



# MOTIFSIM - MOTIF SIMilarity Detection Tool

Version 2.2

## INPUT

### Input Parameters

Number of files:	1
Number of top significant motifs:	2
Number of best matches:	2
Similarity cutoff $\geq$	0.75
Matching motif database:	None
Motif tree:	No
Combined similar motifs:	No
Output file type:	All
Output file format:	All

### Input files and motif counts

File name	Count of motifs	Dataset number
U20230323-stremeR.txt	365	1

## RESULTS

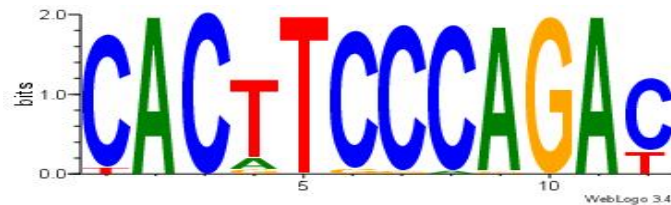
### Top 2 Significant Motifs - Global Matching (Highest to Lowest)

There is no global matching for 1 motif file.

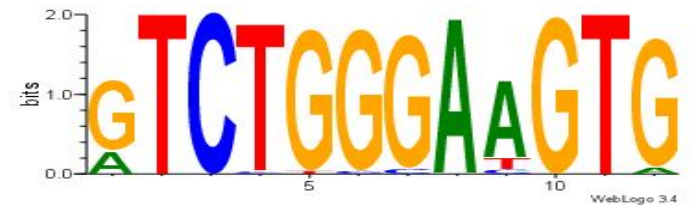
## Significant Motifs - Global and Local Matching (Highest to Lowest)

**Dataset #: 1      Motif ID: 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)

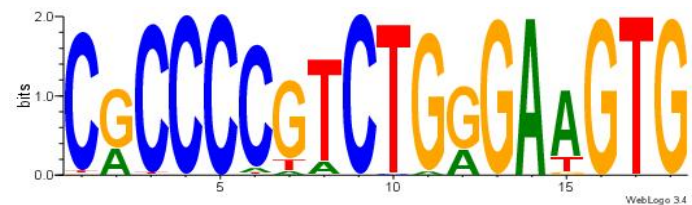
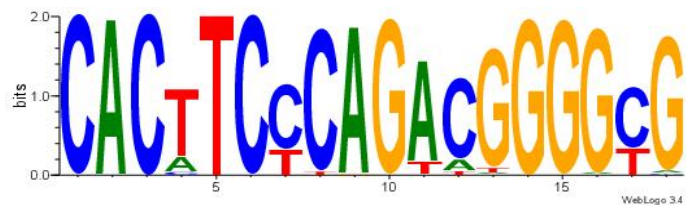
Dataset #:	1
Motif ID:	27
Motif name:	Motif 27
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	7
Number of overlap:	12
Similarity score:	0.00564821

#### Alignment:

```
CACTTCCCAGACGGGGCG
CACTTCCCAGAC-----
```

Original motif      Consensus sequence: CACTTCCCAGACGGGGCG

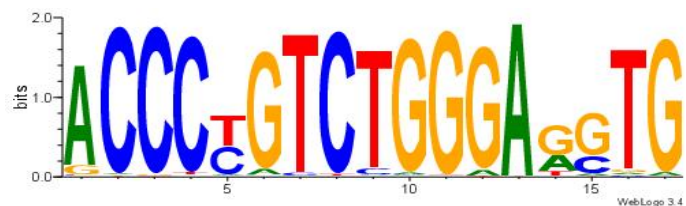
Reverse complement motif      Consensus sequence:  
CGCCCCGTCTGGGAAGTG



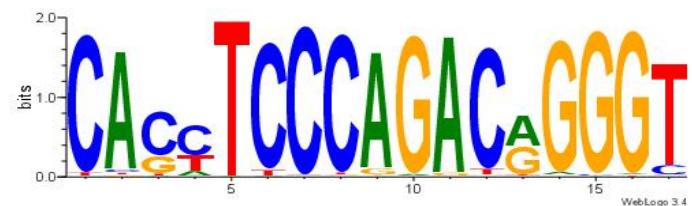
Dataset #: 1  
 Motif ID: 95  
 Motif name: Motif 95  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 6  
 Number of overlap: 12  
 Similarity score: 0.0183065

Alignment:  
 CACCTCCAGACMGGGT  
 -----CACTTCCAGAC

Original motif      Consensus sequence: ACCCYGTCTGGGAGGTG



Reverse complement motif      Consensus sequence: CACCTCCAGACMGGGT

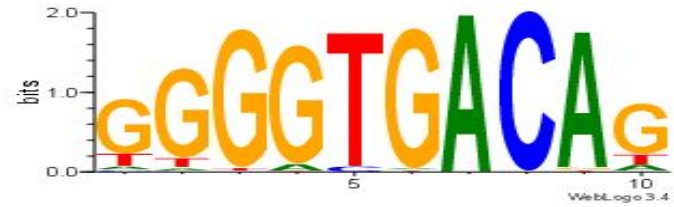


**Dataset #: 1      Motif ID: 146      Motif name: Motif 146**

Original motif      Consensus sequence: CTGTCACCCC



Reverse complement motif      Consensus sequence: GGGGTGACAG



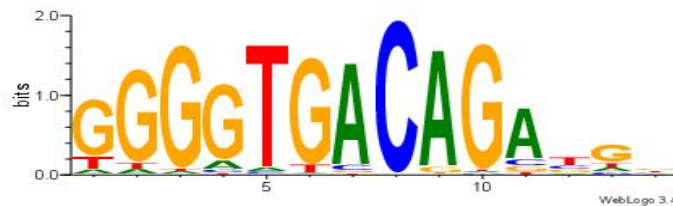
### Best Matches for Significant Motif ID 146 (Highest to Lowest)

Dataset #:	1
Motif ID:	1
Motif name:	Motif 1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	5
Number of overlap:	10
Similarity score:	0.00304976

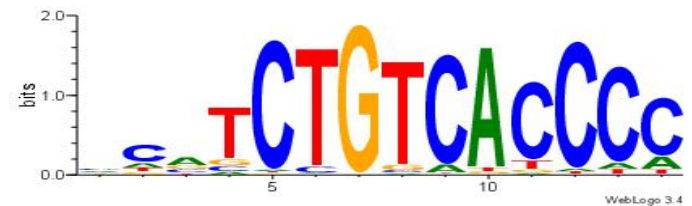
Alignment:

```
GGGGTGACAGABGB
----GGGGTGACAG
```

Original motif      Consensus sequence: GGGGTGACAGABGB



Reverse complement motif      Consensus sequence: BCVTCTGTCACCCC



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

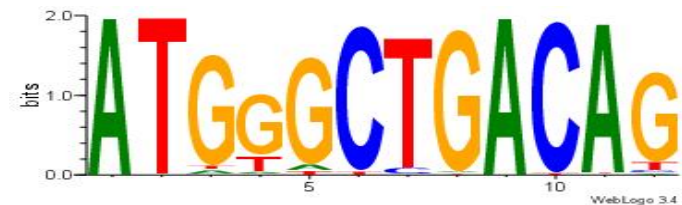
**Alignment:**

ATGGGCTGACAG  
 --GGGGTGACAG

Original motif      Consensus sequence: CTGTCAGCCCAT



Reverse complement motif      Consensus sequence: ATGGGCTGACAG

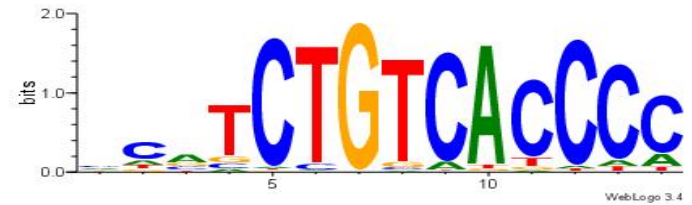
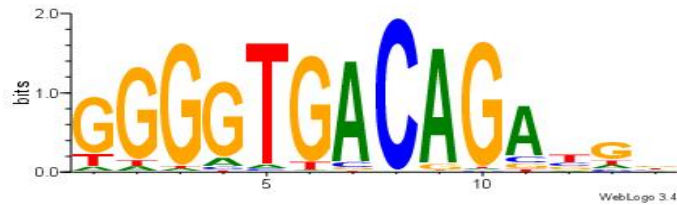


**Best Matches for Each Motif (Highest to Lowest)**

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

Original motif      Consensus sequence: GGGGTGACAGABGB

Reverse complement motif      Consensus sequence: BCVTCTGTACCCG

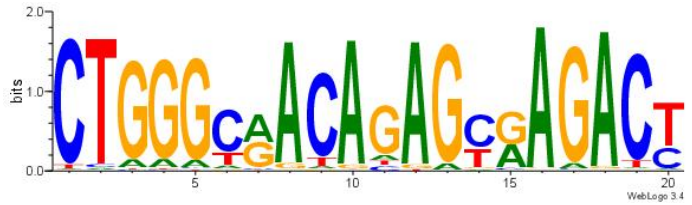


**Best Matches for Motif ID 1 (Highest to Lowest)**

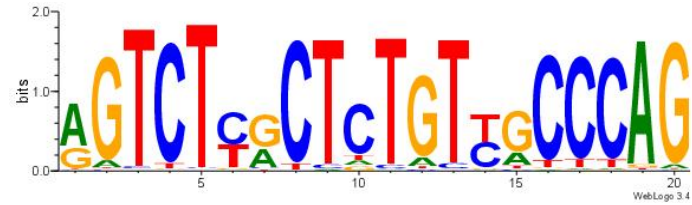
Dataset #: 1  
 Motif ID: 29  
 Motif name: Motif 29  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 6  
 Number of overlap: 14  
 Similarity score: 0.0644652

Alignment:  
 CTGGGCRACAGAGYRAGACY  
 -GGGGTGACAGABGB-----

Original motif      Consensus sequence: CTGGGCRACAGAGYRAGACY



Reverse complement motif      Consensus sequence: MGTCTMKCTCTGKGCCAG

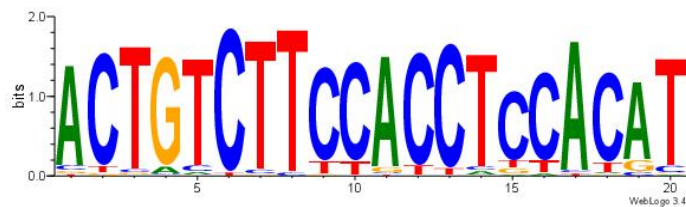


Dataset #: 1  
 Motif ID: 178  
 Motif name: Motif 178  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 6  
 Number of overlap: 14  
 Similarity score: 0.0767787

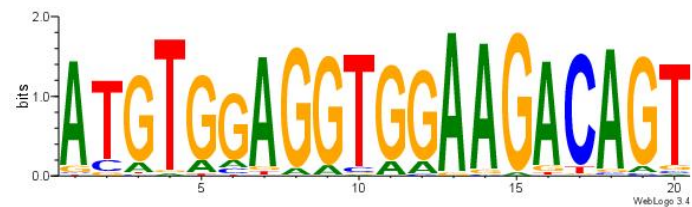
Alignment:

ACTGTCTTCCACCTCCACAT  
 -BCVTCTGTCACCCC-----

Original motif      Consensus sequence: ACTGTCTTCCACCTCCACAT



Reverse complement motif      Consensus sequence: ATGTGGAGGTGGAAGACAGT



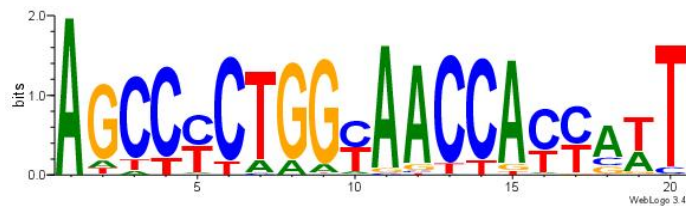
Dataset #: 1  
 Motif ID: 139  
 Motif name: Motif 139  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 6

Number of overlap: 14  
Similarity score: 0.0824915

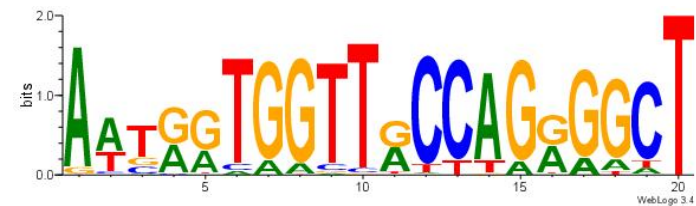
**Alignment:**

AGCCYCTGGYAACCAYYAWT  
-BCVTCTGTCACCCC-----

Original motif      Consensus sequence: AGCCYCTGGYAACCAYYAWT

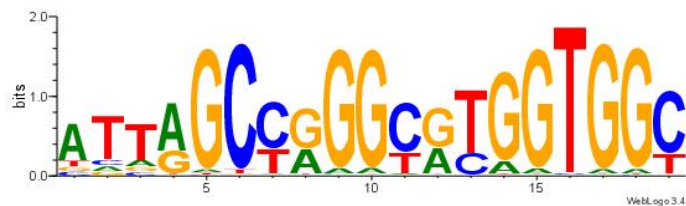


Reverse complement motif      Consensus sequence:  
AWTKKTGGTTKCCAGKGGCT

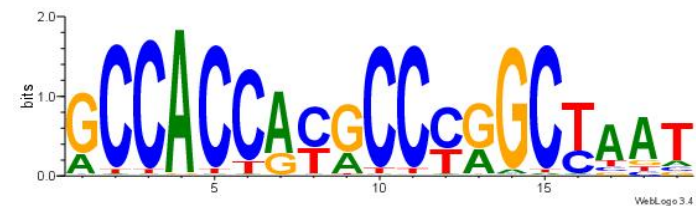


**Dataset #: 1      Motif ID: 2      Motif name: Motif 2**

Original motif      Consensus sequence: ATTAGCYRGGCRTCCTGGTGGC



Reverse complement motif      Consensus sequence:  
GCCACCAMGCCMKGCTAAT



**Best Matches for Motif ID 2 (Highest to Lowest)**

Dataset #: 1  
Motif ID: 155  
Motif name: Motif 155

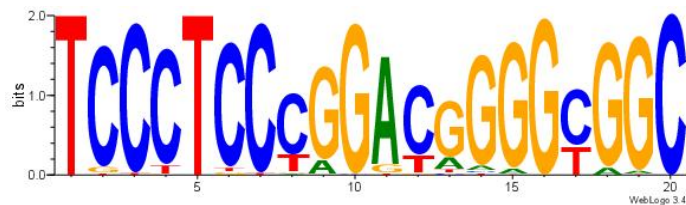


Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	19
Similarity score:	0.0936692

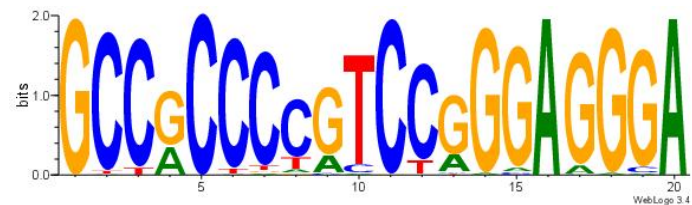
**Alignment:**

```
TCCCTCCCGGACGGGGYGGC
-ATTAGCYRGGCRTGGTGGC
```

Original motif    Consensus sequence: TCCCTCCCGGACGGGGYGGC



Reverse complement motif    Consensus sequence: GCCKCCCCGTCCGGGAGGGA

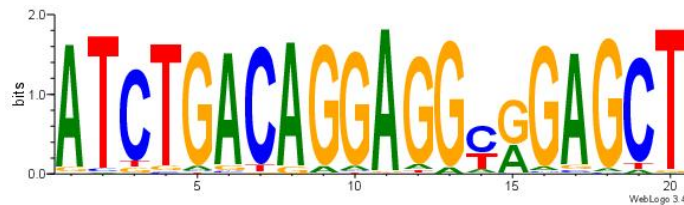


Dataset #:	1
Motif ID:	165
Motif name:	Motif 165
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	19
Similarity score:	0.109865

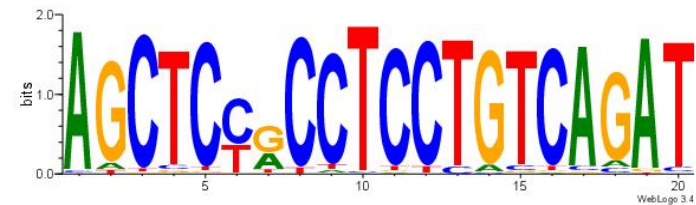
Alignment:

AGCTCMKCCTCCTGTCAGAT  
-GCCACCCAMGCCMKGCTAAT

Original motif      Consensus sequence: ATCTGACAGGAGGYRGAGCT

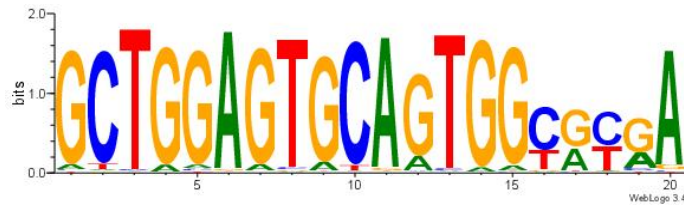


Reverse complement motif      Consensus sequence:  
AGCTCMKCCTCCTGTCAGAT

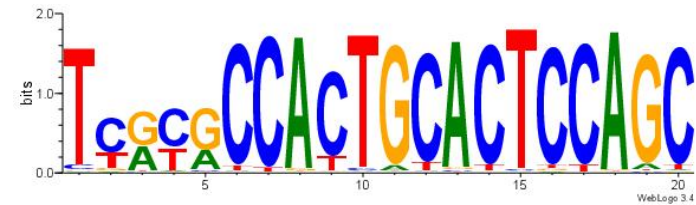


**Dataset #: 1      Motif ID: 3      Motif name: Motif 3**

Original motif      Consensus sequence: GCTGGAGTGCAAGTGG



Reverse complement motif      Consensus sequence:  
TCKMGCCACTGCACTCCAGC



### Best Matches for Motif ID 3 (Highest to Lowest)

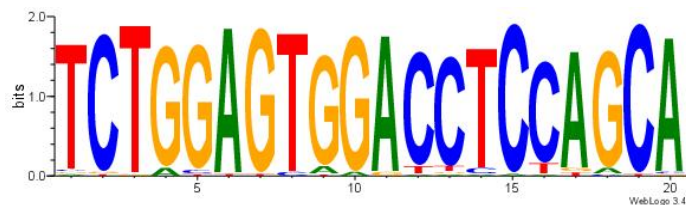
Dataset #:	1
Motif ID:	350
Motif name:	Motif 350
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif

Direction: Forward  
Position number: 1  
Number of overlap: 20  
Similarity score: 0.100707

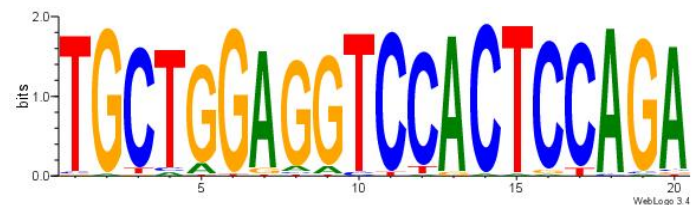
**Alignment:**

TCTGGAGTGGACCTCCAGCA  
GCTGGAGTGCAGTGGCRYGA

Original motif      Consensus sequence: TCTGGAGTGGACCTCCAGCA



Reverse complement motif      Consensus sequence: TGCTGGAGGTCCACTCCAGA

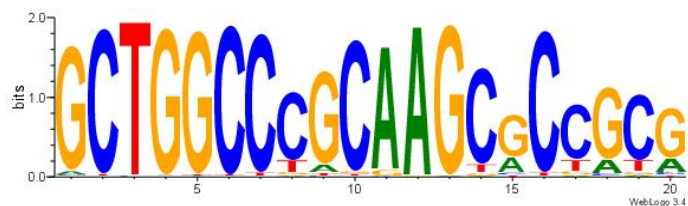


Dataset #: 1  
Motif ID: 100  
Motif name: Motif 100  
Matching format of first motif: Original Motif  
Matching format of second motif: Original Motif  
Direction: Forward  
Position number: 1  
Number of overlap: 20  
Similarity score: 0.113987

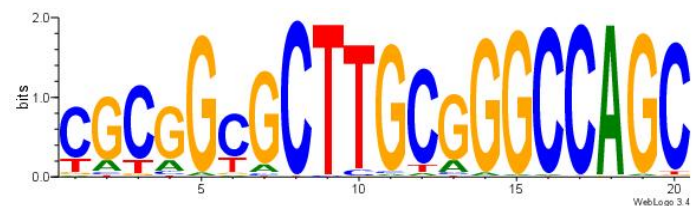
**Alignment:**

GCTGGCCCGCAAGCGCCGCG  
GCTGGAGTGCAGTGGCRYGA

Original motif      Consensus sequence: GCTGGCCCGCAAGCGCCGCG

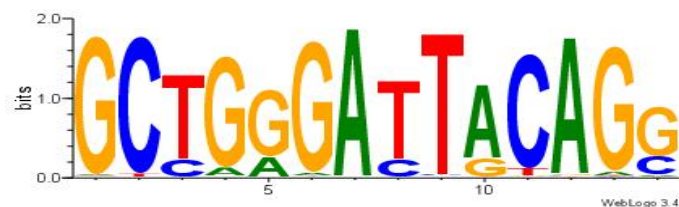


Reverse complement motif      Consensus sequence: CGCGGCGCTTGCGGGCCAGC



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

Original motif      Consensus sequence: GCTGGGATTACAGG



Reverse complement motif      Consensus sequence: CCTGTAATCCAGC



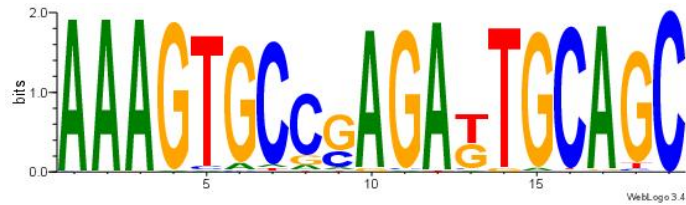
### Best Matches for Motif ID 4 (Highest to Lowest)

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

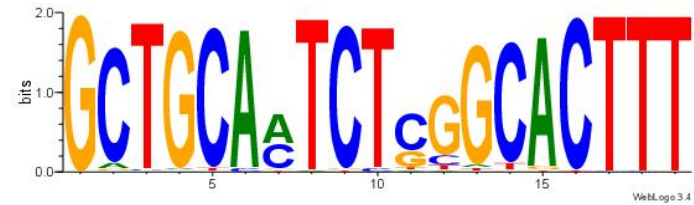
Alignment:

AAAGTGCCGAGAKTGCAGC  
-----GCTGGGATTACAGG

Original motif      Consensus sequence: AAAGTGCCGAGAKTGCAGC



Reverse complement motif      Consensus sequence:  
GCTGCARTCTCGGCACTTT

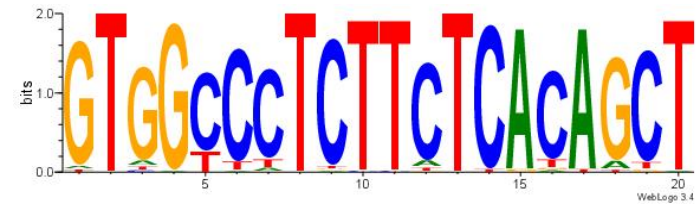
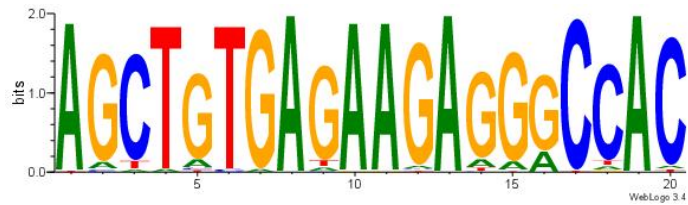


Dataset #: 1  
Motif ID: 294  
Motif name: Motif 294  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Reverse Complement  
Direction: Forward  
Position number: 6  
Number of overlap: 14  
Similarity score: 0.0659358

Alignment:  
GTGGCCCTCTTCTCACAGCT  
-----CCTGTAATCCCAGC-

Original motif      Consensus sequence: AGCTGTGAGAAGAGGGCCAC

Reverse complement motif      Consensus sequence:  
GTGGCCCTCTTCTCACAGCT



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

Original motif      Consensus sequence: CCTCRGCCTCC



Reverse complement motif      Consensus sequence: GGAGGCKGAGG

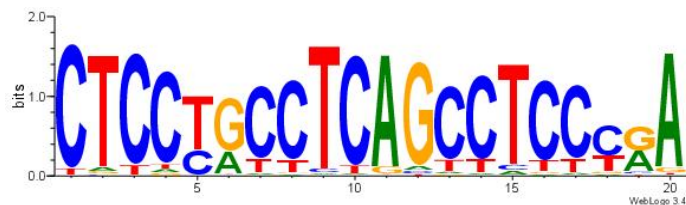


**Best Matches for Motif ID 5 (Highest to Lowest)**

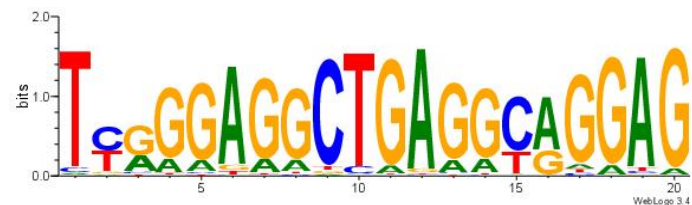
Dataset #:	1
Motif ID:	26
Motif name:	Motif 26
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	4
Number of overlap:	11
Similarity score:	0.0355603

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

Original motif      Consensus sequence: CTCCTGCCTCAGCCTCCRA



Reverse complement motif      Consensus sequence: TMGGGAGGCTGAGGCAGGAG

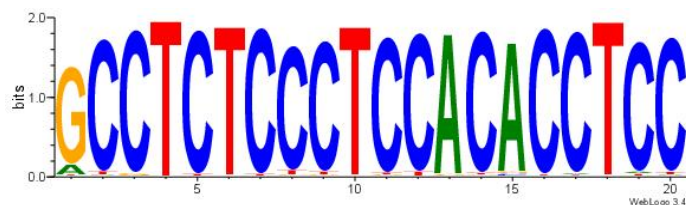


Dataset #: 1  
Motif ID: 105  
Motif name: Motif 105  
Matching format of first motif: Original Motif  
Matching format of second motif: Original Motif  
Direction: Forward  
Position number: 2  
Number of overlap: 11  
Similarity score: 0.0494199

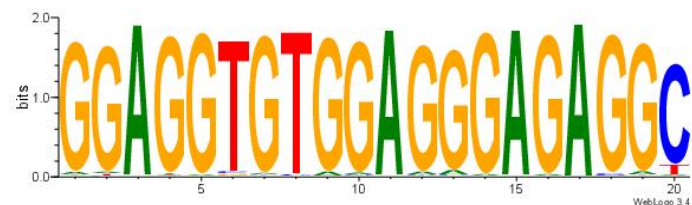
Alignment:

```
GCCTCTCCCTCCACACCTCC  
-CCTCRGCCTCC-----
```

Original motif      Consensus sequence: GCCTCTCCCTCCACACCTCC

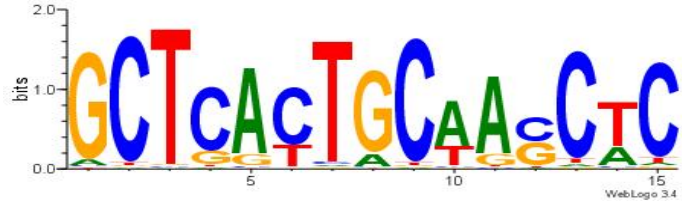


Reverse complement motif      Consensus sequence: GGAGGTGTGGAGGGAGAGGC

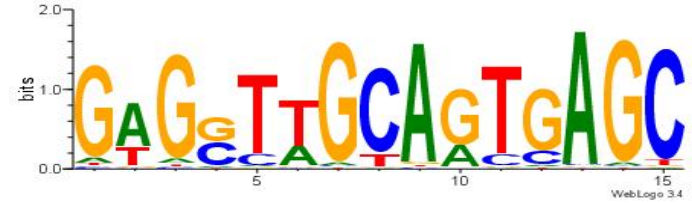


**Dataset #: 1      Motif ID: 6      Motif name: Motif 6**

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

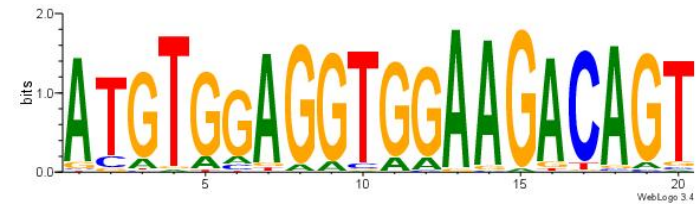
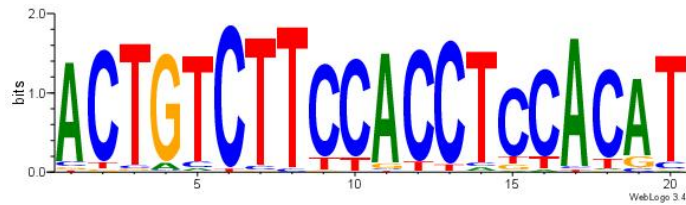
**Alignment:**

```
ATGTGGAGGTGGAAGACAGT
-----GAGSTTGCAGTGAGC
```

Original motif      Consensus sequence: ACTGTCTTCCACCTCCACAT

Reverse complement motif      Consensus sequence:  
ATGTGGAGGTGGAAGACAGT

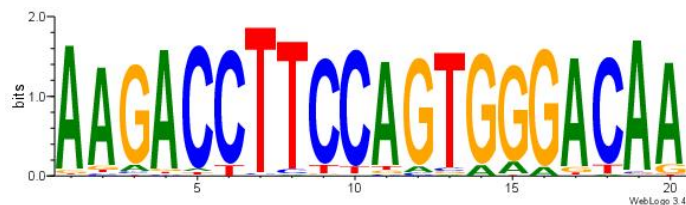




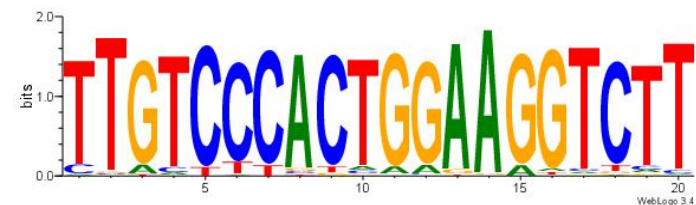
Dataset #: 1  
 Motif ID: 292  
 Motif name: Motif 292  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 3  
 Number of overlap: 15  
 Similarity score: 0.0774202

Alignment:  
 AAGACCTTCCAGTGGGACAA  
 --GAGSTTGCAGTGAGC---

Original motif      Consensus sequence: AAGACCTTCCAGTGGGACAA

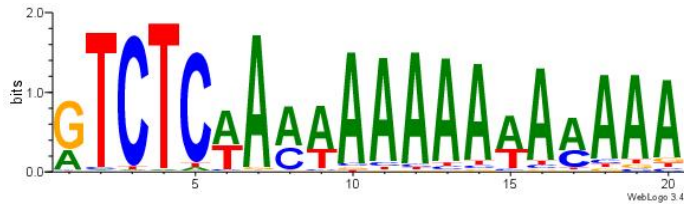


Reverse complement motif      Consensus sequence: TTGTCCCAGTGGGACAA

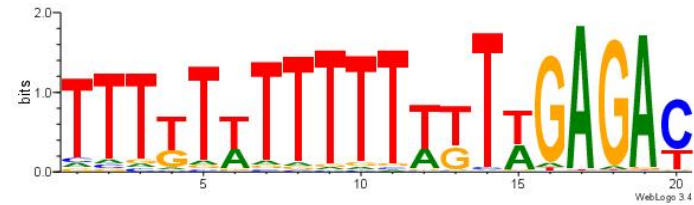


**Dataset #: 1      Motif ID: 7      Motif name: Motif 7**

Original motif      Consensus sequence: GTCTCWAMAAAAAWAMAAA



Reverse complement motif      Consensus sequence: TTTYTWTTTTTYYTWGAGAC



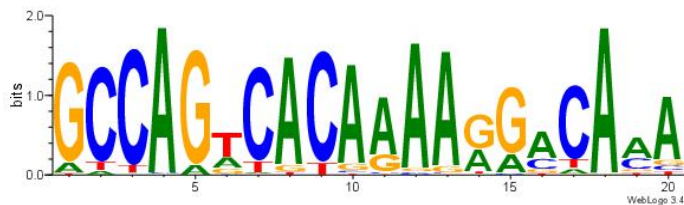
### Best Matches for Motif ID 7 (Highest to Lowest)

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

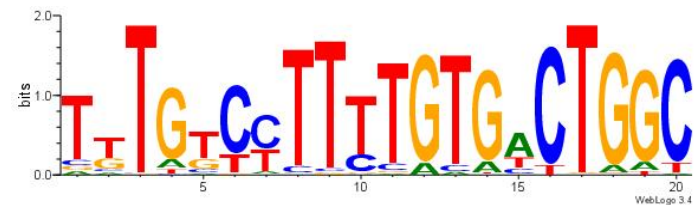
#### Alignment:

GCCAGTCACAAAARGACAMA  
 GTCTCWAMAAAAAWAMAAA

Original motif      Consensus sequence: GCCAGTCACAAAARGACAMA



Reverse complement motif      Consensus sequence: TYTGCMTTTTGTGACTGGC

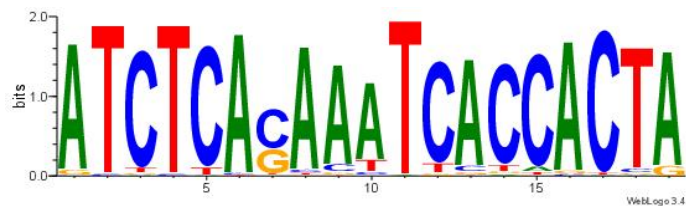


Dataset #: 1  
 Motif ID: 261  
 Motif name: Motif 261  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 19  
 Similarity score: 0.598351

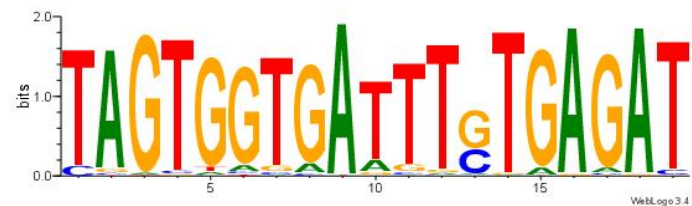
Alignment:

ATCTCASAAATCACCACTA-  
 GTCTCWAMAAAAAWAMAAA

Original motif      Consensus sequence: ATCTCASAAATCACCACTA



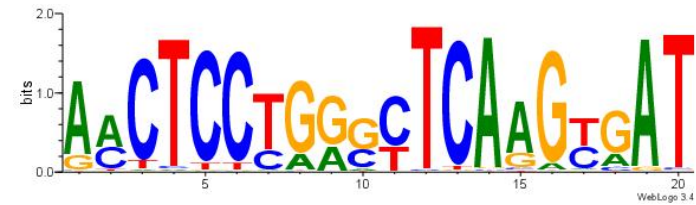
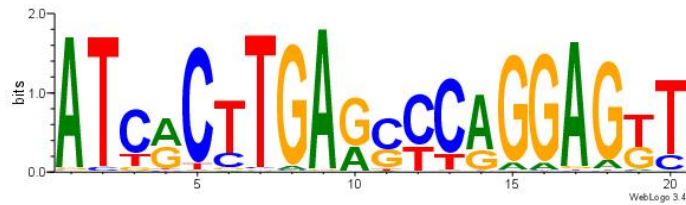
Reverse complement motif      Consensus sequence:  
TAGTGGTGATTSTGAGAT



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

Original motif      Consensus sequence: ATCRCTTGAGSYCAGGAGKT

Reverse complement motif      Consensus sequence:  
ARCTCCTGKSCTCAAGKGAT

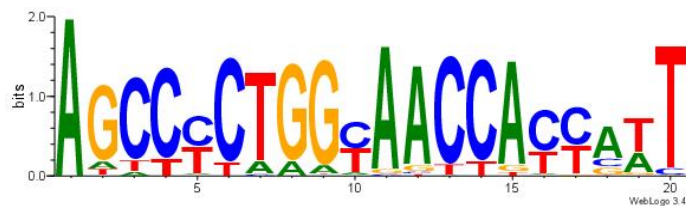


**Best Matches for Motif ID 8 (Highest to Lowest)**

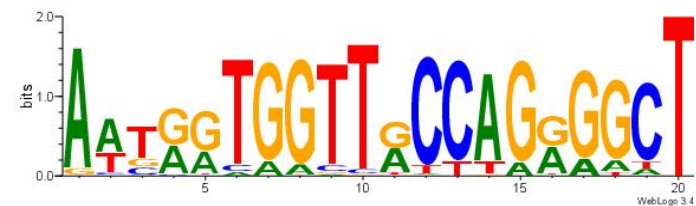
Dataset #: 1  
 Motif ID: 139  
 Motif name: Motif 139  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 20  
 Similarity score: 0.0757564

Alignment:  
 AGCCYCTGGYAACCAYYAWT  
 ARCTCCTGKSCTCAAGKGAT

Original motif      Consensus sequence: AGCCYCTGGYAACCAYYAWT



Reverse complement motif      Consensus sequence: AWTKKTGGTTKCCAGKGGCT

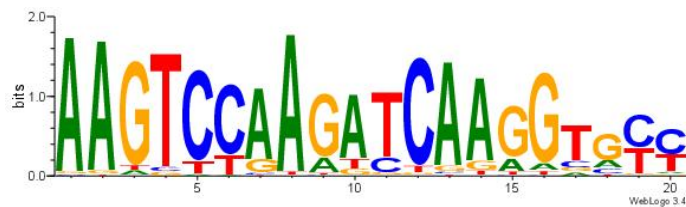


Dataset #: 1  
 Motif ID: 119  
 Motif name: Motif 119  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 20  
 Similarity score: 0.0854742

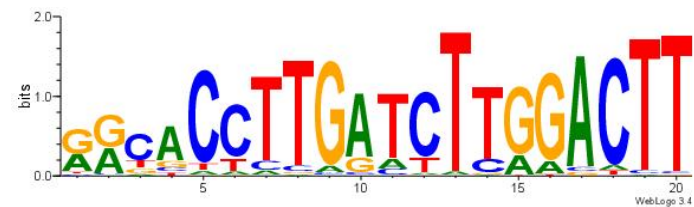
Alignment:

KKCACCTTGATCTTGGACTT  
 ATCRCTTGAGSYCAGGAGKT

Original motif      Consensus sequence: AAGTCCAAGATCAAGGTGYY



Reverse complement motif      Consensus sequence: KKCACCTTGATCTTGGACTT

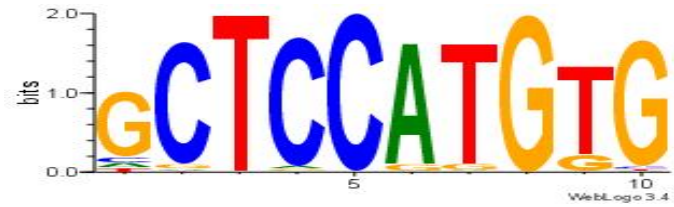



---

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

Original motif      Consensus sequence: CACATGGAGC

Reverse complement motif      Consensus sequence: GCTCCATGTG



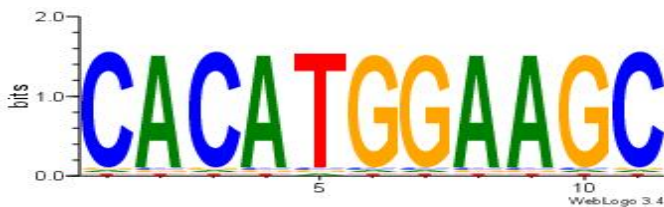
### Best Matches for Motif ID 9 (Highest to Lowest)

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

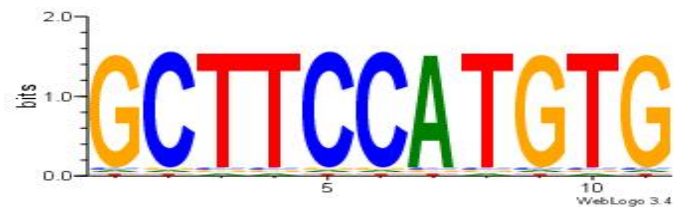
#### Alignment:

GCTTCCATGTG  
 -GCTCCATGTG

Original motif    Consensus sequence: CACATGGAAGC



Reverse complement motif    Consensus sequence: GCTTCCATGTG

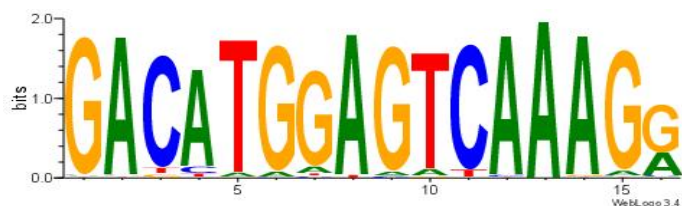


Dataset #: 1

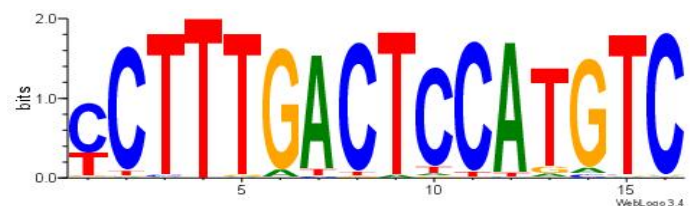
Motif ID: 326  
 Motif name: Motif 326  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 10  
 Similarity score: 0.0461936

Alignment:  
 GACATGGAGTCAAAGG  
 CACATGGAGC-----

Original motif    Consensus sequence: GACATGGAGTCAAAGG

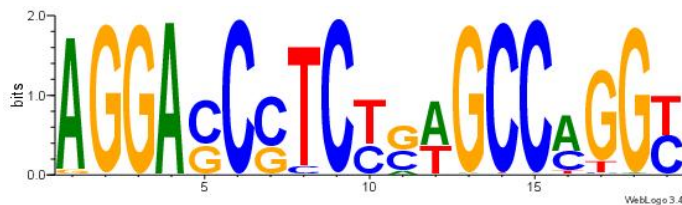


Reverse complement motif    Consensus sequence: CCTTTGACTCCATGTC

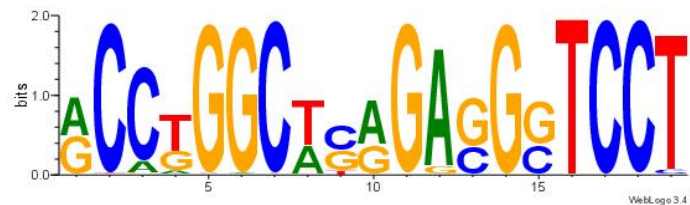


**Dataset #: 1      Motif ID: 10      Motif name: Motif 10**

Original motif    Consensus sequence: AGGASCSTCYSWGCCMGGY



Reverse complement motif    Consensus sequence: MCCYGGCWSMGASGSTCCT



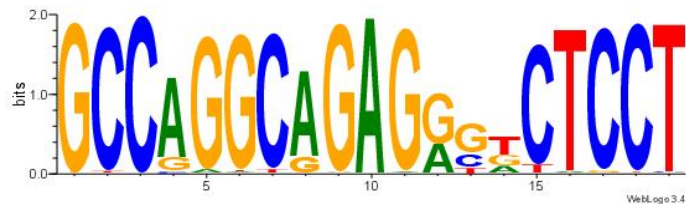
## Best Matches for Motif ID 10 (Highest to Lowest)

Dataset #: 1  
Motif ID: 43  
Motif name: Motif 43  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Original Motif  
Direction: Forward  
Position number: 1  
Number of overlap: 19  
Similarity score: 0.0458009

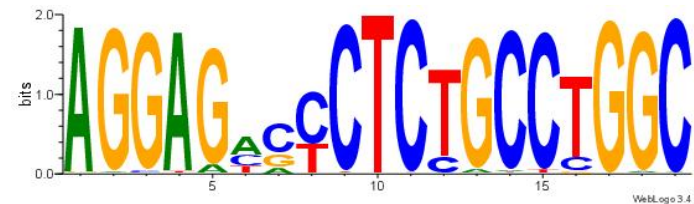
### Alignment:

```
GCCAGGCAGAGRGKCTCCT  
MCCYGGCWSMGASGSTCCT
```

Original motif      Consensus sequence: GCCAGGCAGAGRGKCTCCT



Reverse complement motif      Consensus sequence:  
AGGAGRCMCTCTGCCTGGC



---

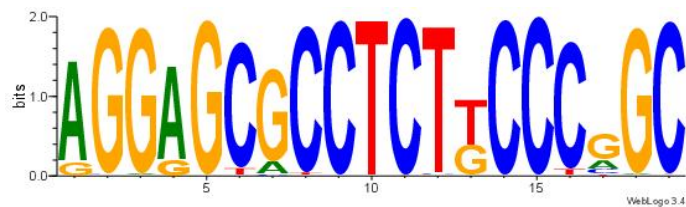
Dataset #: 1  
Motif ID: 30  
Motif name: Motif 30  
Matching format of first motif: Original Motif  
Matching format of second motif: Original Motif



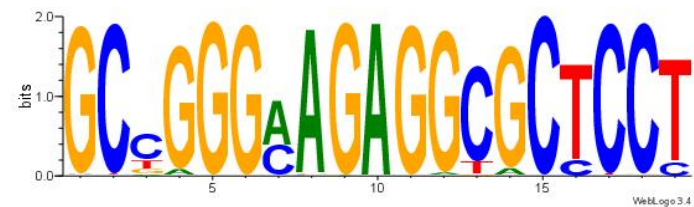
Direction: Forward  
 Position number: 1  
 Number of overlap: 19  
 Similarity score: 0.0489869

Alignment:  
 AGGAGCGCCTCTKCCCGGC  
 AGGASCSTCYSWGCCMGY

Original motif      Consensus sequence: AGGAGCGCCTCTKCCCGGC



Reverse complement motif      Consensus sequence: GCCGGGRAGAGGCGCTCCT

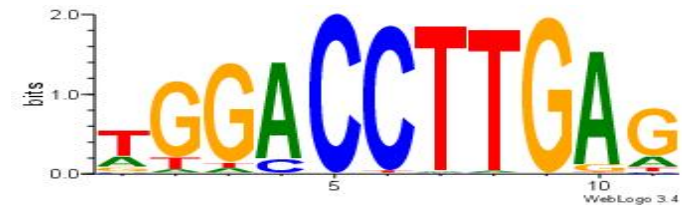


**Dataset #: 1      Motif ID: 11      Motif name: Motif 11**

Original motif      Consensus sequence: CTC AAGTCCA



Reverse complement motif      Consensus sequence: TGGACCTTGAG



**Best Matches for Motif ID 11 (Highest to Lowest)**

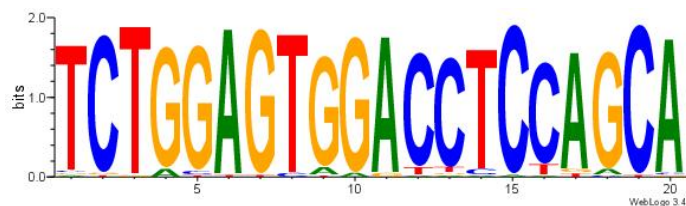
Dataset #: 1  
 Motif ID: 350

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

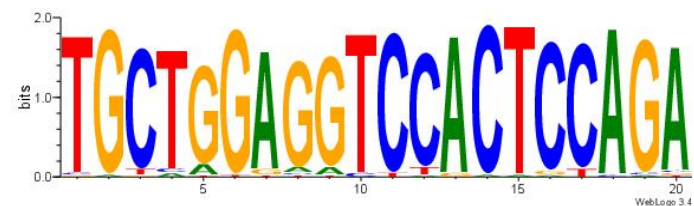
**Alignment:**

TGCTGGAGGTCCACTCCAGA  
 --CTCAAGGTCCA-----

Original motif    Consensus sequence: TCTGGAGTGGACCTCCAGCA



Reverse complement motif    Consensus sequence: TGCTGGAGGTCCACTCCAGA

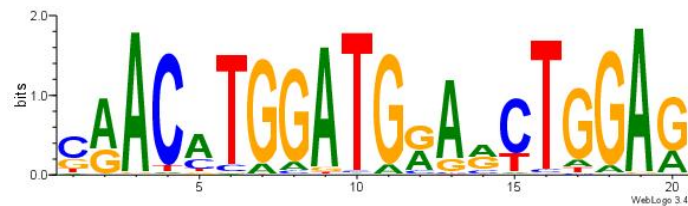


Dataset #: 1  
 Motif ID: 104  
 Motif name: Motif 104  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 10  
 Number of overlap: 11  
 Similarity score: 0.054717

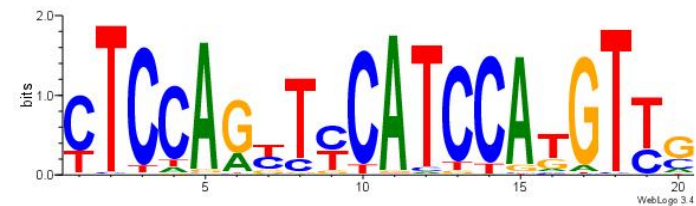
Alignment:

```
CTCCAGKTMCATCCATGTTG
CTCAAGGTCCA-----
```

Original motif      Consensus sequence: CAACATGGATGRARCTGGAG

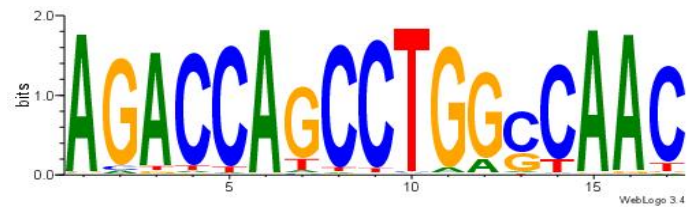


Reverse complement motif      Consensus sequence: CTCCAGKTMCATCCATGTTG

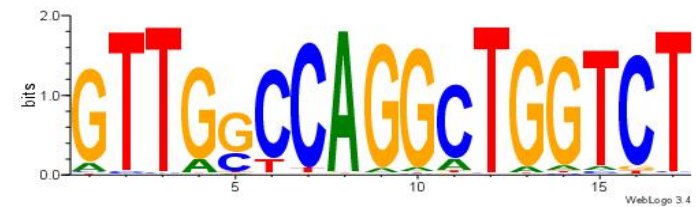


**Dataset #: 1      Motif ID: 12      Motif name: Motif 12**

Original motif      Consensus sequence: AGACCAGCCTGGCCAAC



Reverse complement motif      Consensus sequence: GTTGCCAGGCTGGTCT



**Best Matches for Motif ID 12 (Highest to Lowest)**

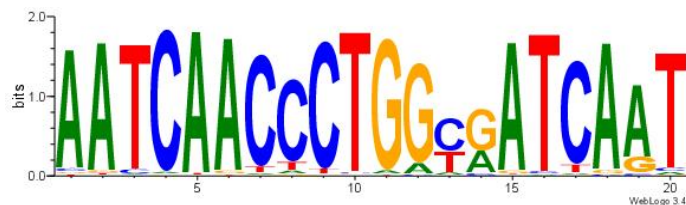
Dataset #:	1
Motif ID:	170
Motif name:	Motif 170
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement

Direction: Backward  
 Position number: 1  
 Number of overlap: 17  
 Similarity score: 0.0789836

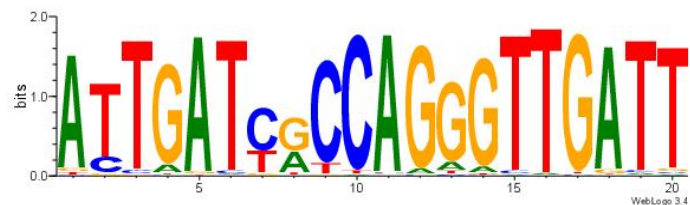
**Alignment:**

ATTGATMKCCAGGGTTGATT  
 ---GTTGGCCAGGCTGGTCT

Original motif      Consensus sequence: AATCAACCCTGGYRATCAAT



Reverse complement motif      Consensus sequence: ATTGATMKCCAGGGTTGATT

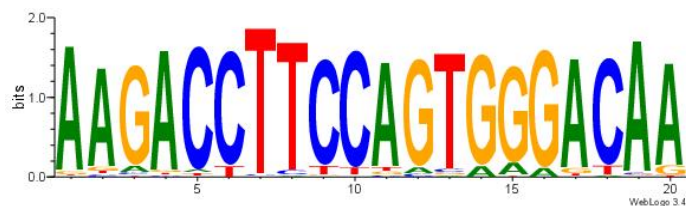


Dataset #: 1  
 Motif ID: 292  
 Motif name: Motif 292  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 2  
 Number of overlap: 17  
 Similarity score: 0.0836974

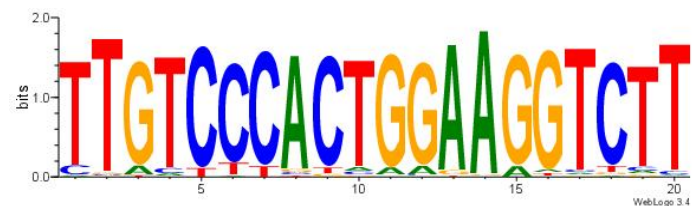
**Alignment:**

AAGACCTTCCAGTGGGACAA  
 -AGACCAGCCTGGCCAAC--

Original motif      Consensus sequence: AAGACCTCCAGTGGGACAA

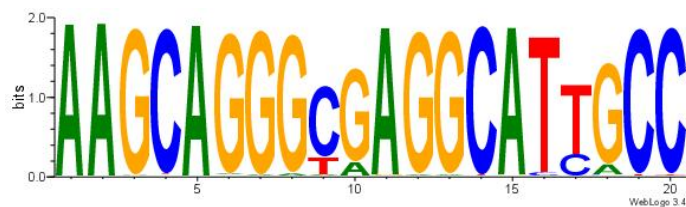


Reverse complement motif      Consensus sequence: TTGTCCCAGTGGAGGTCTT

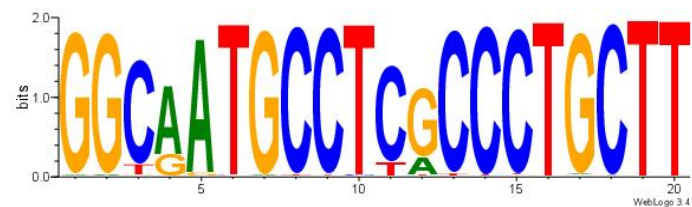


**Dataset #: 1      Motif ID: 13      Motif name: Motif 13**

Original motif      Consensus sequence: AAGCAGGGCGAGGCATTGCC



Reverse complement motif      Consensus sequence: GGCAATGCCTCGCCCTGCTT



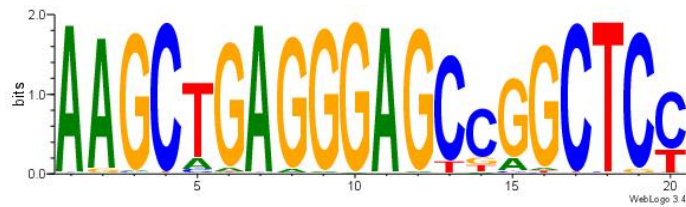
### Best Matches for Motif ID 13 (Highest to Lowest)

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

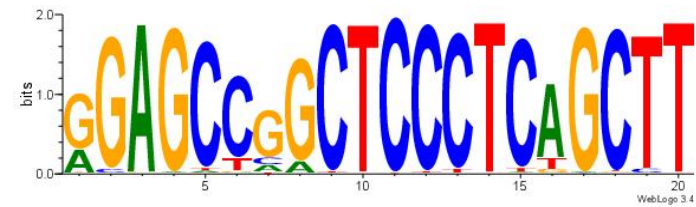
Alignment:

AAGCTGAGGGAGCCGGCTCC  
AAGCAGGGCGAGGCATTGCC

Original motif      Consensus sequence: AAGCTGAGGGAGCCGGCTCC



Reverse complement motif      Consensus sequence:  
GGAGCCGGCTCCCTCAGCTT



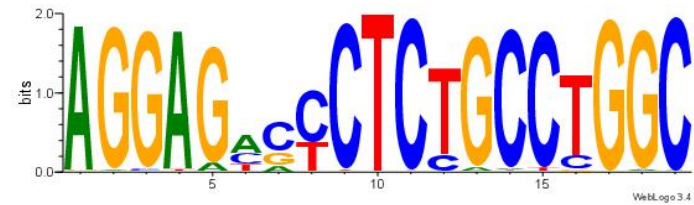
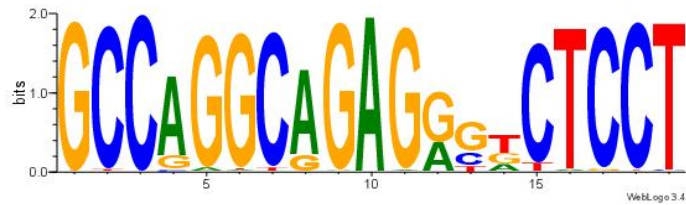
Dataset #: 1  
Motif ID: 43  
Motif name: Motif 43  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Reverse Complement  
Direction: Forward  
Position number: 1  
Number of overlap: 19  
Similarity score: 0.603866

Alignment:

AGGAGRCMCTCTGCCTGGC-  
GGCAATGCCTCGCCCTGCTT

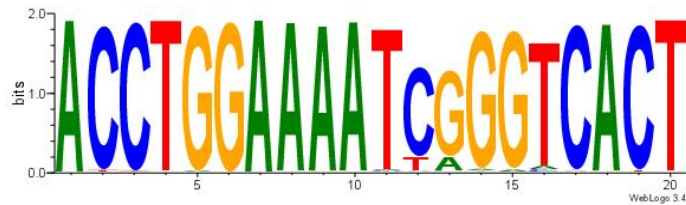
Original motif      Consensus sequence: GCCAGGCAGAGRGKCTCCT

Reverse complement motif      Consensus sequence:  
AGGAGRCMCTCTGCCTGGC

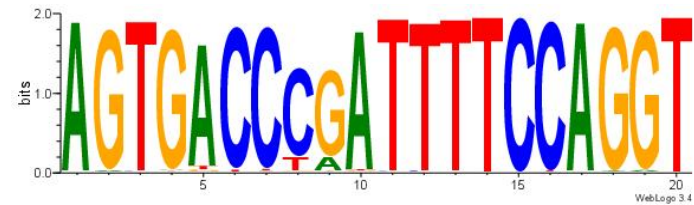


**Dataset #: 1      Motif ID: 14      Motif name: Motif 14**

Original motif      Consensus sequence: ACCTGGAAAATCGGGTCACT



Reverse complement motif      Consensus sequence: AGTGACCCGATTTTCCAGGT



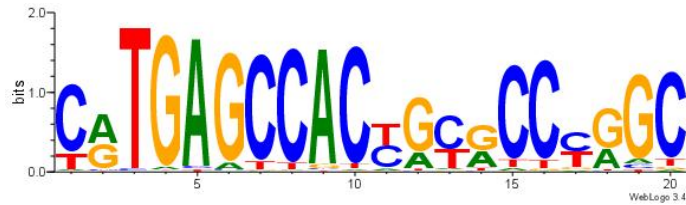
### Best Matches for Motif ID 14 (Highest to Lowest)

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

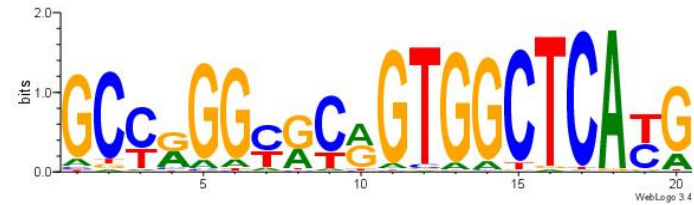
Alignment:

GCCKGGMKCMGTGGCTCAKG  
ACCTGGAAAATCGGGTCACT

Original motif      Consensus sequence: CRTGAGCCACYGYRCCYGGC



Reverse complement motif      Consensus sequence:  
GCCKGGMKCMGTGGCTCAKG



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: 19  
Similarity score: 0.604557

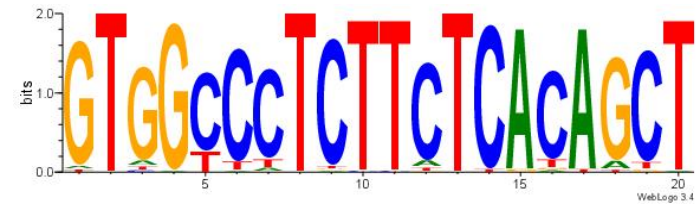
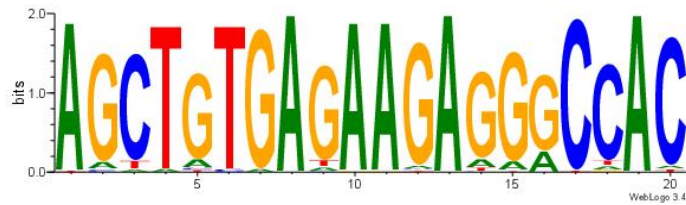
Alignment:

-GTGGCCCTCTTCTCACAGCT  
AGTGACCCGATTTTCCAGGT-

Original motif      Consensus sequence: AGCTGTGAGAAGAGGGCCAC

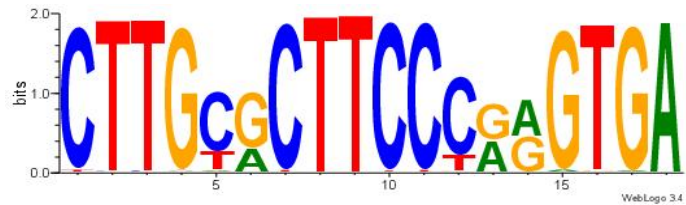
Reverse complement motif      Consensus sequence:  
GTGGCCCTCTTCTCACAGCT



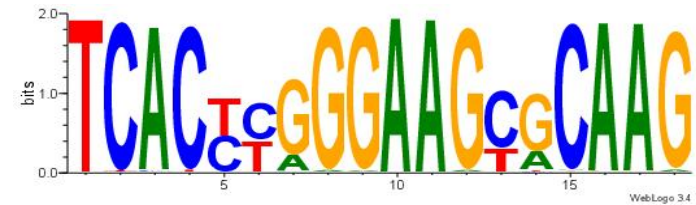


**Dataset #: 1      Motif ID: 15      Motif name: Motif 15**

Original motif      Consensus sequence: CTTGCGCTCCRRGTGA



Reverse complement motif      Consensus sequence: TCACKMGGGAAGCGCAAG



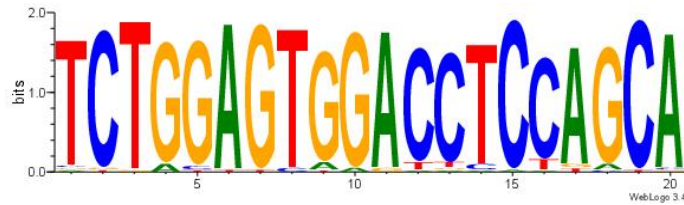
**Best Matches for Motif ID 15 (Highest to Lowest)**

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

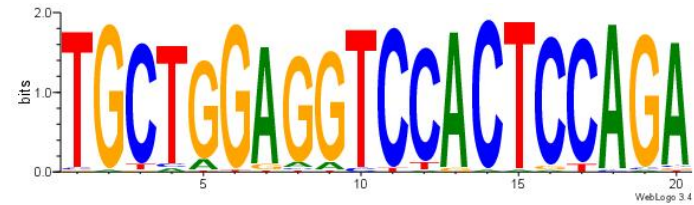
Alignment:

TCTGGAGTGGACCTCCAGCA  
TCACKMGGGAAGCGCAAG--

Original motif      Consensus sequence: TCTGGAGTGGACCTCCAGCA



Reverse complement motif      Consensus sequence:  
TGCTGGAGGTCCACTCCAGA

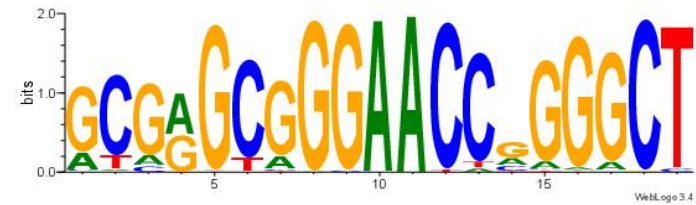
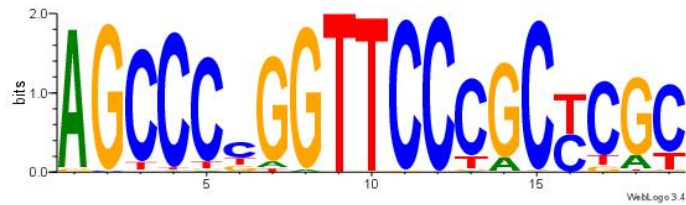


Dataset #: 1  
Motif ID: 164  
Motif name: Motif 164  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Reverse Complement  
Direction: Backward  
Position number: 2  
Number of overlap: 18  
Similarity score: 0.117199

Alignment:  
GCGMGCGGGAACCGGGGCT  
TCACKMGGGAAGCGCAAG-

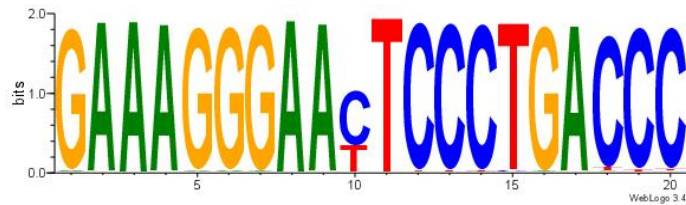
Original motif      Consensus sequence: AGCCCCGGTTCCCGCYCGC

Reverse complement motif      Consensus sequence:  
GCGMGCGGGAACCGGGGCT

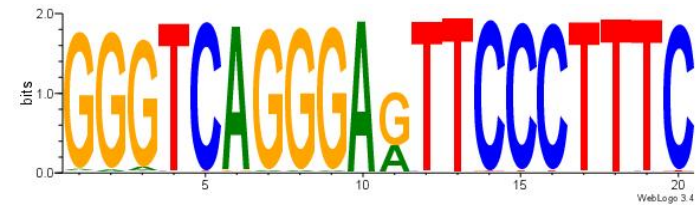


**Dataset #: 1      Motif ID: 16      Motif name: Motif 16**

Original motif      Consensus sequence: GAAAGGGAActCCCTGACCC



Reverse complement motif      Consensus sequence: GGGTCAGGGAGTTCCCTTTC



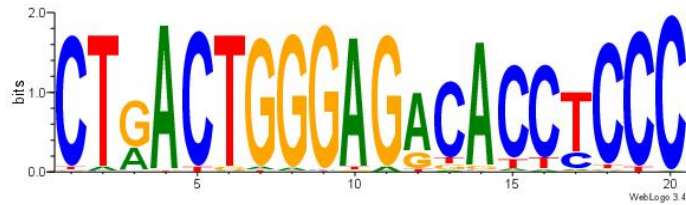
**Best Matches for Motif ID 16 (Highest to Lowest)**

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

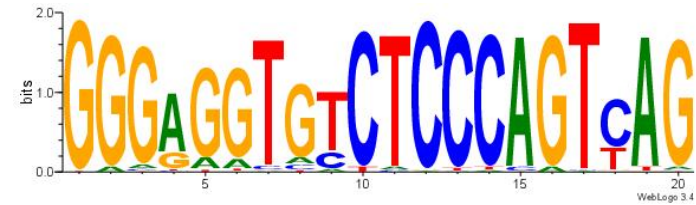
Alignment:

CTGACTGGGAGACACCTCCC  
GGGTCAGGGAGTTCCTTTC

Original motif      Consensus sequence: CTGACTGGGAGACACCTCCC



Reverse complement motif      Consensus sequence:  
GGGAGGTGTCTCCCAGTCAG



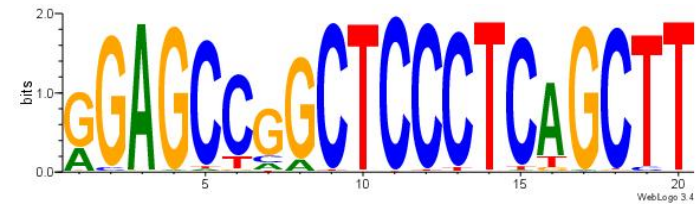
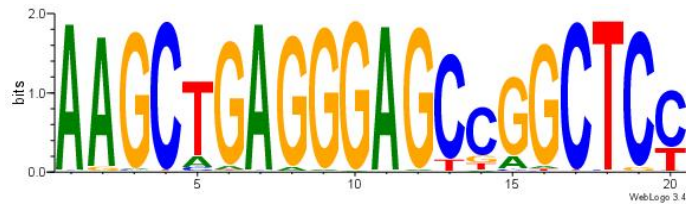
Dataset #: 1  
Motif ID: 96  
Motif name: Motif 96  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Original Motif  
Direction: Forward  
Position number: 2  
Number of overlap: 19  
Similarity score: 0.615331

Alignment:

AAGCTGAGGGAGCCGGCTCC-  
-GGGTCAGGGAGTTCCTTTC

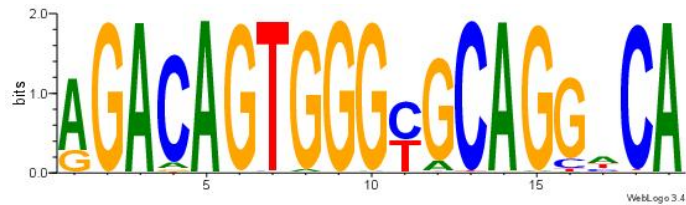
Original motif      Consensus sequence: AAGCTGAGGGAGCCGGCTCC

Reverse complement motif      Consensus sequence:  
GGAGCCGGCTCCCTCAGCTT

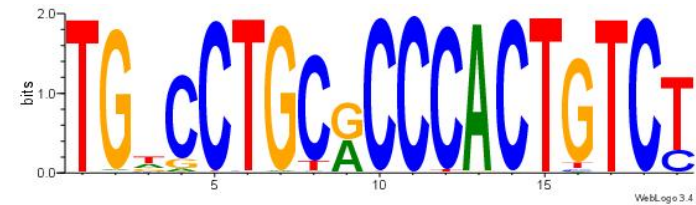


**Dataset #: 1      Motif ID: 17      Motif name: Motif 17**

Original motif      Consensus sequence: AGACAGTGGGYGCAGGHCA



Reverse complement motif      Consensus sequence: TGHCCTGKCCCCTGTCT



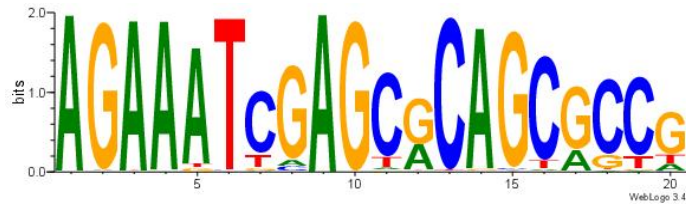
**Best Matches for Motif ID 17 (Highest to Lowest)**

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

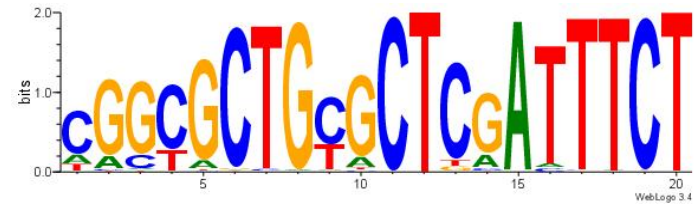
Alignment:

CGGCGCTGMGCTCGATTTCT  
-TGHCTGCKCCCACTGTCT

Original motif      Consensus sequence: AGAAATCGAGCRCAGCGCCG



Reverse complement motif      Consensus sequence:  
CGGCGCTGMGCTCGATTTCT



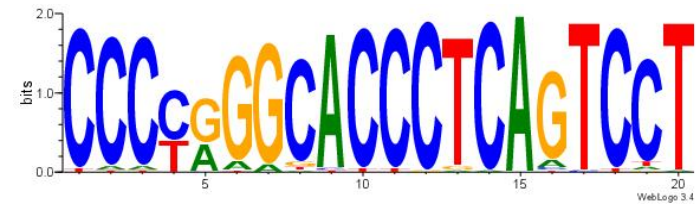
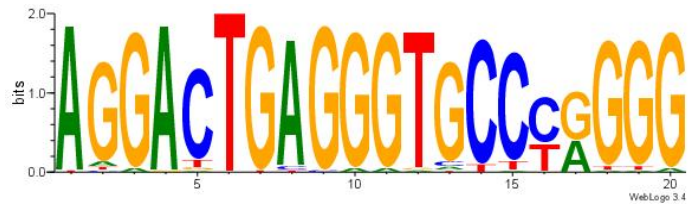
Dataset #: 1  
Motif ID: 312  
Motif name: Motif 312  
Matching format of first motif: Original Motif  
Matching format of second motif: Original Motif  
Direction: Backward  
Position number: 1  
Number of overlap: 19  
Similarity score: 0.0967987

Alignment:

AGGACTGAGGGTGCCYRGGG  
-AGACAGTGGGYGCAGGHCA

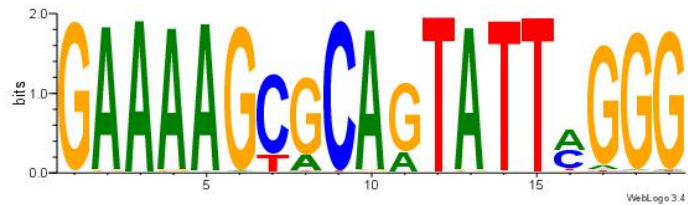
Original motif      Consensus sequence: AGGACTGAGGGTGCCYRGGG

Reverse complement motif      Consensus sequence:  
CCCMKGGCACCCTCAGTCCT

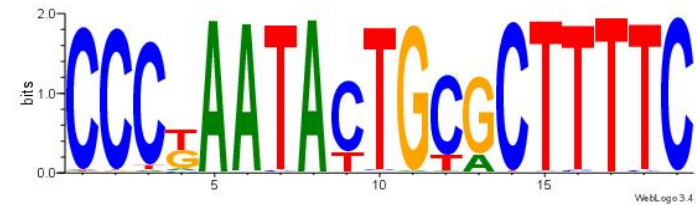


**Dataset #: 1      Motif ID: 18      Motif name: Motif 18**

Original motif      Consensus sequence: GAAAAGCGCAGTATTMGGG



Reverse complement motif      Consensus sequence: CCCYAATACTGCGCTTTTC



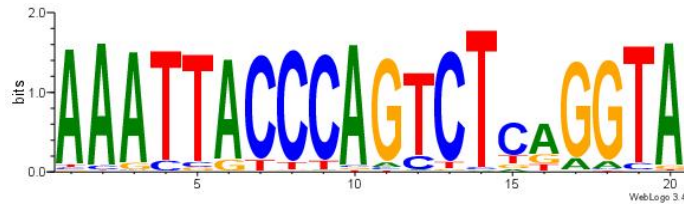
**Best Matches for Motif ID 18 (Highest to Lowest)**

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

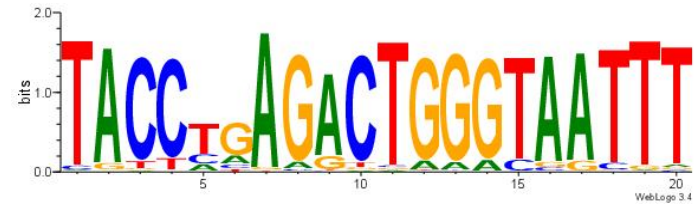
Alignment:

AAATTACCCAGTCTCAGGTA  
GAAAAGCGCAGTATTMGGG-

Original motif      Consensus sequence: AAATTACCCAGTCTCAGGTA



Reverse complement motif      Consensus sequence:  
TACCTGAGACTGGGTAATTT



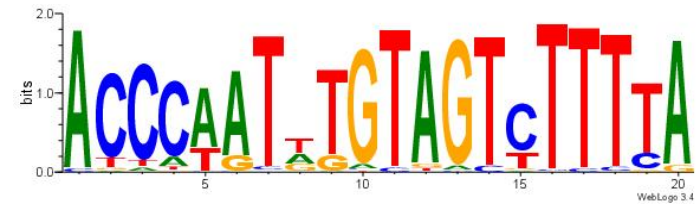
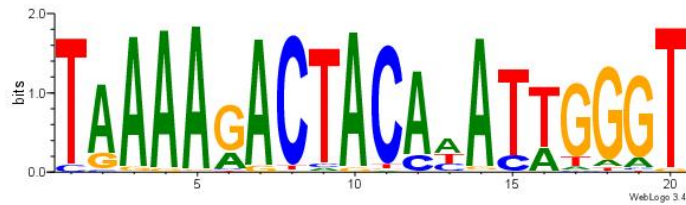
Dataset #: 1  
Motif ID: 195  
Motif name: Motif 195  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Reverse Complement  
Direction: Forward  
Position number: 2  
Number of overlap: 19  
Similarity score: 0.113548

Alignment:  
ACCCAATWTGTAGTCTTTTA  
-CCCYAATACTGCGCTTTTC

Original motif      Consensus sequence: TAAAAGACTACAWATTGGGT

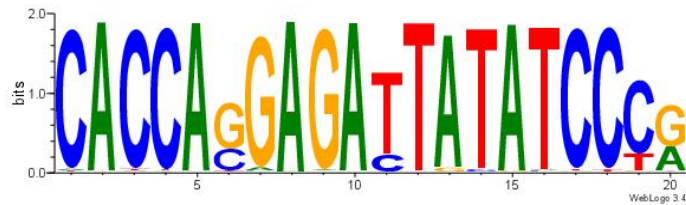
Reverse complement motif      Consensus sequence:  
ACCCAATWTGTAGTCTTTTA



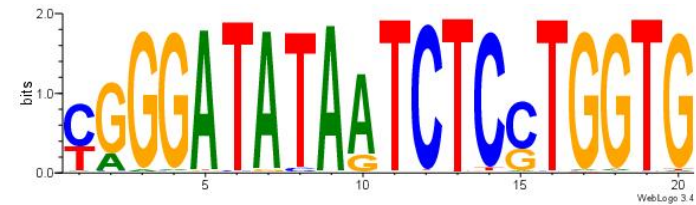


**Dataset #: 1      Motif ID: 19      Motif name: Motif 19**

Original motif      Consensus sequence: CACCAGGAGATTATATCCCR



Reverse complement motif      Consensus sequence: MGGGATATAATCTCCTGGTG



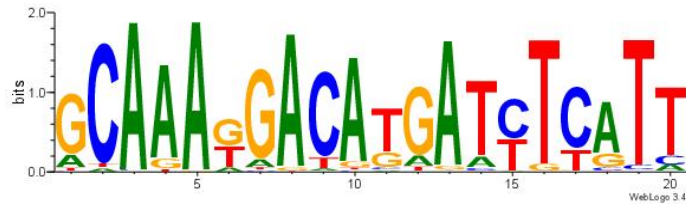
**Best Matches for Motif ID 19 (Highest to Lowest)**

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

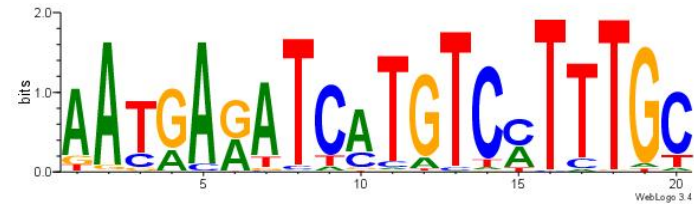
Alignment:

AATGAKATCATGTCYTTTGC  
MGGGATATAATCTCCTGGTG

Original motif      Consensus sequence: GCAAAGACATGATYTCATT



Reverse complement motif      Consensus sequence:  
AATGAKATCATGTCYTTTGC



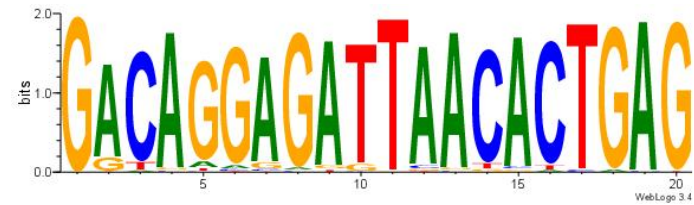
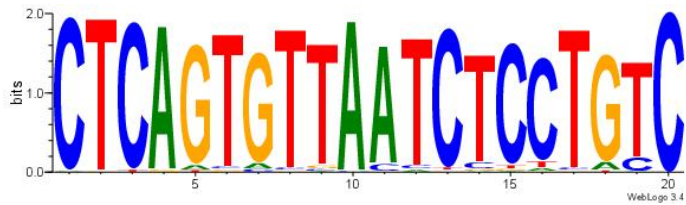
Dataset #:	1
Motif ID:	262
Motif name:	Motif 262
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	2
Number of overlap:	19
Similarity score:	0.601395

Alignment:

-GACAGGAGATTAACACTGAG  
CACCAGGAGATTATATCCCR-

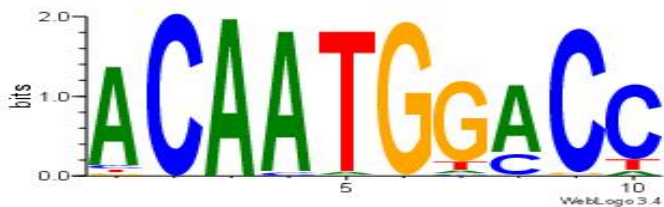
Original motif      Consensus sequence: CTCAGTGTTAATCTCCTGTC

Reverse complement motif      Consensus sequence:  
GACAGGAGATTAACACTGAG

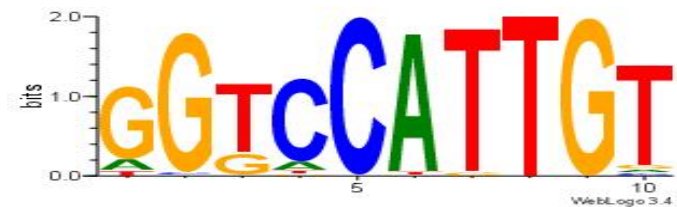


**Dataset #: 1      Motif ID: 20      Motif name: Motif 20**

Original motif      Consensus sequence: ACAATGGACC



Reverse complement motif      Consensus sequence: GTCCATTGT

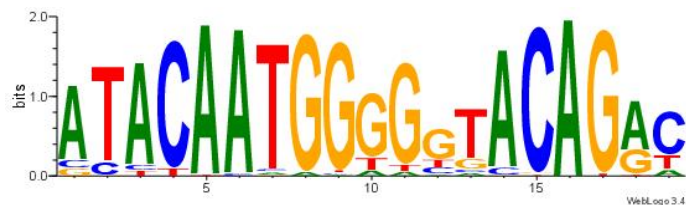


**Best Matches for Motif ID 20 (Highest to Lowest)**

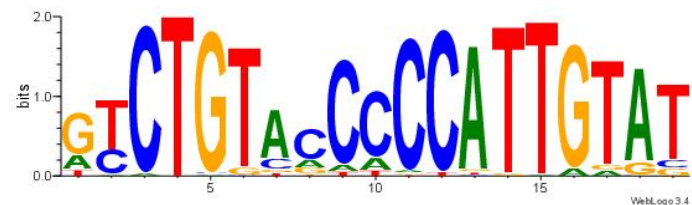
Dataset #:	1
Motif ID:	193
Motif name:	Motif 193
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	3
Number of overlap:	10
Similarity score:	0.0500147

Alignment:  
 GKCTGTACCCCATTTGTAT  
 -----GGTCCATTGT--

Original motif      Consensus sequence: ATACAATGGGGTACAGRC



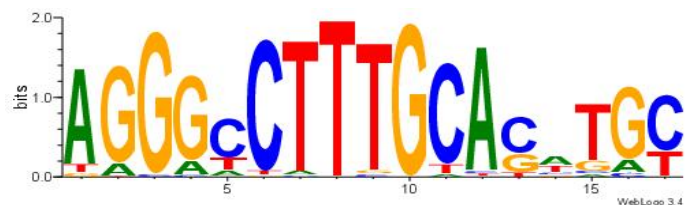
Reverse complement motif      Consensus sequence: GKCTGTACCCCCATTGTAT



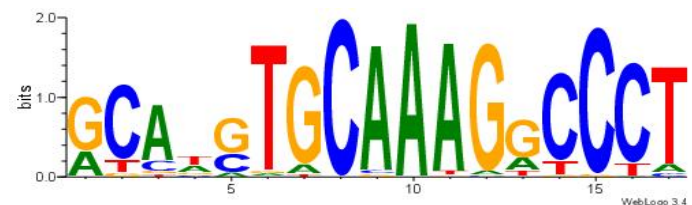
Dataset #: 1  
Motif ID: 322  
Motif name: Motif 322  
Matching format of first motif: Original Motif  
Matching format of second motif: Reverse Complement  
Direction: Forward  
Position number: 7  
Number of overlap: 10  
Similarity score: 0.059291

Alignment:  
GCAWSTGCAAAGGCCCT  
-----ACAATGGACC-

Original motif      Consensus sequence: AGGGCCTTTGCASWTGC

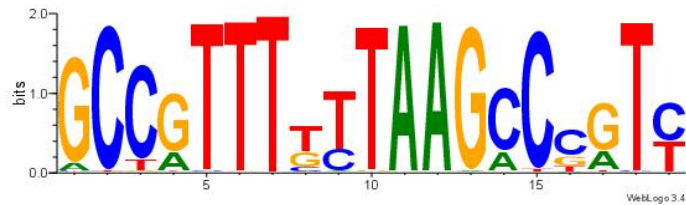


Reverse complement motif      Consensus sequence: GCAWSTGCAAAGGCCCT

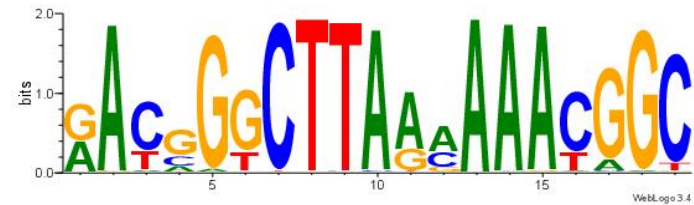


**Dataset #: 1      Motif ID: 21      Motif name: Motif 21**

Original motif      Consensus sequence: GCCGTTTKTTAAGCCCGTY



Reverse complement motif      Consensus sequence: KACGGGCTTAARAAACGGC



### Best Matches for Motif ID 21 (Highest to Lowest)

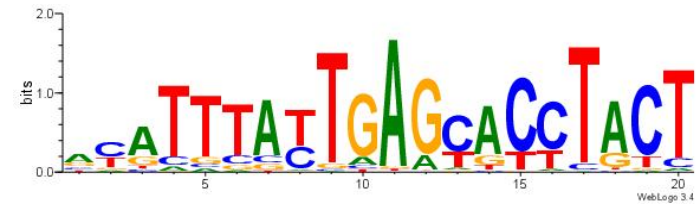
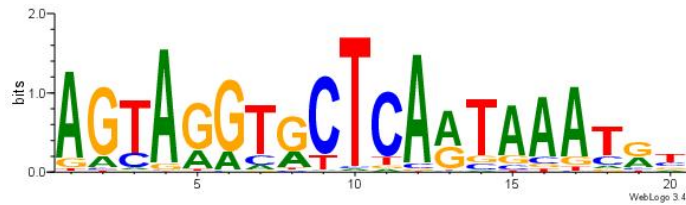
Dataset #:	1
Motif ID:	86
Motif name:	Motif 86
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	3
Number of overlap:	18
Similarity score:	0.0915321

#### Alignment:

```
AGTAGGTGCTCARTAAATRB-  
--KACGGGCTTAARAAACGGC
```

Original motif      Consensus sequence: AGTAGGTGCTCARTAAATRB

Reverse complement motif      Consensus sequence: VMATTTAKTGAGCACCTACT

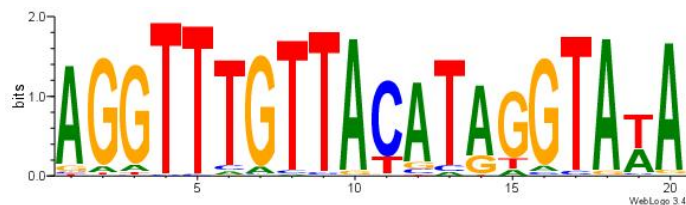


Dataset #: 1  
 Motif ID: 137  
 Motif name: Motif 137  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 3  
 Number of overlap: 18  
 Similarity score: 0.0978691

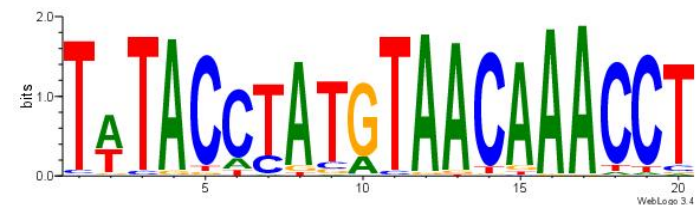
Alignment:

TWTACCTATGTAACAAACCT-  
 --KACGGGCTTAARAAACGGC

Original motif      Consensus sequence: AGGTTTGTACATAGGTAWA



Reverse complement motif      Consensus sequence: TWTACCTATGTAACAAACCT

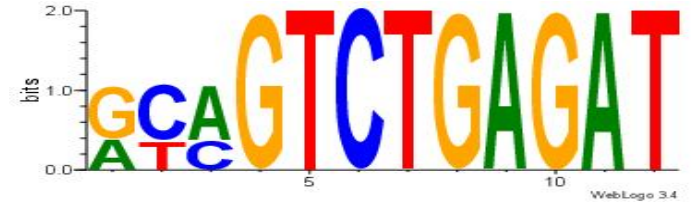


**Dataset #: 1      Motif ID: 22      Motif name: Motif 22**

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

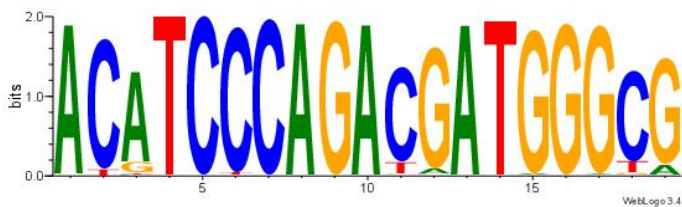
Alignment:

```

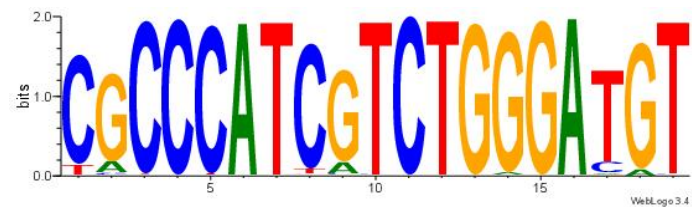
ACATCCCAGACGATGGGCG
--ATCTCAGACKRY-----

```

Original motif    Consensus sequence: ACATCCCAGACGATGGGCG



Reverse complement motif    Consensus sequence: CGCCATCGTCTGGGATGT

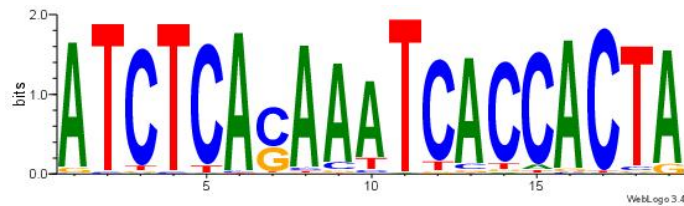


Dataset #: 1  
 Motif ID: 261  
 Motif name: Motif 261  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 8  
 Number of overlap: 12  
 Similarity score: 0.0600848

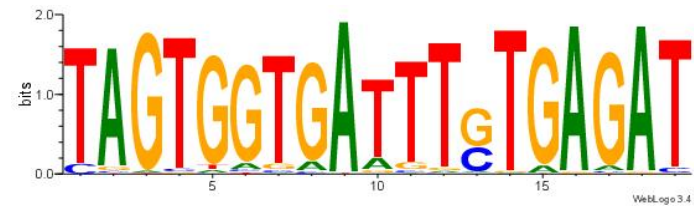
Alignment:

TAGTGGTGATTTSTGAGAT  
 -----KMRGTCTGAGAT

Original motif    Consensus sequence: ATCTCASAAATCACCCTA



Reverse complement motif    Consensus sequence:  
TAGTGGTGATTTSTGAGAT



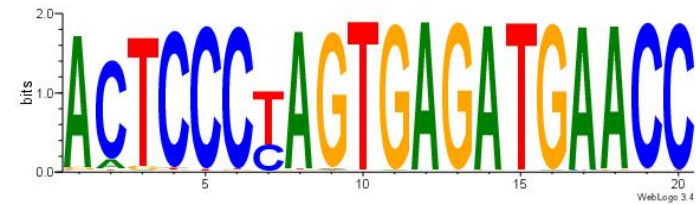
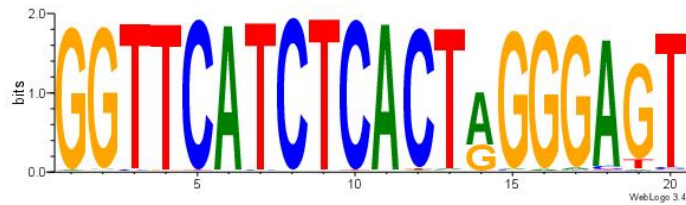

---

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

Original motif    Consensus sequence: GGTCATCTCACTAGGGAGT

Reverse complement motif    Consensus sequence:  
ACTCCCTAGTGAGATGAACC





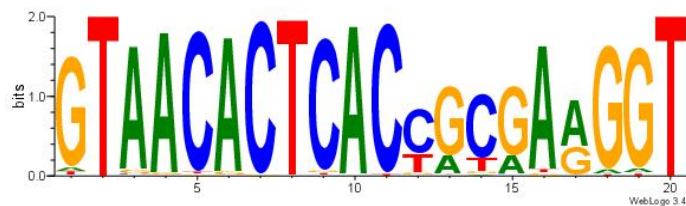
**Best Matches for Motif ID 23 (Highest to Lowest)**

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: 2  
 Number of overlap: 19  
 Similarity score: 0.104804

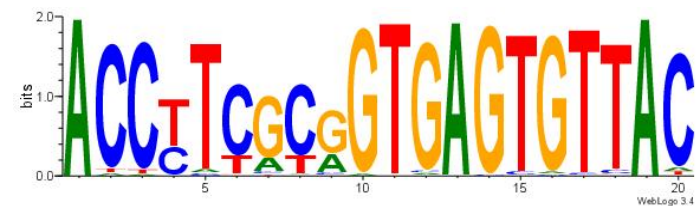
**Alignment:**

-GTAACACTCACCGCGARGGT  
 GGTTTCATCTCACTAGGGAGT-

Original motif      Consensus sequence: GTAACACTCACCGCGARGGT



Reverse complement motif      Consensus sequence: ACCKTCGCGGTGAGTGTTAC

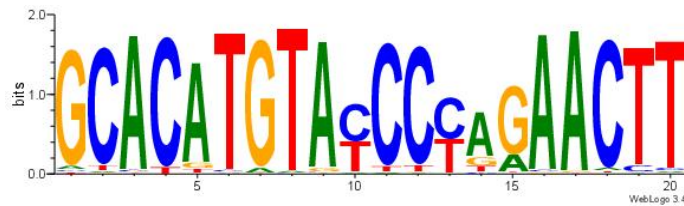


Dataset #: 1  
 Motif ID: 225  
 Motif name: Motif 225  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 2  
 Number of overlap: 19  
 Similarity score: 0.108413

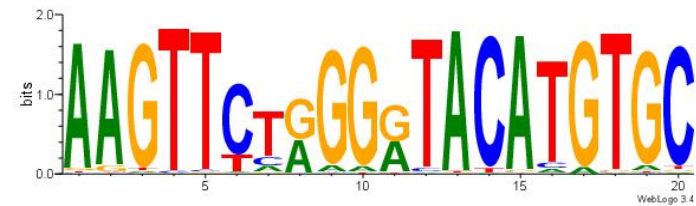
Alignment:

AAGTTCTKGGKTACATGTGC-  
 -ACTCCCTAGTGAGATGAACC

Original motif      Consensus sequence: GCACATGTAYCCYAGAACTT



Reverse complement motif      Consensus sequence: AAGTTCTKGGKTACATGTGC

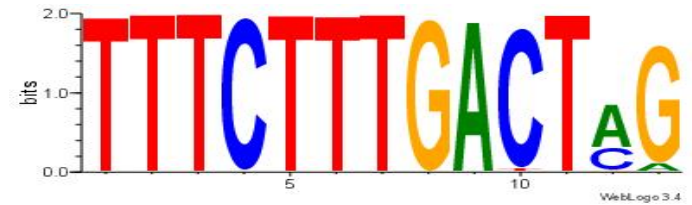
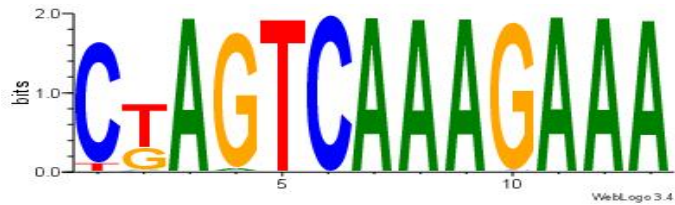



---

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

Original motif      Consensus sequence: CKAGTCAAAGAAA

Reverse complement motif      Consensus sequence: TTTCTTTGACTRG

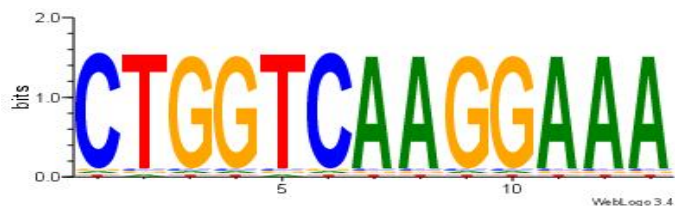


**Best Matches for Motif ID 24 (Highest to Lowest)**

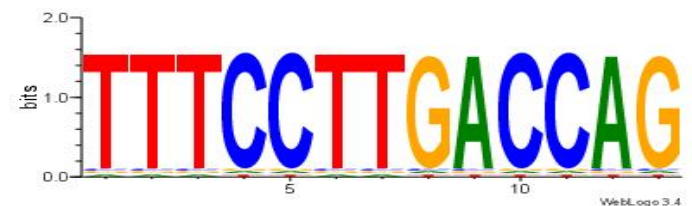
Dataset #: 1  
 Motif ID: 274  
 Motif name: Motif 274  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 13  
 Similarity score: 0.0524968

Alignment:  
 CTGGTCAAGGAAA  
 CKAGTCAAAGAAA

Original motif    Consensus sequence: CTGGTCAAGGAAA



Reverse complement motif    Consensus sequence: TTTCTTTGACCAG



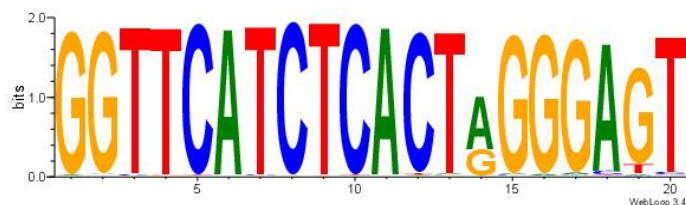
Dataset #: 1

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

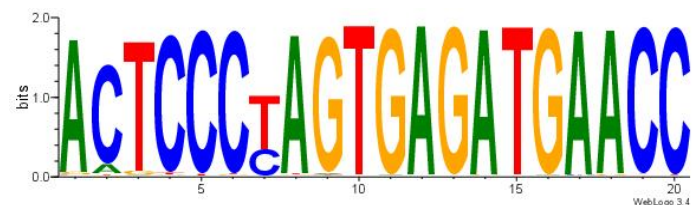
**Alignment:**

ACTCCCTAGTGAGATGAACC  
 --CKAGTCAAAGAAA-----

Original motif    Consensus sequence: GGTTCACTCTCACTAGGGAGT

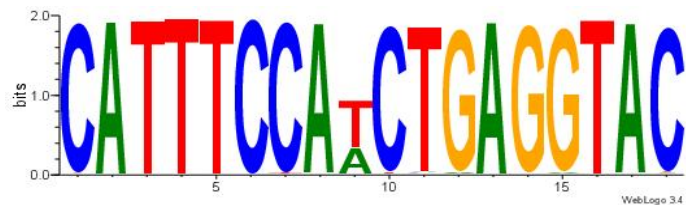


Reverse complement motif    Consensus sequence: ACTCCCTAGTGAGATGAACC

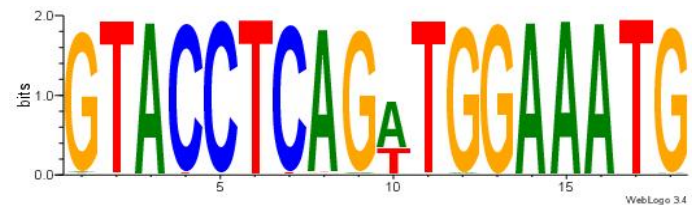


**Dataset #: 1      Motif ID: 25      Motif name: Motif 25**

Original motif    Consensus sequence: CATTCCA<sub>A</sub>CTGAGGTAC



Reverse complement motif    Consensus sequence: GTACCTCAG<sub>A</sub>TGGAAATG



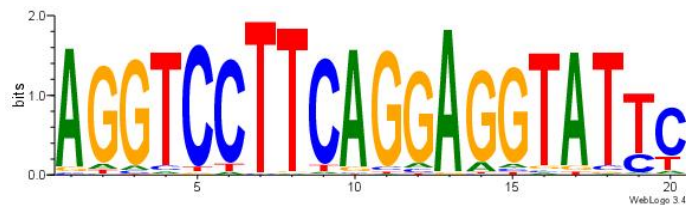
## Best Matches for Motif ID 25 (Highest to Lowest)

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

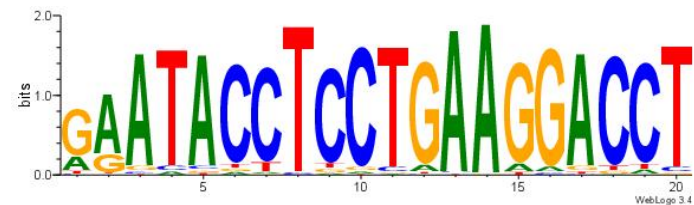
### Alignment:

```
GAATACCTCCTGAAGGACCT  
CATTTCACWCTGAGGTAC--
```

Original motif      Consensus sequence: AGGTCCTCAGGAGGTATTC



Reverse complement motif      Consensus sequence:  
GAATACCTCCTGAAGGACCT

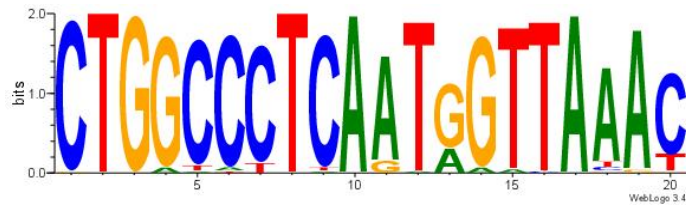


Dataset #: 1  
Motif ID: 332  
Motif name: Motif 332  
Matching format of first motif: Original Motif  
Matching format of second motif: Reverse Complement

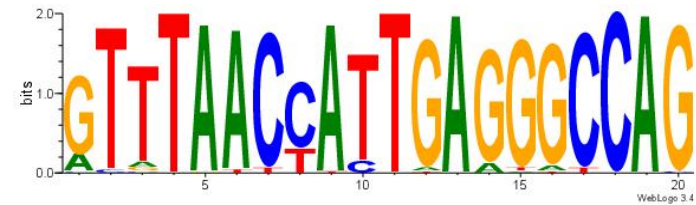
Direction: Forward  
 Position number: 1  
 Number of overlap: 18  
 Similarity score: 0.110707

Alignment:  
 GTTTAACCATTGAGGGCCAG  
 CATTTC CAWCTGAGGTAC--

Original motif      Consensus sequence: CTGGCCCTCAATGGTTAAAC

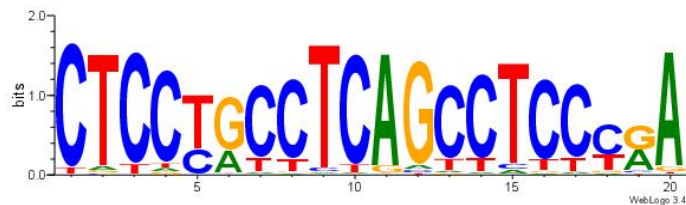


Reverse complement motif      Consensus sequence: GTTTAACCATTGAGGGCCAG

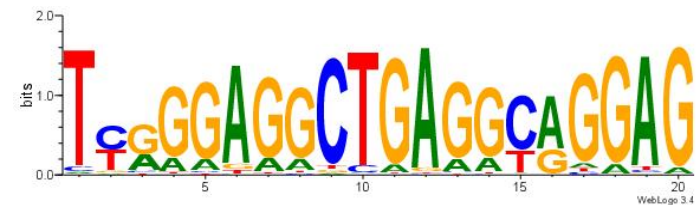


**Dataset #: 1      Motif ID: 26      Motif name: Motif 26**

Original motif      Consensus sequence: CTCCTGCCTCAGCCTCCRA



Reverse complement motif      Consensus sequence: TMGGGAGGCTGAGGCAGGAG



**Best Matches for Motif ID 26 (Highest to Lowest)**

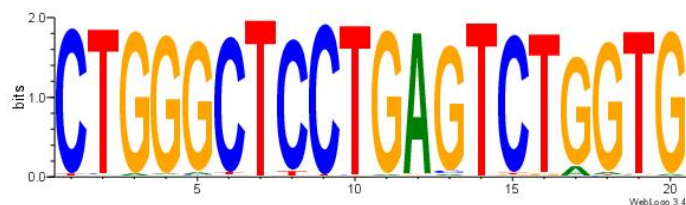
Dataset #: 1

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

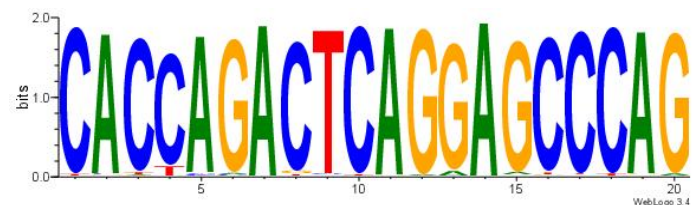
**Alignment:**

CACCAGACTCAGGAGCCCAG  
 CTCCTGCCTCAGCCTCCRA

Original motif    Consensus sequence: CTGGGCTCCTGAGTCTGGTG



Reverse complement motif    Consensus sequence: CACCAGACTCAGGAGCCCAG



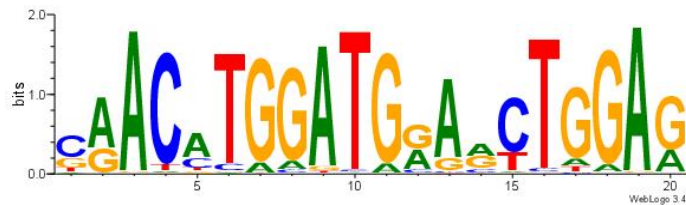
Dataset #: 1  
 Motif ID: 104  
 Motif name: Motif 104  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 20

