motif ID:	178
Motif name:	Motif 178
Matching format of first motif:	Reverse Complement

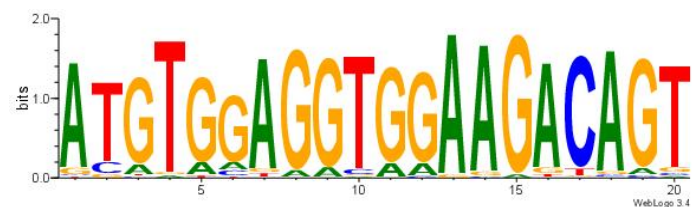
Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 16
 Similarity score: 0.0807607

Alignment:
 ATGTGGAGGTGGAAGACAGT
 ---TTGAGGAGGCAGTCTG-

Original motif Consensus sequence: ACTGTCTTCCACCTCCACAT



Reverse complement motif Consensus sequence: ATGTGGAGGTGGAAGACAGT

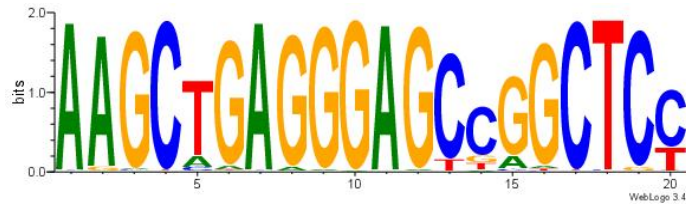


Dataset #: 1
 Motif ID: 96
 Motif name: Motif 96
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 4
 Number of overlap: 16
 Similarity score: 0.0972589

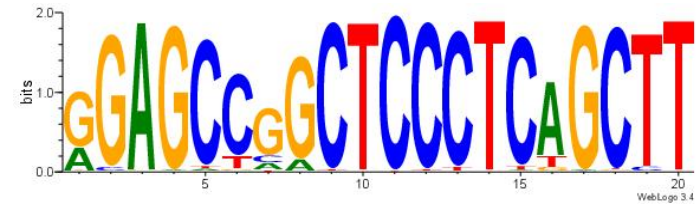
Alignment:

AAGCTGAGGGAGCCGGCTCC
-TTGAGGAGGCAGTCTG---

Original motif Consensus sequence: AAGCTGAGGGAGCCGGCTCC



Reverse complement motif Consensus sequence:
GGAGCCGGCTCCCTCAGCTT

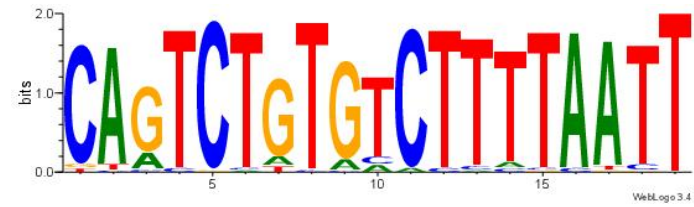
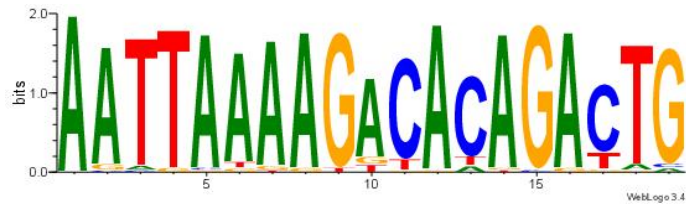


Dataset #: 1
Motif ID: 356
Motif name: Motif 356
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 4
Number of overlap: 16
Similarity score: 0.0988443

Alignment:
AATTAAAAGACACAGACTG
---TTGAGGAGGCAGTCTG

Original motif Consensus sequence: AATTAAAAGACACAGACTG

Reverse complement motif Consensus sequence:
CAGTCTGTGTCTTTTAATT



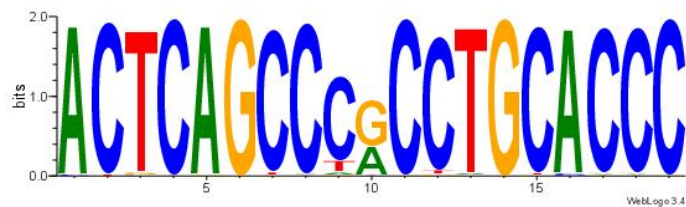
Dataset #: 1
 Motif ID: 149
 Motif name: Motif 149
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 16
 Similarity score: 0.100811

Alignment:

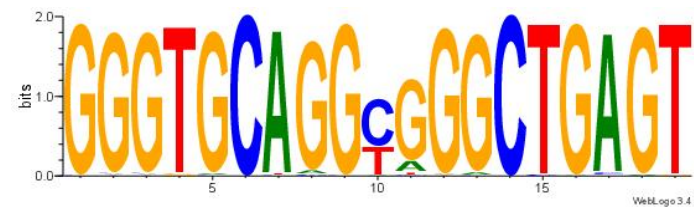
```

ACTCAGCCRCCTGCACCC
---CAGACTGCCTCCTCAA
  
```

Original motif Consensus sequence: ACTCAGCCRCCTGCACCC



Reverse complement motif Consensus sequence: GGGTGCAGGMGGCTGAGT



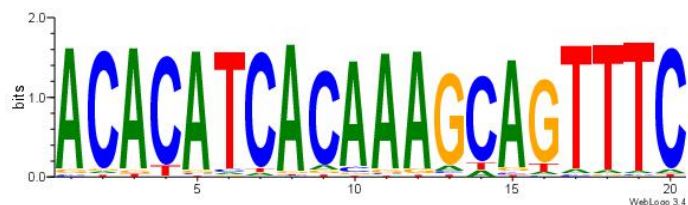
Dataset #: 1

Motif ID: 202
 Motif name: Motif 202
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 5
 Number of overlap: 16
 Similarity score: 0.105987

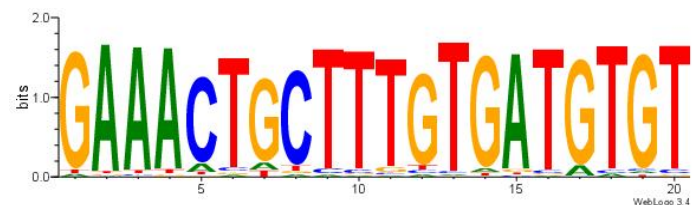
Alignment:

ACACATCACAAAGCAGTTTC
 TTGAGGAGGCAGTCTG-----

Original motif Consensus sequence: ACACATCACAAAGCAGTTTC

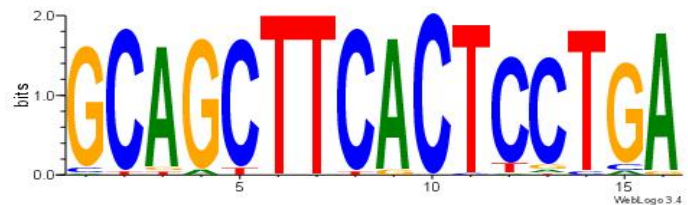


Reverse complement motif Consensus sequence: GAAACTGCTTTGTGATGTGT

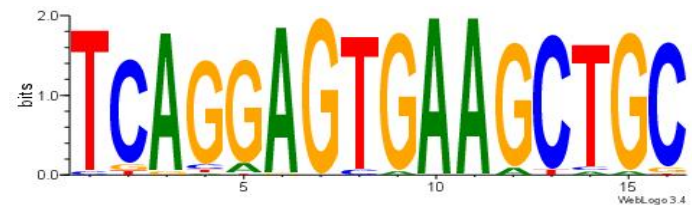


Dataset #: 1 Motif ID: 246 Motif name: Motif 246

Original motif Consensus sequence: GCAGCTTCACTccTGA



Reverse complement motif Consensus sequence: TCAGGAGTGAAAGCTGC



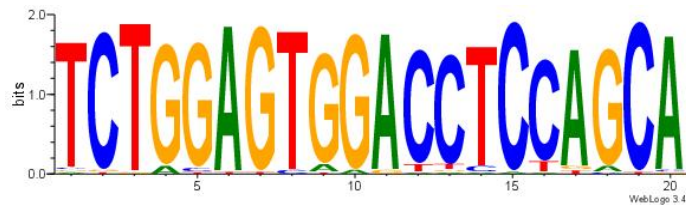
Best Matches for Motif ID 246 (Highest to Lowest)

Dataset #: 1
Motif ID: 350
Motif name: Motif 350
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 16
Similarity score: 0.0626054

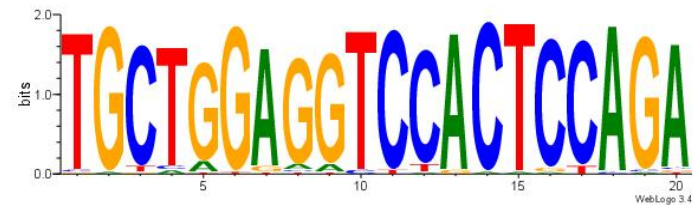
Alignment:

```
TCTGGAGTGGACCTCCAGCA  
TCAGGAGTGAAGCTGC-----
```

Original motif Consensus sequence: TCTGGAGTGGACCTCCAGCA



Reverse complement motif Consensus sequence:
TGCTGGAGGTCCACTCCAGA



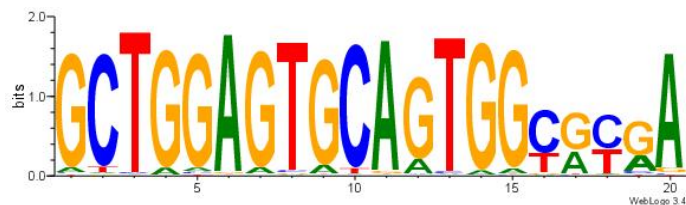
Dataset #: 1
Motif ID: 3
Motif name: Motif 3
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif

Direction: Forward
 Position number: 5
 Number of overlap: 16
 Similarity score: 0.0810673

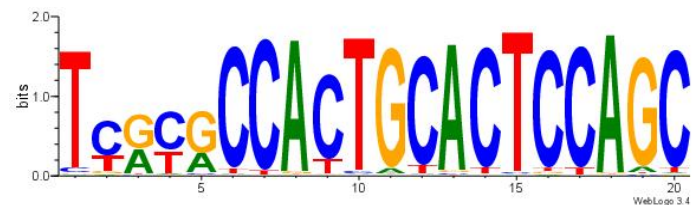
Alignment:

GCTGGAGTGCAGTGGCRYGA
 ----TCAGGAGTGAAGCTGC

Original motif Consensus sequence: GCTGGAGTGCAGTGGCRYGA



Reverse complement motif Consensus sequence: TCKMGCCACTGCACTCCAGC

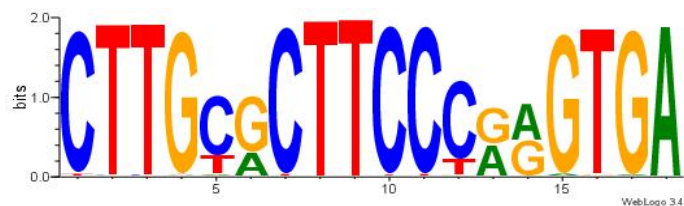


Dataset #: 1
 Motif ID: 15
 Motif name: Motif 15
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 16
 Similarity score: 0.087745

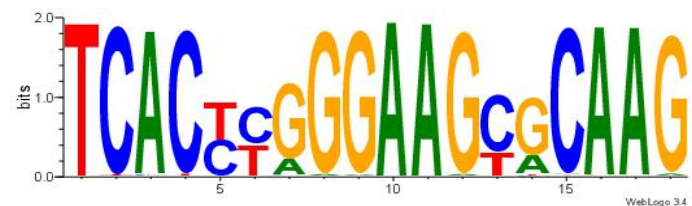
Alignment:

TCACKMGGGAAGCGCAAG
 TCAGGAGTGAAGCTGC--

Original motif Consensus sequence: CTTGCGCTCCCRGTGA



Reverse complement motif Consensus sequence: TCACKMGGGAAGCGCAAG

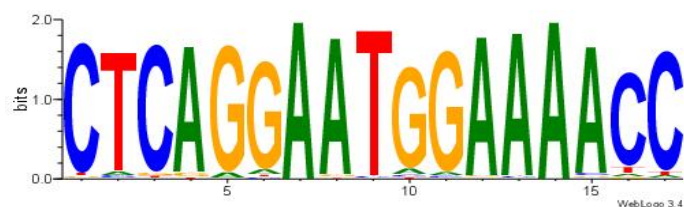


Dataset #: 1
Motif ID: 214
Motif name: Motif 214
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 16
Similarity score: 0.0898189

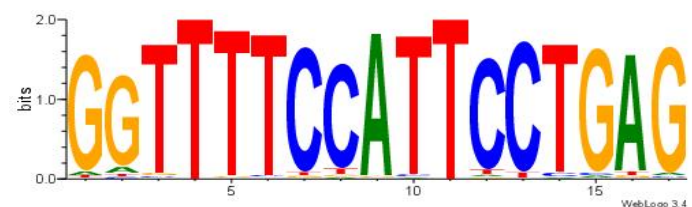
Alignment:

GGTTTTCCATTCCCTGAG
-GCAGCTTCACTCCTGA

Original motif Consensus sequence: CTCAGGAATGGAAAACC



Reverse complement motif Consensus sequence: GGTTTTCCATTCCCTGAG

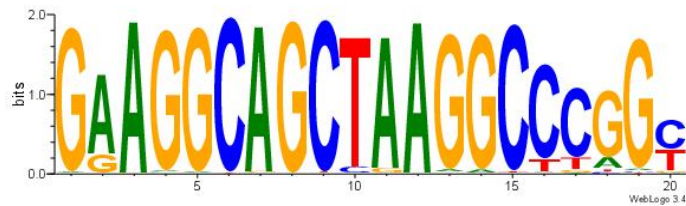


Dataset #: 1
 Motif ID: 64
 Motif name: Motif 64
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 5
 Number of overlap: 16
 Similarity score: 0.0986718

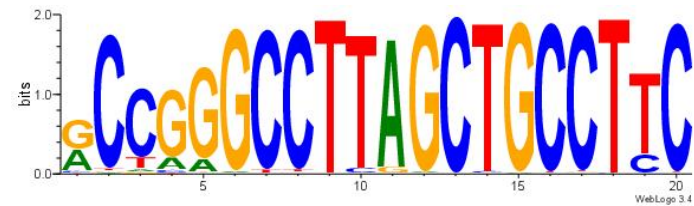
Alignment:

KCCGGGCCTTAGCTGCCTTC
 TCAGGAGTGAAGCTGC-----

Original motif Consensus sequence: GAAGGCAGCTAAGGCCCGY



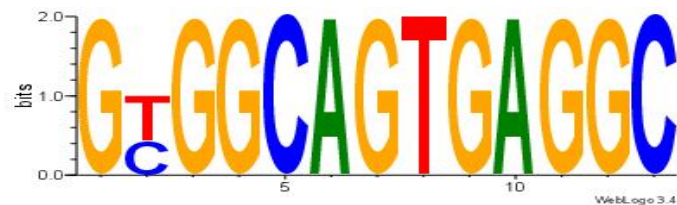
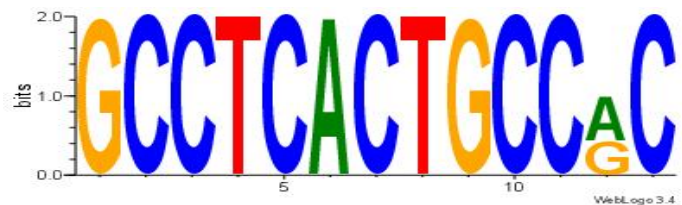
Reverse complement motif Consensus sequence: KCCGGGCCTTAGCTGCCTTC



Dataset #: 1 Motif ID: 247 Motif name: Motif 247

Original motif Consensus sequence: GCCTCACTGCCRC

Reverse complement motif Consensus sequence: GKGGCAGTGAGG

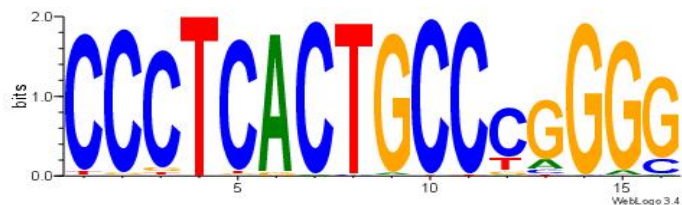


Best Matches for Motif ID 247 (Highest to Lowest)

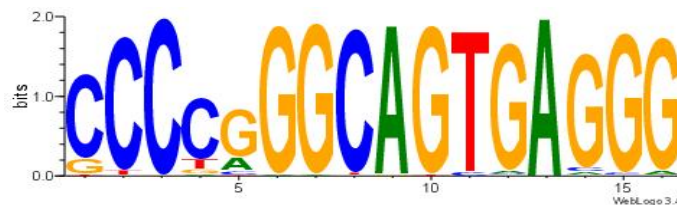
Dataset #: 1
 Motif ID: 136
 Motif name: Motif 136
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 13
 Similarity score: 0.0407776

Alignment:
 CCCCggGCAGTGAGGG
 ---GKGGCAGTGAGGC

Original motif Consensus sequence: CCCTCACTGCCGGGG



Reverse complement motif Consensus sequence: CCCCggGCAGTGAGGG

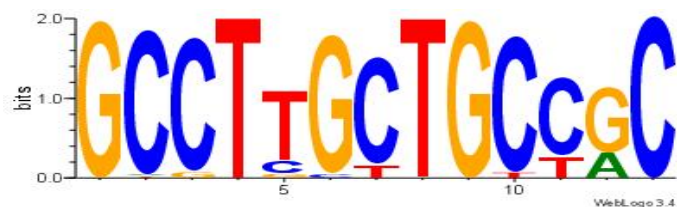


Dataset #: 1
 Motif ID: 229
 Motif name: Motif 229
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 13
 Similarity score: 0.0419595

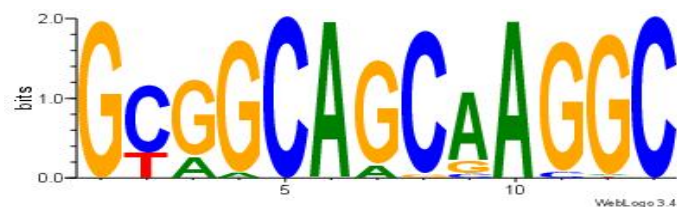
Alignment:

GCCTTGCTGCCGC
 GCCTCACTGCCRC

Original motif Consensus sequence: GCCTTGCTGCCGC



Reverse complement motif Consensus sequence: GCGGCAGCAAGGC



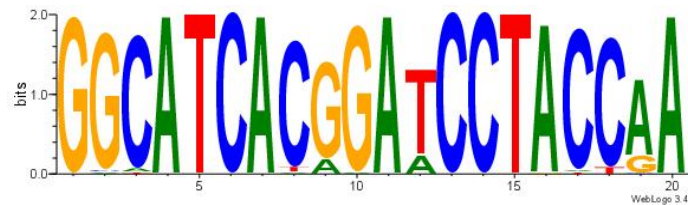
Dataset #: 1
 Motif ID: 311
 Motif name: Motif 311
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 13

Similarity score: 0.0798714

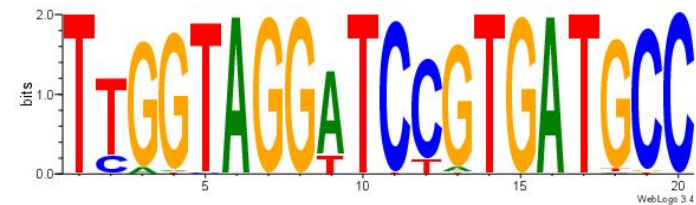
Alignment:

TTGGTAGGATCCGTGATGCC
-----GKGGCAGTGAGGC-

Original motif Consensus sequence: GGCATCACGGATCCTACCAA



Reverse complement motif Consensus sequence:
TTGGTAGGATCCGTGATGCC



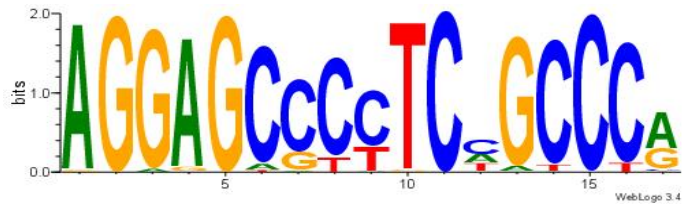
Dataset #: 1
Motif ID: 111
Motif name: Motif 111
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 13
Similarity score: 0.0800588

Alignment:

KGGGCDGAGGGGCTCCT
GKGGCAGTGAGGC----

Original motif Consensus sequence: AGGAGCCCCTCHGCCCR

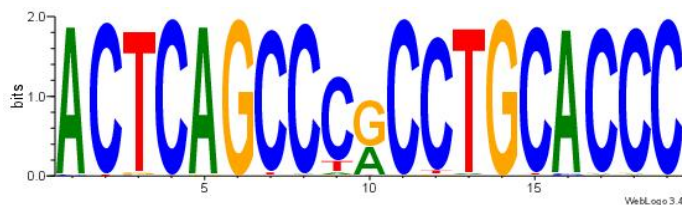
Reverse complement motif Consensus sequence:
KGGGCDGAGGGGCTCCT



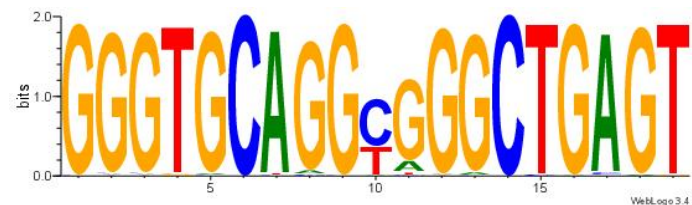
Dataset #: 1
 Motif ID: 149
 Motif name: Motif 149
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 13
 Similarity score: 0.0819712

Alignment:
 GGGTGCAGGMGGGCTGAGT
 -GKGGCAGTGAGGC-----

Original motif Consensus sequence: ACTCAGCCRCCTGCACCC

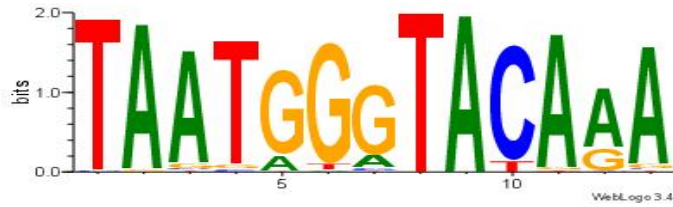


Reverse complement motif Consensus sequence: GGGTGCAGGMGGGCTGAGT

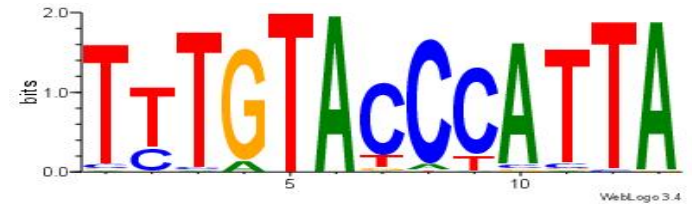


Dataset #: 1 Motif ID: 248 Motif name: Motif 248

Original motif Consensus sequence: TAATGGGTACAAA



Reverse complement motif Consensus sequence: TTTGTACCCATTA



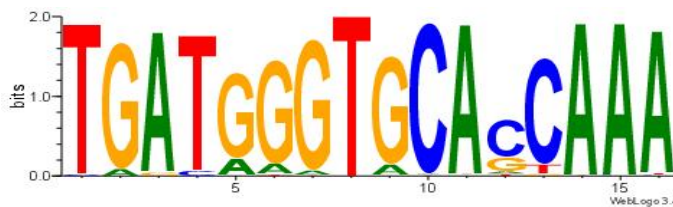
Best Matches for Motif ID 248 (Highest to Lowest)

Dataset #:	1
Motif ID:	289
Motif name:	Motif 289
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	4
Number of overlap:	13
Similarity score:	0.0609387

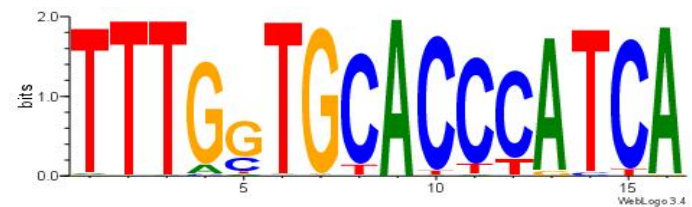
Alignment:

```
TGATGGGTGCACCAA  
TAATGGGTACAAA---
```

Original motif Consensus sequence: TGATGGGTGCACCAA



Reverse complement motif Consensus sequence: TTTGGTGCACCCATCA

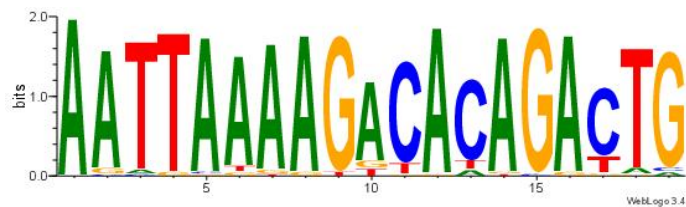


Dataset #: 1
 Motif ID: 356
 Motif name: Motif 356
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 4
 Number of overlap: 13
 Similarity score: 0.0698241

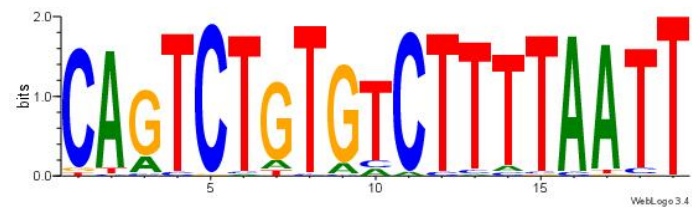
Alignment:

AATTAAAAGACACAGACTG
 ---TAATGGGTACAAA---

Original motif Consensus sequence: AATTAAAAGACACAGACTG



Reverse complement motif Consensus sequence: CAGTCTGTCTTTTAATT



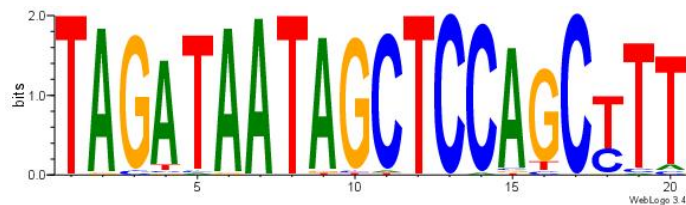
Dataset #: 1
 Motif ID: 333
 Motif name: Motif 333
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 4

Number of overlap: 13
Similarity score: 0.0771988

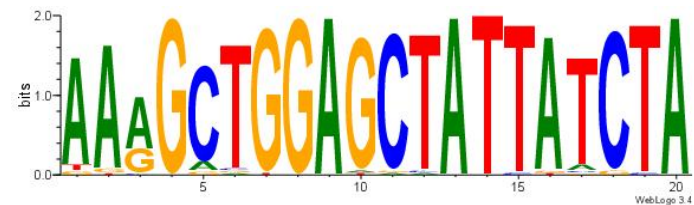
Alignment:

TAGATAATAGCTCCAGCTTT
----TAATGGGTACAAA----

Original motif Consensus sequence: TAGATAATAGCTCCAGCTTT



Reverse complement motif Consensus sequence:
AAAGCTGGAGCTATTATCTA

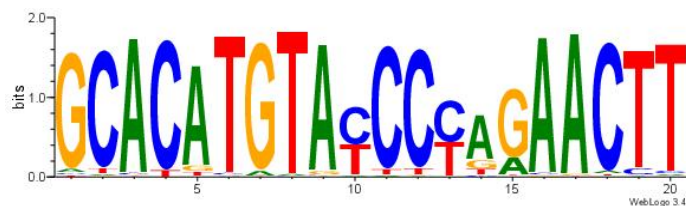


Dataset #: 1
Motif ID: 225
Motif name: Motif 225
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 5
Number of overlap: 13
Similarity score: 0.0773246

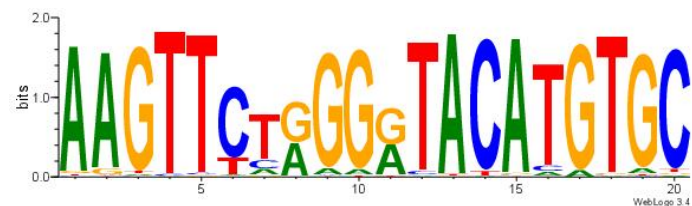
Alignment:

GCACATGTAYCCYAGAACTT
----TTTGTACCCATTA----

Original motif Consensus sequence: GCACATGTAYCCYAGAACTT



Reverse complement motif Consensus sequence:
AAGTTCTKGGKTACATGTGC

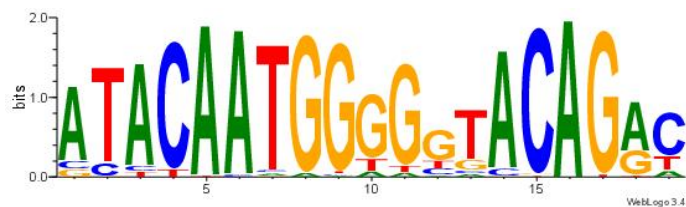


Dataset #: 1
Motif ID: 193
Motif name: Motif 193
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 4
Number of overlap: 13
Similarity score: 0.0779989

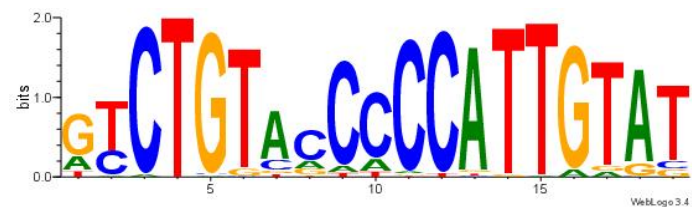
Alignment:

GKCTGTACCCCATTTGTAT
---TTTGTACCCATTA---

Original motif Consensus sequence: ATACAATGGGGGTACAGRC

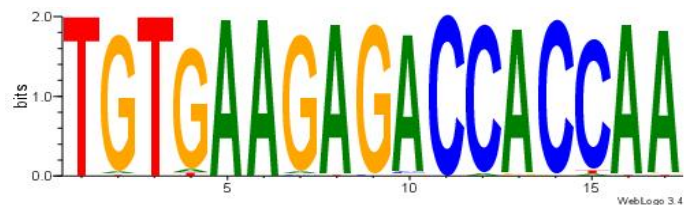


Reverse complement motif Consensus sequence:
GKCTGTACCCCATTTGTAT

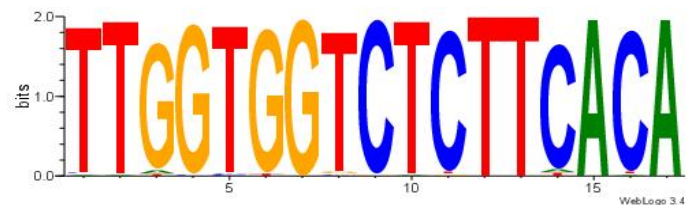


Dataset #: 1 Motif ID: 249 Motif name: Motif 249

Original motif Consensus sequence: TGTGAAGAGACCACCAA



Reverse complement motif Consensus sequence: TTGGTGGTCTCTTCACA



Best Matches for Motif ID 249 (Highest to Lowest)

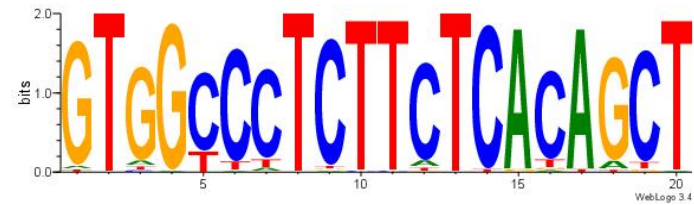
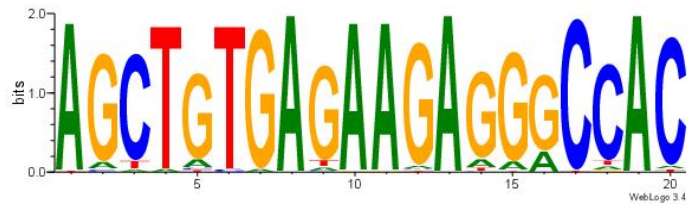
Dataset #:	1
Motif ID:	294
Motif name:	Motif 294
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	4
Number of overlap:	17
Similarity score:	0.0818261

Alignment:

```
AGCTGTGAGAAGAGGGCCAC  
---TGTGAAGAGACCACCAA
```

Original motif Consensus sequence: AGCTGTGAGAAGAGGGCCAC

Reverse complement motif Consensus sequence:
GTGGCCCTCTCTCACAGCT

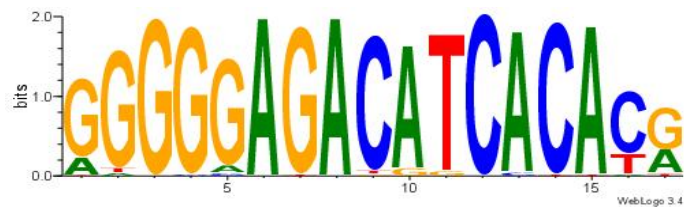


Dataset #: 1
 Motif ID: 279
 Motif name: Motif 279
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 17
 Similarity score: 0.106605

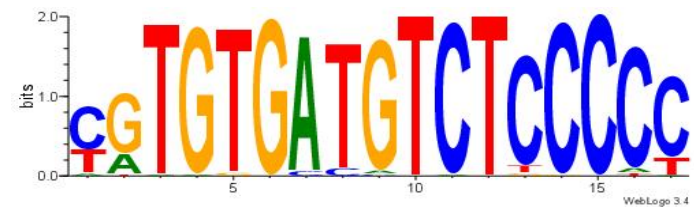
Alignment:

MGTGTGATGTCTCCCC
 TTGGTGGTCTCTCACA

Original motif Consensus sequence: GGGGGAGACATCACACR



Reverse complement motif Consensus sequence: MGTGTGATGTCTCCCC



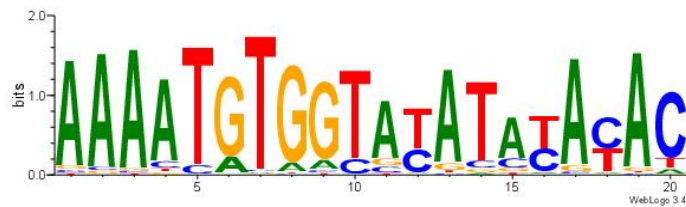
Dataset #: 1

Motif ID: 83
 Motif name: Motif 83
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3
 Number of overlap: 17
 Similarity score: 0.110316

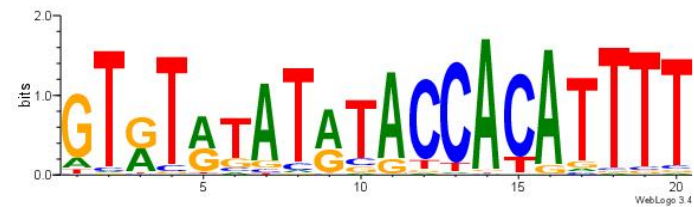
Alignment:

GTKTMTATMTACCACATTTT
 --TGTGAAGAGACCACCAA-

Original motif Consensus sequence: AAAATGTGGTAYATAYAYAC



Reverse complement motif Consensus sequence: GTKTMTATMTACCACATTTT



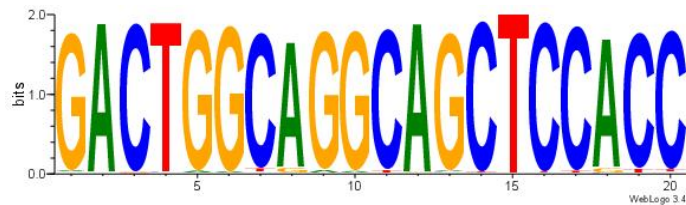
Dataset #: 1
 Motif ID: 52
 Motif name: Motif 52
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 17

Similarity score: 0.112629

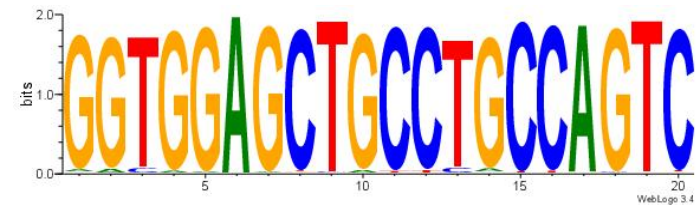
Alignment:

GGTGGAGCTGCCTGCCAGTC
---TGTGAAGAGACCACCAA

Original motif Consensus sequence: GACTGGCAGGCAGCTCCACC



Reverse complement motif Consensus sequence:
GGTGGAGCTGCCTGCCAGTC



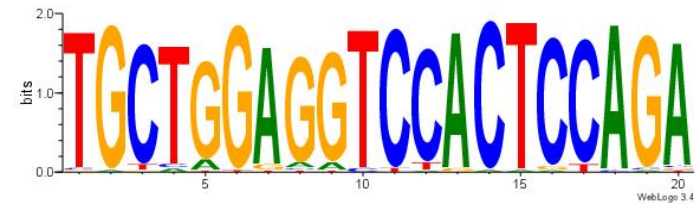
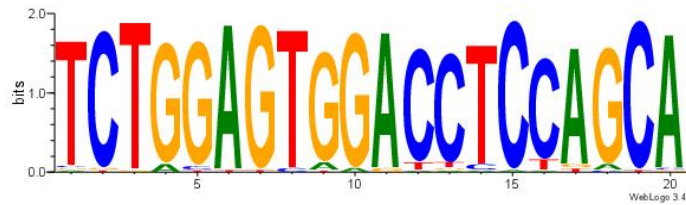
Dataset #: 1
Motif ID: 350
Motif name: Motif 350
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 17
Similarity score: 0.112706

Alignment:

TGCTGGAGGTCCACTCCAGA
---TTGGTGGTCTCTTCACA

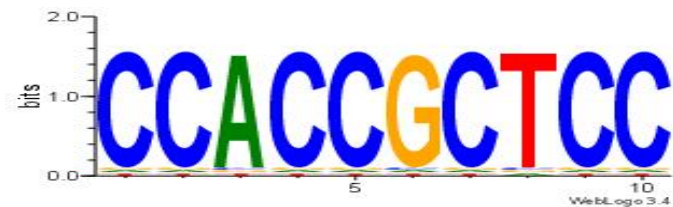
Original motif Consensus sequence: TCTGGAGTGGACCTCCAGCA

Reverse complement motif Consensus sequence:
TGCTGGAGGTCCACTCCAGA

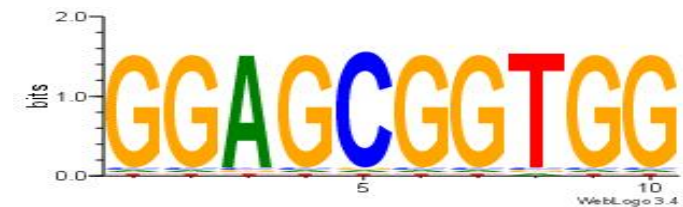


Dataset #: 1 Motif ID: 250 Motif name: Motif 250

Original motif Consensus sequence: CCACCGCTCC



Reverse complement motif Consensus sequence: GGAGCGGTGG

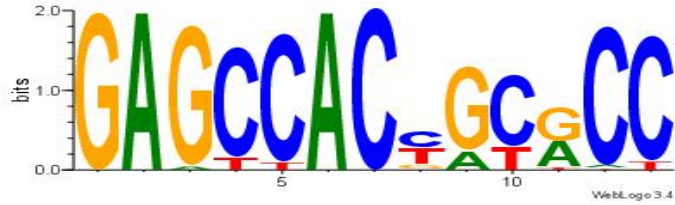


Best Matches for Motif ID 250 (Highest to Lowest)

Dataset #:	1
Motif ID:	107
Motif name:	Motif 107
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	10
Similarity score:	0.03718

Alignment:
GGMGCKGTGGCTC
GGAGCGGTGG----

Original motif Consensus sequence: GAGCCACYGCRCC



Reverse complement motif Consensus sequence: GGMGCKGTGGCTC

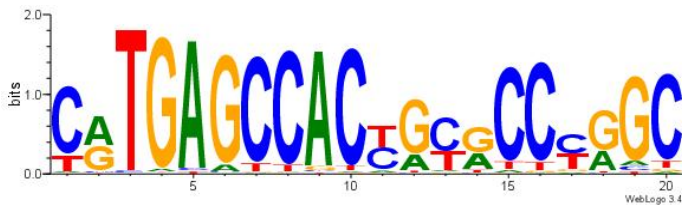


Dataset #: 1
 Motif ID: 56
 Motif name: Motif 56
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 7
 Number of overlap: 10
 Similarity score: 0.0459856

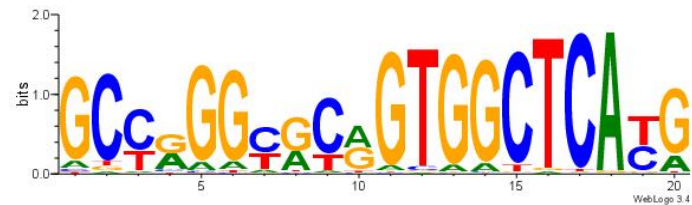
Alignment:

```
CRTGAGCCACYGYRCCYGGC
-----CCACCGCTCC-----
```

Original motif Consensus sequence: CRTGAGCCACYGYRCCYGGC



Reverse complement motif Consensus sequence: GCCKGGMKCMGTGGCTCAKG

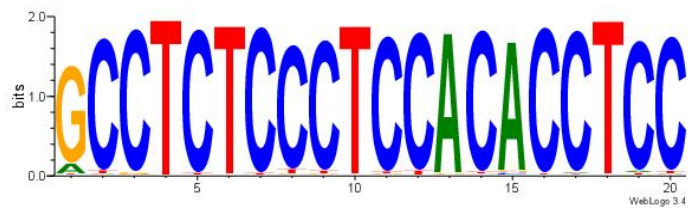


Dataset #: 1
 Motif ID: 105
 Motif name: Motif 105
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 10
 Similarity score: 0.0478436

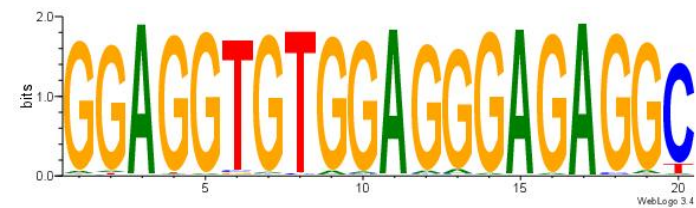
Alignment:

GGAGGTGTGGAGGGAGAGGC
 GGAGCGGTGG-----

Original motif Consensus sequence: GCCTCTCCCTCCACACCTCC



Reverse complement motif Consensus sequence: GGAGGTGTGGAGGGAGAGGC

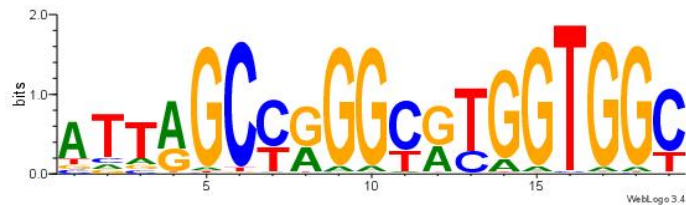


Dataset #: 1
 Motif ID: 2
 Motif name: Motif 2
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2

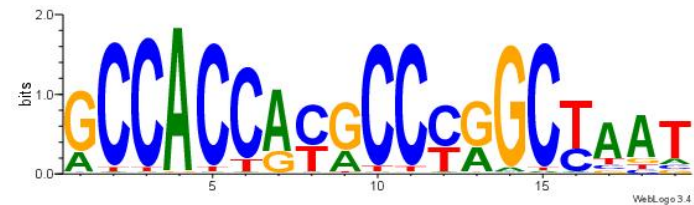
Number of overlap: 10
Similarity score: 0.0491967

Alignment:
ATTAGCYRGGCRTGGTGGC
-GGAGCGGTGG-----

Original motif Consensus sequence: ATTAGCYRGGCRTGGTGGC



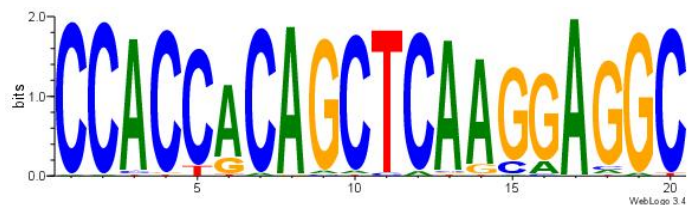
Reverse complement motif Consensus sequence: GCCACCAMGCCMKGCTAAT



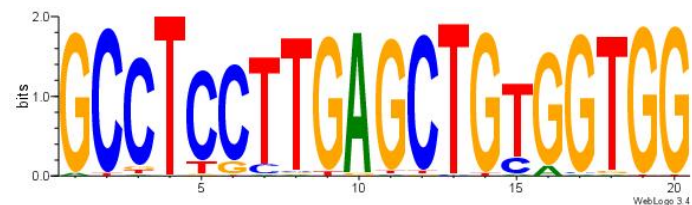
Dataset #: 1
Motif ID: 331
Motif name: Motif 331
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 8
Number of overlap: 10
Similarity score: 0.0519556

Alignment:
GCCTCCTTGAGCTGTGGTGG
-----GGAGCGGTGG---

Original motif Consensus sequence: CCACCACAGCTCAAGGAGGC

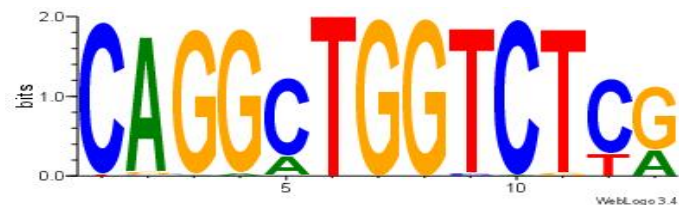


Reverse complement motif Consensus sequence: GCCTCCTTGAGCTGTGGTGG



Dataset #: 1 Motif ID: 251 Motif name: Motif 251

Original motif Consensus sequence: CAGGCTGGTCTCG



Reverse complement motif Consensus sequence: CGAGACCAGCCTG



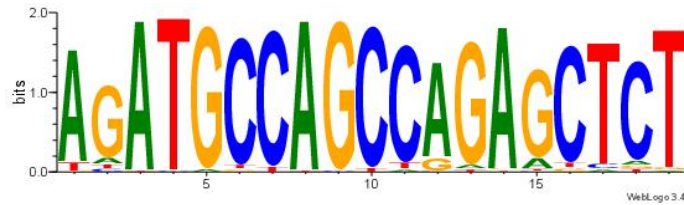
Best Matches for Motif ID 251 (Highest to Lowest)

Dataset #:	1
Motif ID:	307
Motif name:	Motif 307
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	13
Similarity score:	0.0730434

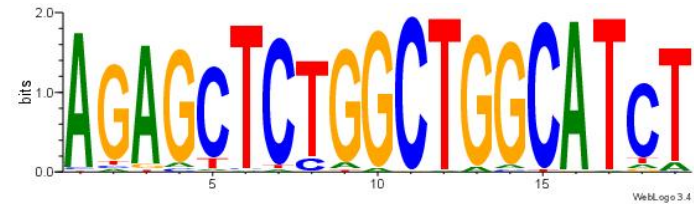
Alignment:

AGATGCCAGCCAGAGCTCT
CGAGACCAGCCTG-----

Original motif Consensus sequence: AGATGCCAGCCAGAGCTCT



Reverse complement motif Consensus sequence:
AGAGCTCTGGCTGGCATCT

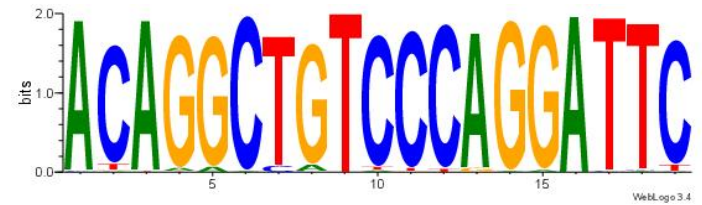
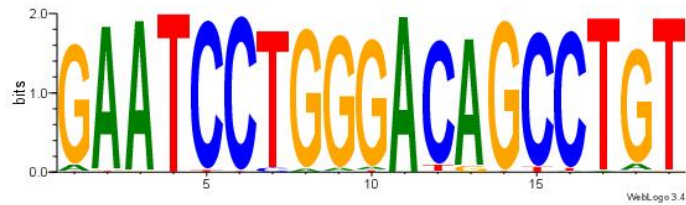


Dataset #: 1
Motif ID: 192
Motif name: Motif 192
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 6
Number of overlap: 13
Similarity score: 0.0761402

Alignment:
ACAGGCTGTCCCAGGATTC
-----CAGGCTGGTCTCG-

Original motif Consensus sequence: GAATCCTGGGACAGCCTGT

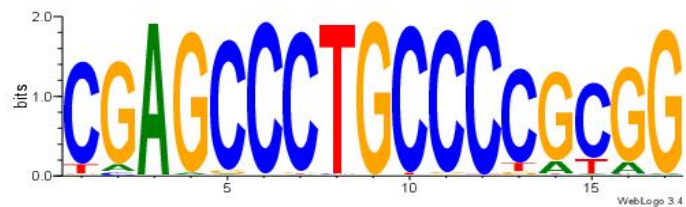
Reverse complement motif Consensus sequence:
ACAGGCTGTCCCAGGATTC



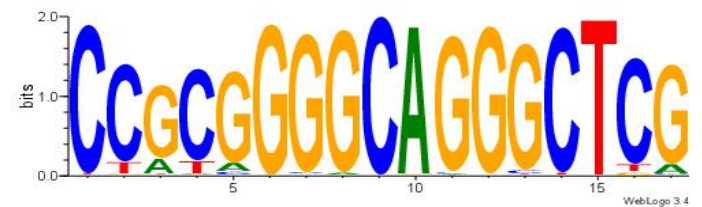
Dataset #: 1
 Motif ID: 78
 Motif name: Motif 78
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 13
 Similarity score: 0.0811019

Alignment:
 CGAGCCCTGCCCCGCGG
 ----CGAGACCAGCCTG

Original motif Consensus sequence: CGAGCCCTGCCCCGCGG



Reverse complement motif Consensus sequence: CCGCGGGGCAGGGCTCG



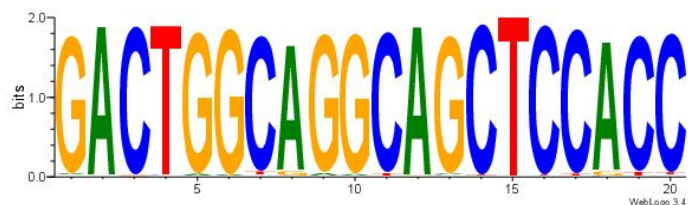
Dataset #: 1

Motif ID: 52
 Motif name: Motif 52
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 7
 Number of overlap: 13
 Similarity score: 0.0865311

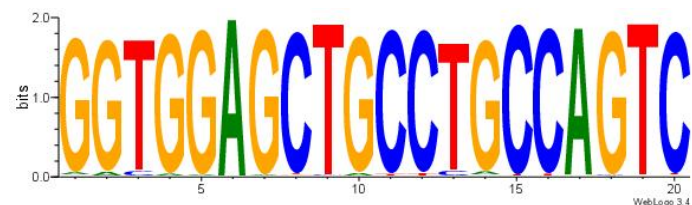
Alignment:

GGTGGAGCTGCCTGCCAGTC
 -CGAGACCAGCCTG-----

Original motif Consensus sequence: GACTGGCAGGCAGCTCCACC



Reverse complement motif Consensus sequence: GGTGGAGCTGCCTGCCAGTC



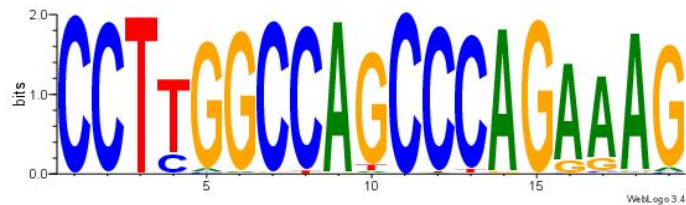
Dataset #: 1
 Motif ID: 122
 Motif name: Motif 122
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 13

Similarity score: 0.0910885

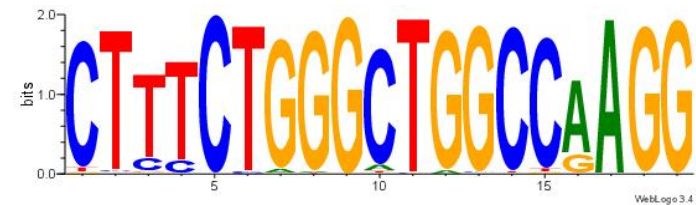
Alignment:

CTTTCTGGGCTGGCCAAGG
-CAGGCTGGTCTCG-----

Original motif Consensus sequence: CCTTGGCCAGCCCAGAAAG



Reverse complement motif Consensus sequence: CTTTCTGGGCTGGCCAAGG



Dataset #: 1 Motif ID: 252 Motif name: Motif 252

Original motif Consensus sequence: AATTAGC_cGG



Reverse complement motif Consensus sequence: CCMKGCTAATT



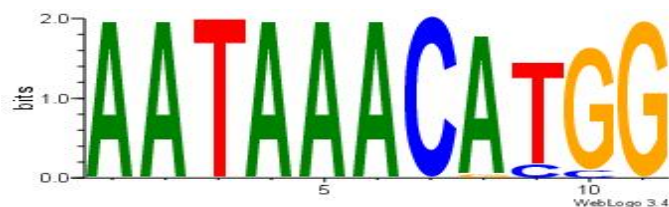
Best Matches for Motif ID 252 (Highest to Lowest)

Dataset #:	1
Motif ID:	226
Motif name:	Motif 226
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement

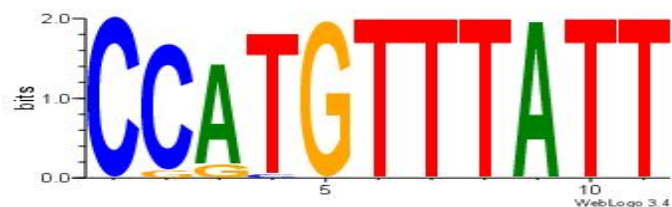
Direction: Forward
Position number: 1
Number of overlap: 11
Similarity score: 0.0630561

Alignment:
CCATGTTTATT
CCMKGCTAATT

Original motif Consensus sequence: AATAACATGG



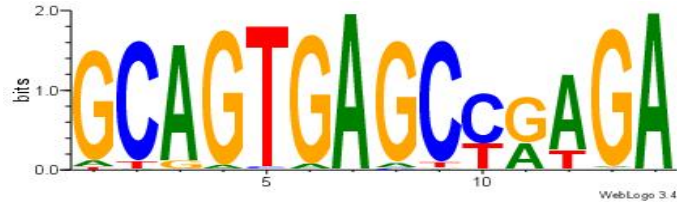
Reverse complement motif Consensus sequence: CCATGTTTATT



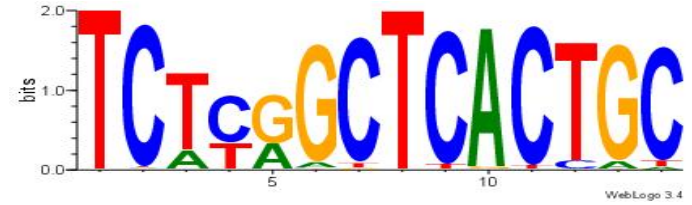
Dataset #: 1
Motif ID: 38
Motif name: Motif 38
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 3
Number of overlap: 11
Similarity score: 0.0649059

Alignment:
TCTMKGCTCACTGC
-CCMKGCTAATT--

Original motif Consensus sequence: GCAGTGAGCYRAGA



Reverse complement motif Consensus sequence: TCTMKGCTCACTG

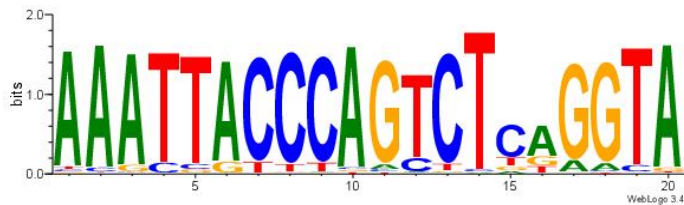


Dataset #: 1
Motif ID: 160
Motif name: Motif 160
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 2
Number of overlap: 11
Similarity score: 0.0702894

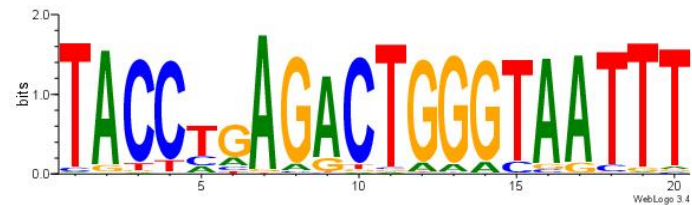
Alignment:

AAATTACCCAGTCTCAGGTA
-AATTAGCYRGG-----

Original motif Consensus sequence: AAATTACCCAGTCTCAGGTA



Reverse complement motif Consensus sequence: TACCTGAGACTGGGTAATTT

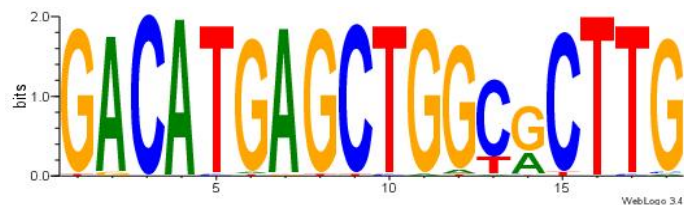


Dataset #: 1
 Motif ID: 306
 Motif name: Motif 306
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 6
 Number of overlap: 11
 Similarity score: 0.0819954

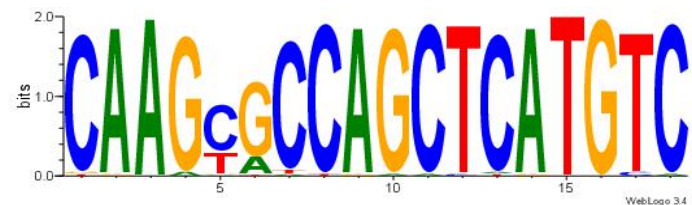
Alignment:

GACATGAGCTGGCGCTTG
 --AATTAGCYRGG-----

Original motif Consensus sequence: GACATGAGCTGGCGCTTG



Reverse complement motif Consensus sequence: CAAGCGCCAGCTCATGTC

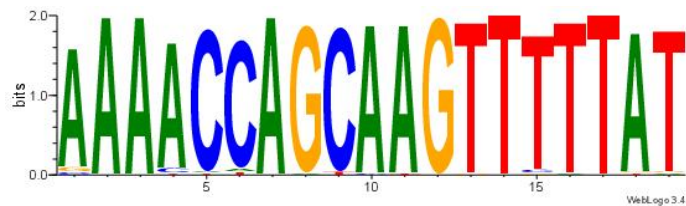


Dataset #: 1
 Motif ID: 330
 Motif name: Motif 330
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 4

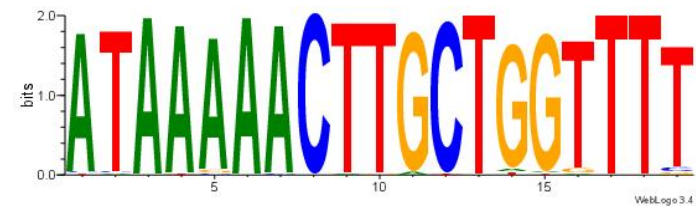
Number of overlap: 11
 Similarity score: 0.0823491

Alignment:
 ATAAAAACTTGCTGGTTTT
 -----AATTAGCYRGG----

Original motif Consensus sequence: AAAACCAGCAAGTTTTTAT

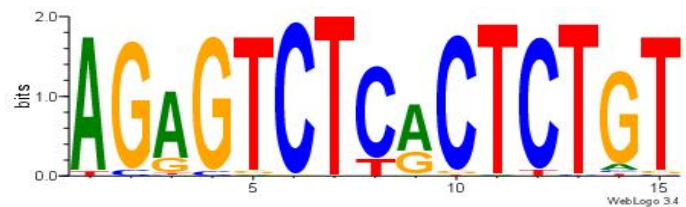


Reverse complement motif Consensus sequence:
 ATAAAAACTTGCTGGTTTT

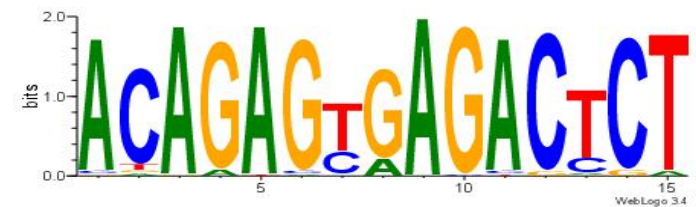


Dataset #: 1 Motif ID: 253 Motif name: Motif 253

Original motif Consensus sequence: AGAGTCTCACTCTGT



Reverse complement motif Consensus sequence: ACAGAGTGAGACTCT



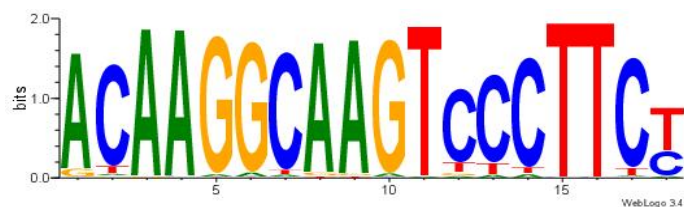
Best Matches for Motif ID 253 (Highest to Lowest)

Dataset #: 1
 Motif ID: 231
 Motif name: Motif 231
 Matching format of first motif: Reverse Complement

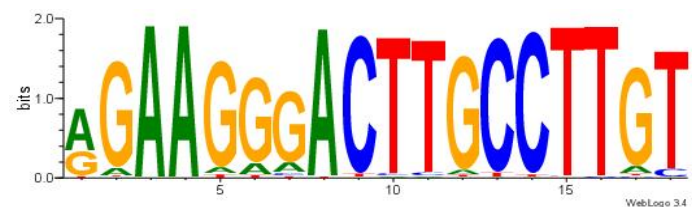
Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 15
 Similarity score: 0.0826494

Alignment:
 ACAAGGCAAGTCCCTTCY
 ---ACAGAGTGAGACTCT

Original motif Consensus sequence: ACAAGGCAAGTCCCTTCY



Reverse complement motif Consensus sequence:
 MGAAGGGACTTGCCTTGT

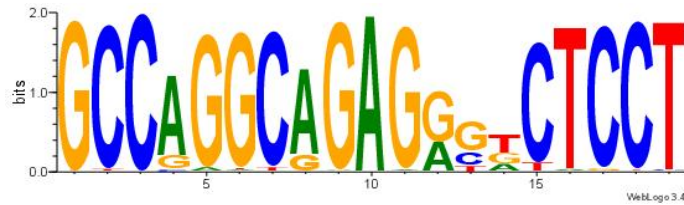


Dataset #: 1
 Motif ID: 43
 Motif name: Motif 43
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 4
 Number of overlap: 15
 Similarity score: 0.0874293

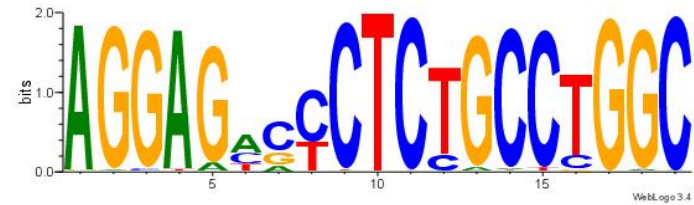
Alignment:

AGGAGRCMCTCTGCCTGGC
-AGAGTCTCACTCTGT---

Original motif Consensus sequence: GCCAGGCAGAGRGKCTCCT



Reverse complement motif Consensus sequence:
AGGAGRCMCTCTGCCTGGC



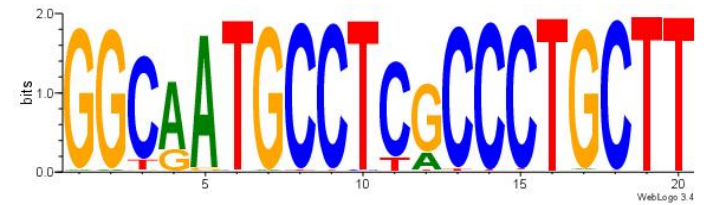
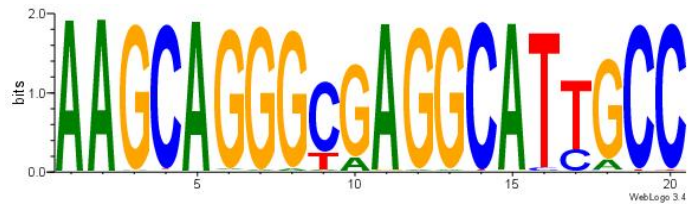
Dataset #: 1
Motif ID: 13
Motif name: Motif 13
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 4
Number of overlap: 15
Similarity score: 0.0917557

Alignment:

AAGCAGGGCGAGGCATTGCC
---ACAGAGTGAGACTCT--

Original motif Consensus sequence: AAGCAGGGCGAGGCATTGCC

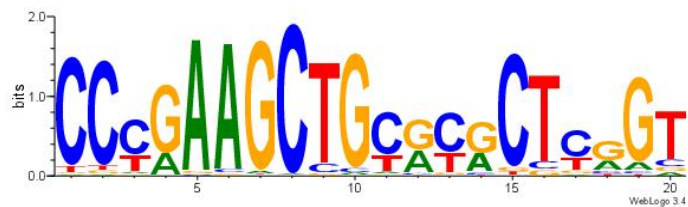
Reverse complement motif Consensus sequence:
GGCAATGCCTCGCCCTGCTT



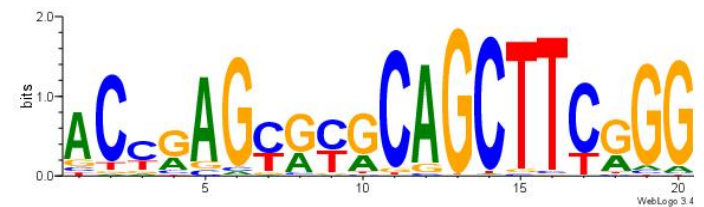
Dataset #: 1
 Motif ID: 177
 Motif name: Motif 177
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 15
 Similarity score: 0.0934943

Alignment:
 ACCGAGMKMGCAGCTTCGGG
 ACAGAGTGAGACTCT-----

Original motif Consensus sequence: CCCGAAGCTGCRYRCTCGGT



Reverse complement motif Consensus sequence: ACCGAGMKMGCAGCTTCGGG

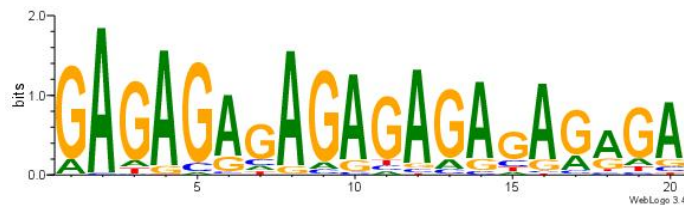


Dataset #: 1

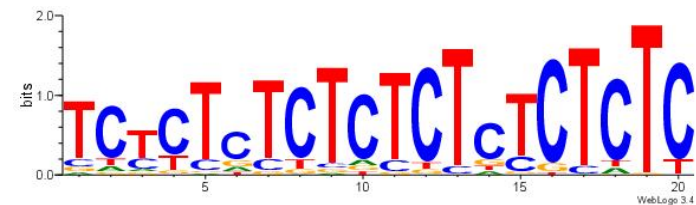
Motif ID: 109
 Motif name: Motif 109
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 15
 Similarity score: 0.0950453

Alignment:
 GAGAGAGAGAGAGAGAGAGA
 --ACAGAGTGAGACTCT---

Original motif Consensus sequence: GAGAGAGAGAGAGAGAGA

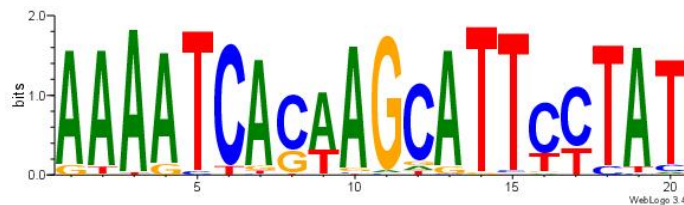


Reverse complement motif Consensus sequence: TCTCTCTCTCTCTCTCTC

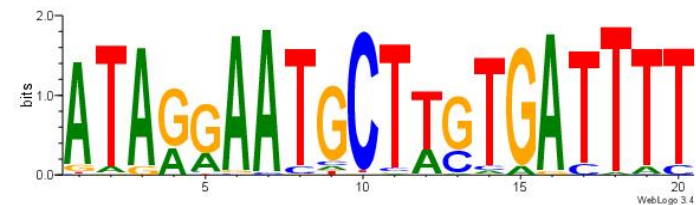


Dataset #: 1 Motif ID: 254 Motif name: Motif 254

Original motif Consensus sequence: AAAATCACAAGCATTCTAT



Reverse complement motif Consensus sequence: ATAGGAATGCTTGATTTT



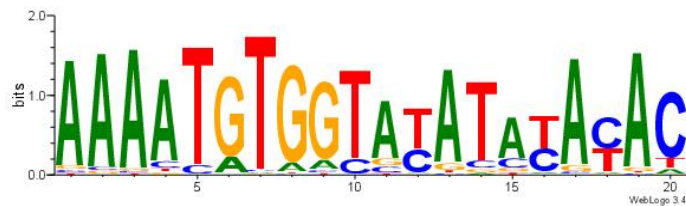
Best Matches for Motif ID 254 (Highest to Lowest)

Dataset #: 1
Motif ID: 83
Motif name: Motif 83
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 20
Similarity score: 0.113683

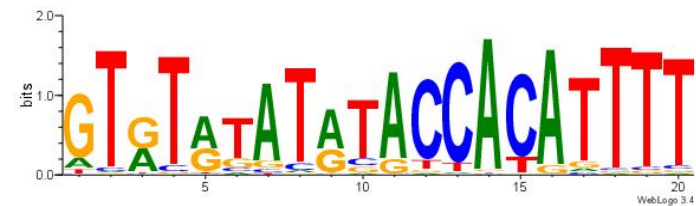
Alignment:

```
AAAATGTGGTAYATAYAYAC  
AAAATCACAAGCATTCTAT
```

Original motif Consensus sequence: AAAATGTGGTAYATAYAYAC



Reverse complement motif Consensus sequence: GTKTMTATMTACCACATTTT



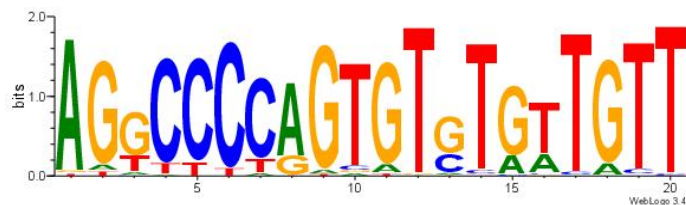
Dataset #: 1
Motif ID: 176
Motif name: Motif 176
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif

Direction: Backward
Position number: 1
Number of overlap: 20
Similarity score: 0.121683

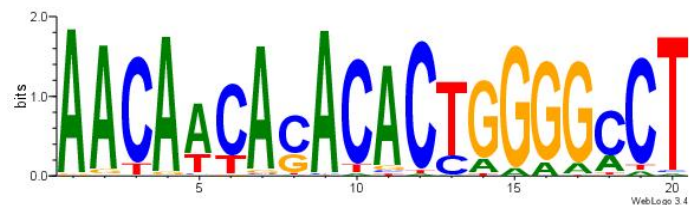
Alignment:

AGGCCCCAGTGTSTGTTGTT
ATAGGAATGCTTGTGATTTT

Original motif Consensus sequence: AGGCCCCAGTGTSTGTTGTT



Reverse complement motif Consensus sequence: AACACASACACTGGGGCCT

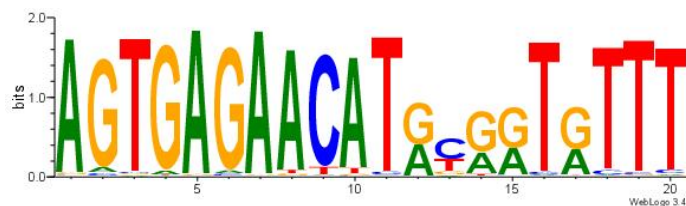


Dataset #: 1
Motif ID: 63
Motif name: Motif 63
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 20
Similarity score: 0.124533

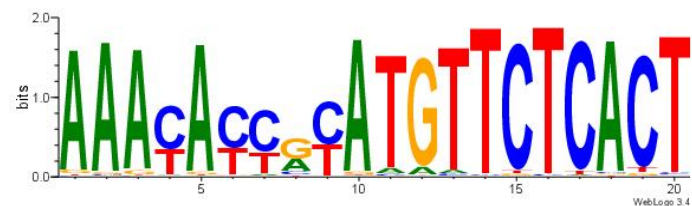
Alignment:

AGTGAGAACATRYRTRTTT
ATAGGAATGCTTGTGATTTT

Original motif Consensus sequence: AGTGAGAACATRYRRTTTT



Reverse complement motif Consensus sequence: AAAMAMMKMATGTTCTCACT

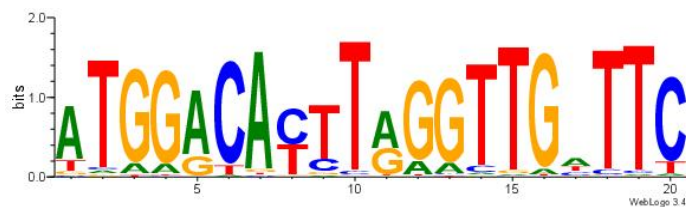


Dataset #: 1
Motif ID: 58
Motif name: Motif 58
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 20
Similarity score: 0.128088

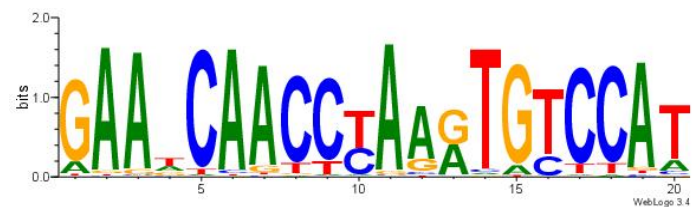
Alignment:

GAAHCAACCKAAKTGTCCAT
AAAATCACAAGCATTCTAT

Original motif Consensus sequence: ATGGACAYTTRGGTTGHTTC



Reverse complement motif Consensus sequence: GAAHCAACCKAAKTGTCCAT

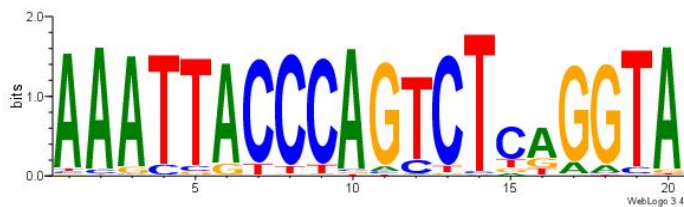


Dataset #: 1
 Motif ID: 160
 Motif name: Motif 160
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.128511

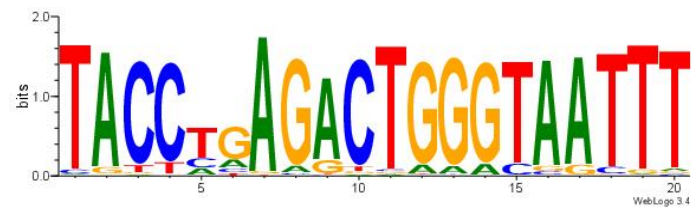
Alignment:

TACCTGAGACTGGGTAATTT
 ATAGGAATGCTTGTGATTTT

Original motif Consensus sequence: AAATTACCCAGTCTCAGGTA



Reverse complement motif Consensus sequence:
TACCTGAGACTGGGTAATTT



Dataset #: 1 Motif ID: 255 Motif name: Motif 255

Original motif Consensus sequence: CTGCTATAACAAA

Reverse complement motif Consensus sequence: TTTGTTATAGCAG

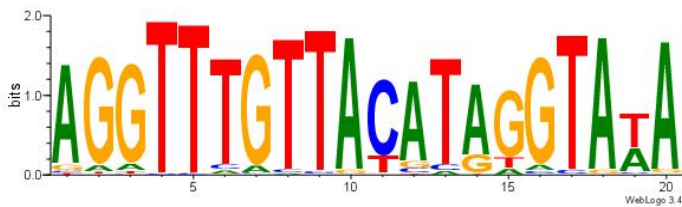


Best Matches for Motif ID 255 (Highest to Lowest)

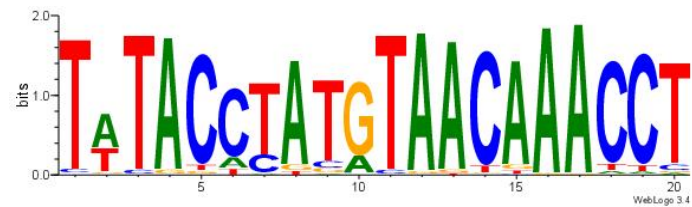
Dataset #: 1
 Motif ID: 137
 Motif name: Motif 137
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 5
 Number of overlap: 13
 Similarity score: 0.0686391

Alignment:
 AGGTTTGTTACATAGGTAWA
 ----TTTGTATAGCAG----

Original motif Consensus sequence: AGGTTTGTTACATAGGTAWA



Reverse complement motif Consensus sequence: TWTACCTATGTAACAAACCT

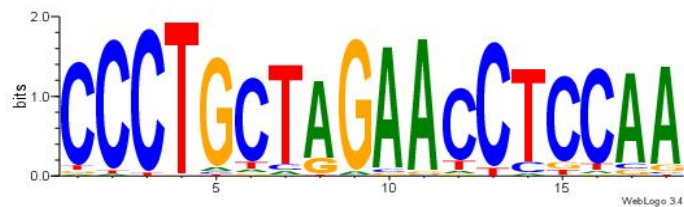


Dataset #: 1
 Motif ID: 299
 Motif name: Motif 299
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 13
 Similarity score: 0.0785239

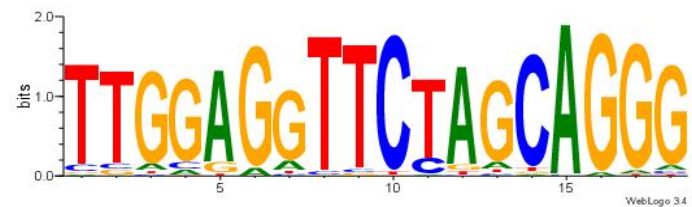
Alignment:

TTGGAGGTTCTAGCAGGG
 ---TTTGTTATAGCAG--

Original motif Consensus sequence: CCCTGCTAGAACCTCCAA



Reverse complement motif Consensus sequence: TTGGAGGTTCTAGCAGGG

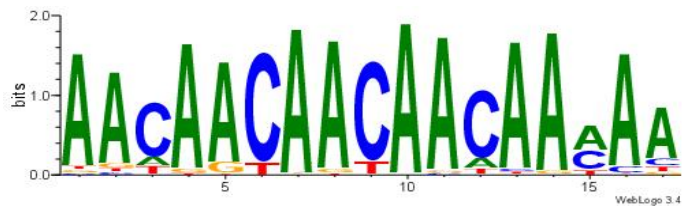


Dataset #: 1
 Motif ID: 117
 Motif name: Motif 117
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3

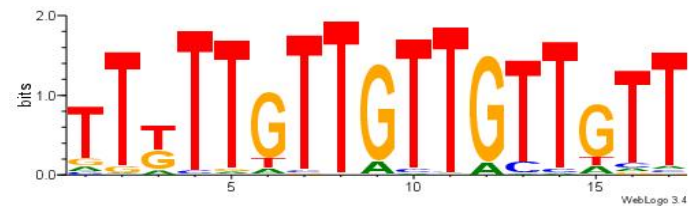
Number of overlap: 13
Similarity score: 0.0860443

Alignment:
AACACAACAACAAMAA
--CTGCTATAACAAA--

Original motif Consensus sequence: AACACAACAACAAMAA



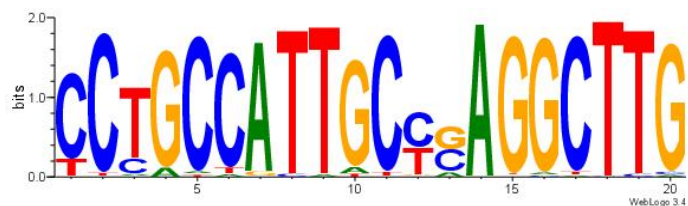
Reverse complement motif Consensus sequence:
TTYTTGTTGTTGTTGTT



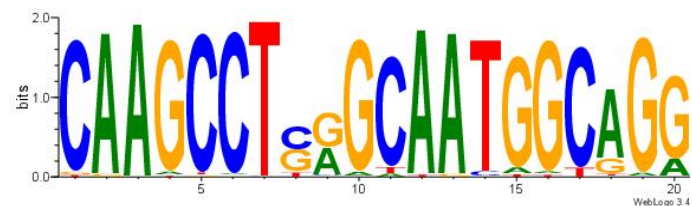
Dataset #: 1
Motif ID: 196
Motif name: Motif 196
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 7
Number of overlap: 13
Similarity score: 0.0860633

Alignment:
CAAGCCTSKGCAATGGCAGG
-----TTTGTTATAGCAG-

Original motif Consensus sequence: CCTGCCATTGCYSAGGCTTG



Reverse complement motif Consensus sequence: CAAGCCTSKGCAATGGCAGG

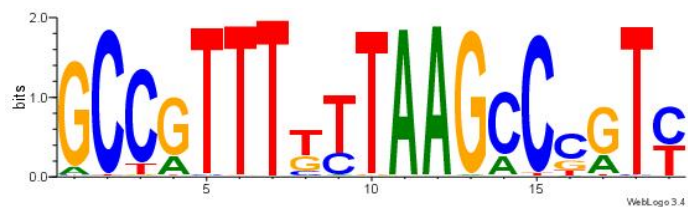


Dataset #: 1
Motif ID: 21
Motif name: Motif 21
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 3
Number of overlap: 13
Similarity score: 0.0907214

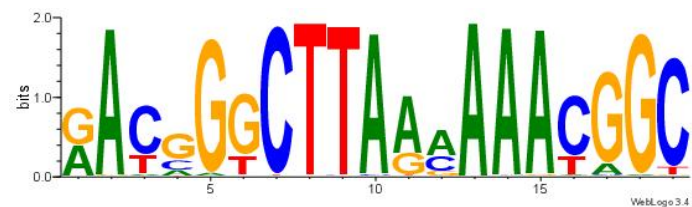
Alignment:

GCCGTTTKTTAAGCCCGTY
--TTTGTTATAGCAG----

Original motif Consensus sequence: GCCGTTTKTTAAGCCCGTY

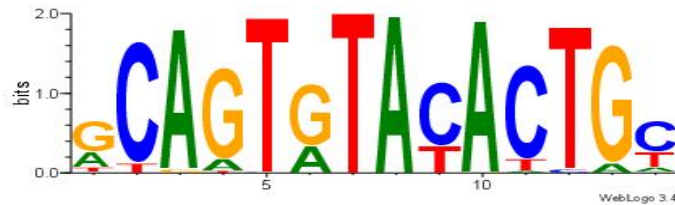


Reverse complement motif Consensus sequence: KACGGGCTTAARAAACGGC

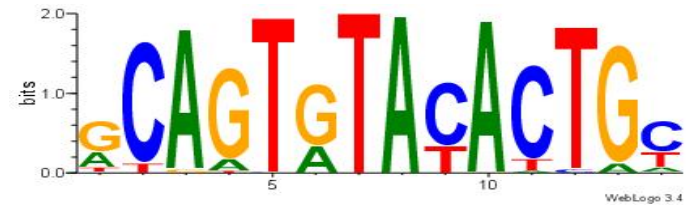


Dataset #: 1 Motif ID: 256 Motif name: Motif 256

Original motif Consensus sequence: RCAGTGTACTGY



Reverse complement motif Consensus sequence: KCAGTGTACTGY



Best Matches for Motif ID 256 (Highest to Lowest)

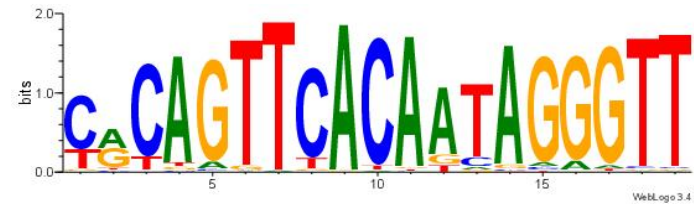
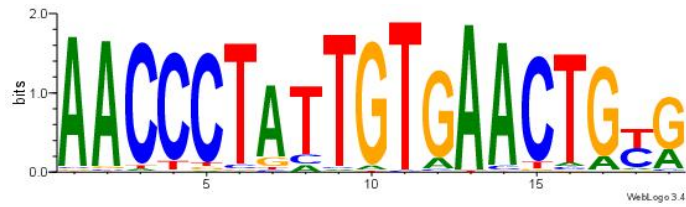
Dataset #:	1
Motif ID:	242
Motif name:	Motif 242
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	5
Number of overlap:	14
Similarity score:	0.0643389

Alignment:

```
AACCCTATTGTGAACTGYG  
----RCAGTGTACTGY-
```

Original motif Consensus sequence: AACCCTATTGTGAACTGYG

Reverse complement motif Consensus sequence:
CMCAGTTCACAATAGGGTT

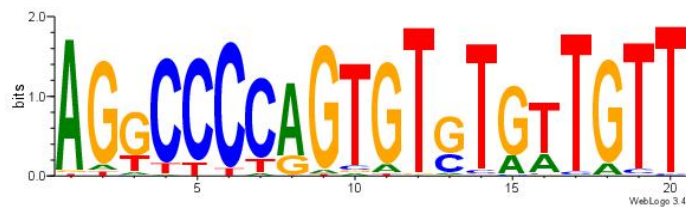


Dataset #: 1
 Motif ID: 176
 Motif name: Motif 176
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 14
 Similarity score: 0.0671024

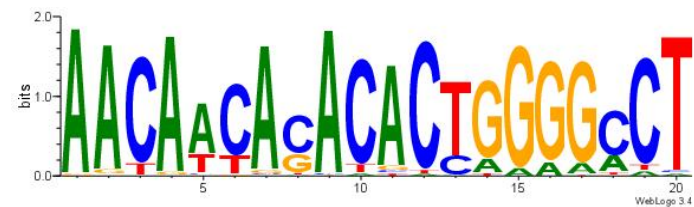
Alignment:

AGGCCCCAGTGTSTGTTGTT
 -----RCAGTGTACTGY-

Original motif Consensus sequence: AGGCCCCAGTGTSTGTTGTT



Reverse complement motif Consensus sequence: AACACASACTGGGGCCT



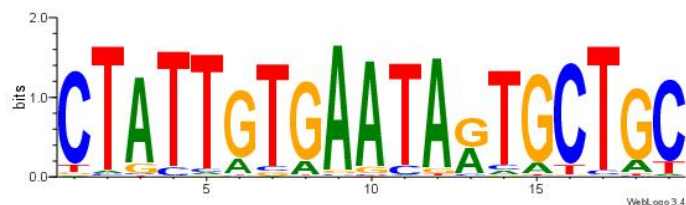
Dataset #: 1

Motif ID: 70
 Motif name: Motif 70
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 14
 Similarity score: 0.0717951

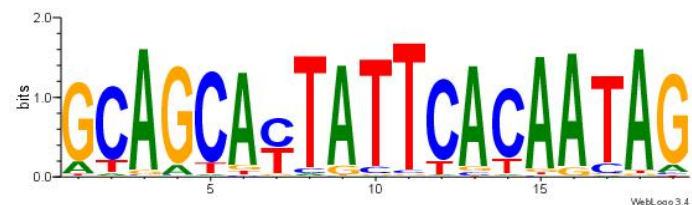
Alignment:

CTATTGTGAATARTGCTGC
 --RCAGTGTACACTGY---

Original motif Consensus sequence: CTATTGTGAATARTGCTGC



Reverse complement motif Consensus sequence: GCAGCAMTATTCACAATAG



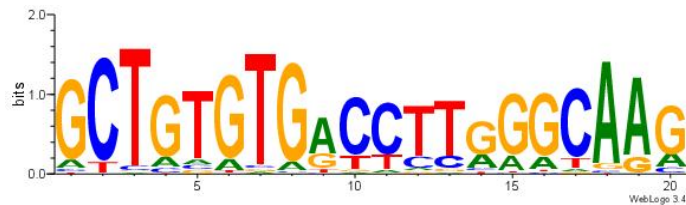
Dataset #: 1
 Motif ID: 112
 Motif name: Motif 112
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 14

Similarity score: 0.0738478

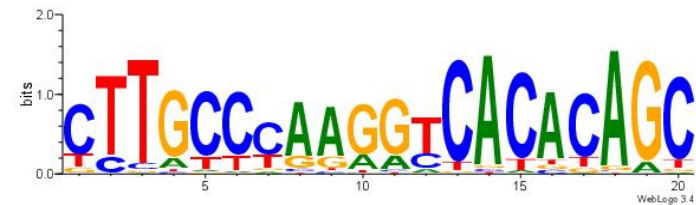
Alignment:

CTTGCCCAAGGTCACACAGC
-----KCAGTGTACTACTGM

Original motif Consensus sequence: GCTGTGTGACCTTGGGCAAG



Reverse complement motif Consensus sequence:
CTTGCCCAAGGTCACACAGC



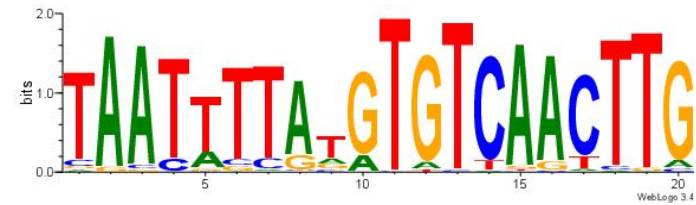
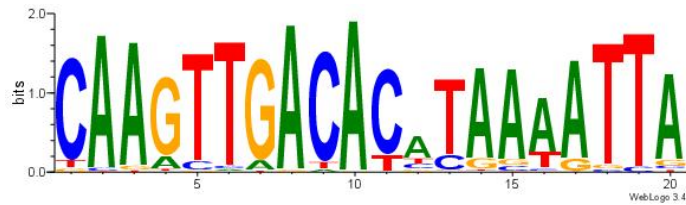
Dataset #: 1
Motif ID: 357
Motif name: Motif 357
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 14
Similarity score: 0.0744746

Alignment:

TAATTTTATGTGTCAACTTG
-----KCAGTGTACTACTGM

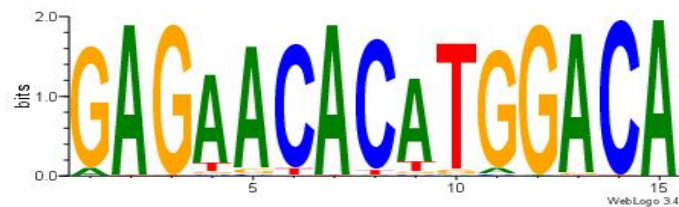
Original motif Consensus sequence: CAAGTTGACACATAAAATTA

Reverse complement motif Consensus sequence:
TAATTTTATGTGTCAACTTG

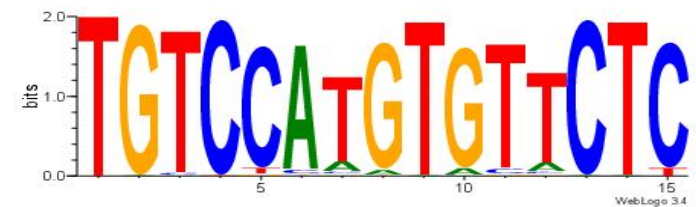


Dataset #: 1 Motif ID: 257 Motif name: Motif 257

Original motif Consensus sequence: GAGAACACATGGACA



Reverse complement motif Consensus sequence: TGCCATGTGTC

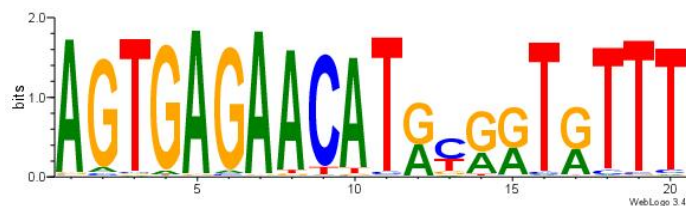


Best Matches for Motif ID 257 (Highest to Lowest)

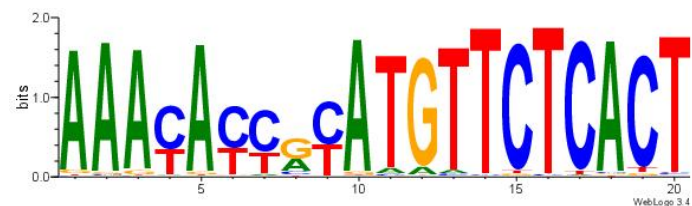
Dataset #:	1
Motif ID:	63
Motif name:	Motif 63
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	3
Number of overlap:	15
Similarity score:	0.0985209

Alignment:
 AGTGAGAACATRYRRTRTTT
 ---GAGAACACATGGACA--

Original motif Consensus sequence: AGTGAGAACATRYRRTTTT



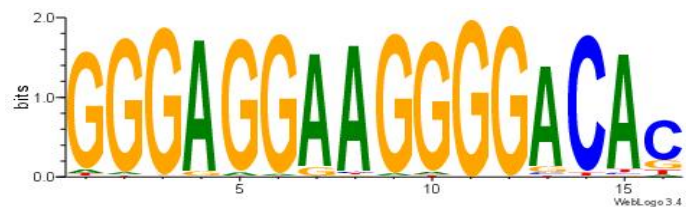
Reverse complement motif Consensus sequence: AAAMAMMKMATGTTCTCACT



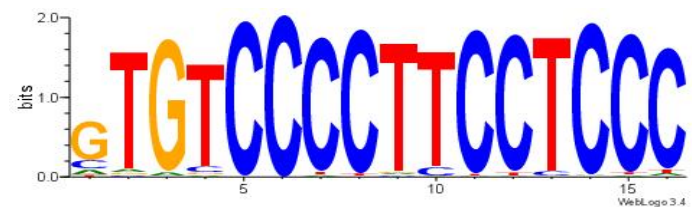
Dataset #: 1
Motif ID: 221
Motif name: Motif 221
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2
Number of overlap: 15
Similarity score: 0.10032

Alignment:
GGGAGGAAGGGGACAC
GAGAACACATGGACA-

Original motif Consensus sequence: GGGAGGAAGGGGACAC



Reverse complement motif Consensus sequence: GTGTCCCTTCTCCC

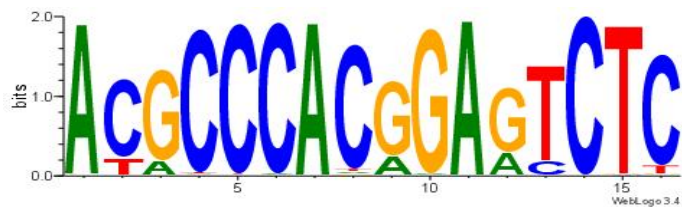


Dataset #: 1
 Motif ID: 33
 Motif name: Motif 33
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 15
 Similarity score: 0.100528

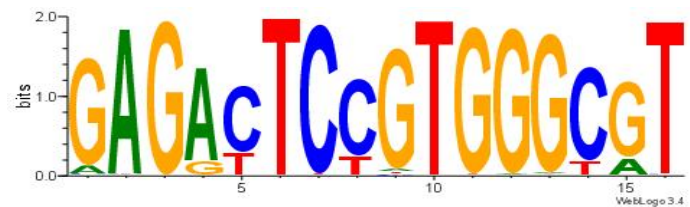
Alignment:

ACGCCACGGAGTCTC
 TGTCCATGTGTTCTC-

Original motif Consensus sequence: ACGCCACGGAGTCTC



Reverse complement motif Consensus sequence: GAGACTCCGTGGGCGT



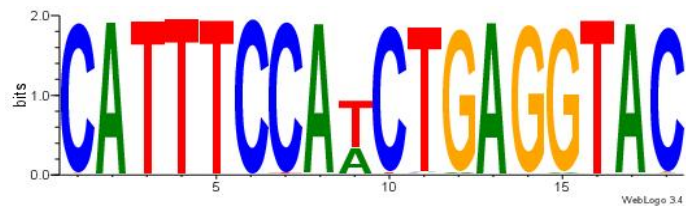
Dataset #: 1
 Motif ID: 25
 Motif name: Motif 25
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3

Number of overlap: 15
Similarity score: 0.102413

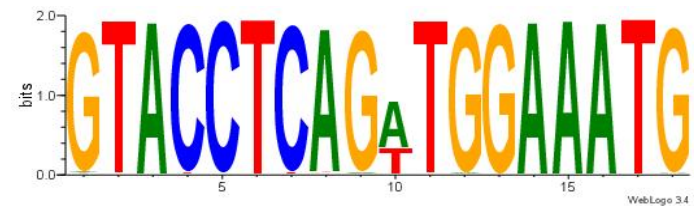
Alignment:

GTACCTCAGWTGGAAATG
--GAGAACACATGGACA-

Original motif Consensus sequence: CATTTCACCTGAGGTAC



Reverse complement motif Consensus sequence:
GTACCTCAGWTGGAAATG

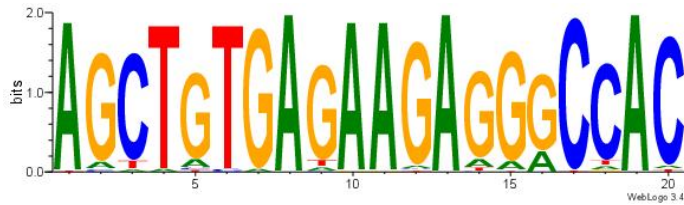


Dataset #: 1
Motif ID: 294
Motif name: Motif 294
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 2
Number of overlap: 15
Similarity score: 0.103591

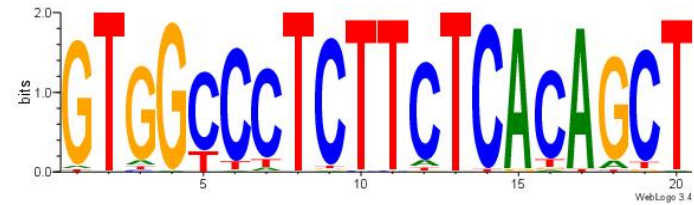
Alignment:

GTGGCCCTCTTCTCACAGCT
-TGTCCATGTGTTCTC----

Original motif Consensus sequence: AGCTGTGAGAAGAGGGCCAC

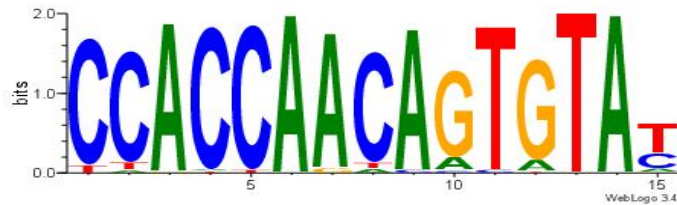


Reverse complement motif Consensus sequence: GTGGCCCTCTTCTCACAGCT

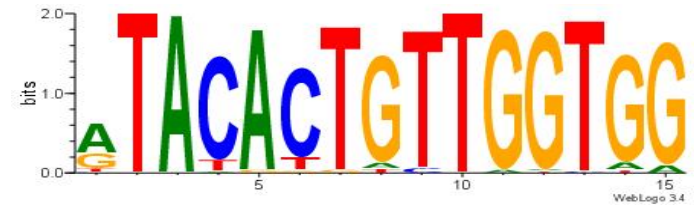


Dataset #: 1 Motif ID: 258 Motif name: Motif 258

Original motif Consensus sequence: CCACCAACAGTGTA



Reverse complement motif Consensus sequence: MTACACTGTTGGT



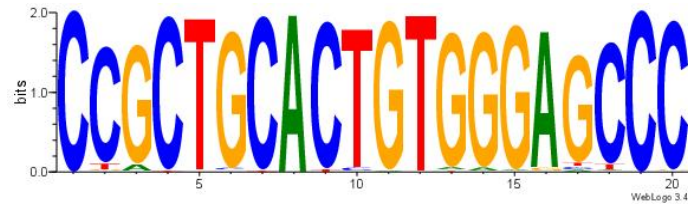
Best Matches for Motif ID 258 (Highest to Lowest)

Dataset #:	1
Motif ID:	144
Motif name:	Motif 144
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	3
Number of overlap:	15
Similarity score:	0.0771788

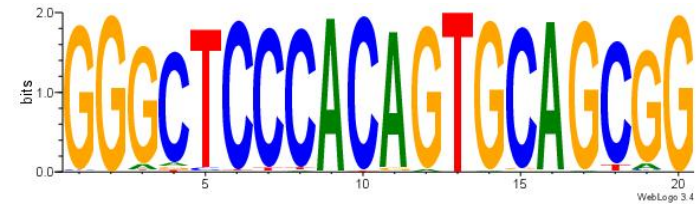
Alignment:

GGGCTCCACAGTGCAGCGG
---CCACCAACAGTGTAY--

Original motif Consensus sequence: CCGCTGCACTGTGGGAGCCC



Reverse complement motif Consensus sequence:
GGGCTCCACAGTGCAGCGG

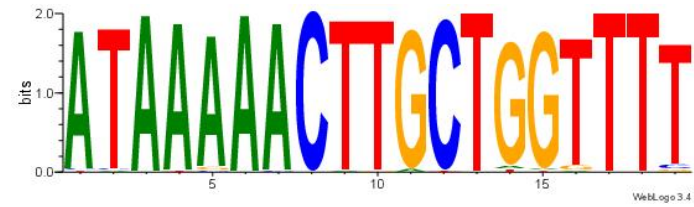
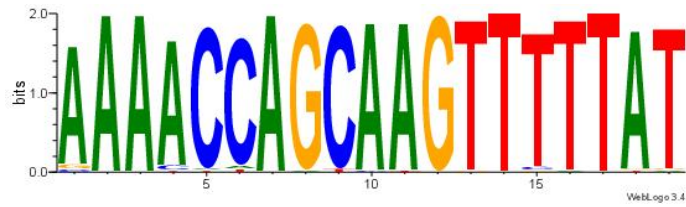


Dataset #: 1
Motif ID: 330
Motif name: Motif 330
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 5
Number of overlap: 15
Similarity score: 0.0810042

Alignment:
ATAAAAAGTTGCTGGTTTT
MTACACTGTTGGTGG----

Original motif Consensus sequence: AAAACCAGCAAGTTTTTAT

Reverse complement motif Consensus sequence:
ATAAAAAGTTGCTGGTTTT

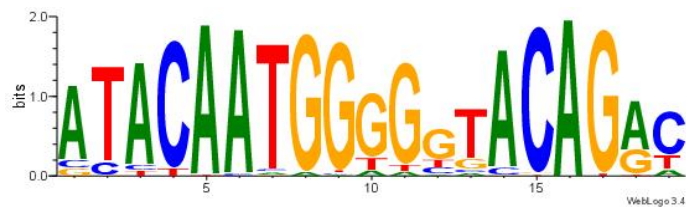


Dataset #: 1
 Motif ID: 193
 Motif name: Motif 193
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 5
 Number of overlap: 15
 Similarity score: 0.0921216

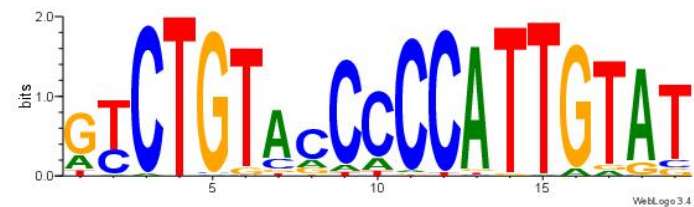
Alignment:

GKCTGTACCCCCATTGTAT
 CCACCAACAGTGTAY----

Original motif Consensus sequence: ATACAATGGGGGTACAGRC



Reverse complement motif Consensus sequence: GKCTGTACCCCCATTGTAT



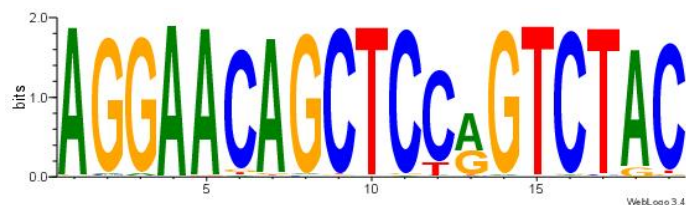
Dataset #: 1

Motif ID: 62
 Motif name: Motif 62
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 15
 Similarity score: 0.0987651

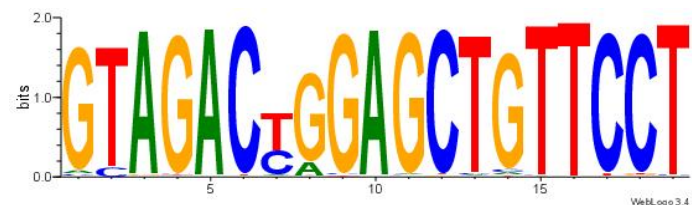
Alignment:

AGGAACAGCTCCRGCTCTAC
 ----CCACCAACAGTGTAY

Original motif Consensus sequence: AGGAACAGCTCCRGCTCTAC



Reverse complement motif Consensus sequence: GTAGACKGGAGCTGTTCCCT



Dataset #: 1
 Motif ID: 33
 Motif name: Motif 33
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 15

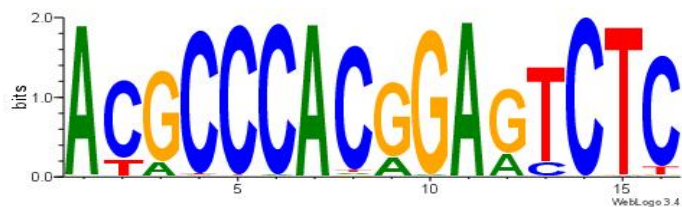
Similarity score: 0.103803

Alignment:

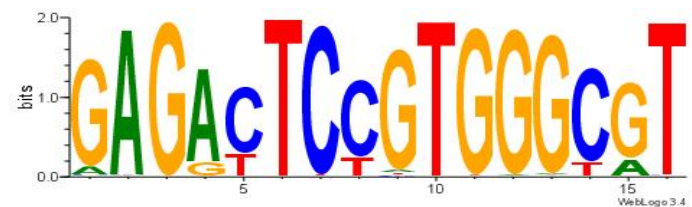
ACGCCCACGGAGTCTC

CCACCAACAGTGTAY-

Original motif Consensus sequence: ACGCCCACGGAGTCTC

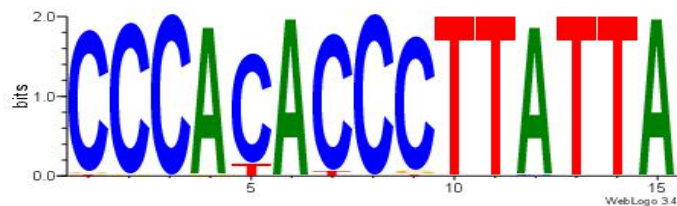


Reverse complement motif Consensus sequence: GAGACTCCGTGGGCGT

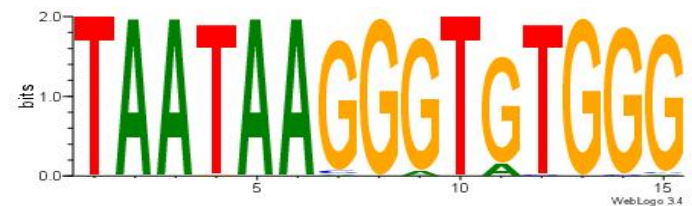


Dataset #: 1 Motif ID: 259 Motif name: Motif 259

Original motif Consensus sequence: CCCACACCCTTATTA



Reverse complement motif Consensus sequence: TAATAAGGGTGTGG



Best Matches for Motif ID 259 (Highest to Lowest)

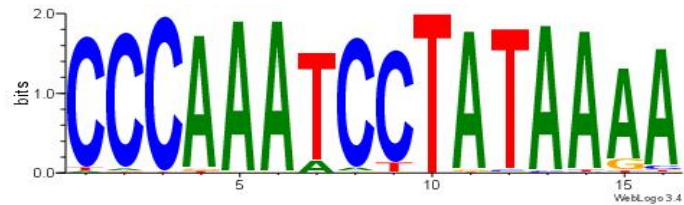
Dataset #:	1
Motif ID:	169
Motif name:	Motif 169
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement

Direction: Forward
 Position number: 2
 Number of overlap: 15
 Similarity score: 0.0922705

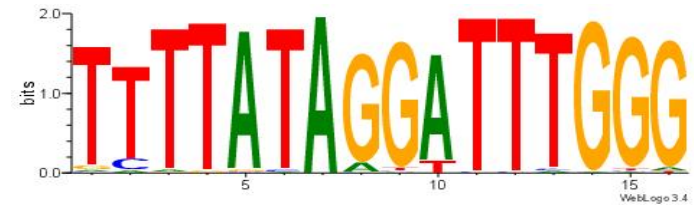
Alignment:

TTTTATAGGATTTGGG
 -TAATAAGGGTGTGGG

Original motif Consensus sequence: CCCAAATCCTATAAAA



Reverse complement motif Consensus sequence: TTTTATAGGATTTGGG

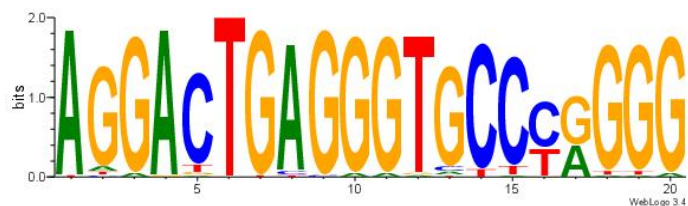


Dataset #: 1
 Motif ID: 312
 Motif name: Motif 312
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 4
 Number of overlap: 15
 Similarity score: 0.0982406

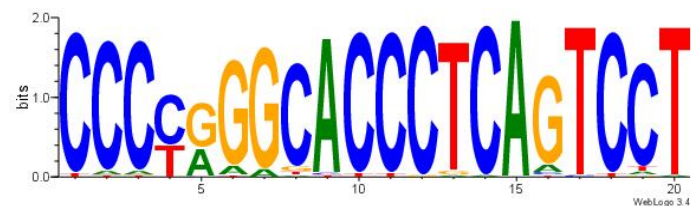
Alignment:

CCCMKGGCACCCCTCAGTCCT
 ---CCCACACCCTTATTA--

Original motif Consensus sequence: AGGACTGAGGGTGCCYRGGG



Reverse complement motif Consensus sequence: CCCMKGGCACCCTCAGTCCT

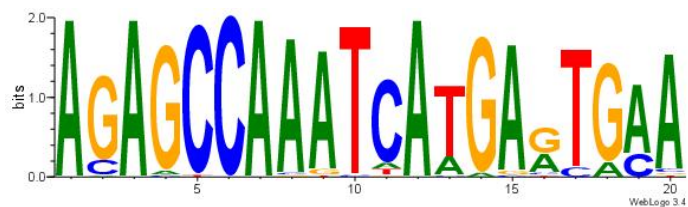


Dataset #: 1
Motif ID: 349
Motif name: Motif 349
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 4
Number of overlap: 15
Similarity score: 0.106051

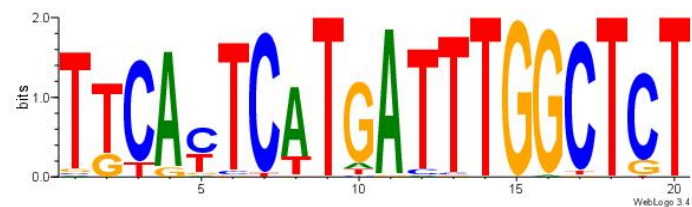
Alignment:

TTCAMTCATGATTTGGCTCT
--TAATAAGGGTGTGGG---

Original motif Consensus sequence: AGAGCCAAATCATGARTGAA



Reverse complement motif Consensus sequence: TTCAMTCATGATTTGGCTCT

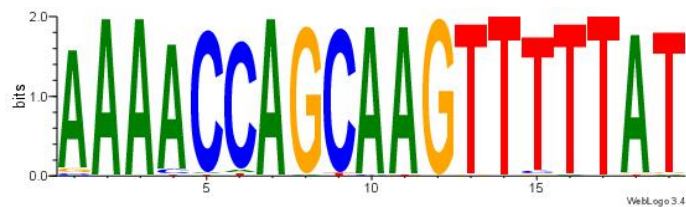


Dataset #: 1
 Motif ID: 330
 Motif name: Motif 330
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 15
 Similarity score: 0.106485

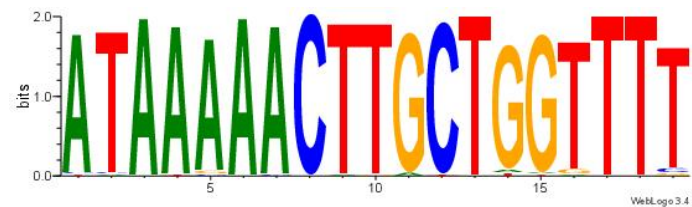
Alignment:

ATAAAACTTGCTGGTTTT
 -TAATAAGGGTGTGGG---

Original motif Consensus sequence: AAAACCAGCAAGTTTTTAT



Reverse complement motif Consensus sequence: ATAAAACTTGCTGGTTTT



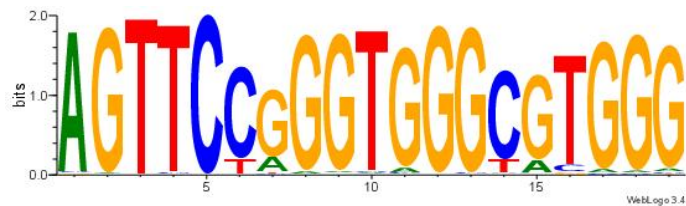
Dataset #: 1
 Motif ID: 98
 Motif name: Motif 98
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1

Number of overlap: 15
Similarity score: 0.107379

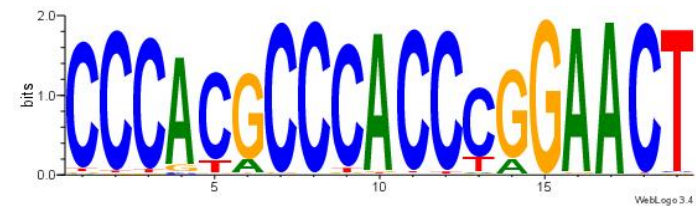
Alignment:

CCCACGCCCACCCGGA
ACT
----CCCACACCCTTATTA

Original motif Consensus sequence: AGTTCCGGGTGGGCGTGGG

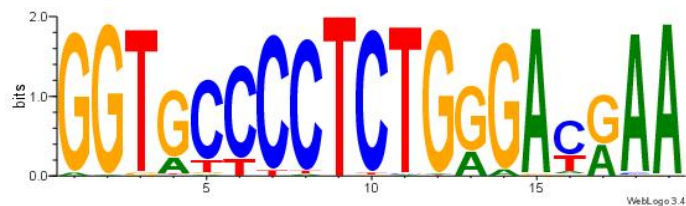


Reverse complement motif Consensus sequence:
CCCACGCCCACCCGGA
ACT

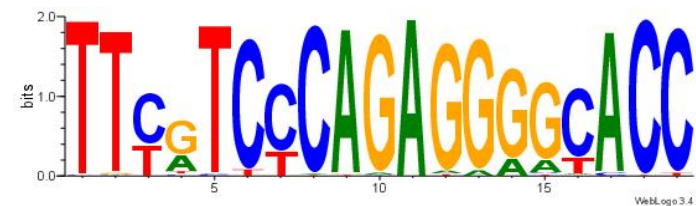


Dataset #: 1 Motif ID: 260 Motif name: Motif 260

Original motif Consensus sequence: GGTGCCCTCTGGGACRAA



Reverse complement motif Consensus sequence:
TTMGTCCCAGAGGGGCACC



Best Matches for Motif ID 260 (Highest to Lowest)