Similarity score: 0.111358

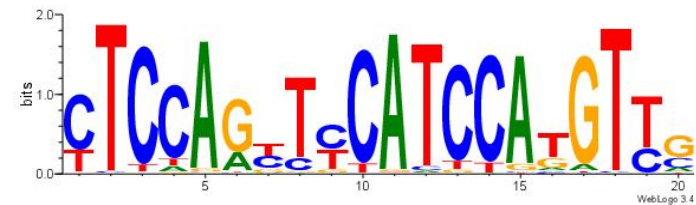
Alignment:

CAACATGGATGRARCTGGAG  
TMGGGAGGCTGAGGCAGGAG

Original motif Consensus sequence: CAACATGGATGRARCTGGAG

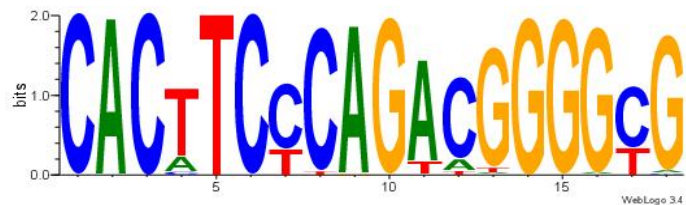


Reverse complement motif Consensus sequence: CTCCAGKTCATCCATGTTG

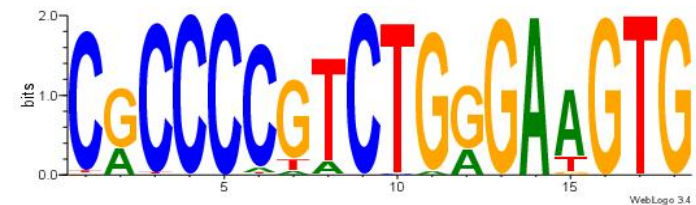


**Dataset #: 1 Motif ID: 27 Motif name: Motif 27**

Original motif Consensus sequence: CACTTCCCAGACGGGGCG



Reverse complement motif Consensus sequence: CGCCCCGTCTGGGAAGTG



**Best Matches for Motif ID 27 (Highest to Lowest)**

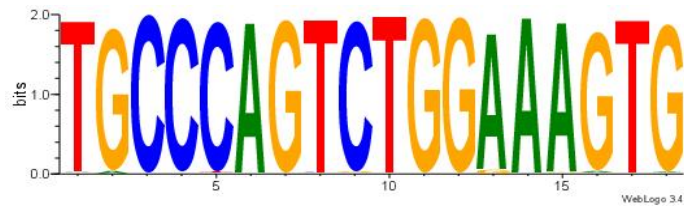
Dataset #: 1  
Motif ID: 45  
Motif name: Motif 45  
Matching format of first motif: Original Motif



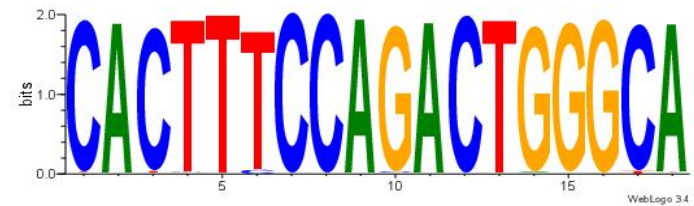
Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 18  
 Similarity score: 0.0413095

Alignment:  
 CACTTTCCAGACTGGGCA  
 CACTTCCCAGACGGGGCG

Original motif      Consensus sequence: TGCCCAGTCTGGAAAGTG



Reverse complement motif      Consensus sequence: CACTTTCCAGACTGGGCA

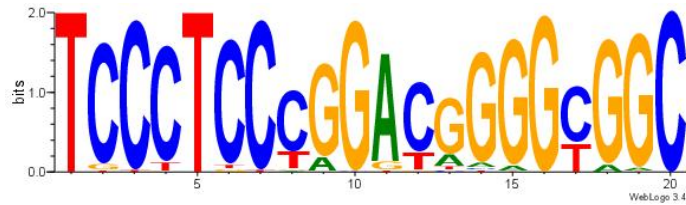


Dataset #: 1  
 Motif ID: 155  
 Motif name: Motif 155  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 3  
 Number of overlap: 18  
 Similarity score: 0.0525092

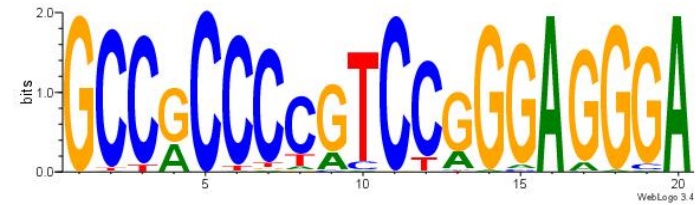
Alignment:

TCCCTCCCGGACGGGGYGGC  
 CACTTCCCAGACGGGGCG--

Original motif    Consensus sequence: TCCCTCCCGGACGGGGYGGC

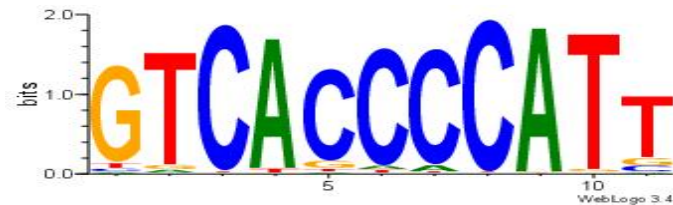


Reverse complement motif    Consensus sequence: GCCKCCCCGTCCGGGAGGGA

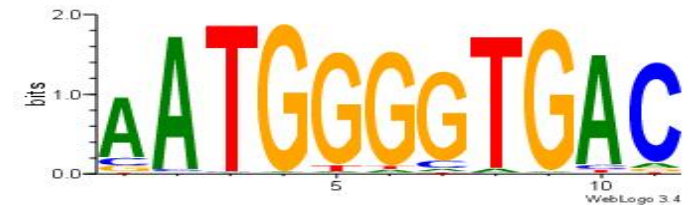


**Dataset #: 1      Motif ID: 28      Motif name: Motif 28**

Original motif    Consensus sequence: GTCACCCCAT



Reverse complement motif    Consensus sequence: AATGGGGTGAC



**Best Matches for Motif ID 28 (Highest to Lowest)**

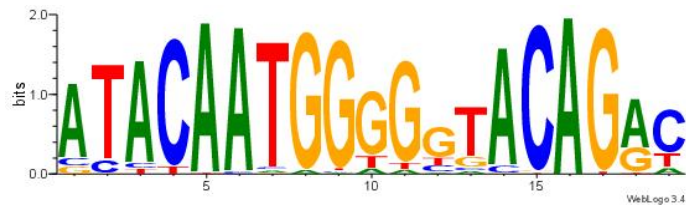
Dataset #:	1
Motif ID:	193
Motif name:	Motif 193
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	5
Number of overlap:	11

Similarity score: 0.0423623

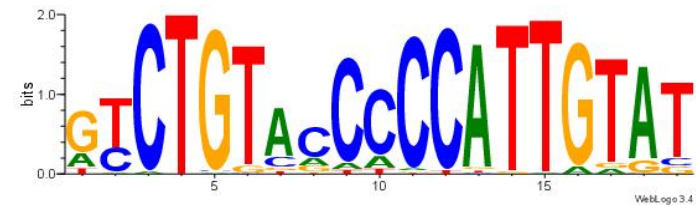
Alignment:

ATACAATGGGGGTACAGRC  
----AATGGGGTGAC----

Original motif      Consensus sequence: ATACAATGGGGGTACAGRC



Reverse complement motif      Consensus sequence:  
GKCTGTACCCCCATTGTAT



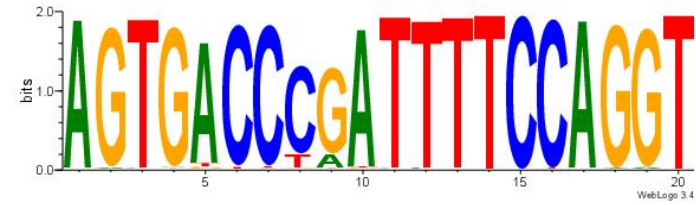
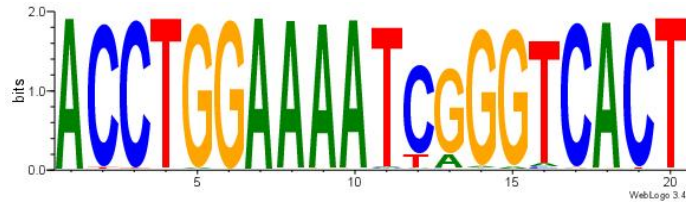
Dataset #: 1  
Motif ID: 14  
Motif name: Motif 14  
Matching format of first motif: Original Motif  
Matching format of second motif: Reverse Complement  
Direction: Backward  
Position number: 2  
Number of overlap: 11  
Similarity score: 0.0486677

Alignment:

AGTGACCCGATTTTCCAGGT  
-----GTCACCCCATT-

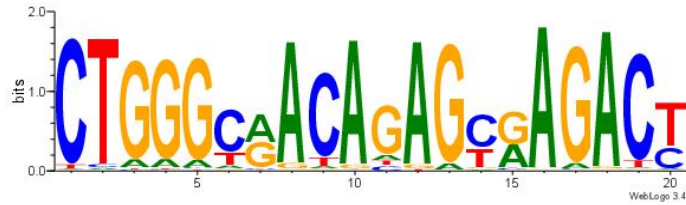
Original motif      Consensus sequence: ACCTGGAAAATCGGGTCACT

Reverse complement motif      Consensus sequence:  
AGTGACCCGATTTTCCAGGT

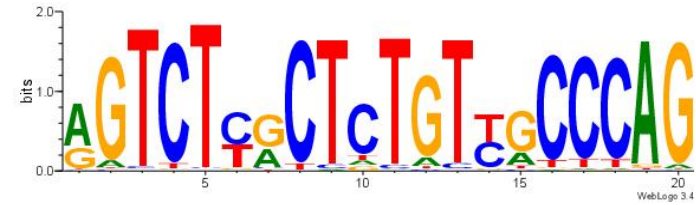


**Dataset #: 1      Motif ID: 29      Motif name: Motif 29**

Original motif      Consensus sequence: CTGGGCRACAGAGYRAGACY



Reverse complement motif      Consensus sequence: MGTCTMKCTCTGKGGCCAG



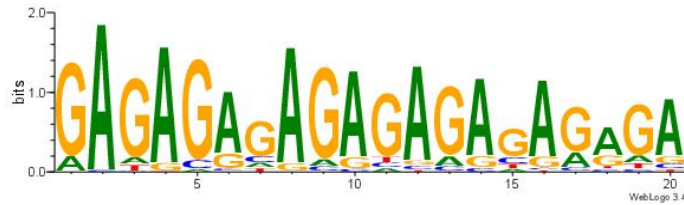
**Best Matches for Motif ID 29 (Highest to Lowest)**

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

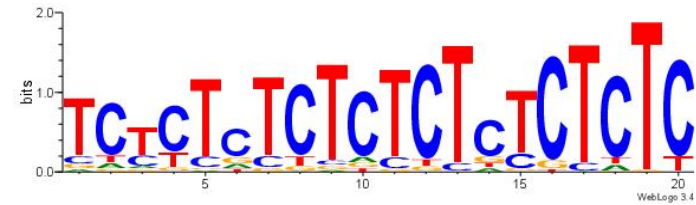
Alignment:

TCTCTCTCTCTCTCTCTCTC  
MGTCTMKCTCTGTKGCCAG

Original motif      Consensus sequence: GAGAGAGAGAGAGAGAGA



Reverse complement motif      Consensus sequence:  
TCTCTCTCTCTCTCTCTCTC

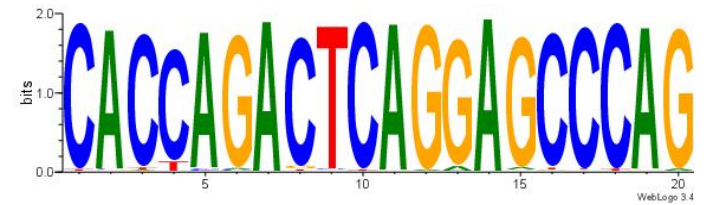
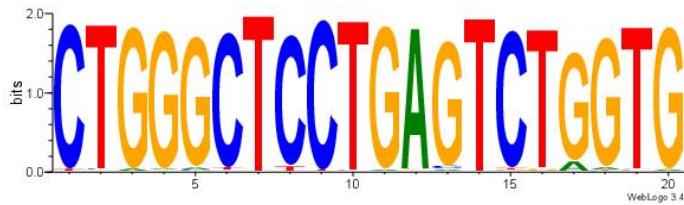


Dataset #: 1  
Motif ID: 67  
Motif name: Motif 67  
Matching format of first motif: Original Motif  
Matching format of second motif: Original Motif  
Direction: Forward  
Position number: 1  
Number of overlap: 20  
Similarity score: 0.100789

Alignment:  
CTGGGCTCCTGAGTCTGGTG  
CTGGGCRACAGAGYRAGACY

Original motif      Consensus sequence: CTGGGCTCCTGAGTCTGGTG

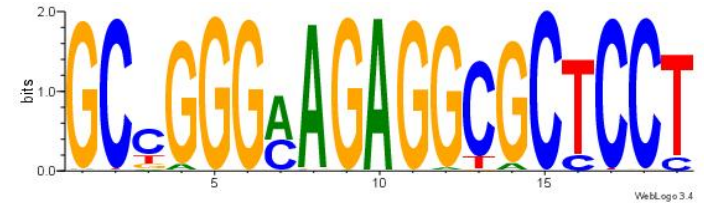
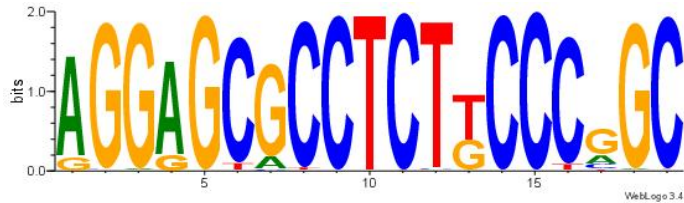
Reverse complement motif      Consensus sequence:  
CACCAGACTCAGGAGCCCAG



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

Original motif      Consensus sequence: AGGAGCGCTCTKCCCGGC

Reverse complement motif      Consensus sequence: GCCGGRAGAGGCGCTCCT



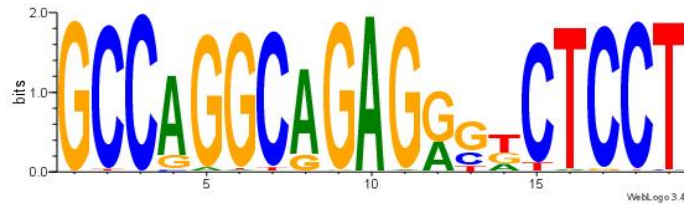
**Best Matches for Motif ID 30 (Highest to Lowest)**

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

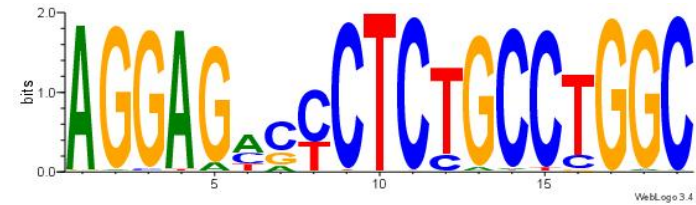
Alignment:

AGGAGRCMCTCTGCCTGGC  
AGGAGCGCCTCTKCCCGGC

Original motif      Consensus sequence: GCCAGGCAGAGRGKCTCCT



Reverse complement motif      Consensus sequence:  
AGGAGRCMCTCTGCCTGGC

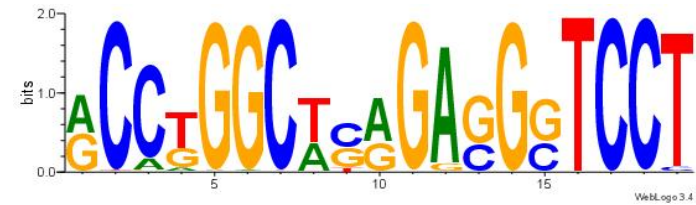
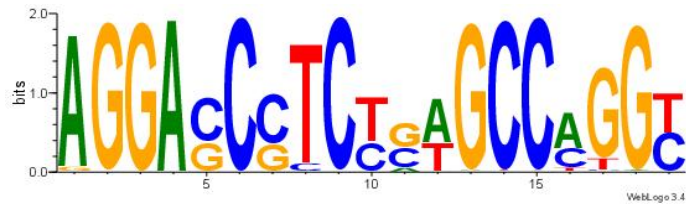


Dataset #: 1  
Motif ID: 10  
Motif name: Motif 10  
Matching format of first motif: Original Motif  
Matching format of second motif: Original Motif  
Direction: Forward  
Position number: 1  
Number of overlap: 19  
Similarity score: 0.0610031

Alignment:  
AGGASCSTCYSWGCCMGGY  
AGGAGCGCCTCTKCCCGGC

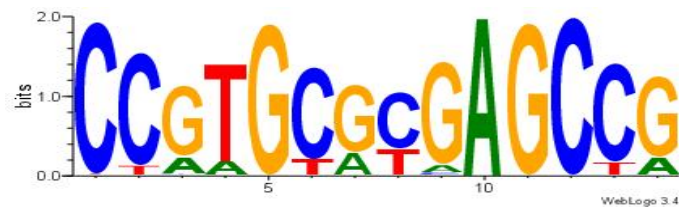
Original motif      Consensus sequence: AGGASCSTCYSWGCCMGGY

Reverse complement motif      Consensus sequence:  
MCCYGGCWSMGASGSTCCT

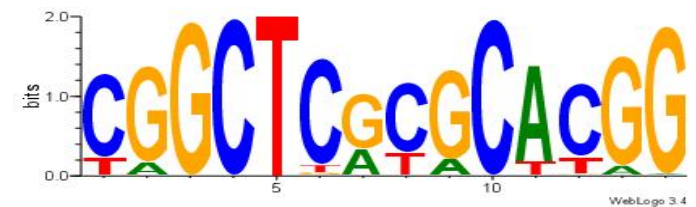


**Dataset #: 1      Motif ID: 31      Motif name: Motif 31**

Original motif      Consensus sequence: CCGTGC GCGAGCCG



Reverse complement motif      Consensus sequence: CGGCTCGCGCACCG



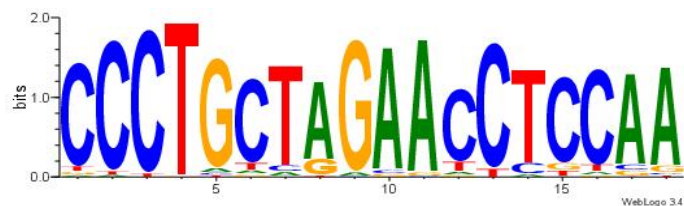
**Best Matches for Motif ID 31 (Highest to Lowest)**

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

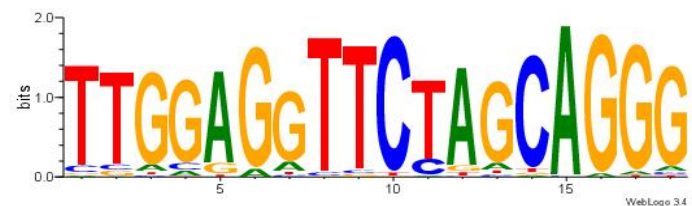
Alignment:  
 TTGGAGGTTCTAGCAGGG  
 ----CGGCTCGCGCACGG



Original motif      Consensus sequence: CCCTGCTAGAACCTCCAA



Reverse complement motif      Consensus sequence: TTGGAGTTCTAGCAGGG

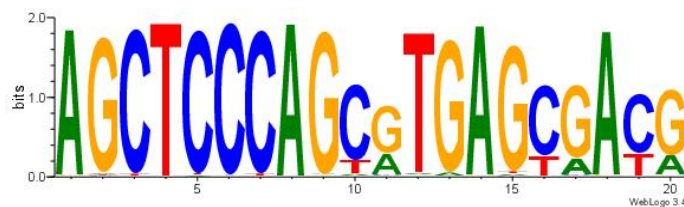


Dataset #: 1  
Motif ID: 48  
Motif name: Motif 48  
Matching format of first motif: Original Motif  
Matching format of second motif: Original Motif  
Direction: Backward  
Position number: 3  
Number of overlap: 14  
Similarity score: 0.0742371

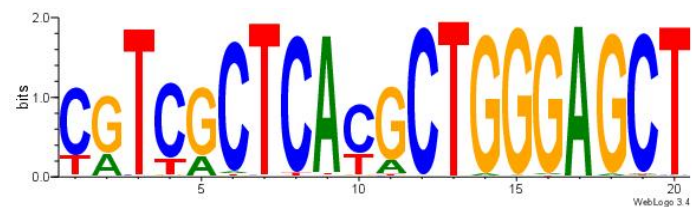
Alignment:

```
AGCTCCCAGCGTGAGCGACG  
----CCGTGCGCGAGCCG--
```

Original motif      Consensus sequence: AGCTCCCAGCGTGAGCGACG



Reverse complement motif      Consensus sequence: CGTCGCTCAGCTGGGAGCT

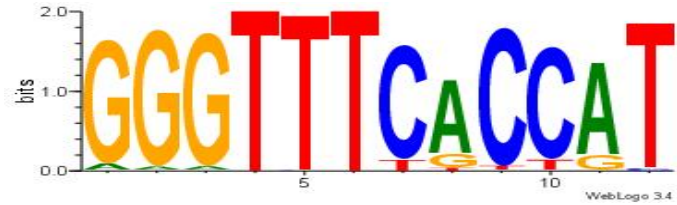


**Dataset #: 1      Motif ID: 32      Motif name: Motif 32**

Original motif      Consensus sequence: ATGGTGAAACCC



Reverse complement motif      Consensus sequence: GGGTTTCACCAT



**Best Matches for Motif ID 32 (Highest to Lowest)**

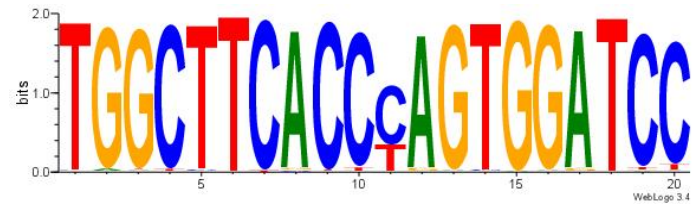
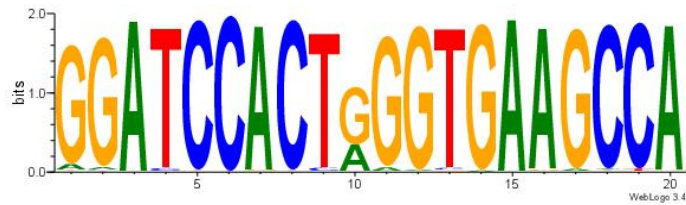
Dataset #:	1
Motif ID:	61
Motif name:	Motif 61
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	9
Number of overlap:	12
Similarity score:	0.0712132

**Alignment:**

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

Original motif      Consensus sequence: GGATCCACTGGGTGAAGCCA

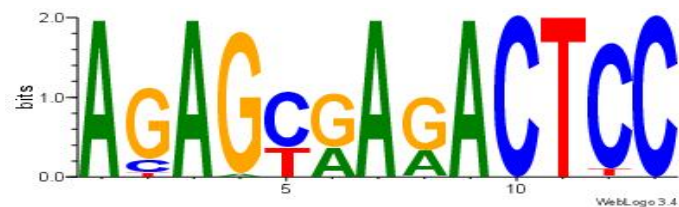
Reverse complement motif      Consensus sequence:  
TGGCTTCACCCAGTGGATCC



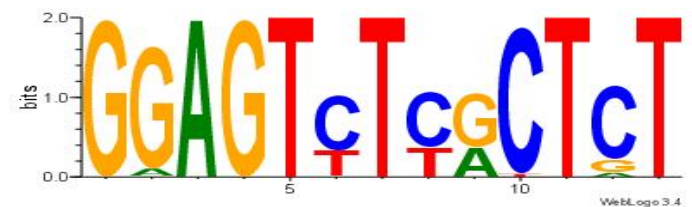
Dataset #: 1  
 Motif ID: 204  
 Motif name: Motif 204  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 2  
 Number of overlap: 12  
 Similarity score: 0.0785008

Alignment:  
 AGAGYRAGACTCC  
 ATGGTGAAACCC-

Original motif      Consensus sequence: AGAGYRAGACTCC

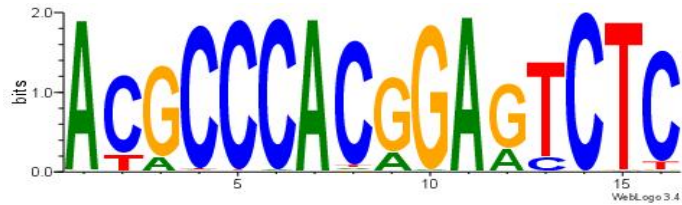


Reverse complement motif      Consensus sequence: GGAGTCTMKCTCT

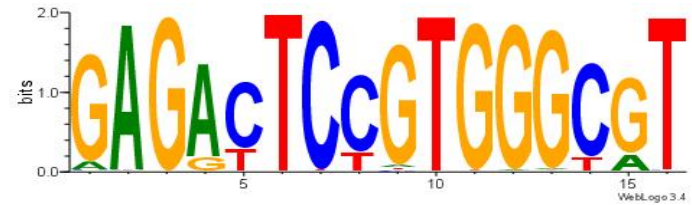


**Dataset #: 1      Motif ID: 33      Motif name: Motif 33**

Original motif    Consensus sequence: ACGCCACGGAGTCTC



Reverse complement motif    Consensus sequence: GAGACTCCGTGGGCGT



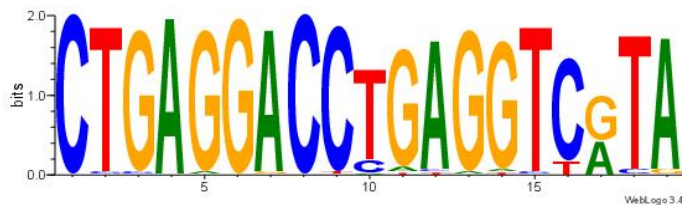
### Best Matches for Motif ID 33 (Highest to Lowest)

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

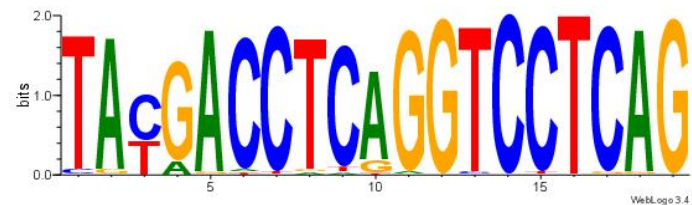
#### Alignment:

```
CTGAGGACCTGAGGTCRTA  
--GAGACTCCGTGGGCGT--
```

Original motif    Consensus sequence: CTGAGGACCTGAGGTCRTA



Reverse complement motif    Consensus sequence: TAMGACCTCAGGTCCTCAG

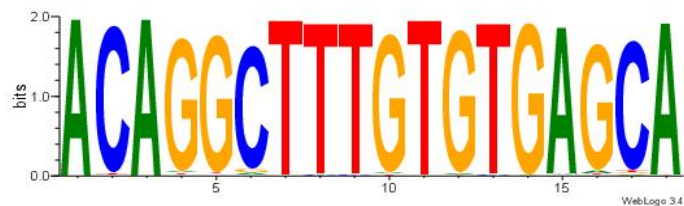


Dataset #: 1  
 Motif ID: 159  
 Motif name: Motif 159  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 2  
 Number of overlap: 16  
 Similarity score: 0.100481

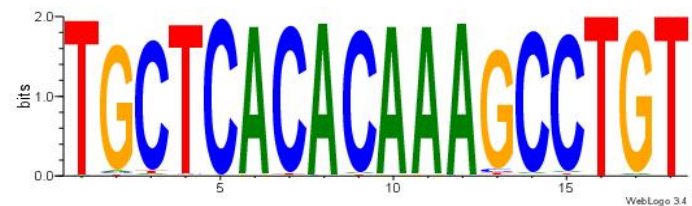
Alignment:

TGCTCACACAAAGCCTGT  
 -ACGCCACGGAGTCTC-

Original motif    Consensus sequence: ACAGGCTTTGTGTGAGCA



Reverse complement motif    Consensus sequence: TGCTCACACAAAGCCTGT



**Dataset #: 1      Motif ID: 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)**

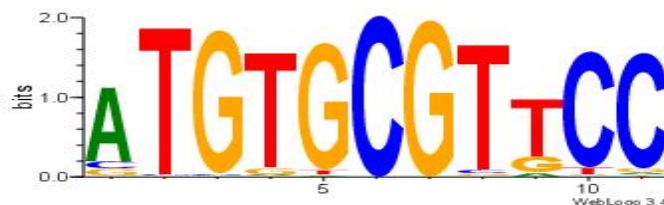
Dataset #: 1  
 Motif ID: 314  
 Motif name: Motif 314  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 2  
 Number of overlap: 9  
 Similarity score: 0.0220227

Alignment:  
 ATGTGCGTTCC  
 -TGTGCGTCC-

Original motif      Consensus sequence: GGAACGCACAT



Reverse complement motif      Consensus sequence: ATGTGCGTTCC



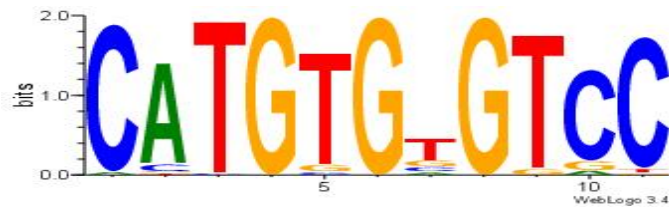
Dataset #: 1

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

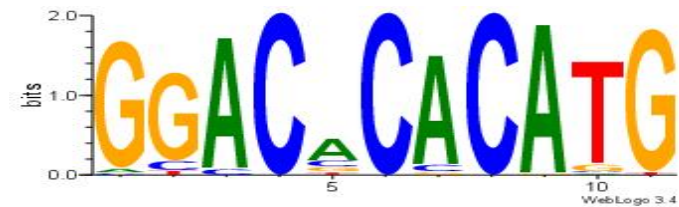
Alignment:

GGACACACATG  
 GGACGCACA--

Original motif      Consensus sequence: CATGTGTGCC

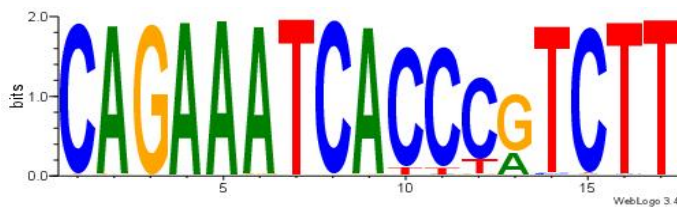


Reverse complement motif      Consensus sequence: GGACACACATG

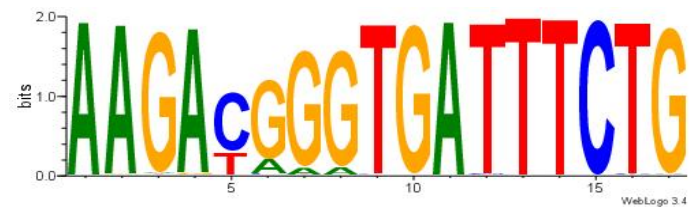


**Dataset #: 1      Motif ID: 35      Motif name: Motif 35**

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

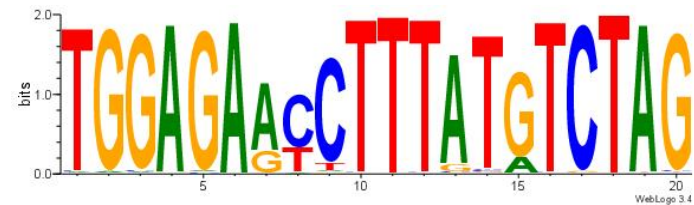
### Alignment:

```
TGGAGAACCTTTATGTCTAG  
--AAGACGGGTGATTTCTG-
```

Original motif      Consensus sequence: CTAGACATAAAGTTCTCCA



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

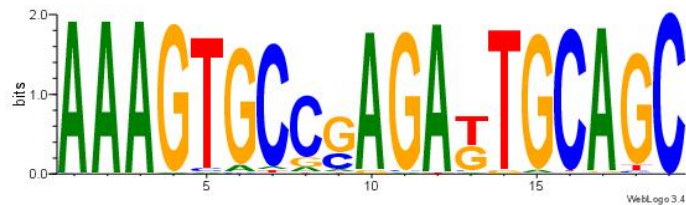


Direction: Backward  
 Position number: 2  
 Number of overlap: 17  
 Similarity score: 0.109156

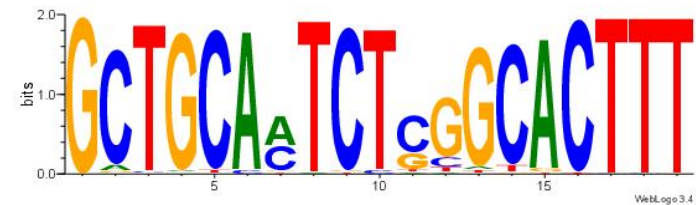
**Alignment:**

GCTGCARTCTCGGCACTTT  
 -CAGAAATCACCCGTCTT-

Original motif      Consensus sequence: AAAGTGCCGAGAKTGCAGC

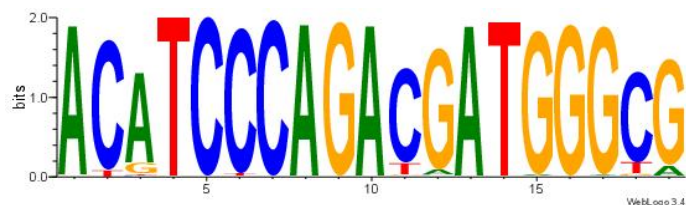


Reverse complement motif      Consensus sequence: GCTGCARTCTCGGCACTTT

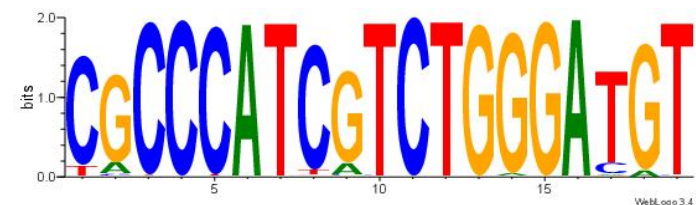


**Dataset #: 1      Motif ID: 36      Motif name: Motif 36**

Original motif      Consensus sequence: ACATCCCAGACGATGGGCG



Reverse complement motif      Consensus sequence: CGCCATCGTCTGGGATGT



**Best Matches for Motif ID 36 (Highest to Lowest)**

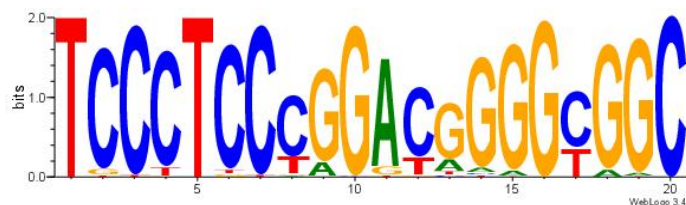
Dataset #: 1

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

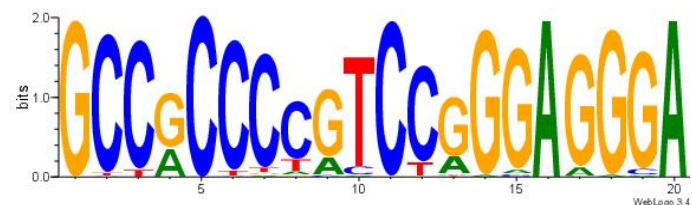
**Alignment:**

GCCKCCCCGTCCGGGAGGGA  
 CGCCCATCGTCTGGGATGT-

Original motif    Consensus sequence: TCCCTCCCGACGGGGYGGC



Reverse complement motif    Consensus sequence: GCCKCCCCGTCCGGGAGGGA



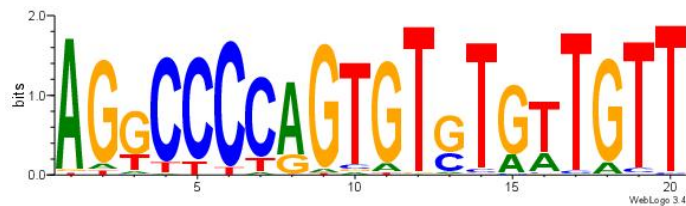
Dataset #: 1  
 Motif ID: 176  
 Motif name: Motif 176  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 19

Similarity score: 0.105478

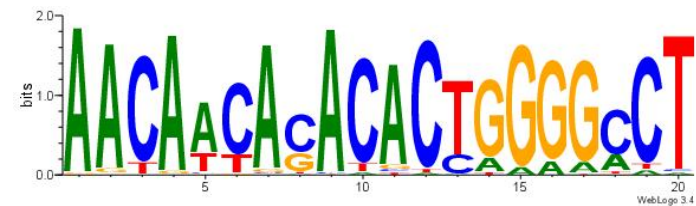
Alignment:

AACAACASACTGGGGCCT  
-ACATCCCAGACGATGGGCG

Original motif    Consensus sequence: AGGCCCCAGTGTSTGTTGTT

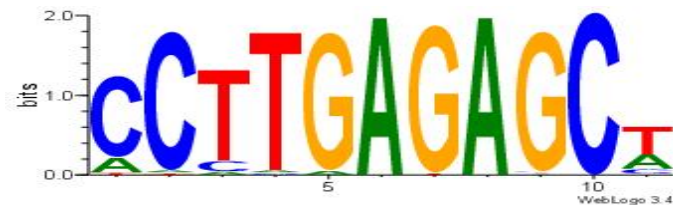


Reverse complement motif    Consensus sequence: AACAACASACTGGGGCCT

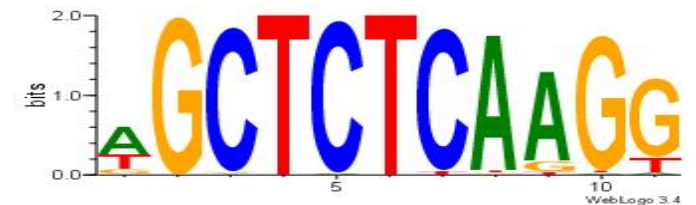


**Dataset #: 1      Motif ID: 37      Motif name: Motif 37**

Original motif    Consensus sequence: CCTTGAGAGCW



Reverse complement motif    Consensus sequence: WGCTCTCAAGG



**Best Matches for Motif ID 37 (Highest to Lowest)**

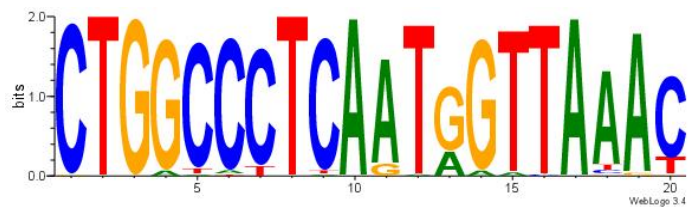
Dataset #:	1
Motif ID:	332
Motif name:	Motif 332
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement

Direction: Backward  
 Position number: 3  
 Number of overlap: 11  
 Similarity score: 0.0617144

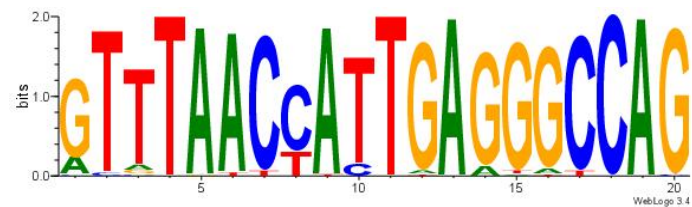
**Alignment:**

GTTTAACCATTGAGGGCCAG  
 -----CCTTGAGAGCW--

Original motif    Consensus sequence: CTGGCCCTCAATGGTTAAAC



Reverse complement motif    Consensus sequence: GTTTAACCATTGAGGGCCAG

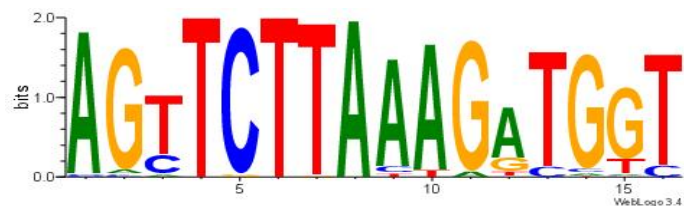


Dataset #: 1  
 Motif ID: 303  
 Motif name: Motif 303  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 11  
 Similarity score: 0.0637615

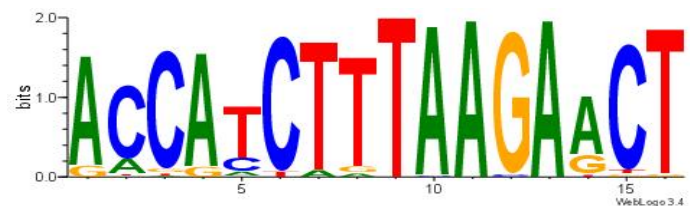
**Alignment:**

AGTTCTTAAAGATGGT  
 WGCTCTCAAGG-----

Original motif      Consensus sequence: AGTTCTTAAAGATGGT



Reverse complement motif      Consensus sequence: ACCATCTTTAAGAACT

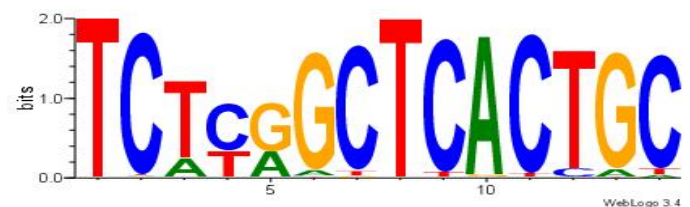


**Dataset #: 1      Motif ID: 38      Motif name: Motif 38**

Original motif      Consensus sequence: GCAGTGAGCCGAGA



Reverse complement motif      Consensus sequence: TCTMKGCTCACTGC



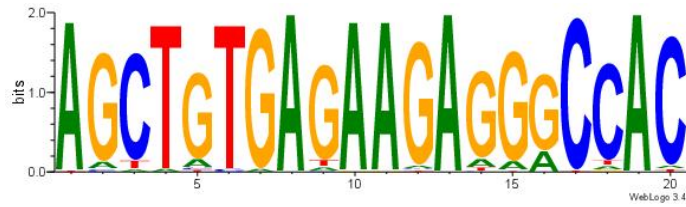
### Best Matches for Motif ID 38 (Highest to Lowest)

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

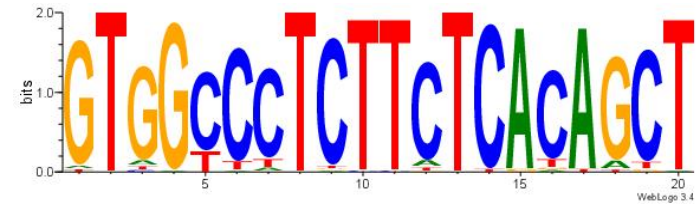
Alignment:

GTGGCCCTCTTCTCACAGCT  
 -----TCTMKGCTCACTGC-

Original motif      Consensus sequence: AGCTGTGAGAAGAGGGCCAC



Reverse complement motif      Consensus sequence:  
 GTGGCCCTCTTCTCACAGCT

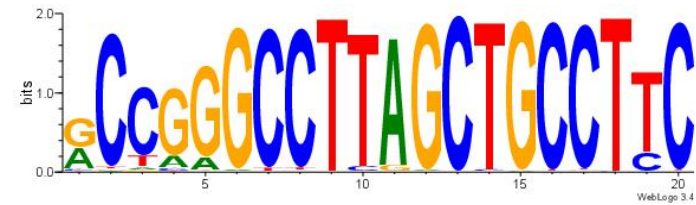
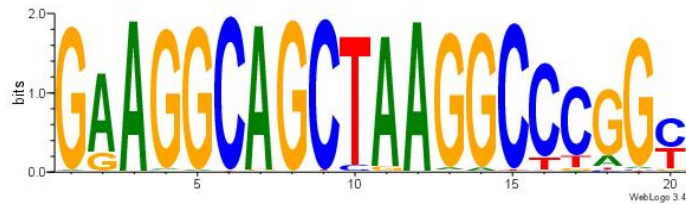


Dataset #:	1
Motif ID:	64
Motif name:	Motif 64
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	7
Number of overlap:	14
Similarity score:	0.0904176

Alignment:  
 GAAGGCAGCTAAGGCCCGGY  
 GCAGTGAGCYRAGA-----

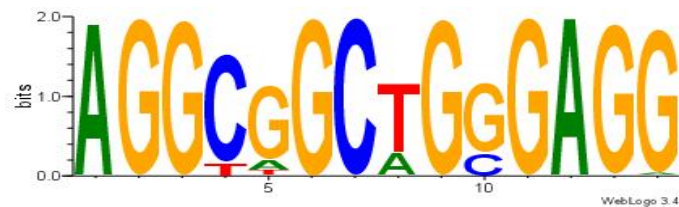
Original motif      Consensus sequence: GAAGGCAGCTAAGGCCCGGY

Reverse complement motif      Consensus sequence:  
 KCCGGGCCTTAGCTGCCTTC



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

Original motif      Consensus sequence: AGGCGGCTGGGAGG



Reverse complement motif      Consensus sequence: CCTCCAGCCGCTT

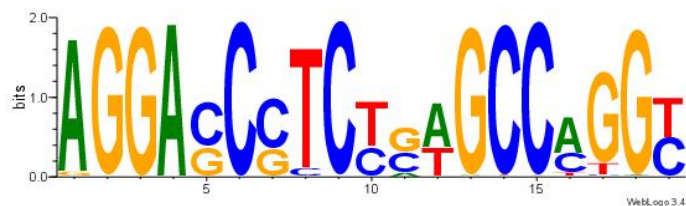


**Best Matches for Motif ID 39 (Highest to Lowest)**

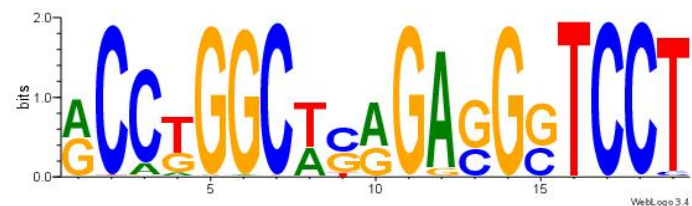
Dataset #:	1
Motif ID:	10
Motif name:	Motif 10
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	14
Similarity score:	0.0839569

Alignment:  
 AGGASCSTCYSWGCCMGY  
 CCTCCAGCCGCT-----

Original motif      Consensus sequence: AGGASCSTCYSWGCCMGGY



Reverse complement motif      Consensus sequence: MCCYGGCWSMGASGSTCCT

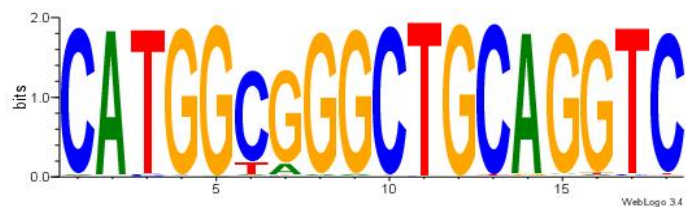


Dataset #: 1  
Motif ID: 68  
Motif name: Motif 68  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Reverse Complement  
Direction: Forward  
Position number: 3  
Number of overlap: 14  
Similarity score: 0.0883656

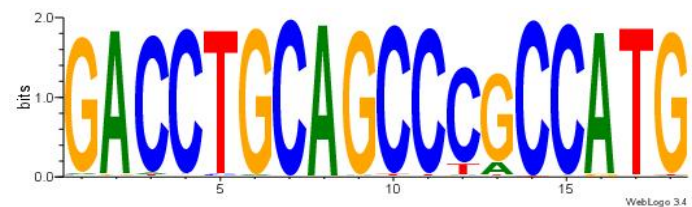
Alignment:

GACCTGCAGCCCGCCATG  
--CCTCCCAGCCGCCT--

Original motif      Consensus sequence: CATGGCGGGCTGCAGGTC



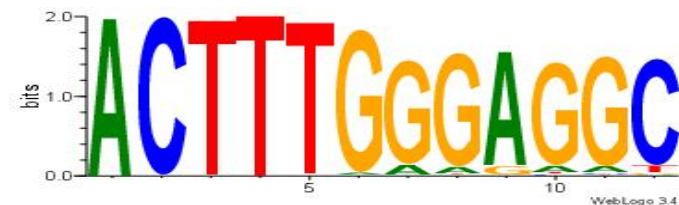
Reverse complement motif      Consensus sequence: GACCTGCAGCCCGCCATG



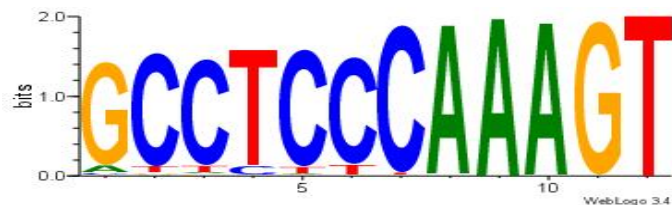


**Dataset #: 1      Motif ID: 40      Motif name: Motif 40**

Original motif      Consensus sequence: ACTTTGGGAGGC



Reverse complement motif      Consensus sequence: GCCTCCCAAAGT



**Best Matches for Motif ID 40 (Highest to Lowest)**

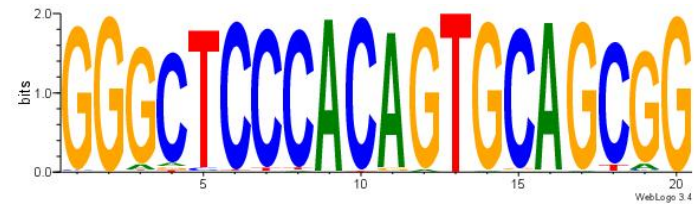
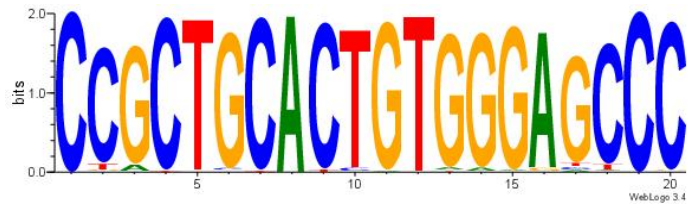
Dataset #:	1
Motif ID:	144
Motif name:	Motif 144
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	2
Number of overlap:	12
Similarity score:	0.0448889

**Alignment:**

```
GGGCTCCACAGTGCAGCGG
-GCCTCCCAAAGT-----
```

Original motif      Consensus sequence: CCGTGCAGTGGGAGCCC

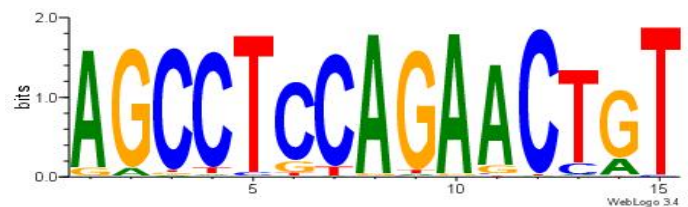
Reverse complement motif      Consensus sequence:  
GGGCTCCACAGTGCAGCGG



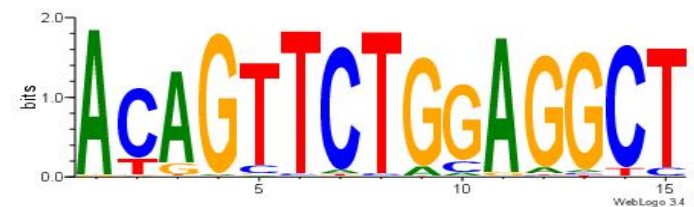
Dataset #: 1  
 Motif ID: 239  
 Motif name: Motif 239  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 3  
 Number of overlap: 12  
 Similarity score: 0.0724344

Alignment:  
 ACAGTTCTGGAGGCT  
 --ACTTTGGGAGGC--

Original motif    Consensus sequence: AGCCTCCAGAACTGT

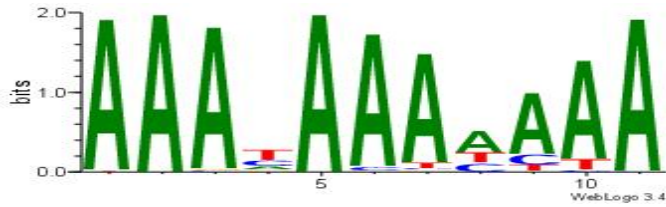


Reverse complement motif    Consensus sequence: ACAGTTCTGGAGGCT

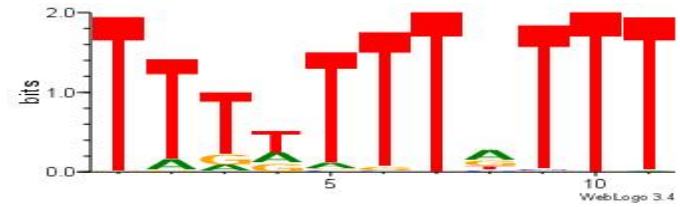


**Dataset #: 1      Motif ID: 41      Motif name: Motif 41**

Original motif      Consensus sequence: AAAYAAAAAA



Reverse complement motif      Consensus sequence: TTTTTTMTTT



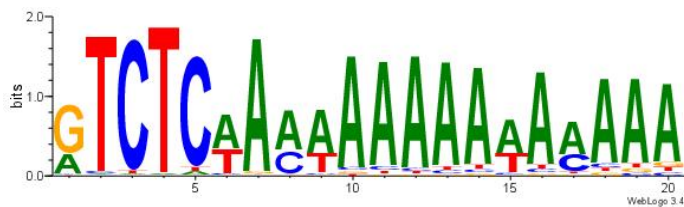
**Best Matches for Motif ID 41 (Highest to Lowest)**

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

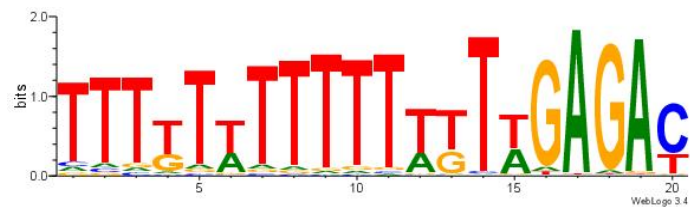
Alignment:

```
GTCTCWAMAAAAAWAMAAA
-----AAAYAAAAAA
```

Original motif      Consensus sequence: GTCTCWAMAAAAAWAMAAA



Reverse complement motif      Consensus sequence: TTTYTWTTTTTYTWGAGAC

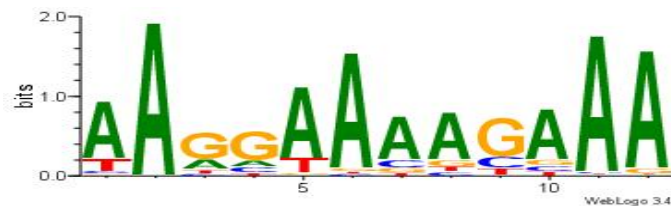


Dataset #: 1  
 Motif ID: 54  
 Motif name: Motif 54  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 11  
 Similarity score: 0.0476983

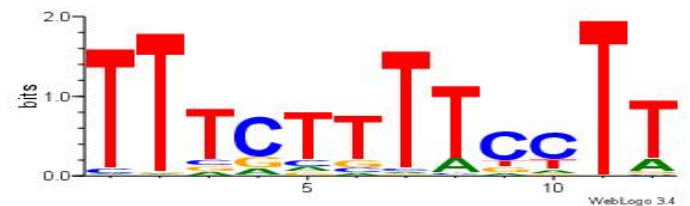
Alignment:

TTTCTTTTCCTT  
 -TTTTTTTMTTT

Original motif      Consensus sequence: AAGGAAAAGAAA

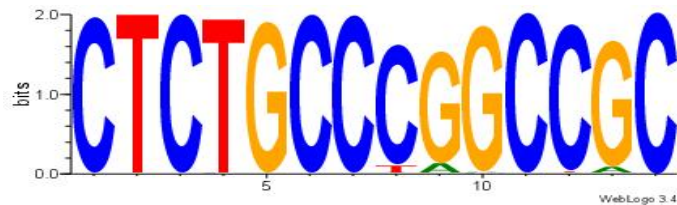


Reverse complement motif      Consensus sequence: TTTCTTTTCCTT

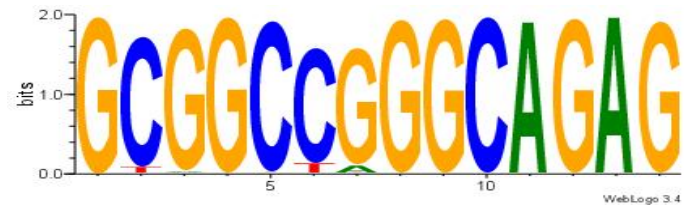


**Dataset #: 1      Motif ID: 42      Motif name: Motif 42**

Original motif      Consensus sequence: CTCTGCCCGGCCGC



Reverse complement motif      Consensus sequence: GCGGCCGGGCAGAG



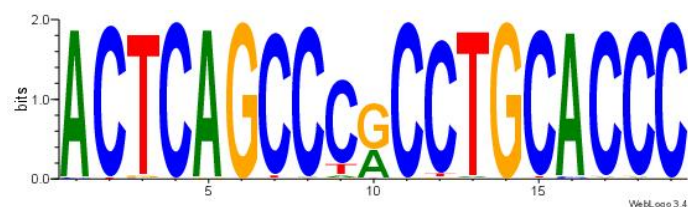
## Best Matches for Motif ID 42 (Highest to Lowest)

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

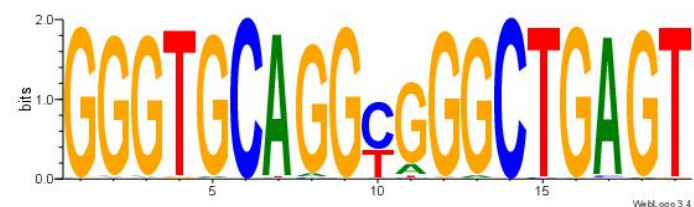
### Alignment:

```
GGGTGCAGGMGGGCTGAGT  
----GCGGCCGGGCAGAG--
```

Original motif      Consensus sequence: ACTCAGCCRCCTGCACCC



Reverse complement motif      Consensus sequence:  
GGGTGCAGGMGGGCTGAGT



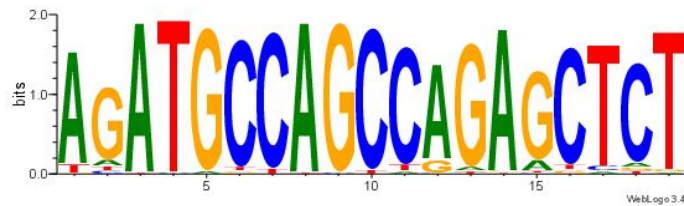
---

Dataset #: 1  
Motif ID: 307  
Motif name: Motif 307  
Matching format of first motif: Original Motif  
Matching format of second motif: Reverse Complement

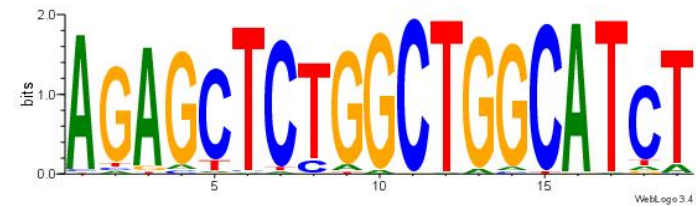
Direction: Backward  
 Position number: 2  
 Number of overlap: 14  
 Similarity score: 0.0775689

Alignment:  
 AGAGCTCTGGCTGGCATCT  
 ----CTCTGCCCCGCCGC--

Original motif      Consensus sequence: AGATGCCAGCCAGAGCTCT

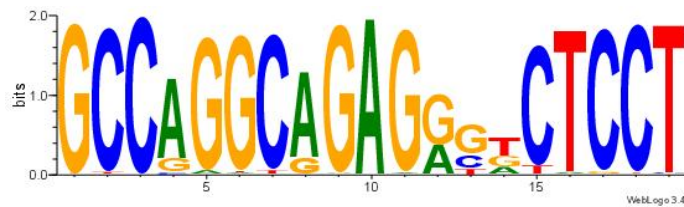


Reverse complement motif      Consensus sequence:  
 AGAGCTCTGGCTGGCATCT

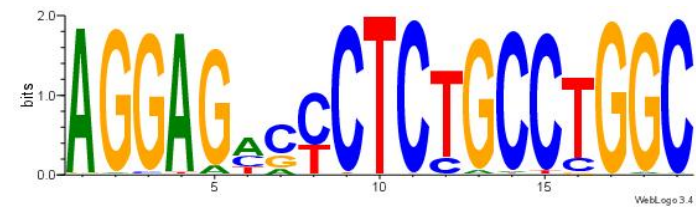


**Dataset #: 1      Motif ID: 43      Motif name: Motif 43**

Original motif      Consensus sequence: GCCAGGCAGAGRGKCTCCT



Reverse complement motif      Consensus sequence:  
 AGGAGRCMCTCTGCCTGGC



**Best Matches for Motif ID 43 (Highest to Lowest)**

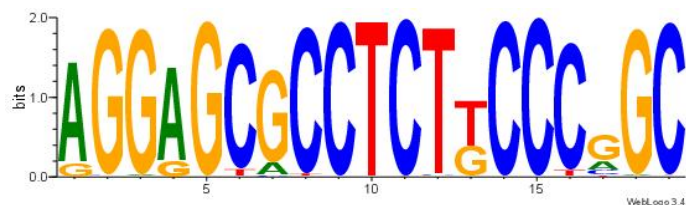
Dataset #: 1

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

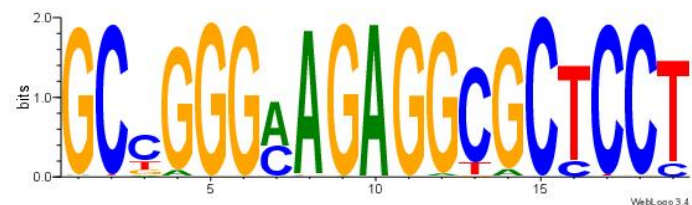
**Alignment:**

GCCGGGRAGAGGCGCTCCT  
 GCCAGGCAGAGRKCTCCT

Original motif    Consensus sequence: AGGAGCGCCTCTKCCCGGC



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

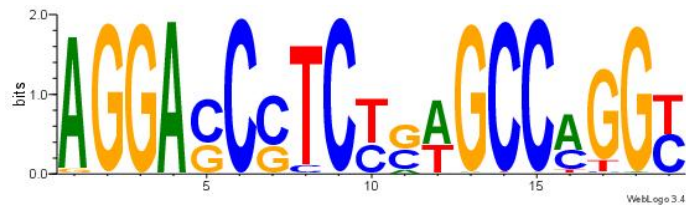
Similarity score: 0.0674635

Alignment:

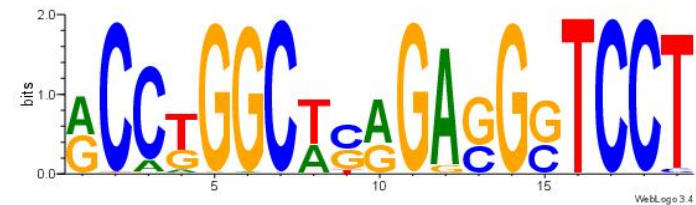
AGGASCSTCYSWGCCMGY

AGGAGRCMCTCTGCCTGGC

Original motif Consensus sequence: AGGASCSTCYSWGCCMGY

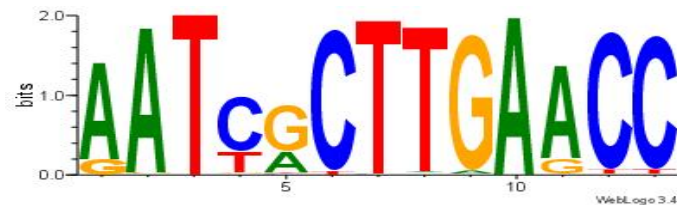


Reverse complement motif Consensus sequence: MCCYGGCWSMGASGSTCCT



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

Original motif Consensus sequence: AATCGCTTGAACC



Reverse complement motif Consensus sequence: GGTTC AAGCGATT



### Best Matches for Motif ID 44 (Highest to Lowest)

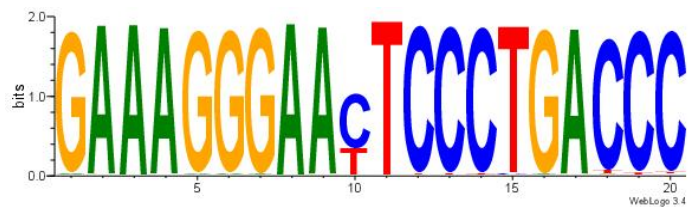
Dataset #:	1
Motif ID:	16
Motif name:	Motif 16
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif



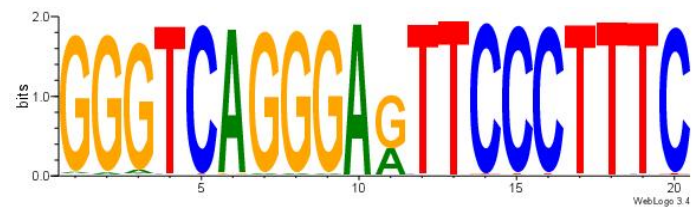
Direction: Backward  
 Position number: 1  
 Number of overlap: 13  
 Similarity score: 0.0728317

Alignment:  
 GAAAGGGA ACTCCCTGACCC  
 -----AATCGCTTGAACC

Original motif Consensus sequence: GAAAGGGA ACTCCCTGACCC



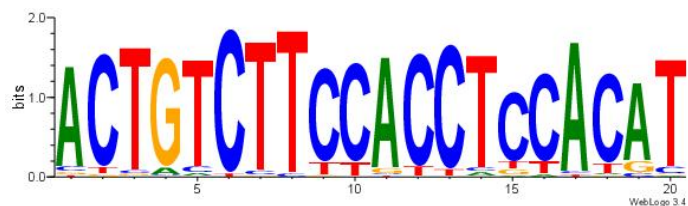
Reverse complement motif Consensus sequence: GGGTCAGGGA GTTCCCTTTC



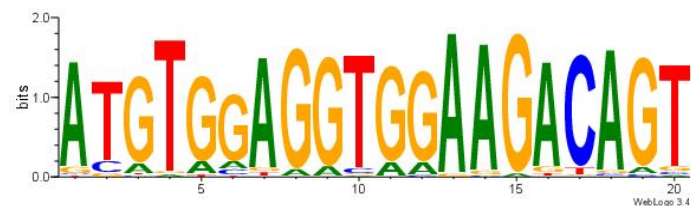
Dataset #: 1  
 Motif ID: 178  
 Motif name: Motif 178  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 8  
 Number of overlap: 13  
 Similarity score: 0.0766097

Alignment:  
 ATGTGGAGGTGGAAGACAGT  
 -----GGTTCAAGCGATT

Original motif      Consensus sequence: ACTGTCTTCCACCTCCACAT

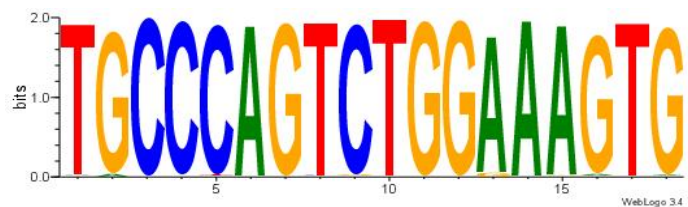


Reverse complement motif      Consensus sequence: ATGTGGAGGTGGAAGACAGT

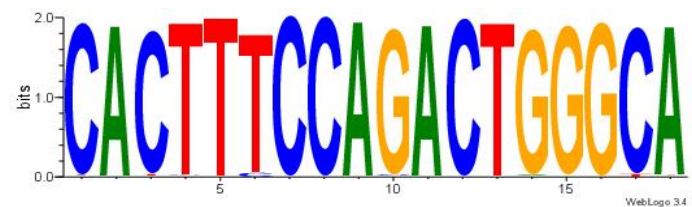


**Dataset #: 1      Motif ID: 45      Motif name: Motif 45**

Original motif      Consensus sequence: TGCCCAGTCTGGAAAGTG



Reverse complement motif      Consensus sequence: CACTTTCAGACTGGGCA



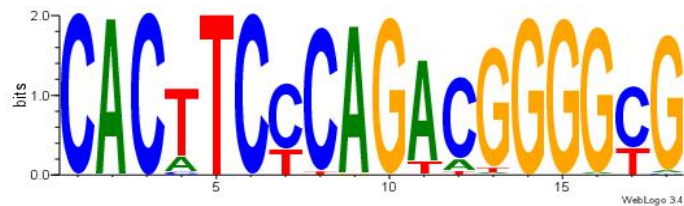
### Best Matches for Motif ID 45 (Highest to Lowest)

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

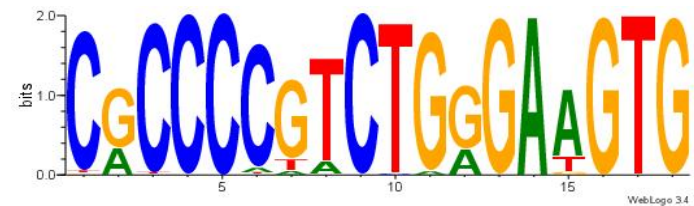
Alignment:

CGCCCCGTCTGGGAAGTG  
TGCCCAGTCTGGAAAGTG

Original motif      Consensus sequence: CACTTCCCAGACGGGGCG



Reverse complement motif      Consensus sequence:  
CGCCCCGTCTGGGAAGTG



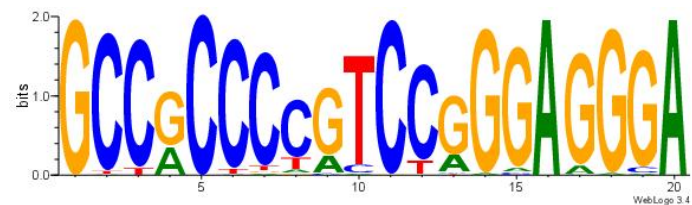
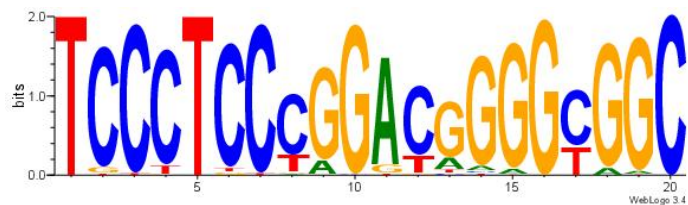
Dataset #: 1  
Motif ID: 155  
Motif name: Motif 155  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Original Motif  
Direction: Forward  
Position number: 1  
Number of overlap: 18  
Similarity score: 0.104002

Alignment:

TCCCTCCCGGACGGGGYGGC  
CACTTCCAGACTGGGCA--

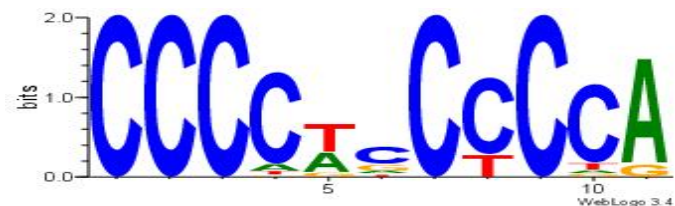
Original motif      Consensus sequence: TCCCTCCCGGACGGGGYGGC

Reverse complement motif      Consensus sequence:  
GCCKCCCCGTCCGGGAGGGA



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

Original motif      Consensus sequence: CCCCWCCCCCA



Reverse complement motif      Consensus sequence: TGGGGWGGGG

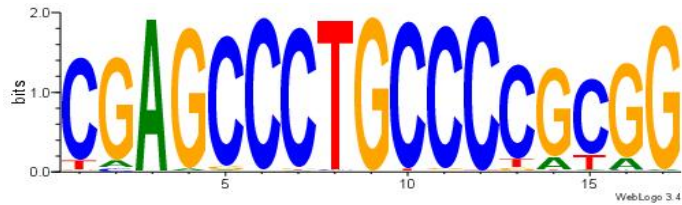


**Best Matches for Motif ID 46 (Highest to Lowest)**

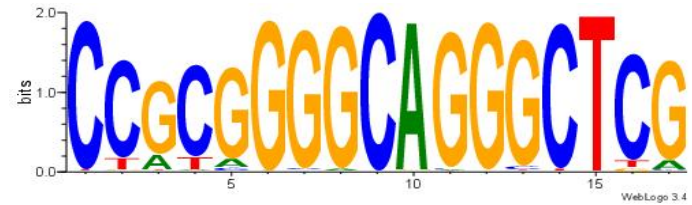
Dataset #:	1
Motif ID:	78
Motif name:	Motif 78
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	4
Number of overlap:	11
Similarity score:	0.0694266

Alignment:  
CGAGCCCTGCCCGCGG  
---CCCWCCCCCA---

Original motif      Consensus sequence: CGAGCCCTGCCCGCGG



Reverse complement motif      Consensus sequence: CCGCGGGGCAGGGCTCG

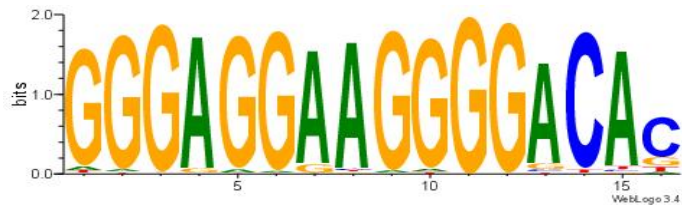


Dataset #: 1  
 Motif ID: 221  
 Motif name: Motif 221  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 5  
 Number of overlap: 11  
 Similarity score: 0.0733808

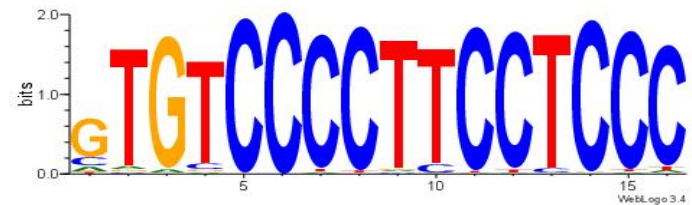
Alignment:

GGGAGGAAGGGGACAC  
 -TGGGGWGGG-----

Original motif      Consensus sequence: GGGAGGAAGGGGACAC

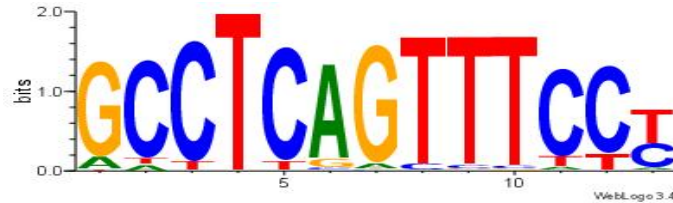


Reverse complement motif      Consensus sequence: GTGCCCCTTCTCCC

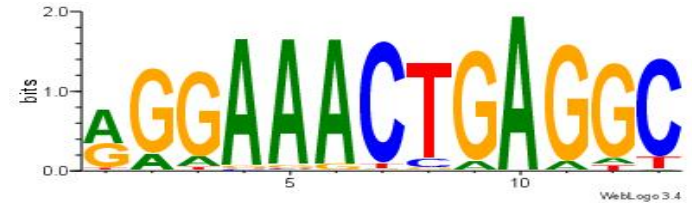


**Dataset #: 1      Motif ID: 47      Motif name: Motif 47**

Original motif      Consensus sequence: GCCTCAGTTTCCY



Reverse complement motif      Consensus sequence: MGGAACTGAGGC



**Best Matches for Motif ID 47 (Highest to Lowest)**

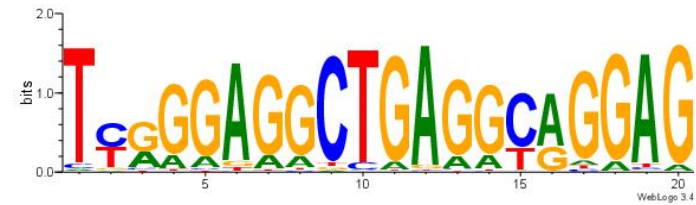
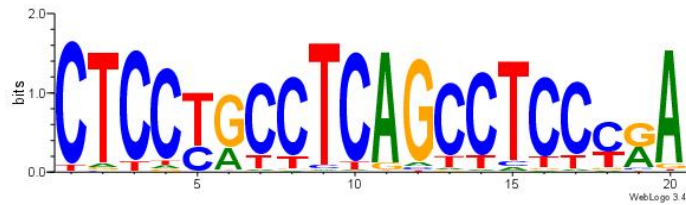
Dataset #:	1
Motif ID:	26
Motif name:	Motif 26
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	6
Number of overlap:	13
Similarity score:	0.0351242

**Alignment:**

```
CTCCTGCCTCAGCCTCCCRA  
-----GCCTCAGTTTCCY--
```

Original motif      Consensus sequence: CTCCTGCCTCAGCCTCCCRA

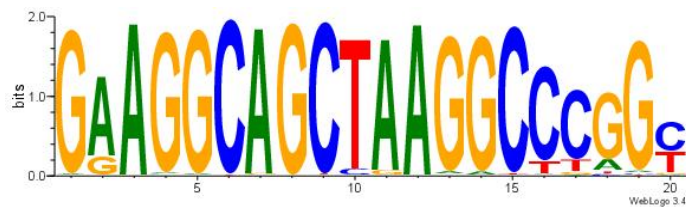
Reverse complement motif      Consensus sequence: TMGGGAGGCTGAGGCAGGAG



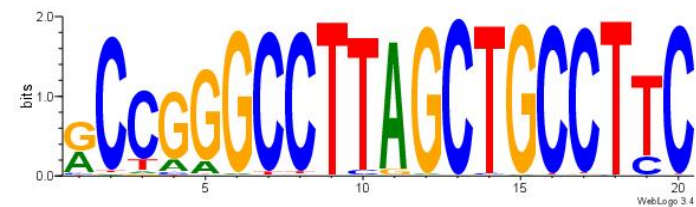
Dataset #: 1  
 Motif ID: 64  
 Motif name: Motif 64  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 6  
 Number of overlap: 13  
 Similarity score: 0.0624672

Alignment:  
 KCCGGGCCTTAGCTGCCTTC  
 -----GCCTCAGTTTCCY--

Original motif      Consensus sequence: GAAGGCAGCTAAGGCCCGG

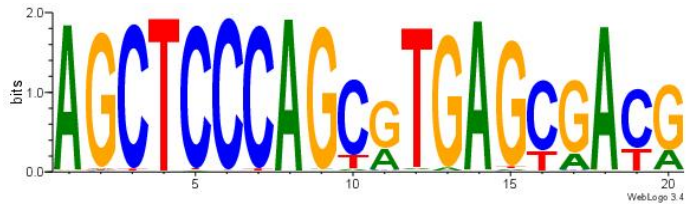


Reverse complement motif      Consensus sequence: KCCGGGCCTTAGCTGCCTTC

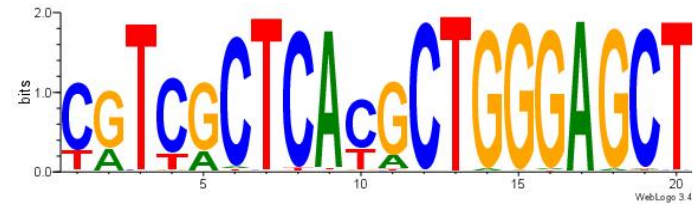


**Dataset #: 1      Motif ID: 48      Motif name: Motif 48**

Original motif      Consensus sequence: AGCTCCCAGCGTGAGCGACG



Reverse complement motif      Consensus sequence: CGTCGCTCACGCTGGGAGCT



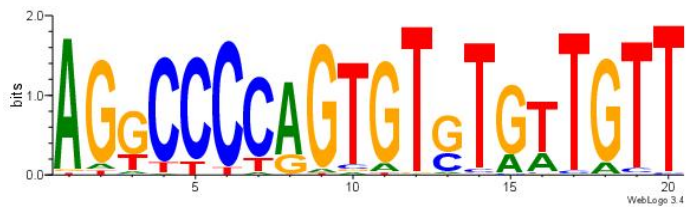
### Best Matches for Motif ID 48 (Highest to Lowest)

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

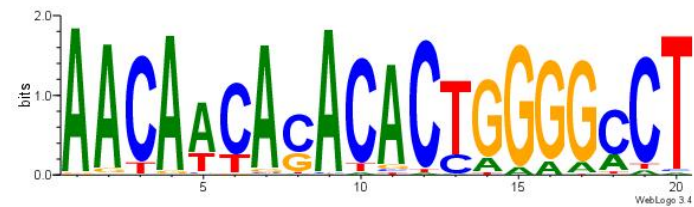
#### Alignment:

```
AGGCCCCAGTGTSTGTTGTT
AGCTCCCAGCGTGAGCGACG
```

Original motif      Consensus sequence: AGGCCCCAGTGTSTGTTGTT



Reverse complement motif      Consensus sequence: AAC AACASACTGGGGCCT



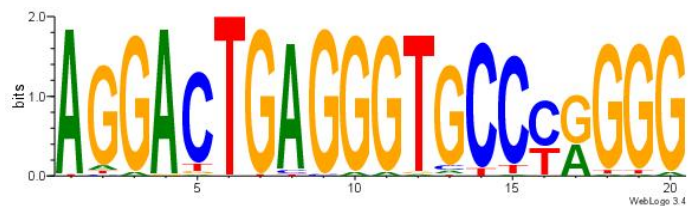


Dataset #: 1  
 Motif ID: 312  
 Motif name: Motif 312  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 20  
 Similarity score: 0.121076

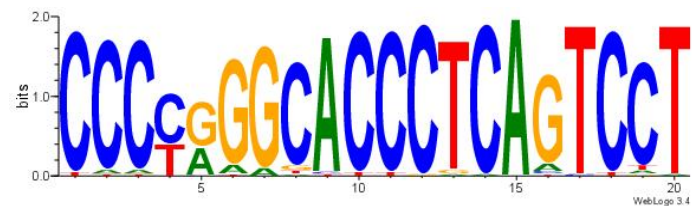
Alignment:

CCCMKGGCACCCCTCAGTCCT  
 CGTCGCTCACGCTGGGAGCT

Original motif      Consensus sequence: AGGACTGAGGGTGCCYRGGG



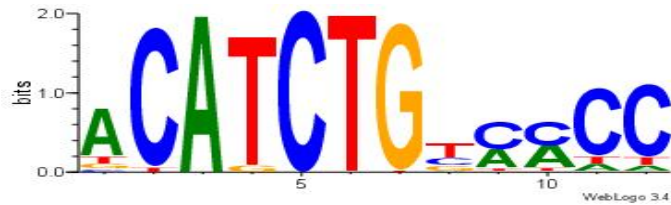
Reverse complement motif      Consensus sequence: CCCMKGGCACCCCTCAGTCCT



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

Original motif      Consensus sequence: ACATCTGYMMCC

Reverse complement motif      Consensus sequence: GRRMCAGATGT

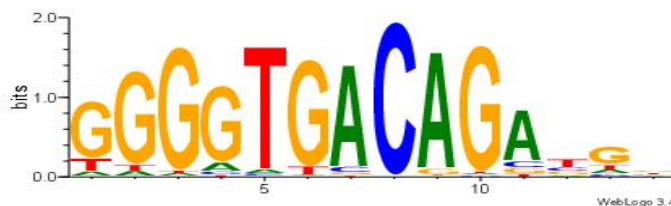


**Best Matches for Motif ID 49 (Highest to Lowest)**

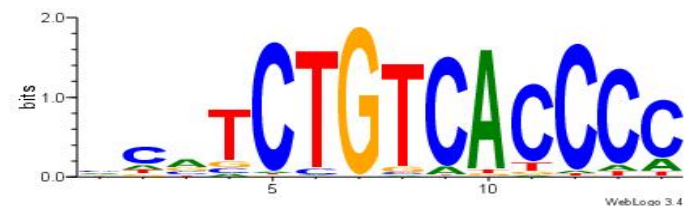
Dataset #: 1  
 Motif ID: 1  
 Motif name: Motif 1  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 12  
 Similarity score: 0.0495311

Alignment:  
 GGGGTGACAGABGB  
 GRRMCAGATGT--

Original motif    Consensus sequence: GGGGTGACAGABGB



Reverse complement motif    Consensus sequence: BCVTCTGTACCC

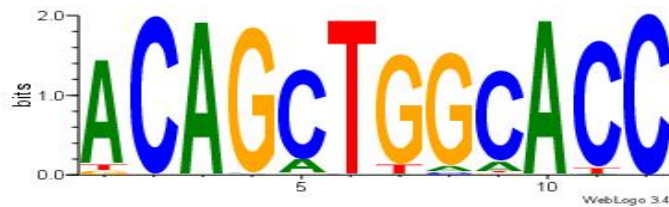


Dataset #: 1

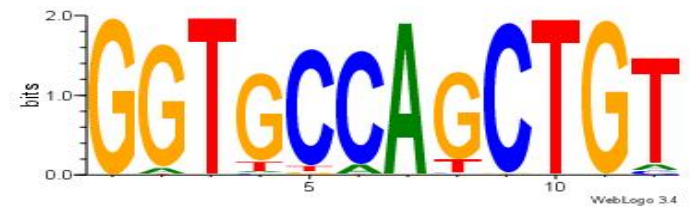
Motif ID: 199  
 Motif name: Motif 199  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 12  
 Similarity score: 0.0505389

Alignment:  
 ACAGCTGGCACC  
 ACATCTGYMMCC

Original motif      Consensus sequence: ACAGCTGGCACC

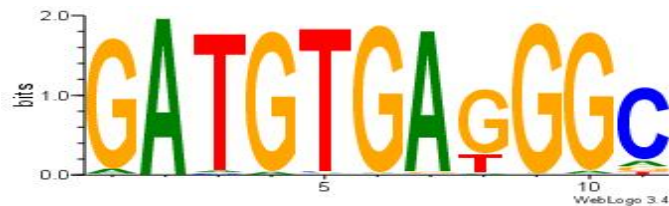


Reverse complement motif      Consensus sequence: GGTGCCAGCTGT

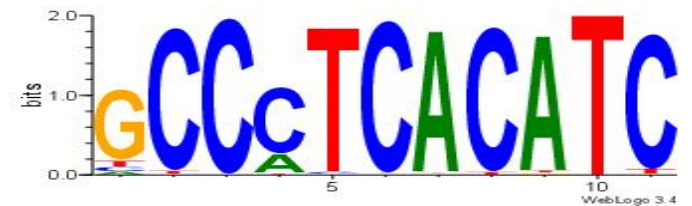


**Dataset #: 1      Motif ID: 50      Motif name: Motif 50**

Original motif      Consensus sequence: GATGTGAGGGC



Reverse complement motif      Consensus sequence: GCCCTCACATC



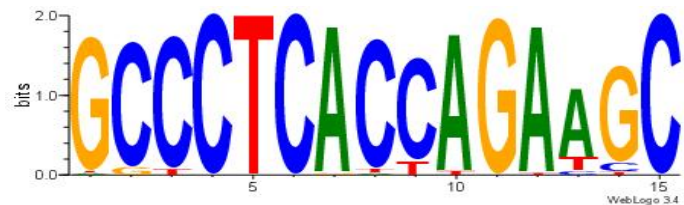
## Best Matches for Motif ID 50 (Highest to Lowest)

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

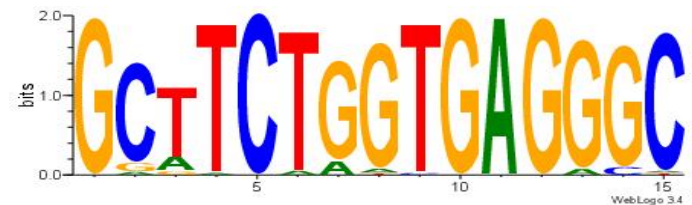
### Alignment:

```
GCTTCTGGTGAGGGC  
----GATGTGAGGGC
```

Original motif    Consensus sequence: GCCCTCACCAGAAGC



Reverse complement motif    Consensus sequence: GCTTCTGGTGAGGGC

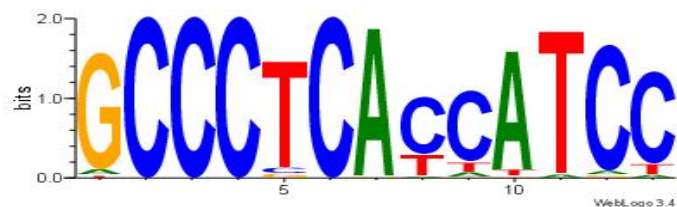


Dataset #: 1  
Motif ID: 283  
Motif name: Motif 283  
Matching format of first motif: Original Motif  
Matching format of second motif: Reverse Complement

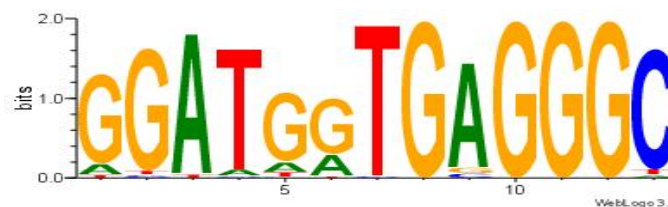
Direction: Forward  
 Position number: 3  
 Number of overlap: 11  
 Similarity score: 0.0702987

Alignment:  
 GGATGGTGAGGGC  
 --GATGTGAGGGC

Original motif      Consensus sequence: GCCCTCACCATCC

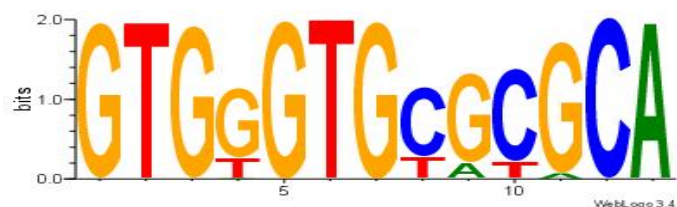


Reverse complement motif      Consensus sequence: GGATGGTGAGGGC



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

Original motif      Consensus sequence: GTGGGTGCGCGCA



Reverse complement motif      Consensus sequence: TGC GCGACCCAC



**Best Matches for Motif ID 51 (Highest to Lowest)**

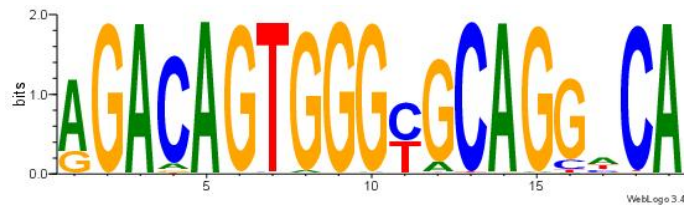
Dataset #: 1  
 Motif ID: 17  
 Motif name: Motif 17

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

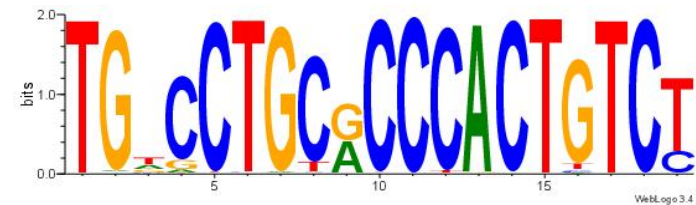
Alignment:

```
TGHCCTGCKCCCCTGTCT
-----TGC GCGCACCCAC-
```

Original motif      Consensus sequence: AGACAGTGGGYGCAGGHCA



Reverse complement motif      Consensus sequence: TGHCCTGCKCCCCTGTCT

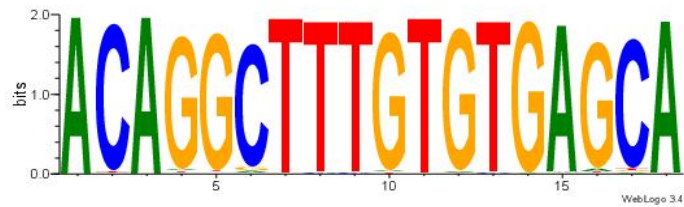


Dataset #:	1
Motif ID:	159
Motif name:	Motif 159
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	6
Number of overlap:	13
Similarity score:	0.0830854

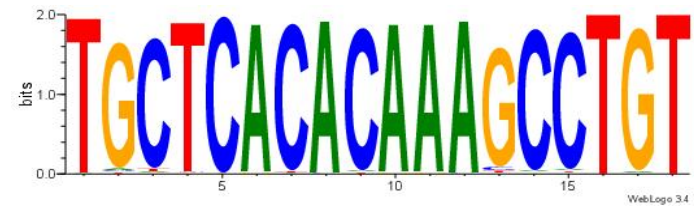
Alignment:

```
ACAGGCTTTGTGTGAGCA
-----GTGGGTGCGCGCA
```

Original motif      Consensus sequence: ACAGGCTTTGTGTGAGCA

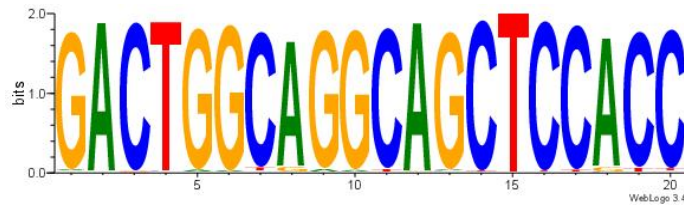


Reverse complement motif      Consensus sequence: TGCTCACACAAAGCCTGT

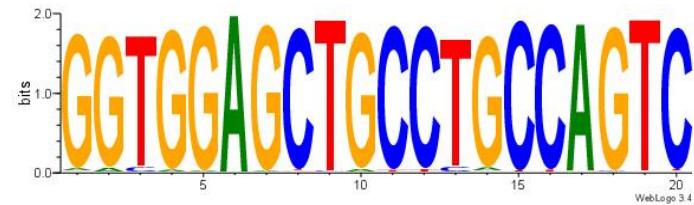


**Dataset #: 1      Motif ID: 52      Motif name: Motif 52**

Original motif      Consensus sequence: GACTGGCAGGCAGCTCCACC



Reverse complement motif      Consensus sequence: GGTGGAGCTGCCAGTC



**Best Matches for Motif ID 52 (Highest to Lowest)**

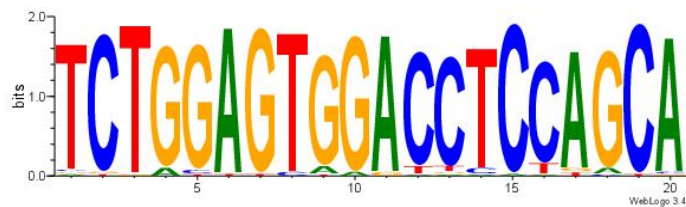
Dataset #:	1
Motif ID:	350
Motif name:	Motif 350
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement

Direction: Forward  
Position number: 1  
Number of overlap: 20  
Similarity score: 0.108621

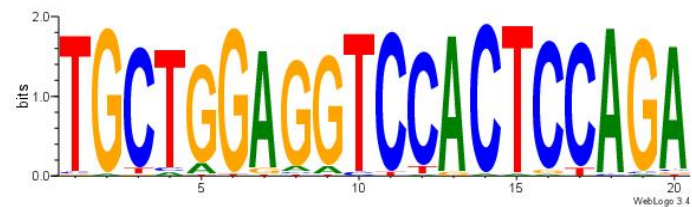
Alignment:

TGCTGGAGGTCCACTCCAGA  
GACTGGCAGGCAGCTCCACC

Original motif    Consensus sequence: TCTGGAGTGGACCTCCAGCA



Reverse complement motif    Consensus sequence: TGCTGGAGGTCCACTCCAGA



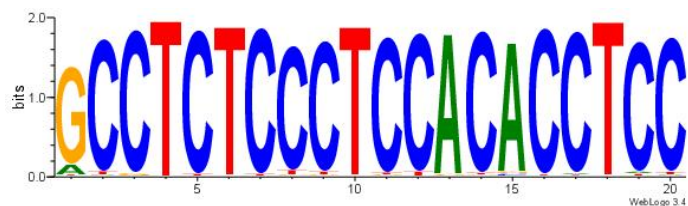
Dataset #: 1  
Motif ID: 105  
Motif name: Motif 105  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Reverse Complement  
Direction: Backward  
Position number: 1  
Number of overlap: 20  
Similarity score: 0.118973

Alignment:

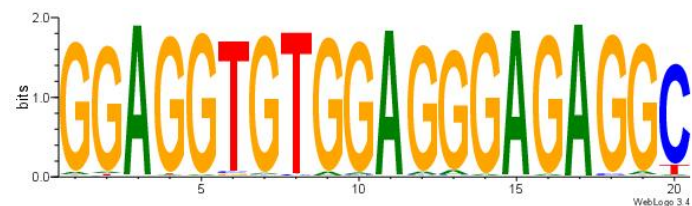
GGAGGTGTGGAGGGAGAGGC  
GGTGGAGCTGCCTGCCAGTC



Original motif      Consensus sequence: GCCTCTCCCTCCACACCTCC

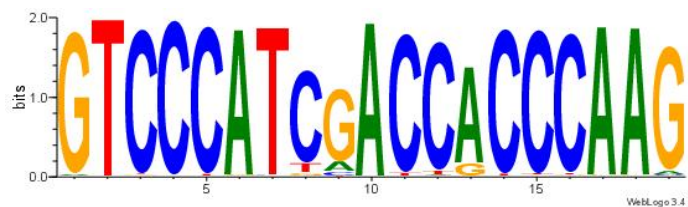


Reverse complement motif      Consensus sequence: GGAGGTGTGGAGGGAGAGGC

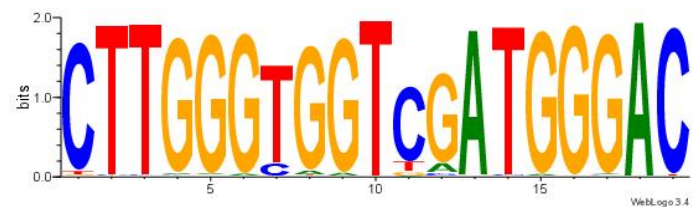


**Dataset #: 1      Motif ID: 53      Motif name: Motif 53**

Original motif      Consensus sequence: GTCCCATCGACCACCCAAG



Reverse complement motif      Consensus sequence: CTTGGGTGGTGGATGGGAC



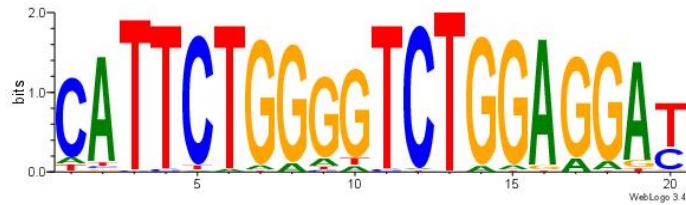
**Best Matches for Motif ID 53 (Highest to Lowest)**

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

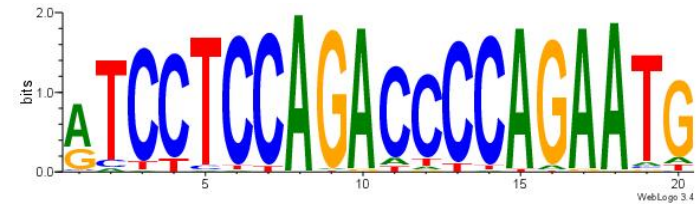
Alignment:

CATTCTGGGGTCTGGAGGAY  
-CTTGGGTGGTCGATGGGAC

Original motif      Consensus sequence: CATTCTGGGGTCTGGAGGAY



Reverse complement motif      Consensus sequence:  
MTCCTCCAGACCCCAGAATG



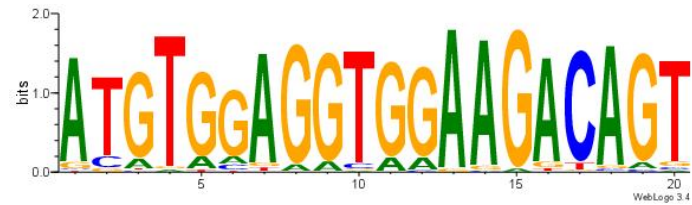
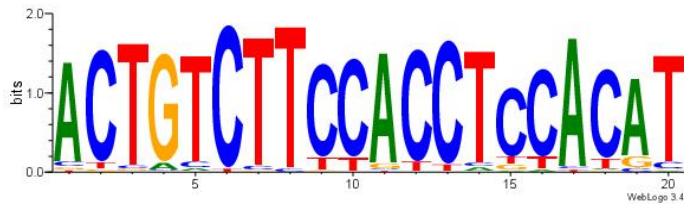
Dataset #: 1  
Motif ID: 178  
Motif name: Motif 178  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Reverse Complement  
Direction: Forward  
Position number: 1  
Number of overlap: 19  
Similarity score: 0.118023

Alignment:

ATGTGGAGGTGGAAGACAGT  
CTTGGGTGGTCGATGGGAC-

Original motif      Consensus sequence: ACTGTCTTCCACCTCCACAT

Reverse complement motif      Consensus sequence:  
ATGTGGAGGTGGAAGACAGT

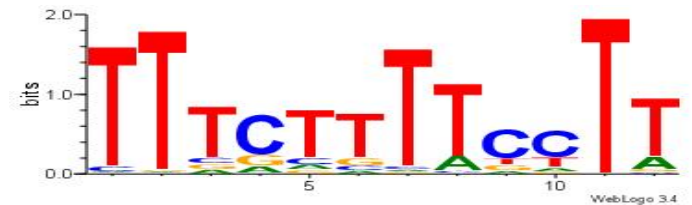


**Dataset #: 1      Motif ID: 54      Motif name: Motif 54**

Original motif      Consensus sequence: AAGGAAAAGAAA



Reverse complement motif      Consensus sequence: TTTCTTTTCCTT

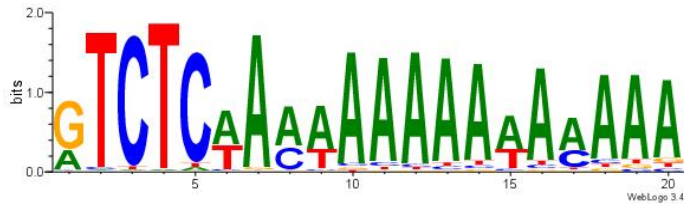


**Best Matches for Motif ID 54 (Highest to Lowest)**

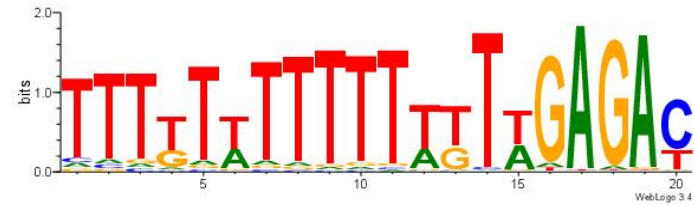
Dataset #:	1
Motif ID:	7
Motif name:	Motif 7
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	9
Number of overlap:	12
Similarity score:	0.0346455

Alignment:  
 GTCTCWAMAAAAAAWAMAAA  
 -----AAGGAAAAGAAA

Original motif      Consensus sequence: GTCTCWAMAAAAAWAMAAA



Reverse complement motif      Consensus sequence: TTTYTWTTTTTYYTWGAGAC

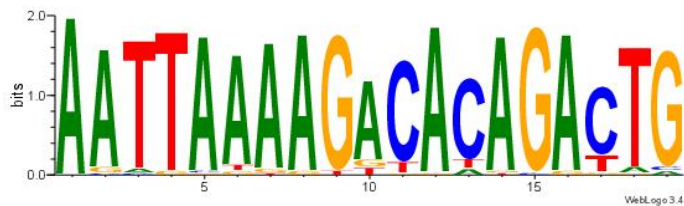


Dataset #: 1  
 Motif ID: 356  
 Motif name: Motif 356  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 12  
 Similarity score: 0.0458962

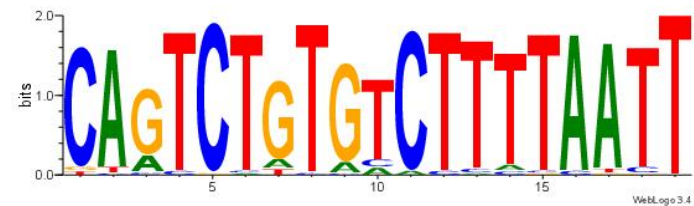
Alignment:

```
CAGTCTGTGTCTTTTAATT
-----TTTCTTTTCCTT
```