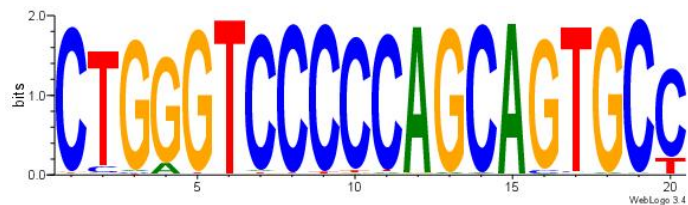
Dataset #: 1
Motif ID: 84
Motif name: Motif 84

Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	19
Similarity score:	0.0961044

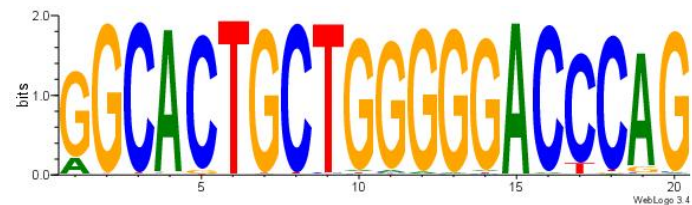
Alignment:

```
CTGGGTCCCCCAGCAGTGCC
TTMGTCCCAGAGGGGCACC-
```

Original motif Consensus sequence: CTGGGTCCCCCAGCAGTGCC



Reverse complement motif Consensus sequence: GGCAGTCTGGGGGACCCAG

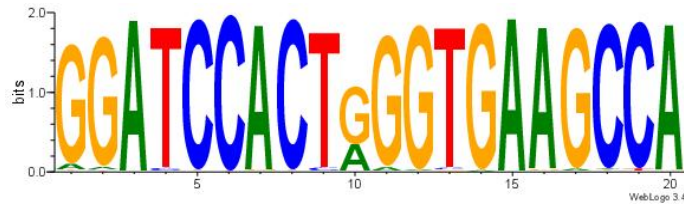


Dataset #:	1
Motif ID:	61
Motif name:	Motif 61
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	2
Number of overlap:	19
Similarity score:	0.100972

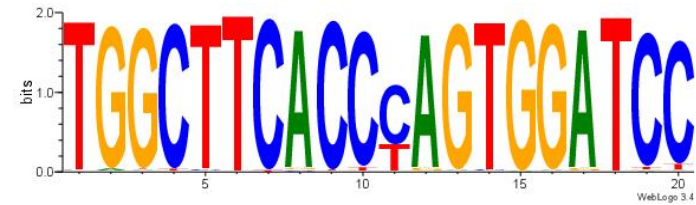
Alignment:

TGGCTTCACCCAGTGGATCC
-TTMGTCCCAGAGGGGCACC

Original motif Consensus sequence: GGATCCACTGGGTGAAGCCA



Reverse complement motif Consensus sequence:
TGGCTTCACCCAGTGGATCC



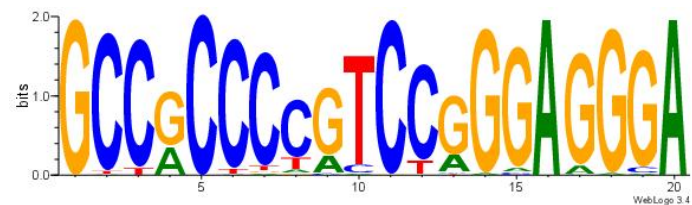
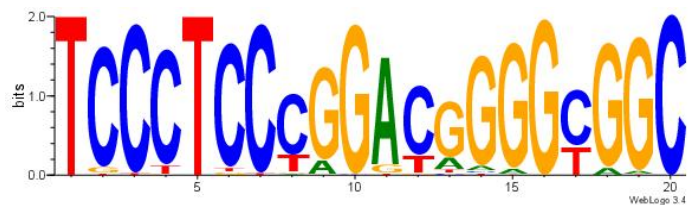
Dataset #: 1
Motif ID: 155
Motif name: Motif 155
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 19
Similarity score: 0.10173

Alignment:

TCCCTCCCGACGGGGYGGC
-TTMGTCCCAGAGGGGCACC

Original motif Consensus sequence: TCCCTCCCGACGGGGYGGC

Reverse complement motif Consensus sequence:
GCCKCCCCGTCCGGGAGGGA

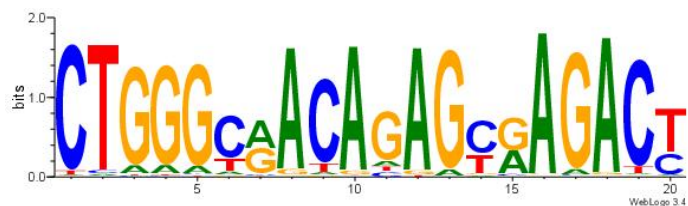


Dataset #: 1
 Motif ID: 29
 Motif name: Motif 29
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 19
 Similarity score: 0.103455

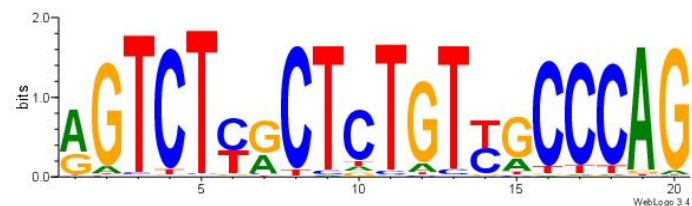
Alignment:

MGTCTMKCTCTGTKGCCAG
 -GGTGCCCTCTGGGACRAA

Original motif Consensus sequence: CTGGGCRACAGAGYRAGACY



Reverse complement motif Consensus sequence: MGTCTMKCTCTGTKGCCAG



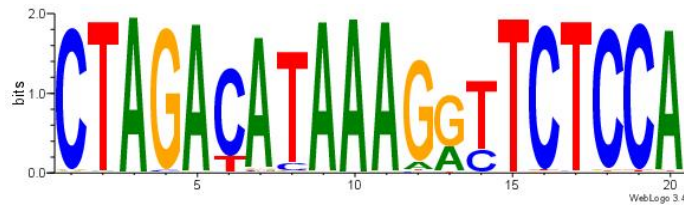
Dataset #: 1

Motif ID: 85
 Motif name: Motif 85
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 19
 Similarity score: 0.103612

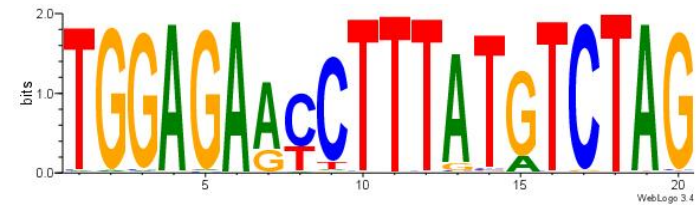
Alignment:

TGGAGAACCTTTATGTCTAG
 GGTGCCCTCTGGGACRAA-

Original motif Consensus sequence: CTAGACATAAAGTTCTCCA

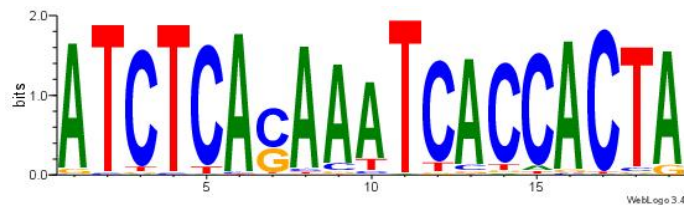


Reverse complement motif Consensus sequence: TGGAGAACCTTTATGTCTAG

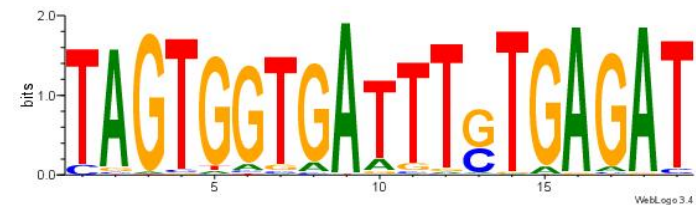


Dataset #: 1 Motif ID: 261 Motif name: Motif 261

Original motif Consensus sequence: ATCTCASAAATCACCCTA



Reverse complement motif Consensus sequence: TAGTGGTGAATTTGAGAT



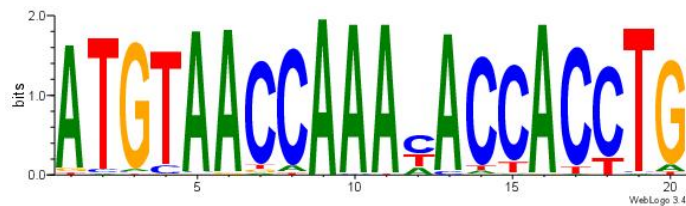
Best Matches for Motif ID 261 (Highest to Lowest)

Dataset #: 1
Motif ID: 336
Motif name: Motif 336
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2
Number of overlap: 19
Similarity score: 0.0782433

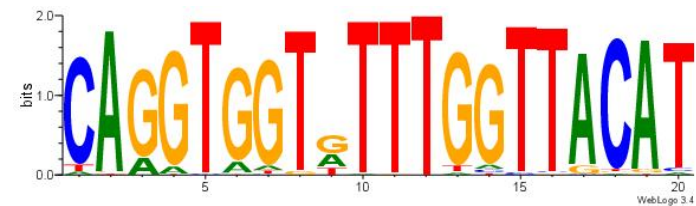
Alignment:

ATGTAACCAAAYACCACCTG
ATCTCASAAATCACCCTA-

Original motif Consensus sequence: ATGTAACCAAAYACCACCTG



Reverse complement motif Consensus sequence:
CAGGTGGTKTTTGGTTACAT

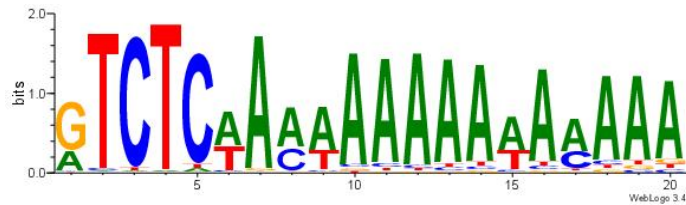


Dataset #: 1
Motif ID: 7
Motif name: Motif 7
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif

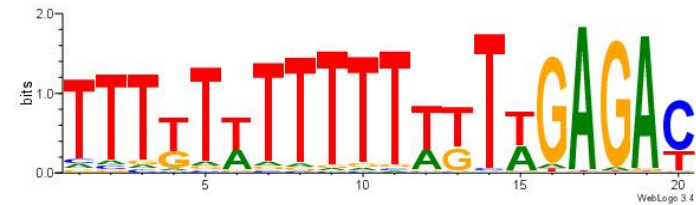
Direction: Forward
 Position number: 1
 Number of overlap: 19
 Similarity score: 0.0942998

Alignment:
 GTCTCWAMAAAAAWAMAAA
 ATCTCASAAATCACCCTA-

Original motif Consensus sequence: GTCTCWAMAAAAAWAMAAA



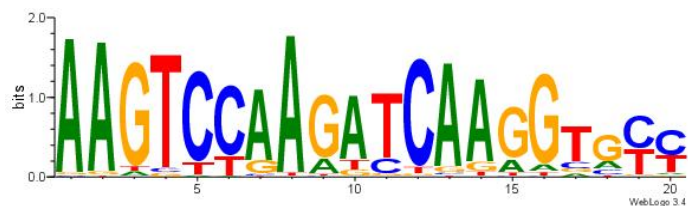
Reverse complement motif Consensus sequence: TTTYTWTTTTTWTGAGAC



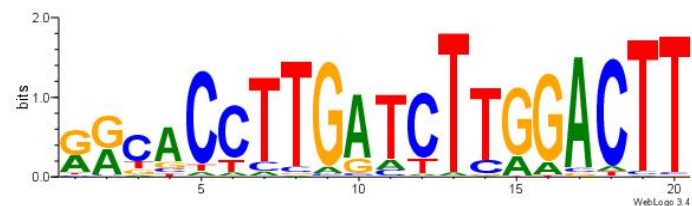
Dataset #: 1
 Motif ID: 119
 Motif name: Motif 119
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 19
 Similarity score: 0.113215

Alignment:
 KKCACCTTGATCTTGGACTT
 -TAGTGGTGATTTSTGAGAT

Original motif Consensus sequence: AAGTCCAAGATCAAGGTGY



Reverse complement motif Consensus sequence: KKCACCTTGATCTTGGACTT

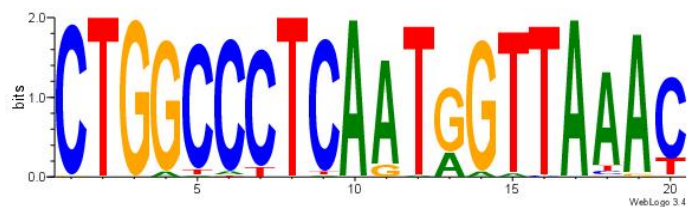


Dataset #: 1
Motif ID: 332
Motif name: Motif 332
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 2
Number of overlap: 19
Similarity score: 0.115495

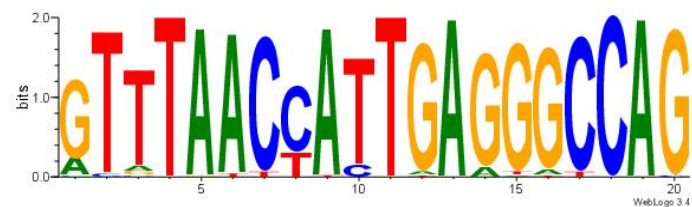
Alignment:

GTTTAACCATTGAGGGCCAG
ATCTCASAAATCACCCTA-

Original motif Consensus sequence: CTGGCCCTCAATGGTTAAAC



Reverse complement motif Consensus sequence: GTTTAACCATTGAGGGCCAG

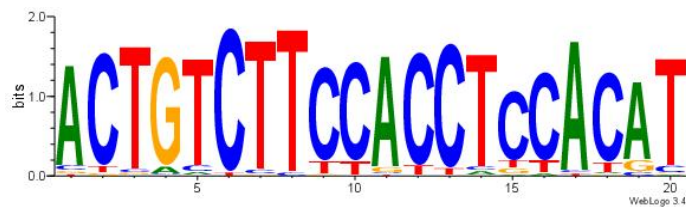


Dataset #: 1
 Motif ID: 178
 Motif name: Motif 178
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 19
 Similarity score: 0.116588

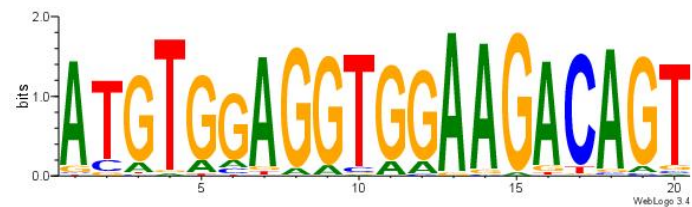
Alignment:

ATGTGGAGGTGGAAGACAGT
 TAGTGGTGATTTSTGAGAT-

Original motif Consensus sequence: ACTGTCTTCCACCTCCACAT



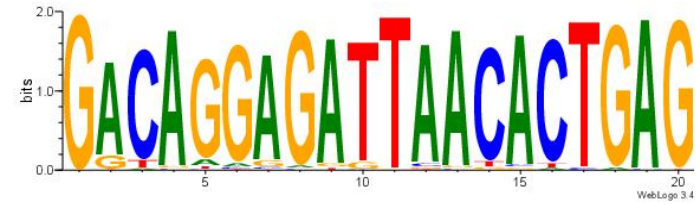
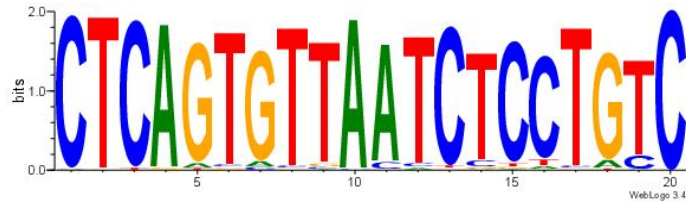
Reverse complement motif Consensus sequence: ATGTGGAGGTGGAAGACAGT



Dataset #: 1 Motif ID: 262 Motif name: Motif 262

Original motif Consensus sequence: CTCAGTGTTAATCTCCTGTC

Reverse complement motif Consensus sequence: GACAGGAGATTAACACTGAG



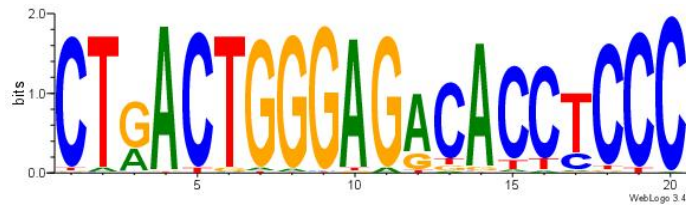
Best Matches for Motif ID 262 (Highest to Lowest)

Dataset #: 1
 Motif ID: 293
 Motif name: Motif 293
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.108944

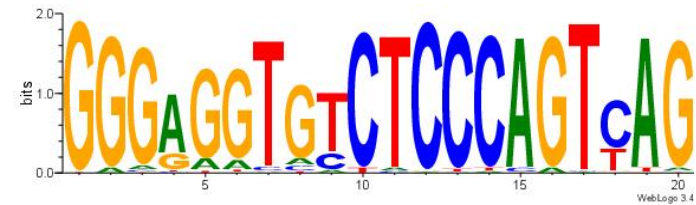
Alignment:

CTGACTGGGAGACACCTCCC
 CTCAGTGTTAATCTCCTGTC

Original motif Consensus sequence: CTGACTGGGAGACACCTCCC



Reverse complement motif Consensus sequence:
 GGGAGGTGTCTCCAGTCAG

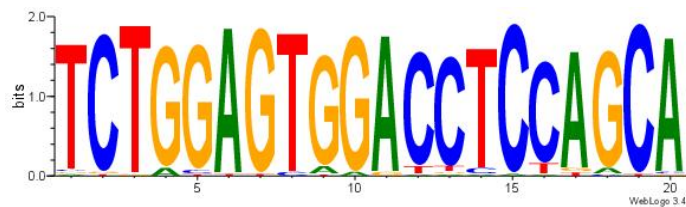


Dataset #: 1
 Motif ID: 350
 Motif name: Motif 350
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.129073

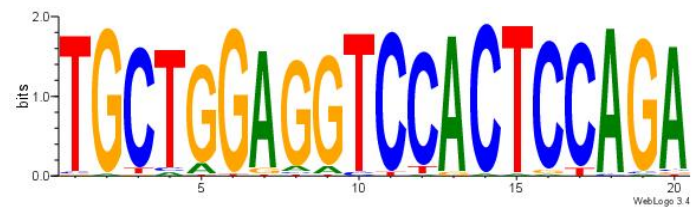
Alignment:

TCTGGAGTGGACCTCCAGCA
 CTCAGTGTTAATCTCCTGTC

Original motif Consensus sequence: TCTGGAGTGGACCTCCAGCA



Reverse complement motif Consensus sequence: TGCTGGAGGTCCACTCCAGA



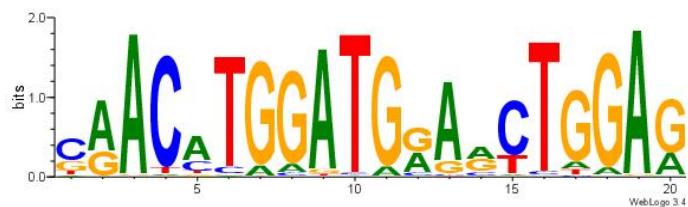
Dataset #: 1
 Motif ID: 104
 Motif name: Motif 104
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1

Number of overlap: 20
Similarity score: 0.131966

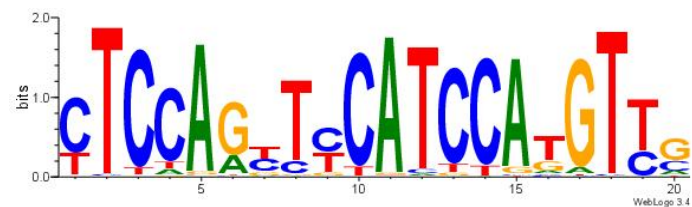
Alignment:

CAACATGGATGRARCTGGAG
GACAGGAGATTAACACTGAG

Original motif Consensus sequence: CAACATGGATGRARCTGGAG



Reverse complement motif Consensus sequence:
CTCCAGKTMCATCCATGTTG

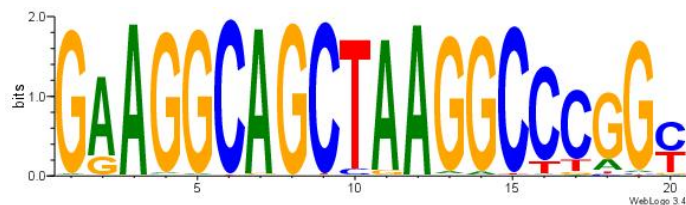


Dataset #: 1
Motif ID: 64
Motif name: Motif 64
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 20
Similarity score: 0.133887

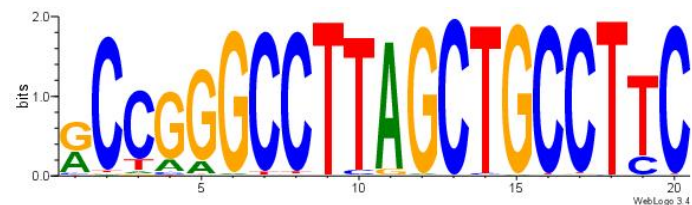
Alignment:

KCCGGGCCTTAGCTGCCTTC
CTCAGTGTTAATCTCCTGTC

Original motif Consensus sequence: GAAGGCAGCTAAGGCCGGY



Reverse complement motif Consensus sequence: KCCGGGCCTTAGCTGCCTTC

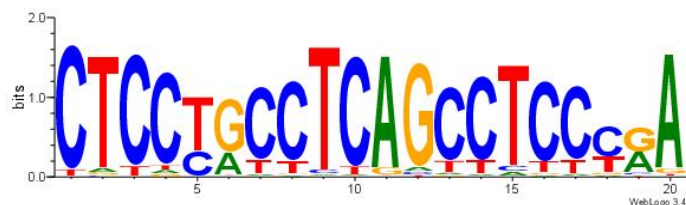


Dataset #: 1
Motif ID: 26
Motif name: Motif 26
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 20
Similarity score: 0.138871

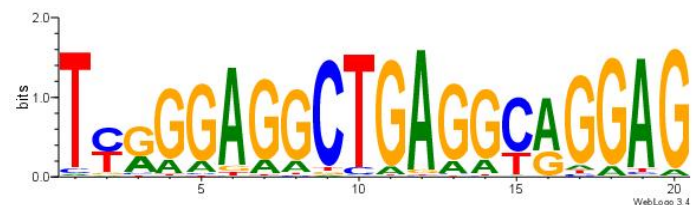
Alignment:

TMGGGAGGCTGAGGCAGGAG
GACAGGAGATTAACACTGAG

Original motif Consensus sequence: CTCCTGCCTCAGCCTCCRA

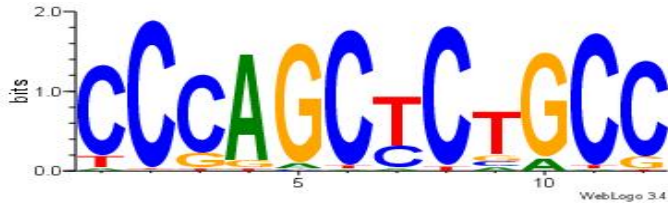


Reverse complement motif Consensus sequence: TMGGGAGGCTGAGGCAGGAG



Dataset #: 1 Motif ID: 263 Motif name: Motif 263

Original motif Consensus sequence: CCCAGCTCTGCC



Reverse complement motif Consensus sequence: GGCAGAGCTGGG



Best Matches for Motif ID 263 (Highest to Lowest)

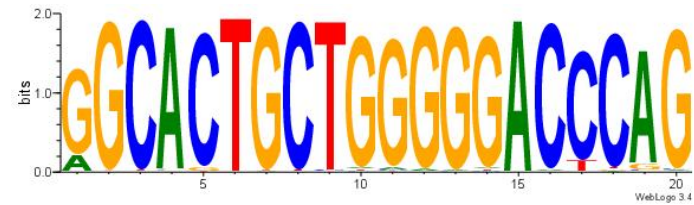
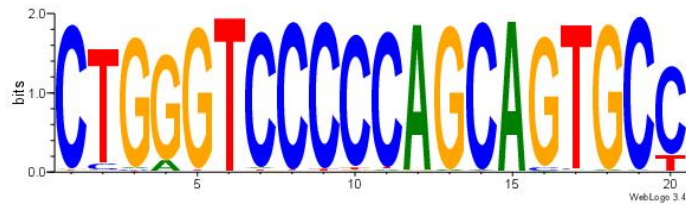
Dataset #:	1
Motif ID:	84
Motif name:	Motif 84
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	12
Similarity score:	0.0427579

Alignment:

```
GGCACTGCTGGGGGACCCAG
GGCAGAGCTGGG-----
```

Original motif Consensus sequence: CTGGGTCCCCCAGCAGTGCC

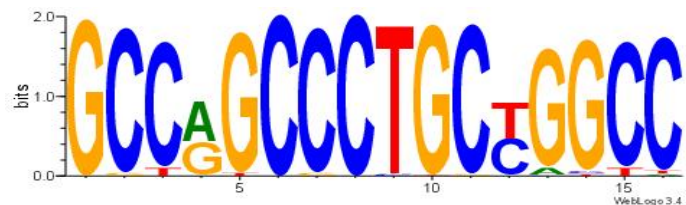
Reverse complement motif Consensus sequence: GGCAGAGCTGGG



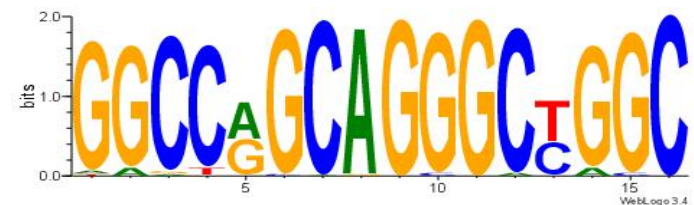
Dataset #: 1
 Motif ID: 183
 Motif name: Motif 183
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 12
 Similarity score: 0.0507335

Alignment:
 GCCRGCCTGCYGGCC
 CCCAGCTCTGCC----

Original motif Consensus sequence: GCCRGCCTGCYGGCC



Reverse complement motif Consensus sequence: GGCCMGCAGGGCKGGC



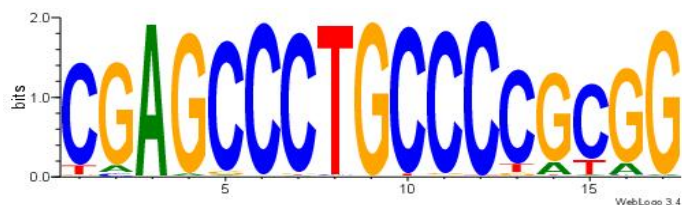
Dataset #: 1

Motif ID: 78
 Motif name: Motif 78
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 5
 Number of overlap: 12
 Similarity score: 0.0634235

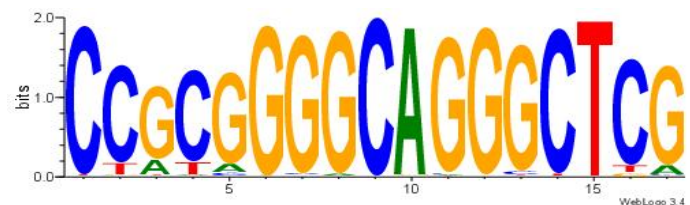
Alignment:

CGAGCCCTGCCCGCGG
 ----CCCAGCTCTGCC-

Original motif Consensus sequence: CGAGCCCTGCCCGCGG



Reverse complement motif Consensus sequence: CCGCGGGGCAGGGCTCG



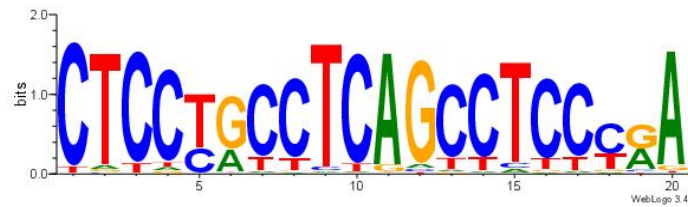
Dataset #: 1
 Motif ID: 26
 Motif name: Motif 26
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 12

Similarity score: 0.0664844

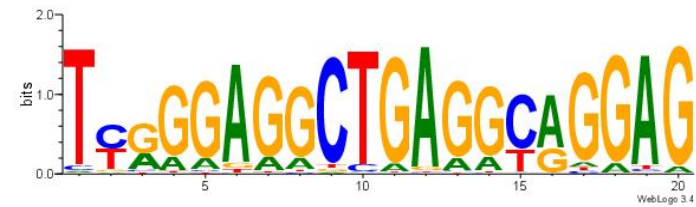
Alignment:

```
CTCCTGCCTCAGCCTCCCRA  
--CCCAGCTCTGCC-----
```

Original motif Consensus sequence: CTCCTGCCTCAGCCTCCCRA



Reverse complement motif Consensus sequence: TMGGGAGGCTGAGGCAGGAG



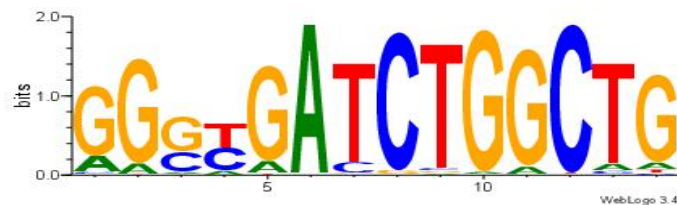
Dataset #: 1
Motif ID: 138
Motif name: Motif 138
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 3
Number of overlap: 12
Similarity score: 0.0690886

Alignment:

```
GGSKGATCTGGCTG  
GGCAGAGCTGGG--
```

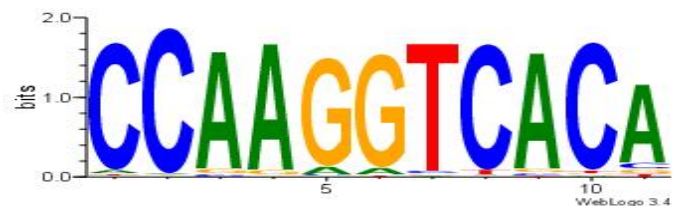
Original motif Consensus sequence: CAGCCAGATCRSCC

Reverse complement motif Consensus sequence: GGSKGATCTGGCT

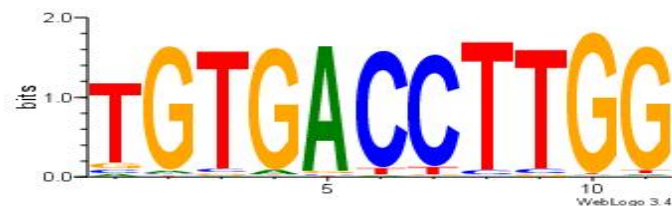


Dataset #: 1 Motif ID: 264 Motif name: Motif 264

Original motif Consensus sequence: CCAAGGCACA



Reverse complement motif Consensus sequence: TGTGACCTTG

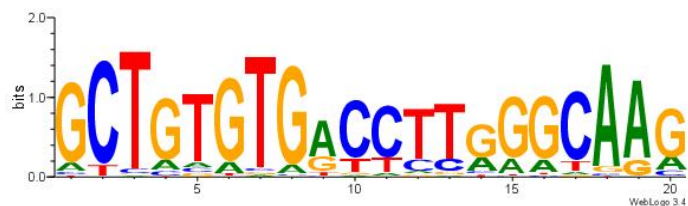


Best Matches for Motif ID 264 (Highest to Lowest)

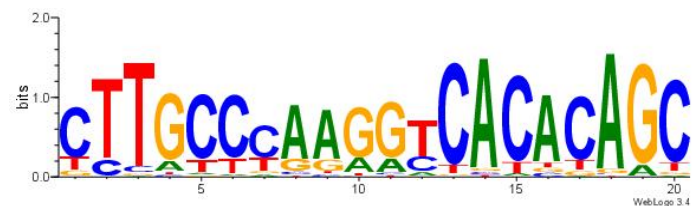
Dataset #:	1
Motif ID:	112
Motif name:	Motif 112
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	5
Number of overlap:	11
Similarity score:	0.0343671

Alignment:
 CTTGCCCAAGGCACACAGC
 ----CCAAGGCACA-----

Original motif Consensus sequence: GCTGTGTGACCTTGGGCAAG



Reverse complement motif Consensus sequence: CTTGCCCAAGGTCACACAGC

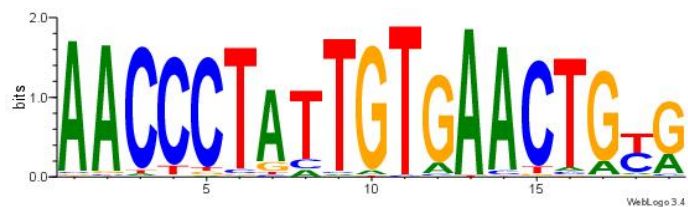


Dataset #: 1
Motif ID: 242
Motif name: Motif 242
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 11
Similarity score: 0.0609262

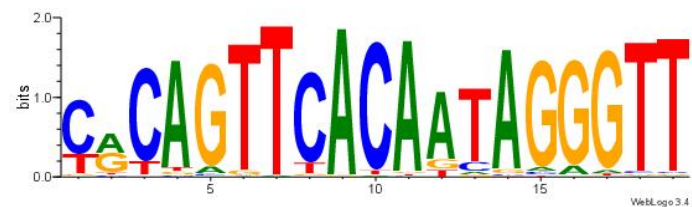
Alignment:

AACCCTATTGTGAACTGYG
TGTGACCTTGG-----

Original motif Consensus sequence: AACCCTATTGTGAACTGG



Reverse complement motif Consensus sequence: CMCAGTTCACAATAGGGTT

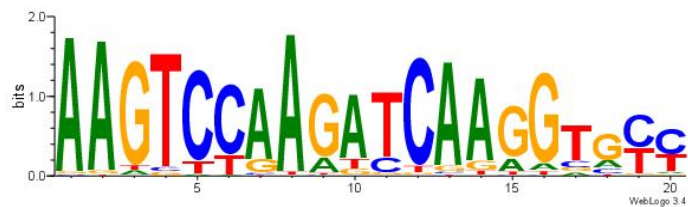


Dataset #: 1
 Motif ID: 119
 Motif name: Motif 119
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 5
 Number of overlap: 11
 Similarity score: 0.0681999

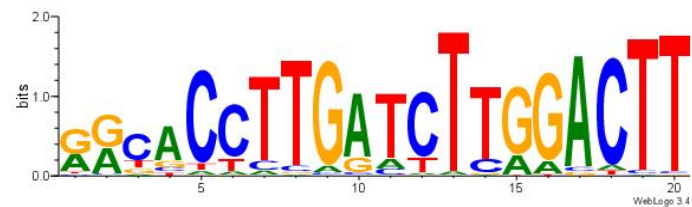
Alignment:

AAGTCCAAGATCAAGGTGY
 ----CCAAGGTCACA-----

Original motif Consensus sequence: AAGTCCAAGATCAAGGTGY



Reverse complement motif Consensus sequence: KKCACCTTGATCTTGGACTT



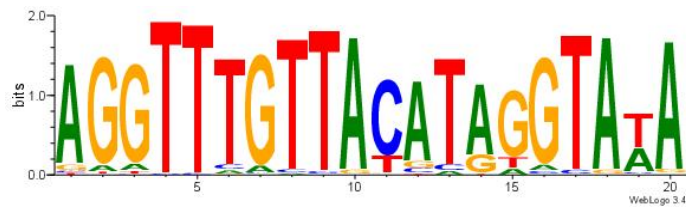
Dataset #: 1
 Motif ID: 137
 Motif name: Motif 137
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 6

Number of overlap: 11
Similarity score: 0.069002

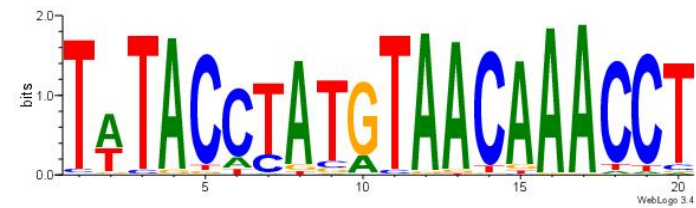
Alignment:

TWTACCTATGTAACAAACCT
-----CCAAGGTCACA-----

Original motif Consensus sequence: AGGTTTGTACATAGGTAWA



Reverse complement motif Consensus sequence:
TWTACCTATGTAACAAACCT

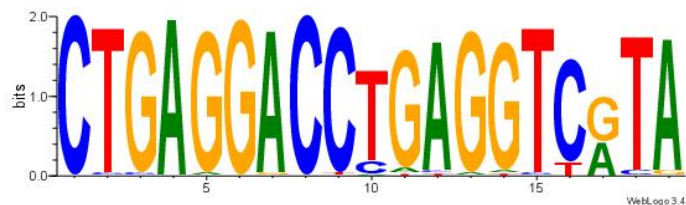


Dataset #: 1
Motif ID: 291
Motif name: Motif 291
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 11
Similarity score: 0.0740266

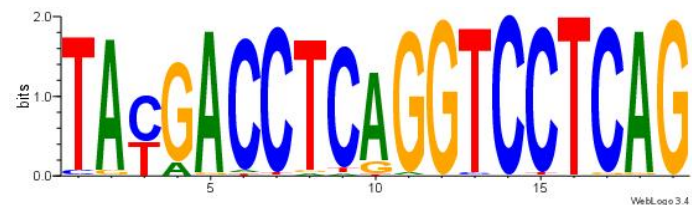
Alignment:

CTGAGGACCTGAGGTCRTA
-----CCAAGGTCACA

Original motif Consensus sequence: CTGAGGACCTGAGGTCRTA



Reverse complement motif Consensus sequence: TAMGACCTCAGGTCCTCAG

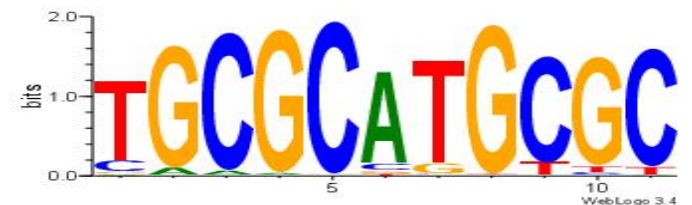


Dataset #: 1 Motif ID: 265 Motif name: Motif 265

Original motif Consensus sequence: GCGCATGCGCA



Reverse complement motif Consensus sequence: TGCGCATGCGC



Best Matches for Motif ID 265 (Highest to Lowest)

Dataset #:	1
Motif ID:	180
Motif name:	Motif 180
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	11
Similarity score:	0.00596496

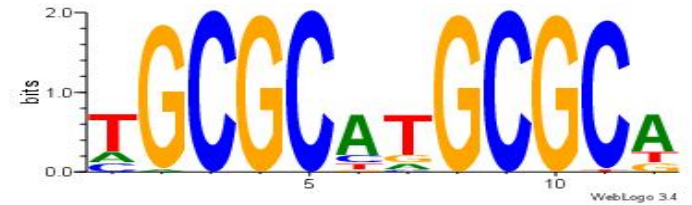
Alignment:

TGCGCATGCGCA
 TGCGCATGCGC-

Original motif Consensus sequence: TGCGCATGCGCA



Reverse complement motif Consensus sequence: TGCGCATGCGCA

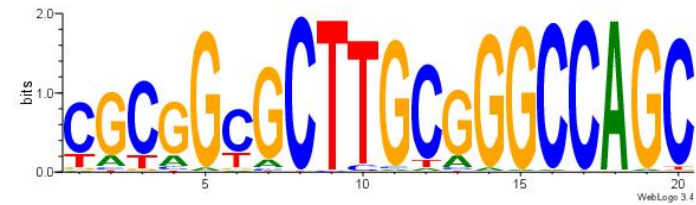
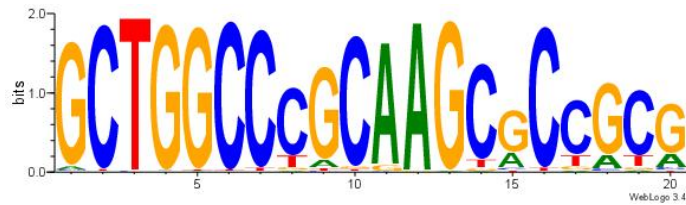


Dataset #: 1
 Motif ID: 100
 Motif name: Motif 100
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 4
 Number of overlap: 11
 Similarity score: 0.0616255

Alignment:
 CGCGGCGCTTGCGGGCCAGC
 ---TGCGCATGCGC-----

Original motif Consensus sequence: GCTGGCCCGCAAGCGCCGCG

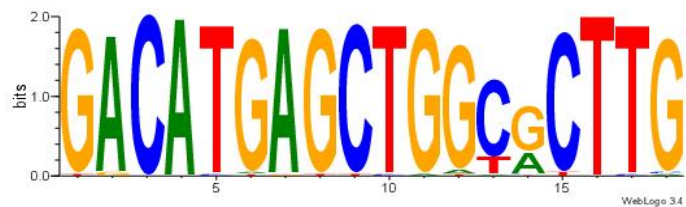
Reverse complement motif Consensus sequence:
 CGCGGCGCTTGCGGGCCAGC



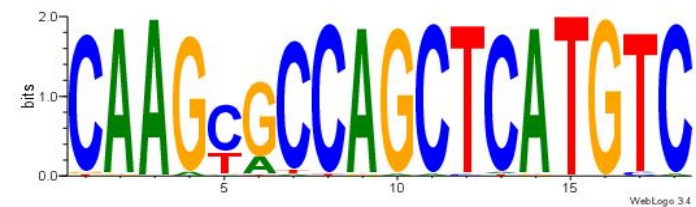
Dataset #: 1
 Motif ID: 306
 Motif name: Motif 306
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 5
 Number of overlap: 11
 Similarity score: 0.0658945

Alignment:
 CAAGCGCCAGCTCATGTC
 ---GCGCATGCGCA----

Original motif Consensus sequence: GACATGAGCTGGCGCTTG



Reverse complement motif Consensus sequence: CAAGCGCCAGCTCATGTC



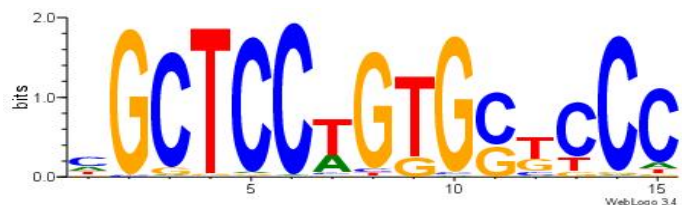
Dataset #: 1

Motif ID: 215
 Motif name: Motif 215
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 5
 Number of overlap: 11
 Similarity score: 0.079487

Alignment:

HGCTCCTGTGSKCCC
 ----TGCGCATGCGC

Original motif Consensus sequence: HGCTCCTGTGSKCCC



Reverse complement motif Consensus sequence: GGGRSCACAGGAGCD



Dataset #: 1
 Motif ID: 51
 Motif name: Motif 51
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 11

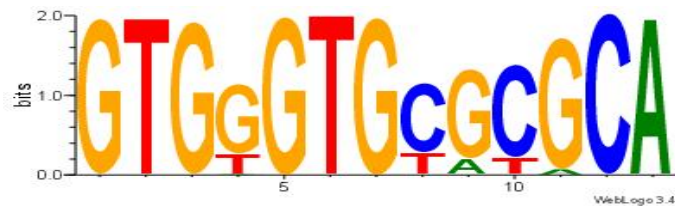
Similarity score: 0.0805098

Alignment:

TGCGCGCACCCAC

-GCGCATGCGCA-

Original motif Consensus sequence: GTGGGTGCGCGCA

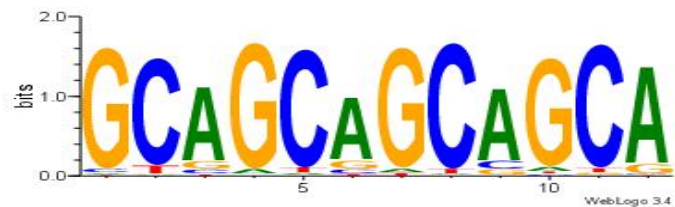


Reverse complement motif Consensus sequence: TGCGCGCACCCAC

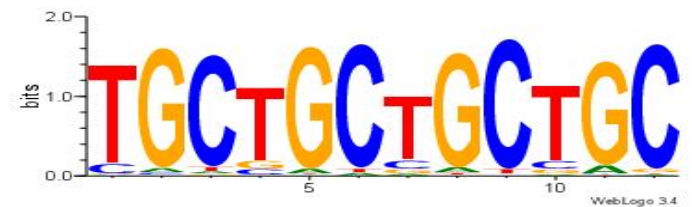


Dataset #: 1 Motif ID: 266 Motif name: Motif 266

Original motif Consensus sequence: GCAGCAGCAGCA



Reverse complement motif Consensus sequence: TGCTGCTGCTGC



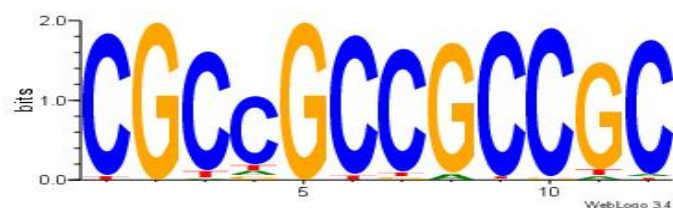
Best Matches for Motif ID 266 (Highest to Lowest)

Dataset #:	1
Motif ID:	101
Motif name:	Motif 101
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward

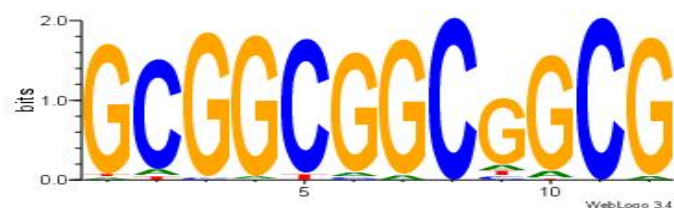
Position number: 1
Number of overlap: 12
Similarity score: 0.0655581

Alignment:
CGCCGCCGCCGC
TGCTGCTGCTGC

Original motif Consensus sequence: CGCCGCCGCCGC



Reverse complement motif Consensus sequence: GCGGCGGCGGCG

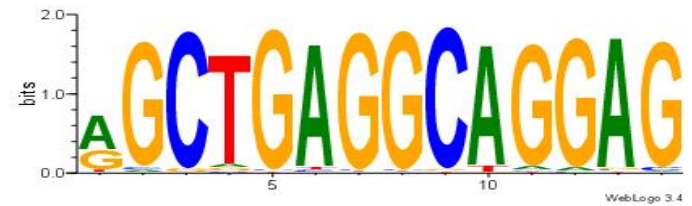
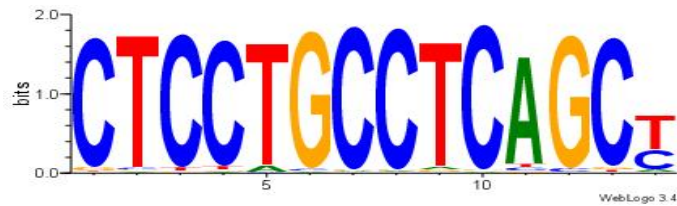


Dataset #: 1
Motif ID: 313
Motif name: Motif 313
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 2
Number of overlap: 12
Similarity score: 0.0732114

Alignment:
MGCTGAGGCAGGAG
-GCAGCAGCAGCA-

Original motif Consensus sequence: CTCCTGCCTCAGCY

Reverse complement motif Consensus sequence: MGCTGAGGCAGGAG

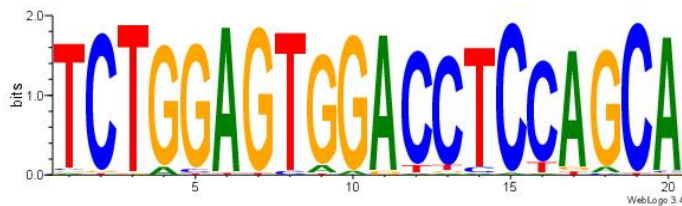


Dataset #: 1
 Motif ID: 350
 Motif name: Motif 350
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 9
 Number of overlap: 12
 Similarity score: 0.0784217

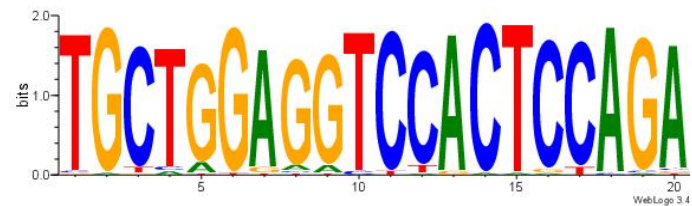
Alignment:

TGCTGGAGGTCCACTCCAGA
 TGCTGCTGCTGC-----

Original motif Consensus sequence: TCTGGAGTGGACCTCCAGCA



Reverse complement motif Consensus sequence: TGCTGGAGGTCCACTCCAGA



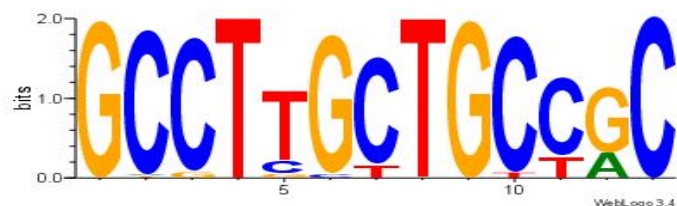
Dataset #: 1

Motif ID: 229
 Motif name: Motif 229
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 12
 Similarity score: 0.0792404

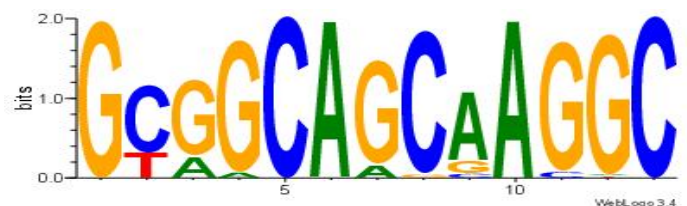
Alignment:

GCGGCAGCAAGGC
 -GCAGCAGCAGCA

Original motif Consensus sequence: GCCTTGCTGCCGC



Reverse complement motif Consensus sequence: GCGGCAGCAAGGC

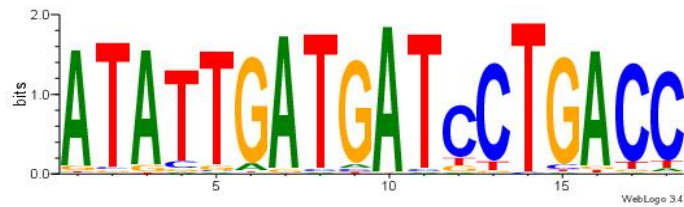


Dataset #: 1
 Motif ID: 184
 Motif name: Motif 184
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 5
 Number of overlap: 12
 Similarity score: 0.0798146

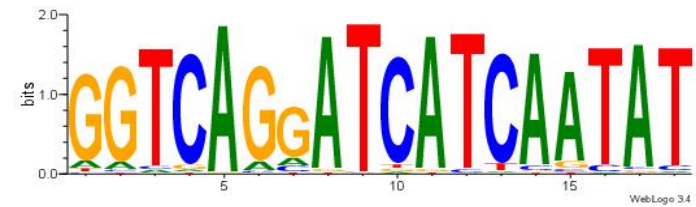
Alignment:

```
GGTCAGGATCATCAATAT
----GCAGCAGCAGCA--
```

Original motif Consensus sequence: ATATTGATGATcCTGACC



Reverse complement motif Consensus sequence: GGTCAGGATCATCAATAT



Dataset #: 1 Motif ID: 267 Motif name: Motif 267

Original motif Consensus sequence: ATGGACTTGAGA



Reverse complement motif Consensus sequence: TCTCAAGTCCAT



Best Matches for Motif ID 267 (Highest to Lowest)

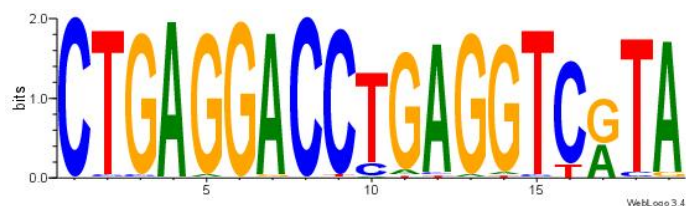
Dataset #:	1
Motif ID:	291
Motif name:	Motif 291
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward

Position number: 6
Number of overlap: 12
Similarity score: 0.0822148

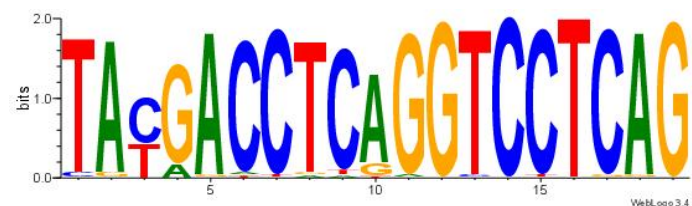
Alignment:

CTGAGGACCTGAGGTCRTA
--ATGGA^cCTTGAGA-----

Original motif Consensus sequence: CTGAGGACCTGAGGTCRTA



Reverse complement motif Consensus sequence: TAMGACCTCAGGTCCTCAG

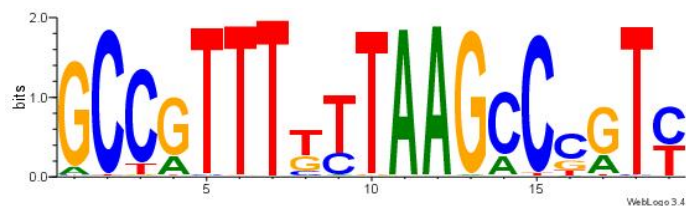


Dataset #: 1
Motif ID: 21
Motif name: Motif 21
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 2
Number of overlap: 12
Similarity score: 0.0832965

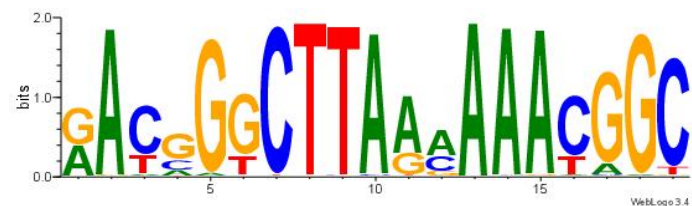
Alignment:

KACGGGCTTAARAAACGGC
-----ATGGA^cCTTGAGA-

Original motif Consensus sequence: GCCGTTTKTTAAGCCCGTY



Reverse complement motif Consensus sequence: KACGGGCTTAARAAACGGC

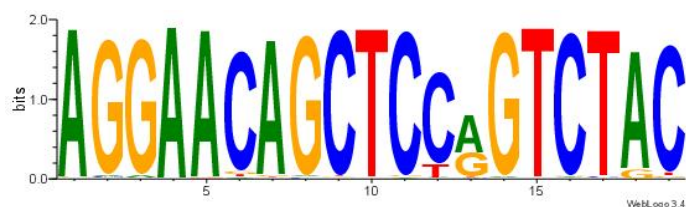


Dataset #: 1
Motif ID: 62
Motif name: Motif 62
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 8
Number of overlap: 12
Similarity score: 0.0857476

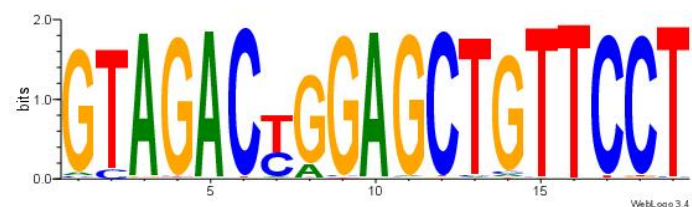
Alignment:

AGGAACAGCTCCRGCTCTAC
TCTCAAGTCCAT-----

Original motif Consensus sequence: AGGAACAGCTCCRGCTCTAC



Reverse complement motif Consensus sequence: GTAGACKGGAGCTGTTCCCT

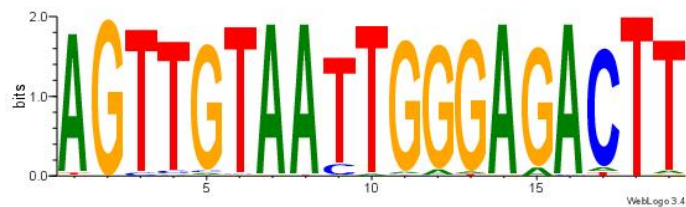


Dataset #: 1
 Motif ID: 232
 Motif name: Motif 232
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 6
 Number of overlap: 12
 Similarity score: 0.0886223

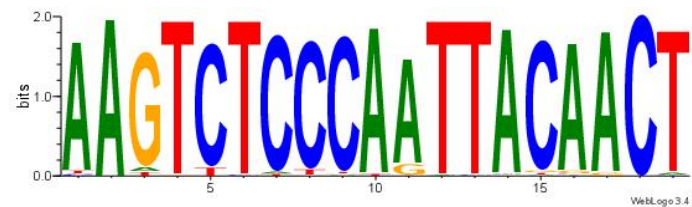
Alignment:

AGTTGTAATTGGGAGACTT
 --ATGGACTTGAGA-----

Original motif Consensus sequence: AGTTGTAATTGGGAGACTT



Reverse complement motif Consensus sequence: AAGTCTCCCAATTACAAC

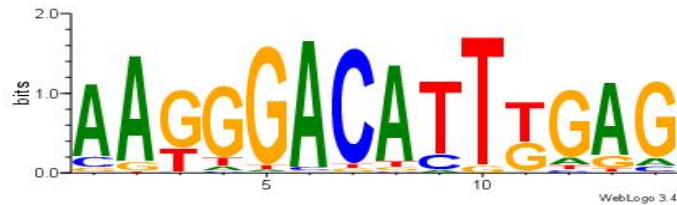


Dataset #: 1
 Motif ID: 166
 Motif name: Motif 166
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2

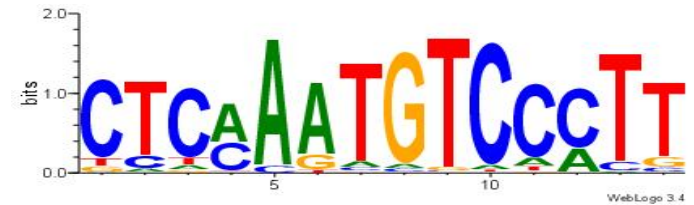
Number of overlap: 12
Similarity score: 0.0887226

Alignment:
AAGGGACATTKGAG
-ATGGA^TTTGAGA-

Original motif Consensus sequence: AAGGGACATTKGAG

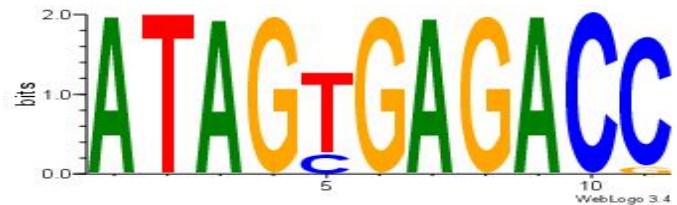


Reverse complement motif Consensus sequence: CTCRAATGTCCT

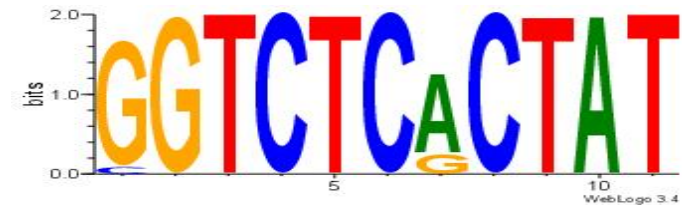


Dataset #: 1 Motif ID: 268 Motif name: Motif 268

Original motif Consensus sequence: ATAGTGAGACC



Reverse complement motif Consensus sequence: GGTCTCACTAT



Best Matches for Motif ID 268 (Highest to Lowest)

Dataset #: 1
Motif ID: 32
Motif name: Motif 32
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif

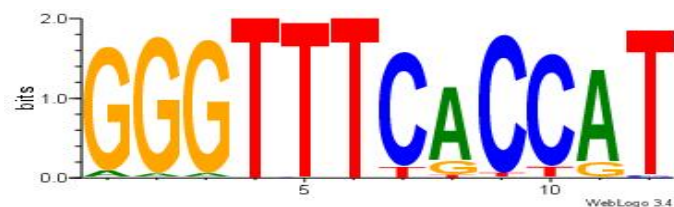
Direction: Forward
Position number: 1
Number of overlap: 11
Similarity score: 0.0513709

Alignment:
ATGGTGAAACCC
ATAGTGAGACC-

Original motif Consensus sequence: ATGGTGAAACCC



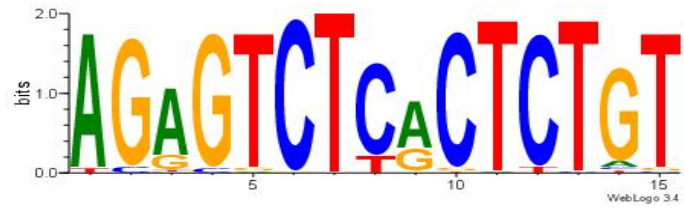
Reverse complement motif Consensus sequence: GGGTTTCACCAT



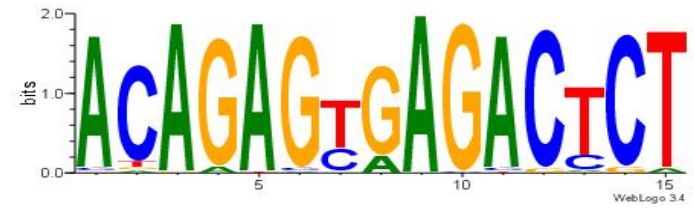
Dataset #: 1
Motif ID: 253
Motif name: Motif 253
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 3
Number of overlap: 11
Similarity score: 0.0539738

Alignment:
ACAGAGTGAGACTCT
--ATAGTGAGACC--

Original motif Consensus sequence: AGAGTCTCACTCTGT



Reverse complement motif Consensus sequence: ACAGAGTGAGACT

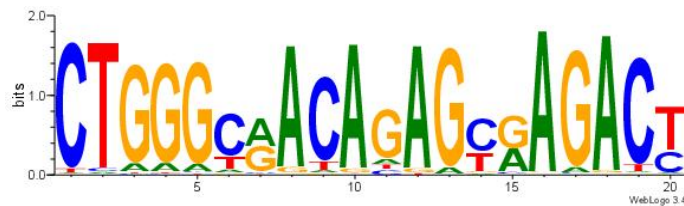


Dataset #: 1
Motif ID: 29
Motif name: Motif 29
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 10
Number of overlap: 11
Similarity score: 0.0624225

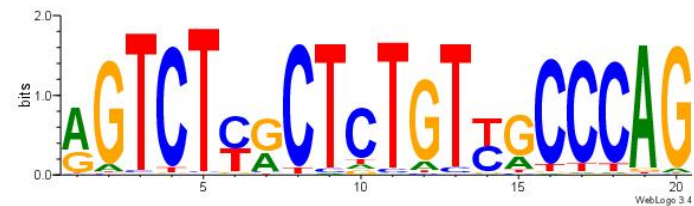
Alignment:

CTGGGCRACAGAGYRAGACY
-----ATAGTGAGACC

Original motif Consensus sequence: CTGGGCRACAGAGYRAGACY



Reverse complement motif Consensus sequence: MGTCTMKCTCTGKGCCAG

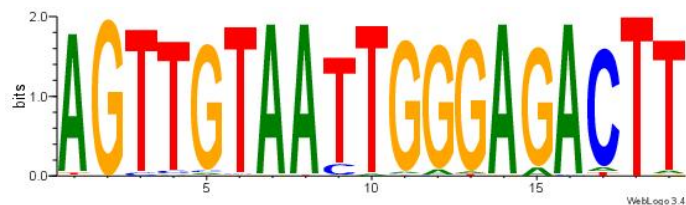


Dataset #: 1
 Motif ID: 232
 Motif name: Motif 232
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 11
 Similarity score: 0.0678548

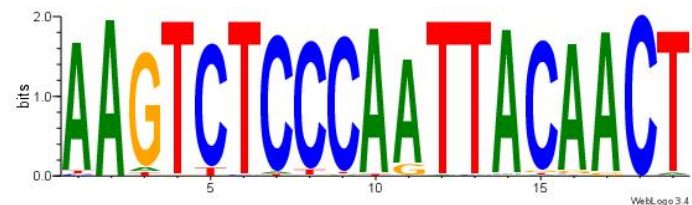
Alignment:

AAGTCTCCCAATTACAAC
 -GGTCTCACTAT-----

Original motif Consensus sequence: AGTTGTAATTGGGAGACTT



Reverse complement motif Consensus sequence: AAGTCTCCCAATTACAAC

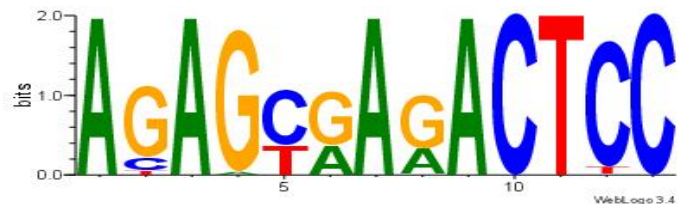


Dataset #: 1
 Motif ID: 204
 Motif name: Motif 204
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3

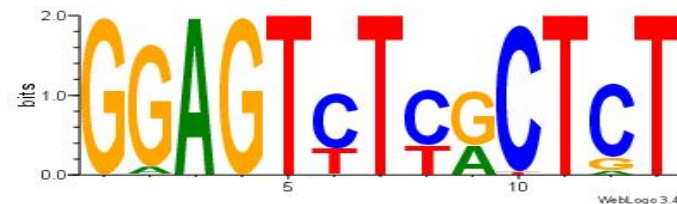
Number of overlap: 11
Similarity score: 0.0686646

Alignment:
AGAGYRAGACTCC
ATAGTGAGACC--

Original motif Consensus sequence: AGAGYRAGACTCC

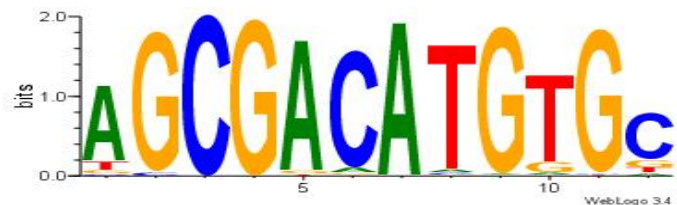


Reverse complement motif Consensus sequence: GGAGTCTMKCTCT

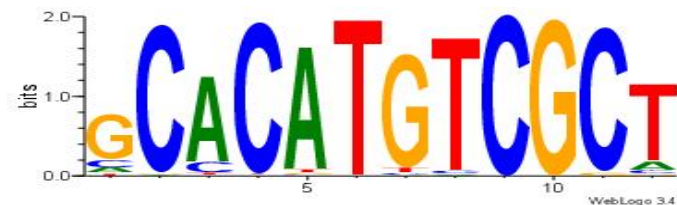


Dataset #: 1 Motif ID: 269 Motif name: Motif 269

Original motif Consensus sequence: AGCGACATGTGC



Reverse complement motif Consensus sequence: GCACATGTCGCT



Best Matches for Motif ID 269 (Highest to Lowest)

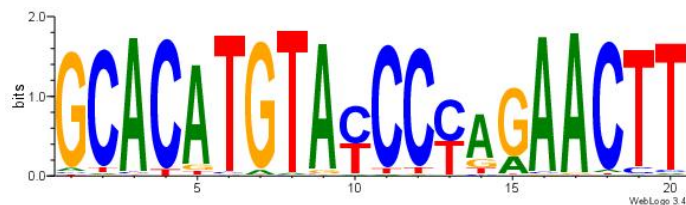
Dataset #:	1
Motif ID:	225
Motif name:	Motif 225
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif

Direction: Backward
Position number: 1
Number of overlap: 12
Similarity score: 0.0483903

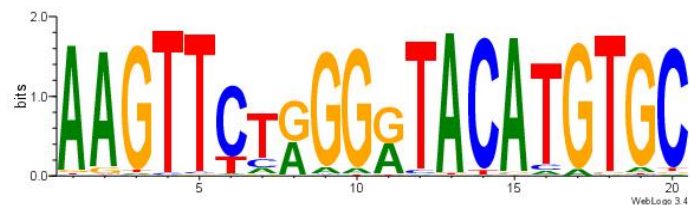
Alignment:

GCACATGTAYCCYAGAACTT
-----GCACATGTCGCT

Original motif Consensus sequence: GCACATGTAYCCYAGAACTT



Reverse complement motif Consensus sequence: AAGTTCTKGGKTACATGTGC

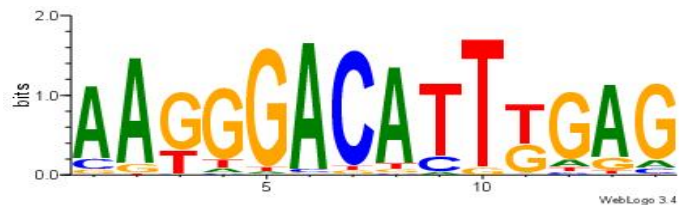


Dataset #: 1
Motif ID: 166
Motif name: Motif 166
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 2
Number of overlap: 12
Similarity score: 0.0581181

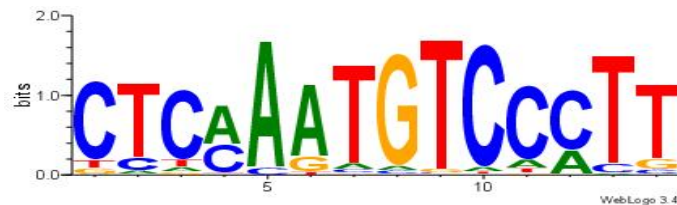
Alignment:

CTCRAATGTCCCTT
-GCACATGTCGCT-

Original motif Consensus sequence: AAGGGACATTKGAG



Reverse complement motif Consensus sequence: CTCRAATGTCCCT

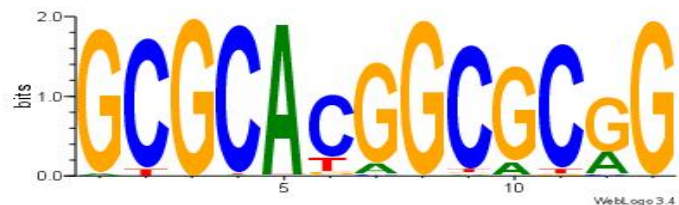


Dataset #: 1
Motif ID: 157
Motif name: Motif 157
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 2
Number of overlap: 12
Similarity score: 0.062288

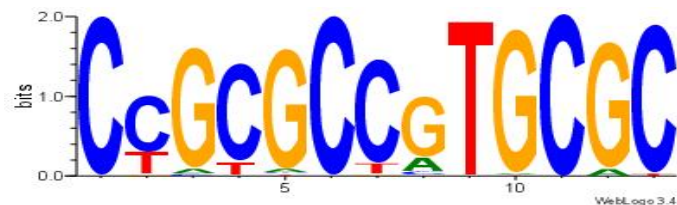
Alignment:

CCGCGCCGTGCGC
AGCGACATGTGC-

Original motif Consensus sequence: GCGCACGGCGCGG



Reverse complement motif Consensus sequence: CCGCGCCGTGCGC

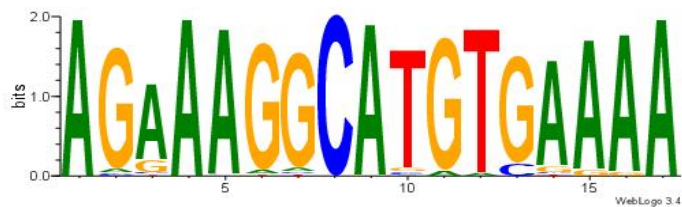


Dataset #: 1
 Motif ID: 230
 Motif name: Motif 230
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 12
 Similarity score: 0.0646389

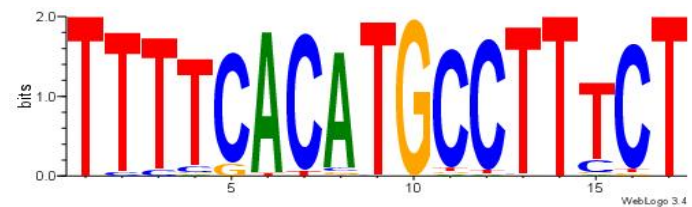
Alignment:

TTTTCACATGCCTTTCT
 ---GCACATGTCGCT--

Original motif Consensus sequence: AGAAAGGCATGTGAAAA



Reverse complement motif Consensus sequence: TTTTCACATGCCTTTCT



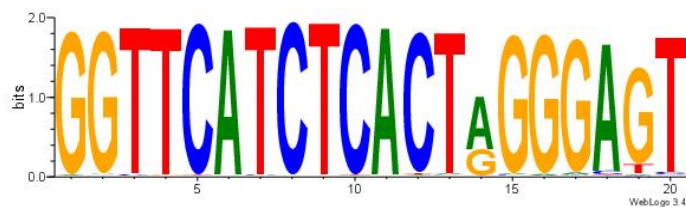
Dataset #: 1
 Motif ID: 23
 Motif name: Motif 23
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 8

Number of overlap: 12
Similarity score: 0.0679249

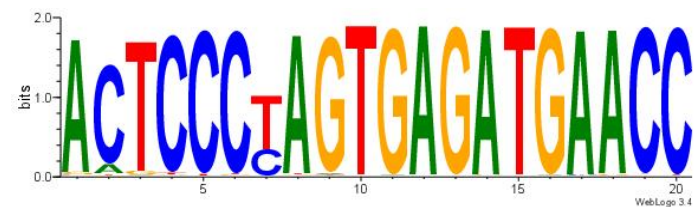
Alignment:

ACTCCCTAGTGAGATGAACC
-AGCGACATGTGC-----

Original motif Consensus sequence: GGTTCACTCTCACTAGGGAGT

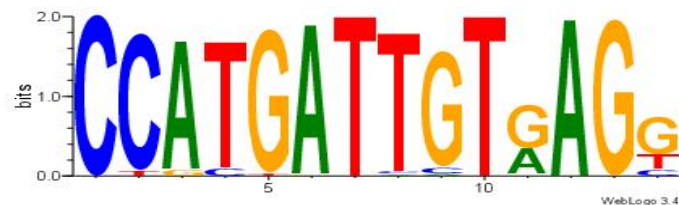


Reverse complement motif Consensus sequence:
ACTCCCTAGTGAGATGAACC

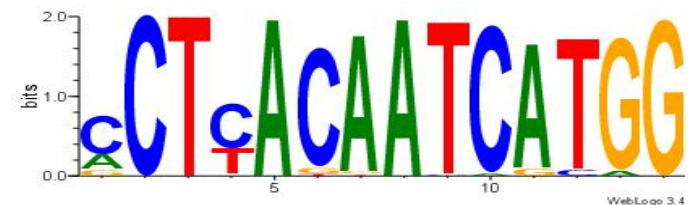


Dataset #: 1 Motif ID: 270 Motif name: Motif 270

Original motif Consensus sequence: CCATGATTGTAGG



Reverse complement motif Consensus sequence: CCTMACAATCATGG



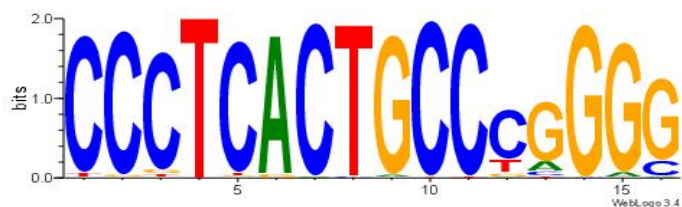
Best Matches for Motif ID 270 (Highest to Lowest)

Dataset #: 1
Motif ID: 136
Motif name: Motif 136
Matching format of first motif: Reverse Complement

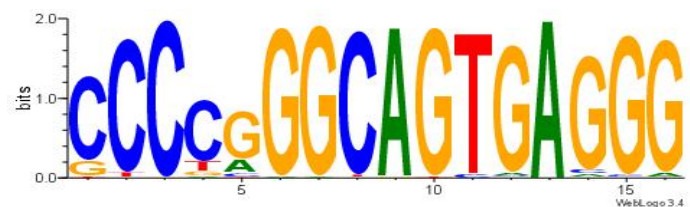
Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 14
 Similarity score: 0.0904714

Alignment:
 CCCTCACTGCCCCGGG
 -CCTMACAATCATGG-

Original motif Consensus sequence: CCCTCACTGCCCCGGG



Reverse complement motif Consensus sequence: CCCCgggCAGTGAGGG

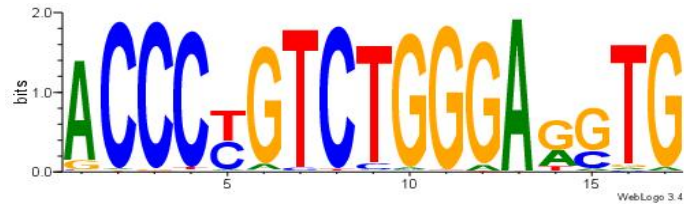


Dataset #: 1
 Motif ID: 95
 Motif name: Motif 95
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3
 Number of overlap: 14
 Similarity score: 0.091519

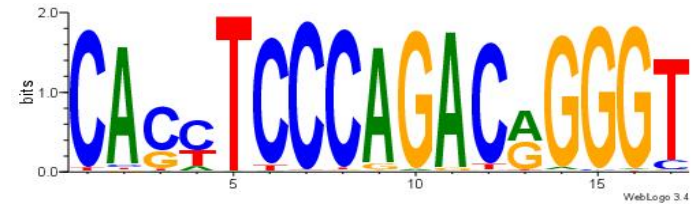
Alignment:

CACCTCCCAGACMGGGT
--CCTMACAATCATGG--

Original motif Consensus sequence: ACCCYGTCTGGGAGGTG



Reverse complement motif Consensus sequence:
CACCTCCCAGACMGGGT

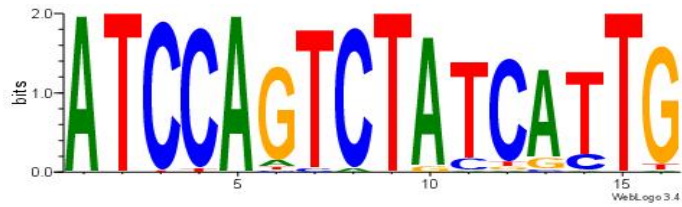


Dataset #:	1
Motif ID:	189
Motif name:	Motif 189
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	3
Number of overlap:	14
Similarity score:	0.0977764

Alignment:
CAATGATAGACTGGAT
--CCATGATTGTRAGG

Original motif Consensus sequence: ATCCAGTCTATCATTG

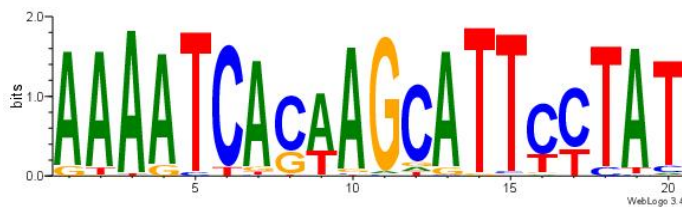
Reverse complement motif Consensus sequence:
CAATGATAGACTGGAT



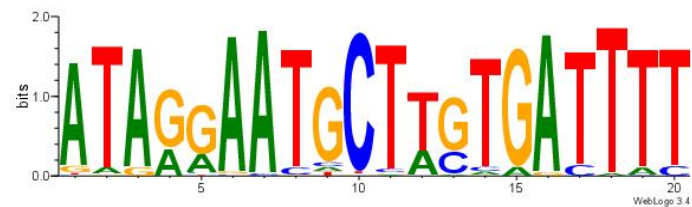
Dataset #: 1
 Motif ID: 254
 Motif name: Motif 254
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 5
 Number of overlap: 14
 Similarity score: 0.0983227

Alignment:
 AAAATCACAAGCATTCTAT
 ----CCTMACAATCATGG--

Original motif Consensus sequence: AAAATCACAAGCATTCTAT



Reverse complement motif Consensus sequence: ATAGGAATGCTTGTGATTTT



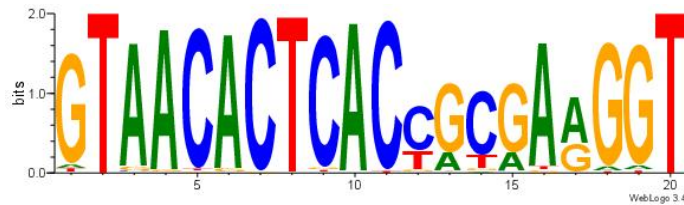
Dataset #: 1

Motif ID: 201
 Motif name: Motif 201
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 6
 Number of overlap: 14
 Similarity score: 0.0984147

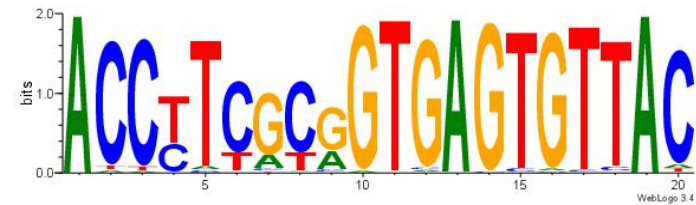
Alignment:

GTAACACTCACCGCGARGGT
 -CCTMACAATCATGG-----

Original motif Consensus sequence: GTAACACTCACCGCGARGGT

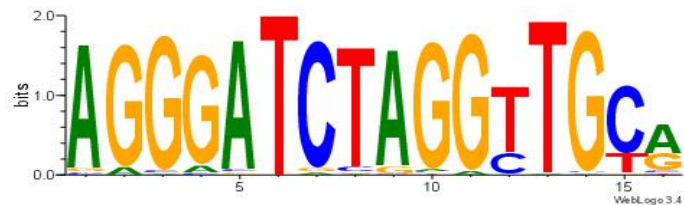


Reverse complement motif Consensus sequence: ACCKTCGCGGTGAGTGTTAC

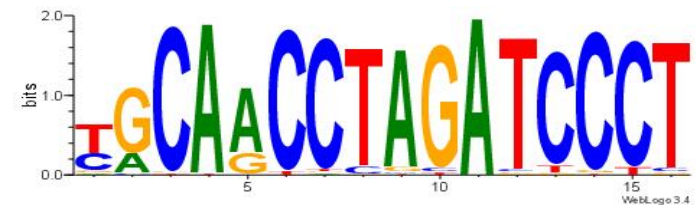


Dataset #: 1 Motif ID: 271 Motif name: Motif 271

Original motif Consensus sequence: AGGGATCTAGGTTGCR



Reverse complement motif Consensus sequence: KGCAACCTAGATCCCT



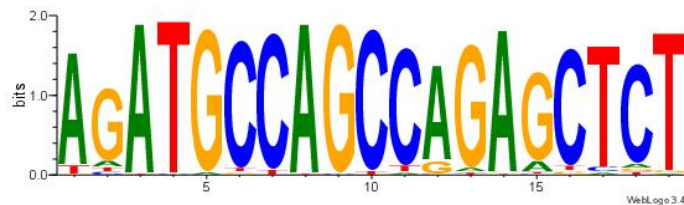
Best Matches for Motif ID 271 (Highest to Lowest)

Dataset #: 1
Motif ID: 307
Motif name: Motif 307
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 4
Number of overlap: 16
Similarity score: 0.0814563

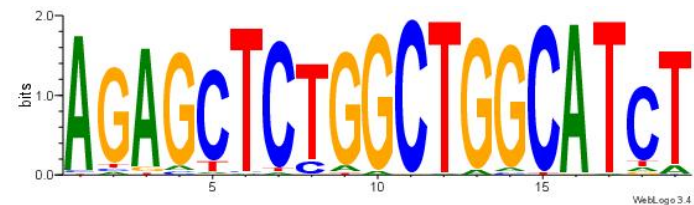
Alignment:

AGAGCTCTGGCTGGCATCT
AGGGATCTAGGTTGCR---

Original motif Consensus sequence: AGATGCCAGCCAGAGCTCT



Reverse complement motif Consensus sequence:
AGAGCTCTGGCTGGCATCT



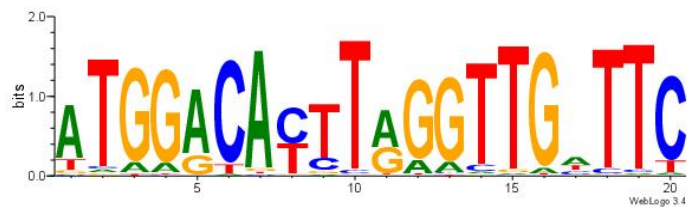
Dataset #: 1
Motif ID: 58
Motif name: Motif 58
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif

Direction: Backward
Position number: 3
Number of overlap: 16
Similarity score: 0.0869615

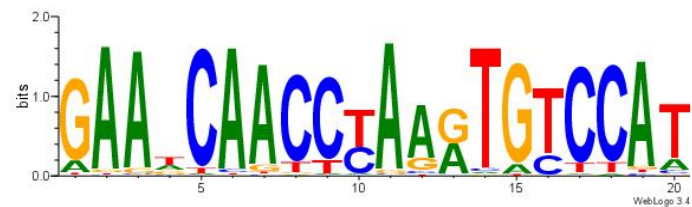
Alignment:

ATGGACAYTTRGGTTGHTTC
--AGGGATCTAGGTTGCR--

Original motif Consensus sequence: ATGGACAYTTRGGTTGHTTC



Reverse complement motif Consensus sequence: GAAHCAACCKAAKTGTCCAT

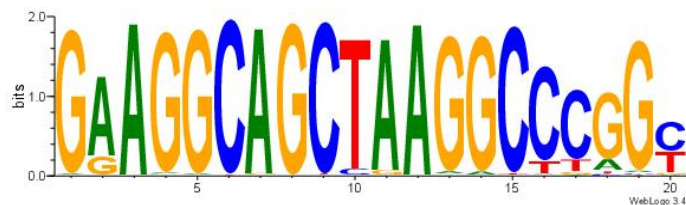


Dataset #: 1
Motif ID: 64
Motif name: Motif 64
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 3
Number of overlap: 16
Similarity score: 0.0921874

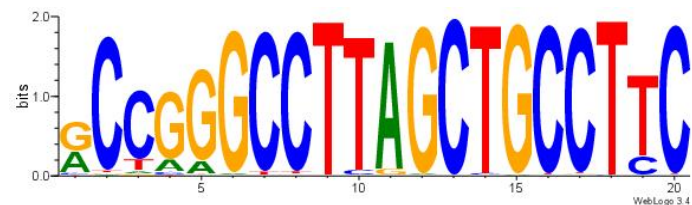
Alignment:

GAAGGCAGCTAAGGCCGGY
--AGGGATCTAGGTTGCR--

Original motif Consensus sequence: GAAGGCAGCTAAGGCCGGY



Reverse complement motif Consensus sequence: KCCGGCCTTAGCTGCCTTC

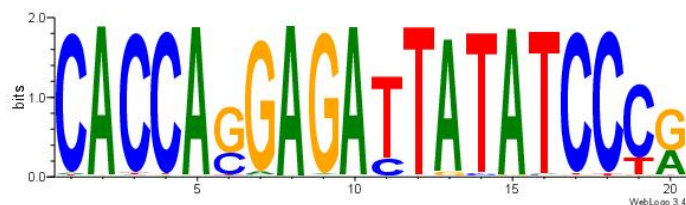


Dataset #: 1
Motif ID: 19
Motif name: Motif 19
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 5
Number of overlap: 16
Similarity score: 0.096154

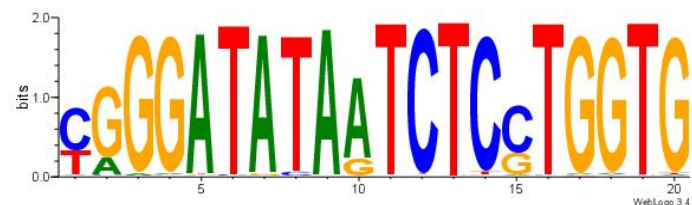
Alignment:

CACCAGGAGATTATATCCCR
KGCAACCTAGATCCCT-----

Original motif Consensus sequence: CACCAGGAGATTATATCCCR



Reverse complement motif Consensus sequence: MGGGATATAATCTCCTGGTG

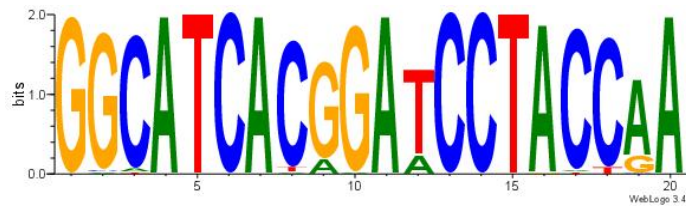


Dataset #: 1
 Motif ID: 311
 Motif name: Motif 311
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 16
 Similarity score: 0.0980366

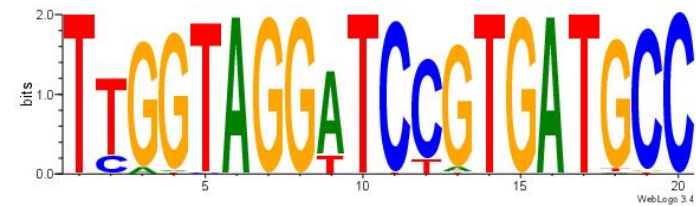
Alignment:

GGCATCACGGATCCTACCAA
 KGCAACCTAGATCCCT----

Original motif Consensus sequence: GGCATCACGGATCCTACCAA



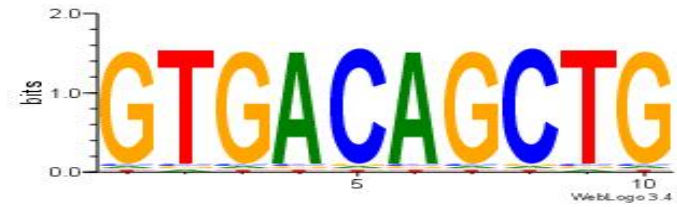
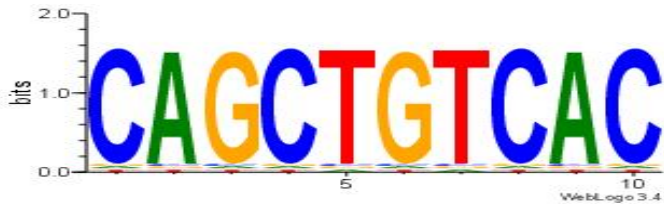
Reverse complement motif Consensus sequence: TTGGTAGGATCCGTGATGCC



Dataset #: 1 Motif ID: 272 Motif name: Motif 272

Original motif Consensus sequence: CAGCTGTCAC

Reverse complement motif Consensus sequence: GTGACAGCTG



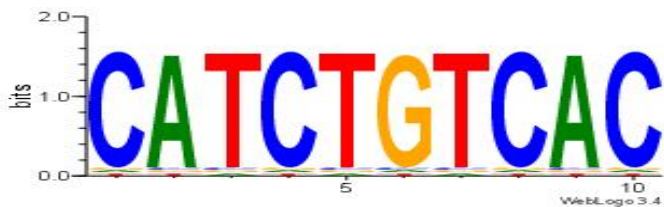
Best Matches for Motif ID 272 (Highest to Lowest)

Dataset #: 1
 Motif ID: 334
 Motif name: Motif 334
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 10
 Similarity score: 0.0227273

Alignment:

CATCTGTCAC
 CAGCTGTCAC

Original motif Consensus sequence: CATCTGTCAC



Reverse complement motif Consensus sequence: GTGACAGATG

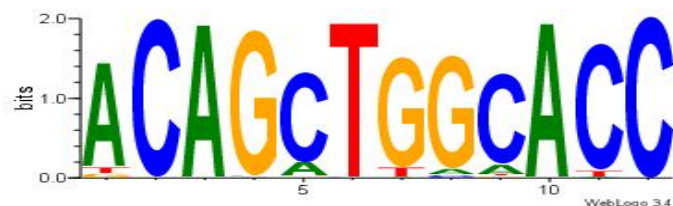


Dataset #: 1

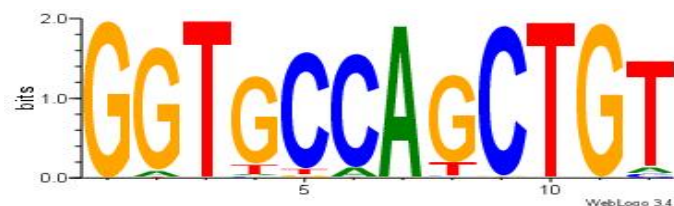
Motif ID: 199
 Motif name: Motif 199
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 10
 Similarity score: 0.037149

Alignment:
 GGTGCCAGCTGT
 -GTGACAGCTG-

Original motif Consensus sequence: ACAGCTGGCACC



Reverse complement motif Consensus sequence: GGTGCCAGCTGT

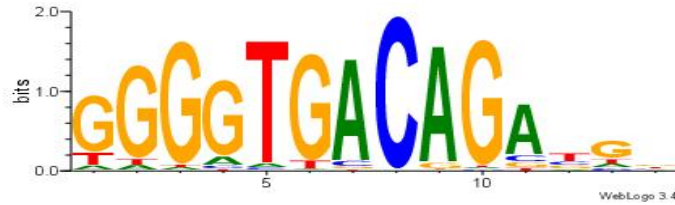


Dataset #: 1
 Motif ID: 1
 Motif name: Motif 1
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 10
 Similarity score: 0.0483787

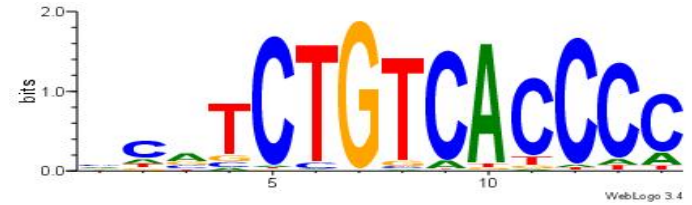
Alignment:

BCVTCTGTCACCCC
---CAGCTGTCAC-

Original motif Consensus sequence: GGGGTGACAGABGB



Reverse complement motif Consensus sequence: BCVTCTGTCACCCC



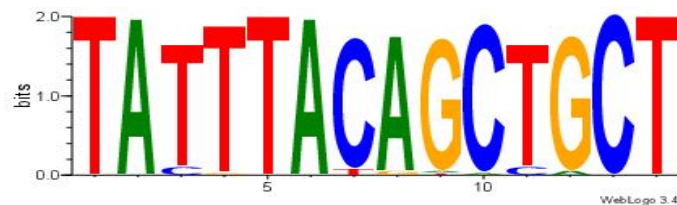
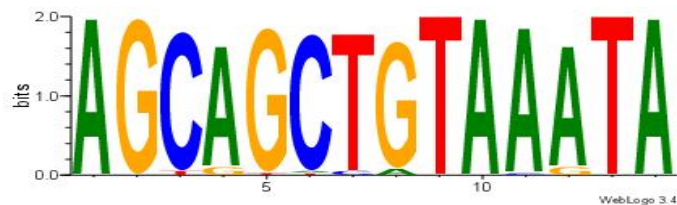
Dataset #: 1
Motif ID: 325
Motif name: Motif 325
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 3
Number of overlap: 10
Similarity score: 0.0565248

Alignment:

TATTTACAGCTGCT
--GTGACAGCTG--

Original motif Consensus sequence: AGCAGCTGTAAATA

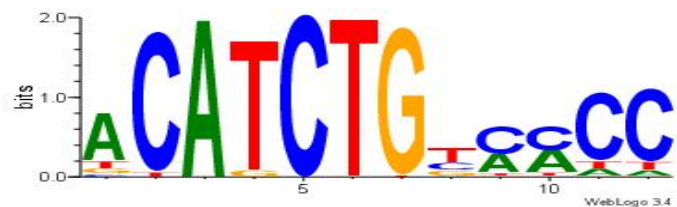
Reverse complement motif Consensus sequence: TATTTACAGCTGCT



Dataset #: 1
 Motif ID: 49
 Motif name: Motif 49
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 10
 Similarity score: 0.0671188

Alignment:
 ACATCTGYMMCC
 -CAGCTGTCAC-

Original motif Consensus sequence: ACATCTGYMMCC

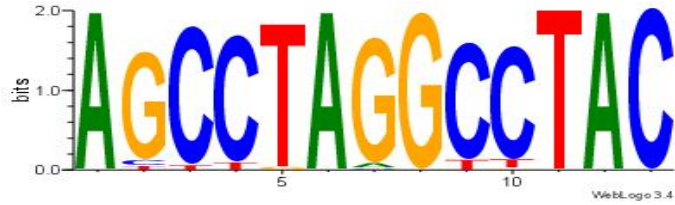


Reverse complement motif Consensus sequence: GRRMCAGATGT

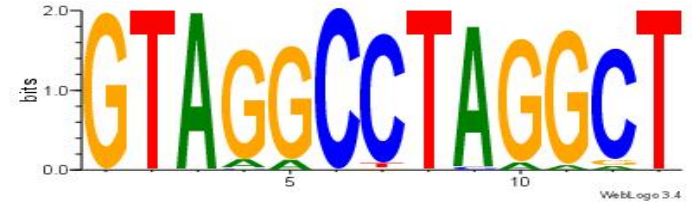


Dataset #: 1 Motif ID: 273 Motif name: Motif 273

Original motif Consensus sequence: AGCCTAGGCCTAC



Reverse complement motif Consensus sequence: GTAGGCCTAGGCT



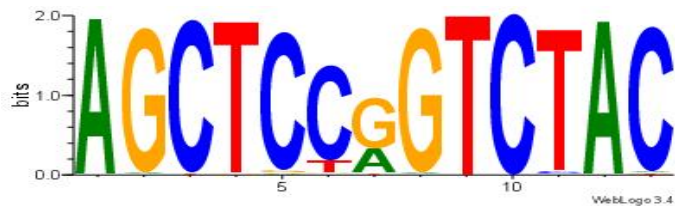
Best Matches for Motif ID 273 (Highest to Lowest)

Dataset #:	1
Motif ID:	365
Motif name:	Motif 365
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	13
Similarity score:	0.0731001

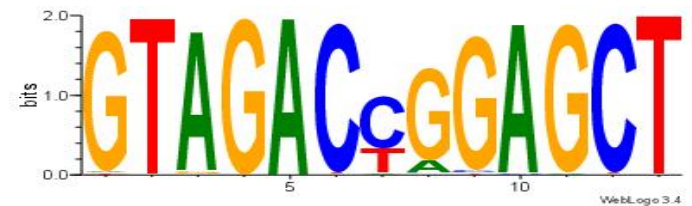
Alignment:

```
AGCTCCGGTCTAC  
AGCCTAGGCCTAC
```

Original motif Consensus sequence: AGCTCCGGTCTAC



Reverse complement motif Consensus sequence: GTAGACCGGAGCT

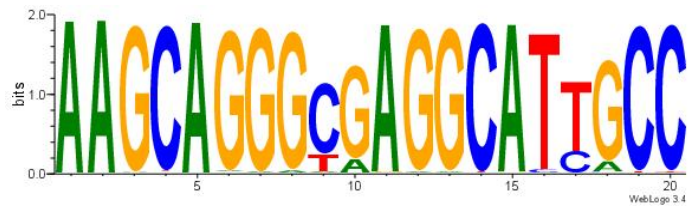


Dataset #: 1
 Motif ID: 13
 Motif name: Motif 13
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 13
 Similarity score: 0.0735654

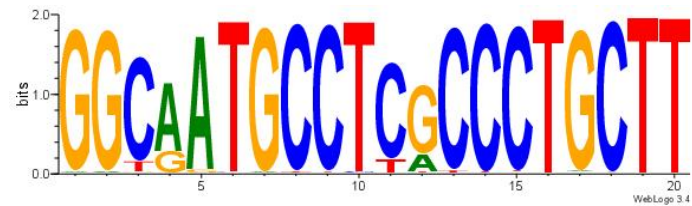
Alignment:

AAGCAGGGCGAGGCATTGCC
 -----GTAGGCCTAGGCT--

Original motif Consensus sequence: AAGCAGGGCGAGGCATTGCC



Reverse complement motif Consensus sequence: GGCAATGCCTCGCCCTGCTT



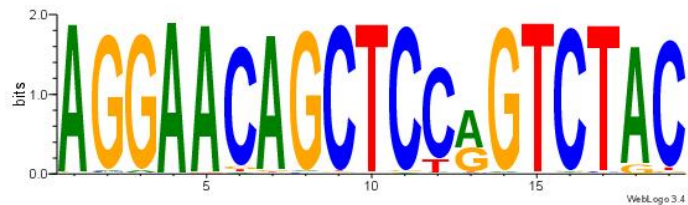
Dataset #: 1
 Motif ID: 62
 Motif name: Motif 62
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 7

Number of overlap: 13
Similarity score: 0.0803293

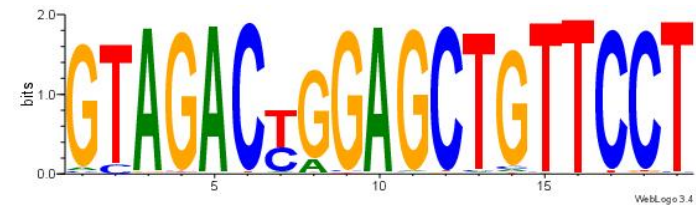
Alignment:

AGGAACAGCTCCRGTCTAC
-----AGCCTAGGCCTAC

Original motif Consensus sequence: AGGAACAGCTCCRGTCTAC



Reverse complement motif Consensus sequence:
GTAGACKGGAGCTGTTCCT

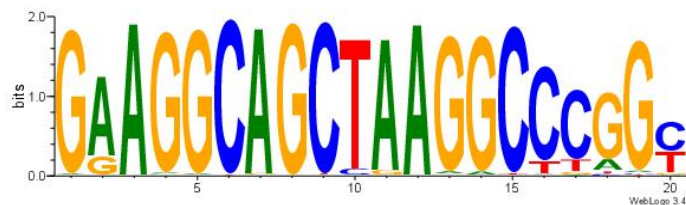


Dataset #: 1
Motif ID: 64
Motif name: Motif 64
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 7
Number of overlap: 13
Similarity score: 0.0829415

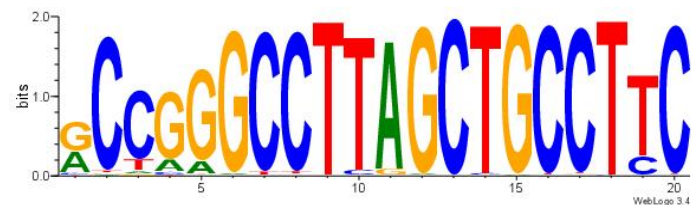
Alignment:

GAAGGCAGCTAAGGCCGGY
-----AGCCTAGGCCTAC-

Original motif Consensus sequence: GAAGGCAGCTAAGGCCGGY



Reverse complement motif Consensus sequence: KCCGGGCCTTAGCTGCCTTC

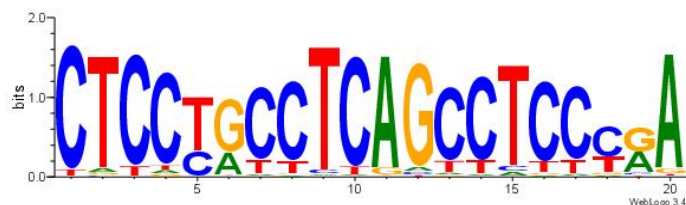


Dataset #: 1
Motif ID: 26
Motif name: Motif 26
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 5
Number of overlap: 13
Similarity score: 0.0838018

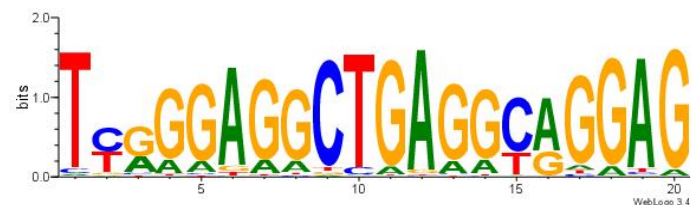
Alignment:

```
TMGGGAGGCTGAGGCAGGAG  
---GTAGGCCTAGGCT----
```

Original motif Consensus sequence: CTCCTGCCTCAGCCTCCRA

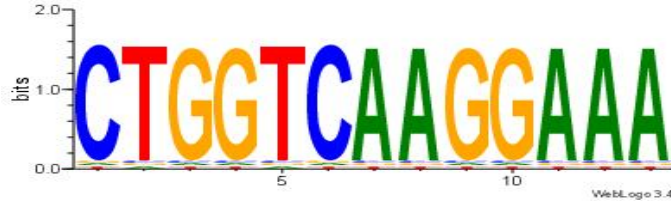


Reverse complement motif Consensus sequence: TMGGGAGGCTGAGGCAGGAG

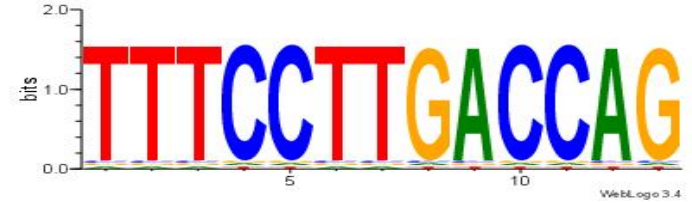


Dataset #: 1 Motif ID: 274 Motif name: Motif 274

Original motif Consensus sequence: CTGGTCAAGGAAA



Reverse complement motif Consensus sequence: TTTCTTGACCAG



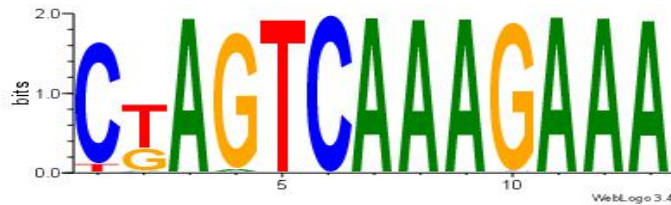
Best Matches for Motif ID 274 (Highest to Lowest)

Dataset #:	1
Motif ID:	24
Motif name:	Motif 24
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	13
Similarity score:	0.0483985

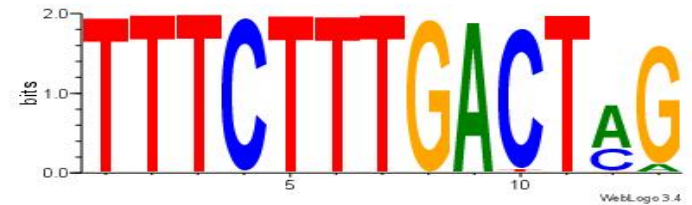
Alignment:

CKAGTCAAAGAAA
CTGGTCAAGGAAA

Original motif Consensus sequence: CKAGTCAAAGAAA



Reverse complement motif Consensus sequence: TTTCTTGACTRG

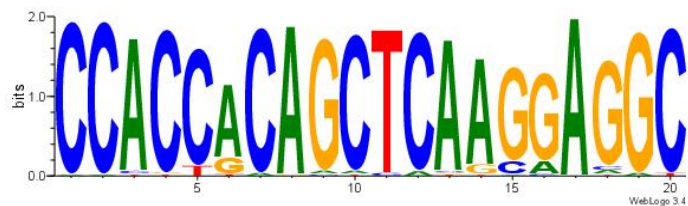


Dataset #: 1
 Motif ID: 331
 Motif name: Motif 331
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 13
 Similarity score: 0.0763683

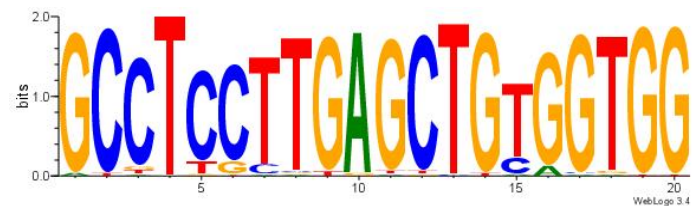
Alignment:

CCACCACAGCTCAAGGAGGC
 -----CTGGTCAAGGAAA-

Original motif Consensus sequence: CCACCACAGCTCAAGGAGGC



Reverse complement motif Consensus sequence: GCCTCCTTGAGCTGTGGTGG



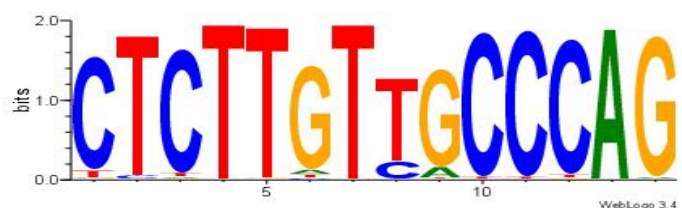
Dataset #: 1
 Motif ID: 135
 Motif name: Motif 135
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward

Position number: 1
Number of overlap: 13
Similarity score: 0.077238

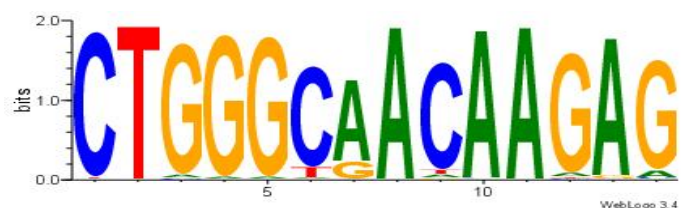
Alignment:

CTGGGCAACAAGAG
-CTGGTCAAGGAAA

Original motif Consensus sequence: CTCTTGTTGCCAG



Reverse complement motif Consensus sequence: CTGGGCAACAAGAG

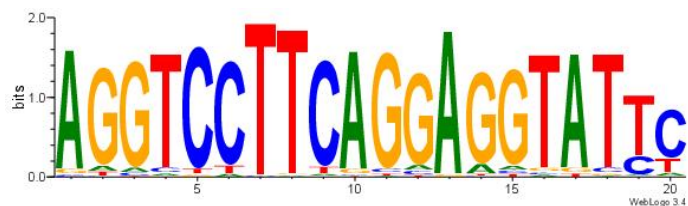


Dataset #: 1
Motif ID: 179
Motif name: Motif 179
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2
Number of overlap: 13
Similarity score: 0.0876128

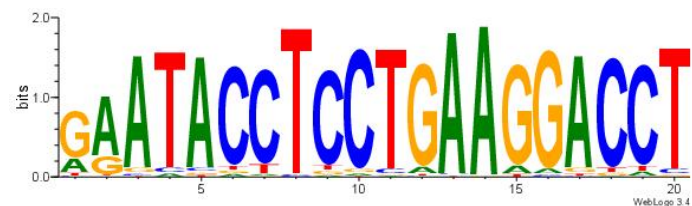
Alignment:

AGGTCCTTCAGGAGGTATTC
-----TTCCTTGACCAG-

Original motif Consensus sequence: AGGTCCTCAGGAGGTATTC



Reverse complement motif Consensus sequence: GAATACCTCCTGAAGGACCT

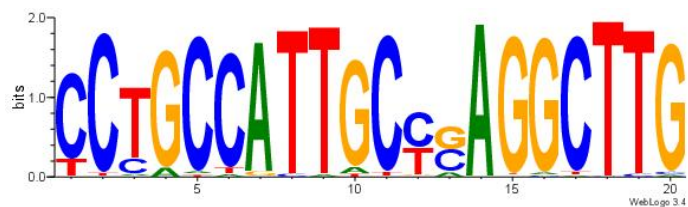


Dataset #: 1
Motif ID: 196
Motif name: Motif 196
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 3
Number of overlap: 13
Similarity score: 0.0913407

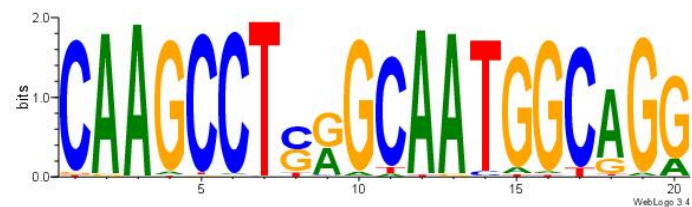
Alignment:

CCTGCCATTGCYSAGGCTTG
-----TTCCTTGACCAG--

Original motif Consensus sequence: CCTGCCATTGCYSAGGCTTG

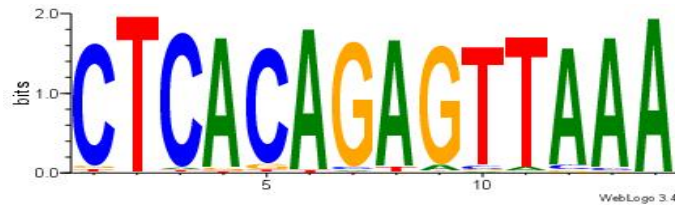


Reverse complement motif Consensus sequence: CAAGCCTSKGCAATGGCAGG

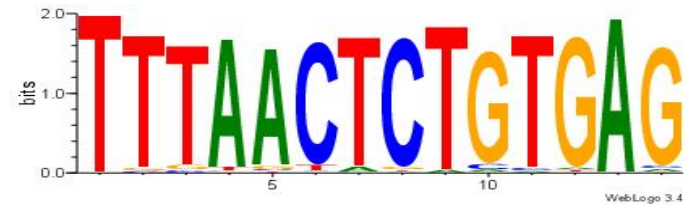


Dataset #: 1 Motif ID: 275 Motif name: Motif 275

Original motif Consensus sequence: CTCACAGAGTTAAA



Reverse complement motif Consensus sequence: TTTAACTCTGTGAG



Best Matches for Motif ID 275 (Highest to Lowest)

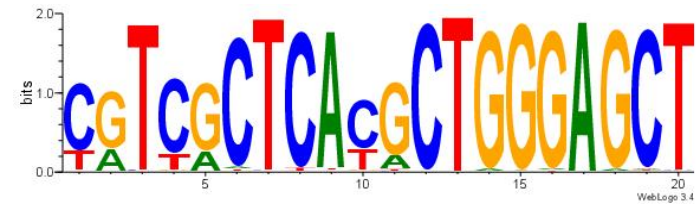
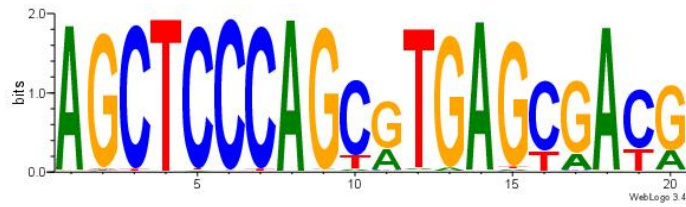
Dataset #:	1
Motif ID:	48
Motif name:	Motif 48
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	3
Number of overlap:	14
Similarity score:	0.0799887

Alignment:

```
CGTCGCTCACGCTGGGAGCT
----TTTAACTCTGTGAG--
```

Original motif Consensus sequence: AGCTCCAGCGTGAGCGACG

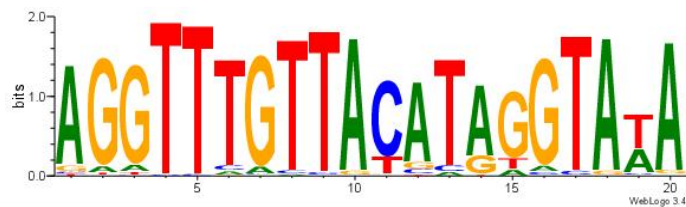
Reverse complement motif Consensus sequence:
CGTCGCTCACGCTGGGAGCT