Original motif      Consensus sequence: AATTAAAGACACAGACTG

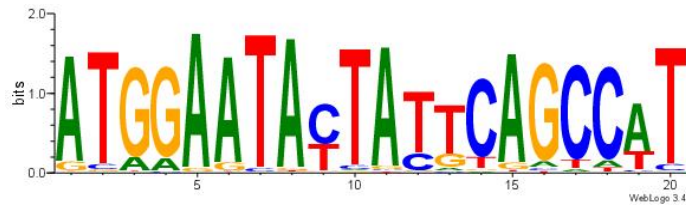


Reverse complement motif      Consensus sequence: CAGTCTGTGTCTTTTAATT

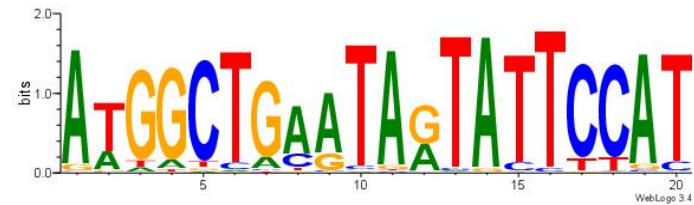


**Dataset #: 1      Motif ID: 55      Motif name: Motif 55**

Original motif      Consensus sequence: ATGGAATAYTATTCAGCCAT



Reverse complement motif      Consensus sequence: ATGGCTGAATAKTATTCCAT



### Best Matches for Motif ID 55 (Highest to Lowest)

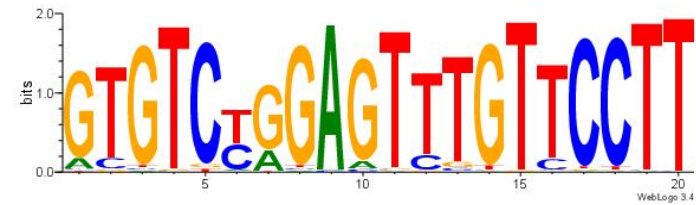
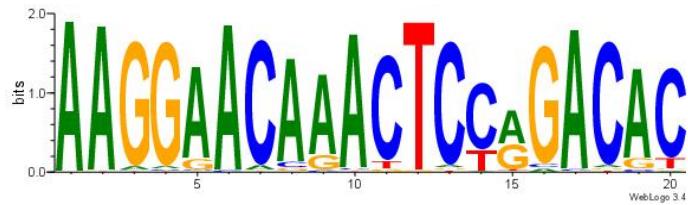
Dataset #:	1
Motif ID:	234
Motif name:	Motif 234
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	20
Similarity score:	0.0832183

#### Alignment:

```
GTGTCKGGAGTTTGTTTCCTT  
ATGGCTGAATAKTATTCCAT
```

Original motif      Consensus sequence: AAGGAACAACTCCRGACAC

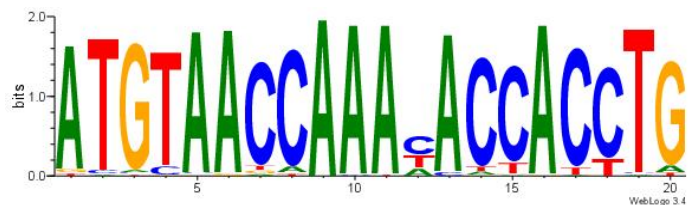
Reverse complement motif      Consensus sequence: GTGTCKGGAGTTTGTTTCCTT



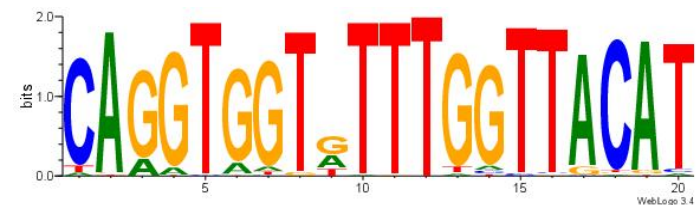
Dataset #: 1  
 Motif ID: 336  
 Motif name: Motif 336  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 20  
 Similarity score: 0.102251

Alignment:  
 CAGGTGGTKTTTGGTTACAT  
 ATGGCTGAATAKTATTCCAT

Original motif      Consensus sequence: ATGTAACCAAAYACCACCTG

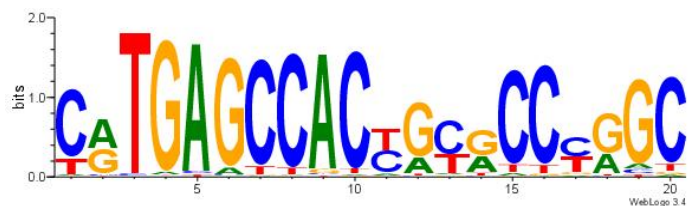


Reverse complement motif      Consensus sequence: CAGGTGGTKTTTGGTTACAT

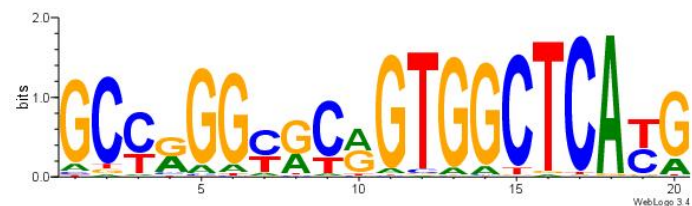


**Dataset #: 1      Motif ID: 56      Motif name: Motif 56**

Original motif      Consensus sequence: CRTGAGCCACYGYRCCYGGC



Reverse complement motif      Consensus sequence: GCCKGGMKCMGTGGCTCAKG



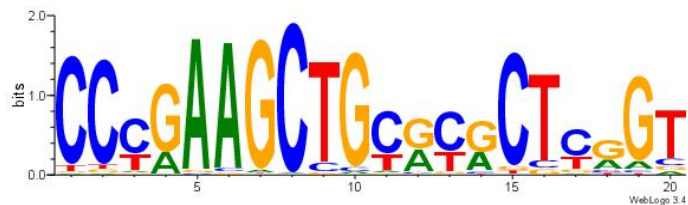
### Best Matches for Motif ID 56 (Highest to Lowest)

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

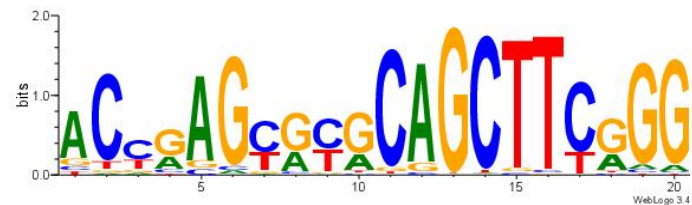
#### Alignment:

```
CCCGAAGCTGCRYRCTCGGT  
CRTGAGCCACYGYRCCYGGC
```

Original motif      Consensus sequence: CCCGAAGCTGCRYRCTCGGT



Reverse complement motif      Consensus sequence: ACCGAGMKMGCAGCTTCGGG

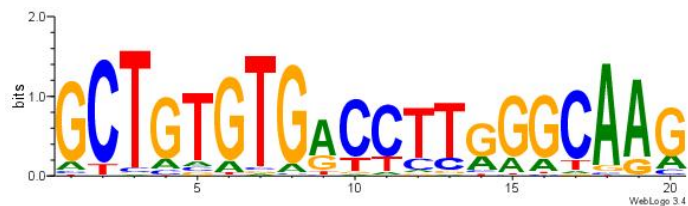


Dataset #: 1  
 Motif ID: 112  
 Motif name: Motif 112  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 20  
 Similarity score: 0.103187

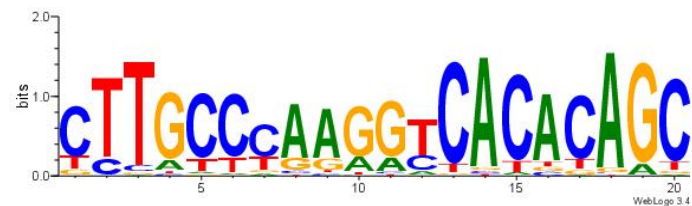
Alignment:

CTTGCCCAAGGTCACACAGC  
 CRTGAGCCACYGYRCCYGGC

Original motif    Consensus sequence: GCTGTGTGACCTTGGGCAAG



Reverse complement motif    Consensus sequence: CTTGCCCAAGGTCACACAGC

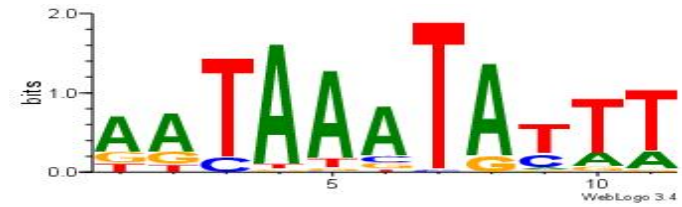
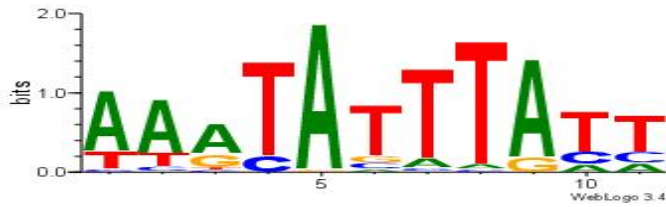


**Dataset #: 1      Motif ID: 57      Motif name: Motif 57**

Original motif    Consensus sequence: AAATATTTATT

Reverse complement motif    Consensus sequence: AATAAATATTT



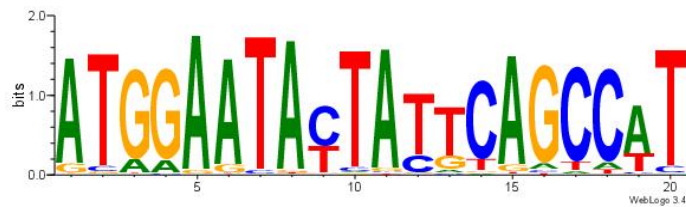


**Best Matches for Motif ID 57 (Highest to Lowest)**

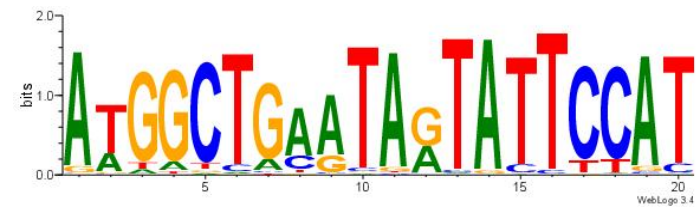
Dataset #: 1  
 Motif ID: 55  
 Motif name: Motif 55  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 4  
 Number of overlap: 11  
 Similarity score: 0.0640425

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

Original motif      Consensus sequence: ATGGAATAYTATTCAGCCAT



Reverse complement motif      Consensus sequence: ATGGCTGAATAKTATTCCAT

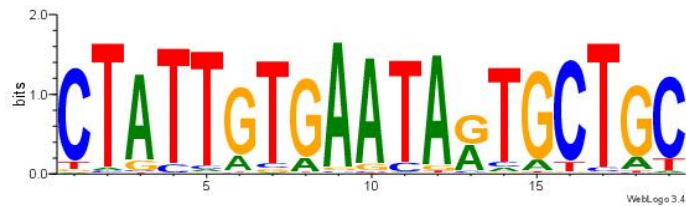


Dataset #: 1  
 Motif ID: 70  
 Motif name: Motif 70  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 5  
 Number of overlap: 11  
 Similarity score: 0.0653502

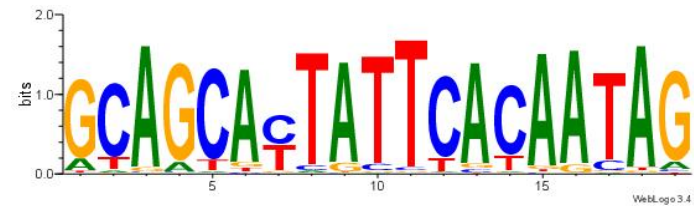
Alignment:

GCAGCAMTATTCCACAATAG  
 ----AAATATTTATT----

Original motif      Consensus sequence: CTATTGTGAATARTGCTGC



Reverse complement motif      Consensus sequence: GCAGCAMTATTCCACAATAG

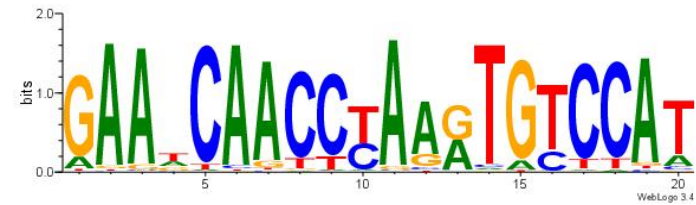
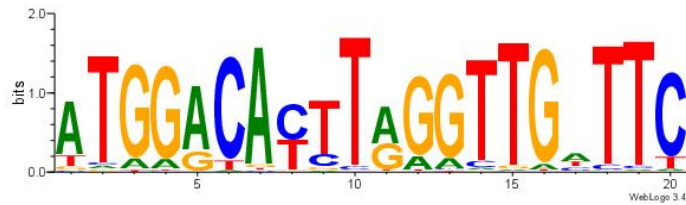



---

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

Original motif      Consensus sequence: ATGGACAYTTRGGTTGHTTC

Reverse complement motif      Consensus sequence: GAAHCAACCKAAKTGTCCAT



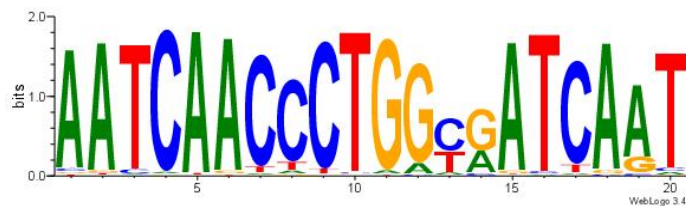
**Best Matches for Motif ID 58 (Highest to Lowest)**

Dataset #: 1  
 Motif ID: 170  
 Motif name: Motif 170  
 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: 0.0796786

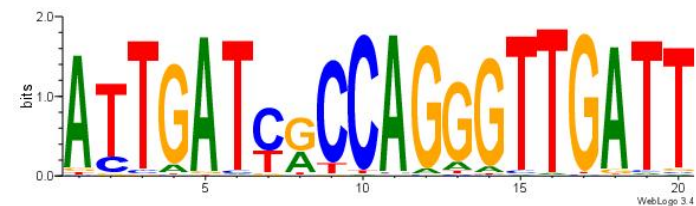
**Alignment:**

ATTGATMKCCAGGGTTGATT-  
 -ATGGACAYTTRGGTTGHTTC

Original motif      Consensus sequence: AATCAACCCTGGYRATCAAT



Reverse complement motif      Consensus sequence: ATTGATMKCCAGGGTTGATT

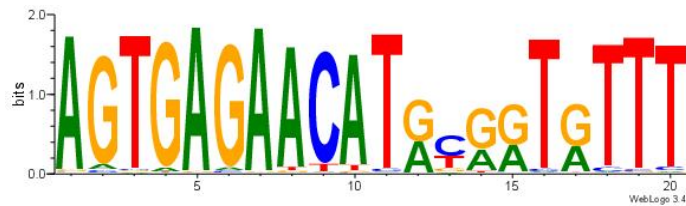


Dataset #: 1  
 Motif ID: 63  
 Motif name: Motif 63  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 2  
 Number of overlap: 19  
 Similarity score: 0.0861321

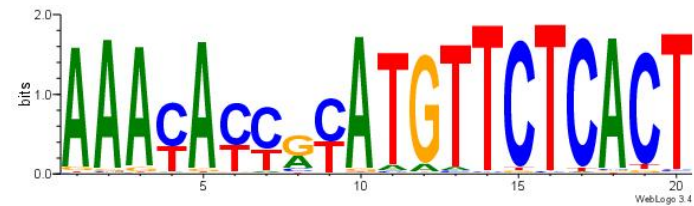
Alignment:

AGTGAGAACATRYRRTRTTT-  
 -ATGGACAYTTRGGTTGHTTC

Original motif      Consensus sequence: AGTGAGAACATRYRRTRTTT



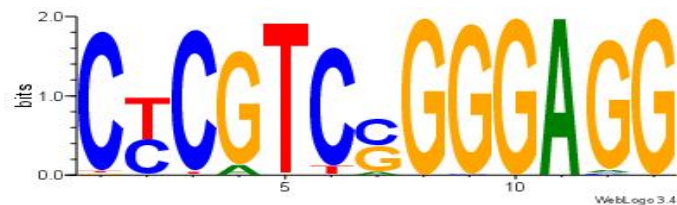
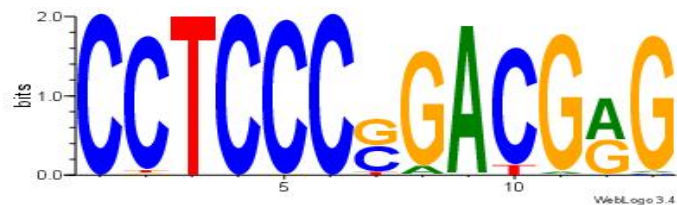
Reverse complement motif      Consensus sequence: AAAMAMMKMATGTTCTCACT



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

Original motif      Consensus sequence: CCTCCCSGACGRG

Reverse complement motif      Consensus sequence: CKCGTCSGGAGG

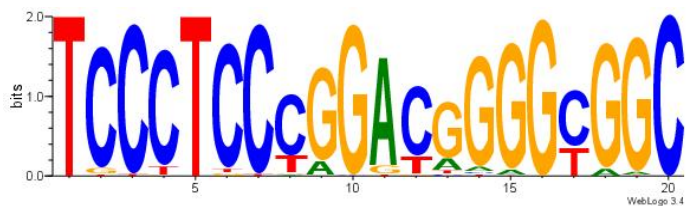


**Best Matches for Motif ID 59 (Highest to Lowest)**

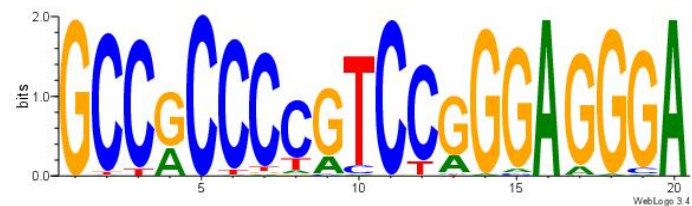
Dataset #: 1  
 Motif ID: 155  
 Motif name: Motif 155  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 3  
 Number of overlap: 13  
 Similarity score: 0.0335165

Alignment:  
 TCCCTCCCGGACGGGGYGGC  
 --CCTCCCSGACGRG-----

Original motif      Consensus sequence: TCCCTCCCGGACGGGGYGGC



Reverse complement motif      Consensus sequence: GCCCCCCGTCCGGGAGGGGA

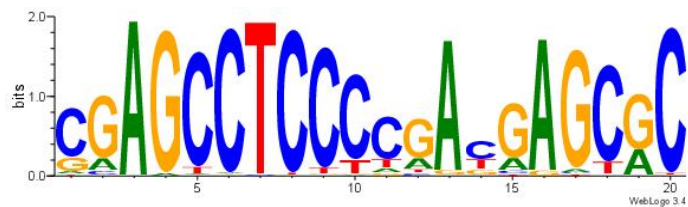


Dataset #: 1  
 Motif ID: 108  
 Motif name: Motif 108  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 4  
 Number of overlap: 13  
 Similarity score: 0.0365108

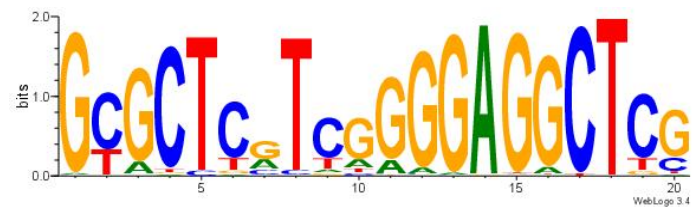
Alignment:

GCGCTCKTCGGGGAGGCTCG  
 ---CKCGTCSGGGAGG----

Original motif      Consensus sequence: CGAGCCTCCCCGAYGAGCGC



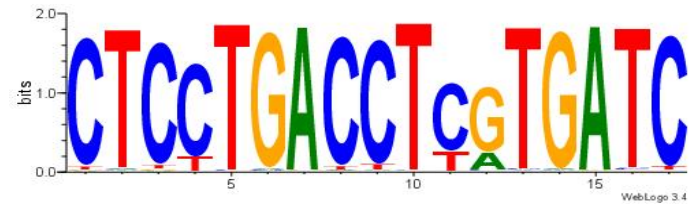
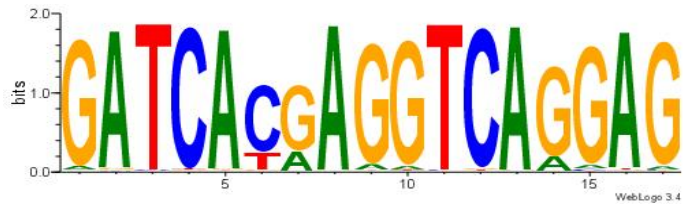
Reverse complement motif      Consensus sequence: GCGCTCKTCGGGGAGGCTCG



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

Original motif      Consensus sequence: GATCACGAGGTCAGGAG

Reverse complement motif      Consensus sequence: CTCCTGACCTCGTGATC

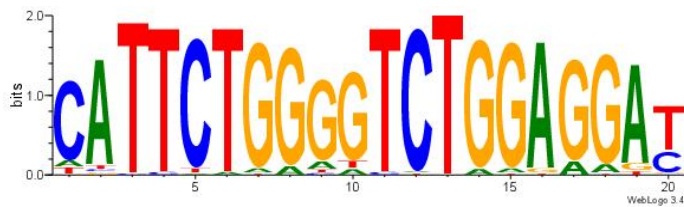


**Best Matches for Motif ID 60 (Highest to Lowest)**

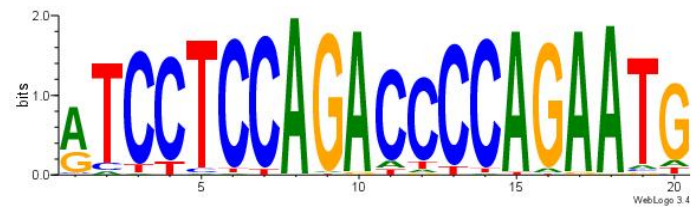
Dataset #: 1  
 Motif ID: 309  
 Motif name: Motif 309  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 4  
 Number of overlap: 17  
 Similarity score: 0.08025

Alignment:  
 CATTCTGGGGTCTGGAGGAY  
 GATCACGAGGTCAGGAG---

Original motif      Consensus sequence: CATTCTGGGGTCTGGAGGAY



Reverse complement motif      Consensus sequence: MTCCTCCAGACCCAGAAATG

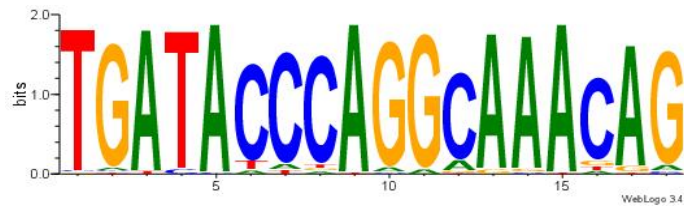


Dataset #: 1  
 Motif ID: 290  
 Motif name: Motif 290  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 2  
 Number of overlap: 17  
 Similarity score: 0.0894593

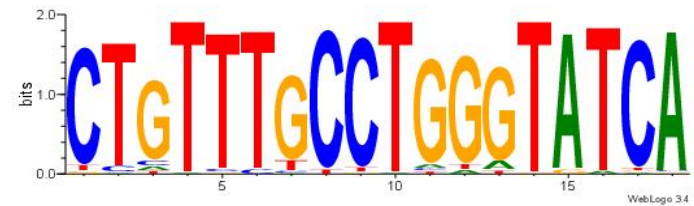
Alignment:

CTGTTTGCCTGGGTATCA  
 CTCCTGACCTCGTGATC-

Original motif      Consensus sequence: TGATACCCAGGCAAACAG



Reverse complement motif      Consensus sequence: CTGTTTGCCTGGGTATCA

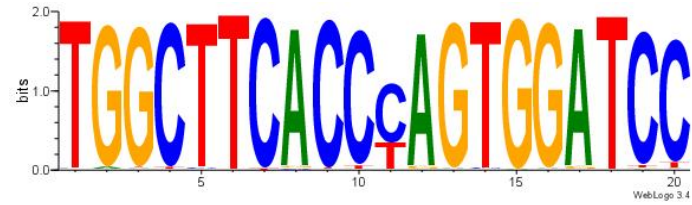
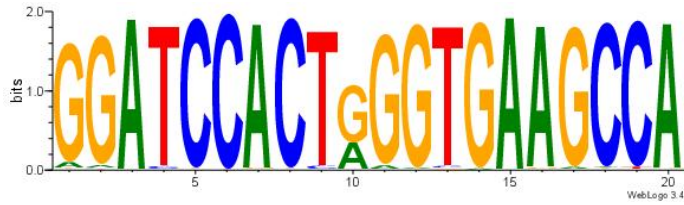


**Dataset #: 1      Motif ID: 61      Motif name: Motif 61**

Original motif      Consensus sequence: GGATCCACTGGGTGAAGCCA

Reverse complement motif      Consensus sequence: TGGCTTCACCCAGTGGATCC



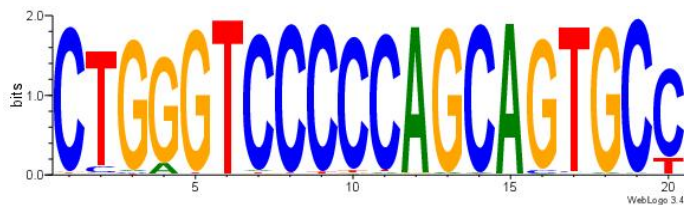


**Best Matches for Motif ID 61 (Highest to Lowest)**

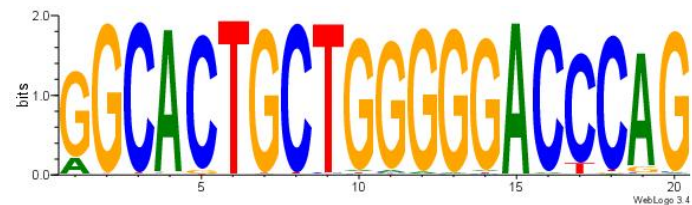
Dataset #: 1  
 Motif ID: 84  
 Motif name: Motif 84  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 20  
 Similarity score: 0.110456

Alignment:  
 GGC ACTGCTGGGGGACCCAG  
 GGATCCACTGGGTGAAGCCA

Original motif    Consensus sequence: CTGGGTCCCCCAGCAGTGCC



Reverse complement motif    Consensus sequence: GGC ACTGCTGGGGGACCCAG

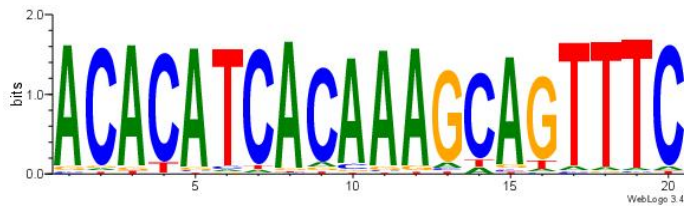


Dataset #: 1  
 Motif ID: 202  
 Motif name: Motif 202  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 20  
 Similarity score: 0.116364

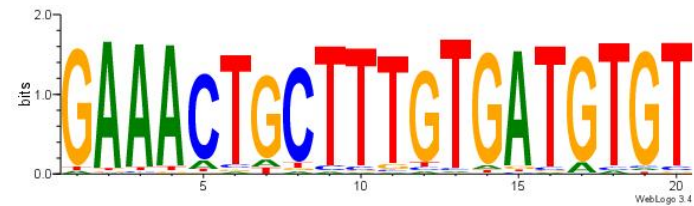
Alignment:

ACACATCACAAAGCAGTTTC  
 TGGCTTCACCCAGTGGATCC

Original motif      Consensus sequence: ACACATCACAAAGCAGTTTC



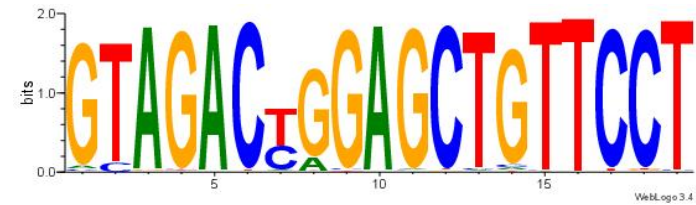
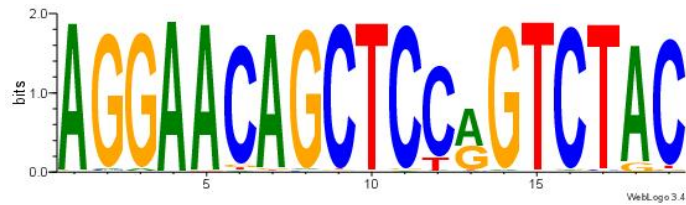
Reverse complement motif      Consensus sequence: GAAACTGCTTTGTGATGTGT



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

Original motif      Consensus sequence: AGGAACAGCTCCRGCTAC

Reverse complement motif      Consensus sequence: GTAGACKGGAGCTGTTCT

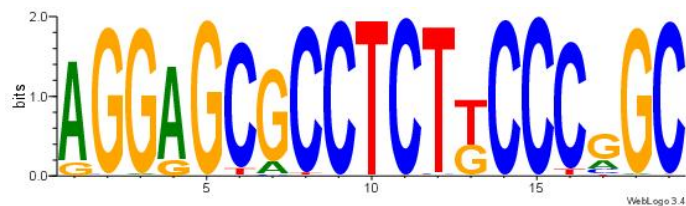


**Best Matches for Motif ID 62 (Highest to Lowest)**

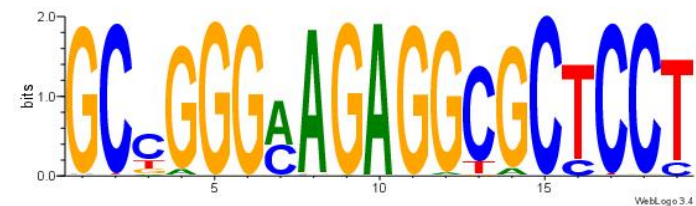
Dataset #: 1  
 Motif ID: 30  
 Motif name: Motif 30  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 19  
 Similarity score: 0.108892

Alignment:  
 AGGAGCGCCTCTKCCCGGC  
 AGGAACAGCTCCRGTCTAC

Original motif      Consensus sequence: AGGAGCGCCTCTKCCCGGC



Reverse complement motif      Consensus sequence: GCCGGGRAGAGGCGCTCT

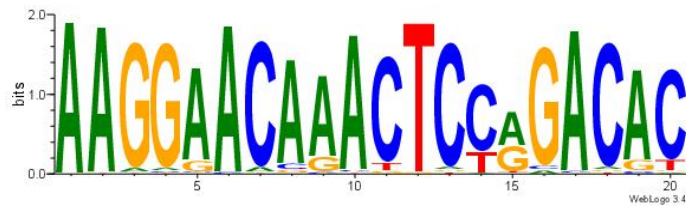


Dataset #: 1  
 Motif ID: 234  
 Motif name: Motif 234  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 2  
 Number of overlap: 19  
 Similarity score: 0.110299

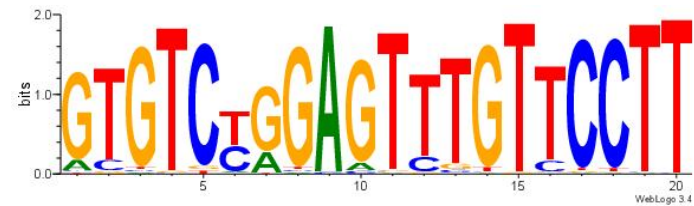
Alignment:

AAGGAACAAACTCCRGACAC  
 -AGGAACAGCTCCRGCTCTAC

Original motif      Consensus sequence: AAGGAACAAACTCCRGACAC



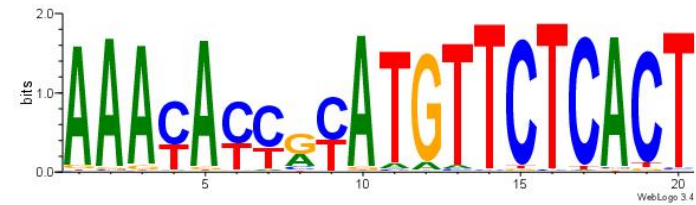
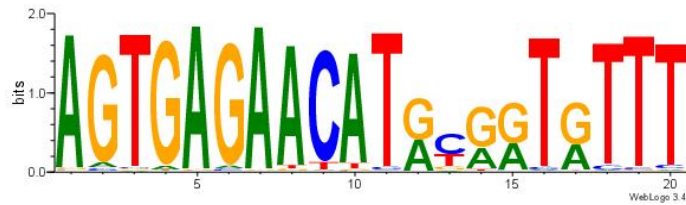
Reverse complement motif      Consensus sequence: GTGTCGGAGTTTGTTCCTT



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

Original motif      Consensus sequence: AGTGAGAACATRYRRTRTTT

Reverse complement motif      Consensus sequence: AAAMAMMKMATGTTCTCACT

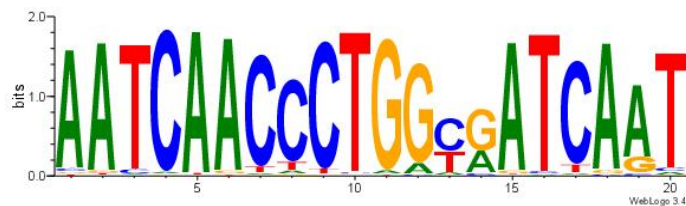


**Best Matches for Motif ID 63 (Highest to Lowest)**

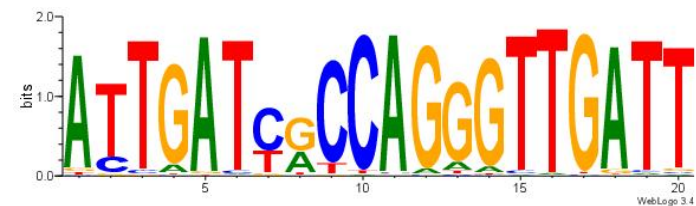
Dataset #: 1  
 Motif ID: 170  
 Motif name: Motif 170  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 20  
 Similarity score: 0.10502

Alignment:  
 AATCAACCCTGGYRATCAAT  
 AAAMAMMKMATGTTCTCACT

Original motif      Consensus sequence: AATCAACCCTGGYRATCAAT



Reverse complement motif      Consensus sequence: ATTGATMKCCAGGGTTGATT

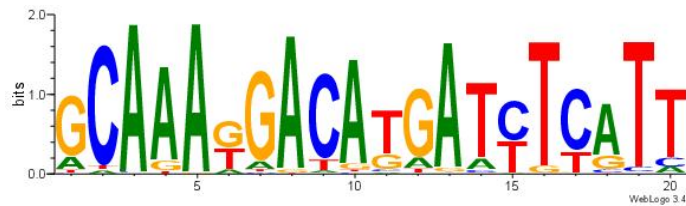


Dataset #: 1  
 Motif ID: 99  
 Motif name: Motif 99  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 20  
 Similarity score: 0.106569

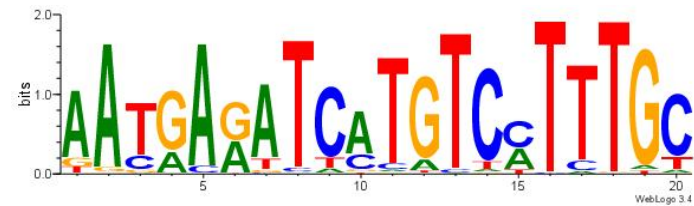
Alignment:

GCAAAGACATGATYTCATT  
 AAAMAMMKMATGTTCTCACT

Original motif      Consensus sequence: GCAAAGACATGATYTCATT



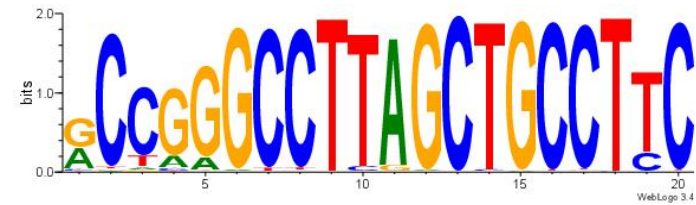
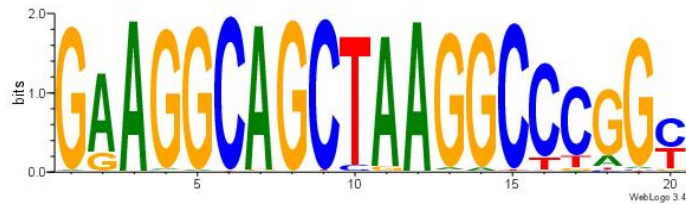
Reverse complement motif      Consensus sequence: AATGAKATCATGTCYTTTGC



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

Original motif      Consensus sequence: GAAGGCAGCTAAGGCCCGGY

Reverse complement motif      Consensus sequence: KCCGGGCCTTAGCTGCCTTC

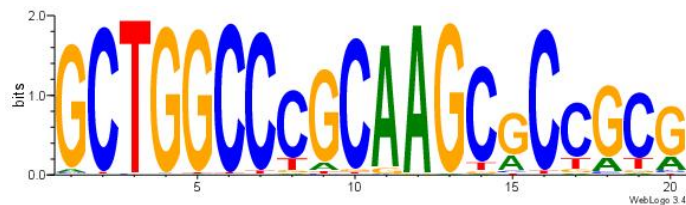


**Best Matches for Motif ID 64 (Highest to Lowest)**

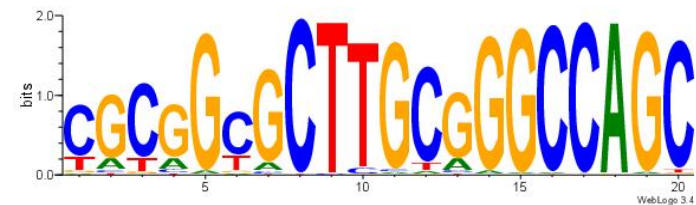
Dataset #: 1  
 Motif ID: 100  
 Motif name: Motif 100  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 20  
 Similarity score: 0.088142

Alignment:  
 CGCGGCGCTTGCGGGCCAGC  
 KCCGGGCCTTAGCTGCCTTC

Original motif      Consensus sequence: GCTGGCCCGCAAGGcGcCcGGcG



Reverse complement motif      Consensus sequence: CGCGGCGCTTGCGGGCCAGC

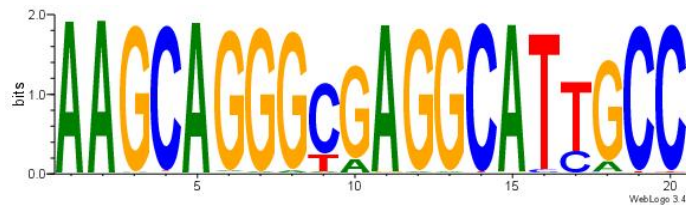


Dataset #: 1  
 Motif ID: 13  
 Motif name: Motif 13  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 2  
 Number of overlap: 19  
 Similarity score: 0.586666

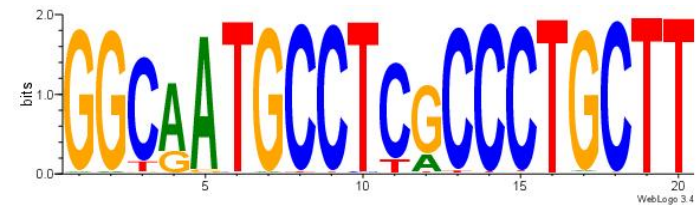
Alignment:

-AAGCAGGGCGAGGCATTGCC  
 GAAGGCAGCTAAGGCCCGY-

Original motif      Consensus sequence: AAGCAGGGCGAGGCATTGCC



Reverse complement motif      Consensus sequence: GGCAATGCCTCGCCCTGCTT

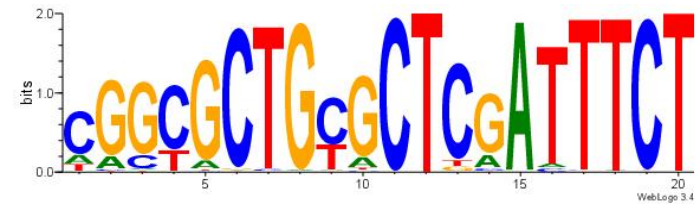
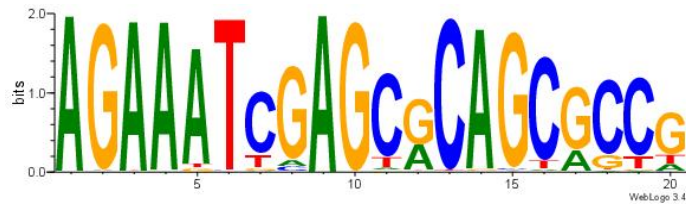


**Dataset #: 1      Motif ID: 65      Motif name: Motif 65**

Original motif      Consensus sequence: AGAAATCGAGCRCAGCGCCG

Reverse complement motif      Consensus sequence: CGGCGCTGMGCTCGATTTCT



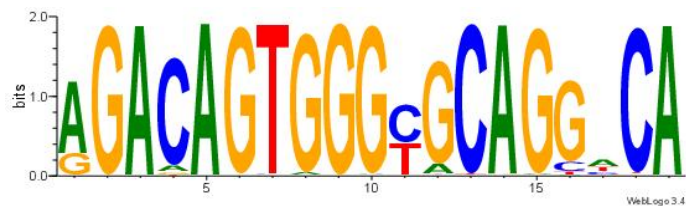


**Best Matches for Motif ID 65 (Highest to Lowest)**

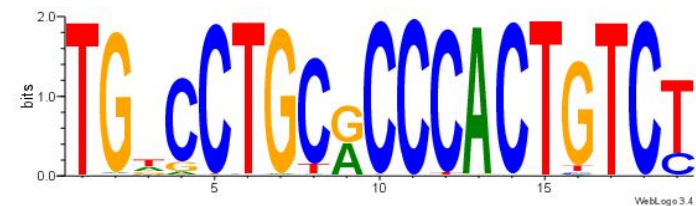
Dataset #: 1  
 Motif ID: 17  
 Motif name: Motif 17  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 19  
 Similarity score: 0.0924478

Alignment:  
 -TGHCCCTGCKCCCCTGTCT  
 CGGCGCTGMGCTCGATTTCT

Original motif      Consensus sequence: AGACAGTGGGYGCAGGHCA



Reverse complement motif      Consensus sequence: TGHCCCTGCKCCCCTGTCT

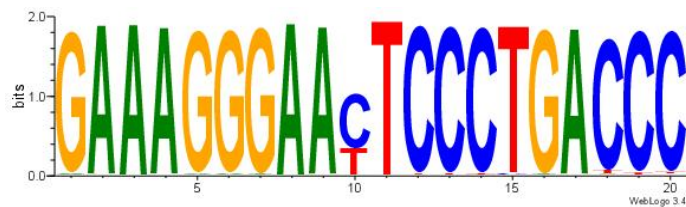


Dataset #: 1  
 Motif ID: 16  
 Motif name: Motif 16  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 2  
 Number of overlap: 19  
 Similarity score: 0.116136

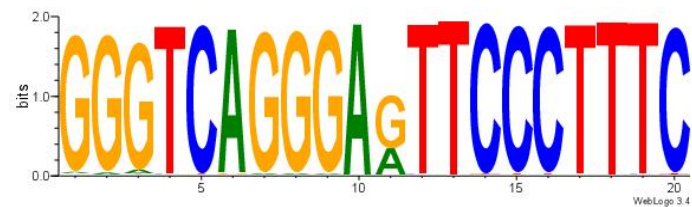
Alignment:

GGGTCAGGGAGTCCCTTTC-  
 -CGGCGCTGMGCTCGATTTCT

Original motif      Consensus sequence: GAAAGGGA ACTCCCTGACCC



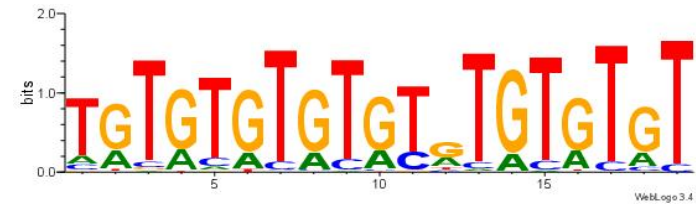
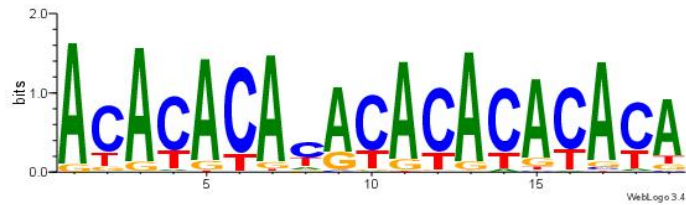
Reverse complement motif      Consensus sequence: GGGTCAGGGAGTCCCTTTC



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

Original motif      Consensus sequence: ACACACAYACACACACA

Reverse complement motif      Consensus sequence: TGTGTGTGTGKTGTGTGT

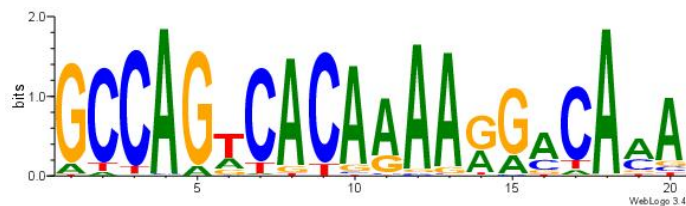


**Best Matches for Motif ID 66 (Highest to Lowest)**

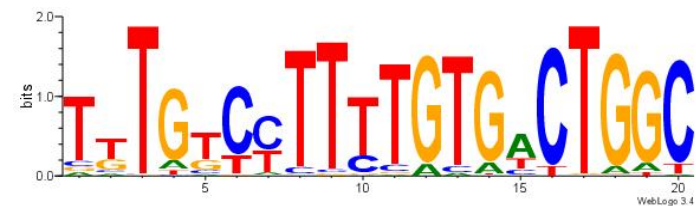
Dataset #: 1  
 Motif ID: 145  
 Motif name: Motif 145  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 19  
 Similarity score: 0.0762936

Alignment:  
 TYTGTCMTTTTGTGACTGGC  
 TGTGTGTGTGKTGTGTGT-

Original motif      Consensus sequence: GCCAGTCACAAAARGACAMA



Reverse complement motif      Consensus sequence: TYTGTCMTTTTGTGACTGGC

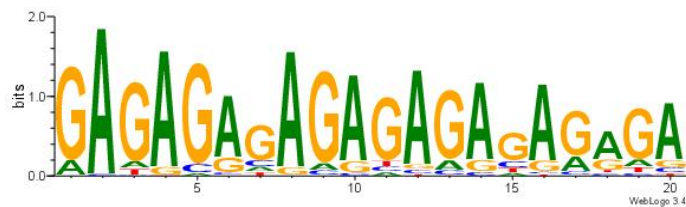


Dataset #: 1  
 Motif ID: 109  
 Motif name: Motif 109  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 19  
 Similarity score: 0.084962

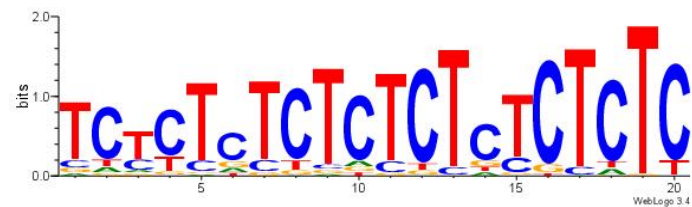
Alignment:

GAGAGAGAGAGAGAGAGAGA  
 -ACACACAYACACACACACA

Original motif      Consensus sequence: GAGAGAGAGAGAGAGAGAGA



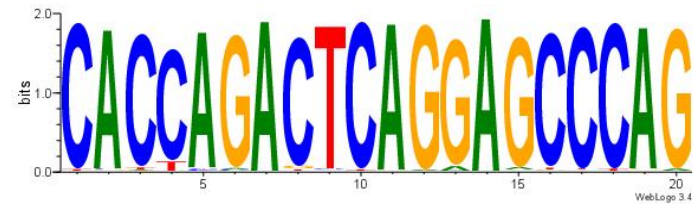
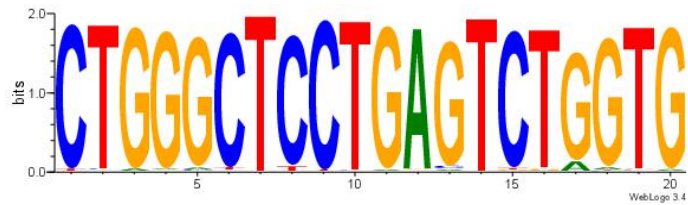
Reverse complement motif      Consensus sequence: TCTCTCTCTCTCTCTCTC



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

Original motif      Consensus sequence: CTGGGCTCCTGAGTCTGGTG

Reverse complement motif      Consensus sequence: CACCAGACTCAGGAGCCCAG



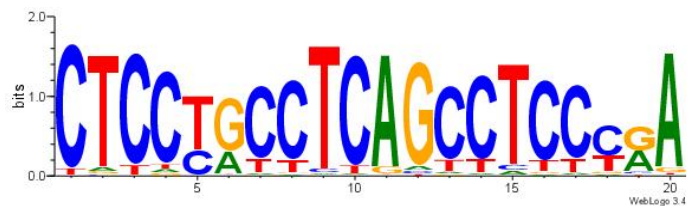
### Best Matches for Motif ID 67 (Highest to Lowest)

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

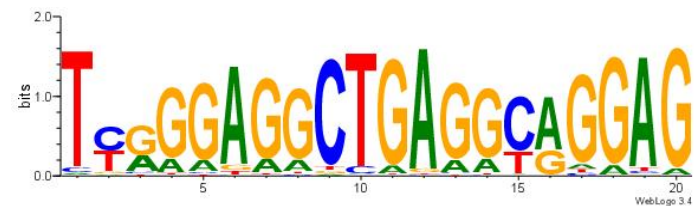
#### Alignment:

TMGGGAGGCTGAGGCAGGAG  
 CTGGGCTCCTGAGTCTGGT

Original motif      Consensus sequence: CTCCTGCCTCAGCCTCCCRA



Reverse complement motif      Consensus sequence: TMGGGAGGCTGAGGCAGGAG

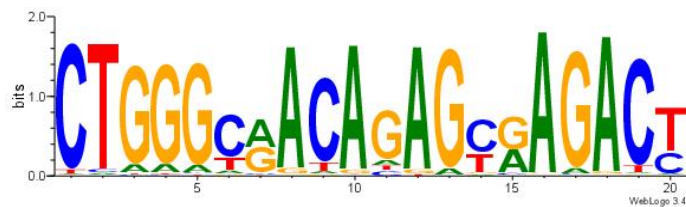


Dataset #: 1  
 Motif ID: 29  
 Motif name: Motif 29  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 20  
 Similarity score: 0.107414

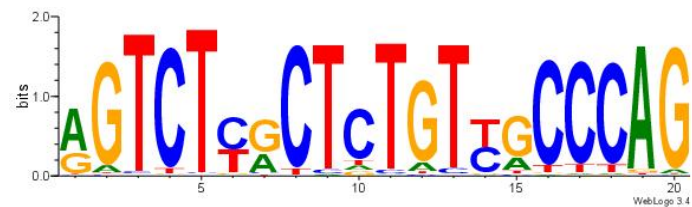
Alignment:

CTGGGCRACAGAGYRAGACY  
 CTGGGCTCCTGAGTCTGGTG

Original motif      Consensus sequence: CTGGGCRACAGAGYRAGACY



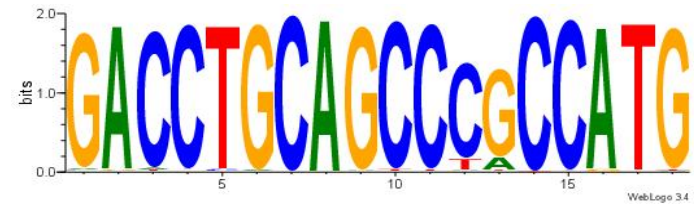
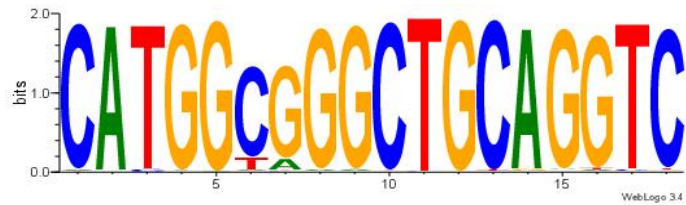
Reverse complement motif      Consensus sequence: MGTCTMKCTCTGKGCCAG



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

Original motif      Consensus sequence: CATGGCGGGCTGCAGGTC

Reverse complement motif      Consensus sequence: GACCTGCAGCCCGCCATG

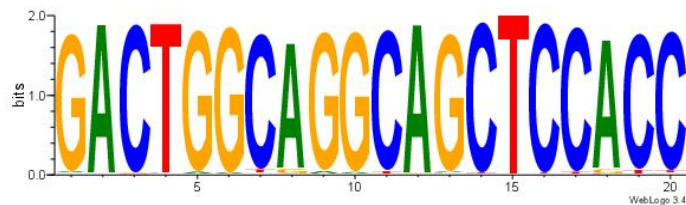


**Best Matches for Motif ID 68 (Highest to Lowest)**

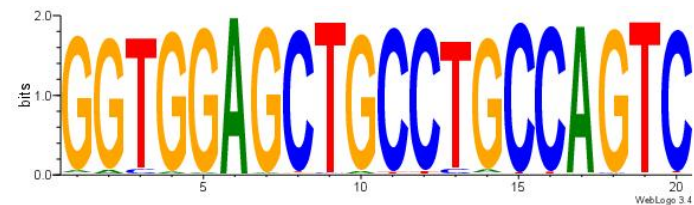
Dataset #: 1  
 Motif ID: 52  
 Motif name: Motif 52  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 2  
 Number of overlap: 18  
 Similarity score: 0.102941

Alignment:  
 GACTGGCAGGCAGCTCCACC  
 -CATGGCGGGCTGCAGGTC-

Original motif      Consensus sequence: GACTGGCAGGCAGCTCCACC



Reverse complement motif      Consensus sequence: GGTGGAGCTGCCAGTC

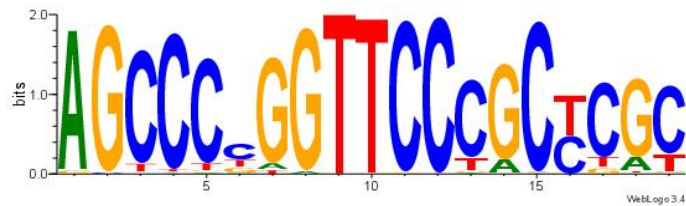


Dataset #: 1  
 Motif ID: 164  
 Motif name: Motif 164  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 2  
 Number of overlap: 18  
 Similarity score: 0.111785

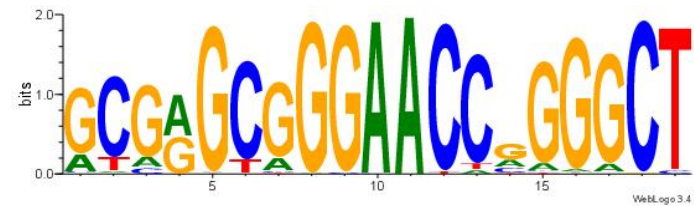
Alignment:

AGCCCCGGTTCCCGCYCGC  
 -GACCTGCAGCCCGCCATG

Original motif      Consensus sequence: AGCCCCGGTTCCCGCYCGC



Reverse complement motif      Consensus sequence: GCGMCGGGAACCGGGCT



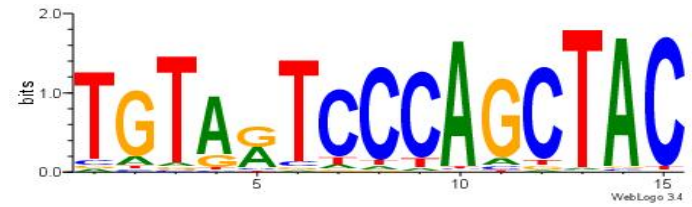
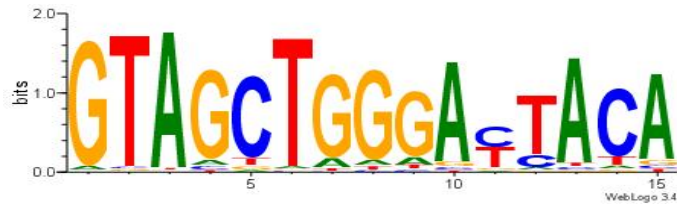

---

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

Original motif      Consensus sequence: GTAGCTGGGAYTACA

Reverse complement motif      Consensus sequence: TGTAKTCCCAGCT



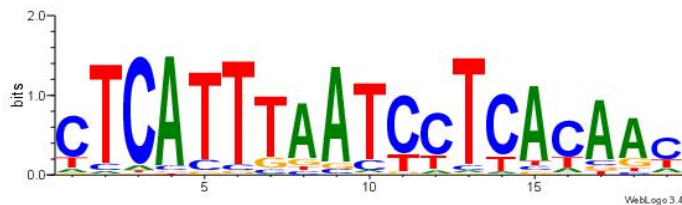


**Best Matches for Motif ID 69 (Highest to Lowest)**

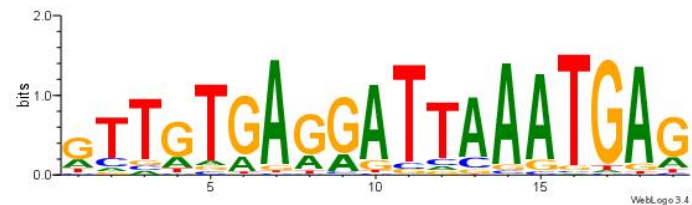
Dataset #: 1  
 Motif ID: 102  
 Motif name: Motif 102  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 5  
 Number of overlap: 15  
 Similarity score: 0.0936422

Alignment:  
 GTTGTGAGGATTAATGAG  
 GTAGCTGGGAYTACA-----

Original motif      Consensus sequence: CTCATTTAATCCACAAC



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

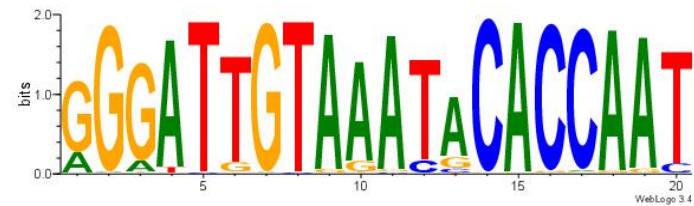
Alignment:

ATTGGTGTATTTACAATCCC  
 GTAGCTGGGAYTACA-----

Original motif      Consensus sequence: ATTGGTGTATTTACAATCCC



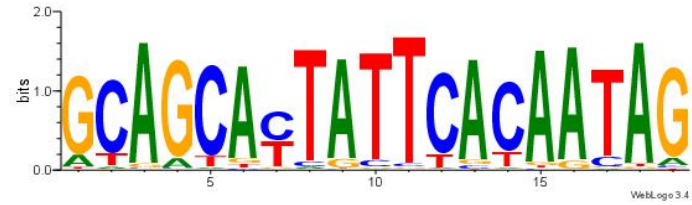
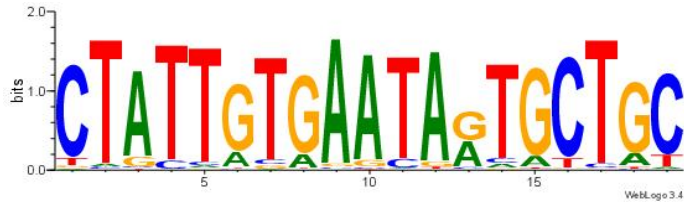
Reverse complement motif      Consensus sequence: GGGATTGTAAATACACCAAT



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

Original motif      Consensus sequence: CTATTGTGAATARTGCTGC

Reverse complement motif      Consensus sequence: GCAGCAMTATTCAATAG

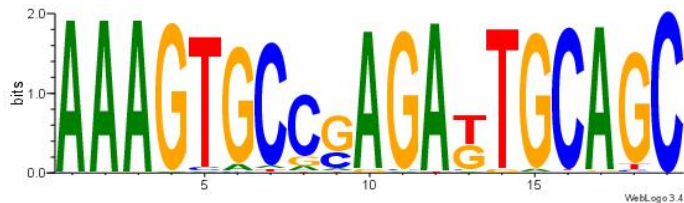


**Best Matches for Motif ID 70 (Highest to Lowest)**

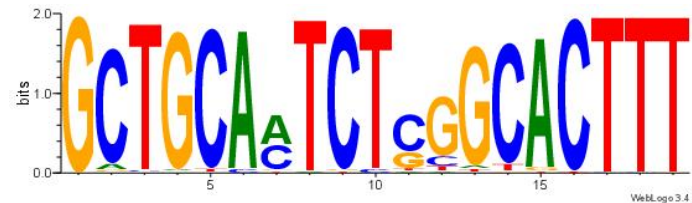
Dataset #: 1  
 Motif ID: 191  
 Motif name: Motif 191  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 19  
 Similarity score: 0.0948966

Alignment:  
 GCTGCARTCTCGGCACTTT  
 GCAGCAMTATTCACAATAG

Original motif      Consensus sequence: AAAGTGCCGAGAKTGCAGC



Reverse complement motif      Consensus sequence: GCTGCARTCTCGGCACTTT

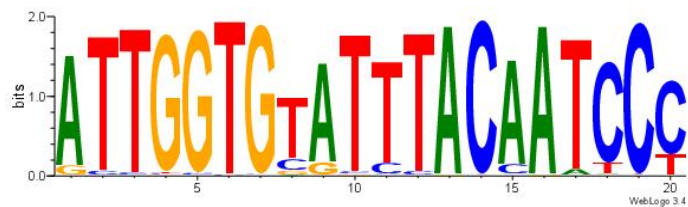


Dataset #: 1  
 Motif ID: 106  
 Motif name: Motif 106  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 19  
 Similarity score: 0.100944

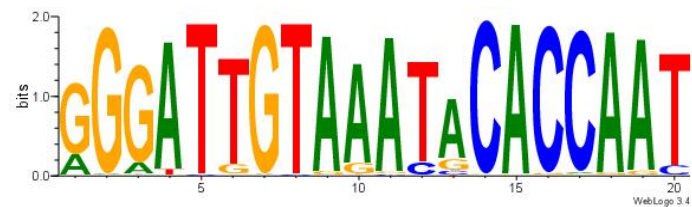
Alignment:

GGGATTGTAAATACACCAAT  
 -CTATTGTGAATARTGCTGC

Original motif      Consensus sequence: ATTGGTGTATTTACAATCCC



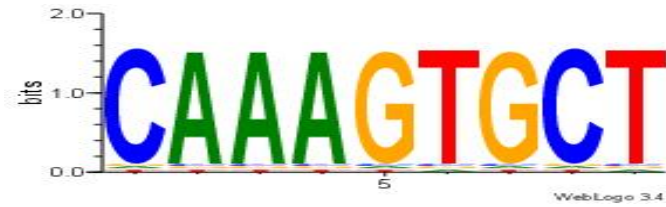
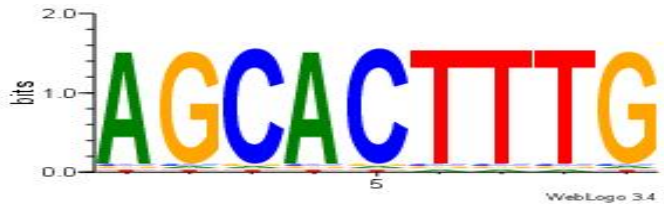
Reverse complement motif      Consensus sequence: GGGATTGTAAATACACCAAT



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

Original motif      Consensus sequence: AGCACTTTG

Reverse complement motif      Consensus sequence: CAAAGTGCT

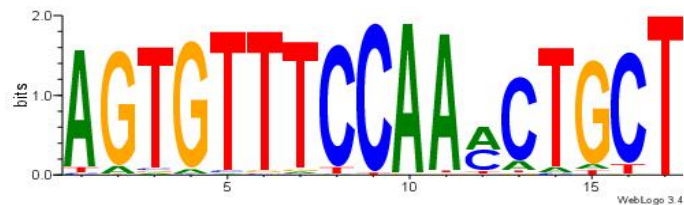


**Best Matches for Motif ID 71 (Highest to Lowest)**

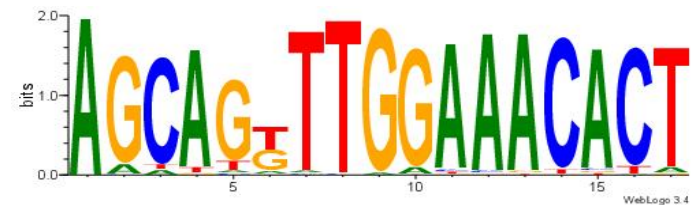
Dataset #: 1  
 Motif ID: 304  
 Motif name: Motif 304  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 9  
 Similarity score: 0.039262

Alignment:  
 AGCAGYTTGGAAACACT  
 AGCACTTTG-----

Original motif      Consensus sequence: AGTGTTTCCAAMCTGCT



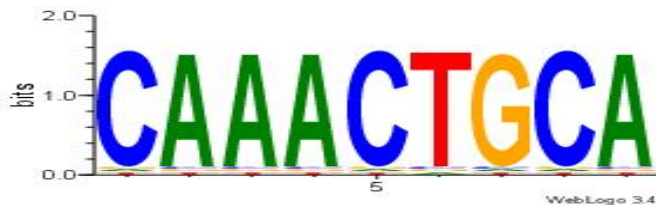
Reverse complement motif      Consensus sequence: AGCAGYTTGGAAACACT



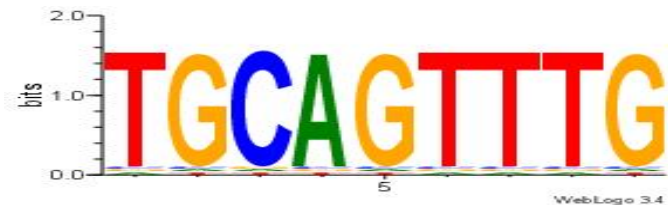
Dataset #: 1  
 Motif ID: 134  
 Motif name: Motif 134  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 9  
 Similarity score: 0.0420544

Alignment:  
 CAAACTGCA  
 CAAAGTGCT

Original motif    Consensus sequence: CAAACTGCA

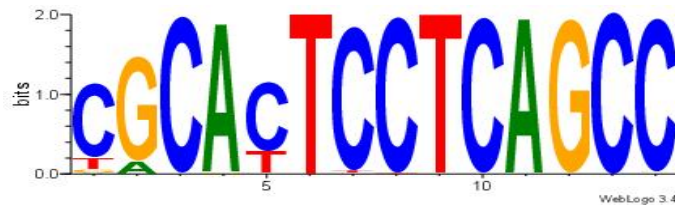


Reverse complement motif    Consensus sequence: TGCAGTTTG



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

Original motif    Consensus sequence: CGCACTCCTCAGCC



Reverse complement motif    Consensus sequence: GGCTGAGGAGTGC



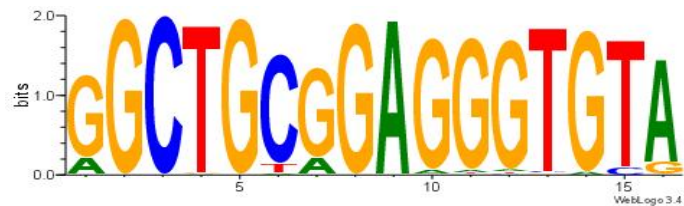
## Best Matches for Motif ID 72 (Highest to Lowest)

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

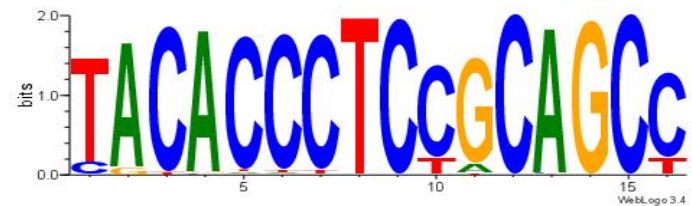
### Alignment:

```
TACACCCTCCGCAGCC  
--CGCACTCCTCAGCC
```

Original motif    Consensus sequence: GGCTGCGGAGGGTGTA



Reverse complement motif    Consensus sequence:  
TACACCCTCCGCAGCC



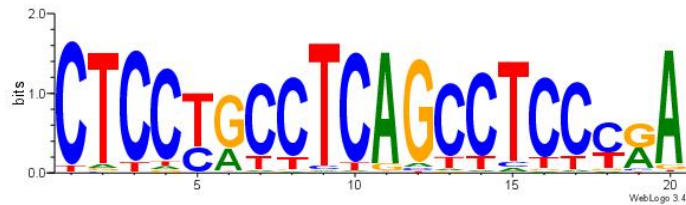
---

Dataset #: 1  
Motif ID: 26  
Motif name: Motif 26  
Matching format of first motif: Original Motif  
Matching format of second motif: Original Motif

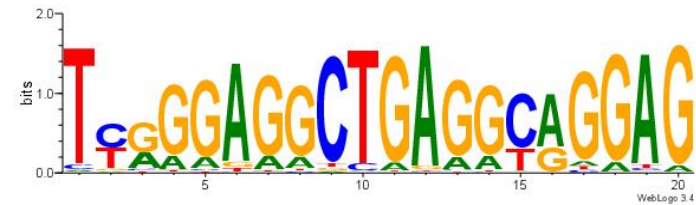
Direction: Forward  
 Position number: 1  
 Number of overlap: 14  
 Similarity score: 0.0793425

Alignment:  
 CTCCTGCCTCAGCCTCCCRA  
 CGCACTCCTCAGCC-----

Original motif      Consensus sequence: CTCCTGCCTCAGCCTCCCRA

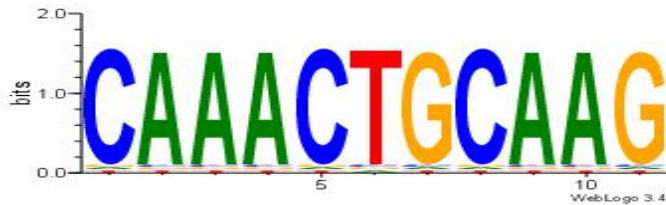


Reverse complement motif      Consensus sequence: TMGGGAGGCTGAGGCAGGAG

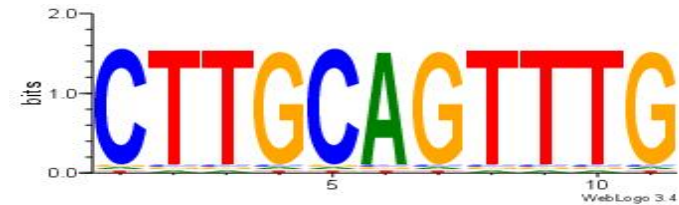


**Dataset #: 1      Motif ID: 73      Motif name: Motif 73**

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

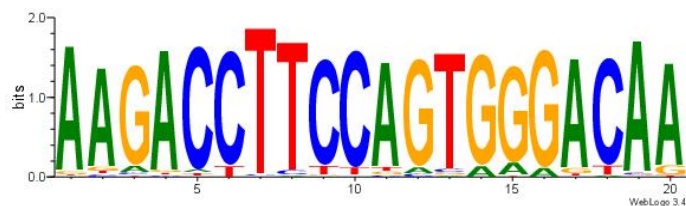


Motif name: Motif 292  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 5  
 Number of overlap: 11  
 Similarity score: 0.0679381

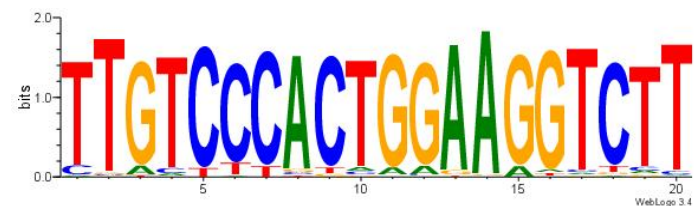
Alignment:

TTGTCCCCTGGAAGGTCTT  
 ----CAAAGTCAAG-----

Original motif      Consensus sequence: AAGACCTTCCAGTGGGACAA



Reverse complement motif      Consensus sequence: TTGTCCCCTGGAAGGTCTT

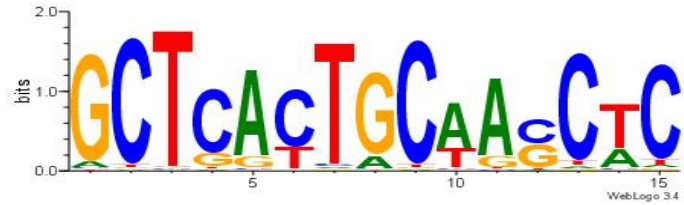


Dataset #: 1  
 Motif ID: 6  
 Motif name: Motif 6  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 2  
 Number of overlap: 11  
 Similarity score: 0.0730245

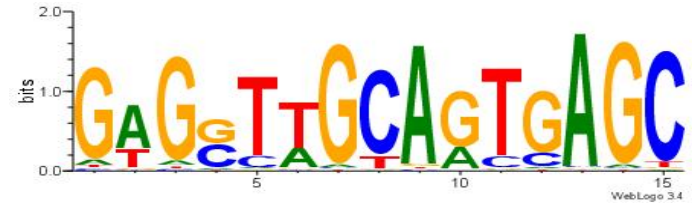
Alignment:

GAGSTTGCAGTGAGC  
---CTTGCAGTTTG-

Original motif      Consensus sequence: GCTCACTGCAASCTC

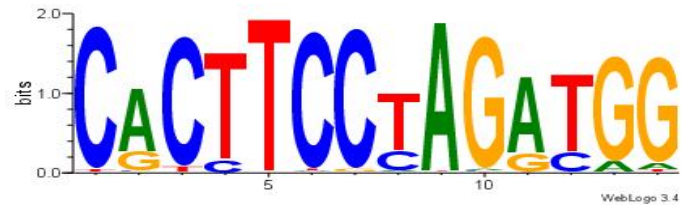


Reverse complement motif      Consensus sequence: GAGSTTGCAGTGAGC

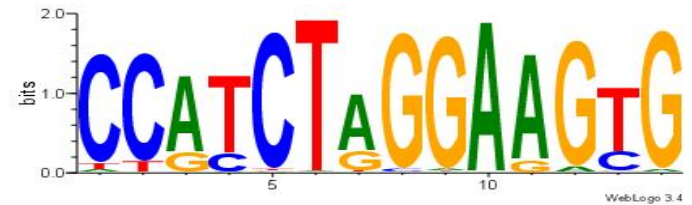


**Dataset #: 1      Motif ID: 74      Motif name: Motif 74**

Original motif      Consensus sequence: CACTTCTAGATGG



Reverse complement motif      Consensus sequence: CCATCTAGGAAGT



**Best Matches for Motif ID 74 (Highest to Lowest)**

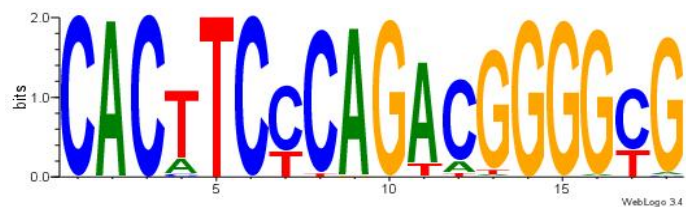
Dataset #:	1
Motif ID:	27
Motif name:	Motif 27
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1

Number of overlap: 14  
Similarity score: 0.0286091

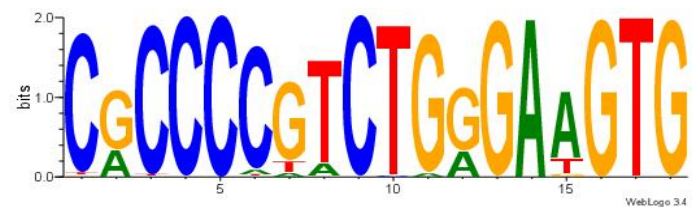
Alignment:

CACTTCCCAGACGGGGCG  
CACTTCTAGATGG-----

Original motif    Consensus sequence: CACTTCCCAGACGGGGCG



Reverse complement motif    Consensus sequence: CGCCCCGTCTGGGAAGTG

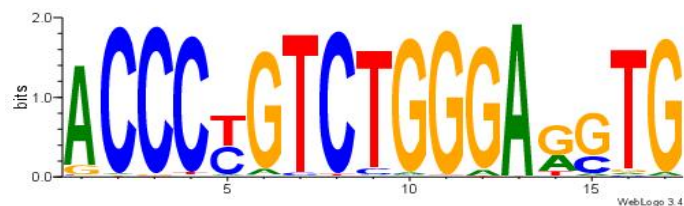


Dataset #: 1  
Motif ID: 95  
Motif name: Motif 95  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Original Motif  
Direction: Backward  
Position number: 1  
Number of overlap: 14  
Similarity score: 0.0523125

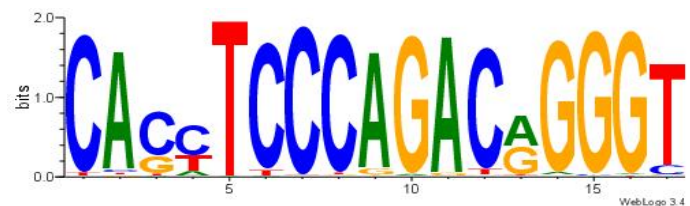
Alignment:

ACCCYGTCTGGGAGGTG  
---CCATCTAGGAAGTG

Original motif      Consensus sequence: ACCCYGTCTGGGAGGTG



Reverse complement motif      Consensus sequence: CACCTCCCAGACMGGGT

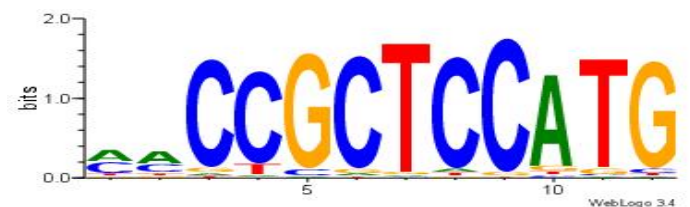


**Dataset #: 1      Motif ID: 75      Motif name: Motif 75**

Original motif      Consensus sequence: CATGGAGCGGK



Reverse complement motif      Consensus sequence: RRCCGCTCCATG



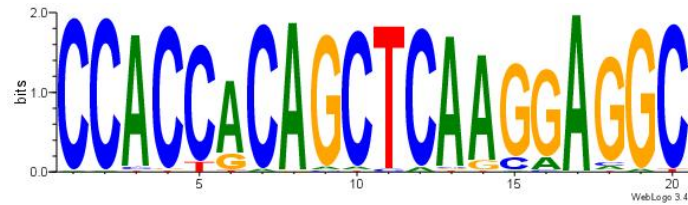
### Best Matches for Motif ID 75 (Highest to Lowest)

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

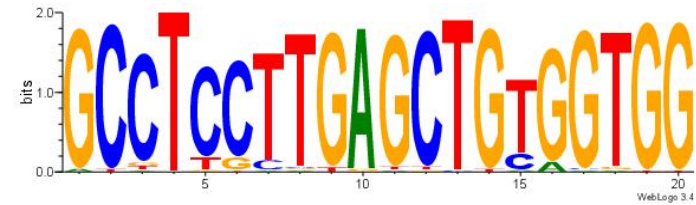
Alignment:

GCCTCCTTGAGCTGTGGTGG  
 ----CATGGAGCGGKK----

Original motif      Consensus sequence: CCACCACAGCTCAAGGAGGC



Reverse complement motif      Consensus sequence:  
 GCCTCCTTGAGCTGTGGTGG

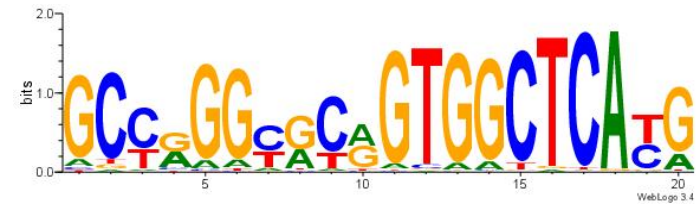
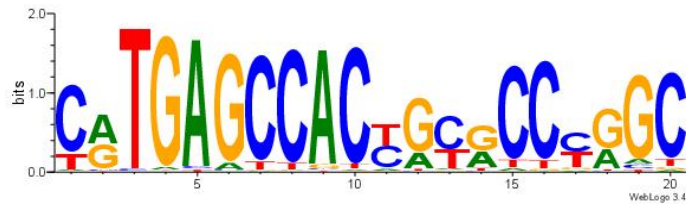


Dataset #: 1  
 Motif ID: 56  
 Motif name: Motif 56  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 2  
 Number of overlap: 12  
 Similarity score: 0.0764369

Alignment:  
 CRTGAGCCACYGYRCCYGGC  
 -RRCCGCTCCATG-----

Original motif      Consensus sequence: CRTGAGCCACYGYRCCYGGC

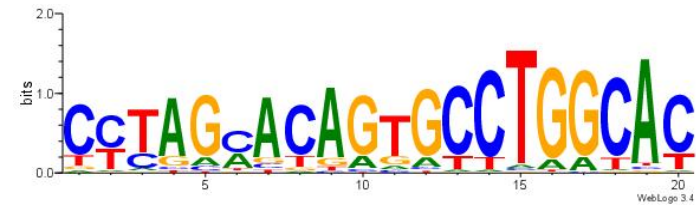
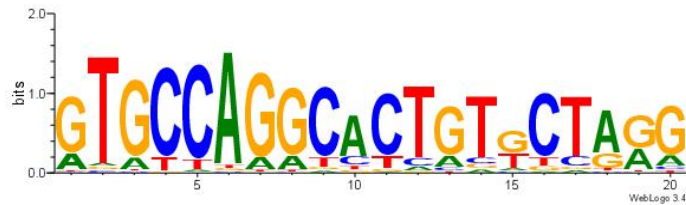
Reverse complement motif      Consensus sequence:  
 GCCKGGMKCMGTGGCTCAKG



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

Original motif      Consensus sequence: GTGCCAGGCACTGKCTARG

Reverse complement motif      Consensus sequence: CMTAGYACAGTGCCTGGCAC



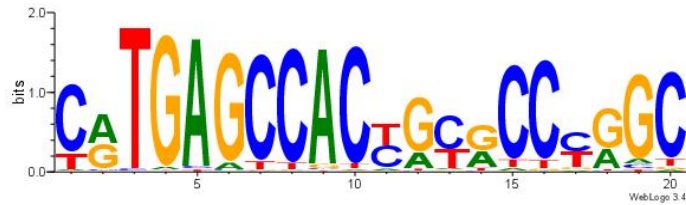
**Best Matches for Motif ID 76 (Highest to Lowest)**

Dataset #:	1
Motif ID:	56
Motif name:	Motif 56
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:	0.0709271

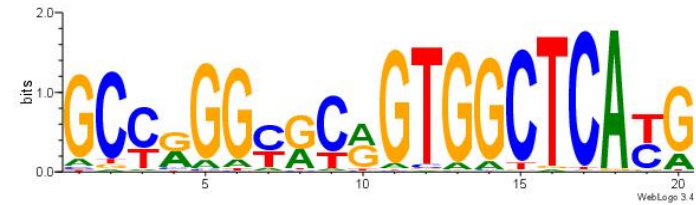
Alignment:

-CRTGAGCCACYGYRCCYGGC  
GTGCCAGGCACTGTKCTARG-

Original motif      Consensus sequence: CRTGAGCCACYGYRCCYGGC



Reverse complement motif      Consensus sequence:  
GCCGGMKCMGTGGCTCAKG



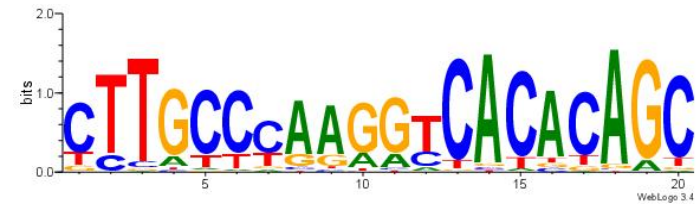
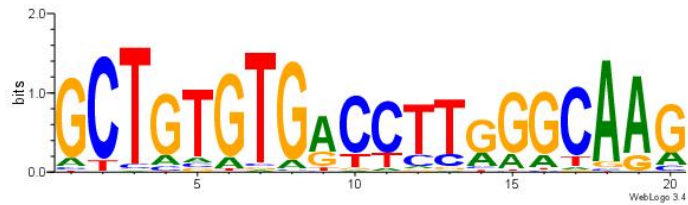
Dataset #: 1  
Motif ID: 112  
Motif name: Motif 112  
Matching format of first motif: Original Motif  
Matching format of second motif: Original Motif  
Direction: Forward  
Position number: 2  
Number of overlap: 19  
Similarity score: 0.0806209

Alignment:

GCTGTGTGACCTTGGGCAAG-  
-GTGCCAGGCACTGTKCTARG

Original motif      Consensus sequence: GCTGTGTGACCTTGGGCAAG

Reverse complement motif      Consensus sequence:  
CTTGCCCAAGGTCACACAGC

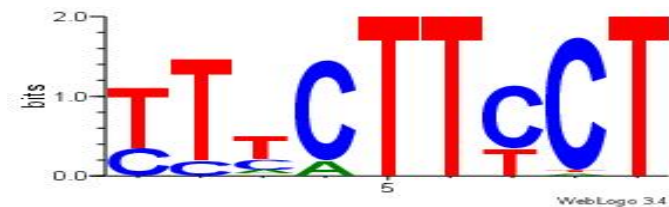


**Dataset #: 1      Motif ID: 77      Motif name: Motif 77**

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

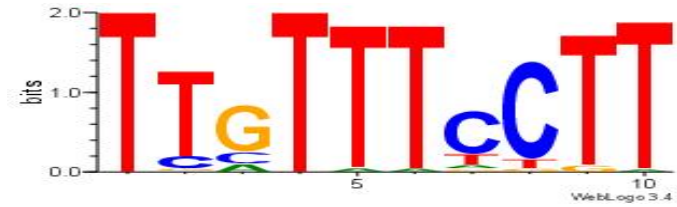
Alignment:  
 TTGTTTCCTT  
 TTTCTTCCT-



Original motif      Consensus sequence: AAGGAAACAA



Reverse complement motif      Consensus sequence: TTGTTTCCTT

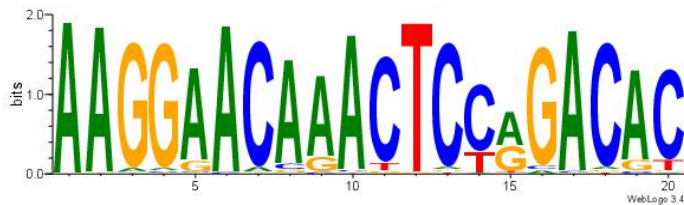


Dataset #: 1  
 Motif ID: 234  
 Motif name: Motif 234  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 11  
 Number of overlap: 9  
 Similarity score: 0.0447051

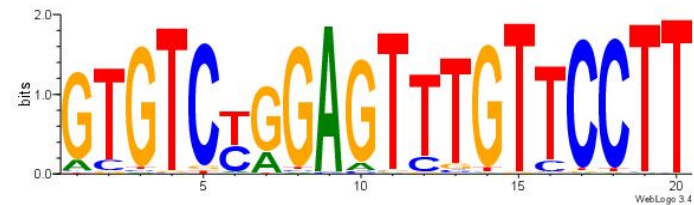
Alignment:

AAGGAACAAACTCCRGACAC  
 -AGGAAGAAA-----

Original motif      Consensus sequence: AAGGAACAAACTCCRGACAC

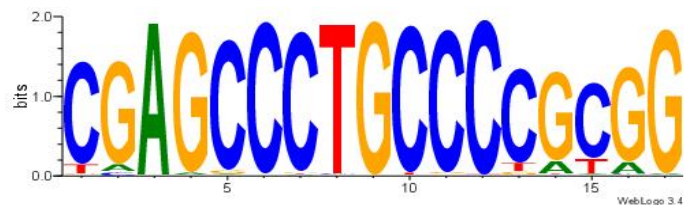


Reverse complement motif      Consensus sequence: GTGTCGGAGTTTGTTCCTT

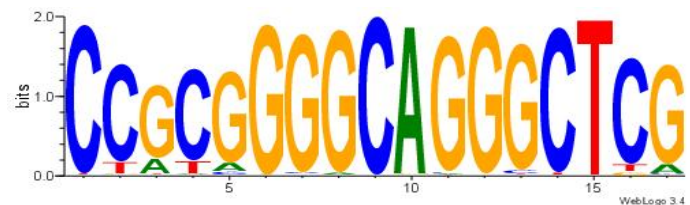


**Dataset #: 1      Motif ID: 78      Motif name: Motif 78**

Original motif      Consensus sequence: CGAGCCCTGCCCGCGG



Reverse complement motif      Consensus sequence: CCGCGGGGCAGGGCTCG



### Best Matches for Motif ID 78 (Highest to Lowest)

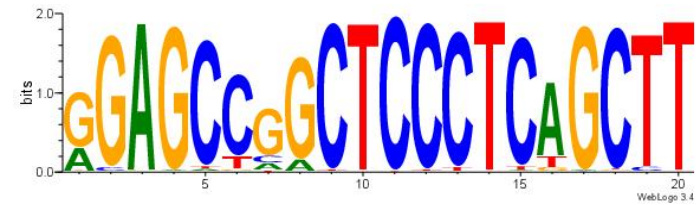
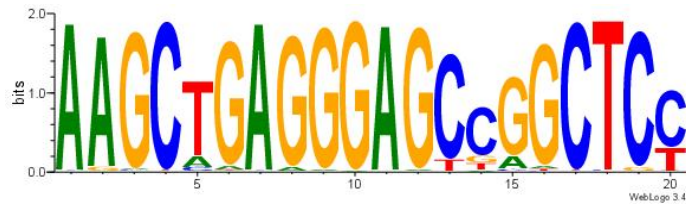
Dataset #:	1
Motif ID:	96
Motif name:	Motif 96
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	17
Similarity score:	0.0803184

#### Alignment:

```
AAGCTGAGGGAGCCGGCTCC  
---CCGCGGGGCAGGGCTCG
```

Original motif      Consensus sequence: AAGCTGAGGGAGCCGGCTCC

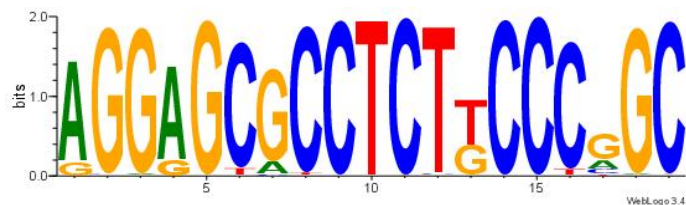
Reverse complement motif      Consensus sequence: GGAGCCGGCTCCCTCAGCTT



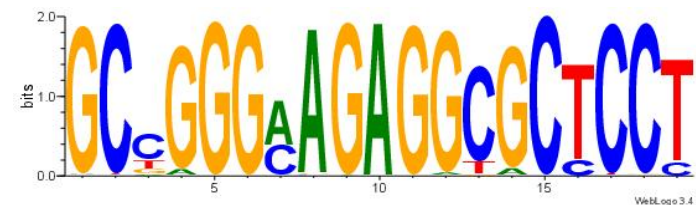
Dataset #: 1  
 Motif ID: 30  
 Motif name: Motif 30  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 2  
 Number of overlap: 17  
 Similarity score: 0.0851642

Alignment:  
 GCCGGGRAGAGGCGCTCCT  
 -CCGCGGGCAGGGCTCG-

Original motif      Consensus sequence: AGGAGCGCTCTKCCCGGC

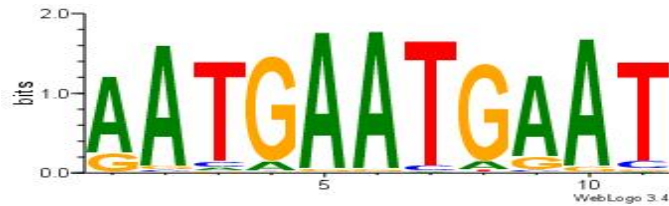


Reverse complement motif      Consensus sequence: GCCGGGRAGAGGCGCTCCT

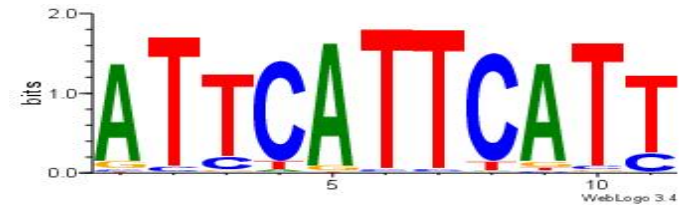


**Dataset #: 1      Motif ID: 79      Motif name: Motif 79**

Original motif    Consensus sequence: AATGAATGAAT



Reverse complement motif    Consensus sequence: ATTCATTCATT



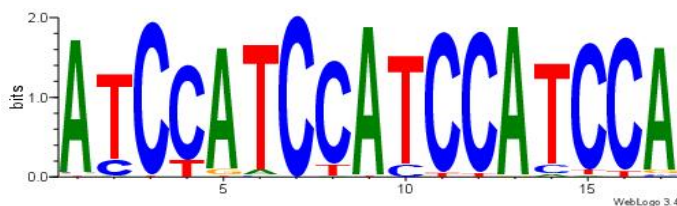
### Best Matches for Motif ID 79 (Highest to Lowest)

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

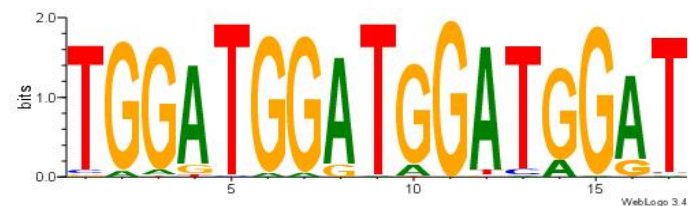
Alignment:

```
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

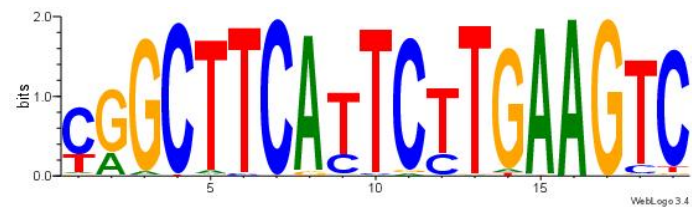
Alignment:

CGGCTTCATTCTTGAAGTC  
 ---ATTCATTCATT-----

Original motif      Consensus sequence: GACTTCAAGAATGAAGCCG



Reverse complement motif      Consensus sequence: CGGCTTCATTCTTGAAGTC

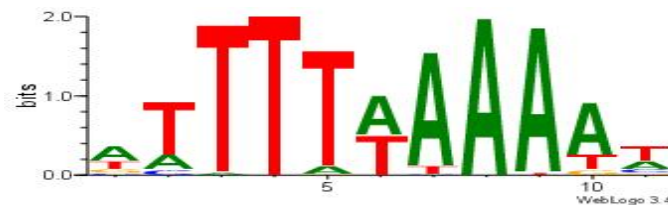
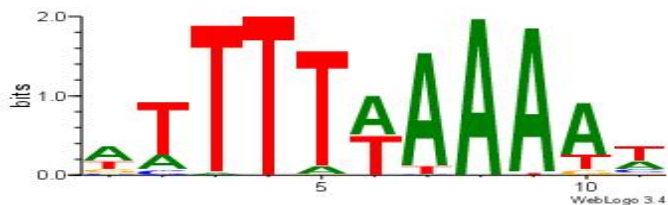



---

**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)

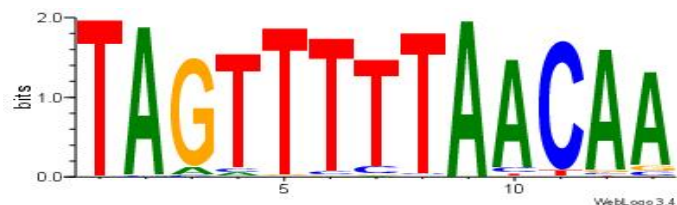
Dataset #: 1  
 Motif ID: 319  
 Motif name: Motif 319  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 3  
 Number of overlap: 11  
 Similarity score: 0.0536456

#### Alignment:

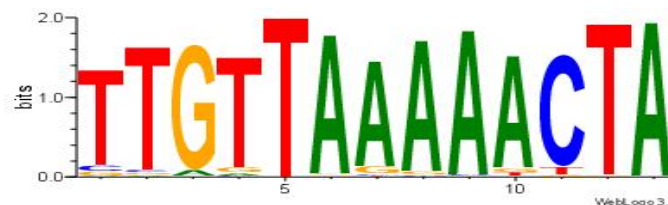
```

TAGTTTTTAACAA
--WTTTTWAAAAW
  
```

Original motif      Consensus sequence: TAGTTTTTAACAA



Reverse complement motif      Consensus sequence: TTGTTAAAACTA

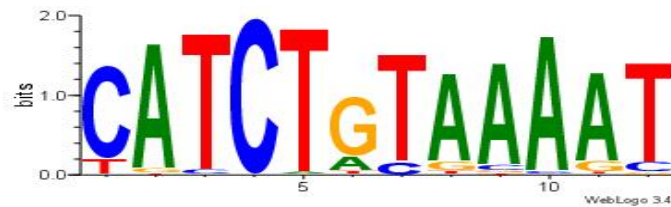


Dataset #: 1

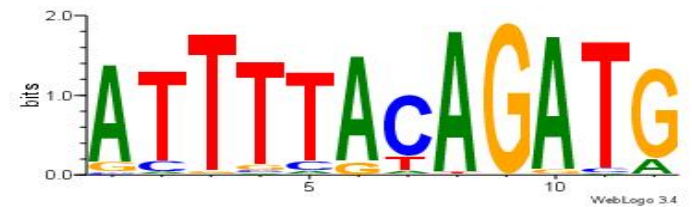
Motif ID: 81  
 Motif name: Motif 81  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 2  
 Number of overlap: 11  
 Similarity score: 0.0558466

Alignment:  
 ATTTTACAGATG  
 WTTTTWAAAAW-

Original motif    Consensus sequence: CATCTGTAAAAT

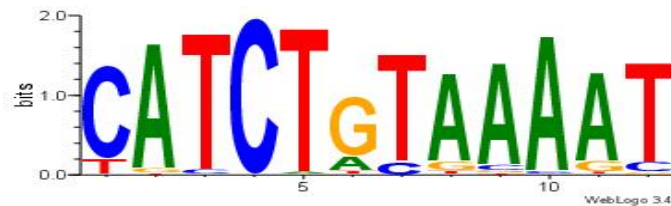


Reverse complement motif    Consensus sequence: ATTTTACAGATG

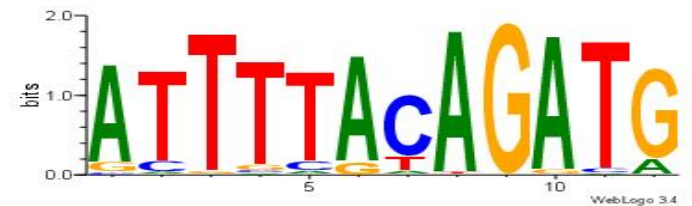


**Dataset #: 1      Motif ID: 81      Motif name: Motif 81**

Original motif    Consensus sequence: CATCTGTAAAAT



Reverse complement motif    Consensus sequence: ATTTTACAGATG



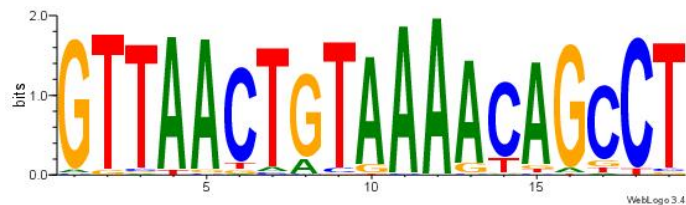
## Best Matches for Motif ID 81 (Highest to Lowest)

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

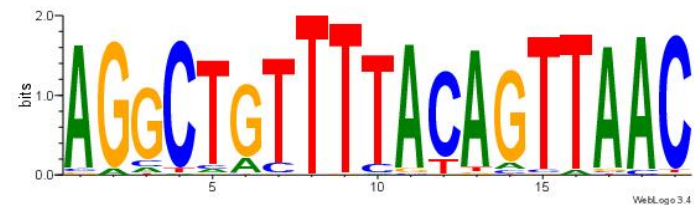
### Alignment:

```
GTAACTGTAAAACAGCCT  
--CATCTGTAAAAT-----
```

Original motif      Consensus sequence: GTAACTGTAAAACAGCCT



Reverse complement motif      Consensus sequence:  
AGGCTGTTTACAGTTAAC



---

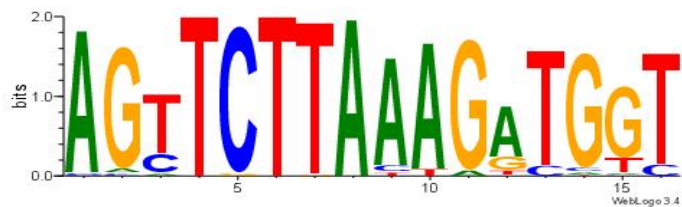
Dataset #: 1  
Motif ID: 303  
Motif name: Motif 303  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Original Motif



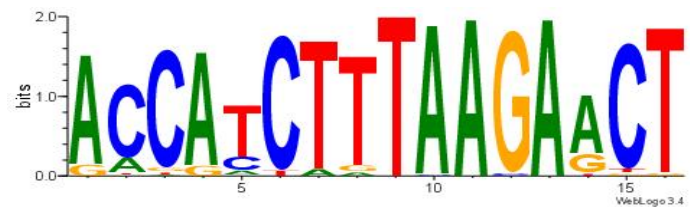
Direction: Forward  
 Position number: 3  
 Number of overlap: 12  
 Similarity score: 0.0658845

Alignment:  
 AGTTCTTAAAGATGGT  
 --ATTTTACAGATG--

Original motif Consensus sequence: AGTTCTTAAAGATGGT

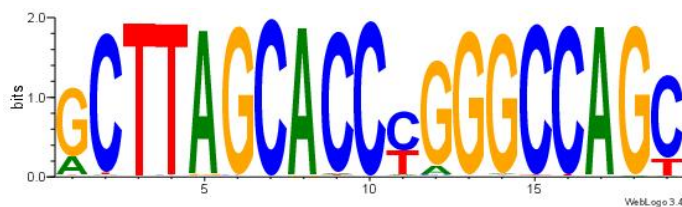


Reverse complement motif Consensus sequence: ACCATCTTTAAGAACT

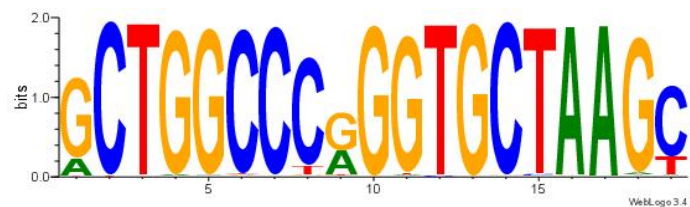


**Dataset #: 1 Motif ID: 82 Motif name: Motif 82**

Original motif Consensus sequence: GCTTAGCACCCGGGCCAGC



Reverse complement motif Consensus sequence: GCTGGCCCKGGTGCTAAGC



**Best Matches for Motif ID 82 (Highest to Lowest)**

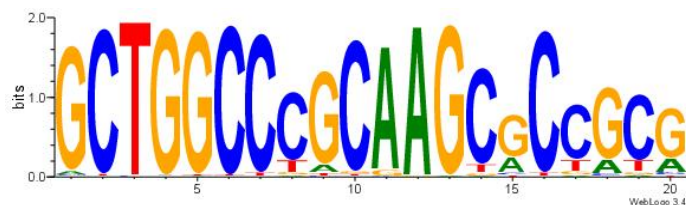
Dataset #: 1

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

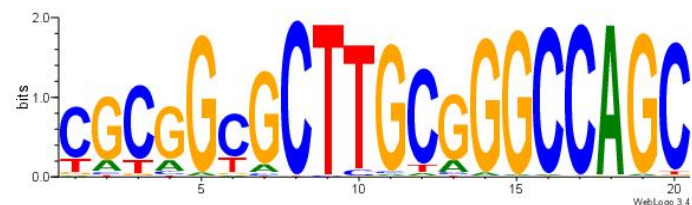
**Alignment:**

CGCGGCGCTTGCGGGCCAGC  
 -GCTTAGCACCYGGGCCAGC

Original motif    Consensus sequence: GCTGGCCCGCAAGCGCCGCG



Reverse complement motif    Consensus sequence: CGCGGCGCTTGCGGGCCAGC



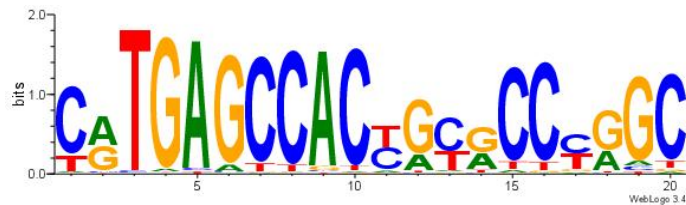
Dataset #: 1  
 Motif ID: 56  
 Motif name: Motif 56  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 19

Similarity score: 0.104947

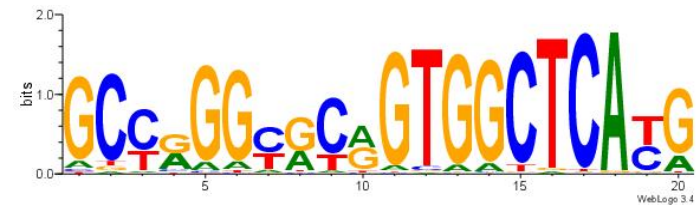
Alignment:

GCCKGGMKCMGTGGCTCAKG  
-GCTGGCCCKGGTGCTAAGC

Original motif      Consensus sequence: CRTGAGCCACYGYRCCYGGC

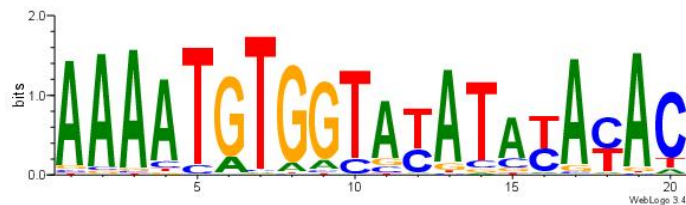


Reverse complement motif      Consensus sequence: GCCKGGMKCMGTGGCTCAKG

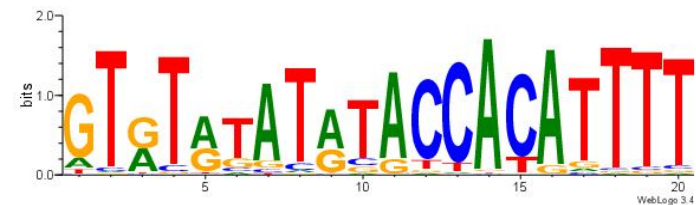


**Dataset #: 1      Motif ID: 83      Motif name: Motif 83**

Original motif      Consensus sequence: AAAATGTGGTAYATAYAYAC



Reverse complement motif      Consensus sequence: GTKTMTATMTACCACATTTT



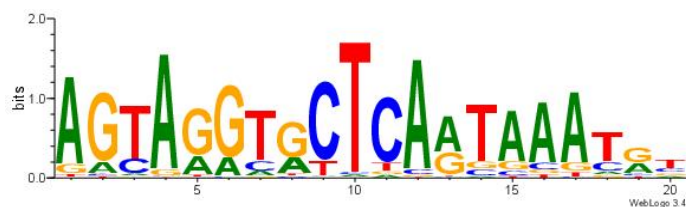
**Best Matches for Motif ID 83 (Highest to Lowest)**

Dataset #:	1
Motif ID:	86
Motif name:	Motif 86
Matching format of first motif:	Original Motif

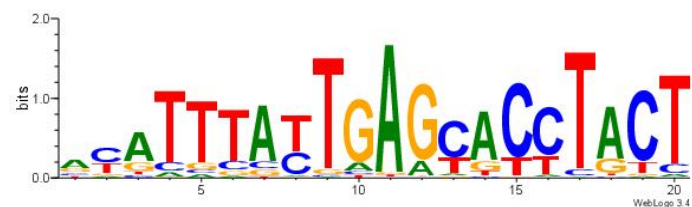
Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 20  
 Similarity score: 0.100064

Alignment:  
 AGTAGGTGCTCARTAAATRB  
 AAAATGTGGTAYATAYAYAC

Original motif Consensus sequence: AGTAGGTGCTCARTAAATRB



Reverse complement motif Consensus sequence:  
 VMATTTAKTGAGCACCTACT

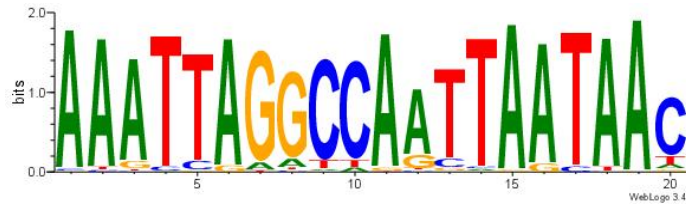


Dataset #: 1  
 Motif ID: 308  
 Motif name: Motif 308  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 20  
 Similarity score: 0.110604

Alignment:

GTTATTAATTGGCCTAATTT  
GKTMTATMTACCACATTTT

Original motif      Consensus sequence: AAATTAGGCCAATTAATAAC

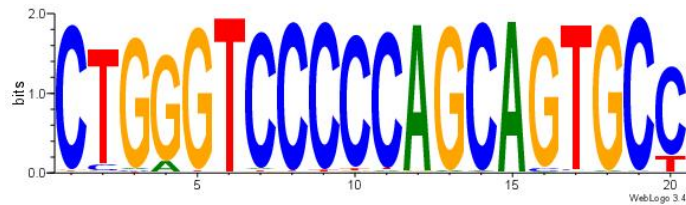


Reverse complement motif      Consensus sequence:  
GTTATTAATTGGCCTAATTT

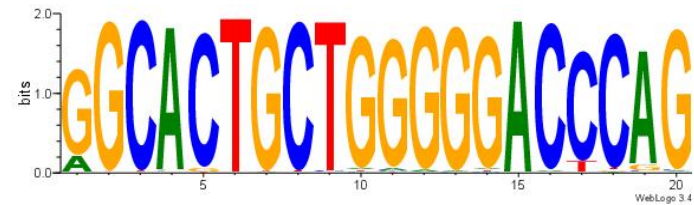


**Dataset #: 1      Motif ID: 84      Motif name: Motif 84**

Original motif      Consensus sequence: CTGGGTCCCCCAGCAGTGCC



Reverse complement motif      Consensus sequence:  
GGCACTGCTGGGGGACCCAG



**Best Matches for Motif ID 84 (Highest to Lowest)**

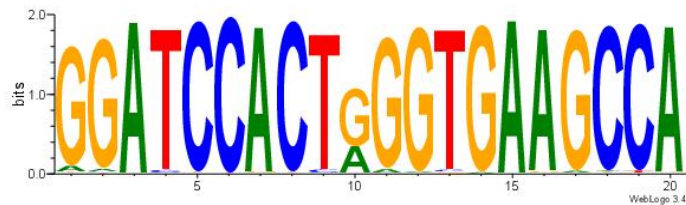
Dataset #:	1
Motif ID:	61
Motif name:	Motif 61
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1

Number of overlap: 20  
Similarity score: 0.106094

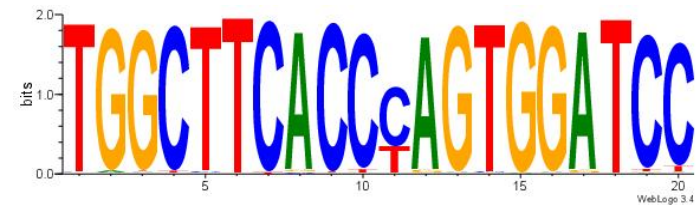
Alignment:

TGGCTTCACCCAGTGGATCC  
CTGGGTCCCCCAGCAGTGCC

Original motif    Consensus sequence: GGATCCACTGGGTGAAGCCA



Reverse complement motif    Consensus sequence: TGGCTTCACCCAGTGGATCC

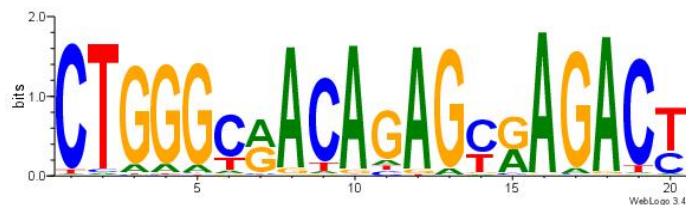


Dataset #: 1  
Motif ID: 29  
Motif name: Motif 29  
Matching format of first motif: Original Motif  
Matching format of second motif: Original Motif  
Direction: Forward  
Position number: 1  
Number of overlap: 20  
Similarity score: 0.107291

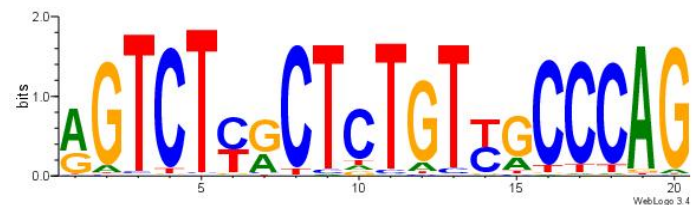
Alignment:

CTGGGCRACAGAGYRAGACY  
CTGGGTCCCCCAGCAGTGCC

Original motif      Consensus sequence: CTGGGCRACAGAGYRAGACY



Reverse complement motif      Consensus sequence: MGTCTMKCTCTGTGCCCCAG

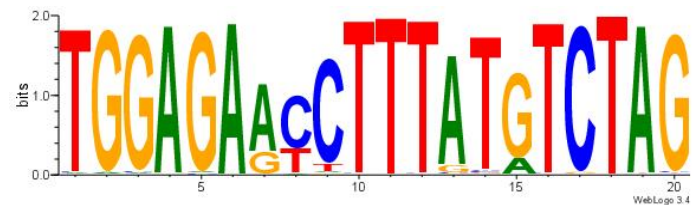


**Dataset #: 1      Motif ID: 85      Motif name: Motif 85**

Original motif      Consensus sequence: CTAGACATAAAGTTCTCCA



Reverse complement motif      Consensus sequence: TGGAGAACCTTTATGTCTAG



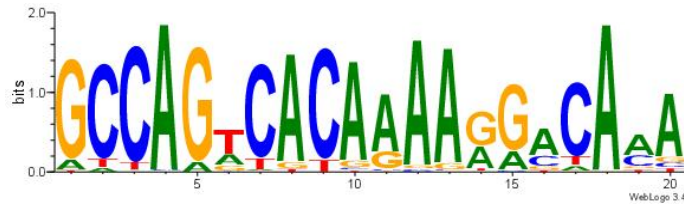
### Best Matches for Motif ID 85 (Highest to Lowest)

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:	2
Number of overlap:	19
Similarity score:	0.110512

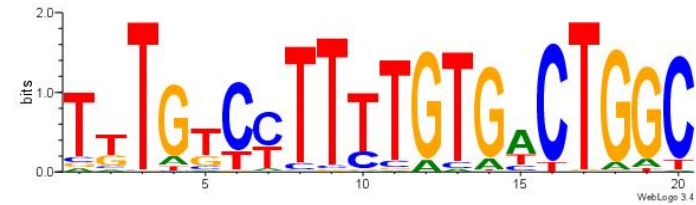
Alignment:

GCCAGTCACAAAARGACAMA-  
-CTAGACATAAAGGTTCTCCA

Original motif      Consensus sequence: GCCAGTCACAAAARGACAMA



Reverse complement motif      Consensus sequence:  
TYTGTCMTTTTGTGACTGGC



Dataset #: 1  
Motif ID: 260  
Motif name: Motif 260  
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: 0.114441

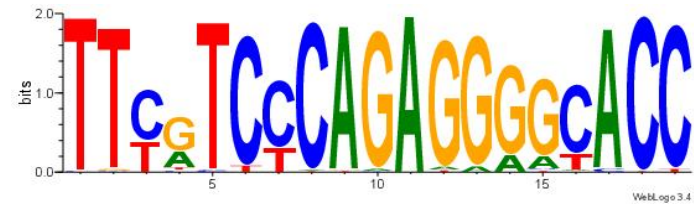
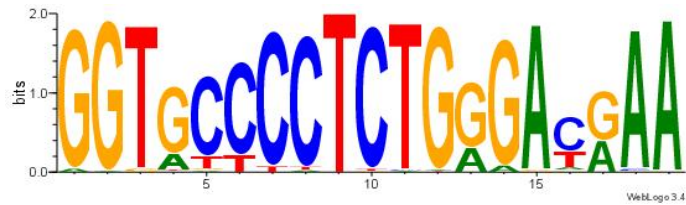
Alignment:

TTMGTCCCAGAGGGGCACC-  
CTAGACATAAAGGTTCTCCA

Original motif      Consensus sequence: GGTGCCCTCTGGGACRAA

Reverse complement motif      Consensus sequence:  
TTMGTCCCAGAGGGGCACC

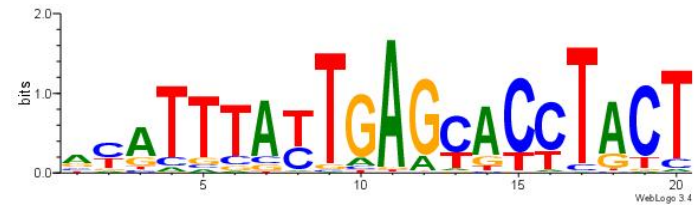
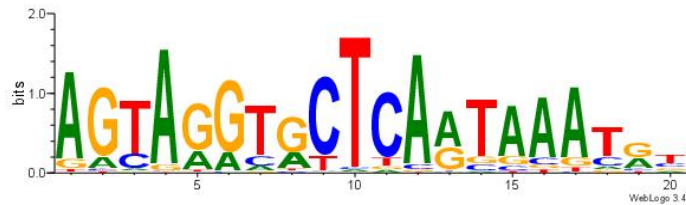




**Dataset #: 1      Motif ID: 86      Motif name: Motif 86**

Original motif      Consensus sequence: AGTAGGTGCTCARTAAATRB

Reverse complement motif      Consensus sequence: VMATTTAKTGAGCACCTACT



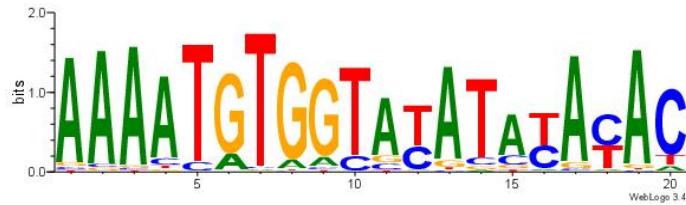
**Best Matches for Motif ID 86 (Highest to Lowest)**

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

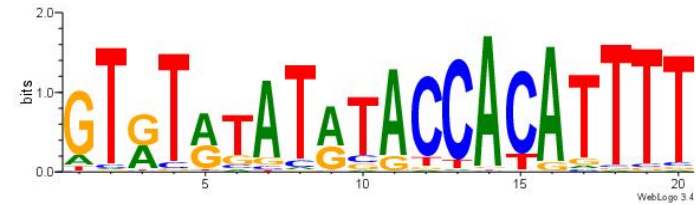
Alignment:

AAAATGTGGTAYATAYAYAC  
AGTAGGTGCTCARTAAATRB

Original motif      Consensus sequence: AAAATGTGGTAYATAYAYAC



Reverse complement motif      Consensus sequence: GTKTMTATMTACCACATTTT



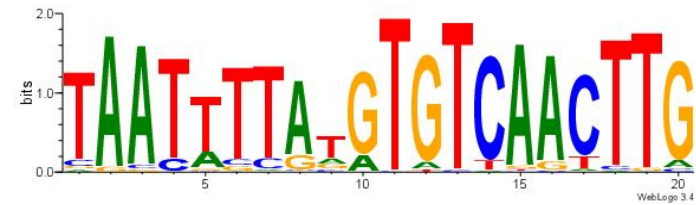
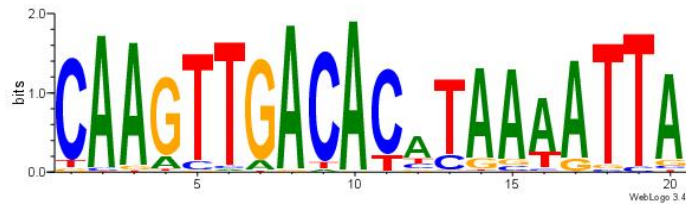
Dataset #: 1  
Motif ID: 357  
Motif name: Motif 357  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Reverse Complement  
Direction: Forward  
Position number: 2  
Number of overlap: 19  
Similarity score: 0.581344

Alignment:

TAATTTTATGTGTCAACTTG-  
-VMATTTAKTGAGCACCTACT

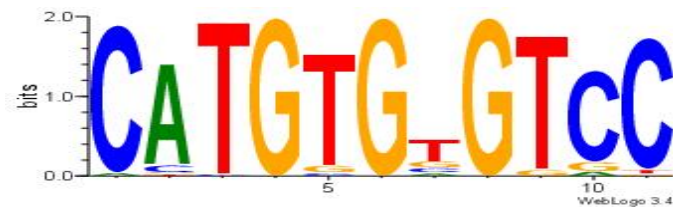
Original motif      Consensus sequence: CAAGTTGACACATAAAATTA

Reverse complement motif      Consensus sequence: TAATTTTATGTGTCAACTTG

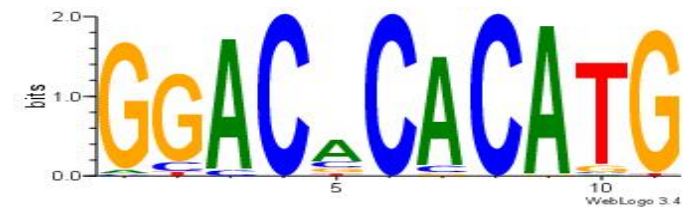


**Dataset #: 1      Motif ID: 87      Motif name: Motif 87**

Original motif      Consensus sequence: CATGTGTGCC



Reverse complement motif      Consensus sequence: GGACACATG

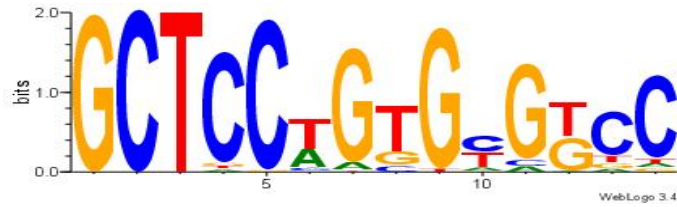


**Best Matches for Motif ID 87 (Highest to Lowest)**

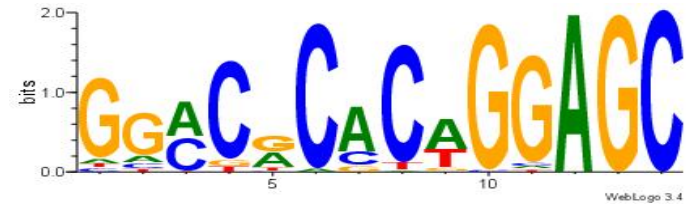
Dataset #:	1
Motif ID:	206
Motif name:	Motif 206
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	4
Number of overlap:	11
Similarity score:	0.0574969

Alignment:  
GCTCCWGTGYGKCC  
---CATGTGTGCC

Original motif      Consensus sequence: GCTCCWGTGYGKCC



Reverse complement motif      Consensus sequence: GGRCKCACWGGAA

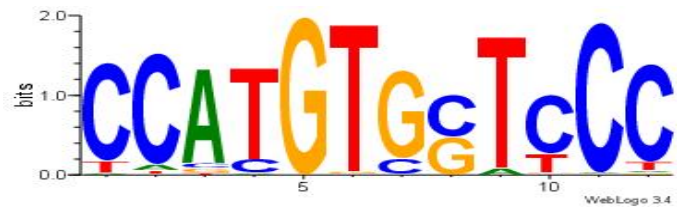


Dataset #: 1  
Motif ID: 120  
Motif name: Motif 120  
Matching format of first motif: Original Motif  
Matching format of second motif: Original Motif  
Direction: Forward  
Position number: 2  
Number of overlap: 11  
Similarity score: 0.062082

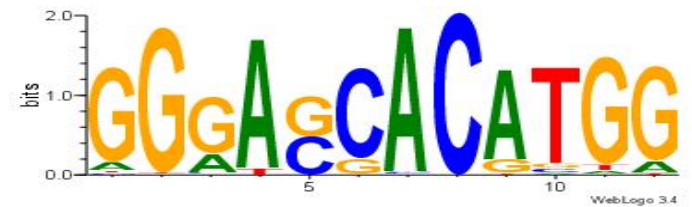
Alignment:

CCATGTGSTCCC  
-CATGTGTGTCC

Original motif      Consensus sequence: CCATGTGSTCCC

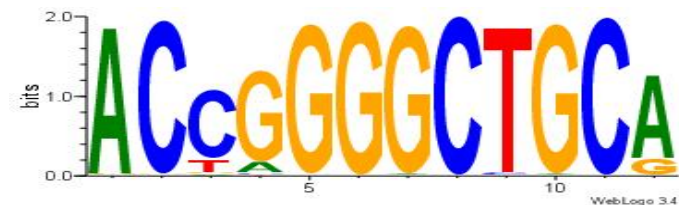


Reverse complement motif      Consensus sequence: GGGASCACATGG

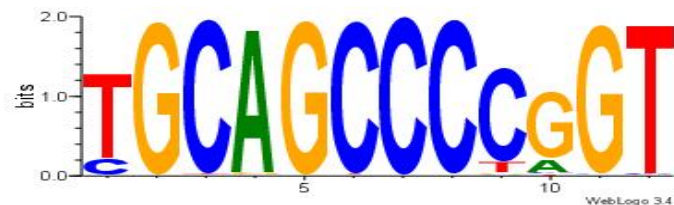


**Dataset #: 1      Motif ID: 88      Motif name: Motif 88**

Original motif      Consensus sequence: ACCGGGGCTGCA



Reverse complement motif      Consensus sequence: TGCAGCCCCGGT



**Best Matches for Motif ID 88 (Highest to Lowest)**

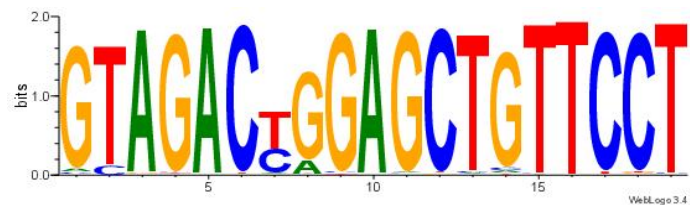
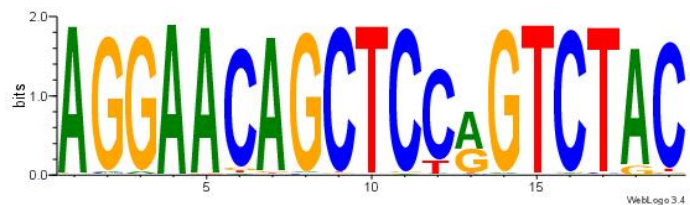
Dataset #:	1
Motif ID:	62
Motif name:	Motif 62
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	4
Number of overlap:	12
Similarity score:	0.0744827

**Alignment:**

```
GTAGACKGGAGCTGTTTCCT  
---ACCGGGGCTGCA----
```

Original motif      Consensus sequence: AGGAACAGCTCCRGCTCTAC

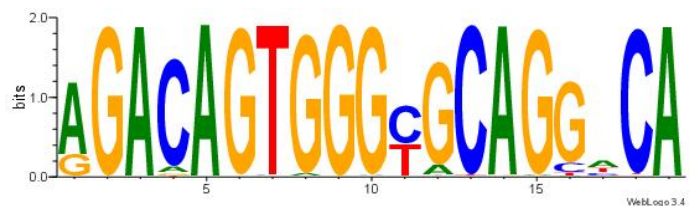
Reverse complement motif      Consensus sequence:  
GTAGACKGGAGCTGTTTCCT



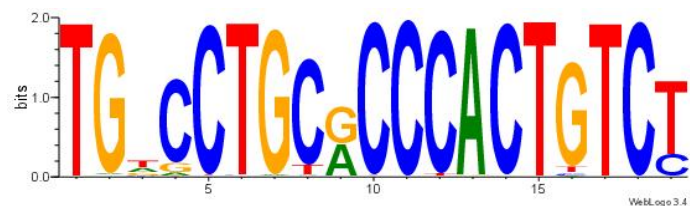
Dataset #: 1  
 Motif ID: 17  
 Motif name: Motif 17  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 3  
 Number of overlap: 12  
 Similarity score: 0.0782839

Alignment:  
 AGACAGTGGGYGCAGGHCA  
 --ACCGGGGCTGCA-----

Original motif      Consensus sequence: AGACAGTGGGYGCAGGHCA

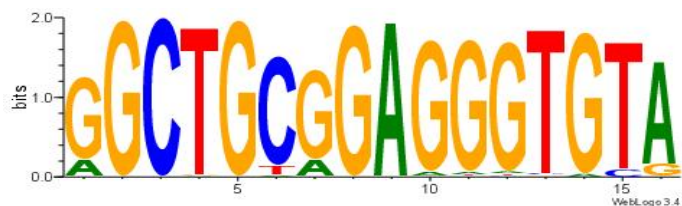


Reverse complement motif      Consensus sequence: TGHCTGCKCCCACTGTCT

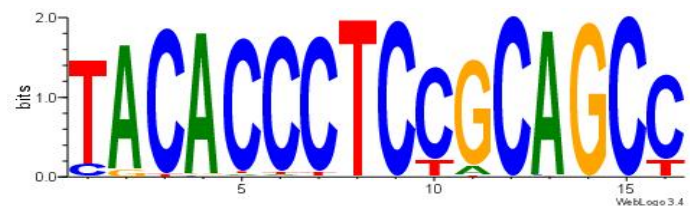


**Dataset #: 1      Motif ID: 89      Motif name: Motif 89**

Original motif    Consensus sequence: GGCTGCGAGGGTGTA



Reverse complement motif    Consensus sequence: TACACCCTCCGCAGCC



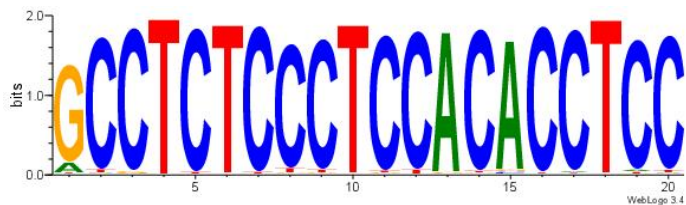
### Best Matches for Motif ID 89 (Highest to Lowest)

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

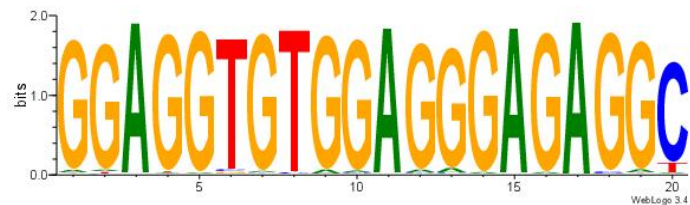
#### Alignment:

```
GGAGGTGTGGAGGGAGAGGC  
--GGCTGCGGAGGGTGTA--
```

Original motif    Consensus sequence: GCCTCTCCCTCCACACCTCC



Reverse complement motif    Consensus sequence: GGAGGTGTGGAGGGAGAGGC

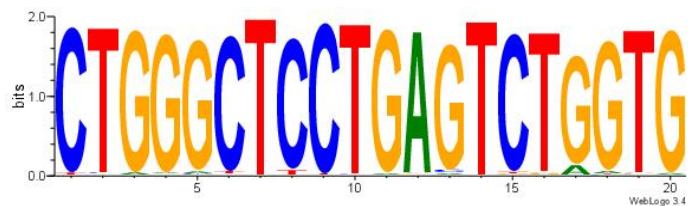


Dataset #: 1  
 Motif ID: 67  
 Motif name: Motif 67  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 4  
 Number of overlap: 16  
 Similarity score: 0.0835227

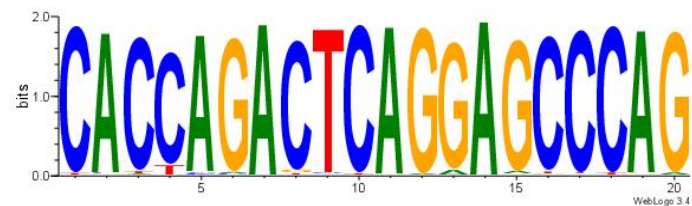
Alignment:

CACCAGACTCAGGAGCCCAG  
 -TACACCCTCCGCAGCC---

Original motif      Consensus sequence: CTGGGCTCCTGAGTCTGGTG



Reverse complement motif      Consensus sequence: CACCAGACTCAGGAGCCCAG

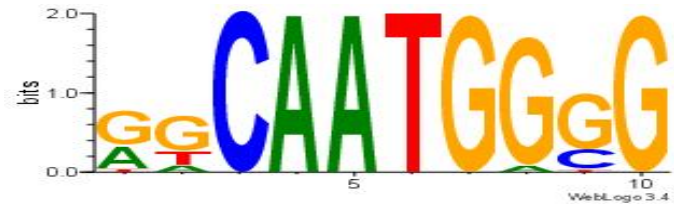
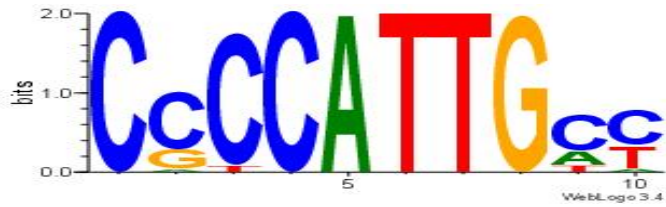


**Dataset #: 1      Motif ID: 90      Motif name: Motif 90**

Original motif      Consensus sequence: CCCATTGCY

Reverse complement motif      Consensus sequence: KGCAATGGGG





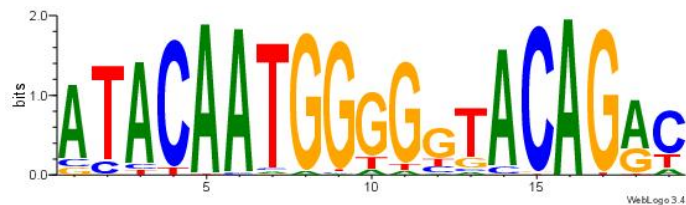
### Best Matches for Motif ID 90 (Highest to Lowest)

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

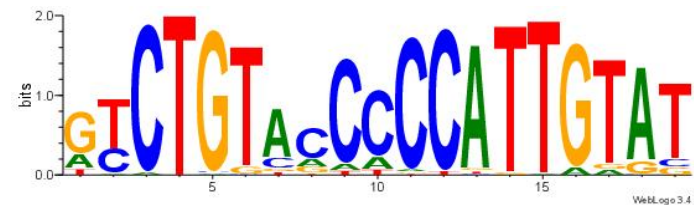
#### Alignment:

ATACAATGGGGGTACAGRC  
 -KGCAATGGGG-----

Original motif      Consensus sequence: ATACAATGGGGGTACAGRC



Reverse complement motif      Consensus sequence: GKCTGTACCCCATTTGTAT

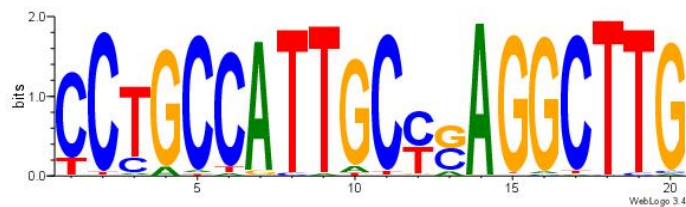


Dataset #: 1  
 Motif ID: 196  
 Motif name: Motif 196  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 9  
 Number of overlap: 10  
 Similarity score: 0.0348826

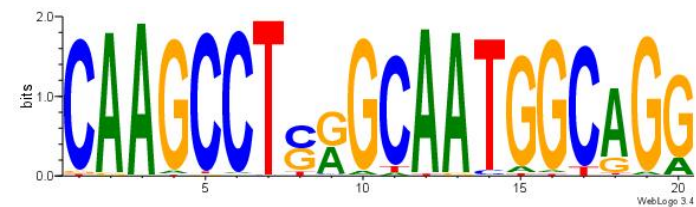
Alignment:

CCTGCCATTGCYSAGGCTTG  
 --CCCCATTGCY-----

Original motif      Consensus sequence: CCTGCCATTGCYSAGGCTTG



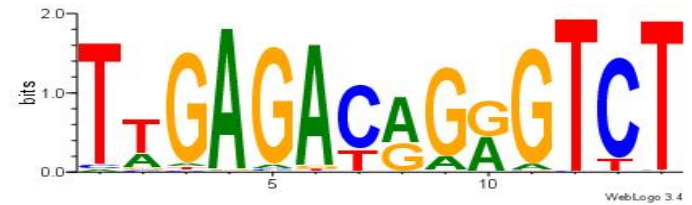
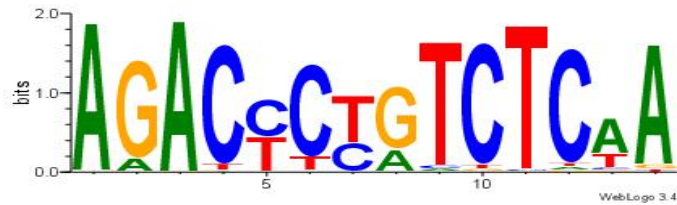
Reverse complement motif      Consensus sequence: CAAGCCTSKGCAATGGCAGG



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

Original motif      Consensus sequence: AGACYCYGTCTCAA

Reverse complement motif      Consensus sequence: TTGAGACMGKGTCT

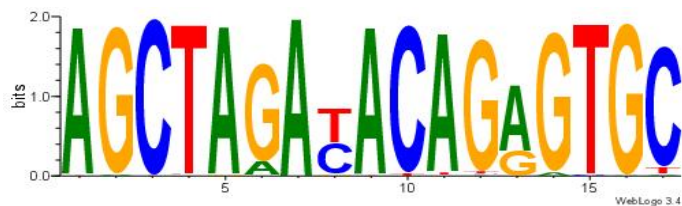


**Best Matches for Motif ID 91 (Highest to Lowest)**

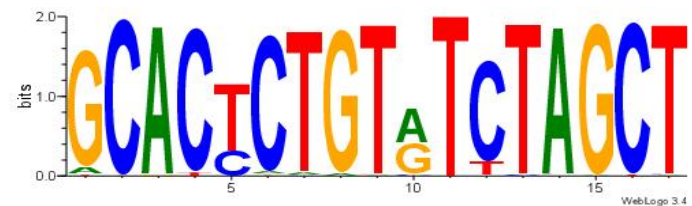
Dataset #: 1  
 Motif ID: 175  
 Motif name: Motif 175  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 4  
 Number of overlap: 14  
 Similarity score: 0.0743241

Alignment:  
 GCACTCTGTMCTAGCT  
 AGACYCYGTCTCAA---

Original motif      Consensus sequence: AGCTAGAYACAGAGTGC



Reverse complement motif      Consensus sequence: GCACTCTGTMCTAGCT

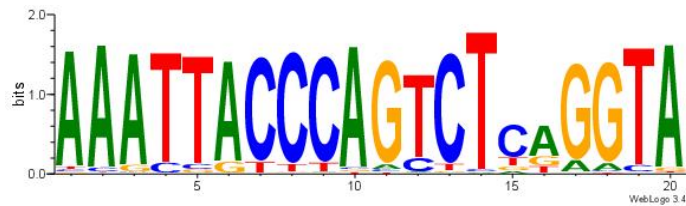


Dataset #: 1  
 Motif ID: 160  
 Motif name: Motif 160  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 4  
 Number of overlap: 14  
 Similarity score: 0.0811922

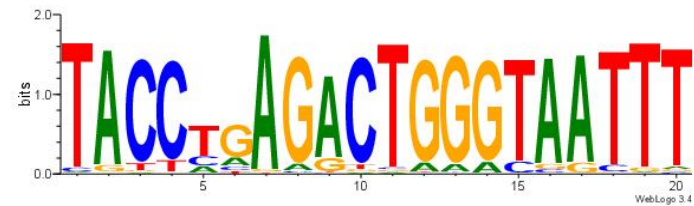
Alignment:

TACCTGAGACTGGGTAATTT  
 ---TTGAGACMGKGTCT---

Original motif      Consensus sequence: AAATTACCCAGTCTCAGGTA



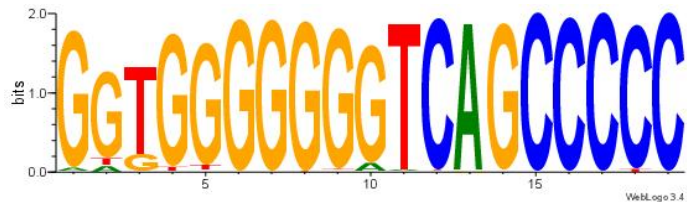
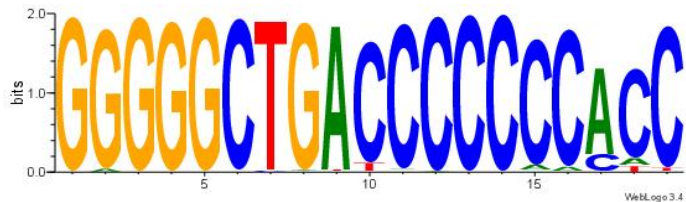
Reverse complement motif      Consensus sequence:  
TACCTGAGACTGGGTAATTT



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

Original motif      Consensus sequence: GGGGCTGACCCCCACC

Reverse complement motif      Consensus sequence:  
GGTGGGGGGTTCAGCCCC

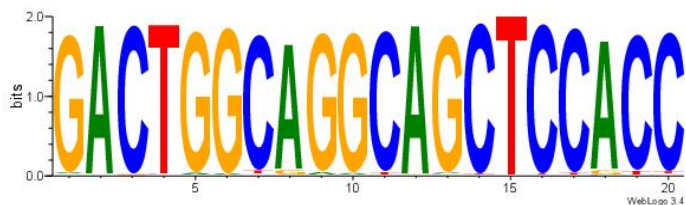


**Best Matches for Motif ID 92 (Highest to Lowest)**

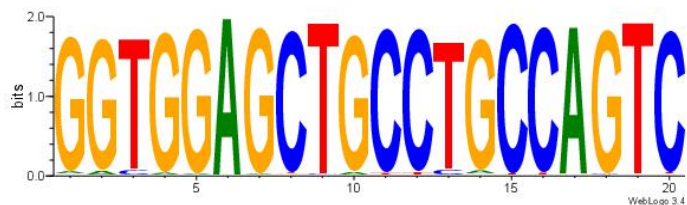
Dataset #: 1  
 Motif ID: 52  
 Motif name: Motif 52  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 2  
 Number of overlap: 19  
 Similarity score: 0.100201

Alignment:  
 GACTGGCAGGCAGCTCCACC  
 -GGGGGCTGACCCCCCCACC

Original motif      Consensus sequence: GACTGGCAGGCAGCTCCACC



Reverse complement motif      Consensus sequence: GGTGGAGCTGCCAGTC

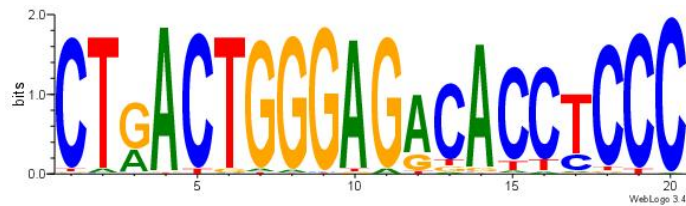


Dataset #: 1  
 Motif ID: 293  
 Motif name: Motif 293  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 19  
 Similarity score: 0.10109

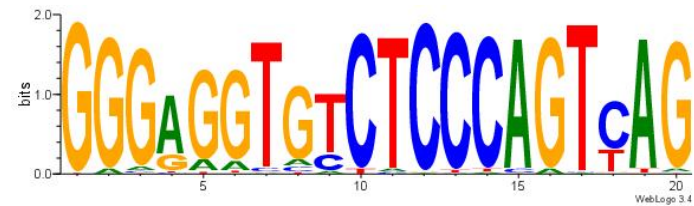
Alignment:

CTGACTGGGAGACACCTCCC  
 -GGTGGGGGGGTCAGCCCCC

Original motif      Consensus sequence: CTGACTGGGAGACACCTCCC



Reverse complement motif      Consensus sequence: GGGAGGTGTCTCCCAGTCAG

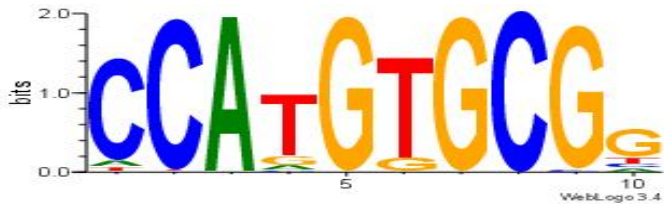



---

**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)

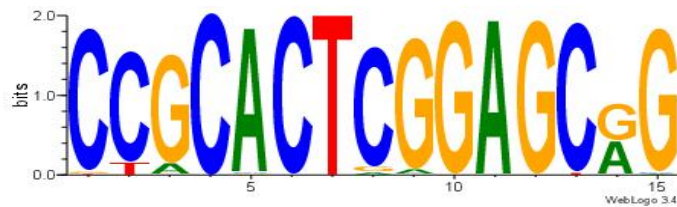
Dataset #: 1  
 Motif ID: 128  
 Motif name: Motif 128  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 10  
 Similarity score: 0.0496914

#### Alignment:

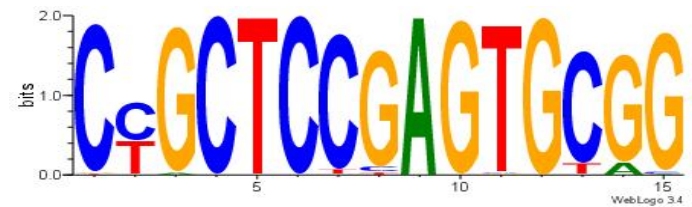
```

CMGCTCCGAGTGCGG
-----CCATGTGCGG
  
```

Original motif      Consensus sequence: CCGCACTCGGAGCG



Reverse complement motif      Consensus sequence: CMGCTCCGAGTGCGG

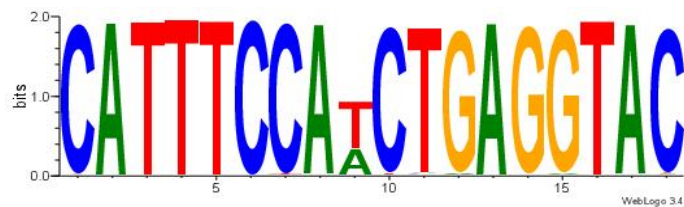


Dataset #: 1  
 Motif ID: 25  
 Motif name: Motif 25  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 6  
 Number of overlap: 10  
 Similarity score: 0.0540497

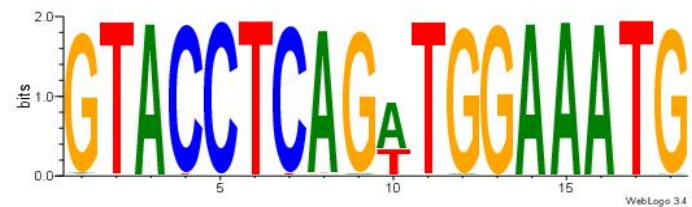
Alignment:

GTACCTCAGWTGGAAATG  
 ---CCGCACATGG-----

Original motif      Consensus sequence: CATTTC~~CA~~CTGAGGTAC



Reverse complement motif      Consensus sequence: GTACCTCAGWTGGAAATG



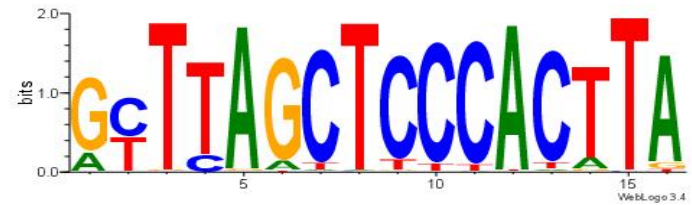
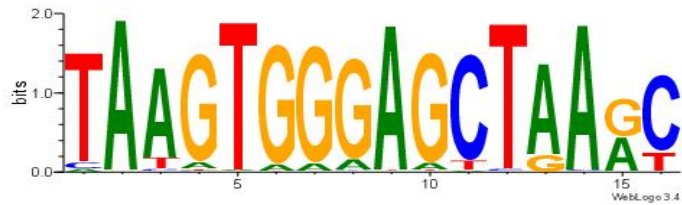

---

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

Original motif      Consensus sequence: TAAGTGGGAGCTAARC

Reverse complement motif      Consensus sequence: G~~MT~~TAGCTCCCACTTA



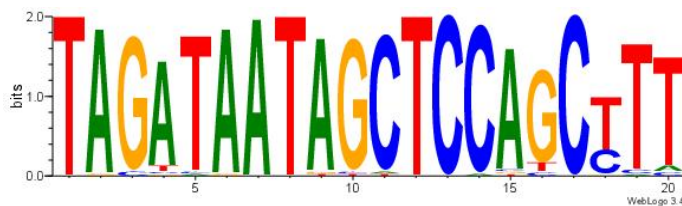


**Best Matches for Motif ID 94 (Highest to Lowest)**

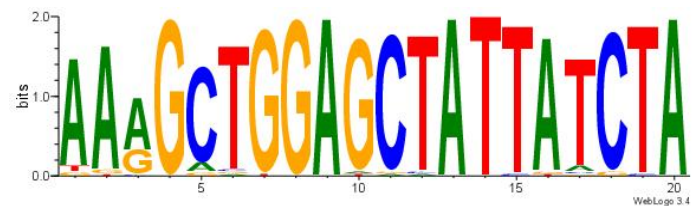
Dataset #: 1  
 Motif ID: 333  
 Motif name: Motif 333  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 5  
 Number of overlap: 16  
 Similarity score: 0.062587

Alignment:  
 TAGATAATAGCTCCAGCTTT  
 ----GMTTAGCTCCC ACTTA

Original motif      Consensus sequence: TAGATAATAGCTCCAGCTTT



Reverse complement motif      Consensus sequence: AAAGCTGGAGCTATTATCTA

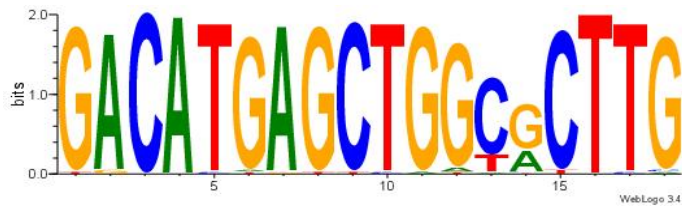


Dataset #: 1  
 Motif ID: 306  
 Motif name: Motif 306  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 16  
 Similarity score: 0.0700236

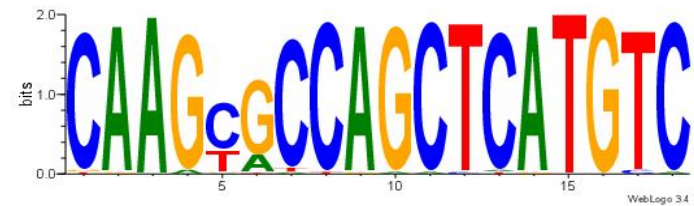
Alignment:

GACATGAGCTGGCGCTTG  
 --GMTTAGCTCCCACTTA

Original motif    Consensus sequence: GACATGAGCTGGCGCTTG



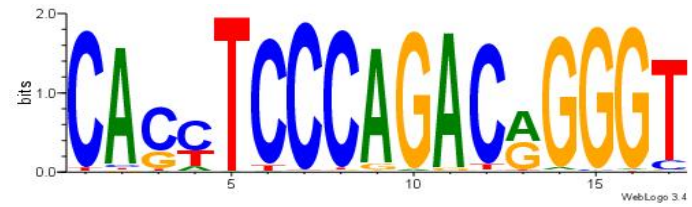
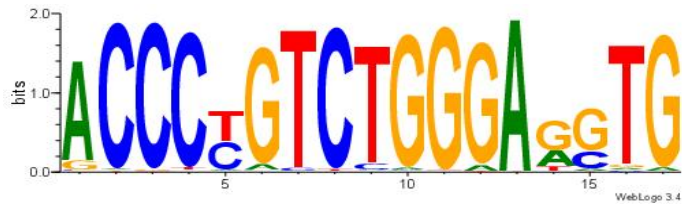
Reverse complement motif    Consensus sequence: CAAGCGCCAGCTCATGTC



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

Original motif    Consensus sequence: ACCCYGTCTGGGAGGTG

Reverse complement motif    Consensus sequence: CACCTCCCAGACMGGGT

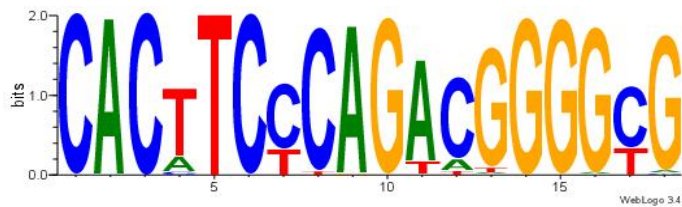


**Best Matches for Motif ID 95 (Highest to Lowest)**

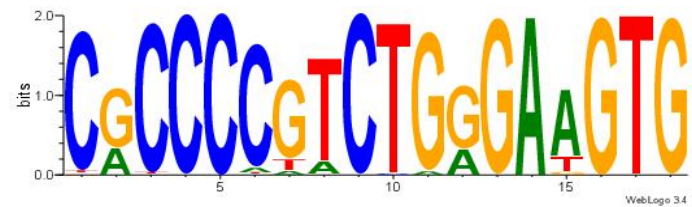
Dataset #: 1  
 Motif ID: 27  
 Motif name: Motif 27  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 17  
 Similarity score: 0.0376618

Alignment:  
 CACTTCCCAGACGGGGCG  
 -CACCTCCCAGACMGGGT

Original motif      Consensus sequence: CACTTCCCAGACGGGGCG



Reverse complement motif      Consensus sequence: CGCCCCGTCTGGGAAGTG

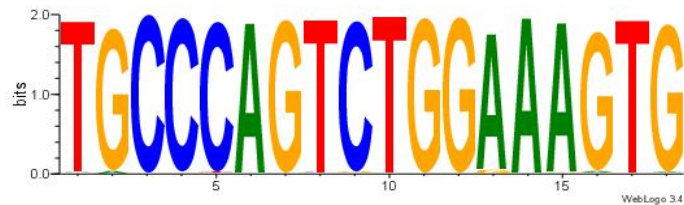


Dataset #: 1  
 Motif ID: 45  
 Motif name: Motif 45  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 17  
 Similarity score: 0.0519023

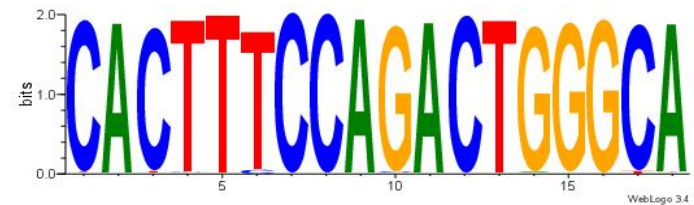
Alignment:

TGCCCAGTCTGGAAAGTG  
 -ACCCYGTCTGGGAGGTG

Original motif      Consensus sequence: TGCCCAGTCTGGAAAGTG



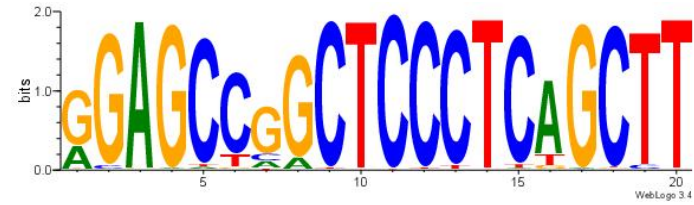
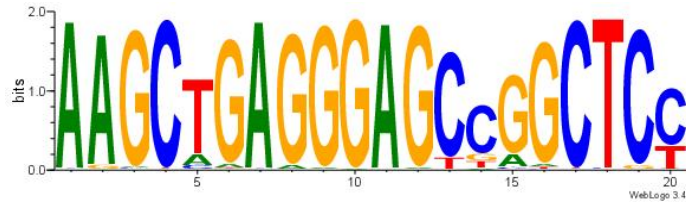
Reverse complement motif      Consensus sequence: CACTTCCAGACTGGGCA



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

Original motif      Consensus sequence: AAGCTGAGGGAGCCGGCTCC

Reverse complement motif      Consensus sequence: GGAGCCGGCTCCCTCAGCTT



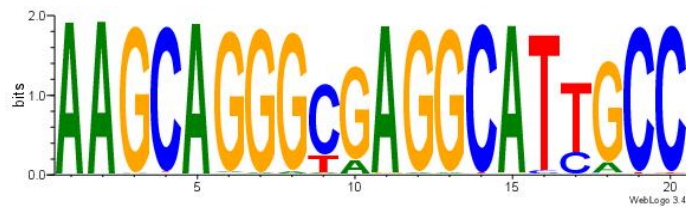
### Best Matches for Motif ID 96 (Highest to Lowest)

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

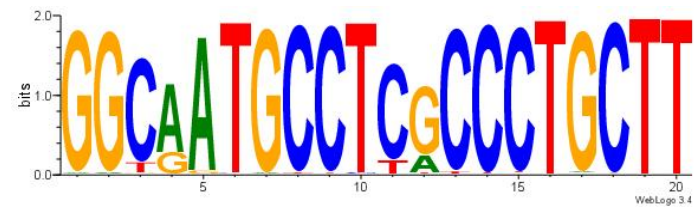
#### Alignment:

AAGCAGGGCGAGGCATTGCC  
 AAGCTGAGGGAGCCGGCTCC

Original motif      Consensus sequence: AAGCAGGGCGAGGCATTGCC



Reverse complement motif      Consensus sequence: GGCAATGCCTCGCCCTGCTT

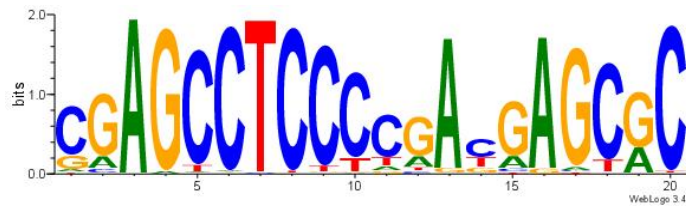


Dataset #: 1  
 Motif ID: 108  
 Motif name: Motif 108  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 20  
 Similarity score: 0.11205

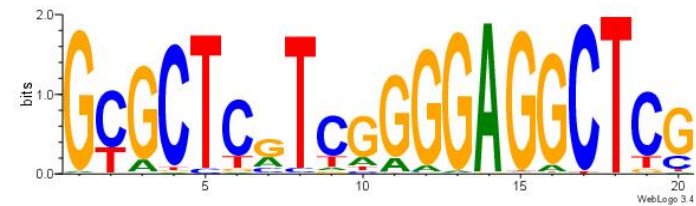
Alignment:

CGAGCCTCCCCGAYGAGCGC  
 GGAGCCGGCTCCCTCAGCTT

Original motif      Consensus sequence: CGAGCCTCCCCGAYGAGCGC



Reverse complement motif      Consensus sequence: GCGCTCKTCGGGGAGGCTCG

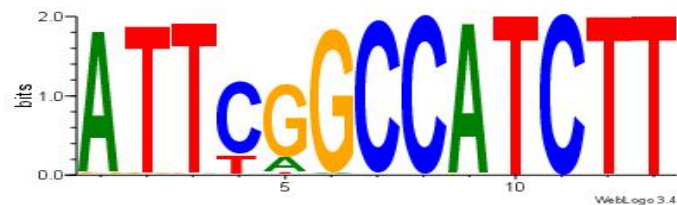
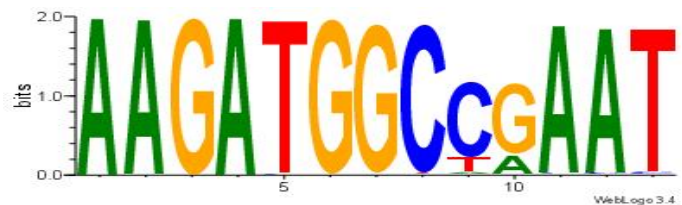



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**Dataset #: 1      Motif ID: 97      Motif name: Motif 97**

Original motif      Consensus sequence: AAGATGGCCGAAT

Reverse complement motif      Consensus sequence: ATTCGGCCATCTT

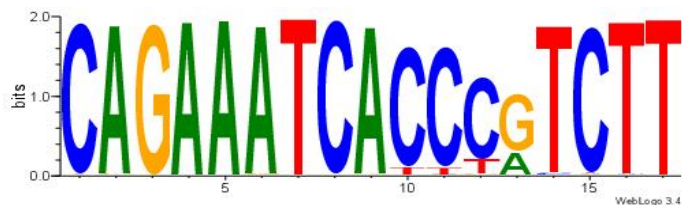


**Best Matches for Motif ID 97 (Highest to Lowest)**

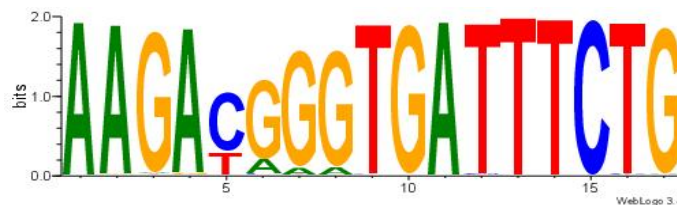
Dataset #: 1  
 Motif ID: 35  
 Motif name: Motif 35  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 13  
 Similarity score: 0.0664224

Alignment:  
 AAGACGGGTGATTTCTG  
 ----AAGATGGCCGAAT

Original motif    Consensus sequence: CAGAAATCACCCGTTCTT



Reverse complement motif    Consensus sequence: AAGACGGGTGATTTCTG

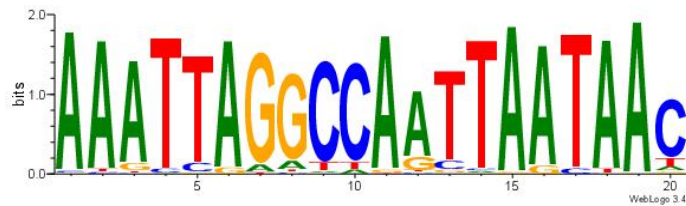


Dataset #: 1  
 Motif ID: 308  
 Motif name: Motif 308  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 6  
 Number of overlap: 13  
 Similarity score: 0.0712075

Alignment:

AAATTAGGCCAATTAATAAC  
 --ATTCGGCCATCTT-----

Original motif      Consensus sequence: AAATTAGGCCAATTAATAAC



Reverse complement motif      Consensus sequence: GTTATTAATTGGCCTAATTT

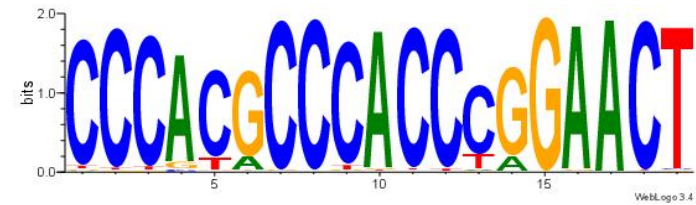
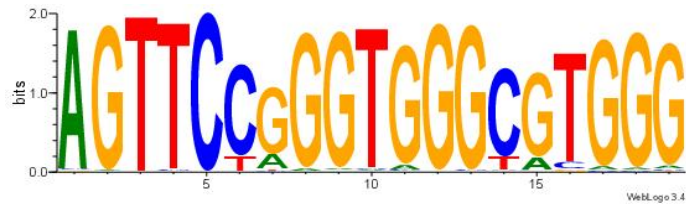


**Dataset #: 1      Motif ID: 98      Motif name: Motif 98**

Original motif      Consensus sequence: AGTTCGGGTGGGCGTGGG

Reverse complement motif      Consensus sequence: CCCACGCCACCCGGAAT





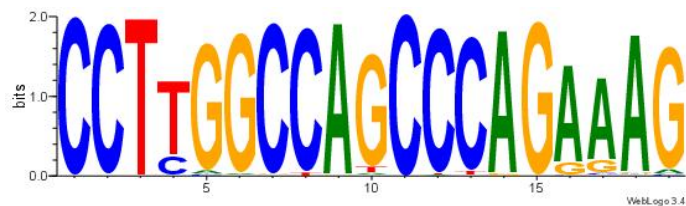
### Best Matches for Motif ID 98 (Highest to Lowest)

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

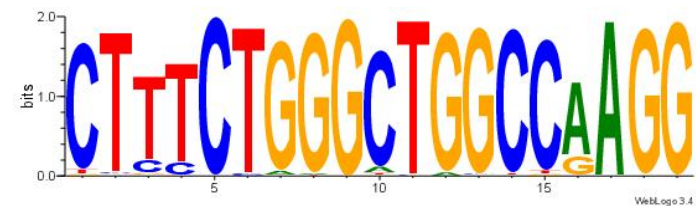
#### Alignment:

CTTTCTGGGCTGGCCAAGG  
 AGTTCCGGGTGGGCGTGGG

Original motif      Consensus sequence: CCTTGGCCAGCCCAGAAAG



Reverse complement motif      Consensus sequence: CTTTCTGGGCTGGCCAAGG

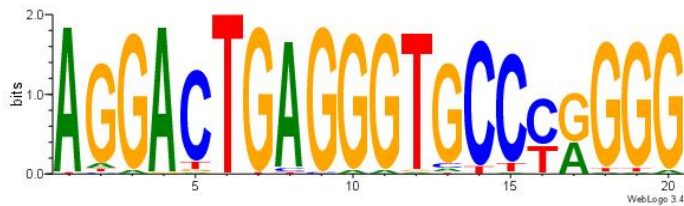


Dataset #: 1  
 Motif ID: 312  
 Motif name: Motif 312  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 19  
 Similarity score: 0.0978875

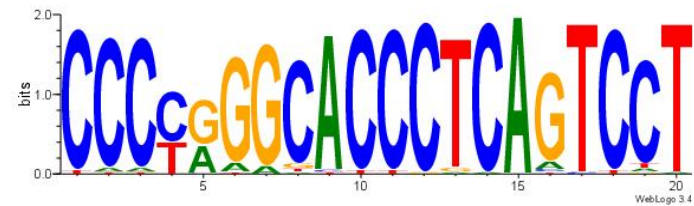
Alignment:

AGGACTGAGGGTGCCYRGGG  
 AGTTCCGGGTGGCGTGGG-

Original motif      Consensus sequence: AGGACTGAGGGTGCCYRGGG



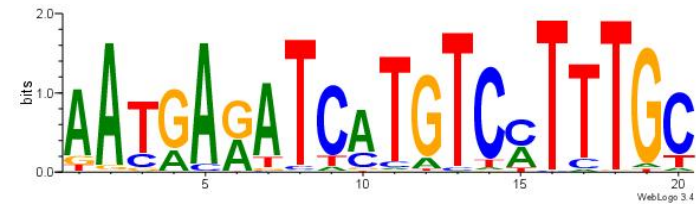
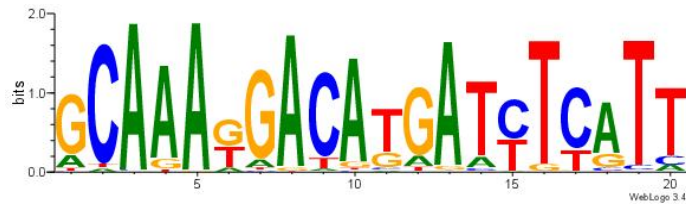
Reverse complement motif      Consensus sequence: CCCMKGGCACCCTCAGTCCT



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

Original motif      Consensus sequence: GCAAAGACATGATYTCATT

Reverse complement motif      Consensus sequence: AATGAKATCATGTCYTTTGC

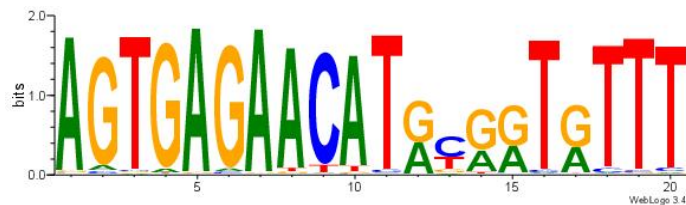


**Best Matches for Motif ID 99 (Highest to Lowest)**

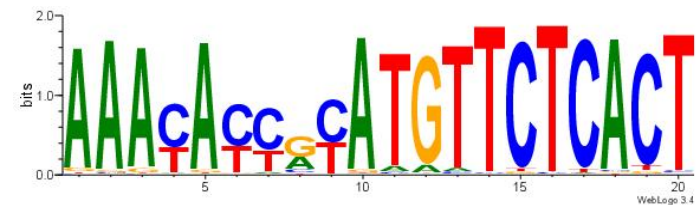
Dataset #: 1  
 Motif ID: 63  
 Motif name: Motif 63  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 20  
 Similarity score: 0.0793398

Alignment:  
 AGTGAGAACATRYRRTRTTT  
 AATGAKATCATGTCYTTTGC

Original motif    Consensus sequence: AGTGAGAACATRYRRTRTTT



Reverse complement motif    Consensus sequence: AAAMAMMKMATGTTCTCACT

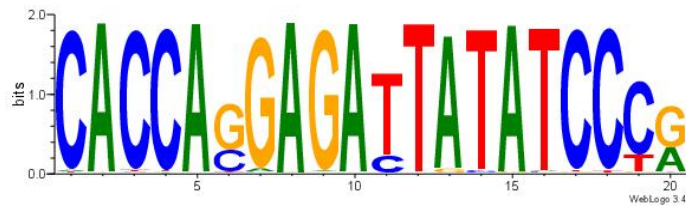


Dataset #: 1  
 Motif ID: 19  
 Motif name: Motif 19  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 20  
 Similarity score: 0.0873595

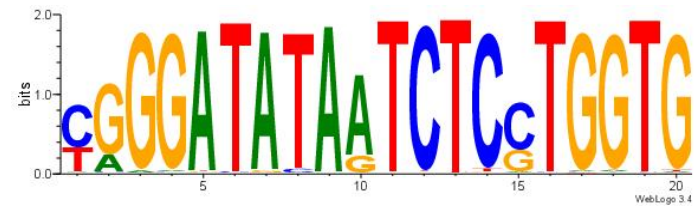
Alignment:

MGGGATATAATCTCCTGGTG  
 AATGAKATCATGTCYTTTGC

Original motif      Consensus sequence: CACCAGGAGATTATATCCCR



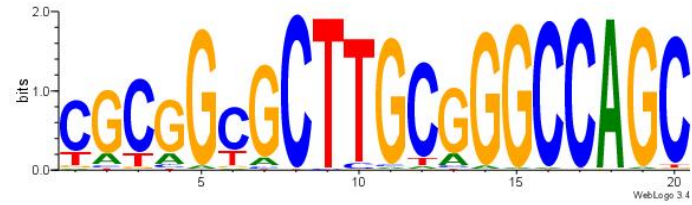
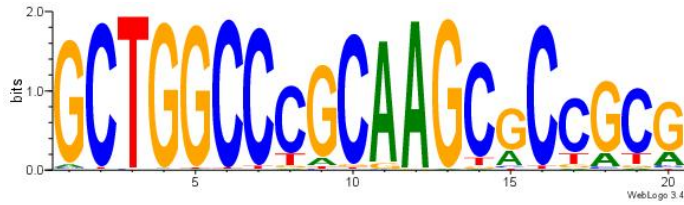
Reverse complement motif      Consensus sequence: MGGGATATAATCTCCTGGTG



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

Original motif      Consensus sequence: GCTGGCCCGCAAGCGCCGCG

Reverse complement motif      Consensus sequence: CGCGGCGCTTGCGGGCCAGC



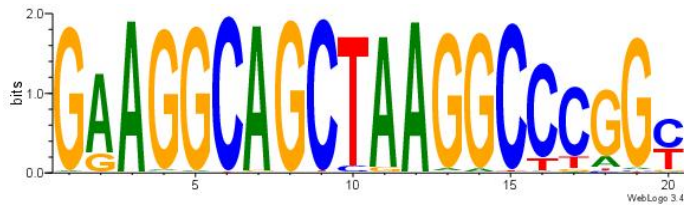
**Best Matches for Motif ID 100 (Highest to Lowest)**

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

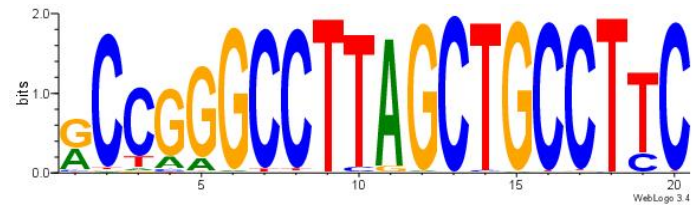
**Alignment:**

KCCGGGCCTTAGCTGCCTTC  
 CGCGGCGCTTGCGGGCCAGC

Original motif      Consensus sequence: GAAGGCAGCTAAGGCCcCGG



Reverse complement motif      Consensus sequence: KCCGGGCCTTAGCTGCCTTC

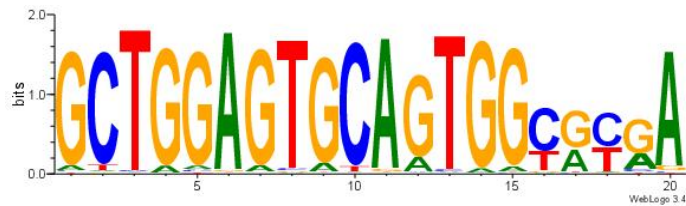


Dataset #: 1  
 Motif ID: 3  
 Motif name: Motif 3  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 20  
 Similarity score: 0.111065

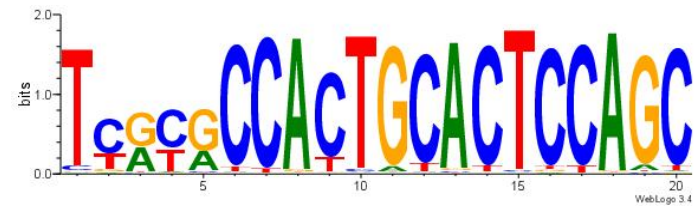
Alignment:

GCTGGAGTGCAGTGGCRYGA  
 GCTGGCCCGCAAGCGCCGCG

Original motif      Consensus sequence: GCTGGAGTGCAGTGGCRYGA



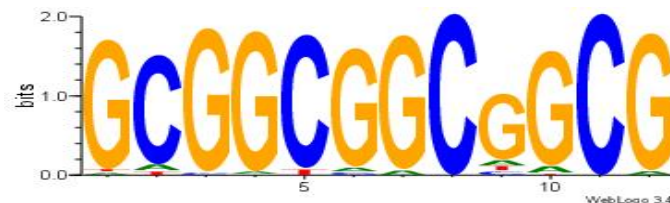
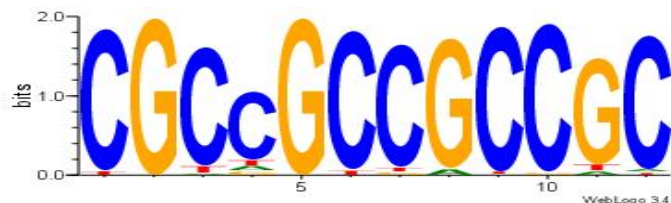
Reverse complement motif      Consensus sequence: TCKMGCCACTGCACTCCAGC



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

Original motif      Consensus sequence: CGCCGCCGCCGC

Reverse complement motif      Consensus sequence: GCGGCGGCGGCG

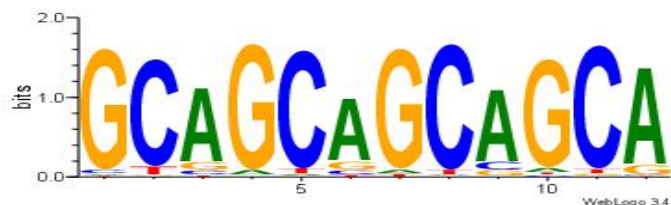


**Best Matches for Motif ID 101 (Highest to Lowest)**

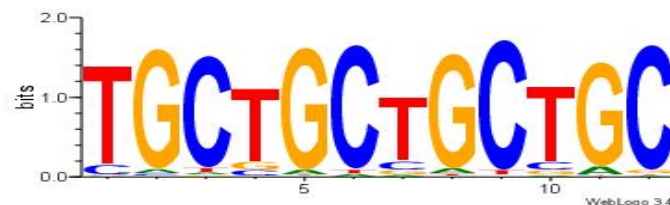
Dataset #: 1  
 Motif ID: 266  
 Motif name: Motif 266  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 12  
 Similarity score: 0.0686683

Alignment:  
 GCAGCAGCAGCA  
 GCGGC GCGGCG

Original motif      Consensus sequence: GCAGCAGCAGCA



Reverse complement motif      Consensus sequence: TGCTGCTGCTGC




---

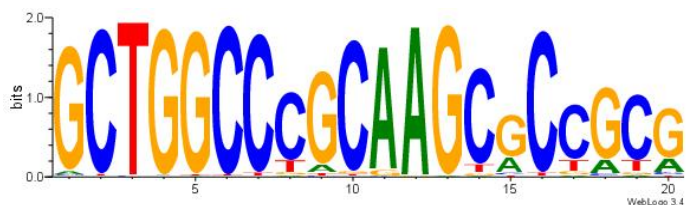
Dataset #: 1

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

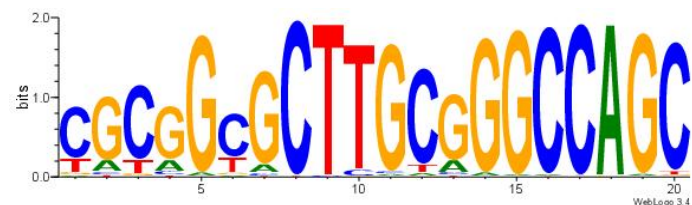
Alignment:

GCTGGCCCGCAAGCGCCGCG  
 -----CGCCGCCGCCGC-

Original motif    Consensus sequence: GCTGGCCCGCAAGCGCCGCG

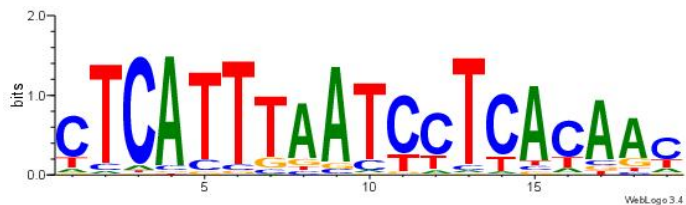


Reverse complement motif    Consensus sequence: CGCGGCGCTTGCGGGCCAGC

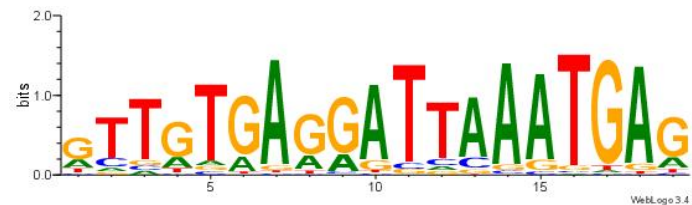


**Dataset #: 1      Motif ID: 102      Motif name: Motif 102**

Original motif    Consensus sequence: CTCATTTAATCCTCACAAC



Reverse complement motif    Consensus sequence: GTTGTGAGGATTAATGAG





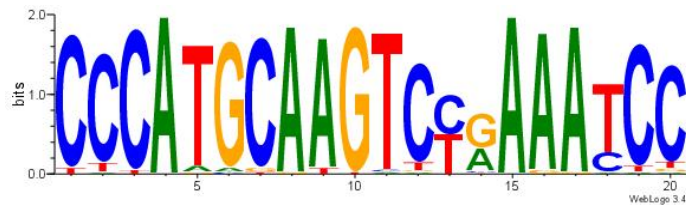
## Best Matches for Motif ID 102 (Highest to Lowest)

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

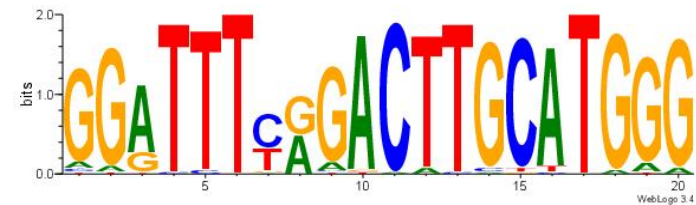
### Alignment:

```
CCCATGCAAGTCYRAAATCC  
CTCATTTAATCCTCACAAC-
```

Original motif      Consensus sequence: CCCATGCAAGTCYRAAATCC



Reverse complement motif      Consensus sequence:  
GGATTTMKGACTTGCATGGG



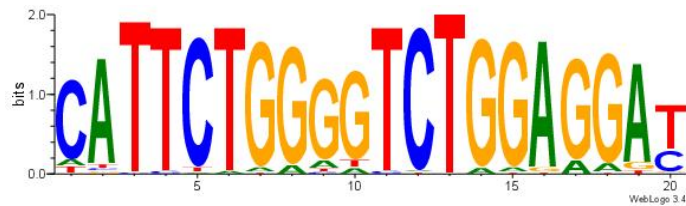
---

Dataset #: 1  
Motif ID: 309  
Motif name: Motif 309  
Matching format of first motif: Original Motif  
Matching format of second motif: Reverse Complement

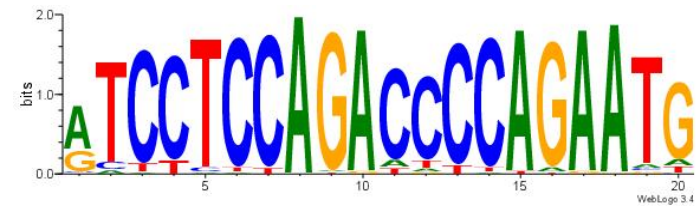
Direction: Forward  
 Position number: 1  
 Number of overlap: 19  
 Similarity score: 0.0968109

Alignment:  
 MTCCTCCAGACCCCAGAATG  
 CTCATTTAATCCTCACAAC-

Original motif Consensus sequence: CATTCTGGGGTCTGGAGGAY

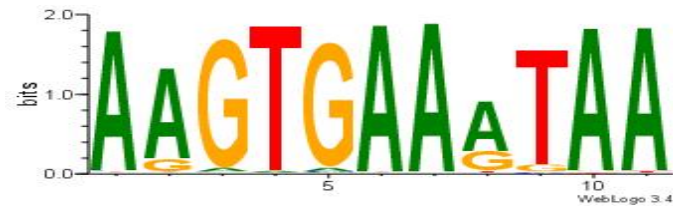


Reverse complement motif Consensus sequence: MTCCTCCAGACCCCAGAATG

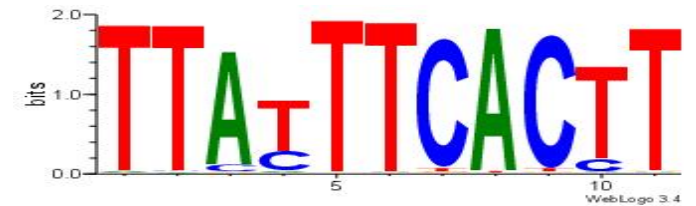


**Dataset #: 1 Motif ID: 103 Motif name: Motif 103**

Original motif Consensus sequence: AAGTGAAATAA



Reverse complement motif Consensus sequence: TTATTTCACTT



**Best Matches for Motif ID 103 (Highest to Lowest)**

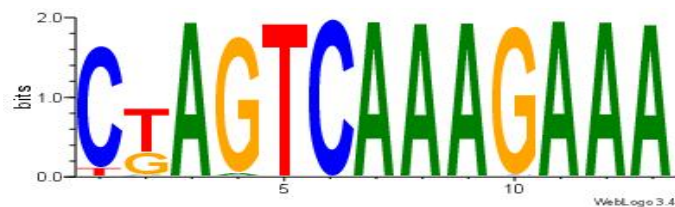
Dataset #: 1  
 Motif ID: 24

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

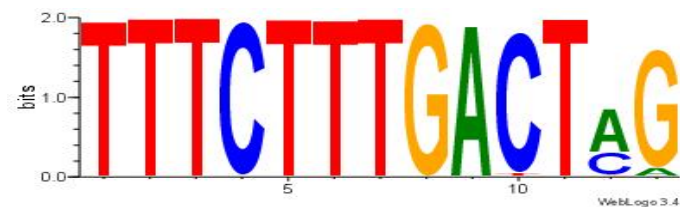
Alignment:

CKAGTCAAAGAAA  
 -AAGTGAAATAA-

Original motif    Consensus sequence: CKAGTCAAAGAAA



Reverse complement motif    Consensus sequence: TTTCTTTGACTRG

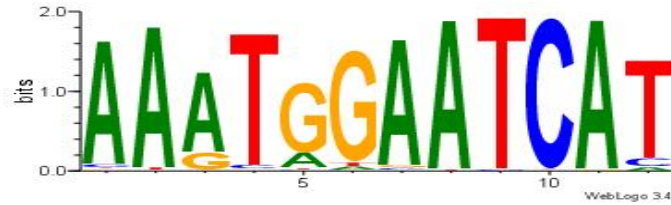


Dataset #: 1  
 Motif ID: 281  
 Motif name: Motif 281  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 11  
 Similarity score: 0.068219

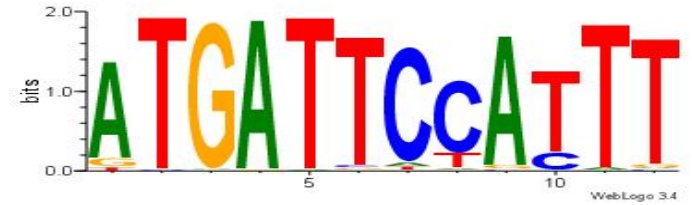
Alignment:

AAATGGAATCAT  
AAGTCAAATAA-

Original motif      Consensus sequence: AAATGGAATCAT

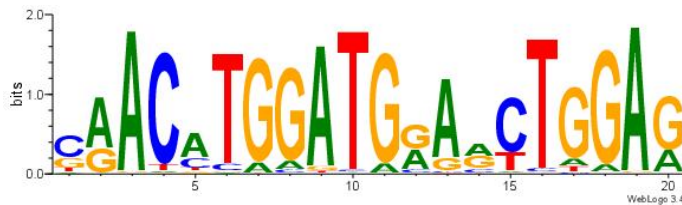


Reverse complement motif      Consensus sequence: ATGATTCCATTT

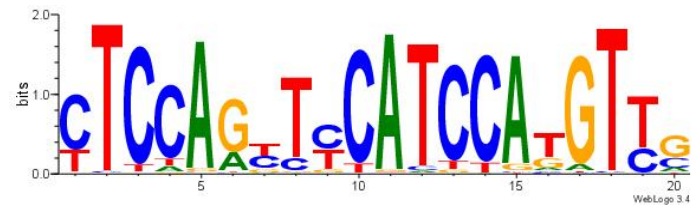


**Dataset #: 1      Motif ID: 104      Motif name: Motif 104**

Original motif      Consensus sequence: CAACATGGATGRARCTGGAG



Reverse complement motif      Consensus sequence: CTCAGKTCATCCATGTTG



**Best Matches for Motif ID 104 (Highest to Lowest)**

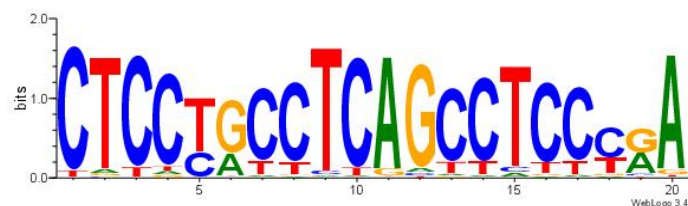
Dataset #:	1
Motif ID:	26
Motif name:	Motif 26
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward

Position number: 1  
Number of overlap: 20  
Similarity score: 0.0969491

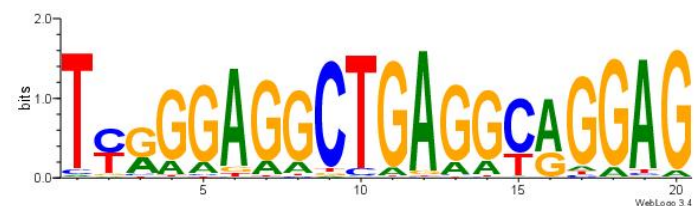
Alignment:

CTCCTGCCTCAGCCTCCCRA  
CTCCAGKTMCATCCATGTTG

Original motif    Consensus sequence: CTCCTGCCTCAGCCTCCCRA



Reverse complement motif    Consensus sequence: TMGGGAGGCTGAGGCAGGAG

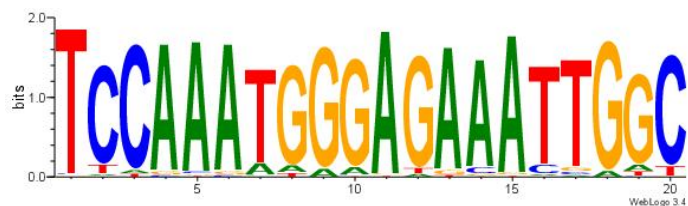


Dataset #: 1  
Motif ID: 235  
Motif name: Motif 235  
Matching format of first motif: Original Motif  
Matching format of second motif: Original Motif  
Direction: Forward  
Position number: 2  
Number of overlap: 19  
Similarity score: 0.576666

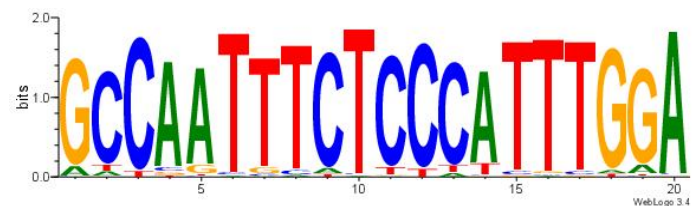
Alignment:

TCCAAATGGGAGAAATTGGC-  
-CAACATGGATGRARCTGGAG

Original motif      Consensus sequence: TCCAATGGGAGAAATTGGC

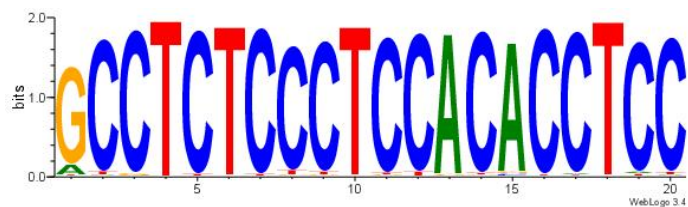


Reverse complement motif      Consensus sequence: GCCAATTTCTCCCATTGGGA

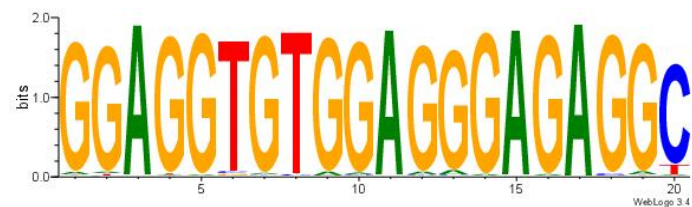


**Dataset #: 1      Motif ID: 105      Motif name: Motif 105**

Original motif      Consensus sequence: GCCTCTCCCTCCACACCTCC



Reverse complement motif      Consensus sequence: GGAGGTGTGGAGGGAGAGGC



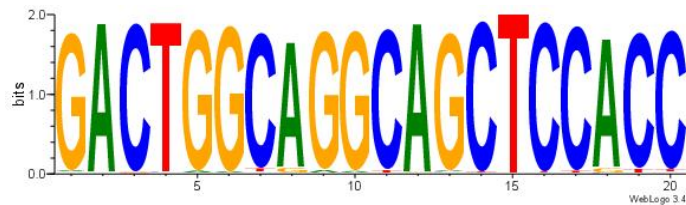
**Best Matches for Motif ID 105 (Highest to Lowest)**

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

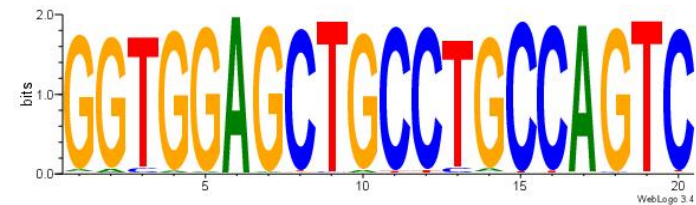
Alignment:

GGTGGAGCTGCCTGCCAGTC  
GGAGGTGTGGAGGGAGAGGC

Original motif      Consensus sequence: GACTGGCAGGCAGCTCCACC



Reverse complement motif      Consensus sequence:  
GGTGGAGCTGCCTGCCAGTC



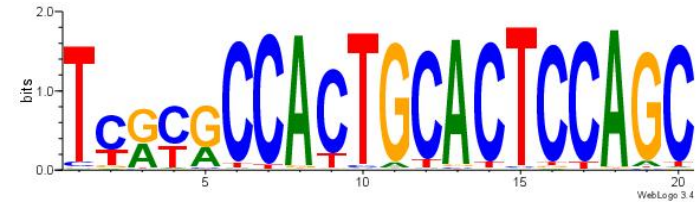
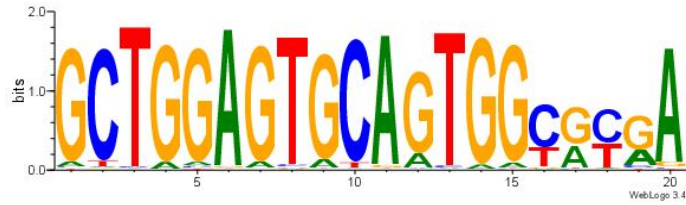
Dataset #:	1
Motif ID:	3
Motif name:	Motif 3
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	20
Similarity score:	0.11947

Alignment:

TCKMGCCACTGCACTCCAGC  
GCCTCTCCCTCCACACCTCC

Original motif      Consensus sequence: GCTGGAGTGCAGTGGCRYGA

Reverse complement motif      Consensus sequence:  
TCKMGCCACTGCACTCCAGC

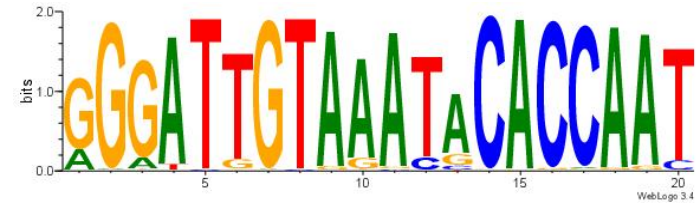


**Dataset #: 1      Motif ID: 106      Motif name: Motif 106**

Original motif      Consensus sequence: ATTGGTGTATTTACAATCCC



Reverse complement motif      Consensus sequence: GGGATTGTAAATACACCAAT



**Best Matches for Motif ID 106 (Highest to Lowest)**

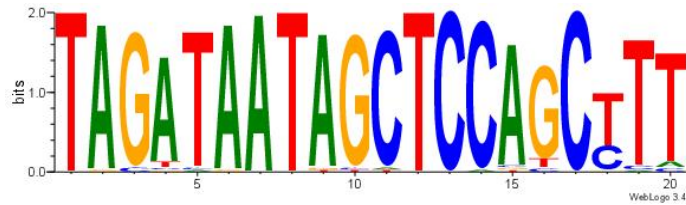
Dataset #:	1
Motif ID:	333
Motif name:	Motif 333
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	20
Similarity score:	0.112321

Alignment:

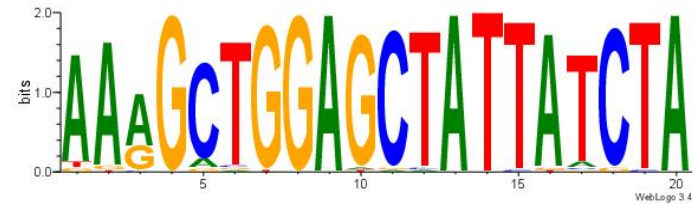


TAGATAATAGCTCCAGCTTT  
GGGATTGTAAATACACCAAT

Original motif      Consensus sequence: TAGATAATAGCTCCAGCTTT



Reverse complement motif      Consensus sequence:  
AAAGCTGGAGCTATTATCTA



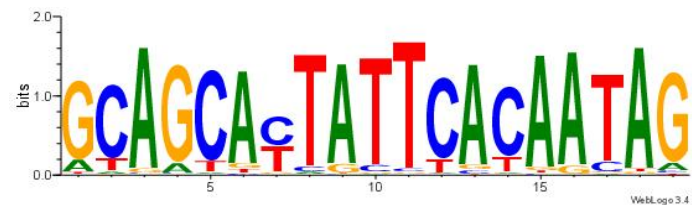
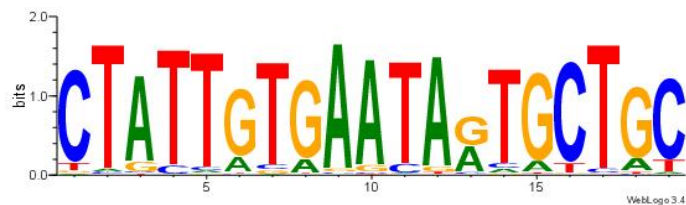
Dataset #:	1
Motif ID:	70
Motif name:	Motif 70
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	19
Similarity score:	0.609937

Alignment:

-GCAGCAMTATTCACAATAG  
ATTGGTGTATTTACAATCCC

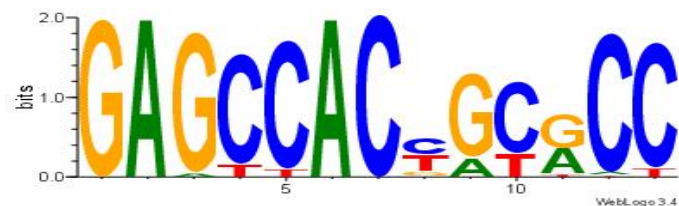
Original motif      Consensus sequence: CTATTGTGAATARTGCTGC

Reverse complement motif      Consensus sequence:  
GCAGCAMTATTCACAATAG

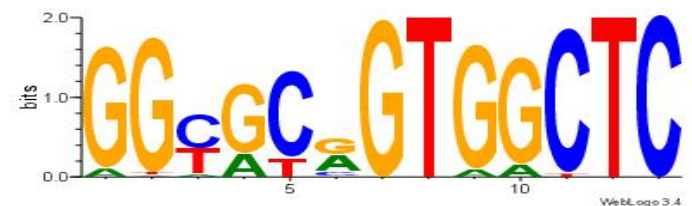


**Dataset #: 1      Motif ID: 107      Motif name: Motif 107**

Original motif      Consensus sequence: GAGCCACYGCRCC



Reverse complement motif      Consensus sequence: GGMGCKGTGGCTC

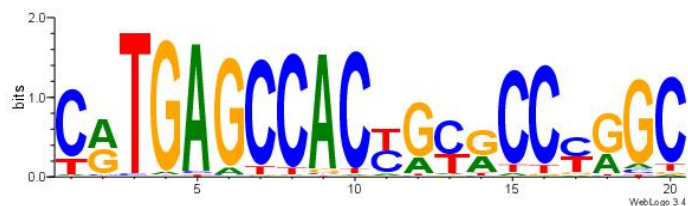


**Best Matches for Motif ID 107 (Highest to Lowest)**

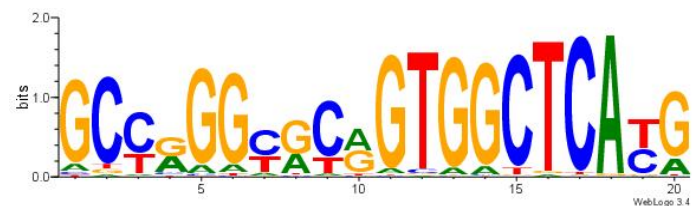
Dataset #:	1
Motif ID:	56
Motif name:	Motif 56
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	5
Number of overlap:	13
Similarity score:	0.00724402

Alignment:  
 CRTGAGCCACYGYRCCYGGC  
 ---GAGCCACYGCRCC----

Original motif      Consensus sequence: CRTGAGCCACYGYRCCYGGC



Reverse complement motif      Consensus sequence: GCCKGGMKCMGTGGCTCAKG

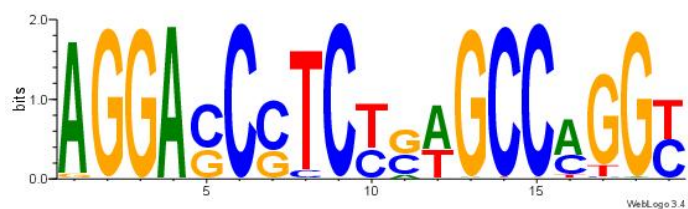


Dataset #: 1  
Motif ID: 10  
Motif name: Motif 10  
Matching format of first motif: Original Motif  
Matching format of second motif: Original Motif  
Direction: Forward  
Position number: 3  
Number of overlap: 13  
Similarity score: 0.0668268

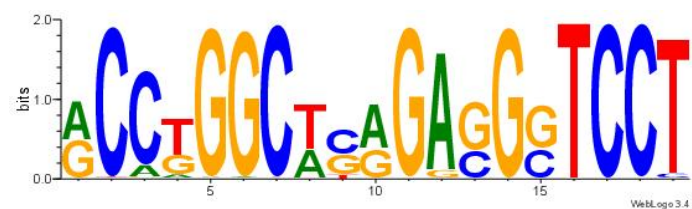
Alignment:

AGGASCSTCYSWGCCMGGY  
--GAGCCACYGCRCC----

Original motif      Consensus sequence: AGGASCSTCYSWGCCMGGY

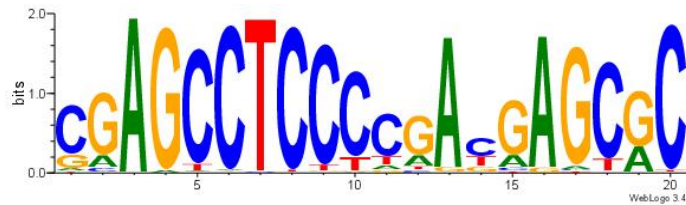


Reverse complement motif      Consensus sequence: MCCYGGCWSMGASGSTCCT

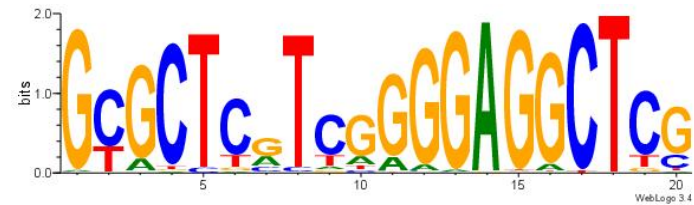


**Dataset #: 1      Motif ID: 108      Motif name: Motif 108**

Original motif      Consensus sequence: CGAGCCTCCCCGAYGAGCGC



Reverse complement motif      Consensus sequence: GCGCTCKTCGGGGAGGCTCG



### Best Matches for Motif ID 108 (Highest to Lowest)

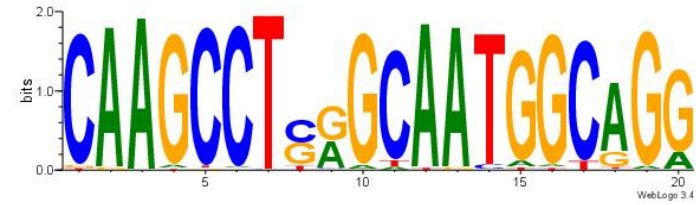
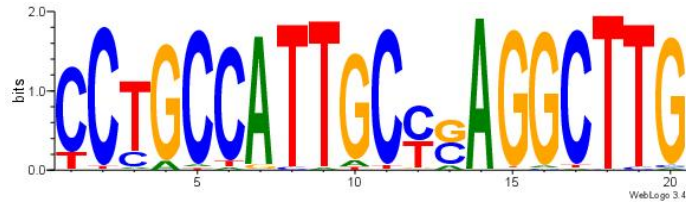
Dataset #:	1
Motif ID:	196
Motif name:	Motif 196
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	20
Similarity score:	0.0943206

#### Alignment:

```
CAAGCCTSKGCAATGGCAGG  
CGAGCCTCCCCGAYGAGCGC
```

Original motif      Consensus sequence: CCTGCCATTGCYSAGGCTTG

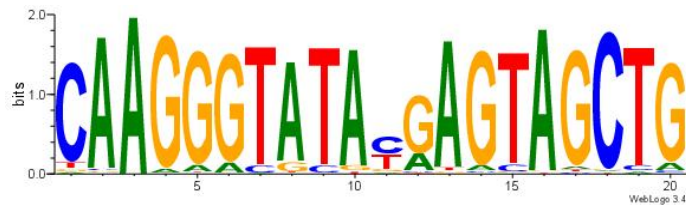
Reverse complement motif      Consensus sequence: CAAGCCTSKGCAATGGCAGG



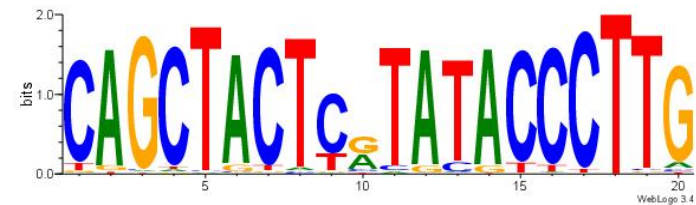
Dataset #: 1  
 Motif ID: 194  
 Motif name: Motif 194  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 20  
 Similarity score: 0.095821

Alignment:  
 CAGCTACTCKTATACCCTTG  
 GCGCTCKTCGGGGAGGCTCG

Original motif      Consensus sequence: CAAGGGTATAYGAGTAGCTG

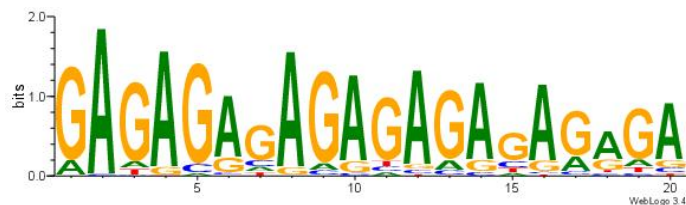


Reverse complement motif      Consensus sequence: CAGCTACTCKTATACCCTTG

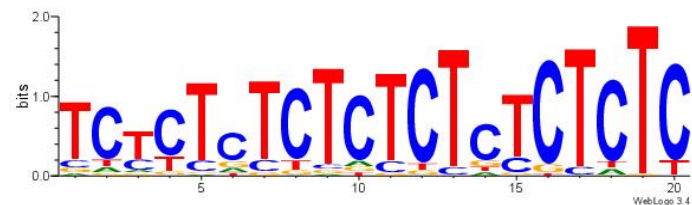


**Dataset #: 1      Motif ID: 109      Motif name: Motif 109**

Original motif      Consensus sequence: GAGAGAGAGAGAGAGAGA



Reverse complement motif      Consensus sequence: TCTCTCTCTCTCTCTCTC



### Best Matches for Motif ID 109 (Highest to Lowest)

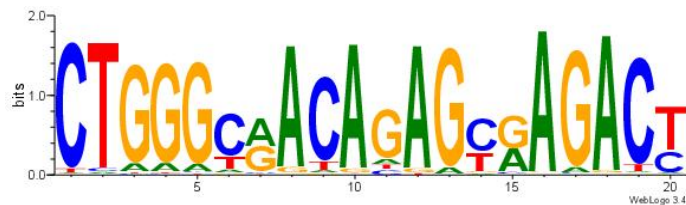
Dataset #:	1
Motif ID:	29
Motif name:	Motif 29
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	20
Similarity score:	0.0851551

#### Alignment:

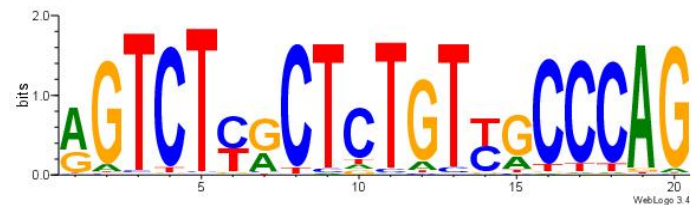
```