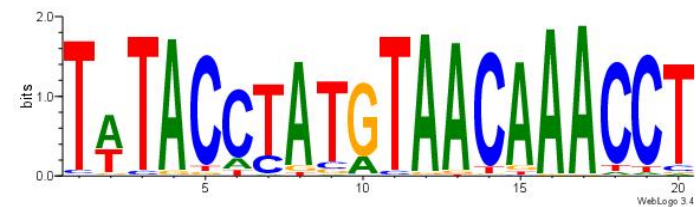
Dataset #: 1
 Motif ID: 137
 Motif name: Motif 137
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 7
 Number of overlap: 14
 Similarity score: 0.0822742

Alignment:
 TWTACCTATGTAACAAACCT
 TTTAACTCTGTGAG-----

Original motif Consensus sequence: AGGTTTGTTACATAGGTAWA



Reverse complement motif Consensus sequence: TWTACCTATGTAACAAACCT



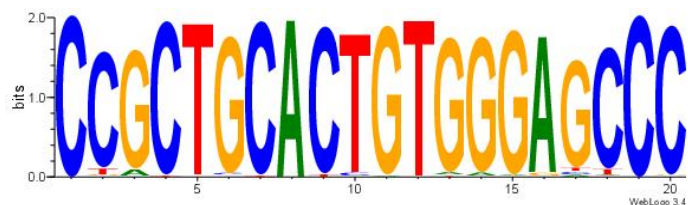
Dataset #: 1

Motif ID: 144
 Motif name: Motif 144
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 4
 Number of overlap: 14
 Similarity score: 0.0838641

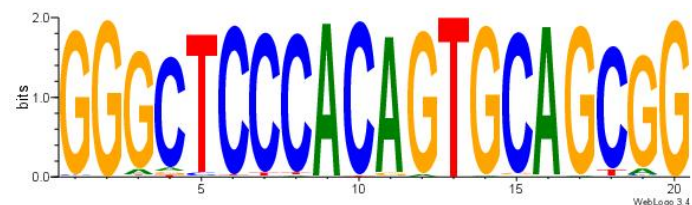
Alignment:

GGGCTCCCACAGTGCAGCGG
 ---CTCACAGAGTTAAA---

Original motif Consensus sequence: CCGCTGCACTGTGGGAGCCC



Reverse complement motif Consensus sequence: GGGCTCCCACAGTGCAGCGG



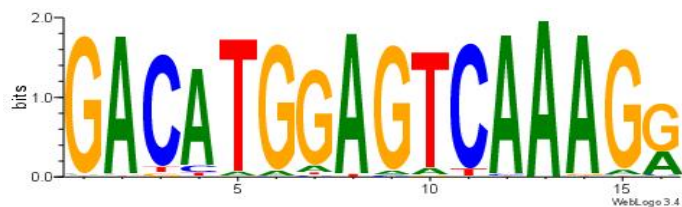
Dataset #: 1
 Motif ID: 326
 Motif name: Motif 326
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 14

Similarity score: 0.0840845

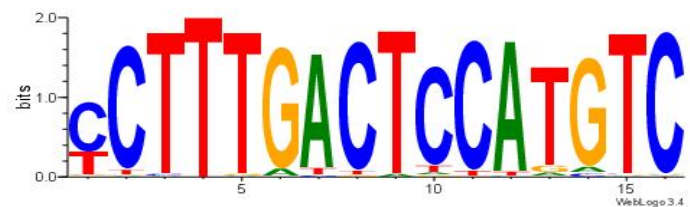
Alignment:

GACATGGAGTCAAAGG
CTCACAGAGTTAAA--

Original motif Consensus sequence: GACATGGAGTCAAAGG



Reverse complement motif Consensus sequence:
CCTTTGACTCCATGTC



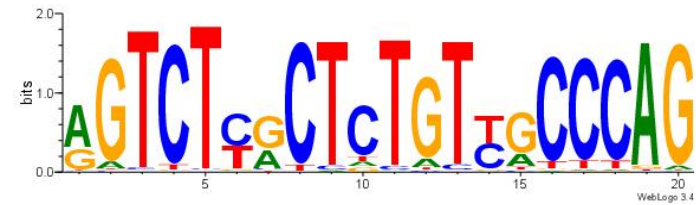
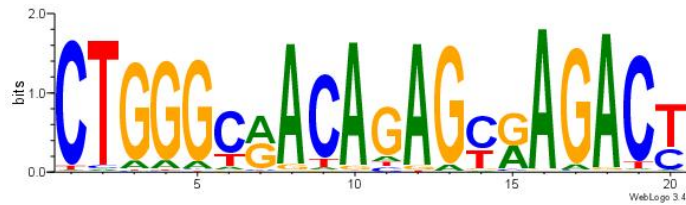
Dataset #: 1
Motif ID: 29
Motif name: Motif 29
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 3
Number of overlap: 14
Similarity score: 0.0858362

Alignment:

MGTCMKCTCTGTKGCCAG
--TTTAACTCTGTGAG----

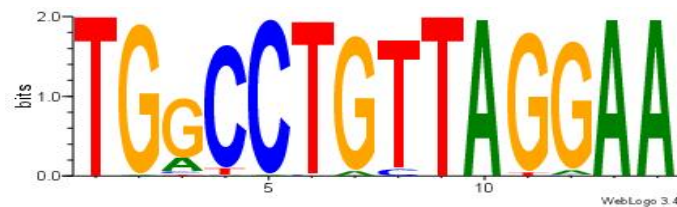
Original motif Consensus sequence: CTGGGCRACAGAGYRAGACY

Reverse complement motif Consensus sequence:
MGTCMKCTCTGTKGCCAG

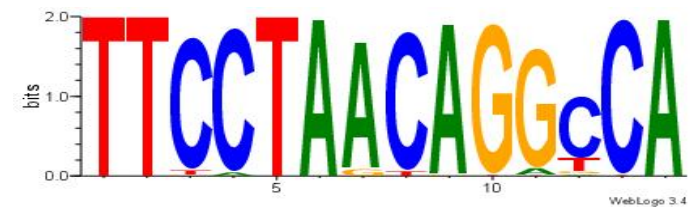


Dataset #: 1 Motif ID: 276 Motif name: Motif 276

Original motif Consensus sequence: TGGCCTGTTAGGAA



Reverse complement motif Consensus sequence: TTCCTAACAGGCC



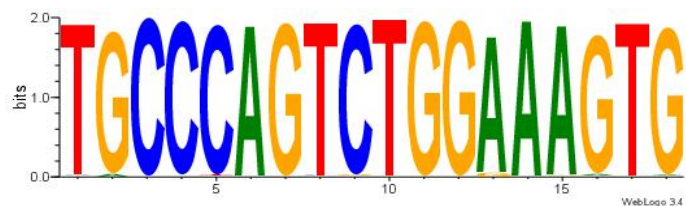
Best Matches for Motif ID 276 (Highest to Lowest)

Dataset #:	1
Motif ID:	45
Motif name:	Motif 45
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	14
Similarity score:	0.0718165

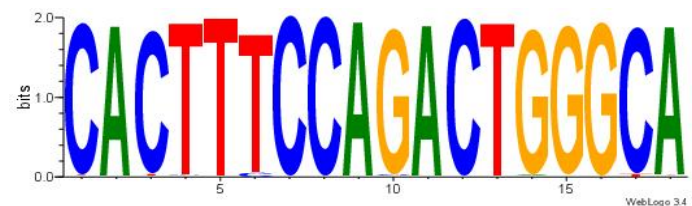
Alignment:

```
TGCCCAGTCTGGAAAGTG
TGGCCTGTTAGGAA----
```

Original motif Consensus sequence: TGCCAGTCTGGAAAGTG



Reverse complement motif Consensus sequence: CACTTCCAGACTGGGCA

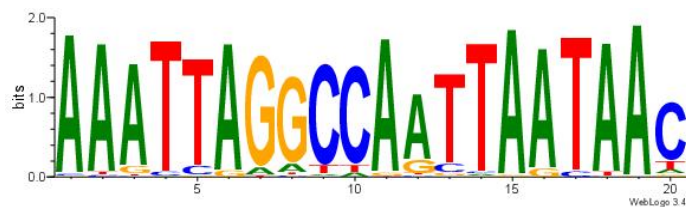


Dataset #: 1
Motif ID: 308
Motif name: Motif 308
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 6
Number of overlap: 14
Similarity score: 0.0893293

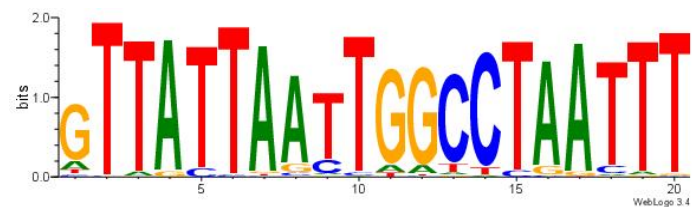
Alignment:

AAATTAGGCCAATTAATAAC
-----TGGCCTGTTAGGAA-

Original motif Consensus sequence: AAATTAGGCCAATTAATAAC



Reverse complement motif Consensus sequence: GTTATTAATTGGCCTAATTT

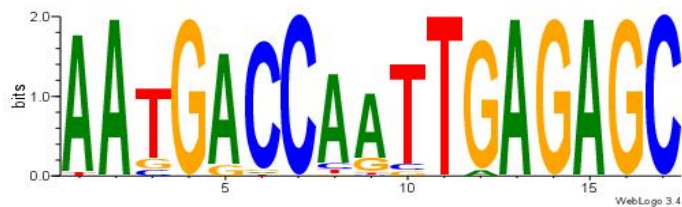


Dataset #: 1
 Motif ID: 305
 Motif name: Motif 305
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 14
 Similarity score: 0.099366

Alignment:

AATGACCAATTGAGAGC
 --TGGCCTGTTAGGAA-

Original motif Consensus sequence: AATGACCAATTGAGAGC



Reverse complement motif Consensus sequence: GCTCTCAATTGGTCATT



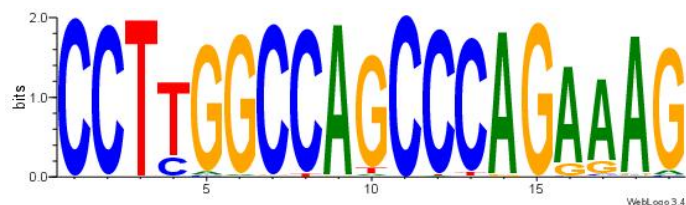
Dataset #: 1
 Motif ID: 122
 Motif name: Motif 122
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3

Number of overlap: 14
Similarity score: 0.100366

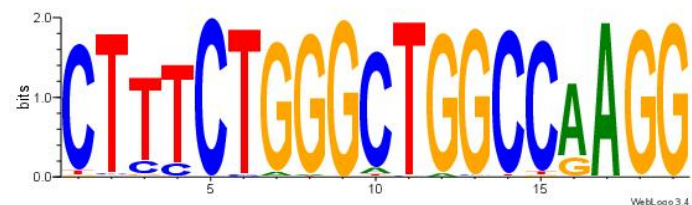
Alignment:

CCTTGGCCAGCCCAGAAAG
---TGGCCTGTTAGGAA--

Original motif Consensus sequence: CCTTGGCCAGCCCAGAAAG



Reverse complement motif Consensus sequence:
CTTCTGGGCTGGCCAAGG

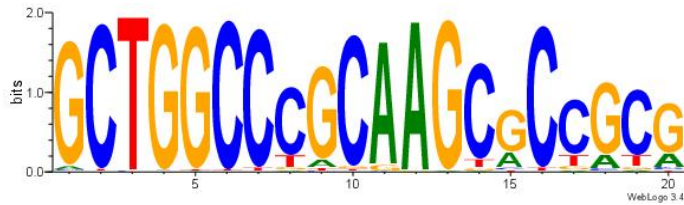


Dataset #: 1
Motif ID: 100
Motif name: Motif 100
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 5
Number of overlap: 14
Similarity score: 0.101376

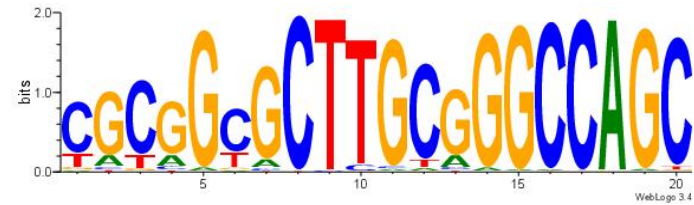
Alignment:

GCTGGCCCGCAAGCGCCGCG
--TGGCCTGTTAGGAA----

Original motif Consensus sequence: GCTGGCCCGCAAGCGCCGCG

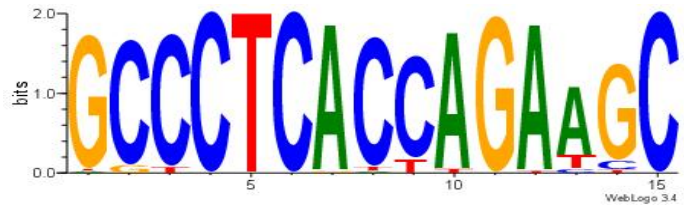


Reverse complement motif Consensus sequence: CGCGGCGCTTGCGGGCCAGC

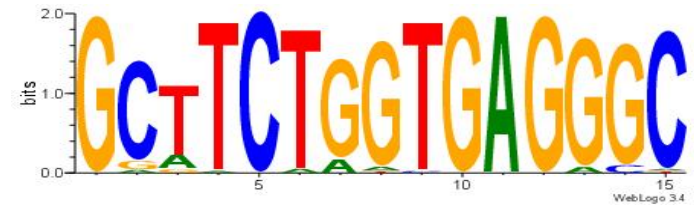


Dataset #: 1 Motif ID: 277 Motif name: Motif 277

Original motif Consensus sequence: GCCCTCACCAGAAGC



Reverse complement motif Consensus sequence: GCTTCTGGTGAGGC



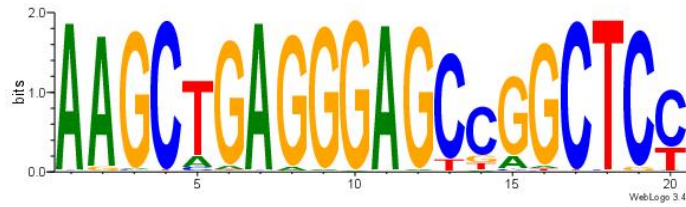
Best Matches for Motif ID 277 (Highest to Lowest)

Dataset #:	1
Motif ID:	96
Motif name:	Motif 96
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	4
Number of overlap:	15
Similarity score:	0.0937412

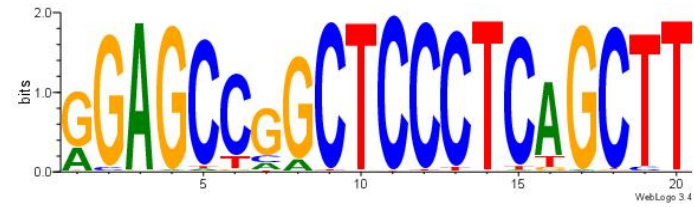
Alignment:

AAGCTGAGGGAGCCGGCTCC
 ---GCTTCTGGTGAGGGC--

Original motif Consensus sequence: AAGCTGAGGGAGCCGGCTCC



Reverse complement motif Consensus sequence:
 GGAGCCGGCTCCCTCAGCTT

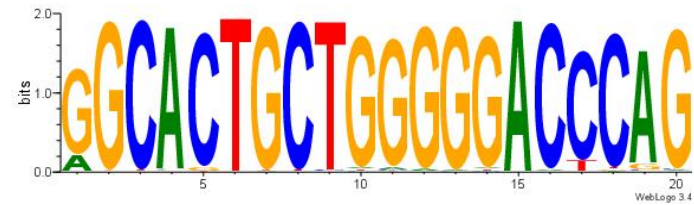
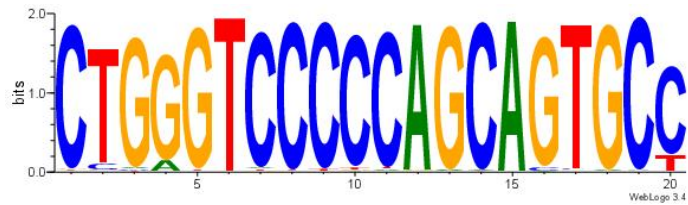


Dataset #: 1
 Motif ID: 84
 Motif name: Motif 84
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 15
 Similarity score: 0.094292

Alignment:
 GGC ACTGCTGGGGGACCCAG
 GCTTCTGGTGAGGGC-----

Original motif Consensus sequence: CTGGTCCCCCAGCAGTGCC

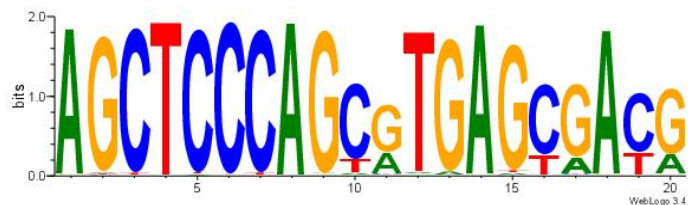
Reverse complement motif Consensus sequence:
 GGC ACTGCTGGGGGACCCAG



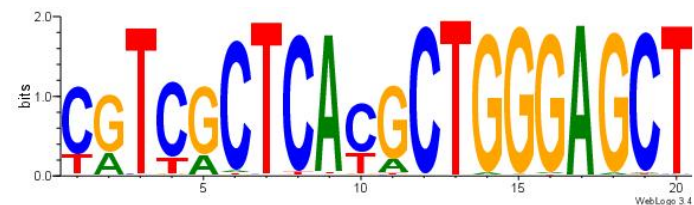
Dataset #: 1
 Motif ID: 48
 Motif name: Motif 48
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 5
 Number of overlap: 15
 Similarity score: 0.0943045

Alignment:
 AGCTCCCAGCGTGAGCGACG
 -GCCCTCACCAGAAGC-----

Original motif Consensus sequence: AGCTCCCAGCGTGAGCGACG



Reverse complement motif Consensus sequence: CGTCGCTCAGCTGGGAGCT



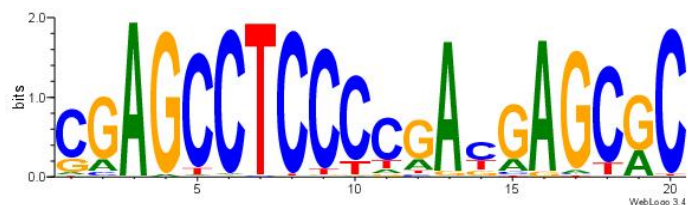
Dataset #: 1

Motif ID: 108
 Motif name: Motif 108
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 15
 Similarity score: 0.0957474

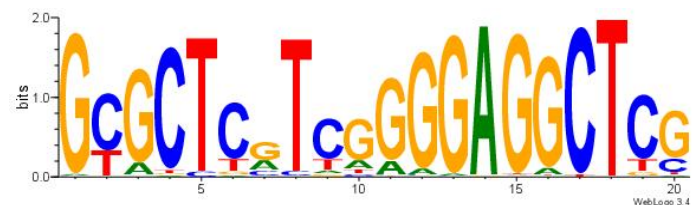
Alignment:

CGAGCCTCCCCGAYGAGCGC
 ---GCCCTCACCAGAAGC--

Original motif Consensus sequence: CGAGCCTCCCCGAYGAGCGC



Reverse complement motif Consensus sequence: GCGCTCKTCGGGGAGGCTCG



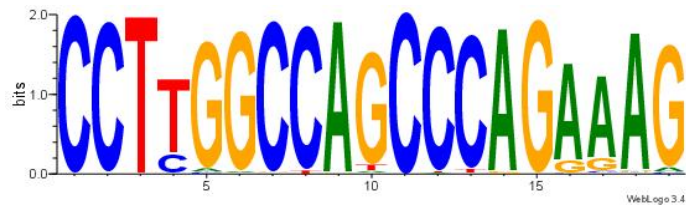
Dataset #: 1
 Motif ID: 122
 Motif name: Motif 122
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 5
 Number of overlap: 15

Similarity score: 0.0961872

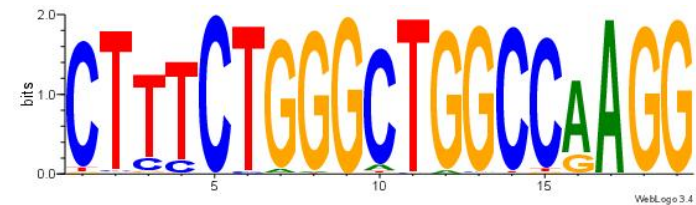
Alignment:

CTTTCTGGGCTGGCCAAGG
GCTTCTGGTGAGGGC-----

Original motif Consensus sequence: CCTTGGCCAGCCCAGAAAG

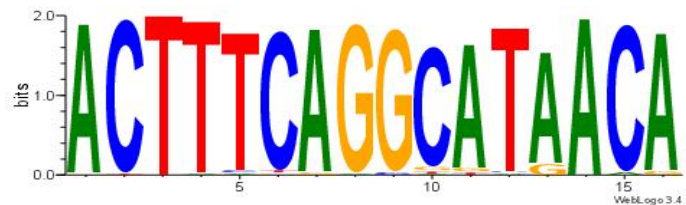


Reverse complement motif Consensus sequence: CTTTCTGGGCTGGCCAAGG

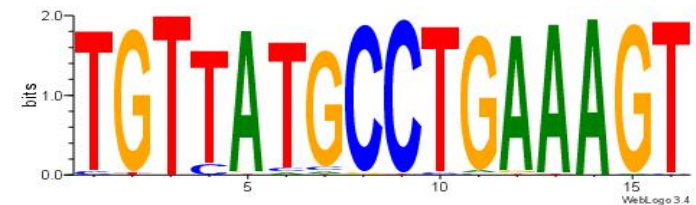


Dataset #: 1 Motif ID: 278 Motif name: Motif 278

Original motif Consensus sequence: ACTTTCAGGCATAACA



Reverse complement motif Consensus sequence: TGTTATGCCTGAAAGT



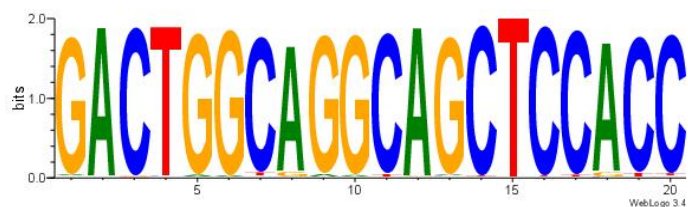
Best Matches for Motif ID 278 (Highest to Lowest)

Dataset #:	1
Motif ID:	52
Motif name:	Motif 52
Matching format of first motif:	Reverse Complement

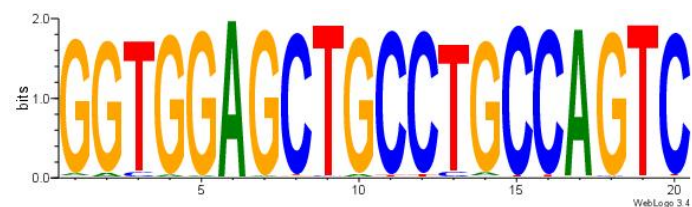
Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 16
 Similarity score: 0.0883057

Alignment:
 GGTGGAGCTGCCTGCCAGTC
 ---TGTTATGCCTGAAAGT-

Original motif Consensus sequence: GACTGGCAGGCAGCTCCACC



Reverse complement motif Consensus sequence:
 GGTGGAGCTGCCTGCCAGTC

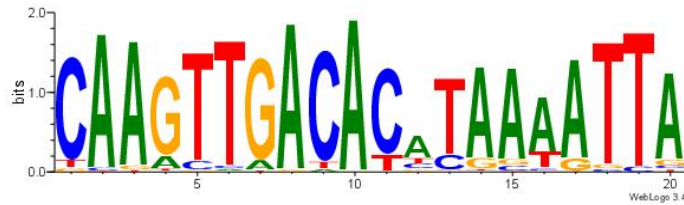


Dataset #: 1
 Motif ID: 357
 Motif name: Motif 357
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 4
 Number of overlap: 16
 Similarity score: 0.101075

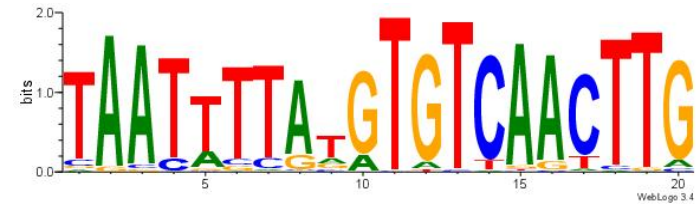
Alignment:

TAATTTTATGTGTCAACTTG
 ---TGTTATGCCTGAAAGT-

Original motif Consensus sequence: CAAGTTGACACATAAAATTA



Reverse complement motif Consensus sequence:
 TAATTTTATGTGTCAACTTG

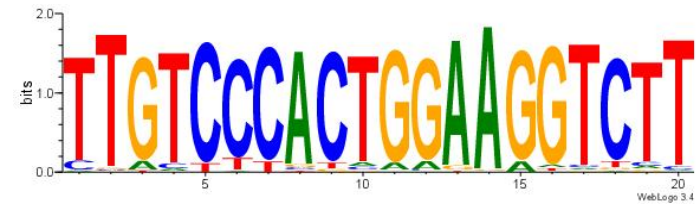
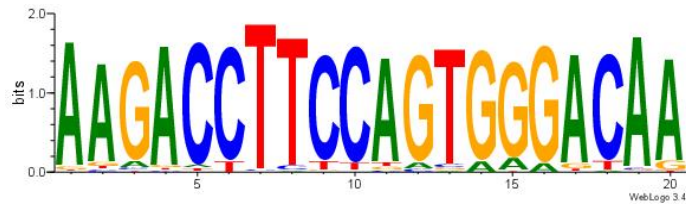


Dataset #:	1
Motif ID:	292
Motif name:	Motif 292
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	4
Number of overlap:	16
Similarity score:	0.102784

Alignment:
 AAGACCTTCCAGTGGGACAA
 ---ACTTTCAGGCATAACA-

Original motif Consensus sequence: AAGACCTTCCAGTGGGACAA

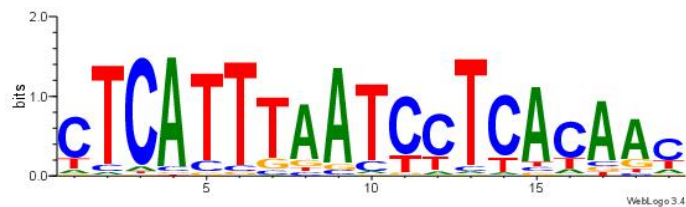
Reverse complement motif Consensus sequence:
 TTGCCCCTGGAAGGTCTT



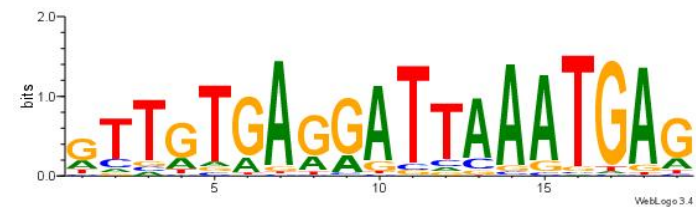
Dataset #: 1
 Motif ID: 102
 Motif name: Motif 102
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 16
 Similarity score: 0.110723

Alignment:
 GTTGTGAGGATTAATGAG
 --TGTTATGCCTGAAAGT--

Original motif Consensus sequence: CTCATTTAATCCACAAC



Reverse complement motif Consensus sequence: GTTGTGAGGATTAATGAG



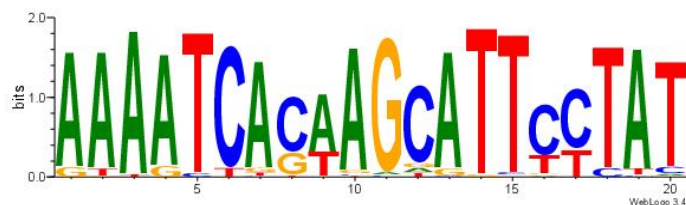
Dataset #: 1

Motif ID: 254
 Motif name: Motif 254
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3
 Number of overlap: 16
 Similarity score: 0.114892

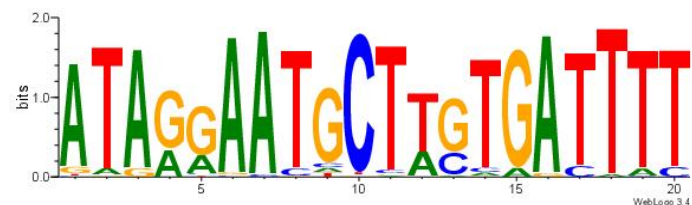
Alignment:

ATAGGAATGCTTGTGATTTT
 --TGTTATGCCTGAAAGT--

Original motif Consensus sequence: AAAATCACAAGCATTCCCTAT

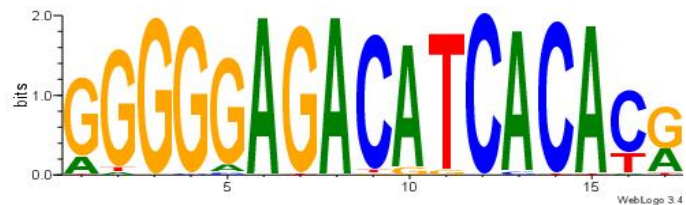


Reverse complement motif Consensus sequence: ATAGGAATGCTTGTGATTTT

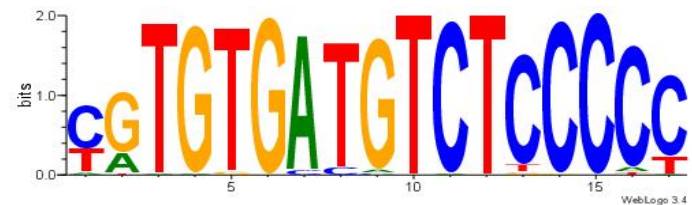


Dataset #: 1 Motif ID: 279 Motif name: Motif 279

Original motif Consensus sequence: GGGGGAGACATCACAC



Reverse complement motif Consensus sequence: MGTGTGATGTCTCCCC



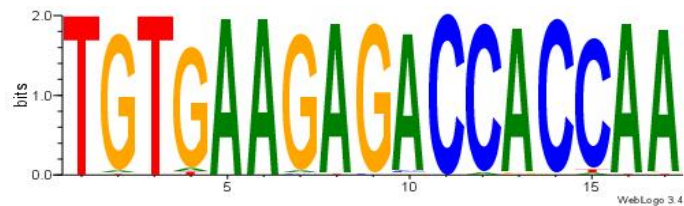
Best Matches for Motif ID 279 (Highest to Lowest)

Dataset #: 1
Motif ID: 249
Motif name: Motif 249
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 17
Similarity score: 0.10127

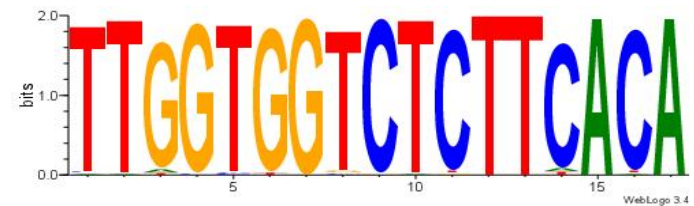
Alignment:

```
TTGGTGGTCTCTTCACA  
MGTGTGATGTCTCCCCC
```

Original motif Consensus sequence: TGTGAAGAGACCACCAA



Reverse complement motif Consensus sequence:
TTGGTGGTCTCTTCACA



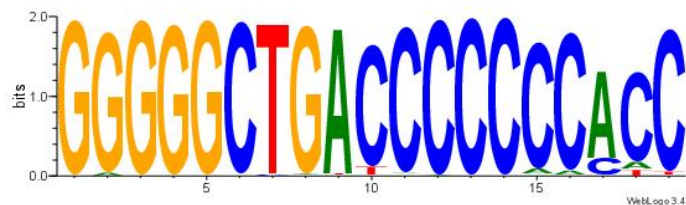
Dataset #: 1
Motif ID: 92
Motif name: Motif 92
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement

Direction: Forward
Position number: 2
Number of overlap: 17
Similarity score: 0.103877

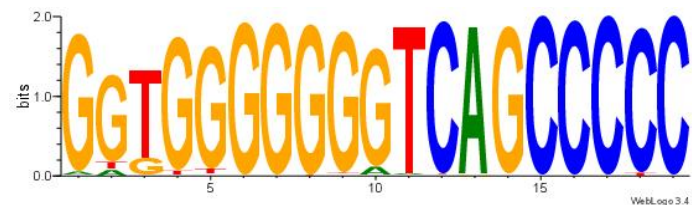
Alignment:

GGTGGGGGGGTCAGCCCC
-MGTGTGATGTCTCCCC-

Original motif Consensus sequence: GGGGGCTGACCCCCCACC



Reverse complement motif Consensus sequence: GGTGGGGGGGTCAGCCCC

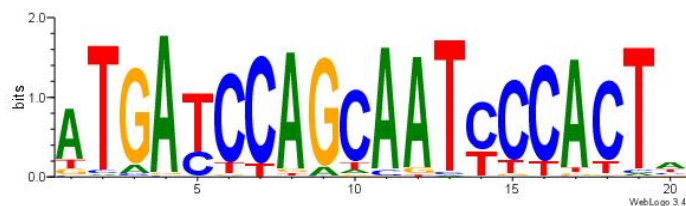


Dataset #: 1
Motif ID: 115
Motif name: Motif 115
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 2
Number of overlap: 17
Similarity score: 0.104422

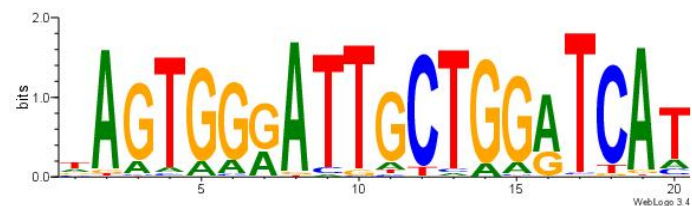
Alignment:

HAGTGGKATTGCTGGATCAT
-MGTGTGATGTCTCCCC--

Original motif Consensus sequence: ATGATCCAGCAATYCCACTH



Reverse complement motif Consensus sequence: HAGTGGKATTGCTGGATCAT

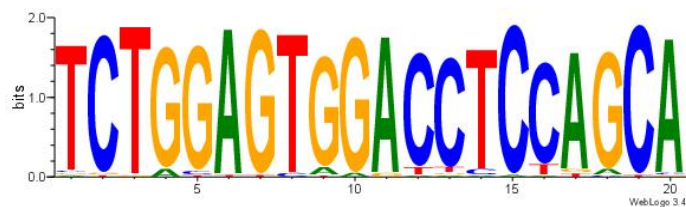


Dataset #: 1
Motif ID: 350
Motif name: Motif 350
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 17
Similarity score: 0.106892

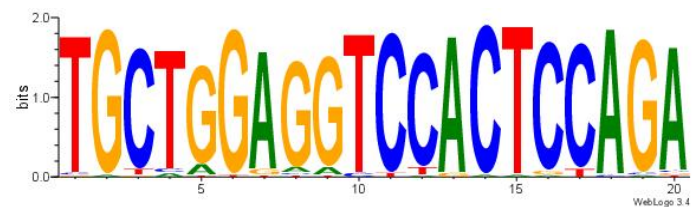
Alignment:

TCTGGAGTGGACCTCCAGCA
---GGGGAGACATCACACR

Original motif Consensus sequence: TCTGGAGTGGACCTCCAGCA



Reverse complement motif Consensus sequence: TGCTGGAGGTCCACTCCAGA

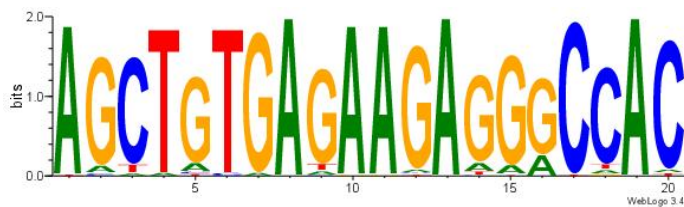


Dataset #: 1
 Motif ID: 294
 Motif name: Motif 294
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 17
 Similarity score: 0.107484

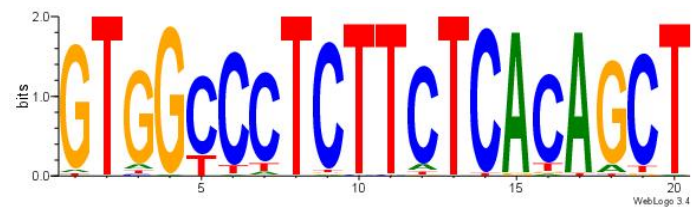
Alignment:

GTGGCCCTCTTCTCACAGCT
 GGGGAGACATCACACR---

Original motif Consensus sequence: AGCTGTGAGAAGAGGGCCAC



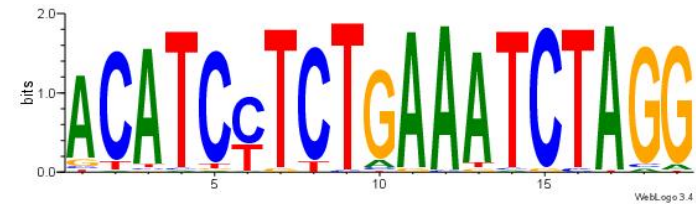
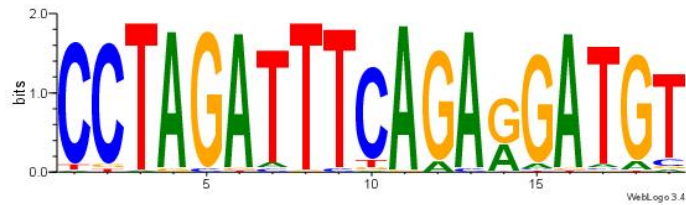
Reverse complement motif Consensus sequence: GTGGCCCTCTTCTCACAGCT



Dataset #: 1 Motif ID: 280 Motif name: Motif 280

Original motif Consensus sequence: CCTAGATTTAGARGATGT

Reverse complement motif Consensus sequence: ACATCMTCTGAAATCTAGG

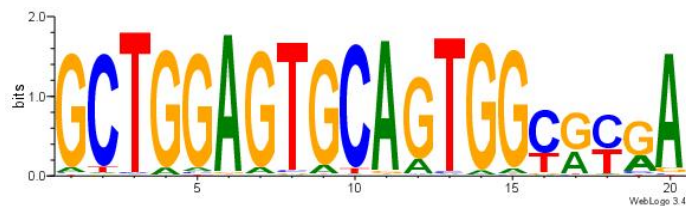


Best Matches for Motif ID 280 (Highest to Lowest)

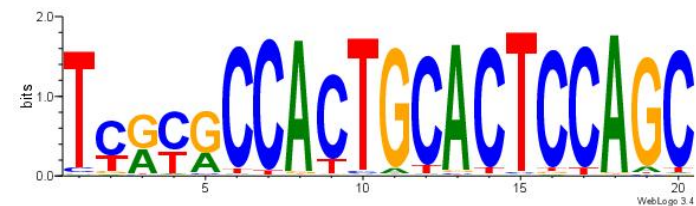
Dataset #: 1
 Motif ID: 3
 Motif name: Motif 3
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 19
 Similarity score: 0.098089

Alignment:
 TCKMGCCACTGCACTCCAGC
 -ACATCMTCTGAAATCTAGG

Original motif Consensus sequence: GCTGGAGTGCAGTGGCRYGA



Reverse complement motif Consensus sequence: TCKMGCCACTGCACTCCAGC

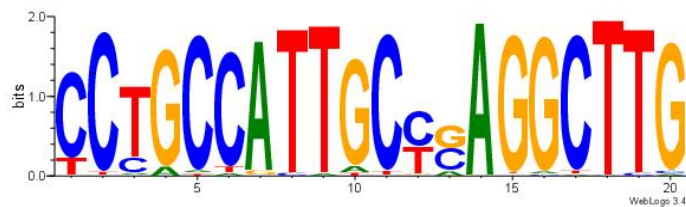


Dataset #: 1
 Motif ID: 196
 Motif name: Motif 196
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 19
 Similarity score: 0.110835

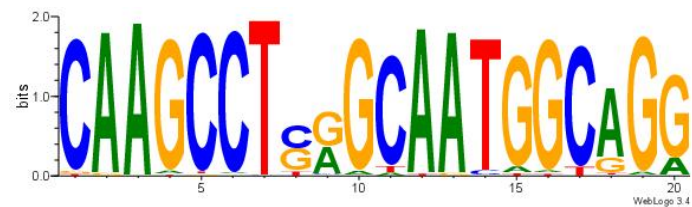
Alignment:

CAAGCCTSKGCAATGGCAGG
 ACATCMTCTGAAATCTAGG-

Original motif Consensus sequence: CCTGCCATTGCYSAGGCTTG



Reverse complement motif Consensus sequence: CAAGCCTSKGCAATGGCAGG



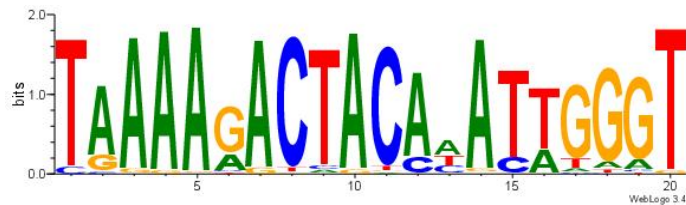
Dataset #: 1
 Motif ID: 195
 Motif name: Motif 195
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1

Number of overlap: 19
Similarity score: 0.112769

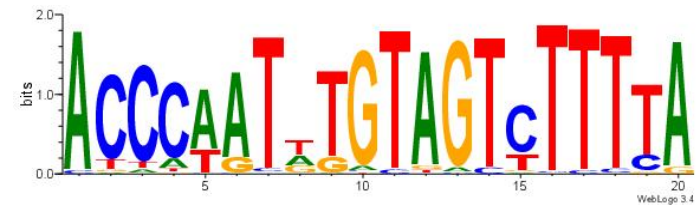
Alignment:

ACCCAATWTGTAGTCTTTTA
ACATCMTCTGAAATCTAGG-

Original motif Consensus sequence: TAAAAGACTACAWATTGGGT



Reverse complement motif Consensus sequence:
ACCCAATWTGTAGTCTTTTA

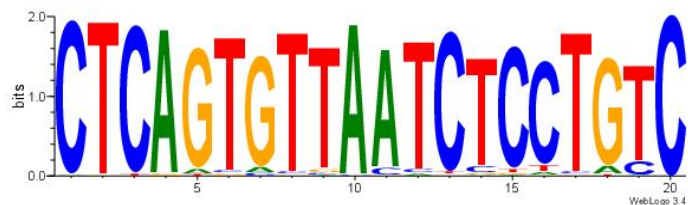


Dataset #: 1
Motif ID: 262
Motif name: Motif 262
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 2
Number of overlap: 19
Similarity score: 0.114054

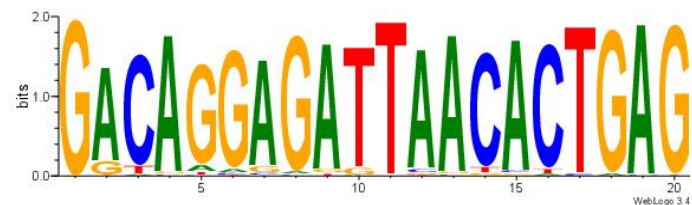
Alignment:

GACAGGAGATTAACACTGAG
-ACATCMTCTGAAATCTAGG

Original motif Consensus sequence: CTCAGTGTTAATCTCCTGTC



Reverse complement motif Consensus sequence: GACAGGAGATTAACACTGAG

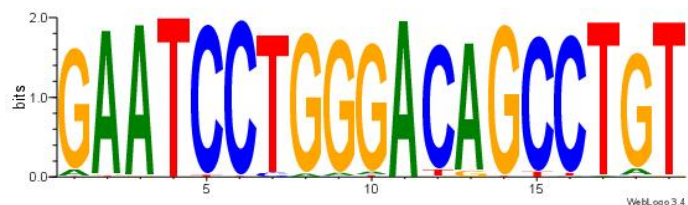


Dataset #: 1
Motif ID: 192
Motif name: Motif 192
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 19
Similarity score: 0.114945

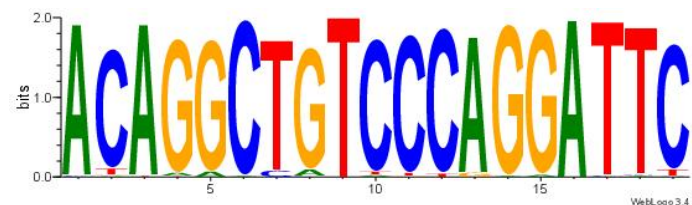
Alignment:

GAATCCTGGGACAGCCTGT
ACATCMTCTGAAATCTAGG

Original motif Consensus sequence: GAATCCTGGGACAGCCTGT

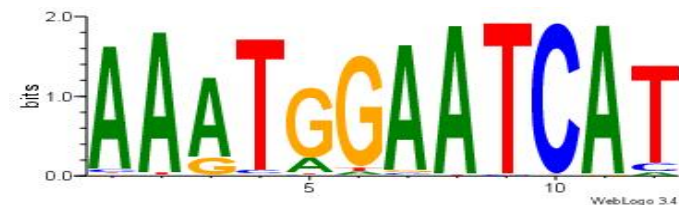


Reverse complement motif Consensus sequence: ACAGGCTGTCCCAGGATTC

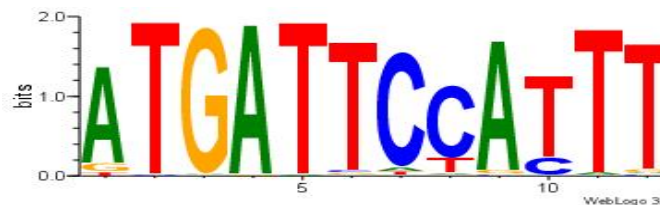


Dataset #: 1 Motif ID: 281 Motif name: Motif 281

Original motif Consensus sequence: AAATGGAATCAT



Reverse complement motif Consensus sequence: ATGATTCCATTT



Best Matches for Motif ID 281 (Highest to Lowest)

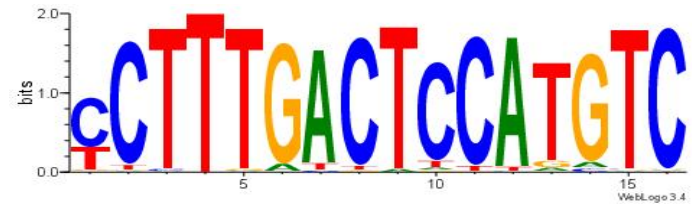
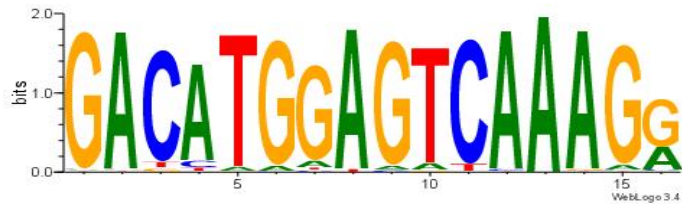
Dataset #:	1
Motif ID:	326
Motif name:	Motif 326
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	2
Number of overlap:	12
Similarity score:	0.0598156

Alignment:

```
CCTTTGACTCCATGTC  
---ATGATTCCATTT-
```

Original motif Consensus sequence: GACATGGAGTCAAAGG

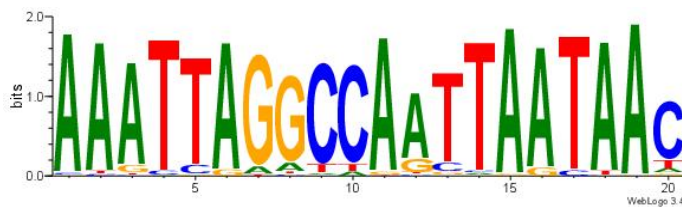
Reverse complement motif Consensus sequence:
CCTTTGACTCCATGTC



Dataset #: 1
 Motif ID: 308
 Motif name: Motif 308
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 7
 Number of overlap: 12
 Similarity score: 0.0709771

Alignment:
 GTTATTAATTGGCCTAATTT
 -----AAATGGAATCAT--

Original motif Consensus sequence: AAATTAGGCCAATTAATAAC



Reverse complement motif Consensus sequence: GTTATTAATTGGCCTAATTT



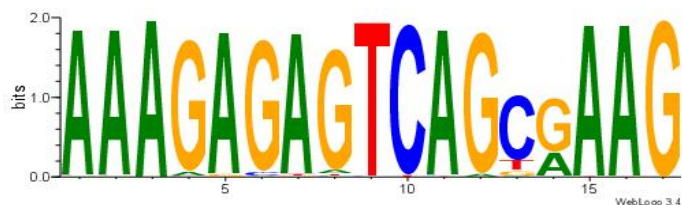
Dataset #: 1

Motif ID: 148
 Motif name: Motif 148
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 12
 Similarity score: 0.0717431

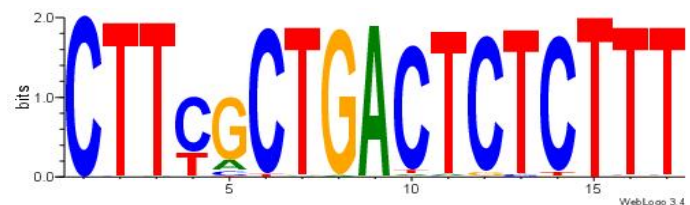
Alignment:

AAAGAGAGTCAGCGAAG
 AAATGGAATCAT-----

Original motif Consensus sequence: AAAGAGAGTCAGCGAAG



Reverse complement motif Consensus sequence: CTTGCTGACTCTCTTT



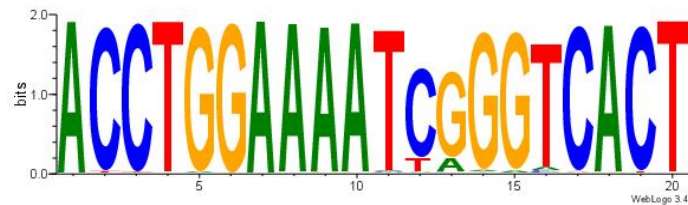
Dataset #: 1
 Motif ID: 14
 Motif name: Motif 14
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 8
 Number of overlap: 12

Similarity score: 0.0745254

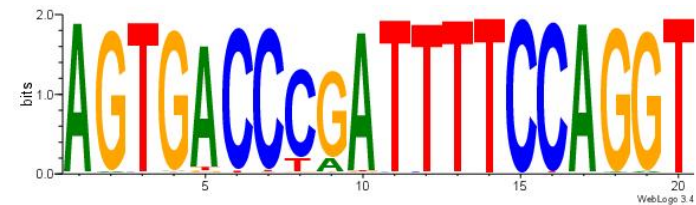
Alignment:

ACCTGGAAAATCGGGTCACT
-----AAATGGAATCAT-

Original motif Consensus sequence: ACCTGGAAAATCGGGTCACT



Reverse complement motif Consensus sequence:
AGTGACCCGATTTTCCAGGT



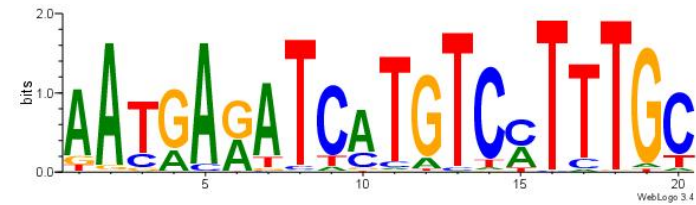
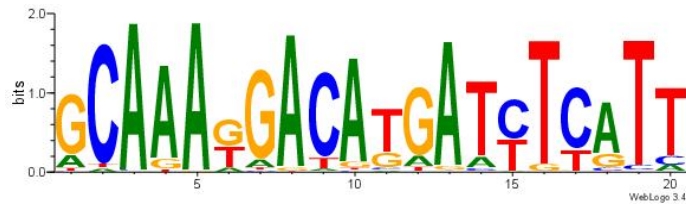
Dataset #: 1
Motif ID: 99
Motif name: Motif 99
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 8
Number of overlap: 12
Similarity score: 0.0765832

Alignment:

AATGAKATCATGTCYTTTGC
-ATGATTCCATTT-----

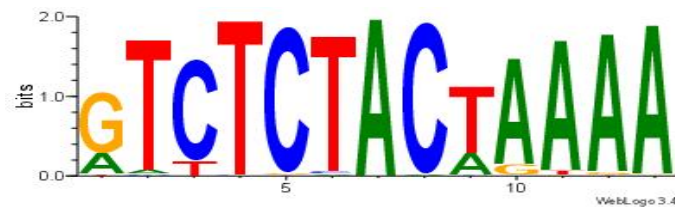
Original motif Consensus sequence: GCAAAGACATGATYTCATT

Reverse complement motif Consensus sequence:
AATGAKATCATGTCYTTTGC

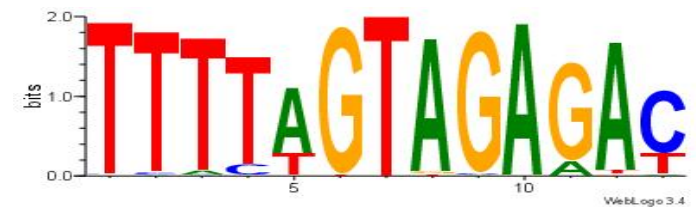


Dataset #: 1 Motif ID: 282 Motif name: Motif 282

Original motif Consensus sequence: GTCTCTACTAAA



Reverse complement motif Consensus sequence: TTTTAGTAGAGAC

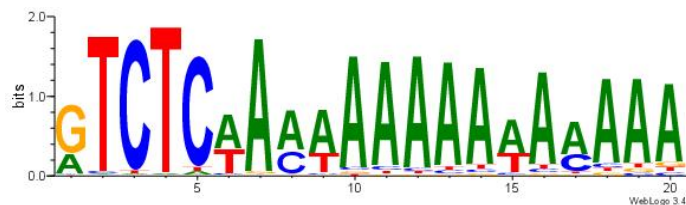


Best Matches for Motif ID 282 (Highest to Lowest)

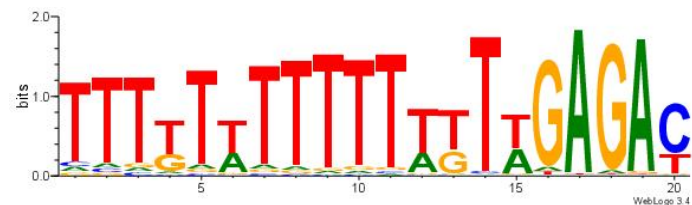
Dataset #:	1
Motif ID:	7
Motif name:	Motif 7
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	13
Similarity score:	0.033043

Alignment:
 GTCTCWAMAAAAAAWAMAAA
 GTCTCTACTAAA-----

Original motif Consensus sequence: GTCTCWAMAAAAAWAMAAA



Reverse complement motif Consensus sequence: TTTYTWTTTTTTTWTGAGAC

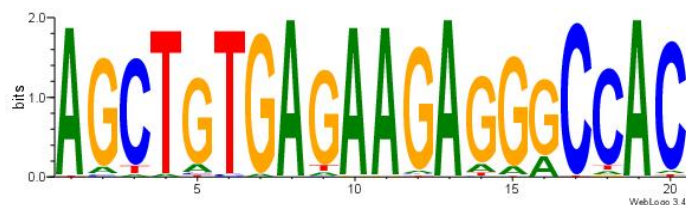


Dataset #: 1
Motif ID: 294
Motif name: Motif 294
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 5
Number of overlap: 13
Similarity score: 0.0894973

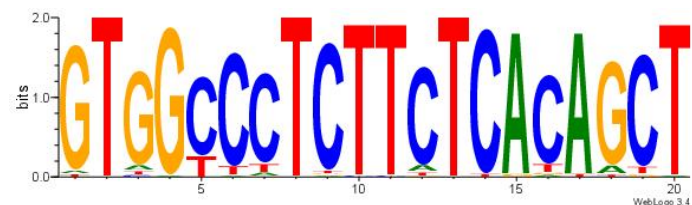
Alignment:

AGCTGTGAGAAGAGGGCCAC
---TTTGTAGTAGAGAC----

Original motif Consensus sequence: AGCTGTGAGAAGAGGGCCAC



Reverse complement motif Consensus sequence: GTGGCCCTCTTCTCACAGCT

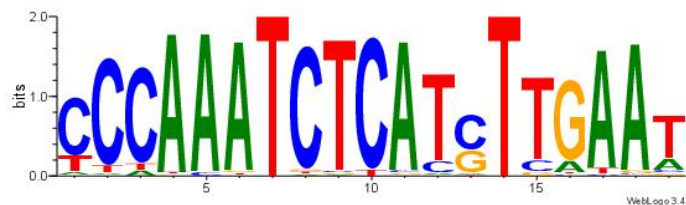


Dataset #: 1
 Motif ID: 227
 Motif name: Motif 227
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 13
 Similarity score: 0.0954988

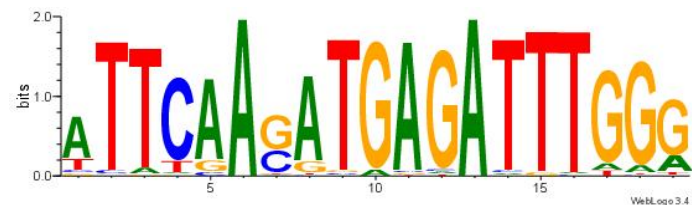
Alignment:

CCCAAATCTCATSTTGAAT
 -----GTCTCTACTAAAA-

Original motif Consensus sequence: CCCAAATCTCATSTTGAAT



Reverse complement motif Consensus sequence: ATTCAASATGAGATTTGGG



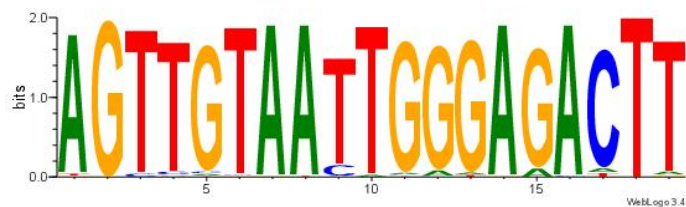
Dataset #: 1
 Motif ID: 232
 Motif name: Motif 232
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3

Number of overlap: 13
Similarity score: 0.0959906

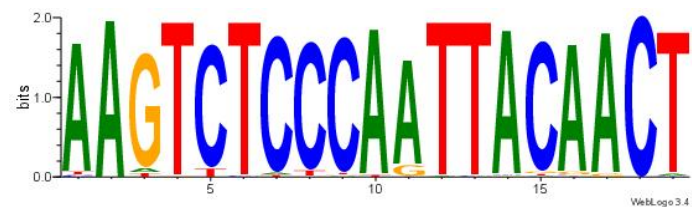
Alignment:

AAGTCTCCCAATTACAAC
--GTCTCTACTAAAA----

Original motif Consensus sequence: AGTTGTAATTGGGAGACTT



Reverse complement motif Consensus sequence:
AAGTCTCCCAATTACAAC

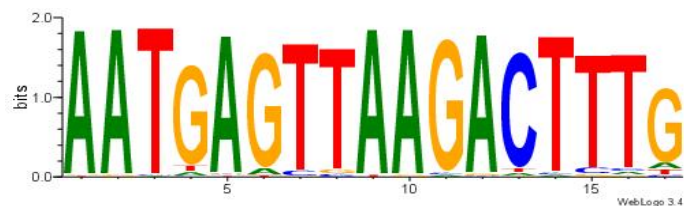


Dataset #: 1
Motif ID: 224
Motif name: Motif 224
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 13
Similarity score: 0.0973832

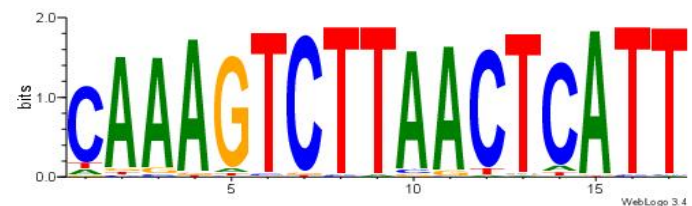
Alignment:

CAAAGTCTTAACTCATT
GTCTCTACTAAAA----

Original motif Consensus sequence: AATGAGTTAAGACTTTG

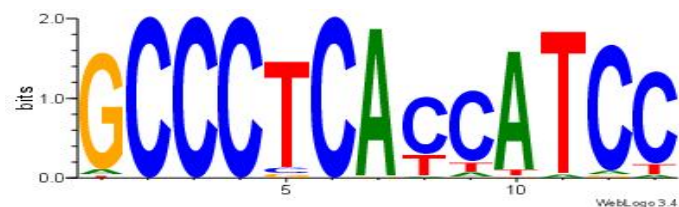


Reverse complement motif Consensus sequence: CAAAGTCTTAACTCATT

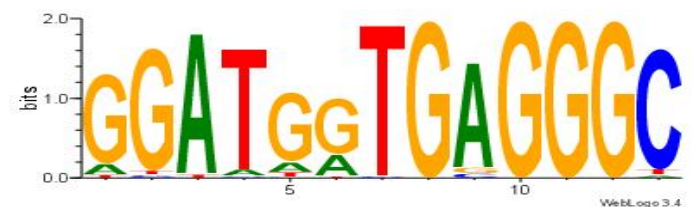


Dataset #: 1 Motif ID: 283 Motif name: Motif 283

Original motif Consensus sequence: GCCCTCACCATCC



Reverse complement motif Consensus sequence: GGATGGTGAGGGC



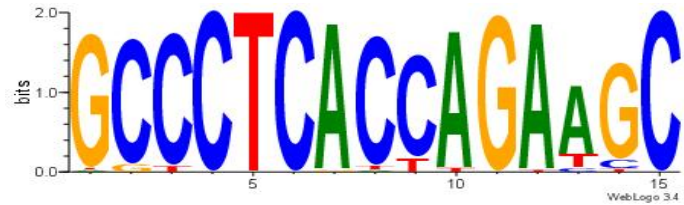
Best Matches for Motif ID 283 (Highest to Lowest)

Dataset #:	1
Motif ID:	277
Motif name:	Motif 277
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	3
Number of overlap:	13
Similarity score:	0.0577529

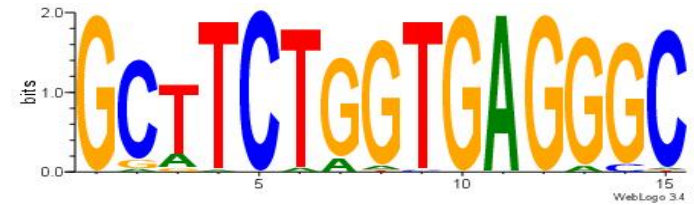
Alignment:

GCCCTCACCAGAAGC
GCCCTCACCATCC--

Original motif Consensus sequence: GCCCTCACCAGAAGC



Reverse complement motif Consensus sequence: GCTTCTGGTGAGG



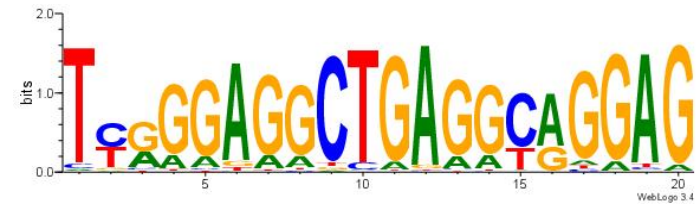
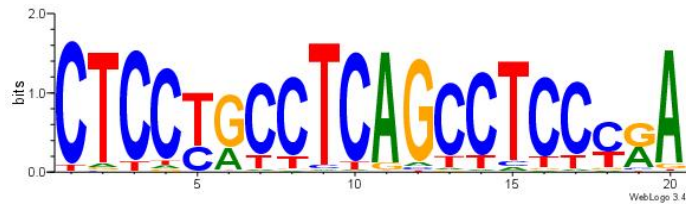
Dataset #: 1
Motif ID: 26
Motif name: Motif 26
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 5
Number of overlap: 13
Similarity score: 0.0747837

Alignment:

TMGGGAGGCTGAGGCAGGAG
---GGATGGTGAGGGC----

Original motif Consensus sequence: CTCCTGCCTCAGCCTCCRA

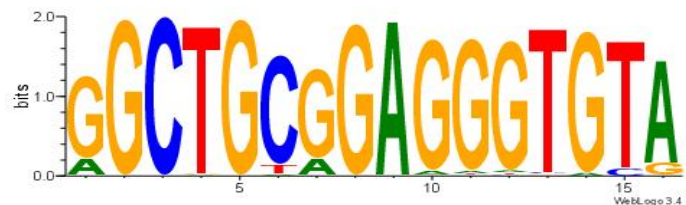
Reverse complement motif Consensus sequence:
TMGGGAGGCTGAGGCAGGAG



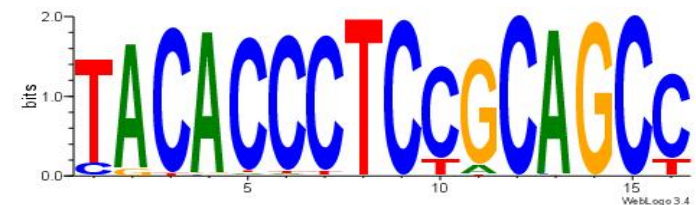
Dataset #: 1
 Motif ID: 89
 Motif name: Motif 89
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 13
 Similarity score: 0.0759531

Alignment:
 GGCTGCGGAGGGTGTA
 ---GGATGGTGAGGGC

Original motif Consensus sequence: GGCTGCGGAGGGTGTA



Reverse complement motif Consensus sequence: TACACCCTCCGAGCC



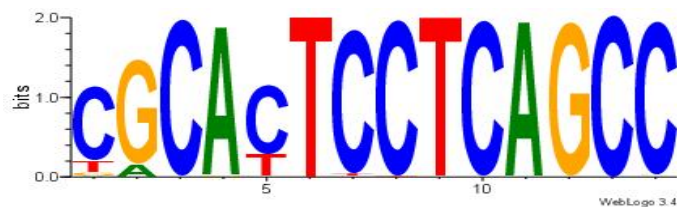
Dataset #: 1

Motif ID: 72
 Motif name: Motif 72
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 13
 Similarity score: 0.0811013

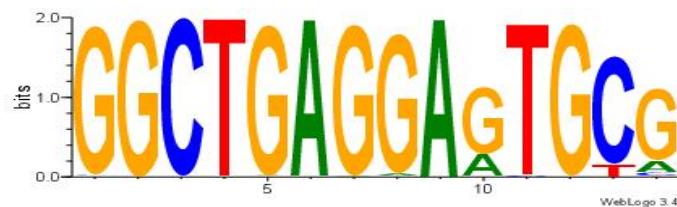
Alignment:

CGCACTCCTCAGCC
 -GCCCTCACCATCC

Original motif Consensus sequence: CGCACTCCTCAGCC



Reverse complement motif Consensus sequence: GGCTGAGGAGTGC

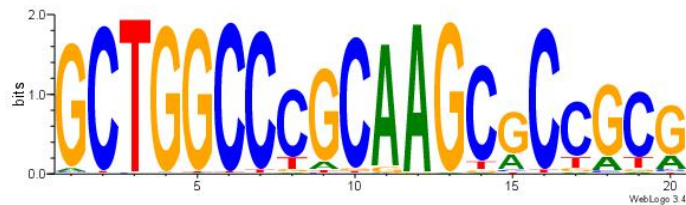


Dataset #: 1
 Motif ID: 100
 Motif name: Motif 100
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 4
 Number of overlap: 13
 Similarity score: 0.0835643

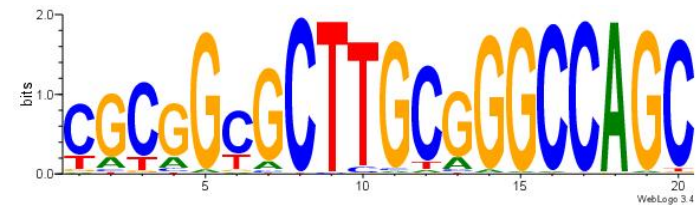
Alignment:

```
CGCGGCGCTTGC GGGCCAGC  
---GGATGGTGAGGGC----
```

Original motif Consensus sequence: GCTGGCCCGCAAGCcGcGcGCG

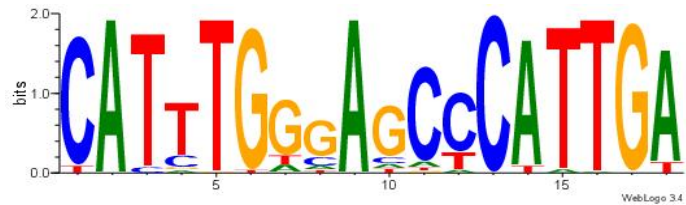


Reverse complement motif Consensus sequence:
CGCGGCGCTTGC GGGCCAGC

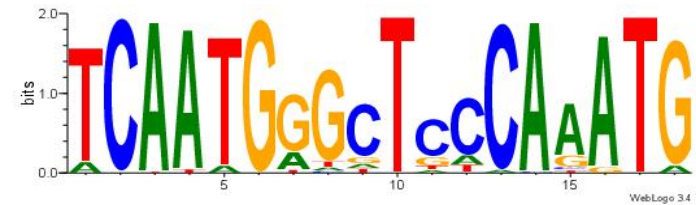


Dataset #: 1 Motif ID: 284 Motif name: Motif 284

Original motif Consensus sequence: CATTGGGAGCCATTGA



Reverse complement motif Consensus sequence:
TCAATGGGCTCCCAAATG



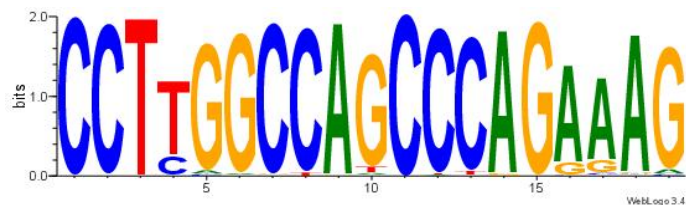
Best Matches for Motif ID 284 (Highest to Lowest)

Dataset #:	1
Motif ID:	122
Motif name:	Motif 122
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif

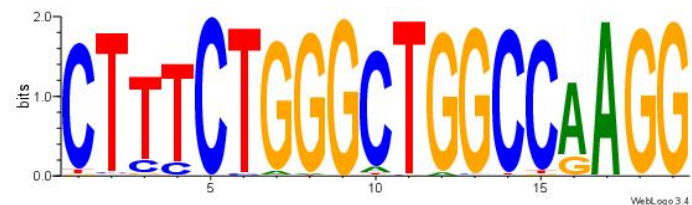
Direction: Forward
 Position number: 1
 Number of overlap: 18
 Similarity score: 0.0934546

Alignment:
 CCTTGGCCAGCCCAGAAAG
 CATTGGGAGCCCATTGA-

Original motif Consensus sequence: CCTTGGCCAGCCCAGAAAG



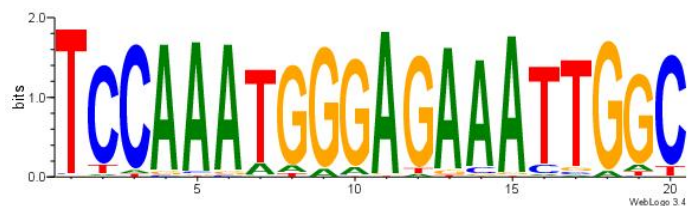
Reverse complement motif Consensus sequence: CTTTCTGGGCTGGCCAAGG



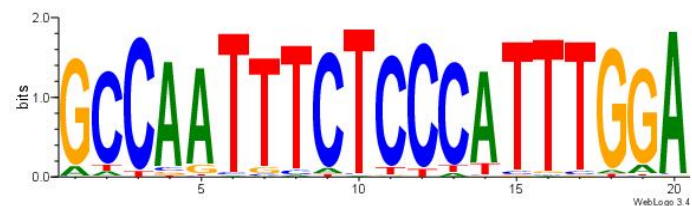
Dataset #: 1
 Motif ID: 235
 Motif name: Motif 235
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 18
 Similarity score: 0.105262

Alignment:
 GCCAATTTCTCCATTGGA
 TCAATGGGCTCCCAAATG--

Original motif Consensus sequence: TCCAATGGGAGAAATTGGC



Reverse complement motif Consensus sequence: GCCAATTTCTCCCATTTGGA

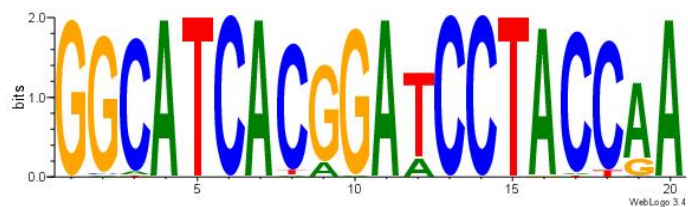


Dataset #: 1
Motif ID: 311
Motif name: Motif 311
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 3
Number of overlap: 18
Similarity score: 0.106572

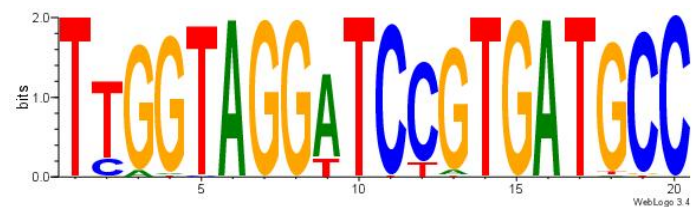
Alignment:

GGCATCACGGATCCTACCAA
--CATTGGGAGCCCATTGA

Original motif Consensus sequence: GGCATCACGGATCCTACCAA



Reverse complement motif Consensus sequence: TTGGTAGGATCCGTGATGCC

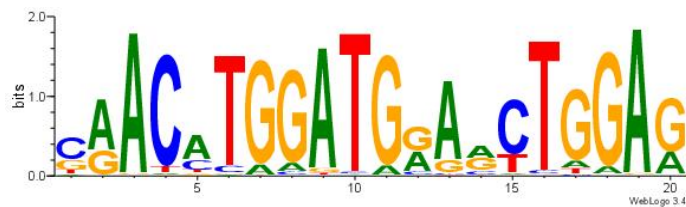


Dataset #: 1
 Motif ID: 104
 Motif name: Motif 104
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 18
 Similarity score: 0.107655

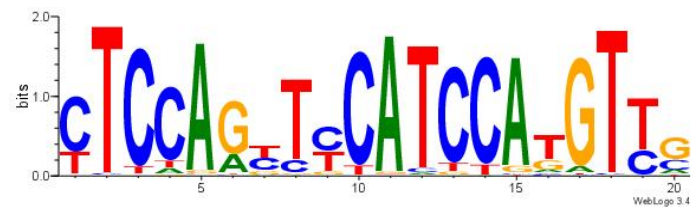
Alignment:

CTCCAGKTMCATCCATGTTG
 -TCAATGGGCTCCCAAATG-

Original motif Consensus sequence: CAACATGGATGRARCTGGAG



Reverse complement motif Consensus sequence: CTCCAGKTMCATCCATGTTG



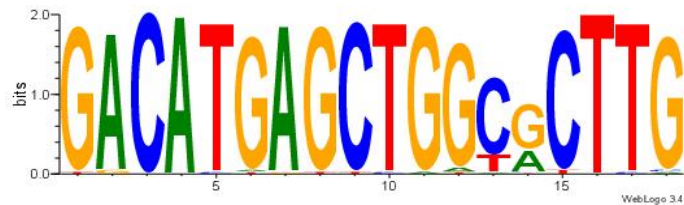
Dataset #: 1
 Motif ID: 306
 Motif name: Motif 306
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1

Number of overlap: 18
Similarity score: 0.111838

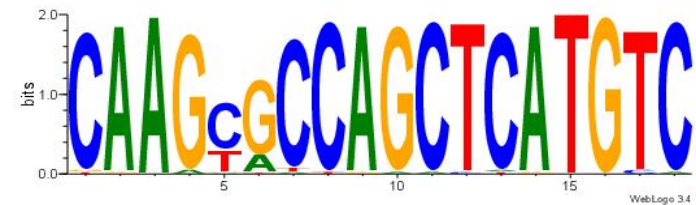
Alignment:

GACATGAGCTGGCGCTTG
TCAATGGGCTCCCAAATG

Original motif Consensus sequence: GACATGAGCTGGCGCTTG

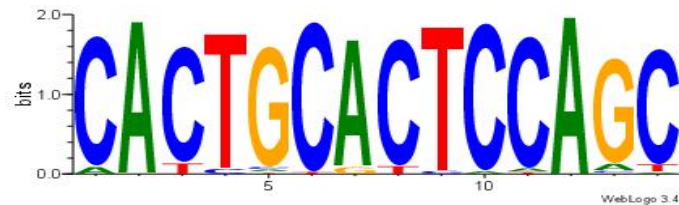


Reverse complement motif Consensus sequence:
CAAGCGCCAGCTCATGTC

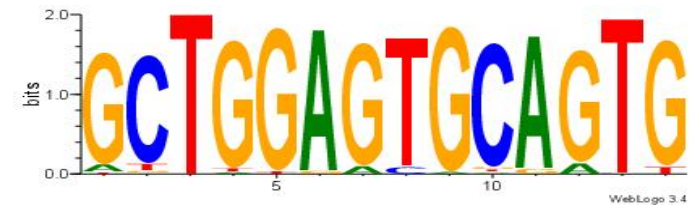


Dataset #: 1 Motif ID: 285 Motif name: Motif 285

Original motif Consensus sequence: CACTGCACTCCAGC



Reverse complement motif Consensus sequence: GCTGGAGTGCAGT



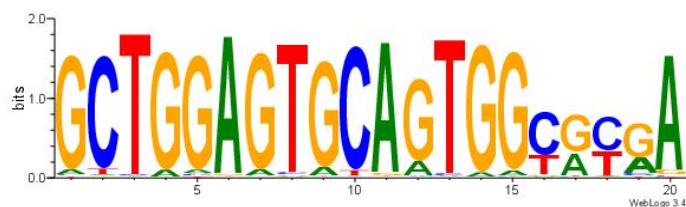
Best Matches for Motif ID 285 (Highest to Lowest)

Dataset #: 1
Motif ID: 3
Motif name: Motif 3
Matching format of first motif: Original Motif

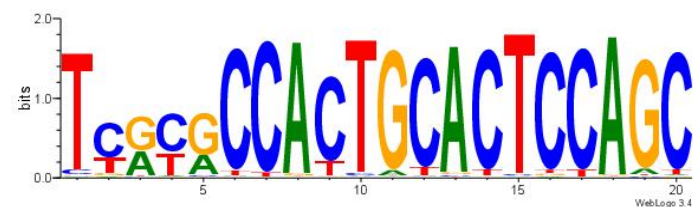
Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0.00211425

Alignment:
 TCKMGCCACTGCACTCCAGC
 CACTGCACTCCAGC-----

Original motif Consensus sequence: GCTGGAGTGCAGTGGCRYGA



Reverse complement motif Consensus sequence: TCKMGCCACTGCACTCCAGC

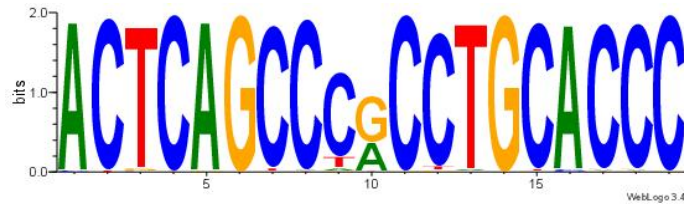


Dataset #: 1
 Motif ID: 149
 Motif name: Motif 149
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 5
 Number of overlap: 14
 Similarity score: 0.0792554

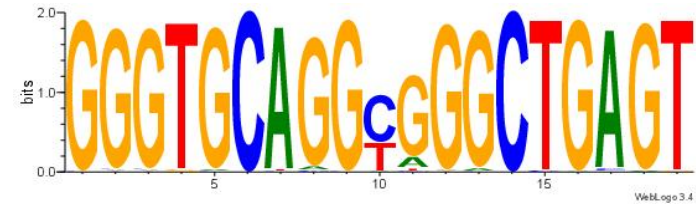
Alignment:

GGGTGCAGGMGGGCTGAGT
----GCTGGAGTGCAGTG--

Original motif Consensus sequence: ACTCAGCCRCCTGCACCC



Reverse complement motif Consensus sequence:
GGGTGCAGGMGGGCTGAGT



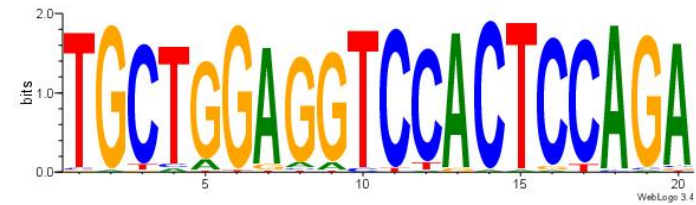
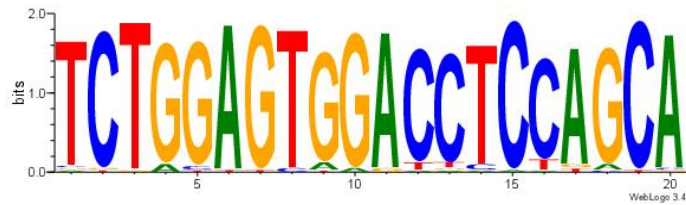
Dataset #: 1
Motif ID: 350
Motif name: Motif 350
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 14
Similarity score: 0.0809977

Alignment:

TGCTGGAGGTCCACTCCAGA
-----CACTGCACTCCAGC

Original motif Consensus sequence: TCTGGAGTGGACCTCCAGCA

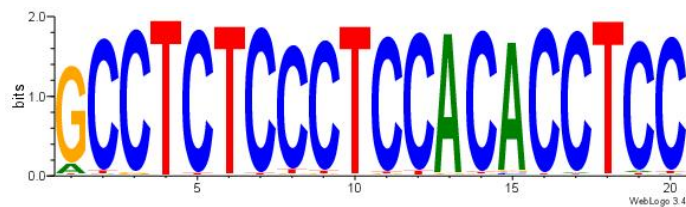
Reverse complement motif Consensus sequence:
TGCTGGAGGTCCACTCCAGA



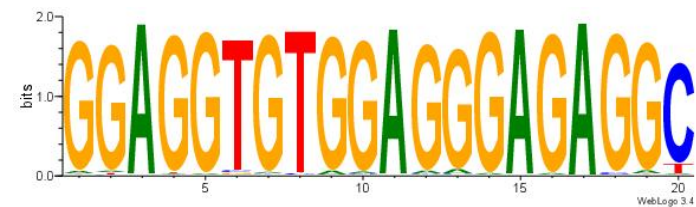
Dataset #: 1
 Motif ID: 105
 Motif name: Motif 105
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0.0818524

Alignment:
 GGAGGTGTGGAGGGAGAGGC
 GCTGGAGTGCAGT-----

Original motif Consensus sequence: GCCTCTCCCTCCACACCTCC



Reverse complement motif Consensus sequence: GGAGGTGTGGAGGGAGAGGC

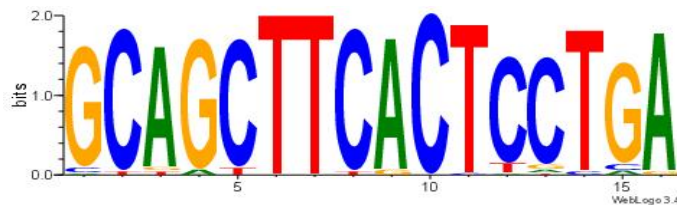


Dataset #: 1

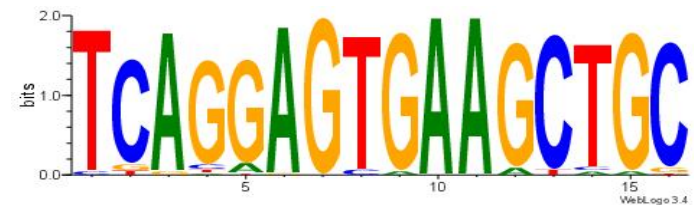
Motif ID: 246
 Motif name: Motif 246
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0.0819031

Alignment:
 TCAGGAGTGAAGCTGC
 GCTGGAGTGCAGTG--

Original motif Consensus sequence: GCAGCTTCACTcctGA

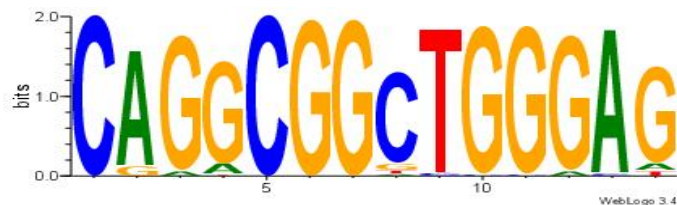


Reverse complement motif Consensus sequence: TCAGGAGTGAAGCTGC



Dataset #: 1 Motif ID: 286 Motif name: Motif 286

Original motif Consensus sequence: CAGGCGGCTGGGAG



Reverse complement motif Consensus sequence: CTCCCAGCCGCTG



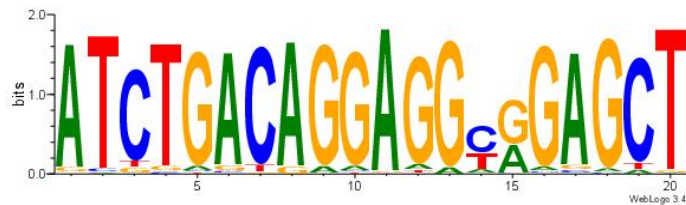
Best Matches for Motif ID 286 (Highest to Lowest)

Dataset #: 1
Motif ID: 165
Motif name: Motif 165
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 7
Number of overlap: 14
Similarity score: 0.0824568

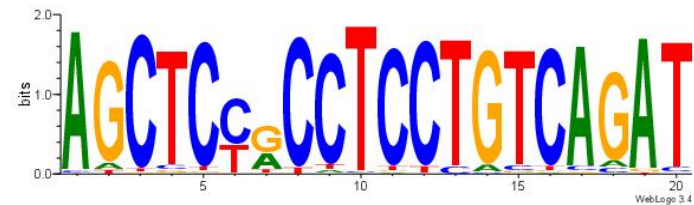
Alignment:

```
AGCTCMKCCTCCTGTCAGAT  
CTCCCAGCCGCTG-----
```

Original motif Consensus sequence: ATCTGACAGGAGGYRGAGCT



Reverse complement motif Consensus sequence: AGCTCMKCCTCCTGTCAGAT



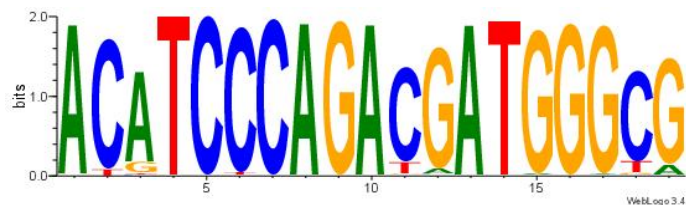
Dataset #: 1
Motif ID: 36
Motif name: Motif 36
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement

Direction: Forward
Position number: 3
Number of overlap: 14
Similarity score: 0.0825275

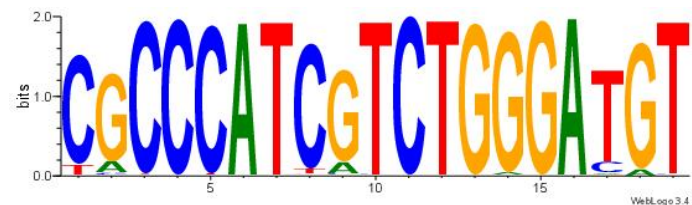
Alignment:

CGCCCATCGTCTGGGATGT
--CAGGCGGCTGGGAG---

Original motif Consensus sequence: ACATCCCAGACGATGGGCG



Reverse complement motif Consensus sequence: CGCCCATCGTCTGGGATGT

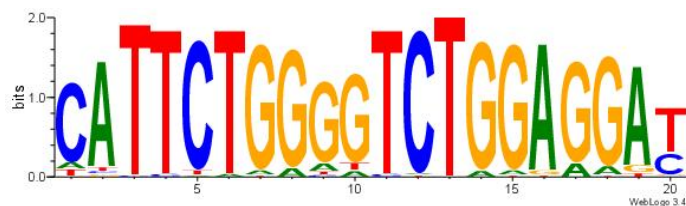


Dataset #: 1
Motif ID: 309
Motif name: Motif 309
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 5
Number of overlap: 14
Similarity score: 0.0841785

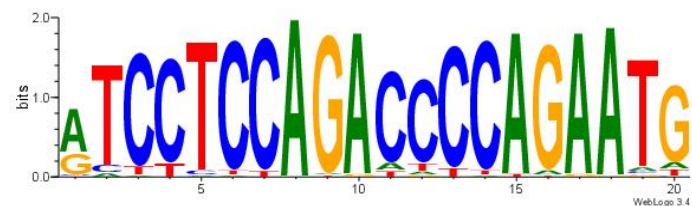
Alignment:

CATTCTGGGGTCTGGAGGAY
----CAGGCGGCTGGGAG--

Original motif Consensus sequence: CATTCTGGGGTCTGGAGGAY



Reverse complement motif Consensus sequence: MTCCTCCAGACCCCAGAATG

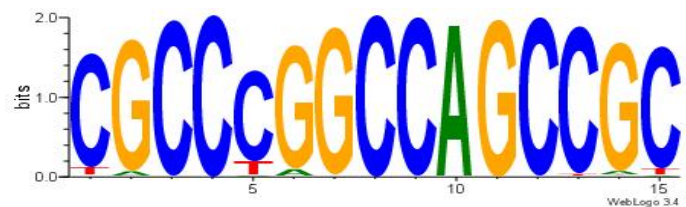


Dataset #: 1
Motif ID: 125
Motif name: Motif 125
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 2
Number of overlap: 14
Similarity score: 0.0849087

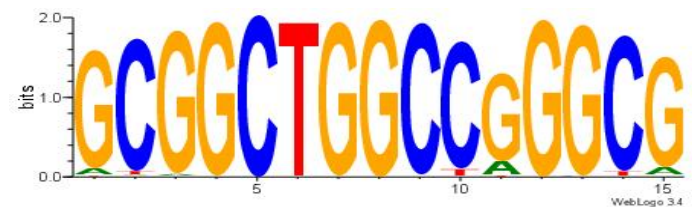
Alignment:

CGCCCGCCAGCCGC
-CTCCCAGCCGCCTG

Original motif Consensus sequence: CGCCCGCCAGCCGC



Reverse complement motif Consensus sequence: GCGGCTGGCCGGCG

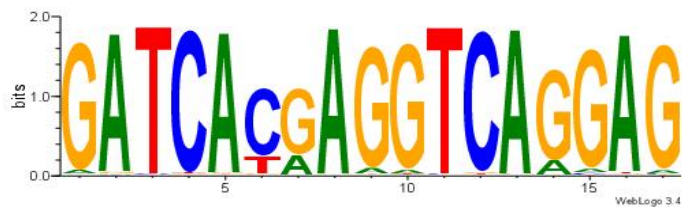


Dataset #: 1
 Motif ID: 60
 Motif name: Motif 60
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0.0884768

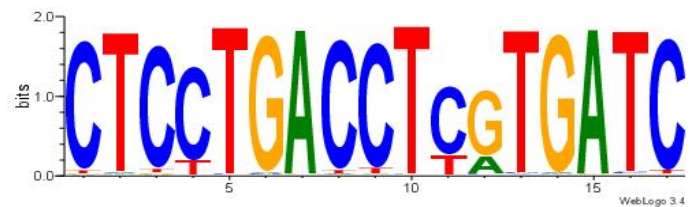
Alignment:

GATCACGAGGTCAGGAG
 ---CAGGCGGCTGGGAG

Original motif Consensus sequence: GATCACGAGGTCAGGAG



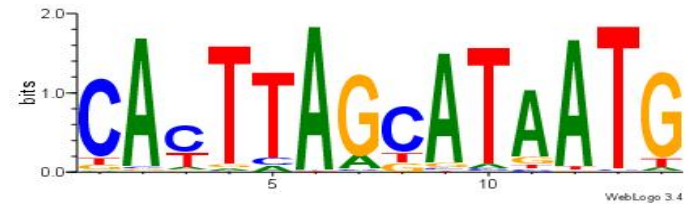
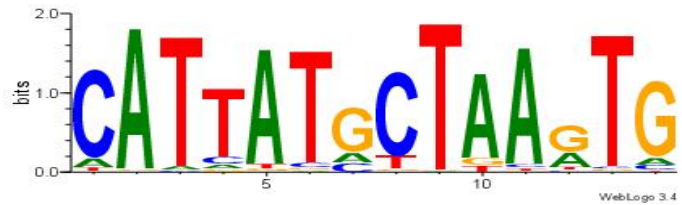
Reverse complement motif Consensus sequence: CTCCTGACCTCGTGATC



Dataset #: 1 Motif ID: 287 Motif name: Motif 287

Original motif Consensus sequence: CATTATGCTAARTG

Reverse complement motif Consensus sequence: CAMTTAGCATAAT

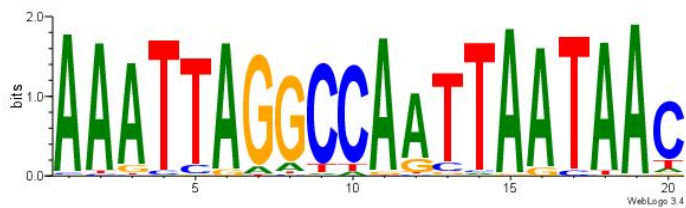


Best Matches for Motif ID 287 (Highest to Lowest)

Dataset #: 1
 Motif ID: 308
 Motif name: Motif 308
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 14
 Similarity score: 0.0753566

Alignment:
 GTTATTAATTGGCCTAATTT
 -----CAMTTAGCATAATG--

Original motif Consensus sequence: AAATTAGGCCAATTAATAAC



Reverse complement motif Consensus sequence: GTTATTAATTGGCCTAATTT

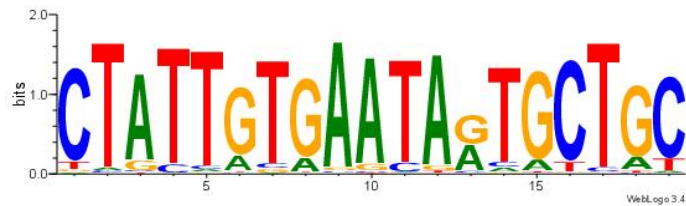


Dataset #: 1
 Motif ID: 70
 Motif name: Motif 70
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 14
 Similarity score: 0.0796028

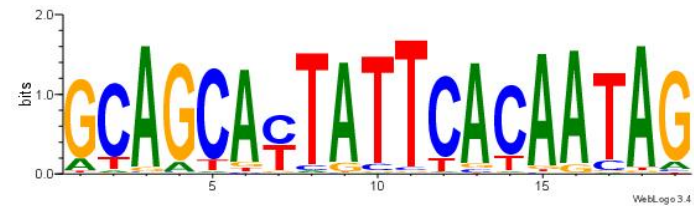
Alignment:

GCAGCAMTATT CACAATAG
 ----CAMTTAGCATAATG-

Original motif Consensus sequence: CTATTGTGAATARTGCTGC



Reverse complement motif Consensus sequence: GCAGCAMTATT CACAATAG



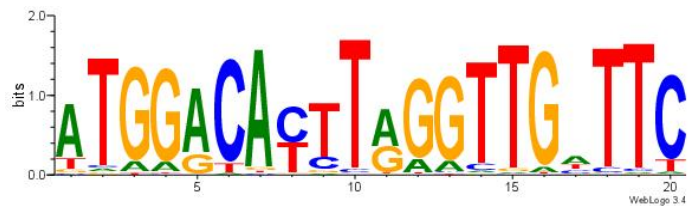
Dataset #: 1
 Motif ID: 58
 Motif name: Motif 58
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2

Number of overlap: 14
Similarity score: 0.0797498

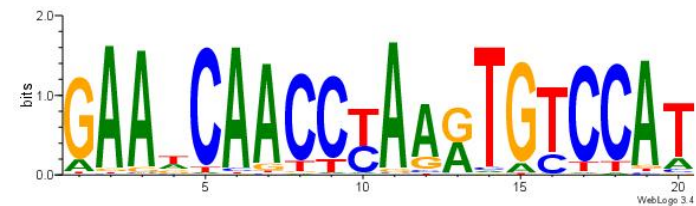
Alignment:

ATGGACAYTTRGGTTGHTTC
-CAMTTAGCATAATG-----

Original motif Consensus sequence: ATGGACAYTTRGGTTGHTTC



Reverse complement motif Consensus sequence:
GAAHCAACCKAAKTGTCCAT

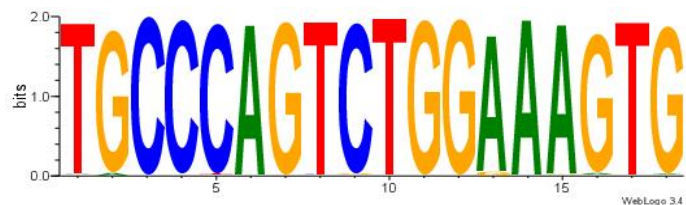


Dataset #: 1
Motif ID: 45
Motif name: Motif 45
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 5
Number of overlap: 14
Similarity score: 0.0807351

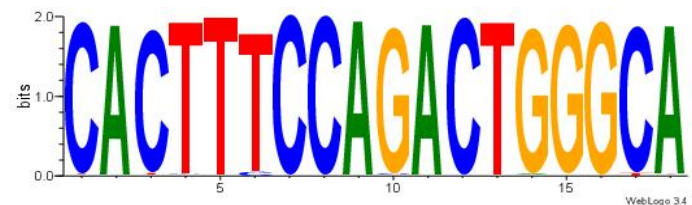
Alignment:

CACTTTCCAGACTGGGCA
CAMTTAGCATAATG-----

Original motif Consensus sequence: TGCCCAGTCTGGAAAGTG



Reverse complement motif Consensus sequence: CACTTTCAGACTGGGCA

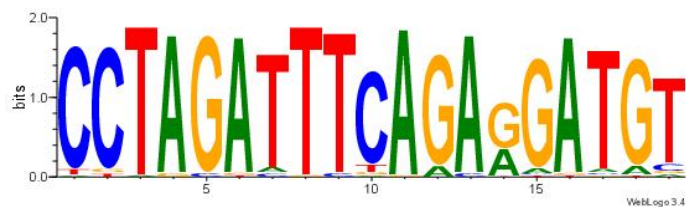


Dataset #: 1
Motif ID: 280
Motif name: Motif 280
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 5
Number of overlap: 14
Similarity score: 0.090033

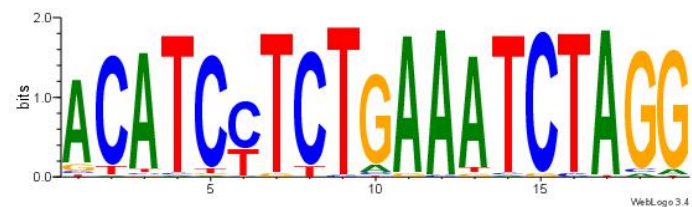
Alignment:

CCTAGATTTTCAGARGATGT
-CAMTTAGCATAATG----

Original motif Consensus sequence: CCTAGATTTTCAGARGATGT



Reverse complement motif Consensus sequence: ACATCCTCTGAAATCTAGG



Dataset #: 1 Motif ID: 288 Motif name: Motif 288

Original motif Consensus sequence: CCCAAGTCCC



Reverse complement motif Consensus sequence: GGGACTTGGG



Best Matches for Motif ID 288 (Highest to Lowest)

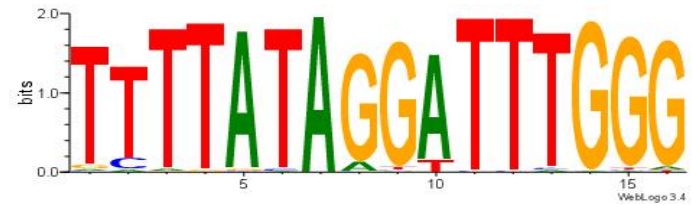
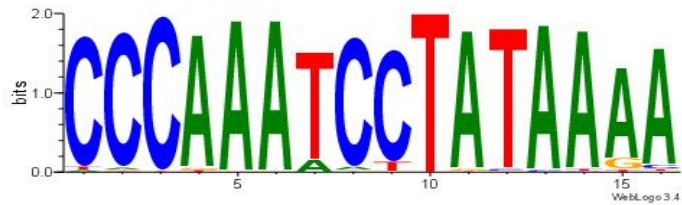
Dataset #:	1
Motif ID:	169
Motif name:	Motif 169
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	7
Number of overlap:	10
Similarity score:	0.0450065

Alignment:

```
CCCAAATCCTATAAAA  
CCCAAGTCCC-----
```

Original motif Consensus sequence: CCCAAATCCTATAAAA

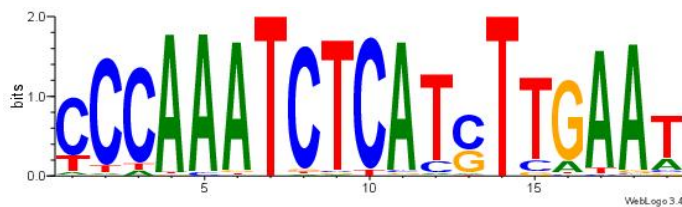
Reverse complement motif Consensus sequence:
TTTTATAGGATTTGGG



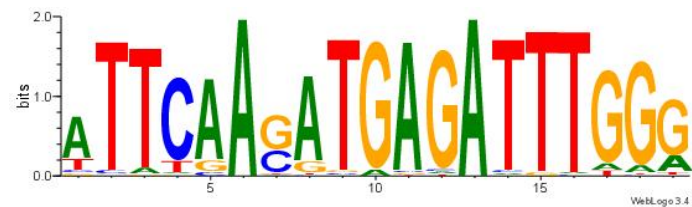
Dataset #: 1
 Motif ID: 227
 Motif name: Motif 227
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 10
 Number of overlap: 10
 Similarity score: 0.0494747

Alignment:
 CCCAAATCTCATSTTGAAT
 CCCAAGTCCC-----

Original motif Consensus sequence: CCCAAATCTCATSTTGAAT



Reverse complement motif Consensus sequence: ATTC AATGAGATTTGGG



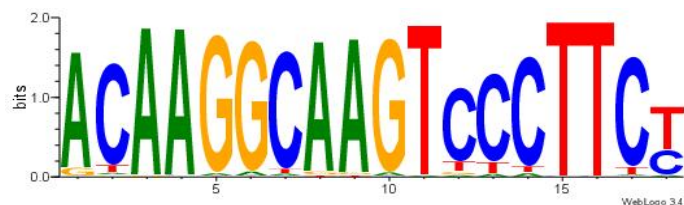
Dataset #: 1

Motif ID: 231
 Motif name: Motif 231
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 5
 Number of overlap: 10
 Similarity score: 0.0498601

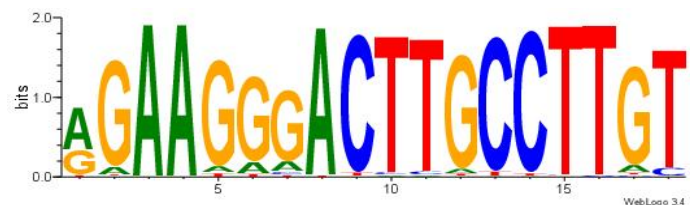
Alignment:

ACAAGGCAAGTCCCTTCY
 ----CCCAAGTCCC----

Original motif Consensus sequence: ACAAGGCAAGTCCCTTCY



Reverse complement motif Consensus sequence: MGAAGGGACTTGCCTTGT



Dataset #: 1
 Motif ID: 267
 Motif name: Motif 267
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 10

Similarity score: 0.0528606

Alignment:

ATGGA CT TGAGA
-GGGACTTGGG-

Original motif Consensus sequence: ATGGA CT TGAGA



Reverse complement motif Consensus sequence: TCTCAAGTCCAT



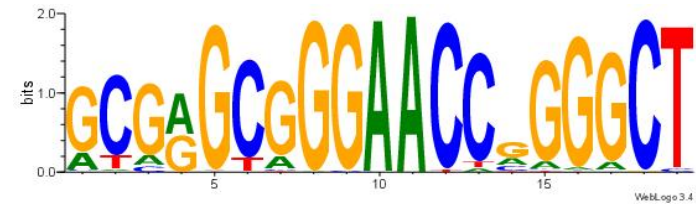
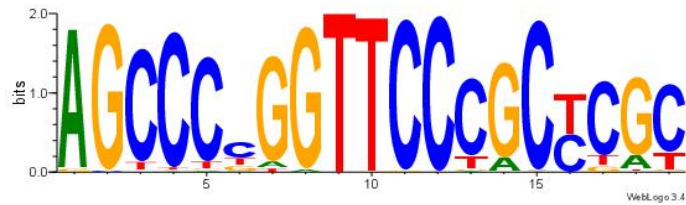
Dataset #: 1
Motif ID: 164
Motif name: Motif 164
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 8
Number of overlap: 10
Similarity score: 0.0606246

Alignment:

GCGMGC G GGAACCGGGGCT
-----GGGACTTGGG--

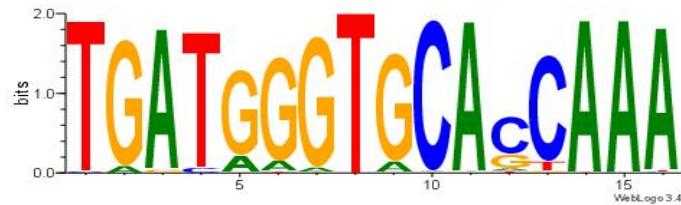
Original motif Consensus sequence: AGCCCCGTTCCCGCYCGC

Reverse complement motif Consensus sequence:
GCGMGC G GGAACCGGGGCT

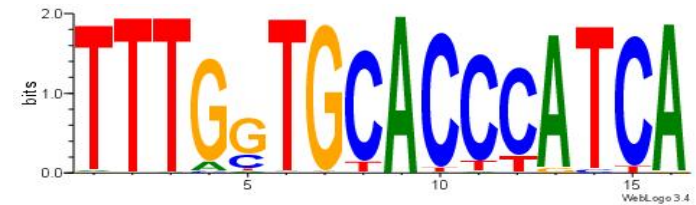


Dataset #: 1 Motif ID: 289 Motif name: Motif 289

Original motif Consensus sequence: TGATGGGTGCACCAA



Reverse complement motif Consensus sequence: TTTGGTGCACCCATCA



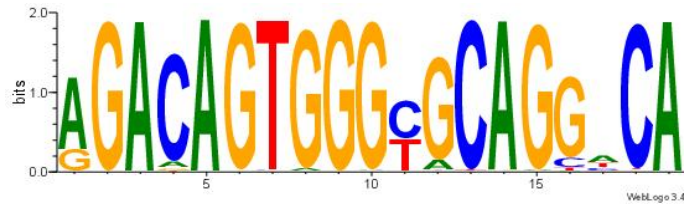
Best Matches for Motif ID 289 (Highest to Lowest)

Dataset #:	1
Motif ID:	17
Motif name:	Motif 17
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	4
Number of overlap:	16
Similarity score:	0.100149

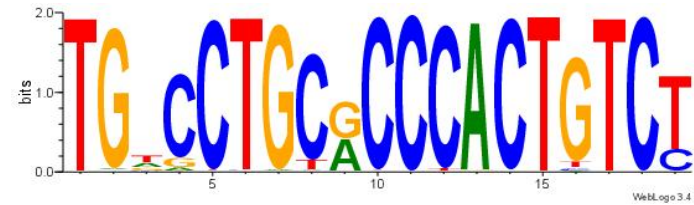
Alignment:

AGACAGTGGGYGCAGGHCA
---TGATGGGTGCACCAAA

Original motif Consensus sequence: AGACAGTGGGYGCAGGHCA



Reverse complement motif Consensus sequence:
TGHCTGCKCCCACTGTCT

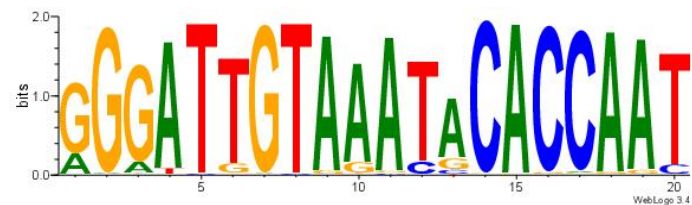
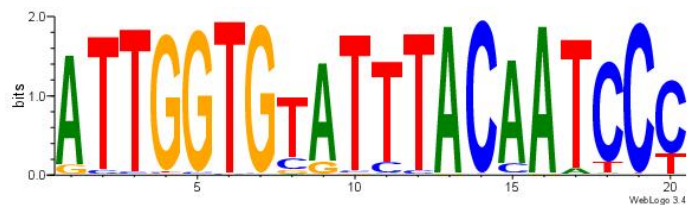


Dataset #: 1
Motif ID: 106
Motif name: Motif 106
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 5
Number of overlap: 16
Similarity score: 0.103791

Alignment:
ATTGGTGTATTTACAATCCC
----TTTGGTGCACCCATCA

Original motif Consensus sequence: ATTGGTGTATTTACAATCCC

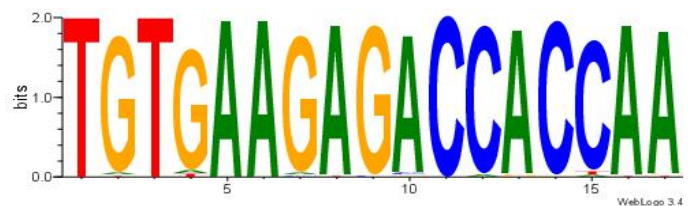
Reverse complement motif Consensus sequence:
GGGATTGTAAATACACCAAT



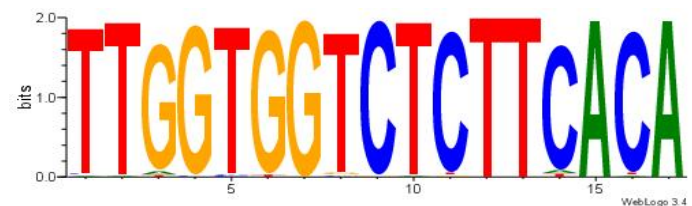
Dataset #: 1
 Motif ID: 249
 Motif name: Motif 249
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 16
 Similarity score: 0.105577

Alignment:
 TTGGTGGTCTCTTCACA
 TGATGGGTGCACCAAA-

Original motif Consensus sequence: TGTGAAGAGACCACCAA



Reverse complement motif Consensus sequence: TTGGTGGTCTCTTCACA



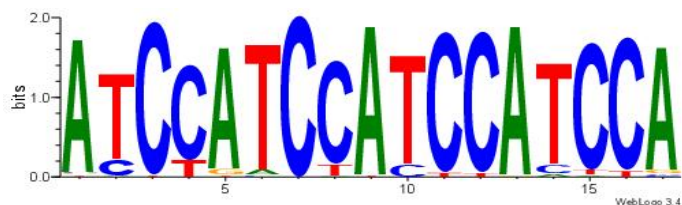
Dataset #: 1

Motif ID: 341
 Motif name: Motif 341
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 16
 Similarity score: 0.107792

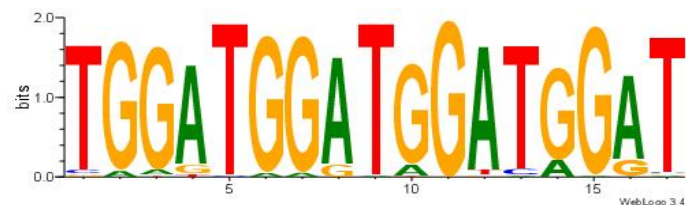
Alignment:

ATCCATCCATCCATCCA
 TTTGGTGCACCCATCA-

Original motif Consensus sequence: ATCCATCCATCCATCCA



Reverse complement motif Consensus sequence: TGGATGGATGGATGGAT



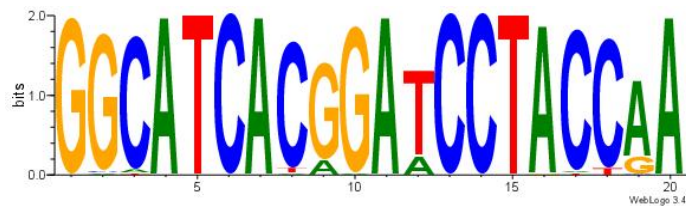
Dataset #: 1
 Motif ID: 311
 Motif name: Motif 311
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 5
 Number of overlap: 16

Similarity score: 0.109184

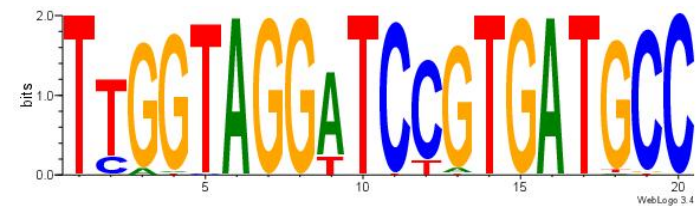
Alignment:

GGCATCACGGATCCTACCAA
----TGATGGGTGCACCAA

Original motif Consensus sequence: GGCATCACGGATCCTACCAA

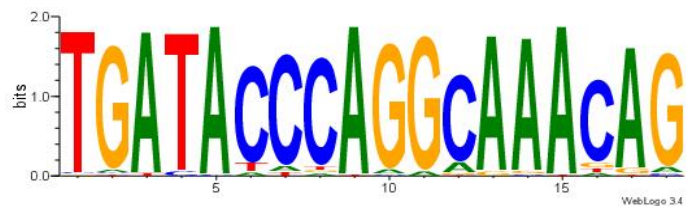


Reverse complement motif Consensus sequence: TTGGTAGGATCCGTGATGCC

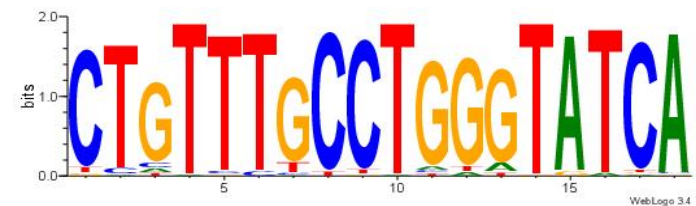


Dataset #: 1 Motif ID: 290 Motif name: Motif 290

Original motif Consensus sequence: TGATACCCAGGCAAACAG



Reverse complement motif Consensus sequence: CTGTTTGCCTGGGTATCA



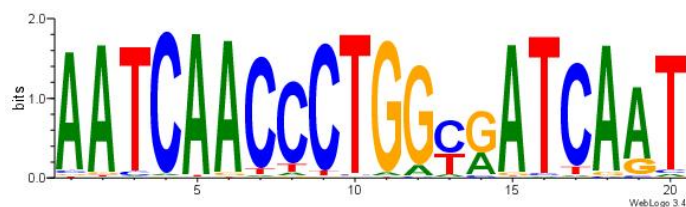
Best Matches for Motif ID 290 (Highest to Lowest)

Dataset #:	1
Motif ID:	170
Motif name:	Motif 170
Matching format of first motif:	Original Motif

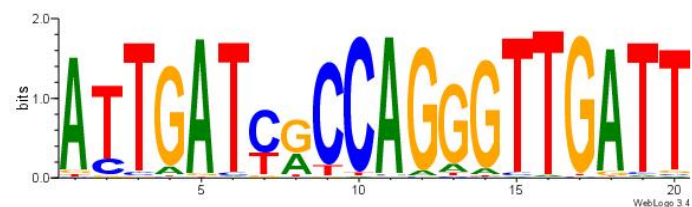
Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 18
 Similarity score: 0.0975901