MGTCTMKCTCTGTKGCCAG
TCTCTCTCTCTCTCTCTC
  
```

Original motif      Consensus sequence: CTGGGCRACAGYRAGACY



Reverse complement motif      Consensus sequence: MGTCTMKCTCTGTKGCCAG

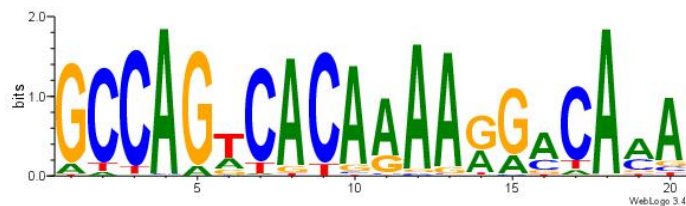


Dataset #: 1  
 Motif ID: 145  
 Motif name: Motif 145  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 20  
 Similarity score: 0.0867304

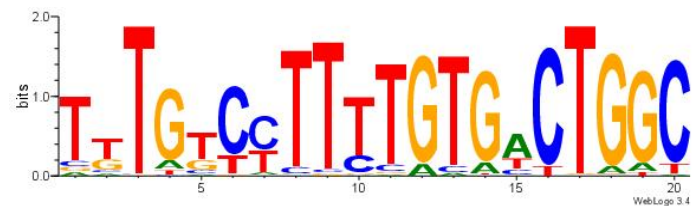
Alignment:

GCCAGTCACAAAARGACAMA  
 GAGAGAGAGAGAGAGAGA

Original motif    Consensus sequence: GCCAGTCACAAAARGACAMA



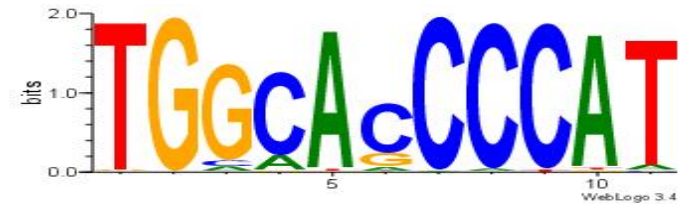
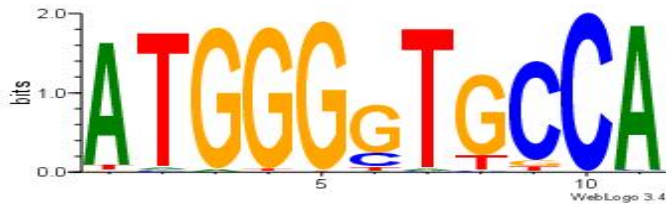
Reverse complement motif    Consensus sequence: TYTGTCMTTTTGTGACTGGC



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

Original motif    Consensus sequence: ATGGGGTGCCA

Reverse complement motif    Consensus sequence: TGGCACCCCAT

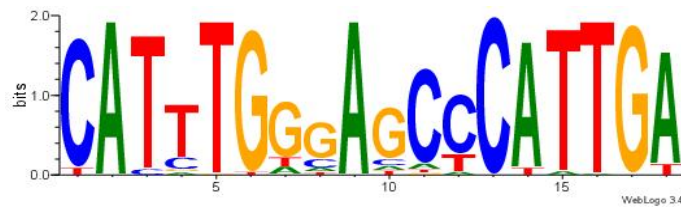


**Best Matches for Motif ID 110 (Highest to Lowest)**

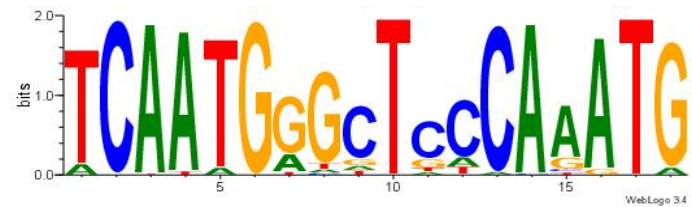
Dataset #: 1  
 Motif ID: 284  
 Motif name: Motif 284  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 5  
 Number of overlap: 11  
 Similarity score: 0.0371465

Alignment:  
 TCAATGGGCTCCCAAATG  
 ---ATGGGGTGCCA----

Original motif      Consensus sequence: CATTGGGAGCCATTGA



Reverse complement motif      Consensus sequence: TCAATGGGCTCCCAAATG



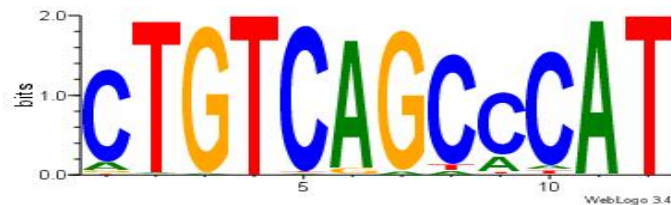


Dataset #: 1  
 Motif ID: 209  
 Motif name: Motif 209  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 11  
 Similarity score: 0.0451831

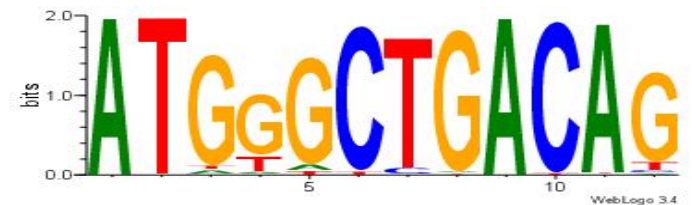
Alignment:

CTGTCAGCCCAT  
 -TGGCACCCCAT

Original motif      Consensus sequence: CTGTCAGCCCAT



Reverse complement motif      Consensus sequence: ATGGGCTGACAG

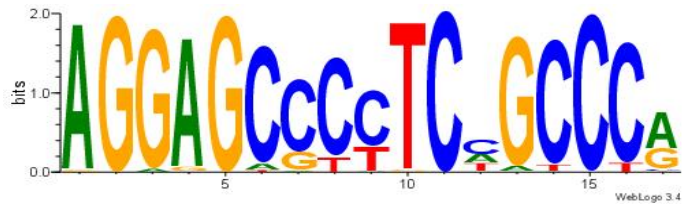



---

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

Original motif      Consensus sequence: AGGAGCCCCTCHGCCCR

Reverse complement motif      Consensus sequence:  
KGGCDGAGGGGCTCCT

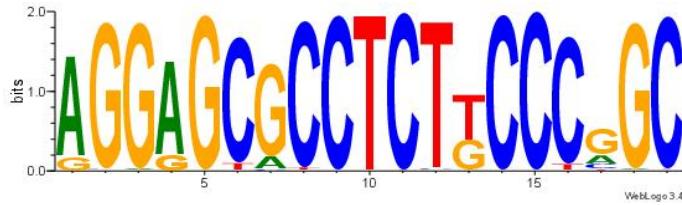


**Best Matches for Motif ID 111 (Highest to Lowest)**

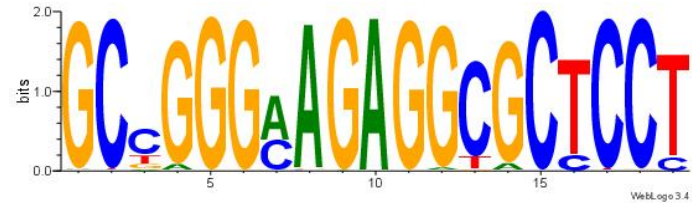
Dataset #: 1  
 Motif ID: 30  
 Motif name: Motif 30  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 17  
 Similarity score: 0.0374525

Alignment:  
 AGGAGCGCCTCTKCCCGGC  
 AGGAGCCCCTCHGCCCR--

Original motif      Consensus sequence: AGGAGCGCCTCTKCCCGGC



Reverse complement motif      Consensus sequence: GCCGGGRAGAGGCGCTCCT

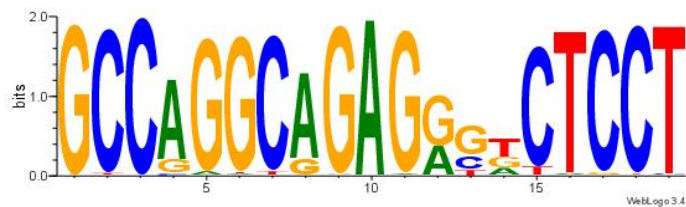


Dataset #: 1  
 Motif ID: 43  
 Motif name: Motif 43  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 3  
 Number of overlap: 17  
 Similarity score: 0.0498697

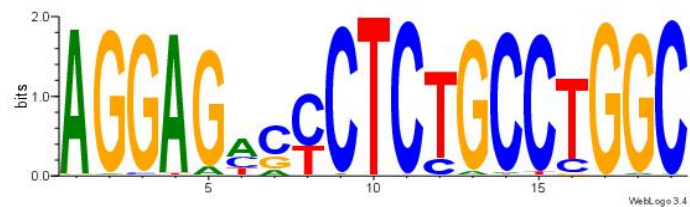
Alignment:

AGGAGRCMCTCTGCCTGGC  
 --AGGAGCCCCTCHGCCCR

Original motif      Consensus sequence: GCCAGGCAGAGRGKCTCCT



Reverse complement motif      Consensus sequence: AGGAGRCMCTCTGCCTGGC

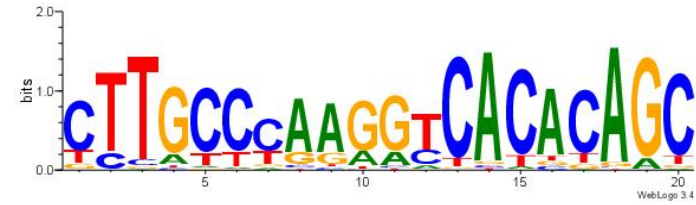
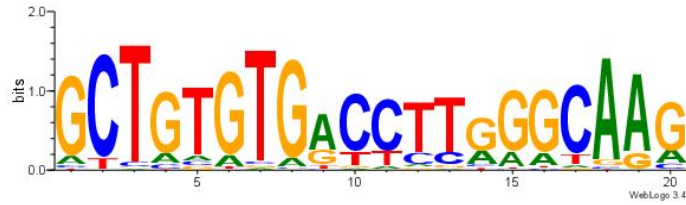



---

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

Original motif      Consensus sequence: GCTGTGTGACCTTGGGCAAG

Reverse complement motif      Consensus sequence: CTTGCCCAAGGTCACACAGC

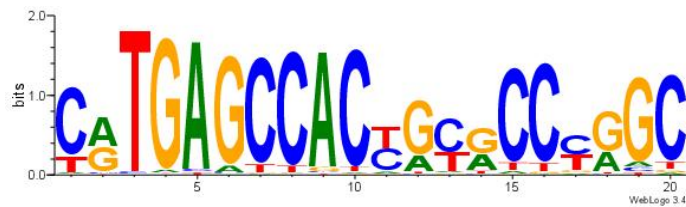


**Best Matches for Motif ID 112 (Highest to Lowest)**

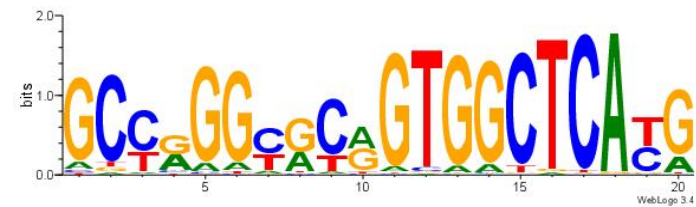
Dataset #: 1  
 Motif ID: 56  
 Motif name: Motif 56  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 20  
 Similarity score: 0.100531

Alignment:  
 GCCKGGMKCMGTGGCTCAKG  
 GCTGTGTGACCTTGGGCAAG

Original motif      Consensus sequence: CRTGAGCCACYGYRCCYGGC



Reverse complement motif      Consensus sequence: GCCKGGMKCMGTGGCTCAKG

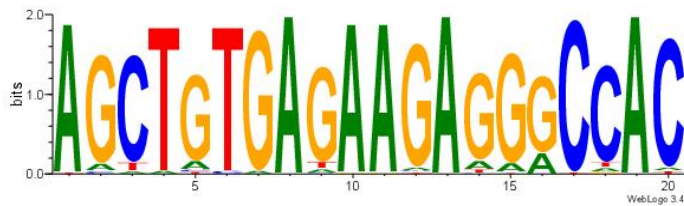


Dataset #: 1  
 Motif ID: 294  
 Motif name: Motif 294  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 2  
 Number of overlap: 19  
 Similarity score: 0.580817

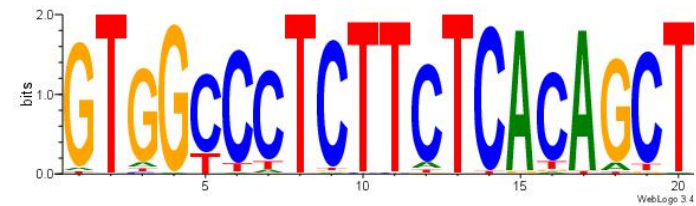
Alignment:

-GTGGCCCTCTTCTCACAGCT  
 CTTGCCCAAGGTCACACAGC-

Original motif      Consensus sequence: AGCTGTGAGAAGAGGGCCAC



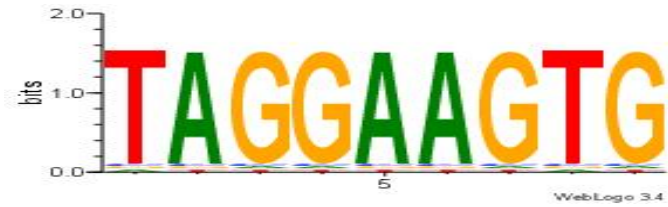
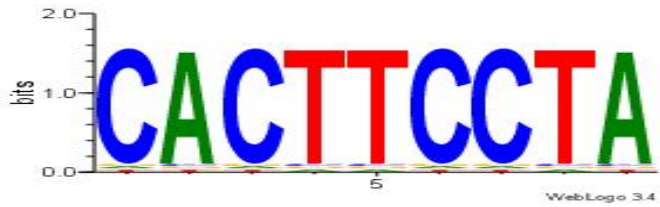
Reverse complement motif      Consensus sequence: GTGGCCCTCTTCTCACAGCT



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

Original motif      Consensus sequence: CACTTCCTA

Reverse complement motif      Consensus sequence: TAGGAAGTG

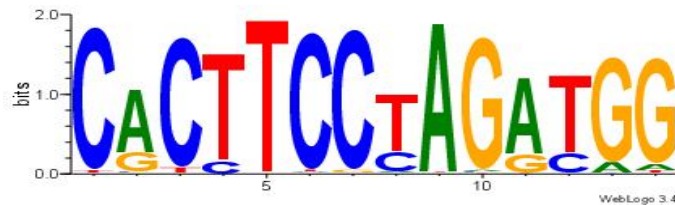


### Best Matches for Motif ID 113 (Highest to Lowest)

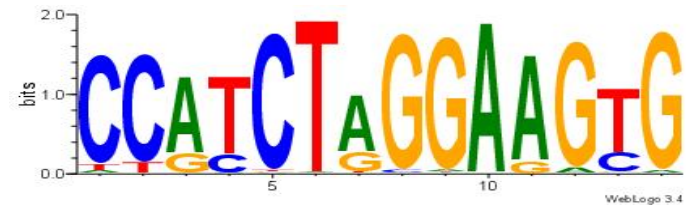
Dataset #: 1  
 Motif ID: 74  
 Motif name: Motif 74  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 9  
 Similarity score: 0.0147795

Alignment:  
 CCATCTAGGAAGTG  
 -----TAGGAAGTG

Original motif      Consensus sequence: CACTTCCTAGATGG



Reverse complement motif      Consensus sequence: CCATCTAGGAAGTG

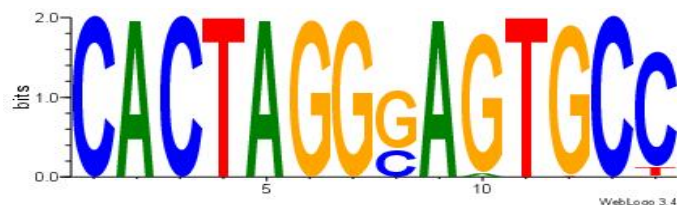


Dataset #: 1

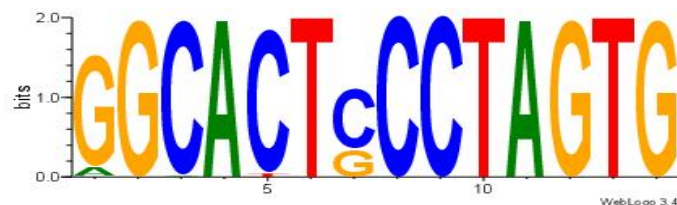
Motif ID: 153  
 Motif name: Motif 153  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 3  
 Number of overlap: 9  
 Similarity score: 0.0332374

Alignment:  
 CACTAGGGAGTGCC  
 ---TAGGAAGTG--

Original motif      Consensus sequence: CACTAGGGAGTGCC

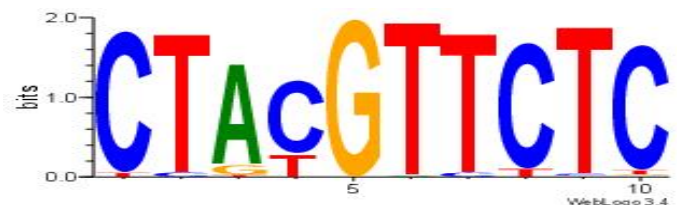


Reverse complement motif      Consensus sequence: GGCACCTCCTAGTG



**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)

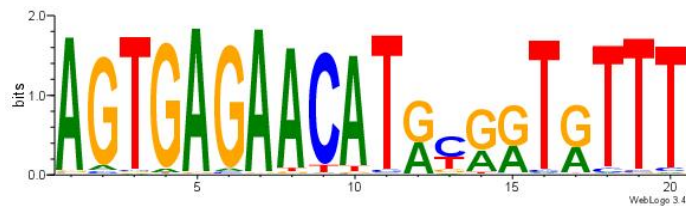
Dataset #: 1  
 Motif ID: 63  
 Motif name: Motif 63  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 4  
 Number of overlap: 10  
 Similarity score: 0.0559267

### Alignment:

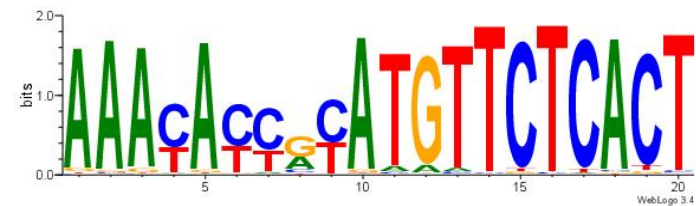
```

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

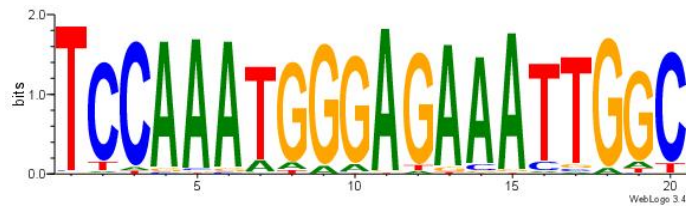


Direction: Backward  
 Position number: 2  
 Number of overlap: 10  
 Similarity score: 0.0641267

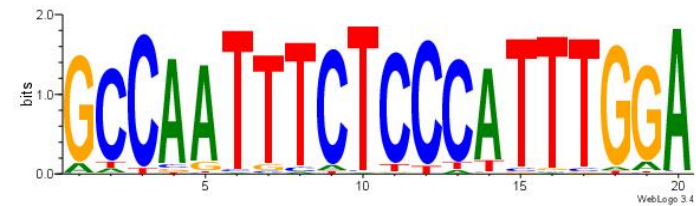
**Alignment:**

TCCAAATGGGAGAAATTGGC  
 -----GAGAACGTAG--

Original motif      Consensus sequence: TCCAAATGGGAGAAATTGGC

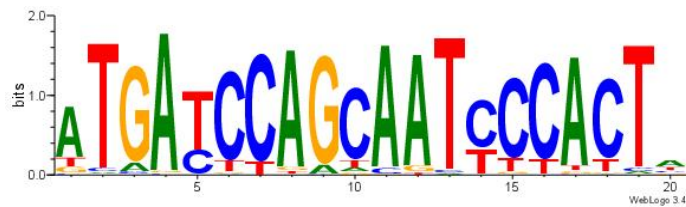


Reverse complement motif      Consensus sequence:  
 GCCAATTTCTCCCATTTGGA

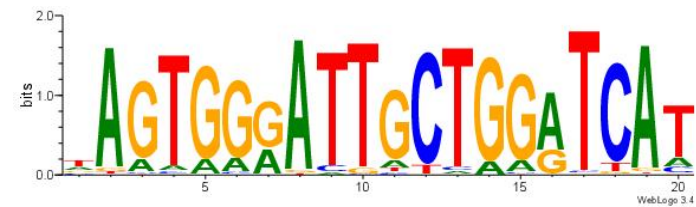


**Dataset #: 1      Motif ID: 115      Motif name: Motif 115**

Original motif      Consensus sequence: ATGATCCAGCAATYCCACTH



Reverse complement motif      Consensus sequence:  
 HAGTGGKATTGCTGGATCAT



**Best Matches for Motif ID 115 (Highest to Lowest)**

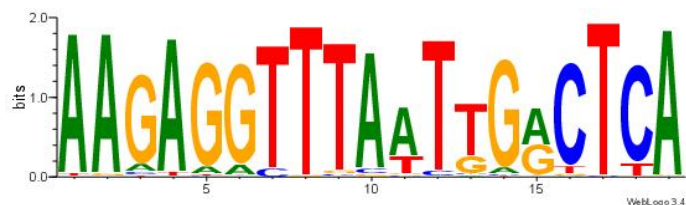
Dataset #: 1

Motif ID: 129  
 Motif name: Motif 129  
 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: 0.0868585

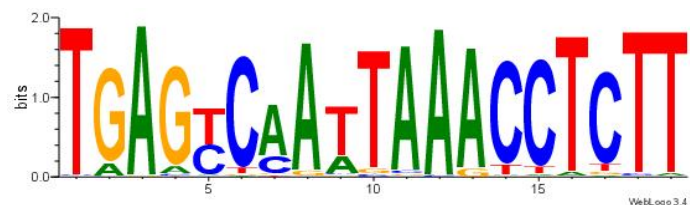
Alignment:

AAGAGGTTTAATTGRCTCA-  
 HAGTGGKATTGCTGGATCAT

Original motif    Consensus sequence: AAGAGGTTTAATTGRCTCA



Reverse complement motif    Consensus sequence: TGAGKCAATTAACCTCTT



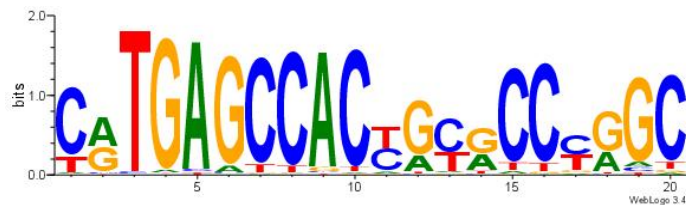
Dataset #: 1  
 Motif ID: 56  
 Motif name: Motif 56  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 2  
 Number of overlap: 19

Similarity score: 0.0917072

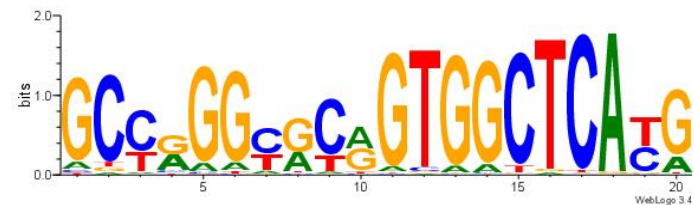
Alignment:

CRTGAGCCACYGYRCCYGGC-  
-ATGATCCAGCAATYCCACTH

Original motif      Consensus sequence: CRTGAGCCACYGYRCCYGGC

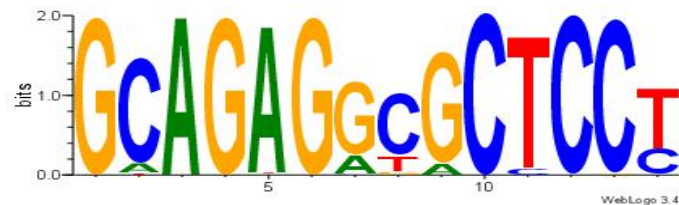


Reverse complement motif      Consensus sequence: GCCKGGMKCMGTGGCTCAKG

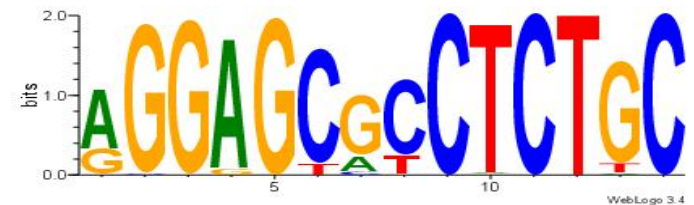


**Dataset #: 1      Motif ID: 116      Motif name: Motif 116**

Original motif      Consensus sequence: GCAGAGGCGCTCCT



Reverse complement motif      Consensus sequence: AGGAGCGCCTCTG



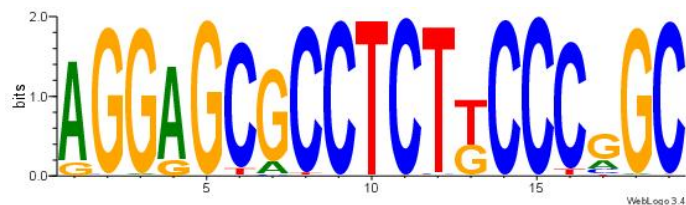
**Best Matches for Motif ID 116 (Highest to Lowest)**

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

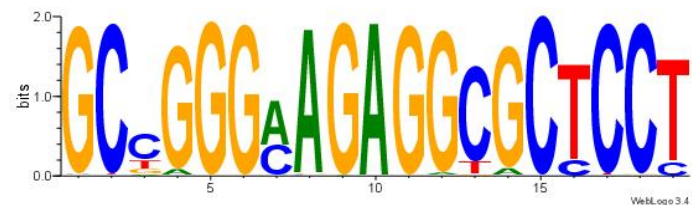
Direction: Forward  
 Position number: 1  
 Number of overlap: 14  
 Similarity score: 0.023579

Alignment:  
 GCCGGGRAGAGGCGCTCCT  
 GCAGAGGCGCTCCT-----

Original motif      Consensus sequence: AGGAGCGCCTCTKCCCGGC



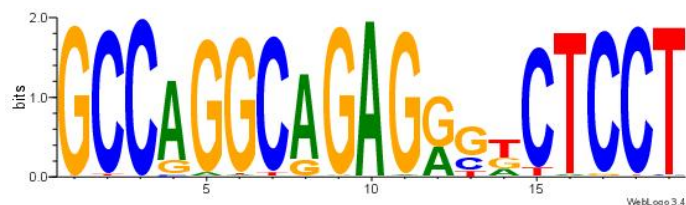
Reverse complement motif      Consensus sequence: GCCGGGRAGAGGCGCTCCT



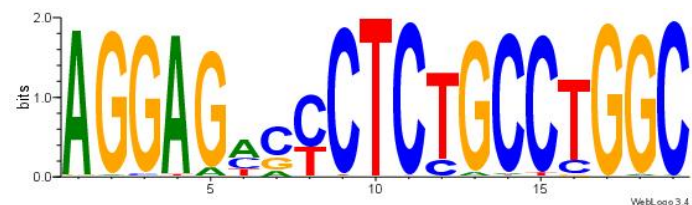
Dataset #: 1  
 Motif ID: 43  
 Motif name: Motif 43  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 6  
 Number of overlap: 14  
 Similarity score: 0.0315071

Alignment:  
 GCCAGGCAGAGRKCTCCT  
 -----GCAGAGGCGCTCCT

Original motif      Consensus sequence: GCCAGGCAGAGRGKCTCCT

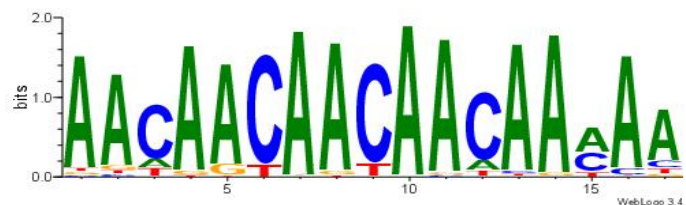


Reverse complement motif      Consensus sequence: AGGAGRCMCTCTGCCTGGC

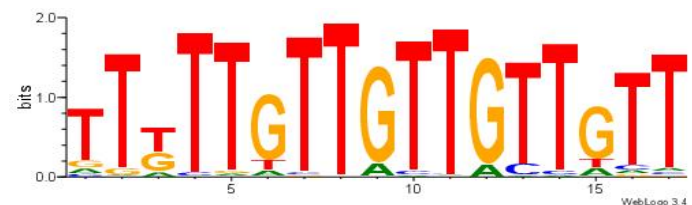


**Dataset #: 1      Motif ID: 117      Motif name: Motif 117**

Original motif      Consensus sequence: AACAACAACAAMAA



Reverse complement motif      Consensus sequence: TTYTTGTTGTTGTT



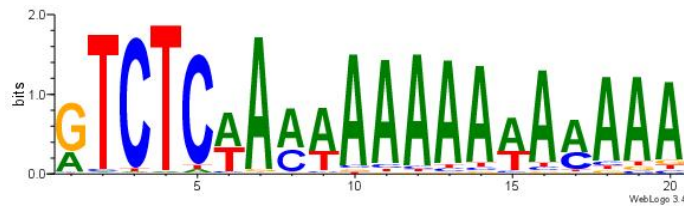
**Best Matches for Motif ID 117 (Highest to Lowest)**

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

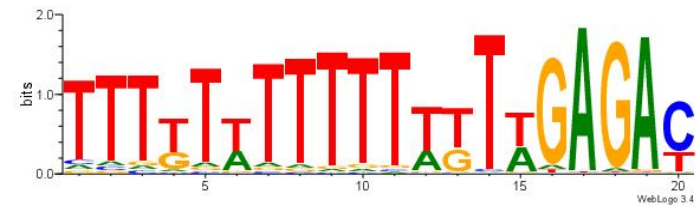
Alignment:

GTCTCWAMAAAAAWAMAAA  
--ACAACAACAACAAMAA-

Original motif      Consensus sequence: GTCTCWAMAAAAAWAMAAA



Reverse complement motif      Consensus sequence:  
TTTTWTTTTTTTWTGAGAC



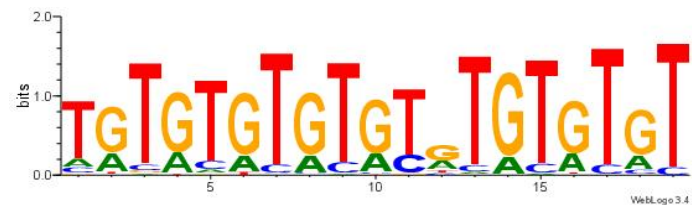
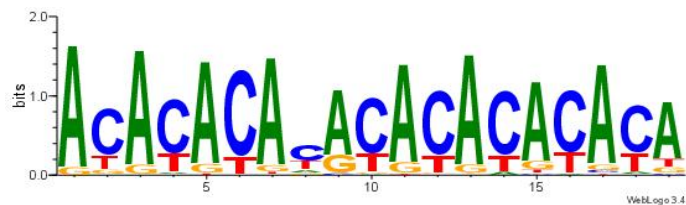
Dataset #: 1  
Motif ID: 66  
Motif name: Motif 66  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Reverse Complement  
Direction: Forward  
Position number: 3  
Number of overlap: 17  
Similarity score: 0.0820961

Alignment:

TGTGTGTGTGKTGTGTGT  
--TTYTTGTTGTTGTTGTT

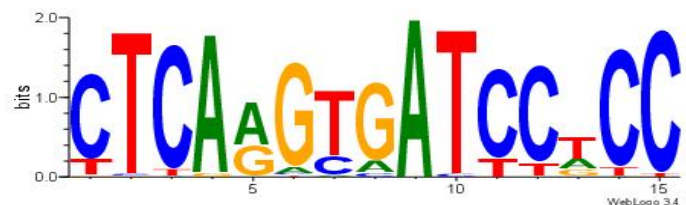
Original motif      Consensus sequence: ACACACAYACACACACA

Reverse complement motif      Consensus sequence:  
TGTGTGTGTGKTGTGTGT



**Dataset #: 1      Motif ID: 118      Motif name: Motif 118**

Original motif      Consensus sequence: CTCARGTGATCCTCC



Reverse complement motif      Consensus sequence: GGAGGATCACTGAG

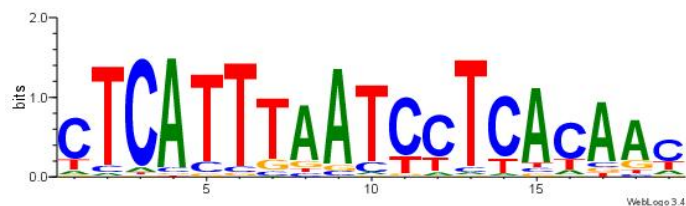


**Best Matches for Motif ID 118 (Highest to Lowest)**

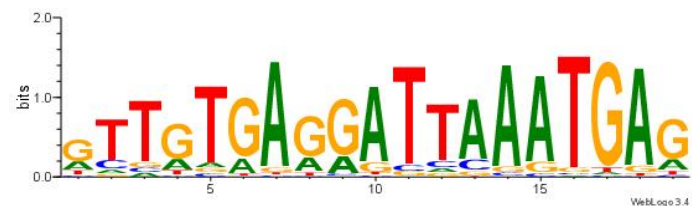
Dataset #:	1
Motif ID:	102
Motif name:	Motif 102
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	5
Number of overlap:	15
Similarity score:	0.0724382

Alignment:  
 CTCATTTAATCCTCACAAC  
 CTCARGTGATCCTCC----

Original motif      Consensus sequence: CTCATTTAATCCTCACAAC



Reverse complement motif      Consensus sequence: GTTGTGAGGATTAATGAG

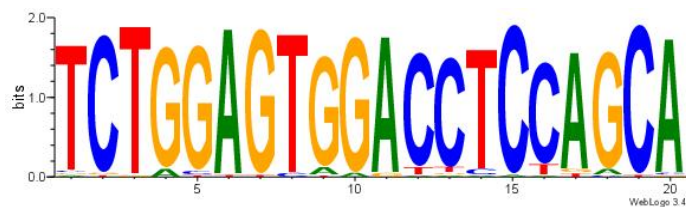


Dataset #: 1  
Motif ID: 350  
Motif name: Motif 350  
Matching format of first motif: Original Motif  
Matching format of second motif: Original Motif  
Direction: Forward  
Position number: 2  
Number of overlap: 15  
Similarity score: 0.0817171

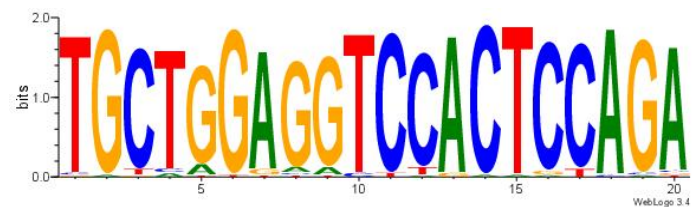
Alignment:

TCTGGAGTGGACCTCCAGCA  
-CTCARGTGATCCTCC-----

Original motif      Consensus sequence: TCTGGAGTGGACCTCCAGCA



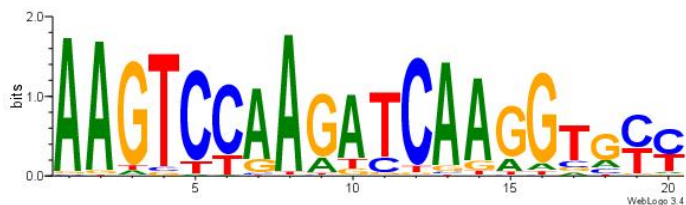
Reverse complement motif      Consensus sequence: TGCTGGAGTCCACTCCAGA



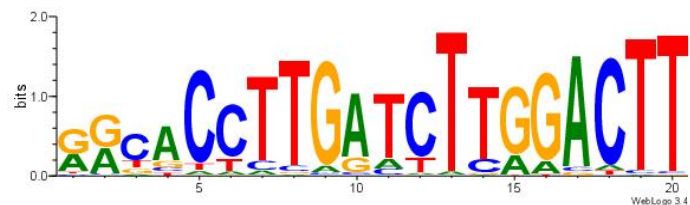


**Dataset #: 1      Motif ID: 119      Motif name: Motif 119**

Original motif      Consensus sequence: AAGTCCAAGATCAAGGTGY



Reverse complement motif      Consensus sequence: KKCACCTTGATCTTGGACTT



**Best Matches for Motif ID 119 (Highest to Lowest)**

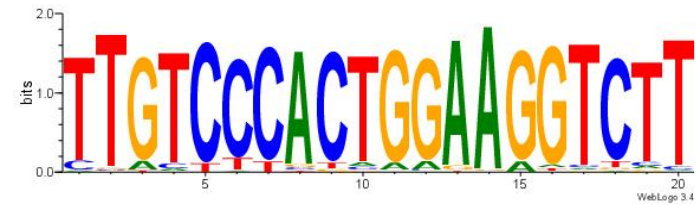
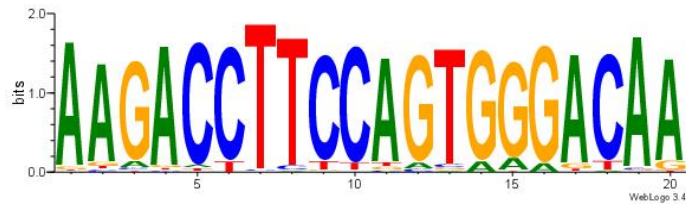
Dataset #:	1
Motif ID:	292
Motif name:	Motif 292
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	20
Similarity score:	0.103662

**Alignment:**

TTGTCCCACTGGAAGGTCTT  
AAGTCCAAGATCAAGGTGY

Original motif      Consensus sequence: AAGACCTTCCAGTGGGACAA

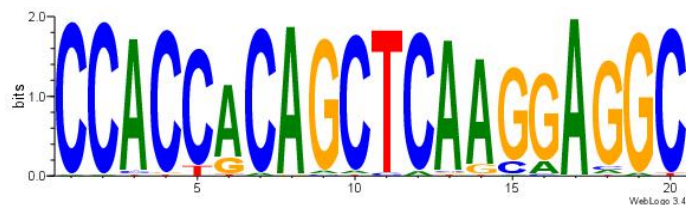
Reverse complement motif      Consensus sequence: TTGTCCCACTGGAAGGTCTT



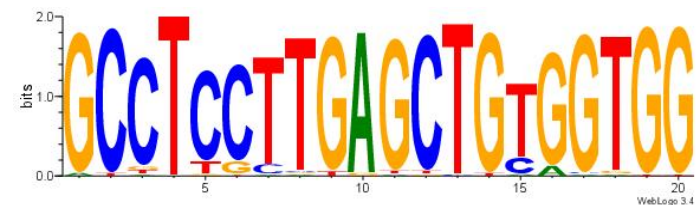
Dataset #: 1  
 Motif ID: 331  
 Motif name: Motif 331  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 20  
 Similarity score: 0.107278

Alignment:  
 GCCTCCTTGAGCTGTGGTGG  
 KKCACCTTGATCTTGGACTT

Original motif      Consensus sequence: CCACCACAGCTCAAGGAGGC

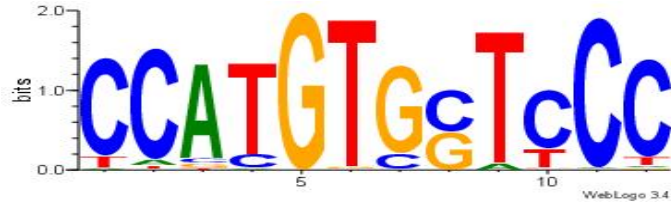


Reverse complement motif      Consensus sequence: GCCTCCTTGAGCTGTGGTGG

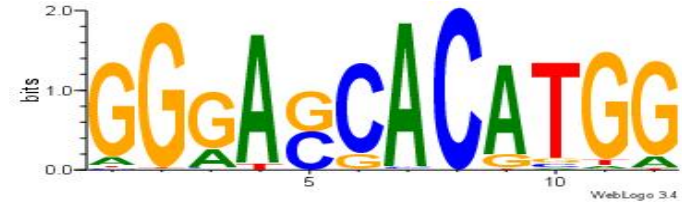


**Dataset #: 1      Motif ID: 120      Motif name: Motif 120**

Original motif      Consensus sequence: CCATGTGcTcCc



Reverse complement motif      Consensus sequence: GGGASCACATGG



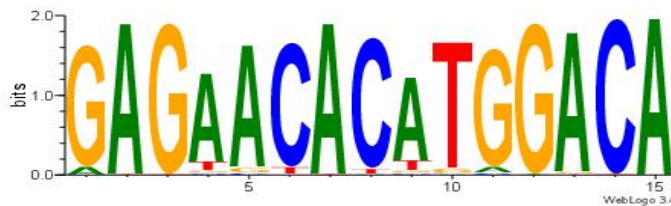
### Best Matches for Motif ID 120 (Highest to Lowest)

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

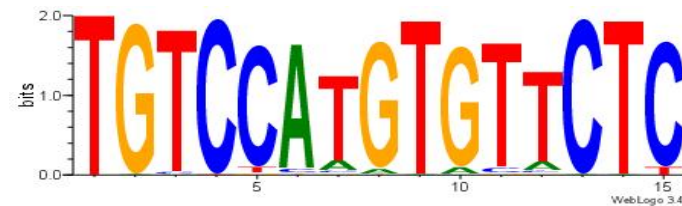
#### Alignment:

```
GAGAACACATGGACA  
GGGASCACATGG---
```

Original motif      Consensus sequence: GAGAACACATGGACA



Reverse complement motif      Consensus sequence: TGTCCATGTGTTCTC

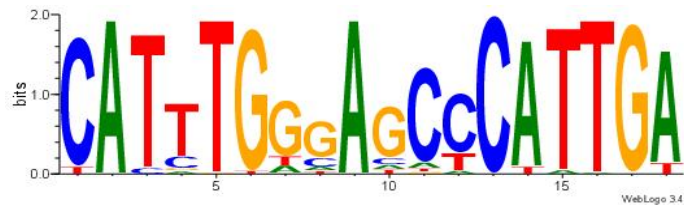


Dataset #: 1  
 Motif ID: 284  
 Motif name: Motif 284  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 6  
 Number of overlap: 12  
 Similarity score: 0.0509107

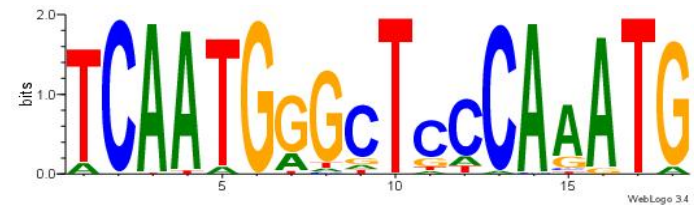
Alignment:

TCAATGGGCTCCCAAATG  
 -CCATGTGSTCCC-----

Original motif      Consensus sequence: CATTGGGAGCCATTGA



Reverse complement motif      Consensus sequence: TCAATGGGCTCCCAAATG

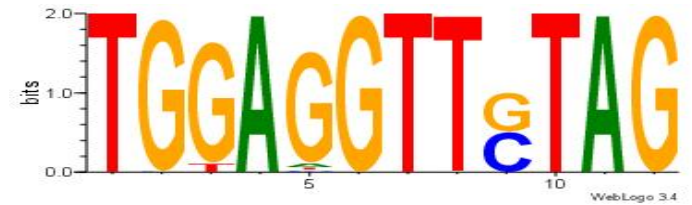



---

**Dataset #: 1      Motif ID: 121      Motif name: Motif 121**

Original motif      Consensus sequence: CTASAACCTCCA

Reverse complement motif      Consensus sequence: TGGAGGTTSTAG

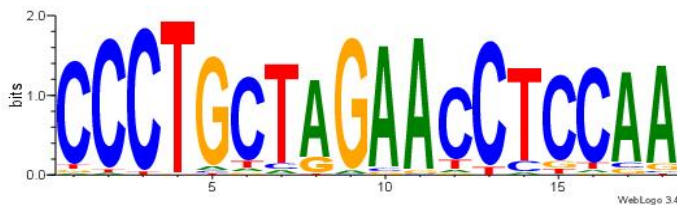


**Best Matches for Motif ID 121 (Highest to Lowest)**

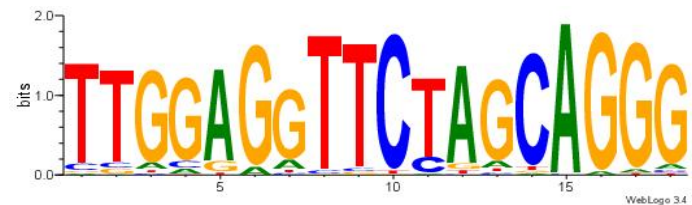
Dataset #: 1  
 Motif ID: 299  
 Motif name: Motif 299  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 6  
 Number of overlap: 12  
 Similarity score: 0.0292892

Alignment:  
 CCCTGCTAGAACCTCCAA  
 -----CTASAACCTCCA-

Original motif      Consensus sequence: CCCTGCTAGAACCTCCAA



Reverse complement motif      Consensus sequence: TTGGAGGTTCTAGCAGGG

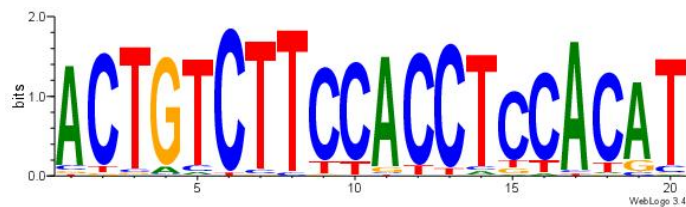


Dataset #: 1  
 Motif ID: 178  
 Motif name: Motif 178  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 4  
 Number of overlap: 12  
 Similarity score: 0.0571056

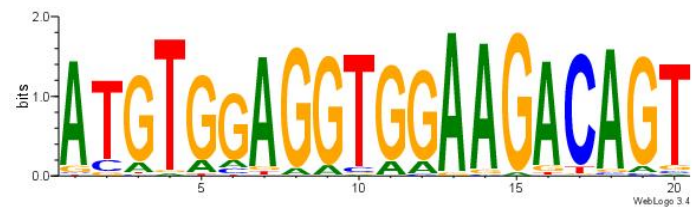
Alignment:

ATGTGGAGGTGGAAGACAGT  
 ---TGGAGGTTSTAG-----

Original motif      Consensus sequence: ACTGTCTTCCACCTCCACAT



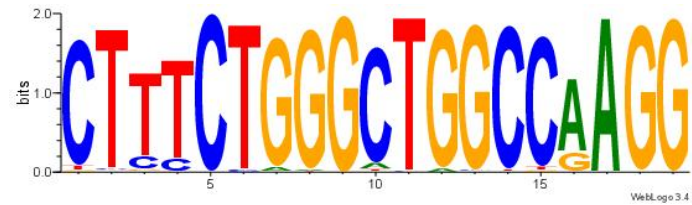
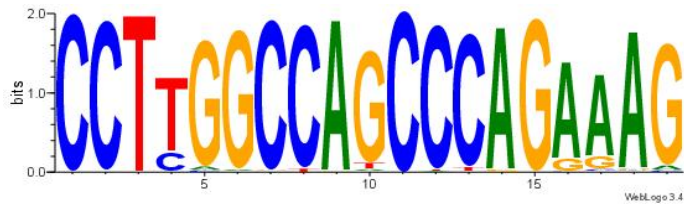
Reverse complement motif      Consensus sequence: ATGTGGAGGTGGAAGACAGT



**Dataset #: 1      Motif ID: 122      Motif name: Motif 122**

Original motif      Consensus sequence: CCTTGGCCAGCCCAGAAAG

Reverse complement motif      Consensus sequence: CTTTCTGGGCTGGCCAAGG

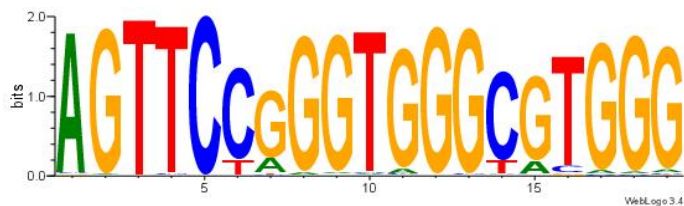


**Best Matches for Motif ID 122 (Highest to Lowest)**

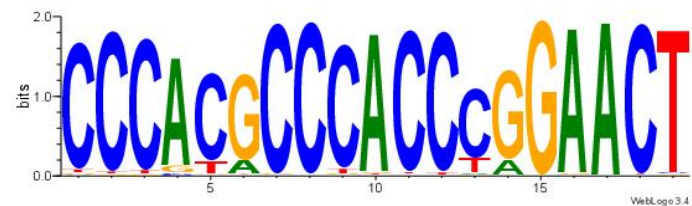
Dataset #: 1  
 Motif ID: 98  
 Motif name: Motif 98  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 19  
 Similarity score: 0.0950931

Alignment:  
 CCCACGCCACCCGGA  
 CCTTGGCCAGCCCAGAAAG

Original motif      Consensus sequence: AGTTCCGGTGGGCGTGGG



Reverse complement motif      Consensus sequence: CCCACGCCACCCGGA

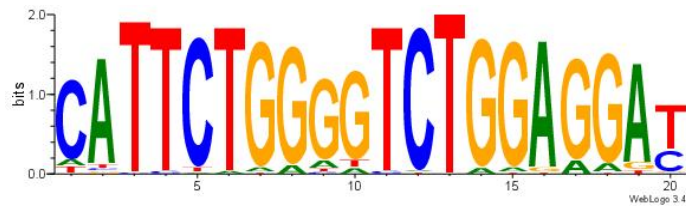


Dataset #: 1  
 Motif ID: 309  
 Motif name: Motif 309  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 2  
 Number of overlap: 19  
 Similarity score: 0.0996139

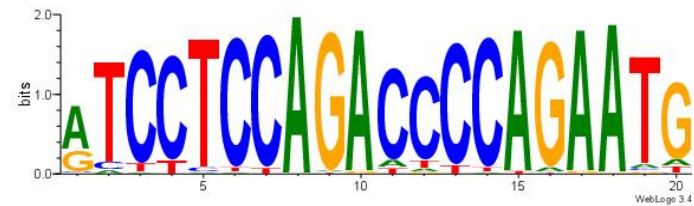
Alignment:

CATTCTGGGGTCTGGAGGAY  
 CTTTCTGGGCTGGCCAAGG-

Original motif      Consensus sequence: CATTCTGGGGTCTGGAGGAY



Reverse complement motif      Consensus sequence: MTCCTCCAGACCCCAAGAATG



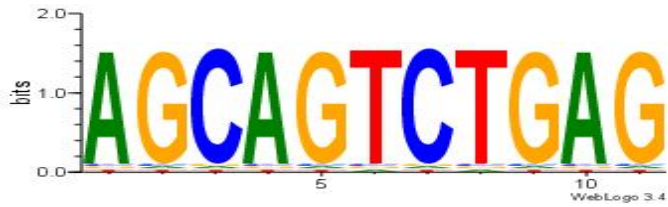

---

**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)

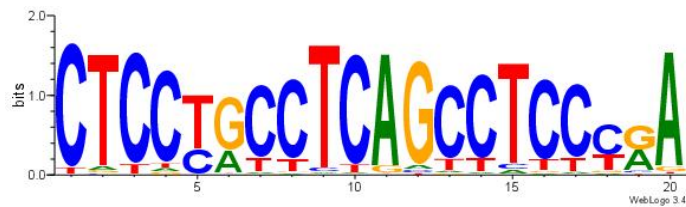
Dataset #: 1  
 Motif ID: 26  
 Motif name: Motif 26  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 8  
 Number of overlap: 11  
 Similarity score: 0.0598949

#### Alignment:

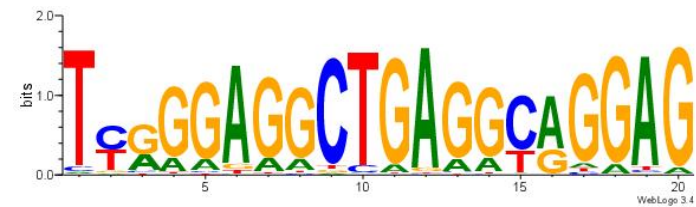
```

TMGGGAGGCTGAGGCAGGAG
-----AGCAGTCTGAG--
  
```

Original motif      Consensus sequence: CTCCTGCCTCAGCCTCCCRA



Reverse complement motif      Consensus sequence: TMGGGAGGCTGAGGCAGGAG

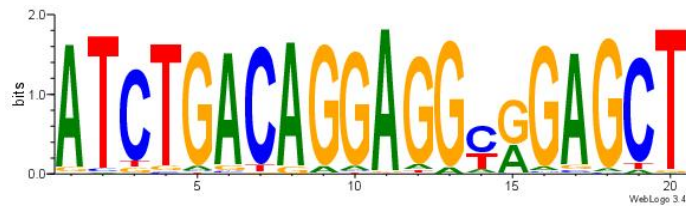


Dataset #: 1  
 Motif ID: 165  
 Motif name: Motif 165  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 8  
 Number of overlap: 11  
 Similarity score: 0.0609349

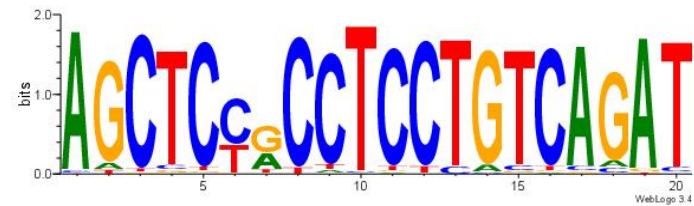
Alignment:

AGCTCMKCCTCCTGTCAGAT  
 --CTCAGACTGCT-----

Original motif      Consensus sequence: ATCTGACAGGAGGYRGAGCT



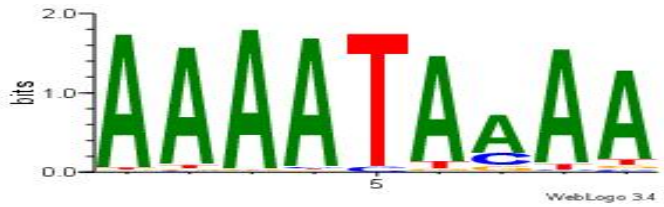
Reverse complement motif      Consensus sequence: AGCTCMKCCTCCTGTCAGAT



**Dataset #: 1      Motif ID: 124      Motif name: Motif 124**

Original motif      Consensus sequence: AAAATAAAA

Reverse complement motif      Consensus sequence: TTTATTTT

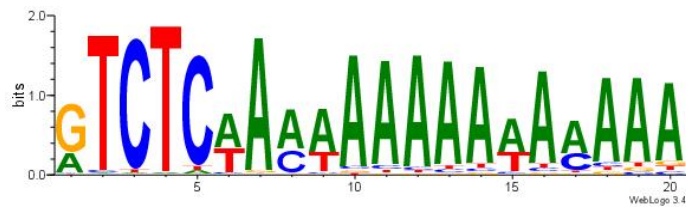


**Best Matches for Motif ID 124 (Highest to Lowest)**

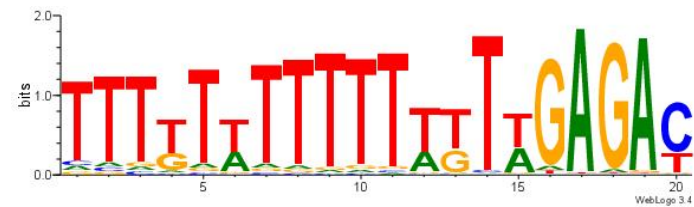
Dataset #: 1  
 Motif ID: 7  
 Motif name: Motif 7  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 2  
 Number of overlap: 9  
 Similarity score: 0.021153

Alignment:  
 GTCTCWAMAAAAAAWAMAAA  
 -----AAAATAAAA-

Original motif      Consensus sequence: GTCTCWAMAAAAAAWAMAAA



Reverse complement motif      Consensus sequence: TTTYTWTTTTTYYTWGAGAC

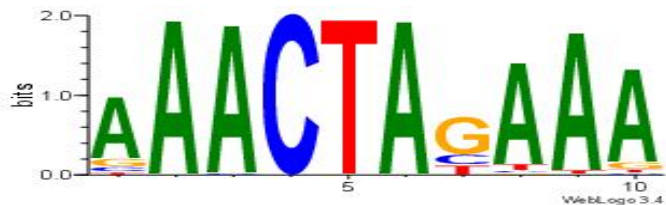


Dataset #: 1  
 Motif ID: 337  
 Motif name: Motif 337  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 9  
 Similarity score: 0.0464816

Alignment:

TTTCTAGTTT  
 -TTTTATTTT

Original motif      Consensus sequence: AACTAGAAA



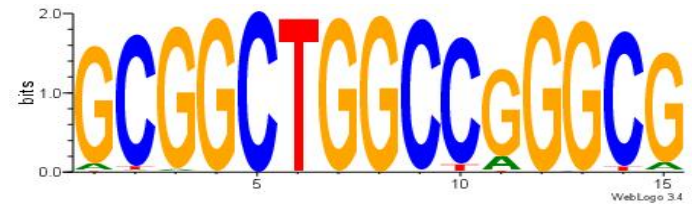
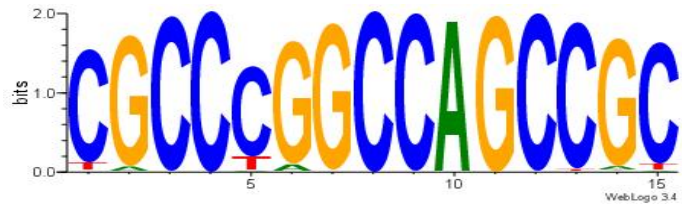
Reverse complement motif      Consensus sequence: TTTCTAGTTT



**Dataset #: 1      Motif ID: 125      Motif name: Motif 125**

Original motif      Consensus sequence: CGCCGGCCAGCCGC

Reverse complement motif      Consensus sequence:  
GCGGCTGGCCGGCG

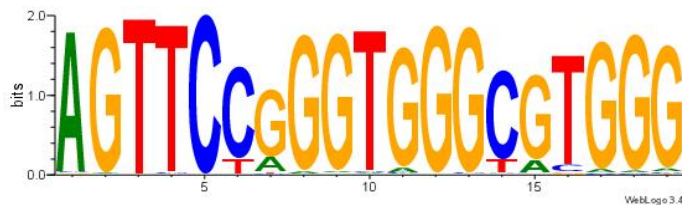


**Best Matches for Motif ID 125 (Highest to Lowest)**

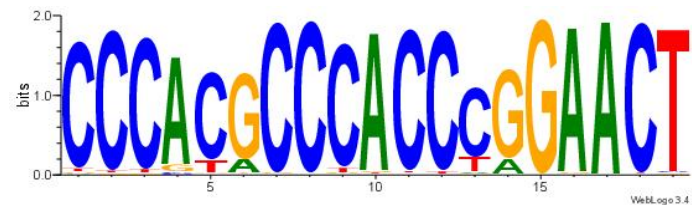
Dataset #: 1  
 Motif ID: 98  
 Motif name: Motif 98  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 5  
 Number of overlap: 15  
 Similarity score: 0.0866862

Alignment:  
 AGTTCGGGTGGCGTGGG  
 GCGGCTGGCCGGCG-----

Original motif      Consensus sequence: AGTTCGGGTGGCGTGGG



Reverse complement motif      Consensus sequence: CCCACGCCACCCGGAAC

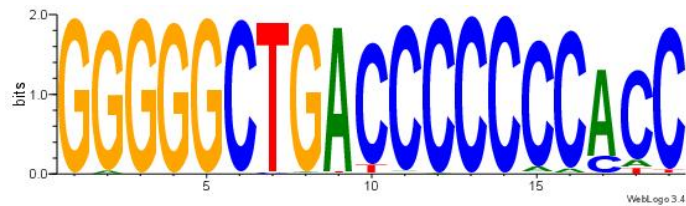


Dataset #: 1  
 Motif ID: 92  
 Motif name: Motif 92  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 4  
 Number of overlap: 15  
 Similarity score: 0.0950761

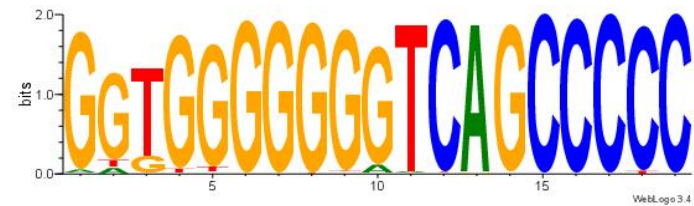
Alignment:

GGTGGGGGGGTCAGCCCC  
 -CGCCCGGCCAGCCGC---

Original motif      Consensus sequence: GGGGGCTGACCCCCCACC



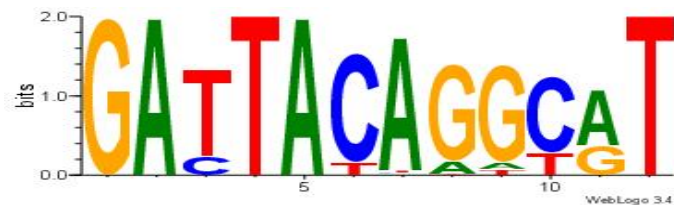
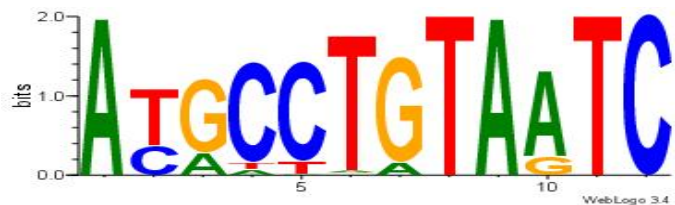
Reverse complement motif      Consensus sequence: GGTGGGGGGGTCAGCCCC



**Dataset #: 1      Motif ID: 126      Motif name: Motif 126**

Original motif      Consensus sequence: AYGCTGTAATC

Reverse complement motif      Consensus sequence: GATTACAGGCMT

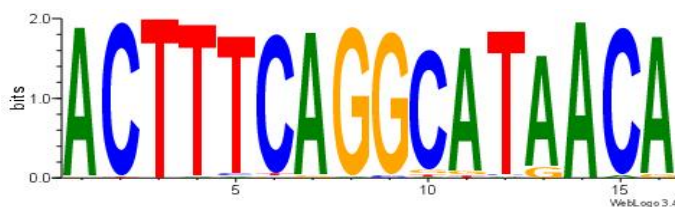


### Best Matches for Motif ID 126 (Highest to Lowest)

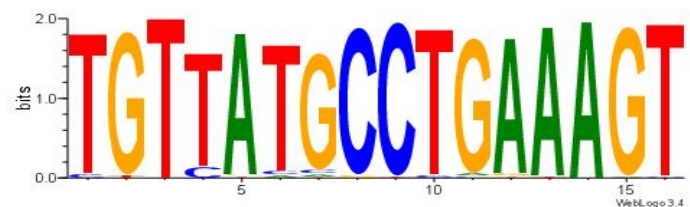
Dataset #: 1  
 Motif ID: 278  
 Motif name: Motif 278  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 12  
 Similarity score: 0.0669992

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

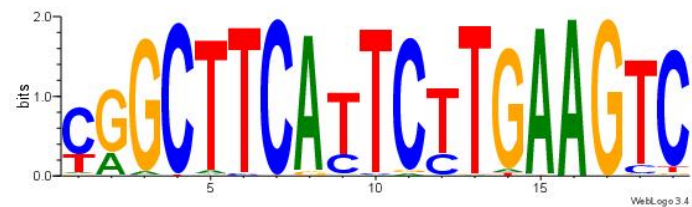
Alignment:

GACTTCAAGAATGAAGCCG  
 GATTACAGGCMT-----

Original motif      Consensus sequence: GACTTCAAGAATGAAGCCG



Reverse complement motif      Consensus sequence: CGGCTTCATTCTTGAAGTC



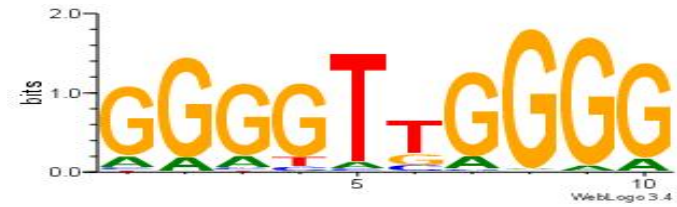
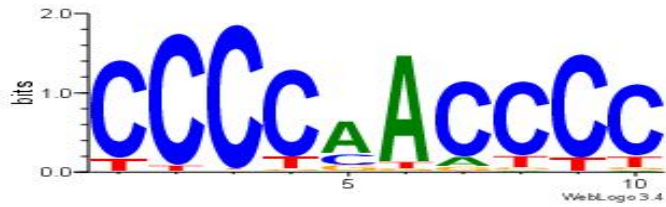

---

**Dataset #: 1      Motif ID: 127      Motif name: Motif 127**

Original motif      Consensus sequence: CCCCAACCCC

Reverse complement motif      Consensus sequence: GGGGTTGGGG



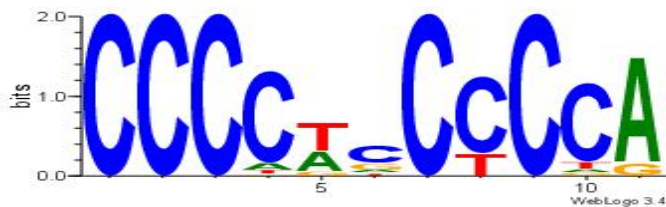


### Best Matches for Motif ID 127 (Highest to Lowest)

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



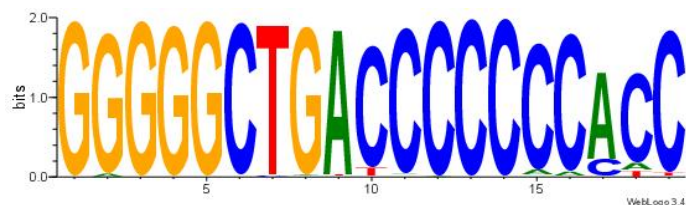
Dataset #: 1

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

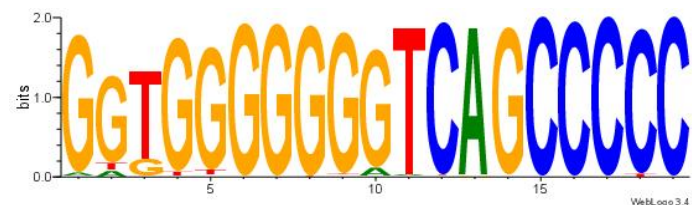
Alignment:

GGGGGCTGACCCCCCACC  
 -----CCCCAACCCC

Original motif    Consensus sequence: GGGGGCTGACCCCCCACC

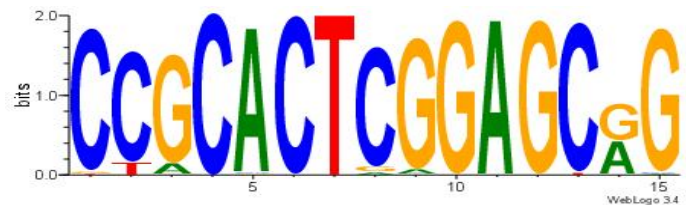


Reverse complement motif    Consensus sequence: GGTGGGGGGGTCAGCCCCC

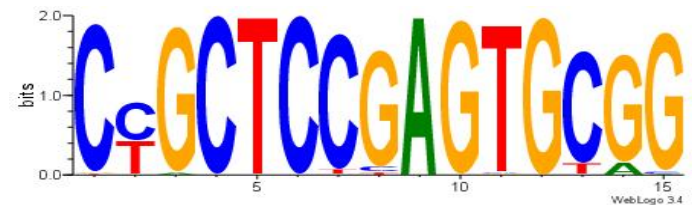


**Dataset #: 1      Motif ID: 128      Motif name: Motif 128**

Original motif    Consensus sequence: CCGCACTCGGAGCRG



Reverse complement motif    Consensus sequence: CMGCTCCGAGTGCGG



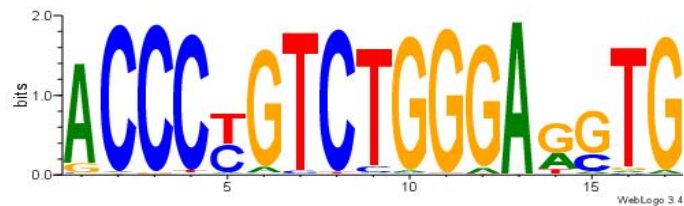
## Best Matches for Motif ID 128 (Highest to Lowest)

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

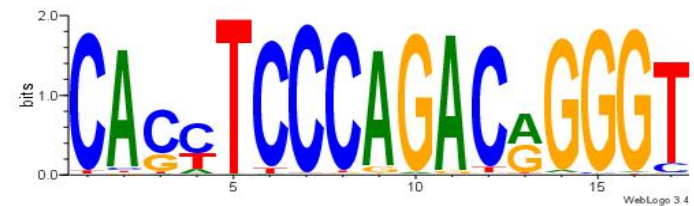
### Alignment:

```
CACCTCCCAGACMGGGT  
CMGCTCCGAGTGCGG--
```

Original motif      Consensus sequence: ACCYGTCTGGGAGGTG



Reverse complement motif      Consensus sequence: CACCTCCCAGACMGGGT



---

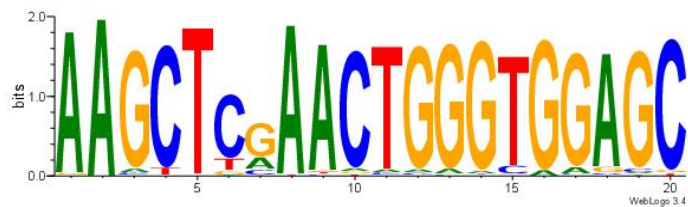
Dataset #: 1  
Motif ID: 321  
Motif name: Motif 321  
Matching format of first motif: Original Motif  
Matching format of second motif: Original Motif

Direction: Backward  
 Position number: 2  
 Number of overlap: 15  
 Similarity score: 0.0895427

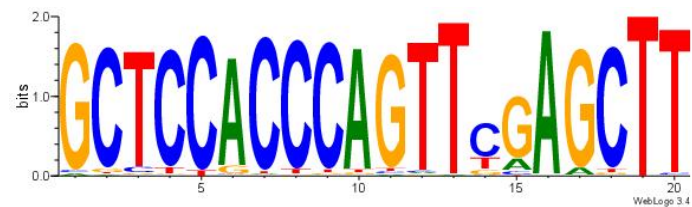
**Alignment:**

AAGCTCGAACTGGGTGGAGC  
 ----CCGCACTCGGAGCRG--

Original motif      Consensus sequence: AAGCTCGAACTGGGTGGAGC

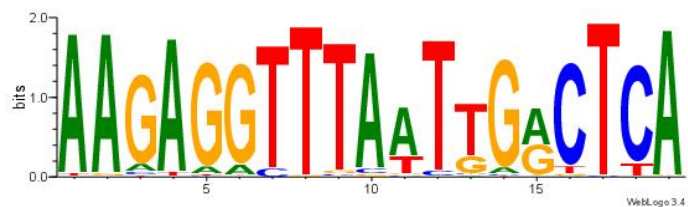


Reverse complement motif      Consensus sequence: GCTCCACCCAGTTCGAGCTT

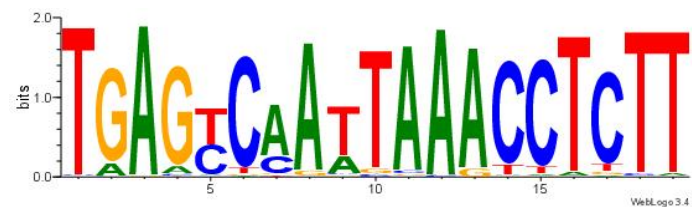


**Dataset #: 1      Motif ID: 129      Motif name: Motif 129**

Original motif      Consensus sequence: AAGAGGTTTAATTGRCTCA



Reverse complement motif      Consensus sequence: TGAGKCAATTAACCTCTT



**Best Matches for Motif ID 129 (Highest to Lowest)**

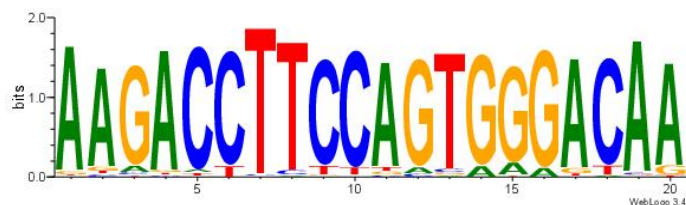
Dataset #: 1

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

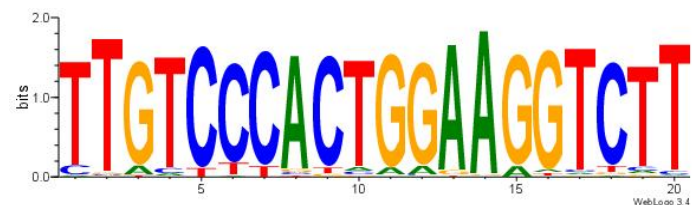
**Alignment:**

AAGACCTTCCAGTGGGACAA  
 AAGAGGTTTAAATTGRCTCA-

Original motif    Consensus sequence: AAGACCTTCCAGTGGGACAA



Reverse complement motif    Consensus sequence: TTGTCCCCTGGAAGGTCTT



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:

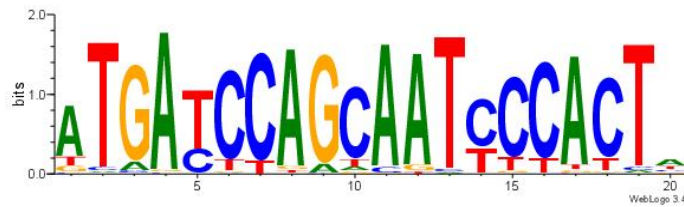
0.0969481

Alignment:

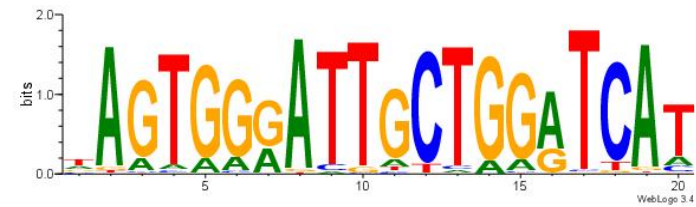
ATGATCCAGCAATYCCACTH

TGAGKCAATTAAACCTCTT-

Original motif      Consensus sequence: ATGATCCAGCAATYCCACTH

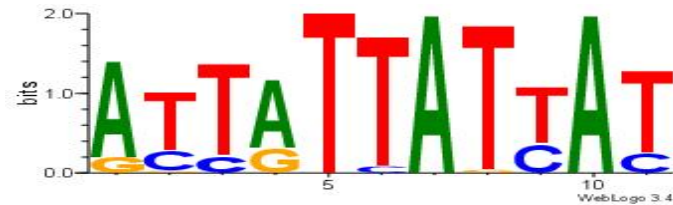


Reverse complement motif      Consensus sequence: HAGTGGKATTGCTGGATCAT

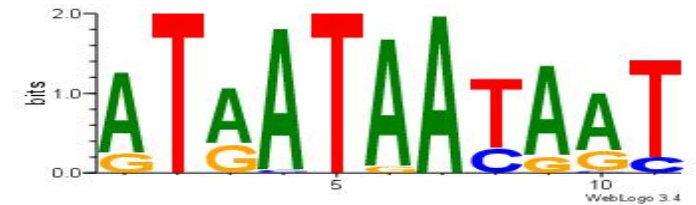


**Dataset #: 1      Motif ID: 130      Motif name: Motif 130**

Original motif      Consensus sequence: ATTATTATYAT



Reverse complement motif      Consensus sequence: ATMATAATAAT



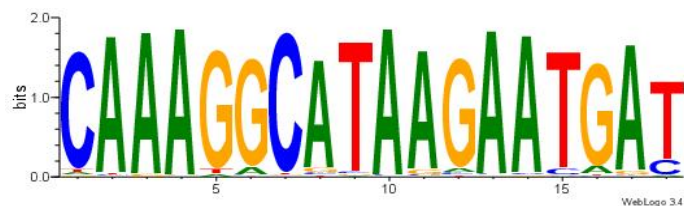
### Best Matches for Motif ID 130 (Highest to Lowest)

Dataset #:	1
Motif ID:	190
Motif name:	Motif 190
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement

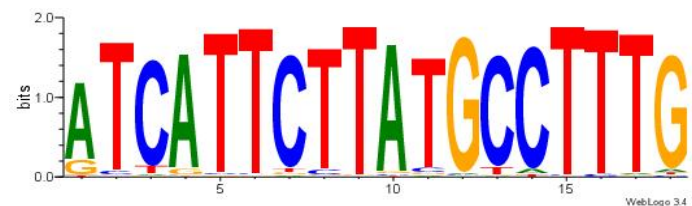
Direction: Forward  
Position number: 1  
Number of overlap: 11  
Similarity score: 0.0362259

Alignment:  
ATCATTCTTATGCCTTTG  
ATTATTATYAT-----

Original motif      Consensus sequence: CAAAGGCATAAGAATGAT



Reverse complement motif      Consensus sequence: ATCATTCTTATGCCTTTG



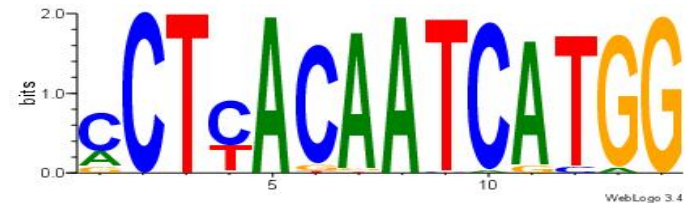
Dataset #: 1  
Motif ID: 270  
Motif name: Motif 270  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Reverse Complement  
Direction: Forward  
Position number: 2  
Number of overlap: 11  
Similarity score: 0.0458076

Alignment:  
CCTMACAATCATGG  
-ATMATAATAAT--

Original motif      Consensus sequence: CCATGATTGTRAGG

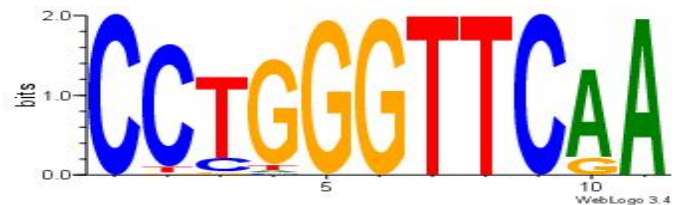


Reverse complement motif      Consensus sequence: CCTMACAATCATGG



**Dataset #: 1      Motif ID: 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)**

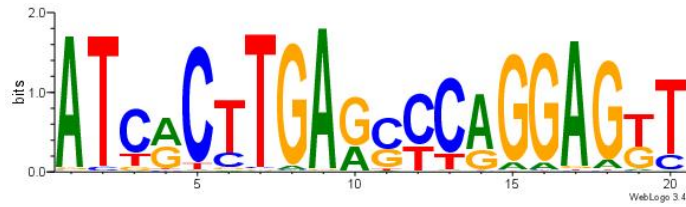
Dataset #:	1
Motif ID:	8
Motif name:	Motif 8
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	6
Number of overlap:	11
Similarity score:	0.044498

Alignment:

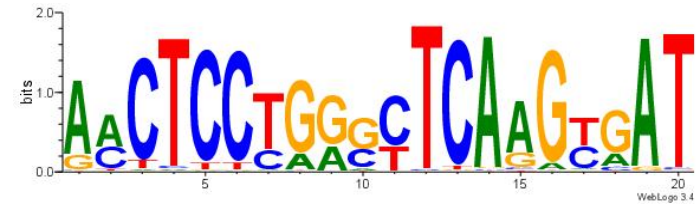


ARCTCCTGKSCTCAAGKGAT  
 -----CCTGGGTCAA-----

Original motif      Consensus sequence: ATCRCTTGAGSYCAGGAGKT



Reverse complement motif      Consensus sequence:  
 ARCTCCTGKSCTCAAGKGAT

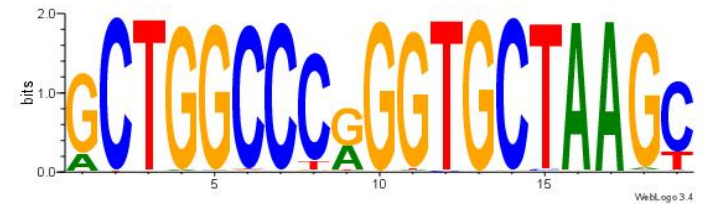
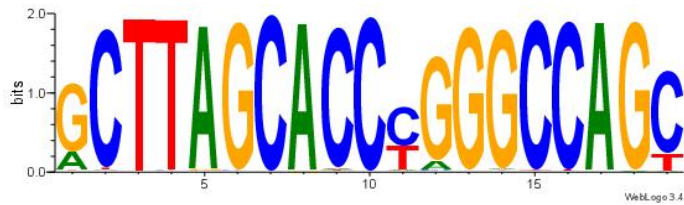


Dataset #:	1
Motif ID:	82
Motif name:	Motif 82
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	6
Number of overlap:	11
Similarity score:	0.0639634

Alignment:  
 GCTTAGCACCYGGGCCAGC  
 -----TTGAACCCAGG---

Original motif      Consensus sequence: GCTTAGCACCYGGGCCAGC

Reverse complement motif      Consensus sequence:  
 GCTGGCCCKGGTGCTAAGC

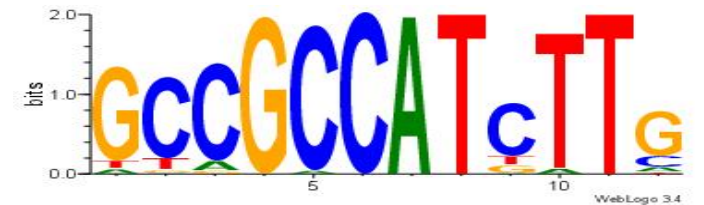


**Dataset #: 1      Motif ID: 132      Motif name: Motif 132**

Original motif      Consensus sequence: CAAGATGGCGGC



Reverse complement motif      Consensus sequence: GCCGCCATCTTG

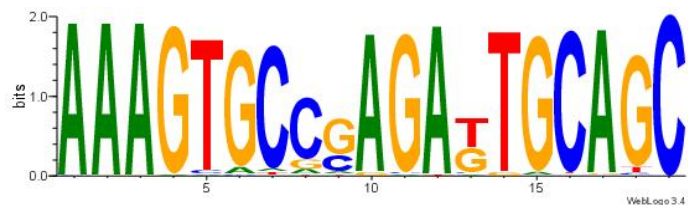


**Best Matches for Motif ID 132 (Highest to Lowest)**

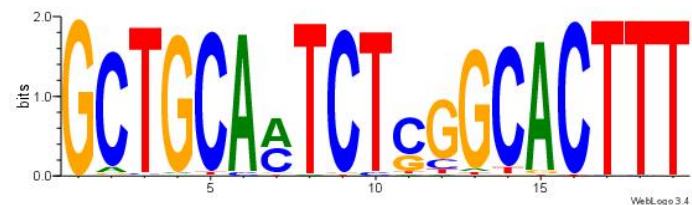
Dataset #:	1
Motif ID:	191
Motif name:	Motif 191
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	8
Number of overlap:	12
Similarity score:	0.0630794

Alignment:  
GCTGCARTCTCGGCACTTT  
GCCGCCATCTTG-----

Original motif      Consensus sequence: AAAGTGCCGAGAKTGCAGC



Reverse complement motif      Consensus sequence: GCTGCARTCTCGGCACTTT

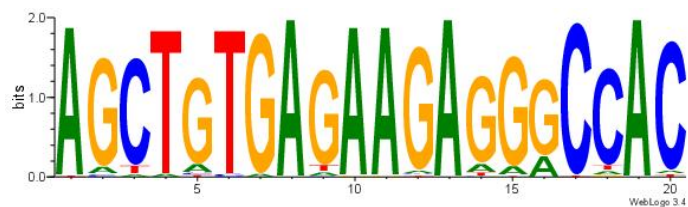


Dataset #: 1  
Motif ID: 294  
Motif name: Motif 294  
Matching format of first motif: Original Motif  
Matching format of second motif: Original Motif  
Direction: Forward  
Position number: 9  
Number of overlap: 12  
Similarity score: 0.0641012

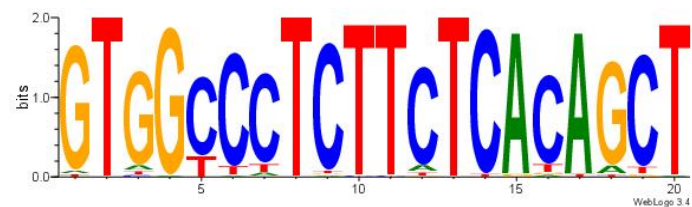
Alignment:

```
AGCTGTGAGAAGAGGGCCAC  
-----CAAGATGGCGGC
```

Original motif      Consensus sequence: AGCTGTGAGAAGAGGGCCAC



Reverse complement motif      Consensus sequence: GTGGCCCTCTTCTCACAGCT



**Dataset #: 1      Motif ID: 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)**

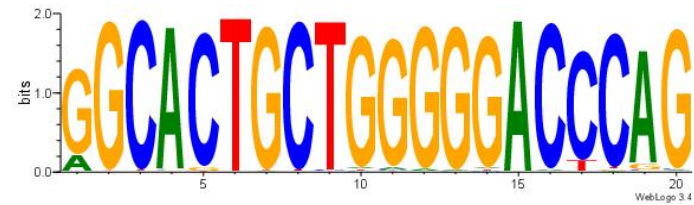
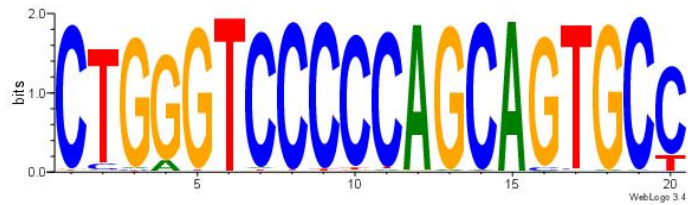
Dataset #:	1
Motif ID:	84
Motif name:	Motif 84
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	11
Similarity score:	0.0319466

**Alignment:**

```
GGCACTGCTGGGGGACCCAG
-----TGGGGACMCAG
```

Original motif      Consensus sequence: CTGGGTCCCCCAGCAGTGCC

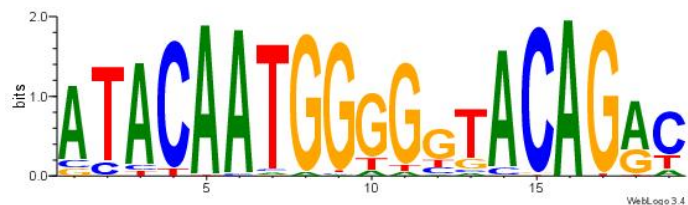
Reverse complement motif      Consensus sequence: GGCACTGCTGGGGGACCCAG



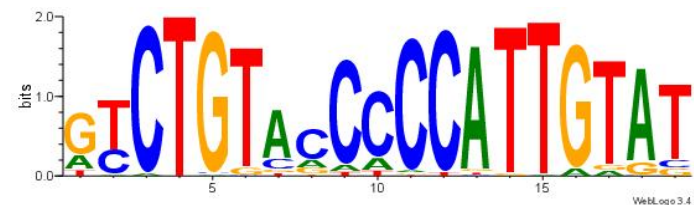
Dataset #: 1  
 Motif ID: 193  
 Motif name: Motif 193  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 3  
 Number of overlap: 11  
 Similarity score: 0.0508347

Alignment:  
 GKCTGTACCCCCATTGTAT  
 --CTGYGTCCCA-----

Original motif      Consensus sequence: ATACAATGGGGGTACAGRC

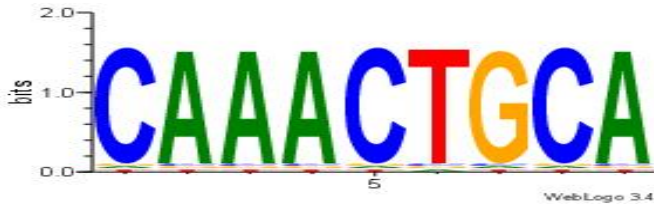


Reverse complement motif      Consensus sequence: GKCTGTACCCCCATTGTAT

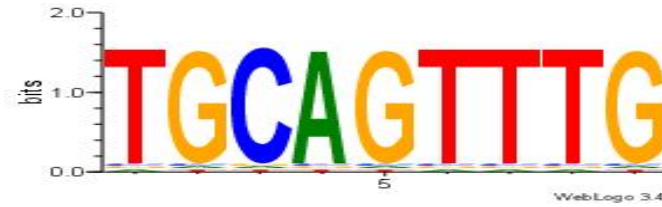


**Dataset #: 1      Motif ID: 134      Motif name: Motif 134**

Original motif    Consensus sequence: CAAACTGCA



Reverse complement motif    Consensus sequence: TGCAGTTTG



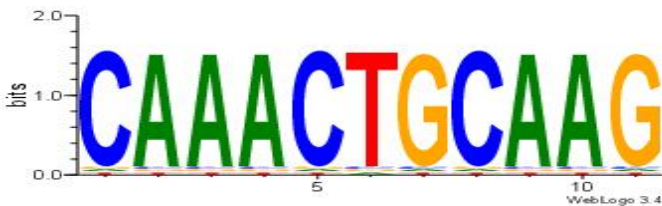
### Best Matches for Motif ID 134 (Highest to Lowest)

Dataset #:	1
Motif ID:	73
Motif name:	Motif 73
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	9
Similarity score:	0

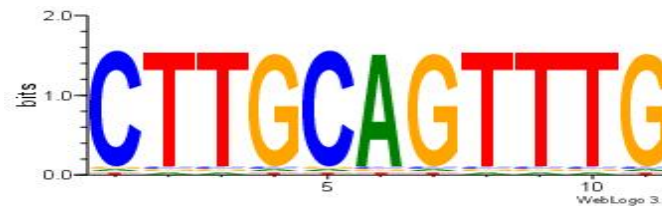
Alignment:

```
CTTGCAGTTTG  
--TGCAGTTTG
```

Original motif    Consensus sequence: CAAACTGCAAG



Reverse complement motif    Consensus sequence: CTTGCAGTTTG

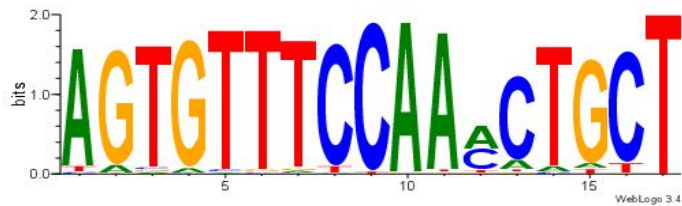


Dataset #: 1  
 Motif ID: 304  
 Motif name: Motif 304  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 9  
 Similarity score: 0.0499634

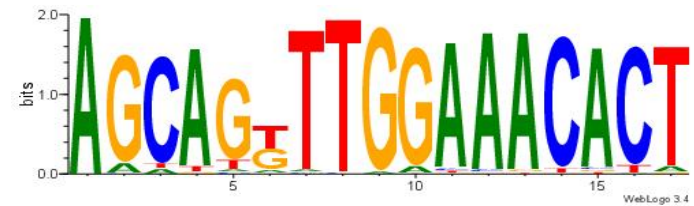
Alignment:

AGTGTTTCCAAMCTGCT  
 -----CAAAC TGCA

Original motif      Consensus sequence: AGTGTTTCCAAMCTGCT



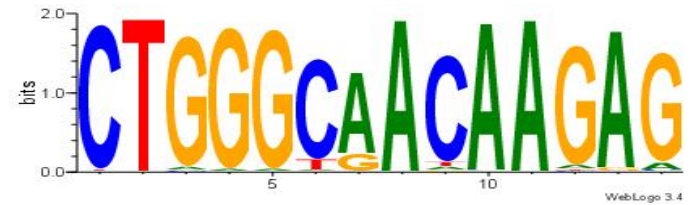
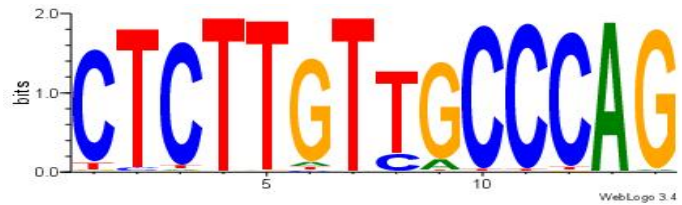
Reverse complement motif      Consensus sequence: AGCAGYTTGGAAACACT



**Dataset #: 1      Motif ID: 135      Motif name: Motif 135**

Original motif      Consensus sequence: CTCTGTTGCCAG

Reverse complement motif      Consensus sequence: CTGGCAACAAGA

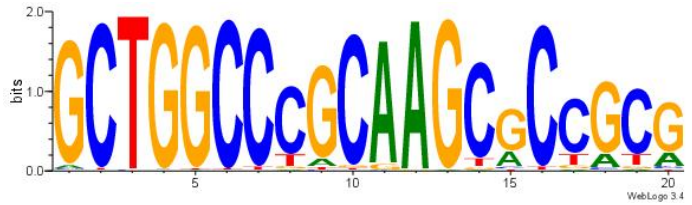


**Best Matches for Motif ID 135 (Highest to Lowest)**

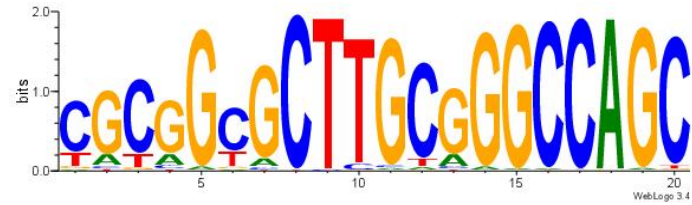
Dataset #: 1  
 Motif ID: 100  
 Motif name: Motif 100  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 2  
 Number of overlap: 14  
 Similarity score: 0.0668647

Alignment:  
 GCTGGCCCGCAAGCGCCGCG  
 -----CTGGGCAACAAGAG--

Original motif      Consensus sequence: GCTGGCCCGCAAGCGCCGCG



Reverse complement motif      Consensus sequence: CGCGGCGCTTGCGGGCCAGC



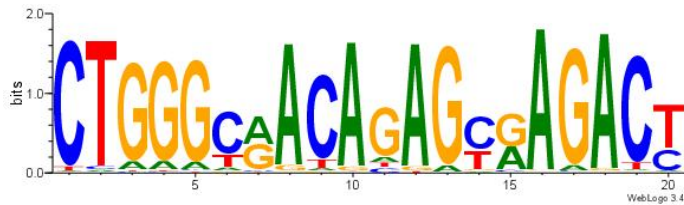


Dataset #: 1  
 Motif ID: 29  
 Motif name: Motif 29  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 7  
 Number of overlap: 14  
 Similarity score: 0.0777944

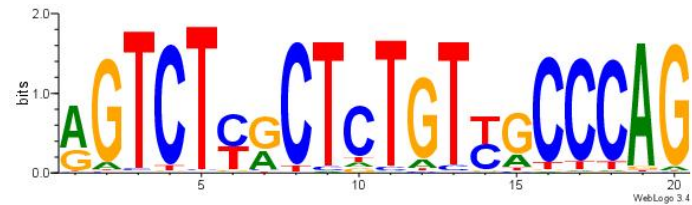
Alignment:

MGTCTMKCTCTGTKGCCCAG  
 CTCTTGTTGCCAG-----

Original motif      Consensus sequence: CTGGGCRACAGAGYRAGACY



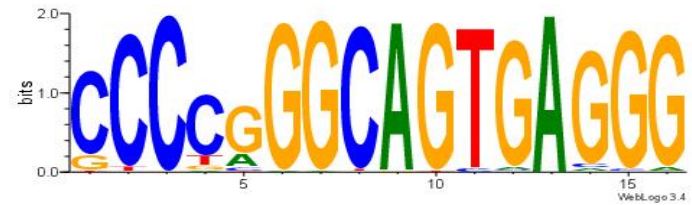
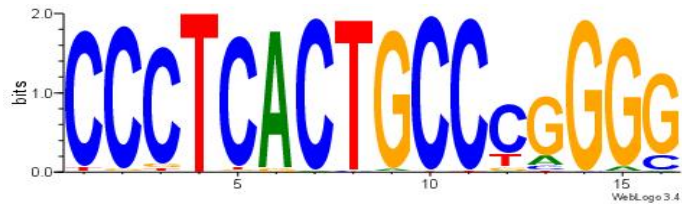
Reverse complement motif      Consensus sequence: MGTCTMKCTCTGTKGCCCAG



**Dataset #: 1      Motif ID: 136      Motif name: Motif 136**

Original motif      Consensus sequence: CCCTCACTGCCCGGGG

Reverse complement motif      Consensus sequence: CCCCGGCAGTGAGGG

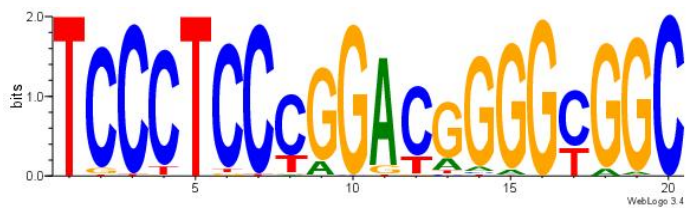


**Best Matches for Motif ID 136 (Highest to Lowest)**

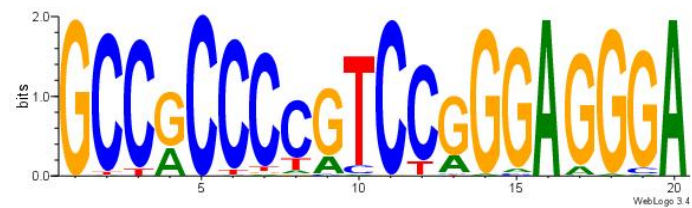
Dataset #: 1  
 Motif ID: 155  
 Motif name: Motif 155  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 4  
 Number of overlap: 16  
 Similarity score: 0.0741545

Alignment:  
 GCCKCCCCGTCCGGGAGGGA  
 ---CCCCGGGCAGTGAGGG--

Original motif      Consensus sequence: TCCCTCCCGGACGGGGYGGC



Reverse complement motif      Consensus sequence: GCCKCCCCGTCCGGGAGGGA

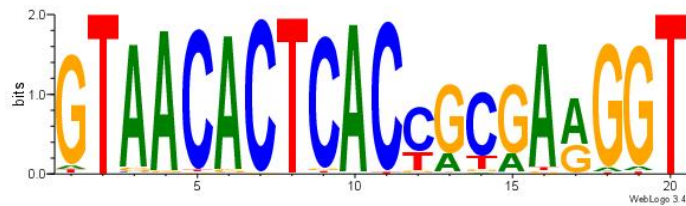


Dataset #: 1  
 Motif ID: 201  
 Motif name: Motif 201  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 5  
 Number of overlap: 16  
 Similarity score: 0.0805996

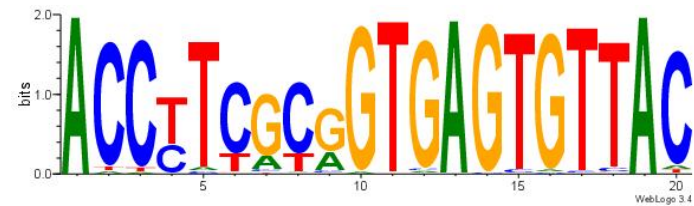
Alignment:

GTAACACTCACCGCGARGGT  
 ----CCCTCACTGCCCGGGG

Original motif      Consensus sequence: GTAACACTCACCGCGARGGT



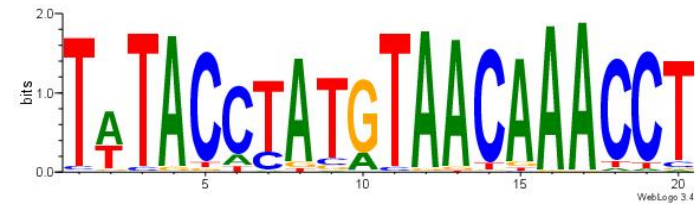
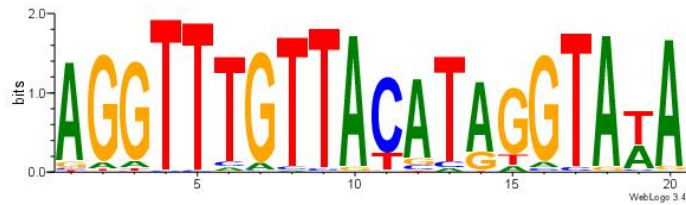
Reverse complement motif      Consensus sequence: ACCKTCGCGGTGAGTGTTAC



**Dataset #: 1      Motif ID: 137      Motif name: Motif 137**

Original motif      Consensus sequence: AGGTTTGTACATAGGTAWA

Reverse complement motif      Consensus sequence: TWTACCTATGTAACAAACCT

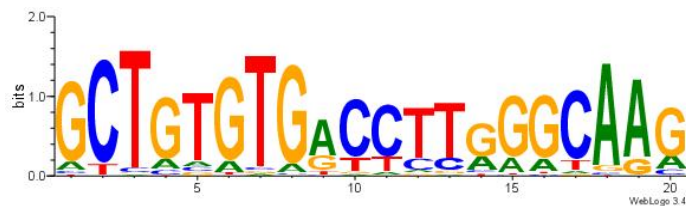


**Best Matches for Motif ID 137 (Highest to Lowest)**

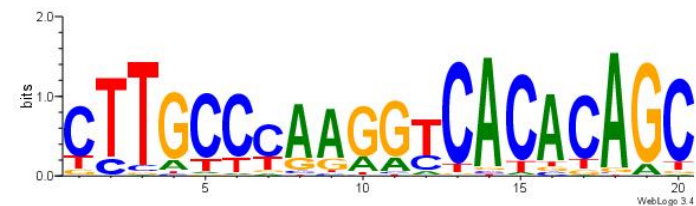
Dataset #: 1  
 Motif ID: 112  
 Motif name: Motif 112  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 2  
 Number of overlap: 19  
 Similarity score: 0.0884615

Alignment:  
 CTTGCCCAAGGTCACACAGC-  
 -TWTACCTATGTAACAAACCT

Original motif      Consensus sequence: GCTGTGTGACCTGGGCAAG



Reverse complement motif      Consensus sequence: CTTGCCCAAGGTCACACAGC

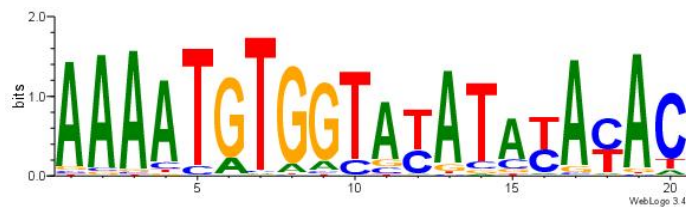


Dataset #: 1  
 Motif ID: 83  
 Motif name: Motif 83  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 2  
 Number of overlap: 19  
 Similarity score: 0.0899122

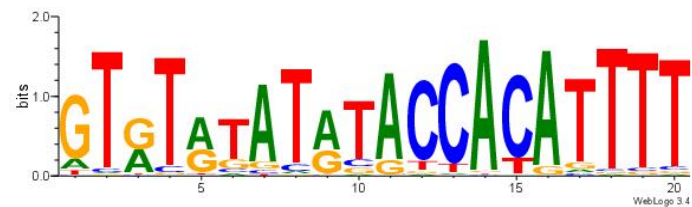
Alignment:

AAAATGTGGTAYATAYAYAC-  
 -AGGTTTGTTCATAGGTAWA

Original motif      Consensus sequence: AAAATGTGGTAYATAYAYAC



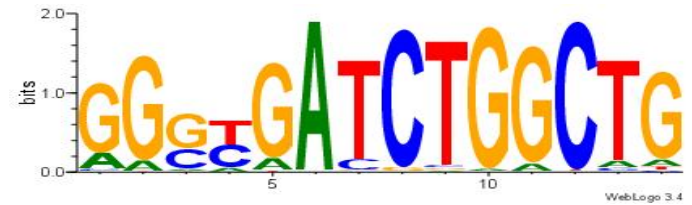
Reverse complement motif      Consensus sequence: GTKTMTATMTACCACATTTT



**Dataset #: 1      Motif ID: 138      Motif name: Motif 138**

Original motif      Consensus sequence: CAGCCAGATCRSCC

Reverse complement motif      Consensus sequence: GSKGATCTGGCT

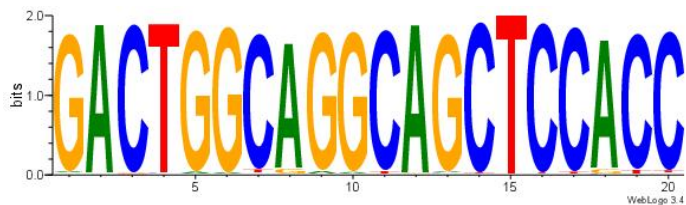


**Best Matches for Motif ID 138 (Highest to Lowest)**

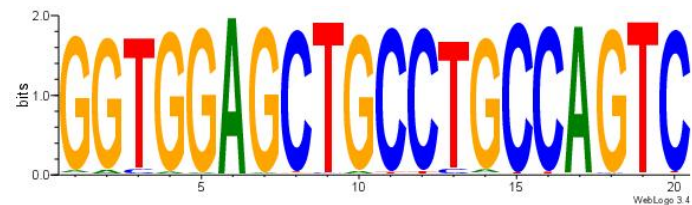
Dataset #: 1  
 Motif ID: 52  
 Motif name: Motif 52  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 7  
 Number of overlap: 14  
 Similarity score: 0.0576267

Alignment:  
 GGTGGAGCTGCCAGTC  
 GSKGATCTGGCTG-----

Original motif      Consensus sequence: GACTGGCAGGCAGCTCCACC



Reverse complement motif      Consensus sequence: GGTGGAGCTGCCAGTC

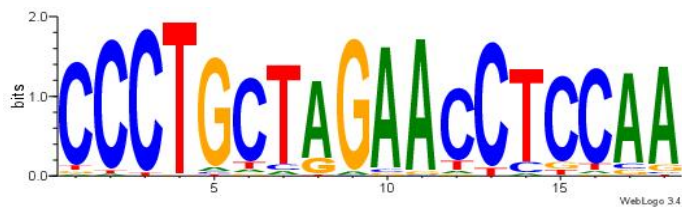


Dataset #: 1  
 Motif ID: 299  
 Motif name: Motif 299  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 3  
 Number of overlap: 14  
 Similarity score: 0.0761753

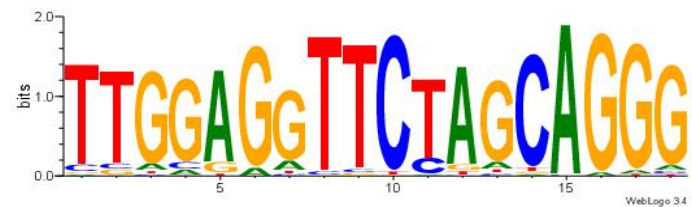
Alignment:

TTGGAGGTTCTAGCAGGG  
 --GSKGATCTGGCTG--

Original motif      Consensus sequence: CCCTGCTAGAACCTCCAA



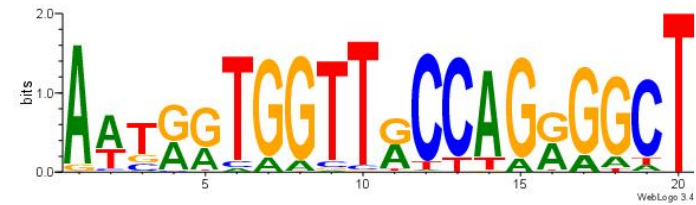
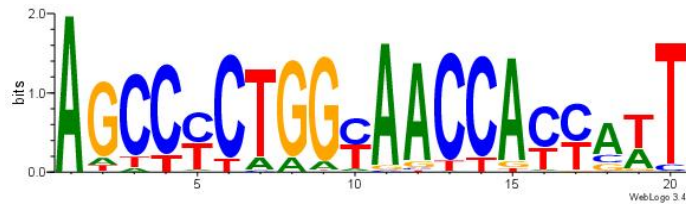
Reverse complement motif      Consensus sequence: TTGGAGGTTCTAGCAGGG



**Dataset #: 1      Motif ID: 139      Motif name: Motif 139**

Original motif      Consensus sequence: AGCCYCTGGYAACCAYYAWT

Reverse complement motif      Consensus sequence: AWTKKTGGTTKCCAGKGGCT

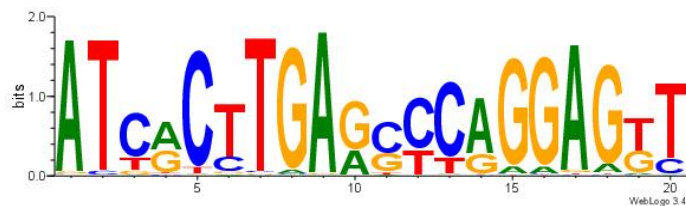


**Best Matches for Motif ID 139 (Highest to Lowest)**

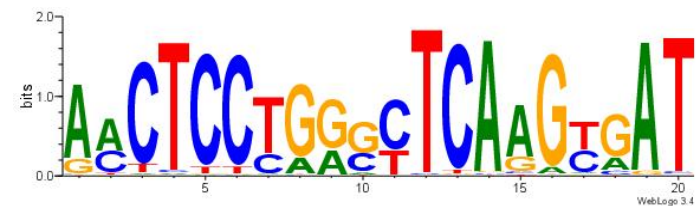
Dataset #: 1  
 Motif ID: 8  
 Motif name: Motif 8  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 20  
 Similarity score: 0.087556