Alignment:
 AATCAACCCTGGYRATCAAT
 -TGATACCCAGGCAAACAG-

Original motif Consensus sequence: AATCAACCCTGGYRATCAAT



Reverse complement motif Consensus sequence:
 ATTGATMKCCAGGGTTGATT

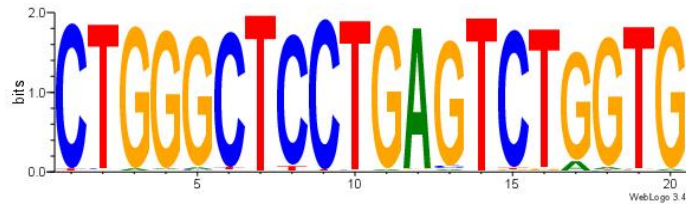


Dataset #: 1
 Motif ID: 67
 Motif name: Motif 67
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 18
 Similarity score: 0.0999158

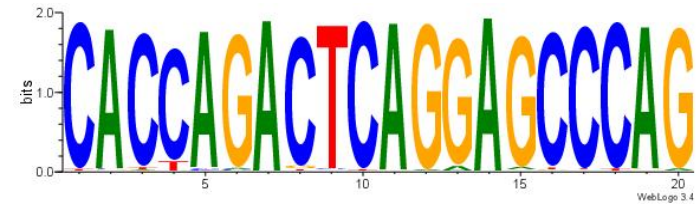
Alignment:

CTGGGCTCCTGAGTCTGGTG
--CTGTTTGCCTGGGTATCA

Original motif Consensus sequence: CTGGGCTCCTGAGTCTGGTG



Reverse complement motif Consensus sequence:
CACCAGACTCAGGAGCCCAG



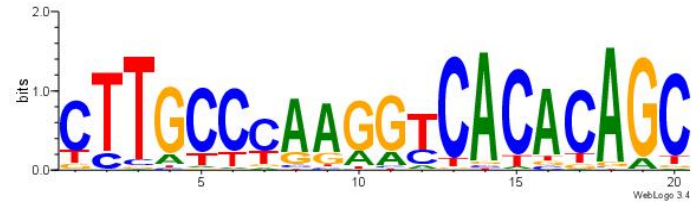
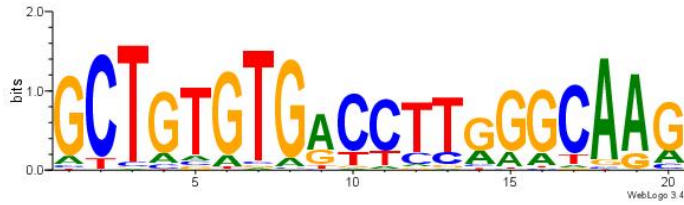
Dataset #:	1
Motif ID:	112
Motif name:	Motif 112
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2
Number of overlap:	18
Similarity score:	0.107254

Alignment:

GCTGTGTGACCTTGGGCAAG
-CTGTTTGCCTGGGTATCA-

Original motif Consensus sequence: GCTGTGTGACCTTGGGCAAG

Reverse complement motif Consensus sequence:
CTTGCCCAAGGTCACACAGC

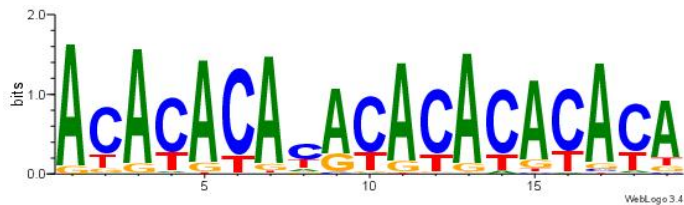


Dataset #: 1
 Motif ID: 66
 Motif name: Motif 66
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 18
 Similarity score: 0.10792

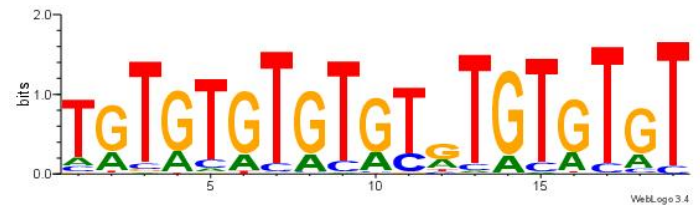
Alignment:

ACACACAYACACACACACA
 TGATACCCAGGCAAACAG-

Original motif Consensus sequence: ACACACAYACACACACACA



Reverse complement motif Consensus sequence: TGTGTGTGTGTGTGTGT



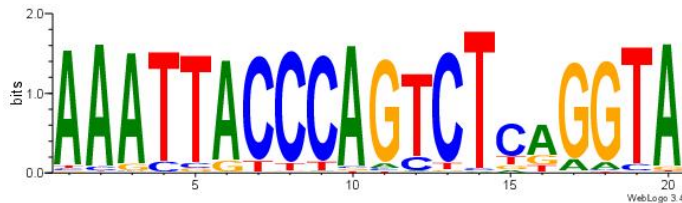
Dataset #: 1

Motif ID: 160
 Motif name: Motif 160
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 18
 Similarity score: 0.112251

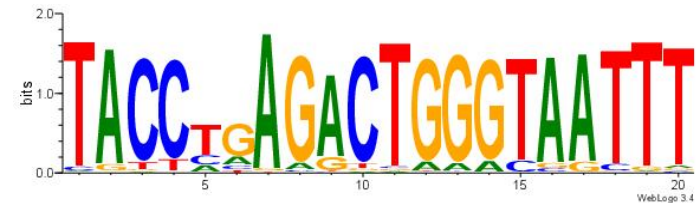
Alignment:

TACCTGAGACTGGGTAATTT
 -CTGTTTGCCTGGGTATCA-

Original motif Consensus sequence: AAATTACCCAGTCTCAGGTA

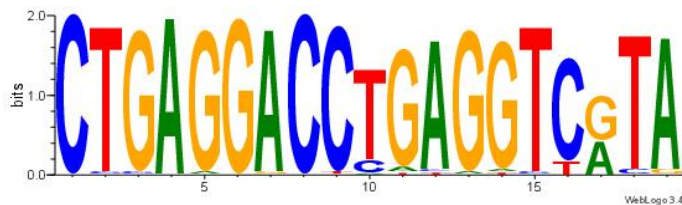


Reverse complement motif Consensus sequence: TACCTGAGACTGGGTAATTT

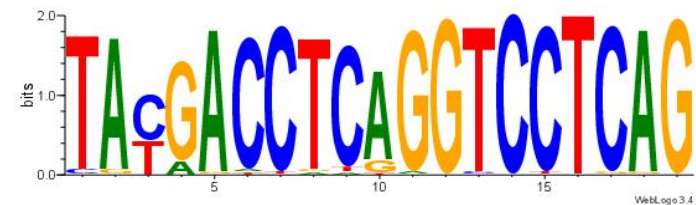


Dataset #: 1 Motif ID: 291 Motif name: Motif 291

Original motif Consensus sequence: CTGAGGACCTGAGGTCRTA



Reverse complement motif Consensus sequence: TAMGACCTCAGGTCCTCAG



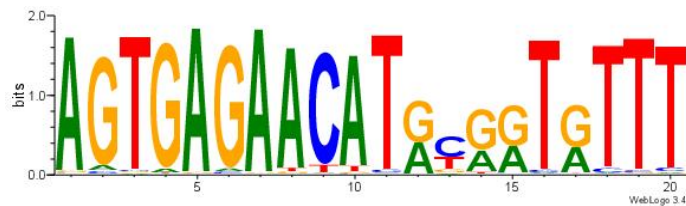
Best Matches for Motif ID 291 (Highest to Lowest)

Dataset #: 1
Motif ID: 63
Motif name: Motif 63
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 2
Number of overlap: 19
Similarity score: 0.0928513

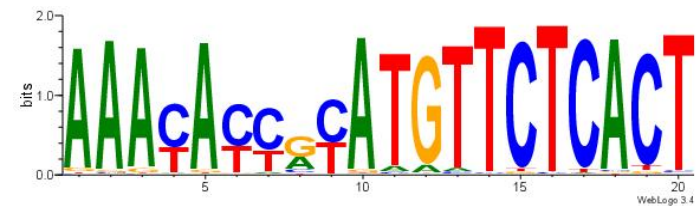
Alignment:

```
AAAMAMMKMATGTTCTCACT  
TAMGACCTCAGGTCCTCAG-
```

Original motif Consensus sequence: AGTGAGAACATRYRRTTTT



Reverse complement motif Consensus sequence:
AAAMAMMKMATGTTCTCACT



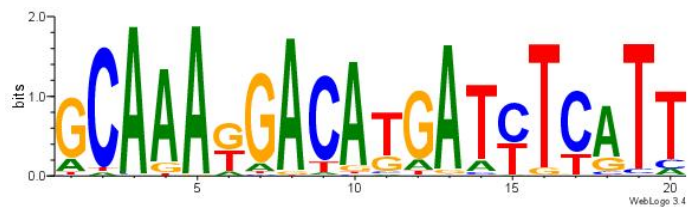
Dataset #: 1
Motif ID: 99
Motif name: Motif 99
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif

Direction: Forward
Position number: 2
Number of overlap: 19
Similarity score: 0.0929924

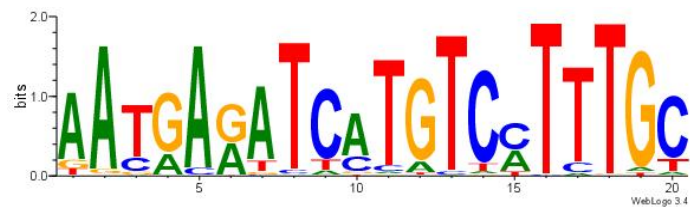
Alignment:

GCAAAGACATGATYTCATT
-CTGAGGACCTGAGGTCRTA

Original motif Consensus sequence: GCAAAGACATGATYTCATT



Reverse complement motif Consensus sequence: AATGAKATCATGTCYTTTGC

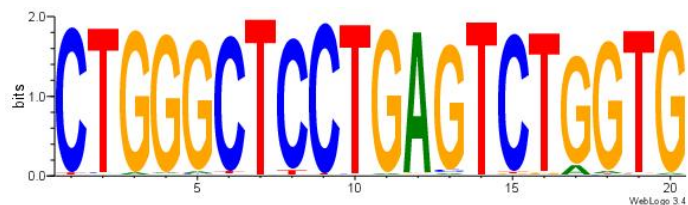


Dataset #: 1
Motif ID: 67
Motif name: Motif 67
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 19
Similarity score: 0.105301

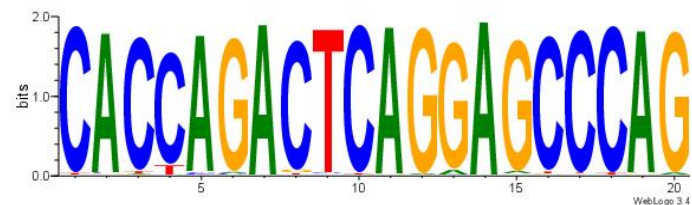
Alignment:

CTGGGCTCCTGAGTCTGGTG
CTGAGGACCTGAGGTCRTA-

Original motif Consensus sequence: CTGGGCTCCTGAGTCTGGTG



Reverse complement motif Consensus sequence: CACCAGACTCAGGAGCCCAG

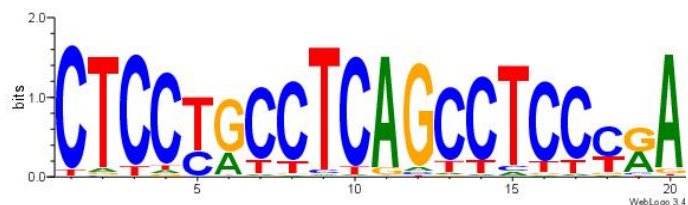


Dataset #: 1
Motif ID: 26
Motif name: Motif 26
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 2
Number of overlap: 19
Similarity score: 0.114654

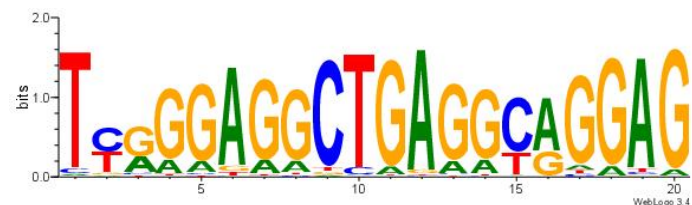
Alignment:

TMGGGAGGCTGAGGCAGGAG
-CTGAGGACCTGAGGTCRТА

Original motif Consensus sequence: CTCCTGCCTCAGCCTCCRA



Reverse complement motif Consensus sequence: TMGGGAGGCTGAGGCAGGAG

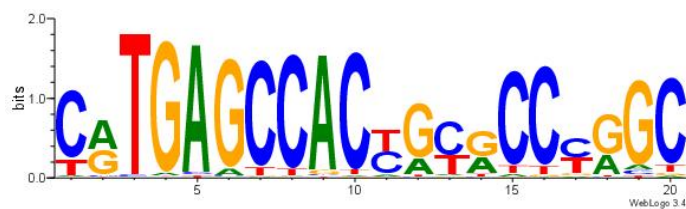


Dataset #: 1
 Motif ID: 56
 Motif name: Motif 56
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 19
 Similarity score: 0.117941

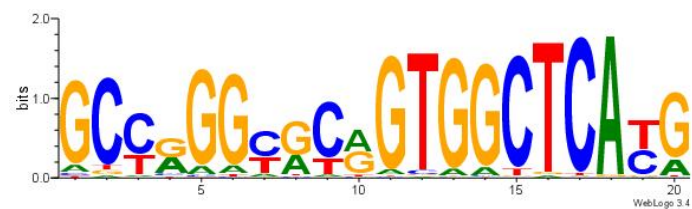
Alignment:

GCCKGGMKCMGTGGCTCAKG
 TAMGACCTCAGGTCCTCAG-

Original motif Consensus sequence: CRTGAGCCACYGYRCCYGGC



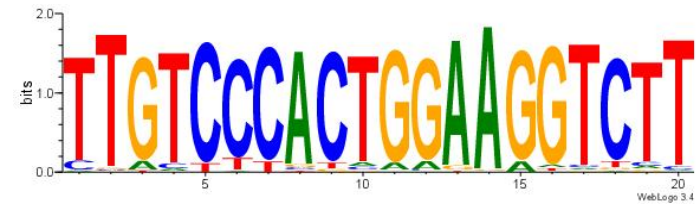
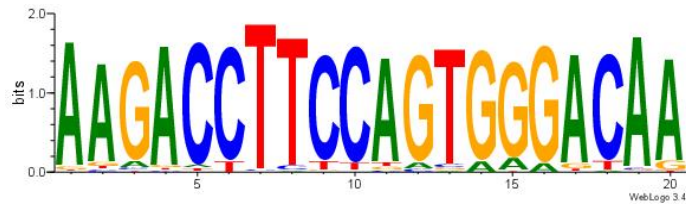
Reverse complement motif Consensus sequence: GCCKGGMKCMGTGGCTCAKG



Dataset #: 1 Motif ID: 292 Motif name: Motif 292

Original motif Consensus sequence: AAGACCTTCCAGTGGGACAA

Reverse complement motif Consensus sequence: TTGTCCCACTGGAAGGTCTT

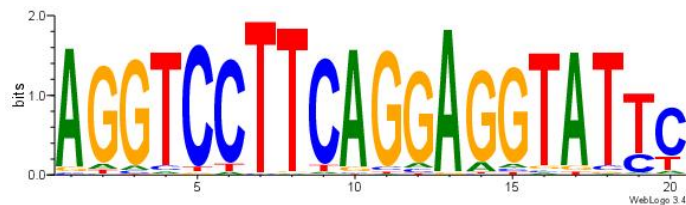


Best Matches for Motif ID 292 (Highest to Lowest)

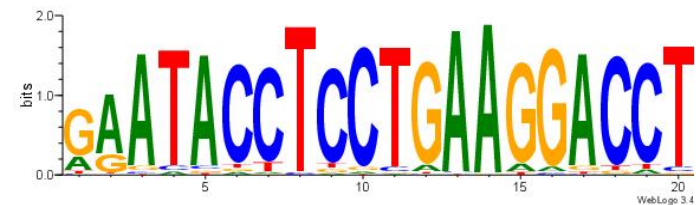
Dataset #: 1
 Motif ID: 179
 Motif name: Motif 179
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.094932

Alignment:
 GAATACCTCCTGAAGGACCT
 TTGTCCCAGTGGAGGTCTT

Original motif Consensus sequence: AGGTCCTCAGGAGGTATTC



Reverse complement motif Consensus sequence: GAATACCTCCTGAAGGACCT

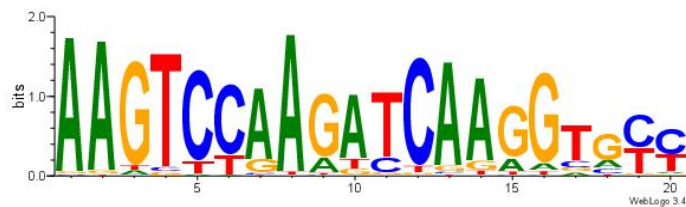


Dataset #: 1
 Motif ID: 119
 Motif name: Motif 119
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.106872

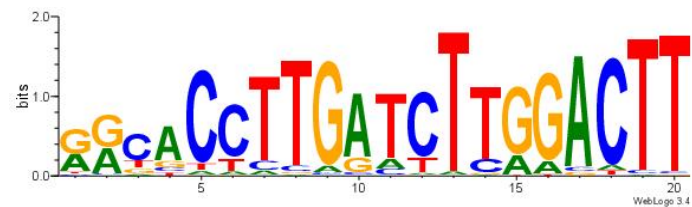
Alignment:

KKCACCTTGATCTTGGACTT
 AAGACCTTCCAGTGGGACAA

Original motif Consensus sequence: AAGTCCAAGATCAAGGTGY



Reverse complement motif Consensus sequence: KKCACCTTGATCTTGGACTT



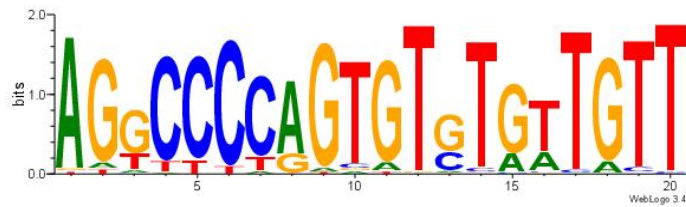
Dataset #: 1
 Motif ID: 176
 Motif name: Motif 176
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1

Number of overlap: 20
Similarity score: 0.109322

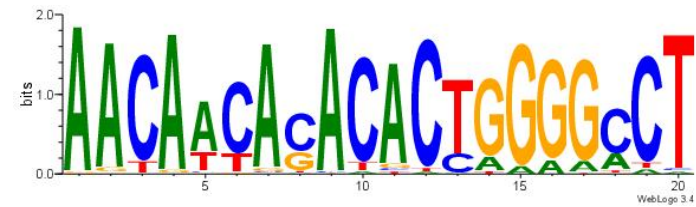
Alignment:

AACAACASACTGGGGCCT
AAGACCTTCCAGTGGGACAA

Original motif Consensus sequence: AGGCCCCAGTGTSTGTTGTT



Reverse complement motif Consensus sequence:
AACAACASACTGGGGCCT

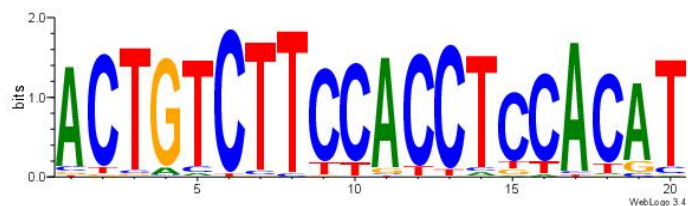


Dataset #: 1
Motif ID: 178
Motif name: Motif 178
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 20
Similarity score: 0.112394

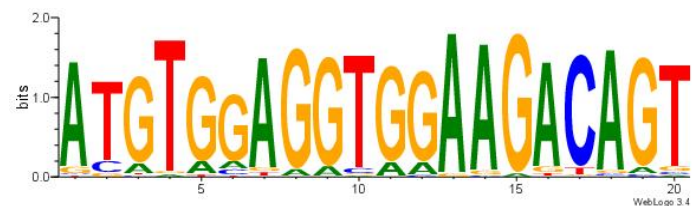
Alignment:

ATGTGGAGGTGGAAGACAGT
TTGTCCCACTGGAAGGTCTT

Original motif Consensus sequence: ACTGTCTTCCACCTCCACAT



Reverse complement motif Consensus sequence: ATGTGGAGGTGGAAGACAGT

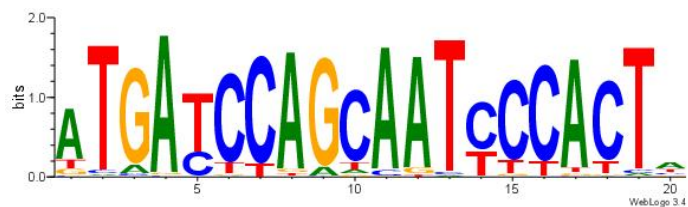


Dataset #: 1
Motif ID: 115
Motif name: Motif 115
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 20
Similarity score: 0.11745

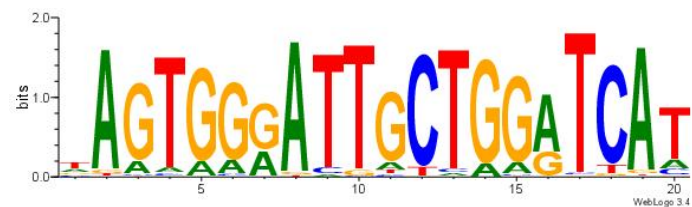
Alignment:

ATGATCCAGCAATYCCACTH
AAGACCTTCCAGTGGGACAA

Original motif Consensus sequence: ATGATCCAGCAATYCCACTH

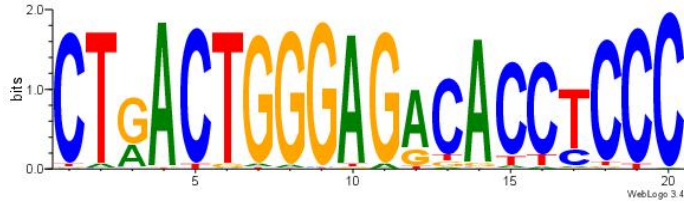


Reverse complement motif Consensus sequence: HAGTGGKATTGCTGGATCAT

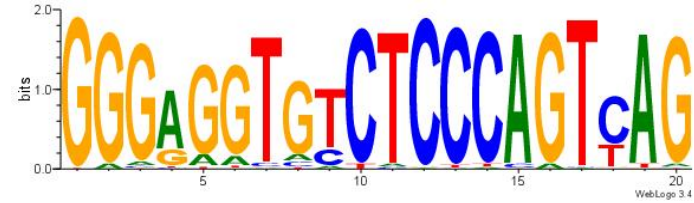


Dataset #: 1 Motif ID: 293 Motif name: Motif 293

Original motif Consensus sequence: CTGACTGGGAGACACCTCCC



Reverse complement motif Consensus sequence: GGGAGGTGTCTCCCAGTCAG



Best Matches for Motif ID 293 (Highest to Lowest)

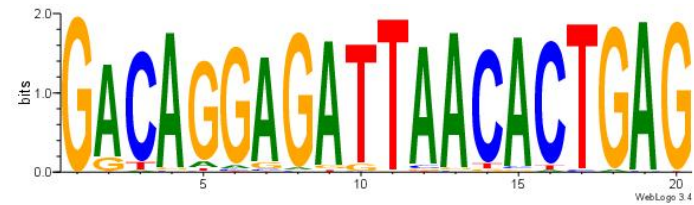
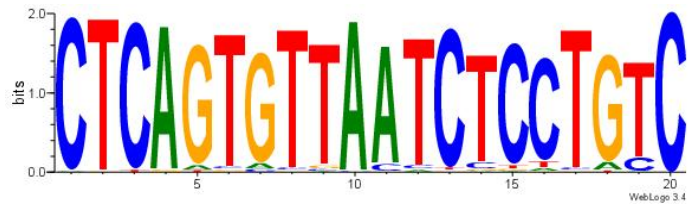
Dataset #:	1
Motif ID:	262
Motif name:	Motif 262
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	20
Similarity score:	0.106264

Alignment:

```
CTCAGTGTTAATCTCCTGTC  
CTGACTGGGAGACACCTCCC
```

Original motif Consensus sequence: CTCAGTGTTAATCTCCTGTC

Reverse complement motif Consensus sequence: GACAGGAGATTAACACTGAG

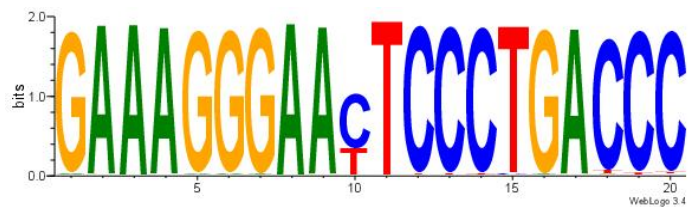


Dataset #: 1
 Motif ID: 16
 Motif name: Motif 16
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.115344

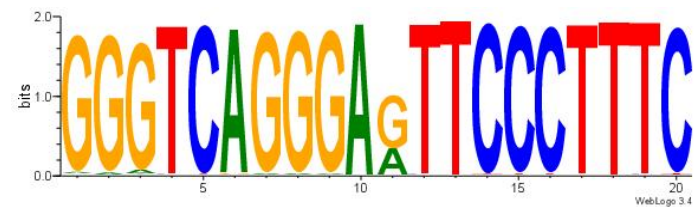
Alignment:

GAAAGGGA ACTCCCTGACCC
 GGGAGGTGTCTCC CAGTCAG

Original motif Consensus sequence: GAAAGGGA ACTCCCTGACCC



Reverse complement motif Consensus sequence: GGGTCAGGGA GTTCCCTTTC



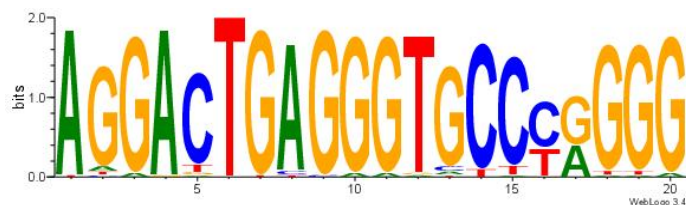
Dataset #: 1

Motif ID: 312
 Motif name: Motif 312
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.123537

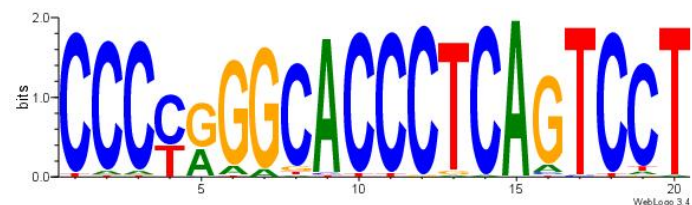
Alignment:

CCCMKGGCACCCCTCAGTCCT
 GGGAGGTGTCTCCAGTCAG

Original motif Consensus sequence: AGGACTGAGGGTGCCYRGGG



Reverse complement motif Consensus sequence: CCCMKGGCACCCCTCAGTCCT



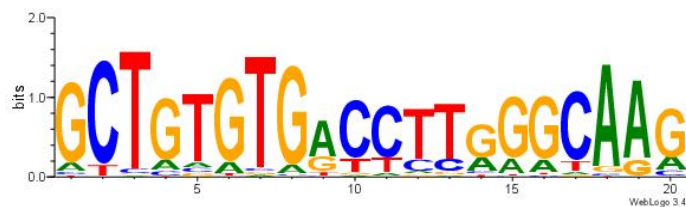
Dataset #: 1
 Motif ID: 112
 Motif name: Motif 112
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 20

Similarity score: 0.126725

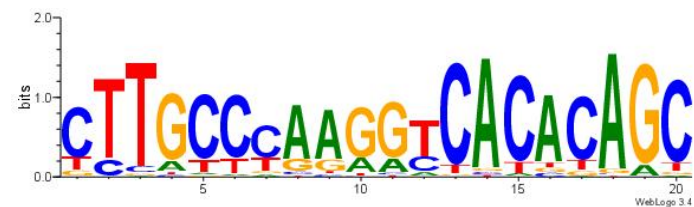
Alignment:

CTTGCCCAAGGTCACACAGC
CTGACTGGGAGACACCTCCC

Original motif Consensus sequence: GCTGTGTGACCTGGGCAAG



Reverse complement motif Consensus sequence:
CTTGCCCAAGGTCACACAGC



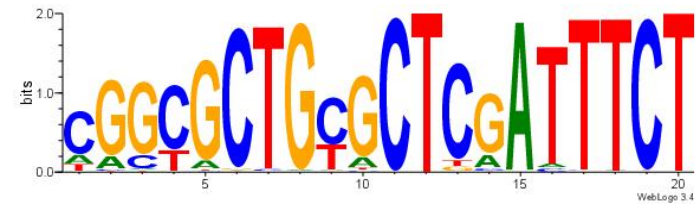
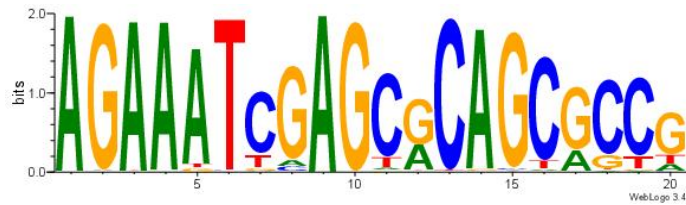
Dataset #: 1
Motif ID: 65
Motif name: Motif 65
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 20
Similarity score: 0.133644

Alignment:

AGAAATCGAGCRCAGCGCCG
CTGACTGGGAGACACCTCCC

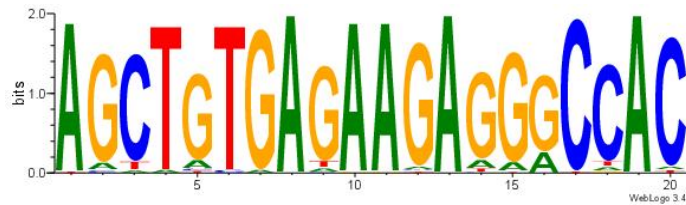
Original motif Consensus sequence: AGAAATCGAGCRCAGCGCCG

Reverse complement motif Consensus sequence:
CGGCGCTGMGCTCGATTCT

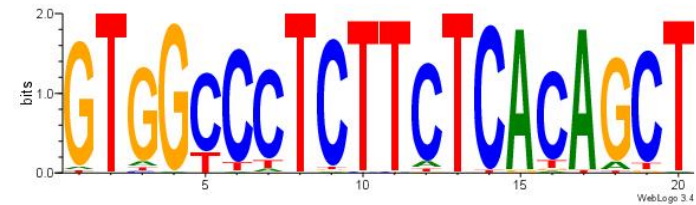


Dataset #: 1 Motif ID: 294 Motif name: Motif 294

Original motif Consensus sequence: AGCTGTGAGAAGAGGGCCAC



Reverse complement motif Consensus sequence: GTGGCCCTCTTCTCACAGCT



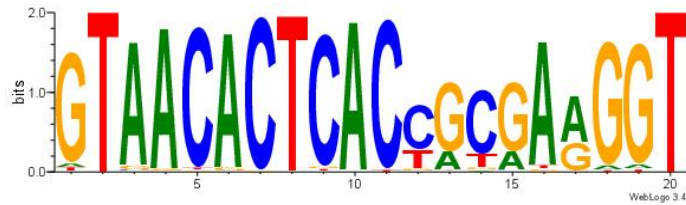
Best Matches for Motif ID 294 (Highest to Lowest)

Dataset #:	1
Motif ID:	201
Motif name:	Motif 201
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	20
Similarity score:	0.113168

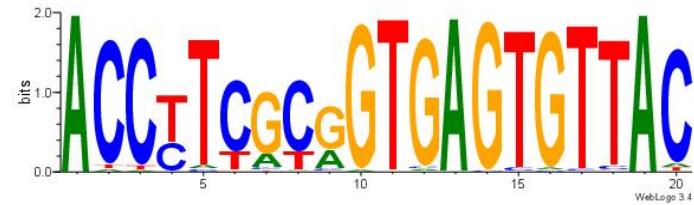
Alignment:

ACCKTCGCGGTGAGTGTTAC
AGCTGTGAGAAGAGGGCCAC

Original motif Consensus sequence: GTAACACTCACCGCGARGGT



Reverse complement motif Consensus sequence:
ACCKTCGCGGTGAGTGTTAC

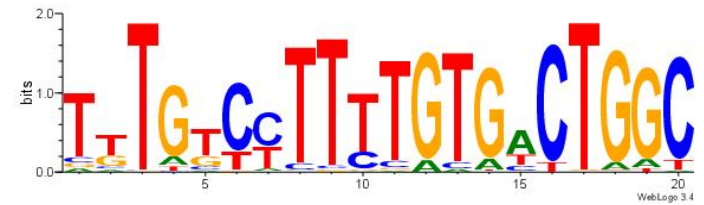
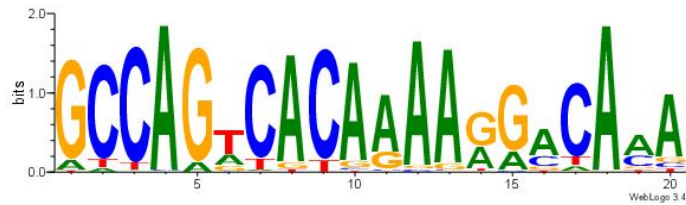


Dataset #: 1
Motif ID: 145
Motif name: Motif 145
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 20
Similarity score: 0.119835

Alignment:
GCCAGTCACAAAARGACAMA
AGCTGTGAGAAGAGGGCCAC

Original motif Consensus sequence: GCCAGTCACAAAARGACAMA

Reverse complement motif Consensus sequence:
TYGTCTTTTTGTGACTGGC

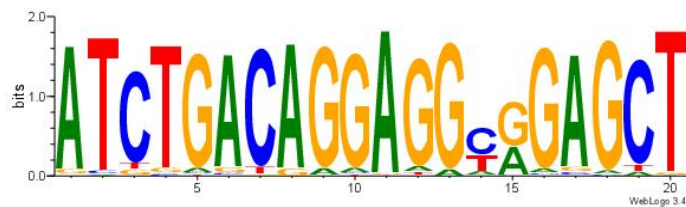


Dataset #: 1
 Motif ID: 165
 Motif name: Motif 165
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.122097

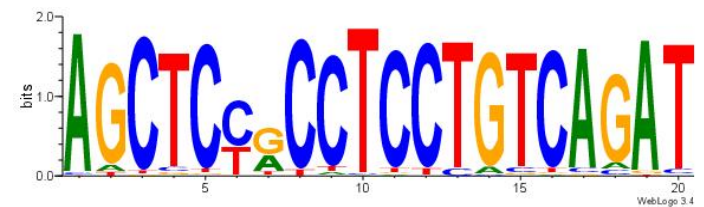
Alignment:

AGCTCMKCCTCCTGTCAGAT
 GTGGCCCTCTTCTCACAGCT

Original motif Consensus sequence: ATCTGACAGGAGGYRGAGCT



Reverse complement motif Consensus sequence: AGCTCMKCCTCCTGTCAGAT



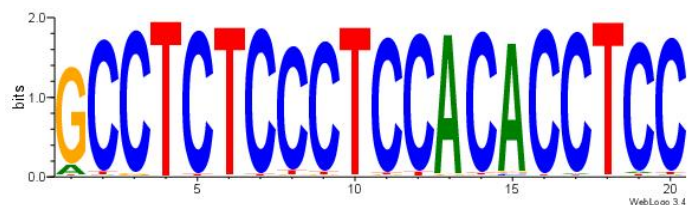
Dataset #: 1

Motif ID: 105
 Motif name: Motif 105
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.122268

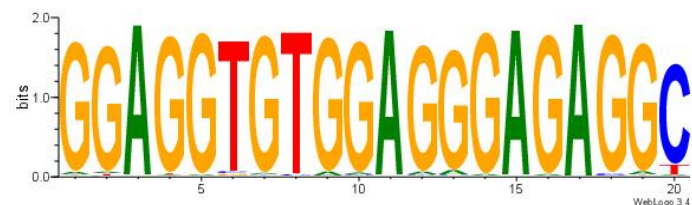
Alignment:

GGAGGTGTGGAGGGAGAGGC
 AGCTGTGAGAAGAGGGCCAC

Original motif Consensus sequence: GCCTCTCCCTCCACACCTCC



Reverse complement motif Consensus sequence: GGAGGTGTGGAGGGAGAGGC



Dataset #: 1
 Motif ID: 179
 Motif name: Motif 179
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 20

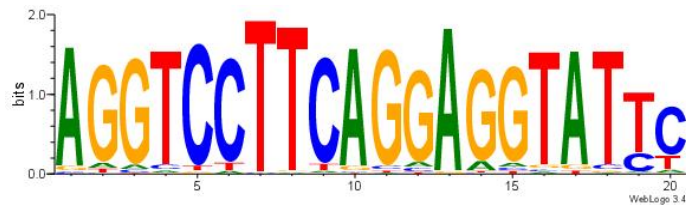
Similarity score: 0.127957

Alignment:

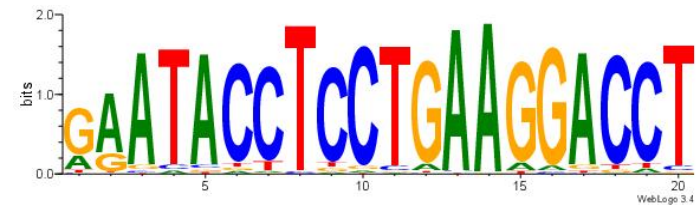
GAATACCTCCTGAAGGACCT

GTGGCCCTCTTCTCACAGCT

Original motif Consensus sequence: AGGTCCTCAGGAGGTATTC



Reverse complement motif Consensus sequence: GAATACCTCCTGAAGGACCT



Dataset #: 1 Motif ID: 295 Motif name: Motif 295

Original motif Consensus sequence: CCCC GCCC



Reverse complement motif Consensus sequence: GGGG CGGG



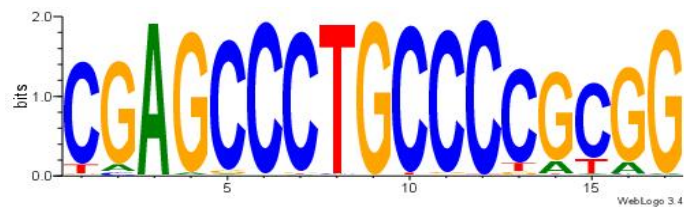
Best Matches for Motif ID 295 (Highest to Lowest)

Dataset #:	1
Motif ID:	78
Motif name:	Motif 78
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif

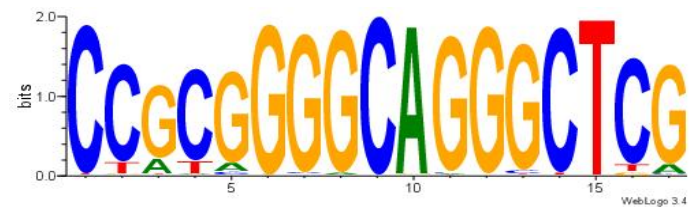
Direction: Backward
Position number: 5
Number of overlap: 9
Similarity score: 0.02574

Alignment:
CGAGCCCTGCCCGCGG
----CCCGCCCC----

Original motif Consensus sequence: CGAGCCCTGCCCGCGG



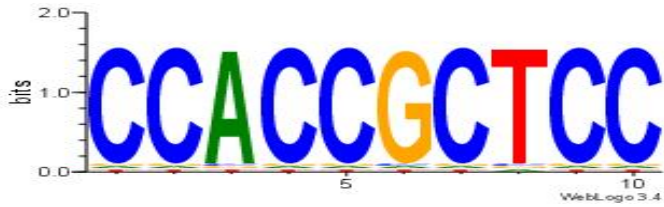
Reverse complement motif Consensus sequence: CCGCGGGGCAGGGCTCG



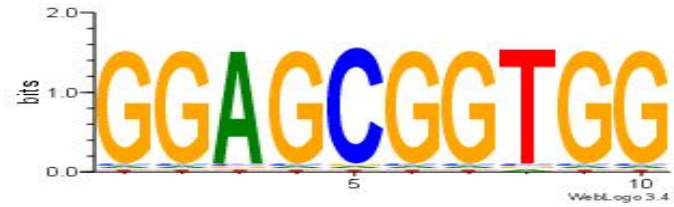
Dataset #: 1
Motif ID: 250
Motif name: Motif 250
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 2
Number of overlap: 9
Similarity score: 0.0380756

Alignment:
CCACCGCTCC
-CCCGCCCC

Original motif Consensus sequence: CCACCGCTCC



Reverse complement motif Consensus sequence: GGAGCGGTGG

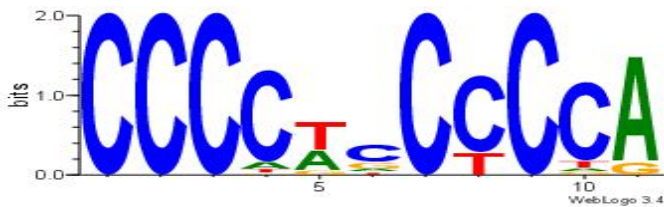


Dataset #: 1
Motif ID: 46
Motif name: Motif 46
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 3
Number of overlap: 9
Similarity score: 0.0387901

Alignment:

CCCCWCCCCCA
CCCCGCCCC--

Original motif Consensus sequence: CCCCWCCCCCA



Reverse complement motif Consensus sequence: TGGGGGWGGGG

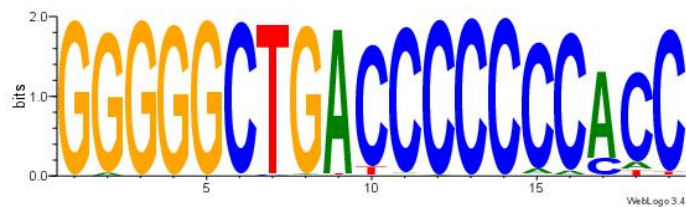


Dataset #: 1
 Motif ID: 92
 Motif name: Motif 92
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 9
 Similarity score: 0.047748

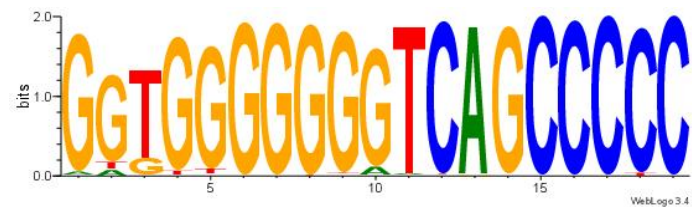
Alignment:

GGGGGCTGACCCCCCACC
 -----CCCGCCCC

Original motif Consensus sequence: GGGGGCTGACCCCCCACC



Reverse complement motif Consensus sequence: GGTGGGGGGGTCAGCCCCC



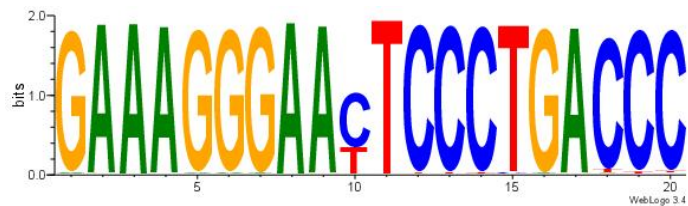
Dataset #: 1
 Motif ID: 16
 Motif name: Motif 16
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1

Number of overlap: 9
Similarity score: 0.0495574

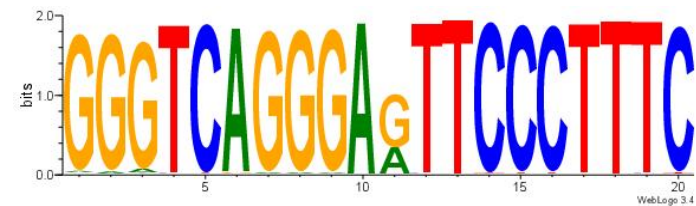
Alignment:

GAAAGGGA ACTCCCTGACCC
-----CCCGCCCC

Original motif Consensus sequence: GAAAGGGA ACTCCCTGACCC



Reverse complement motif Consensus sequence:
GGGTCAGGGAGTTCCTTTC



Dataset #: 1 Motif ID: 296 Motif name: Motif 296

Original motif Consensus sequence: CCACGTGG



Reverse complement motif Consensus sequence: CCACGTGG



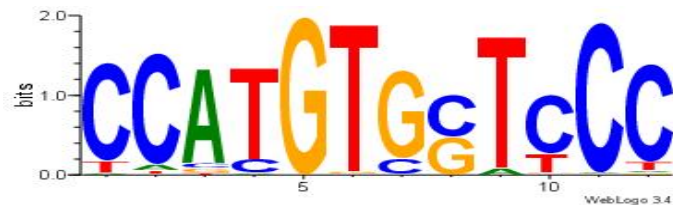
Best Matches for Motif ID 296 (Highest to Lowest)

Dataset #: 1
Motif ID: 120
Motif name: Motif 120
Matching format of first motif: Original Motif

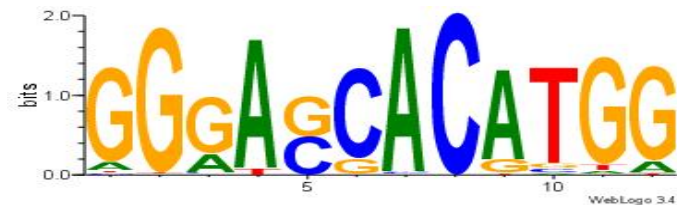
Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 5
 Number of overlap: 8
 Similarity score: 0.0506234

Alignment:
 CCATGTGSTCCC
 CCACGTGG-----

Original motif Consensus sequence: CCATGTGSTCCC



Reverse complement motif Consensus sequence: GGGASCACATGG

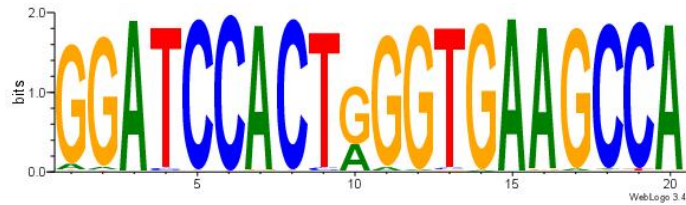


Dataset #: 1
 Motif ID: 61
 Motif name: Motif 61
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 5
 Number of overlap: 8
 Similarity score: 0.0551535

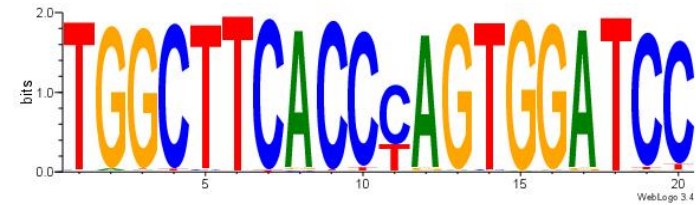
Alignment:

GGATCCACTGGGTGAAGCCA
-----CCACGTGG-----

Original motif Consensus sequence: GGATCCACTGGGTGAAGCCA



Reverse complement motif Consensus sequence:
TGGCTTCACCCAGTGGATCC

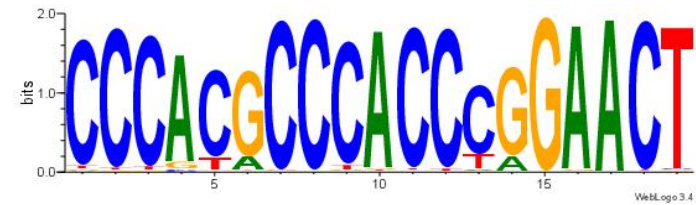
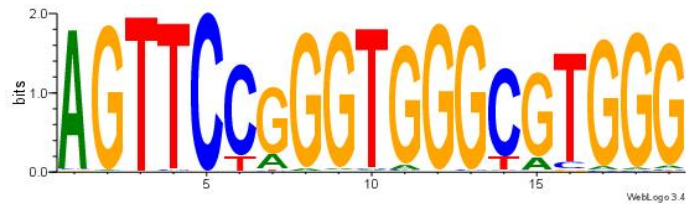


Dataset #:	1
Motif ID:	98
Motif name:	Motif 98
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	8
Number of overlap:	8
Similarity score:	0.0566616

Alignment:
CCCACGCCACCCGGA
-----CCACGTGG-----

Original motif Consensus sequence: AGTTCCGGGTGGGCGTGGG

Reverse complement motif Consensus sequence:
CCCACGCCACCCGGA

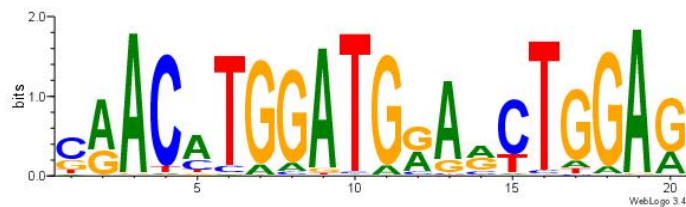


Dataset #: 1
 Motif ID: 104
 Motif name: Motif 104
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 13
 Number of overlap: 8
 Similarity score: 0.0583814

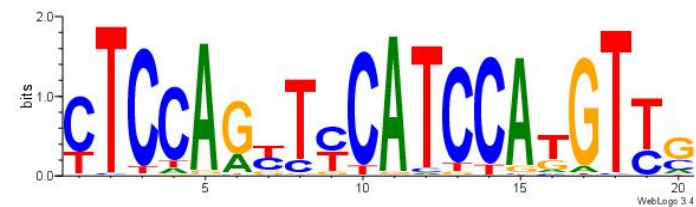
Alignment:

CAACATGGATGRARCTGGAG
 -----CCACGTGG

Original motif Consensus sequence: CAACATGGATGRARCTGGAG



Reverse complement motif Consensus sequence: CTCCAGKTCATCCATGTTG



Dataset #: 1

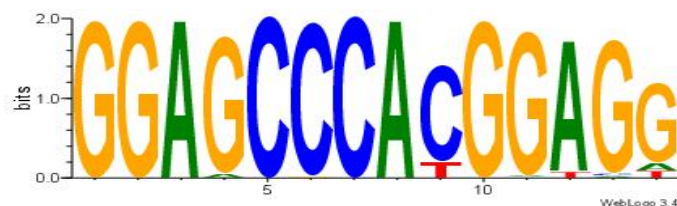
Motif ID: 163
 Motif name: Motif 163
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 6
 Number of overlap: 8
 Similarity score: 0.0613138

Alignment:
 GGAGCCCACGGAGG
 -----CCACGTGG--

Original motif Consensus sequence: CCTCCGTGGGCTCC

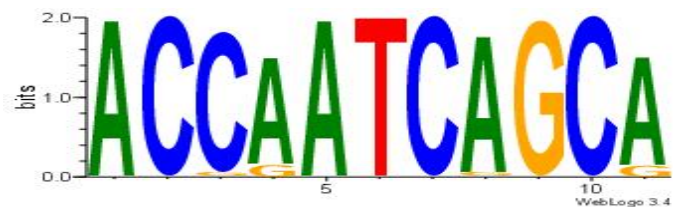


Reverse complement motif Consensus sequence: GGAGCCCACGGAGG

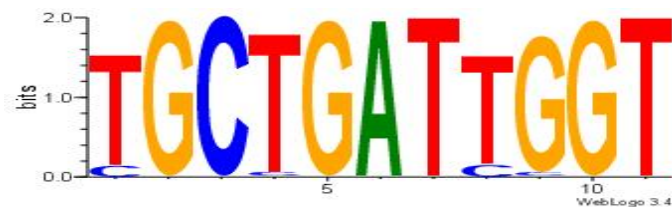


Dataset #: 1 Motif ID: 297 Motif name: Motif 297

Original motif Consensus sequence: ACCAATCAGCA



Reverse complement motif Consensus sequence: TGCTGATTGGT



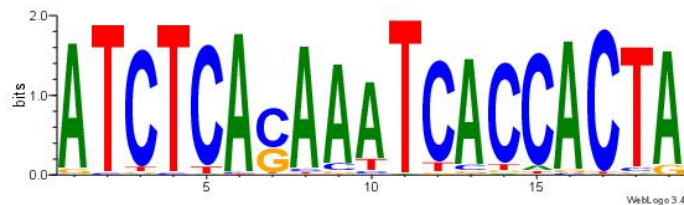
Best Matches for Motif ID 297 (Highest to Lowest)

Dataset #: 1
Motif ID: 261
Motif name: Motif 261
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 4
Number of overlap: 11
Similarity score: 0.0606967

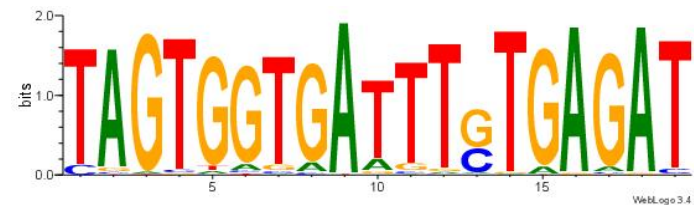
Alignment:

```
TAGTGGTGATTTSTGAGAT  
---TGCTGATTGGT-----
```

Original motif Consensus sequence: ATCTCASAAATCACCCTA



Reverse complement motif Consensus sequence:
TAGTGGTGATTTSTGAGAT



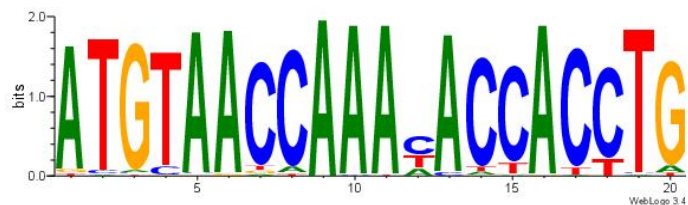
Dataset #: 1
Motif ID: 336
Motif name: Motif 336
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement

Direction: Forward
 Position number: 5
 Number of overlap: 11
 Similarity score: 0.0632904

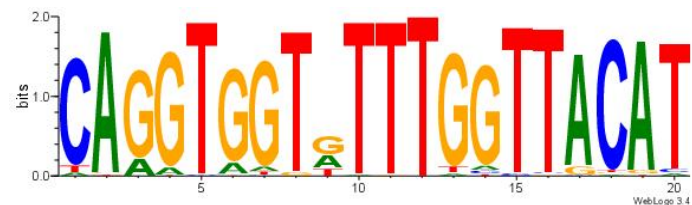
Alignment:

CAGGTGGTKTTTGGTTACAT
 ----TGCTGATTGGT-----

Original motif Consensus sequence: ATGTAACCAAAYACCACCTG



Reverse complement motif Consensus sequence: CAGGTGGTKTTTGGTTACAT

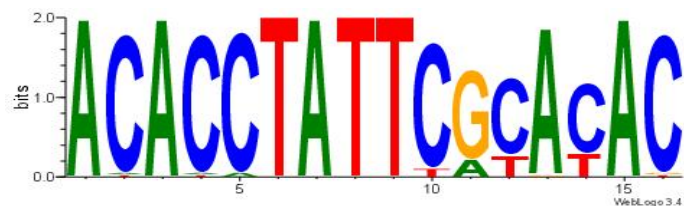


Dataset #: 1
 Motif ID: 347
 Motif name: Motif 347
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 4
 Number of overlap: 11
 Similarity score: 0.0719846

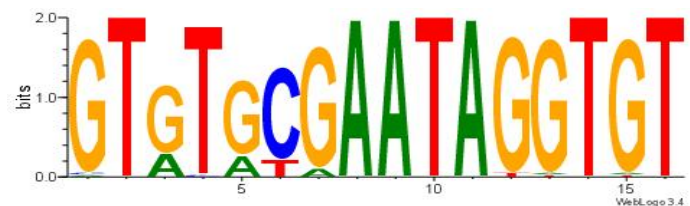
Alignment:

GTGTGCGAATAGGTGT
 ---TGCTGATTGGT--

Original motif Consensus sequence: ACACCTATTCGCACAC



Reverse complement motif Consensus sequence:
GTGTGCGAATAGGTGT

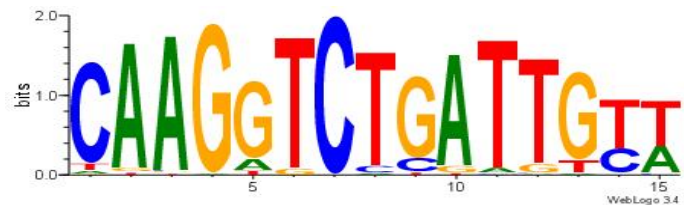


Dataset #: 1
Motif ID: 363
Motif name: Motif 363
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 11
Similarity score: 0.0728365

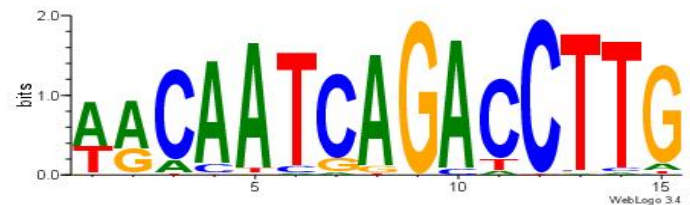
Alignment:

WACAATCAGACCTTG
ACCAATCAGCA-----

Original motif Consensus sequence: CAAGGTCTGATTGTW



Reverse complement motif Consensus sequence: WACAATCAGACCTTG

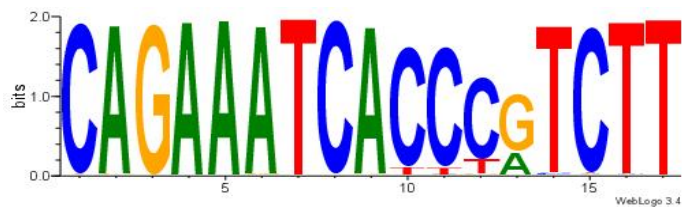


Dataset #: 1
 Motif ID: 35
 Motif name: Motif 35
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 11
 Similarity score: 0.0840444

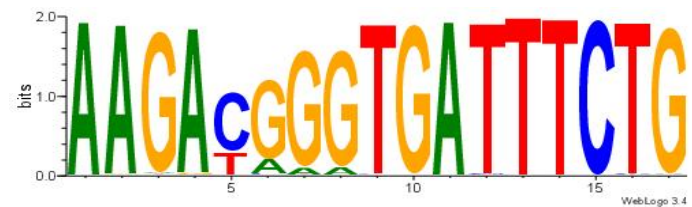
Alignment:

AAGACGGGTGATTTCTG
 -----TGCTGATTGGT-

Original motif Consensus sequence: CAGAAATCACCCGTCTT



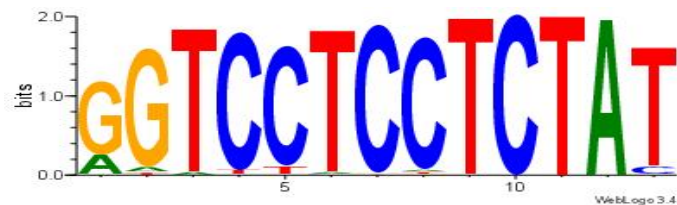
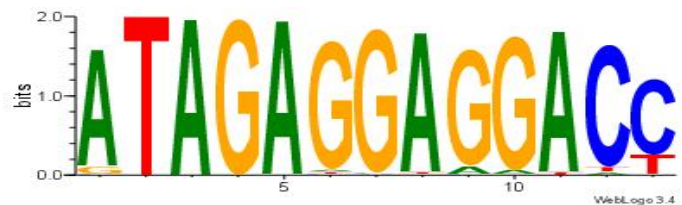
Reverse complement motif Consensus sequence: AAGACGGGTGATTTCTG



Dataset #: 1 Motif ID: 298 Motif name: Motif 298

Original motif Consensus sequence: ATAGAGGAGGACC

Reverse complement motif Consensus sequence: GTCCTCCTCTAT

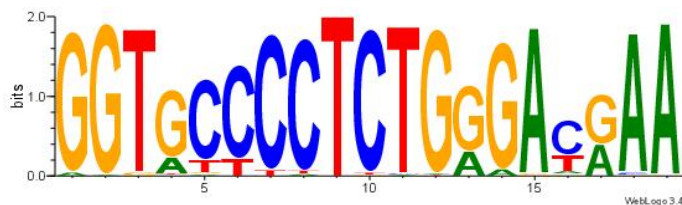


Best Matches for Motif ID 298 (Highest to Lowest)

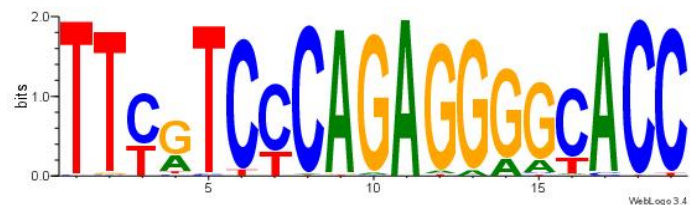
Dataset #: 1
 Motif ID: 260
 Motif name: Motif 260
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 13
 Similarity score: 0.0631665

Alignment:
 GGTGCCCTCTGGGACRAA
 -----GGTCCTCCTCTAT

Original motif Consensus sequence: GGTGCCCTCTGGGACRAA



Reverse complement motif Consensus sequence: TTMGTCCCAGAGGGGCACC

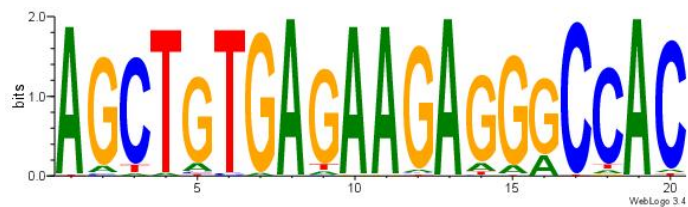


Dataset #: 1
 Motif ID: 294
 Motif name: Motif 294
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 6
 Number of overlap: 13
 Similarity score: 0.0642679

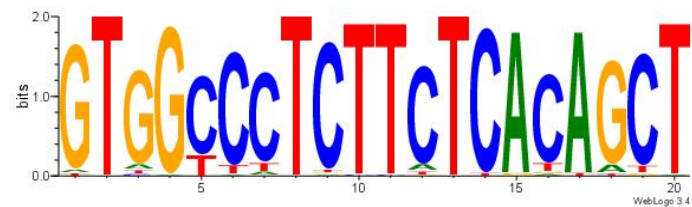
Alignment:

AGCTGTGAGAAGAGGGCCAC
 -----ATAGAGGAGGACC--

Original motif Consensus sequence: AGCTGTGAGAAGAGGGCCAC



Reverse complement motif Consensus sequence: GTGGCCCTCTTCTCACAGCT



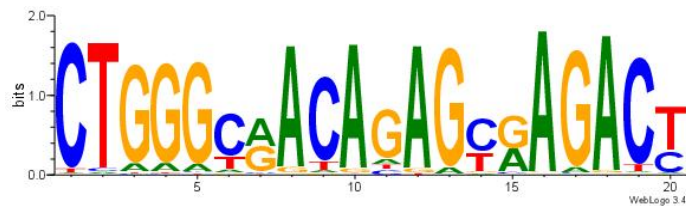
Dataset #: 1
 Motif ID: 29
 Motif name: Motif 29
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 8

Number of overlap: 13
Similarity score: 0.0658365

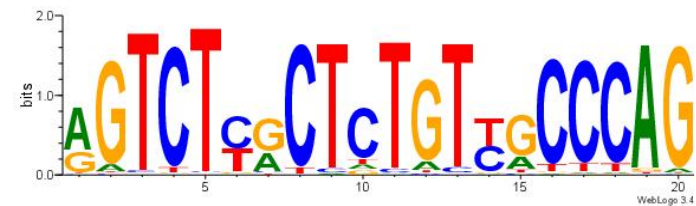
Alignment:

CTGGGCRACAGAGYRAGACY
-----ATAGAGGAGGACC

Original motif Consensus sequence: CTGGGCRACAGAGYRAGACY



Reverse complement motif Consensus sequence:
MGTCTMKCTCTGKGGCCAG



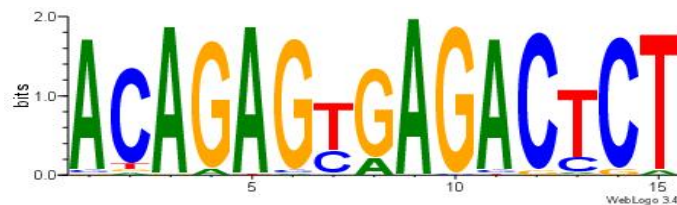
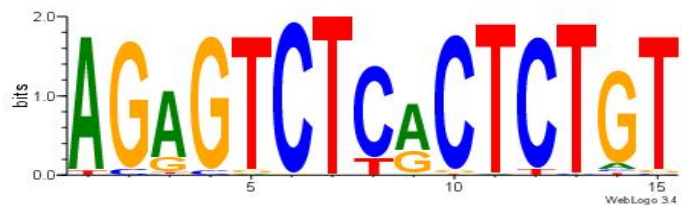
Dataset #: 1
Motif ID: 253
Motif name: Motif 253
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 3
Number of overlap: 13
Similarity score: 0.0707264

Alignment:

AGAGTCTCACTCTGT
GGTCCTCCTCTAT--

Original motif Consensus sequence: AGAGTCTCACTCTGT

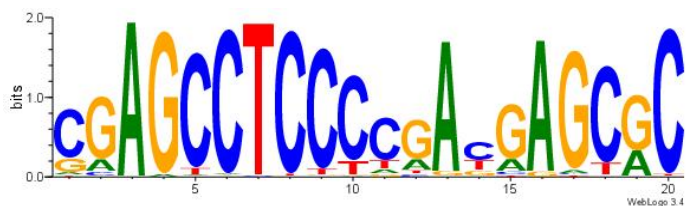
Reverse complement motif Consensus sequence: ACAGAGTGAGACT



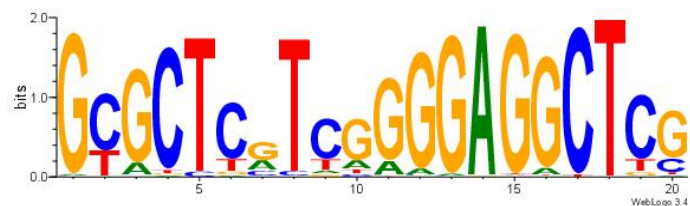
Dataset #: 1
 Motif ID: 108
 Motif name: Motif 108
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 13
 Similarity score: 0.0811499

Alignment:
 GCGCTCKTCGGGGAGGCTCG
 -ATAGAGGAGGACC-----

Original motif Consensus sequence: CGAGCCTCCCGAYGAGCGC

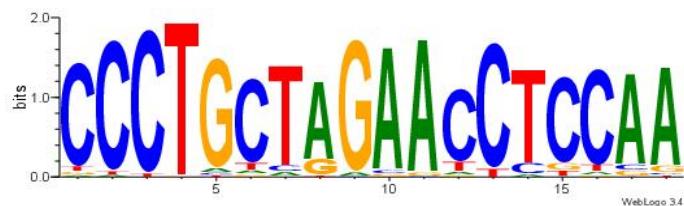


Reverse complement motif Consensus sequence: GCGCTCKTCGGGGAGGCTCG

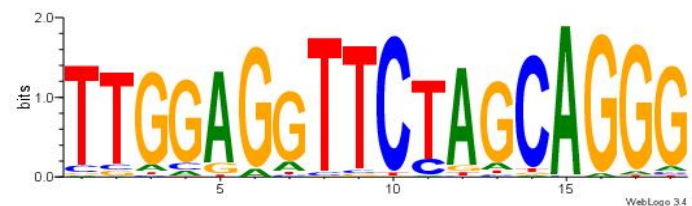


Dataset #: 1 Motif ID: 299 Motif name: Motif 299

Original motif Consensus sequence: CCCTGCTAGAACCTCCAA



Reverse complement motif Consensus sequence: TTGGAGGTTCTAGCAGGG



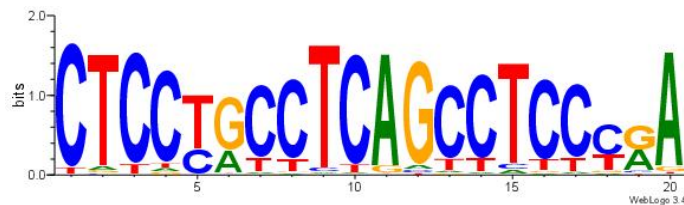
Best Matches for Motif ID 299 (Highest to Lowest)

Dataset #:	1
Motif ID:	26
Motif name:	Motif 26
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	18
Similarity score:	0.0856135

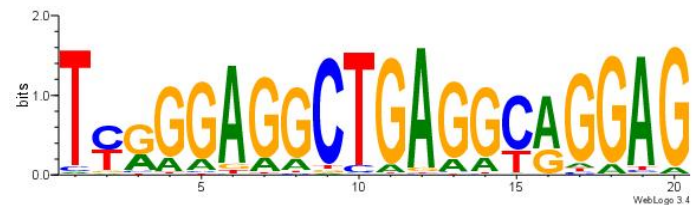
Alignment:

```
CTCCTGCCTCAGCCTCCCRA  
-CCCTGCTAGAACCTCCAA-
```

Original motif Consensus sequence: CTCCTGCCTCAGCCTCCCRA



Reverse complement motif Consensus sequence: TMGGGAGGCTGAGGCAGGAG

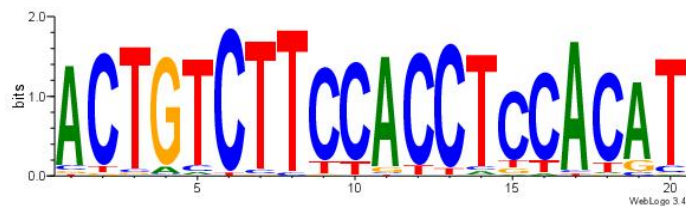


Dataset #: 1
 Motif ID: 178
 Motif name: Motif 178
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 18
 Similarity score: 0.097377

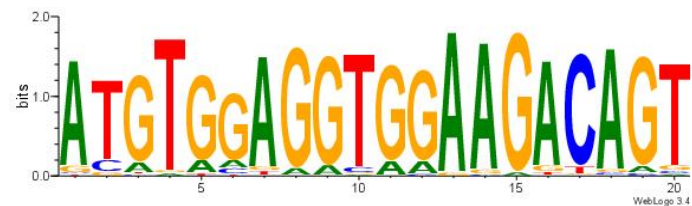
Alignment:

ATGTGGAGGTGGAAGACAGT
 --TTGGAGGTTCTAGCAGGG

Original motif Consensus sequence: ACTGTCTTCCACCTCCACAT



Reverse complement motif Consensus sequence: ATGTGGAGGTGGAAGACAGT



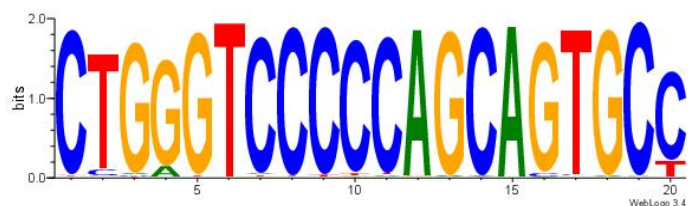
Dataset #: 1
 Motif ID: 84
 Motif name: Motif 84
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward

Position number: 1
Number of overlap: 18
Similarity score: 0.100452

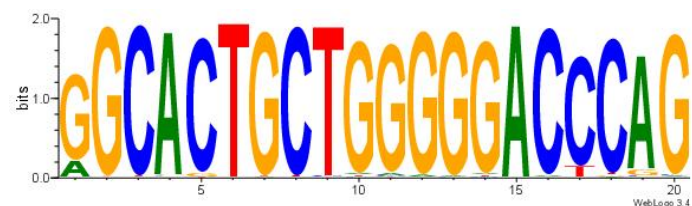
Alignment:

CTGGGTCCCCCAGCAGTGCC
--TTGGAGGTTCTAGCAGGG

Original motif Consensus sequence: CTGGGTCCCCCAGCAGTGCC



Reverse complement motif Consensus sequence: GGCAGTCTGGGGGACCCAG

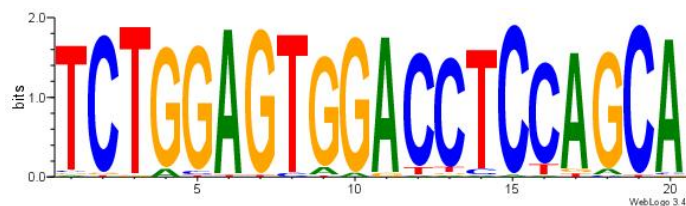


Dataset #: 1
Motif ID: 350
Motif name: Motif 350
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 18
Similarity score: 0.100799

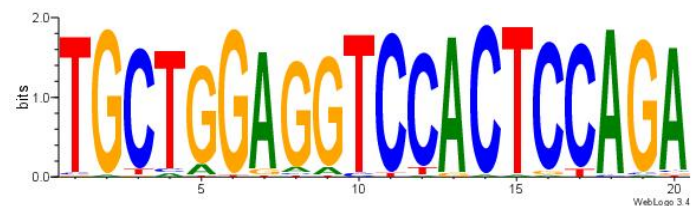
Alignment:

TCTGGAGTGGACCTCCAGCA
CCCTGCTAGAACCTCCAA--

Original motif Consensus sequence: TCTGGAGTGGACCTCCAGCA



Reverse complement motif Consensus sequence: TGCTGGAGGTCCACTCCAGA

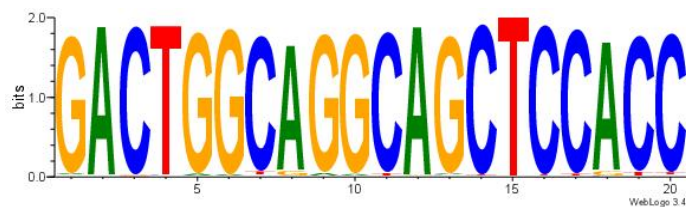


Dataset #: 1
Motif ID: 52
Motif name: Motif 52
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2
Number of overlap: 18
Similarity score: 0.102664

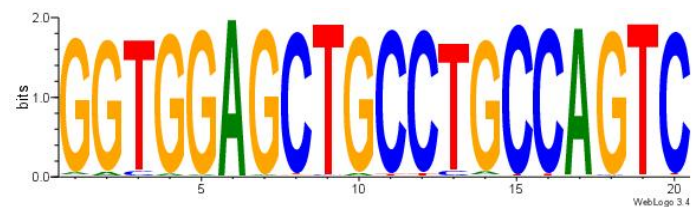
Alignment:

GACTGGCAGGCAGCTCCACC
-CCCTGCTAGAACCTCCAA-

Original motif Consensus sequence: GACTGGCAGGCAGCTCCACC

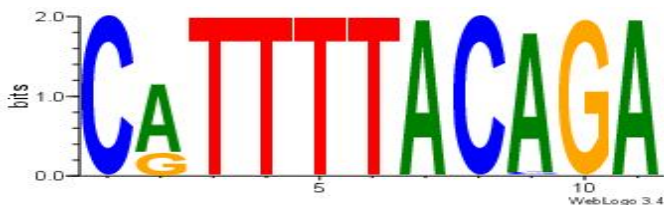


Reverse complement motif Consensus sequence: GGTGGAGCTGCCTGCCAGTC



Dataset #: 1 Motif ID: 300 Motif name: Motif 300

Original motif Consensus sequence: CATTTTACAGA



Reverse complement motif Consensus sequence: TCTGTAAAATG



Best Matches for Motif ID 300 (Highest to Lowest)

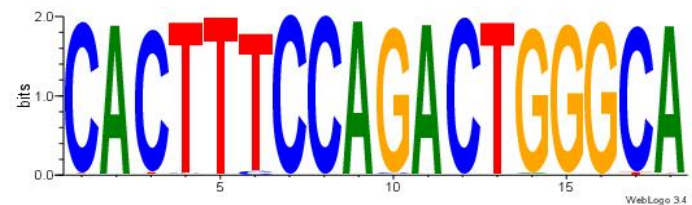
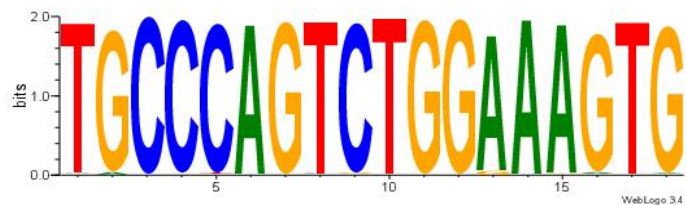
Dataset #:	1
Motif ID:	45
Motif name:	Motif 45
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	11
Similarity score:	0.0501861

Alignment:

```
CACTTTCCAGACTGGGCA  
-----CATTTTACAGA
```

Original motif Consensus sequence: TGCCAGTCTGGAAAGTG

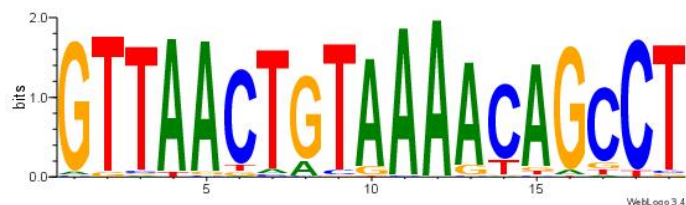
Reverse complement motif Consensus sequence:
CACTTTCCAGACTGGGCA



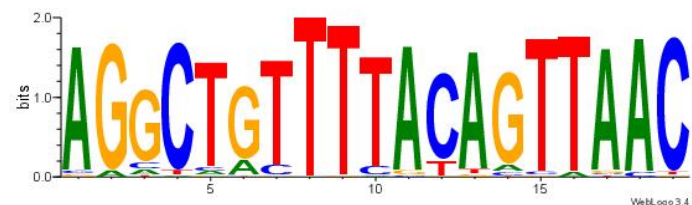
Dataset #: 1
 Motif ID: 233
 Motif name: Motif 233
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 5
 Number of overlap: 11
 Similarity score: 0.071946

Alignment:
 GTTAACTGTAAAACAGCCT
 ----TCTGTAAAATG----

Original motif Consensus sequence: GTTAACTGTAAAACAGCCT



Reverse complement motif Consensus sequence: AGGCTGTTTACAGTTAAC



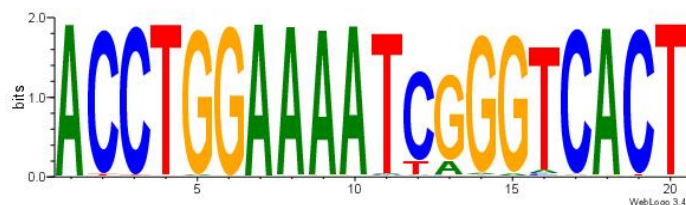
Dataset #: 1

Motif ID: 14
 Motif name: Motif 14
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 9
 Number of overlap: 11
 Similarity score: 0.0723755

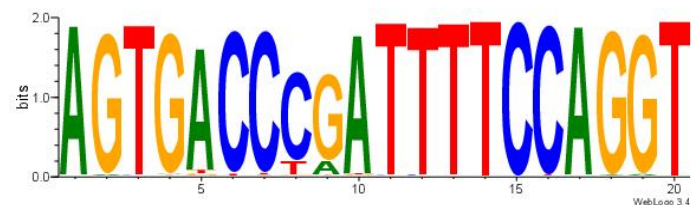
Alignment:

AGTGACCCGATTTTCCAGGT
 -CATTTTACAGA-----

Original motif Consensus sequence: ACCTGGAAAATCGGGTCACT



Reverse complement motif Consensus sequence: AGTGACCCGATTTTCCAGGT



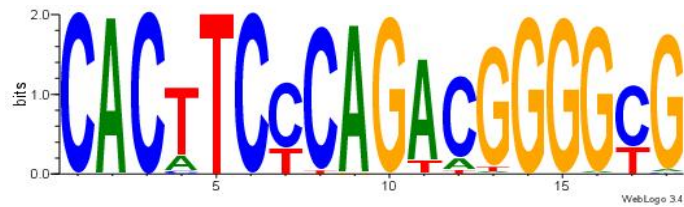
Dataset #: 1
 Motif ID: 27
 Motif name: Motif 27
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 11

Similarity score: 0.0735422

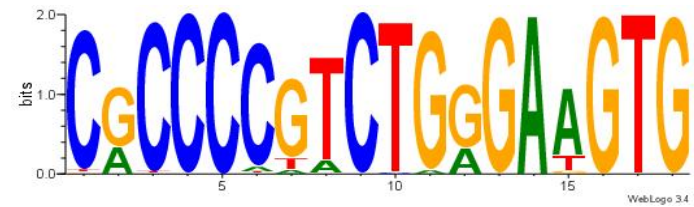
Alignment:

CGCCCCGTCTGGGAAGTG
-----TCTGTAAAATG

Original motif Consensus sequence: CACTTCCCAGACGGGGCG



Reverse complement motif Consensus sequence: CGCCCCGTCTGGGAAGTG



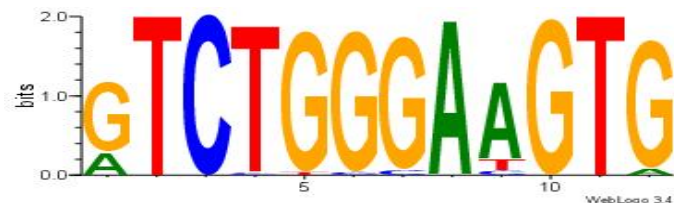
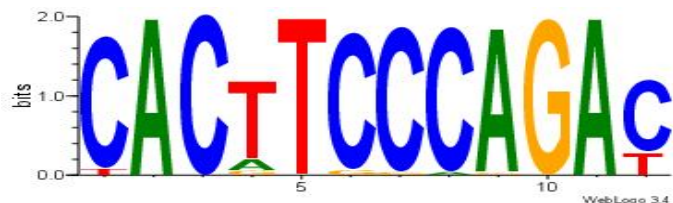
Dataset #: 1
Motif ID: 156
Motif name: Motif 156
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 11
Similarity score: 0.0773708

Alignment:

GTCTGGGAAGTG
-TCTGTAAAATG

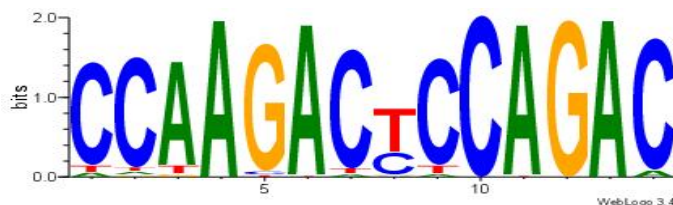
Original motif Consensus sequence: CACTTCCCAGAC

Reverse complement motif Consensus sequence: GTCTGGGAAGTG



Dataset #: 1 Motif ID: 301 Motif name: Motif 301

Original motif Consensus sequence: CCAAGACYCCAGAC



Reverse complement motif Consensus sequence: GTCTGGMGTCCTTG



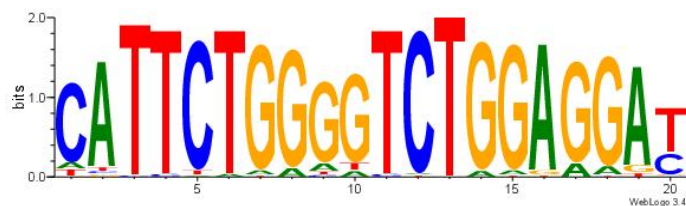
Best Matches for Motif ID 301 (Highest to Lowest)

Dataset #:	1
Motif ID:	309
Motif name:	Motif 309
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	3
Number of overlap:	14
Similarity score:	0.0547706

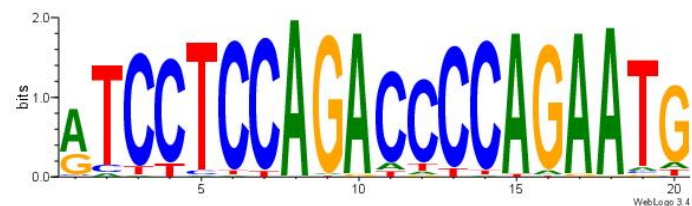
Alignment:

```
MTCCTCCAGACCCCAGAATG
-----CCAAGACYCCAGAC--
```

Original motif Consensus sequence: CATTCTGGGGTCTGGAGGAY



Reverse complement motif Consensus sequence: MTCCTCCAGACCCCAGAATG

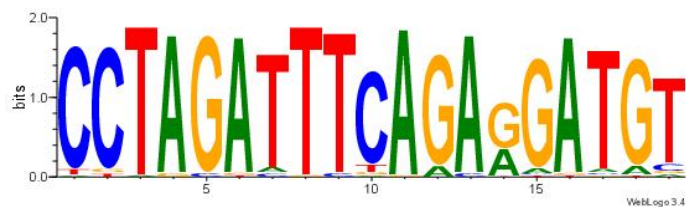


Dataset #: 1
Motif ID: 280
Motif name: Motif 280
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 14
Similarity score: 0.0659934

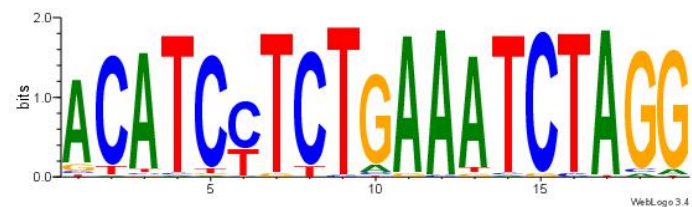
Alignment:

CCTAGATTTTCAGARGATGT
CCAAGACYCCAGAC-----

Original motif Consensus sequence: CCTAGATTTTCAGARGATGT



Reverse complement motif Consensus sequence: ACATCCTCTGAAATCTAGG

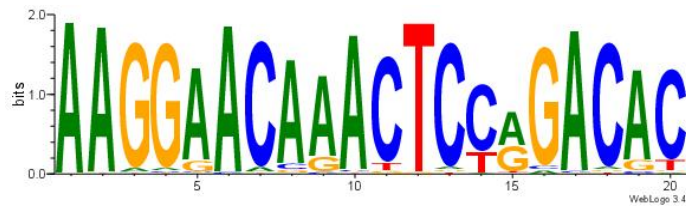


Dataset #: 1
 Motif ID: 234
 Motif name: Motif 234
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3
 Number of overlap: 14
 Similarity score: 0.0768046

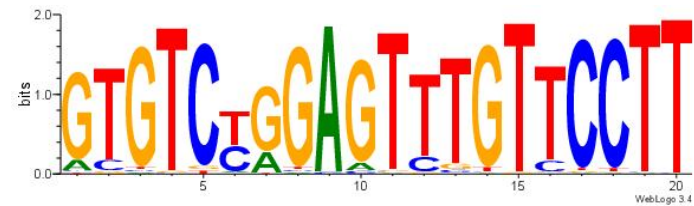
Alignment:

GTGTCKGGAGTTTGTTTCCTT
 --GTCTGGMGTCTTGG-----

Original motif Consensus sequence: AAGGAACAACTCCRGACAC



Reverse complement motif Consensus sequence: GTGTCKGGAGTTTGTTTCCTT



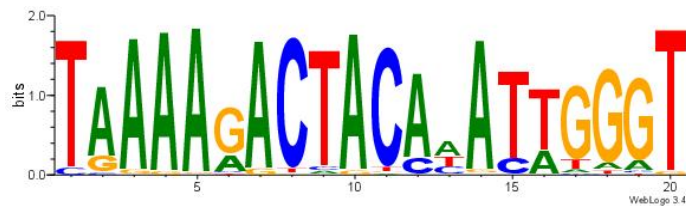
Dataset #: 1
 Motif ID: 195
 Motif name: Motif 195
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 6

Number of overlap: 14
Similarity score: 0.0814768

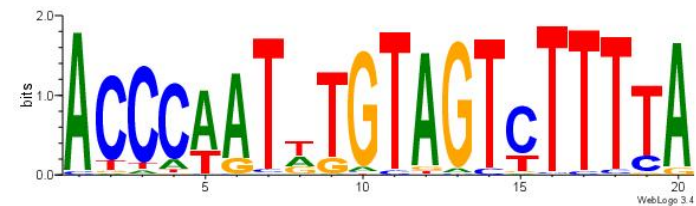
Alignment:

ACCCAATWTGTAGTCTTTTA
-----GTCTGGMGTCTTGG-

Original motif Consensus sequence: TAAAAGACTACAWATTGGGT



Reverse complement motif Consensus sequence:
ACCCAATWTGTAGTCTTTTA

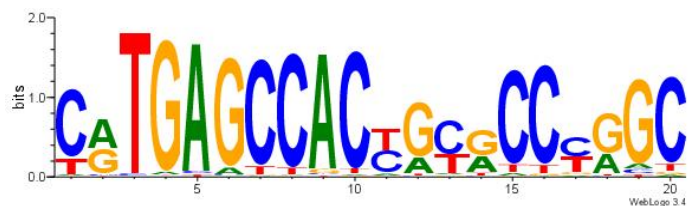


Dataset #: 1
Motif ID: 56
Motif name: Motif 56
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 7
Number of overlap: 14
Similarity score: 0.0823107

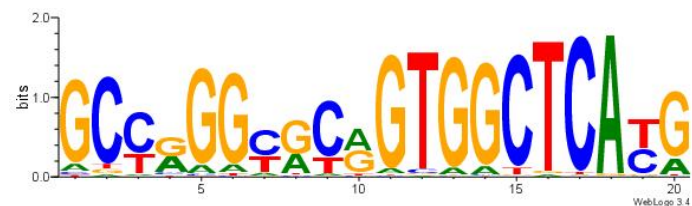
Alignment:

GCCKGGMKCMGTGGCTCAKG
GTCTGGMGTCTTGG-----

Original motif Consensus sequence: CRTGAGCCACYGYRCCYGGC

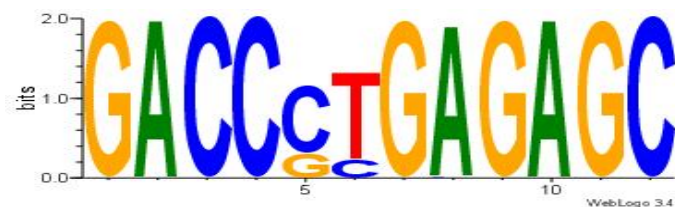


Reverse complement motif Consensus sequence: GCCKGGMKCMGTGGCTCAKG

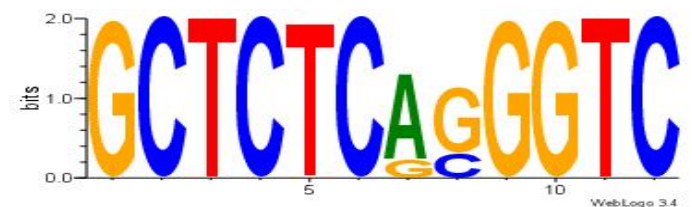


Dataset #: 1 Motif ID: 302 Motif name: Motif 302

Original motif Consensus sequence: GACCCTGAGAGC



Reverse complement motif Consensus sequence: GCTCTCAGGGTC



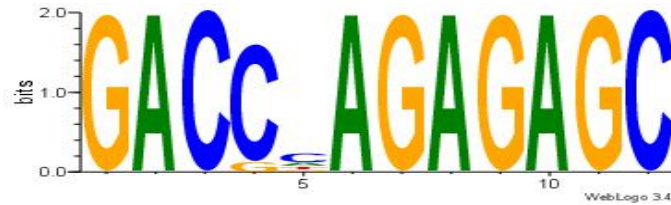
Best Matches for Motif ID 302 (Highest to Lowest)

Dataset #:	1
Motif ID:	340
Motif name:	Motif 340
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	12
Similarity score:	0.0268873

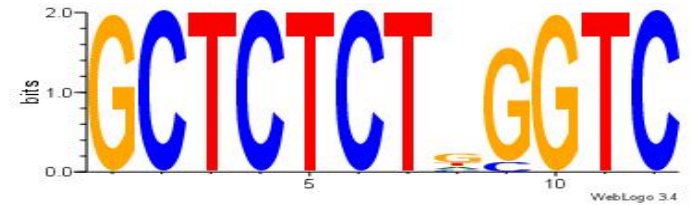
Alignment:

GACCCAGAGAGC
GACCCTGAGAGC

Original motif Consensus sequence: GACCCAGAGAGC



Reverse complement motif Consensus sequence: GCTCTCTGGGTC

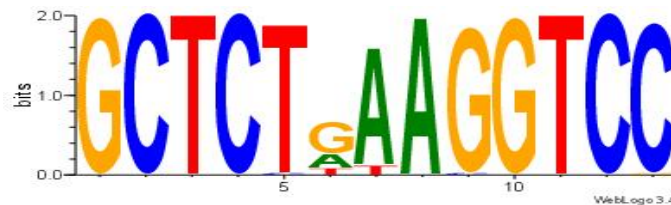


Dataset #: 1
Motif ID: 362
Motif name: Motif 362
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 12
Similarity score: 0.0423209

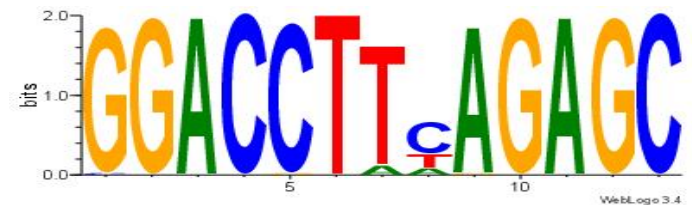
Alignment:

GGACCTTCAGAGC
-GACCCTGAGAGC

Original motif Consensus sequence: GCTCTGAAGGTCC



Reverse complement motif Consensus sequence: GGACCTTCAGAGC

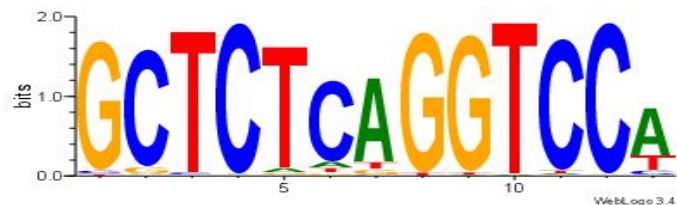


Dataset #: 1
Motif ID: 323
Motif name: Motif 323
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2
Number of overlap: 12
Similarity score: 0.0548786

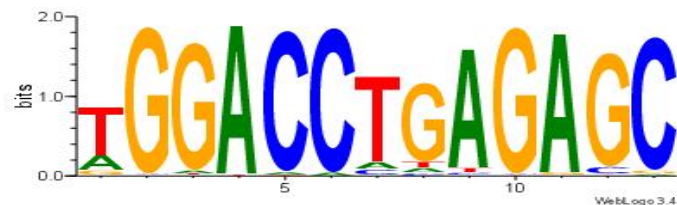
Alignment:

GCTCTCAGGTCCA
GCTCTCAGGGTC-

Original motif Consensus sequence: GCTCTCAGGTCCA



Reverse complement motif Consensus sequence: TGGACCTGAGAGC

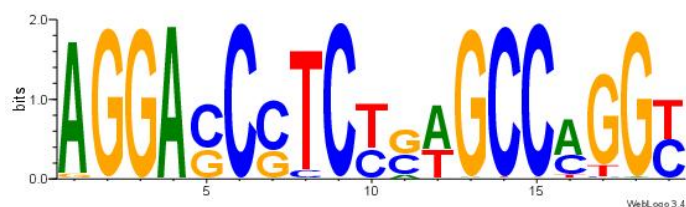


Dataset #: 1
Motif ID: 10
Motif name: Motif 10
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 3

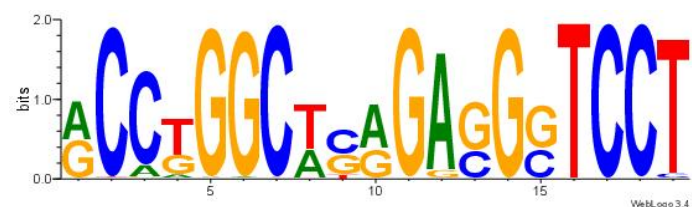
Number of overlap: 12
Similarity score: 0.0701639

Alignment:
AGGASCSTCYSWGCCMGY
--GACCCTGAGAGC-----

Original motif Consensus sequence: AGGASCSTCYSWGCCMGY



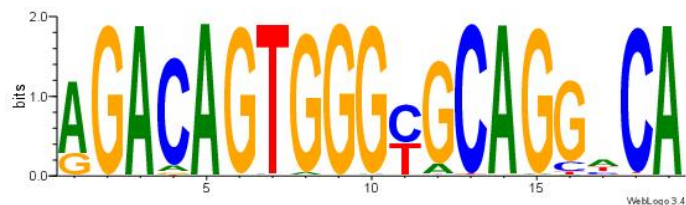
Reverse complement motif Consensus sequence:
MCCYGGCWSMGASGSTCCT



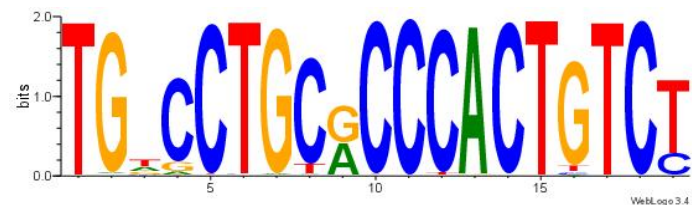
Dataset #: 1
Motif ID: 17
Motif name: Motif 17
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 2
Number of overlap: 12
Similarity score: 0.0731393

Alignment:
TGHCCCTGCKCCCCTGTCT
-----GCTCTCAGGGTC-

Original motif Consensus sequence: AGACAGTGGGYGCAGGHCA

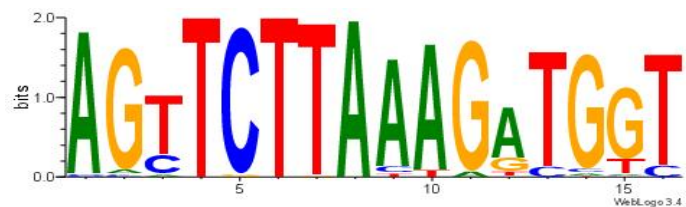


Reverse complement motif Consensus sequence: TGHCCTGCKCCCACTGTCT

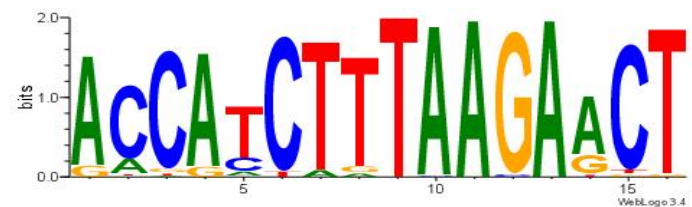


Dataset #: 1 Motif ID: 303 Motif name: Motif 303

Original motif Consensus sequence: AGTTCTTAAAGATGGT



Reverse complement motif Consensus sequence: ACCATCTTTAAGAACT



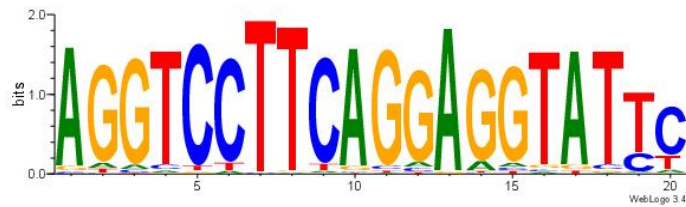
Best Matches for Motif ID 303 (Highest to Lowest)

Dataset #:	1
Motif ID:	179
Motif name:	Motif 179
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	5
Number of overlap:	16
Similarity score:	0.0731282

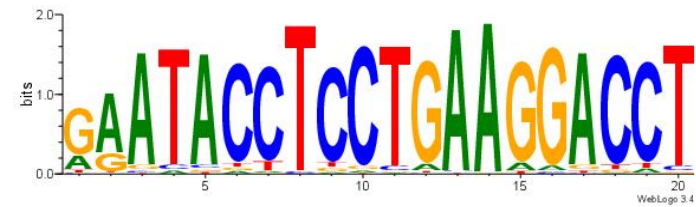
Alignment:

GAATACCTCCTGAAGGACCT
----ACCATCTTTAAGAACT

Original motif Consensus sequence: AGGTCCTTCAGGAGGTATTC



Reverse complement motif Consensus sequence:
GAATACCTCCTGAAGGACCT



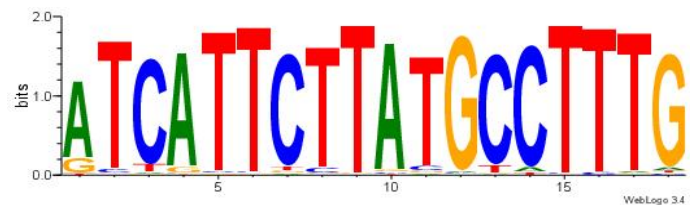
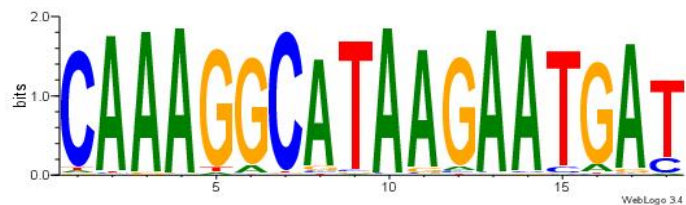
Dataset #: 1
Motif ID: 190
Motif name: Motif 190
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 3
Number of overlap: 16
Similarity score: 0.0867922

Alignment:

ATCATTCTTATGCCTTTG
ACCATCTTTAAGAACT--

Original motif Consensus sequence: CAAAGGCATAAGAATGAT

Reverse complement motif Consensus sequence:
ATCATTCTTATGCCTTTG

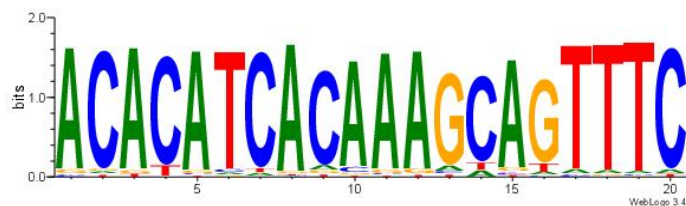


Dataset #: 1
 Motif ID: 202
 Motif name: Motif 202
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 16
 Similarity score: 0.0876942

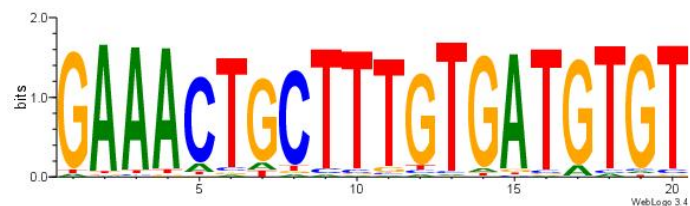
Alignment:

GAAACTGCTTTGTGATGTGT
 --ACCATCTTTAAGAACT--

Original motif Consensus sequence: ACACATCACAAAGCAGTTTC



Reverse complement motif Consensus sequence: GAAACTGCTTTGTGATGTGT



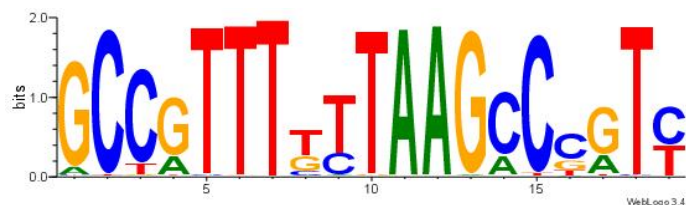
Dataset #: 1

Motif ID: 21
 Motif name: Motif 21
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 16
 Similarity score: 0.0880938

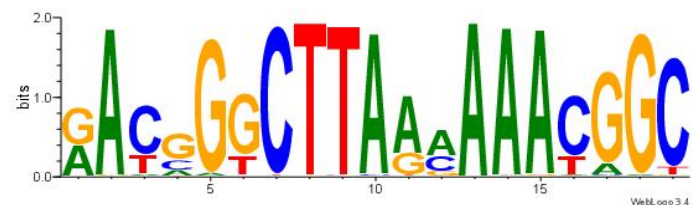
Alignment:

KACGGGCTTAARAAACGGC
 -ACCATCTTTAAGAACT--

Original motif Consensus sequence: GCCGTTTKTTAAGCCCGTY



Reverse complement motif Consensus sequence: KACGGGCTTAARAAACGGC



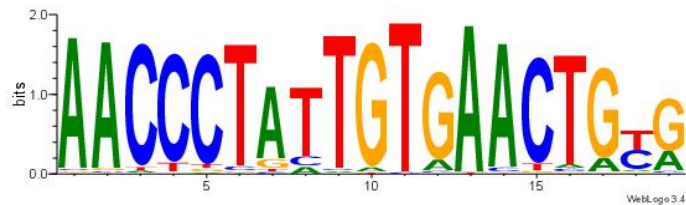
Dataset #: 1
 Motif ID: 242
 Motif name: Motif 242
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 16

Similarity score: 0.088173

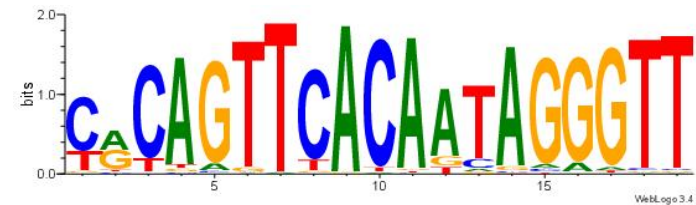
Alignment:

AACCCTATTGTGAACTGYG
---ACCATCTTTAAGAACT

Original motif Consensus sequence: AACCCTATTGTGAACTGYG

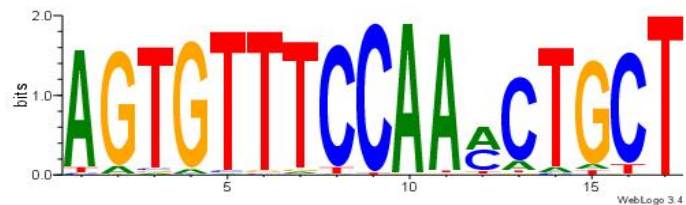


Reverse complement motif Consensus sequence: CMCAGTTCACAATAGGGTT

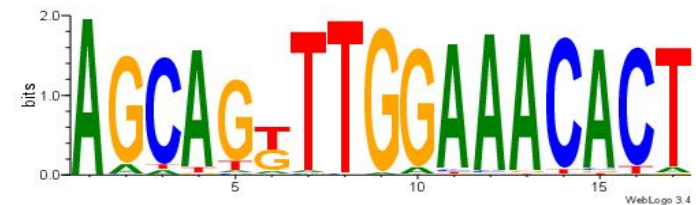


Dataset #: 1 Motif ID: 304 Motif name: Motif 304

Original motif Consensus sequence: AGTGTTTCCAAMCTGCT



Reverse complement motif Consensus sequence: AGCAGTTGGAAACACT



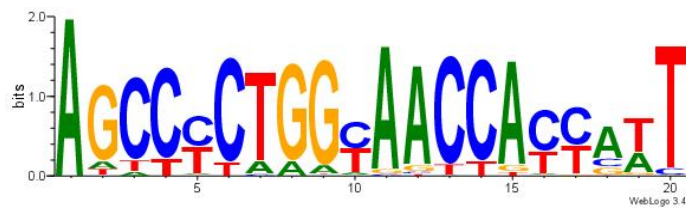
Best Matches for Motif ID 304 (Highest to Lowest)

Dataset #:	1
Motif ID:	139
Motif name:	Motif 139
Matching format of first motif:	Original Motif

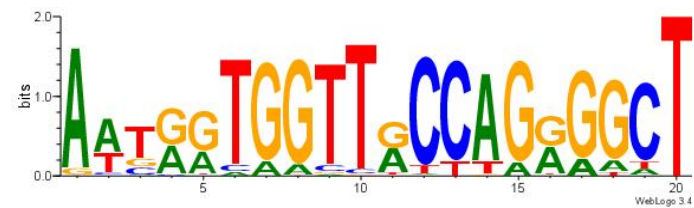
Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 17
 Similarity score: 0.0916595

Alignment:
 AWTKKTGGTTKCCAGKGGCT
 AGTGTTCCTCAAMCTGCT---

Original motif Consensus sequence: AGCCYCTGGYAACCAYYAWT



Reverse complement motif Consensus sequence:
 AWTKKTGGTTKCCAGKGGCT

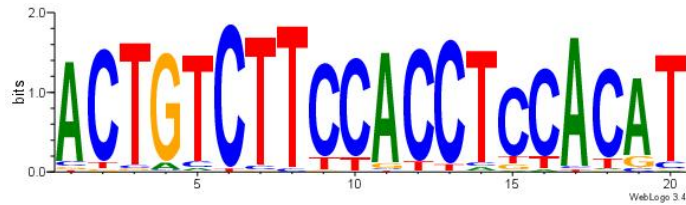


Dataset #: 1
 Motif ID: 178
 Motif name: Motif 178
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 4
 Number of overlap: 17
 Similarity score: 0.0916702

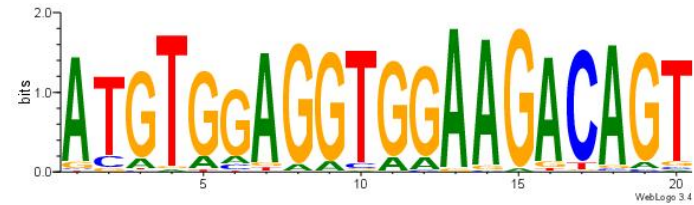
Alignment:

ACTGTCTTCCACCTCCACAT
AGTGTTTCCAAMCTGCT---

Original motif Consensus sequence: ACTGTCTTCCACCTCCACAT



Reverse complement motif Consensus sequence:
ATGTGGAGGTGGAAGACAGT

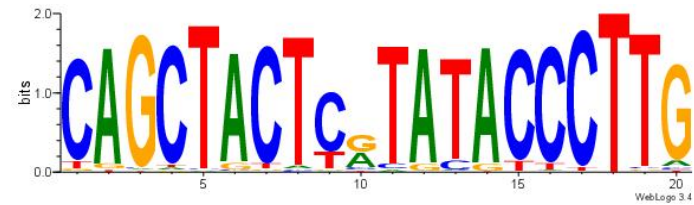
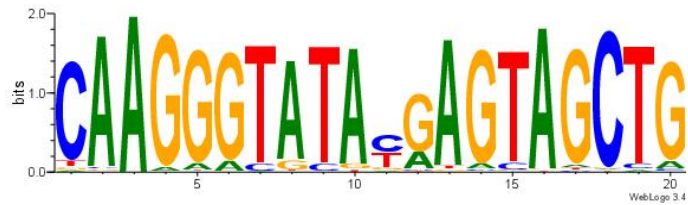


Dataset #: 1
Motif ID: 194
Motif name: Motif 194
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 3
Number of overlap: 17
Similarity score: 0.095632

Alignment:
CAGCTACTCKTATACCCTTG
-AGCAGYTTGGAAACACT--

Original motif Consensus sequence: CAAGGGTATAYGAGTAGCTG

Reverse complement motif Consensus sequence:
CAGCTACTCKTATACCCTTG

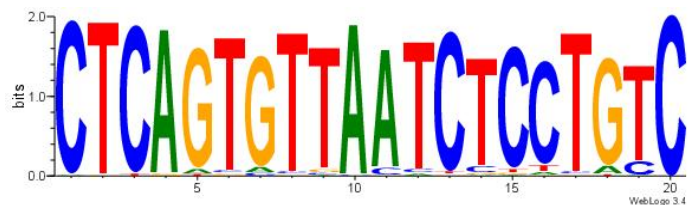


Dataset #: 1
 Motif ID: 262
 Motif name: Motif 262
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 17
 Similarity score: 0.102026

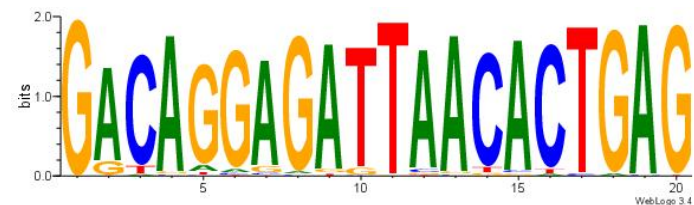
Alignment:

CTCAGTGTTAATCTCCTGTC
 ---AGTGTTTCCAAMCTGCT

Original motif Consensus sequence: CTCAGTGTTAATCTCCTGTC



Reverse complement motif Consensus sequence: GACAGGAGATTAACACTGAG



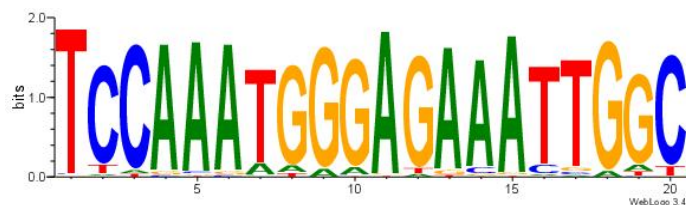
Dataset #: 1

Motif ID: 235
 Motif name: Motif 235
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 4
 Number of overlap: 17
 Similarity score: 0.107468

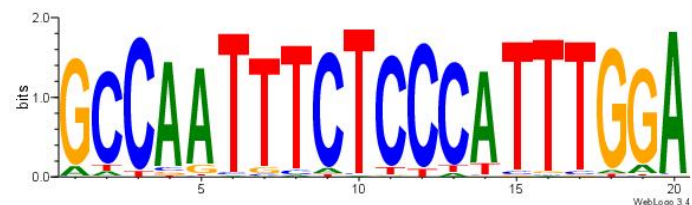
Alignment:

GCCAATTTCTCCCATTGGA
 AGTGTTTCCAAMCTGCT---

Original motif Consensus sequence: TCCAATGGGAGAAATTGGC

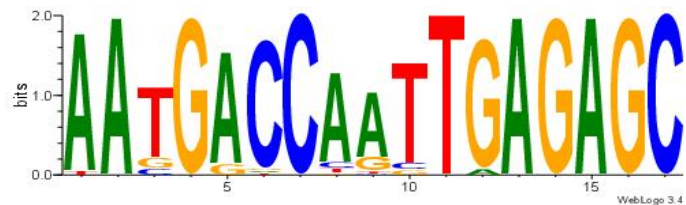


Reverse complement motif Consensus sequence: GCCAATTTCTCCCATTGGA



Dataset #: 1 Motif ID: 305 Motif name: Motif 305

Original motif Consensus sequence: AATGACCAATTGAGAGC



Reverse complement motif Consensus sequence: GCTCTCAATTGGTCATT



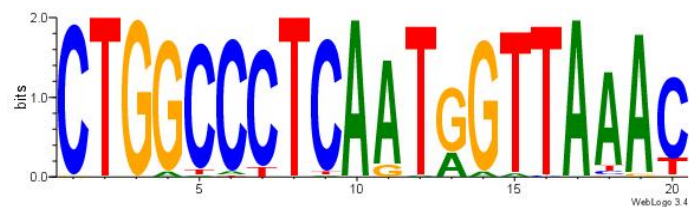
Best Matches for Motif ID 305 (Highest to Lowest)

Dataset #: 1
Motif ID: 332
Motif name: Motif 332
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 4
Number of overlap: 17
Similarity score: 0.0848872

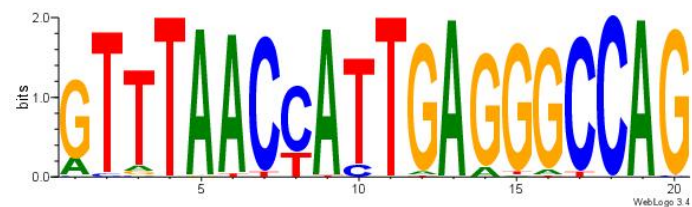
Alignment:

```
GTTTAACCATTGAGGGCCAG  
AATGACCAATTGAGAGC---
```

Original motif Consensus sequence: CTGGCCCTCAATGGTTAAAC



Reverse complement motif Consensus sequence: GTTTAACCATTGAGGGCCAG



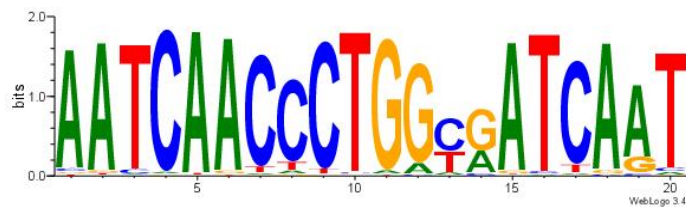
Dataset #: 1
Motif ID: 170
Motif name: Motif 170
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement

Direction: Backward
 Position number: 1
 Number of overlap: 17
 Similarity score: 0.0979755

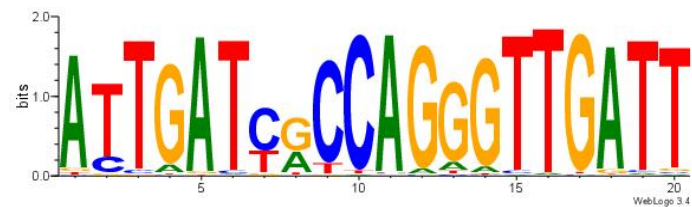
Alignment:

ATTGATMKCCAGGGTTGATT
 ---GCTCTCAATTGGTCATT

Original motif Consensus sequence: AATCAACCCTGGYRATCAAT



Reverse complement motif Consensus sequence: ATTGATMKCCAGGGTTGATT

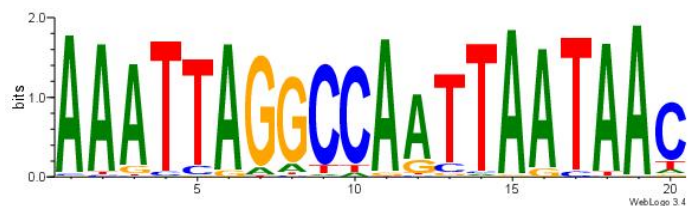


Dataset #: 1
 Motif ID: 308
 Motif name: Motif 308
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 17
 Similarity score: 0.101217

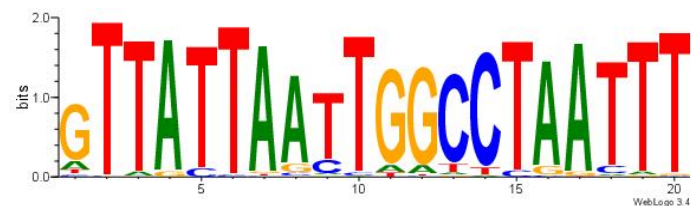
Alignment:

AAATTAGGCCAATTAATAAC
 ---AATGACCAATTGAGAGC

Original motif Consensus sequence: AAATTAGGCCAATTAATAAC



Reverse complement motif Consensus sequence: GTTATTAATTGGCCTAATTT

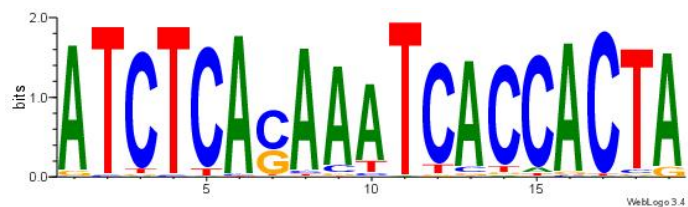


Dataset #: 1
Motif ID: 261
Motif name: Motif 261
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2
Number of overlap: 17
Similarity score: 0.103313

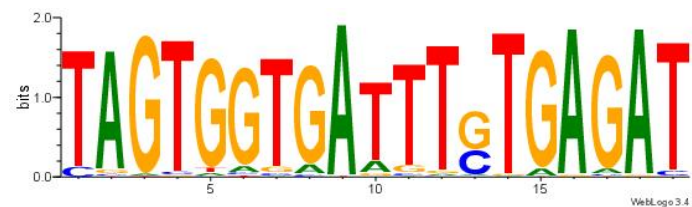
Alignment:

ATCTCASAAATCACCCTA
-GCTCTCAATTGGTCATT-

Original motif Consensus sequence: ATCTCASAAATCACCCTA



Reverse complement motif Consensus sequence: TAGTGGTGAATTTGAGAT

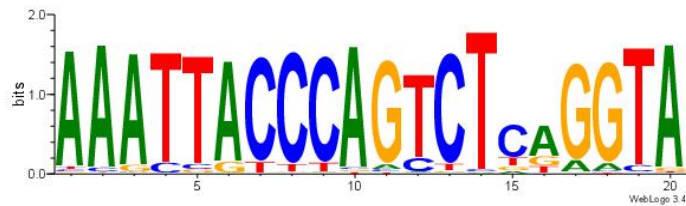


Dataset #: 1
 Motif ID: 160
 Motif name: Motif 160
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 17
 Similarity score: 0.106625

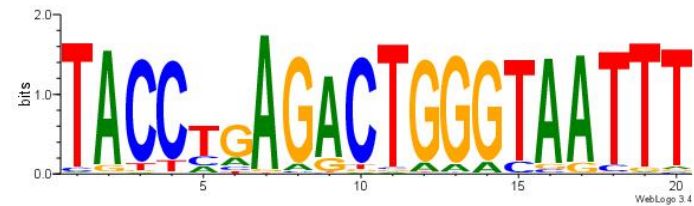
Alignment:

TACCTGAGACTGGGTAATTT
 --GCTCTCAATTGGTCATT-

Original motif Consensus sequence: AAATTACCCAGTCTCAGGTA



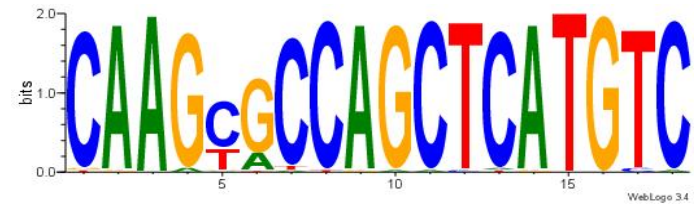
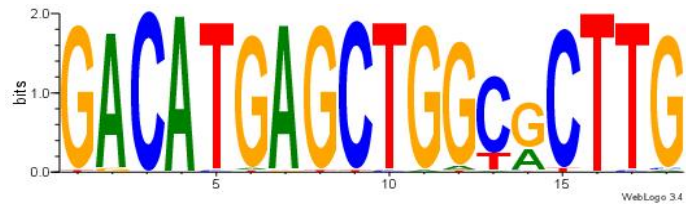
Reverse complement motif Consensus sequence: TACCTGAGACTGGGTAATTT



Dataset #: 1 Motif ID: 306 Motif name: Motif 306

Original motif Consensus sequence: GACATGAGCTGGCGCTTG

Reverse complement motif Consensus sequence: CAAGCGCCAGCTCATGTC

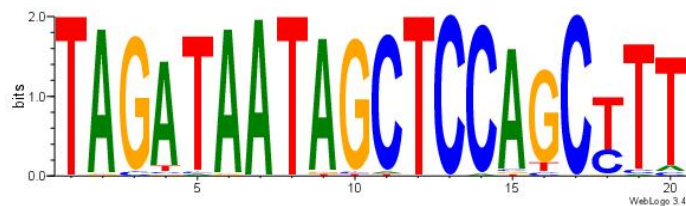


Best Matches for Motif ID 306 (Highest to Lowest)

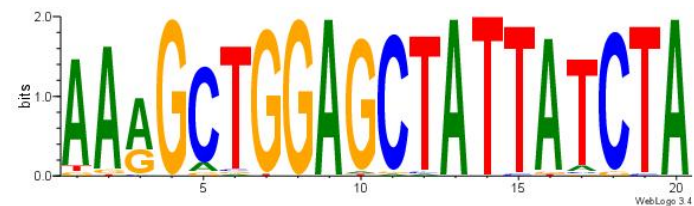
Dataset #: 1
 Motif ID: 333
 Motif name: Motif 333
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 18
 Similarity score: 0.102628

Alignment:
 AAAGCTGGAGCTATTATCTA
 CAAGCGCCAGCTCATGTC--

Original motif Consensus sequence: TAGATAATAGCTCCAGCTTT



Reverse complement motif Consensus sequence: AAAGCTGGAGCTATTATCTA

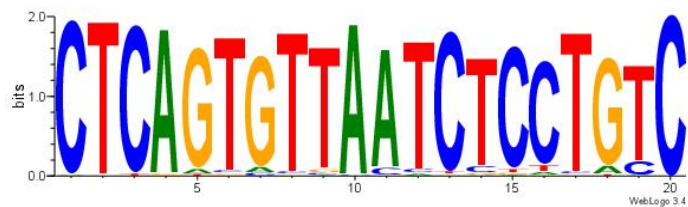


Dataset #: 1
 Motif ID: 262
 Motif name: Motif 262
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3
 Number of overlap: 18
 Similarity score: 0.107908

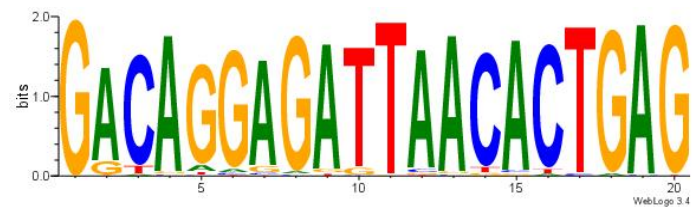
Alignment:

GACAGGAGATTAACACTGAG
 --GACATGAGCTGGCGCTTG

Original motif Consensus sequence: CTCAGTGTTAATCTCCTGTC



Reverse complement motif Consensus sequence: GACAGGAGATTAACACTGAG



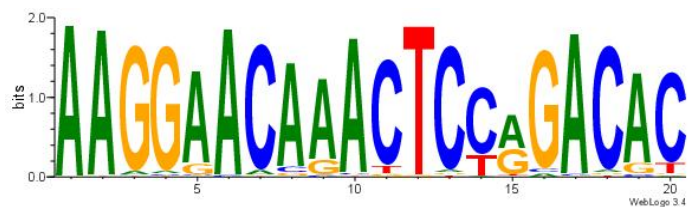
Dataset #: 1
 Motif ID: 234
 Motif name: Motif 234
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3

Number of overlap: 18
Similarity score: 0.118321

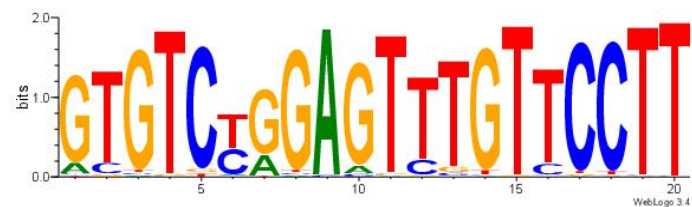
Alignment:

AAGGAACAAACTCCRGACAC
--CAAGCGCCAGCTCATGTC

Original motif Consensus sequence: AAGGAACAAACTCCRGACAC



Reverse complement motif Consensus sequence:
GTGTCKGGAGTTTGTTCCTT

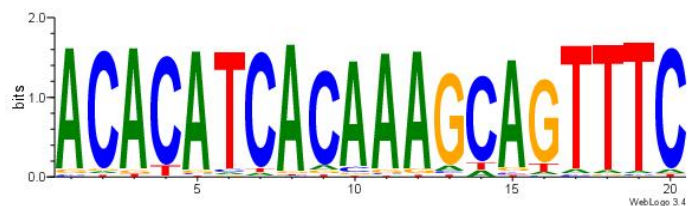


Dataset #: 1
Motif ID: 202
Motif name: Motif 202
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 2
Number of overlap: 18
Similarity score: 0.118931

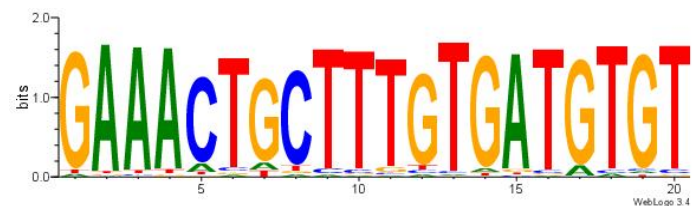
Alignment:

ACACATCACAAAGCAGTTTC
-GACATGAGCTGGCGCTTG-

Original motif Consensus sequence: ACACATCACAAGCAGTTTC



Reverse complement motif Consensus sequence: GAAACTGCTTTGTGATGTGT

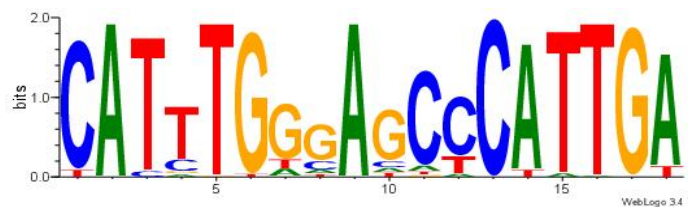


Dataset #: 1
Motif ID: 284
Motif name: Motif 284
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 18
Similarity score: 0.119654

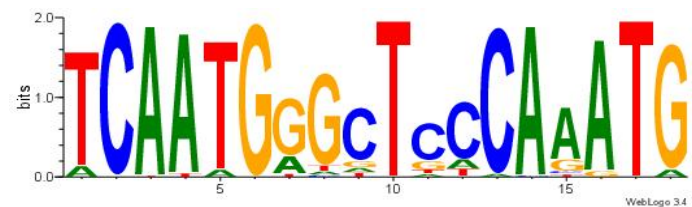
Alignment:

CATTTGGGAGCCCATTGA
CAAGCGCCAGCTCATGTC

Original motif Consensus sequence: CATTTGGGAGCCCATTGA

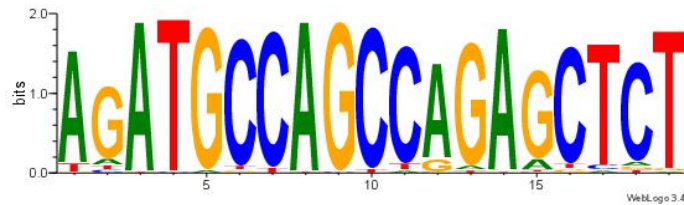


Reverse complement motif Consensus sequence: TCAATGGGCTCCCAAATG

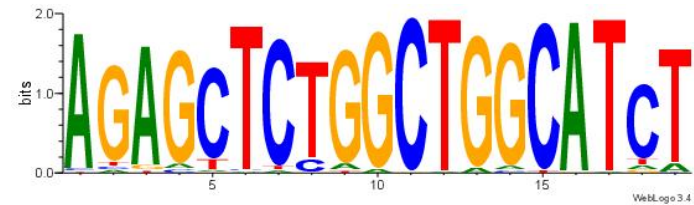


Dataset #: 1 Motif ID: 307 Motif name: Motif 307

Original motif Consensus sequence: AGATGCCAGCCAGAGCTCT



Reverse complement motif Consensus sequence: AGAGCTCTGGCTGGCATCT



Best Matches for Motif ID 307 (Highest to Lowest)

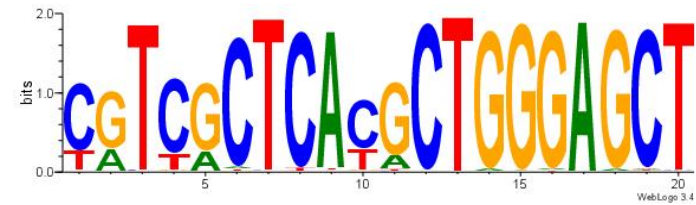
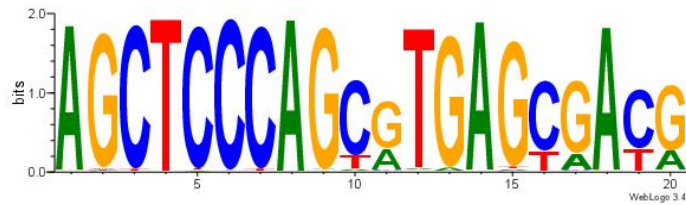
Dataset #:	1
Motif ID:	48
Motif name:	Motif 48
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	19
Similarity score:	0.0871974

Alignment:

```
AGCTCCCAGCGTGAGCGACG  
AGATGCCAGCCAGAGCTCT-
```

Original motif Consensus sequence: AGCTCCCAGCGTGAGCGACG

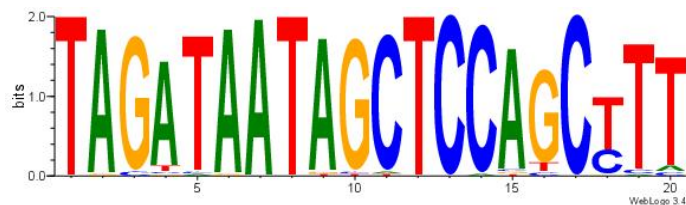
Reverse complement motif Consensus sequence: CGTCGCTCAGCTGGGAGCT



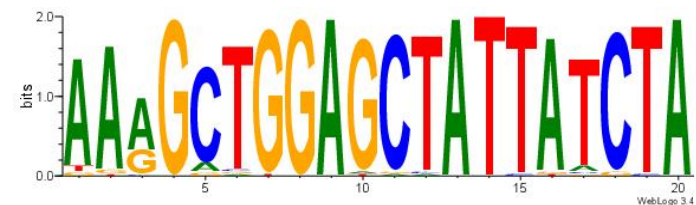
Dataset #: 1
 Motif ID: 333
 Motif name: Motif 333
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 19
 Similarity score: 0.0921664

Alignment:
 AAAGCTGGAGCTATTATCTA
 AGAGCTCTGGCTGGCATCT-

Original motif Consensus sequence: TAGATAATAGCTCCAGCTTT



Reverse complement motif Consensus sequence: AAAGCTGGAGCTATTATCTA



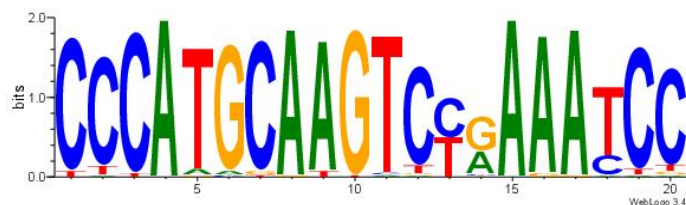
Dataset #: 1

Motif ID: 310
 Motif name: Motif 310
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 19
 Similarity score: 0.0945368

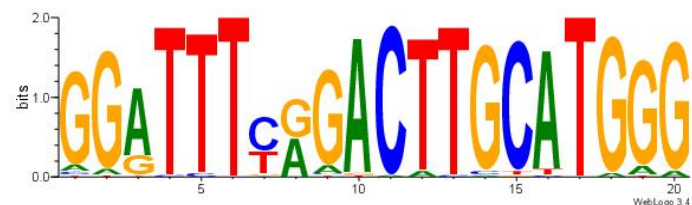
Alignment:

GGATTTMKGACTTGCATGGG
 AGAGCTCTGGCTGGCATCT-

Original motif Consensus sequence: CCCATGCAAGTCYRAAATCC



Reverse complement motif Consensus sequence: GGATTTMKGACTTGCATGGG



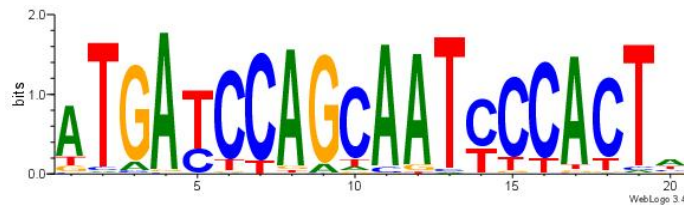
Dataset #: 1
 Motif ID: 115
 Motif name: Motif 115
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 19

Similarity score: 0.107882

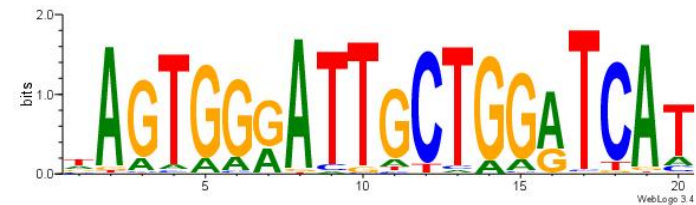
Alignment:

HAGTGGKATTGCTGGATCAT
-AGAGCTCTGGCTGGCATCT

Original motif Consensus sequence: ATGATCCAGCAATYCCACTH



Reverse complement motif Consensus sequence:
HAGTGGKATTGCTGGATCAT



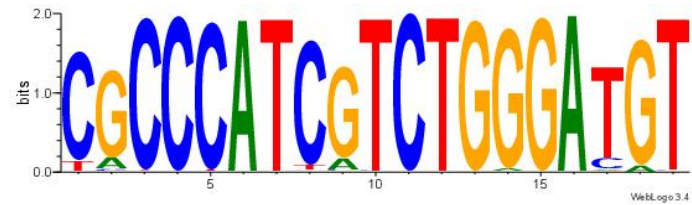
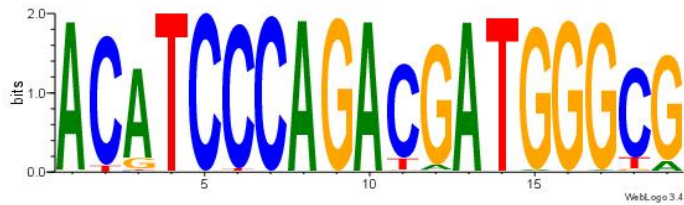
Dataset #: 1
Motif ID: 36
Motif name: Motif 36
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 19
Similarity score: 0.112048

Alignment:

ACATCCCAGACGATGGGCG
AGATGCCAGCCAGAGCTCT

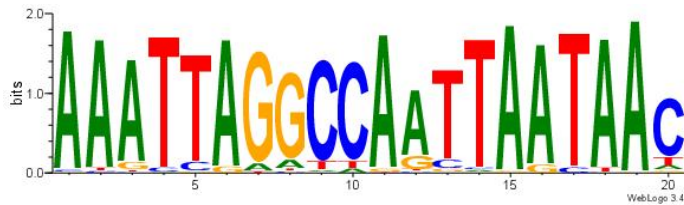
Original motif Consensus sequence: ACATCCCAGACGATGGGCG

Reverse complement motif Consensus sequence:
CGCCATCGTCTGGGATGT



Dataset #: 1 Motif ID: 308 Motif name: Motif 308

Original motif Consensus sequence: AAATTAGGCCAATTAATAAC



Reverse complement motif Consensus sequence: GTTATTAATTGGCCTAATTT



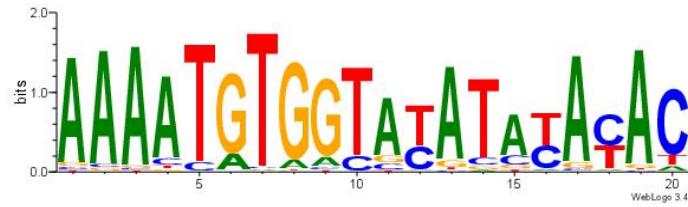
Best Matches for Motif ID 308 (Highest to Lowest)

Dataset #:	1
Motif ID:	83
Motif name:	Motif 83
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	20
Similarity score:	0.109629

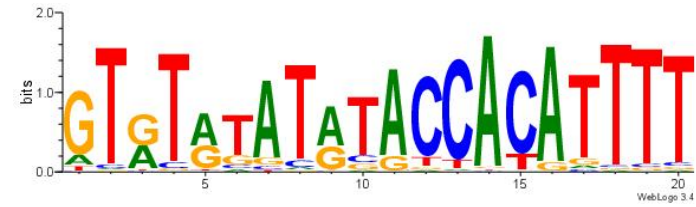
Alignment:

GTKTMTATMTACCACATTTT
GTTATTAATTGGCCTAATTT

Original motif Consensus sequence: AAAATGTGGTAYATAYAYAC



Reverse complement motif Consensus sequence:
GTKTMTATMTACCACATTTT



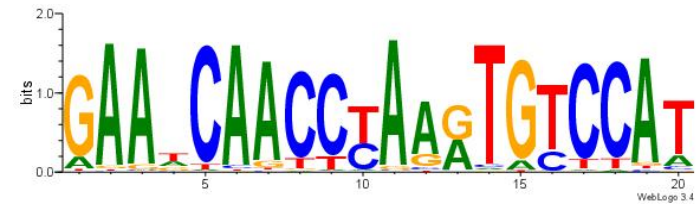
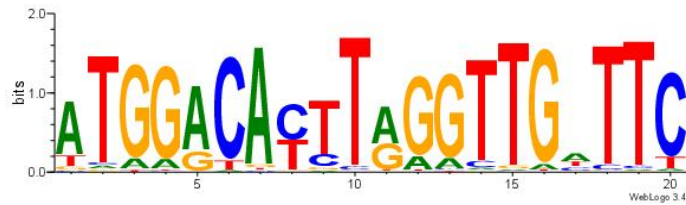
Dataset #: 1
Motif ID: 58
Motif name: Motif 58
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 20
Similarity score: 0.116375

Alignment:

GAAHCAACCKAAKTGTCCAT
AAATTAGGCCAATTAATAAC

Original motif Consensus sequence: ATGGACAYTTRGGTTGHTTC

Reverse complement motif Consensus sequence:
GAAHCAACCKAAKTGTCCAT

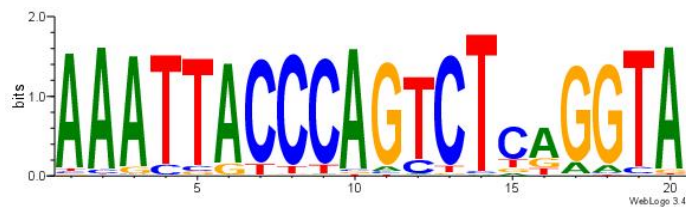


Dataset #: 1
 Motif ID: 160
 Motif name: Motif 160
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.118957

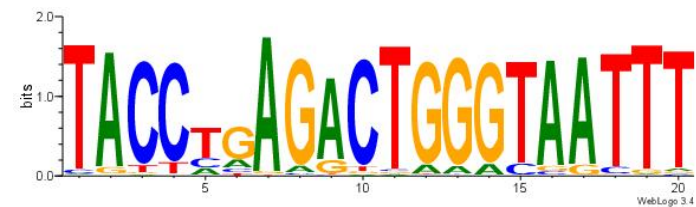
Alignment:

TACCTGAGACTGGGTAATTT
 GTTATTAATTGGCCTAATTT

Original motif Consensus sequence: AAATTACCCAGTCTCA GGTA



Reverse complement motif Consensus sequence: TACCTGAGACTGGGTAATTT



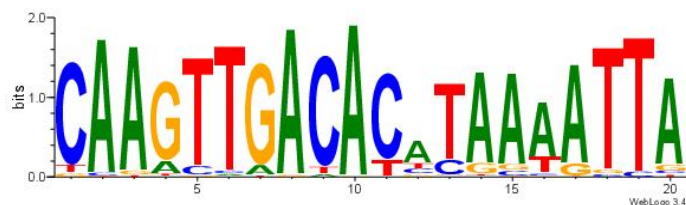
Dataset #: 1

Motif ID: 357
 Motif name: Motif 357
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.121938

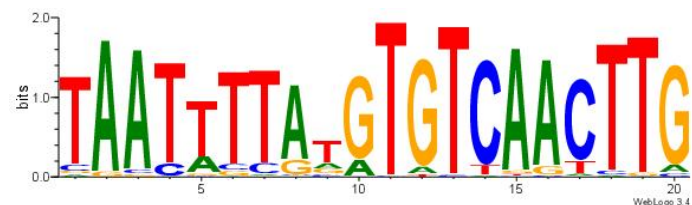
Alignment:

TAATTTTATGTGTCAACTTG
 GTTATTAATTGGCCTAATTT

Original motif Consensus sequence: CAAGTTGACACATAAAATTA



Reverse complement motif Consensus sequence: TAATTTTATGTGTCAACTTG



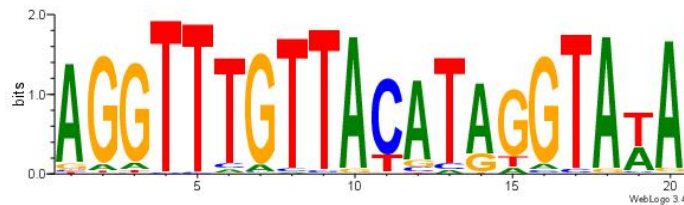
Dataset #: 1
 Motif ID: 137
 Motif name: Motif 137
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 20

Similarity score: 0.124013

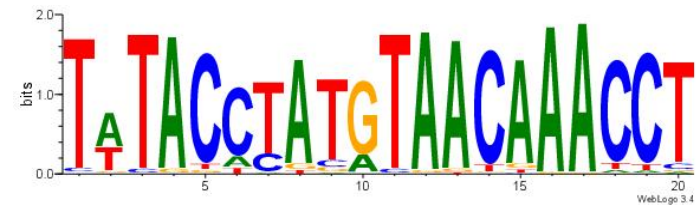
Alignment:

TWTACCTATGTAACAAACCT
GTTATTAATTGGCCTAATTT

Original motif Consensus sequence: AGGTTTGTTACATAGGTAWA

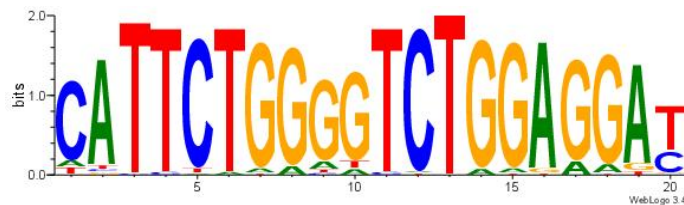


Reverse complement motif Consensus sequence:
TWTACCTATGTAACAAACCT

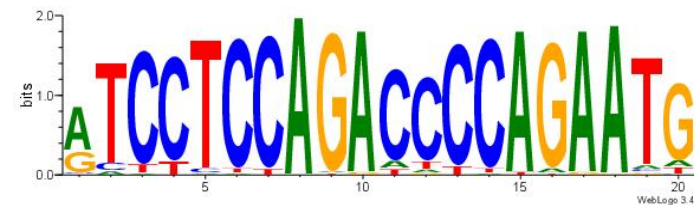


Dataset #: 1 Motif ID: 309 Motif name: Motif 309

Original motif Consensus sequence: CATTCTGGGGTCTGGAGGAY



Reverse complement motif Consensus sequence:
MTCCTCCAGACCCAGAAATG



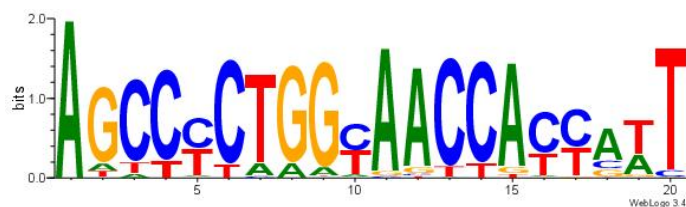
Best Matches for Motif ID 309 (Highest to Lowest)

Dataset #:	1
Motif ID:	139
Motif name:	Motif 139
Matching format of first motif:	Reverse Complement

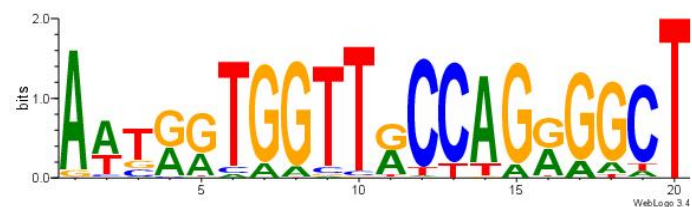
Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.116685

Alignment:
 AGCCYCTGGYAACCAYYAWT
 MTCCTCCAGACCCCAGAATG

Original motif Consensus sequence: AGCCYCTGGYAACCAYYAWT



Reverse complement motif Consensus sequence:
 AWTKKTGGTTKCCAGKGGCT

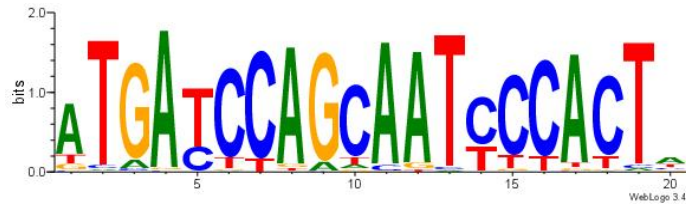


Dataset #: 1
 Motif ID: 115
 Motif name: Motif 115
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.118752

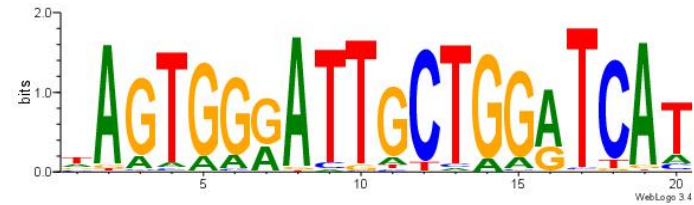
Alignment:

ATGATCCAGCAATYCCACTH
MTCCTCCAGACCCCAGAATG

Original motif Consensus sequence: ATGATCCAGCAATYCCACTH



Reverse complement motif Consensus sequence:
HAGTGGKATTGCTGGATCAT

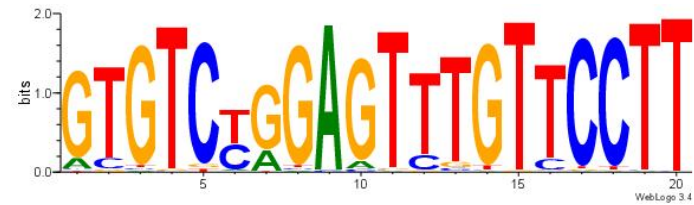
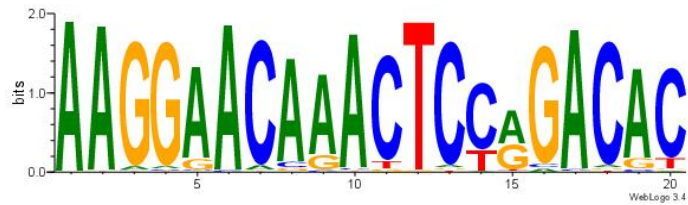


Dataset #: 1
Motif ID: 234
Motif name: Motif 234
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 20
Similarity score: 0.122145

Alignment:
GTGTCKGGAGTTTGTTCCTT
CATTCTGGGGTCTGGAGGAY

Original motif Consensus sequence: AAGGAACAACTCCRGACAC

Reverse complement motif Consensus sequence:
GTGTCKGGAGTTTGTTCCTT

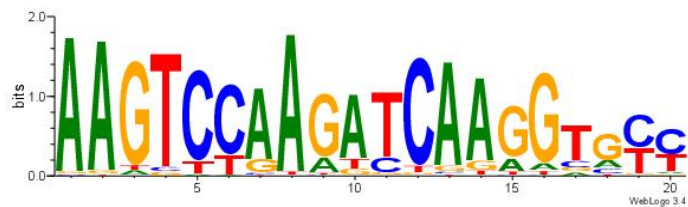


Dataset #: 1
 Motif ID: 119
 Motif name: Motif 119
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.126441

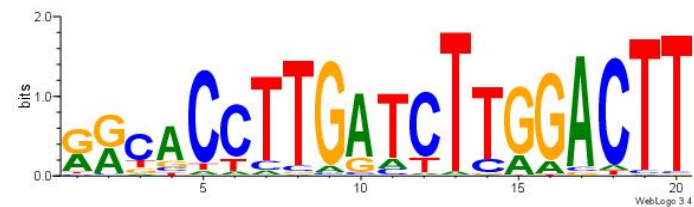
Alignment:

AAGTCCAAGATCAAGGTGYY
 CATTCTGGGGTCTGGAGGAY

Original motif Consensus sequence: AAGTCCAAGATCAAGGTGYY



Reverse complement motif Consensus sequence: KKCACCTTGATCTTGGACTT



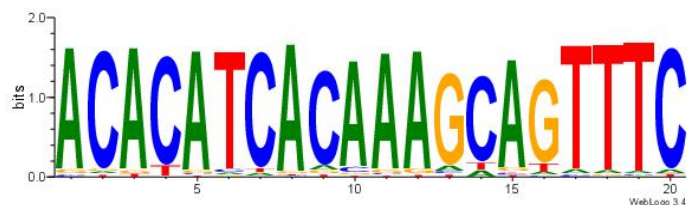
Dataset #: 1

Motif ID: 202
 Motif name: Motif 202
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.127396

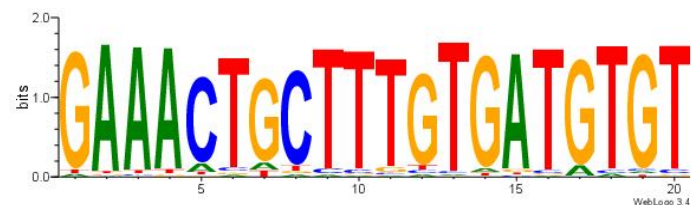
Alignment:

ACACATCACAAAGCAGTTTC
 MTCCTCCAGACCCCAGAATG

Original motif Consensus sequence: ACACATCACAAAGCAGTTTC

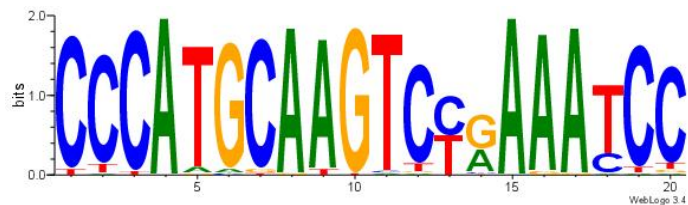


Reverse complement motif Consensus sequence: GAAACTGCTTTGTGATGTGT

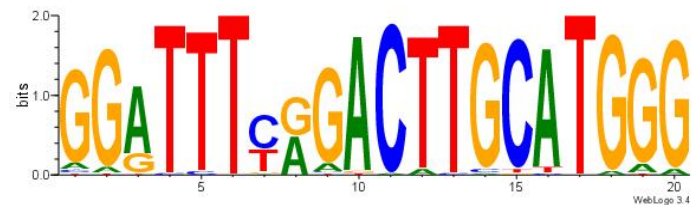


Dataset #: 1 Motif ID: 310 Motif name: Motif 310

Original motif Consensus sequence: CCCATGCAAGTC_CG_AAAA_CTCC



Reverse complement motif Consensus sequence: GGATTTMKGACTTGCATGGG



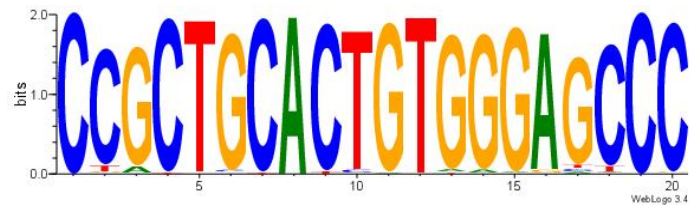
Best Matches for Motif ID 310 (Highest to Lowest)

Dataset #: 1
Motif ID: 144
Motif name: Motif 144
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 20
Similarity score: 0.119136

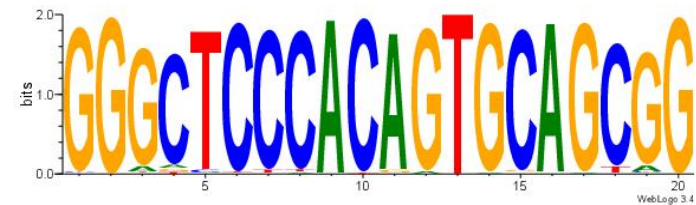
Alignment:

```
CCGCTGCACTGTGGGAGCCC  
CCCATGCAAGTCYRAAATCC
```

Original motif Consensus sequence: CCGCTGCACTGTGGGAGCCC



Reverse complement motif Consensus sequence: GGGCTCCCACAGTGCAGCGG



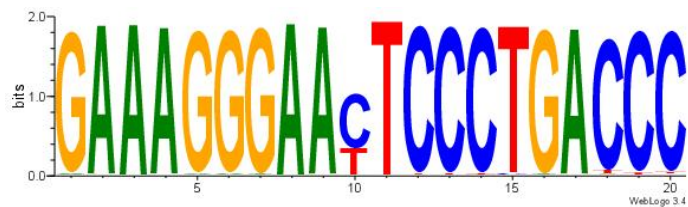
Dataset #: 1
Motif ID: 16
Motif name: Motif 16
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif

Direction: Forward
Position number: 1
Number of overlap: 20
Similarity score: 0.119991

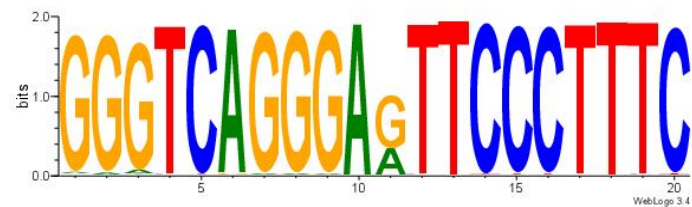
Alignment:

GAAAGGGA ACTCCCTGACCC
CCCATGCAAGTCYRAAATCC

Original motif Consensus sequence: GAAAGGGA ACTCCCTGACCC



Reverse complement motif Consensus sequence: GGGTCAGGGA GTTCCCTTTC

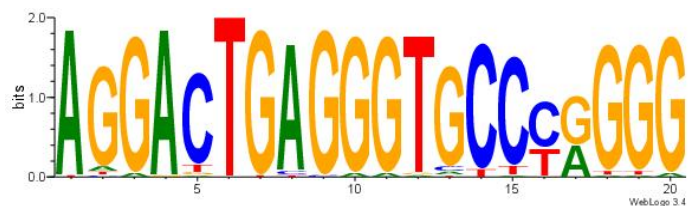


Dataset #: 1
Motif ID: 312
Motif name: Motif 312
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 20
Similarity score: 0.121495

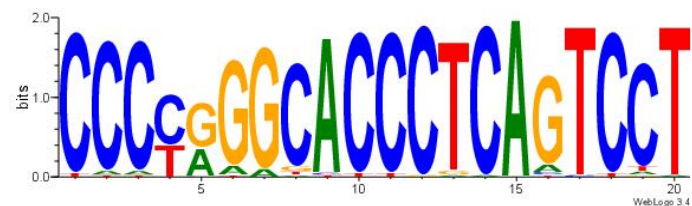
Alignment:

CCCMKGGCACCTCAGTCCT
CCCATGCAAGTCYRAAATCC

Original motif Consensus sequence: AGGACTGAGGGTGCCYRGGG



Reverse complement motif Consensus sequence: CCCMKGGCACCCTCAGTCCT

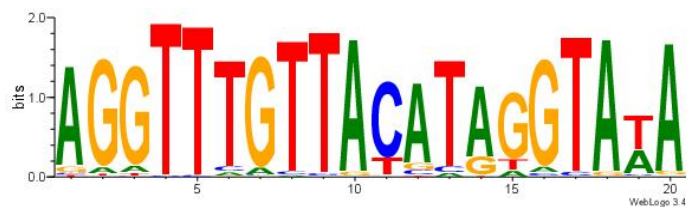


Dataset #: 1
Motif ID: 137
Motif name: Motif 137
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 20
Similarity score: 0.128302

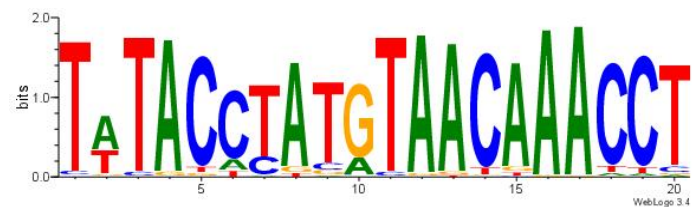
Alignment:

TWTACCTATGTAACAAACCT
CCCATGCAAGTCYRAAATCC

Original motif Consensus sequence: AGGTTTGTACATAGGTAA



Reverse complement motif Consensus sequence: TWTACCTATGTAACAAACCT

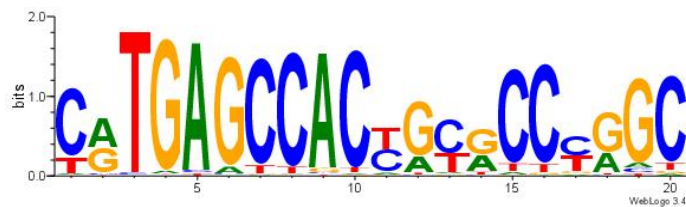


Dataset #: 1
 Motif ID: 56
 Motif name: Motif 56
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.128336

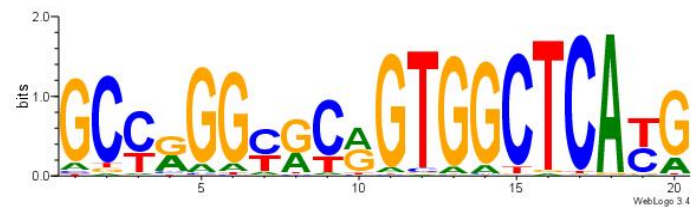
Alignment:

GCCKGGMKCMGTGGCTCAKG
 GGATTTMKGACTTGCATGGG

Original motif Consensus sequence: CRTGAGCCACYGYRCCYGGC



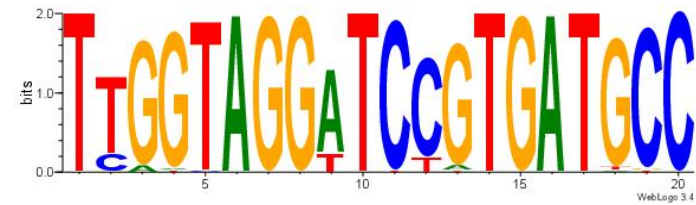
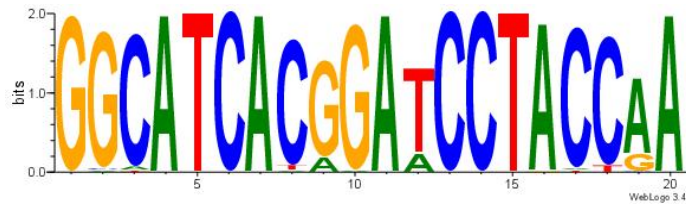
Reverse complement motif Consensus sequence: GCCKGGMKCMGTGGCTCAKG



Dataset #: 1 Motif ID: 311 Motif name: Motif 311

Original motif Consensus sequence: GGCATCACGGATCCTACCAA

Reverse complement motif Consensus sequence: TTGGTAGGATCCGTGATGCC

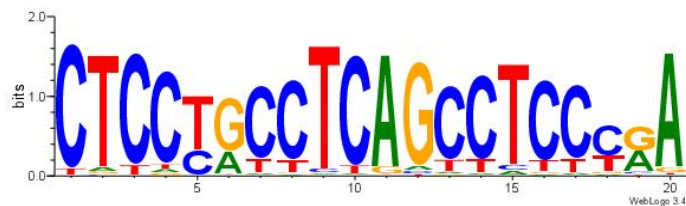


Best Matches for Motif ID 311 (Highest to Lowest)

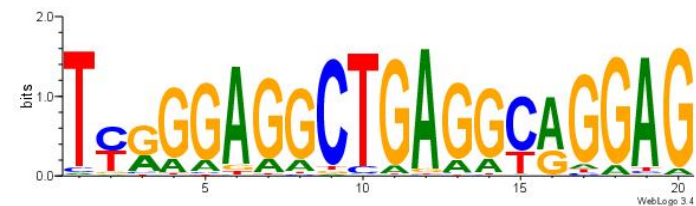
Dataset #: 1
 Motif ID: 26
 Motif name: Motif 26
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.129928

Alignment:
 CTCCTGCCTCAGCCTCCCRA
 GGCATCACGGATCCTACCAA

Original motif Consensus sequence: CTCCTGCCTCAGCCTCCCRA



Reverse complement motif Consensus sequence: TMGGGAGGCTGAGGCAGGAG

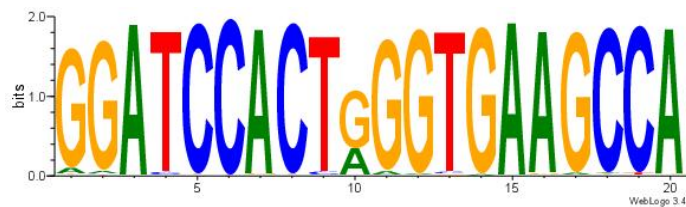


Dataset #: 1
 Motif ID: 61
 Motif name: Motif 61
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.134094

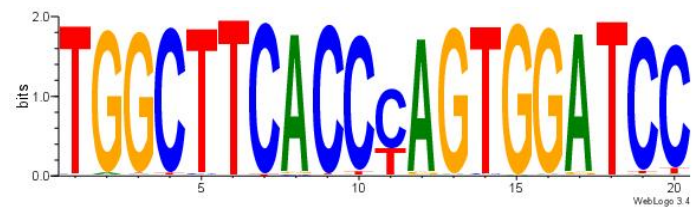
Alignment:

TGGCTTCACCCAGTGGATCC
 TTGGTAGGATCCGTGATGCC

Original motif Consensus sequence: GGATCCACTGGGTGAAGCCA



Reverse complement motif Consensus sequence: TGGCTTCACCCAGTGGATCC



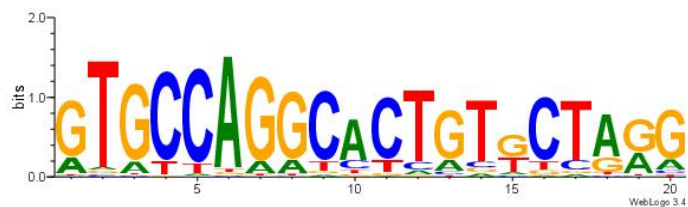
Dataset #: 1
 Motif ID: 76
 Motif name: Motif 76
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1

Number of overlap: 20
Similarity score: 0.134531

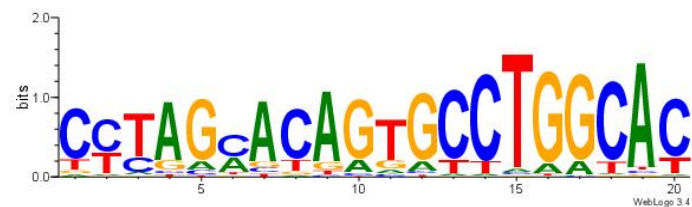
Alignment:

GTGCCAGGCACTGTKCTARG
TTGGTAGGATCCGTGATGCC

Original motif Consensus sequence: GTGCCAGGCACTGTKCTARG



Reverse complement motif Consensus sequence: CMTAGYACAGTGCTGGCAC

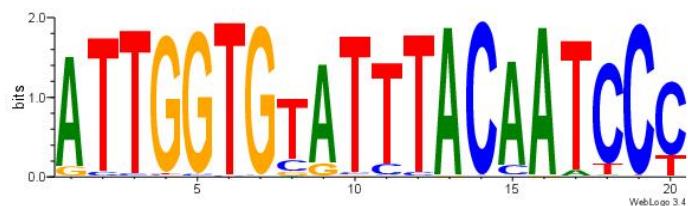


Dataset #: 1
Motif ID: 106
Motif name: Motif 106
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 20
Similarity score: 0.136164

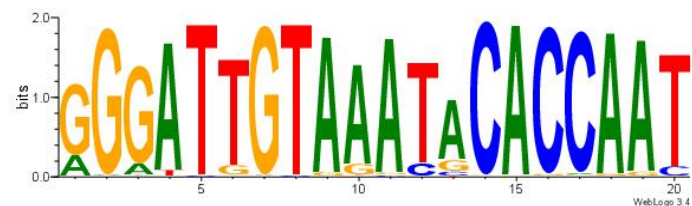
Alignment:

ATTGGTGTATTTACAATCCC
TTGGTAGGATCCGTGATGCC

Original motif Consensus sequence: ATTGGTGTATTACAATCCC



Reverse complement motif Consensus sequence: GGGATTGTAAATACACCAAT

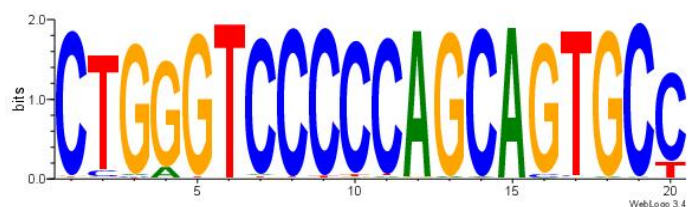


Dataset #: 1
Motif ID: 84
Motif name: Motif 84
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 20
Similarity score: 0.137635

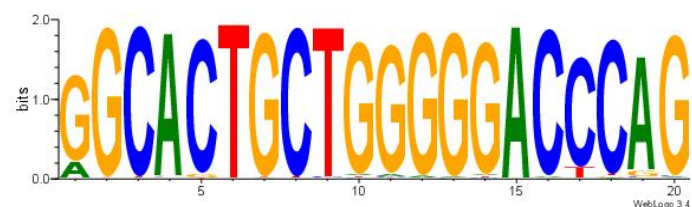
Alignment:

GGCACTGCTGGGGGACCCAG
GGCATCACGGATCCTACCAA

Original motif Consensus sequence: CTGGGTCCCCCAGCAGTGCC

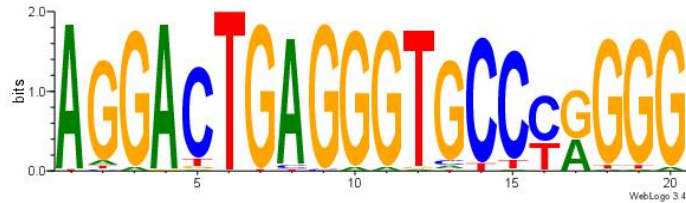


Reverse complement motif Consensus sequence: GGCACTGCTGGGGGACCCAG

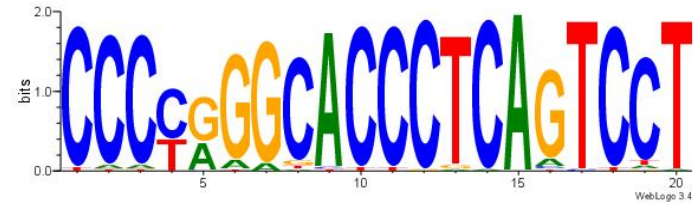


Dataset #: 1 Motif ID: 312 Motif name: Motif 312

Original motif Consensus sequence: AGGACTGAGGGTGCCYRGGG



Reverse complement motif Consensus sequence: CCCMKGGCACCCTCAGTCCT



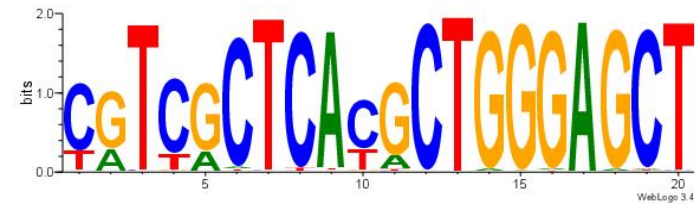
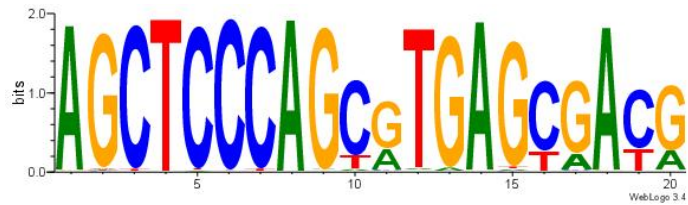
Best Matches for Motif ID 312 (Highest to Lowest)

Dataset #:	1
Motif ID:	48
Motif name:	Motif 48
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	20
Similarity score:	0.104551

Alignment:
CGTCGCTCACGCTGGGAGCT
CCCMKGGCACCCTCAGTCCT

Original motif Consensus sequence: AGCTCCAGCGTGAGCGACG

Reverse complement motif Consensus sequence:
CGTCGCTCACGCTGGGAGCT

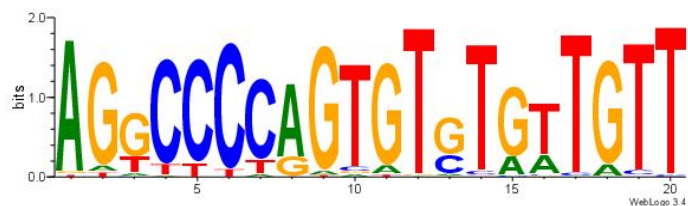


Dataset #: 1
 Motif ID: 176
 Motif name: Motif 176
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.105418

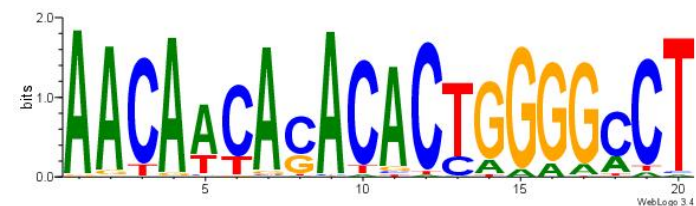
Alignment:

AAC AACASACTGGGGCCT
 CCCMKGGCACCTCAGTCCT

Original motif Consensus sequence: AGGCCCCAGTGTSTGTTGTT



Reverse complement motif Consensus sequence: AAC AACASACTGGGGCCT



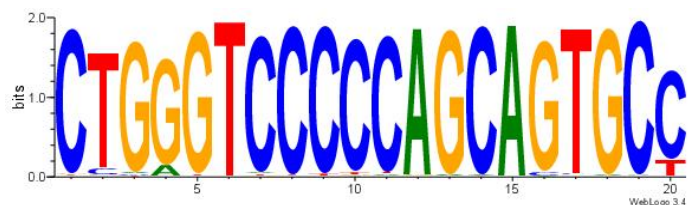
Dataset #: 1

Motif ID: 84
 Motif name: Motif 84
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.107814

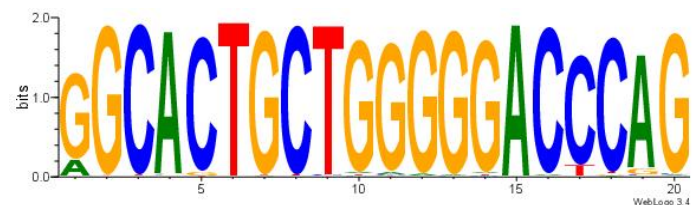
Alignment:

GGCCTGCTGGGGGACCCAG
 AGGACTGAGGGTGCCYRGGG

Original motif Consensus sequence: CTGGGTCCCCCAGCAGTGCC



Reverse complement motif Consensus sequence: GGCCTGCTGGGGGACCCAG



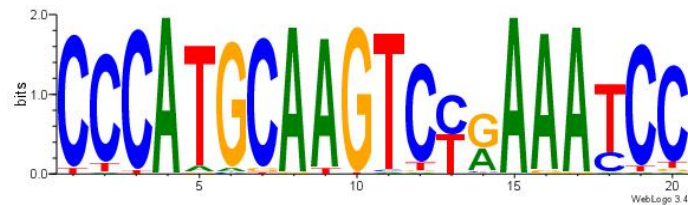
Dataset #: 1
 Motif ID: 310
 Motif name: Motif 310
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 20

Similarity score: 0.11163

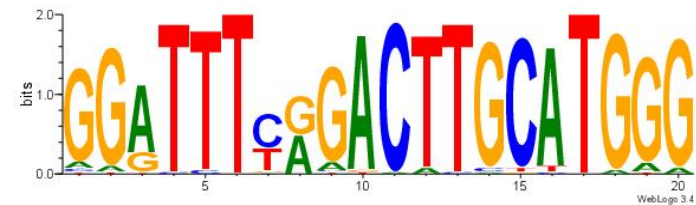
Alignment:

GGATTTMKGACTTGCATGGG
AGGACTGAGGGTGCCYRGGG

Original motif Consensus sequence: CCCATGCAAGTCYRAAATCC



Reverse complement motif Consensus sequence:
GGATTTMKGACTTGCATGGG



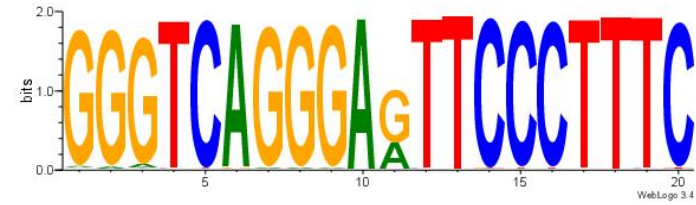
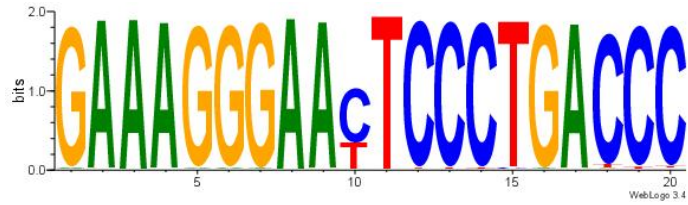
Dataset #: 1
Motif ID: 16
Motif name: Motif 16
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 20
Similarity score: 0.112186

Alignment:

GGGTCAGGGAGTTCCTTTC
AGGACTGAGGGTGCCYRGGG

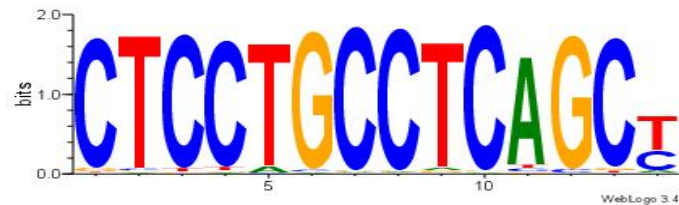
Original motif Consensus sequence: GAAAGGGA ACTCCCTGACCC

Reverse complement motif Consensus sequence:
GGGTCAGGGAGTTCCTTTC

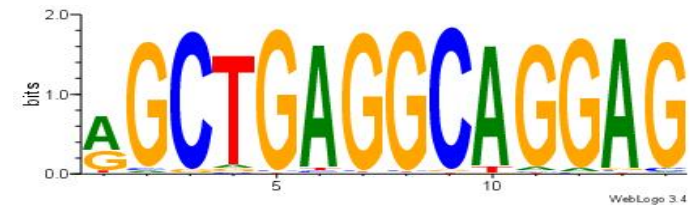


Dataset #: 1 Motif ID: 313 Motif name: Motif 313

Original motif Consensus sequence: CTCCTGCCTCAGCY



Reverse complement motif Consensus sequence: MGCTGAGGCAGG

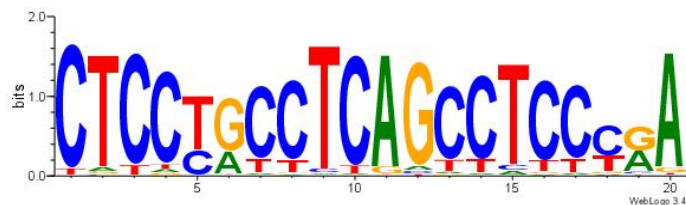


Best Matches for Motif ID 313 (Highest to Lowest)

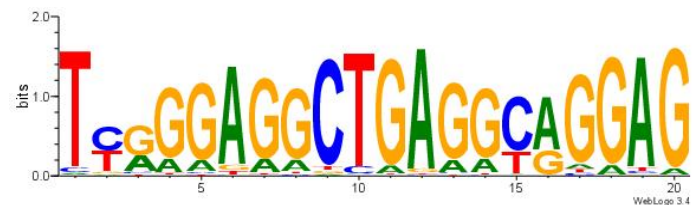
Dataset #:	1
Motif ID:	26
Motif name:	Motif 26
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	14
Similarity score:	0.0298178

Alignment:
 CTCCTGCCTCAGCCTCCCRA
 CTCCTGCCTCAGCY-----

Original motif Consensus sequence: CTCCTGCCTCAGCCTCCRA



Reverse complement motif Consensus sequence: TMGGGAGGCTGAGGCAGGAG

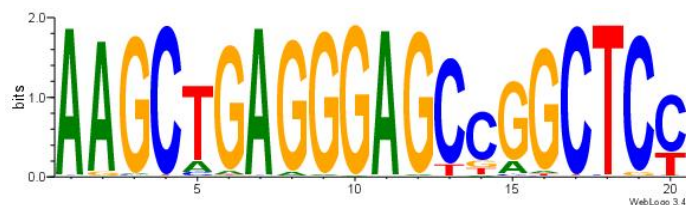


Dataset #: 1
Motif ID: 96
Motif name: Motif 96
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2
Number of overlap: 14
Similarity score: 0.0599095

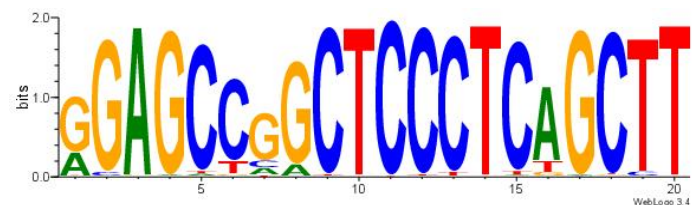
Alignment:

AAGCTGAGGGAGCCGGCTCC
-----MGCTGAGGCAGGAG-

Original motif Consensus sequence: AAGCTGAGGGAGCCGGCTCC



Reverse complement motif Consensus sequence: GGAGCCGGCTCCCTCAGCTT

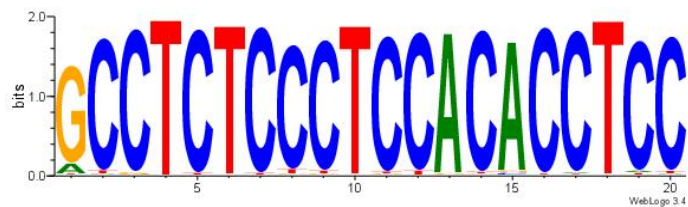


Dataset #: 1
 Motif ID: 105
 Motif name: Motif 105
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 5
 Number of overlap: 14
 Similarity score: 0.0742075

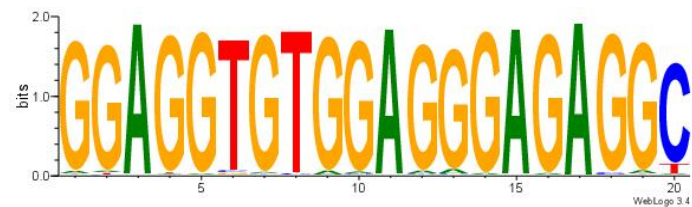
Alignment:

GGAGGTGTGGAGGGAGAGGC
 --MGCTGAGGCAGGAG----

Original motif Consensus sequence: GCCTCTCCCTCCACACCTCC



Reverse complement motif Consensus sequence: GGAGGTGTGGAGGGAGAGGC



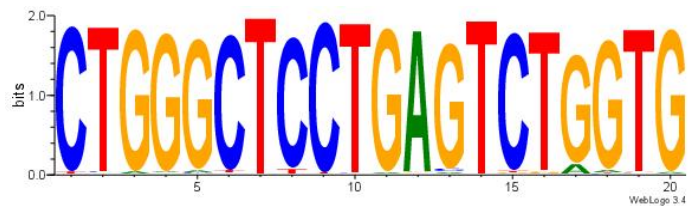
Dataset #: 1
 Motif ID: 67
 Motif name: Motif 67
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 6

Number of overlap: 14
Similarity score: 0.0752599

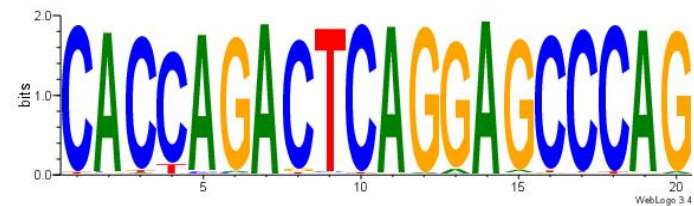
Alignment:

CTGGGCTCCTGAGTCTGGTG
-----CTCCTGCCTCAGCY-

Original motif Consensus sequence: CTGGGCTCCTGAGTCTGGTG



Reverse complement motif Consensus sequence:
CACCAGACTCAGGAGCCCAG



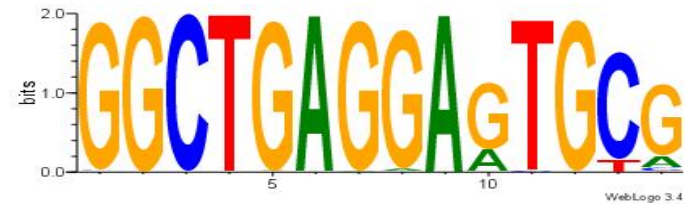
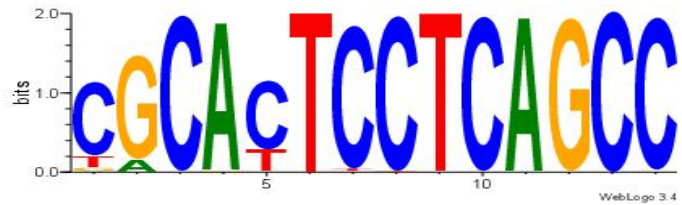
Dataset #: 1
Motif ID: 72
Motif name: Motif 72
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 14
Similarity score: 0.0799645

Alignment:

CGCACTCCTCAGCC
CTCCTGCCTCAGCY

Original motif Consensus sequence: CGCACTCCTCAGCC

Reverse complement motif Consensus sequence: GGCTGAGGAGTGC

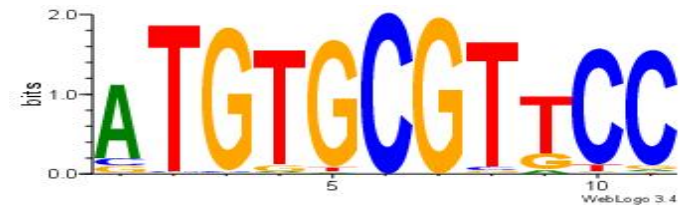


Dataset #: 1 Motif ID: 314 Motif name: Motif 314

Original motif Consensus sequence: GGAACGCACAT



Reverse complement motif Consensus sequence: ATGTGCGTTCC

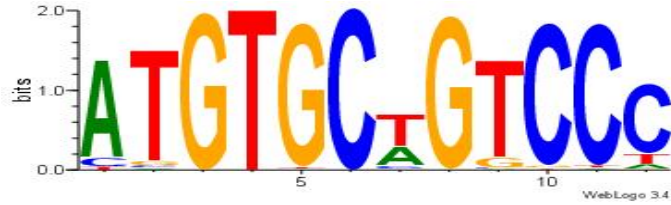


Best Matches for Motif ID 314 (Highest to Lowest)

Dataset #:	1
Motif ID:	240
Motif name:	Motif 240
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	11
Similarity score:	0.0430601

Alignment:
 ATGTGCWGTCCC
 -ATGTGCGTTCC

Original motif Consensus sequence: ATGTGCWGTCCC



Reverse complement motif Consensus sequence: GGGACWGCACAT

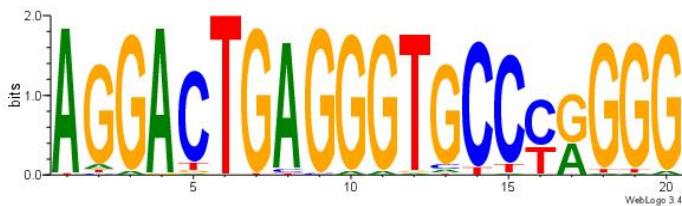


Dataset #: 1
Motif ID: 312
Motif name: Motif 312
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 6
Number of overlap: 11
Similarity score: 0.0705974

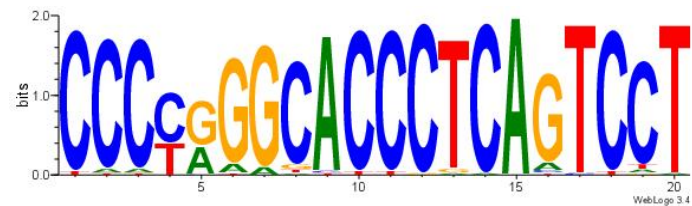
Alignment:

```
AGGACTGAGGGTGCCYRGGG  
-----ATGTGCGTTCC-----
```

Original motif Consensus sequence: AGGACTGAGGGTGCCYRGGG



Reverse complement motif Consensus sequence: CCCMKGGCACCCTCAGTCCT

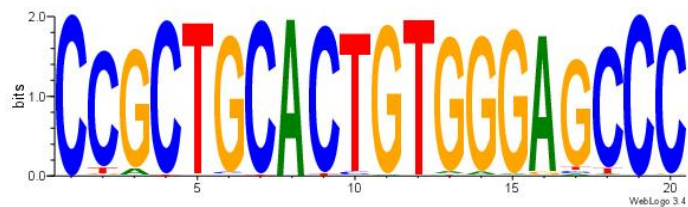


Dataset #: 1
 Motif ID: 144
 Motif name: Motif 144
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 11
 Similarity score: 0.0731257

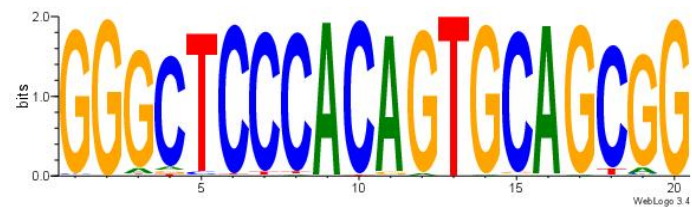
Alignment:

CCGCTGCACTGTGGGAGCCC
 -ATGTGCGTTCC-----

Original motif Consensus sequence: CCGCTGCACTGTGGGAGCCC



Reverse complement motif Consensus sequence: GGGCTCCCACAGTGCAGCGG



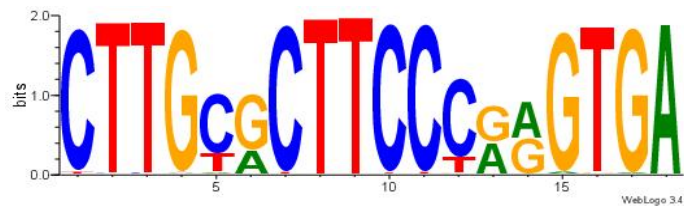
Dataset #: 1
 Motif ID: 15
 Motif name: Motif 15
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2

Number of overlap: 11
Similarity score: 0.0769547

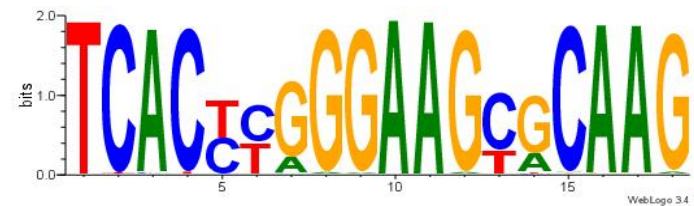
Alignment:

TCACKMGGGAAGCGCAAG
-GGAACGCACAT-----

Original motif Consensus sequence: CTTGCGCTCCRRGTGA



Reverse complement motif Consensus sequence:
TCACKMGGGAAGCGCAAG

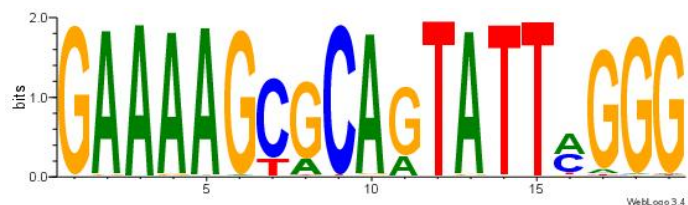


Dataset #: 1
Motif ID: 18
Motif name: Motif 18
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 11
Similarity score: 0.0796102

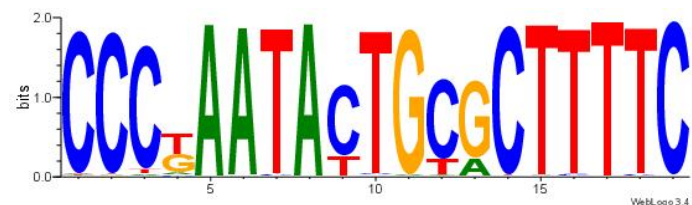
Alignment:

CCCYAATACTGCGCTTTTC
-----ATGTGCGTTCC

Original motif Consensus sequence: GAAAAGCGCAGTATTMGGG

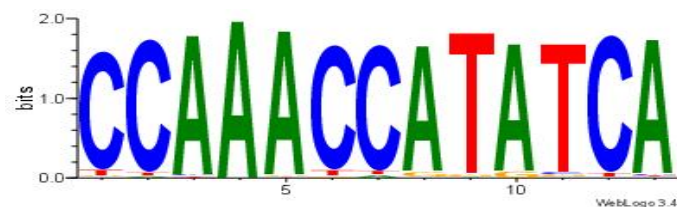


Reverse complement motif Consensus sequence: CCCYAATACTGCGCTTTTC

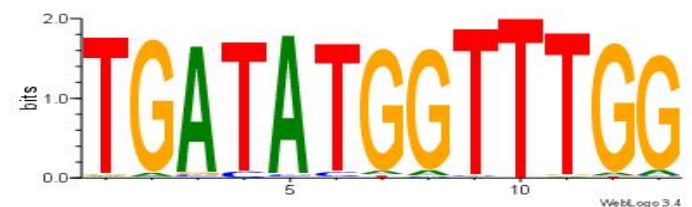


Dataset #: 1 Motif ID: 315 Motif name: Motif 315

Original motif Consensus sequence: CCAAACCATATCA



Reverse complement motif Consensus sequence: TGATATGGTTTGG



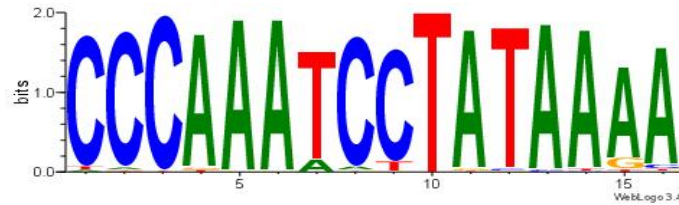
Best Matches for Motif ID 315 (Highest to Lowest)

Dataset #:	1
Motif ID:	169
Motif name:	Motif 169
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	3
Number of overlap:	13
Similarity score:	0.0520963

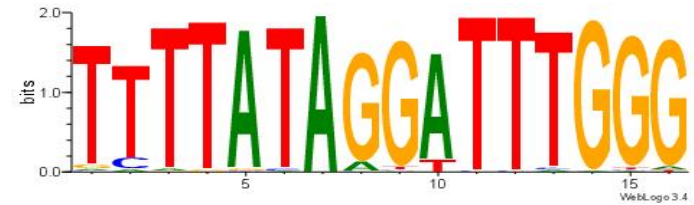
Alignment:

TTTTATAGGATTTGGG
--TGATATGGTTTGG--

Original motif Consensus sequence: CCCAAATCCTATAAAA



Reverse complement motif Consensus sequence:
TTTTATAGGATTTGGG



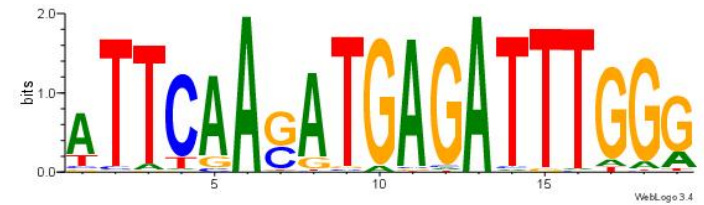
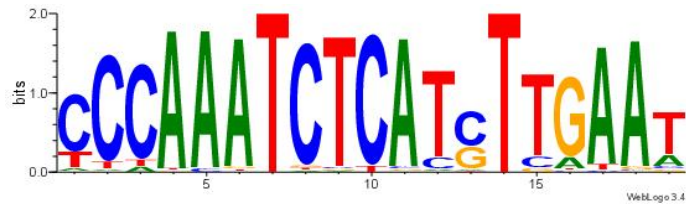
Dataset #: 1
Motif ID: 227
Motif name: Motif 227
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 2
Number of overlap: 13
Similarity score: 0.0822582

Alignment:

CCCAAATCTCATSTTGAAT
-CCAAACCATATCA-----

Original motif Consensus sequence: CCCAAATCTCATSTTGAAT

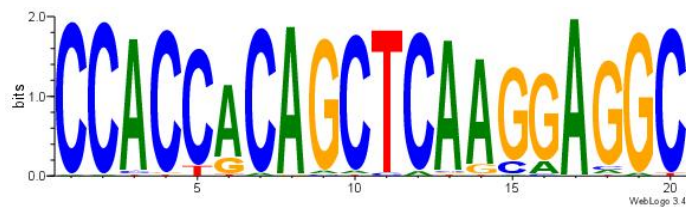
Reverse complement motif Consensus sequence:
ATCAASATGAGATTTGGG



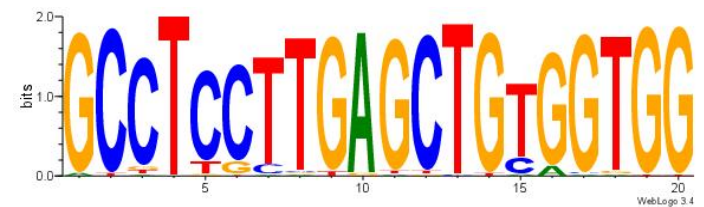
Dataset #: 1
 Motif ID: 331
 Motif name: Motif 331
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 13
 Similarity score: 0.0861727

Alignment:
 GCCTCCTTGAGCTGTGGTGG
 -----TGATATGGTTTGG

Original motif Consensus sequence: CCACCACAGCTCAAGGAGGC



Reverse complement motif Consensus sequence: GCCTCCTTGAGCTGTGGTGG



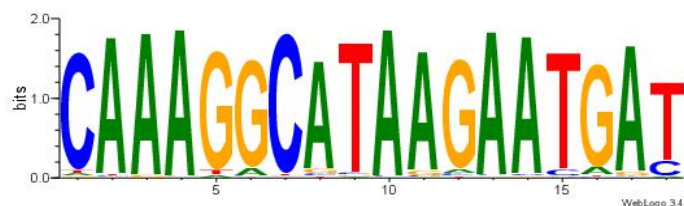
Dataset #: 1

Motif ID: 190
 Motif name: Motif 190
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 6
 Number of overlap: 13
 Similarity score: 0.090194

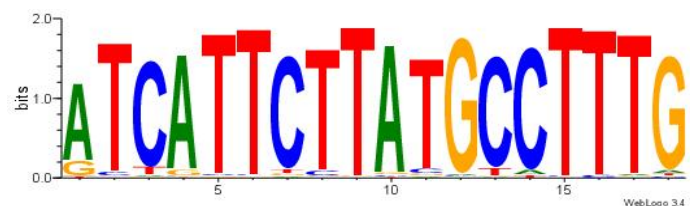
Alignment:

ATCATTCTTATGCCTTTG
 -----TGATATGGTTTGG

Original motif Consensus sequence: CAAAGGCATAAGAATGAT



Reverse complement motif Consensus sequence: ATCATTCTTATGCCTTTG



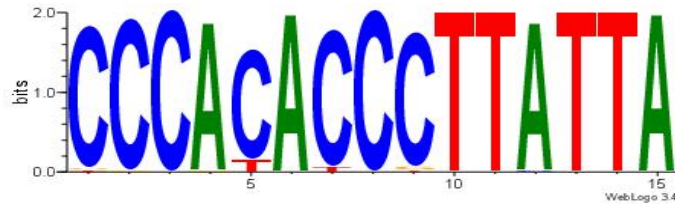
Dataset #: 1
 Motif ID: 259
 Motif name: Motif 259
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 13

Similarity score: 0.0922621

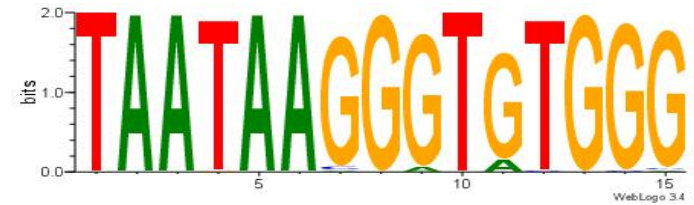
Alignment:

TAATAAGGGTGTGGG
TGATATGGTTTGG--

Original motif Consensus sequence: CCCACACCCTTATTA



Reverse complement motif Consensus sequence: TAATAAGGGTGTGGG

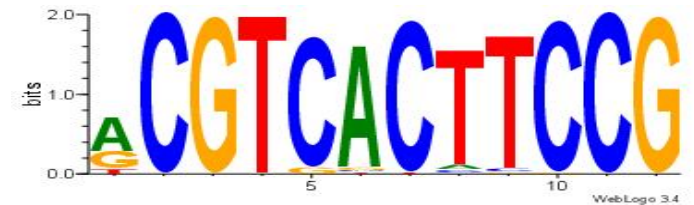


Dataset #: 1 Motif ID: 316 Motif name: Motif 316

Original motif Consensus sequence: CGGAAGTGACGT



Reverse complement motif Consensus sequence: ACGTCACTTCCG



Best Matches for Motif ID 316 (Highest to Lowest)

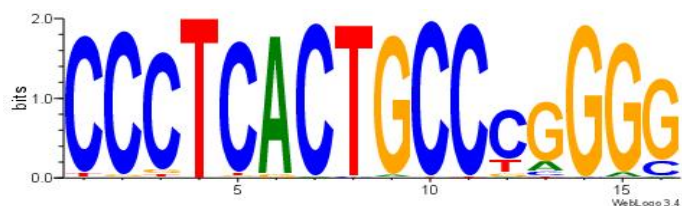
Dataset #:	1
Motif ID:	136
Motif name:	Motif 136
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward

Position number: 1
Number of overlap: 12
Similarity score: 0.0580654

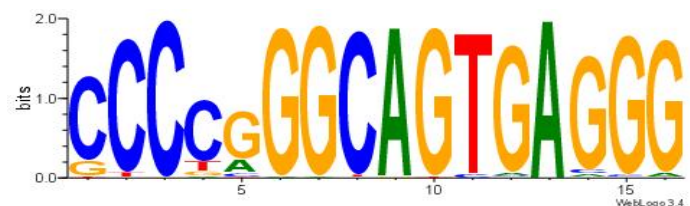
Alignment:

CCCCGGGCAGTGAGGG
CGGAAGTGACGT-----

Original motif Consensus sequence: CCCTCACTGCCCGGGG



Reverse complement motif Consensus sequence: CCCCgggcagtgaggg

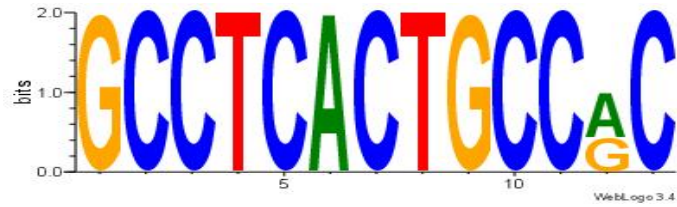


Dataset #: 1
Motif ID: 247
Motif name: Motif 247
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 12
Similarity score: 0.0581297

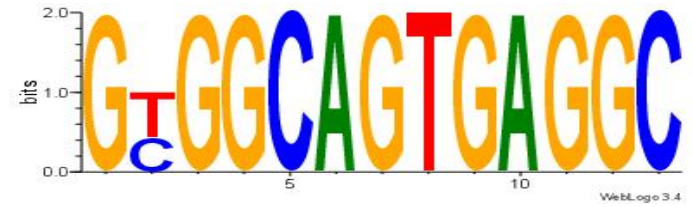
Alignment:

GKGGCAGTGAGGC
CGGAAGTGACGT-

Original motif Consensus sequence: GCCTCACTGCCRC



Reverse complement motif Consensus sequence: GKGGCAGTGAGGC

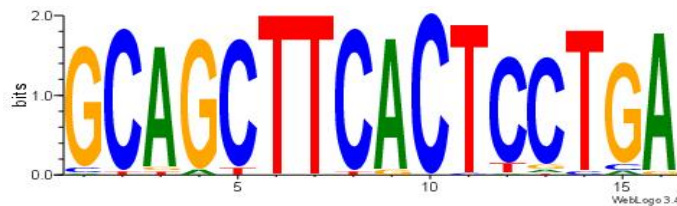


Dataset #: 1
Motif ID: 246
Motif name: Motif 246
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 2
Number of overlap: 12
Similarity score: 0.0638384

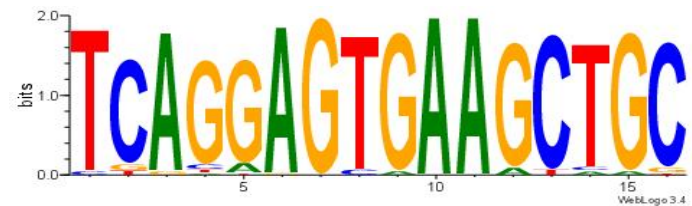
Alignment:

GCAGCTTCACTCCTGA
-ACGTCACTTCCG---

Original motif Consensus sequence: GCAGCTTCACTCCTGA



Reverse complement motif Consensus sequence: TCAGGAGTGAAGCTGC

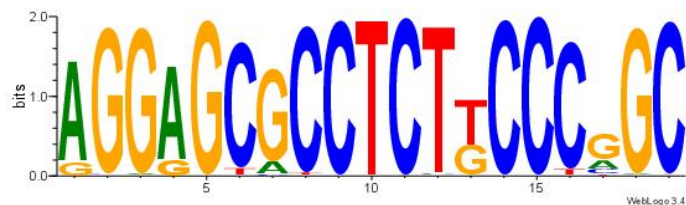


Dataset #: 1
 Motif ID: 30
 Motif name: Motif 30
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 12
 Similarity score: 0.0713677

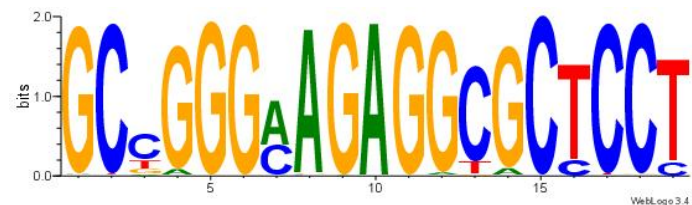
Alignment:

AGGAGCGCCTCTKCCCGGC
 ---ACGTCACCTTCCG----

Original motif Consensus sequence: AGGAGCGCCTCTKCCCGGC



Reverse complement motif Consensus sequence: GCCGGGAGAGGCGCTCCT

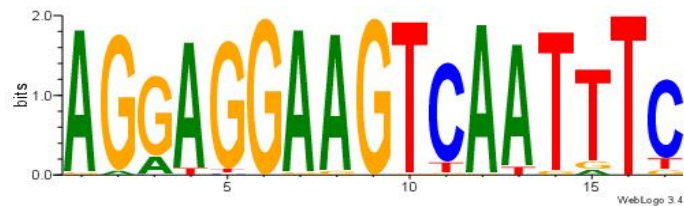


Dataset #: 1
 Motif ID: 327
 Motif name: Motif 327
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4

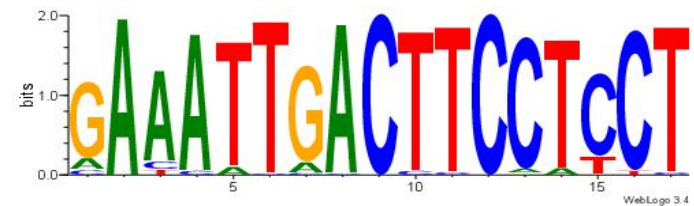
Number of overlap: 12
Similarity score: 0.0721835

Alignment:
AGGAGGAAGTCAATTC
---CGGAAGTGACGT--

Original motif Consensus sequence: AGGAGGAAGTCAATTC

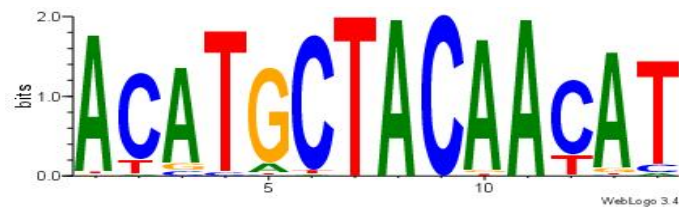


Reverse complement motif Consensus sequence:
GAAATTGACTTCCTCCT

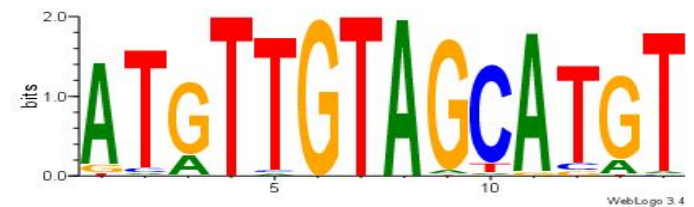


Dataset #: 1 Motif ID: 317 Motif name: Motif 317

Original motif Consensus sequence: ACATGCTACAACAT



Reverse complement motif Consensus sequence: ATGTTGTAGCATGT



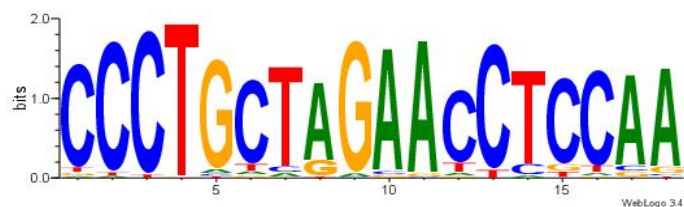
Best Matches for Motif ID 317 (Highest to Lowest)

Dataset #: 1
Motif ID: 299
Motif name: Motif 299
Matching format of first motif: Reverse Complement

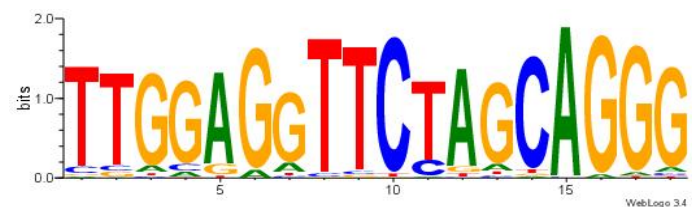
Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 5
 Number of overlap: 14
 Similarity score: 0.0691153

Alignment:
 TTGGAGGTTCTAGCAGGG
 ----ATGTTGTAGCATGT

Original motif Consensus sequence: CCCTGCTAGAACCTCCAA



Reverse complement motif Consensus sequence: TTGGAGGTTCTAGCAGGG

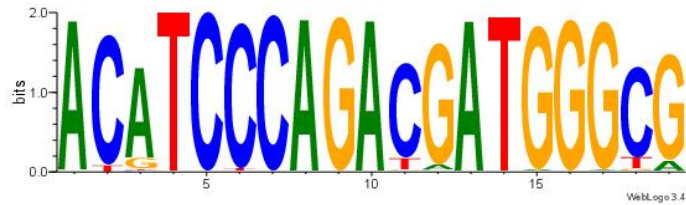


Dataset #: 1
 Motif ID: 36
 Motif name: Motif 36
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0.0828209

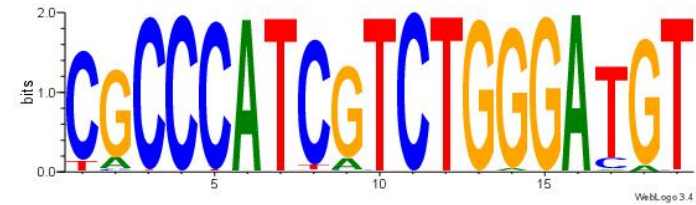
Alignment:

CGCCCATCGTCTGGGATGT
-----ATGTTGTAGCATGT

Original motif Consensus sequence: ACATCCCAGACGATGGGCG



Reverse complement motif Consensus sequence:
CGCCCATCGTCTGGGATGT



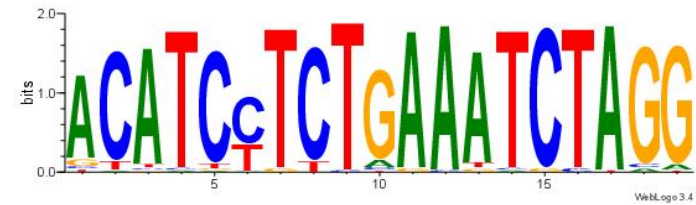
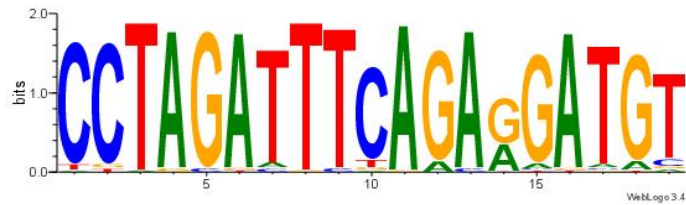
Dataset #:	1
Motif ID:	280
Motif name:	Motif 280
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	6
Number of overlap:	14
Similarity score:	0.0862934

Alignment:

ACATCMTCTGAAATCTAGG
-----ACATGCTACAACAT

Original motif Consensus sequence: CCTAGATTTGAGARGATGT

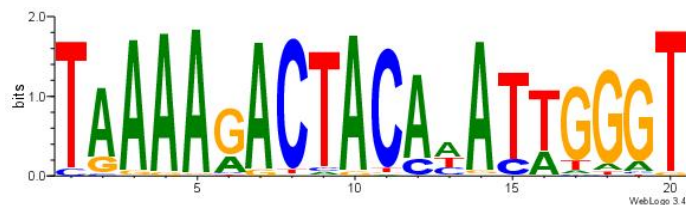
Reverse complement motif Consensus sequence:
ACATCMTCTGAAATCTAGG



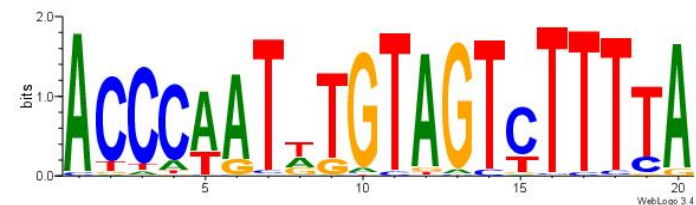
Dataset #: 1
 Motif ID: 195
 Motif name: Motif 195
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 5
 Number of overlap: 14
 Similarity score: 0.0870528

Alignment:
 ACCCAATWTGTAGTCTTTTA
 ----ATGTTGTAGCATGT--

Original motif Consensus sequence: TAAAAGACTACAWATTGGGT



Reverse complement motif Consensus sequence: ACCCAATWTGTAGTCTTTTA



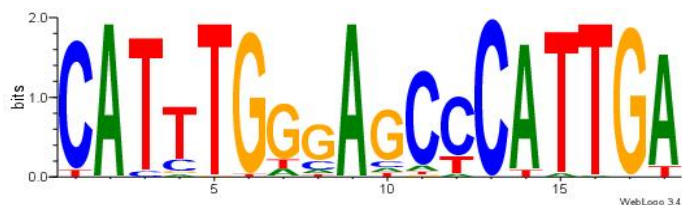
Dataset #: 1

Motif ID: 284
 Motif name: Motif 284
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 14
 Similarity score: 0.0936287

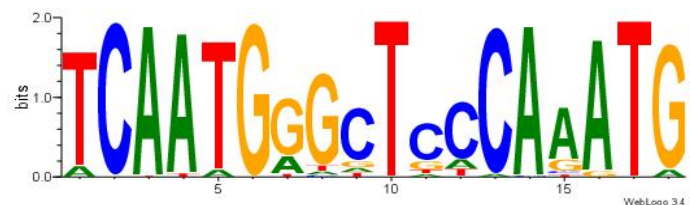
Alignment:

CATTGGGAGCCCATTGA
 ---ATGTTGTAGCATGT-

Original motif Consensus sequence: CATTGGGAGCCCATTGA



Reverse complement motif Consensus sequence: TCAATGGGCTCCCAAATG



Dataset #: 1 Motif ID: 318 Motif name: Motif 318

Original motif Consensus sequence: CAGCCCCG



Reverse complement motif Consensus sequence: CGGGGCTG



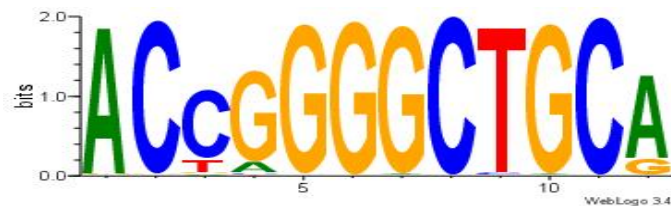
Best Matches for Motif ID 318 (Highest to Lowest)

Dataset #: 1
Motif ID: 88
Motif name: Motif 88
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 3
Number of overlap: 8
Similarity score: 0.00509921

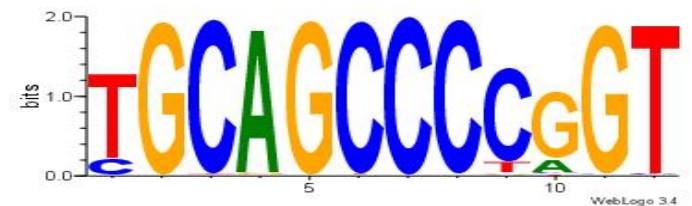
Alignment:

```
ACCGGGGCTGCA  
--CGGGGCTG--
```

Original motif Consensus sequence: ACCGGGGCTGCA



Reverse complement motif Consensus sequence: TGCAGCCCCGGT

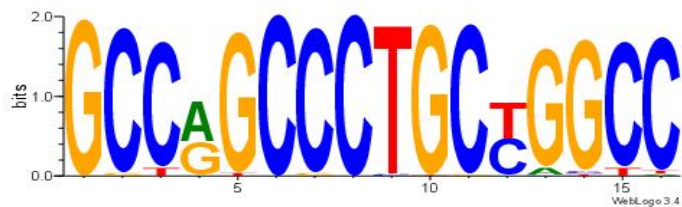


Dataset #: 1
Motif ID: 183
Motif name: Motif 183
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif

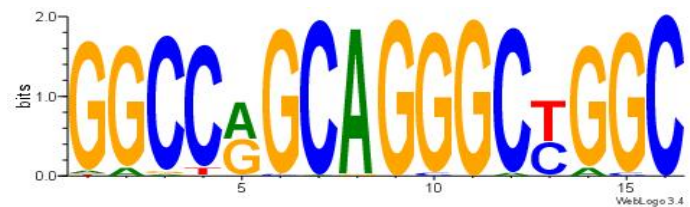
Direction: Forward
Position number: 3
Number of overlap: 8
Similarity score: 0.0248687

Alignment:
GCCRGCCCTGCYGGCC
--CAGCCCCG-----

Original motif Consensus sequence: GCCRGCCCTGCYGGCC



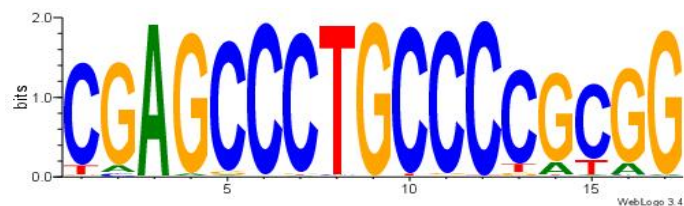
Reverse complement motif Consensus sequence: GGCCMGCAGGGCKGGC



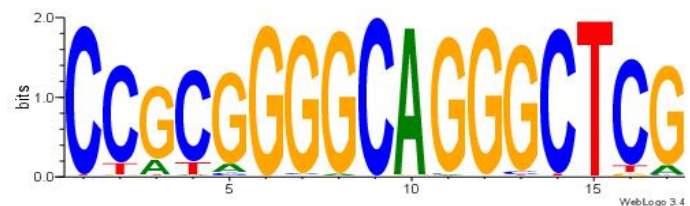
Dataset #: 1
Motif ID: 78
Motif name: Motif 78
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 4
Number of overlap: 8
Similarity score: 0.026456

Alignment:
CGAGCCCTGCCCGCGG
-----CAGCCCCG---

Original motif Consensus sequence: CGAGCCCTGCCCGCGG



Reverse complement motif Consensus sequence: CCGCGGGGCAGGGCTCG

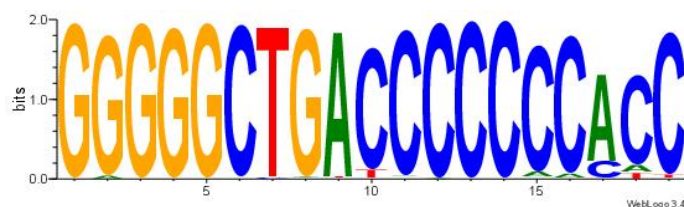


Dataset #: 1
Motif ID: 92
Motif name: Motif 92
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 12
Number of overlap: 8
Similarity score: 0.0266885

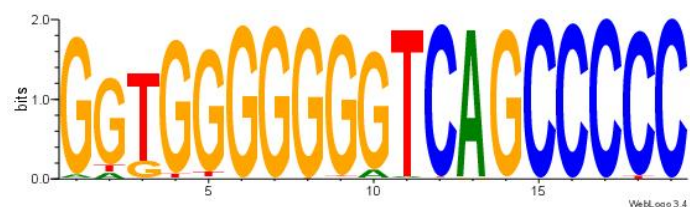
Alignment:

```
GGGGGCTGACCCCCCACC  
-----CGGGGCTG
```

Original motif Consensus sequence: GGGGGCTGACCCCCCACC



Reverse complement motif Consensus sequence: GGTGGGGGGGTCAGCCCCC

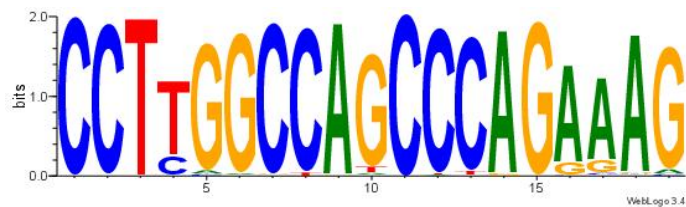


Dataset #: 1
 Motif ID: 122
 Motif name: Motif 122
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 8
 Number of overlap: 8
 Similarity score: 0.0291045

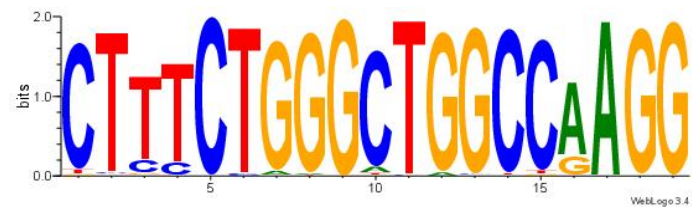
Alignment:

CTTTCTGGGCTGGCCAAGG
 ----CGGGGCTG-----

Original motif Consensus sequence: CCTTGGCCAGCCCAGAAAG



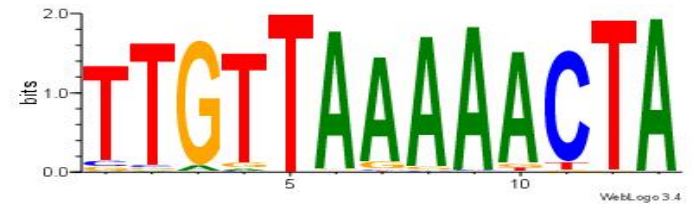
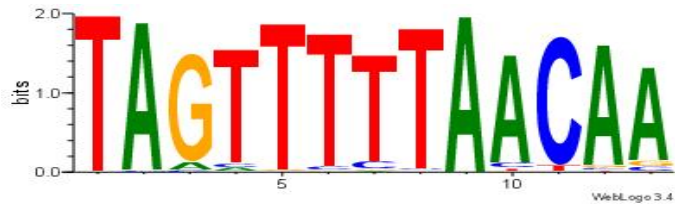
Reverse complement motif Consensus sequence: CTTTCTGGGCTGGCCAAGG



Dataset #: 1 Motif ID: 319 Motif name: Motif 319

Original motif Consensus sequence: TAGTTTTTAACAA

Reverse complement motif Consensus sequence: TTGTTAAAACTA

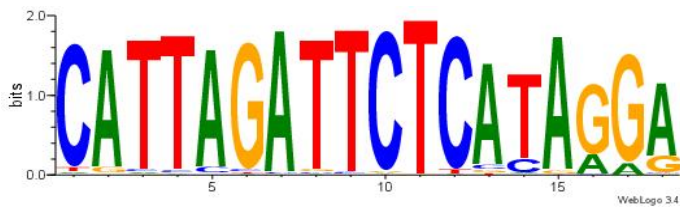


Best Matches for Motif ID 319 (Highest to Lowest)

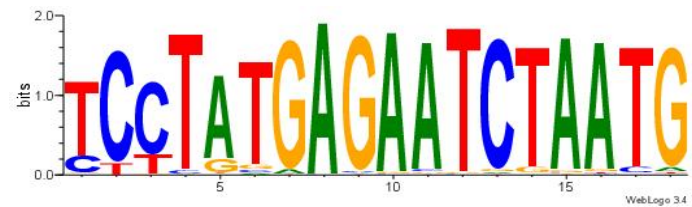
Dataset #: 1
 Motif ID: 154
 Motif name: Motif 154
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 13
 Similarity score: 0.0753436

Alignment:
 CATTAGATTCTCATAGGA
 ---TAGTTTTTAACAA--

Original motif Consensus sequence: CATTAGATTCTCATAGGA



Reverse complement motif Consensus sequence: TCCTATGAGAATCTAATG

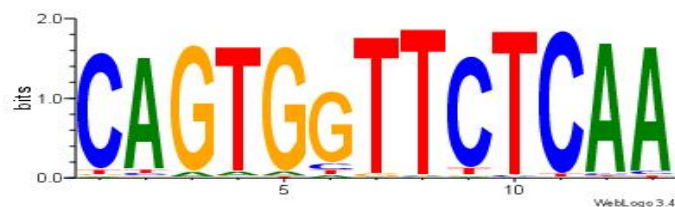


Dataset #: 1
 Motif ID: 243
 Motif name: Motif 243
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 13
 Similarity score: 0.0843202

Alignment:

TTGAGAACCACTG
 TTGTTAAAACTA

Original motif Consensus sequence: CAGTGGTTCTCAA



Reverse complement motif Consensus sequence: TTGAGAACCACTG



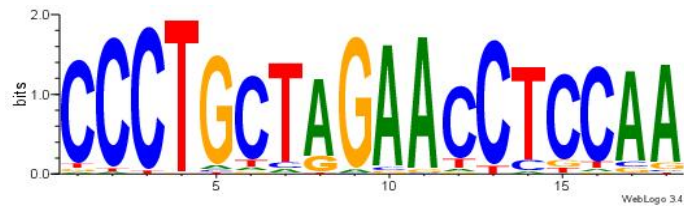
Dataset #: 1
 Motif ID: 299
 Motif name: Motif 299
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 13

Similarity score: 0.084899

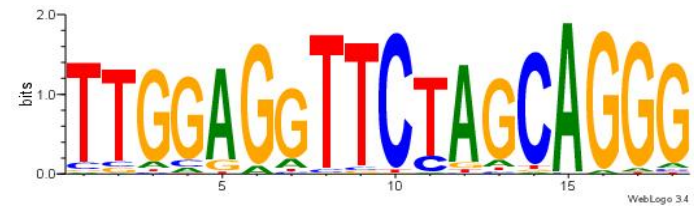
Alignment:

CCCTGCTAGAACCTCCAA
---TTGTTAAAACTA--

Original motif Consensus sequence: CCCTGCTAGAACCTCCAA



Reverse complement motif Consensus sequence:
TTGGAGTTCTAGCAGGG



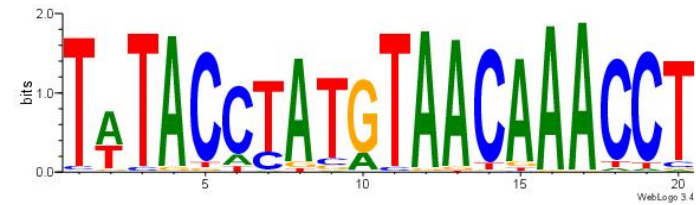
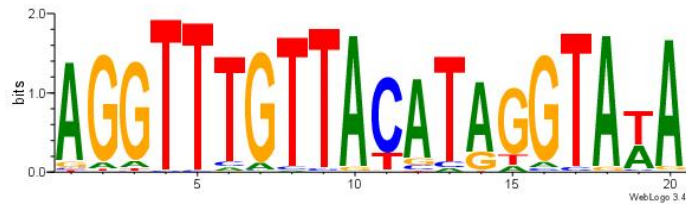
Dataset #: 1
Motif ID: 137
Motif name: Motif 137
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 13
Similarity score: 0.0861013

Alignment:

TWTACCTATGTAACAAACCT
-----TTGTTAAAACTA

Original motif Consensus sequence: AGGTTTGTACATAGGTAWA

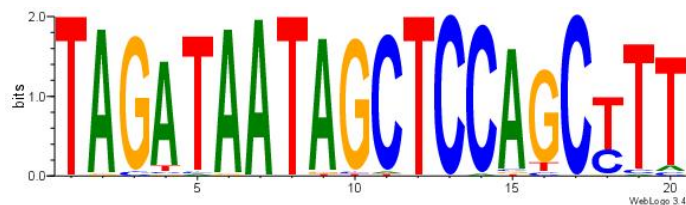
Reverse complement motif Consensus sequence:
TWTACCTATGTAACAAACCT



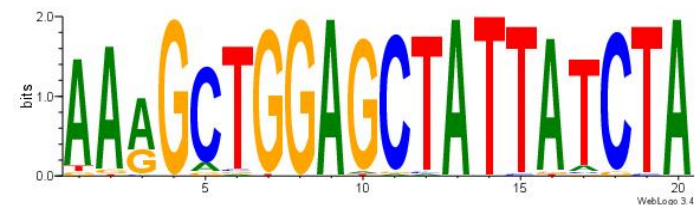
Dataset #: 1
 Motif ID: 333
 Motif name: Motif 333
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 8
 Number of overlap: 13
 Similarity score: 0.08657

Alignment:
 AAAGCTGGAGCTATTATCTA
 -----TAGTTTTTAACAA

Original motif Consensus sequence: TAGATAATAGCTCCAGCTTT

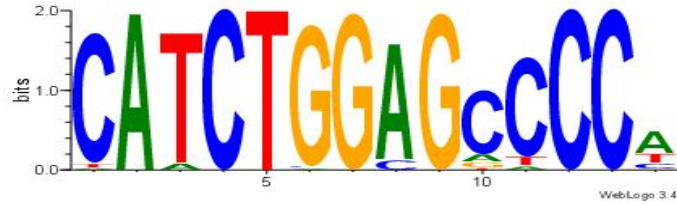


Reverse complement motif Consensus sequence: AAAGCTGGAGCTATTATCTA

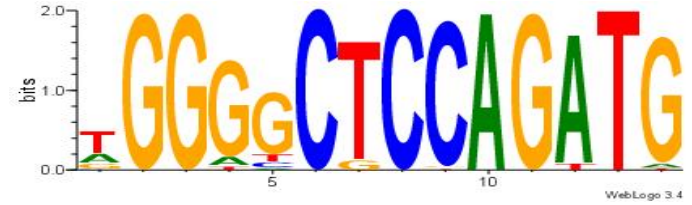


Dataset #: 1 Motif ID: 320 Motif name: Motif 320

Original motif Consensus sequence: CATCTGGAGCCCCA



Reverse complement motif Consensus sequence: TGGGGCTCCAGATG



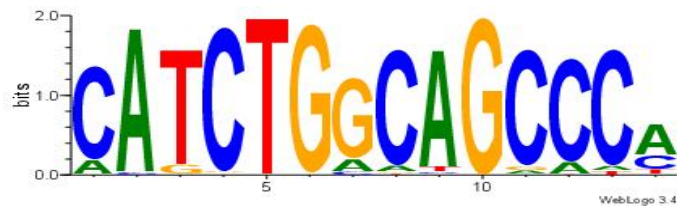
Best Matches for Motif ID 320 (Highest to Lowest)

Dataset #:	1
Motif ID:	205
Motif name:	Motif 205
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	14
Similarity score:	0.057175

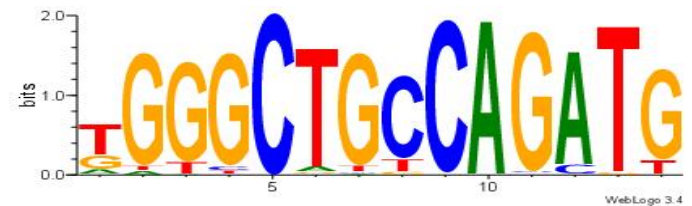
Alignment:

```
CATCTGGCAGCCCA  
CATCTGGAGCCCA
```

Original motif Consensus sequence: CATCTGGCAGCCCA



Reverse complement motif Consensus sequence: TGGGCTGCCAGATG

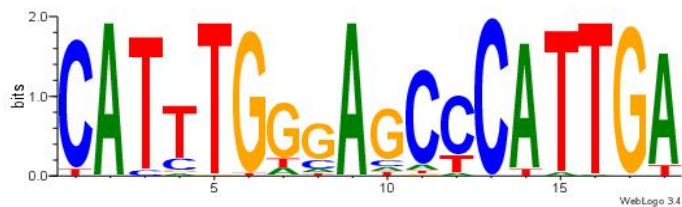


Dataset #: 1
 Motif ID: 284
 Motif name: Motif 284
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0.071304

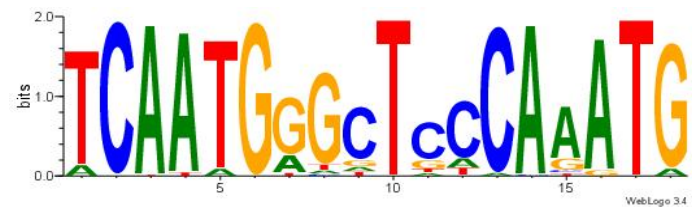
Alignment:

CATTGGGAGCCCATTGA
 CATCTGGAGCCCCA----

Original motif Consensus sequence: CATTGGGAGCCCATTGA



Reverse complement motif Consensus sequence: TCAATGGGCTCCCAAATG



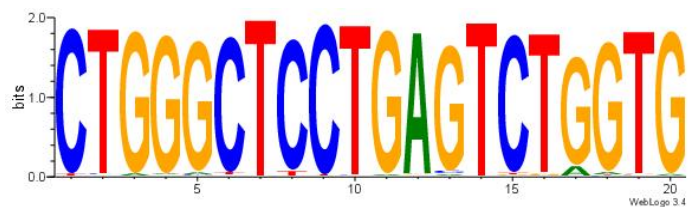
Dataset #: 1
 Motif ID: 67
 Motif name: Motif 67
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1

Number of overlap: 14
Similarity score: 0.0870604

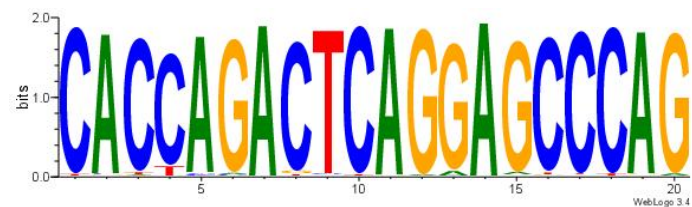
Alignment:

CACCAGACTCAGGAGCCCAG
CATCTGGAGCCCCA-----

Original motif Consensus sequence: CTGGGCTCCTGAGTCTGGTG



Reverse complement motif Consensus sequence:
CACCAGACTCAGGAGCCCAG

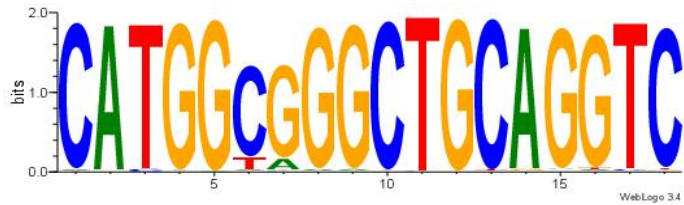


Dataset #: 1
Motif ID: 68
Motif name: Motif 68
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 5
Number of overlap: 14
Similarity score: 0.087898

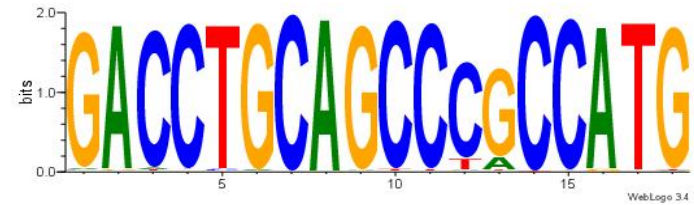
Alignment:

CATGGCGGGCTGCAGGTC
TGGGGCTCCAGATG-----

Original motif Consensus sequence: CATGGCGGGCTGCAGGTC



Reverse complement motif Consensus sequence: GACCTGCAGCCCGCCATG

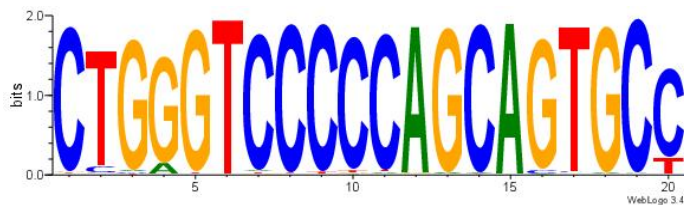


Dataset #: 1
Motif ID: 84
Motif name: Motif 84
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 5
Number of overlap: 14
Similarity score: 0.0974135

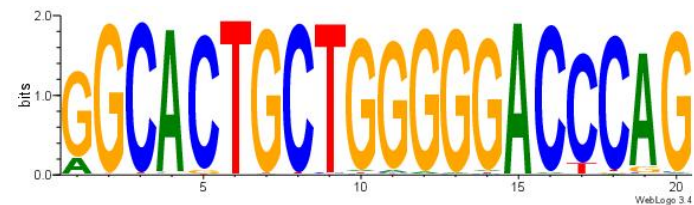
Alignment:

```
G G C A C T G C T G G G G G A C C C A G  
-- C A T C T G G A G C C C C A -----
```

Original motif Consensus sequence: CTGGGTCCCCCAGCAGTGCC

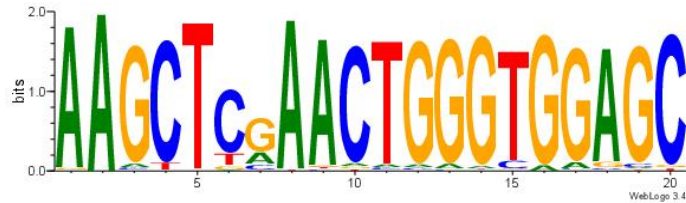


Reverse complement motif Consensus sequence: GGC ACTGCTGGGGGACCCAG

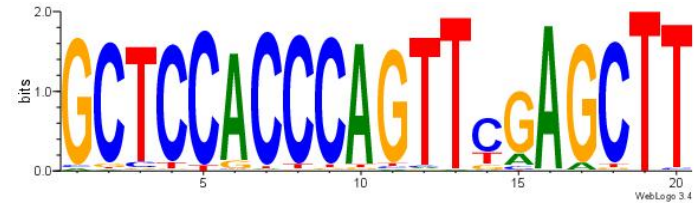


Dataset #: 1 Motif ID: 321 Motif name: Motif 321

Original motif Consensus sequence: AAGCTCGAACTGGGTGGAGC



Reverse complement motif Consensus sequence: GCTCCACCCAGTTCGAGCTT



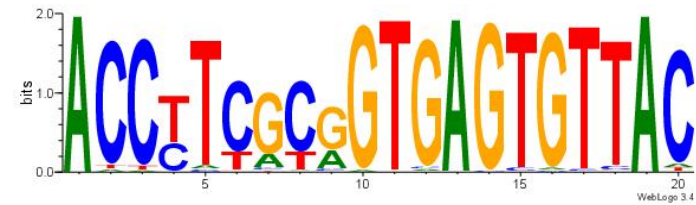
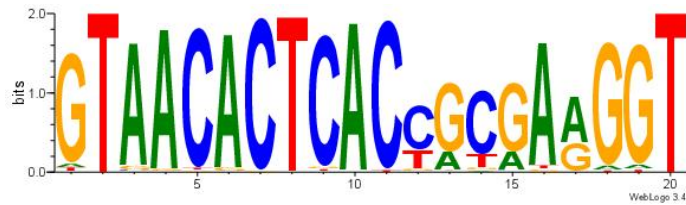
Best Matches for Motif ID 321 (Highest to Lowest)

Dataset #:	1
Motif ID:	201
Motif name:	Motif 201
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	20
Similarity score:	0.114862

Alignment:
ACCKTCGCGGTGAGTGTTAC
AAGCTCGAACTGGGTGGAGC

Original motif Consensus sequence: GTAACACTCACCGCGARGGT

Reverse complement motif Consensus sequence: ACCKTCGCGGTGAGTGTTAC

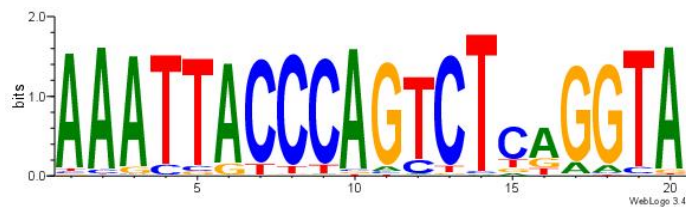


Dataset #: 1
 Motif ID: 160
 Motif name: Motif 160
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.117485

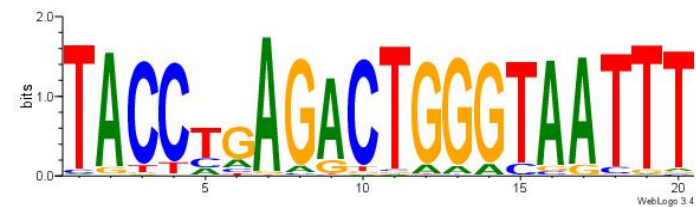
Alignment:

AAATTACCCAGTCTCAGGTA
 GCTCCACCCAGTTCGAGCTT

Original motif Consensus sequence: AAATTACCCAGTCTCAGGTA



Reverse complement motif Consensus sequence: TACCTGAGACTGGGTAATTT



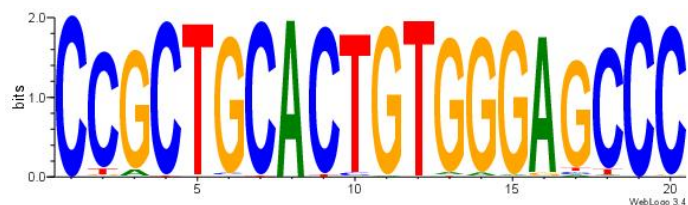
Dataset #: 1

Motif ID: 144
Motif name: Motif 144
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 20
Similarity score: 0.118909

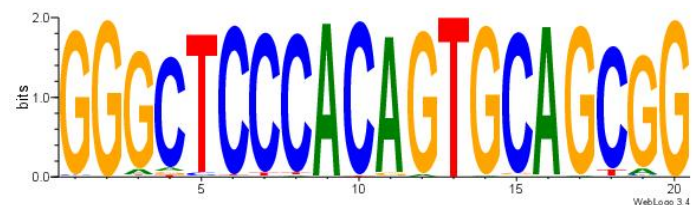
Alignment:

CCGCTGCACTGTGGGAGCCC
GCTCCACCCAGTTCGAGCTT

Original motif Consensus sequence: CCGCTGCACTGTGGGAGCCC



Reverse complement motif Consensus sequence: GGGCTCCACAGTGCAGCGG



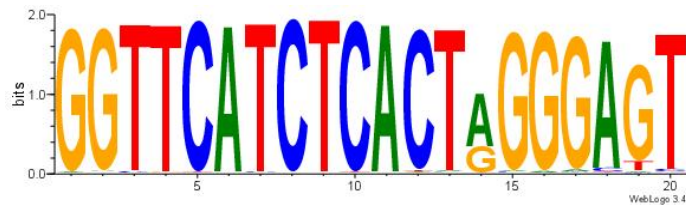
Dataset #: 1
Motif ID: 23
Motif name: Motif 23
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 20

Similarity score: 0.12743

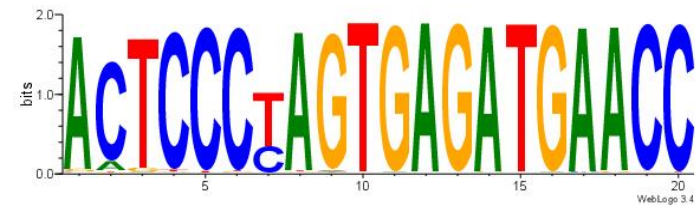
Alignment:

ACTCCCTAGTGAGATGAACC
AAGCTCGAACTGGGTGGAGC

Original motif Consensus sequence: GGTTCACTCACTAGGGAGT



Reverse complement motif Consensus sequence:
ACTCCCTAGTGAGATGAACC



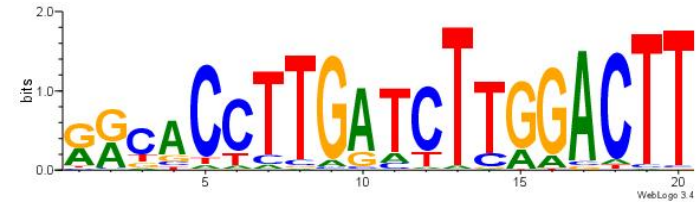
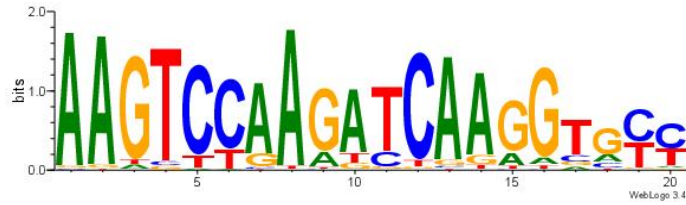
Dataset #: 1
Motif ID: 119
Motif name: Motif 119
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 20
Similarity score: 0.130736

Alignment:

AAGTCCAAGATCAAGGTGY
AAGCTCGAACTGGGTGGAGC

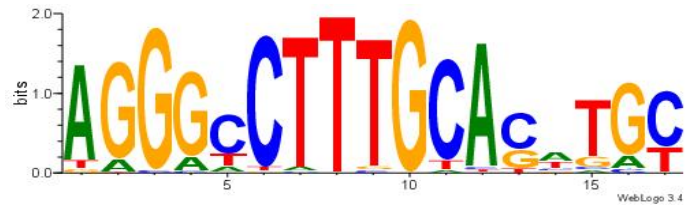
Original motif Consensus sequence: AAGTCCAAGATCAAGGTGY

Reverse complement motif Consensus sequence:
KKCACCTTGATCTTGGACTT

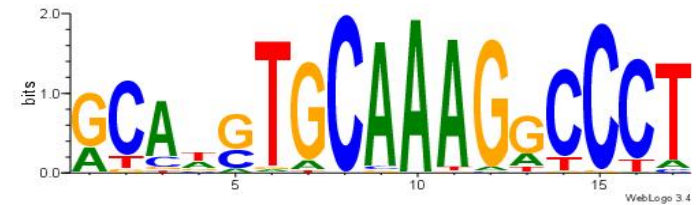


Dataset #: 1 Motif ID: 322 Motif name: Motif 322

Original motif Consensus sequence: AGGGCCTTGCASWTGC



Reverse complement motif Consensus sequence: GCAWSTGCAAAGGCCCT



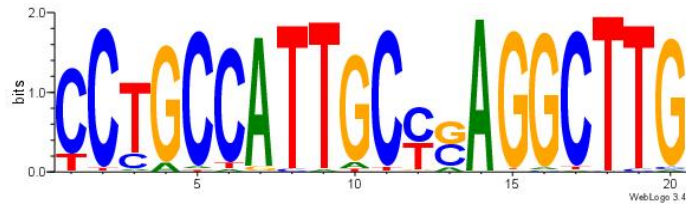
Best Matches for Motif ID 322 (Highest to Lowest)

Dataset #:	1
Motif ID:	196
Motif name:	Motif 196
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	17
Similarity score:	0.0779611

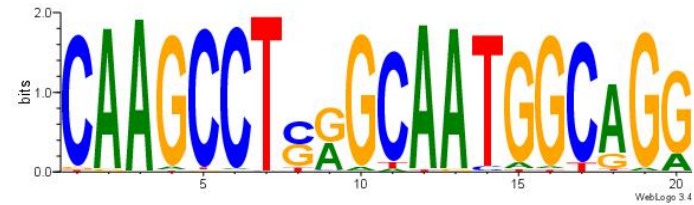
Alignment:

CAAGCCTSKGCAATGGCAGG
---GCAWSTGCAAAGGCCCT

Original motif Consensus sequence: CCTGCCATTGCYSAGGCTTG



Reverse complement motif Consensus sequence:
CAAGCCTSKGCAATGGCAGG



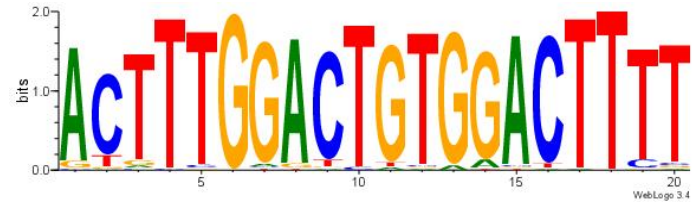
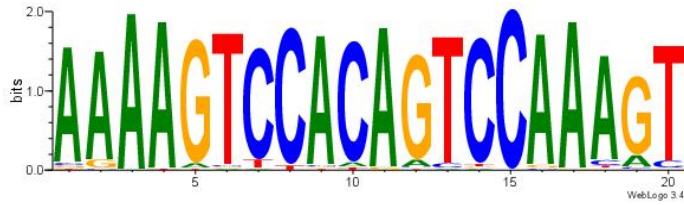
Dataset #:	1
Motif ID:	171
Motif name:	Motif 171
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	17
Similarity score:	0.0904024

Alignment:

ACTTTGGACTGTGGACTTTT
AGGGCCTTTGCASWTGC---

Original motif Consensus sequence: AAAAGTCCACAGTCCAAAGT

Reverse complement motif Consensus sequence:
ACTTTGGACTGTGGACTTTT

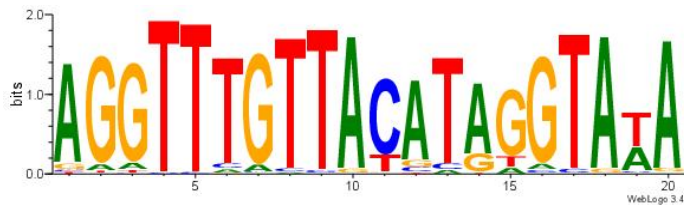


Dataset #: 1
 Motif ID: 137
 Motif name: Motif 137
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 4
 Number of overlap: 17
 Similarity score: 0.0909504

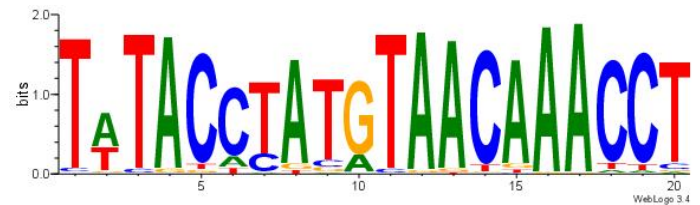
Alignment:

AGGTTTGTTACATAGGTAWA
 AGGGCCTTTGCASWTGC---

Original motif Consensus sequence: AGGTTTGTTACATAGGTAWA



Reverse complement motif Consensus sequence: TWTACCTATGTAACAAACCT



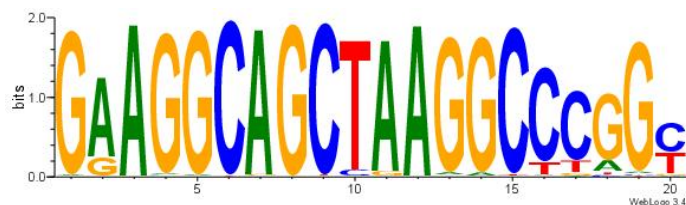
Dataset #: 1

Motif ID: 64
 Motif name: Motif 64
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 17
 Similarity score: 0.0915142

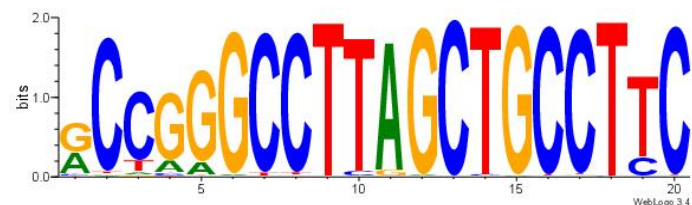
Alignment:

KCCGGGCCTTAGCTGCCTTC
 -AGGGCCTTTGCASWTGC--

Original motif Consensus sequence: GAAGGCAGCTAAGGCCGGY



Reverse complement motif Consensus sequence: KCCGGGCCTTAGCTGCCTTC



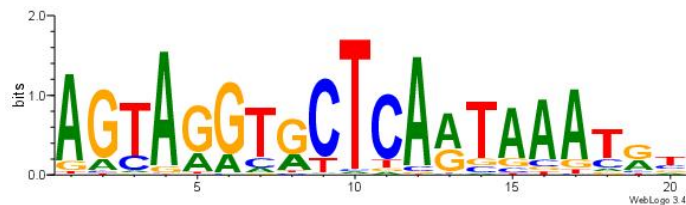
Dataset #: 1
 Motif ID: 86
 Motif name: Motif 86
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 17

Similarity score: 0.0922727

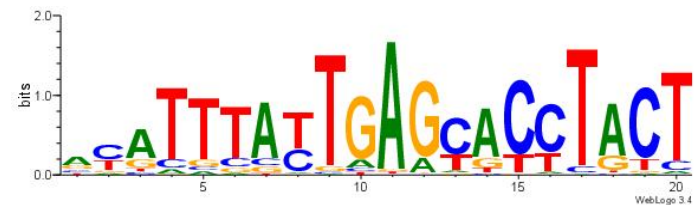
Alignment:

AGTAGGTGCTCARTAAATRB
---AGGGCCTTTGCASWTGC

Original motif Consensus sequence: AGTAGGTGCTCARTAAATRB

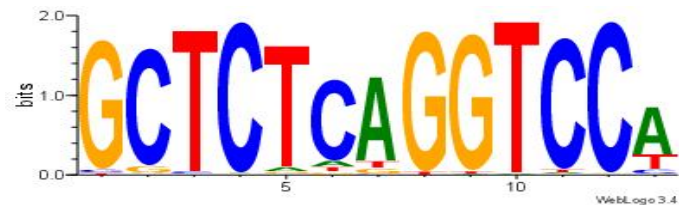


Reverse complement motif Consensus sequence: VMATTTAKTGAGCACCTACT

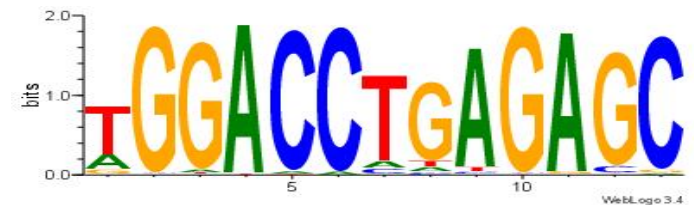


Dataset #: 1 Motif ID: 323 Motif name: Motif 323

Original motif Consensus sequence: GCTCTCAGGTCCA



Reverse complement motif Consensus sequence: TGGACCTGAGAGC



Best Matches for Motif ID 323 (Highest to Lowest)

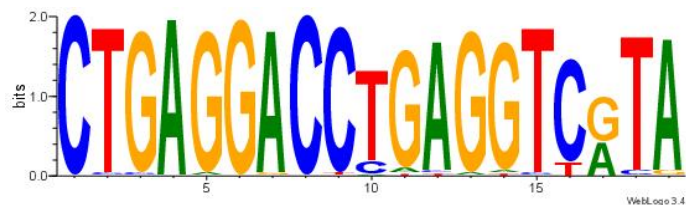
Dataset #:	1
Motif ID:	291
Motif name:	Motif 291
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif

Direction: Backward
Position number: 4
Number of overlap: 13
Similarity score: 0.0533584

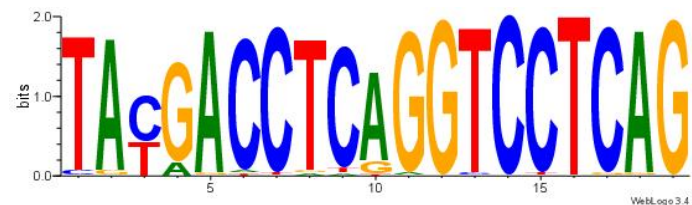
Alignment:

CTGAGGACCTGAGGTCRTA
---TGGACCTGAGAGC---

Original motif Consensus sequence: CTGAGGACCTGAGGTCRTA



Reverse complement motif Consensus sequence: TAMGACCTCAGGTCCTCAG

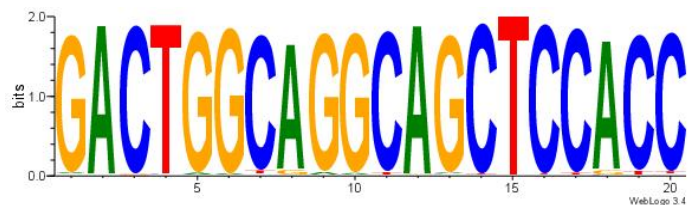


Dataset #: 1
Motif ID: 52
Motif name: Motif 52
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 6
Number of overlap: 13
Similarity score: 0.0809407

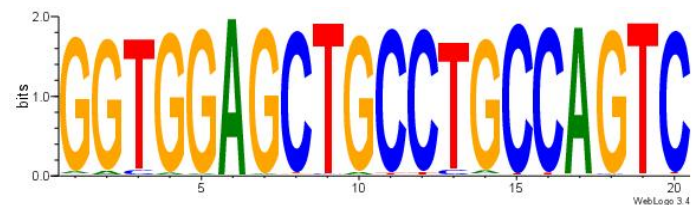
Alignment:

GACTGGCAGGCAGCTCCACC
-----GCTCTCAGGTCCA--

Original motif Consensus sequence: GACTGGCAGGCAGCTCCACC



Reverse complement motif Consensus sequence: GGTGGAGCTGCCTGCCAGTC

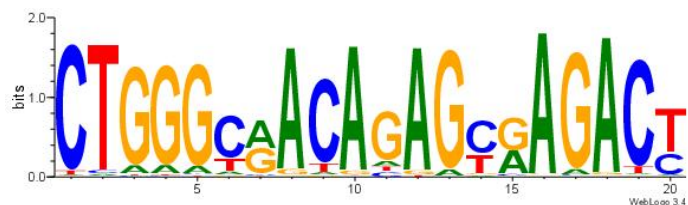


Dataset #: 1
Motif ID: 29
Motif name: Motif 29
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2
Number of overlap: 13
Similarity score: 0.0818999

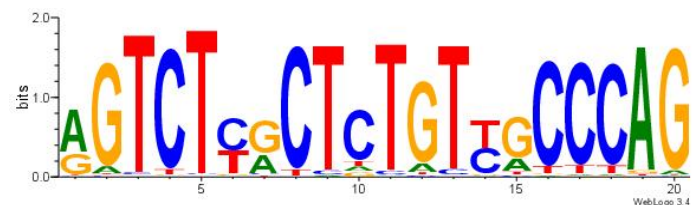
Alignment:

CTGGGCRACAGAGYRAGACY
-----TGGACCTGAGAGC--

Original motif Consensus sequence: CTGGGCRACAGAGYRAGACY



Reverse complement motif Consensus sequence: MGTCTMKCTCTGKGCCAG

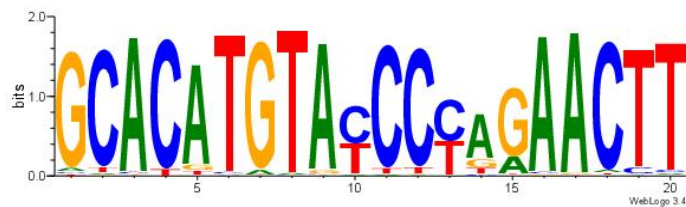


Dataset #: 1
 Motif ID: 225
 Motif name: Motif 225
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 13
 Similarity score: 0.0879728

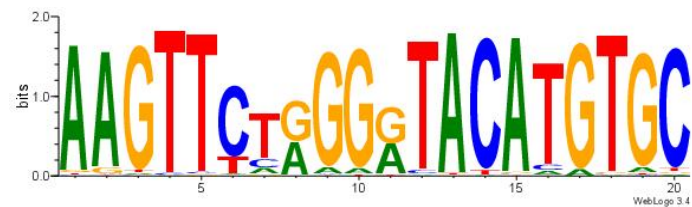
Alignment:

GCACATGTAYCCYAGAACTT
 --TGGACCTGAGAGC-----

Original motif Consensus sequence: GCACATGTAYCCYAGAACTT



Reverse complement motif Consensus sequence: AAGTTCTKGGKTACATGTGC



Dataset #: 1
 Motif ID: 362
 Motif name: Motif 362
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1

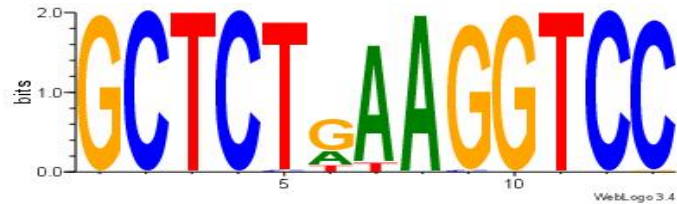
Number of overlap: 13
Similarity score: 0.0895644

Alignment:

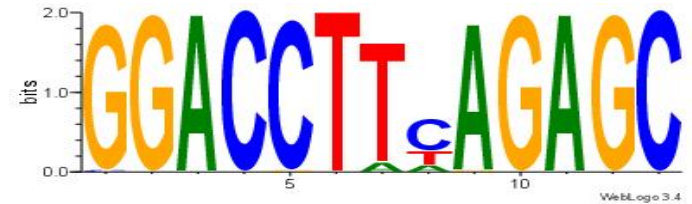
GCTCTGAAGGTCC

GCTCTCAGGTCCA

Original motif Consensus sequence: GCTCTGAAGGTCC

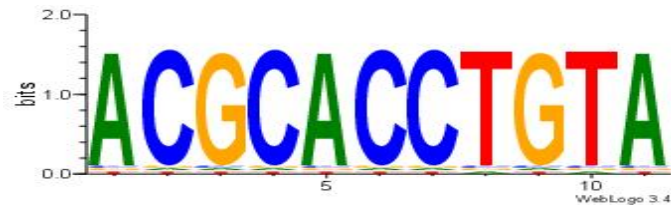


Reverse complement motif Consensus sequence: GGACCTTCAGAGC

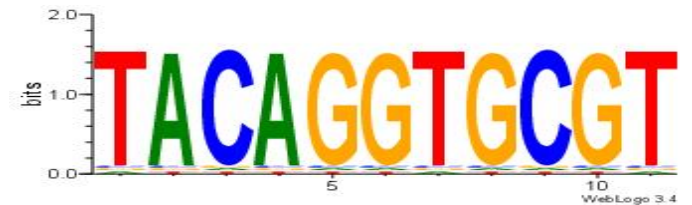


Dataset #: 1 Motif ID: 324 Motif name: Motif 324

Original motif Consensus sequence: ACGCACCTGTA



Reverse complement motif Consensus sequence: TACAGGTGCGT



Best Matches for Motif ID 324 (Highest to Lowest)

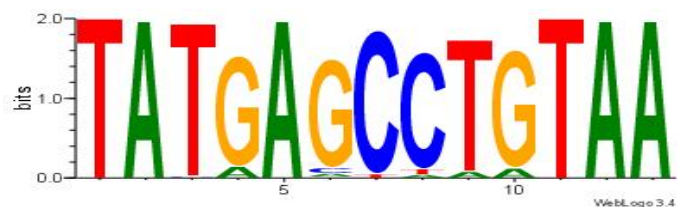
Dataset #: 1
Motif ID: 355
Motif name: Motif 355
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif

Direction: Backward
Position number: 2
Number of overlap: 11
Similarity score: 0.0752538

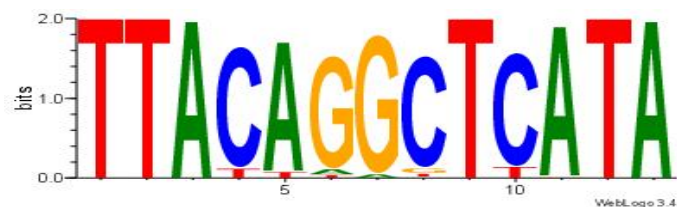
Alignment:

TATGAGCCTGTAA
-ACGCACCTGTA-

Original motif Consensus sequence: TATGAGCCTGTAA



Reverse complement motif Consensus sequence: TTACAGGCTCATA

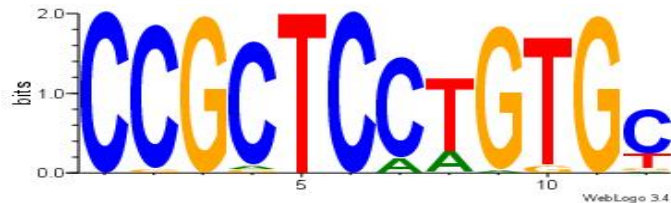


Dataset #: 1
Motif ID: 167
Motif name: Motif 167
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 11
Similarity score: 0.0802613

Alignment:

GCACAGGAGCGG
-TACAGGTGCGT

Original motif Consensus sequence: CCGCTCCTGTGC



Reverse complement motif Consensus sequence: GCACAGGAGCGG

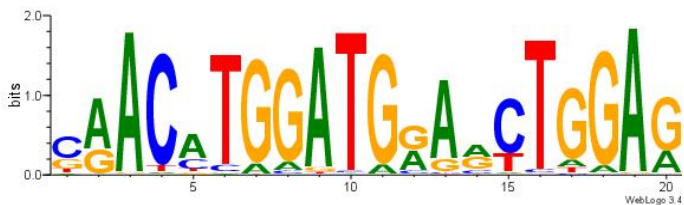


Dataset #: 1
Motif ID: 104
Motif name: Motif 104
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 9
Number of overlap: 11
Similarity score: 0.0876733

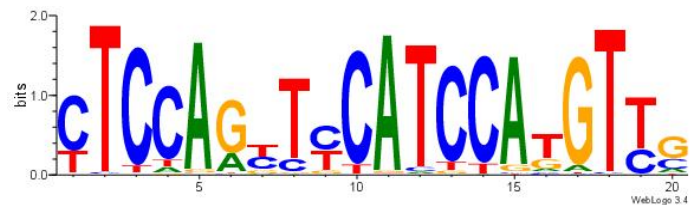
Alignment:

```
CTCCAGKTMCATCCATGTTG  
-TACAGGTGCGT-----
```

Original motif Consensus sequence: CAACATGGATGRARCTGGAG



Reverse complement motif Consensus sequence: CTCCAGKTMCATCCATGTTG

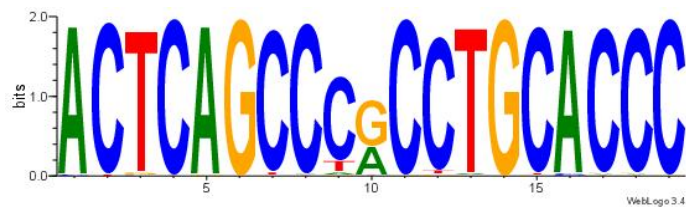


Dataset #: 1
 Motif ID: 149
 Motif name: Motif 149
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 4
 Number of overlap: 11
 Similarity score: 0.088024

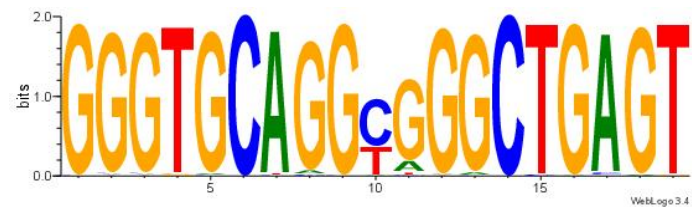
Alignment:

ACTCAGCCRCCTGCACCC
 -----ACGCACCTGTA----

Original motif Consensus sequence: ACTCAGCCRCCTGCACCC



Reverse complement motif Consensus sequence: GGGTGCAGGMGGCTGAGT

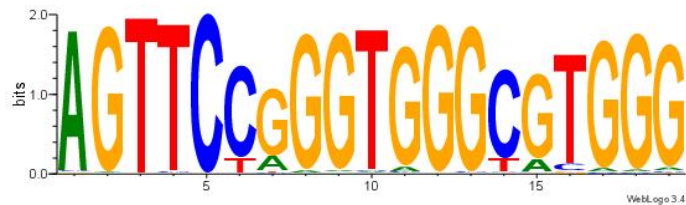


Dataset #: 1
 Motif ID: 98
 Motif name: Motif 98
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 6

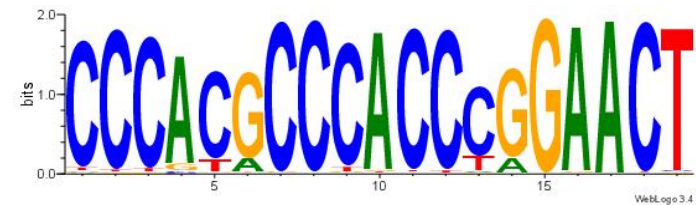
Number of overlap: 11
 Similarity score: 0.0887977

Alignment:
 CCCACGCCCACCCGGA
 ACT
 ---ACGCACCTGTA-----

Original motif Consensus sequence: AGTTCCGGGTGGGCGTGGG

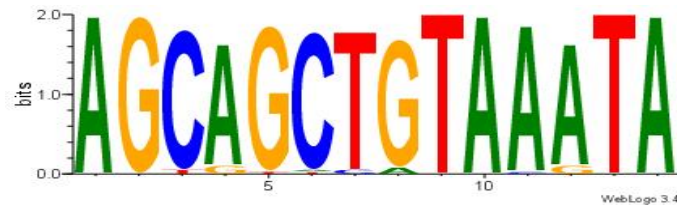


Reverse complement motif Consensus sequence:
 CCCACGCCCACCCGGA
 ACT

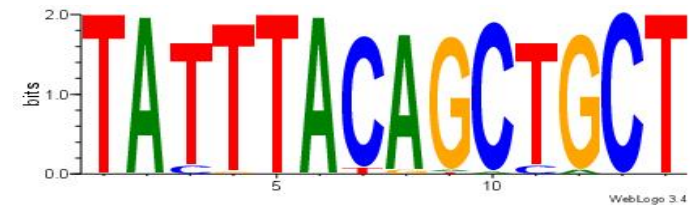


Dataset #: 1 Motif ID: 325 Motif name: Motif 325

Original motif Consensus sequence: AGCAGCTGTAAATA



Reverse complement motif Consensus sequence: TATTTACAGCTGCT



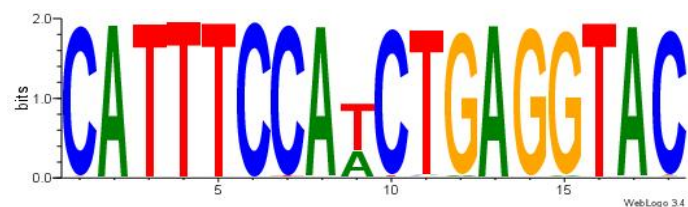
Best Matches for Motif ID 325 (Highest to Lowest)

Dataset #: 1
 Motif ID: 25
 Motif name: Motif 25
 Matching format of first motif: Original Motif

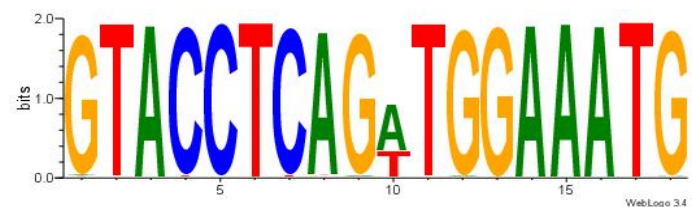
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 5
Number of overlap: 14
Similarity score: 0.087674

Alignment:
GTACCTCAGWTGGAAATG
AGCAGCTGTAAATA-----

Original motif Consensus sequence: CATTCCA^WCTGAGGTAC



Reverse complement motif Consensus sequence: GTACCTCAGWTGGAAATG

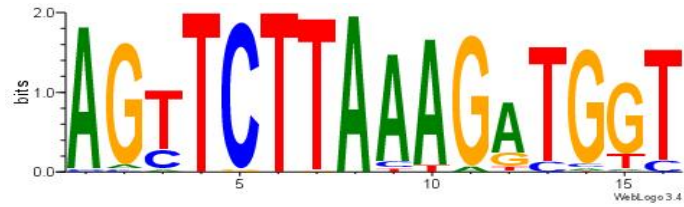


Dataset #: 1
Motif ID: 303
Motif name: Motif 303
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 14
Similarity score: 0.0891021

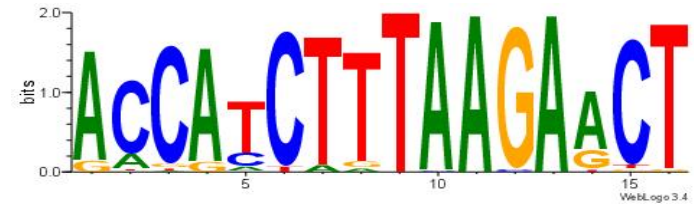
Alignment:

AGTTCTTAAAGATGGT
TATTTACAGCTGCT--

Original motif Consensus sequence: AGTTCTTAAAGATGGT



Reverse complement motif Consensus sequence:
ACCATCTTTAAGAACT



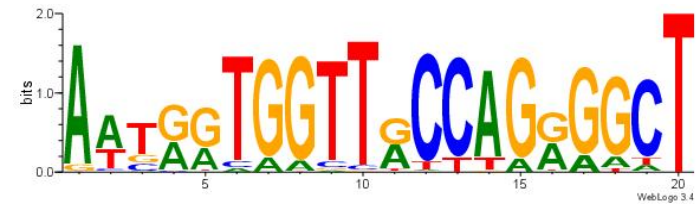
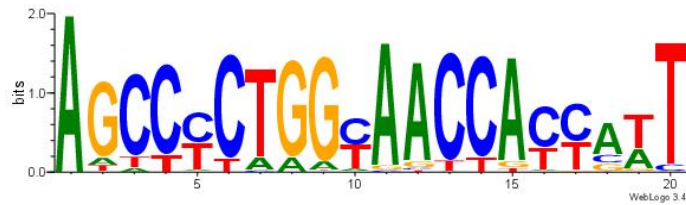
Dataset #:	1
Motif ID:	139
Motif name:	Motif 139
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	7
Number of overlap:	14
Similarity score:	0.0976016

Alignment:

AWTKKTGGTTKCCAGKGGCT
-----TATTTACAGCTGCT

Original motif Consensus sequence: AGCCYCTGGYAACCAYYAWT

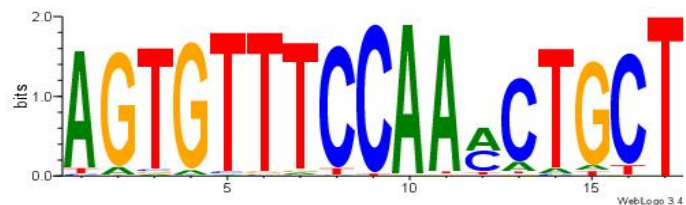
Reverse complement motif Consensus sequence:
AWTKKTGGTTKCCAGKGGCT



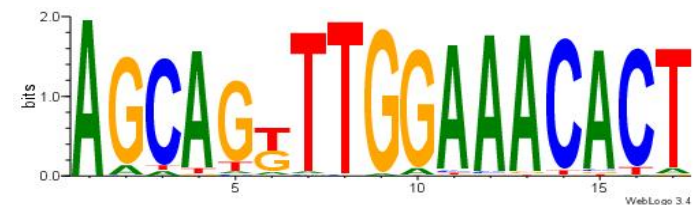
Dataset #: 1
 Motif ID: 304
 Motif name: Motif 304
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 4
 Number of overlap: 14
 Similarity score: 0.100233

Alignment:
 AGTGTTTCCAAMCTGCT
 TATTTACAGCTGCT---

Original motif Consensus sequence: AGTGTTTCCAAMCTGCT



Reverse complement motif Consensus sequence: AGCAGTTGGAAACACT



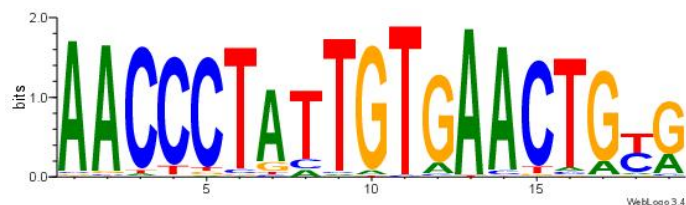
Dataset #: 1

Motif ID: 242
 Motif name: Motif 242
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0.104976

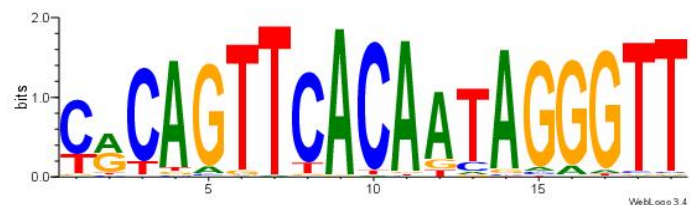
Alignment:

CMCAGTTCACAATAGGGTT
 -----AGCAGCTGTAAATA

Original motif Consensus sequence: AACCTATTGTGAACTGYG

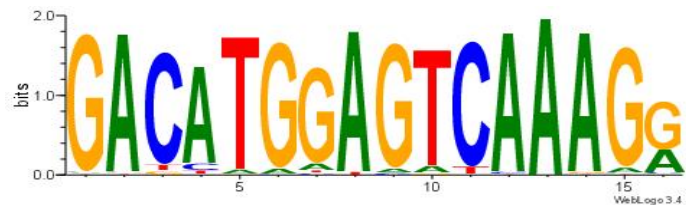


Reverse complement motif Consensus sequence: CMCAGTTCACAATAGGGTT

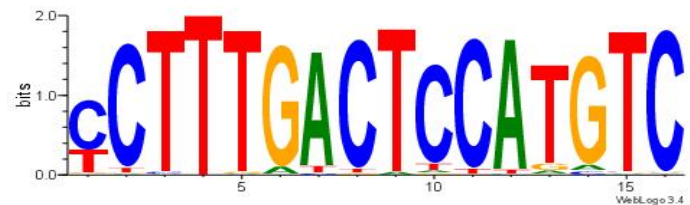


Dataset #: 1 Motif ID: 326 Motif name: Motif 326

Original motif Consensus sequence: GACATGGAGTCAAAGG



Reverse complement motif Consensus sequence: CCTTGACTCCATGTC



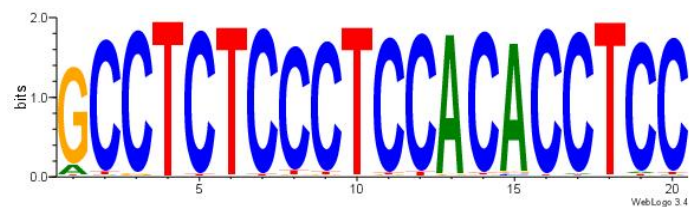
Best Matches for Motif ID 326 (Highest to Lowest)

Dataset #: 1
Motif ID: 105
Motif name: Motif 105
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 2
Number of overlap: 16
Similarity score: 0.0861073

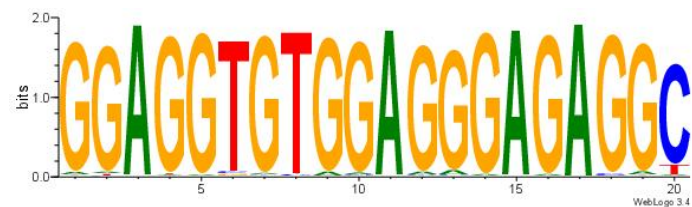
Alignment:

```
GGAGGTGTGGAGGGAGAGGC  
-GACATGGAGTCAAAGG---
```

Original motif Consensus sequence: GCCTCTCCCTCCACACCTCC



Reverse complement motif Consensus sequence:
GGAGGTGTGGAGGGAGAGGC

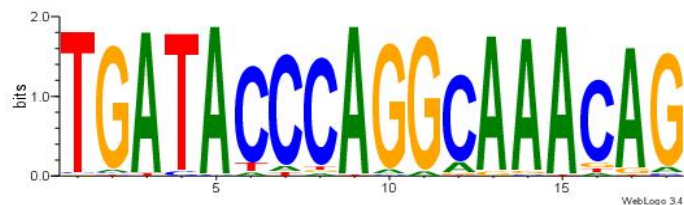


Dataset #: 1
Motif ID: 290
Motif name: Motif 290
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif

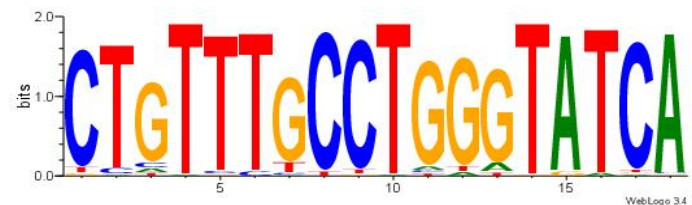
Direction: Forward
Position number: 2
Number of overlap: 16
Similarity score: 0.0886417

Alignment:
TGATACCCAGGCAAACAG
-GACATGGAGTCAAAGG-

Original motif Consensus sequence: TGATACCCAGGCAAACAG



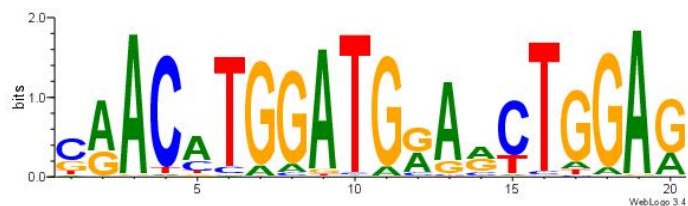
Reverse complement motif Consensus sequence: CTGTTTGCCTGGGTATCA



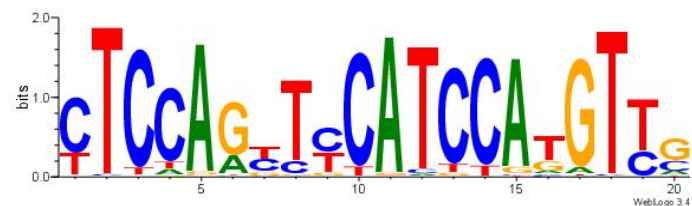
Dataset #: 1
Motif ID: 104
Motif name: Motif 104
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 2
Number of overlap: 16
Similarity score: 0.0935769

Alignment:
CTCCAGKTMCATCCATGTTG
---CCTTTGACTCCATGTC-

Original motif Consensus sequence: CAACATGGATGRARCTGGAG



Reverse complement motif Consensus sequence: CTCAGKTMCATCCATGTTG

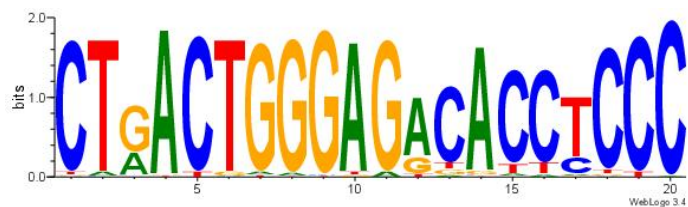


Dataset #: 1
Motif ID: 293
Motif name: Motif 293
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 3
Number of overlap: 16
Similarity score: 0.0948138

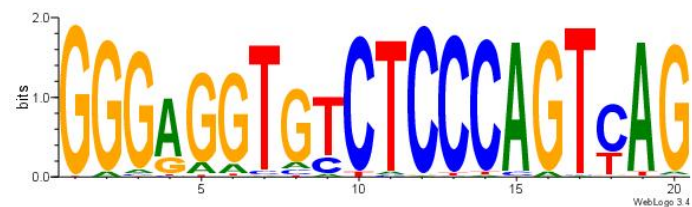
Alignment:

```
GGGAGGTGTCTCCCAGTCAG  
--CCTTTGACTCCATGTC--
```

Original motif Consensus sequence: CTGACTGGGAGACACCTCCC



Reverse complement motif Consensus sequence: GGGAGGTGTCTCCCAGTCAG

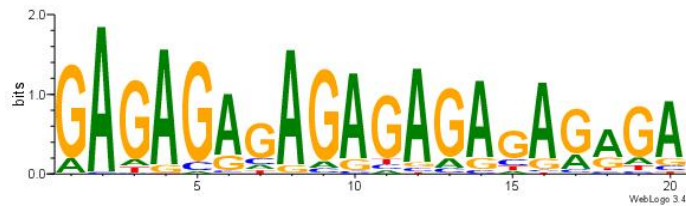


Dataset #: 1
 Motif ID: 109
 Motif name: Motif 109
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 16
 Similarity score: 0.0957162

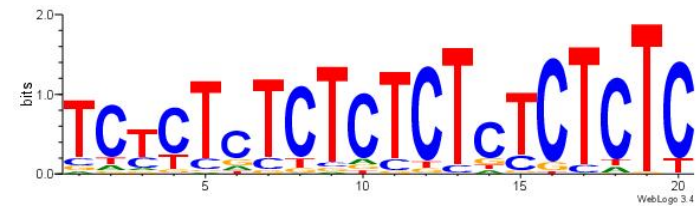
Alignment:

GAGAGAGAGAGAGAGAGAGA
 GACATGGAGTCAAAGG-----

Original motif Consensus sequence: GAGAGAGAGAGAGAGAGAGA



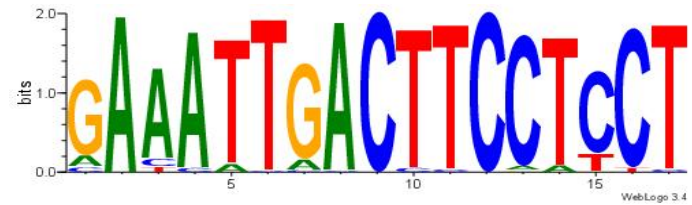
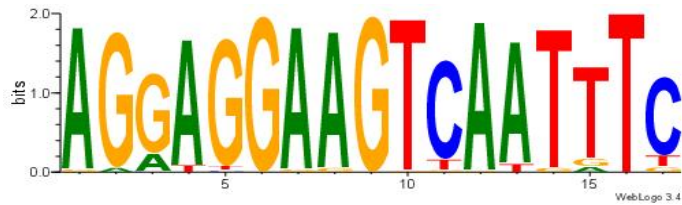
Reverse complement motif Consensus sequence: TCTCTCTCTCTCTCTCTC



Dataset #: 1 Motif ID: 327 Motif name: Motif 327

Original motif Consensus sequence: AGGAGGAAGTCAATTC

Reverse complement motif Consensus sequence: GAAATTGACTTCCTCT

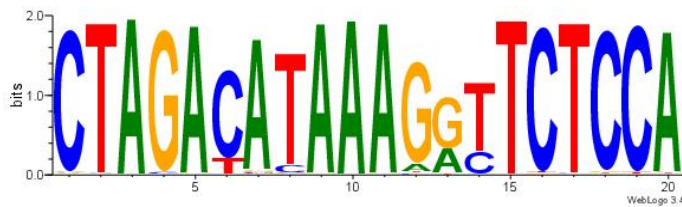


Best Matches for Motif ID 327 (Highest to Lowest)

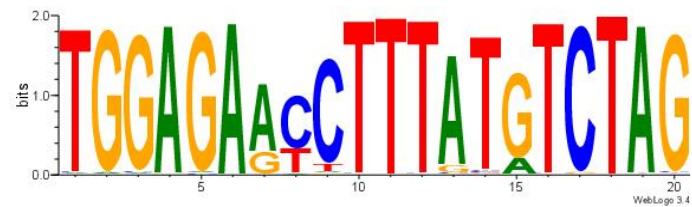
Dataset #: 1
 Motif ID: 85
 Motif name: Motif 85
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 4
 Number of overlap: 17
 Similarity score: 0.087633

Alignment:
 CTAGACATAAAGGTTCTCCA
 GAAATTGACTTCCCT---

Original motif Consensus sequence: CTAGACATAAAGGTTCTCCA



Reverse complement motif Consensus sequence: TGGAGAACCTTTATGTCTAG

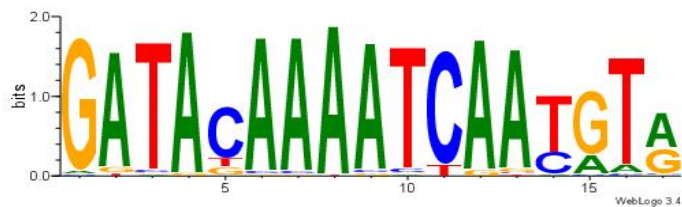


Dataset #: 1
 Motif ID: 328
 Motif name: Motif 328
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 17
 Similarity score: 0.0921863

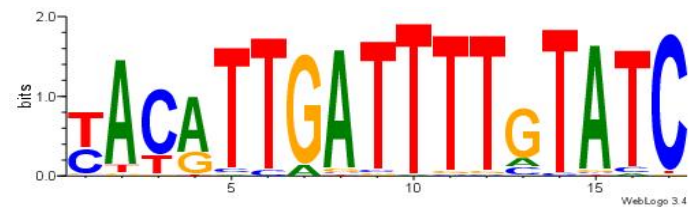
Alignment:

KACATTGATTTTGTATC
 GAAATTGACTTCCTCCT

Original motif Consensus sequence: GATACAAAATCAATGTR



Reverse complement motif Consensus sequence: KACATTGATTTTGTATC



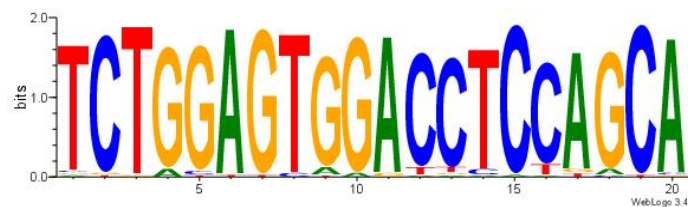
Dataset #: 1
 Motif ID: 350
 Motif name: Motif 350
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1

Number of overlap: 17
Similarity score: 0.0926364

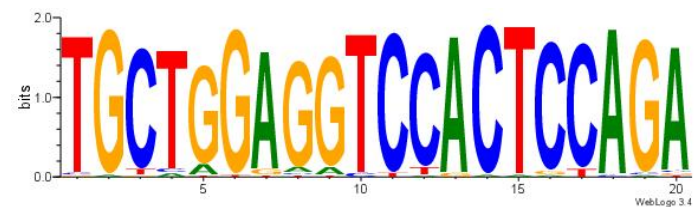
Alignment:

TGCTGGAGGTCCACTCCAGA
AGGAGGAAGTCAATTC---

Original motif Consensus sequence: TCTGGAGTGGACCTCCAGCA



Reverse complement motif Consensus sequence:
TGCTGGAGGTCCACTCCAGA

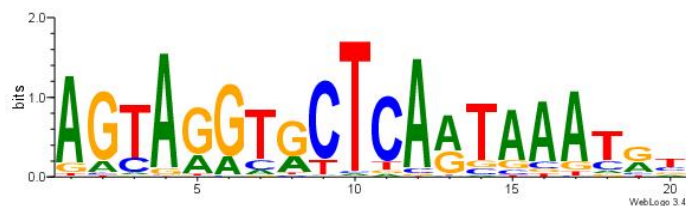


Dataset #: 1
Motif ID: 86
Motif name: Motif 86
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 4
Number of overlap: 17
Similarity score: 0.094205

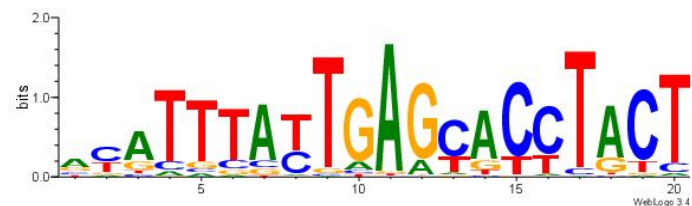
Alignment:

VMATTTAKTGAGCACCTACT
---GAAATTGACTTCCTCCT

Original motif Consensus sequence: AGTAGGTGCTCARTAAATRB



Reverse complement motif Consensus sequence: VMATTTAKTGAGCACCTACT

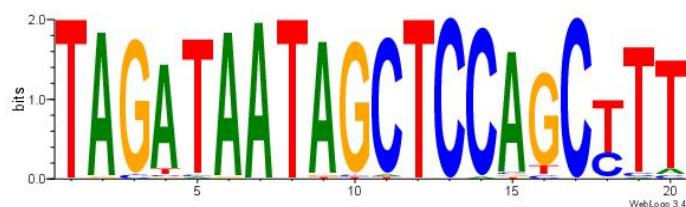


Dataset #: 1
Motif ID: 333
Motif name: Motif 333
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 3
Number of overlap: 17
Similarity score: 0.100031

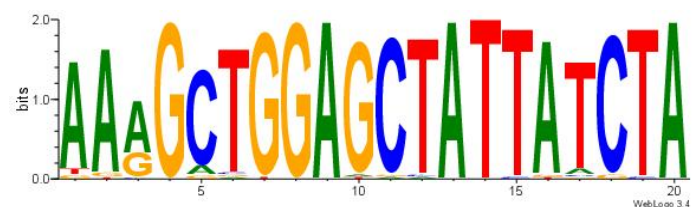
Alignment:

TAGATAATAGCTCCAGCTTT
--GAAATTGACTTCCTCCT--

Original motif Consensus sequence: TAGATAATAGCTCCAGCTTT

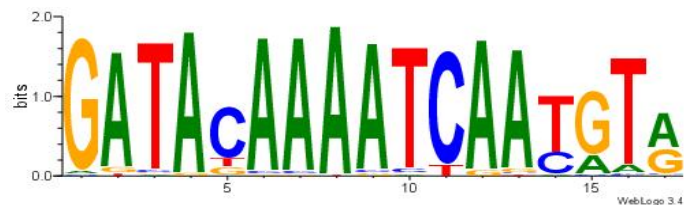


Reverse complement motif Consensus sequence: AAAGCTGGAGCTATTATCTA

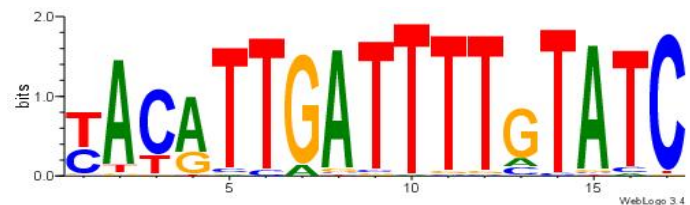


Dataset #: 1 Motif ID: 328 Motif name: Motif 328

Original motif Consensus sequence: GATACAAAATCAATGTR



Reverse complement motif Consensus sequence: KACATTGATTTTGTATC



Best Matches for Motif ID 328 (Highest to Lowest)

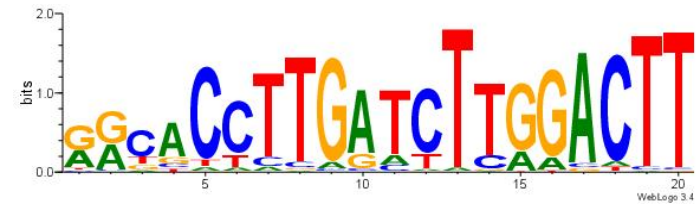
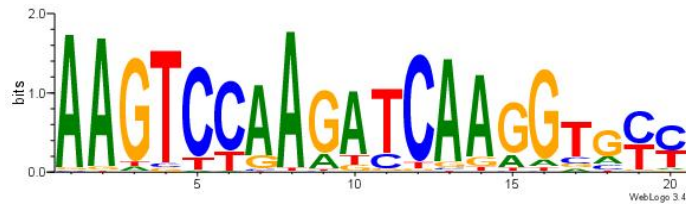
Dataset #:	1
Motif ID:	119
Motif name:	Motif 119
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	17
Similarity score:	0.0460385

Alignment:

```
AAGTCCAAGATCAAGGTGY  
-GATACAAAATCAATGTR--
```

Original motif Consensus sequence: AAGTCCAAGATCAAGGTGY

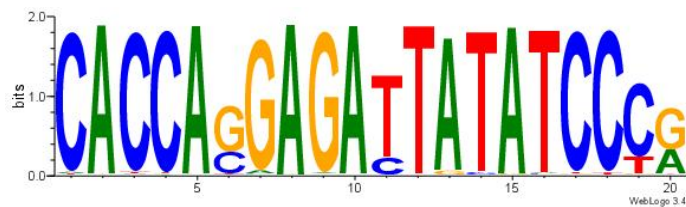
Reverse complement motif Consensus sequence: KKCACCTTGATCTTGACTT



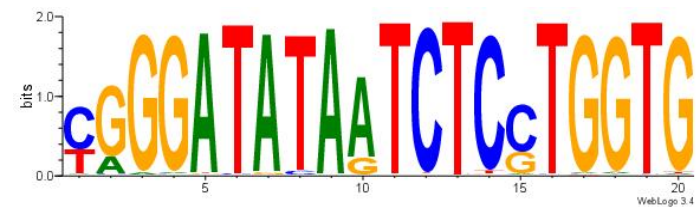
Dataset #: 1
 Motif ID: 19
 Motif name: Motif 19
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 17
 Similarity score: 0.0587823

Alignment:
 CACCAGGAGATTATATCCCR
 ---KACATTGATTTTGTATC

Original motif Consensus sequence: CACCAGGAGATTATATCCCR



Reverse complement motif Consensus sequence: MGGGATATAATCTCCTGGTG



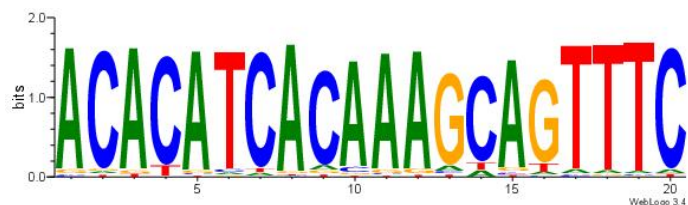
Dataset #: 1

Motif ID: 202
 Motif name: Motif 202
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 4
 Number of overlap: 17
 Similarity score: 0.0635566

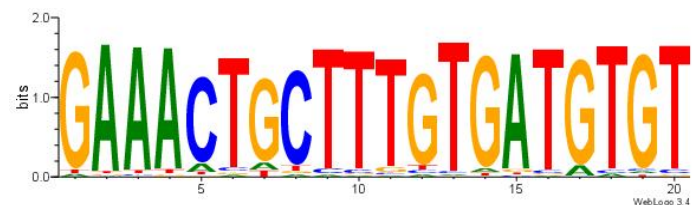
Alignment:

GAAACTGCTTTGTGATGTGT
 KACATTGATTTTGTATC---

Original motif Consensus sequence: ACACATCACAAGCAGTTTC



Reverse complement motif Consensus sequence: GAAACTGCTTTGTGATGTGT



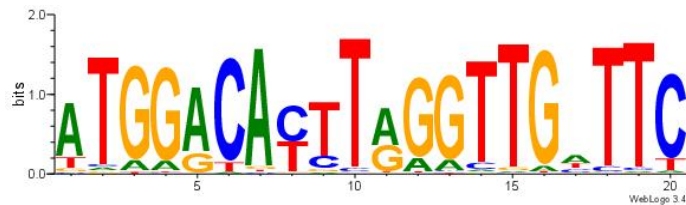
Dataset #: 1
 Motif ID: 58
 Motif name: Motif 58
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 17

Similarity score: 0.0636486

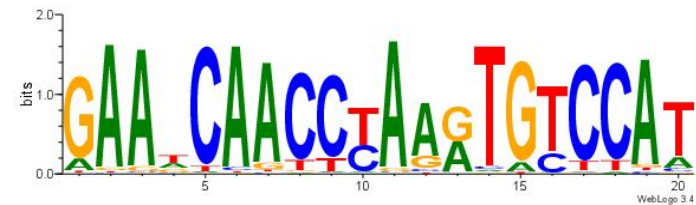
Alignment:

GAAHCAACCKAAKTGTCCAT
---GATACAAAATCAATGTR

Original motif Consensus sequence: ATGGACAYTTRGGTTGHTTC



Reverse complement motif Consensus sequence:
GAAHCAACCKAAKTGTCCAT



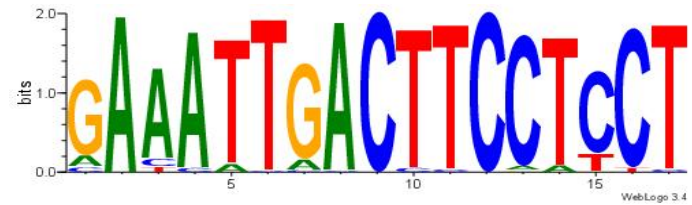
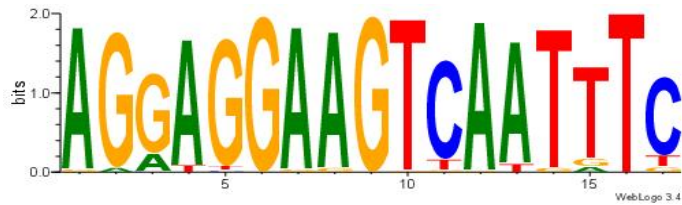
Dataset #: 1
Motif ID: 327
Motif name: Motif 327
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 17
Similarity score: 0.0643479

Alignment:

GAAATTGACTTCCTCCT
KACATTGATTTTGTATC

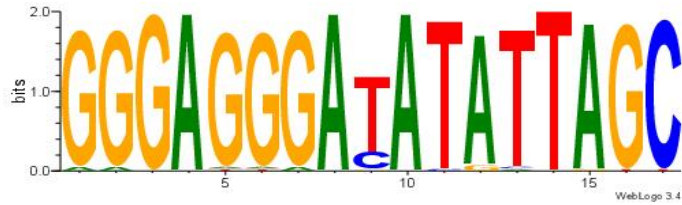
Original motif Consensus sequence: AGGAGGAAGTCAATTC

Reverse complement motif Consensus sequence:
GAAATTGACTTCCTCCT

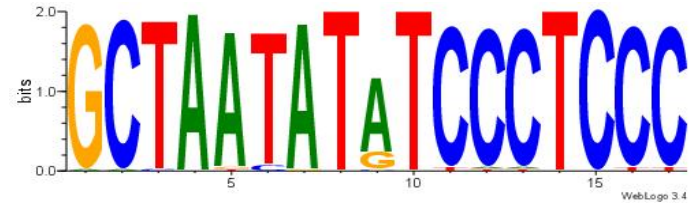


Dataset #: 1 Motif ID: 329 Motif name: Motif 329

Original motif Consensus sequence: GGGAGGGATATATTAGC



Reverse complement motif Consensus sequence: GCTAATATCCCTCCC



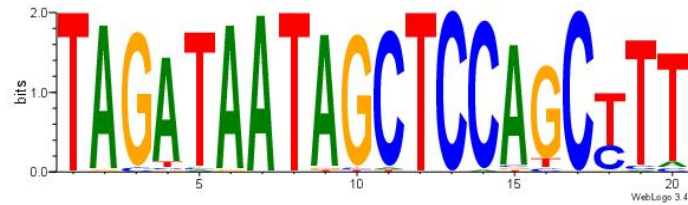
Best Matches for Motif ID 329 (Highest to Lowest)

Dataset #:	1
Motif ID:	333
Motif name:	Motif 333
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	3
Number of overlap:	17
Similarity score:	0.0923491

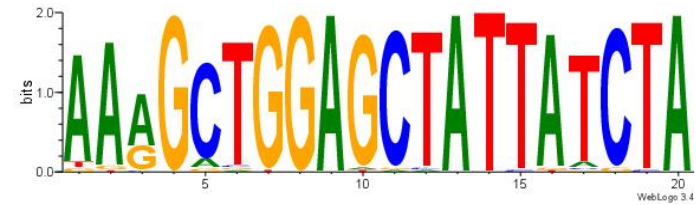
Alignment:

TAGATAATAGCTCCAGCTTT
--GCTAATATATCCCTCCC--

Original motif Consensus sequence: TAGATAATAGCTCCAGCTTT



Reverse complement motif Consensus sequence:
AAAGCTGGAGCTATTATCTA



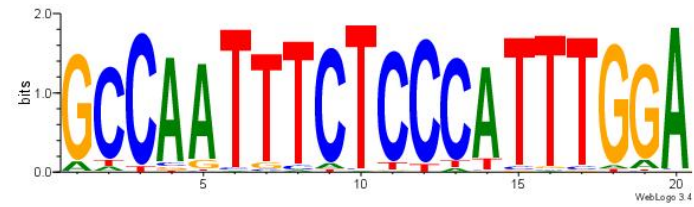
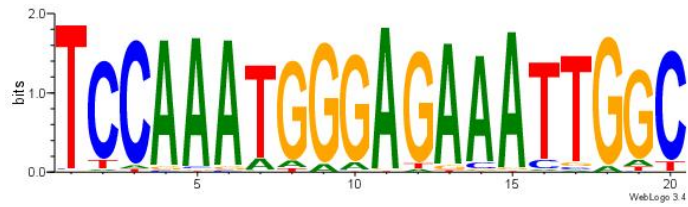
Dataset #: 1
Motif ID: 235
Motif name: Motif 235
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 17
Similarity score: 0.102804

Alignment:

GCCAATTTCTCCCATTTGGA
GCTAATATATCCCTCCC---

Original motif Consensus sequence: TCCAATGGGAGAAATTGGC

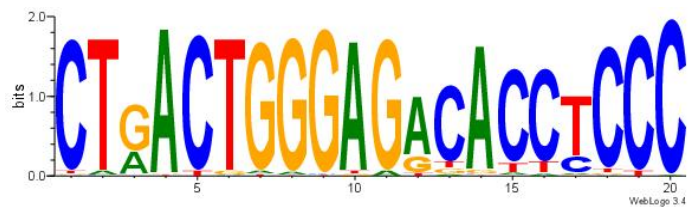
Reverse complement motif Consensus sequence:
GCCAATTTCTCCCATTTGGA



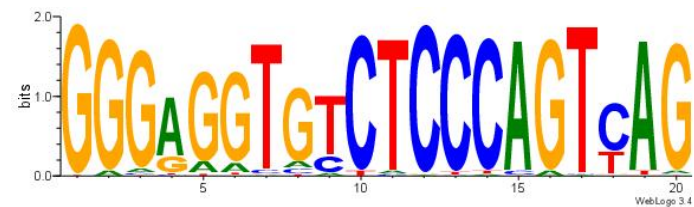
Dataset #: 1
 Motif ID: 293
 Motif name: Motif 293
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 4
 Number of overlap: 17
 Similarity score: 0.109545

Alignment:
 GGGAGGTGTCTCCCAGTCAG
 ---GGGAGGGATATATTAGC

Original motif Consensus sequence: CTGACTGGGAGACACCTCCC



Reverse complement motif Consensus sequence: GGGAGGTGTCTCCCAGTCAG



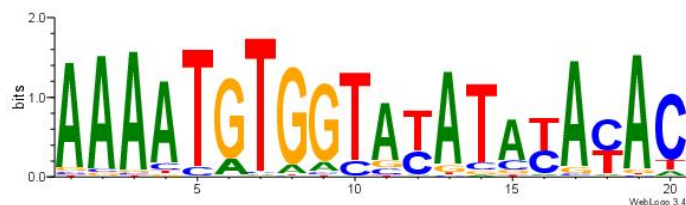
Dataset #: 1

Motif ID: 83
 Motif name: Motif 83
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 4
 Number of overlap: 17
 Similarity score: 0.114728

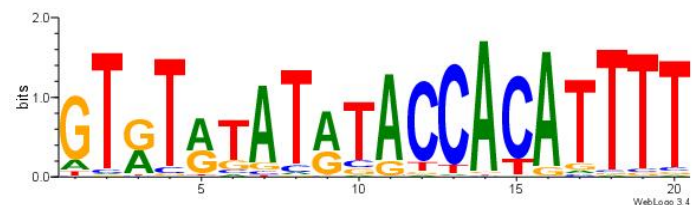
Alignment:

GTKTMTATMTACCACATTTT
 GCTAATATATCCCTCCC---

Original motif Consensus sequence: AAAATGTGGTAYATAYAYAC



Reverse complement motif Consensus sequence: GTKTMTATMTACCACATTTT



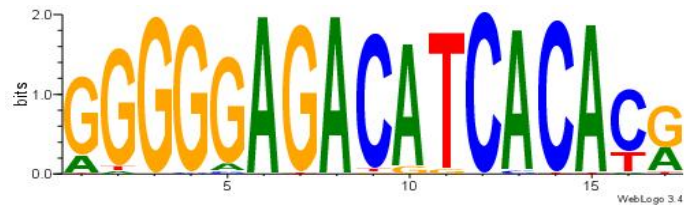
Dataset #: 1
 Motif ID: 279
 Motif name: Motif 279
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 17

Similarity score: 0.115902

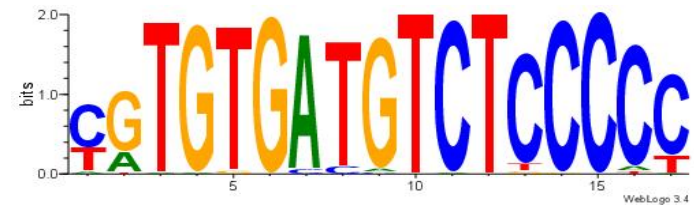
Alignment:

GGGGGAGACATCACACR
GGGAGGGATATATTAGC

Original motif Consensus sequence: GGGGGAGACATCACACR

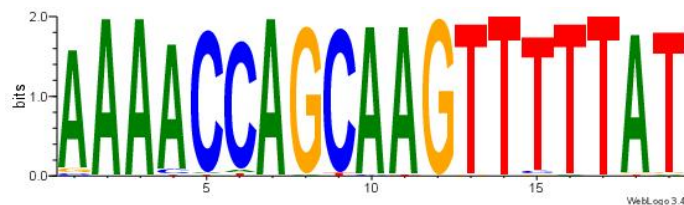


Reverse complement motif Consensus sequence: MGTGTGATGTCTCCCC

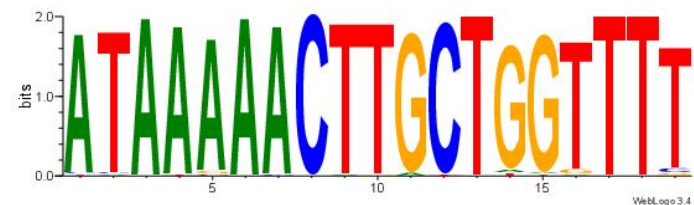


Dataset #: 1 Motif ID: 330 Motif name: Motif 330

Original motif Consensus sequence: AAAACCAGCAAGTTTTTAT



Reverse complement motif Consensus sequence: ATAAAACTTGCTGGTTTT



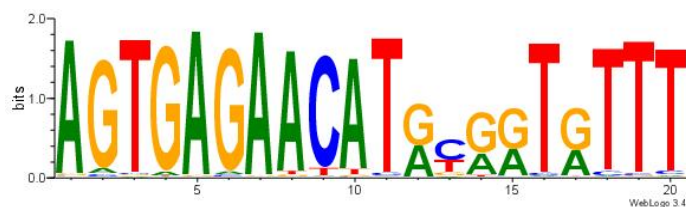
Best Matches for Motif ID 330 (Highest to Lowest)

Dataset #:	1
Motif ID:	63
Motif name:	Motif 63
Matching format of first motif:	Reverse Complement

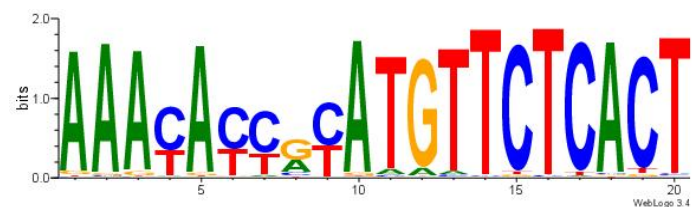
Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 19
 Similarity score: 0.0925249

Alignment:
 AGTGAGAACATRYRRTRTTT
 ATAAAAACTTGCTGGTTTT-

Original motif Consensus sequence: AGTGAGAACATRYRRTRTTT



Reverse complement motif Consensus sequence: AAAMAMMKMATGTTCTCACT

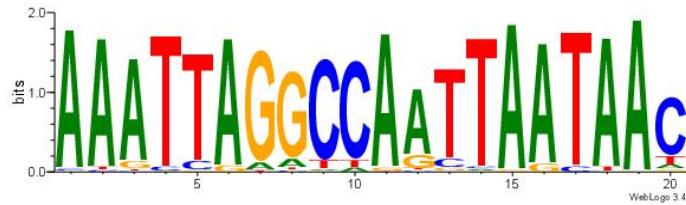


Dataset #: 1
 Motif ID: 308
 Motif name: Motif 308
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 19
 Similarity score: 0.112206

Alignment:

AAATTAGGCCAATTAATAAC
AAAACCAGCAAGTTTTTAT-

Original motif Consensus sequence: AAATTAGGCCAATTAATAAC



Reverse complement motif Consensus sequence:
GTTATTAATTGGCCTAATTT

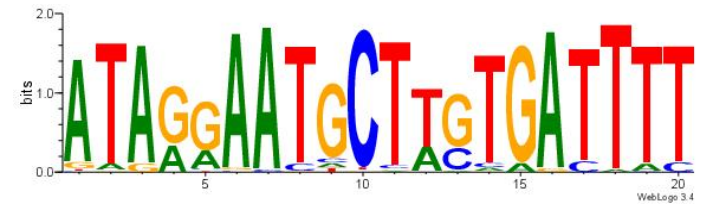
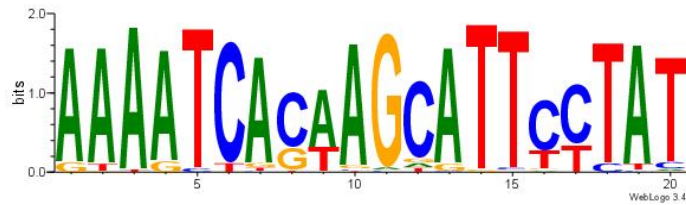


Dataset #: 1
Motif ID: 254
Motif name: Motif 254
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 19
Similarity score: 0.114461

Alignment:
AAAATCACAAGCATTTCCTAT
AAAACCAGCAAGTTTTTAT-

Original motif Consensus sequence: AAAATCACAAGCATTTCCTAT

Reverse complement motif Consensus sequence:
ATAGGAATGCTTGTGATTTT

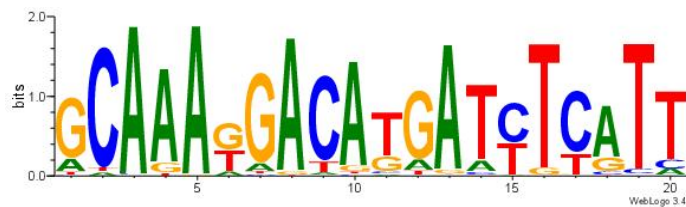


Dataset #: 1
 Motif ID: 99
 Motif name: Motif 99
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 19
 Similarity score: 0.121081

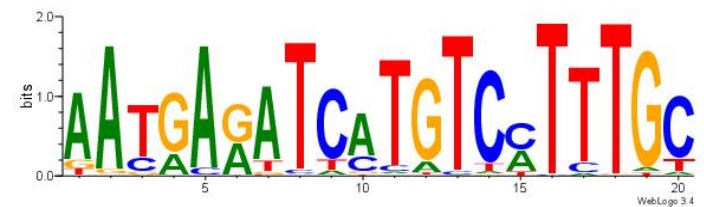
Alignment:

GCAAAGACATGATYTCATT
 AAAACCAGCAAGTTTTTAT-

Original motif Consensus sequence: GCAAAGACATGATYTCATT



Reverse complement motif Consensus sequence: AATGAKATCATGTCYTTTGC



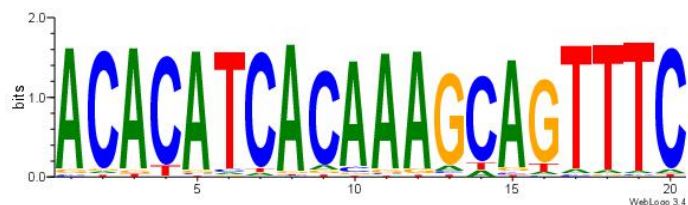
Dataset #: 1

Motif ID: 202
 Motif name: Motif 202
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 19
 Similarity score: 0.121875

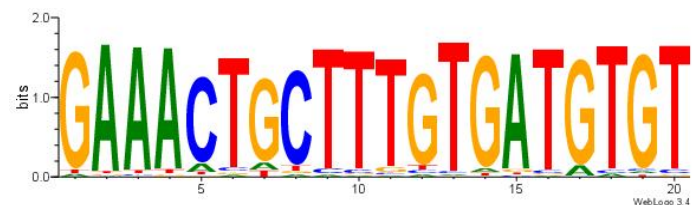
Alignment:

GAAACTGCTTTGTGATGTGT
 ATAAAACTTGCTGGTTTT-

Original motif Consensus sequence: ACACATCACAAGCAGTTTC

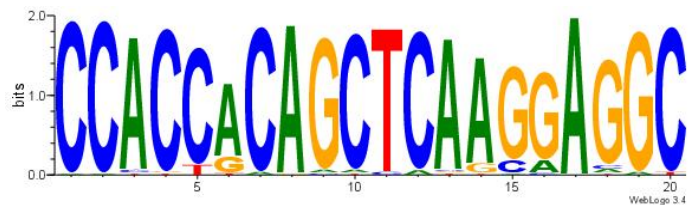


Reverse complement motif Consensus sequence: GAAACTGCTTTGTGATGTGT

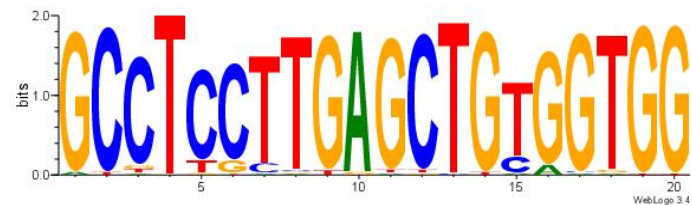


Dataset #: 1 Motif ID: 331 Motif name: Motif 331

Original motif Consensus sequence: CCACCACAGCTCAAGGAGGC



Reverse complement motif Consensus sequence: GCCTCTGAGCTGTGGTGG



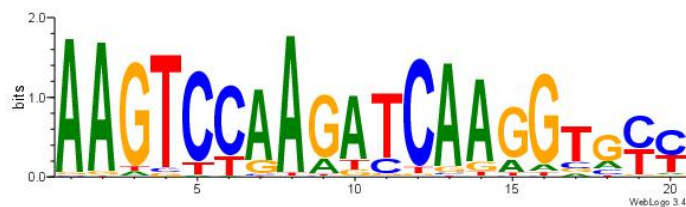
Best Matches for Motif ID 331 (Highest to Lowest)

Dataset #: 1
Motif ID: 119
Motif name: Motif 119
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 20
Similarity score: 0.112645

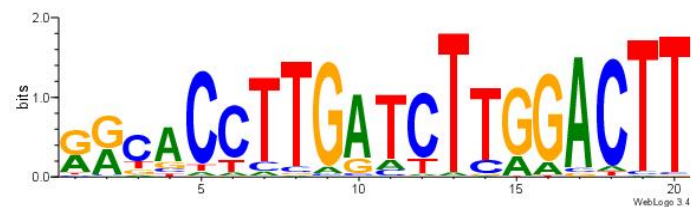
Alignment:

```
KKCACCTTGATCTTGGACTT  
GCCTCCTTGAGCTGTGGTGG
```

Original motif Consensus sequence: AAGTCCAAGATCAAGGTGY



Reverse complement motif Consensus sequence: KKCACCTTGATCTTGGACTT



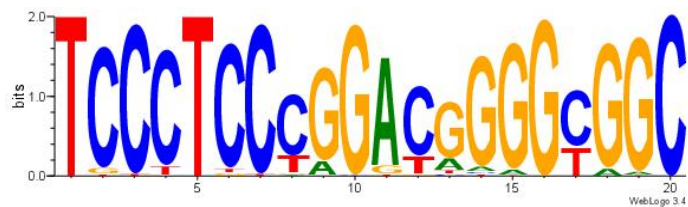
Dataset #: 1
Motif ID: 155
Motif name: Motif 155
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement

Direction: Forward
Position number: 1
Number of overlap: 20
Similarity score: 0.115101

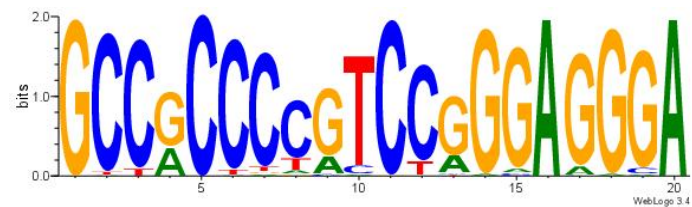
Alignment:

GCCKCCCCGTCCGGGAGGGA
GCCTCCTTGAGCTGTGGTGG

Original motif Consensus sequence: TCCCTCCCGGACGGGGYGGC



Reverse complement motif Consensus sequence: GCCKCCCCGTCCGGGAGGGA

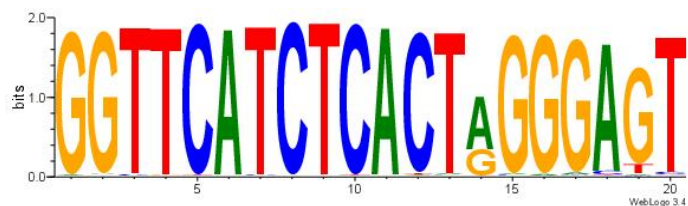


Dataset #: 1
Motif ID: 23
Motif name: Motif 23
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 20
Similarity score: 0.126303

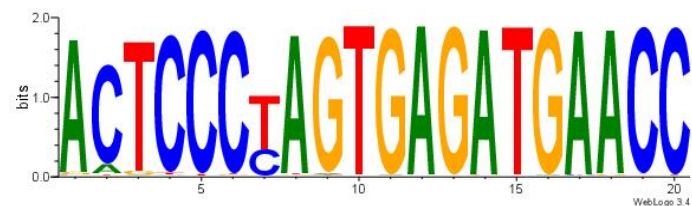
Alignment:

ACTCCCTAGTGAGATGAACC
CCACCACAGCTCAAGGAGGC

Original motif Consensus sequence: GGTTTCATCTCACTAGGGAGT



Reverse complement motif Consensus sequence: ACTCCCTAGTGAGATGAACC

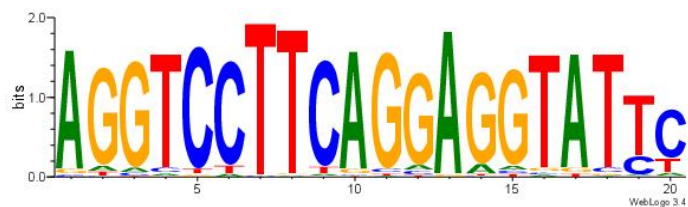


Dataset #: 1
Motif ID: 179
Motif name: Motif 179
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 20
Similarity score: 0.127958

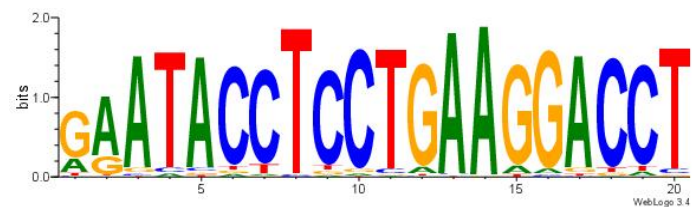
Alignment:

GAATACCTCCTGAAGGACCT
CCACCACAGCTCAAGGAGGC

Original motif Consensus sequence: AGGTCCTTCAGGAGGTATTC



Reverse complement motif Consensus sequence: GAATACCTCCTGAAGGACCT

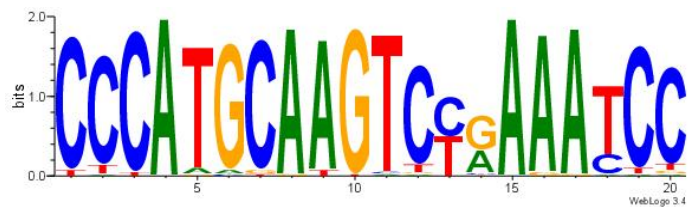


Dataset #: 1
 Motif ID: 310
 Motif name: Motif 310
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.132863

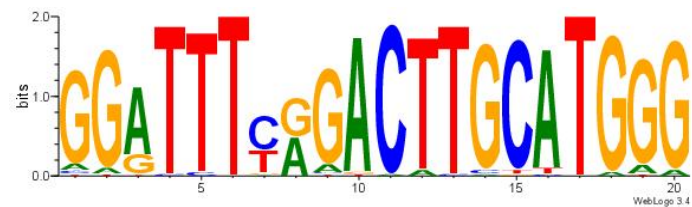
Alignment:

CCCATGCAAGTCYRAAATCC
 CCACCACAGCTCAAGGAGGC

Original motif Consensus sequence: CCCATGCAAGTCYRAAATCC



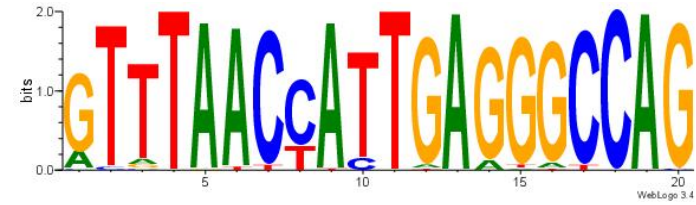
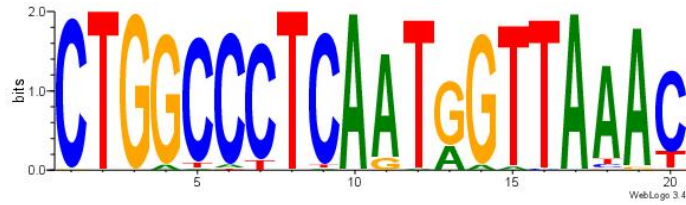
Reverse complement motif Consensus sequence: GGATTTMKGACTTGCATGGG



Dataset #: 1 Motif ID: 332 Motif name: Motif 332

Original motif Consensus sequence: CTGGCCCTCAATGGTTAAAC

Reverse complement motif Consensus sequence: GTTTAACCATTGAGGGCCAG

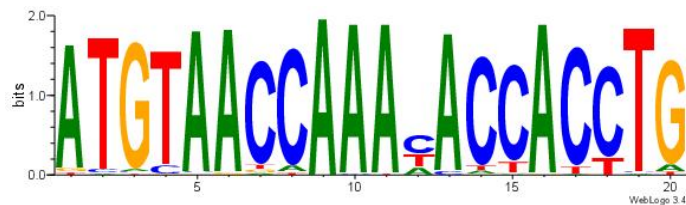


Best Matches for Motif ID 332 (Highest to Lowest)

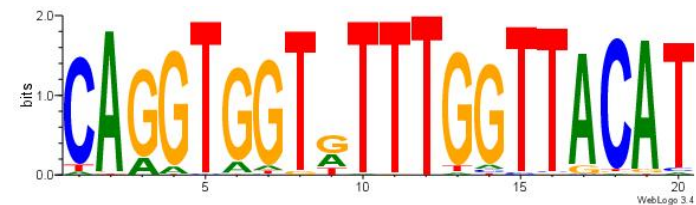
Dataset #: 1
 Motif ID: 336
 Motif name: Motif 336
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.102201

Alignment:
 CAGGTGGTKTTTGGTTACAT
 CTGGCCCTCAATGGTTAAAC

Original motif Consensus sequence: ATGTAACCAAAYACCACCTG



Reverse complement motif Consensus sequence: CAGGTGGTKTTTGGTTACAT

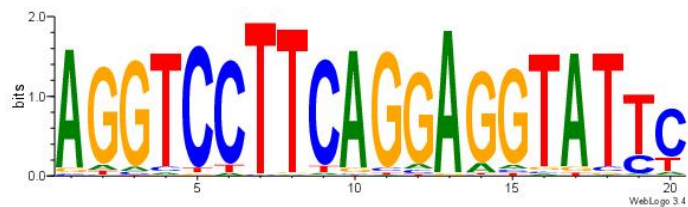


Dataset #: 1
 Motif ID: 179
 Motif name: Motif 179
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.106854

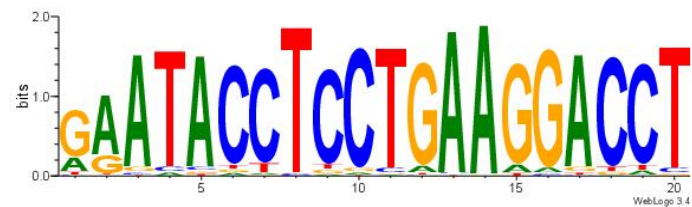
Alignment:

AGGTCCTTCAGGAGGTATTC
 CTGGCCCTCAATGGTTAAAC

Original motif Consensus sequence: AGGTCCTTCAGGAGGTATTC



Reverse complement motif Consensus sequence: GAATACCTCTGAAGGACCT



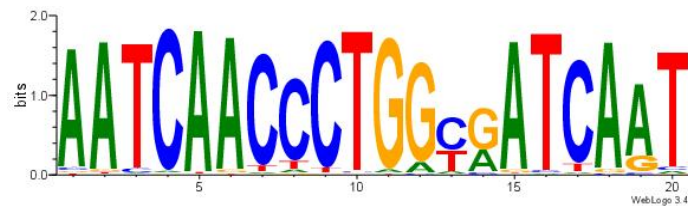
Dataset #: 1
 Motif ID: 170
 Motif name: Motif 170
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1

Number of overlap: 20
Similarity score: 0.115252

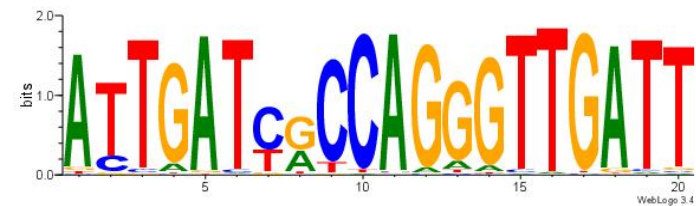
Alignment:

AATCAACCCTGGYRATCAAT
GTTTAACCATTGAGGGCCAG

Original motif Consensus sequence: AATCAACCCTGGYRATCAAT



Reverse complement motif Consensus sequence:
ATTGATMKCCAGGGTTGATT

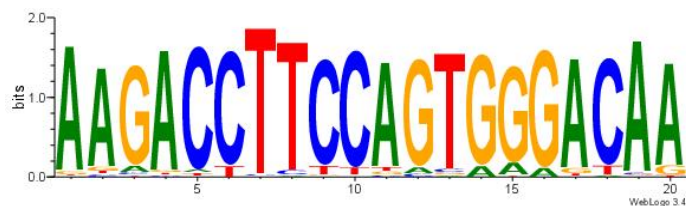


Dataset #: 1
Motif ID: 292
Motif name: Motif 292
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 20
Similarity score: 0.115516

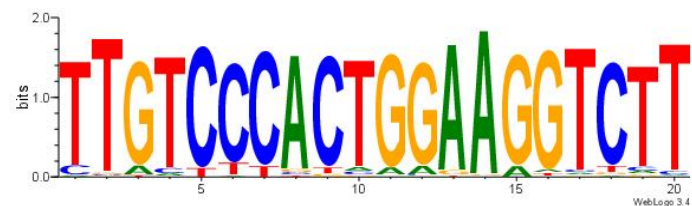
Alignment:

TTGTCCCACTGGAAGGTCTT
GTTTAACCATTGAGGGCCAG

Original motif Consensus sequence: AAGACCTCCAGTGGGACAA



Reverse complement motif Consensus sequence: TTGTCCTGGAAGGTCTT

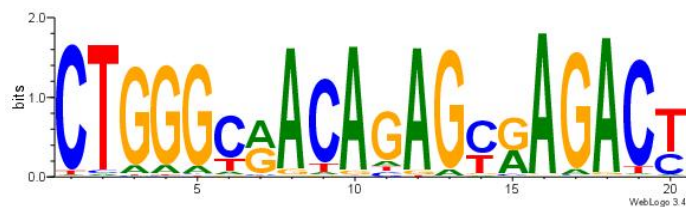


Dataset #: 1
Motif ID: 29
Motif name: Motif 29
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 20
Similarity score: 0.117502

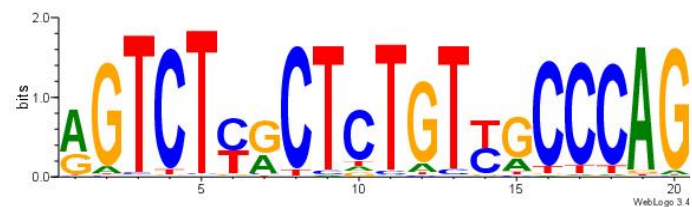
Alignment:

MGTCMKCTCTGTKGCCAG
GTTTAACCATTGAGGGCCAG

Original motif Consensus sequence: CTGGGCRACAGAGAC

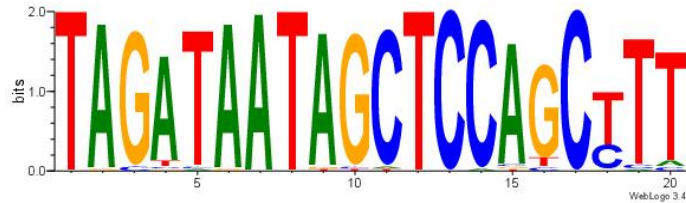


Reverse complement motif Consensus sequence: MGTCMKCTCTGTKGCCAG

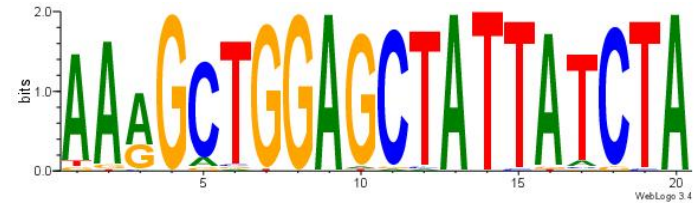


Dataset #: 1 Motif ID: 333 Motif name: Motif 333

Original motif Consensus sequence: TAGATAATAGCTCCAGCTTT



Reverse complement motif Consensus sequence: AAAGCTGGAGCTATTATCTA



Best Matches for Motif ID 333 (Highest to Lowest)

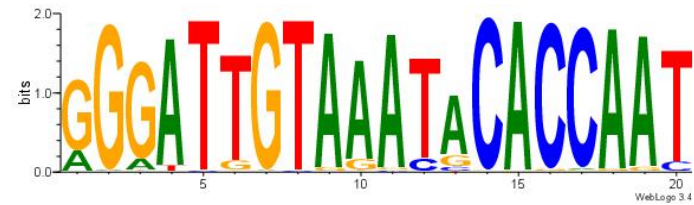
Dataset #:	1
Motif ID:	106
Motif name:	Motif 106
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	20
Similarity score:	0.0856788

Alignment:

```
ATTGGTGTATTTACAATCCC
AAAGCTGGAGCTATTATCTA
```

Original motif Consensus sequence: ATTGGTGTATTTACAATCCC

Reverse complement motif Consensus sequence: GGGATTGTAAATACACCAAT

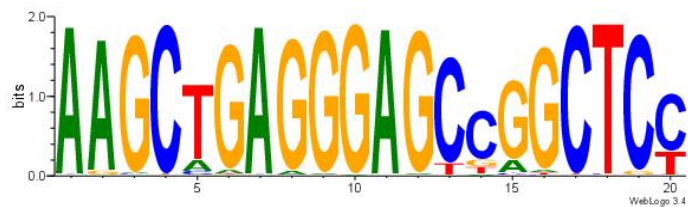


Dataset #: 1
 Motif ID: 96
 Motif name: Motif 96
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.0904379

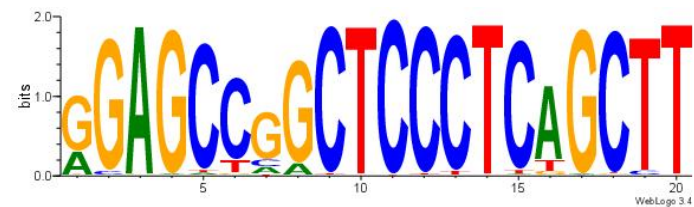
Alignment:

AAGCTGAGGGAGCCGGCTCC
 TAGATAATAGCTCCAGCTTT

Original motif Consensus sequence: AAGCTGAGGGAGCCGGCTCC



Reverse complement motif Consensus sequence: GGAGCCGGCTCCCTCAGCTT



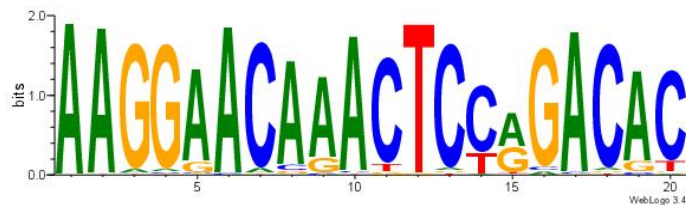
Dataset #: 1

Motif ID: 234
 Motif name: Motif 234
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.0912488

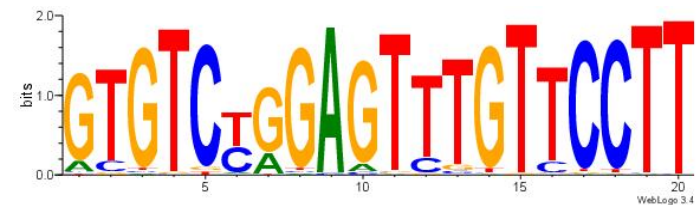
Alignment:

AAGGAACAAACTCCRGACAC
 TAGATAATAGCTCCAGCTTT

Original motif Consensus sequence: AAGGAACAAACTCCRGACAC



Reverse complement motif Consensus sequence: GTGTCGGAGTTTGTTCCTT



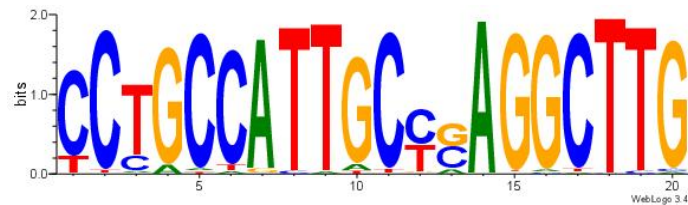
Dataset #: 1
 Motif ID: 196
 Motif name: Motif 196
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 20

Similarity score: 0.102365

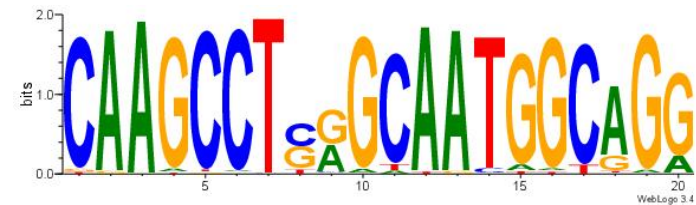
Alignment:

CCTGCCATTGCYSAGGCTTG
TAGATAATAGCTCCAGCTTT

Original motif Consensus sequence: CCTGCCATTGCYSAGGCTTG



Reverse complement motif Consensus sequence:
CAAGCCTSKGCAATGGCAGG



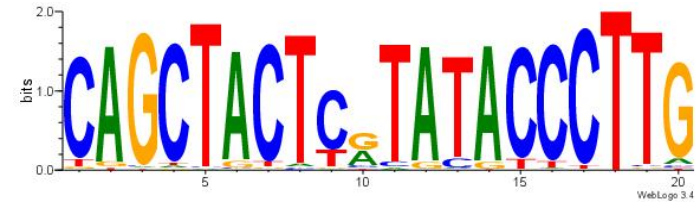
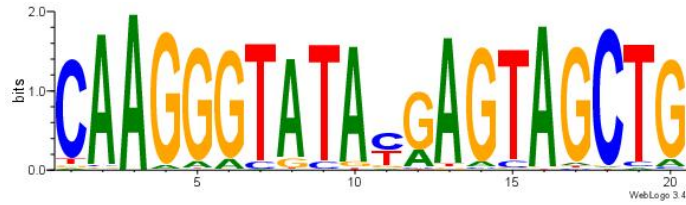
Dataset #: 1
Motif ID: 194
Motif name: Motif 194
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 20
Similarity score: 0.103421

Alignment:

CAAGGGTATAYGAGTAGCTG
AAAGCTGGAGCTATTATCTA

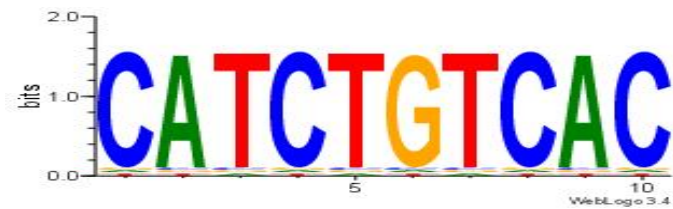
Original motif Consensus sequence: CAAGGGTATAYGAGTAGCTG

Reverse complement motif Consensus sequence:
CAGCTACTCKTATACCCTTG

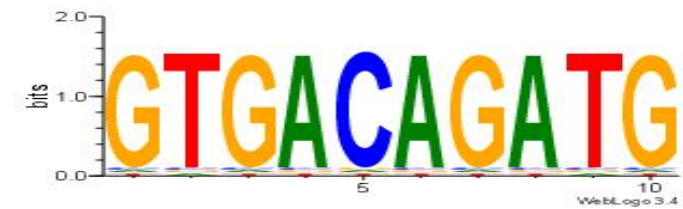


Dataset #: 1 Motif ID: 334 Motif name: Motif 334

Original motif Consensus sequence: CATCTGTCAC



Reverse complement motif Consensus sequence: GTGACAGATG



Best Matches for Motif ID 334 (Highest to Lowest)

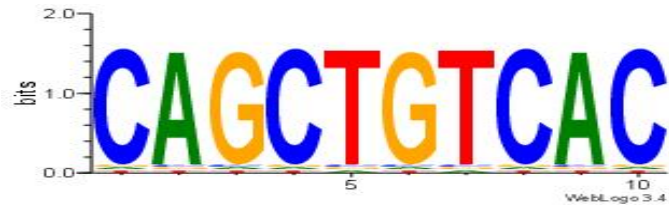
Dataset #:	1
Motif ID:	272
Motif name:	Motif 272
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	10
Similarity score:	0.0227273

Alignment:

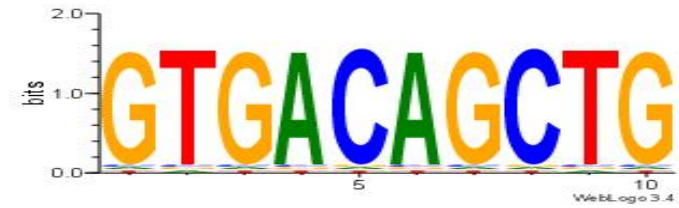
CAGCTGTCAC

CATCTGTCAC

Original motif Consensus sequence: CAGCTGTCAC



Reverse complement motif Consensus sequence: GTGACAGCTG

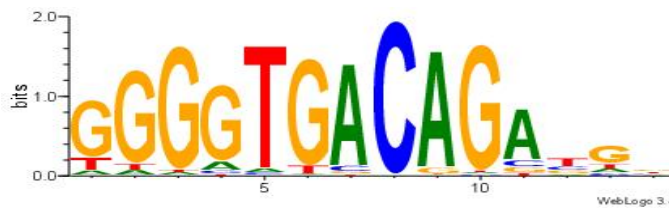


Dataset #: 1
Motif ID: 1
Motif name: Motif 1
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 2
Number of overlap: 10
Similarity score: 0.0317788

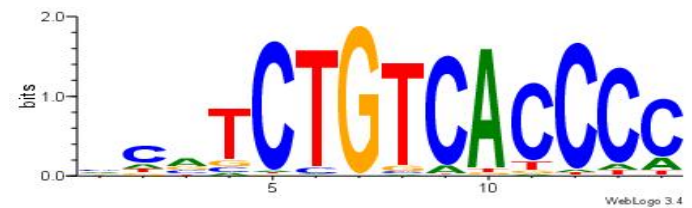
Alignment:

```
BCVTCTGTCACCCC  
---CATCTGTCAC--
```

Original motif Consensus sequence: GGGGTGACAGABGB



Reverse complement motif Consensus sequence: BCVTCTGTCACCCC

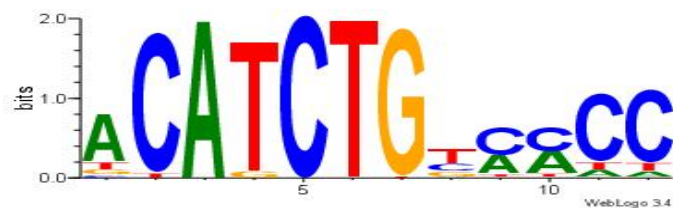


Dataset #: 1
 Motif ID: 49
 Motif name: Motif 49
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 10
 Similarity score: 0.0451613

Alignment:

ACATCTGYMMCC
 -CATCTGTCAC-

Original motif Consensus sequence: ACATCTGYMMCC



Reverse complement motif Consensus sequence: GRRMCAGATGT



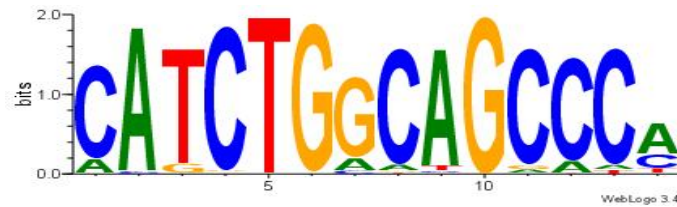
Dataset #: 1
 Motif ID: 205
 Motif name: Motif 205
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 5
 Number of overlap: 10

Similarity score: 0.0558301

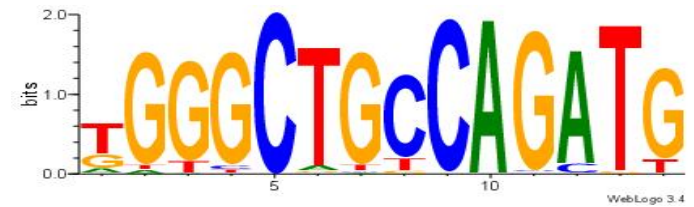
Alignment:

TGGGCTGCCAGATG
----GTGACAGATG

Original motif Consensus sequence: CATCTGGCAGCCCA



Reverse complement motif Consensus sequence: TGGGCTGCCAGATG



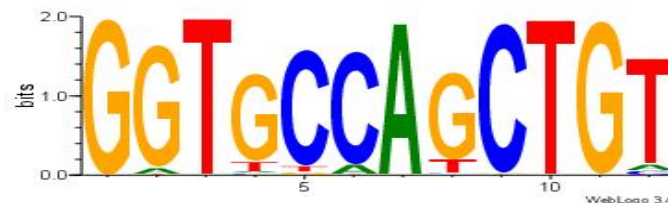
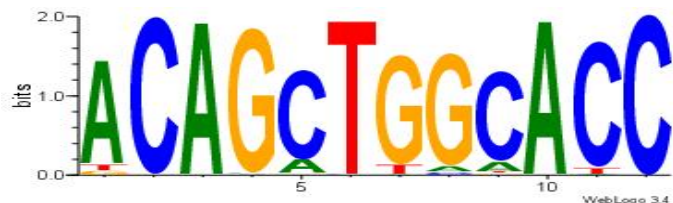
Dataset #: 1
Motif ID: 199
Motif name: Motif 199
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 2
Number of overlap: 10
Similarity score: 0.0598762

Alignment:

GGTGCCAGCTGT
-GTGACAGATG-

Original motif Consensus sequence: ACAGCTGGCACC

Reverse complement motif Consensus sequence: GGTGCCAGCTGT



Dataset #: 1 Motif ID: 335 Motif name: Motif 335

Original motif Consensus sequence: GTTAATGCTGA



Reverse complement motif Consensus sequence: TCAGCATT AAC

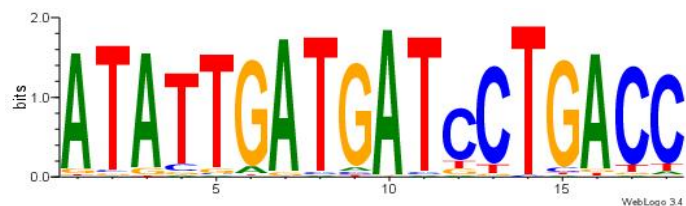


Best Matches for Motif ID 335 (Highest to Lowest)

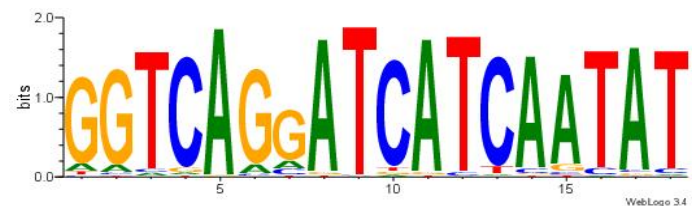
Dataset #:	1
Motif ID:	184
Motif name:	Motif 184
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	6
Number of overlap:	11
Similarity score:	0.054088

Alignment:
 ATATTGATGATCCTGACC
 -----GTTAATGCTGA--

Original motif Consensus sequence: ATATTGATGATCCTGACC



Reverse complement motif Consensus sequence: GGTCAGGATCATCAATAT

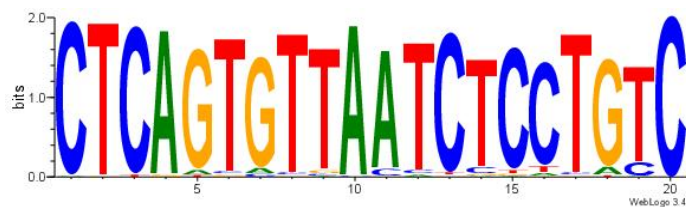


Dataset #: 1
Motif ID: 262
Motif name: Motif 262
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 9
Number of overlap: 11
Similarity score: 0.0564195

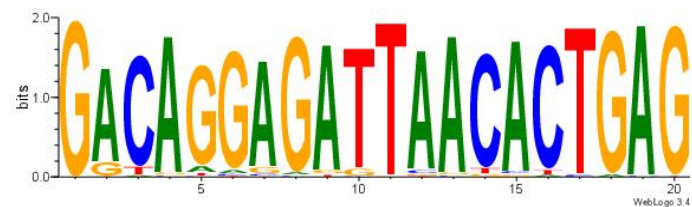
Alignment:

GACAGGAGATTAACACTGAG
-GTTAATGCTGA-----

Original motif Consensus sequence: CTCAGTGTTAATCTCCCTGTC



Reverse complement motif Consensus sequence: GACAGGAGATTAACACTGAG

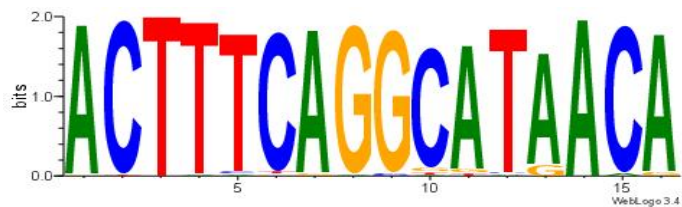


Dataset #: 1
 Motif ID: 278
 Motif name: Motif 278
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 5
 Number of overlap: 11
 Similarity score: 0.0591879

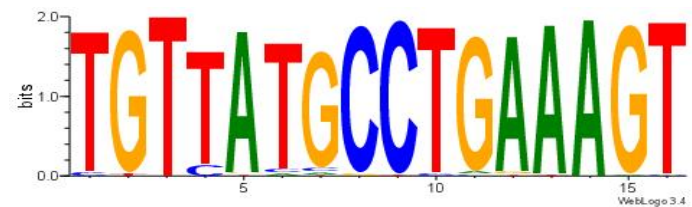
Alignment:

TGTTATGCCTGAAAGT
 ----GTTAATGCTGA-

Original motif Consensus sequence: ACTTTCAGGCATAACA



Reverse complement motif Consensus sequence: TGTTATGCCTGAAAGT



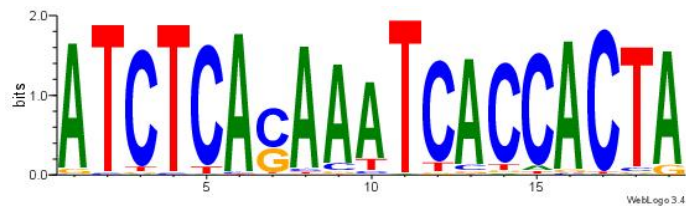
Dataset #: 1
 Motif ID: 261
 Motif name: Motif 261
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 6

Number of overlap: 11
Similarity score: 0.0655056

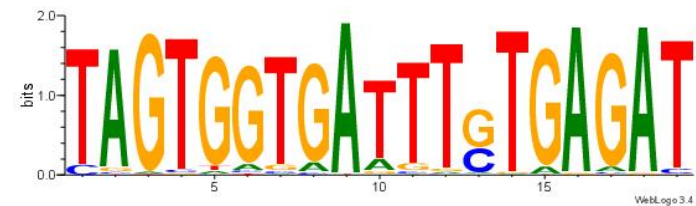
Alignment:

ATCTCASAAATCACCACTA
-----TCAGCATTAAC----

Original motif Consensus sequence: ATCTCASAAATCACCACTA



Reverse complement motif Consensus sequence:
TAGTGGTGAATTTGAGAT

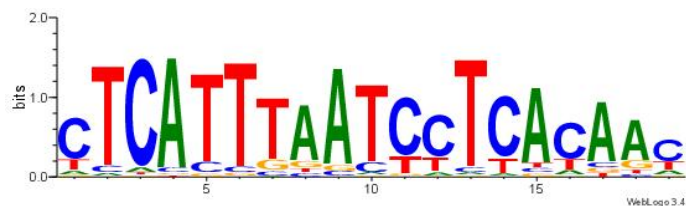


Dataset #: 1
Motif ID: 102
Motif name: Motif 102
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 5
Number of overlap: 11
Similarity score: 0.0670851

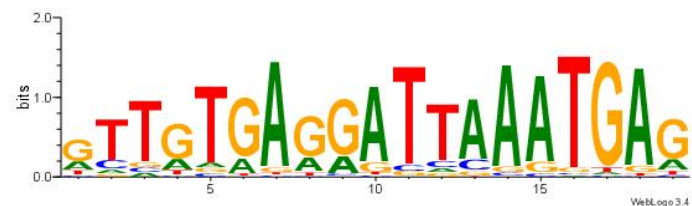
Alignment:

GTTGTGAGGATTAAATGAG
-----TCAGCATTAAC-----

Original motif Consensus sequence: CTCATTTAATCCTCACAAC

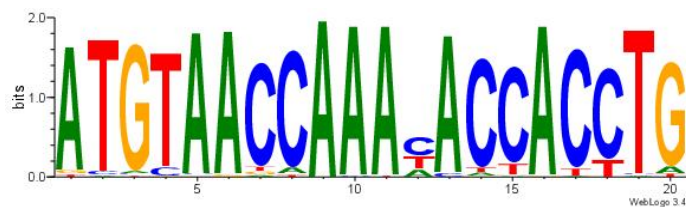


Reverse complement motif Consensus sequence: GTTGTGAGGATTAATGAG

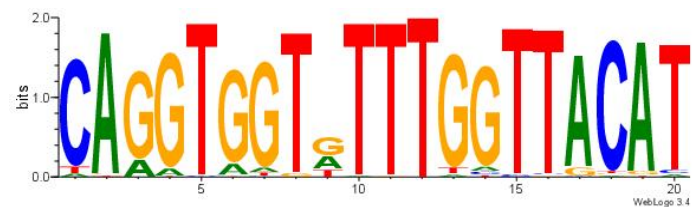


Dataset #: 1 Motif ID: 336 Motif name: Motif 336

Original motif Consensus sequence: ATGTAACCAAAYACCACCTG



Reverse complement motif Consensus sequence: CAGGTGGTKTTTGGTTACAT



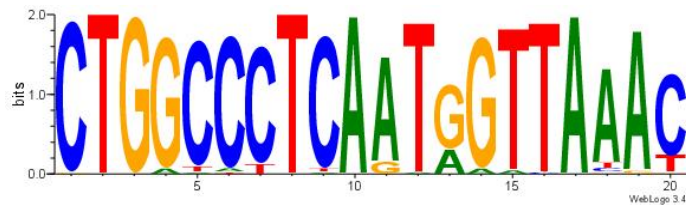
Best Matches for Motif ID 336 (Highest to Lowest)

Dataset #:	1
Motif ID:	332
Motif name:	Motif 332
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	20
Similarity score:	0.108577

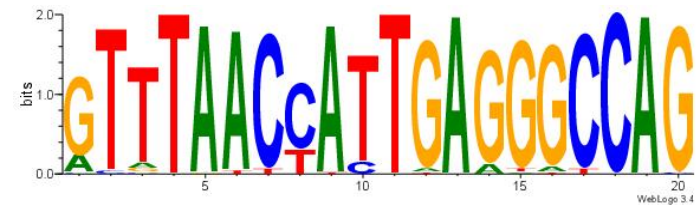
Alignment:

GTTTAACCATTGAGGGCCAG
ATGTAACCAAAYACCACCTG

Original motif Consensus sequence: CTGGCCCTCAATGGTTAAAC



Reverse complement motif Consensus sequence:
GTTTAACCATTGAGGGCCAG



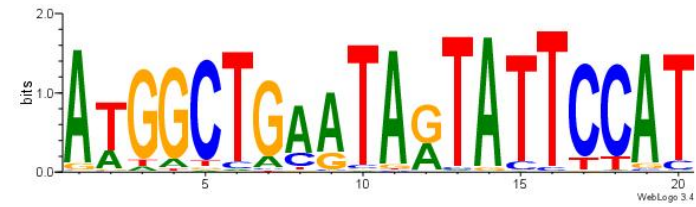
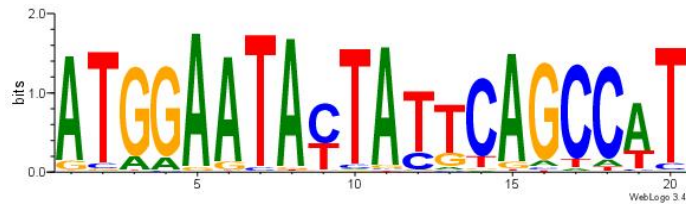
Dataset #: 1
Motif ID: 55
Motif name: Motif 55
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 20
Similarity score: 0.115891

Alignment:

ATGGCTGAATAKTATTCCAT
CAGGTGGTKTTTGGTTACAT

Original motif Consensus sequence: ATGGAATAYATTTCAGCCAT

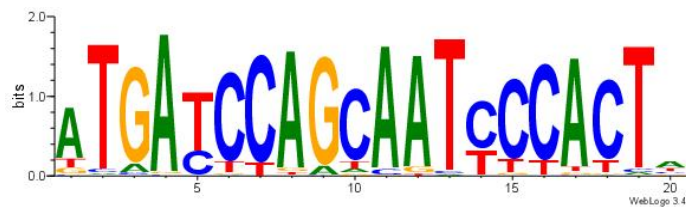
Reverse complement motif Consensus sequence:
ATGGCTGAATAKTATTCCAT



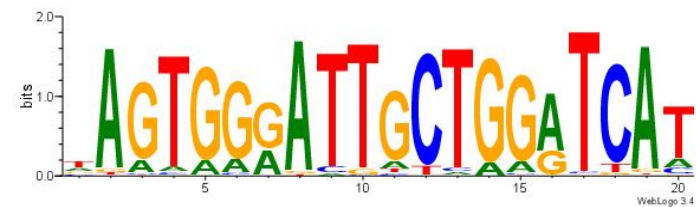
Dataset #: 1
 Motif ID: 115
 Motif name: Motif 115
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.123315

Alignment:
 HAGTGGKATTGCTGGATCAT
 CAGGTGGTKTTTGGTTACAT

Original motif Consensus sequence: ATGATCCAGCAATYCCACTH



Reverse complement motif Consensus sequence: HAGTGGKATTGCTGGATCAT



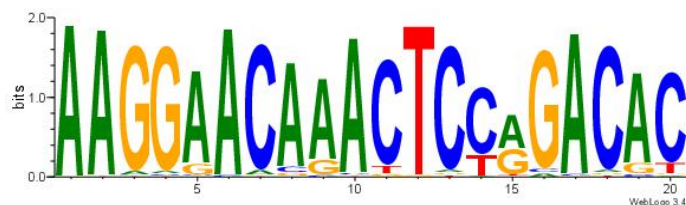
Dataset #: 1

Motif ID: 234
 Motif name: Motif 234
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.123723

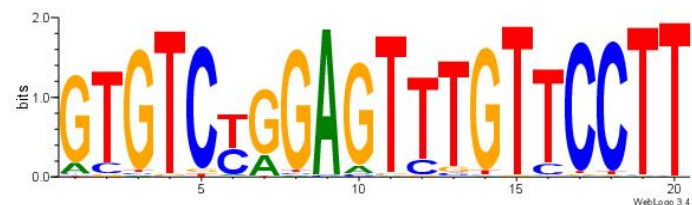
Alignment:

GTGTCKGGAGTTTGTTTCCTT
 CAGGTGGTKTTTGTTACAT

Original motif Consensus sequence: AAGGAACAACTCCRGACAC



Reverse complement motif Consensus sequence: GTGTCKGGAGTTTGTTTCCTT



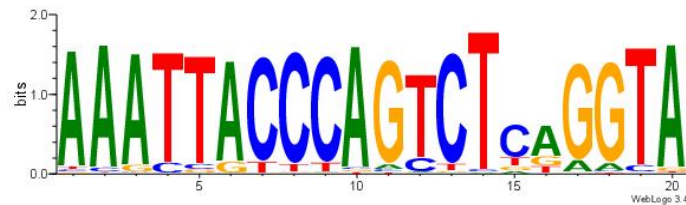
Dataset #: 1
 Motif ID: 160
 Motif name: Motif 160
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 20

Similarity score: 0.127587

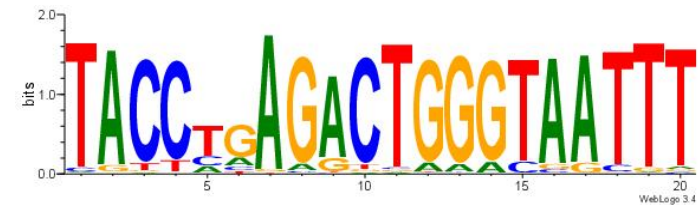
Alignment:

AAATTACCCAGTCTCAGGTA
ATGTAACCAAYACCACCTG

Original motif Consensus sequence: AAATTACCCAGTCTCAGGTA

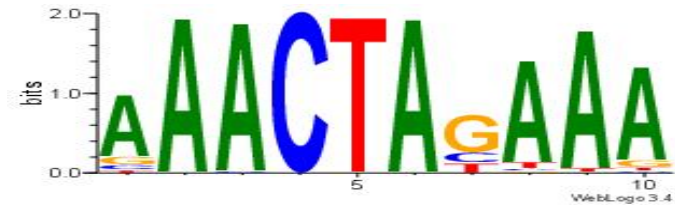


Reverse complement motif Consensus sequence: TACCTGAGACTGGGTAATTT



Dataset #: 1 Motif ID: 337 Motif name: Motif 337

Original motif Consensus sequence: AACTAGAAA



Reverse complement motif Consensus sequence: TTTCTAGTTT



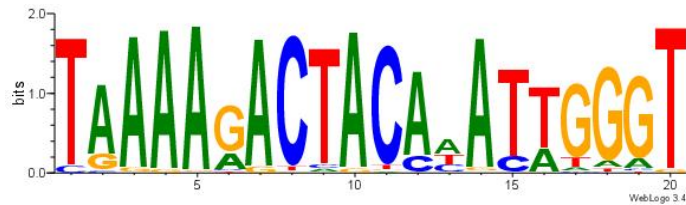
Best Matches for Motif ID 337 (Highest to Lowest)

Dataset #:	1
Motif ID:	195
Motif name:	Motif 195
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif

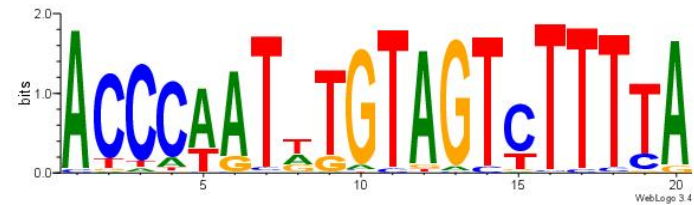
Direction: Backward
Position number: 7
Number of overlap: 10
Similarity score: 0.0563059

Alignment:
TAAAAGACTACAWATTGGGT
----AAACTAGAAA-----

Original motif Consensus sequence: TAAAAGACTACAWATTGGGT



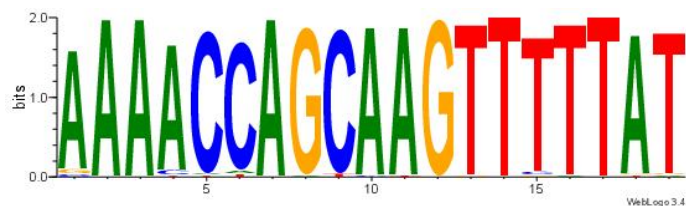
Reverse complement motif Consensus sequence: ACCCAATWTGTAGTCTTTTA



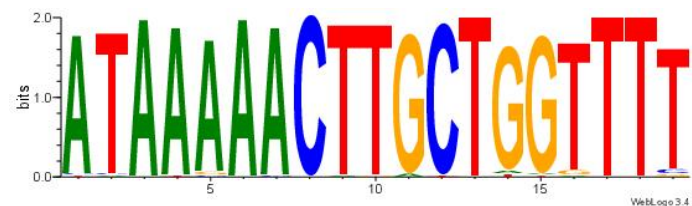
Dataset #: 1
Motif ID: 330
Motif name: Motif 330
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 2
Number of overlap: 10
Similarity score: 0.0573722

Alignment:
ATAAAAAGTTGCTGGTTTT
-----TTTCTAGTTT-

Original motif Consensus sequence: AAAACCAGCAAGTTTTTAT



Reverse complement motif Consensus sequence: ATAAAACTTGCTGGTTTT

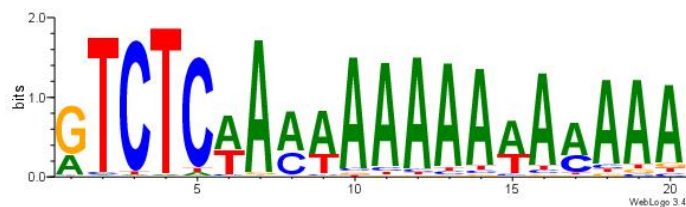


Dataset #: 1
Motif ID: 7
Motif name: Motif 7
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 10
Similarity score: 0.0579018

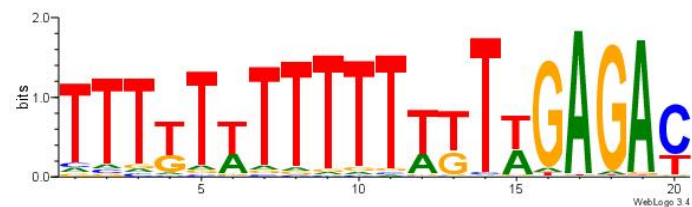
Alignment:

TTTTWTTTTTTTTWTGAGAC
TTTCTAGTTT-----

Original motif Consensus sequence: GTCTWAMAAAAAWAMAAA



Reverse complement motif Consensus sequence: TTTYTWTTTTTTTWTGAGAC

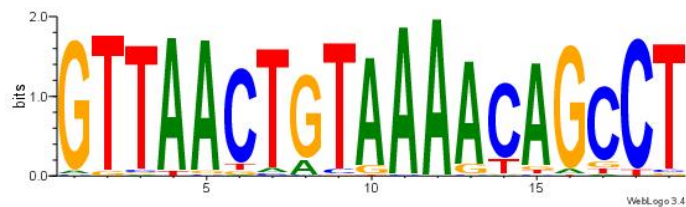


Dataset #: 1
 Motif ID: 233
 Motif name: Motif 233
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 10
 Similarity score: 0.0651653

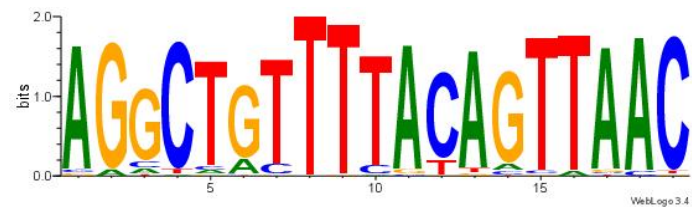
Alignment:

GTTAACTGTAAAACAGCCT
 --AAACTAGAAA-----

Original motif Consensus sequence: GTTAACTGTAAAACAGCCT



Reverse complement motif Consensus sequence: AGGCTGTTTACAGTTAAC

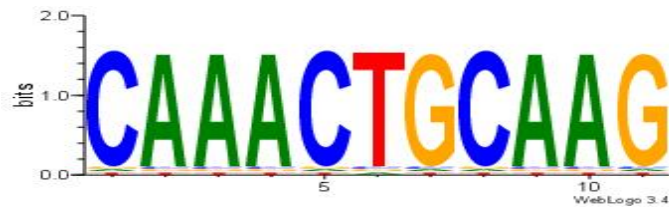


Dataset #: 1
 Motif ID: 73
 Motif name: Motif 73
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1

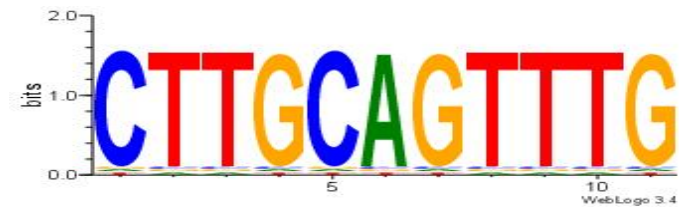
Number of overlap: 10
Similarity score: 0.0679233

Alignment:
CAAAGTCAAG
-AAACTAGAAA

Original motif Consensus sequence: CAAACTGCAAG

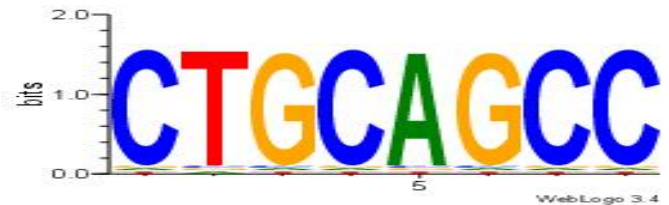


Reverse complement motif Consensus sequence: CTTGCAGTTTG



Dataset #: 1 Motif ID: 338 Motif name: Motif 338

Original motif Consensus sequence: CTGCAGCC



Reverse complement motif Consensus sequence: GGCTGCAG



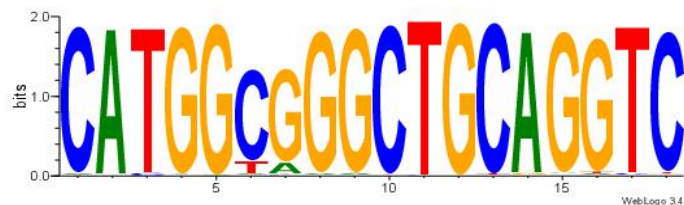
Best Matches for Motif ID 338 (Highest to Lowest)

Dataset #: 1
Motif ID: 68
Motif name: Motif 68
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif

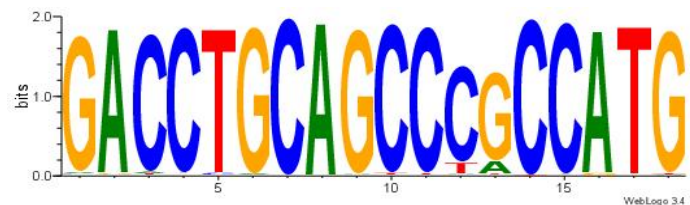
Direction: Forward
Position number: 4
Number of overlap: 8
Similarity score: 0.0130204

Alignment:
CATGGCGGGCTGCAGGTC
---GGCTGCAG-----

Original motif Consensus sequence: CATGGCGGGCTGCAGGTC



Reverse complement motif Consensus sequence: GACCTGCAGCCCGCCATG



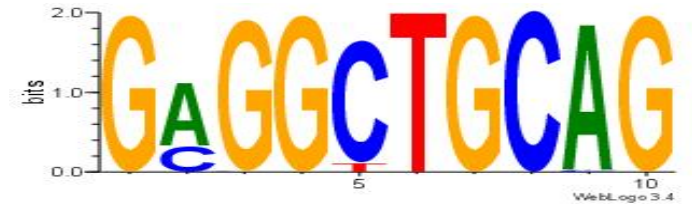
Dataset #: 1
Motif ID: 219
Motif name: Motif 219
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 8
Similarity score: 0.0154581

Alignment:
CTGCAGCCTC
CTGCAGCC--

Original motif Consensus sequence: CTGCAGCCTC



Reverse complement motif Consensus sequence: GAGGCTGCAG

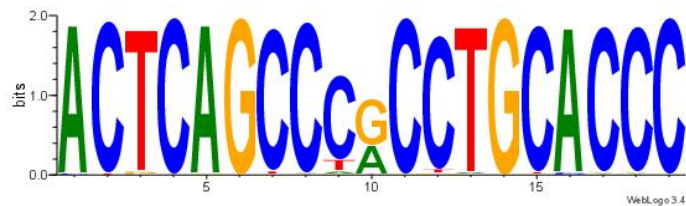


Dataset #: 1
Motif ID: 149
Motif name: Motif 149
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 12
Number of overlap: 8
Similarity score: 0.0406936

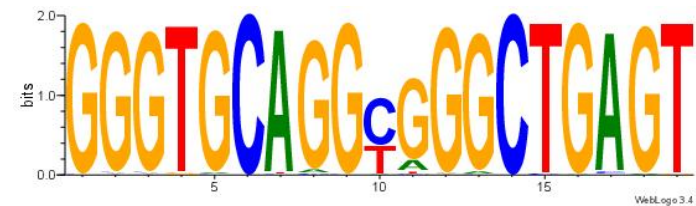
Alignment:

GGGTGCAGGMGGGCTGAGT
GGCTGCAG-----

Original motif Consensus sequence: ACTCAGCCRCCTGCACCC



Reverse complement motif Consensus sequence: GGGTGCAGGMGGGCTGAGT

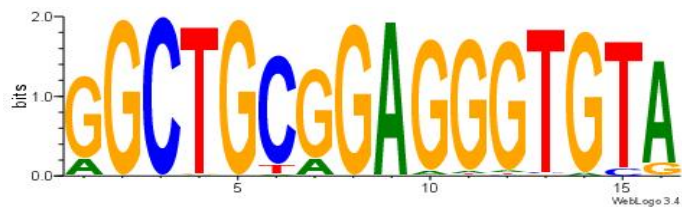


Dataset #: 1
 Motif ID: 89
 Motif name: Motif 89
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 9
 Number of overlap: 8
 Similarity score: 0.0413146

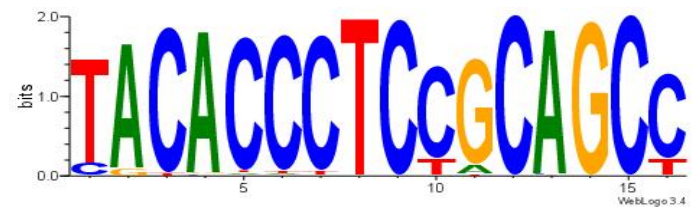
Alignment:

TACACCCTCCGCAGCC
 CTGCAGCC-----

Original motif Consensus sequence: GGCTGCGGAGGGTGTA



Reverse complement motif Consensus sequence: TACACCCTCCGCAGCC

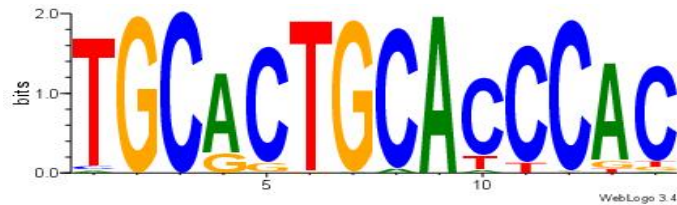


Dataset #: 1
 Motif ID: 220
 Motif name: Motif 220
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3

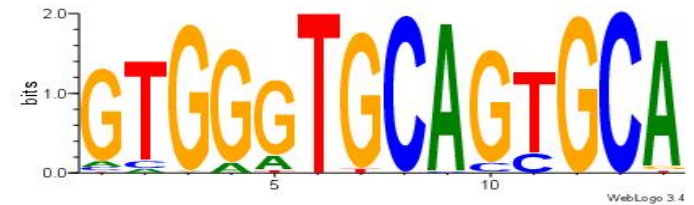
Number of overlap: 8
Similarity score: 0.0415555

Alignment:
GTGGGTGCAGTGCA
--GGCTGCAG-----

Original motif Consensus sequence: TGCACTGCACCCAC

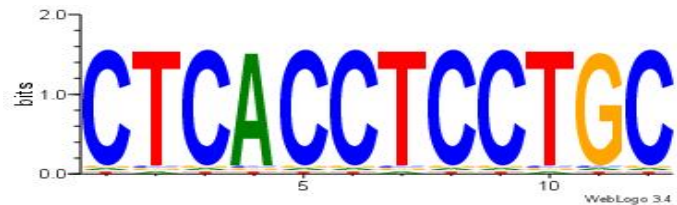


Reverse complement motif Consensus sequence: GTGGGTGCAGTGCA

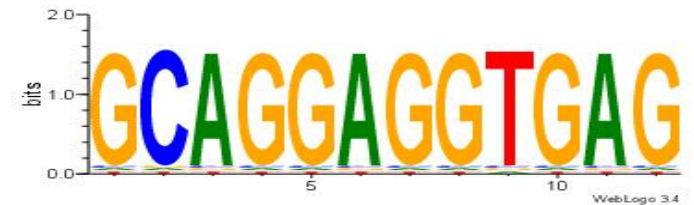


Dataset #: 1 Motif ID: 339 Motif name: Motif 339

Original motif Consensus sequence: CTCACCTCCTGC



Reverse complement motif Consensus sequence: GCAGGAGGTGAG



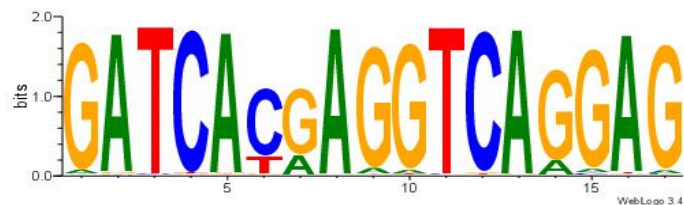
Best Matches for Motif ID 339 (Highest to Lowest)

Dataset #:	1
Motif ID:	60
Motif name:	Motif 60
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement

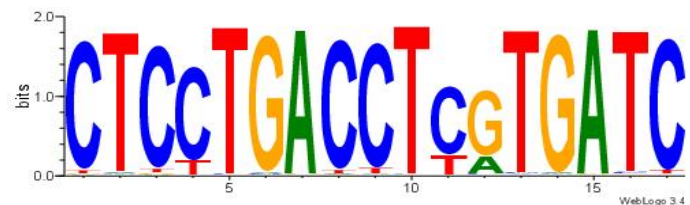
Direction: Forward
Position number: 3
Number of overlap: 12
Similarity score: 0.0722162

Alignment:
CTCCTGACCTCGTGATC
--CTCACCTCCTGC---

Original motif Consensus sequence: GATCACGAGGTCAGGAG



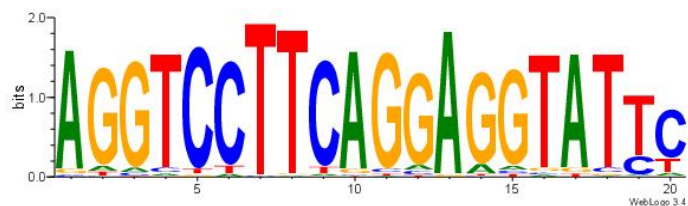
Reverse complement motif Consensus sequence: CTCCTGACCTCGTGATC



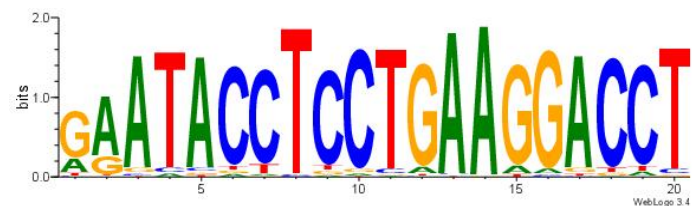
Dataset #: 1
Motif ID: 179
Motif name: Motif 179
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 2
Number of overlap: 12
Similarity score: 0.0795057

Alignment:
AGGTCCTTCAGGAGGTATTC
-GCAGGAGGTGAG-----

Original motif Consensus sequence: AGGTCCTTCAGGAGGTATTC



Reverse complement motif Consensus sequence: GAATACCTCCTGAAGGACCT

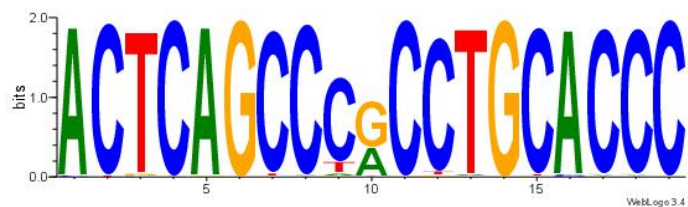


Dataset #: 1
Motif ID: 149
Motif name: Motif 149
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 4
Number of overlap: 12
Similarity score: 0.0820882

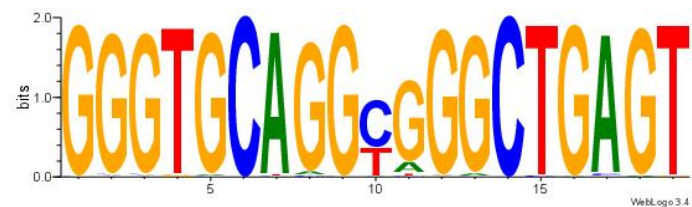
Alignment:

GGGTGCAGGMGGCTGAGT
----GCAGGAGGTGAG---

Original motif Consensus sequence: ACTCAGCCRCCTGCACCC



Reverse complement motif Consensus sequence: GGGTGCAGGMGGCTGAGT

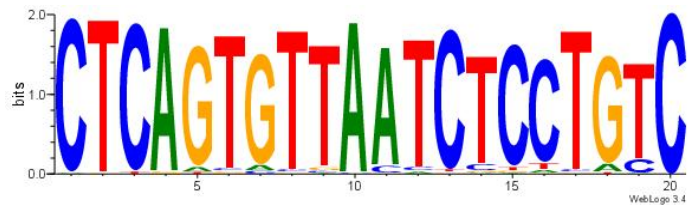


Dataset #: 1
 Motif ID: 262
 Motif name: Motif 262
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 12
 Similarity score: 0.0822961

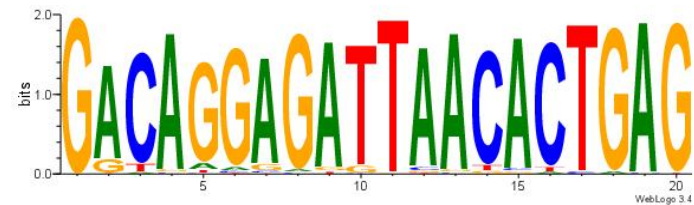
Alignment:

CTCAGTGTTAATCTCCTGTC
 -----CTCACCTCCTGC-

Original motif Consensus sequence: CTCAGTGTTAATCTCCTGTC



Reverse complement motif Consensus sequence: GACAGGAGATTAACACTGAG

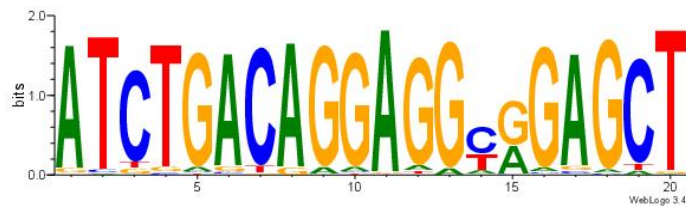


Dataset #: 1
 Motif ID: 165
 Motif name: Motif 165
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 4

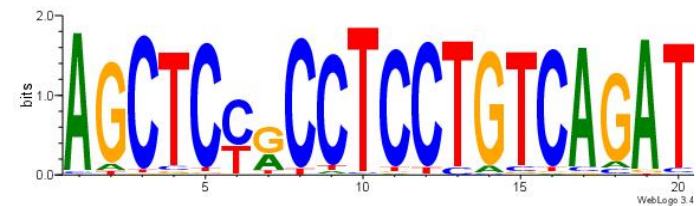
Number of overlap: 12
 Similarity score: 0.082371

Alignment:
 AGCTCMKCCTCCTGTCAGAT
 -----CTCACCTCCTGC----

Original motif Consensus sequence: ATCTGACAGGAGGYRGAGCT

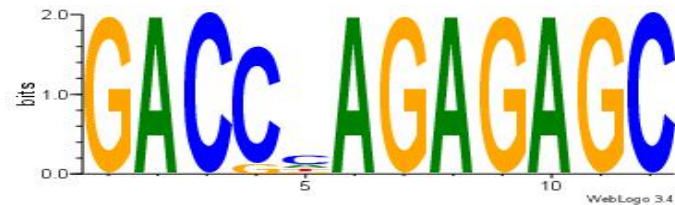


Reverse complement motif Consensus sequence:
 AGCTCMKCCTCCTGTCAGAT

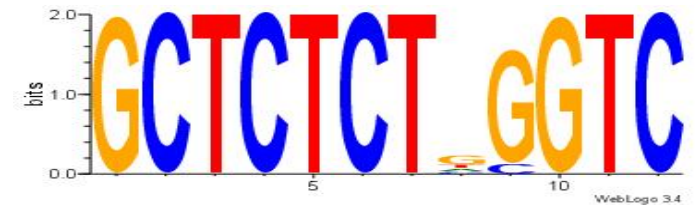


Dataset #: 1 Motif ID: 340 Motif name: Motif 340

Original motif Consensus sequence: GACCCAGAGAGC



Reverse complement motif Consensus sequence: GCTCTCTGGGTC



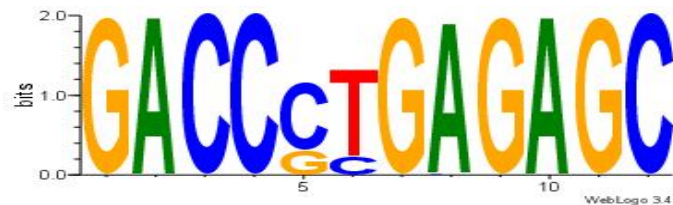
Best Matches for Motif ID 340 (Highest to Lowest)

Dataset #: 1
 Motif ID: 302
 Motif name: Motif 302
 Matching format of first motif: Original Motif

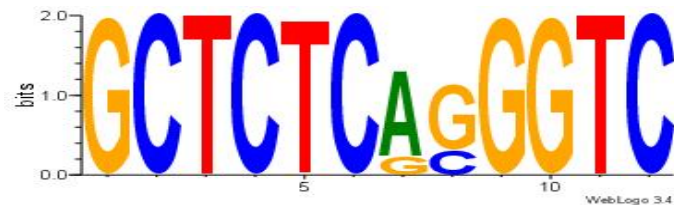
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 12
Similarity score: 0.0285197

Alignment:
GACCCTGAGAGC
GACCCAGAGAGC

Original motif Consensus sequence: GACCCTGAGAGC



Reverse complement motif Consensus sequence: GCTCTCAGGGTC

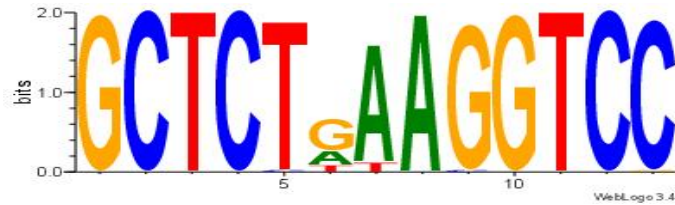


Dataset #: 1
Motif ID: 362
Motif name: Motif 362
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2
Number of overlap: 12
Similarity score: 0.0566001

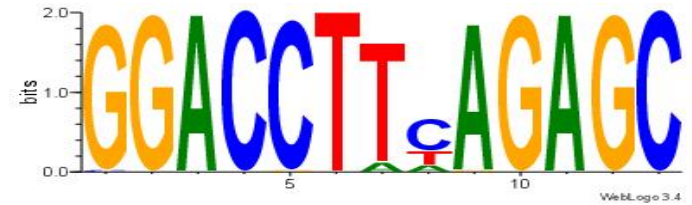
Alignment:

GCTCTGAAGGTCC
GCTCTCTGGGTC-

Original motif Consensus sequence: GCTCTGAAGGTCC



Reverse complement motif Consensus sequence: GGACCTTCAGAGC



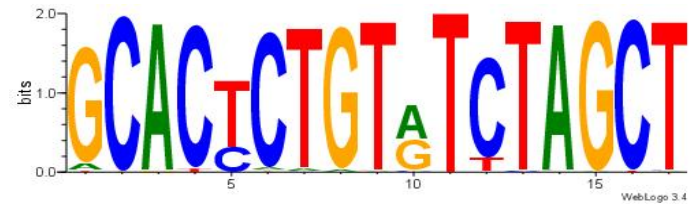
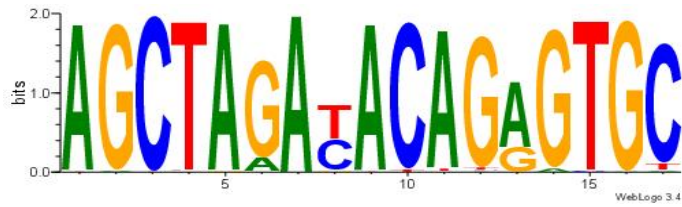
Dataset #: 1
Motif ID: 175
Motif name: Motif 175
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 12
Similarity score: 0.0723494

Alignment:

AGCTAGAYACAGAGTGC
-----GACCCAGAGAGC

Original motif Consensus sequence: AGCTAGAYACAGAGTGC

Reverse complement motif Consensus sequence:
GCACTCTGTMCTAGCT



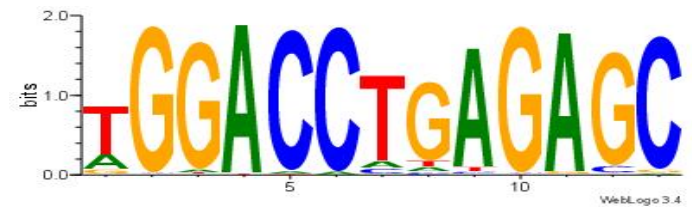
Dataset #: 1
 Motif ID: 323
 Motif name: Motif 323
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 12
 Similarity score: 0.0776328

Alignment:
 TGGACCTGAGAGC
 GACCCAGAGAGC-

Original motif Consensus sequence: GCTCTCAGGTCCA



Reverse complement motif Consensus sequence: TGGACCTGAGAGC



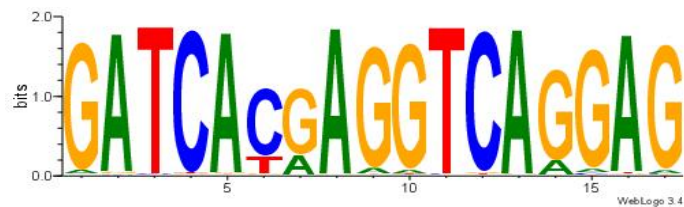
Dataset #: 1
 Motif ID: 60

Motif name:	Motif 60
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	12
Similarity score:	0.0825042

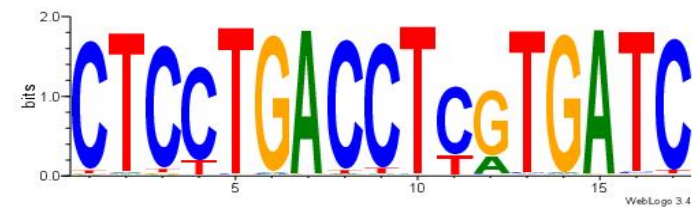
Alignment:

```
GATCACGAGGTCAGGAG
-----GCTCTCTGGGTC
```

Original motif Consensus sequence: GATCACGAGGTCAGGAG

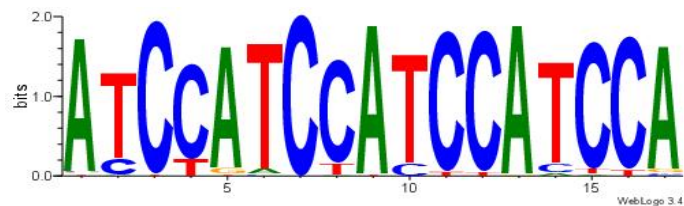


Reverse complement motif Consensus sequence: CTCCTGACCTCGTGATC

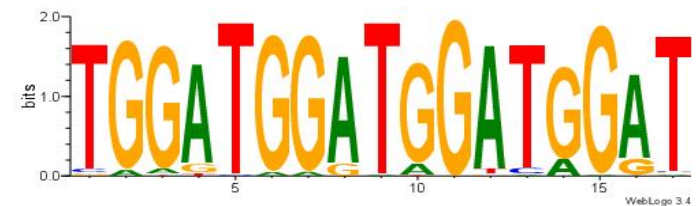


Dataset #: 1 Motif ID: 341 Motif name: Motif 341

Original motif Consensus sequence: ATCCATCCATCCATCCA



Reverse complement motif Consensus sequence: TGGATGGATGGATGGAT



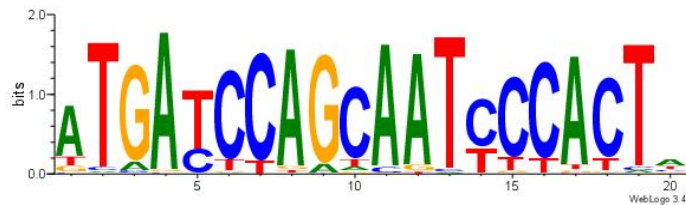
Best Matches for Motif ID 341 (Highest to Lowest)

Dataset #: 1
Motif ID: 115
Motif name: Motif 115
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 17
Similarity score: 0.0809092

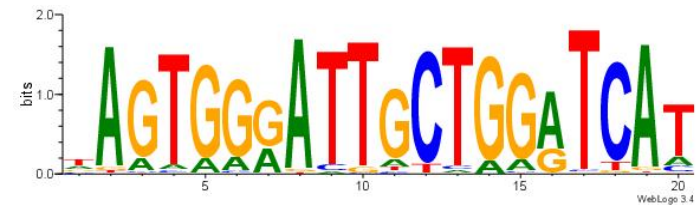
Alignment:

```
HAGTGGKATTGCTGGATCAT  
TGGATGGATGGATGGAT---
```

Original motif Consensus sequence: ATGATCCAGCAATYCCACTH



Reverse complement motif Consensus sequence:
HAGTGGKATTGCTGGATCAT



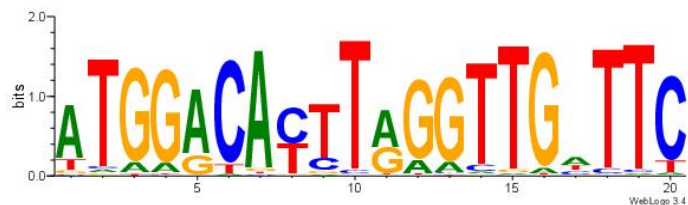
Dataset #: 1
Motif ID: 58
Motif name: Motif 58
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement

Direction: Forward
Position number: 2
Number of overlap: 17
Similarity score: 0.0940608

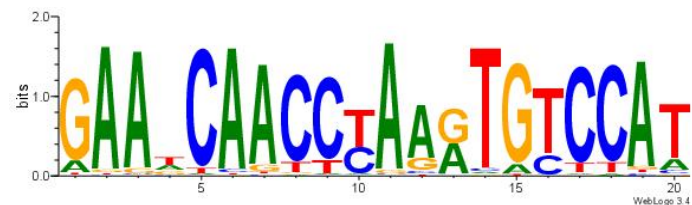
Alignment:

GAAHCAACCKAAKTGTCCAT
-ATCCATCCATCCATCCA--

Original motif Consensus sequence: ATGGACAYTTRGGTTGHTTC



Reverse complement motif Consensus sequence: GAAHCAACCKAAKTGTCCAT

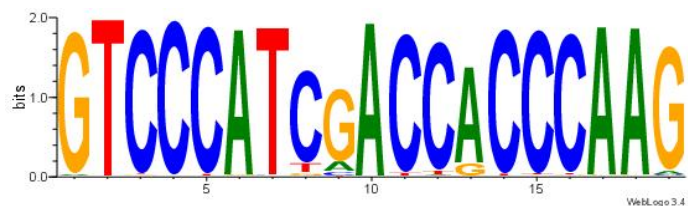


Dataset #: 1
Motif ID: 53
Motif name: Motif 53
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 3
Number of overlap: 17
Similarity score: 0.0958074

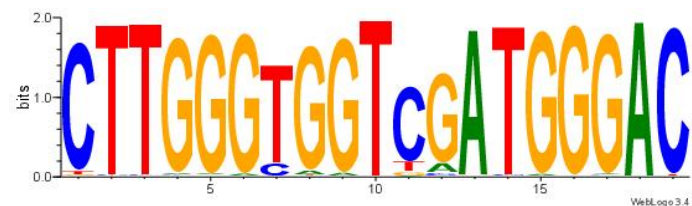
Alignment:

GTCCCATCGACCACCCAAG
ATCCATCCATCCATCCA--

Original motif Consensus sequence: GTCCCATCGACCACCCAAG



Reverse complement motif Consensus sequence: CTTGGGTGGTTCGATGGGAC

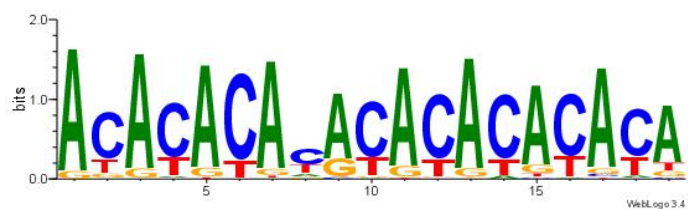


Dataset #: 1
Motif ID: 66
Motif name: Motif 66
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 3
Number of overlap: 17
Similarity score: 0.100906

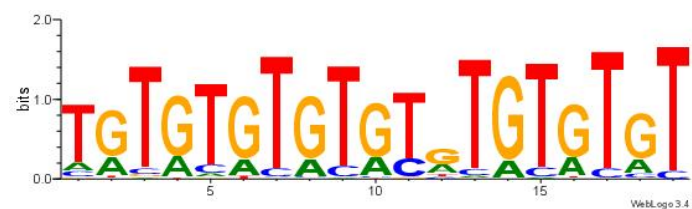
Alignment:

ACACACAYACACACACACA
--ATCCATCCATCCATCCA

Original motif Consensus sequence: ACACACAYACACACACACA



Reverse complement motif Consensus sequence: TGTGTGTGTGKTGTGTGT

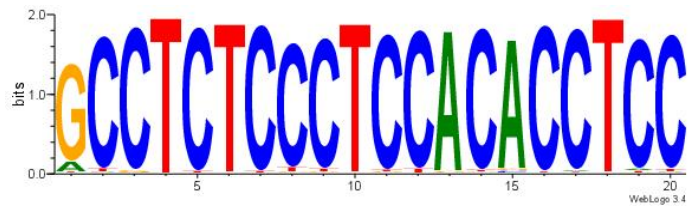


Dataset #: 1
 Motif ID: 105
 Motif name: Motif 105
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 17
 Similarity score: 0.101118

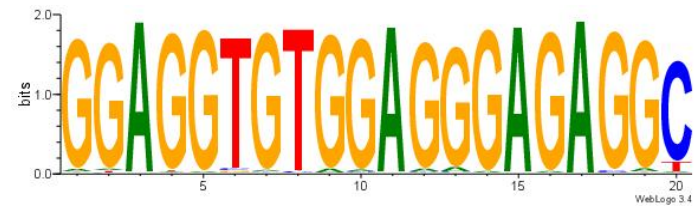
Alignment:

GCCTCTCCCTCCACACCTCC
 ATCCATCCATCCATCCA---

Original motif Consensus sequence: GCCTCTCCCTCCACACCTCC



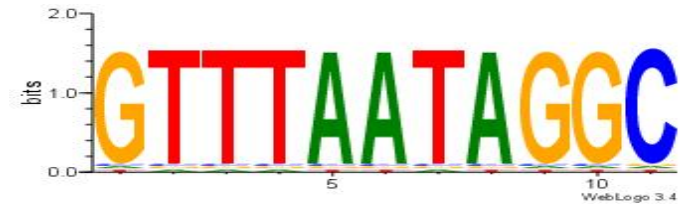
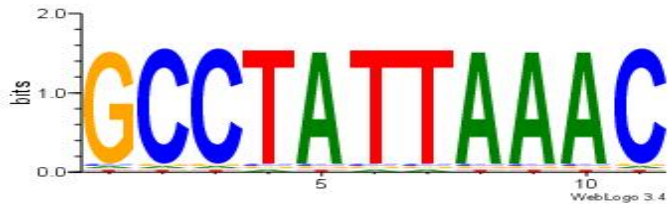
Reverse complement motif Consensus sequence: GGAGGTGTGGAGGGAGAGGC



Dataset #: 1 Motif ID: 342 Motif name: Motif 342

Original motif Consensus sequence: GCCTATTAAC

Reverse complement motif Consensus sequence: GTTTAATAGGC

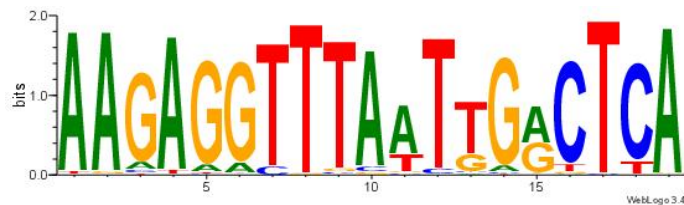


Best Matches for Motif ID 342 (Highest to Lowest)

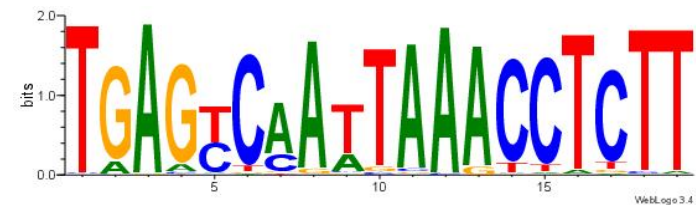
Dataset #: 1
 Motif ID: 129
 Motif name: Motif 129
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 4
 Number of overlap: 11
 Similarity score: 0.032945

Alignment:
 TGAGKCAATTAAACCTCTT
 -----GCCTATTAAAC----

Original motif Consensus sequence: AAGAGGTTTAATTGRCTCA



Reverse complement motif Consensus sequence: TGAGKCAATTAAACCTCTT

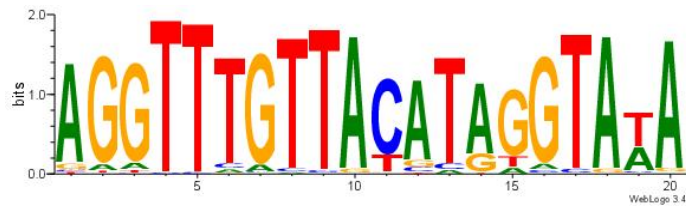


Dataset #: 1
 Motif ID: 137
 Motif name: Motif 137
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 7
 Number of overlap: 11
 Similarity score: 0.0624203

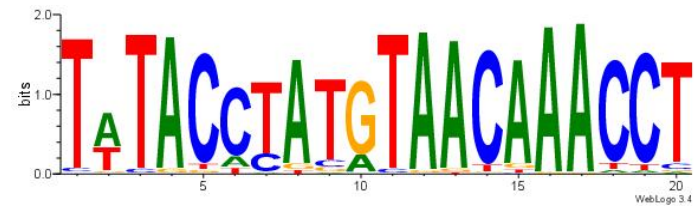
Alignment:

AGGTTTGTTACATAGGTAWA
 ---GTTTAATAGGC-----

Original motif Consensus sequence: AGGTTTGTTACATAGGTAWA



Reverse complement motif Consensus sequence: TWTACCTATGTAACAAACCT



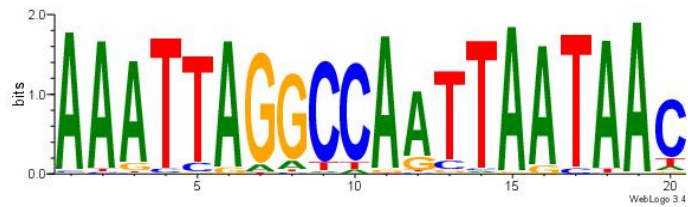
Dataset #: 1
 Motif ID: 308
 Motif name: Motif 308
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3

Number of overlap: 11
Similarity score: 0.0647175

Alignment:

GTTATTAATTGGCCTAATTT
--GTTTAATAGGC-----

Original motif Consensus sequence: AAATTAGGCCAATTAATAAC



Reverse complement motif Consensus sequence:
GTTATTAATTGGCCTAATTT

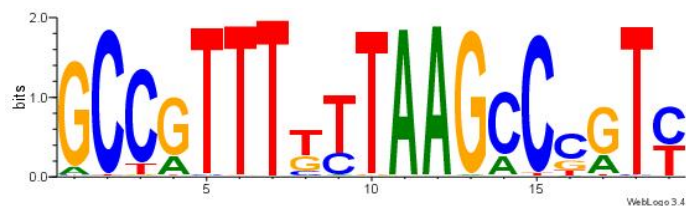


Dataset #: 1
Motif ID: 21
Motif name: Motif 21
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 4
Number of overlap: 11
Similarity score: 0.0690668

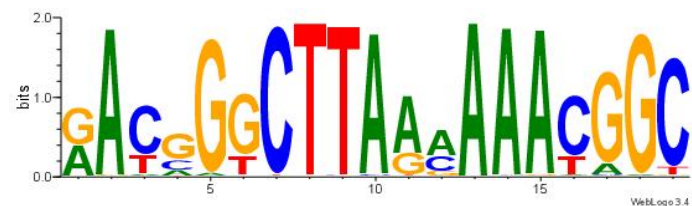
Alignment:

GCCGTTTKTTAAGCCCGTY
-----GTTTAATAGGC---

Original motif Consensus sequence: GCCGTTTKTTAAGCCCGTY



Reverse complement motif Consensus sequence: KACGGGCTTAARAAACGGC

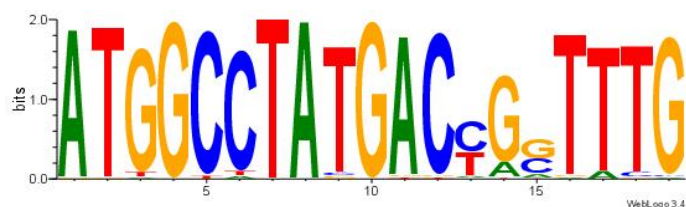


Dataset #: 1
Motif ID: 348
Motif name: Motif 348
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 4
Number of overlap: 11
Similarity score: 0.0723689

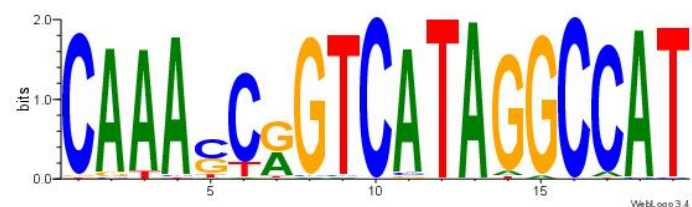
Alignment:

CAAASCKGTCATAGGCCAT
-----GTTTAATAGGC---

Original motif Consensus sequence: ATGGCCTATGACYGSTTTG

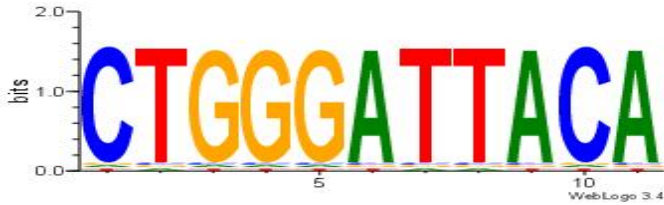


Reverse complement motif Consensus sequence: CAAASCKGTCATAGGCCAT

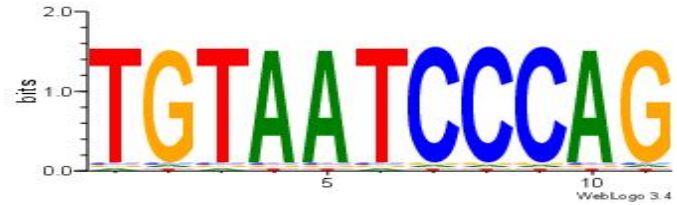


Dataset #: 1 Motif ID: 343 Motif name: Motif 343

Original motif Consensus sequence: CTGGGATTACA



Reverse complement motif Consensus sequence: TGTAATCCCAG



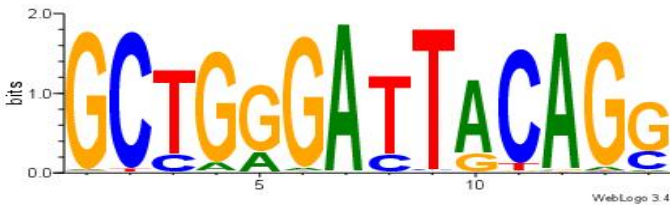
Best Matches for Motif ID 343 (Highest to Lowest)

Dataset #:	1
Motif ID:	4
Motif name:	Motif 4
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	11
Similarity score:	0.022272

Alignment:

GCTGGGATTACAGG
-CTGGGATTACA--

Original motif Consensus sequence: GCTGGGATTACAGG



Reverse complement motif Consensus sequence: CCTGTAATCCCAG

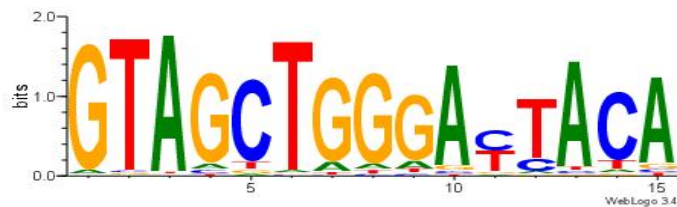


Dataset #: 1
 Motif ID: 69
 Motif name: Motif 69
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.0277108

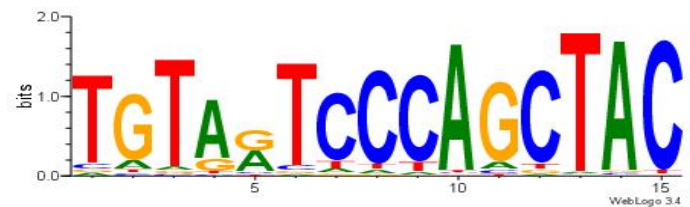
Alignment:

GTAGCTGGGAYTACA
 ----CTGGGATTACA

Original motif Consensus sequence: GTAGCTGGGAYTACA



Reverse complement motif Consensus sequence: TGTAKTCCCAGCT



Dataset #: 1
 Motif ID: 345
 Motif name: Motif 345
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1

Number of overlap: 11
Similarity score: 0.0604855

Alignment:
CTGGGAATCCAAC
CTGGGATTACA--

Original motif Consensus sequence: CTGGGAATCCAAC



Reverse complement motif Consensus sequence: GTTGGATTCCAG

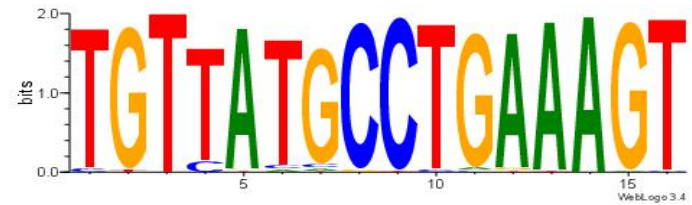
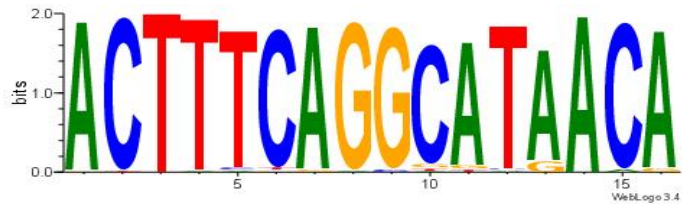


Dataset #: 1
Motif ID: 278
Motif name: Motif 278
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 11
Similarity score: 0.0725854

Alignment:
ACTTTCAGGCATAACA
-----CTGGGATTACA

Original motif Consensus sequence: ACTTTCAGGCATAACA

Reverse complement motif Consensus sequence:
TGTTATGCCTGAAAGT



Dataset #: 1
 Motif ID: 255
 Motif name: Motif 255
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.0732372

Alignment:
 TTTGTTATAGCAG
 --TGTAATCCAG

Original motif Consensus sequence: CTGCTATAACAAA



Reverse complement motif Consensus sequence: TTTGTTATAGCAG

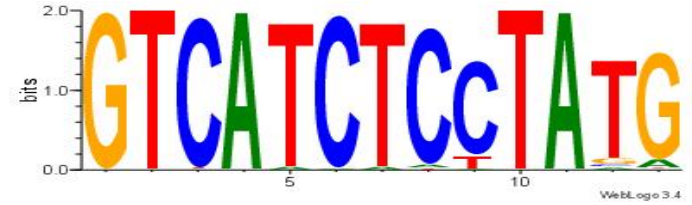


Dataset #: 1 Motif ID: 344 Motif name: Motif 344

Original motif Consensus sequence: CATAGGAGATGAC



Reverse complement motif Consensus sequence: GTCATCTCCTATG



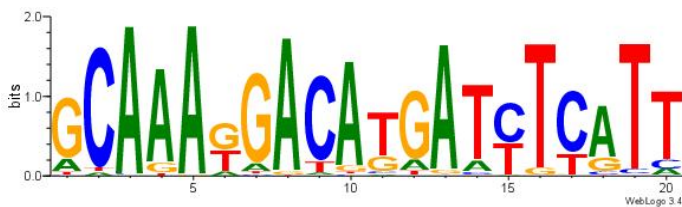
Best Matches for Motif ID 344 (Highest to Lowest)

Dataset #: 1
 Motif ID: 99
 Motif name: Motif 99
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 7
 Number of overlap: 13
 Similarity score: 0.0765815

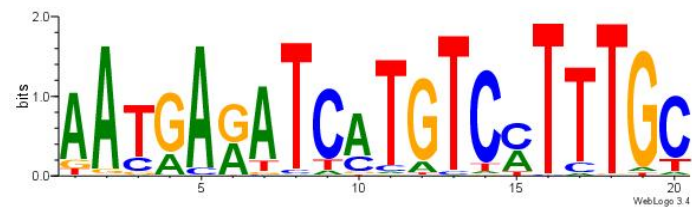
Alignment:

GCAAAGACATGATYTCATT
 -CATAGGAGATGAC-----

Original motif Consensus sequence: GCAAAGACATGATYTCATT



Reverse complement motif Consensus sequence: AATGAKATCATGTCYTTTGC

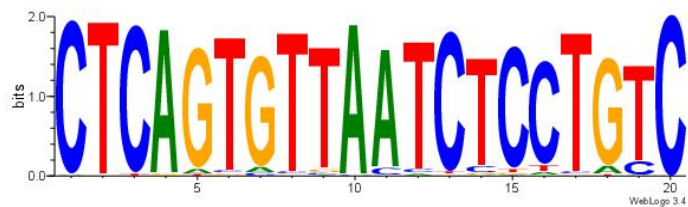


Dataset #: 1
 Motif ID: 262
 Motif name: Motif 262
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 8
 Number of overlap: 13
 Similarity score: 0.0805293

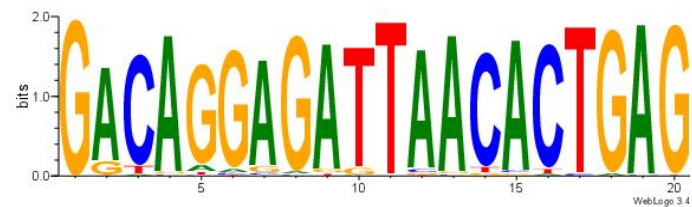
Alignment:

GACAGGAGATTAACACTGAG
 -----CATAGGAGATGAC

Original motif Consensus sequence: CTCAGTGTTAATCTCCTGTC



Reverse complement motif Consensus sequence: GACAGGAGATTAACACTGAG



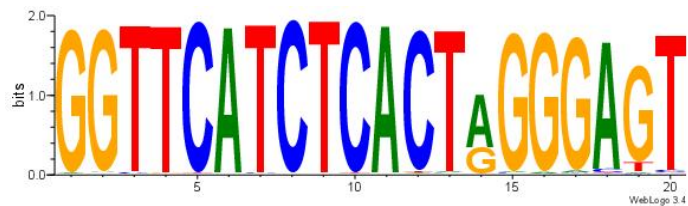
Dataset #: 1
 Motif ID: 23
 Motif name: Motif 23
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 6

Number of overlap: 13
Similarity score: 0.0919284

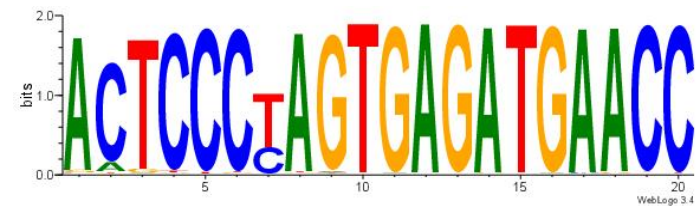
Alignment:

ACTCCCTAGTGAGATGAACC
--CATAGGAGATGAC-----

Original motif Consensus sequence: GGTTTCATCTCACTAGGGAGT



Reverse complement motif Consensus sequence:
ACTCCCTAGTGAGATGAACC

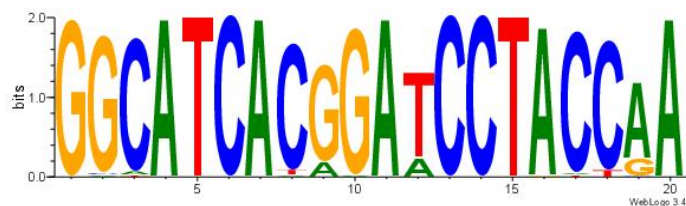


Dataset #: 1
Motif ID: 311
Motif name: Motif 311
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 13
Similarity score: 0.0937575

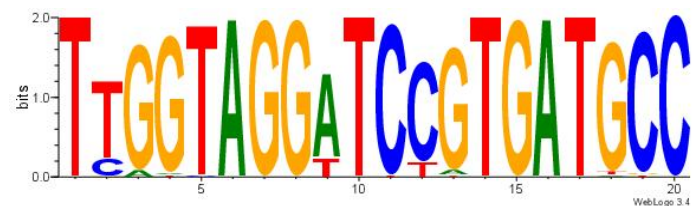
Alignment:

GGCATCACGGATCCTACCAA
-----GTCATCTCCTATG

Original motif Consensus sequence: GGCATCACGGATCCTACCAA



Reverse complement motif Consensus sequence: TTGGTAGGATCCGTGATGCC

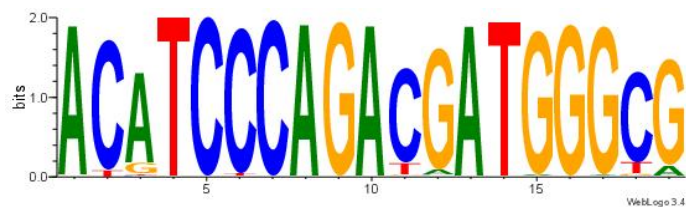


Dataset #: 1
Motif ID: 36
Motif name: Motif 36
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 6
Number of overlap: 13
Similarity score: 0.0944053

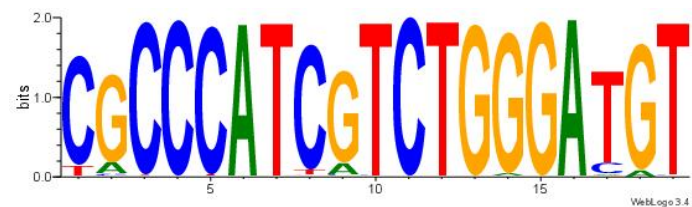
Alignment:

ACATCCCAGACGATGGGCG
-CATAGGAGATGAC-----

Original motif Consensus sequence: ACATCCCAGACGATGGGCG



Reverse complement motif Consensus sequence: CGCCCATCGTCTGGGATGT

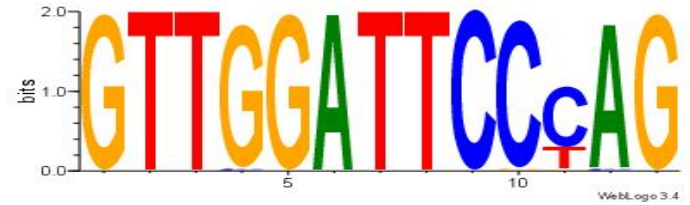


Dataset #: 1 Motif ID: 345 Motif name: Motif 345

Original motif Consensus sequence: CTGGGAATCCAAC



Reverse complement motif Consensus sequence: GTTGGATTCCcAG



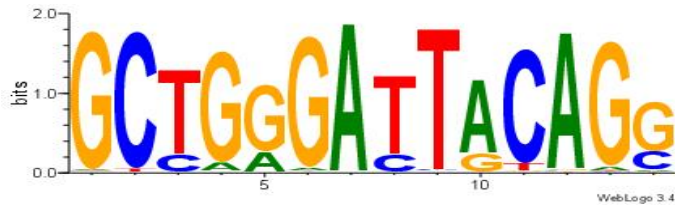
Best Matches for Motif ID 345 (Highest to Lowest)

Dataset #:	1
Motif ID:	4
Motif name:	Motif 4
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	2
Number of overlap:	13
Similarity score:	0.0624846

Alignment:

CCTGTAATCCCAGC
GTTGGATTCCCAG-

Original motif Consensus sequence: GCTGGGATTACAGG



Reverse complement motif Consensus sequence: CCTGTAATCCCAGC

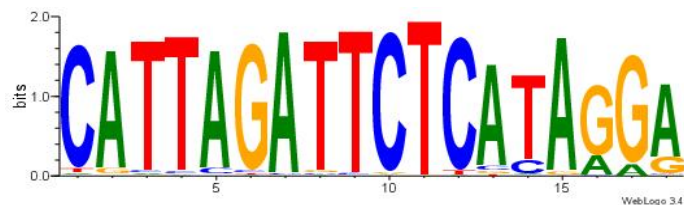


Dataset #: 1
 Motif ID: 154
 Motif name: Motif 154
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 5
 Number of overlap: 13
 Similarity score: 0.0631163

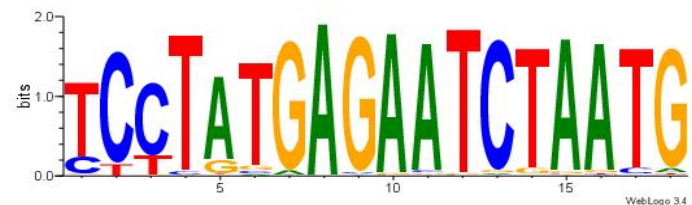
Alignment:

CATTAGATTCTCATAGGA
 ----GTTGGATTCCCAG-

Original motif Consensus sequence: CATTAGATTCTCATAGGA



Reverse complement motif Consensus sequence: TCCTATGAGAATCTAATG



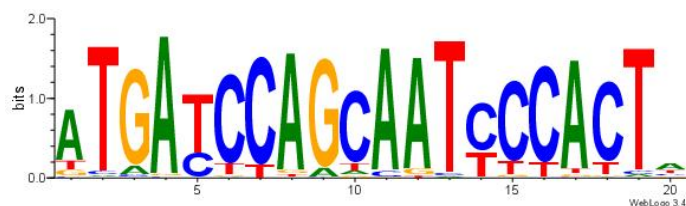
Dataset #: 1
 Motif ID: 115
 Motif name: Motif 115
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward

Position number: 6
 Number of overlap: 13
 Similarity score: 0.070058

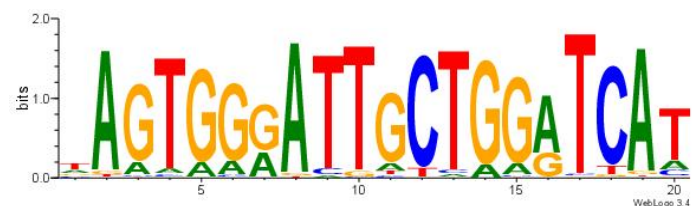
Alignment:

ATGATCCAGCAATYCCACTH
 -----CTGGGAATCCAAC--

Original motif Consensus sequence: ATGATCCAGCAATYCCACTH



Reverse complement motif Consensus sequence: HAGTGGKATTGCTGGATCAT

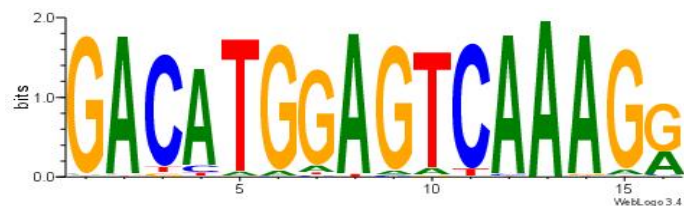


Dataset #: 1
 Motif ID: 326
 Motif name: Motif 326
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3
 Number of overlap: 13
 Similarity score: 0.0766159

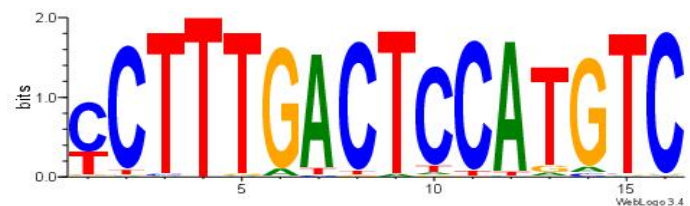
Alignment:

CCTTTGACTCCATGTC
 --CTGGGAATCCAAC-

Original motif Consensus sequence: GACATGGAGTCAAAGG



Reverse complement motif Consensus sequence: CCTTTGACTCCATGTC

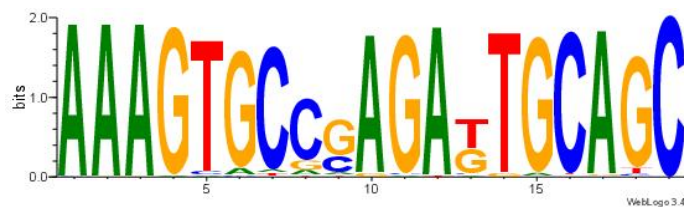


Dataset #: 1
Motif ID: 191
Motif name: Motif 191
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 7
Number of overlap: 13
Similarity score: 0.0805023

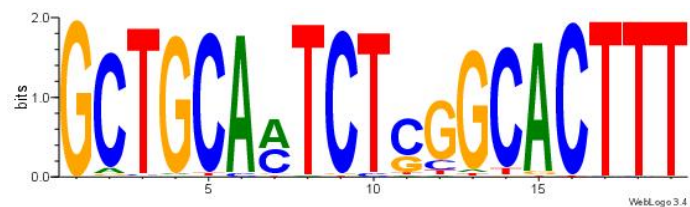
Alignment:

GCTGCARTCTCGGCACTTT
GTTGGATTCCCAG-----

Original motif Consensus sequence: AAAGTGCCAGATGCAGC

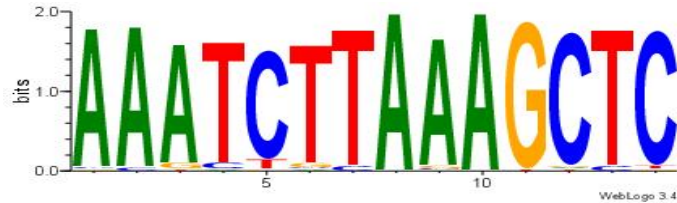


Reverse complement motif Consensus sequence: GCTGCARTCTCGGCACTTT

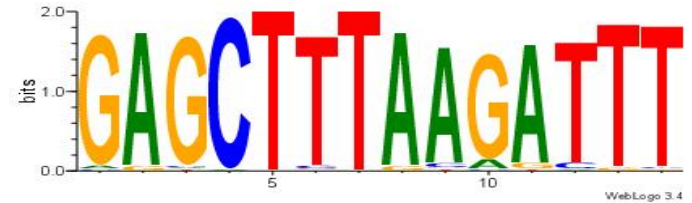


Dataset #: 1 Motif ID: 346 Motif name: Motif 346

Original motif Consensus sequence: AAATCTTAAAGCTC



Reverse complement motif Consensus sequence: GAGCTTTAAGATTT



Best Matches for Motif ID 346 (Highest to Lowest)

Dataset #:	1
Motif ID:	303
Motif name:	Motif 303
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	14
Similarity score:	0.0682748

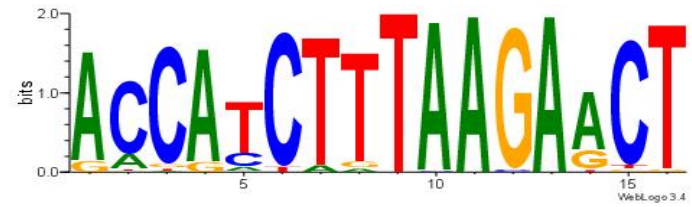
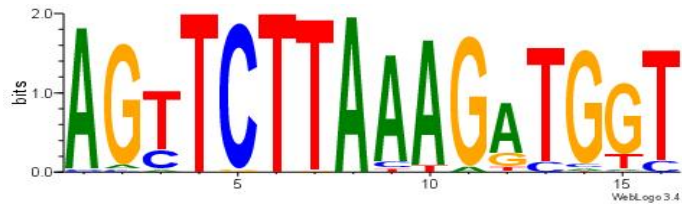
Alignment:

```

ACCATCTTTAAGAACT
--GAGCTTTAAGATTT
    
```

Original motif Consensus sequence: AGTTCTTAAAGATGGT

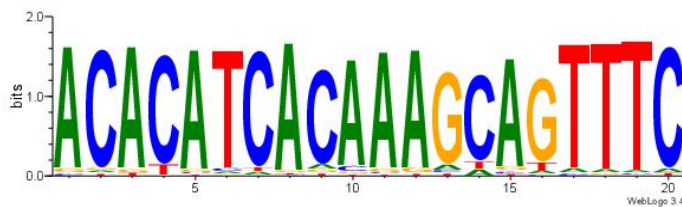
Reverse complement motif Consensus sequence:
ACCATCTTTAAGAACT



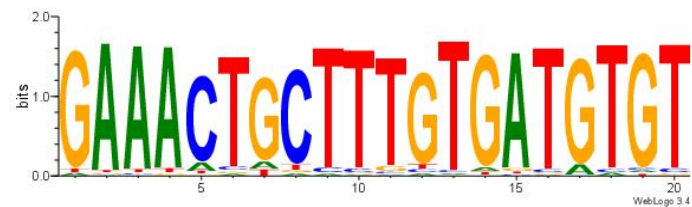
Dataset #: 1
 Motif ID: 202
 Motif name: Motif 202
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 14
 Similarity score: 0.0876662

Alignment:
 GAACTGCTTTGTGATGTGT
 ----GAGCTTTAAGATTT--

Original motif Consensus sequence: ACACATCACAAGCAGTTTC



Reverse complement motif Consensus sequence: GAACTGCTTTGTGATGTGT



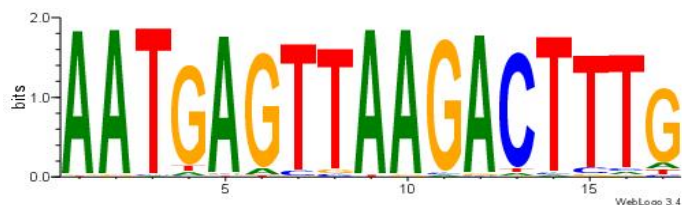
Dataset #: 1

Motif ID: 224
 Motif name: Motif 224
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 14
 Similarity score: 0.0880907

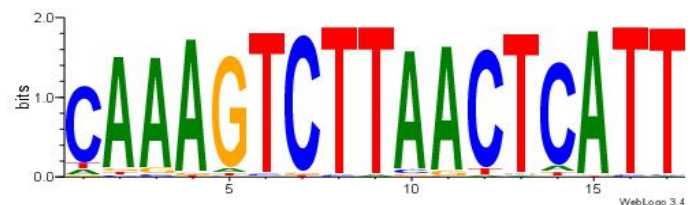
Alignment:

AATGAGTTAAGACTTTG
 --GAGCTTTAAGATTT--

Original motif Consensus sequence: AATGAGTTAAGACTTTG



Reverse complement motif Consensus sequence: CAAAGTCTTAACTCATT



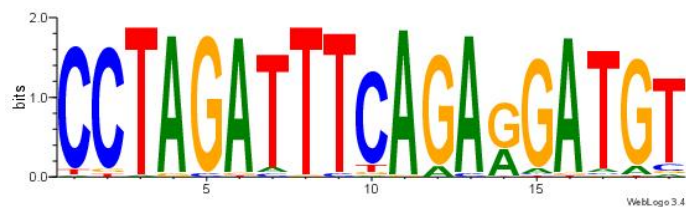
Dataset #: 1
 Motif ID: 280
 Motif name: Motif 280
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 14

Similarity score: 0.0973462

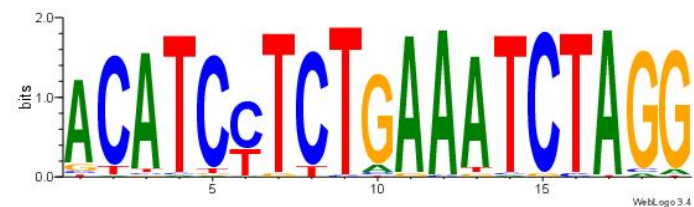
Alignment:

CCTAGATTTTCAGARGATGT
---GAGCTTTAAGATTT---

Original motif Consensus sequence: CCTAGATTTTCAGARGATGT



Reverse complement motif Consensus sequence:
ACATCMTCTGAAATCTAGG



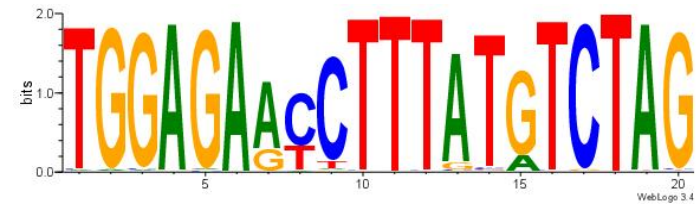
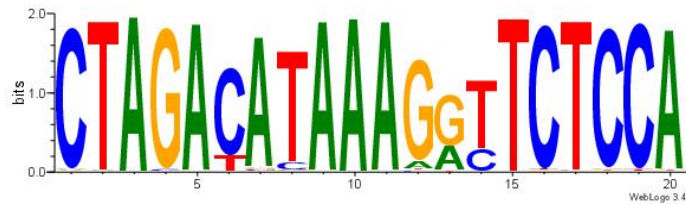
Dataset #: 1
Motif ID: 85
Motif name: Motif 85
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 5
Number of overlap: 14
Similarity score: 0.100914

Alignment:

CTAGACATAAAGGTTCTCCA
--AAATCTTAAAGCTC----

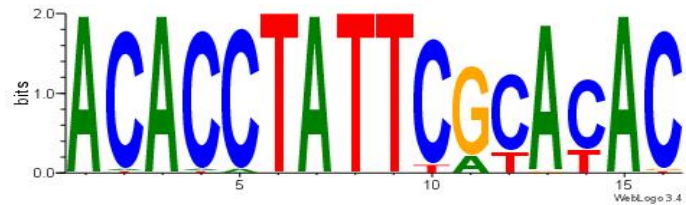
Original motif Consensus sequence: CTAGACATAAAGGTTCTCCA

Reverse complement motif Consensus sequence:
TGGAGAACCTTTATGTCTAG

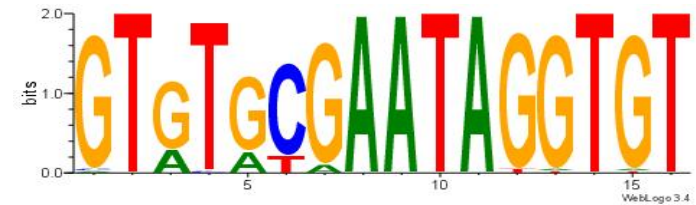


Dataset #: 1 Motif ID: 347 Motif name: Motif 347

Original motif Consensus sequence: ACACCTATTCGCACAC



Reverse complement motif Consensus sequence: GTGTGCGAATAGGTGT



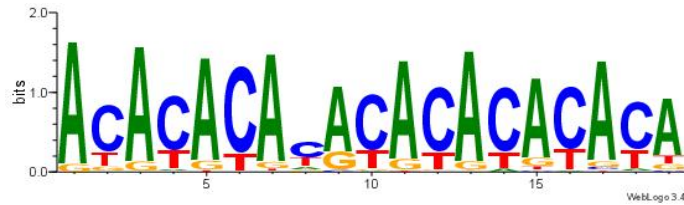
Best Matches for Motif ID 347 (Highest to Lowest)

Dataset #:	1
Motif ID:	66
Motif name:	Motif 66
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	16
Similarity score:	0.0719682

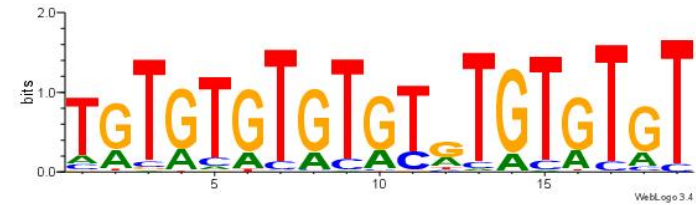
Alignment:

ACACACAYACACACACACA
ACACCTATTCGCACAC---

Original motif Consensus sequence: ACACACAYACACACACACA



Reverse complement motif Consensus sequence:
TGTGTGTGTGKTGTGTGT



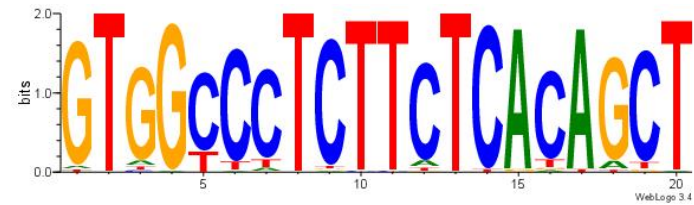
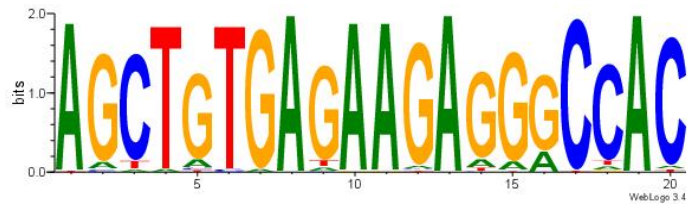
Dataset #: 1
Motif ID: 294
Motif name: Motif 294
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 3
Number of overlap: 16
Similarity score: 0.0824744

Alignment:

AGCTGTGAGAAGAGGGCCAC
--GTGTGCGAATAGGTGT--

Original motif Consensus sequence: AGCTGTGAGAAGAGGGCCAC

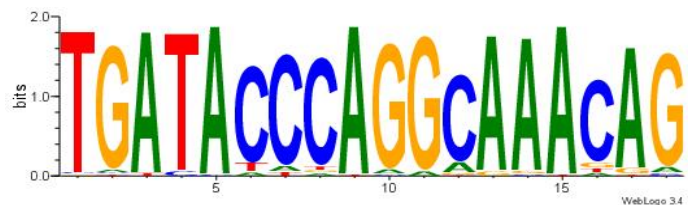
Reverse complement motif Consensus sequence:
GTGGCCCTCTTCTCACAGCT



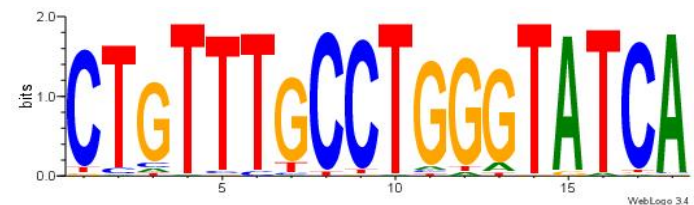
Dataset #: 1
 Motif ID: 290
 Motif name: Motif 290
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 16
 Similarity score: 0.0947322

Alignment:
 CTGTTTGCCTGGGTATCA
 GTGTGCGAATAGGTGT--

Original motif Consensus sequence: TGATACCAGGCAAACAG



Reverse complement motif Consensus sequence: CTGTTTGCCTGGGTATCA



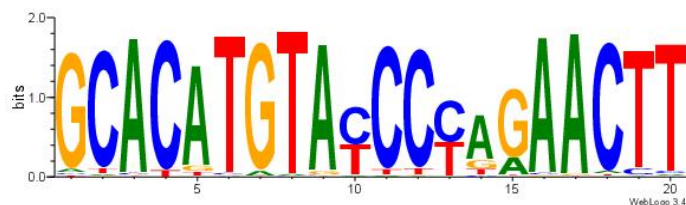
Dataset #: 1

Motif ID: 225
 Motif name: Motif 225
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 16
 Similarity score: 0.0975498

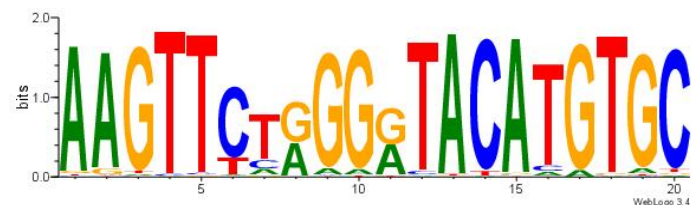
Alignment:

GCACATGTAYCCYAGAACTT
 --ACACCTATTTCGCACAC--

Original motif Consensus sequence: GCACATGTAYCCYAGAACTT



Reverse complement motif Consensus sequence: AAGTTCTKGGKTACATGTGC



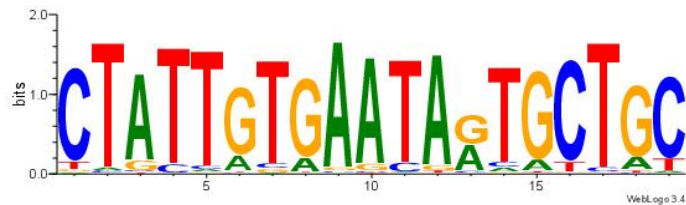
Dataset #: 1
 Motif ID: 70
 Motif name: Motif 70
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 16

Similarity score: 0.102565

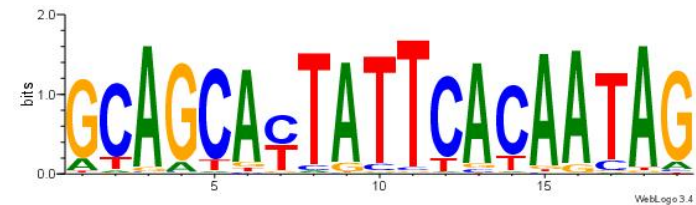
Alignment:

CTATTGTGAATARTGCTGC
--GTGTGCGAATAGGTGT--

Original motif Consensus sequence: CTATTGTGAATARTGCTGC

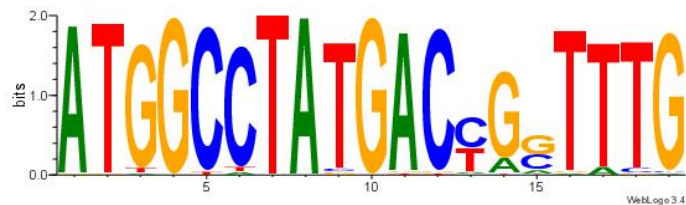


Reverse complement motif Consensus sequence: GCAGCAMTATTCACAATAG

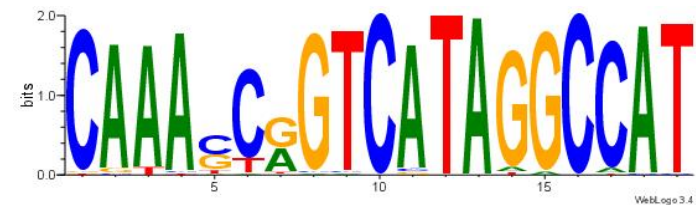


Dataset #: 1 Motif ID: 348 Motif name: Motif 348

Original motif Consensus sequence: ATGGCCTATGACCGTTTG



Reverse complement motif Consensus sequence: CAAASCKGTCATAGGCCAT



Best Matches for Motif ID 348 (Highest to Lowest)

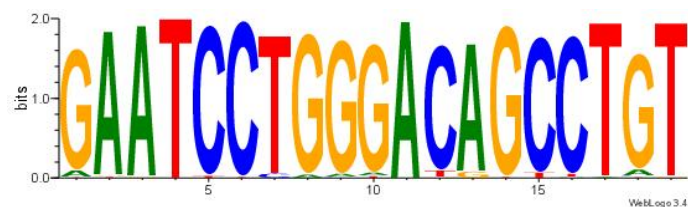
Dataset #:	1
Motif ID:	192
Motif name:	Motif 192
Matching format of first motif:	Original Motif

Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 19
 Similarity score: 0.115392

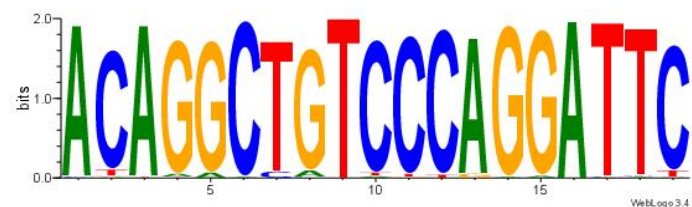
Alignment:

ACAGGCTGTCCCAGGATTC
 ATGGCCTATGACYGSTTTG

Original motif Consensus sequence: GAATCCTGGGACAGCCTGT



Reverse complement motif Consensus sequence:
 ACAGGCTGTCCCAGGATTC

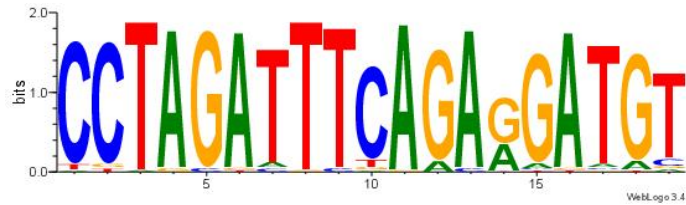


Dataset #: 1
 Motif ID: 280
 Motif name: Motif 280
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 19
 Similarity score: 0.117513

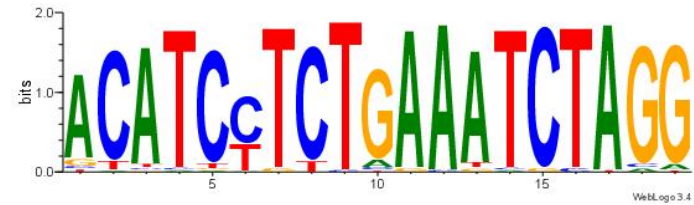
Alignment:

ACATCMTCTGAAATCTAGG
ATGGCCTATGACYGSTTTG

Original motif Consensus sequence: CCTAGATTTcAGARGATGT



Reverse complement motif Consensus sequence:
ACATCMTCTGAAATCTAGG

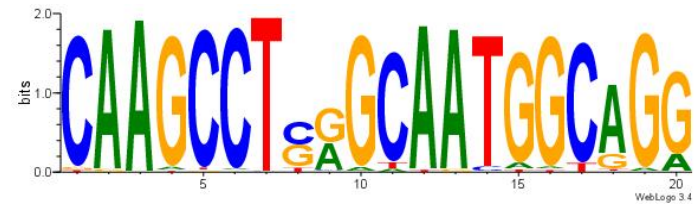
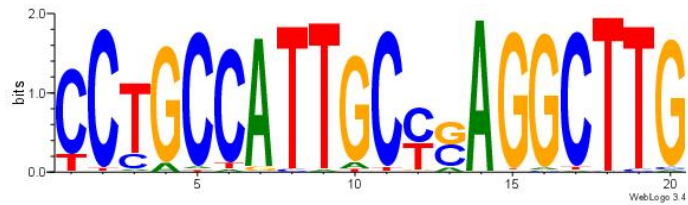


Dataset #: 1
Motif ID: 196
Motif name: Motif 196
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 2
Number of overlap: 19
Similarity score: 0.118

Alignment:
CAAGCCTSKGCAATGGCAGG
CAAASCKGTCATAGGCCAT-

Original motif Consensus sequence: CTGCCATTGCYSAGGCTTG

Reverse complement motif Consensus sequence:
CAAGCCTSKGCAATGGCAGG

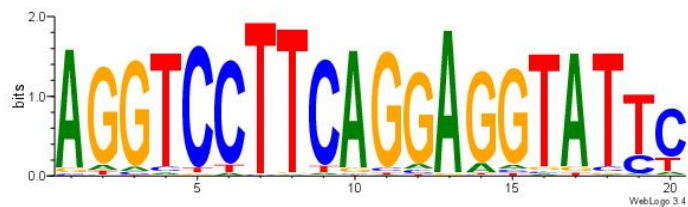


Dataset #: 1
 Motif ID: 179
 Motif name: Motif 179
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 19
 Similarity score: 0.120128

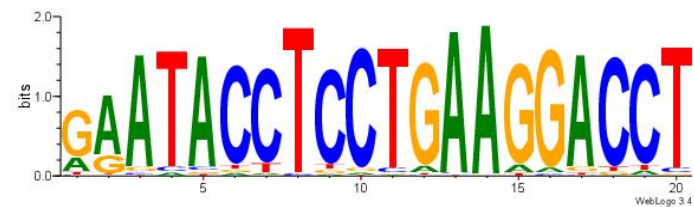
Alignment:

GAATACCTCCTGAAGGACCT
 -CAAASCKGTCATAGGCCAT

Original motif Consensus sequence: AGGTCCTCAGGAGGTATTC



Reverse complement motif Consensus sequence: GAATACCTCCTGAAGGACCT



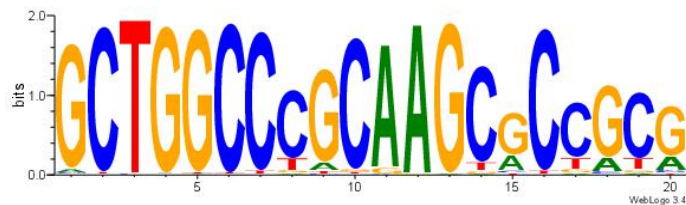
Dataset #: 1

Motif ID: 100
 Motif name: Motif 100
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 19
 Similarity score: 0.120655

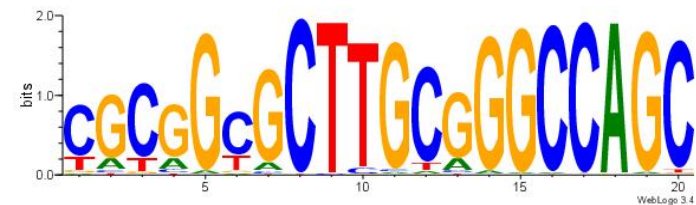
Alignment:

GCTGGCCCGCAAGCGCCGCG
 -ATGGCCTATGACYGSTTTG

Original motif Consensus sequence: GCTGGCCCGCAAGCGCCGCG

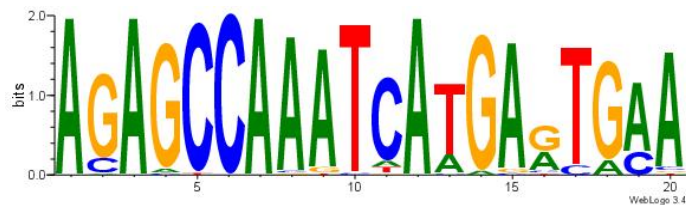


Reverse complement motif Consensus sequence: CGCGGCGCTTGC GGGCCAGC

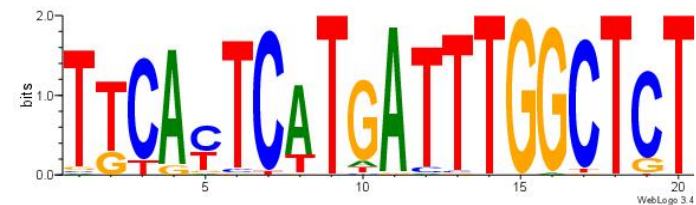


Dataset #: 1 Motif ID: 349 Motif name: Motif 349

Original motif Consensus sequence: AGAGCCAAATCATGARTGAA



Reverse complement motif Consensus sequence: TTCAMTCATGATTTGGCTCT



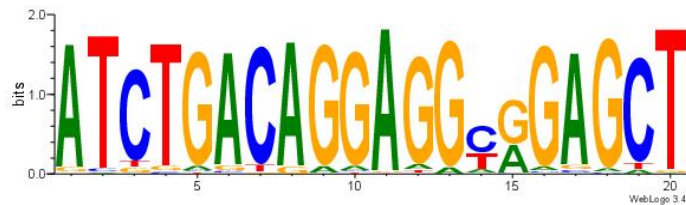
Best Matches for Motif ID 349 (Highest to Lowest)

Dataset #: 1
Motif ID: 165
Motif name: Motif 165
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 20
Similarity score: 0.121011

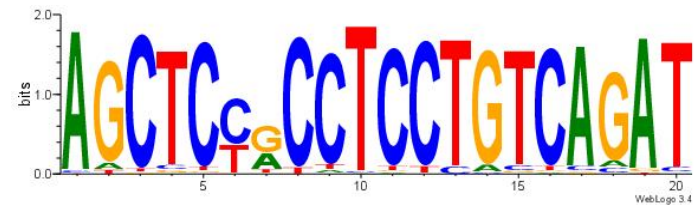
Alignment:

AGCTCMKCCTCCTGTCAGAT
AGAGCCAAATCATGARTGAA

Original motif Consensus sequence: ATCTGACAGGAGGYRGAGCT



Reverse complement motif Consensus sequence:
AGCTCMKCCTCCTGTCAGAT



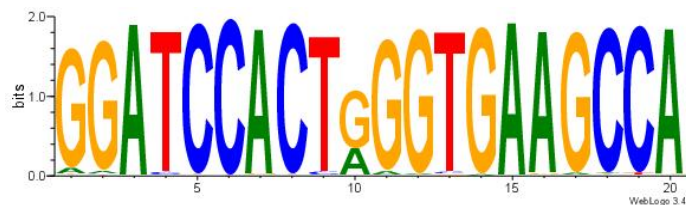
Dataset #: 1
Motif ID: 61
Motif name: Motif 61
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif

Direction: Forward
Position number: 1
Number of overlap: 20
Similarity score: 0.121473

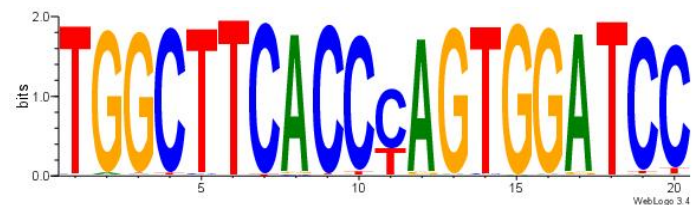
Alignment:

GGATCCACTGGGTGAAGCCA
AGAGCCAAATCATGARTGAA

Original motif Consensus sequence: GGATCCACTGGGTGAAGCCA



Reverse complement motif Consensus sequence: TGGCTTCACCCAGTGGATCC

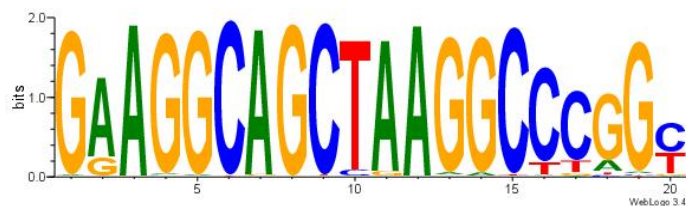


Dataset #: 1
Motif ID: 64
Motif name: Motif 64
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 20
Similarity score: 0.124741

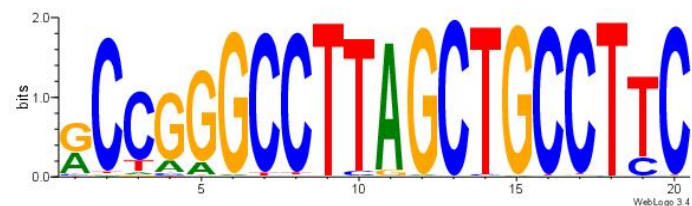
Alignment:

KCCGGGCCTTAGCTGCCTTC
TTCAMTCATGATTTGGCTCT

Original motif Consensus sequence: GAAGGCAGCTAAGGCCGGY



Reverse complement motif Consensus sequence: KCCGGGCCTTAGCTGCCTTC

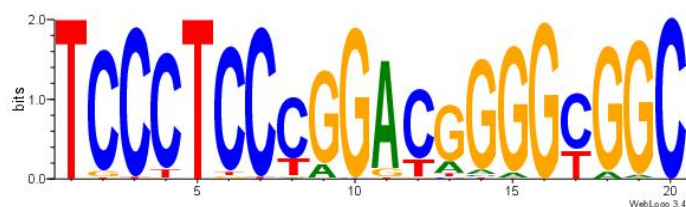


Dataset #: 1
Motif ID: 155
Motif name: Motif 155
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 20
Similarity score: 0.13108

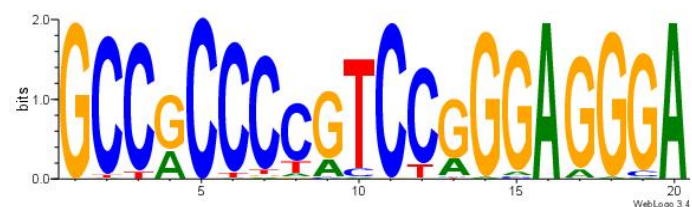
Alignment:

TCCCTCCCGGACGGGGYGGC
TTCAMTCATGATTTGGCTCT

Original motif Consensus sequence: TCCCTCCCGGACGGGGYGGC



Reverse complement motif Consensus sequence: GCCKCCCCGTCCGGGAGGGA

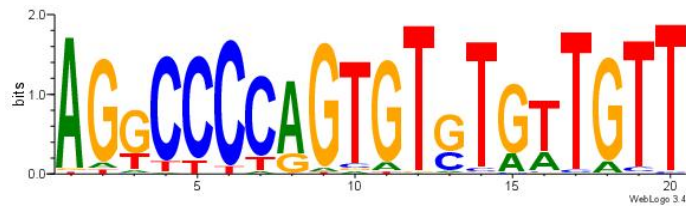


Dataset #: 1
 Motif ID: 176
 Motif name: Motif 176
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.131454

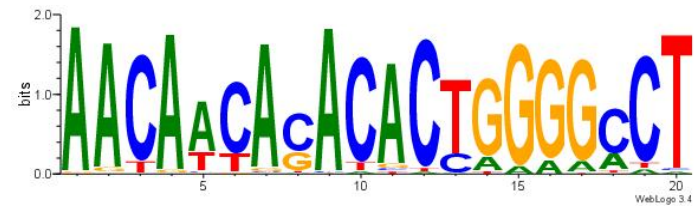
Alignment:

AAC AACASACTGGGGCCT
 TTCAMTCATGATTTGGCTCT

Original motif Consensus sequence: AGGCCCCAGTGTSTGTTGTT



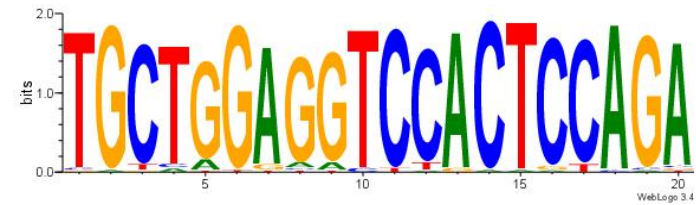
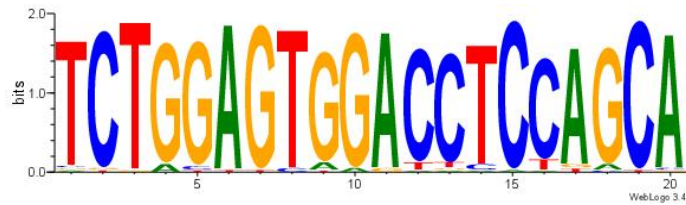
Reverse complement motif Consensus sequence: AAC AACASACTGGGGCCT



Dataset #: 1 Motif ID: 350 Motif name: Motif 350

Original motif Consensus sequence: TCTGGAGTGGACCTCCAGCA

Reverse complement motif Consensus sequence: TGCTGGAGTCCACTCCAGA



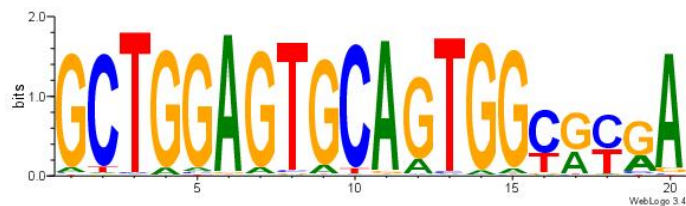
Best Matches for Motif ID 350 (Highest to Lowest)

Dataset #: 1
 Motif ID: 3
 Motif name: Motif 3
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.100512

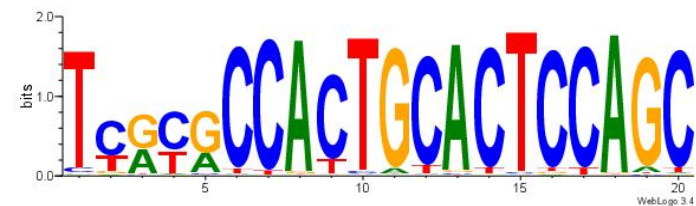
Alignment:

GCTGGAGTGCAGTGGCRYGA
 TCTGGAGTGGACCTCCAGCA

Original motif Consensus sequence: GCTGGAGTGCAGTGGCRYGA



Reverse complement motif Consensus sequence: TCKMGCCACTGCACTCCAGC

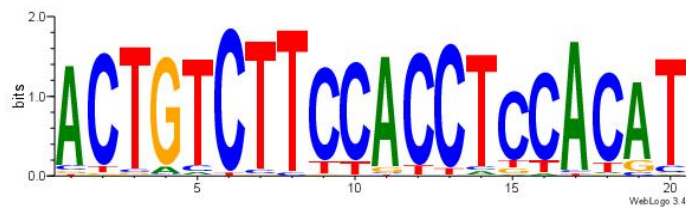


Dataset #: 1
 Motif ID: 178
 Motif name: Motif 178
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.103785

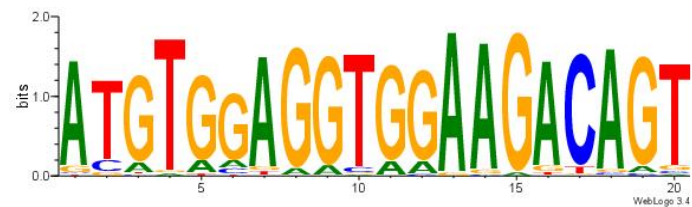
Alignment:

ATGTGGAGGTGGAAGACAGT
 TGCTGGAGGTCCACTCCAGA

Original motif Consensus sequence: ACTGTCTTCCACCTCCACAT



Reverse complement motif Consensus sequence: ATGTGGAGGTGGAAGACAGT



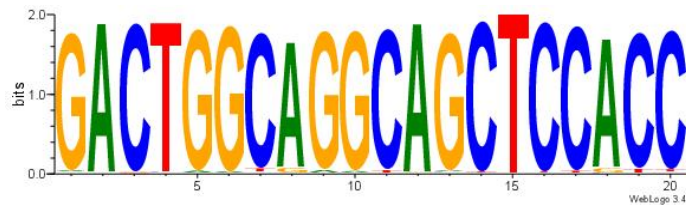
Dataset #: 1
 Motif ID: 52
 Motif name: Motif 52
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1

Number of overlap: 20
Similarity score: 0.104962

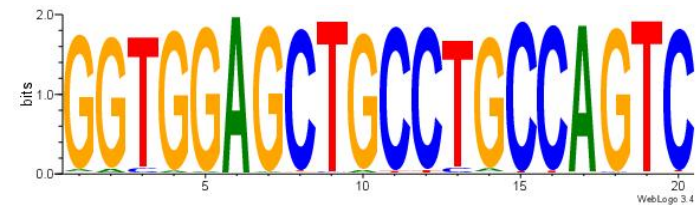
Alignment:

GGTGGAGCTGCCTGCCAGTC
TCTGGAGTGGACCTCCAGCA

Original motif Consensus sequence: GACTGGCAGGCAGCTCCACC



Reverse complement motif Consensus sequence:
GGTGGAGCTGCCTGCCAGTC

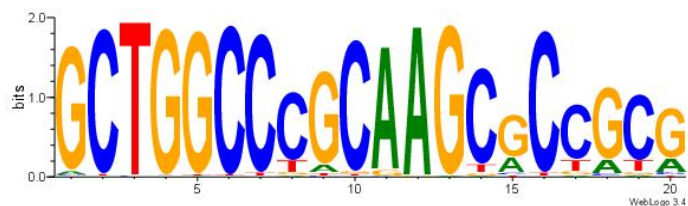


Dataset #: 1
Motif ID: 100
Motif name: Motif 100
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 20
Similarity score: 0.125531

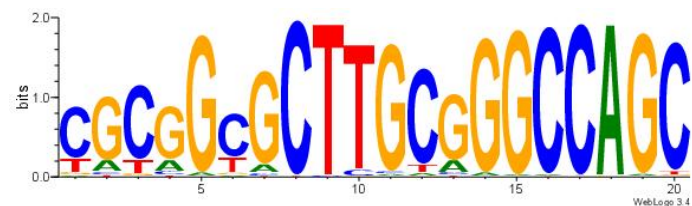
Alignment:

GCTGGCCCGCAAGCGCCGCG
TCTGGAGTGGACCTCCAGCA

Original motif Consensus sequence: GCTGGCCCGCAAGCGCCGCG



Reverse complement motif Consensus sequence: CGCGGCGCTTGCGGGCCAGC

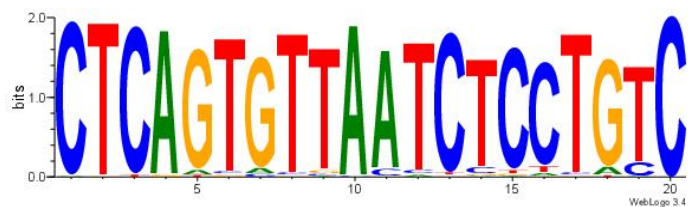


Dataset #: 1
Motif ID: 262
Motif name: Motif 262
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 20
Similarity score: 0.12666

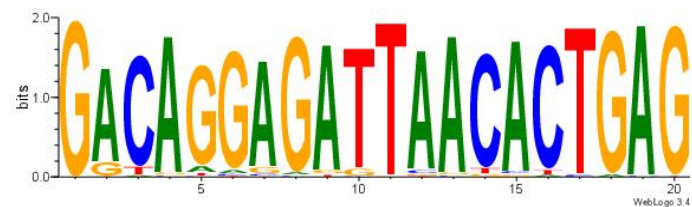
Alignment:

CTCAGTGTTAATCTCCTGTC
TCTGGAGTGGACCTCCAGCA

Original motif Consensus sequence: CTCAGTGTTAATCTCCTGTC

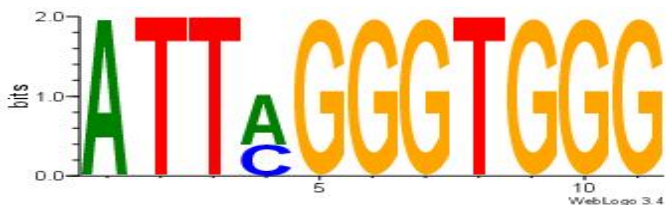


Reverse complement motif Consensus sequence: GACAGGAGATTAACACTGAG

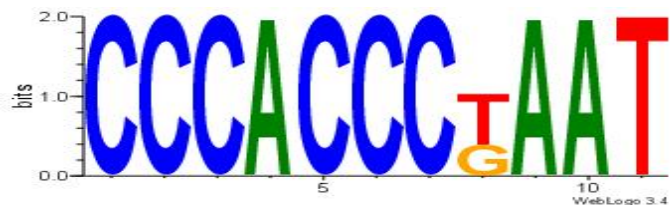


Dataset #: 1 Motif ID: 351 Motif name: Motif 351

Original motif Consensus sequence: ATTMGGGTGGG



Reverse complement motif Consensus sequence: CCCACCCYAAT



Best Matches for Motif ID 351 (Highest to Lowest)

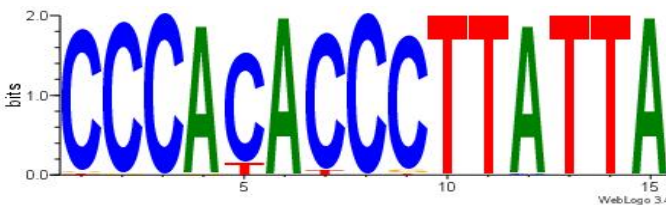
Dataset #:	1
Motif ID:	259
Motif name:	Motif 259
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	3
Number of overlap:	11
Similarity score:	0.0511125

Alignment:

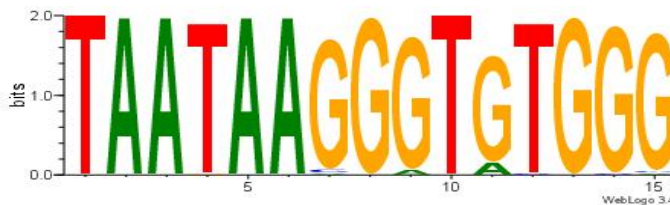
```

CCCACACCCTTATTA
--CCCACCCYAAT--
    
```

Original motif Consensus sequence: CCCACACCCTTATTA



Reverse complement motif Consensus sequence: TAATAAGGGTGTGGG

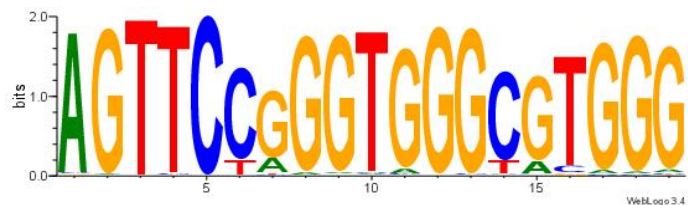


Dataset #: 1
 Motif ID: 98
 Motif name: Motif 98
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 7
 Number of overlap: 11
 Similarity score: 0.0610932

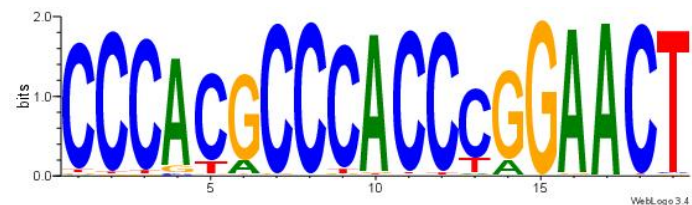
Alignment:

AGTTCCGGGTGGGCGTGGG
 --ATTMGGGTGGG-----

Original motif Consensus sequence: AGTTCCGGGTGGGCGTGGG



Reverse complement motif Consensus sequence: CCCACGCCACCCGGAAC



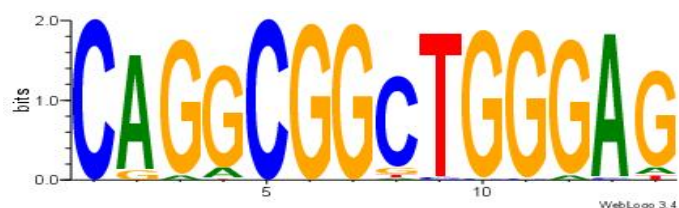
Dataset #: 1
 Motif ID: 286
 Motif name: Motif 286
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward

Position number: 2
Number of overlap: 11
Similarity score: 0.0771299

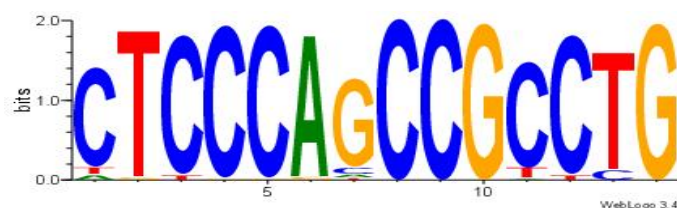
Alignment:

CAGGCGGCTGGGAG
-ATTMGGGTGGG--

Original motif Consensus sequence: CAGGCGGCTGGGAG



Reverse complement motif Consensus sequence: CTCCCAGCCGCCTG



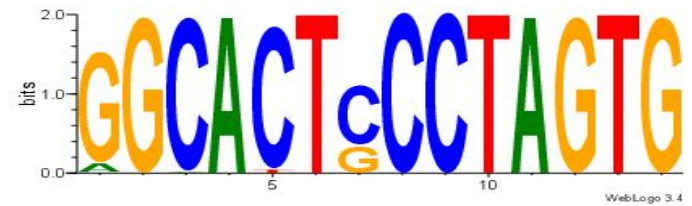
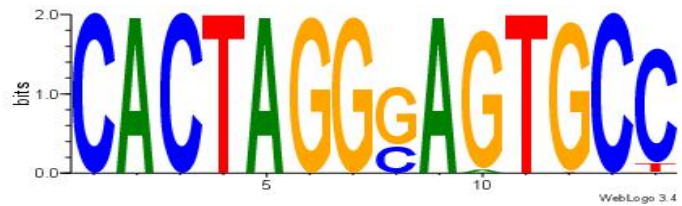
Dataset #: 1
Motif ID: 153
Motif name: Motif 153
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 3
Number of overlap: 11
Similarity score: 0.0778643

Alignment:

GCACTCCCTAGTG
--CCCACCCYAAT-

Original motif Consensus sequence: CACTAGGGAGTGCC

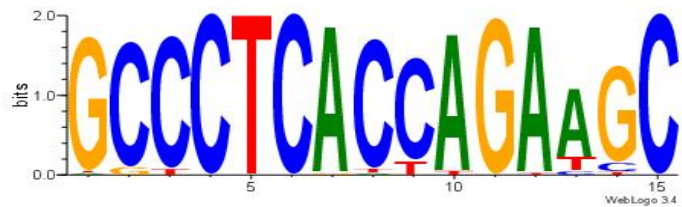
Reverse complement motif Consensus sequence: GCACTCCCTAGTG



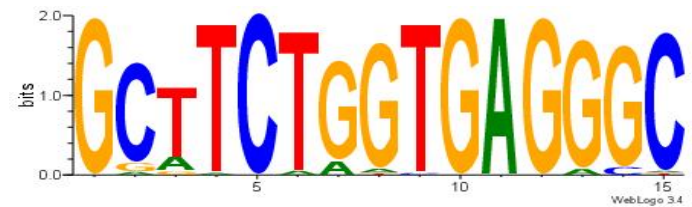
Dataset #: 1
 Motif ID: 277
 Motif name: Motif 277
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 4
 Number of overlap: 11
 Similarity score: 0.0845161

Alignment:
 GCCCTCACCAGAAGC
 -CCCACCCYAAT---

Original motif Consensus sequence: GCCCTCACCAGAAGC



Reverse complement motif Consensus sequence: GCTTCTGGTGAGG



Dataset #: 1 Motif ID: 352 Motif name: Motif 352

Original motif Consensus sequence: CATCTTCA



Reverse complement motif Consensus sequence: TGAAGATG



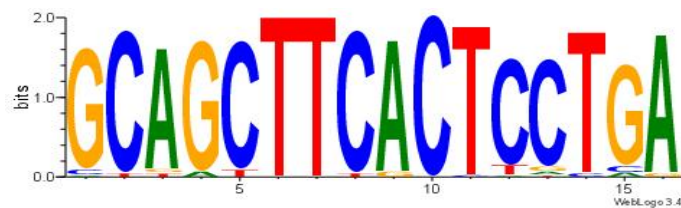
Best Matches for Motif ID 352 (Highest to Lowest)

Dataset #:	1
Motif ID:	246
Motif name:	Motif 246
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	8
Number of overlap:	8
Similarity score:	0.0276887

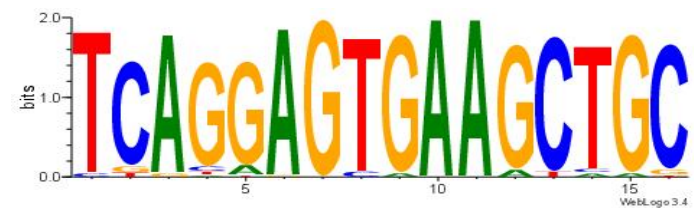
Alignment:

```
TCAGGAGTGAAGCTGC
-----TGAAGATG-
```

Original motif Consensus sequence: GCAGCTTCACTccTGA



Reverse complement motif Consensus sequence: TCAGGAGTGAAGCTGC

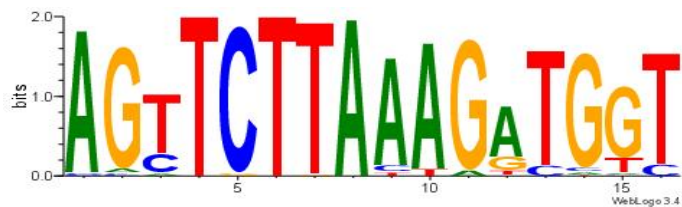


Dataset #: 1
 Motif ID: 303
 Motif name: Motif 303
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 8
 Similarity score: 0.0334876

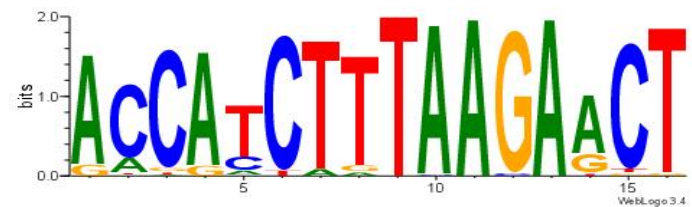
Alignment:

AGTTCTTAAAGATGGT
 --TGAAGATG-----

Original motif Consensus sequence: AGTTCTTAAAGATGGT



Reverse complement motif Consensus sequence: ACCATCTTAAAGAACT

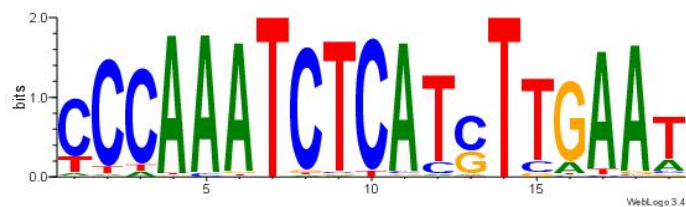


Dataset #: 1
 Motif ID: 227
 Motif name: Motif 227
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3

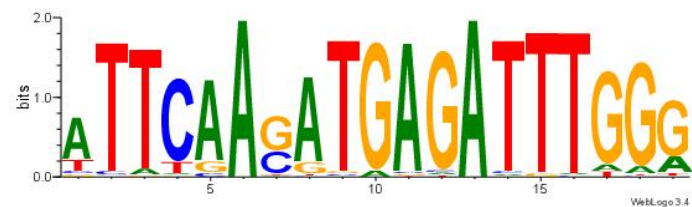
Number of overlap: 8
Similarity score: 0.0397493

Alignment:
CCCAAATCTCATSTTGAAT
-----CATCTTCA--

Original motif Consensus sequence: CCCAAATCTCATSTTGAAT



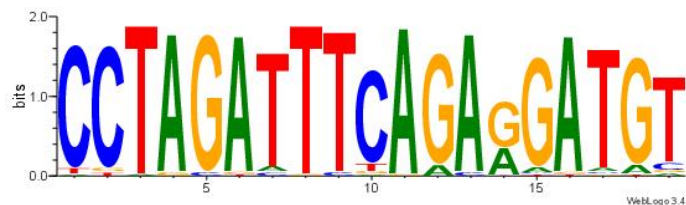
Reverse complement motif Consensus sequence:
ATTC AASATGAGATTTGGG



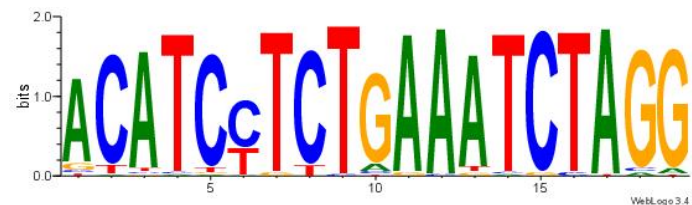
Dataset #: 1
Motif ID: 280
Motif name: Motif 280
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 2
Number of overlap: 8
Similarity score: 0.0443445

Alignment:
ACATCMTCTGAAATCTAGG
-----CATCTTCA--

Original motif Consensus sequence: CCTAGATTCAGARGATGT



Reverse complement motif Consensus sequence: ACATCMTCTGAAATCTAGG

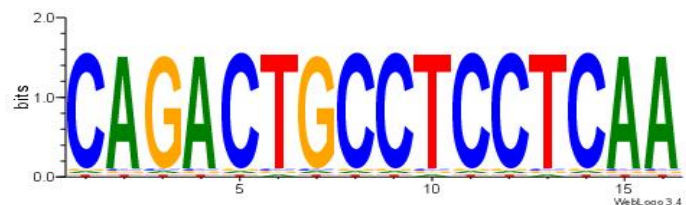


Dataset #: 1
Motif ID: 245
Motif name: Motif 245
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 8
Number of overlap: 8
Similarity score: 0.0449237

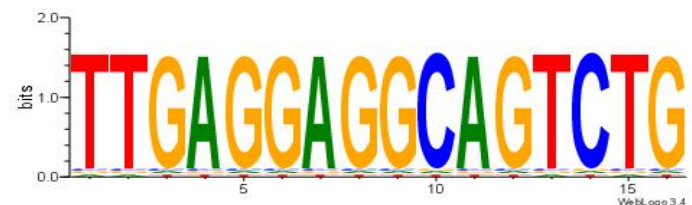
Alignment:

CAGACTGCCTCCTCAA
-----CATCTTCA--

Original motif Consensus sequence: CAGACTGCCTCCTCAA

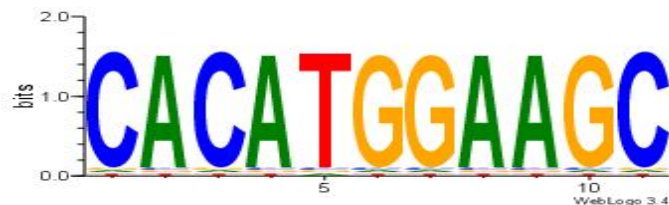


Reverse complement motif Consensus sequence: TTGAGGAGGCAGTCTG

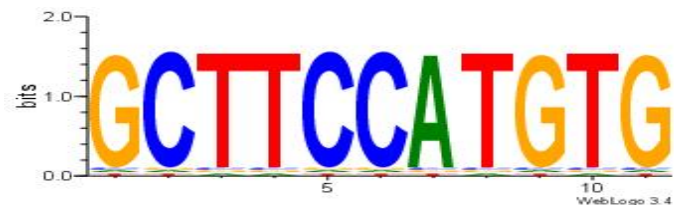


Dataset #: 1 Motif ID: 353 Motif name: Motif 353

Original motif Consensus sequence: CACATGGAAGC



Reverse complement motif Consensus sequence: GCTTCCATGTG



Best Matches for Motif ID 353 (Highest to Lowest)

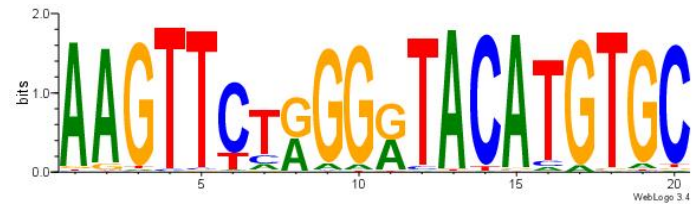
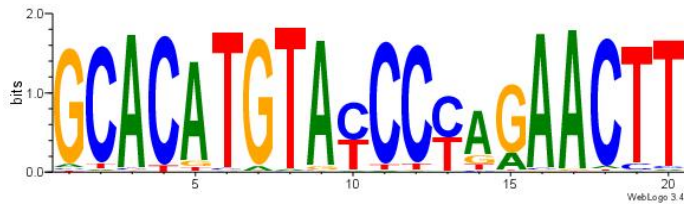
Dataset #:	1
Motif ID:	225
Motif name:	Motif 225
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	2
Number of overlap:	11
Similarity score:	0.0523615

Alignment:

```
AAGTTCTKGGKTACATGTGC  
-----GCTTCCATGTG-
```

Original motif Consensus sequence: GCACATGTAYCCYAGAACTT

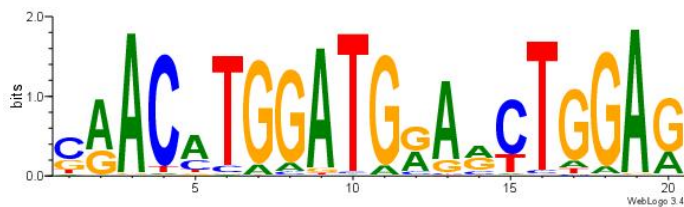
Reverse complement motif Consensus sequence:
AAGTTCTKGGKTACATGTGC



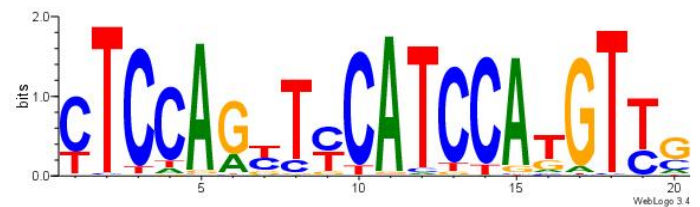
Dataset #: 1
 Motif ID: 104
 Motif name: Motif 104
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 11
 Similarity score: 0.0616894

Alignment:
 CTCCAGKTMCATCCATGTTG
 -----GCTTCCATGTG--

Original motif Consensus sequence: CAACATGGATGRARCTGGAG



Reverse complement motif Consensus sequence: CTCCAGKTMCATCCATGTTG



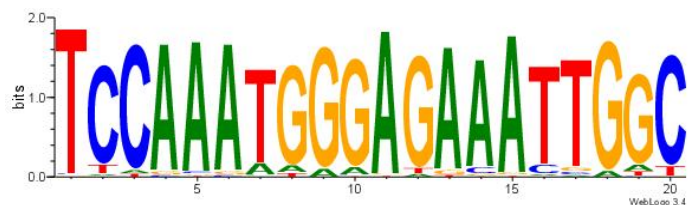
Dataset #: 1

Motif ID: 235
 Motif name: Motif 235
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 8
 Number of overlap: 11
 Similarity score: 0.0617739

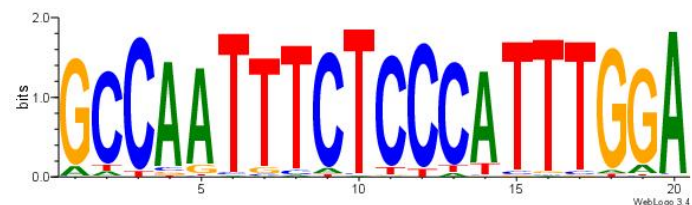
Alignment:

TCCAAATGGGAGAAATTGGC
 --CACATGGAAGC-----

Original motif Consensus sequence: TCCAAATGGGAGAAATTGGC



Reverse complement motif Consensus sequence: GCCAATTTCTCCCATTTGGA



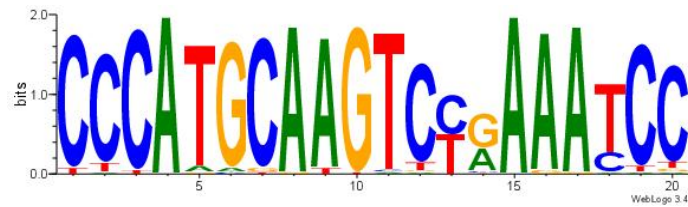
Dataset #: 1
 Motif ID: 310
 Motif name: Motif 310
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 11

Similarity score: 0.0618096

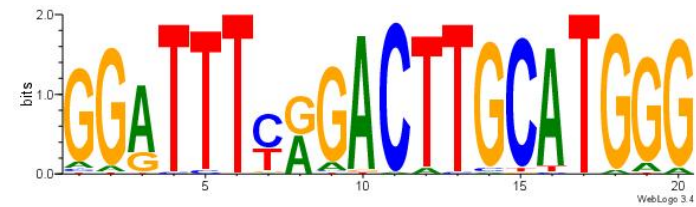
Alignment:

```
GGATTTMKGACTTGCATGGG  
-----GCTTCCATGTG
```

Original motif Consensus sequence: CCCATGCAAGTCYRAAATCC



Reverse complement motif Consensus sequence:
GGATTTMKGACTTGCATGGG



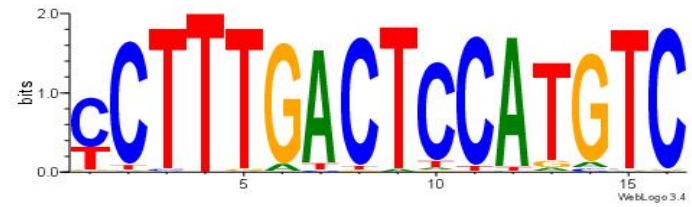
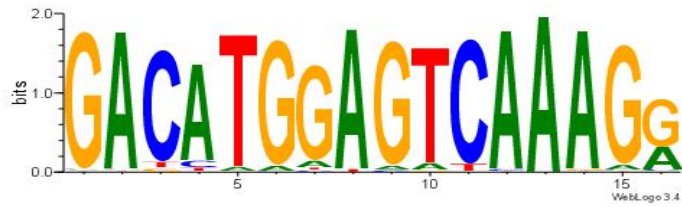
Dataset #: 1
Motif ID: 326
Motif name: Motif 326
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 11
Similarity score: 0.0627655

Alignment:

```
GACATGGAGTCAAAGG  
CACATGGAAGC-----
```

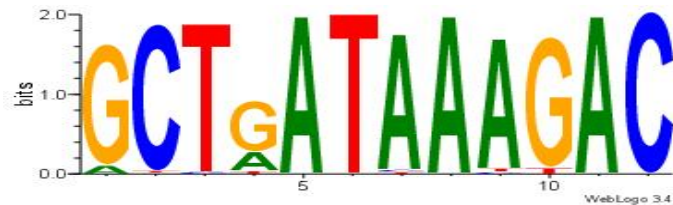
Original motif Consensus sequence: GACATGGAGTCAAAGG

Reverse complement motif Consensus sequence:
CCTTTGACTCCATGTC

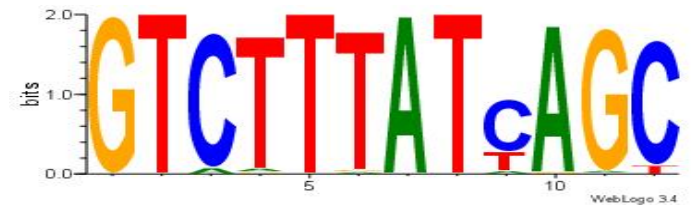


Dataset #: 1 Motif ID: 354 Motif name: Motif 354

Original motif Consensus sequence: GCTGATAAAGAC



Reverse complement motif Consensus sequence: GTCTTTATCAGC

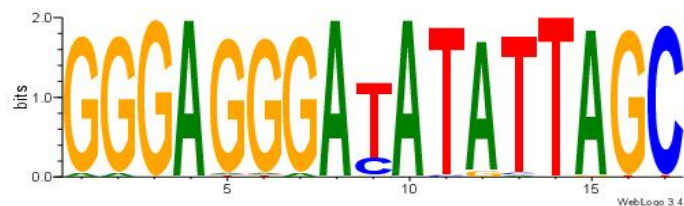


Best Matches for Motif ID 354 (Highest to Lowest)

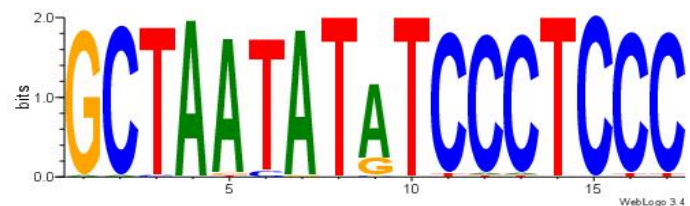
Dataset #:	1
Motif ID:	329
Motif name:	Motif 329
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	6
Number of overlap:	12
Similarity score:	0.0760989

Alignment:
 GGGAGGGATATATTAGC
 GTCTTTATCAGC-----

Original motif Consensus sequence: GGGAGGGATATATTAGC



Reverse complement motif Consensus sequence: GCTAATATATCCCTCCC

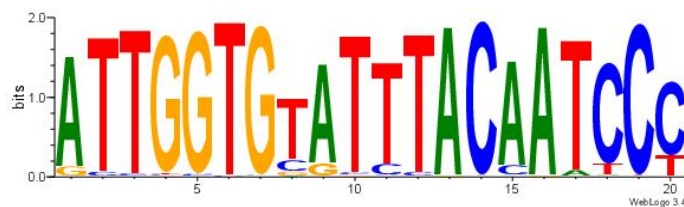


Dataset #: 1
Motif ID: 106
Motif name: Motif 106
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 7
Number of overlap: 12
Similarity score: 0.0776121

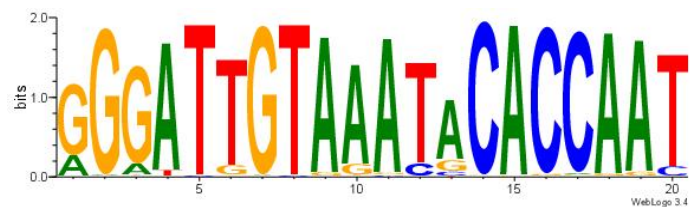
Alignment:

```
GGGATTGTAAATACACCAAT  
-----GCTGATAAAGAC--
```

Original motif Consensus sequence: ATTGGTGTATTACAATCCC



Reverse complement motif Consensus sequence: GGGATTGTAAATACACCAAT

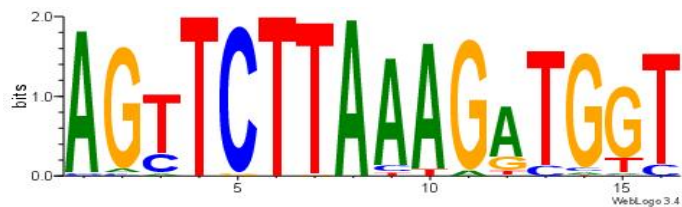


Dataset #: 1
 Motif ID: 303
 Motif name: Motif 303
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 12
 Similarity score: 0.0781258

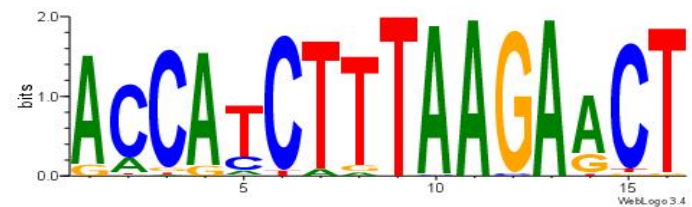
Alignment:

AGTTCTTAAAGATGGT
 -GCTGATAAAGAC---

Original motif Consensus sequence: AGTTCTTAAAGATGGT



Reverse complement motif Consensus sequence: ACCATCTTAAAGAACT



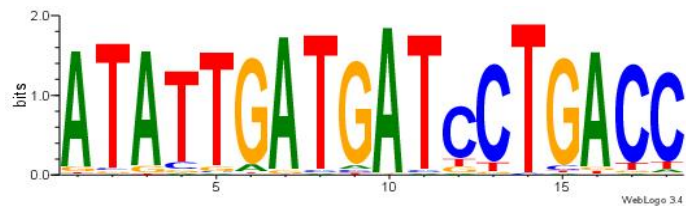
Dataset #: 1
 Motif ID: 184
 Motif name: Motif 184
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2

Number of overlap: 12
Similarity score: 0.0799308

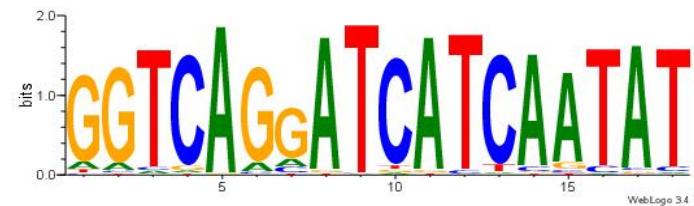
Alignment:

GGTCAGGATCATCAATAT
-GTCTTTATCAGC-----

Original motif Consensus sequence: ATATTGATGATCCTGACC



Reverse complement motif Consensus sequence:
GGTCAGGATCATCAATAT

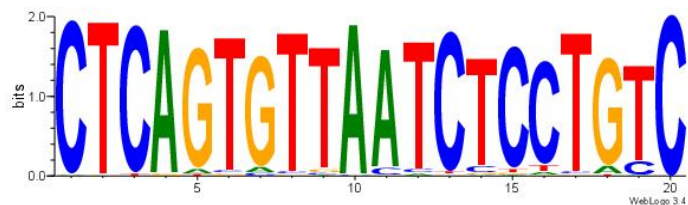


Dataset #: 1
Motif ID: 262
Motif name: Motif 262
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 5
Number of overlap: 12
Similarity score: 0.0859716

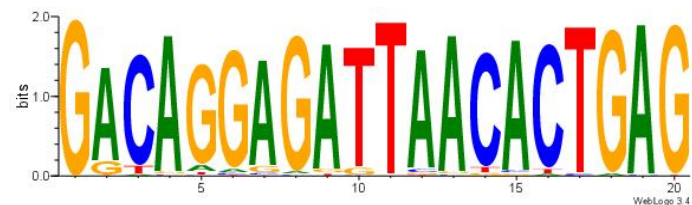
Alignment:

GACAGGAGATTAACACTGAG
----GCTGATAAAGAC----

Original motif Consensus sequence: CTCAGTGTTAATCTCCTGTC

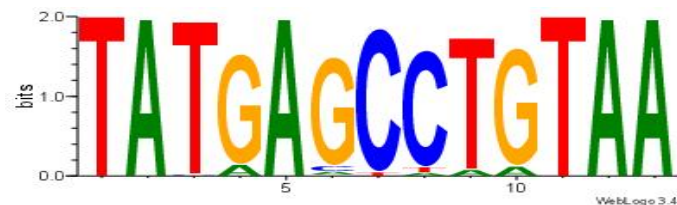


Reverse complement motif Consensus sequence: GACAGGAGATTAACACTGAG

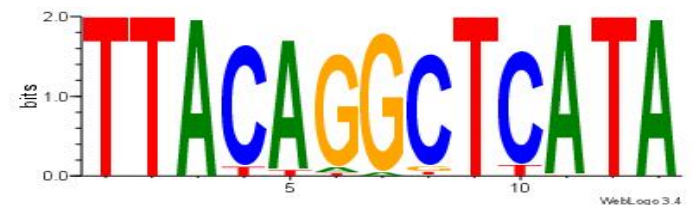


Dataset #: 1 Motif ID: 355 Motif name: Motif 355

Original motif Consensus sequence: TATGAGCCTGTAA



Reverse complement motif Consensus sequence: TTACAGGCTCATA



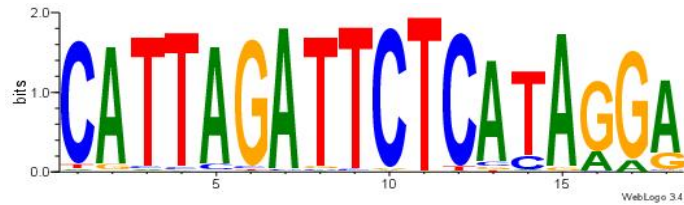
Best Matches for Motif ID 355 (Highest to Lowest)

Dataset #:	1
Motif ID:	154
Motif name:	Motif 154
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	3
Number of overlap:	13
Similarity score:	0.059588

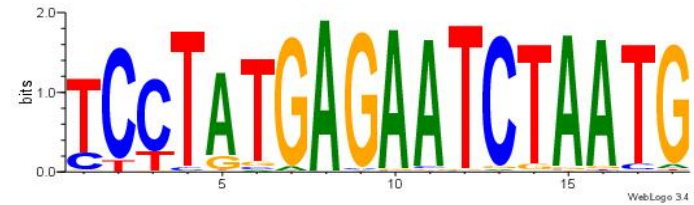
Alignment:

TCCTATGAGAATCTAATG
--TATGAGCCTGTAA---

Original motif Consensus sequence: CATTAGATTCTCATAGGA



Reverse complement motif Consensus sequence:
TCCTATGAGAATCTAATG

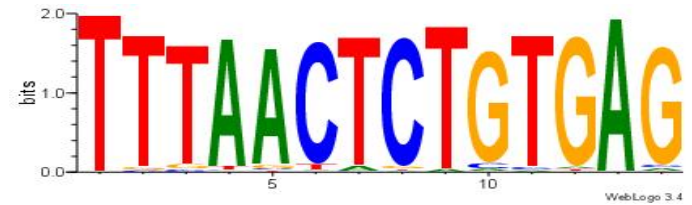
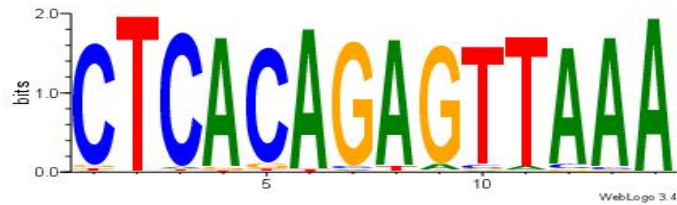


Dataset #:	1
Motif ID:	275
Motif name:	Motif 275
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	13
Similarity score:	0.0903624

Alignment:
CTCACAGAGTTAAA
TTACAGGCTCATA-

Original motif Consensus sequence: CTCACAGAGTTAAA

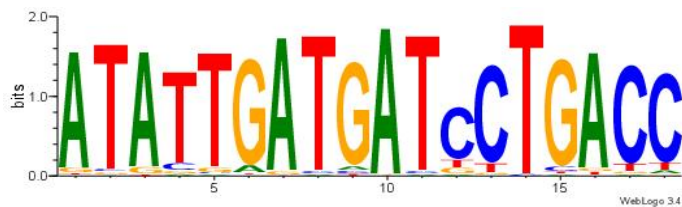
Reverse complement motif Consensus sequence: TTTAACTCTGTGAA



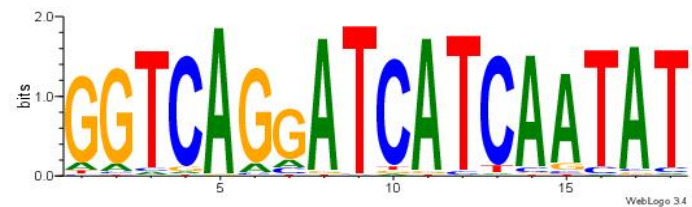
Dataset #: 1
 Motif ID: 184
 Motif name: Motif 184
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 6
 Number of overlap: 13
 Similarity score: 0.0930991

Alignment:
 GGTCAGGATCATCAATAT
 TTACAGGCTCATA-----

Original motif Consensus sequence: ATATTGATGATcCTGACC



Reverse complement motif Consensus sequence: GGTCAGGATCATCAATAT



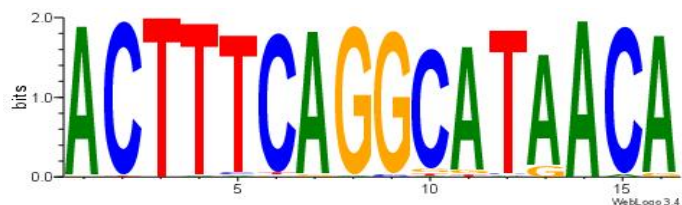
Dataset #: 1

Motif ID: 278
Motif name: Motif 278
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 2
Number of overlap: 13
Similarity score: 0.0931692

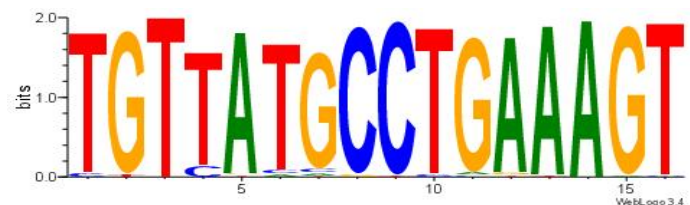
Alignment:

ACTTTCAGGCATAACA
-TTACAGGCTCATA--

Original motif Consensus sequence: ACTTTCAGGCATAACA



Reverse complement motif Consensus sequence: TGTTATGCCTGAAAGT



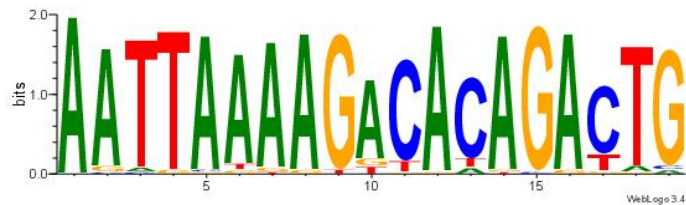
Dataset #: 1
Motif ID: 356
Motif name: Motif 356
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 4
Number of overlap: 13

Similarity score: 0.0940052

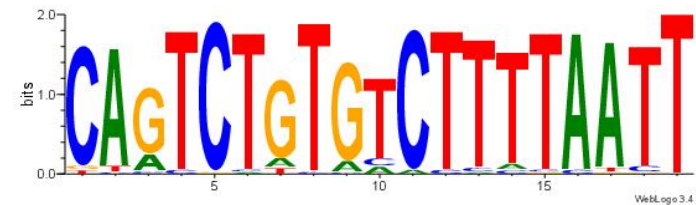
Alignment:

AATTAAAAGACACAGACTG
---TTACAGGCTCATA---

Original motif Consensus sequence: AATTAAAAGACACAGACTG

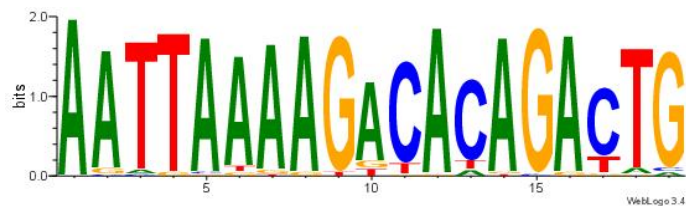


Reverse complement motif Consensus sequence:
CAGTCTGTGCTTTTAATT

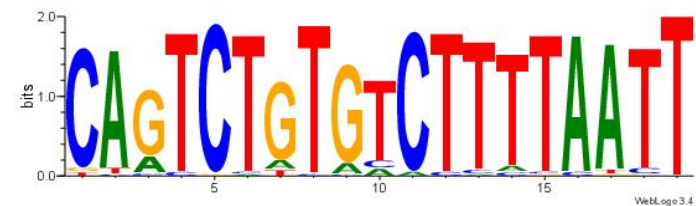


Dataset #: 1 Motif ID: 356 Motif name: Motif 356

Original motif Consensus sequence: AATTAAAAGACACAGACTG



Reverse complement motif Consensus sequence:
CAGTCTGTGCTTTTAATT



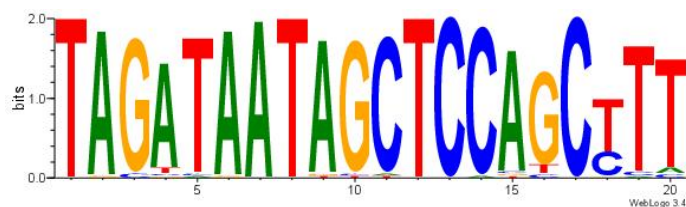
Best Matches for Motif ID 356 (Highest to Lowest)

Dataset #:	1
Motif ID:	333
Motif name:	Motif 333
Matching format of first motif:	Original Motif

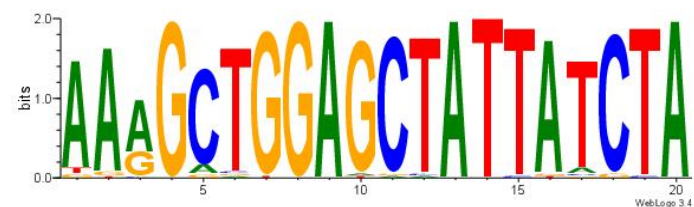
Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 19
 Similarity score: 0.10357

Alignment:
 TAGATAATAGCTCCAGCTTT
 -AATTAAAAGACACAGACTG

Original motif Consensus sequence: TAGATAATAGCTCCAGCTTT



Reverse complement motif Consensus sequence:
 AAAGCTGGAGCTATTATCTA

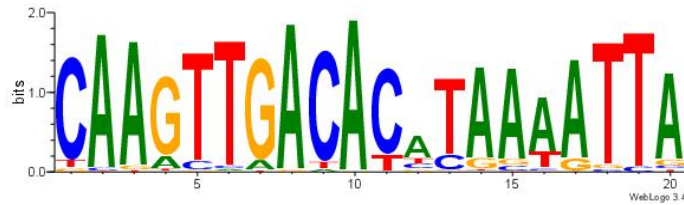


Dataset #: 1
 Motif ID: 357
 Motif name: Motif 357
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 19
 Similarity score: 0.10942

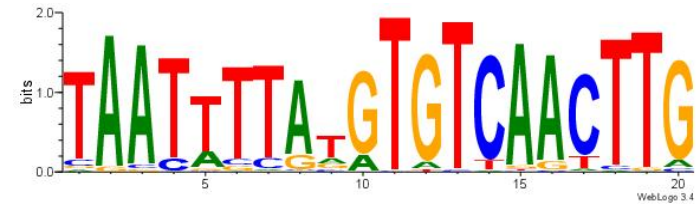
Alignment:

TAATTTTATGTGCTCAACTTG
-AATTAAAAGACACAGACTG

Original motif Consensus sequence: CAAGTTGACACATAAAATTA



Reverse complement motif Consensus sequence:
TAATTTTATGTGCTCAACTTG



Dataset #: 1
Motif ID: 232
Motif name: Motif 232
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 19
Similarity score: 0.110112

Alignment:

AGTTGTAATTGGGAGACTT
AATTAAAAGACACAGACTG

Original motif Consensus sequence: AGTTGTAATTGGGAGACTT

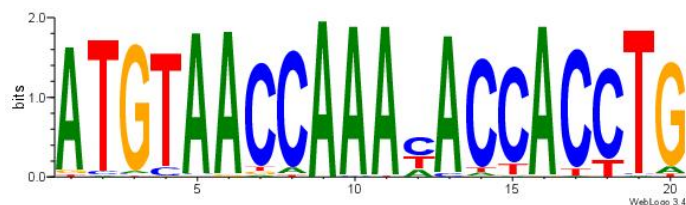
Reverse complement motif Consensus sequence:
AAGTCTCCAATTACAAC

Motif ID: 336
 Motif name: Motif 336
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 19
 Similarity score: 0.115507

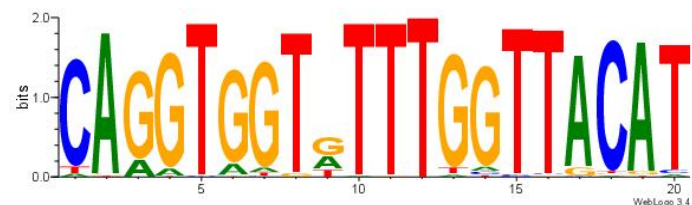
Alignment:

CAGGTGGTKTTTGGTTACAT
 CAGTCTGTGTCTTTTAATT-

Original motif Consensus sequence: ATGTAACCAAAYACCACCTG

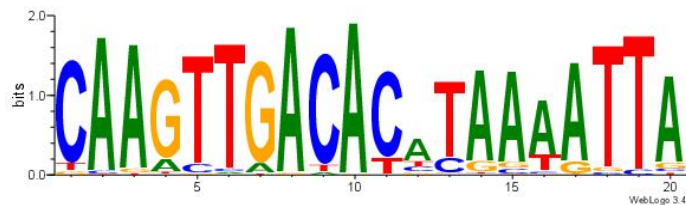


Reverse complement motif Consensus sequence: CAGGTGGTKTTTGGTTACAT

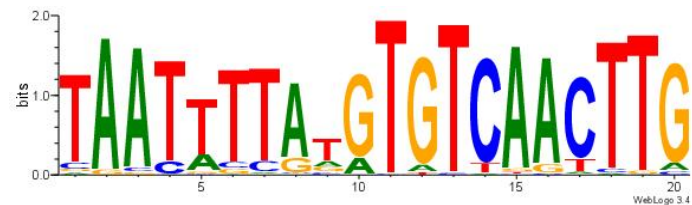


Dataset #: 1 Motif ID: 357 Motif name: Motif 357

Original motif Consensus sequence: CAAGTTGACACATAAAATTA



Reverse complement motif Consensus sequence: TAATTTATGTGCAACTTG



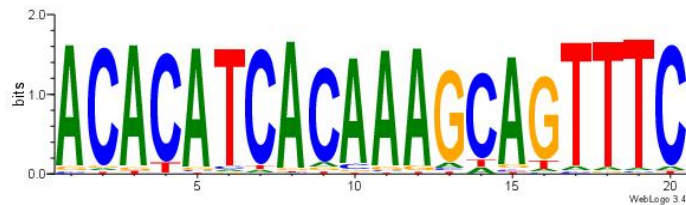
Best Matches for Motif ID 357 (Highest to Lowest)

Dataset #: 1
Motif ID: 202
Motif name: Motif 202
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 20
Similarity score: 0.114196

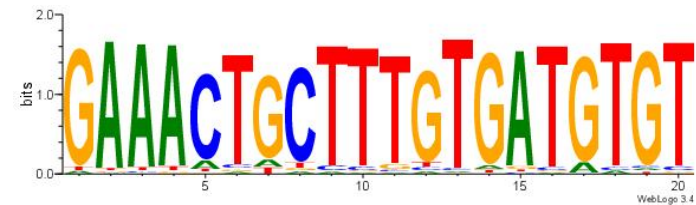
Alignment:

```
GAAACTGCTTTGTGATGTGT  
TAATTTTATGTGTCAACTTG
```

Original motif Consensus sequence: ACACATCACAAGCAGTTTC



Reverse complement motif Consensus sequence:
GAAACTGCTTTGTGATGTGT



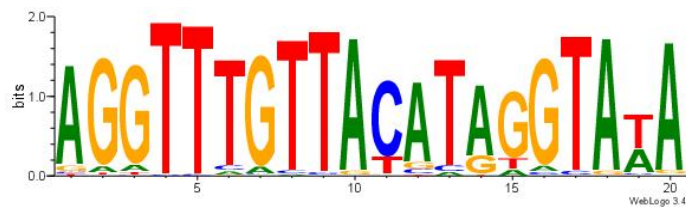
Dataset #: 1
Motif ID: 137
Motif name: Motif 137
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement

Direction: Forward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.114845

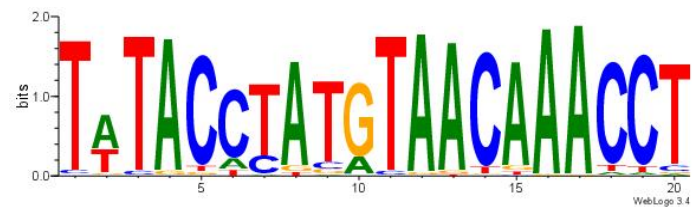
Alignment:

TWTACCTATGTAACAAACCT
 TAATTTTATGTGCTCAACTG

Original motif Consensus sequence: AGGTTTGTTACATAGGTAWA



Reverse complement motif Consensus sequence: TWTACCTATGTAACAAACCT

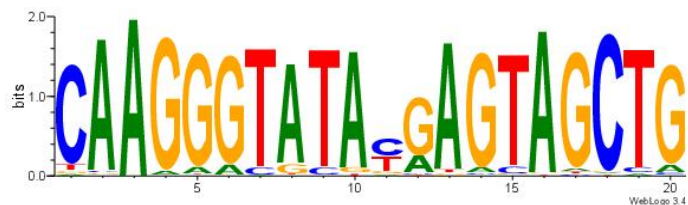


Dataset #: 1
 Motif ID: 194
 Motif name: Motif 194
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.119939

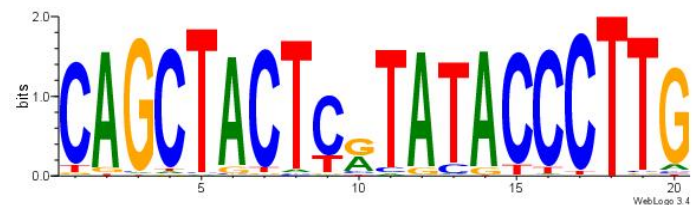
Alignment:

CAAGGGTATAYGAGTAGCTG
 CAAGTTGACACATAAAATTA

Original motif Consensus sequence: CAAGGGTATAYGAGTAGCTG



Reverse complement motif Consensus sequence: CAGCTACTCKTATACCCTTG

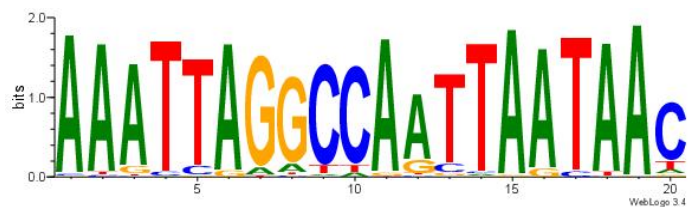


Dataset #: 1
Motif ID: 308
Motif name: Motif 308
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 20
Similarity score: 0.120519

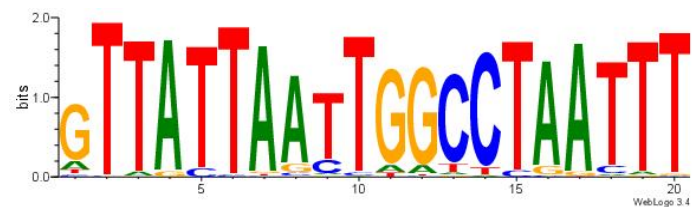
Alignment:

GTTATTAATTGGCCTAATTT
TAATTTTATGTGCAACTTG

Original motif Consensus sequence: AAATTAGGCCAATTAATAAC



Reverse complement motif Consensus sequence: GTTATTAATTGGCCTAATTT

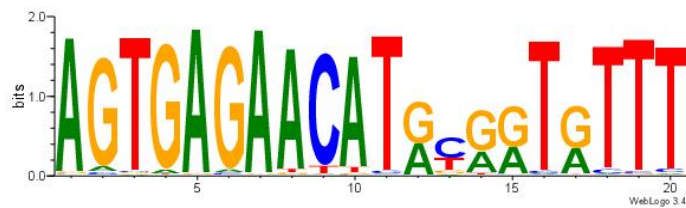


Dataset #: 1
 Motif ID: 63
 Motif name: Motif 63
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.122947

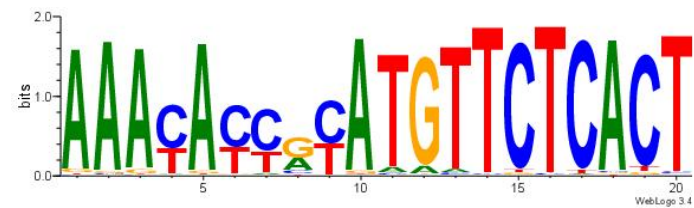
Alignment:

AGTGAGAACATRYRRTRTTT
 CAAGTTGACACATAAAATTA

Original motif Consensus sequence: AGTGAGAACATRYRRTRTTT



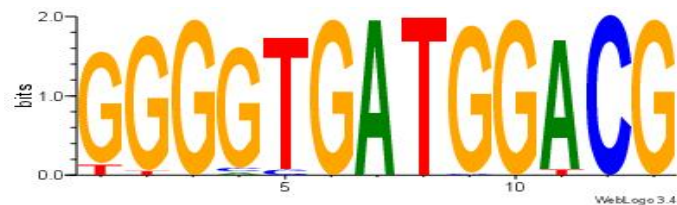
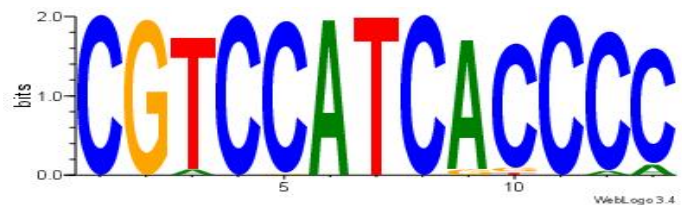
Reverse complement motif Consensus sequence: AAAMAMMKMATGTTCTCACT



Dataset #: 1 Motif ID: 358 Motif name: Motif 358

Original motif Consensus sequence: CGTCCATCACCCC

Reverse complement motif Consensus sequence: GGGTGATGGACCC

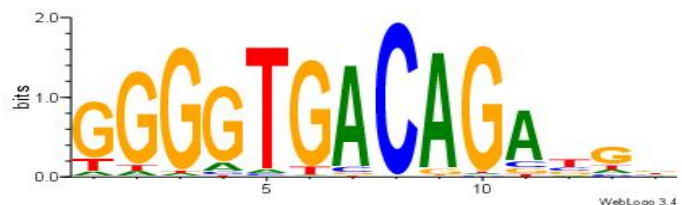


Best Matches for Motif ID 358 (Highest to Lowest)

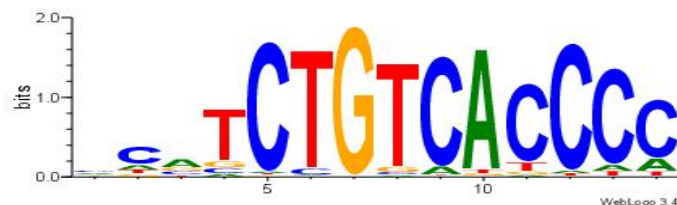
Dataset #: 1
 Motif ID: 1
 Motif name: Motif 1
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 13
 Similarity score: 0.0685601

Alignment:
 BCVTCTGTCACCCC
 CGTCCATCACCCC-

Original motif Consensus sequence: GGGGTGACAGABGB



Reverse complement motif Consensus sequence: BCVTCTGTCACCCC



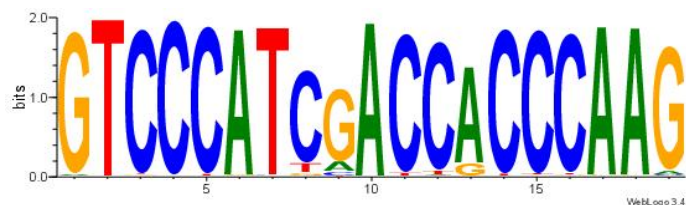
Dataset #: 1

Motif ID: 53
 Motif name: Motif 53
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 13
 Similarity score: 0.0721847

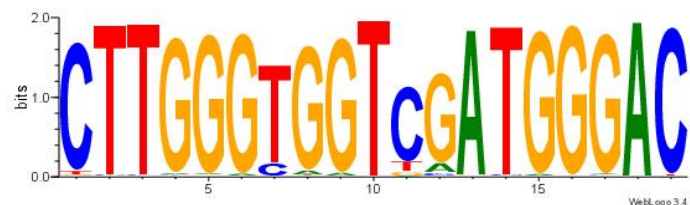
Alignment:

GTCCCATCGACCACCCAAG
 ----CGTCCATCACCCC--

Original motif Consensus sequence: GTCCCATCGACCACCCAAG



Reverse complement motif Consensus sequence: CTTGGGTGGTTCGATGGGAC



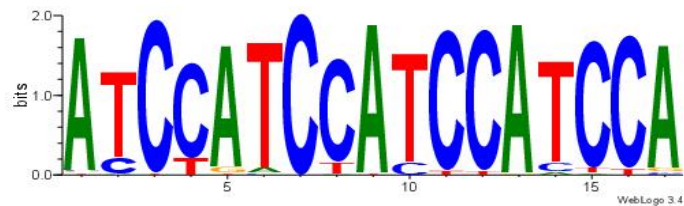
Dataset #: 1
 Motif ID: 341
 Motif name: Motif 341
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 13

Similarity score: 0.0757831

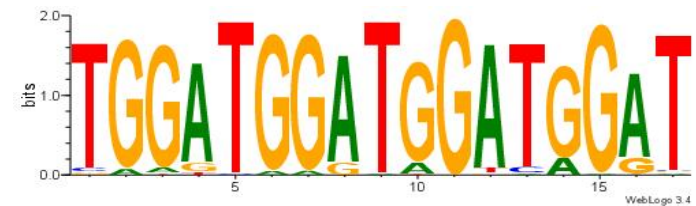
Alignment:

ATCCATCCATCCATCCA
---CGTCCATCACCCC-

Original motif Consensus sequence: ATCCATCCATCCATCCA



Reverse complement motif Consensus sequence:
TGGATGGATGGATGGAT



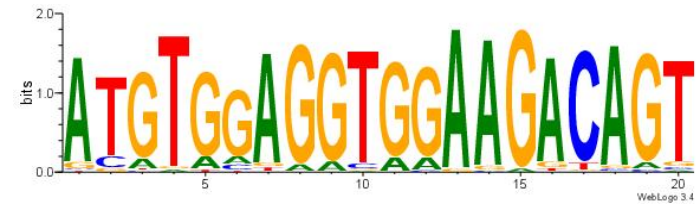
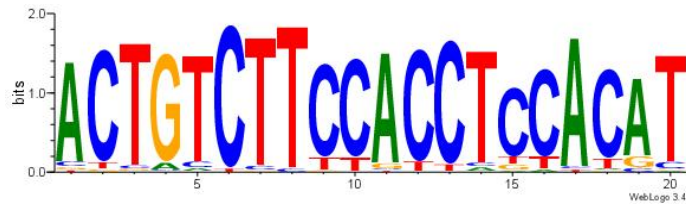
Dataset #: 1
Motif ID: 178
Motif name: Motif 178
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 6
Number of overlap: 13
Similarity score: 0.0810183

Alignment:

ACTGTCTTCCACCTCCACAT
-----CGTCCATCACCCC--

Original motif Consensus sequence: ACTGTCTTCCACCTCCACAT

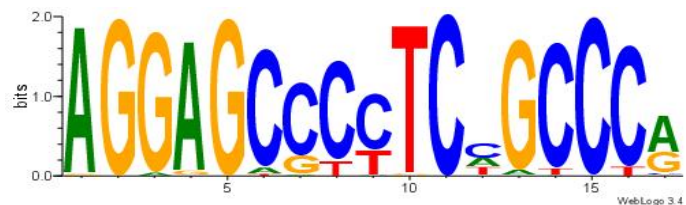
Reverse complement motif Consensus sequence:
ATGTGGAGGTGGAAGACAGT



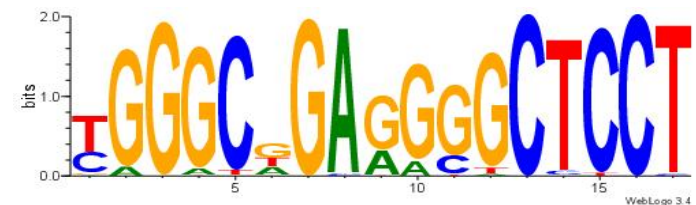
Dataset #: 1
 Motif ID: 111
 Motif name: Motif 111
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 4
 Number of overlap: 13
 Similarity score: 0.083582

Alignment:
 KGGGCDGAGGGGCTCCT
 -GGGGTGATGGACG---

Original motif Consensus sequence: AGGAGCCCCTCHGCCCR

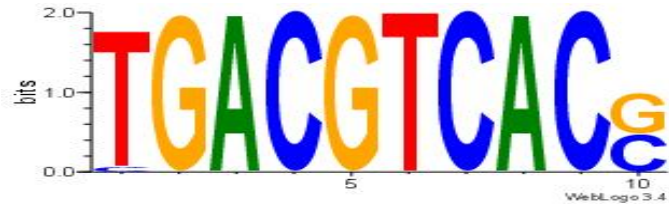


Reverse complement motif Consensus sequence: KGGGCDGAGGGGCTCCT

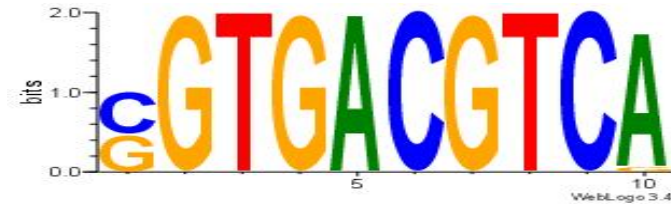


Dataset #: 1 Motif ID: 359 Motif name: Motif 359

Original motif Consensus sequence: TGACGTCACS



Reverse complement motif Consensus sequence: SGTGACGTCA



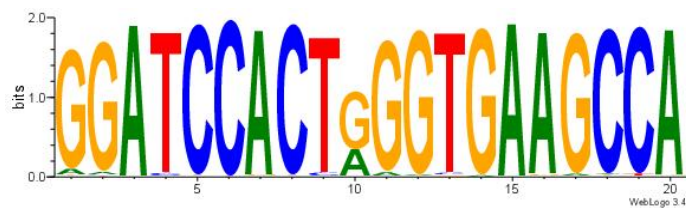
Best Matches for Motif ID 359 (Highest to Lowest)

Dataset #:	1
Motif ID:	61
Motif name:	Motif 61
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	10
Similarity score:	0.0622858

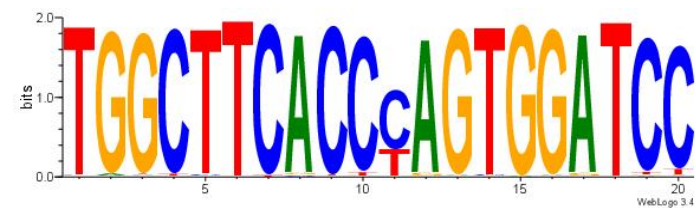
Alignment:

```
GGATCCACTGGGTGAAGCCA
SGTGACGTCA-----
```

Original motif Consensus sequence: GGATCCACTGGGTGAAGCCA



Reverse complement motif Consensus sequence: TGGCTTCAACCCAGTGGATCC

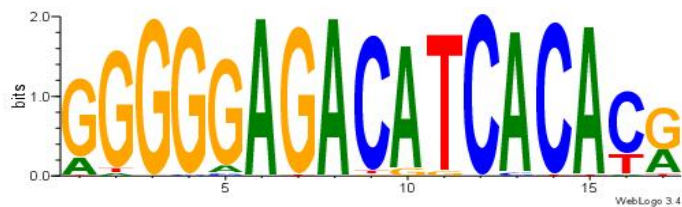


Dataset #: 1
 Motif ID: 279
 Motif name: Motif 279
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 4
 Number of overlap: 10
 Similarity score: 0.0624843

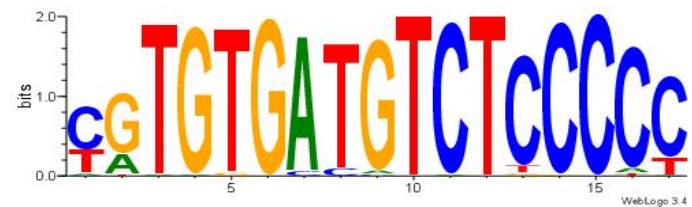
Alignment:

MGTGTGATGTCTCCCC
 ---TGACGTCACS-----

Original motif Consensus sequence: GGGGGAGACATCACACR



Reverse complement motif Consensus sequence: MGTGTGATGTCTCCCC

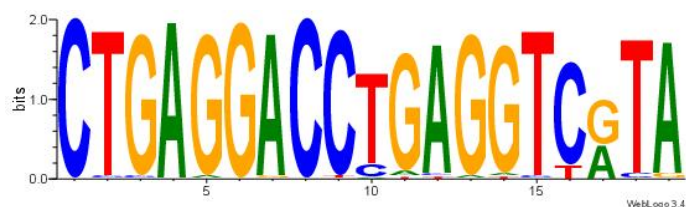


Dataset #: 1
 Motif ID: 291
 Motif name: Motif 291
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3

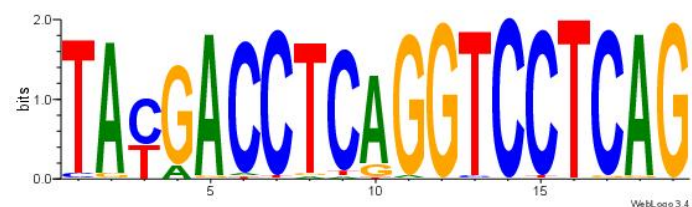
Number of overlap: 10
Similarity score: 0.0832463

Alignment:
TAMGACCTCAGGTCCTCAG
-----TGACGTCACS--

Original motif Consensus sequence: CTGAGGACCTGAGGTCRTA



Reverse complement motif Consensus sequence:
TAMGACCTCAGGTCCTCAG

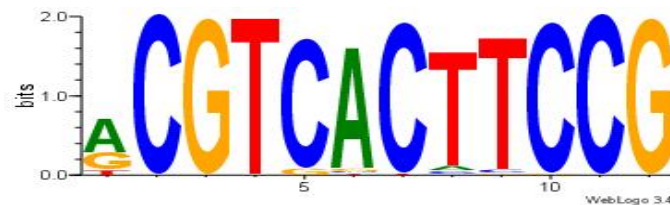


Dataset #: 1
Motif ID: 316
Motif name: Motif 316
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 2
Number of overlap: 10
Similarity score: 0.0833695

Alignment:
ACGTCACTTCCG
-SGTGACGTCA-

Original motif Consensus sequence: CGGAAGTGACGT

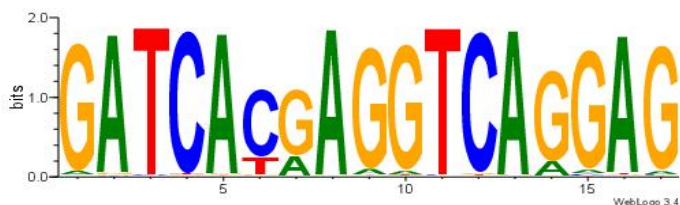
Reverse complement motif Consensus sequence: ACGTCACTTCCG



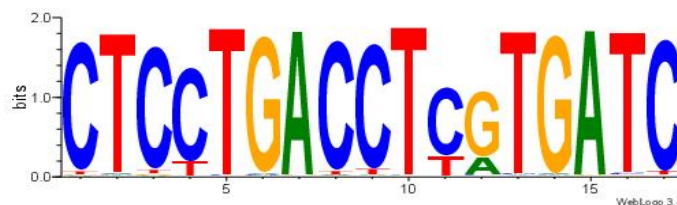
Dataset #: 1
 Motif ID: 60
 Motif name: Motif 60
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 10
 Similarity score: 0.0854535

Alignment:
 GATCACGAGGTCAGGAG
 -----TGACGTCACS--

Original motif Consensus sequence: GATCACGAGGTCAGGAG

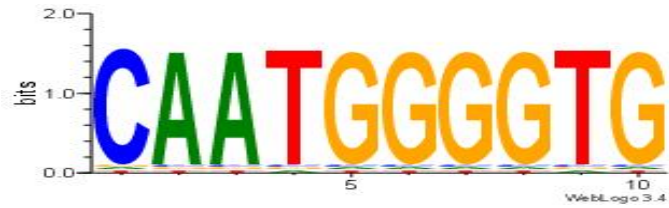


Reverse complement motif Consensus sequence: CTCCTGACCTCGTGATC

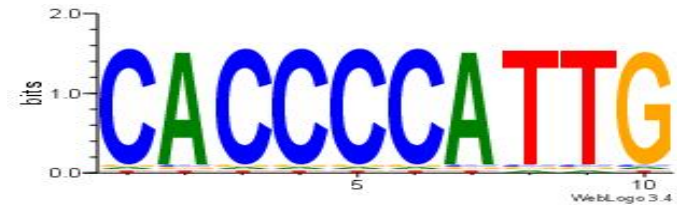


Dataset #: 1 Motif ID: 360 Motif name: Motif 360

Original motif Consensus sequence: CAATGGGGTG



Reverse complement motif Consensus sequence: CACCCCATTTG



Best Matches for Motif ID 360 (Highest to Lowest)

Dataset #:	1
Motif ID:	193
Motif name:	Motif 193
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	4
Number of overlap:	10
Similarity score:	0.0498627

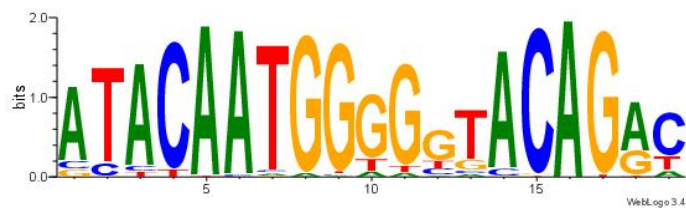
Alignment:

```

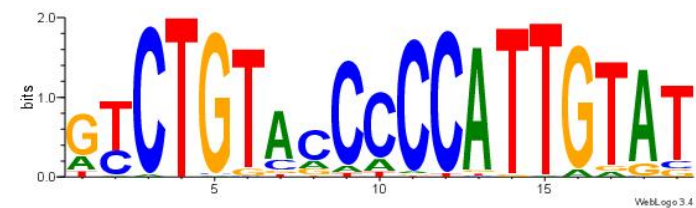
ATACAATGGGGGTACAGRC
---CAATGGGGTG-----

```

Original motif Consensus sequence: ATACAATGGGGGTACAGRC



Reverse complement motif Consensus sequence: GKCTGTACCCCATTTGTAT

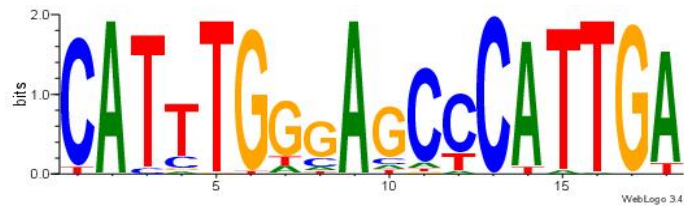


Dataset #: 1
 Motif ID: 284
 Motif name: Motif 284
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 10
 Similarity score: 0.0546882

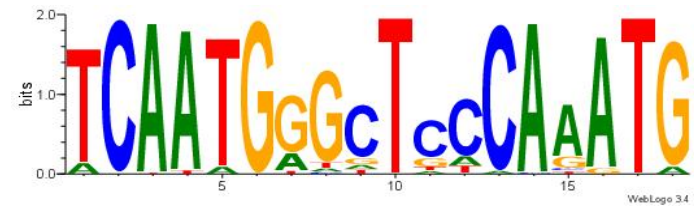
Alignment:

TCAATGGGCTCCCAAATG
 -----CAATGGGGTG--

Original motif Consensus sequence: CATTGGGAGCCATTGA



Reverse complement motif Consensus sequence: TCAATGGGCTCCCAAATG



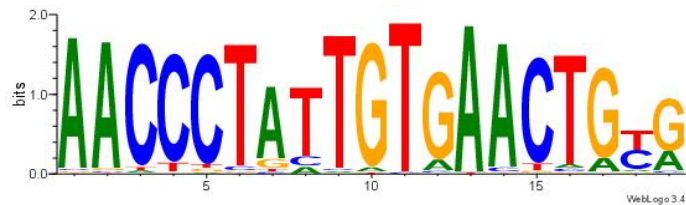
Dataset #: 1
 Motif ID: 242
 Motif name: Motif 242
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 10

Number of overlap: 10
Similarity score: 0.0575203

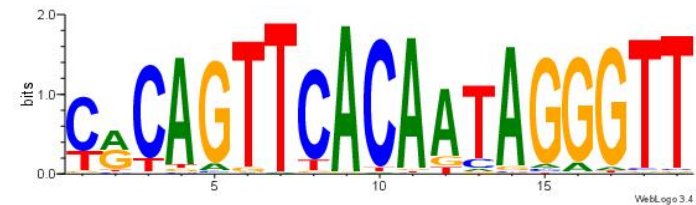
Alignment:

CMCAGTTCACAATAGGGTT
CAATGGGGTG-----

Original motif Consensus sequence: AACCTATTGTGAACTGYG



Reverse complement motif Consensus sequence: CMCAGTTCACAATAGGGTT

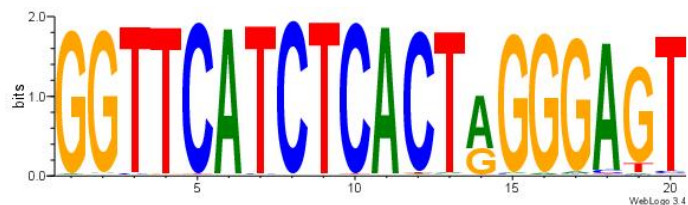


Dataset #: 1
Motif ID: 23
Motif name: Motif 23
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2
Number of overlap: 10
Similarity score: 0.0718758

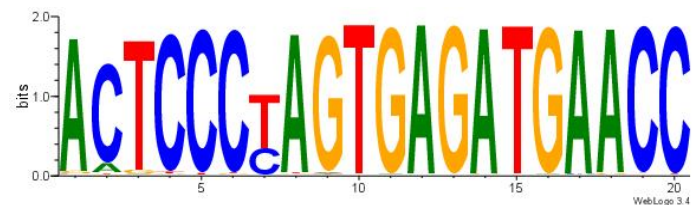
Alignment:

GGTTCATCTCACTAGGGAGT
-----CAATGGGGTG--

Original motif Consensus sequence: GGTTTCATCTCACTAGGGAGT



Reverse complement motif Consensus sequence: ACTCCCTAGTGAGATGAACC

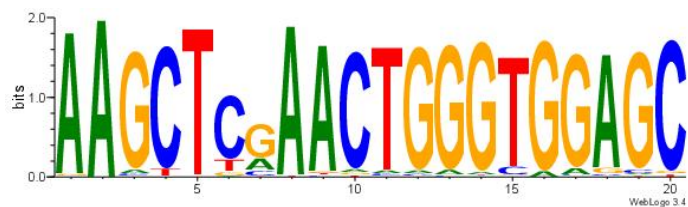


Dataset #: 1
Motif ID: 321
Motif name: Motif 321
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 7
Number of overlap: 10
Similarity score: 0.0732908

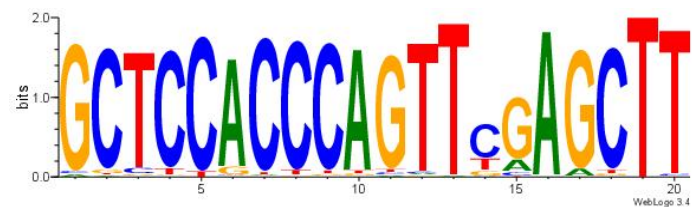
Alignment:

GCTCCACCCAGTTCGAGCTT
----CACCCCATTTG-----

Original motif Consensus sequence: AAGCTCGAACTGGGTGGAGC

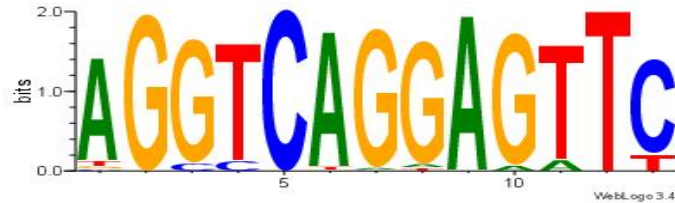


Reverse complement motif Consensus sequence: GCTCCACCCAGTTCGAGCTT

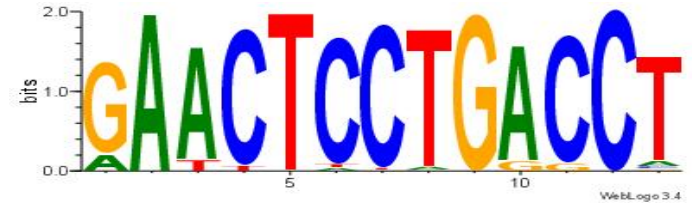


Dataset #: 1 Motif ID: 361 Motif name: Motif 361

Original motif Consensus sequence: AGGTCAGGAGTTC



Reverse complement motif Consensus sequence: GAACTCCTGACCT



Best Matches for Motif ID 361 (Highest to Lowest)

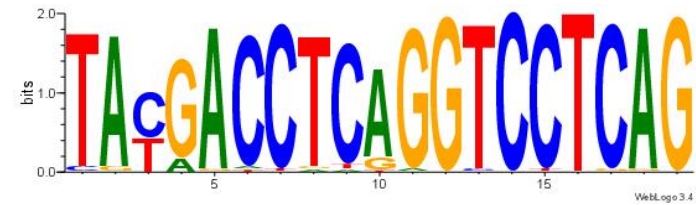
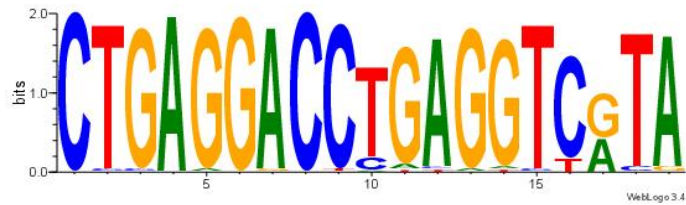
Dataset #:	1
Motif ID:	291
Motif name:	Motif 291
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	4
Number of overlap:	13
Similarity score:	0.0663108

Alignment:

```
TAMGACCTCAGGTCCTCAG  
---GAACTCCTGACCT---
```

Original motif Consensus sequence: CTGAGGACCTGAGGTCRTA

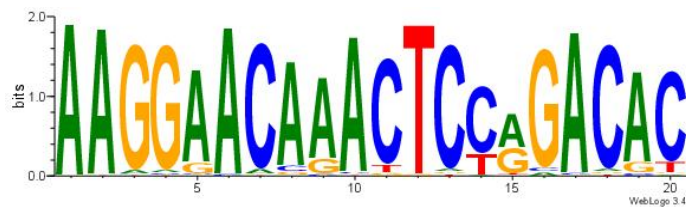
Reverse complement motif Consensus sequence:
TAMGACCTCAGGTCCTCAG



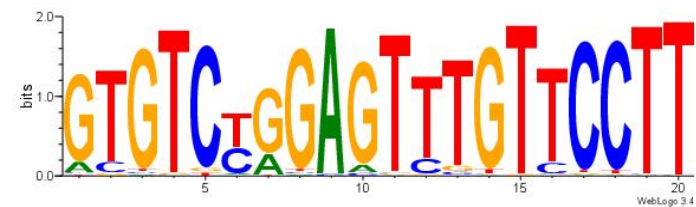
Dataset #: 1
 Motif ID: 234
 Motif name: Motif 234
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 8
 Number of overlap: 13
 Similarity score: 0.0705628

Alignment:
 AAGGAACAAACTCCRGACAC
 GAACTCCTGACCT-----

Original motif Consensus sequence: AAGGAACAAACTCCRGACAC



Reverse complement motif Consensus sequence: GTGTCGGAGTTTGTTCCTT



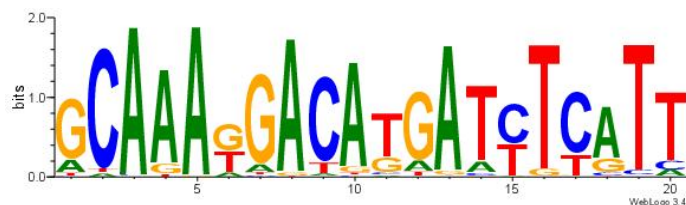
Dataset #: 1

Motif ID: 99
 Motif name: Motif 99
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 4
 Number of overlap: 13
 Similarity score: 0.0735746

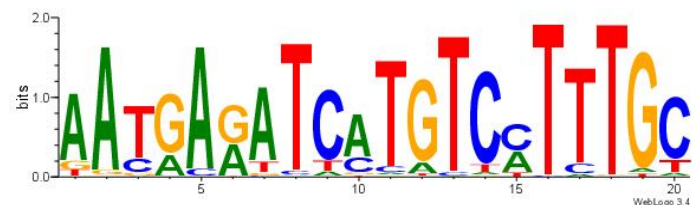
Alignment:

GCAAAGACATGATYTCATT
 ----AGGTCAGGAGTTC----

Original motif Consensus sequence: GCAAAGACATGATYTCATT



Reverse complement motif Consensus sequence: AATGAKATCATGTCYTTTGC



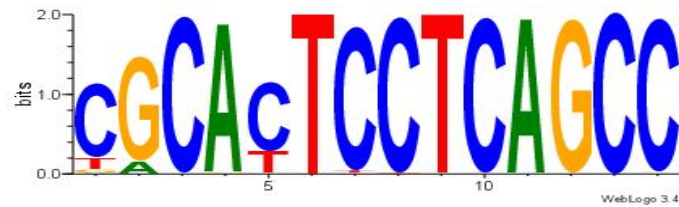
Dataset #: 1
 Motif ID: 72
 Motif name: Motif 72
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 13

Similarity score: 0.0755173

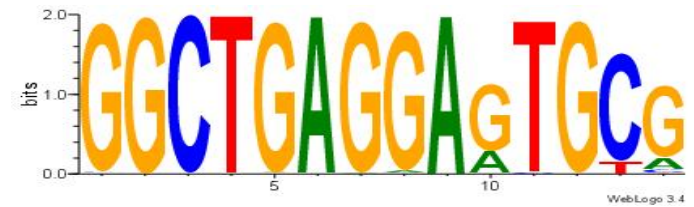
Alignment:

CGCACTCCTCAGCC
GAACTCCTGACCT-

Original motif Consensus sequence: CGCACTCCTCAGCC



Reverse complement motif Consensus sequence: GGCTGAGGAGTGC



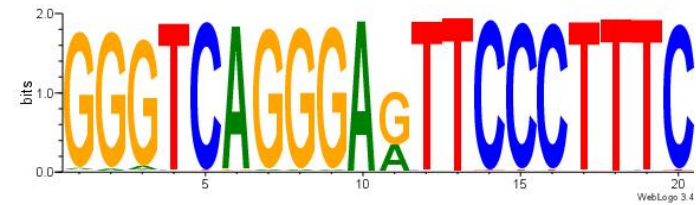
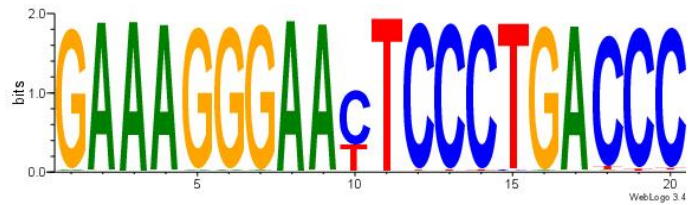
Dataset #: 1
Motif ID: 16
Motif name: Motif 16
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 13
Similarity score: 0.0777779

Alignment:

GAAAGGGA ACTCCCTGACCC
GAACTCCTGACCT-----

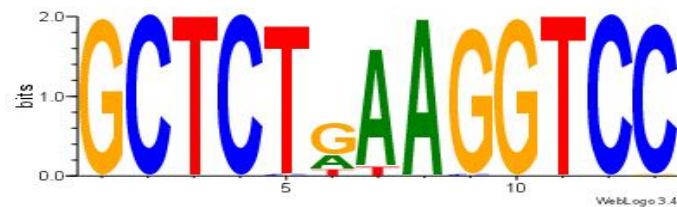
Original motif Consensus sequence: GAAAGGGA ACTCCCTGACCC

Reverse complement motif Consensus sequence:
GGTCAGG GAGTCCCTTTC

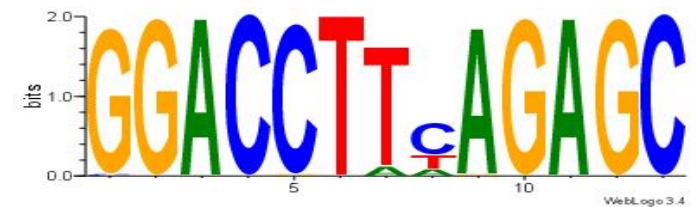


Dataset #: 1 Motif ID: 362 Motif name: Motif 362

Original motif Consensus sequence: GCTCTGAAGGTCC



Reverse complement motif Consensus sequence: GGACCTTCAGAGC

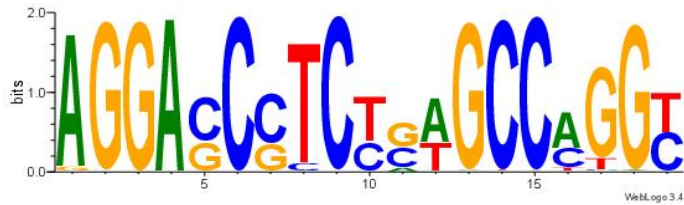


Best Matches for Motif ID 362 (Highest to Lowest)

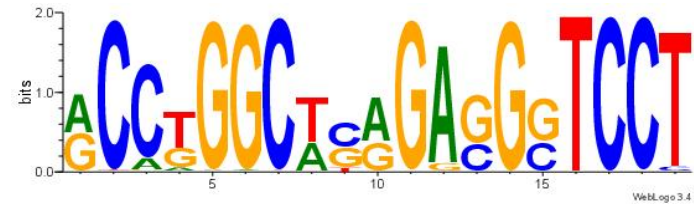
Dataset #:	1
Motif ID:	10
Motif name:	Motif 10
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	2
Number of overlap:	13
Similarity score:	0.0695238

Alignment:
MCCYGGCWSMGASGSTCCT
-GCTCTGAAGGTCC-----

Original motif Consensus sequence: AGGASCSTCYSWGCCMGGY



Reverse complement motif Consensus sequence: MCCYGGCWSMGASGSTCCT

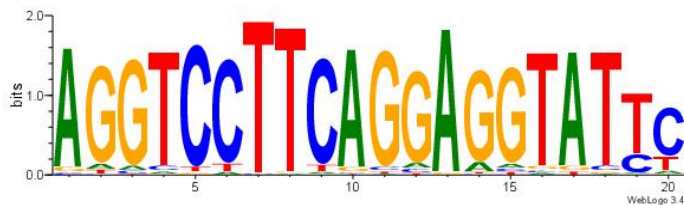


Dataset #: 1
Motif ID: 179
Motif name: Motif 179
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 2
Number of overlap: 13
Similarity score: 0.0873004

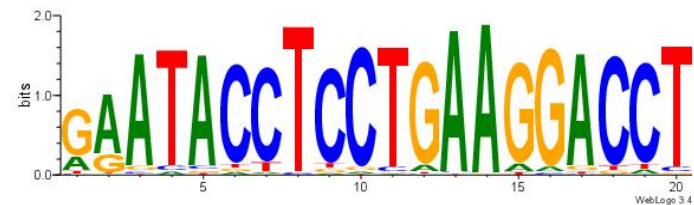
Alignment:

GAATACCTCCTGAAGGACCT
-GCTCTGAAGGTCC-----

Original motif Consensus sequence: AGGTCCTTCAGGAGGTATTC



Reverse complement motif Consensus sequence: GAATACCTCCTGAAGGACCT

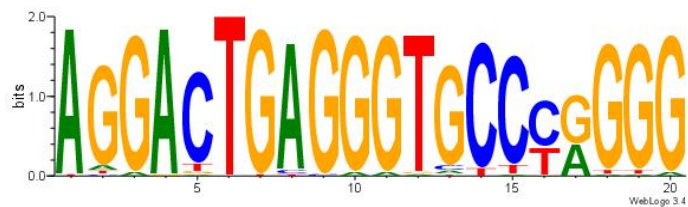


Dataset #: 1
 Motif ID: 312
 Motif name: Motif 312
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 7
 Number of overlap: 13
 Similarity score: 0.088213

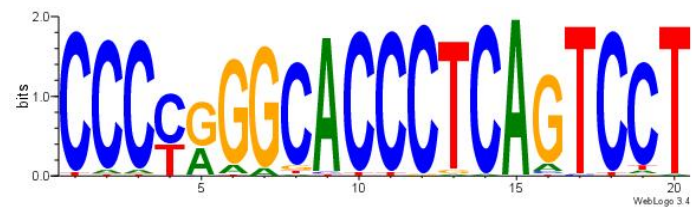
Alignment:

CCCMKGGCACCCCTCAGTCCT
 -----GGACCTTCAGAGC-

Original motif Consensus sequence: AGGACTGAGGGTGCCYRGGG



Reverse complement motif Consensus sequence: CCCMKGGCACCCCTCAGTCCT

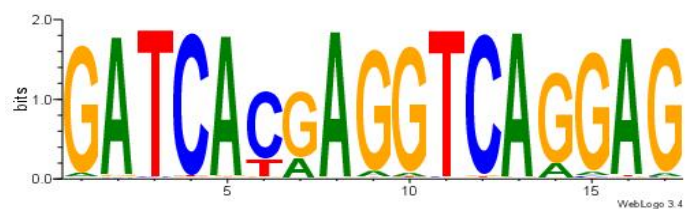


Dataset #: 1
 Motif ID: 60
 Motif name: Motif 60
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1

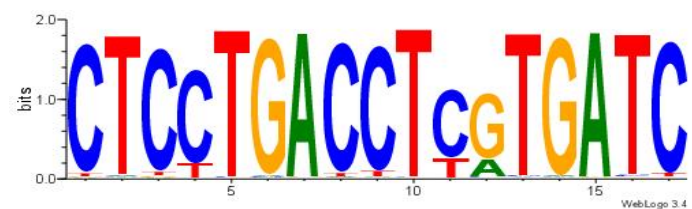
Number of overlap: 13
Similarity score: 0.0888302

Alignment:
GATCACGAGGTCAGGAG
GCTCTGAAGGTCC----

Original motif Consensus sequence: GATCACGAGGTCAGGAG



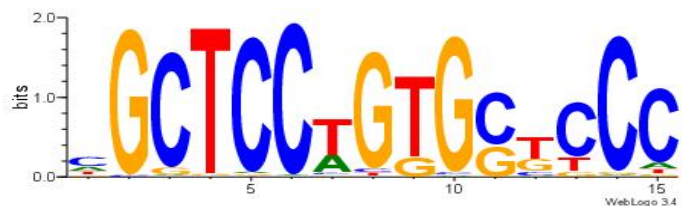
Reverse complement motif Consensus sequence:
CTCCTGACCTCGTGATC



Dataset #: 1
Motif ID: 215
Motif name: Motif 215
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 2
Number of overlap: 13
Similarity score: 0.0929872

Alignment:
GGRSCACAGGAGCD
-GGACCTTCAGAGC-

Original motif Consensus sequence: HGCTCCTGTGSKCCC

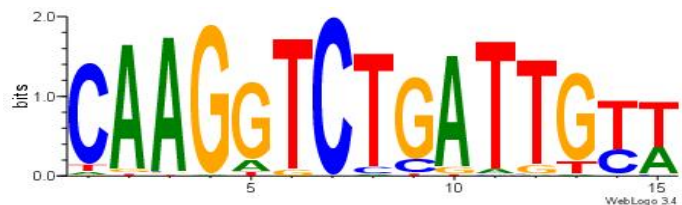


Reverse complement motif Consensus sequence: GGRSCACAGGAGCD



Dataset #: 1 Motif ID: 363 Motif name: Motif 363

Original motif Consensus sequence: CAAGGTCCTGATTGTW



Reverse complement motif Consensus sequence: WACAATCAGACCTTG



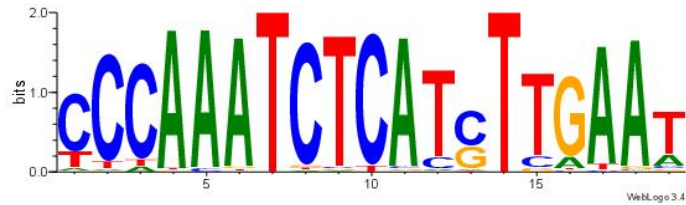
Best Matches for Motif ID 363 (Highest to Lowest)

Dataset #:	1
Motif ID:	227
Motif name:	Motif 227
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	4
Number of overlap:	15
Similarity score:	0.0937179

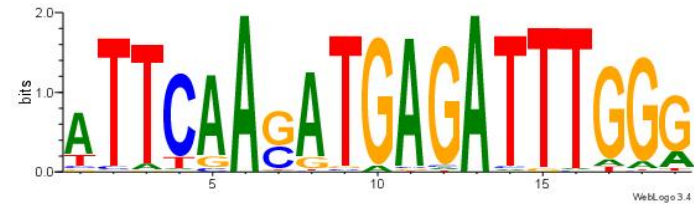
Alignment:

ATTCAASATGAGATTTGGG
-CAAGGTCTGATTGTW---

Original motif Consensus sequence: CCCAAATCTCATSTTGAAT



Reverse complement motif Consensus sequence:
ATTCAASATGAGATTTGGG

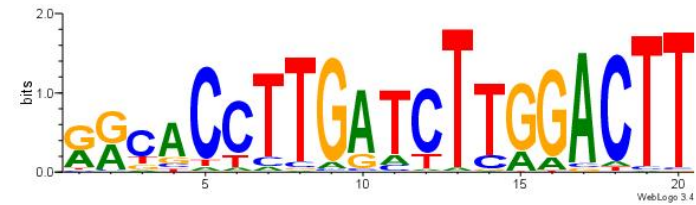
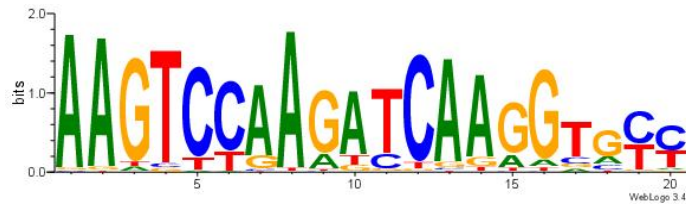


Dataset #: 1
Motif ID: 119
Motif name: Motif 119
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 6
Number of overlap: 15
Similarity score: 0.0941068

Alignment:
AAGTCCAAGATCAAGGTGYY
-----CAAGGTCTGATTGTW

Original motif Consensus sequence: AAGTCCAAGATCAAGGTGYY

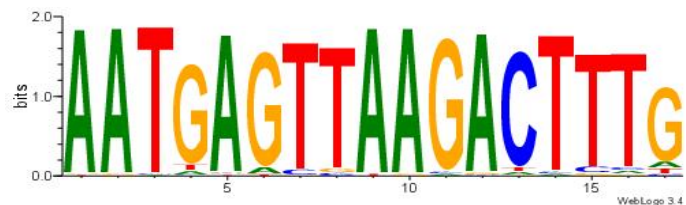
Reverse complement motif Consensus sequence:
KKCACCTTGATCTTGGACTT



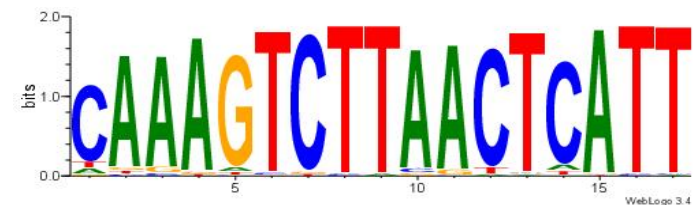
Dataset #: 1
 Motif ID: 224
 Motif name: Motif 224
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 15
 Similarity score: 0.0959593

Alignment:
 AATGAGTTAAGACTTTG
 WACAATCAGACCTTG--

Original motif Consensus sequence: AATGAGTTAAGACTTTG



Reverse complement motif Consensus sequence: CAAAGTCTTAACCTATT



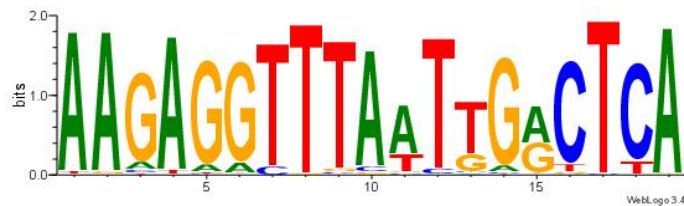
Dataset #: 1

Similarity score: 0.0975054

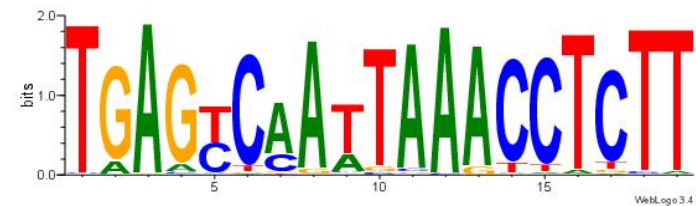
Alignment:

TGAGKCAATTAAACCTCTT
---WACAATCAGACCTTG-

Original motif Consensus sequence: AAGAGGTTTAATTGRCTCA



Reverse complement motif Consensus sequence: TGAGKCAATTAAACCTCTT

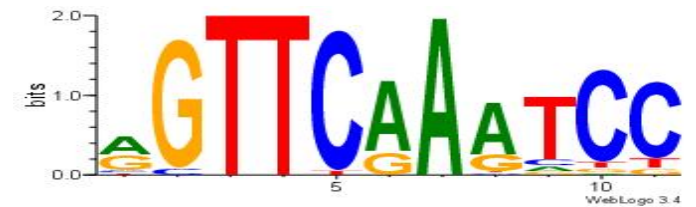


Dataset #: 1 Motif ID: 364 Motif name: Motif 364

Original motif Consensus sequence: GGATTTGAACY



Reverse complement motif Consensus sequence: MGTTCAAATCC



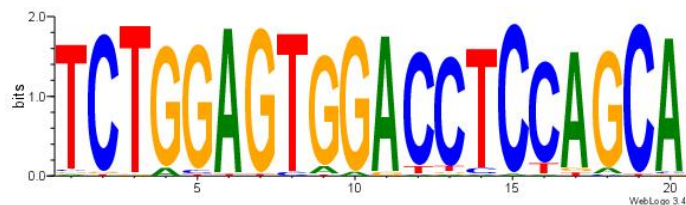
Best Matches for Motif ID 364 (Highest to Lowest)

Dataset #:	1
Motif ID:	350
Motif name:	Motif 350
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement

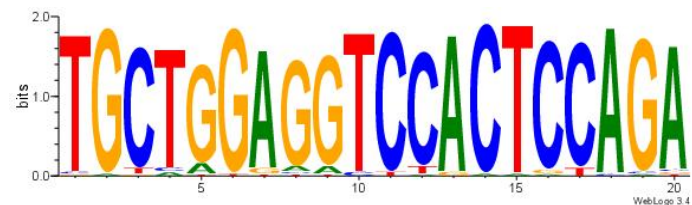
Direction: Backward
Position number: 4
Number of overlap: 11
Similarity score: 0.0565307

Alignment:
TGCTGGAGGTCCACTCCAGA
-----MGTTC AAATCC----

Original motif Consensus sequence: TCTGGAGTGGACCTCCAGCA



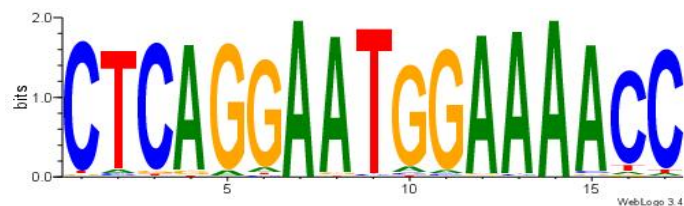
Reverse complement motif Consensus sequence: TGCTGGAGGTCCACTCCAGA



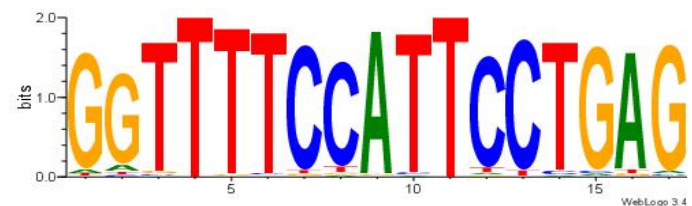
Dataset #: 1
Motif ID: 214
Motif name: Motif 214
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 3
Number of overlap: 11
Similarity score: 0.0725975

Alignment:
GGTTTTCCATTCCTGAG
--MGTTC AAATCC----

Original motif Consensus sequence: CTCAGGAATGGAAAACC



Reverse complement motif Consensus sequence: GGTTTCCATTCCCTGAG

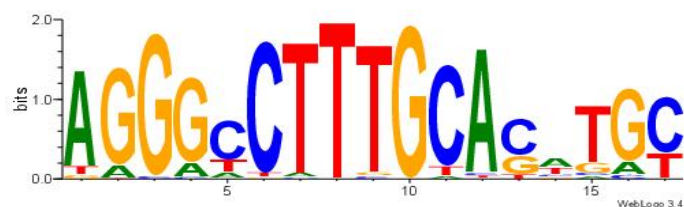


Dataset #: 1
Motif ID: 322
Motif name: Motif 322
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 4
Number of overlap: 11
Similarity score: 0.0730291

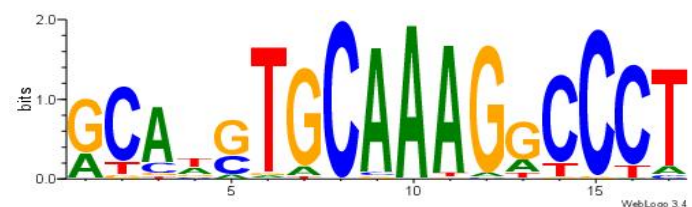
Alignment:

GCAWSTGCAAAGGCCCT
---MGTTCAAATCC---

Original motif Consensus sequence: AGGGCCTTTGCASWTGC



Reverse complement motif Consensus sequence: GCAWSTGCAAAGGCCCT

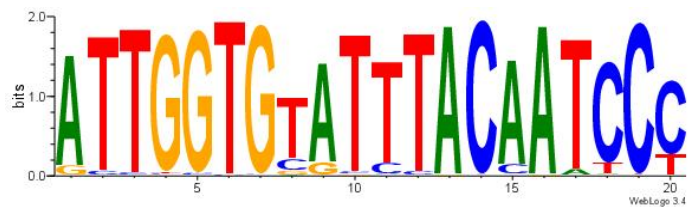


Dataset #: 1
 Motif ID: 106
 Motif name: Motif 106
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 9
 Number of overlap: 11
 Similarity score: 0.0730743

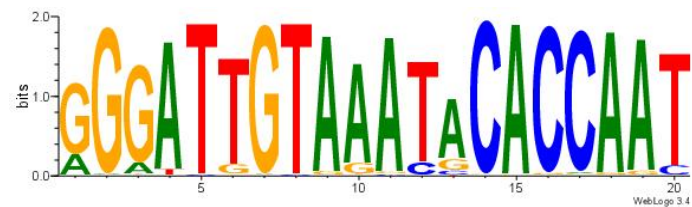
Alignment:

GGGATTGTAAATACACCAAT
 -----GGATTTGAACY-

Original motif Consensus sequence: ATTGGTGTATTTACAATCCC



Reverse complement motif Consensus sequence: GGGATTGTAAATACACCAAT

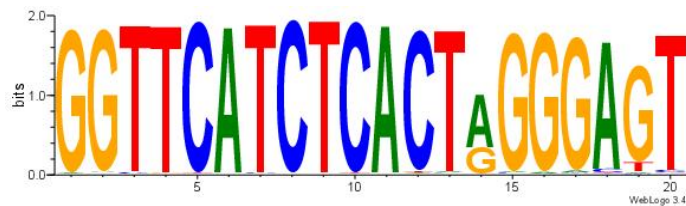


Dataset #: 1
 Motif ID: 23
 Motif name: Motif 23
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 10

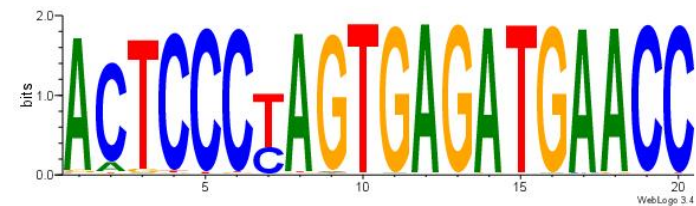
Number of overlap: 11
 Similarity score: 0.0767707

Alignment:
 GGTTTCATCTCACTAGGGAGT
 -----MGTTCAAATCC

Original motif Consensus sequence: GGTTTCATCTCACTAGGGAGT

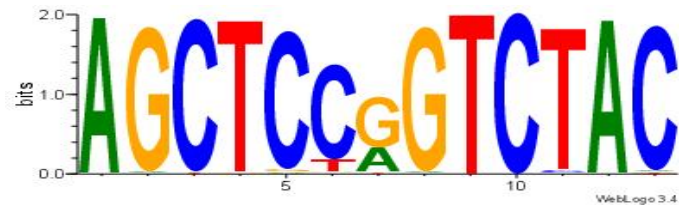


Reverse complement motif Consensus sequence:
 ACTCCCTAGTGAGATGAACC

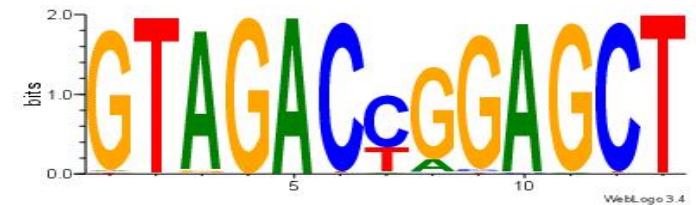


Dataset #: 1 Motif ID: 365 Motif name: Motif 365

Original motif Consensus sequence: AGCTCCGGTCTAC



Reverse complement motif Consensus sequence: GTAGACCGGAGCT



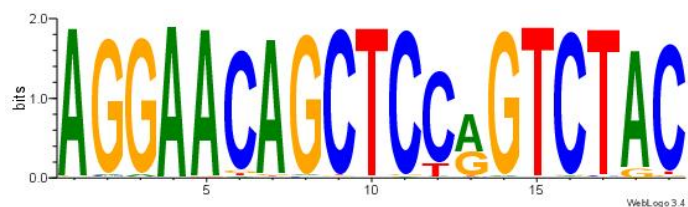
Best Matches for Motif ID 365 (Highest to Lowest)

Dataset #: 1
 Motif ID: 62
 Motif name: Motif 62
 Matching format of first motif: Original Motif

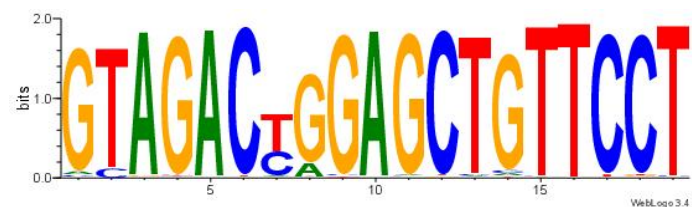
Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 7
 Number of overlap: 13
 Similarity score: 0.00780309

Alignment:
 AGGAACAGCTCCRGCTCTAC
 -----AGCTCCGGTCTAC

Original motif Consensus sequence: AGGAACAGCTCCRGCTCTAC



Reverse complement motif Consensus sequence:
 GTAGACKGGAGCTGTTTCCT

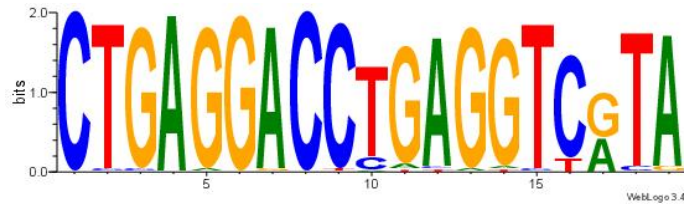


Dataset #: 1
 Motif ID: 291
 Motif name: Motif 291
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 13
 Similarity score: 0.0802174

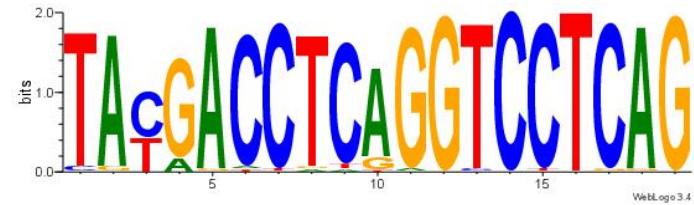
Alignment:

CTGAGGACCTGAGGTCRTA
----GTAGACCGGAGCT--

Original motif Consensus sequence: CTGAGGACCTGAGGTCRTA



Reverse complement motif Consensus sequence: TAMGACCTCAGGTCCTCAG

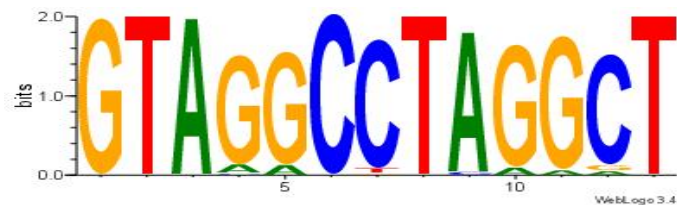
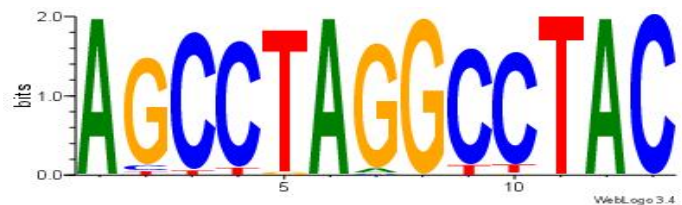


Dataset #: 1
Motif ID: 273
Motif name: Motif 273
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 13
Similarity score: 0.0814755

Alignment:
AGCCTAGGCCTAC
AGCTCCGGTCTAC

Original motif Consensus sequence: AGCCTAGGCCTAC

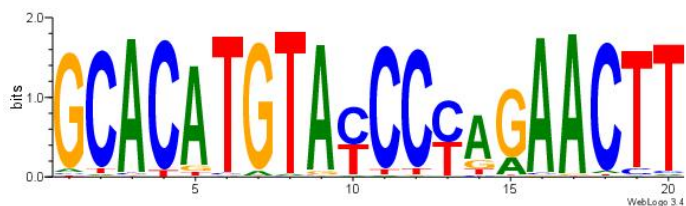
Reverse complement motif Consensus sequence: GTAGGCCTAGGCT



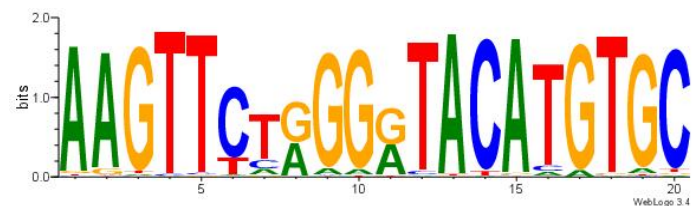
Dataset #: 1
 Motif ID: 225
 Motif name: Motif 225
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 7
 Number of overlap: 13
 Similarity score: 0.0853406

Alignment:
 AAGTTCTKGGKTACATGTGC
 -----AGCTCCGGTCTAC-

Original motif Consensus sequence: GCACATGTAYCCYAGAACTT



Reverse complement motif Consensus sequence: AAGTTCTKGGKTACATGTGC



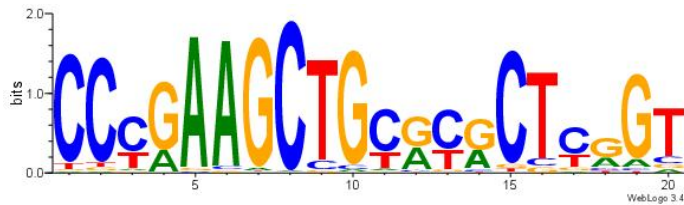
Dataset #: 1

Motif ID: 177
 Motif name: Motif 177
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3
 Number of overlap: 13
 Similarity score: 0.0899013

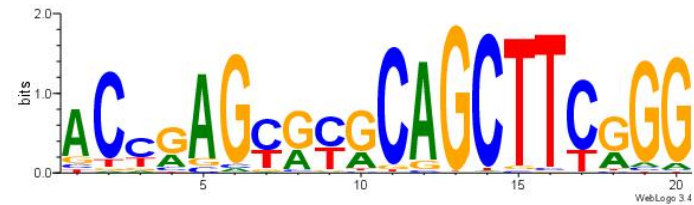
Alignment:

ACCGAGMKMGCAGCTTCGGG
 --GTAGACCGGAGCT-----

Original motif Consensus sequence: CCCGAAGCTGCRYRCTCGGT



Reverse complement motif Consensus sequence: ACCGAGMKMGCAGCTTCGGG



Results created by MOTIFSIM on 03-28-2023 08:14:22
 Runtime: 573.345 seconds

MOTIFSIM is written by Ngoc Tam L. Tran
 Motif logo generated by [weblogo](http://weblogo.threebio.com)