Alignment:  
 ATCRCTTGAGSYCAGGAGKT  
 AWTkKtGGTTKCCAGKGGCT

Original motif      Consensus sequence: ATCRCTTGAGSYCAGGAGKT



Reverse complement motif      Consensus sequence: ARCTCCTGKsCTCAAGKgat



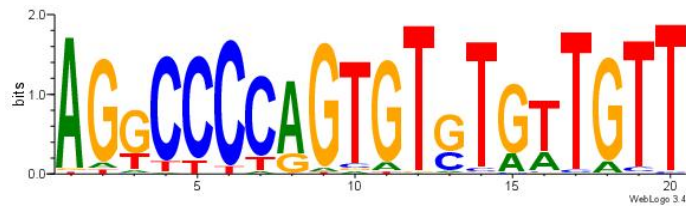


Dataset #: 1  
 Motif ID: 176  
 Motif name: Motif 176  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 20  
 Similarity score: 0.0947311

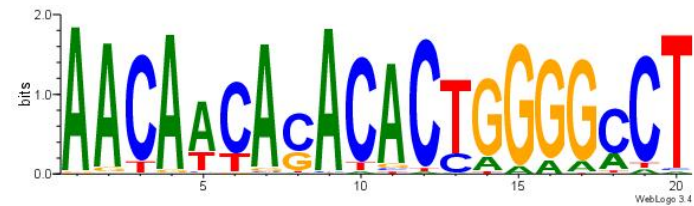
Alignment:

AGGCCCCAGTGTSTGTTGTT  
 AGCCYCTGGYAACCAYYAWT

Original motif      Consensus sequence: AGGCCCCAGTGTSTGTTGTT



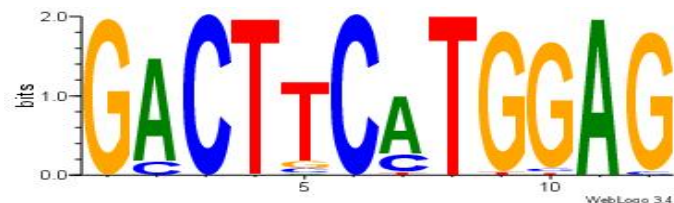
Reverse complement motif      Consensus sequence: AACACASACACTGGGGCCT



**Dataset #: 1      Motif ID: 140      Motif name: Motif 140**

Original motif      Consensus sequence: CTCCATGAAGTC

Reverse complement motif      Consensus sequence: GACTTCATGGAG



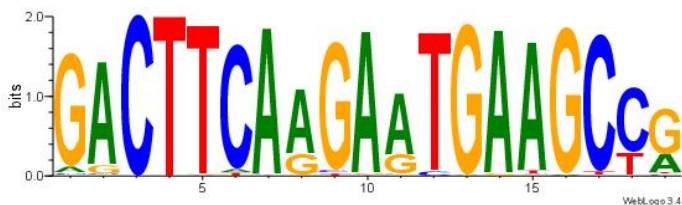
### Best Matches for Motif ID 140 (Highest to Lowest)

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

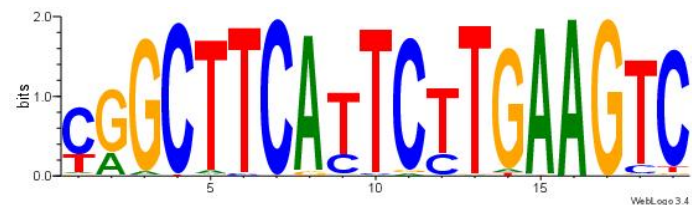
#### Alignment:

```
GACTTCAAGAATGAAGCCG
GACTTCATGGAG-----
```

Original motif      Consensus sequence: GACTTCAAGAATGAAGCCG



Reverse complement motif      Consensus sequence: CGGCTTCATTCTTGAAGTC

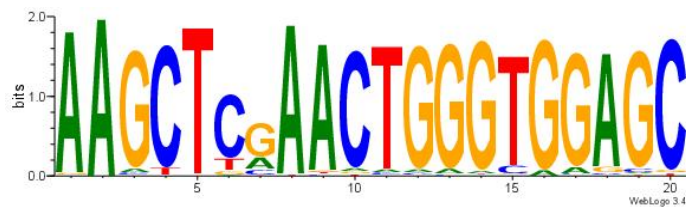


Dataset #: 1  
 Motif ID: 321  
 Motif name: Motif 321  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 2  
 Number of overlap: 12  
 Similarity score: 0.0805058

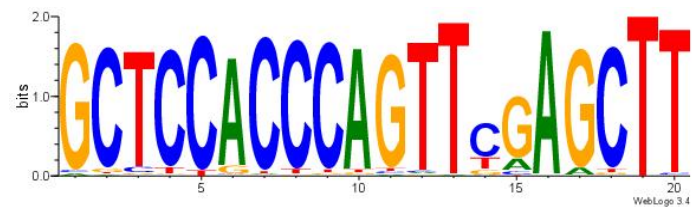
Alignment:

AAGCTCGAACTGGGTGGAGC  
 -----GACTTCATGGAG--

Original motif      Consensus sequence: AAGCTCGAACTGGGTGGAGC



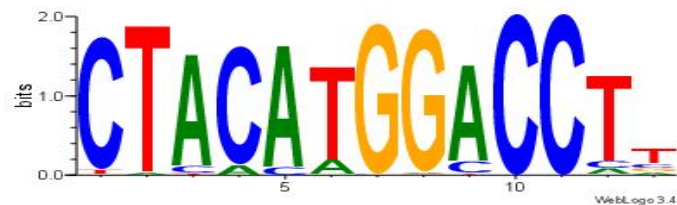
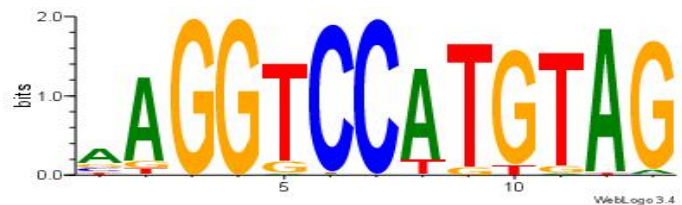
Reverse complement motif      Consensus sequence: GCTCCACCCAGTTCGAGCTT



**Dataset #: 1      Motif ID: 141      Motif name: Motif 141**

Original motif      Consensus sequence: AAGGTCCATGTAG

Reverse complement motif      Consensus sequence: CTACATGGACCTT

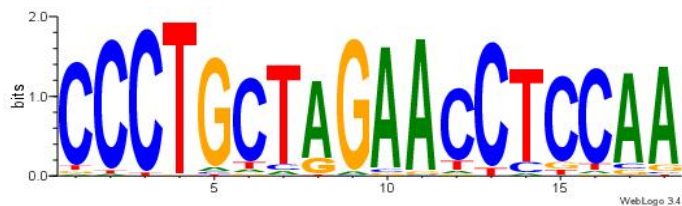


**Best Matches for Motif ID 141 (Highest to Lowest)**

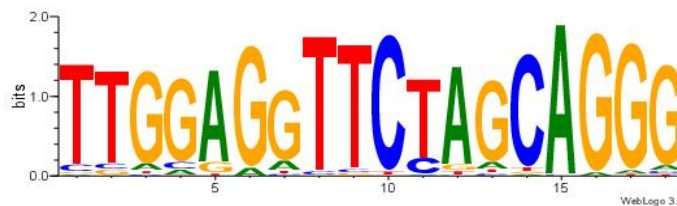
Dataset #: 1  
 Motif ID: 299  
 Motif name: Motif 299  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 4  
 Number of overlap: 13  
 Similarity score: 0.0879979

Alignment:  
 CCCTGCTAGAACCTCCAA  
 --CTACATGGACCTT---

Original motif      Consensus sequence: CCCTGCTAGAACCTCCAA



Reverse complement motif      Consensus sequence: TTGGAGTTCTAGCAGGG

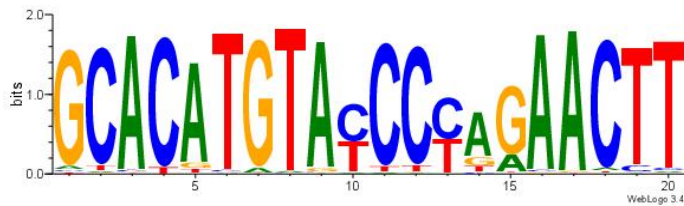


Dataset #: 1  
 Motif ID: 225  
 Motif name: Motif 225  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 8  
 Number of overlap: 13  
 Similarity score: 0.0909434

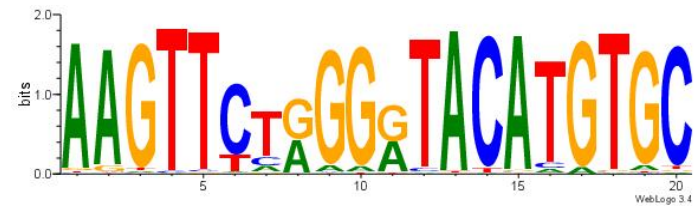
Alignment:

GCACATGTAYCCYAGAACTT  
 CTACATGGACCTT-----

Original motif      Consensus sequence: GCACATGTAYCCYAGAACTT



Reverse complement motif      Consensus sequence: AAGTTCTKGGKTACATGTGC

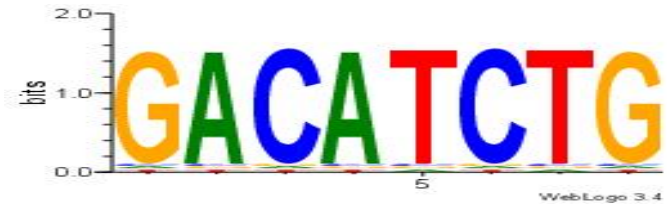



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**Dataset #: 1      Motif ID: 142      Motif name: Motif 142**

Original motif      Consensus sequence: CAGATGTC

Reverse complement motif      Consensus sequence: GACATCTG

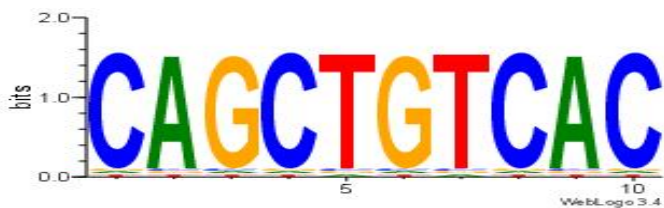


### Best Matches for Motif ID 142 (Highest to Lowest)

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



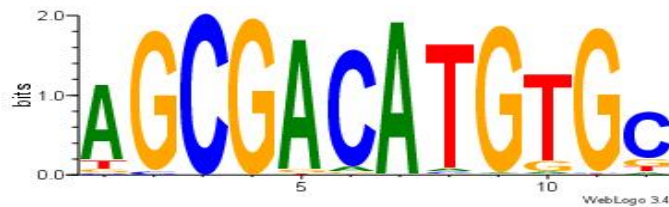

---

Dataset #: 1

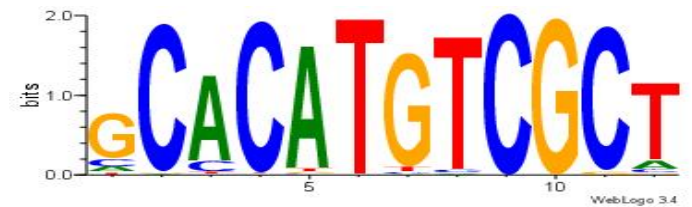
Motif ID: 269  
 Motif name: Motif 269  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 2  
 Number of overlap: 8  
 Similarity score: 0.0407488

Alignment:  
 GCACATGTCGCT  
 -CAGATGTC---

Original motif    Consensus sequence: AGCGACATGTGC

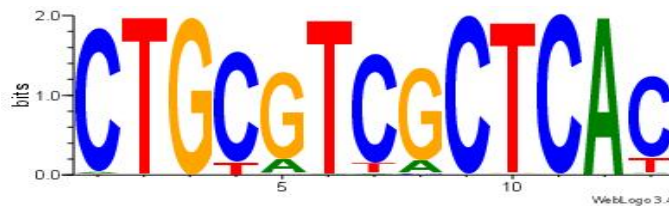


Reverse complement motif    Consensus sequence: GCACATGTCGCT

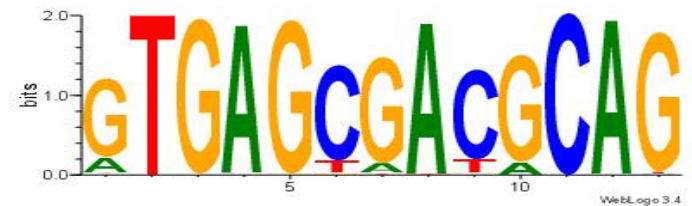


**Dataset #: 1      Motif ID: 143      Motif name: Motif 143**

Original motif    Consensus sequence: CTGCGTCGCTCAC



Reverse complement motif    Consensus sequence: GTGAGCGACGCA



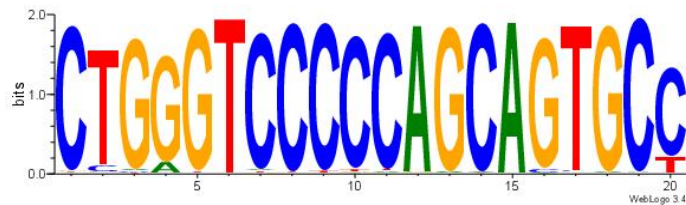
## Best Matches for Motif ID 143 (Highest to Lowest)

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

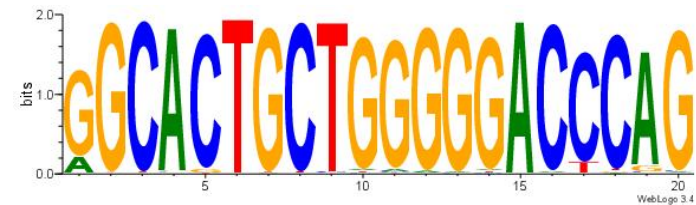
### Alignment:

```
CTGGGTCCCCCAGCAGTGCC  
CTGCGTCGCTCAC-----
```

Original motif      Consensus sequence: CTGGGTCCCCCAGCAGTGCC



Reverse complement motif      Consensus sequence: GGCACTGCTGGGGGACCCAG



---

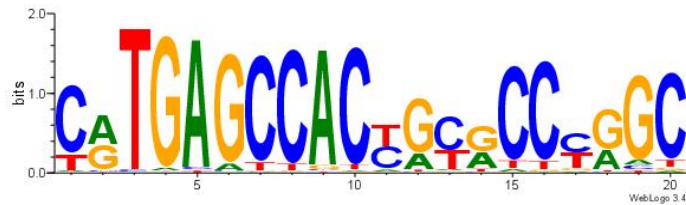
Dataset #: 1  
Motif ID: 56  
Motif name: Motif 56  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Original Motif



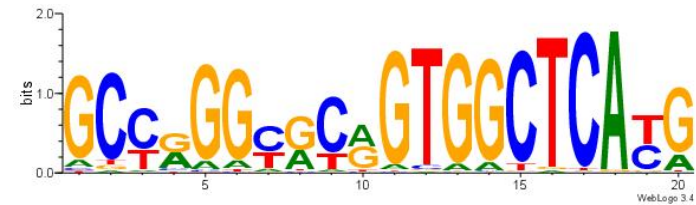
Direction: Forward  
 Position number: 7  
 Number of overlap: 13  
 Similarity score: 0.0789125

Alignment:  
 CRTGAGCCACYGYRCCYGGC  
 -----GTGAGCGACGCAG--

Original motif      Consensus sequence: CRTGAGCCACYGYRCCYGGC

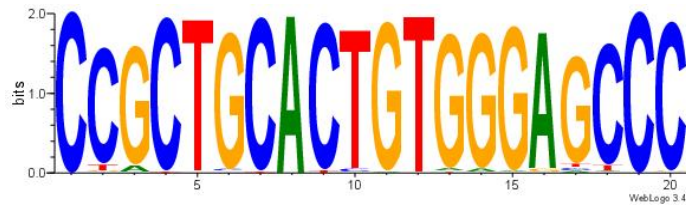


Reverse complement motif      Consensus sequence: GCCKGGMKCMGTGGCTCAKG

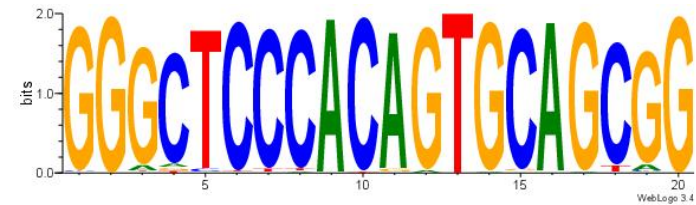


**Dataset #: 1      Motif ID: 144      Motif name: Motif 144**

Original motif      Consensus sequence: CCGCTGCACTGTGGGAGCCC



Reverse complement motif      Consensus sequence: GGGCTCCCACAGTGCAGCGG



**Best Matches for Motif ID 144 (Highest to Lowest)**

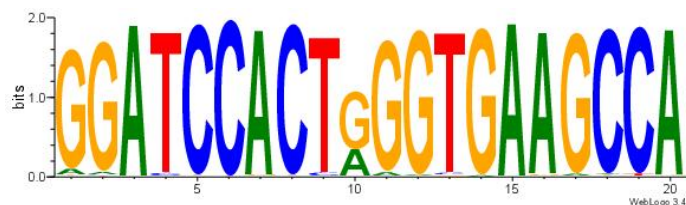
Dataset #: 1

Motif ID: 61  
 Motif name: Motif 61  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 2  
 Number of overlap: 19  
 Similarity score: 0.0905032

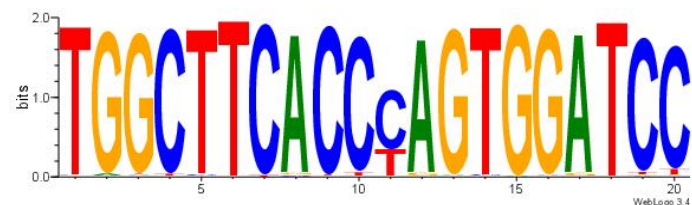
**Alignment:**

TGGCTTCACCCAGTGGATCC-  
 -GGGCTCCCACAGTGCAGCGG

Original motif    Consensus sequence: GGATCCACTGGGTGAAGCCA



Reverse complement motif    Consensus sequence: TGGCTTCACCCAGTGGATCC



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: 1  
 Number of overlap: 19

Similarity score: 0.0928981

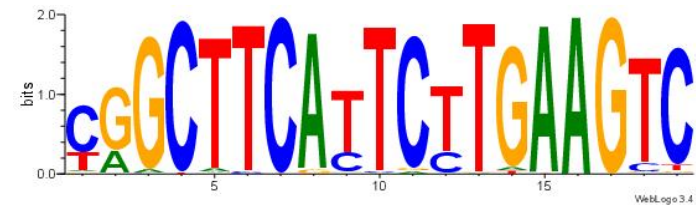
Alignment:

-GACTTCAAGAATGAAGCCG  
GGGCTCCCACAGTGCAGCGG

Original motif      Consensus sequence: GACTTCAAGAATGAAGCCG

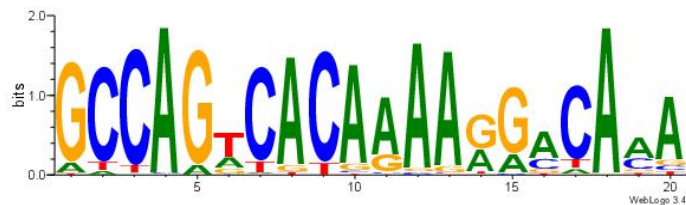


Reverse complement motif      Consensus sequence: CGGCTTCATTCTGAAGTC

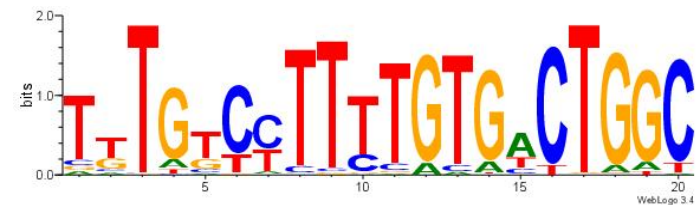


**Dataset #: 1      Motif ID: 145      Motif name: Motif 145**

Original motif      Consensus sequence: GCCAGTCACAAAARGACAMA



Reverse complement motif      Consensus sequence: TYTGTCTTTTGTGACTGGC



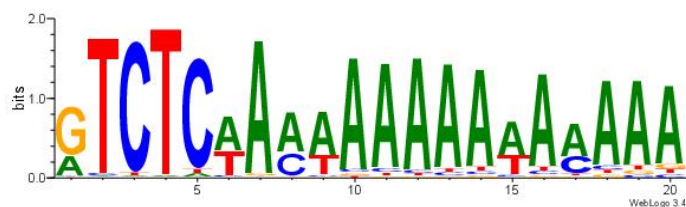
**Best Matches for Motif ID 145 (Highest to Lowest)**

Dataset #:	1
Motif ID:	7
Motif name:	Motif 7
Matching format of first motif:	Original Motif

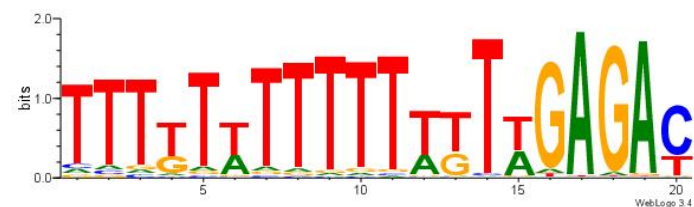
Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 20  
 Similarity score: 0.0929275

Alignment:  
 GTCTCWAMAAAAAWAMAAA  
 GCCAGTCACAAAARGACAMA

Original motif      Consensus sequence: GTCTCWAMAAAAAWAMAAA



Reverse complement motif      Consensus sequence: TTTYTWTTTTTWTGAGAC

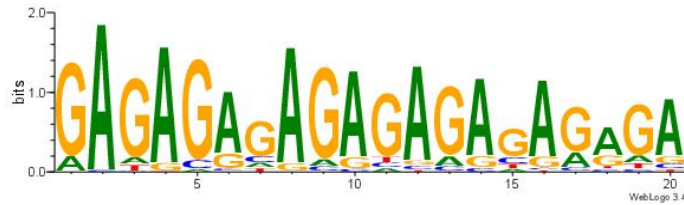


Dataset #: 1  
 Motif ID: 109  
 Motif name: Motif 109  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 20  
 Similarity score: 0.0984643

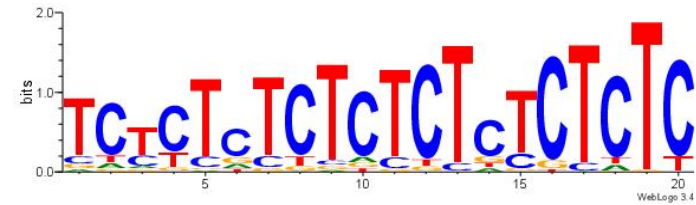
Alignment:

GAGAGAGAGAGAGAGAGAGA  
GCCAGTCACAAAARGACAMA

Original motif      Consensus sequence: GAGAGAGAGAGAGAGAGA



Reverse complement motif      Consensus sequence: TCTCTCTCTCTCTCTCTC

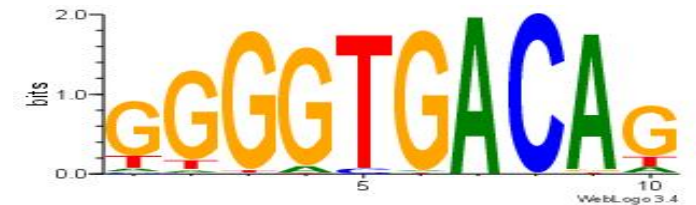


**Dataset #: 1      Motif ID: 146      Motif name: Motif 146**

Original motif      Consensus sequence: CTGTCACCCC



Reverse complement motif      Consensus sequence: GGGGTGACAG



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

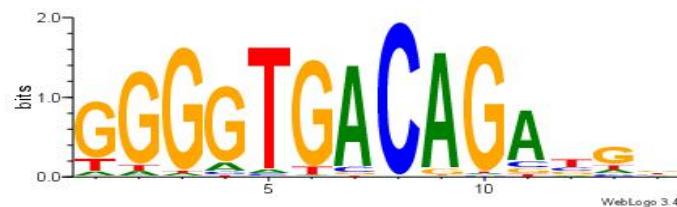
Dataset #:	1
Motif ID:	1
Motif name:	Motif 1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	5
Number of overlap:	10

Similarity score: 0.00304976

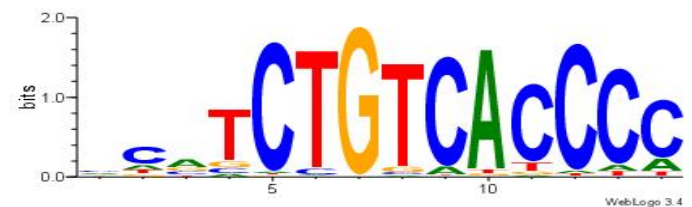
Alignment:

GGGGTGACAGABGB  
----GGGGTGACAG

Original motif    Consensus sequence: GGGGTGACAGABGB



Reverse complement motif    Consensus sequence: BCVTCTGTCACCC



---

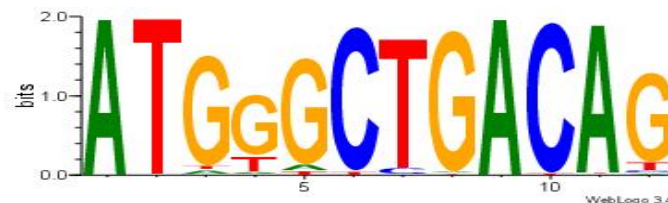
Dataset #: 1  
Motif ID: 209  
Motif name: Motif 209  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Reverse Complement  
Direction: Backward  
Position number: 1  
Number of overlap: 10  
Similarity score: 0.021009

Alignment:

ATGGGCTGACAG  
--GGGGTGACAG

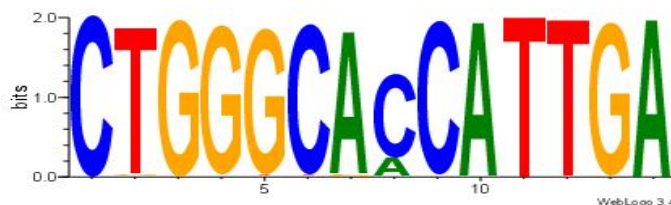
Original motif    Consensus sequence: CTGTCAGCCCAT

Reverse complement motif    Consensus sequence: ATGGGCTGACAG

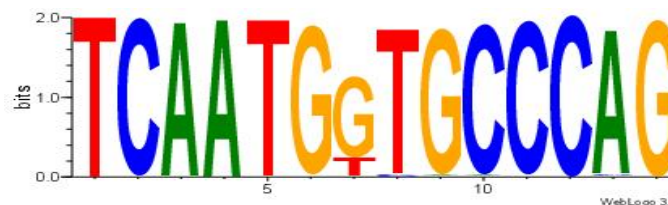


**Dataset #: 1      Motif ID: 147      Motif name: Motif 147**

Original motif      Consensus sequence: CTGGGCACCATTGA



Reverse complement motif      Consensus sequence: TCAATGGTGCCCA



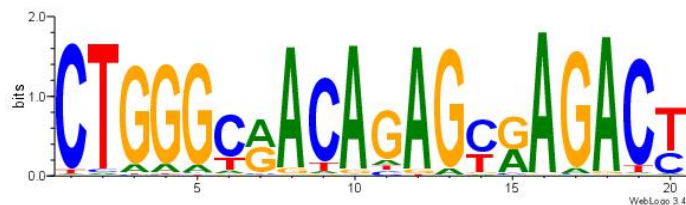
**Best Matches for Motif ID 147 (Highest to Lowest)**

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

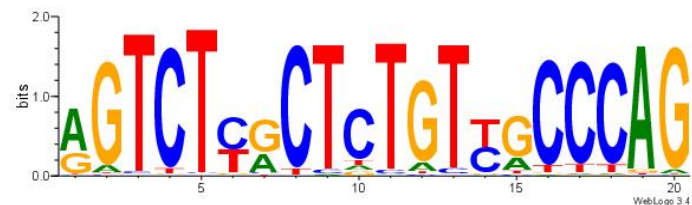
**Alignment:**

```
MGTCTMKCTCTGTKGCCAG
-----TCAATGGTGCCAG
```

Original motif      Consensus sequence: CTGGGCRACAGAGYRAGACY



Reverse complement motif      Consensus sequence: MGTCTMKCTCTGTGKCCCAG

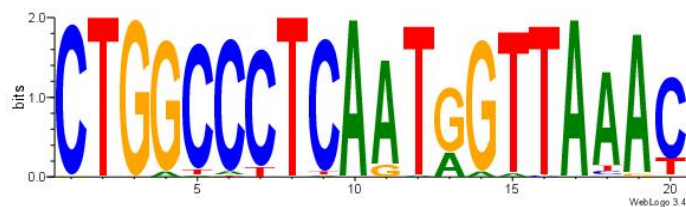


Dataset #: 1  
Motif ID: 332  
Motif name: Motif 332  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Reverse Complement  
Direction: Backward  
Position number: 1  
Number of overlap: 14  
Similarity score: 0.088413

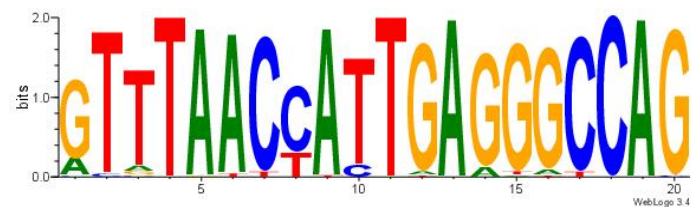
Alignment:

GTTTAACCATTGAGGGCCAG  
-----TCAATGGTGCCCAG

Original motif      Consensus sequence: CTGGCCCTCAATGGTTAAAC



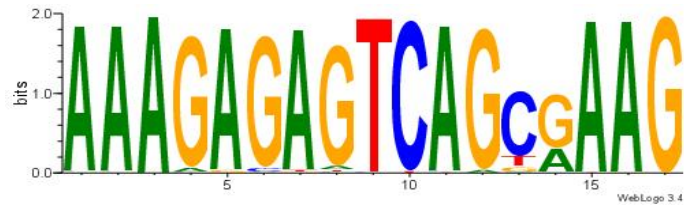
Reverse complement motif      Consensus sequence: GTTTAACCATTGAGGGCCAG



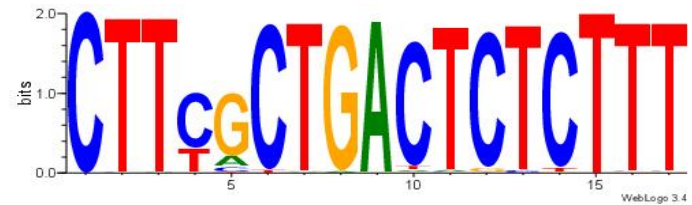


**Dataset #: 1      Motif ID: 148      Motif name: Motif 148**

Original motif      Consensus sequence: AAAGAGAGTCAGCGAAG



Reverse complement motif      Consensus sequence: CTTCGCTGACTCTCTTT



**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

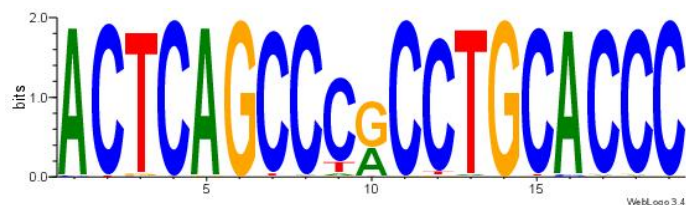
Alignment:  
GAGAGAGAGAGAGAGAGAGA  
-AAAGAGAGTCAGCGAAG--

Original motif      Consensus sequence: GAGAGAGAGAGAGAGAGA

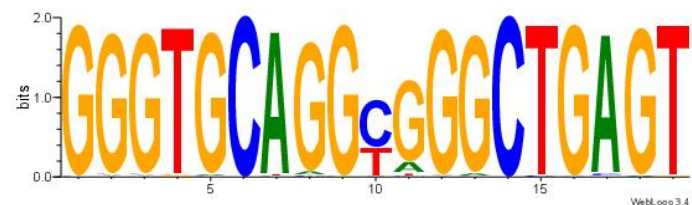
Reverse complement motif      Consensus sequence: TCTCTCTCTCTCTCTCTC



Original motif      Consensus sequence: ACTCAGCCRCCTGCACCC



Reverse complement motif      Consensus sequence: GGGTGCAGMGGGCTGAGT



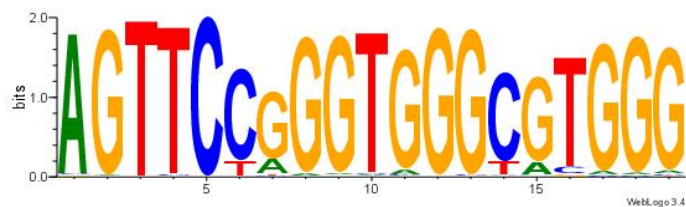
### Best Matches for Motif ID 149 (Highest to Lowest)

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

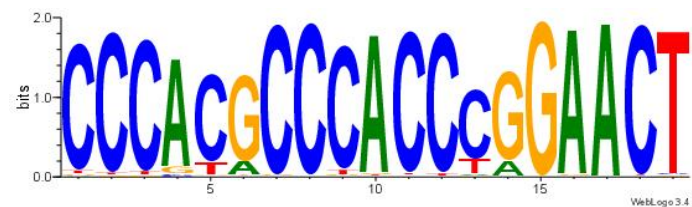
#### Alignment:

```
AGTTCCGGGTGGGCGTGGG  
GGGTGCAGGMGGGCTGAGT
```

Original motif      Consensus sequence: AGTTCCGGGTGGGCGTGGG



Reverse complement motif      Consensus sequence: CCCACGCCACCCGGAAT

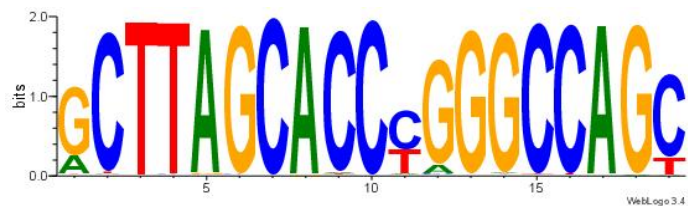


Dataset #: 1  
 Motif ID: 82  
 Motif name: Motif 82  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 19  
 Similarity score: 0.11583

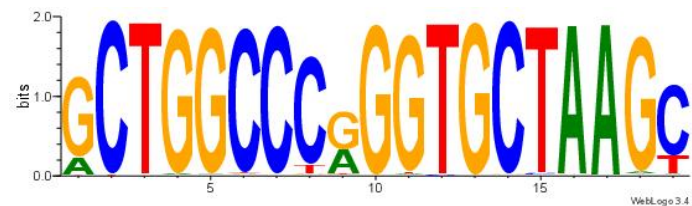
Alignment:

GCTTAGCACCYGGGCCAGC  
 ACTCAGCCRCCTGCACCC

Original motif    Consensus sequence: GCTTAGCACCYGGGCCAGC



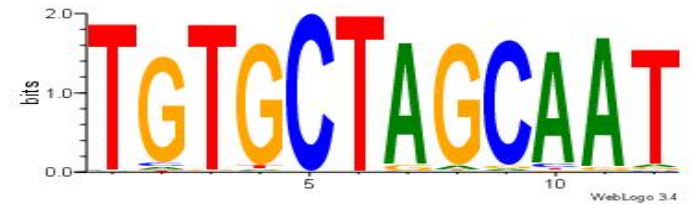
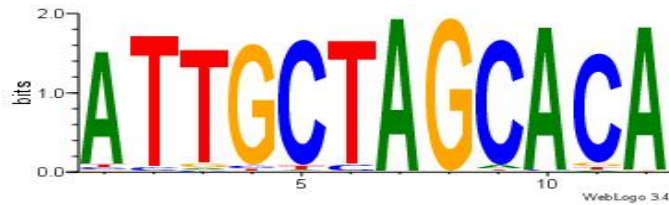
Reverse complement motif    Consensus sequence:  
GCTGGCCCKGGTGCTAAGC



**Dataset #: 1      Motif ID: 150      Motif name: Motif 150**

Original motif    Consensus sequence: ATTGCTAGCACA

Reverse complement motif    Consensus sequence: TGTGCTAGCAAT

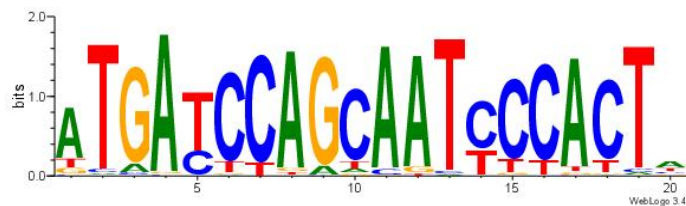


**Best Matches for Motif ID 150 (Highest to Lowest)**

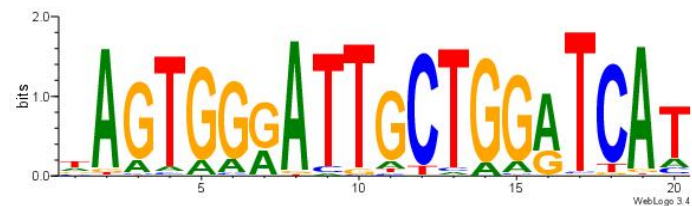
Dataset #: 1  
 Motif ID: 115  
 Motif name: Motif 115  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 2  
 Number of overlap: 12  
 Similarity score: 0.0632108

Alignment:  
 ATGATCCAGCAATYCCACTH  
 -----TGTGCTAGCAAT--

Original motif      Consensus sequence: ATGATCCAGCAATYCCACTH



Reverse complement motif      Consensus sequence: HAGTGGKATTGCTGGATCAT

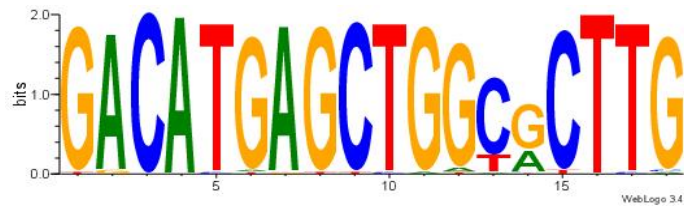


Dataset #: 1  
 Motif ID: 306  
 Motif name: Motif 306  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 5  
 Number of overlap: 12  
 Similarity score: 0.0772146

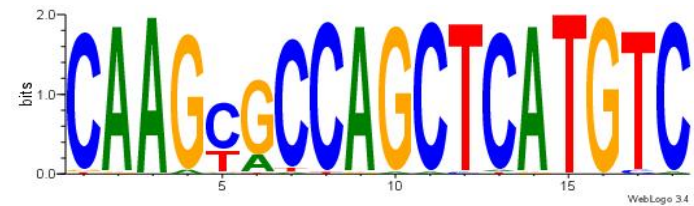
Alignment:

GACATGAGCTGGCGCTTG  
 ----TGTGCTAGCAAT--

Original motif    Consensus sequence: GACATGAGCTGGCGCTTG



Reverse complement motif    Consensus sequence: CAAGCGCCAGCTCATGTC

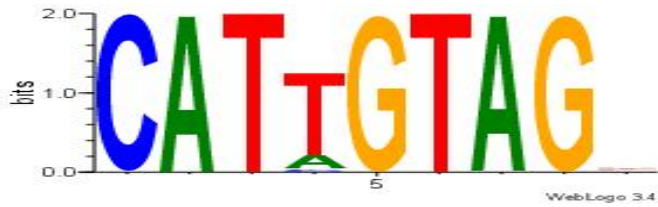



---

**Dataset #: 1      Motif ID: 151      Motif name: Motif 151**

Original motif    Consensus sequence: CATTGTAGB

Reverse complement motif    Consensus sequence: BCTACAATG

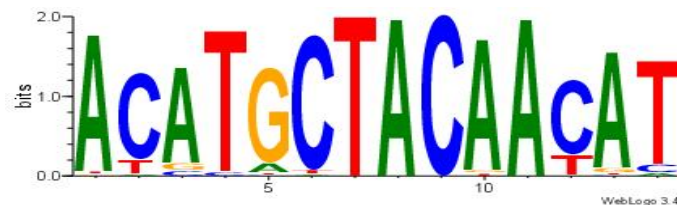


**Best Matches for Motif ID 151 (Highest to Lowest)**

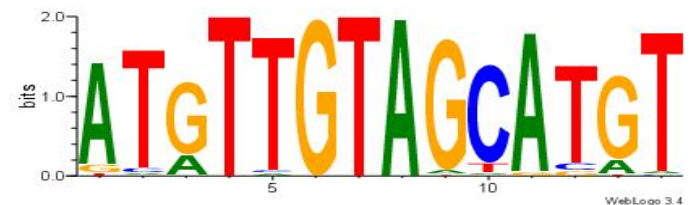
Dataset #: 1  
 Motif ID: 317  
 Motif name: Motif 317  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 2  
 Number of overlap: 9  
 Similarity score: 0.0584909

Alignment:  
 ACATGCTACAACAT  
 ----BCTACAATG--

Original motif      Consensus sequence: ACATGCTACAACAT



Reverse complement motif      Consensus sequence: ATGTTGTAGCATG



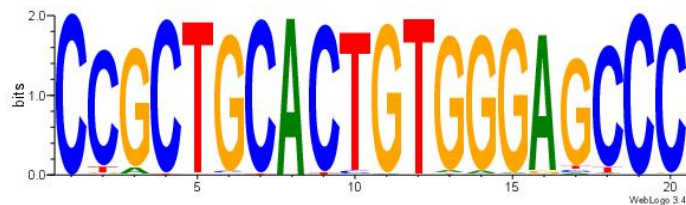
Dataset #: 1

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

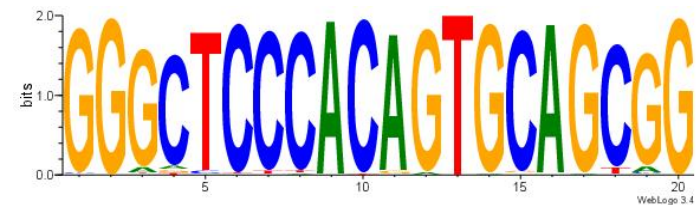
**Alignment:**

CCGCTGCACTGTGGGAGCCC  
 -----CATTGTAGB-----

Original motif    Consensus sequence: CCGCTGCACTGTGGGAGCCC



Reverse complement motif    Consensus sequence: GGGCTCCCACAGTGCAGCGG

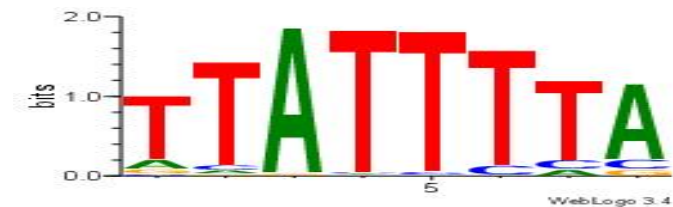


**Dataset #: 1      Motif ID: 152      Motif name: Motif 152**

Original motif    Consensus sequence: TAAAATAA



Reverse complement motif    Consensus sequence: TTATTTTA





## Best Matches for Motif ID 152 (Highest to Lowest)

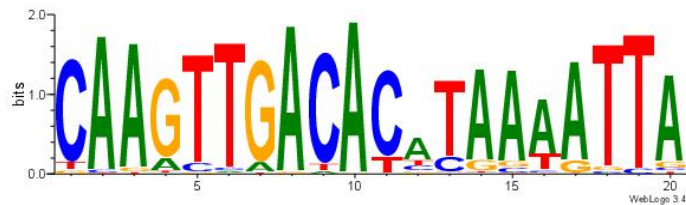
Dataset #: 1  
 Motif ID: 357  
 Motif name: Motif 357  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 8  
 Similarity score: 0.0340112

### Alignment:

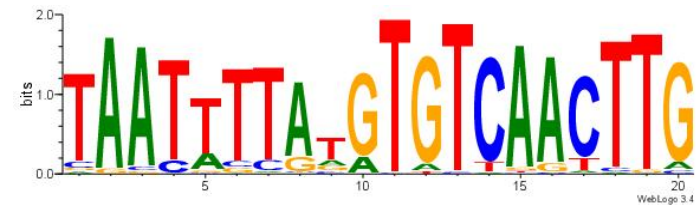
```

TAATTTTATGTGTCAACTTG
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

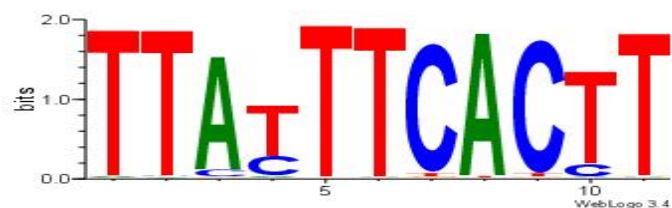
Direction: Backward  
 Position number: 1  
 Number of overlap: 8  
 Similarity score: 0.0363851

Alignment:  
 AAGTGAAATAA  
 ---TAAAATAA

Original motif Consensus sequence: AAGTGAAATAA

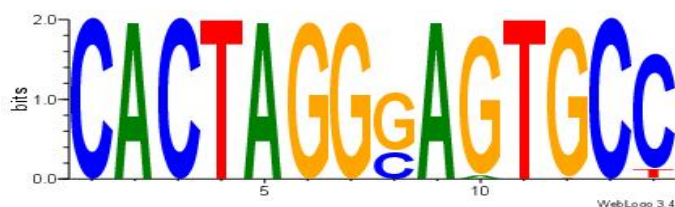


Reverse complement motif Consensus sequence: TTATTTCACTT

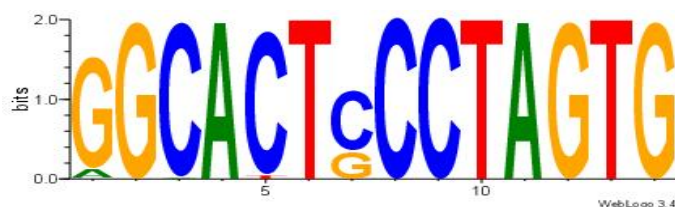


**Dataset #: 1 Motif ID: 153 Motif name: Motif 153**

Original motif Consensus sequence: CACTAGGGAGTGCC



Reverse complement motif Consensus sequence: GGCACTCCCTAGTG



**Best Matches for Motif ID 153 (Highest to Lowest)**

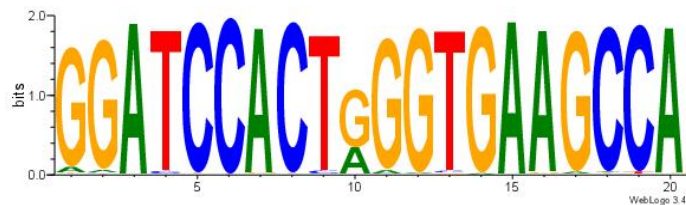
Dataset #: 1  
 Motif ID: 61  
 Motif name: Motif 61

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

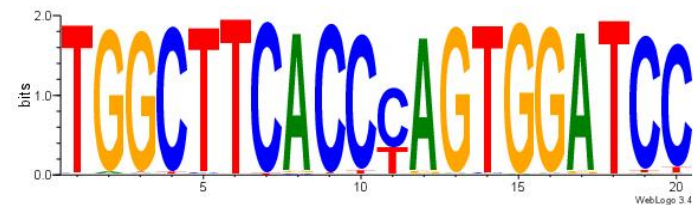
Alignment:

```
GGATCCACTGGGTGAAGCCA
-----CACTAGGGAGTGCC-
```

Original motif      Consensus sequence: GGATCCACTGGGTGAAGCCA



Reverse complement motif      Consensus sequence: TGGCTTCACCCAGTGGATCC

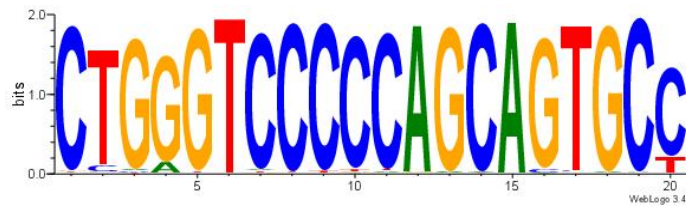


Dataset #:	1
Motif ID:	84
Motif name:	Motif 84
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	14
Similarity score:	0.082834

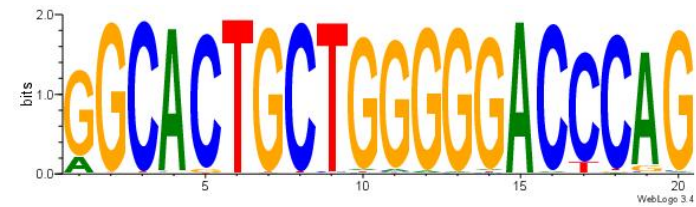
Alignment:

CTGGGTCCCCCAGCAGTGCC  
-----CACTAGGGAGTGCC

Original motif      Consensus sequence: CTGGGTCCCCCAGCAGTGCC

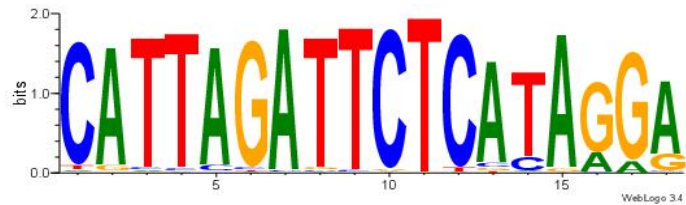


Reverse complement motif      Consensus sequence: GGCACTGCTGGGGACCCAG

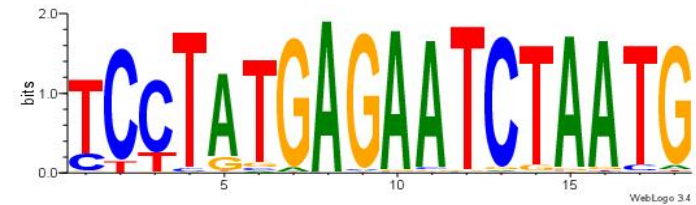


**Dataset #: 1      Motif ID: 154      Motif name: Motif 154**

Original motif      Consensus sequence: CATTAGATTCTCATAGGA



Reverse complement motif      Consensus sequence: TCCTATGAGAATCTAATG



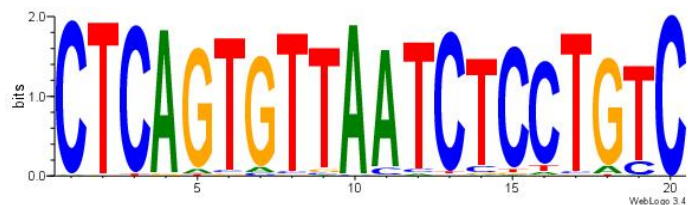
**Best Matches for Motif ID 154 (Highest to Lowest)**

Dataset #:	1
Motif ID:	262
Motif name:	Motif 262
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement

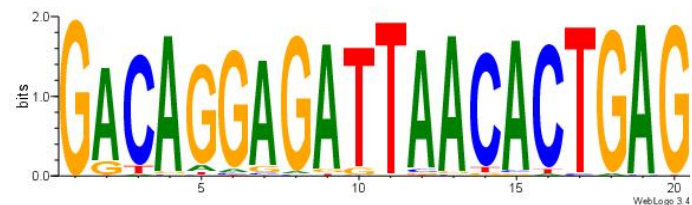
Direction: Backward  
 Position number: 1  
 Number of overlap: 18  
 Similarity score: 0.100102

Alignment:  
 GACAGGAGATTAACACTGAG  
 --CATTAGATTCTCATAGGA

Original motif      Consensus sequence: CTCAGTGTTAATCTCCTGTC



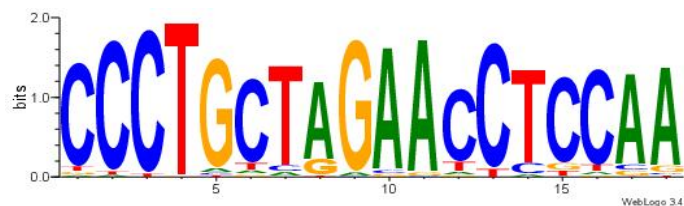
Reverse complement motif      Consensus sequence: GACAGGAGATTAACACTGAG



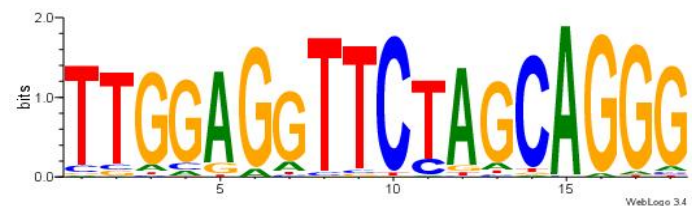
Dataset #: 1  
 Motif ID: 299  
 Motif name: Motif 299  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 18  
 Similarity score: 0.111266

Alignment:  
 TTGGAGGTTCTAGCAGGG  
 CATTAGATTCTCATAGGA

Original motif      Consensus sequence: CCCTGCTAGAACCTCCAA

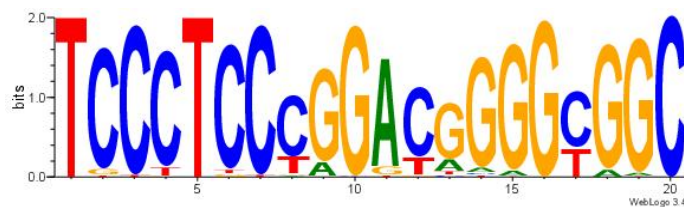


Reverse complement motif      Consensus sequence: TTGGAGTTCTAGCAGGG

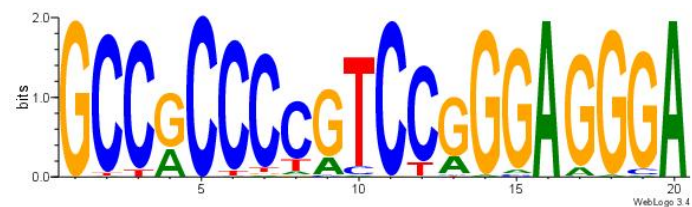


**Dataset #: 1      Motif ID: 155      Motif name: Motif 155**

Original motif      Consensus sequence: TCCCTCCGGACGGGGYGGC



Reverse complement motif      Consensus sequence: GCCKCCCCGTCGGGAGGGA



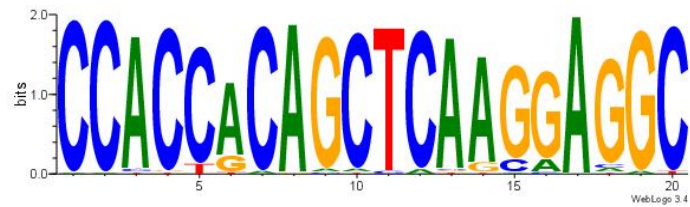
**Best Matches for Motif ID 155 (Highest to Lowest)**

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

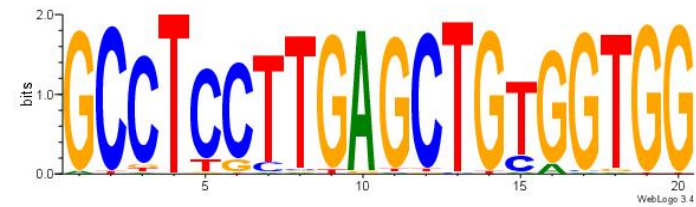
Alignment:

GCCTCCTTGAGCTGTGGTGG  
GCCKCCCCGTCCGGGAGGGA

Original motif      Consensus sequence: CCACCACAGCTCAAGGAGGC



Reverse complement motif      Consensus sequence:  
GCCTCCTTGAGCTGTGGTGG



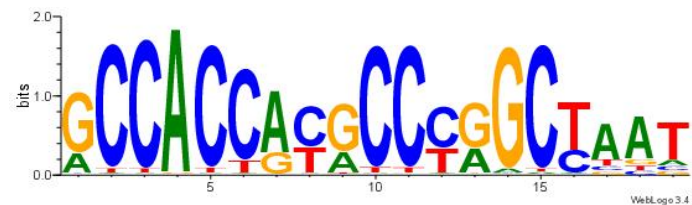
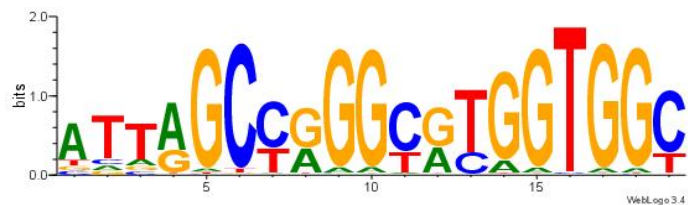
Dataset #: 1  
Motif ID: 2  
Motif name: Motif 2  
Matching format of first motif: Original Motif  
Matching format of second motif: Original Motif  
Direction: Backward  
Position number: 1  
Number of overlap: 19  
Similarity score: 0.597996

Alignment:

-ATTAGCYRGGCRTCRTGGTGGC  
TCCCTCCCGGACGGGGYGGC

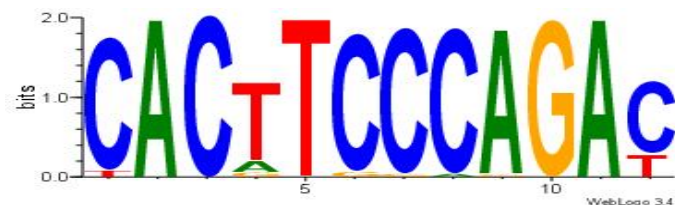
Original motif      Consensus sequence: ATTAGCYRGGCRTCRTGGTGGC

Reverse complement motif      Consensus sequence:  
GCCACCAMGCCMKGCTAAT

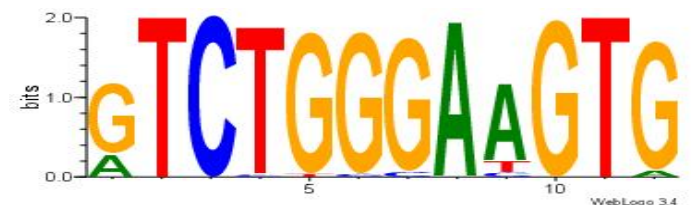


**Dataset #: 1      Motif ID: 156      Motif name: Motif 156**

Original motif      Consensus sequence: CACTTCCCAGAC



Reverse complement motif      Consensus sequence: GTCTGGGAAGTG



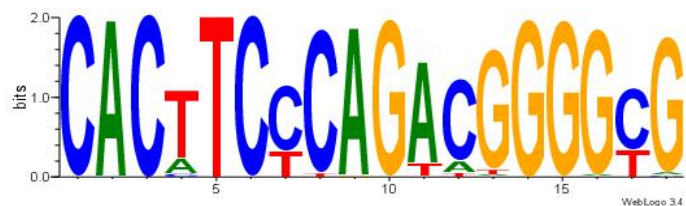
**Best Matches for Motif ID 156 (Highest to Lowest)**

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

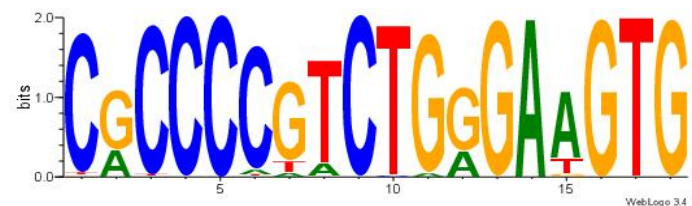
Alignment:  
 CACTTCCCAGACGGGGCG  
 CACTTCCCAGAC-----



Original motif      Consensus sequence: CACTTCCCAGACGGGGCG



Reverse complement motif      Consensus sequence: CGCCCCGTCTGGGAAGTG

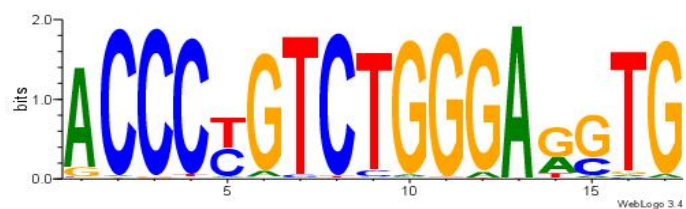


Dataset #: 1  
Motif ID: 95  
Motif name: Motif 95  
Matching format of first motif: Original Motif  
Matching format of second motif: Reverse Complement  
Direction: Forward  
Position number: 6  
Number of overlap: 12  
Similarity score: 0.0183065

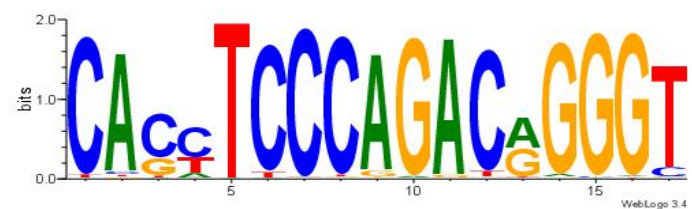
Alignment:

```
CACCTCCCAGACMGGGT  
-----CACTTCCCAGAC
```

Original motif      Consensus sequence: ACCYGTCTGGGAGGTG

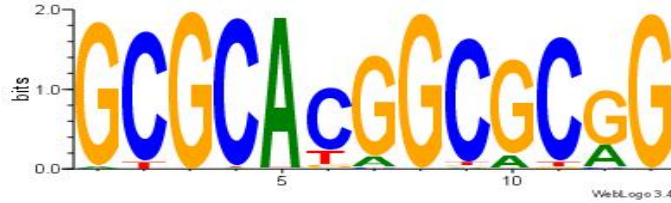


Reverse complement motif      Consensus sequence: CACCTCCCAGACMGGGT

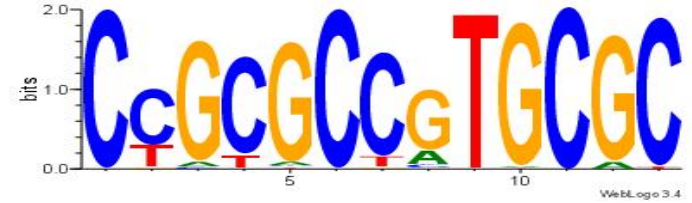


**Dataset #: 1      Motif ID: 157      Motif name: Motif 157**

Original motif      Consensus sequence: GCGCACGGCGCGG



Reverse complement motif      Consensus sequence: CCGCGCCGTGCGG



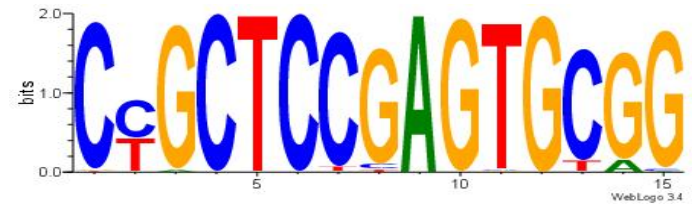
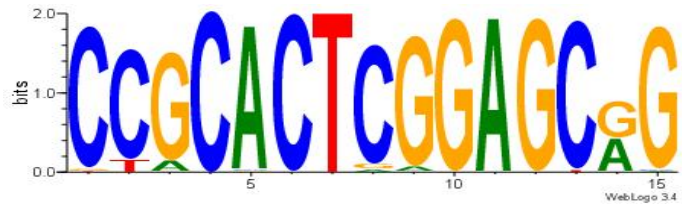
**Best Matches for Motif ID 157 (Highest to Lowest)**

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

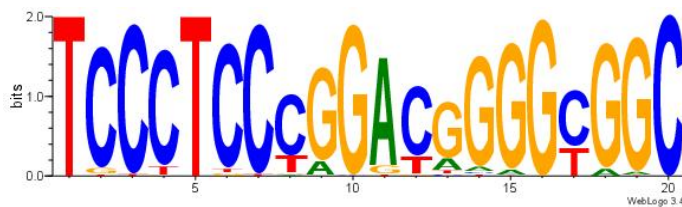
Reverse complement motif      Consensus sequence:  
CMGCTCCGAGTGCGG



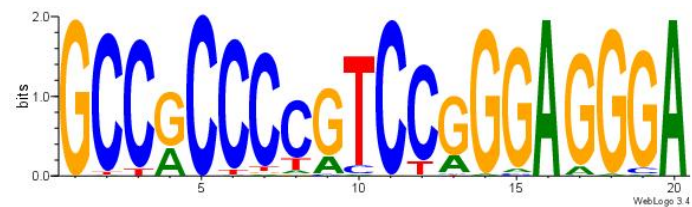
Dataset #: 1  
 Motif ID: 155  
 Motif name: Motif 155  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 2  
 Number of overlap: 13  
 Similarity score: 0.0678809

Alignment:  
 GCCKCCCCGTCCGGGAGGGA  
 -CCGCGCCGTGCGC-----

Original motif      Consensus sequence: TCCCTCCCGGACGGGGYGGC

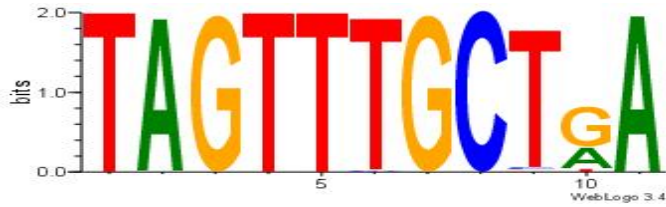


Reverse complement motif      Consensus sequence: GCCKCCCCGTCCGGGAGGGA



**Dataset #: 1      Motif ID: 158      Motif name: Motif 158**

Original motif      Consensus sequence: TAGTTTGCTGA



Reverse complement motif      Consensus sequence: TCAGCAAATA



### 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:	Backward
Position number:	3
Number of overlap:	11
Similarity score:	0.0721214

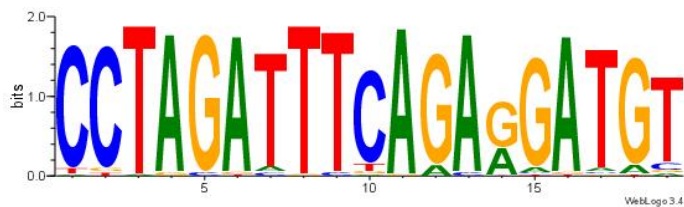
Alignment:

```

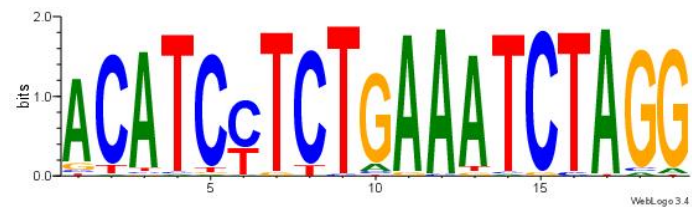
ACATCMTCTGAAATCTAGG
-----TCAGCAAATA--

```

Original motif      Consensus sequence: CCTAGATTTAGAGATGT



Reverse complement motif      Consensus sequence: ACATCMTCTGAAATCTAGG

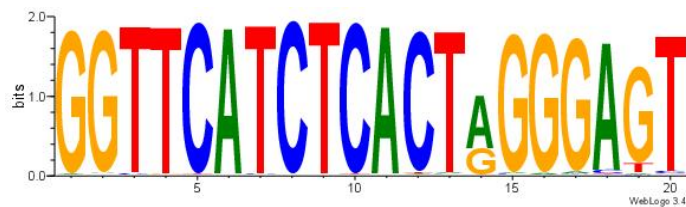


Dataset #: 1  
 Motif ID: 23  
 Motif name: Motif 23  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 4  
 Number of overlap: 11  
 Similarity score: 0.077411

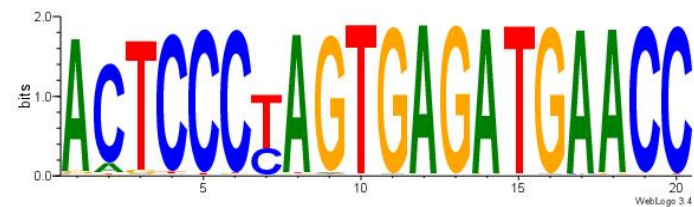
Alignment:

GGTTTCATCTCACTAGGGAGT  
 -----TCAGCAAACATA----

Original motif      Consensus sequence: GGTTTCATCTCACTAGGGAGT



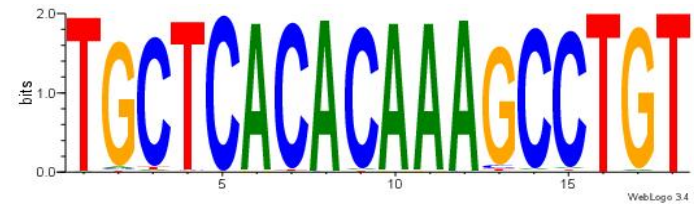
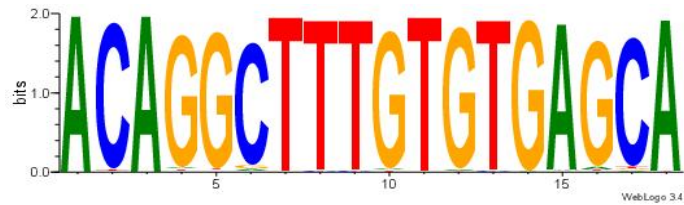
Reverse complement motif      Consensus sequence: ACTCCCTAGTGAGATGAACC



**Dataset #: 1      Motif ID: 159      Motif name: Motif 159**

Original motif      Consensus sequence: ACAGGCTTTGTGTGAGCA

Reverse complement motif      Consensus sequence: TGCTCACACAAAGCCTGT

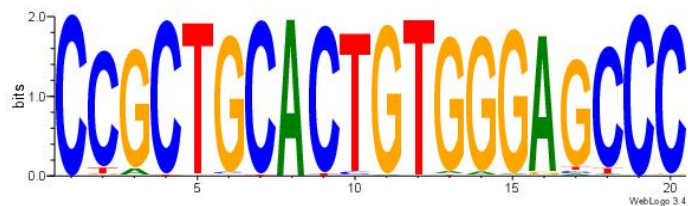


**Best Matches for Motif ID 159 (Highest to Lowest)**

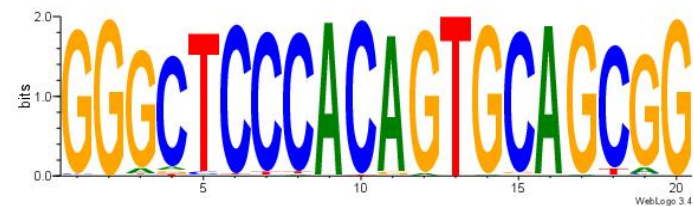
Dataset #: 1  
 Motif ID: 144  
 Motif name: Motif 144  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 2  
 Number of overlap: 18  
 Similarity score: 0.104283

Alignment:  
 GGGCTCCCACAGTGCAGCGG  
 -TGCTCACACAAAGCCTGT-

Original motif      Consensus sequence: CCGCTGCACTGTGGGAGCCC



Reverse complement motif      Consensus sequence: GGGCTCCCACAGTGCAGCGG

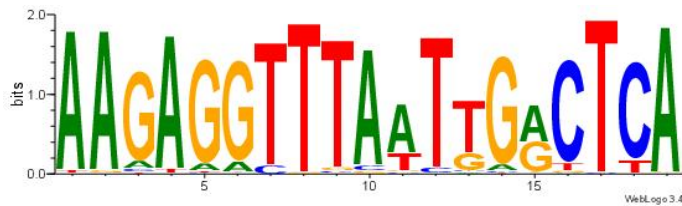


Dataset #: 1  
 Motif ID: 129  
 Motif name: Motif 129  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 2  
 Number of overlap: 18  
 Similarity score: 0.109531

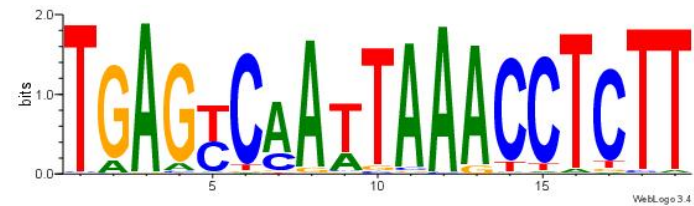
Alignment:

AAGAGGTTTAATTGRCTCA  
 -ACAGGCTTTGTGTGAGCA

Original motif      Consensus sequence: AAGAGGTTTAATTGRCTCA



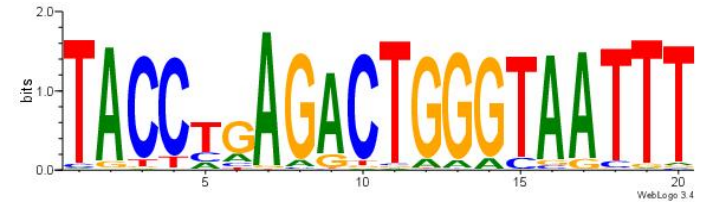
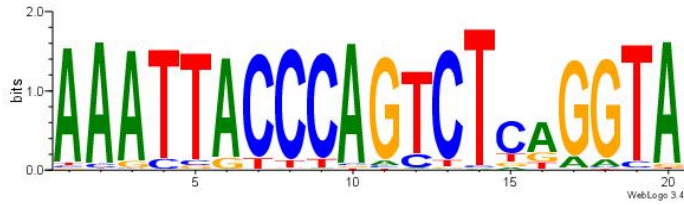
Reverse complement motif      Consensus sequence: TGAGKCAATTAACCTCTT



**Dataset #: 1      Motif ID: 160      Motif name: Motif 160**

Original motif      Consensus sequence: AAATTACCCAGTCTCAGGTA

Reverse complement motif      Consensus sequence: TACCTGAGACTGGGTAATTT



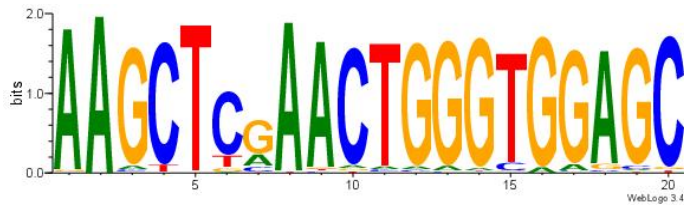
### Best Matches for Motif ID 160 (Highest to Lowest)

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

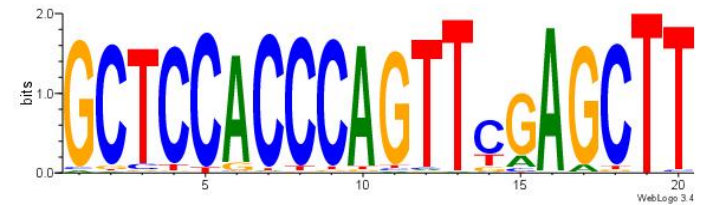
#### Alignment:

AAGCTCGAACTGGGTGGAGC  
 TACCTGAGACTGGGTAATTT

Original motif      Consensus sequence: AAGCTCGAACTGGGTGGAGC



Reverse complement motif      Consensus sequence: GCTCCACCCAGTTCGAGCTT



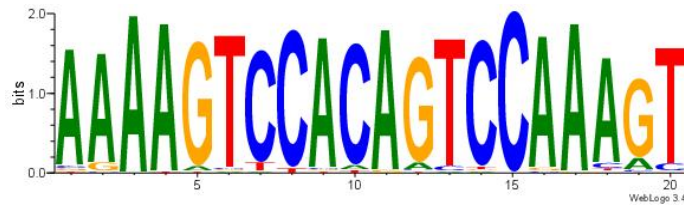


Dataset #: 1  
 Motif ID: 171  
 Motif name: Motif 171  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 2  
 Number of overlap: 19  
 Similarity score: 0.573795

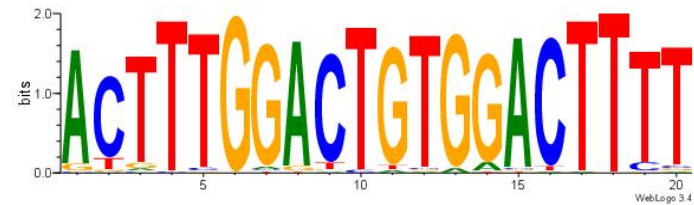
Alignment:

-ACTTTGGACTGTGGACTTTT  
 TACCTGAGACTGGGTAATTT-

Original motif      Consensus sequence: AAAAGTCCACAGTCCAAAGT



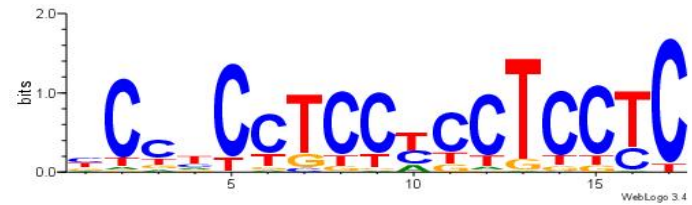
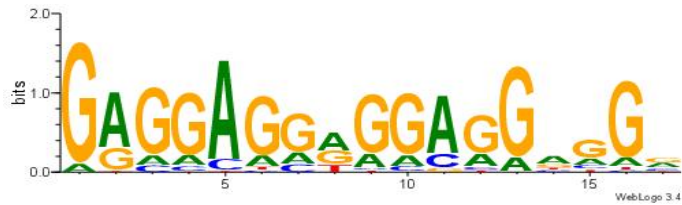
Reverse complement motif      Consensus sequence: ACTTTGGACTGTGGACTTTT



**Dataset #: 1      Motif ID: 161      Motif name: Motif 161**

Original motif      Consensus sequence: GAGGAGGRGGAGGDGGV

Reverse complement motif      Consensus sequence: VCCDCCTCCKCCTCCTC

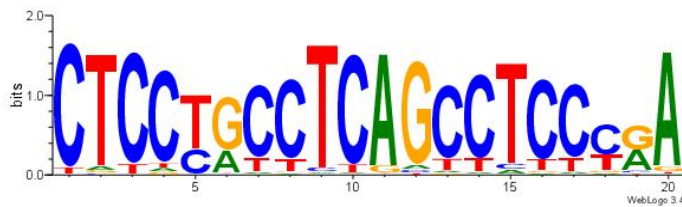


**Best Matches for Motif ID 161 (Highest to Lowest)**

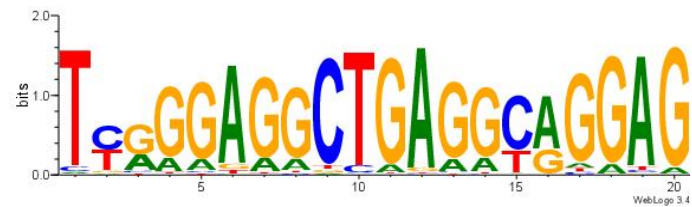
Dataset #: 1  
 Motif ID: 26  
 Motif name: Motif 26  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 2  
 Number of overlap: 17  
 Similarity score: 0.0527497

Alignment:  
 TMGGGAGGCTGAGGCAGGAG  
 --GAGGAGGRGGAGGDGGV--

Original motif      Consensus sequence: CTCCTGCCTCAGCCTCCRA



Reverse complement motif      Consensus sequence: TMGGGAGGCTGAGGCAGGAG

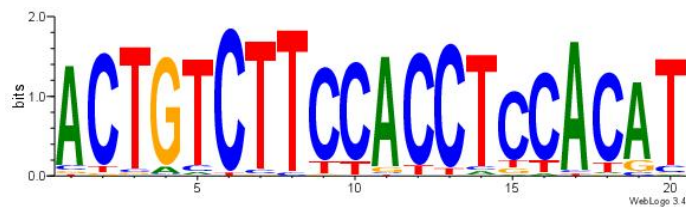


Dataset #: 1  
 Motif ID: 178  
 Motif name: Motif 178  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 2  
 Number of overlap: 17  
 Similarity score: 0.0591495

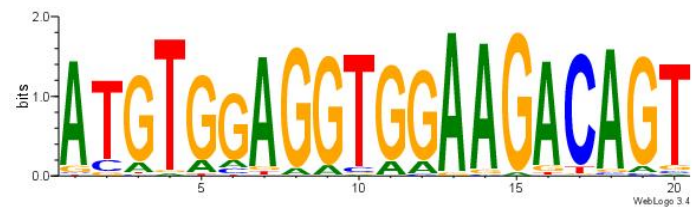
Alignment:

ATGTGGAGGTGGAAGACAGT  
 --GAGGAGGRGGAGGDGGV-

Original motif    Consensus sequence: ACTGTCTTCCACCTCCACAT



Reverse complement motif    Consensus sequence: ATGTGGAGGTGGAAGACAGT

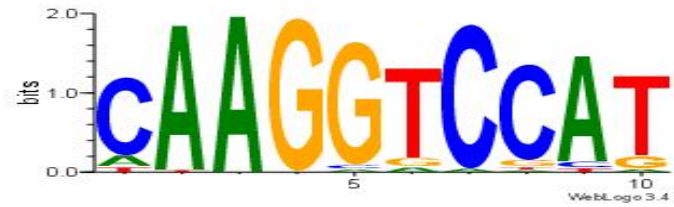
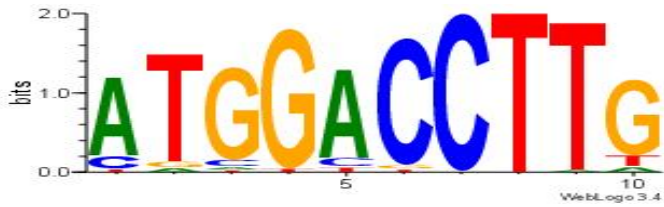



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**Dataset #: 1      Motif ID: 162      Motif name: Motif 162**

Original motif    Consensus sequence: ATGGACCTTG

Reverse complement motif    Consensus sequence: CAAGGTCCAT



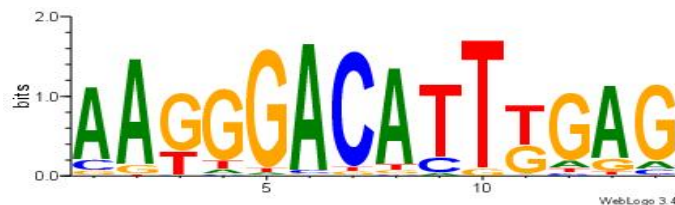
### Best Matches for Motif ID 162 (Highest to Lowest)

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

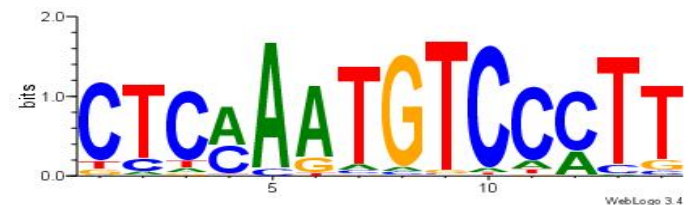
#### Alignment:

AAGGGACATTKGAG  
 -ATGGACCTTG---

Original motif      Consensus sequence: AAGGGACATTKGAG



Reverse complement motif      Consensus sequence: CTCRAATGTCCCT



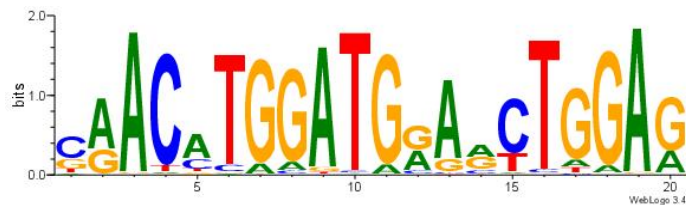
Dataset #: 1

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

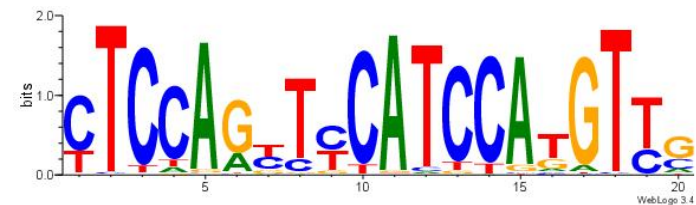
Alignment:

CTCCAGKTMCATCCATGTTG  
 --CAAGGTCCAT-----

Original motif      Consensus sequence: CAACATGGATGRARCTGGAG



Reverse complement motif      Consensus sequence: CTCCAGKTMCATCCATGTTG



**Dataset #: 1      Motif ID: 163      Motif name: Motif 163**

Original motif      Consensus sequence: CCTCCGTGGGCTCC



Reverse complement motif      Consensus sequence: GGAGCCACGGAGG



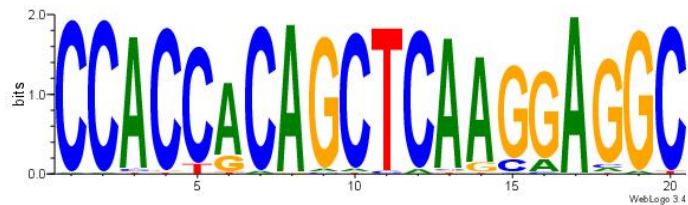
## Best Matches for Motif ID 163 (Highest to Lowest)

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

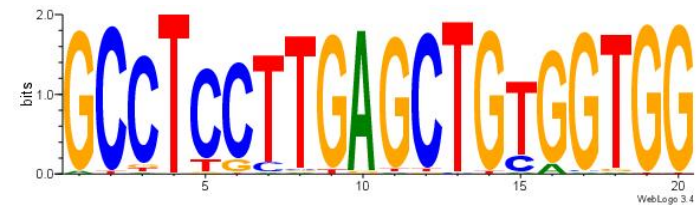
### Alignment:

```
CCACCACAGCTCAAGGAGGC  
-----GGAGCCCACGGAGG--
```

Original motif      Consensus sequence: CCACCACAGCTCAAGGAGGC



Reverse complement motif      Consensus sequence: GCCTCCTTGAGCTGTGGTGG



---

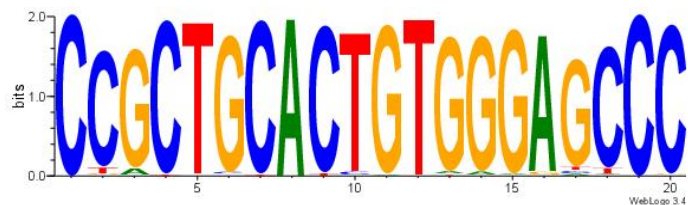
Dataset #: 1  
Motif ID: 144  
Motif name: Motif 144  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Reverse Complement

Direction: Forward  
 Position number: 2  
 Number of overlap: 14  
 Similarity score: 0.0899923

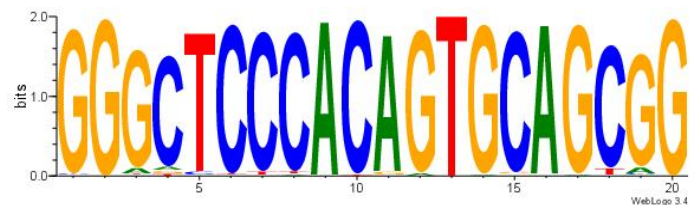
**Alignment:**

GGGCTCCCACAGTGCAGCGG  
 -GGAGCCCACGGAGG-----

Original motif      Consensus sequence: CCGCTGCACTGTGGGAGCCC

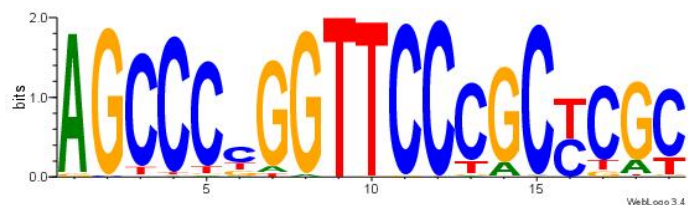


Reverse complement motif      Consensus sequence: GGGCTCCCACAGTGCAGCGG

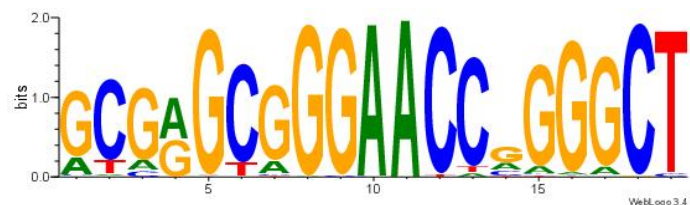


**Dataset #: 1      Motif ID: 164      Motif name: Motif 164**

Original motif      Consensus sequence: AGCCCCGGTTCCCGCYCGC



Reverse complement motif      Consensus sequence: GCGMCGGGAACCGGGGCT



**Best Matches for Motif ID 164 (Highest to Lowest)**

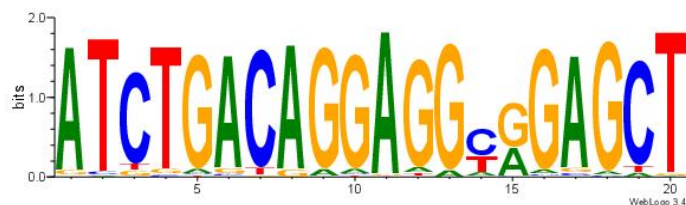
Dataset #: 1

Motif ID: 165  
 Motif name: Motif 165  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 19  
 Similarity score: 0.102596

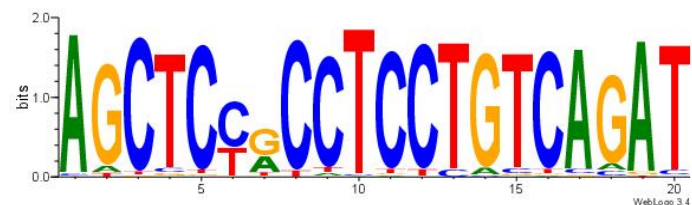
**Alignment:**

AGCTCMKCCTCCTGTCAGAT  
 AGCCCCGGTTCCCGCYCGC-

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

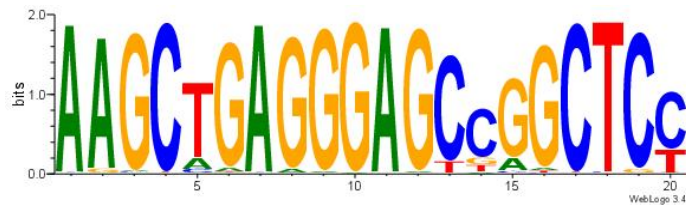


Similarity score: 0.111018

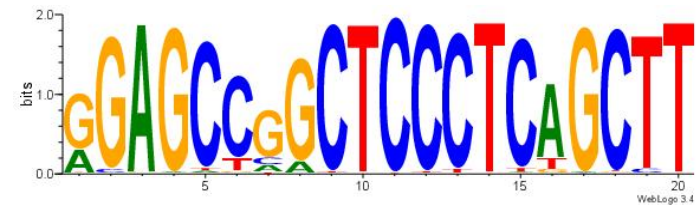
Alignment:

```
GGAGCCGGCTCCCTCAGCTT  
-AGCCCCGGTTCCCGCYCGC
```

Original motif      Consensus sequence: AAGCTGAGGGAGCCGGCTCC

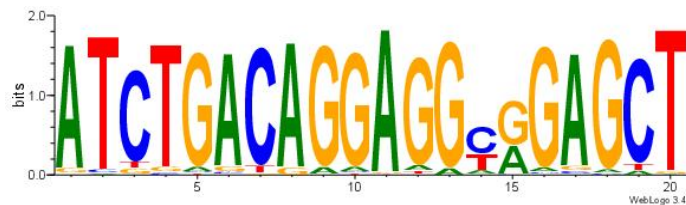


Reverse complement motif      Consensus sequence: GGAGCCGGCTCCCTCAGCTT

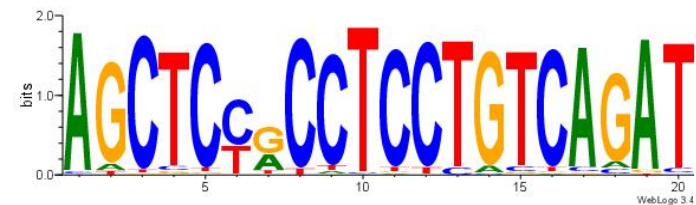


**Dataset #: 1      Motif ID: 165      Motif name: Motif 165**

Original motif      Consensus sequence: ATCTGACAGGAGGAGGAGCT



Reverse complement motif      Consensus sequence: AGCTCMKCTCCTGTCAGAT



**Best Matches for Motif ID 165 (Highest to Lowest)**

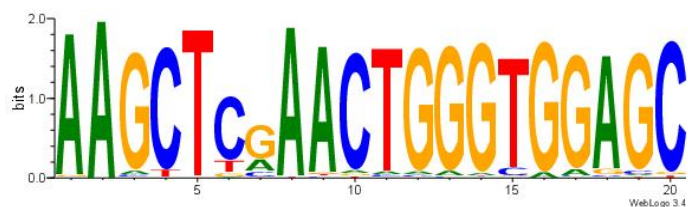
Dataset #:	1
Motif ID:	321
Motif name:	Motif 321
Matching format of first motif:	Original Motif

Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 2  
 Number of overlap: 19  
 Similarity score: 0.0925429

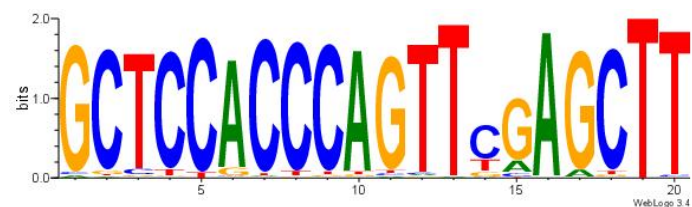
Alignment:

AAGCTCGAACTGGGTGGAGC-  
 -ATCTGACAGGAGGYRGAGCT

Original motif      Consensus sequence: AAGCTCGAACTGGGTGGAGC



Reverse complement motif      Consensus sequence:  
 GCTCCACCCAGTTCGAGCTT

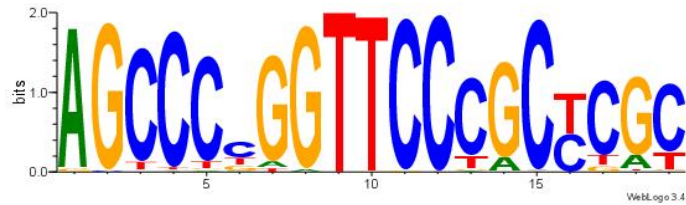


Dataset #: 1  
 Motif ID: 164  
 Motif name: Motif 164  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 19  
 Similarity score: 0.10248

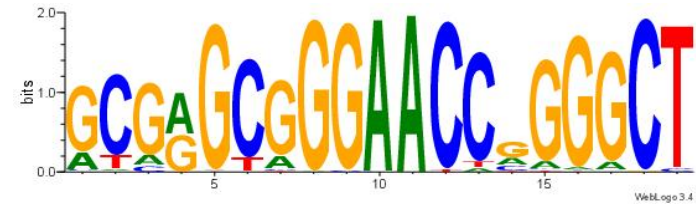
Alignment:

GCGMGCGGGAACCGGGGCT-  
 ATCTGACAGGAGGYRGAGCT

Original motif      Consensus sequence: AGCCCCGGTTCCCGCYCGC

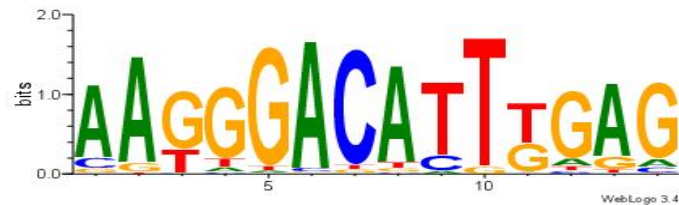


Reverse complement motif      Consensus sequence: GCGMGCGGGAACCGGGGCT

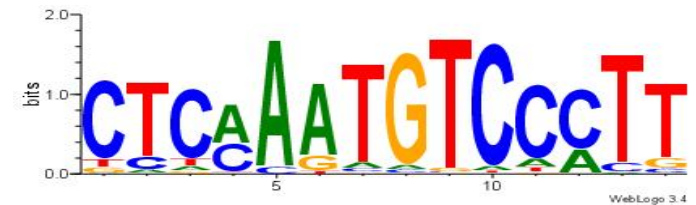


**Dataset #: 1      Motif ID: 166      Motif name: Motif 166**

Original motif      Consensus sequence: AAGGGACATTKGAG



Reverse complement motif      Consensus sequence: CTCRAATGTCCTT



**Best Matches for Motif ID 166 (Highest to Lowest)**

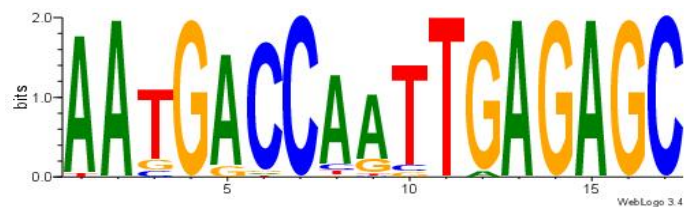
Dataset #:	1
Motif ID:	305
Motif name:	Motif 305
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	4
Number of overlap:	14

Similarity score: 0.0470693

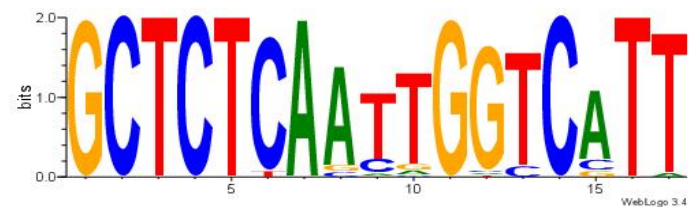
Alignment:

AATGACCAATTGAGAGC  
AAGGGACATTKGAG---

Original motif      Consensus sequence: AATGACCAATTGAGAGC



Reverse complement motif      Consensus sequence:  
GCTCTCAATTGGTCATT



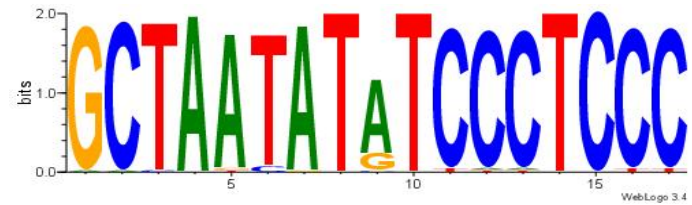
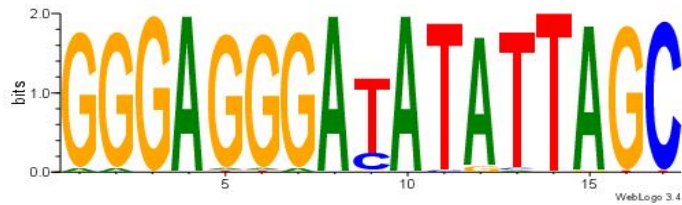
Dataset #: 1  
Motif ID: 329  
Motif name: Motif 329  
Matching format of first motif: Original Motif  
Matching format of second motif: Original Motif  
Direction: Backward  
Position number: 2  
Number of overlap: 14  
Similarity score: 0.0535951

Alignment:

GGGAGGGATATATTAGC  
--AAGGGACATTKGAG-

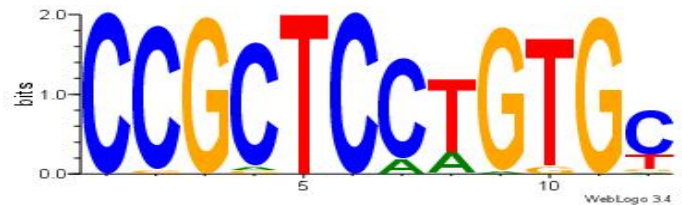
Original motif      Consensus sequence: GGGAGGGATATATTAGC

Reverse complement motif      Consensus sequence:  
GCTAATATATCCCTCCC

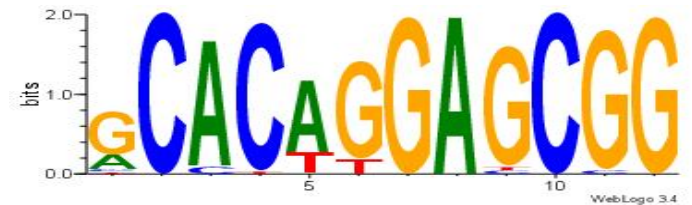


**Dataset #: 1      Motif ID: 167      Motif name: Motif 167**

Original motif      Consensus sequence: CCGCTCCTGTGC



Reverse complement motif      Consensus sequence: GCACAGGAGCGG

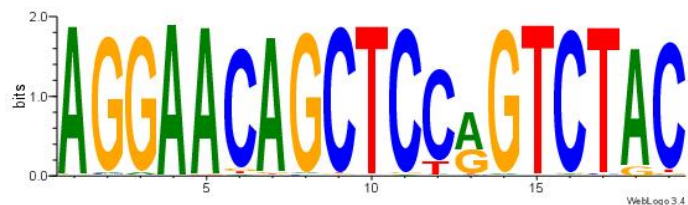


**Best Matches for Motif ID 167 (Highest to Lowest)**

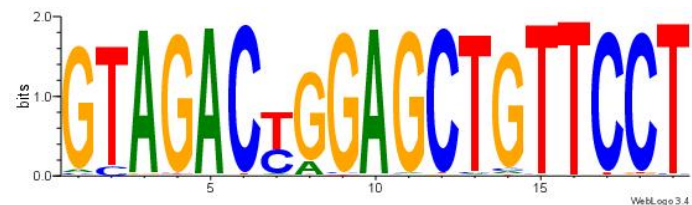
Dataset #:	1
Motif ID:	62
Motif name:	Motif 62
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	3
Number of overlap:	12
Similarity score:	0.0721943

Alignment:  
 AGGAACAGCTCCRGCTCTAC  
 -----CCGCTCCTGTGC--

Original motif      Consensus sequence: AGGAACAGCTCCGAGCTAC



Reverse complement motif      Consensus sequence: GTAGACKGGAGCTGTTCCCT

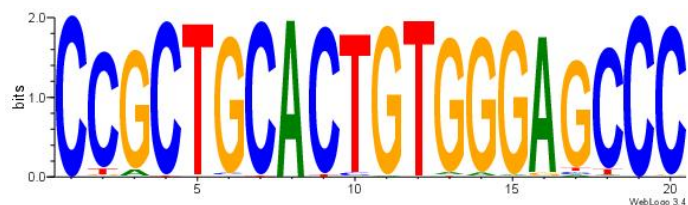


Dataset #: 1  
Motif ID: 144  
Motif name: Motif 144  
Matching format of first motif: Original Motif  
Matching format of second motif: Original Motif  
Direction: Forward  
Position number: 1  
Number of overlap: 12  
Similarity score: 0.0736876

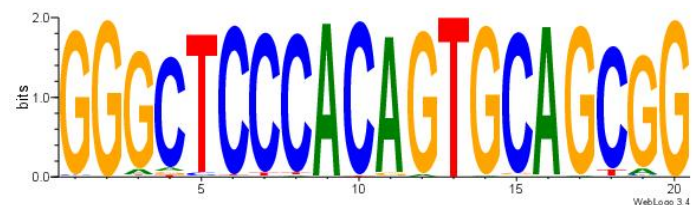
Alignment:

```
CCGCTGCACTGTGGGAGCCC  
CCGCTCCTGTGC-----
```

Original motif      Consensus sequence: CCGCTGCACTGTGGGAGCCC

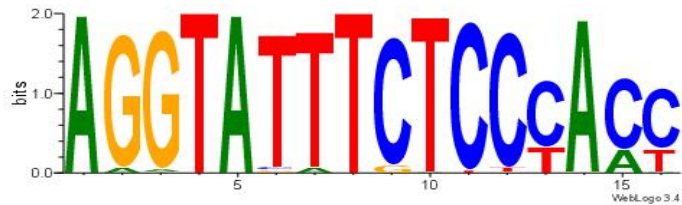


Reverse complement motif      Consensus sequence: GGGCTCCCACAGTGCAGCGG

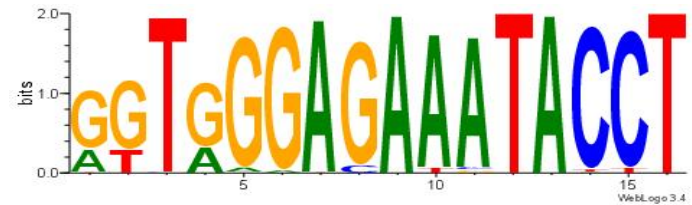


**Dataset #: 1      Motif ID: 168      Motif name: Motif 168**

Original motif      Consensus sequence: AGGTATTTCTCCCACC



Reverse complement motif      Consensus sequence: GGTGGGAGAAATACCT



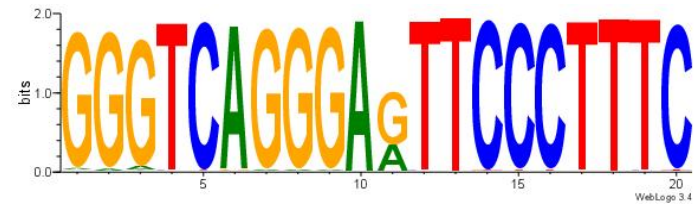
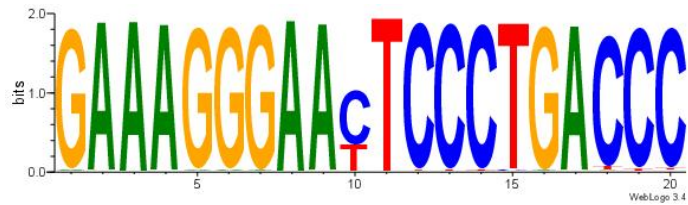
**Best Matches for Motif ID 168 (Highest to Lowest)**

Dataset #:	1
Motif ID:	16
Motif name:	Motif 16
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2
Number of overlap:	16
Similarity score:	0.0930663

Alignment:  
GAAAGGGA ACTCCCTGACCC  
---AGGTATTTCTCCCACC---

Original motif      Consensus sequence: GAAAGGGA ACTCCCTGACCC

Reverse complement motif      Consensus sequence: GGTTCAGGGAGTTCCCTTC

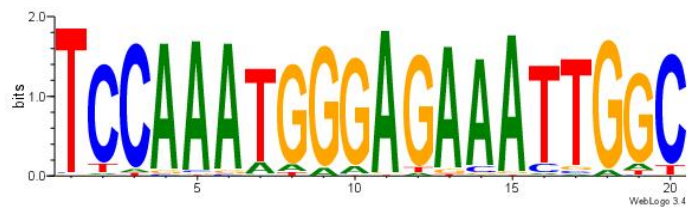


Dataset #: 1  
 Motif ID: 235  
 Motif name: Motif 235  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 16  
 Similarity score: 0.0952107

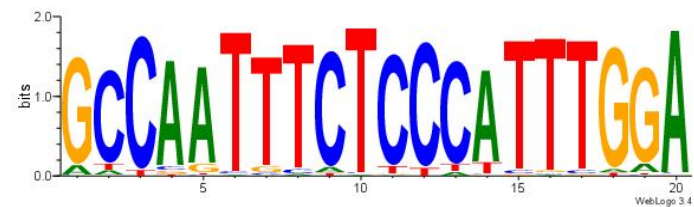
Alignment:

TCCAAATGGGAGAAATTGGC  
 ----GGTGGGAGAAATACCT

Original motif      Consensus sequence: TCCAAATGGGAGAAATTGGC



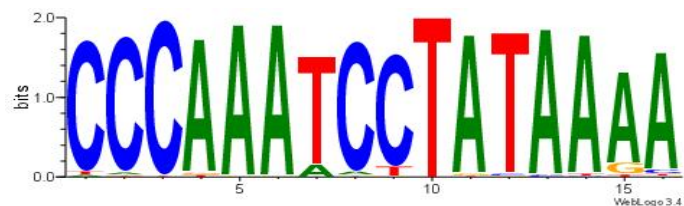
Reverse complement motif      Consensus sequence: GCCAATTTCTCCCATTTGGA



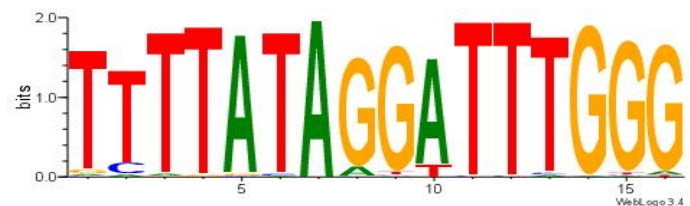
**Dataset #: 1      Motif ID: 169      Motif name: Motif 169**



Original motif      Consensus sequence: CCCAATCCTATAAAA



Reverse complement motif      Consensus sequence: TTTTATAGGATTTGGG



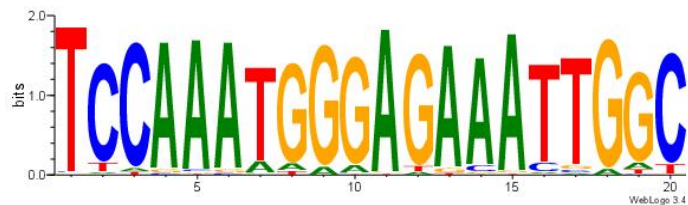
### Best Matches for Motif ID 169 (Highest to Lowest)

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

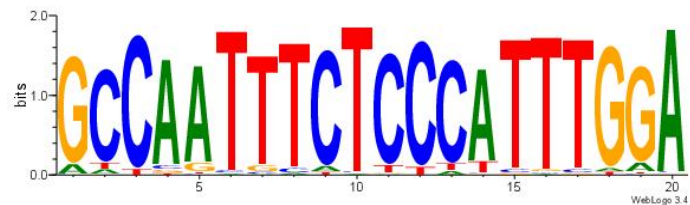
#### Alignment:

```
GCCAATTTCTCCCATTTGGA  
----TTTTATAGGATTTGGG
```

Original motif      Consensus sequence: TCCAATGGGAGAAATTGGC



Reverse complement motif      Consensus sequence: GCCAATTTCTCCCATTTGGA

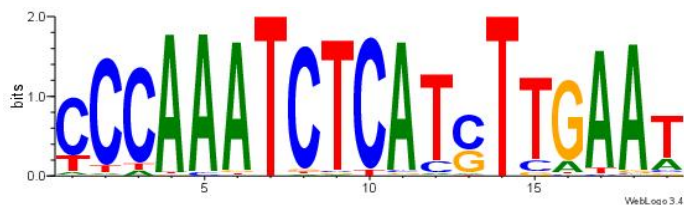


Dataset #: 1  
 Motif ID: 227  
 Motif name: Motif 227  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 16  
 Similarity score: 0.0879004

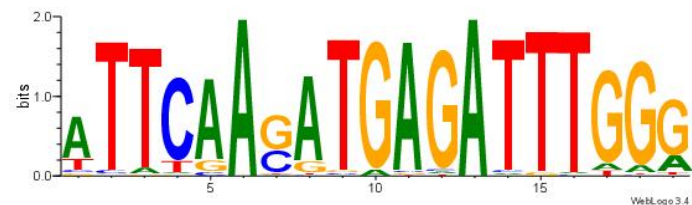
Alignment:

CCCAAATCTCATSTTGAAT  
 CCCAAATCCTATAAAA---

Original motif    Consensus sequence: CCCAAATCTCATSTTGAAT



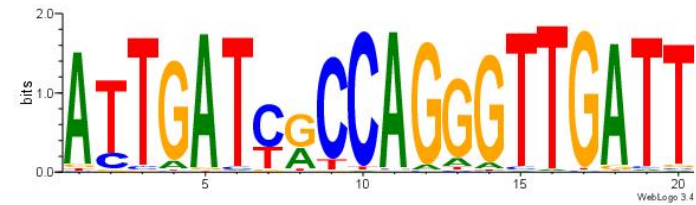
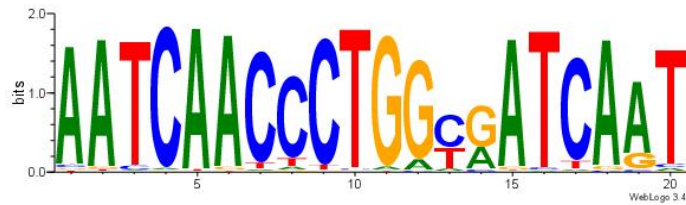
Reverse complement motif    Consensus sequence:  
 ATCAASATGAGATTTGGG



**Dataset #: 1      Motif ID: 170      Motif name: Motif 170**

Original motif    Consensus sequence: AATCAACCCTGGYRATCAAT

Reverse complement motif    Consensus sequence:  
 ATTGATMKCCAGGGTTGATT

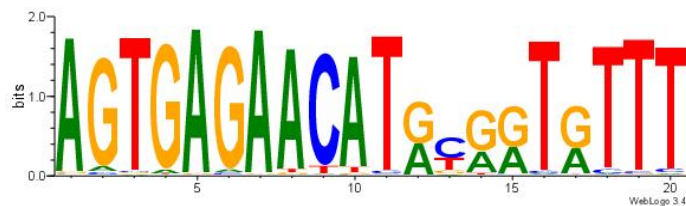


**Best Matches for Motif ID 170 (Highest to Lowest)**

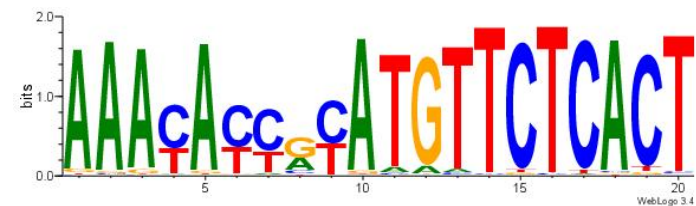
Dataset #: 1  
 Motif ID: 63  
 Motif name: Motif 63  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 20  
 Similarity score: 0.0971686

Alignment:  
 AGTGAGAACATRYRRTRTTT  
 ATTGATMKCCAGGGTTGATT

Original motif      Consensus sequence: AGTGAGAACATRYRRTRTTT



Reverse complement motif      Consensus sequence: AAAMAMMKMATGTTCTCACT

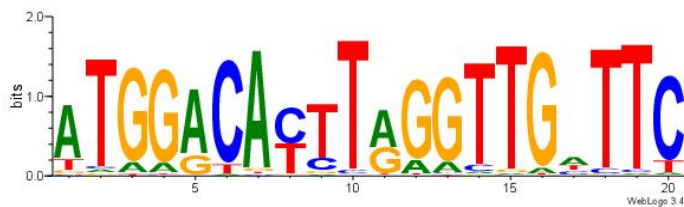


Dataset #: 1  
 Motif ID: 58  
 Motif name: Motif 58  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 2  
 Number of overlap: 19  
 Similarity score: 0.584752

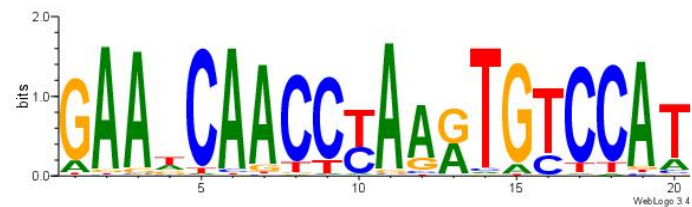
Alignment:

-GAAHCAACCKAAKTGTCCAT  
 AATCAACCCTGGYRATCAAT-

Original motif      Consensus sequence: ATGGACAYTTRGGTTGHTTC



Reverse complement motif      Consensus sequence: GAAHCAACCKAAKTGTCCAT

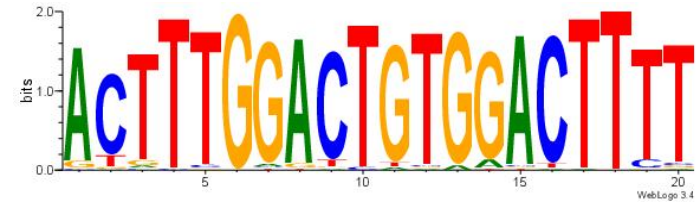
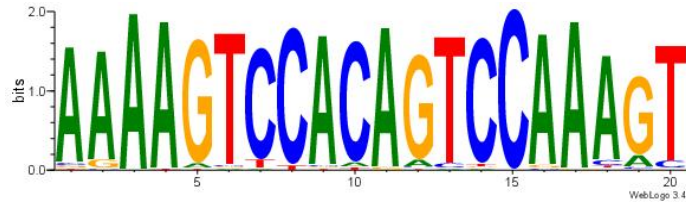



---

**Dataset #: 1      Motif ID: 171      Motif name: Motif 171**

Original motif      Consensus sequence: AAAAGTCCACAGTCCAAAGT

Reverse complement motif      Consensus sequence: ACTTTGGACTGTGGACTTTT

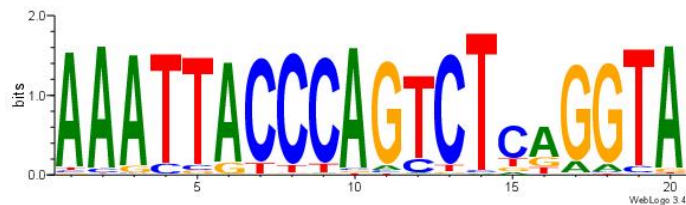


**Best Matches for Motif ID 171 (Highest to Lowest)**

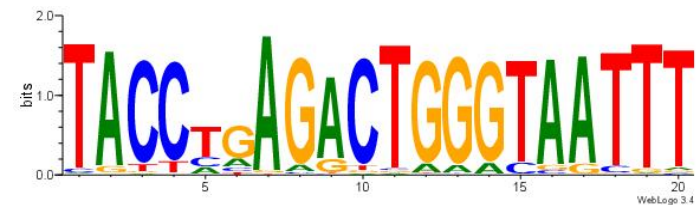
Dataset #: 1  
 Motif ID: 160  
 Motif name: Motif 160  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 2  
 Number of overlap: 19  
 Similarity score: 0.0755123

Alignment:  
 TACCTGAGACTGGGTAATTT-  
 -ACTTTGGACTGTGGACTTTT

Original motif      Consensus sequence: AAATTACCCAGTCTCAGGTA



Reverse complement motif      Consensus sequence: TACCTGAGACTGGGTAATTT

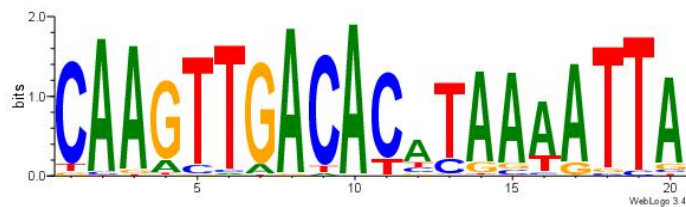


Dataset #: 1  
 Motif ID: 357  
 Motif name: Motif 357  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 2  
 Number of overlap: 19  
 Similarity score: 0.0980025

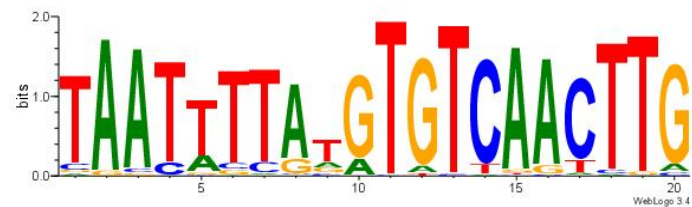
Alignment:

TAATTTTATGTGTCAACTTG-  
 -ACTTTGGACTGTGGACTTTT

Original motif      Consensus sequence: CAAGTTGACACATAAAATTA



Reverse complement motif      Consensus sequence: TAATTTTATGTGTCAACTTG

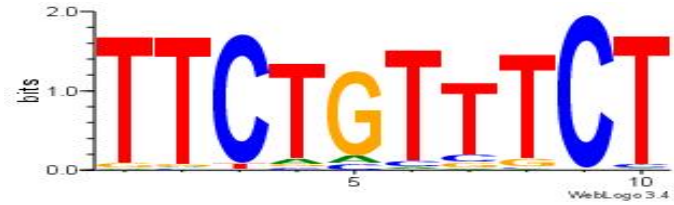



---

**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)

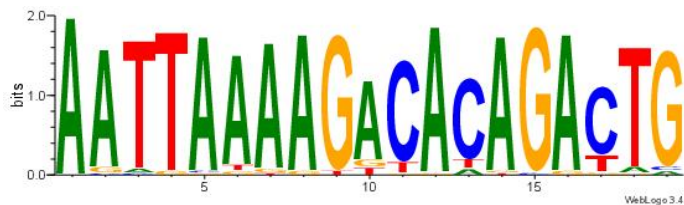
Dataset #: 1  
 Motif ID: 356  
 Motif name: Motif 356  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 8  
 Number of overlap: 10  
 Similarity score: 0.0394673

#### Alignment:

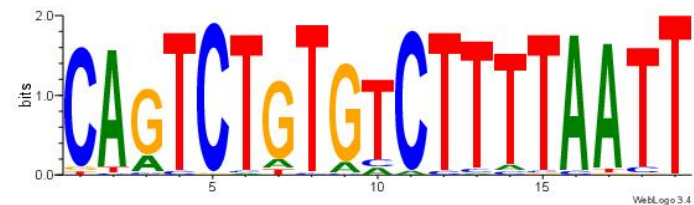
```

CAGTCTGTGTCTTTTAATT
--TTCTGTTTCT-----
  
```

Original motif      Consensus sequence: AATTAAGACACAGACTG



Reverse complement motif      Consensus sequence: CAGTCTGTGTCTTTTAATT

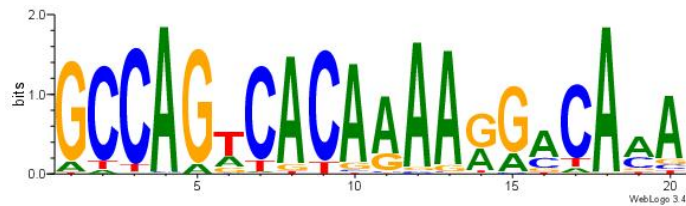


Dataset #: 1  
 Motif ID: 145  
 Motif name: Motif 145  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 8  
 Number of overlap: 10  
 Similarity score: 0.0541669

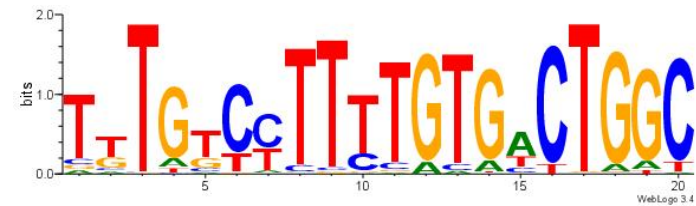
Alignment:

GCCAGTCACAAAARGACAMA  
 ---AGAAACAGAA-----

Original motif      Consensus sequence: GCCAGTCACAAAARGACAMA



Reverse complement motif      Consensus sequence: TYTGCMTTTTGTGACTGGC



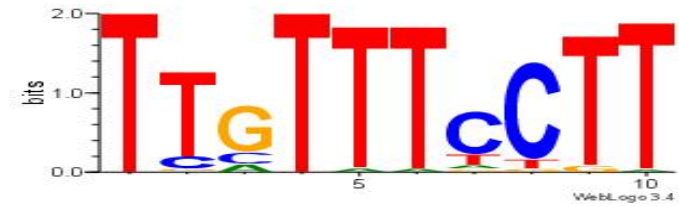

---

**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)

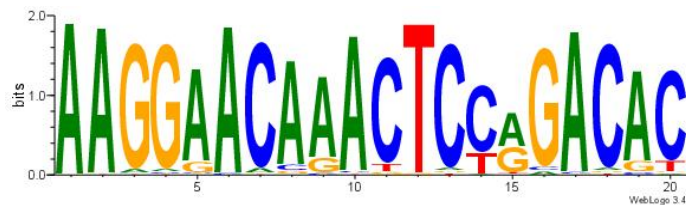
Dataset #: 1  
 Motif ID: 234  
 Motif name: Motif 234  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 11  
 Number of overlap: 10  
 Similarity score: 0.043227

#### Alignment:

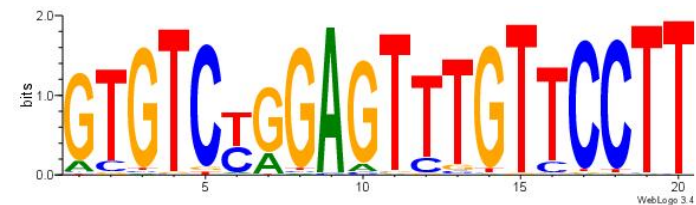
```

GTGTCKGGAGTTTGTTTCCTT
-----TTGTTTCCTT
  
```

Original motif      Consensus sequence: AAGGAACAACTCCRGACAC



Reverse complement motif      Consensus sequence: GTGTCKGGAGTTTGTTTCCTT

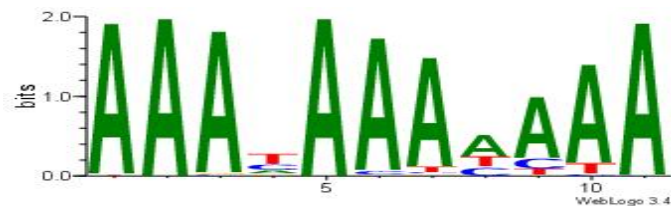


Dataset #: 1  
 Motif ID: 41  
 Motif name: Motif 41  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 2  
 Number of overlap: 10  
 Similarity score: 0.0491703

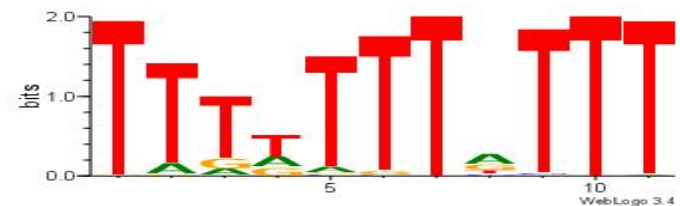
Alignment:

TTTTTTMTTT  
 -TTGTTTCCTT

Original motif      Consensus sequence: AAAYAAAAAA

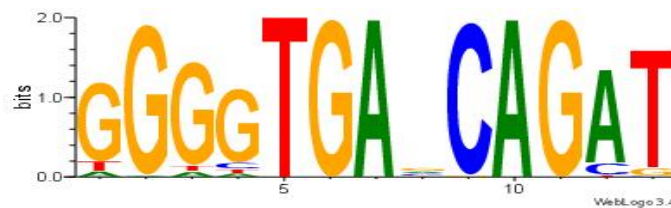


Reverse complement motif      Consensus sequence: TTTTTTMTTT

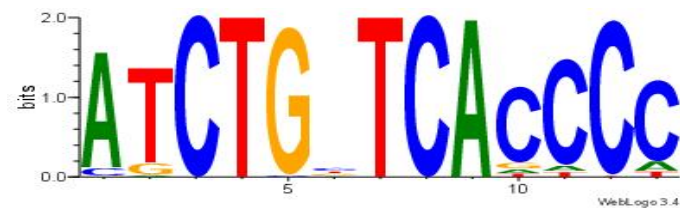


**Dataset #: 1      Motif ID: 174      Motif name: Motif 174**

Original motif      Consensus sequence: GGGGTGAVCAGAT



Reverse complement motif      Consensus sequence: ATCTGVTACCCC



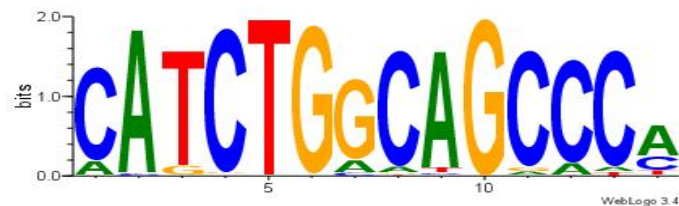
## Best Matches for Motif ID 174 (Highest to Lowest)

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

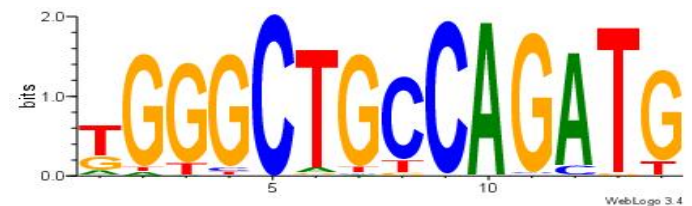
### Alignment:

```
CATCTGGCAGCCCA  
-ATCTGVTACACCC
```

Original motif      Consensus sequence: CATCTGGCAGCCCA



Reverse complement motif      Consensus sequence: TGGGCTGCCAGAT

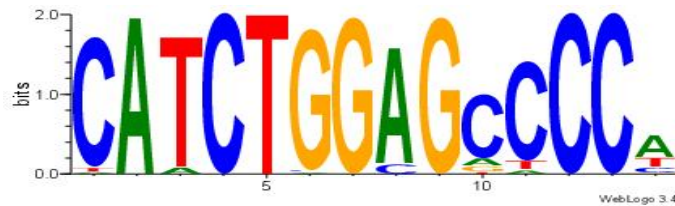


Dataset #: 1  
Motif ID: 320  
Motif name: Motif 320  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Original Motif

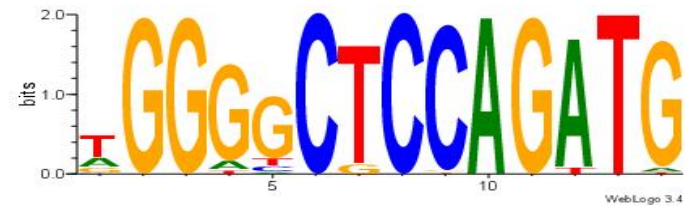
Direction: Backward  
 Position number: 1  
 Number of overlap: 13  
 Similarity score: 0.0766821

Alignment:  
 CATCTGGAGCCCCA  
 -ATCTGVTCACCCC

Original motif      Consensus sequence: CATCTGGAGCCCCA

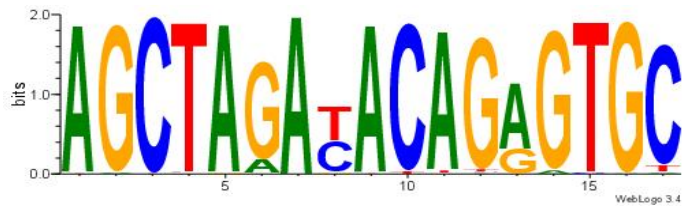


Reverse complement motif      Consensus sequence: TGGGGCTCCAGATG

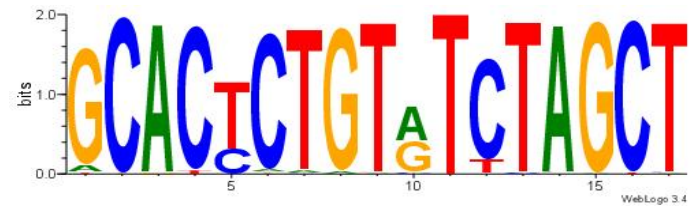


**Dataset #: 1      Motif ID: 175      Motif name: Motif 175**

Original motif      Consensus sequence: AGCTAGAYACAGAGTGC



Reverse complement motif      Consensus sequence: GCACTCTGMTCTAGCT



**Best Matches for Motif ID 175 (Highest to Lowest)**

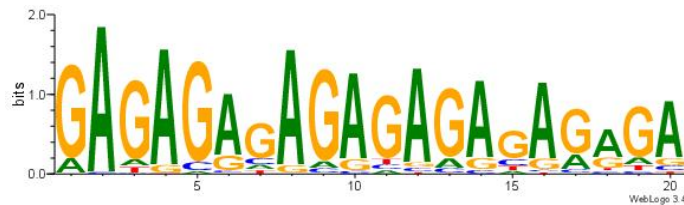
Dataset #: 1  
 Motif ID: 109

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

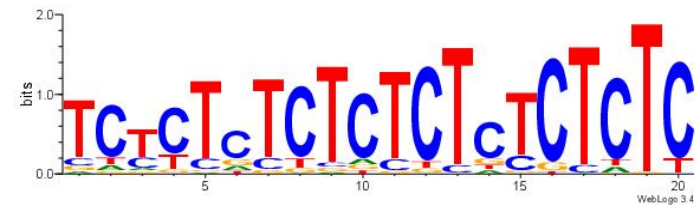
**Alignment:**

TCTCTCTCTCTCTCTCTCTC  
 GCACTCTGTMTCTAGCT---

Original motif      Consensus sequence: GAGAGAGAGAGAGAGAGA



Reverse complement motif      Consensus sequence: TCTCTCTCTCTCTCTCTC

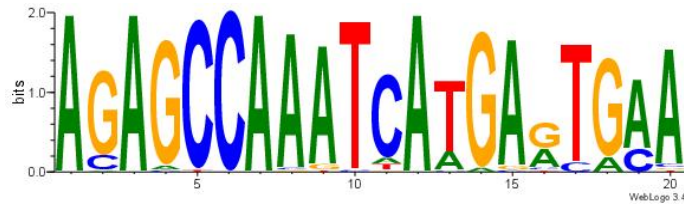


Dataset #: 1  
 Motif ID: 349  
 Motif name: Motif 349  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 2  
 Number of overlap: 17  
 Similarity score: 0.0970004

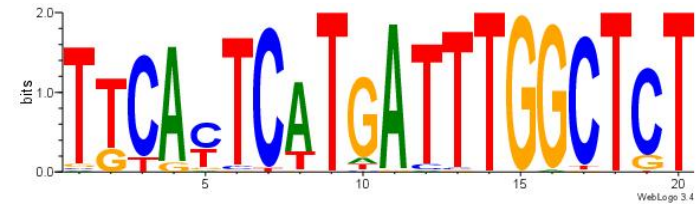
Alignment:

AGAGCCAAATCATGARTGAA  
--AGCTAGAYACAGAGTGC--

Original motif      Consensus sequence: AGAGCCAAATCATGARTGAA

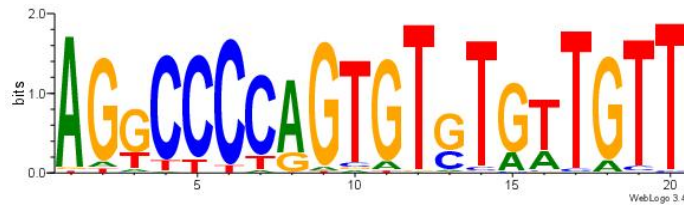


Reverse complement motif      Consensus sequence:  
TTCAMTCATGATTTGGCTCT

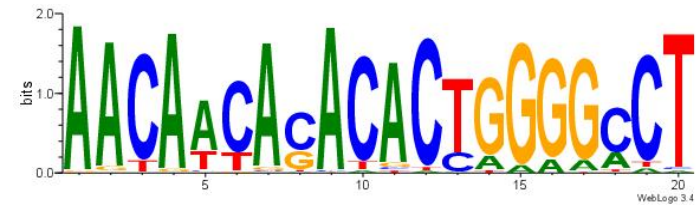


**Dataset #: 1      Motif ID: 176      Motif name: Motif 176**

Original motif      Consensus sequence: AGGCCCCAGTGTSTGTTGTT



Reverse complement motif      Consensus sequence:  
AACACASACTGGGGCCT



**Best Matches for Motif ID 176 (Highest to Lowest)**

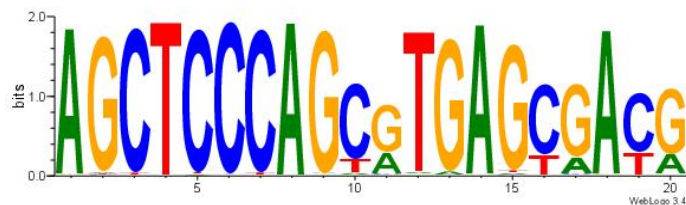
Dataset #:	1
Motif ID:	48
Motif name:	Motif 48
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif

Direction: Forward  
Position number: 1  
Number of overlap: 20  
Similarity score: 0.100522

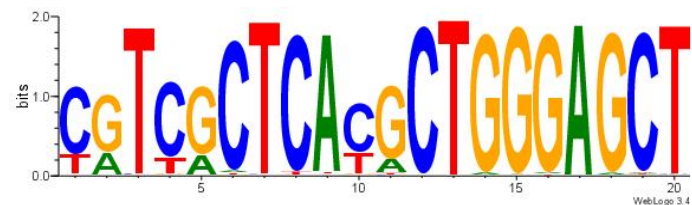
Alignment:

AGCTCCCAGCGTGAGCGACG  
AGGCCCCAGTGTSTGTTGTT

Original motif      Consensus sequence: AGCTCCCAGCGTGAGCGACG



Reverse complement motif      Consensus sequence: CGTCGCTCACGCTGGGAGCT

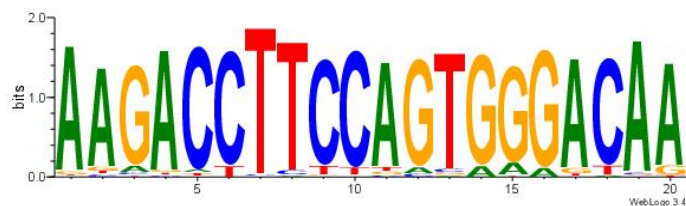


Dataset #: 1  
Motif ID: 292  
Motif name: Motif 292  
Matching format of first motif: Original Motif  
Matching format of second motif: Reverse Complement  
Direction: Forward  
Position number: 1  
Number of overlap: 20  
Similarity score: 0.103197

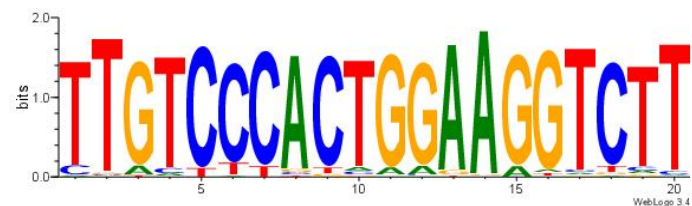
Alignment:

TTGTCCCCTGGAAGGTCTT  
AGGCCCCAGTGTSTGTTGTT

Original motif      Consensus sequence: AAGACCTCCAGTGGGACAA

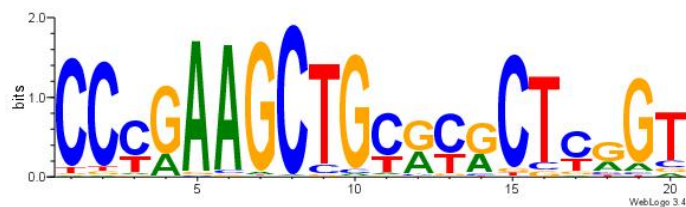


Reverse complement motif      Consensus sequence: TTGTCCCAGTGGGACAA

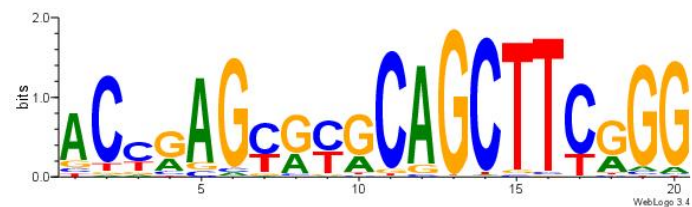


**Dataset #: 1      Motif ID: 177      Motif name: Motif 177**

Original motif      Consensus sequence: CCCGAAGCTGCRYRCTCGGT



Reverse complement motif      Consensus sequence: ACCGAGMKMGCAGCTTCGGG



### Best Matches for Motif ID 177 (Highest to Lowest)

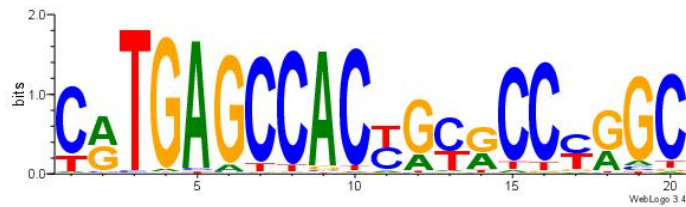
Dataset #:	1
Motif ID:	56
Motif name:	Motif 56
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	20
Similarity score:	0.0760829



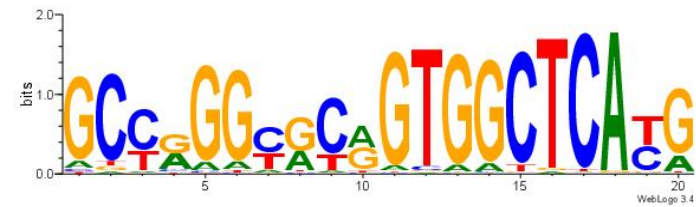
Alignment:

CRTGAGCCACYGYRCCYGGC  
CCCGAAGCTGCRYRCTCGGT

Original motif      Consensus sequence: CRTGAGCCACYGYRCCYGGC



Reverse complement motif      Consensus sequence:  
GCCKGGMKCMGTGGCTCAKG



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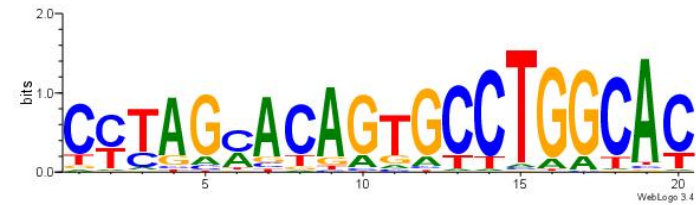
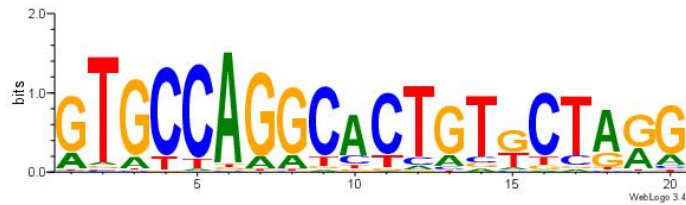
Dataset #:	1
Motif ID:	76
Motif name:	Motif 76
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	19
Similarity score:	0.590313

Alignment:

GTGCCAGGCACTGTKCTARG-  
-CCCGAAGCTGCRYRCTCGGT

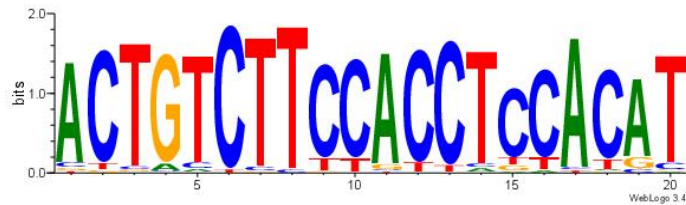
Original motif      Consensus sequence: GTGCCAGGCACTGTKCTARG

Reverse complement motif      Consensus sequence:  
CMTAGYACAGTGCCTGGCAC

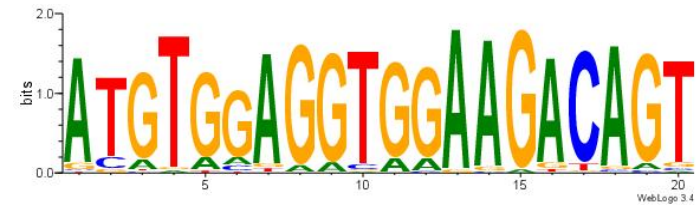


**Dataset #: 1      Motif ID: 178      Motif name: Motif 178**

Original motif      Consensus sequence: ACTGTCTTCCACCTCCACAT



Reverse complement motif      Consensus sequence: ATGTGGAGGTGGAAGACAGT



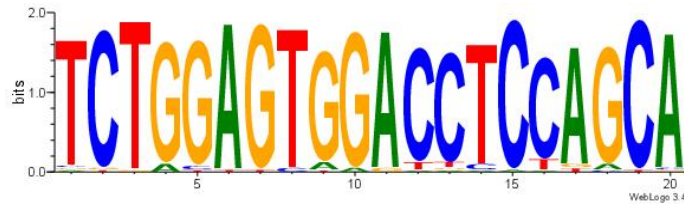
**Best Matches for Motif ID 178 (Highest to Lowest)**

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

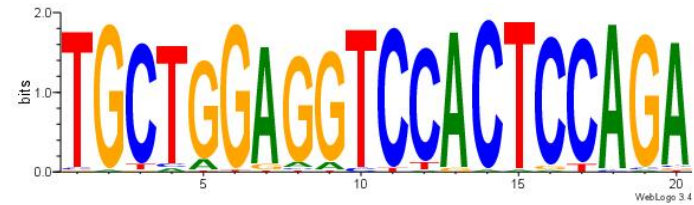
Alignment:

TGCTGGAGGTCCACTCCAGA  
ATGTGGAGGTGGAAGACAGT

Original motif      Consensus sequence: TCTGGAGTGGACCTCCAGCA



Reverse complement motif      Consensus sequence:  
TGCTGGAGGTCCACTCCAGA



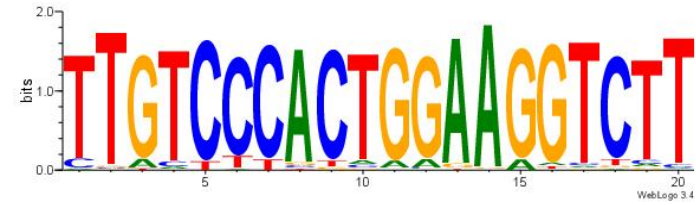
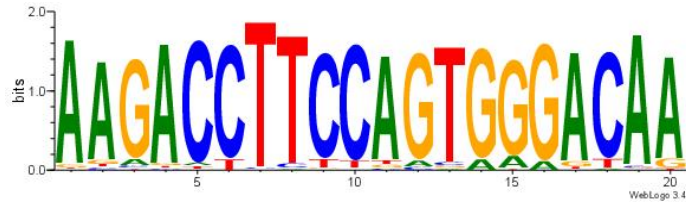
Dataset #: 1  
Motif ID: 292  
Motif name: Motif 292  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Reverse Complement  
Direction: Forward  
Position number: 1  
Number of overlap: 20  
Similarity score: 0.111286

**Alignment:**

TTGTCCCACTGGAAGGTCTT  
ATGTGGAGGTGGAAGACAGT

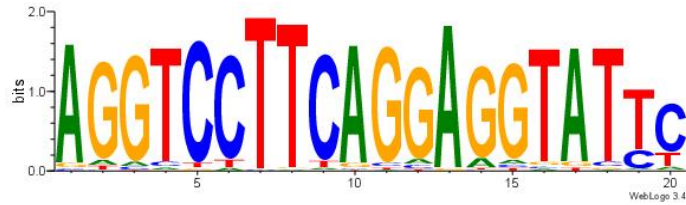
Original motif      Consensus sequence: AAGACCTCCAGTGGGACAA

Reverse complement motif      Consensus sequence:  
TTGTCCCACTGGAAGGTCTT

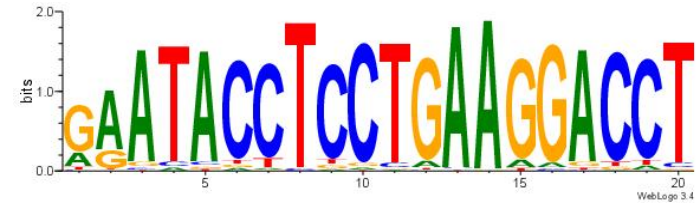


**Dataset #: 1      Motif ID: 179      Motif name: Motif 179**

Original motif      Consensus sequence: AGGTCCTTCAGGAGGTATTC



Reverse complement motif      Consensus sequence: GAATACCTCCTGAAGGACCT



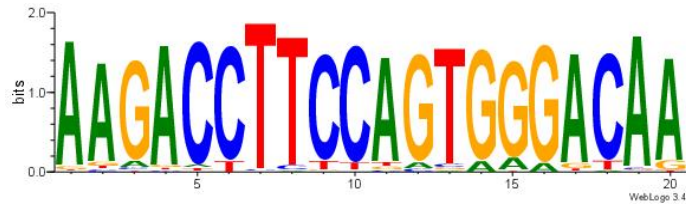
**Best Matches for Motif ID 179 (Highest to Lowest)**

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

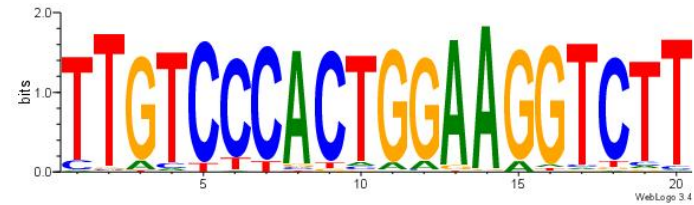
Alignment:

TTGTCCCCTGGAAGGTCTT  
GAATACCTCCTGAAGGACCT

Original motif      Consensus sequence: AAGACCTTCCAGTGGGACAA



Reverse complement motif      Consensus sequence:  
TTGTCCCCTGGAAGGTCTT

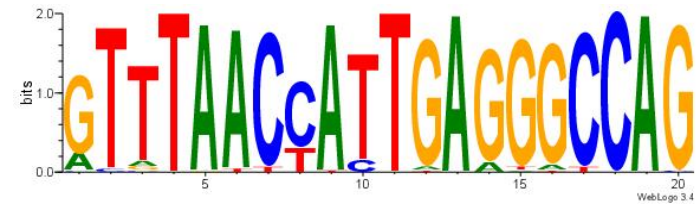
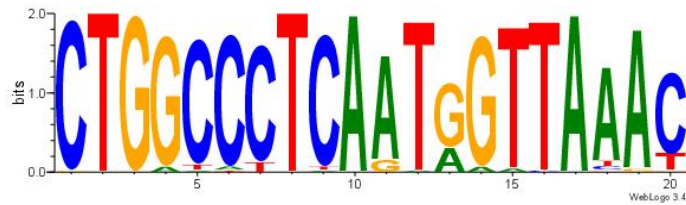


Dataset #: 1  
Motif ID: 332  
Motif name: Motif 332  
Matching format of first motif: Original Motif  
Matching format of second motif: Original Motif  
Direction: Backward  
Position number: 1  
Number of overlap: 20  
Similarity score: 0.114535

Alignment:  
CTGGCCCTCAATGGTTAAAC  
AGGTCCTTCAGGAGGTATTC

Original motif      Consensus sequence: CTGGCCCTCAATGGTTAAAC

Reverse complement motif      Consensus sequence:  
GTTTAAACCATTGAGGGCCAG



**Dataset #: 1      Motif ID: 180      Motif name: Motif 180**

Original motif      Consensus sequence: TGCGCATGCGCA



Reverse complement motif      Consensus sequence: TGCGCATGCGCA

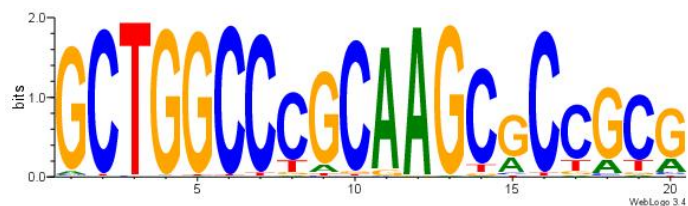


**Best Matches for Motif ID 180 (Highest to Lowest)**

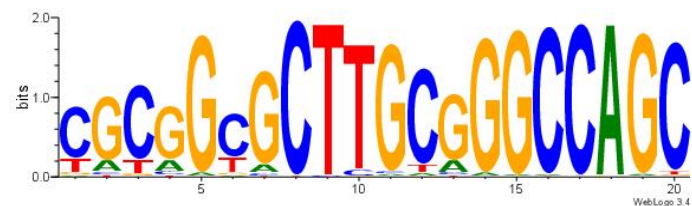
Dataset #:	1
Motif ID:	100
Motif name:	Motif 100
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	4
Number of overlap:	12
Similarity score:	0.0728388

Alignment:  
GCTGGCCCGCAAGCGCCGCG  
---TGCGCATGCGCA-----

Original motif    Consensus sequence: GCTGGCCCGCAAGCGCCGCG



Reverse complement motif    Consensus sequence: CGCGGCGCTTGCGGGCCAGC

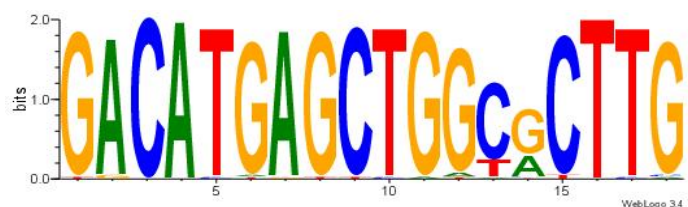


Dataset #: 1  
Motif ID: 306  
Motif name: Motif 306  
Matching format of first motif: Original Motif  
Matching format of second motif: Original Motif  
Direction: Forward  
Position number: 5  
Number of overlap: 12  
Similarity score: 0.0731846

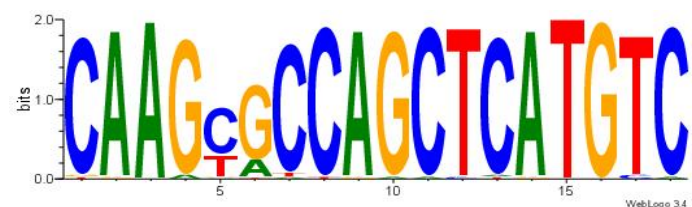
Alignment:

GACATGAGCTGGCGCTTG  
----TGCGCATGCGCA--

Original motif    Consensus sequence: GACATGAGCTGGCGCTTG

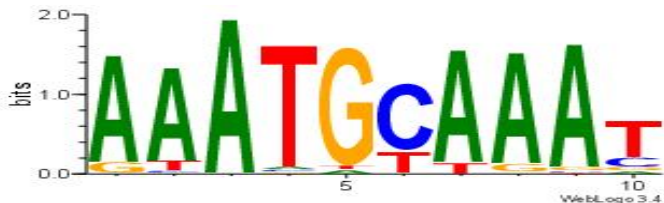


Reverse complement motif    Consensus sequence: CAAGCGCCAGCTCATGTC

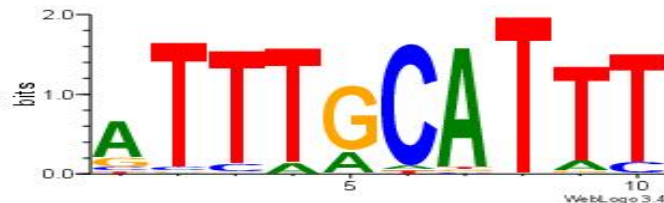


**Dataset #: 1      Motif ID: 181      Motif name: Motif 181**

Original motif      Consensus sequence: AAATGCAAAT



Reverse complement motif      Consensus sequence: ATTTGCATTT



**Best Matches for Motif ID 181 (Highest to Lowest)**

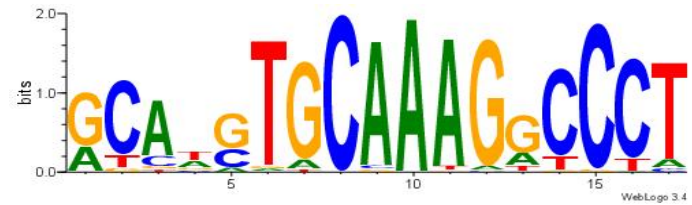
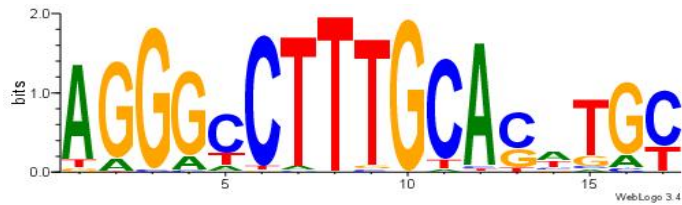
Dataset #:	1
Motif ID:	322
Motif name:	Motif 322
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	6
Number of overlap:	10
Similarity score:	0.0560732

Alignment:  
 AGGGCCTTTGCASWTGC  
 -----ATTTGCATTT--

Original motif      Consensus sequence: AGGGCCTTTGCASWTGC

Reverse complement motif      Consensus sequence:  
 GCAWSTGCAAAGGCCCT

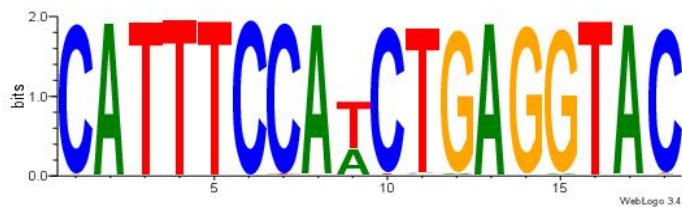




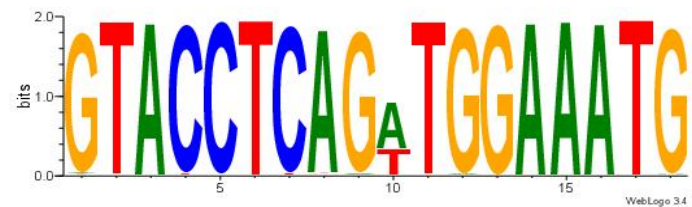
Dataset #: 1  
 Motif ID: 25  
 Motif name: Motif 25  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 2  
 Number of overlap: 10  
 Similarity score: 0.0591841

Alignment:  
 GTACCTCAGWTGGAAATG  
 -AAATGCAAAT-----

Original motif      Consensus sequence: CATTCCA WCTGAGGTAC

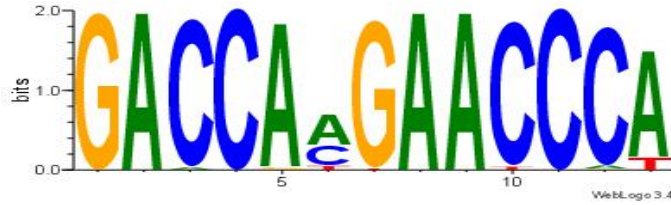


Reverse complement motif      Consensus sequence: GTACCTCAG WTGGAAATG

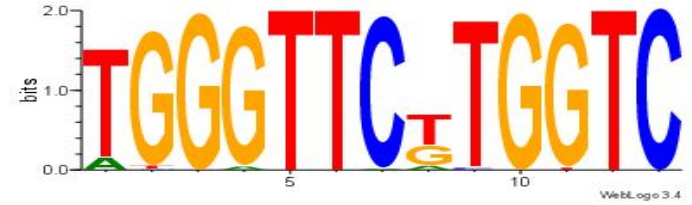


**Dataset #: 1      Motif ID: 182      Motif name: Motif 182**

Original motif    Consensus sequence: GACCAMGAACCCA



Reverse complement motif    Consensus sequence: TGGGTTCTGGTC



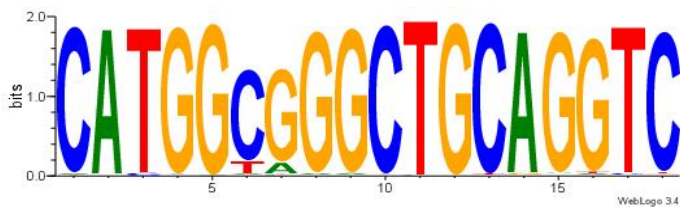
### Best Matches for Motif ID 182 (Highest to Lowest)

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

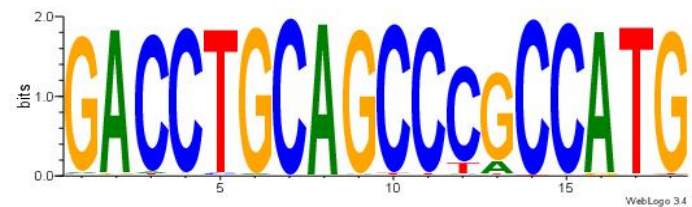
Alignment:

```
GACCTGCAGCCCGCCATG
-----GACCAMGAACCCA
```

Original motif    Consensus sequence: CATGGCGGGCTGCAGGTC



Reverse complement motif    Consensus sequence: GACCTGCAGCCCGCCATG

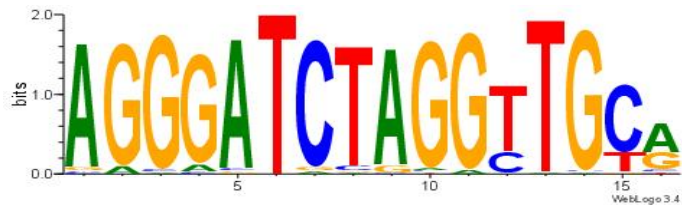


Dataset #: 1  
 Motif ID: 271  
 Motif name: Motif 271  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 13  
 Similarity score: 0.0870886

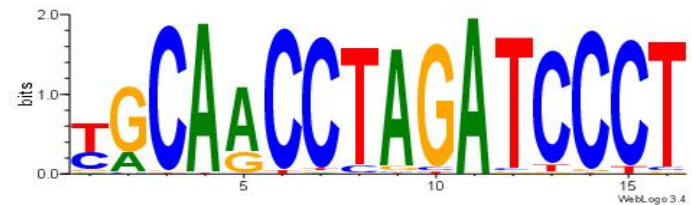
Alignment:

AGGGATCTAGGTTGCR  
 TGGGTTTCYTGGTC---

Original motif      Consensus sequence: AGGGATCTAGGTTGCR



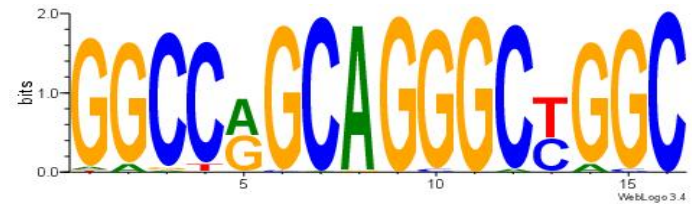
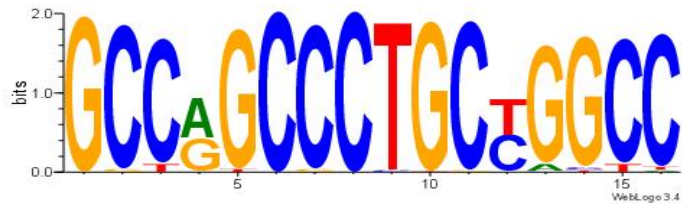
Reverse complement motif      Consensus sequence: KGCAACCTAGATCCCT



**Dataset #: 1      Motif ID: 183      Motif name: Motif 183**

Original motif      Consensus sequence: GCCRGCCTGCYGGCC

Reverse complement motif      Consensus sequence: GGCCMGCAGGGCKGGC

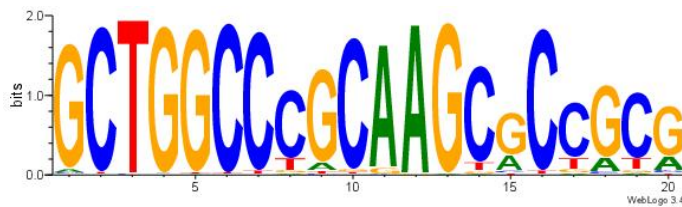


**Best Matches for Motif ID 183 (Highest to Lowest)**

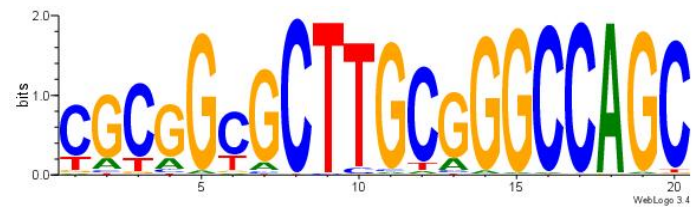
Dataset #: 1  
 Motif ID: 100  
 Motif name: Motif 100  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 4  
 Number of overlap: 16  
 Similarity score: 0.0673082

Alignment:  
 GCTGGCCCGCAAGCGCCGCG  
 -GGCCMGCAGGGCKGGC----

Original motif      Consensus sequence: GCTGGCCCGCAAGCGCCGCG



Reverse complement motif      Consensus sequence: CGCGGCGCTTGCGGCCAGC

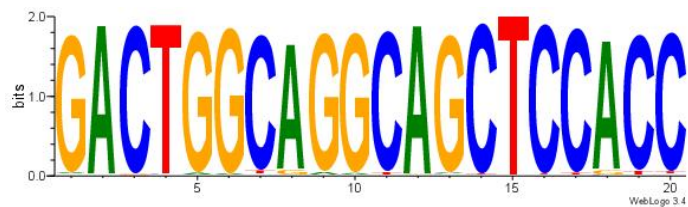


Dataset #: 1  
 Motif ID: 52  
 Motif name: Motif 52  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 5  
 Number of overlap: 16  
 Similarity score: 0.0703996

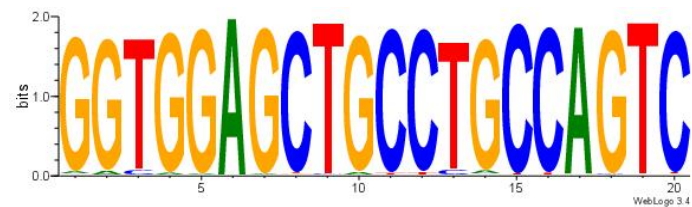
Alignment:

GACTGGCAGGCAGCTCCACC  
 GGCCMGCAGGGCKGGC-----

Original motif      Consensus sequence: GACTGGCAGGCAGCTCCACC



Reverse complement motif      Consensus sequence: GGTGGAGCTGCCTGCCAGTC

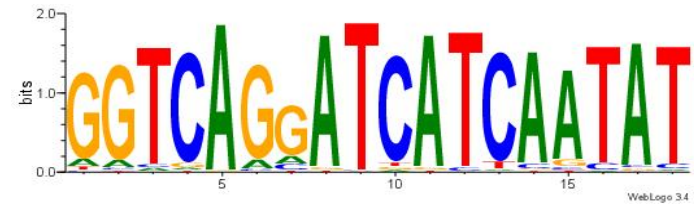
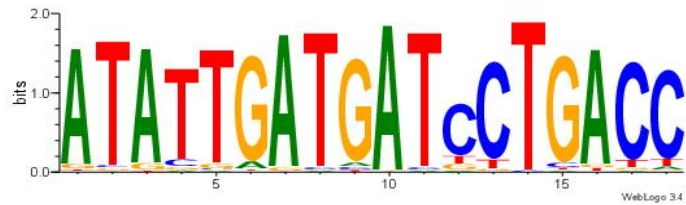



---

**Dataset #: 1      Motif ID: 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)

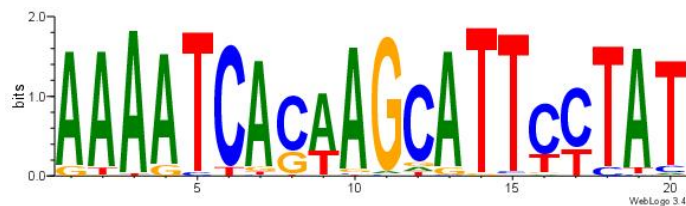
Dataset #: 1  
 Motif ID: 254  
 Motif name: Motif 254  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 18  
 Similarity score: 0.08828

#### Alignment:

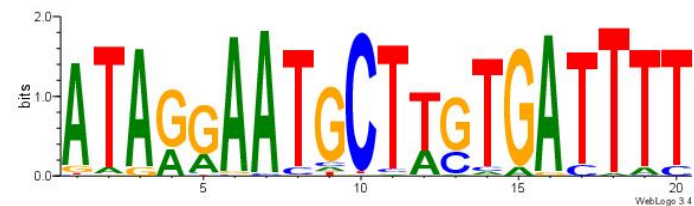
```

ATAGGAATGCTTGTGATTTT
ATATTGATGATCCTGACC--
  
```

Original motif      Consensus sequence: AAAATCACAAGCATTCTAT



Reverse complement motif      Consensus sequence: ATAGGAATGCTTGTGATTTT

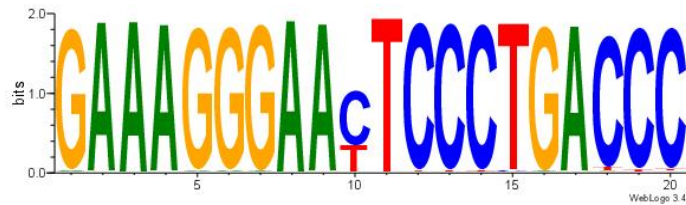


Dataset #: 1  
 Motif ID: 16  
 Motif name: Motif 16  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 2  
 Number of overlap: 18  
 Similarity score: 0.0954042

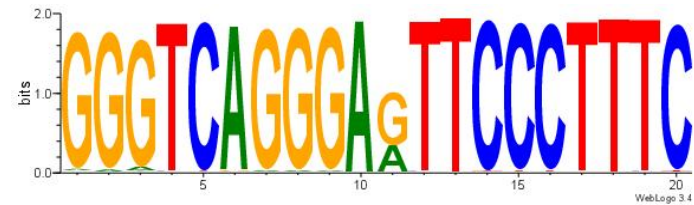
Alignment:

GAAAGGGA ACTCCCTGACCC  
 -ATATTGATGATCCTGACC-

Original motif      Consensus sequence: GAAAGGGA ACTCCCTGACCC



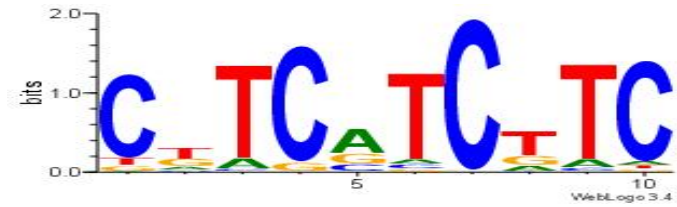
Reverse complement motif      Consensus sequence: GGGTCAGGGA GTTCCCTTTC



**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)

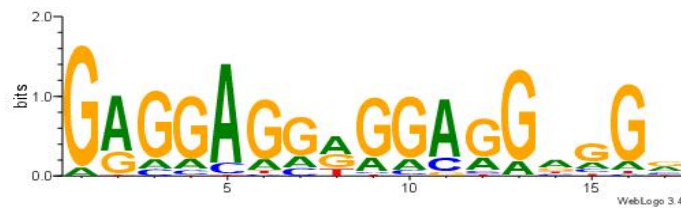
Dataset #: 1  
 Motif ID: 161  
 Motif name: Motif 161  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 4  
 Number of overlap: 10  
 Similarity score: 0.038579

#### Alignment:

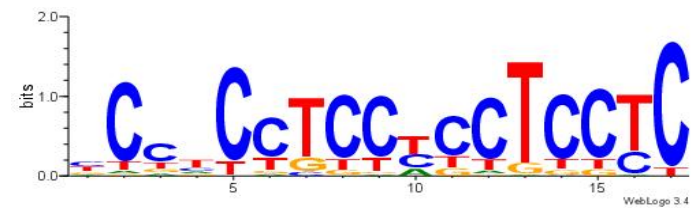
```

VCCDCCTCCKCCTCCTC
----CYTCATCTTC----
  
```

Original motif      Consensus sequence: GAGGAGGRGGAGGDGGV



Reverse complement motif      Consensus sequence: VCCDCCTCCKCCTCCTC



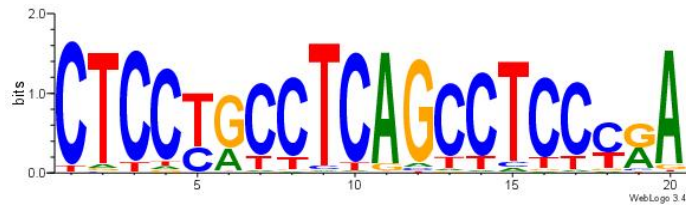


Dataset #: 1  
 Motif ID: 26  
 Motif name: Motif 26  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 7  
 Number of overlap: 10  
 Similarity score: 0.0396628

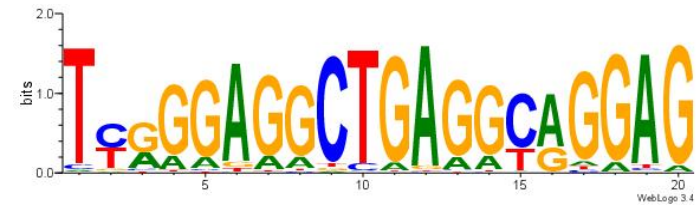
Alignment:

TMGGGAGGCTGAGGCAGGAG  
 -----GAAGATGAMG-----

Original motif    Consensus sequence: CTCCTGCCTCAGCCTCCCRA



Reverse complement motif    Consensus sequence: TMGGGAGGCTGAGGCAGGAG

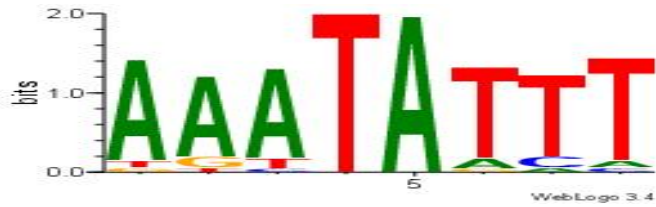



---

**Dataset #: 1      Motif ID: 186      Motif name: Motif 186**

Original motif    Consensus sequence: AAATATTT

Reverse complement motif    Consensus sequence: AAATATTT

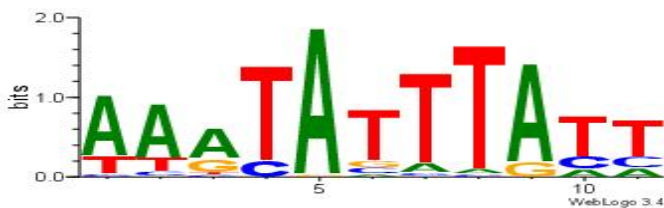


### Best Matches for Motif ID 186 (Highest to Lowest)

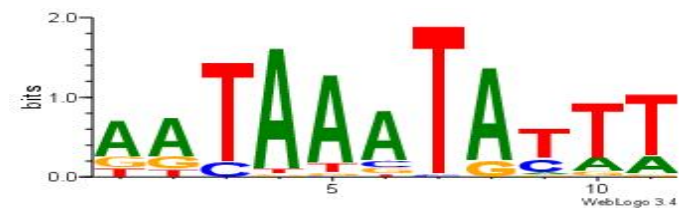
Dataset #: 1  
 Motif ID: 57  
 Motif name: Motif 57  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 8  
 Similarity score: 0.0174942

Alignment:  
 AATAAATATTT  
 AAATATTT---

Original motif      Consensus sequence: AAATATTTATT



Reverse complement motif      Consensus sequence: AATAAATATTT

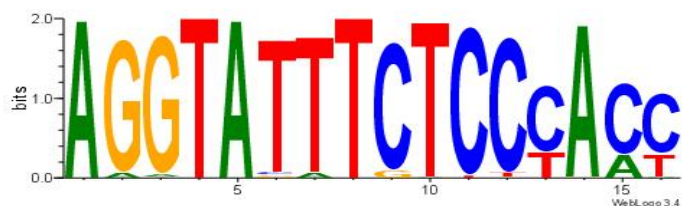


Dataset #: 1

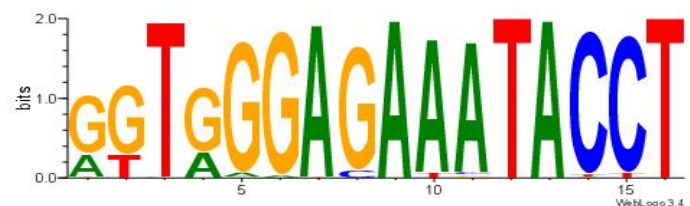
Motif ID: 168  
 Motif name: Motif 168  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 9  
 Number of overlap: 8  
 Similarity score: 0.0532506

Alignment:  
 AGGTATTTCTCCCACC  
 AAATATTT-----

Original motif    Consensus sequence: AGGTATTTCTCCCACC

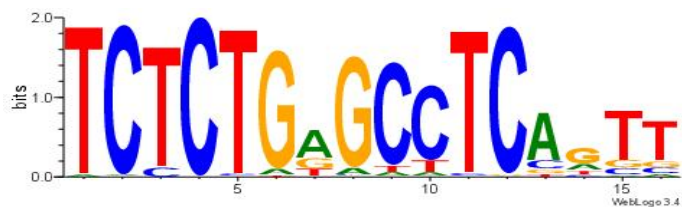


Reverse complement motif    Consensus sequence: GGTGGGAGAAATACCT

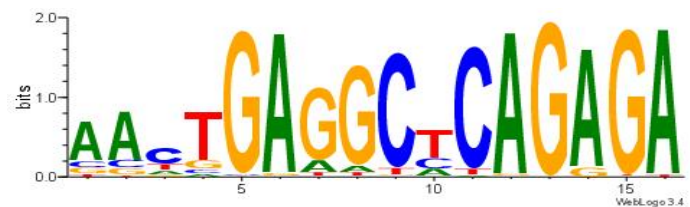


**Dataset #: 1      Motif ID: 187      Motif name: Motif 187**

Original motif    Consensus sequence: TCTCTGAGCCTCAGTT



Reverse complement motif    Consensus sequence: AACTGAGGCTCAGAGA



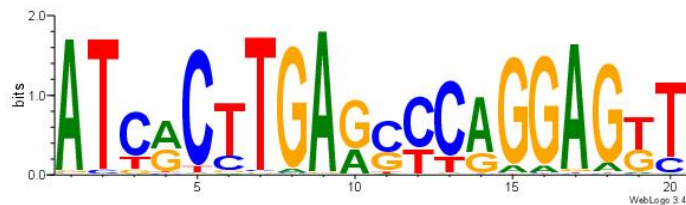
## Best Matches for Motif ID 187 (Highest to Lowest)

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

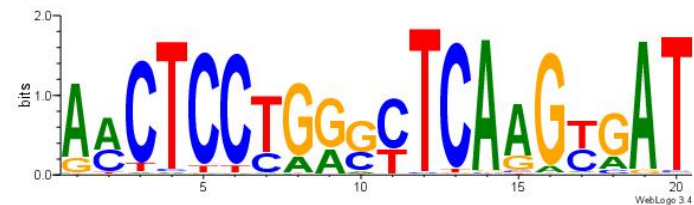
### Alignment:

```
ATCRCTTGAGSYCAGGAGKT  
-AACTGAGGCTCAGAGA---
```

Original motif      Consensus sequence: ATCRCTTGAGSYCAGGAGKT



Reverse complement motif      Consensus sequence: ARCTCCTGKSCTCAAGKGAT



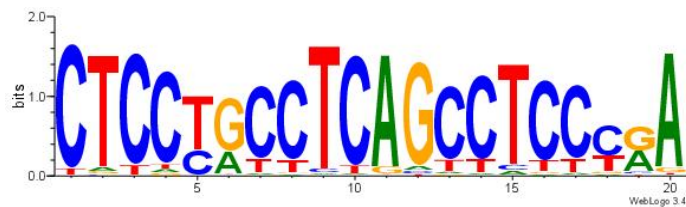
---

Dataset #: 1  
Motif ID: 26  
Motif name: Motif 26  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Reverse Complement

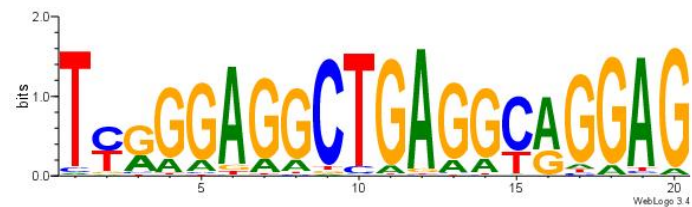
Direction: Forward  
 Position number: 1  
 Number of overlap: 16  
 Similarity score: 0.0936416

Alignment:  
 TMGGGAGGCTGAGGCAGGAG  
 AACTGAGGCTCAGAGA-----

Original motif    Consensus sequence: CTCCTGCCTCAGCCTCCCRA

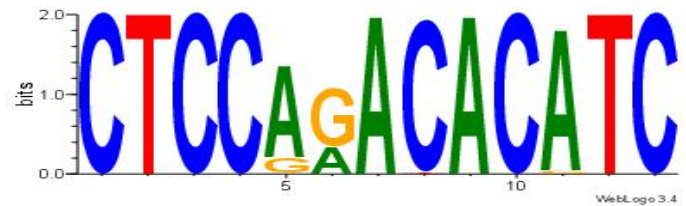


Reverse complement motif    Consensus sequence: TMGGGAGGCTGAGGCAGGAG

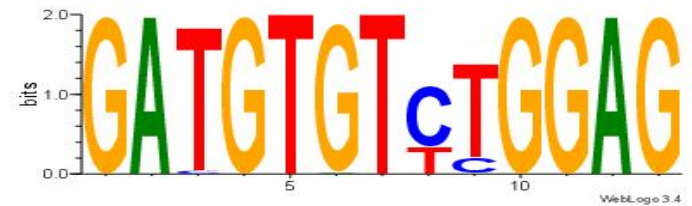


**Dataset #: 1    Motif ID: 188    Motif name: Motif 188**

Original motif    Consensus sequence: CTCCAGACACATC



Reverse complement motif    Consensus sequence: GATGTGTCTGGAG



**Best Matches for Motif ID 188 (Highest to Lowest)**

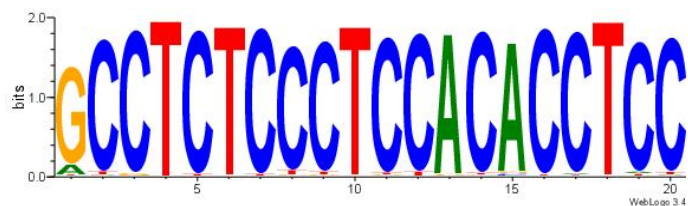
Dataset #: 1  
 Motif ID: 105

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

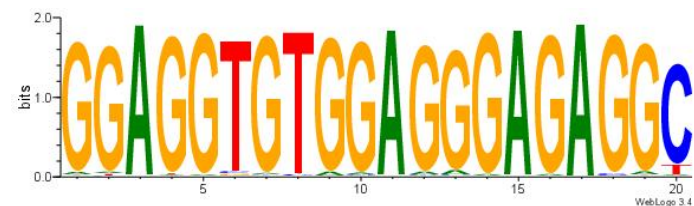
**Alignment:**

GGAGGTGTGGAGGGAGAGGC  
 ---GATGTGTCTGGAG----

Original motif    Consensus sequence: GCCTCTCCCTCCACACCTCC



Reverse complement motif    Consensus sequence: GGAGGTGTGGAGGGAGAGGC

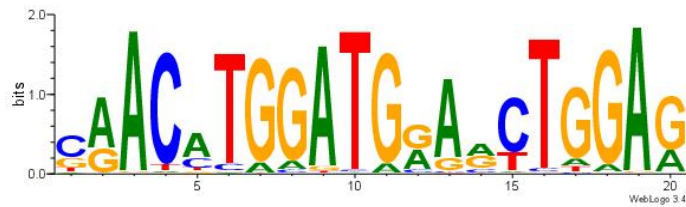


Dataset #: 1  
 Motif ID: 104  
 Motif name: Motif 104  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 8  
 Number of overlap: 13  
 Similarity score: 0.0708894

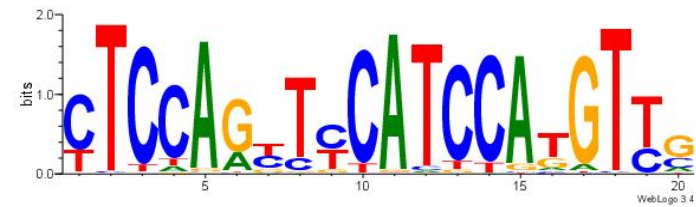
Alignment:

CAACATGGATGRARCTGGAG  
GATGTGTCTGGAG-----

Original motif      Consensus sequence: CAACATGGATGRARCTGGAG

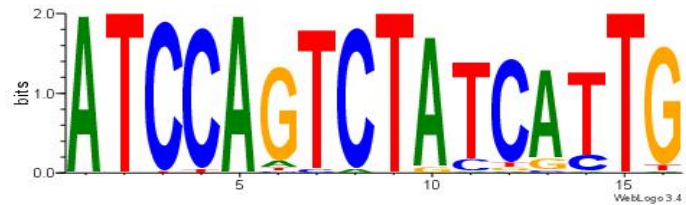


Reverse complement motif      Consensus sequence:  
CTCCAGKTCATCCATGTTG

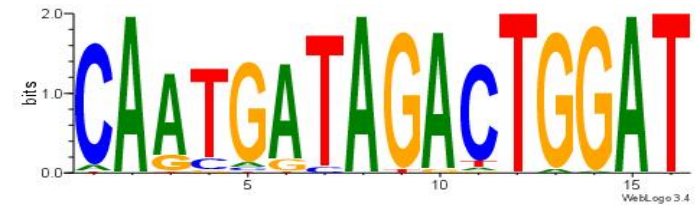


**Dataset #: 1      Motif ID: 189      Motif name: Motif 189**

Original motif      Consensus sequence: ATCCAGTCTATCATTG



Reverse complement motif      Consensus sequence:  
CAATGATAGACTGGAT



**Best Matches for Motif ID 189 (Highest to Lowest)**

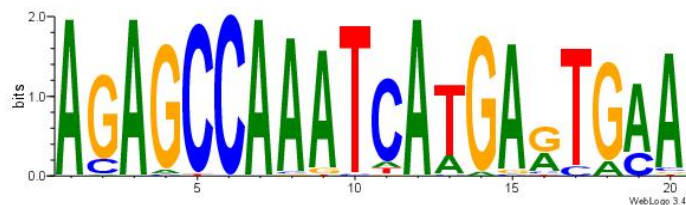
Dataset #:	1
Motif ID:	349
Motif name:	Motif 349
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement

Direction: Forward  
 Position number: 3  
 Number of overlap: 16  
 Similarity score: 0.0977739

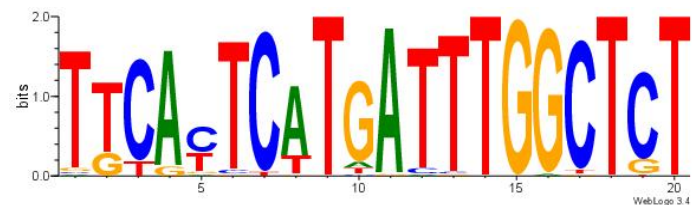
**Alignment:**

TTCAMTCATGATTTGGCTCT  
 --CAATGATAGACTGGAT--

Original motif      Consensus sequence: AGAGCCAAATCATGARTGAA



Reverse complement motif      Consensus sequence: TTCAMTCATGATTTGGCTCT



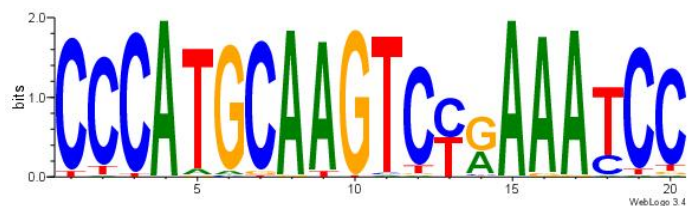
Dataset #: 1  
 Motif ID: 310  
 Motif name: Motif 310  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 2  
 Number of overlap: 16  
 Similarity score: 0.106334

**Alignment:**

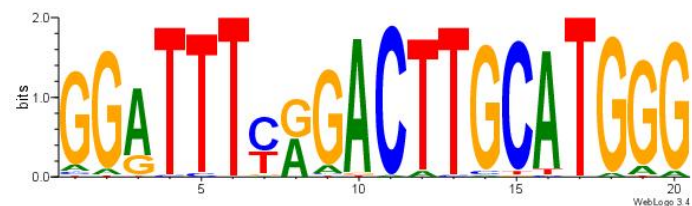
CCCATGCAAGTCYRAAATCC  
 -CAATGATAGACTGGAT---



Original motif      Consensus sequence: CCCATGCAAGTCYRAAATCC

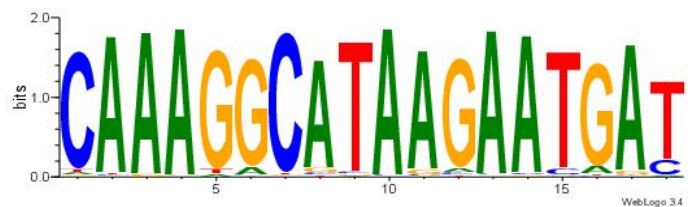


Reverse complement motif      Consensus sequence: GGATTTMKGACTTGCATGGG

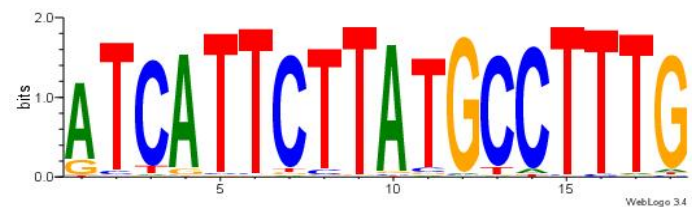


**Dataset #: 1      Motif ID: 190      Motif name: Motif 190**

Original motif      Consensus sequence: CAAAGGCATAAGAATGAT



Reverse complement motif      Consensus sequence: ATCATTCTTATGCCTTTG



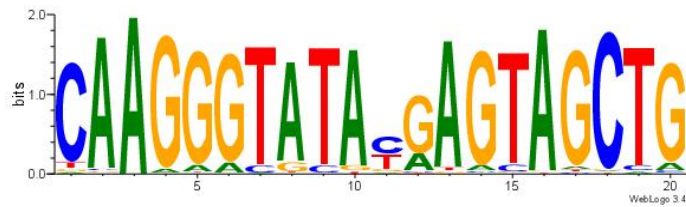
### Best Matches for Motif ID 190 (Highest to Lowest)

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

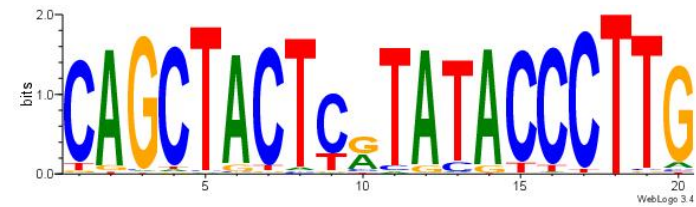
Alignment:

CAAGGGTATAYGAGTAGCTG  
CAAAGGCATAAGAATGAT--

Original motif      Consensus sequence: CAAGGGTATAYGAGTAGCTG



Reverse complement motif      Consensus sequence:  
CAGCTACTCKTATACCCTTG



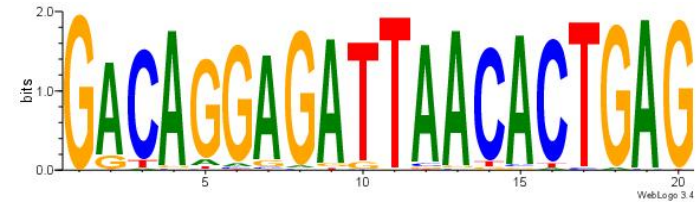
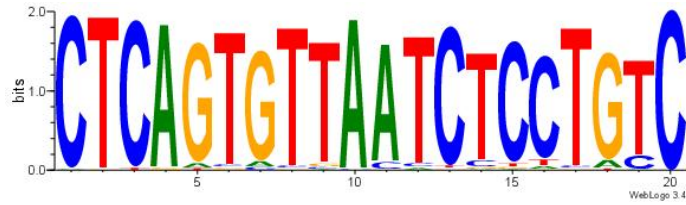
Dataset #: 1  
Motif ID: 262  
Motif name: Motif 262  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Original Motif  
Direction: Backward  
Position number: 3  
Number of overlap: 18  
Similarity score: 0.101423

Alignment:

CTCAGTGTTAATCTCCTGTC  
ATCATTCTTATGCCTTTG--

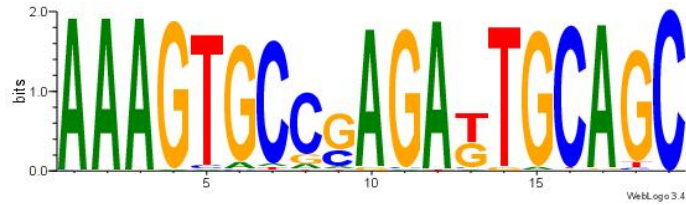
Original motif      Consensus sequence: CTCAGTGTTAATCTCCTGTC

Reverse complement motif      Consensus sequence:  
GACAGGAGATTAACACTGAG

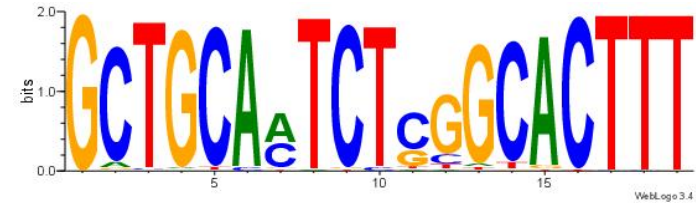


**Dataset #: 1      Motif ID: 191      Motif name: Motif 191**

Original motif      Consensus sequence: AAAGTGCCGAGAKTGCAGC



Reverse complement motif      Consensus sequence: GCTGCARTCTCGGCACTTT



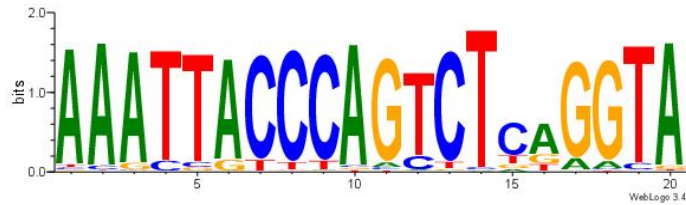
**Best Matches for Motif ID 191 (Highest to Lowest)**

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

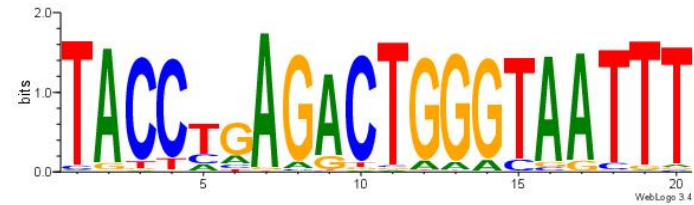
Alignment:

TACCTGAGACTGGGTAATTT  
-GCTGCARTCTCGGCACTTT

Original motif      Consensus sequence: AAATTACCCAGTCTCAGGTA



Reverse complement motif      Consensus sequence:  
TACCTGAGACTGGGTAATTT



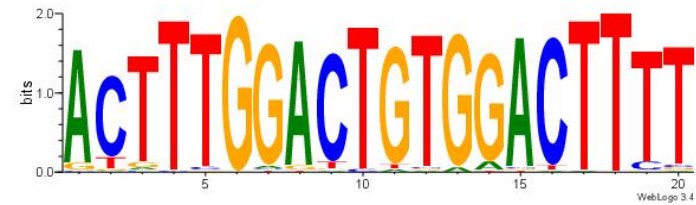
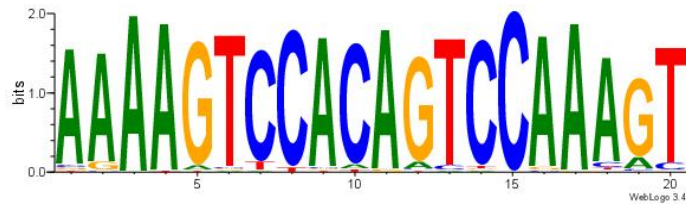
Dataset #: 1  
Motif ID: 171  
Motif name: Motif 171  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Reverse Complement  
Direction: Backward  
Position number: 2  
Number of overlap: 19  
Similarity score: 0.106747

Alignment:

ACTTTGGACTGTGGACTTTT  
GCTGCARTCTCGGCACTTT-

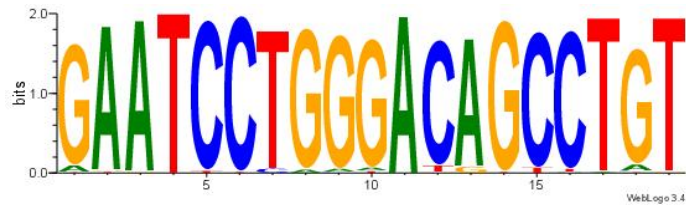
Original motif      Consensus sequence: AAAAGTCCACAGTCCAAAGT

Reverse complement motif      Consensus sequence:  
ACTTTGGACTGTGGACTTTT

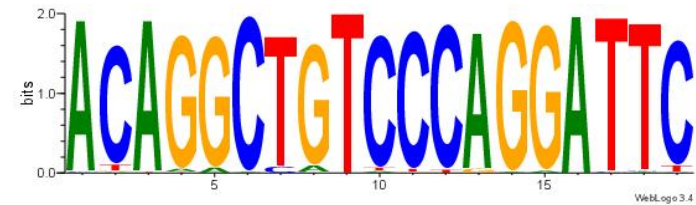


**Dataset #: 1      Motif ID: 192      Motif name: Motif 192**

Original motif      Consensus sequence: GAATCCTGGGACAGCCTGT



Reverse complement motif      Consensus sequence: ACAGGCTGTCCCAGGATTC



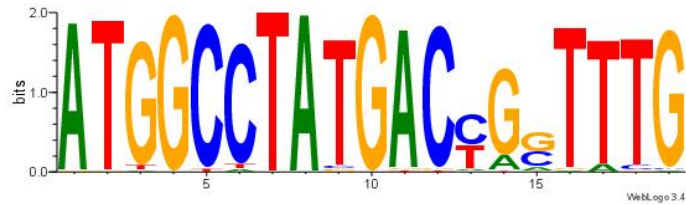
**Best Matches for Motif ID 192 (Highest to Lowest)**

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

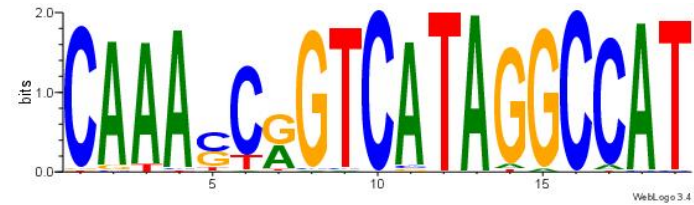
Alignment:

CAAASCKGTCATAGGCCAT  
GAATCCTGGGACAGCCTGT

Original motif      Consensus sequence: ATGGCCTATGACYGSTTTG



Reverse complement motif      Consensus sequence:  
CAAASCKGTCATAGGCCAT



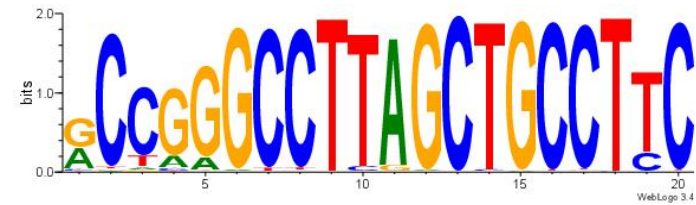
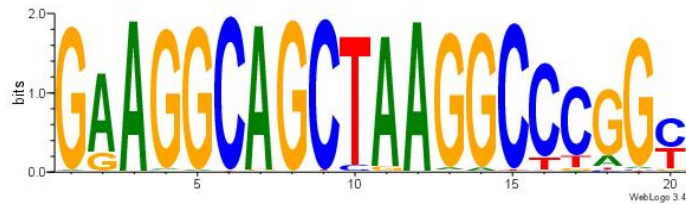
Dataset #: 1  
Motif ID: 64  
Motif name: Motif 64  
Matching format of first motif: Original Motif  
Matching format of second motif: Original Motif  
Direction: Forward  
Position number: 1  
Number of overlap: 19  
Similarity score: 0.111948

Alignment:

GAAGGCAGCTAAGGCCCGY  
GAATCCTGGGACAGCCTGT-

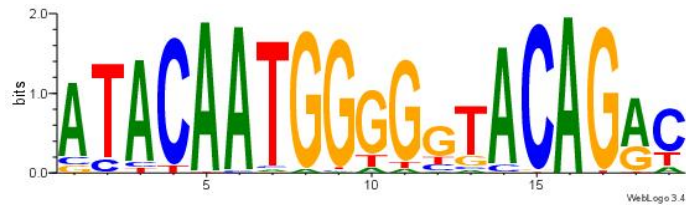
Original motif      Consensus sequence: GAAGGCAGCTAAGGCCCGY

Reverse complement motif      Consensus sequence:  
KCCGGGCCTTAGCTGCCTC

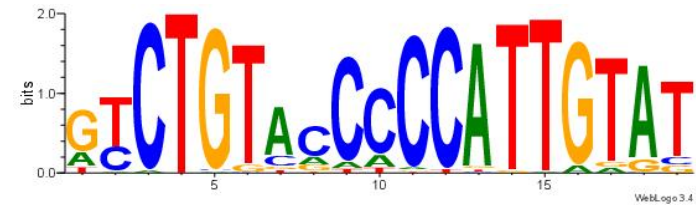


**Dataset #: 1      Motif ID: 193      Motif name: Motif 193**

Original motif      Consensus sequence: ATACAATGGGGTACAGRC



Reverse complement motif      Consensus sequence: GKCTGTACCCCATTTGTAT



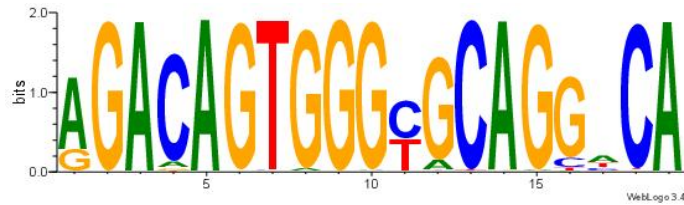
**Best Matches for Motif ID 193 (Highest to Lowest)**

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

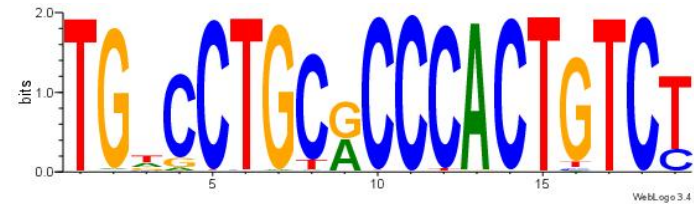
Alignment:

TGHCCTGCKCCCCTGTCT  
GKCTGTACCCCATTTGTAT

Original motif      Consensus sequence: AGACAGTGGGCGCAGGCA



Reverse complement motif      Consensus sequence:  
TGHCCTGCKCCCCTGTCT



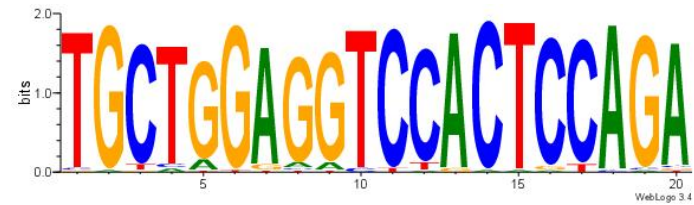
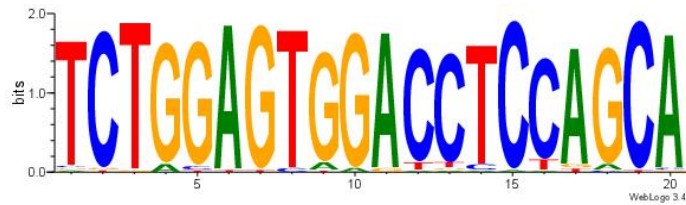
Dataset #: 1  
Motif ID: 350  
Motif name: Motif 350  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Reverse Complement  
Direction: Forward  
Position number: 1  
Number of overlap: 19  
Similarity score: 0.0979844

Alignment:  
TGCTGGAGGTCCACTCCAGA  
GKCTGTACCCCATTTGTAT-

Original motif      Consensus sequence: TCTGGAGTGGACCTCCAGCA

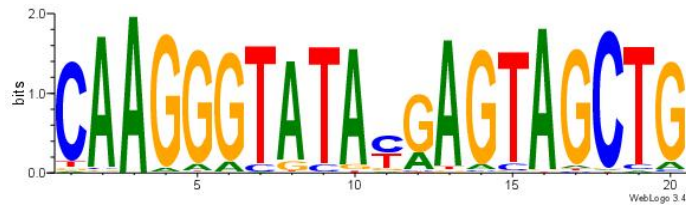
Reverse complement motif      Consensus sequence:  
TGCTGGAGGTCCACTCCAGA



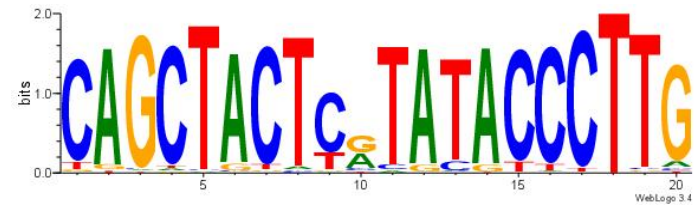


**Dataset #: 1      Motif ID: 194      Motif name: Motif 194**

Original motif      Consensus sequence: CAAGGGTATAYGAGTAGCTG



Reverse complement motif      Consensus sequence: CAGCTACTCKTATACCCTTG



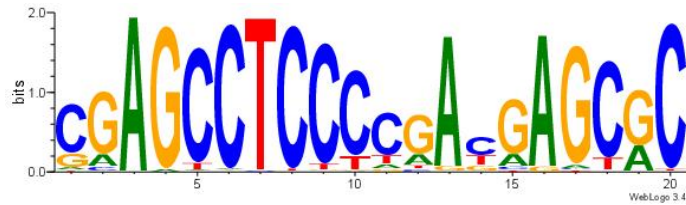
**Best Matches for Motif ID 194 (Highest to Lowest)**

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

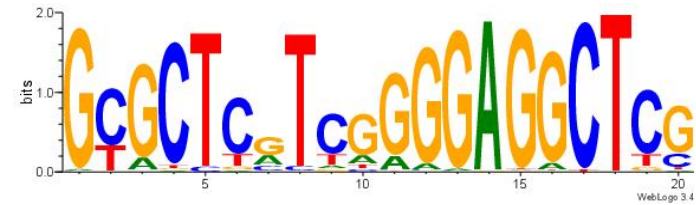
Alignment:

GCGCTCKTCGGGGAGGCTCG  
CAGCTACTCKTATACCCTTG

Original motif      Consensus sequence: CGAGCCTCCCCGAYGAGCGC



Reverse complement motif      Consensus sequence:  
GCGCTCKTCGGGGAGGCTCG



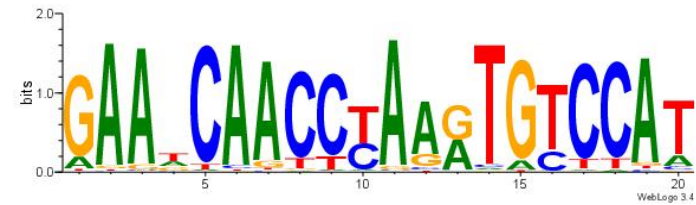
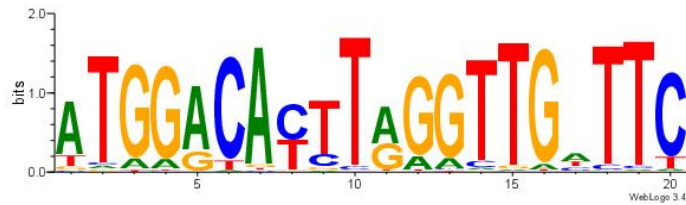
Dataset #:	1
Motif ID:	58
Motif name:	Motif 58
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2
Number of overlap:	19
Similarity score:	0.608266

Alignment:

-ATGGACAYTTRGGTTGHTTC  
CAAGGGTATAYGAGTAGCTG-

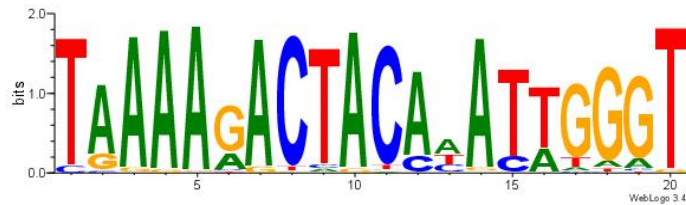
Original motif      Consensus sequence: ATGGACAYTTRGGTTGHTTC

Reverse complement motif      Consensus sequence:  
GAAHCAACCKAAKTGTCCAT

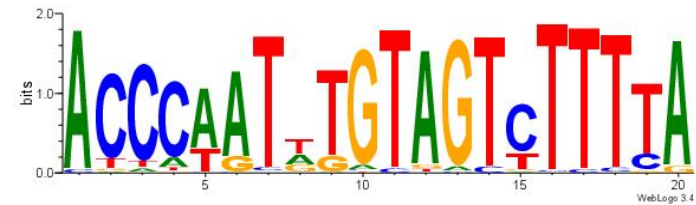


**Dataset #: 1      Motif ID: 195      Motif name: Motif 195**

Original motif      Consensus sequence: TAAAAGACTACAWATTGGGT



Reverse complement motif      Consensus sequence: ACCCAATWTGTAGTCTTTTA



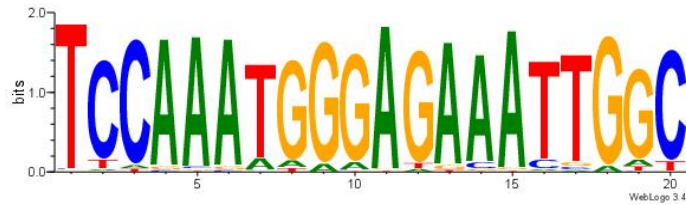
**Best Matches for Motif ID 195 (Highest to Lowest)**

Dataset #:	1
Motif ID:	235
Motif name:	Motif 235
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:	0.093741

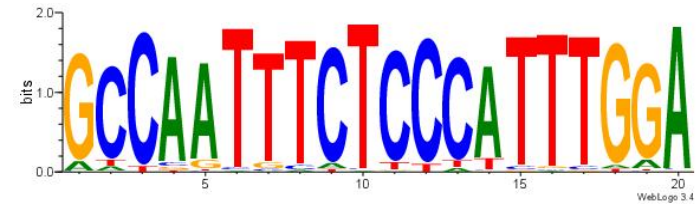
Alignment:

-GCCAATTTCTCCCATTTGGA  
ACCCAATWTGTAGTCTTTTA-

Original motif      Consensus sequence: TCCAATGGGAGAAATTGGC



Reverse complement motif      Consensus sequence:  
GCCAATTTCTCCCATTTGGA



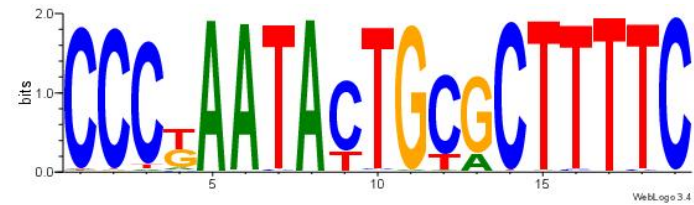
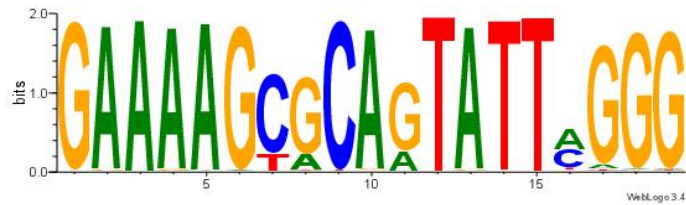
Dataset #:	1
Motif ID:	18
Motif name:	Motif 18
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	19
Similarity score:	0.0994352

Alignment:

-CCCYAATACTGCGCTTTTC  
ACCCAATWTGTAGTCTTTTA

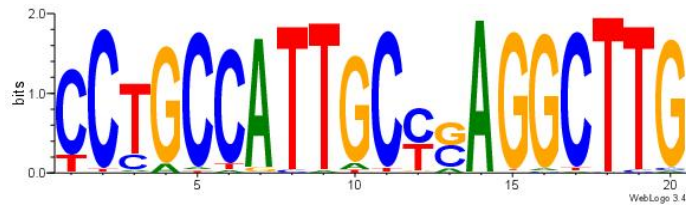
Original motif      Consensus sequence: GAAAAGCGCAGTATTMGGG

Reverse complement motif      Consensus sequence:  
CCCYAATACTGCGCTTTTC

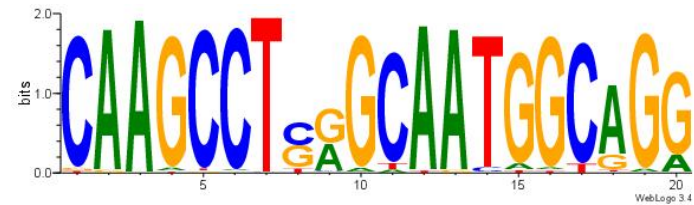


**Dataset #: 1      Motif ID: 196      Motif name: Motif 196**

Original motif      Consensus sequence: **CCTGCCATTGCYSAGGCTTG**



Reverse complement motif      Consensus sequence: **CAAGCCTSKGCAATGGCAGG**



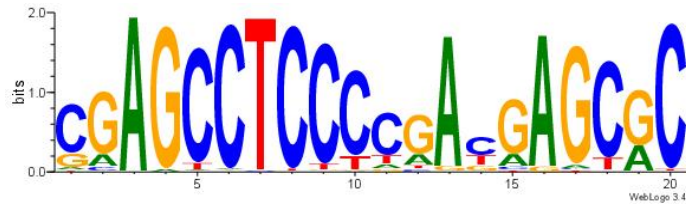
**Best Matches for Motif ID 196 (Highest to Lowest)**

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

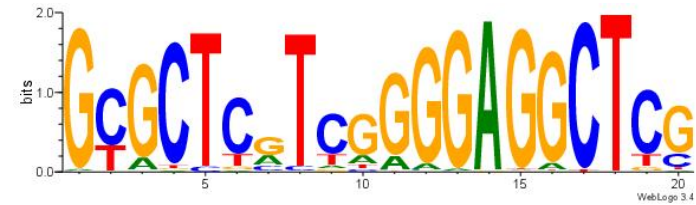
Alignment:

GCGCTCKTCGGGGAGGCTCG  
CCTGCCATTGCYSAGGCTTG

Original motif      Consensus sequence: CGAGCCTCCCCGAYGAGCGC



Reverse complement motif      Consensus sequence:  
GCGCTCKTCGGGGAGGCTCG



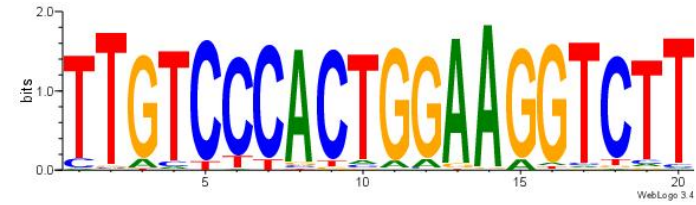
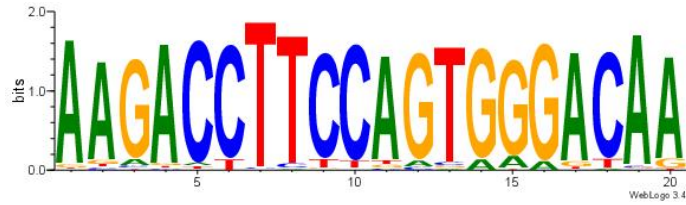
Dataset #:	1
Motif ID:	292
Motif name:	Motif 292
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2
Number of overlap:	19
Similarity score:	0.612012

Alignment:

-AAGACCTTCCAGTGGGACAA  
CAAGCCTSKGCAATGGCAGG-

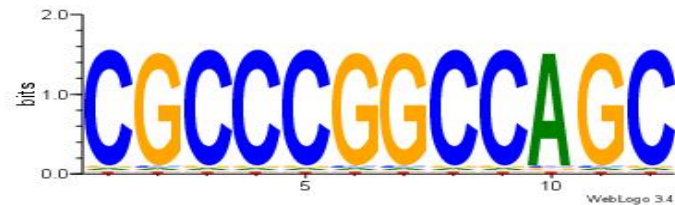
Original motif      Consensus sequence: AAGACCTTCCAGTGGGACAA

Reverse complement motif      Consensus sequence:  
TTGTCCCACTGGAAGGTCTT

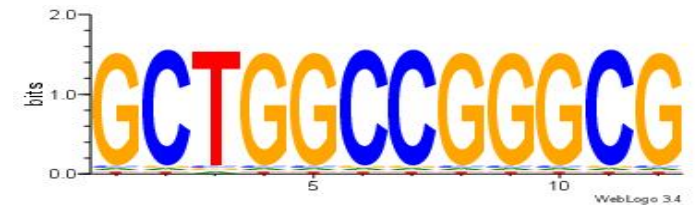


**Dataset #: 1      Motif ID: 197      Motif name: Motif 197**

Original motif      Consensus sequence: CGCCCGCCAGC



Reverse complement motif      Consensus sequence: GCTGGCCGGGCG

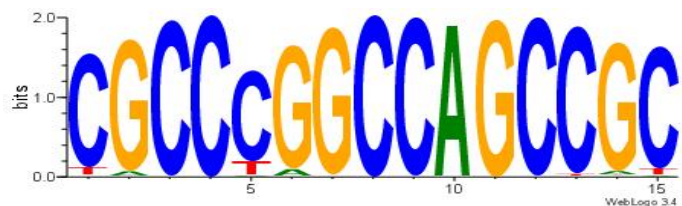


**Best Matches for Motif ID 197 (Highest to Lowest)**

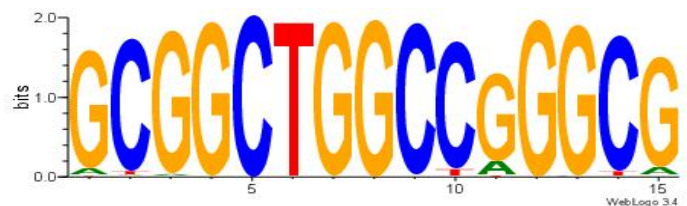
Dataset #:	1
Motif ID:	125
Motif name:	Motif 125
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	12
Similarity score:	0.0154405

Alignment:  
 CGCCCGCCAGCCGC  
 CGCCCGCCAGC---

Original motif      Consensus sequence: CGCCCGCCAGCCGC



Reverse complement motif      Consensus sequence: GCGGCTGGCCGGCG

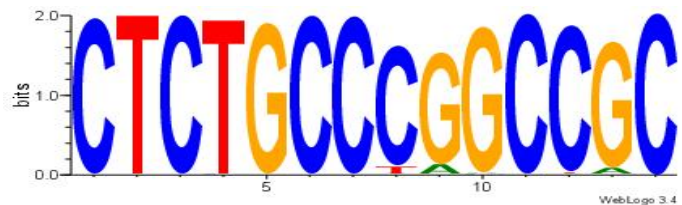


Dataset #: 1  
Motif ID: 42  
Motif name: Motif 42  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Original Motif  
Direction: Backward  
Position number: 2  
Number of overlap: 12  
Similarity score: 0.0710698

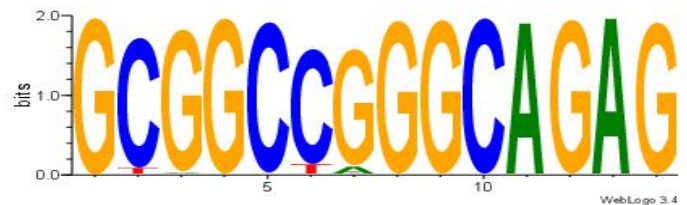
Alignment:

CTCTGCCCGGCCGC  
-GCTGGCCGGGCG-

Original motif      Consensus sequence: CTCTGCCCGGCCGC



Reverse complement motif      Consensus sequence: GCGGCCGGGCAG



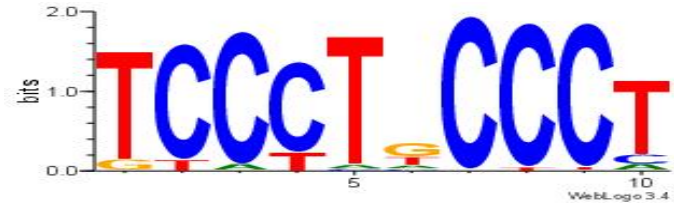


**Dataset #: 1      Motif ID: 198      Motif name: Motif 198**

Original motif      Consensus sequence: AGGGMAGGGA



Reverse complement motif      Consensus sequence: TCCCTRCCCT



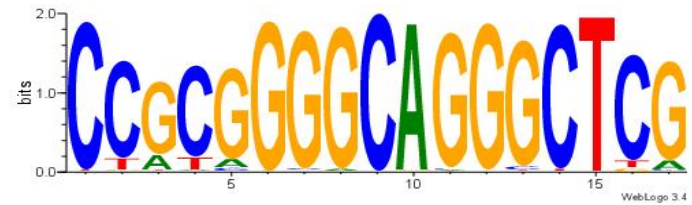
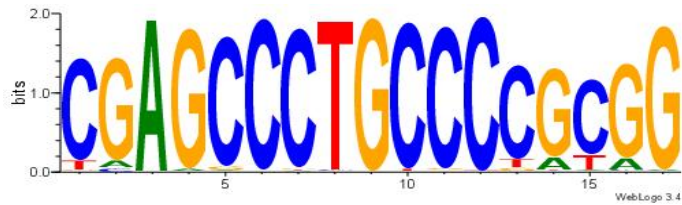
**Best Matches for Motif ID 198 (Highest to Lowest)**

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

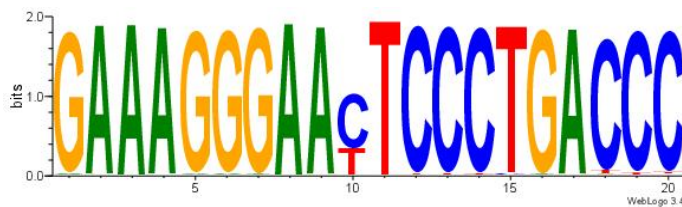
Reverse complement motif      Consensus sequence:  
CCGCGGGGCAGGGCTCG



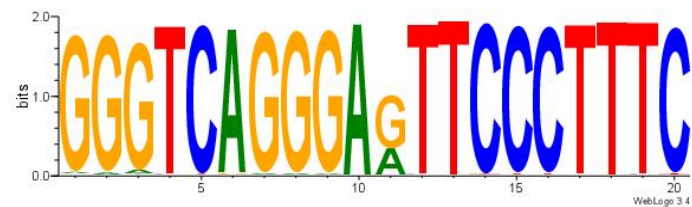
Dataset #: 1  
 Motif ID: 16  
 Motif name: Motif 16  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 10  
 Similarity score: 0.0554968

Alignment:  
 GAAAGGGA ACTCCCTGACCC  
 TCCCTRCCCT-----

Original motif      Consensus sequence: GAAAGGGA ACTCCCTGACCC

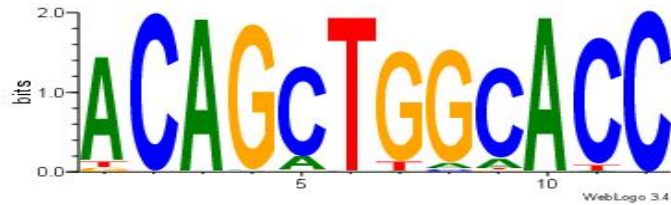


Reverse complement motif      Consensus sequence: GGGTCAGGGAGTTCCCTTTC

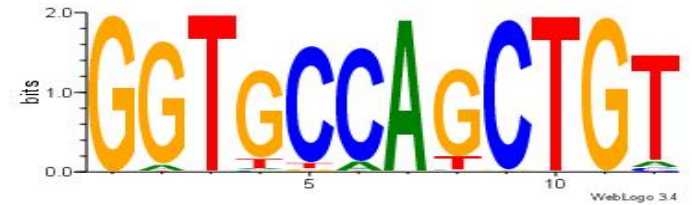


**Dataset #: 1      Motif ID: 199      Motif name: Motif 199**

Original motif      Consensus sequence: ACAGCTGGCACC



Reverse complement motif      Consensus sequence: GGTGCCAGCTGT



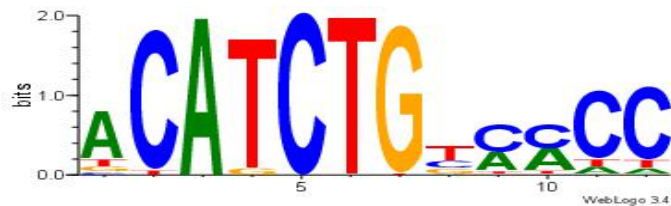
### Best Matches for Motif ID 199 (Highest to Lowest)

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

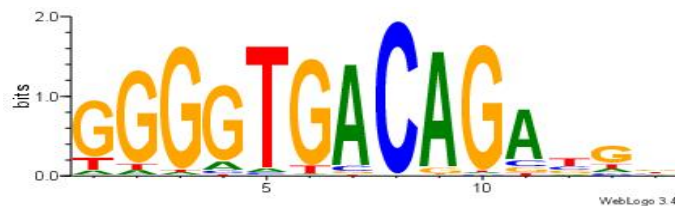


Dataset #: 1  
 Motif ID: 1  
 Motif name: Motif 1  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 12  
 Similarity score: 0.0698583

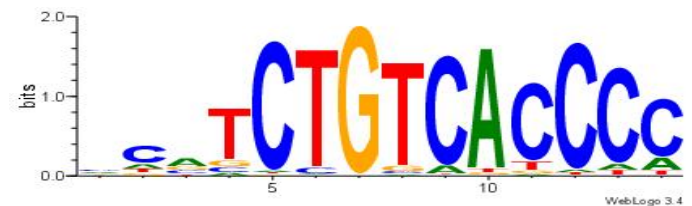
Alignment:

BCVTCTGTCACCCC  
 --ACAGCTGGCACC

Original motif      Consensus sequence: GGGGTGACAGABGB

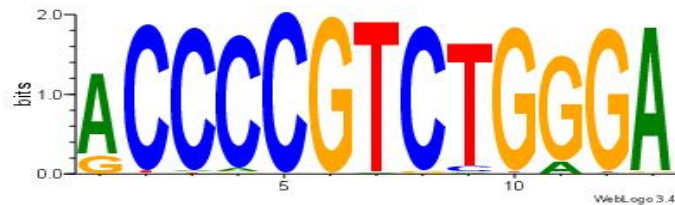


Reverse complement motif      Consensus sequence: BCVTCTGTCACCCC

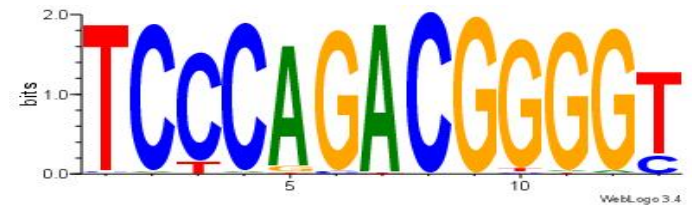


**Dataset #: 1      Motif ID: 200      Motif name: Motif 200**

Original motif      Consensus sequence: ACCCGTCTGGGA



Reverse complement motif      Consensus sequence: TCCAGACGGGGT



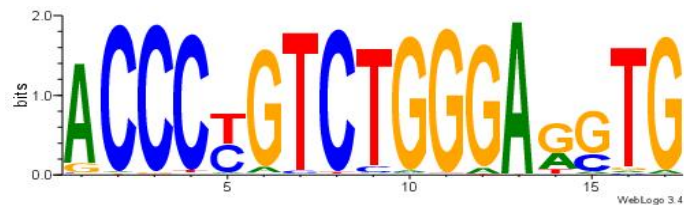
## Best Matches for Motif ID 200 (Highest to Lowest)

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

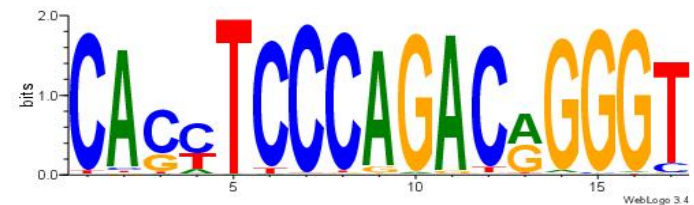
### Alignment:

```
ACCCYGTCTGGGAGGTG  
ACCCCGTCTGGGA-----
```

Original motif      Consensus sequence: ACCCYGTCTGGGAGGTG



Reverse complement motif      Consensus sequence:  
CACCTCCCAGACMGGGT



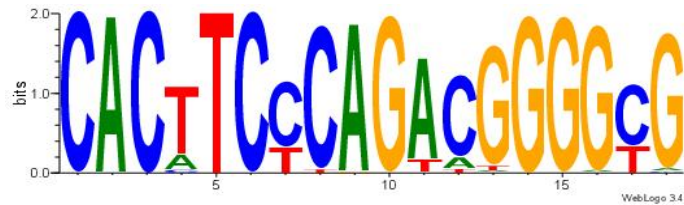
---

Dataset #: 1  
Motif ID: 27  
Motif name: Motif 27  
Matching format of first motif: Original Motif  
Matching format of second motif: Reverse Complement

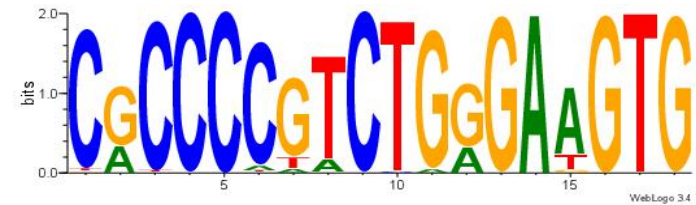
Direction: Forward  
 Position number: 5  
 Number of overlap: 13  
 Similarity score: 0.0207173

Alignment:  
 CGCCCCGTCTGGGAAGTG  
 ----ACCCCGTCTGGGA--

Original motif      Consensus sequence: CACTTCCCAGACGGGGCG

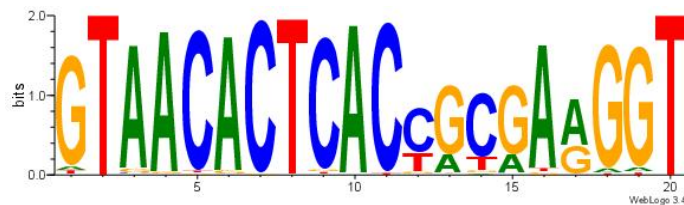


Reverse complement motif      Consensus sequence: CGCCCCGTCTGGGAAGTG

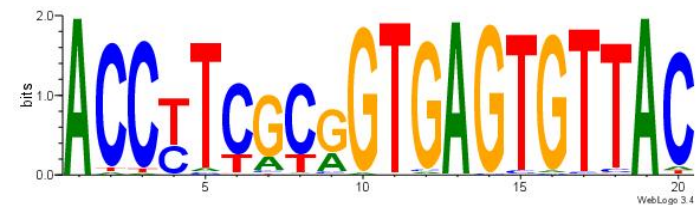


**Dataset #: 1      Motif ID: 201      Motif name: Motif 201**

Original motif      Consensus sequence: GTAACACTCACCGCGARGGT



Reverse complement motif      Consensus sequence: ACCKTCGCGGTGAGTGTTAC



**Best Matches for Motif ID 201 (Highest to Lowest)**

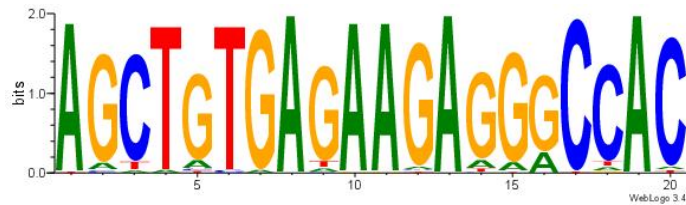
Dataset #: 1

Motif ID: 294  
 Motif name: Motif 294  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 20  
 Similarity score: 0.11338

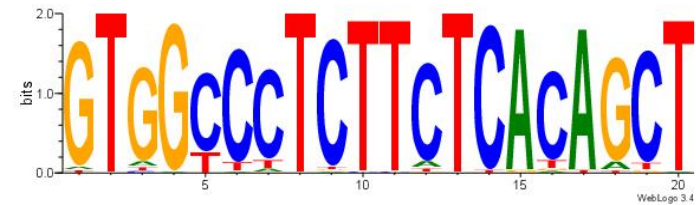
**Alignment:**

GTGGCCCTCTTCTCACAGCT  
 GTAACACTCACCGCGARGGT

Original motif    Consensus sequence: AGCTGTGAGAAGAGGGCCAC



Reverse complement motif    Consensus sequence: GTGGCCCTCTTCTCACAGCT



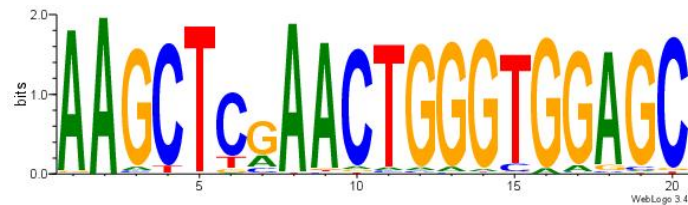
Dataset #: 1  
 Motif ID: 321  
 Motif name: Motif 321  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 20

Similarity score: 0.114848

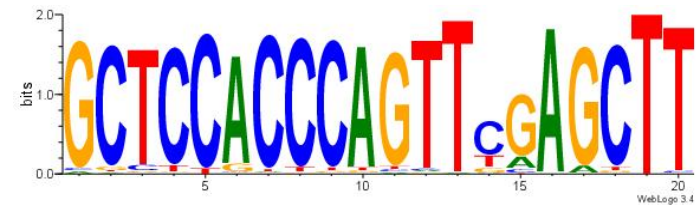
Alignment:

GCTCCACCCAGTTCGAGCTT  
GTAACACTCACCGCGARGGT

Original motif      Consensus sequence: AAGCTCGAACTGGGTGGAGC

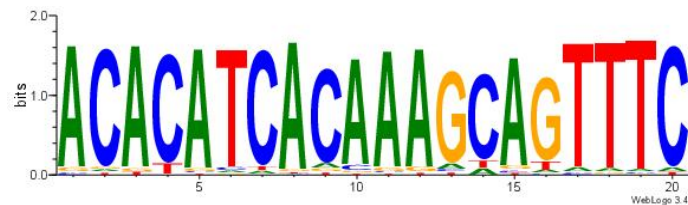


Reverse complement motif      Consensus sequence:  
GCTCCACCCAGTTCGAGCTT

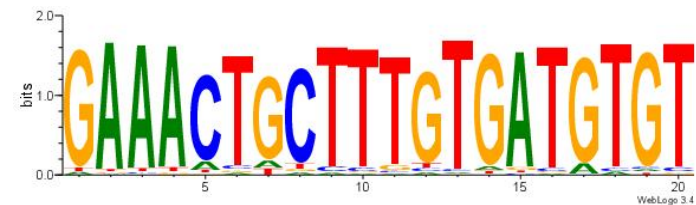


**Dataset #: 1      Motif ID: 202      Motif name: Motif 202**

Original motif      Consensus sequence: ACACATCACAAAGCAGTTTC



Reverse complement motif      Consensus sequence:  
GAAACTGCTTTGTGATGTGT



**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

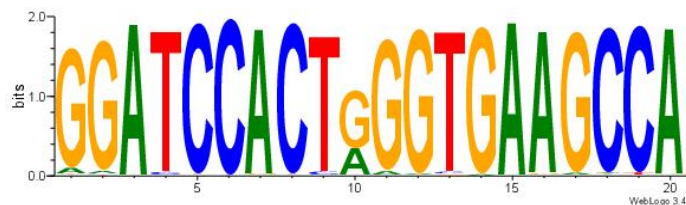


Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	20
Similarity score:	0.117486

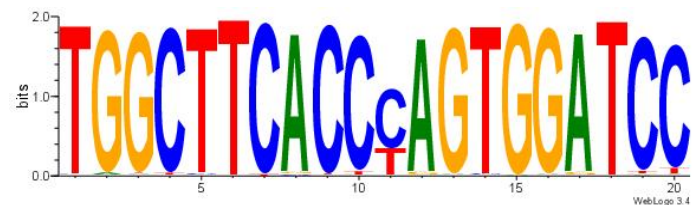
Alignment:

```
GGATCCACTGGGTGAAGCCA
GAAACTGCTTTGTGATGTGT
```

Original motif      Consensus sequence: GGATCCACTGGGTGAAGCCA



Reverse complement motif      Consensus sequence: TGGCTTCACCCAGTGGATCC

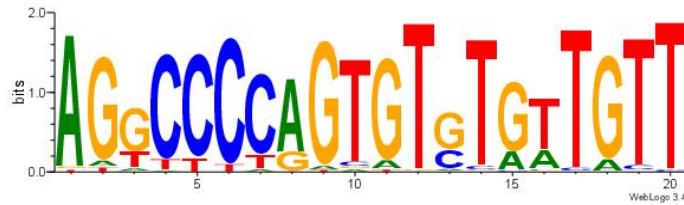


Dataset #:	1
Motif ID:	176
Motif name:	Motif 176
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2
Number of overlap:	19
Similarity score:	0.607495

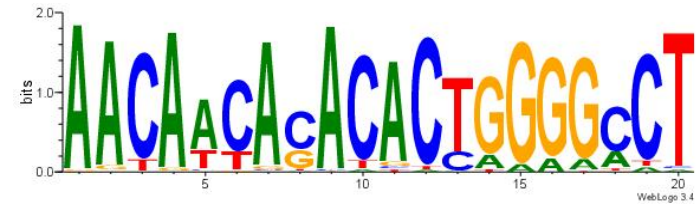
Alignment:

-AGGCCCCAGTGTSTGTTGTT  
 GAAACTGCTTTGTGATGTGT-

Original motif    Consensus sequence: AGGCCCCAGTGTSTGTTGTT



Reverse complement motif    Consensus sequence: AACACASACACTGGGGCCT



**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)**

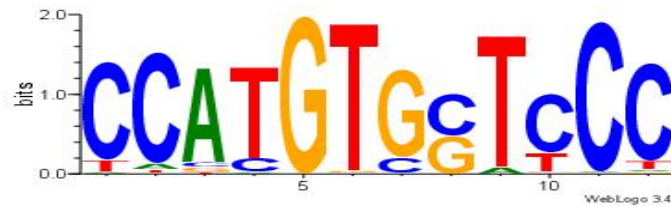
Dataset #:	1
Motif ID:	120
Motif name:	Motif 120
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	2
Number of overlap:	11

Similarity score: 0.0640975

Alignment:

GGGASCACATGG  
-GGACGCCATGG

Original motif      Consensus sequence: CCATGTGSTCCC



Reverse complement motif      Consensus sequence: GGGASCACATGG



---

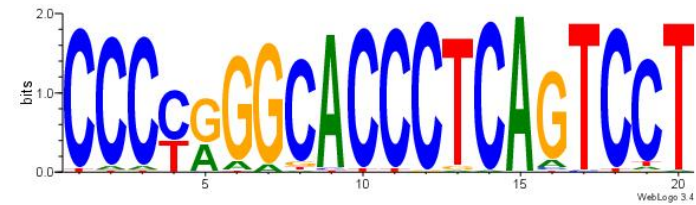
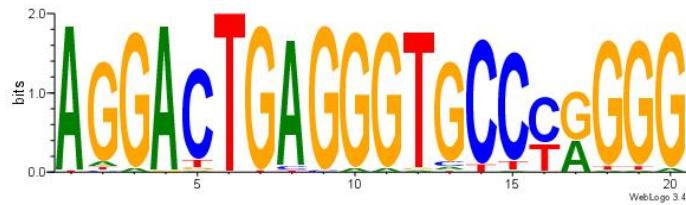
Dataset #: 1  
Motif ID: 312  
Motif name: Motif 312  
Matching format of first motif: Original Motif  
Matching format of second motif: Reverse Complement  
Direction: Backward  
Position number: 9  
Number of overlap: 11  
Similarity score: 0.0662761

Alignment:

CCCMKGGCACCCTCAGTCCT  
-CCATGGCGTCC-----

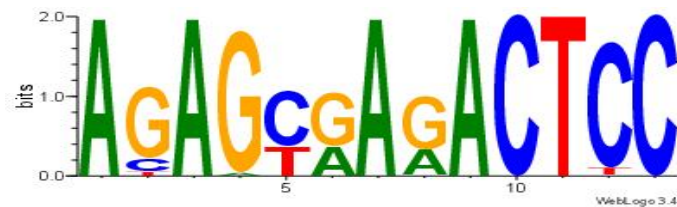
Original motif      Consensus sequence: AGGACTGAGGGTGCCYRGGG

Reverse complement motif      Consensus sequence:  
CCCMKGGCACCCTCAGTCCT

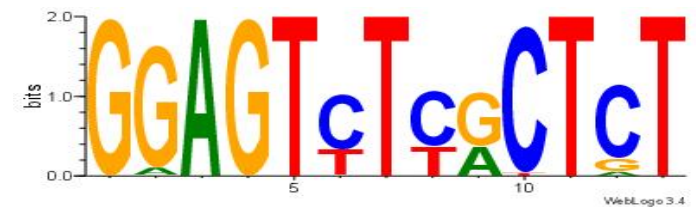


**Dataset #: 1      Motif ID: 204      Motif name: Motif 204**

Original motif      Consensus sequence: AGAGYRAGACTCC



Reverse complement motif      Consensus sequence: GGAGTCMKCTCT

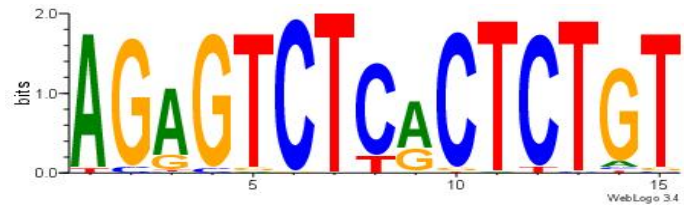


**Best Matches for Motif ID 204 (Highest to Lowest)**

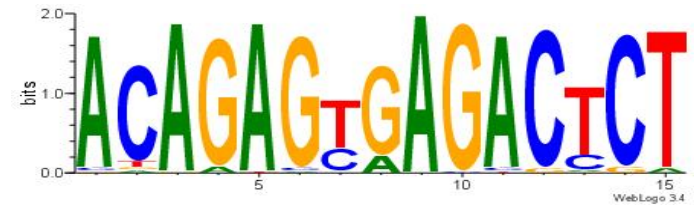
Dataset #:	1
Motif ID:	253
Motif name:	Motif 253
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	3
Number of overlap:	13
Similarity score:	0.0513045

Alignment:  
ACAGAGTGAGACTCT  
--AGAGYRAGACTCC

Original motif      Consensus sequence: AGAGTCTCACTCTGT



Reverse complement motif      Consensus sequence: ACAGAGTGAGACT

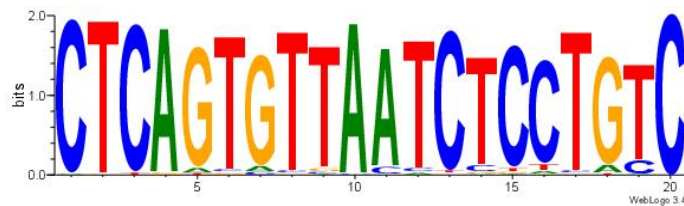


Dataset #: 1  
Motif ID: 262  
Motif name: Motif 262  
Matching format of first motif: Original Motif  
Matching format of second motif: Original Motif  
Direction: Forward  
Position number: 4  
Number of overlap: 13  
Similarity score: 0.0874128

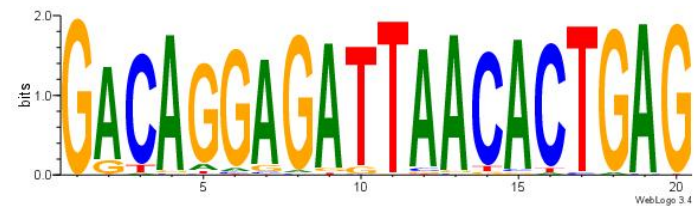
Alignment:

CTCAGTGTTAATCTCCTGTC  
---AGAGYRAGACTCC----

Original motif      Consensus sequence: CTCAGTGTTAATCTCCTGTC

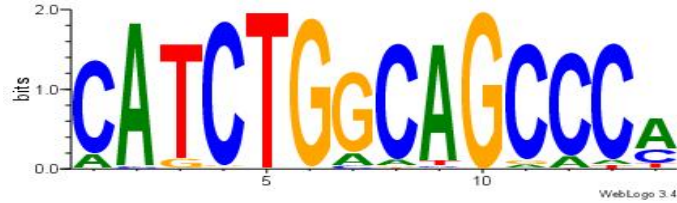


Reverse complement motif      Consensus sequence: GACAGGAGATTAACACTGAG

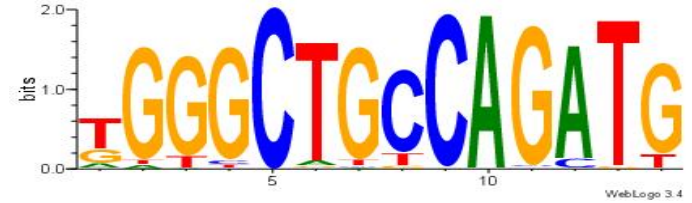


**Dataset #: 1      Motif ID: 205      Motif name: Motif 205**

Original motif      Consensus sequence: CATCTGGCAGCCCA



Reverse complement motif      Consensus sequence: TGGGCTGCCAGAT



**Best Matches for Motif ID 205 (Highest to Lowest)**

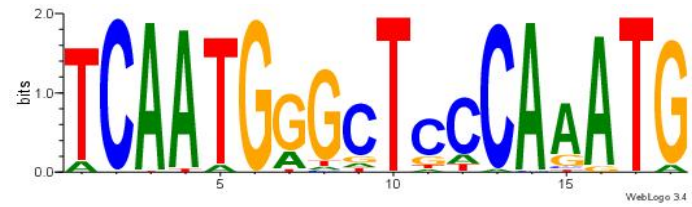
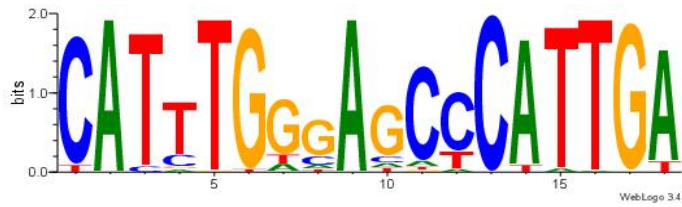
Dataset #:	1
Motif ID:	284
Motif name:	Motif 284
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	5
Number of overlap:	14
Similarity score:	0.036398

**Alignment:**

```
CATTTGGGAGCCCATTGA
CATCTGGCAGCCCA-----
```

Original motif      Consensus sequence: CATTTGGGAGCCCATTGA

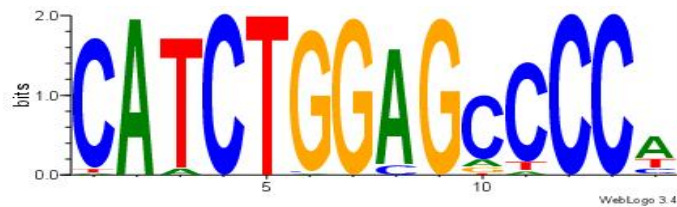
Reverse complement motif      Consensus sequence:  
TCAATGGGCTCCCAAATG



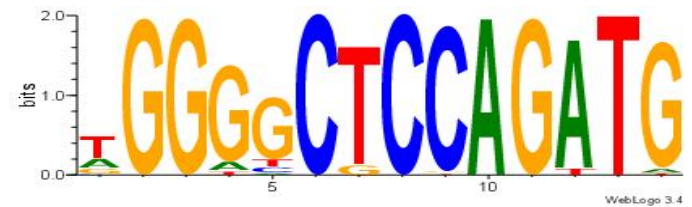
Dataset #: 1  
 Motif ID: 320  
 Motif name: Motif 320  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 14  
 Similarity score: 0.0491079

Alignment:  
 CATCTGGAGCCCCA  
 CATCTGGCAGCCCCA

Original motif      Consensus sequence: CATCTGGAGCCCCA

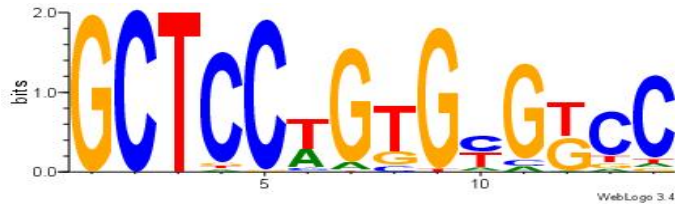


Reverse complement motif      Consensus sequence: TGGGGCTCCAGATG

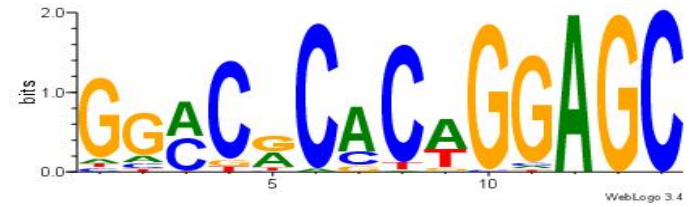


**Dataset #: 1      Motif ID: 206      Motif name: Motif 206**

Original motif      Consensus sequence: GCTCCWGTGYGKCC



Reverse complement motif      Consensus sequence: GGRCKCACWGGAA



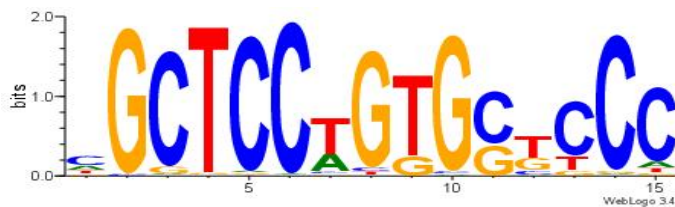
### Best Matches for Motif ID 206 (Highest to Lowest)

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

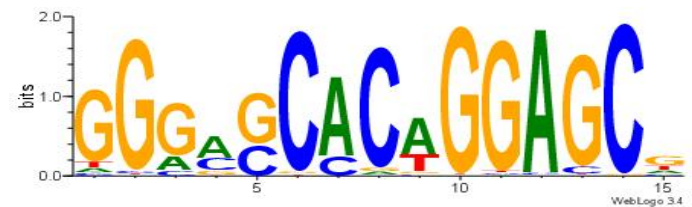
Alignment:

```
GGGRSCACAGGAGCD
GGRCKCACWGGAGC-
```

Original motif      Consensus sequence: HGCTCCTGTGSKCCC



Reverse complement motif      Consensus sequence: GGRSCACAGGAGCD



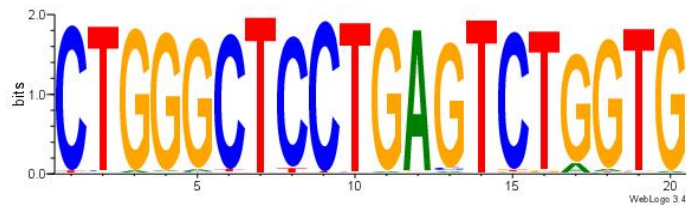


Dataset #: 1  
 Motif ID: 67  
 Motif name: Motif 67  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 3  
 Number of overlap: 14  
 Similarity score: 0.0894523

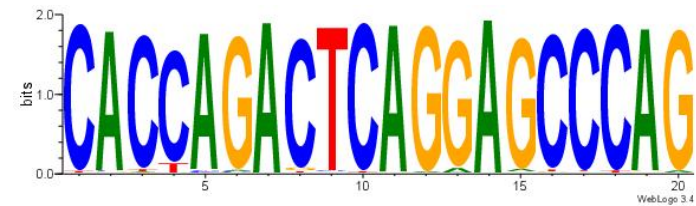
Alignment:

CTGGGCTCCTGAGTCTGGTG  
 ----GCTCCWGTGYGKCC--

Original motif      Consensus sequence: CTGGGCTCCTGAGTCTGGTG



Reverse complement motif      Consensus sequence: CACCAGACTCAGGAGCCCAG

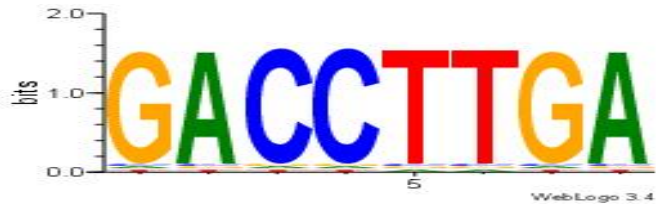



---

**Dataset #: 1      Motif ID: 207      Motif name: Motif 207**

Original motif      Consensus sequence: GACCTTGA

Reverse complement motif      Consensus sequence: TCAAGGTC

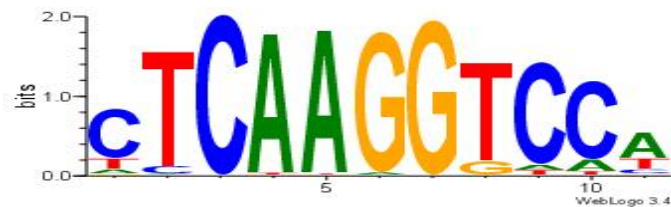


### Best Matches for Motif ID 207 (Highest to Lowest)

Dataset #: 1  
 Motif ID: 11  
 Motif name: Motif 11  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 3  
 Number of overlap: 8  
 Similarity score: 0.0145765

Alignment:  
 CTCAAGGTCCA  
 --TCAAGGTC--

Original motif      Consensus sequence: CTCAAGGTCCA



Reverse complement motif      Consensus sequence: TGGACCTTGAG

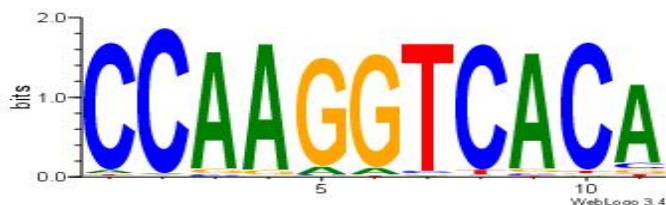


Dataset #: 1

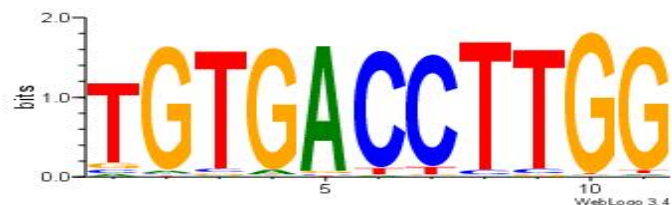
Motif ID: 264  
 Motif name: Motif 264  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 8  
 Similarity score: 0.0364604

Alignment:  
 TGTGACCTTGG  
 ---GACCTTGA

Original motif    Consensus sequence: CCAAGGTCACA

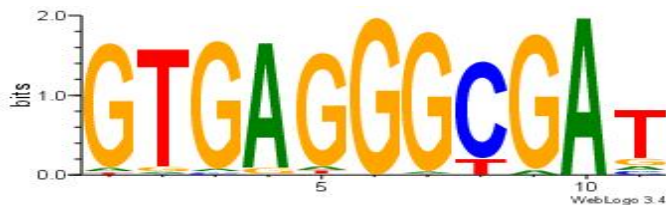


Reverse complement motif    Consensus sequence: TGTGACCTTGG



**Dataset #: 1      Motif ID: 208      Motif name: Motif 208**

Original motif    Consensus sequence: GTGAGGGCGAT



Reverse complement motif    Consensus sequence: ATGCCCTCAC



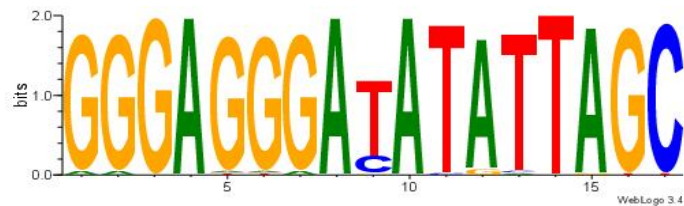
## Best Matches for Motif ID 208 (Highest to Lowest)

Dataset #: 1  
Motif ID: 329  
Motif name: Motif 329  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Reverse Complement  
Direction: Backward  
Position number: 1  
Number of overlap: 11  
Similarity score: 0.0622115

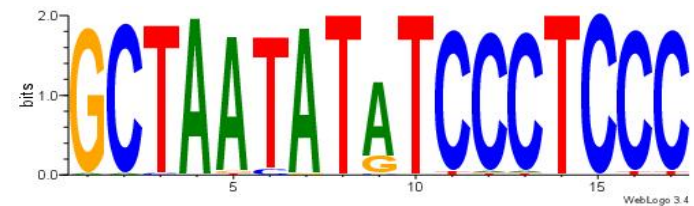
### Alignment:

```
GCTAATATATCCCTCCC  
-----ATCGCCCTCAC
```

Original motif      Consensus sequence: GGGAGGGATATATTAGC



Reverse complement motif      Consensus sequence:  
GCTAATATATCCCTCCC



---

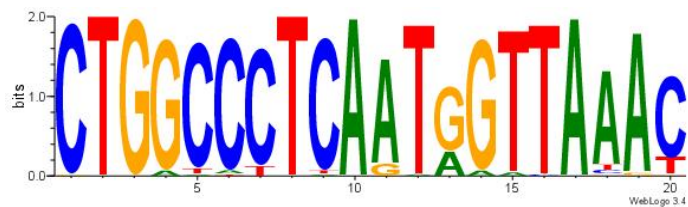
Dataset #: 1  
Motif ID: 332  
Motif name: Motif 332  
Matching format of first motif: Original Motif  
Matching format of second motif: Reverse Complement

Direction: Forward  
 Position number: 10  
 Number of overlap: 11  
 Similarity score: 0.0654927

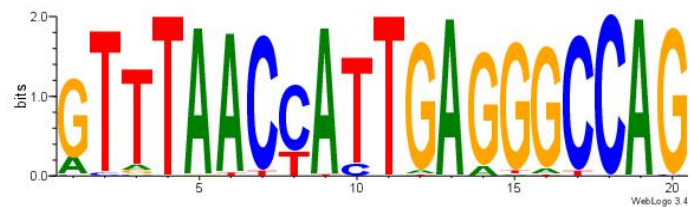
Alignment:

GTTTAACCATTGAGGGCCAG  
 -----GTGAGGGCGAT

Original motif      Consensus sequence: CTGGCCCTCAATGGTTAAAC



Reverse complement motif      Consensus sequence: GTTTAACcATTGAGGGCCAG

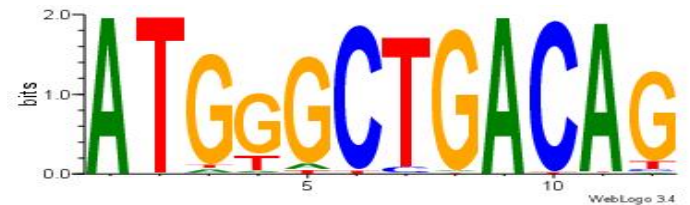


**Dataset #: 1      Motif ID: 209      Motif name: Motif 209**

Original motif      Consensus sequence: CTGTCAGCCCAT



Reverse complement motif      Consensus sequence: ATGGGCTGACAG



**Best Matches for Motif ID 209 (Highest to Lowest)**

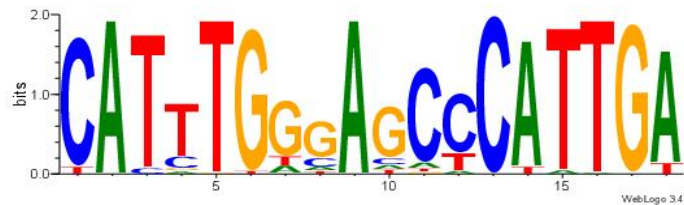
Dataset #: 1  
 Motif ID: 284

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

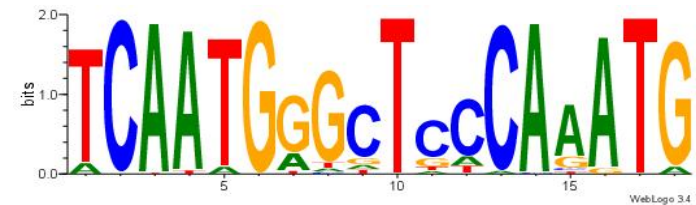
**Alignment:**

CATTGGGAGCCCATTGA  
 ---CTGTCAGCCCAT---

Original motif    Consensus sequence: CATTGGGAGCCCATTGA



Reverse complement motif    Consensus sequence: TCAATGGGCTCCCAAATG

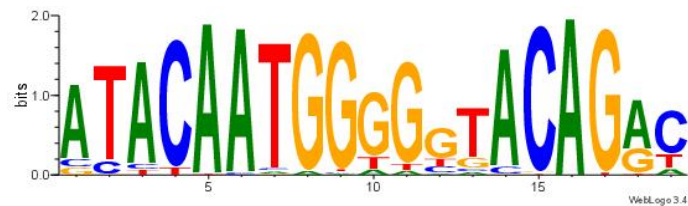


Dataset #: 1  
 Motif ID: 193  
 Motif name: Motif 193  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 6  
 Number of overlap: 12  
 Similarity score: 0.0594073

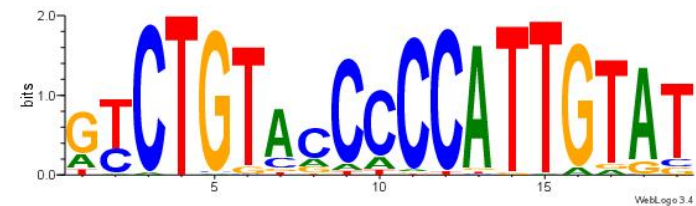
Alignment:

```
GKCTGTACCCCCATTGTAT
-----CTGTCAGCCCAT--
```

Original motif      Consensus sequence: ATACAATGGGGGTACAGRC

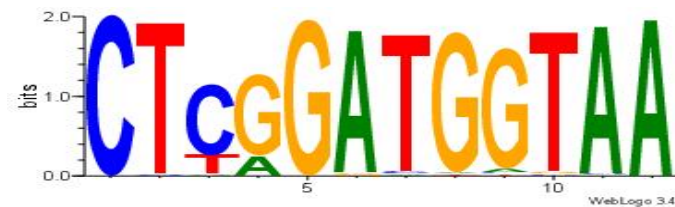


Reverse complement motif      Consensus sequence: GKCTGTACCCCCATTGTAT

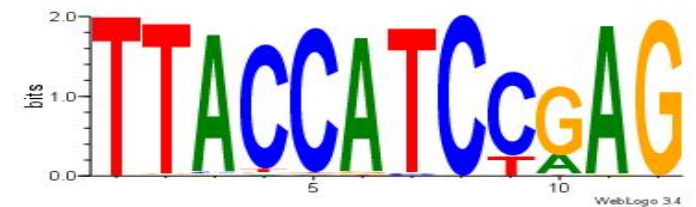


**Dataset #: 1      Motif ID: 210      Motif name: Motif 210**

Original motif      Consensus sequence: CTCGGATGGTAA



Reverse complement motif      Consensus sequence: TTACCATCCGAG



**Best Matches for Motif ID 210 (Highest to Lowest)**

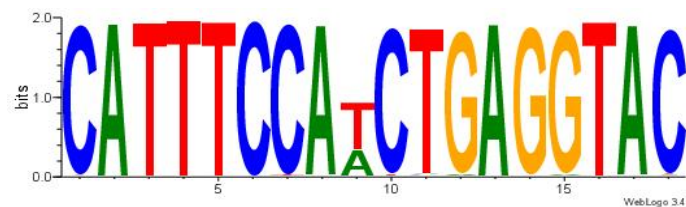
Dataset #:	1
Motif ID:	25
Motif name:	Motif 25
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward

Position number: 3  
Number of overlap: 12  
Similarity score: 0.0447432

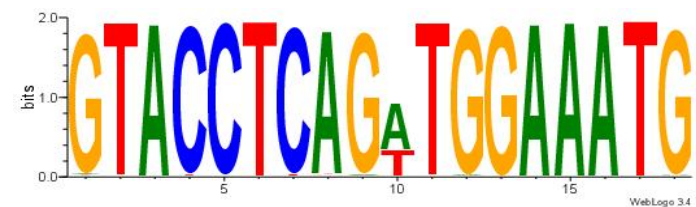
Alignment:

CATTTCCAWCTGAGGTAC  
-----TTACCATCCGAG--

Original motif      Consensus sequence: CATTTCCAWCTGAGGTAC



Reverse complement motif      Consensus sequence:  
GTACCTCAGWTGGAAATG



---

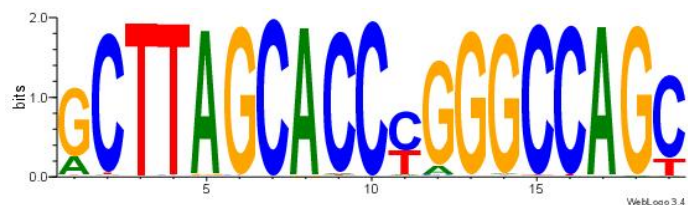
Dataset #: 1  
Motif ID: 82  
Motif name: Motif 82  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Original Motif  
Direction: Backward  
Position number: 3  
Number of overlap: 12  
Similarity score: 0.0679752

Alignment:

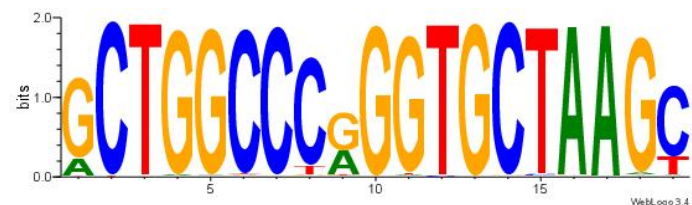
GCTTAGCACCYGGGCCAGC  
-----TTACCATCCGAG--



Original motif      Consensus sequence: GCTTAGCACCYGGGCCAGC

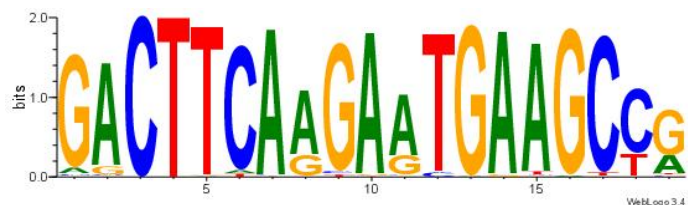


Reverse complement motif      Consensus sequence: GCTGGCCCKGGTGCTAAGC

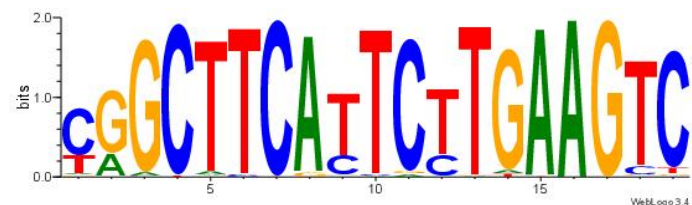


**Dataset #: 1      Motif ID: 211      Motif name: Motif 211**

Original motif      Consensus sequence: GACTTCAAGAATGAAGCCG



Reverse complement motif      Consensus sequence: CGGCTTCATTCTTGAAGTC



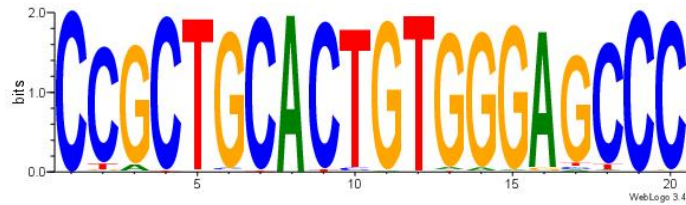
### Best Matches for Motif ID 211 (Highest to Lowest)

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

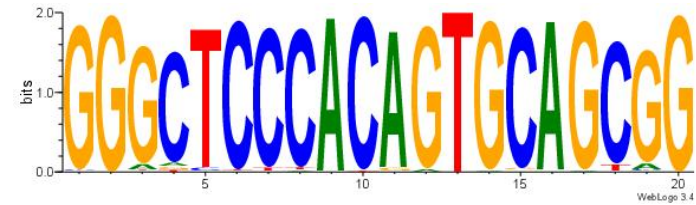
Alignment:

CCGCTGCACTGTGGGAGCCC  
-CGGCTTCATTCTTGAAGTC

Original motif      Consensus sequence: CCGCTGCACTGTGGGAGCCC



Reverse complement motif      Consensus sequence:  
GGGCTCCCACAGTGCAGCGG



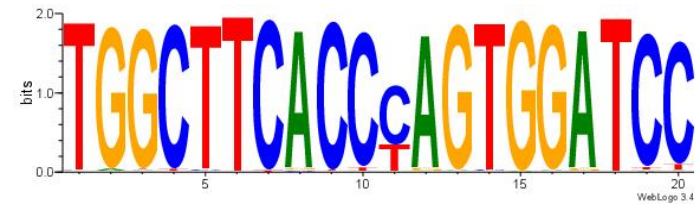
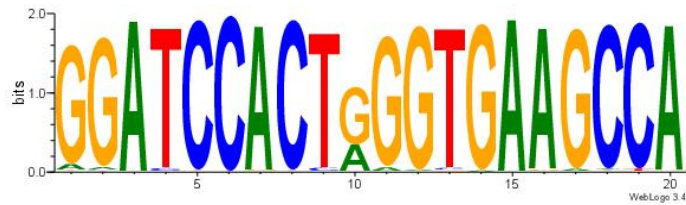
Dataset #: 1  
Motif ID: 61  
Motif name: Motif 61  
Matching format of first motif: Original Motif  
Matching format of second motif: Original Motif  
Direction: Forward  
Position number: 2  
Number of overlap: 19  
Similarity score: 0.109235

Alignment:

GGATCCACTGGGTGAAGCCA  
-GACTTCAAGAATGAAGCCG

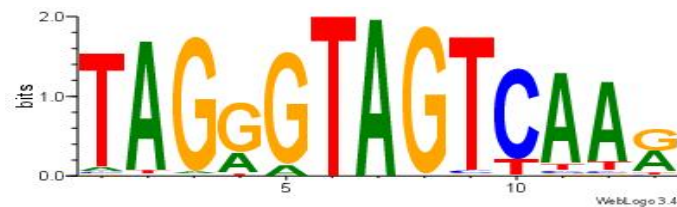
Original motif      Consensus sequence: GGATCCACTGGGTGAAGCCA

Reverse complement motif      Consensus sequence:  
TGGCTTCAACCCAGTGGATCC

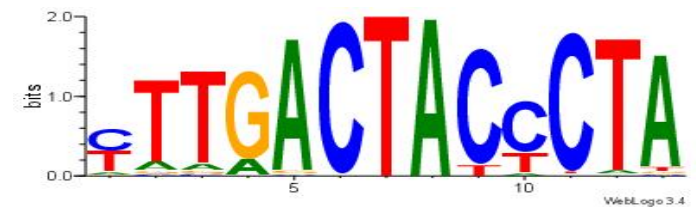


**Dataset #: 1      Motif ID: 212      Motif name: Motif 212**

Original motif      Consensus sequence: TAGGGTAGTCAAR



Reverse complement motif      Consensus sequence: MTTGACTACCCTA



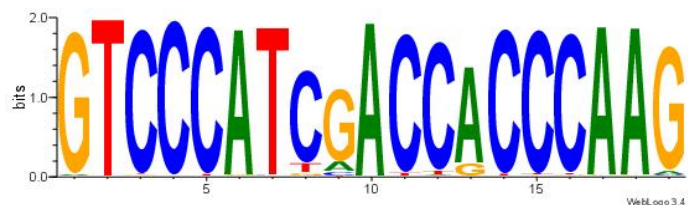
**Best Matches for Motif ID 212 (Highest to Lowest)**

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

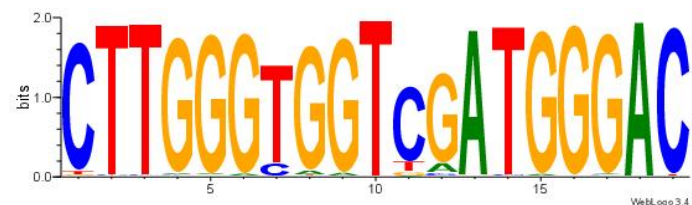
**Alignment:**

```
CTTGGGTGGTCGATGGGAC
-----TAGGGTAGTCAAR-
```

Original motif      Consensus sequence: GTCCCATCGACCACCCAAG



Reverse complement motif      Consensus sequence: CTTGGGTGGTTCGATGGGAC

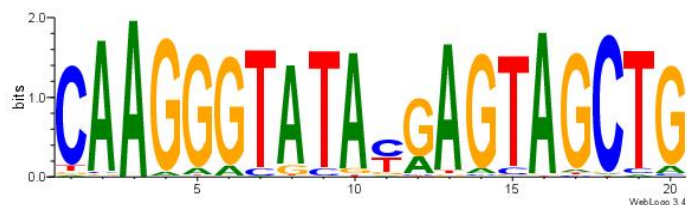


Dataset #: 1  
Motif ID: 194  
Motif name: Motif 194  
Matching format of first motif: Original Motif  
Matching format of second motif: Original Motif  
Direction: Forward  
Position number: 2  
Number of overlap: 13  
Similarity score: 0.0722477

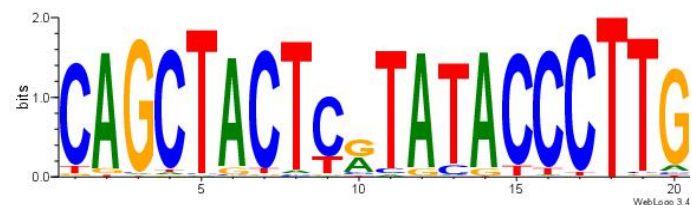
Alignment:

CAAGGGTATAYGAGTAGCTG  
-TAGGGTAGTCAAR-----

Original motif      Consensus sequence: CAAGGGTATAYGAGTAGCTG

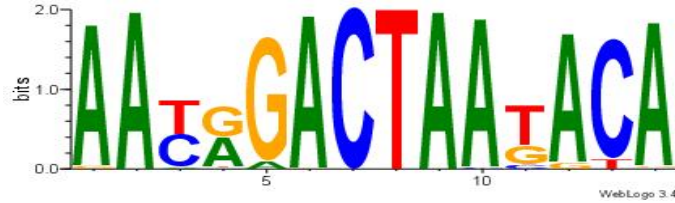


Reverse complement motif      Consensus sequence: CAGCTACTCKTATACCCTTG

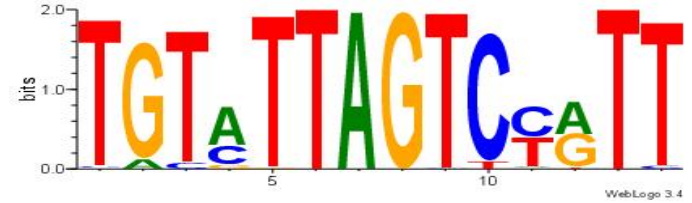


**Dataset #: 1      Motif ID: 213      Motif name: Motif 213**

Original motif      Consensus sequence: AAYRGACTAATACA



Reverse complement motif      Consensus sequence: TGTATTAGTCMMT



**Best Matches for Motif ID 213 (Highest to Lowest)**

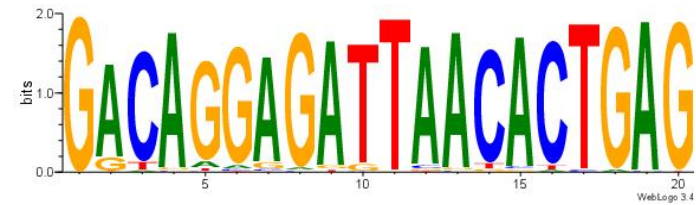
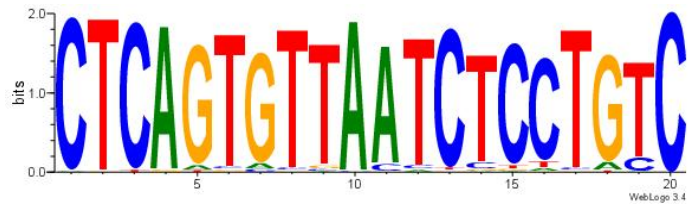
Dataset #:	1
Motif ID:	262
Motif name:	Motif 262
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	4
Number of overlap:	14
Similarity score:	0.0676805

**Alignment:**

```
CTCAGTGTTAATCTCCTGTC
---TGTATTAGTCMMTT---
```

Original motif      Consensus sequence: CTCAGTGTTAATCTCCTGTC

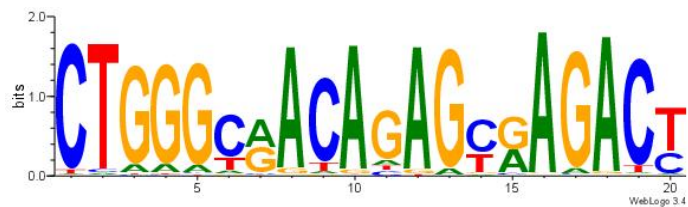
Reverse complement motif      Consensus sequence:  
GACAGGAGATTAACACTGAG



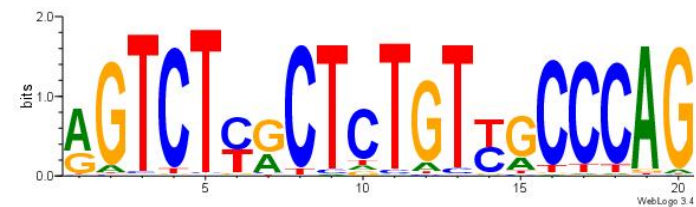
Dataset #: 1  
 Motif ID: 29  
 Motif name: Motif 29  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 7  
 Number of overlap: 14  
 Similarity score: 0.0742206

Alignment:  
 CTGGGCRACAGAGYRAGACY  
 -----AAYRGACTAATACA

Original motif      Consensus sequence: CTGGGCRACAGAGYRAGACY

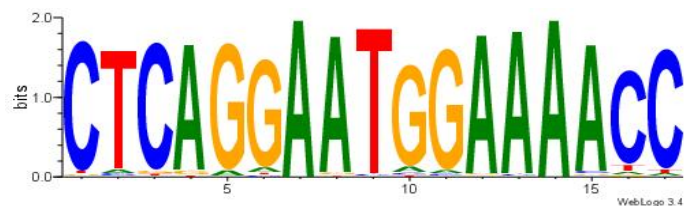


Reverse complement motif      Consensus sequence: MGTCTMKCTCTGKGCCAG

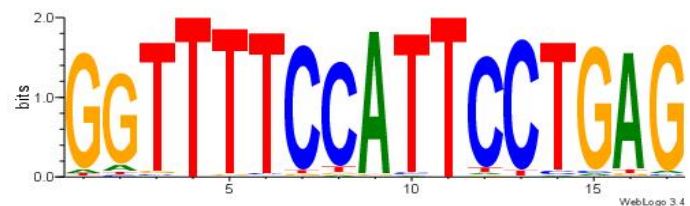


**Dataset #: 1      Motif ID: 214      Motif name: Motif 214**

Original motif      Consensus sequence: CTCAGGAATGGAAAACC



Reverse complement motif      Consensus sequence: GGTTTCCATTCCCTGAG



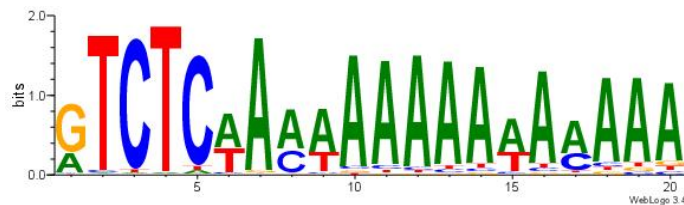
### Best Matches for Motif ID 214 (Highest to Lowest)

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

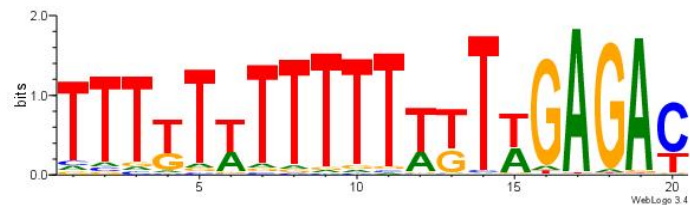
#### Alignment:

```
TTTTWTTTTTTTTWTGAGAC  
-GGTTTCCATTCCCTGAG--
```

Original motif      Consensus sequence: GTCTWAMAAAAAWAMAAA



Reverse complement motif      Consensus sequence: TTTYTWTTTTTTTWTGAGAC

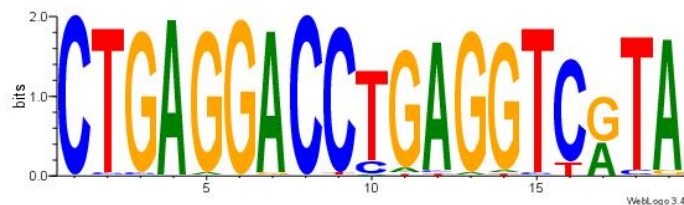


Dataset #: 1  
 Motif ID: 291  
 Motif name: Motif 291  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 3  
 Number of overlap: 17  
 Similarity score: 0.109842

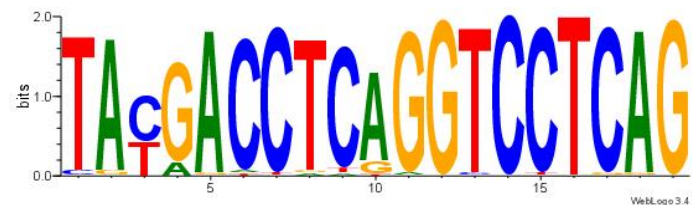
Alignment:

TAMGACCTCAGGTCCTCAG  
 --GGTTTTCCATTCTGAG

Original motif    Consensus sequence: CTGAGGACCTGAGGTCRTA



Reverse complement motif    Consensus sequence:  
TAMGACCTCAGGTCCTCAG

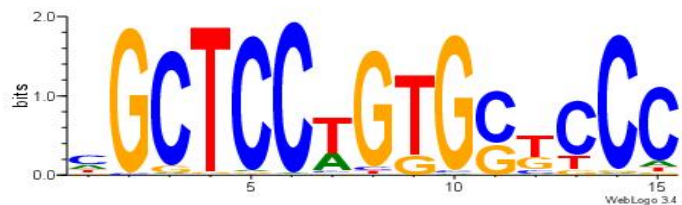


**Dataset #: 1      Motif ID: 215      Motif name: Motif 215**

Original motif    Consensus sequence: HGCTCCTGTGSKCCC

Reverse complement motif    Consensus sequence:  
GGRSCACAGGAGCD



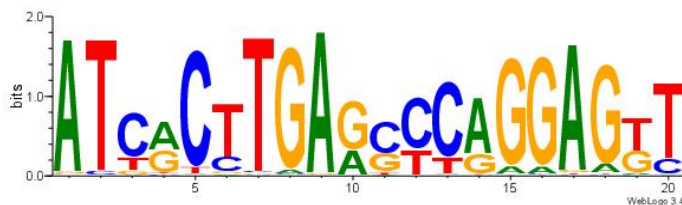


**Best Matches for Motif ID 215 (Highest to Lowest)**

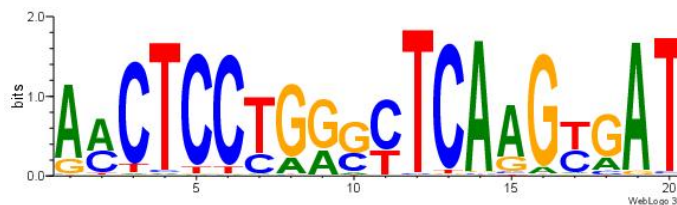
Dataset #: 1  
 Motif ID: 8  
 Motif name: Motif 8  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 6  
 Number of overlap: 15  
 Similarity score: 0.0619315

Alignment:  
 ATCRCTTGAGSYCAGGAGKT  
 GGRSCACAGGAGCD-----

Original motif      Consensus sequence: ATCRCTTGAGSYCAGGAGKT



Reverse complement motif      Consensus sequence: ARCTCCTGKSCTCAAGKGAT

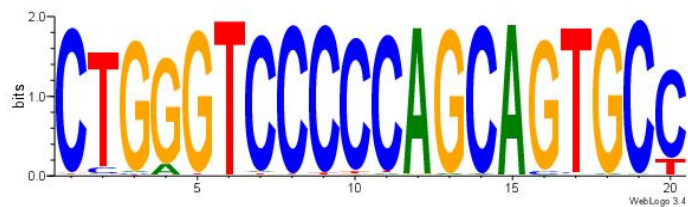


Dataset #: 1  
 Motif ID: 84  
 Motif name: Motif 84  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 4  
 Number of overlap: 15  
 Similarity score: 0.0736896

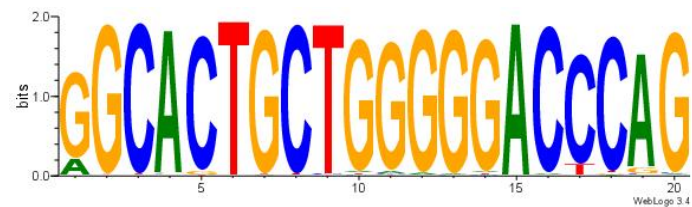
Alignment:

CTGGGTCCCCCAGCAGTGCC  
 --GGRSCACAGGAGCD---

Original motif      Consensus sequence: CTGGGTCCCCCAGCAGTGCC



Reverse complement motif      Consensus sequence: GGCAGTCTGGGGGACCCAG

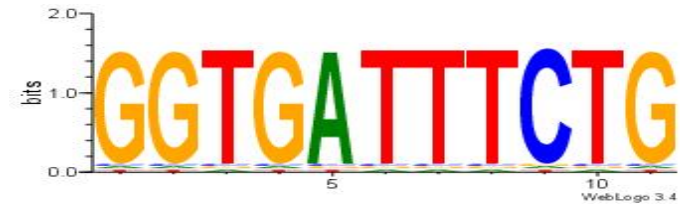



---

**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)

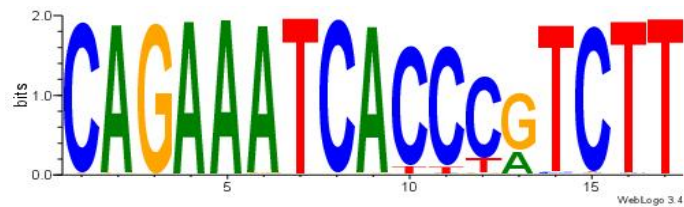
Dataset #: 1  
 Motif ID: 35  
 Motif name: Motif 35  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 7  
 Number of overlap: 11  
 Similarity score: 0.0137887

#### Alignment:

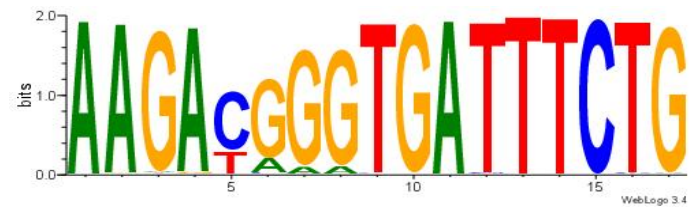
```

CAGAAATCACCCGTCTT
CAGAAATCACC-----
  
```

Original motif      Consensus sequence: CAGAAATCACCCGTCTT



Reverse complement motif      Consensus sequence: AAGACGGGTGATTTCTG

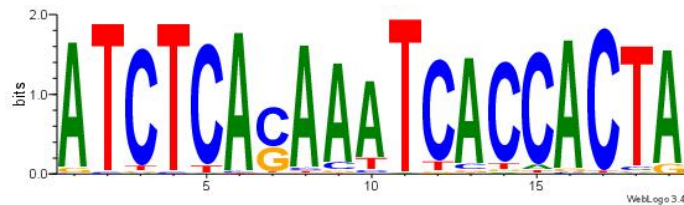


Dataset #: 1  
 Motif ID: 261  
 Motif name: Motif 261  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 5  
 Number of overlap: 11  
 Similarity score: 0.0239476

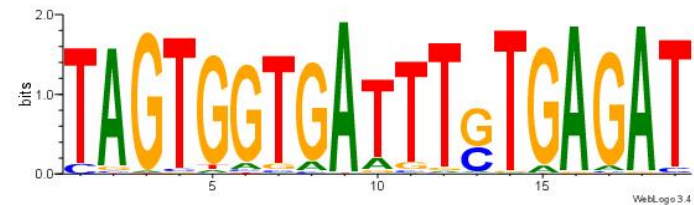
Alignment:

TAGTGGTGATTTSTGAGAT  
 ----GGTGATTTCTG----

Original motif    Consensus sequence: ATCTCASAAATCACCCTA



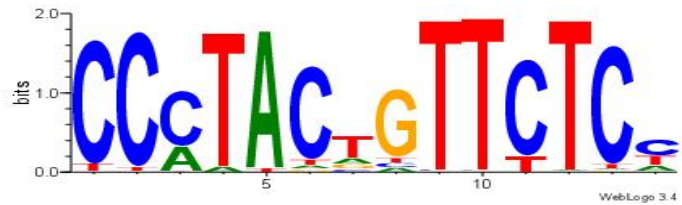
Reverse complement motif    Consensus sequence: TAGTGGTGATTTSTGAGAT



**Dataset #: 1      Motif ID: 217      Motif name: Motif 217**

Original motif    Consensus sequence: CCCTACTGTTCTCY

Reverse complement motif    Consensus sequence: KGAGAACAGTAGG

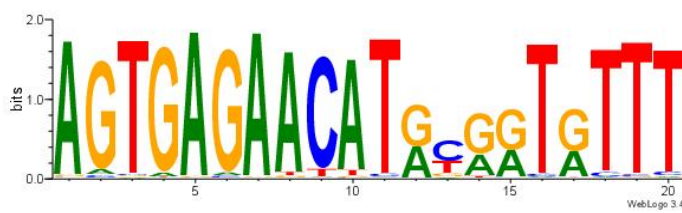


**Best Matches for Motif ID 217 (Highest to Lowest)**

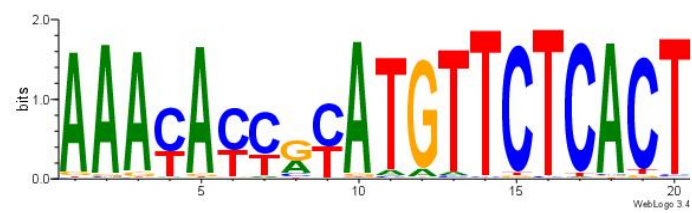
Dataset #: 1  
 Motif ID: 63  
 Motif name: Motif 63  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 5  
 Number of overlap: 14  
 Similarity score: 0.0624984

Alignment:  
 AGTGAGAACATRYRRTRTTT  
 ----KGAGAACAGTAGGG--

Original motif      Consensus sequence: AGTGAGAACATRYRRTRTTT



Reverse complement motif      Consensus sequence: AAAMAMMKMATGTTCTCACT

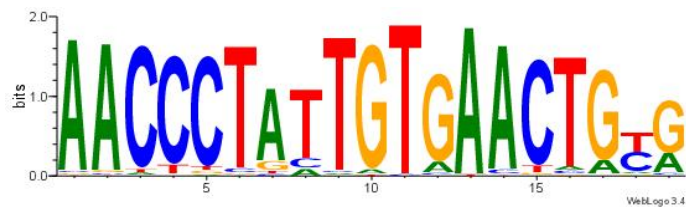


Dataset #: 1  
 Motif ID: 242  
 Motif name: Motif 242  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 4  
 Number of overlap: 14  
 Similarity score: 0.070491

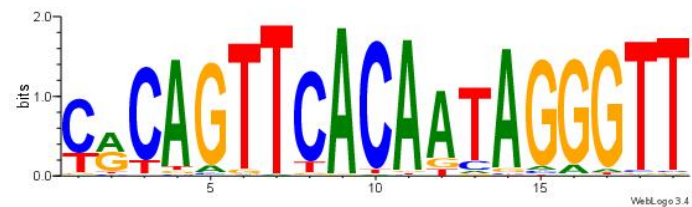
Alignment:

CMCAGTTCACAATAGGGTT  
 ---KGAGAACAGTAGGG--

Original motif    Consensus sequence: AACCTATTGTGAACTGYG



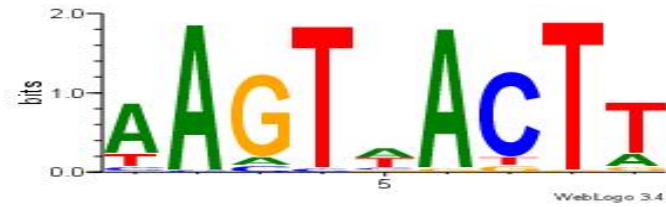
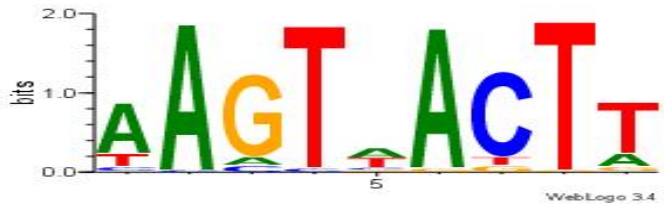
Reverse complement motif    Consensus sequence: CMCAGTTCACAATAGGGTT



**Dataset #: 1      Motif ID: 218      Motif name: Motif 218**

Original motif    Consensus sequence: AAGTWACTT

Reverse complement motif    Consensus sequence: AAGTWACTT

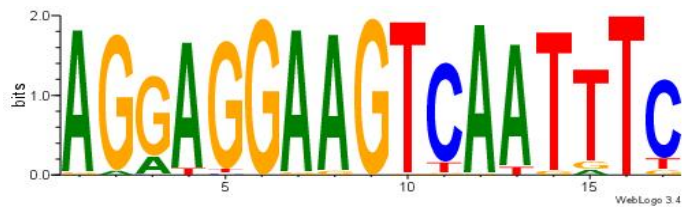


**Best Matches for Motif ID 218 (Highest to Lowest)**

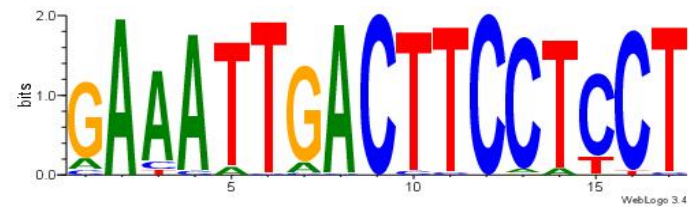
Dataset #: 1  
 Motif ID: 327  
 Motif name: Motif 327  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 7  
 Number of overlap: 9  
 Similarity score: 0.0387296

Alignment:  
 GAAATTGACTTCCTCCT  
 --AAGTWACTT-----

Original motif      Consensus sequence: AGGAGGAAGTCAATTC



Reverse complement motif      Consensus sequence: GAAATTGACTTCCTCCT

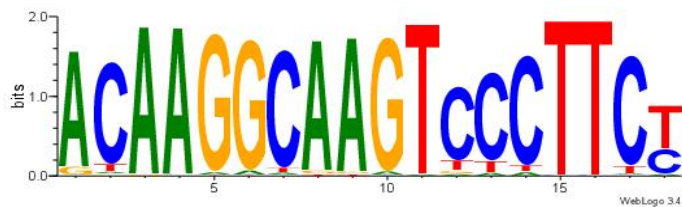


Dataset #: 1  
 Motif ID: 231  
 Motif name: Motif 231  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 8  
 Number of overlap: 9  
 Similarity score: 0.0394637

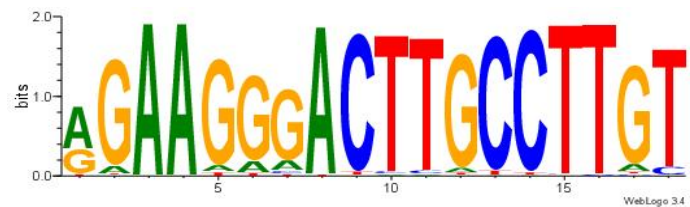
Alignment:

MGAAGGGACTTGCCTTGT  
 --AAGTWACTT-----

Original motif    Consensus sequence: ACAAGGCAAGTCCCTTCY



Reverse complement motif    Consensus sequence: MGAAGGGACTTGCCTTGT



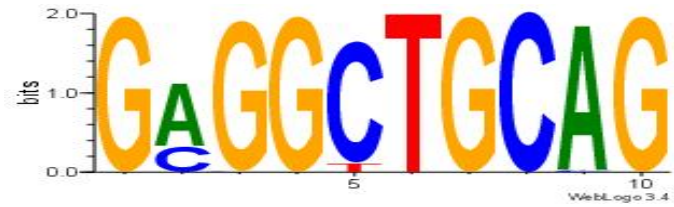

---

**Dataset #: 1      Motif ID: 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)

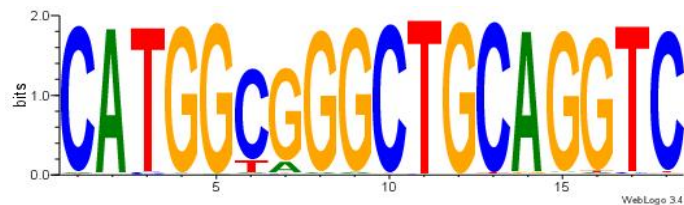
Dataset #: 1  
 Motif ID: 68  
 Motif name: Motif 68  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 6  
 Number of overlap: 10  
 Similarity score: 0.0362773

#### Alignment:

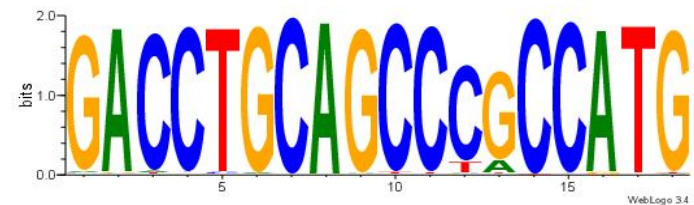
```

GACCTGCAGCCCGCCATG
-----CTGCAGCCTC-----
  
```

Original motif      Consensus sequence: CATGGCGGGCTGCAGGTC



Reverse complement motif      Consensus sequence: GACCTGCAGCCCGCCATG

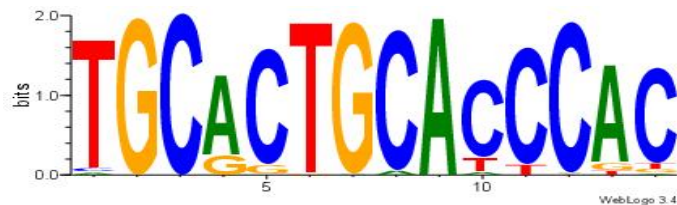


Dataset #: 1  
 Motif ID: 220  
 Motif name: Motif 220  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 10  
 Similarity score: 0.0471481

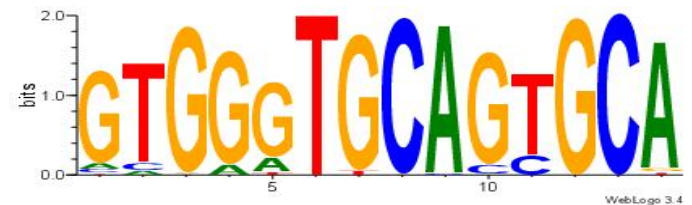
Alignment:

GTGGGTGCAGTGCA  
 GAGGCTGCAG-----

Original motif      Consensus sequence: TGCACTGCACCCAC

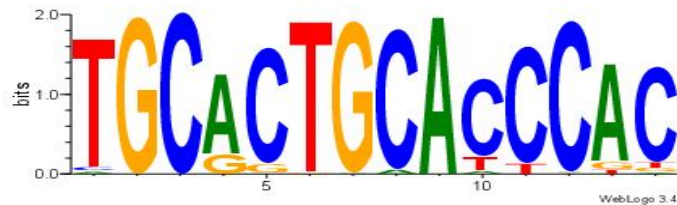


Reverse complement motif      Consensus sequence: GTGGGTGCAGTGCA

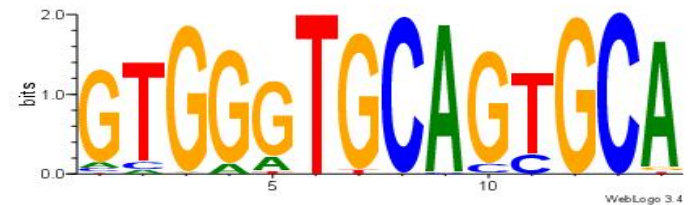


**Dataset #: 1      Motif ID: 220      Motif name: Motif 220**

Original motif      Consensus sequence: TGCACTGCACCCAC



Reverse complement motif      Consensus sequence: GTGGGTGCAGTGCA



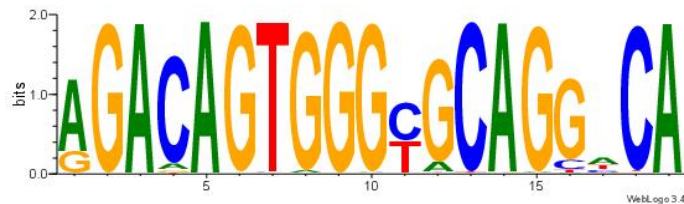
## Best Matches for Motif ID 220 (Highest to Lowest)

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

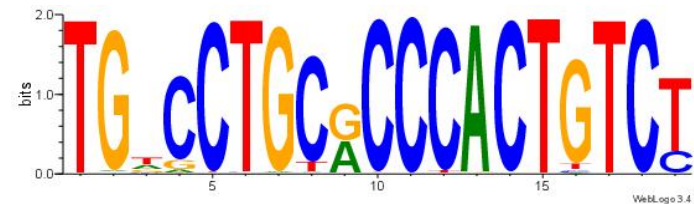
### Alignment:

```
TGHCCTGCKCCCCTGTCT  
-----TGCCTGCACCCAC
```

Original motif      Consensus sequence: AGACAGTGGGYGCAGGHCA



Reverse complement motif      Consensus sequence:  
TGHCCTGCKCCCCTGTCT



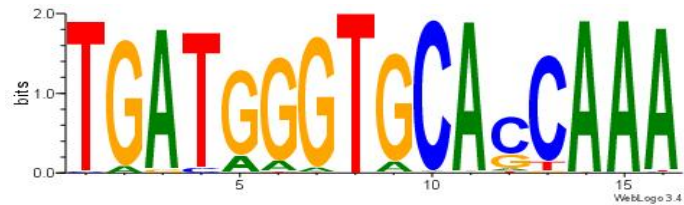
---

Dataset #: 1  
Motif ID: 289  
Motif name: Motif 289  
Matching format of first motif: Original Motif  
Matching format of second motif: Reverse Complement

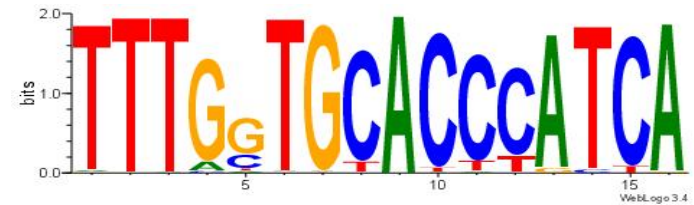
Direction: Backward  
 Position number: 3  
 Number of overlap: 14  
 Similarity score: 0.0840846

Alignment:  
 TTTGGTGCACCCATCA  
 TGCACTGCACCCAC--

Original motif    Consensus sequence: TGATGGGTGCACAAA

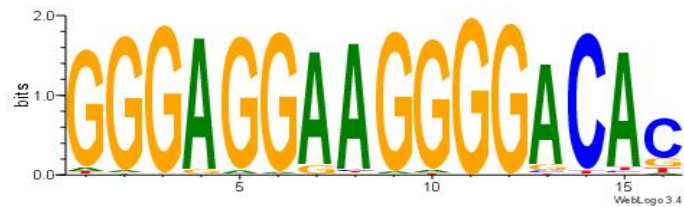


Reverse complement motif    Consensus sequence: TTTGGTGCACCCATCA

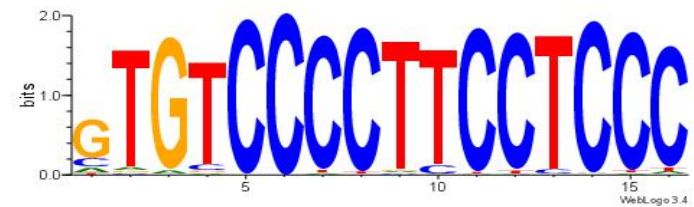


**Dataset #: 1      Motif ID: 221      Motif name: Motif 221**

Original motif    Consensus sequence: GGGAGGAAGGGGACAC



Reverse complement motif    Consensus sequence: GTGTCCCCTTCTCCC



**Best Matches for Motif ID 221 (Highest to Lowest)**

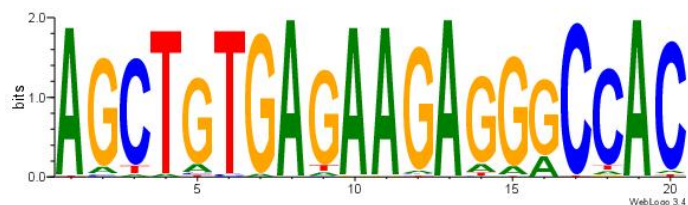
Dataset #: 1

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

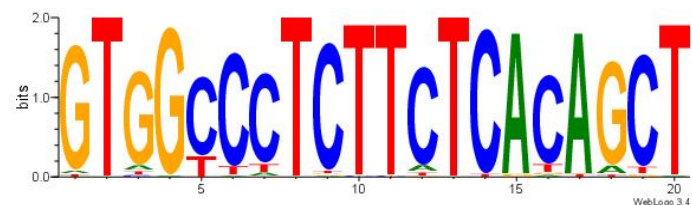
**Alignment:**

GTGGCCCTCTTCTCACAGCT  
 GTGTCCCCTTCTCCC-----

Original motif      Consensus sequence: AGCTGTGAGAAGAGGGCCAC



Reverse complement motif      Consensus sequence: GTGGCCCTCTTCTCACAGCT



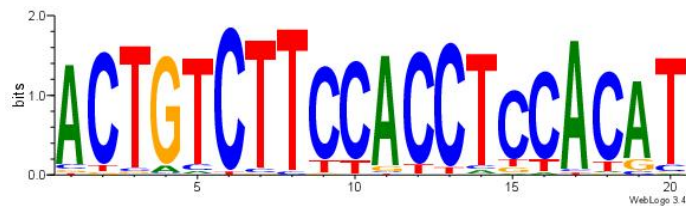
Dataset #: 1  
 Motif ID: 178  
 Motif name: Motif 178  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 4  
 Number of overlap: 16

Similarity score: 0.0878739

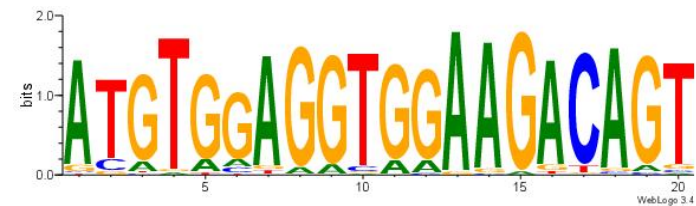
Alignment:

ATGTGGAGGTGGAAGACAGT  
-GGGAGGAAGGGGACAC---

Original motif      Consensus sequence: ACTGTCTTCCACCTCCACAT

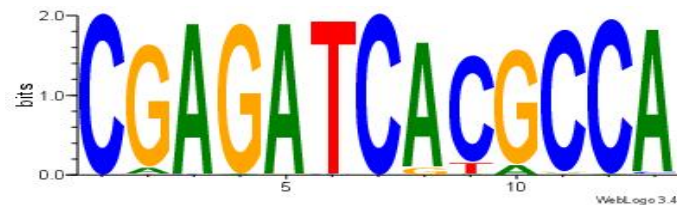


Reverse complement motif      Consensus sequence: ATGTGGAGGTGGAAGACAGT



**Dataset #: 1      Motif ID: 222      Motif name: Motif 222**

Original motif      Consensus sequence: CGAGATCACGCCA



Reverse complement motif      Consensus sequence: TGGCGTGATCTCG



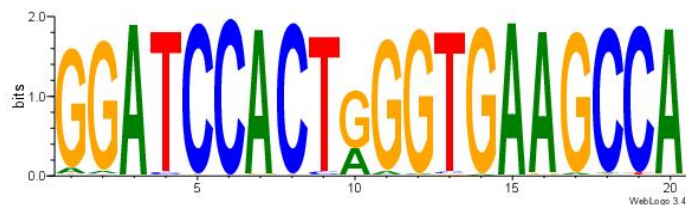
### Best Matches for Motif ID 222 (Highest to Lowest)

Dataset #:	1
Motif ID:	61
Motif name:	Motif 61
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif

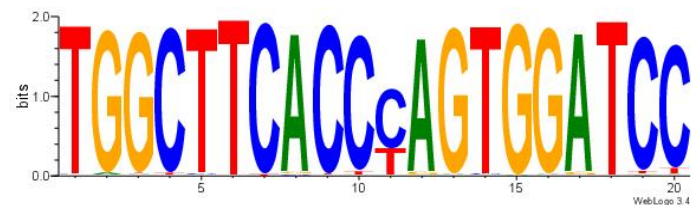
Direction: Forward  
 Position number: 8  
 Number of overlap: 13  
 Similarity score: 0.0800547

Alignment:  
 GGATCCACTGGGTGAAGCCA  
 -----CGAGATCACGCCA

Original motif    Consensus sequence: GGATCCACTGGGTGAAGCCA



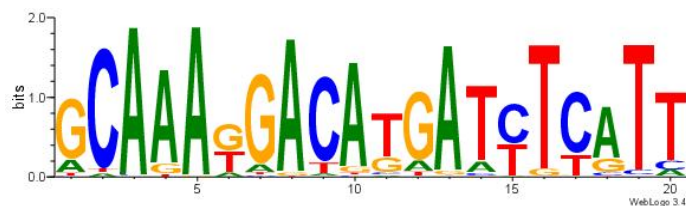
Reverse complement motif    Consensus sequence: TGGCTTCACCCAGTGGATCC



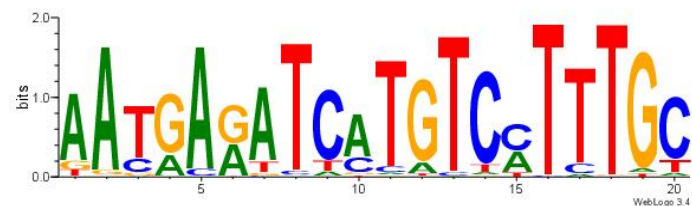
Dataset #: 1  
 Motif ID: 99  
 Motif name: Motif 99  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 6  
 Number of overlap: 13  
 Similarity score: 0.0816199

Alignment:  
 AATGAKATCATGTCYTTTGC  
 -----CGAGATCACGCCA--

Original motif      Consensus sequence: GCAAAGACATGATYTCATT

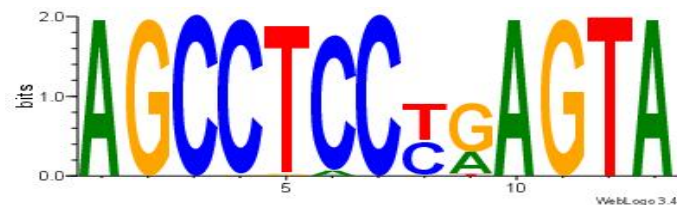


Reverse complement motif      Consensus sequence: AATGAKATCATGTCYTTTGC

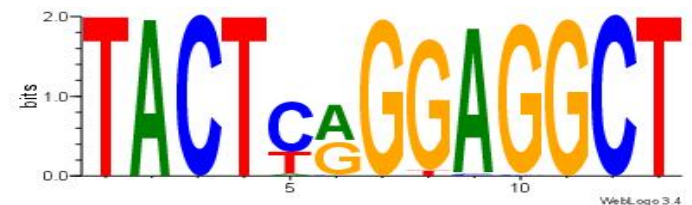


**Dataset #: 1      Motif ID: 223      Motif name: Motif 223**

Original motif      Consensus sequence: AGCCTCCYGAGTA



Reverse complement motif      Consensus sequence: TACTCMGGAGGCT



### Best Matches for Motif ID 223 (Highest to Lowest)

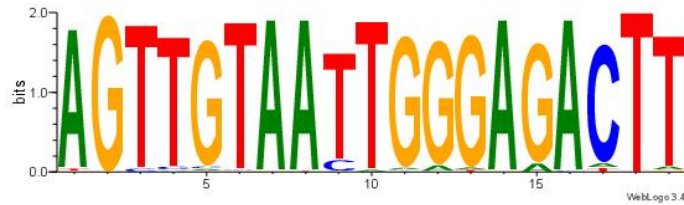
Dataset #:	1
Motif ID:	232
Motif name:	Motif 232
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	2
Number of overlap:	13
Similarity score:	0.0672113

Alignment:

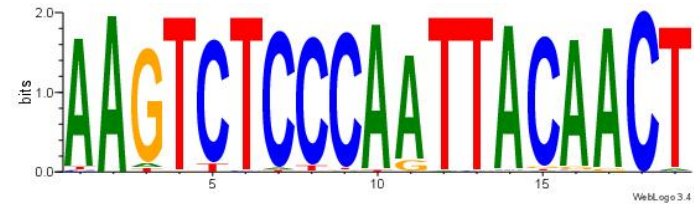


AAGTCTCCCAATTACAAC T  
-AGCCTCCYGAGTA-----

Original motif      Consensus sequence: AGTTGTAATTGGGAGACTT



Reverse complement motif      Consensus sequence:  
AAGTCTCCCAATTACAAC T



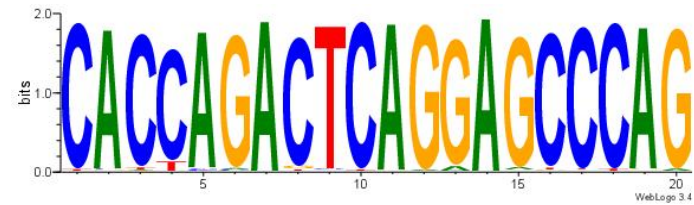
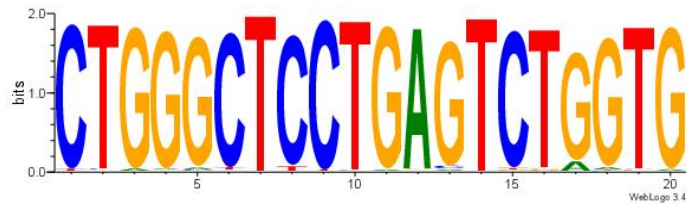
Dataset #: 1  
Motif ID: 67  
Motif name: Motif 67  
Matching format of first motif: Original Motif  
Matching format of second motif: Original Motif  
Direction: Forward  
Position number: 3  
Number of overlap: 13  
Similarity score: 0.075298

Alignment:

CTGGGCTCCTGAGTCTGGTG  
--AGCCTCCYGAGTA-----

Original motif      Consensus sequence: CTGGGCTCCTGAGTCTGGTG

Reverse complement motif      Consensus sequence:  
CACCAGACTCAGGAGCCCAG

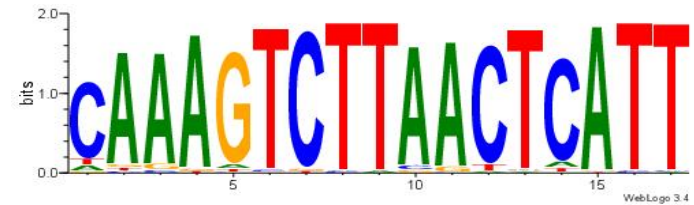


**Dataset #: 1      Motif ID: 224      Motif name: Motif 224**

Original motif      Consensus sequence: AATGAGTTAAGACTTTG



Reverse complement motif      Consensus sequence: CAAAGTCTTAACTCATT



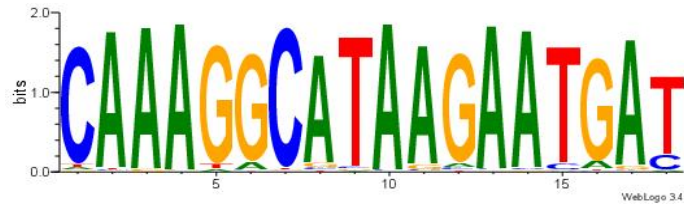
**Best Matches for Motif ID 224 (Highest to Lowest)**

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

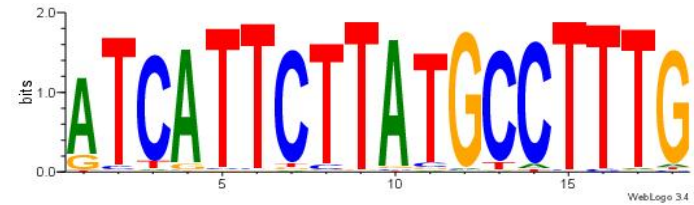
Alignment:

ATCATTCTTATGCCTTTG  
CAAAGTCTTAACTCATT-

Original motif      Consensus sequence: CAAAGGCATAAGAATGAT



Reverse complement motif      Consensus sequence:  
ATCATTCTTATGCCTTTG

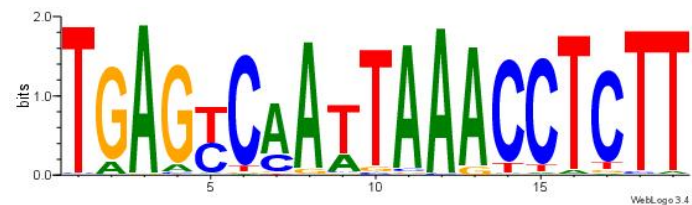
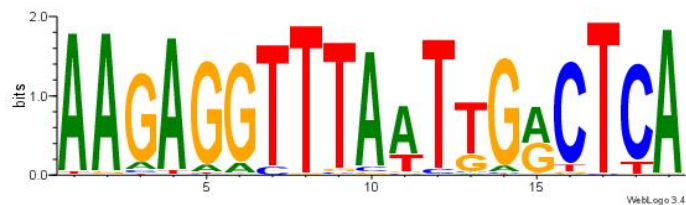


Dataset #: 1  
Motif ID: 129  
Motif name: Motif 129  
Matching format of first motif: Original Motif  
Matching format of second motif: Reverse Complement  
Direction: Forward  
Position number: 1  
Number of overlap: 17  
Similarity score: 0.103511

Alignment:  
TGAGKCAATTAAACCTCTT  
AATGAGTTAAGACTTTG--

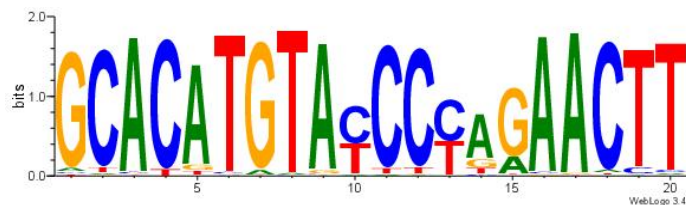
Original motif      Consensus sequence: AAGAGTTTAATTGRCTCA

Reverse complement motif      Consensus sequence:  
TGAGKCAATTAAACCTCTT

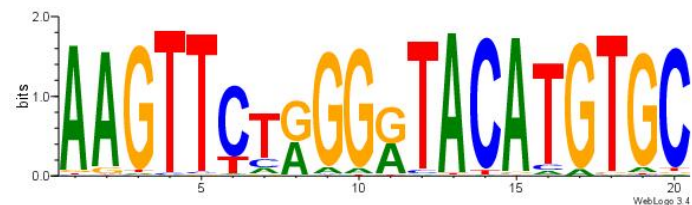


**Dataset #: 1      Motif ID: 225      Motif name: Motif 225**

Original motif      Consensus sequence: GCACATGTAYCCYAGAACTT



Reverse complement motif      Consensus sequence: AAGTTCTKGGKTACATGTGC



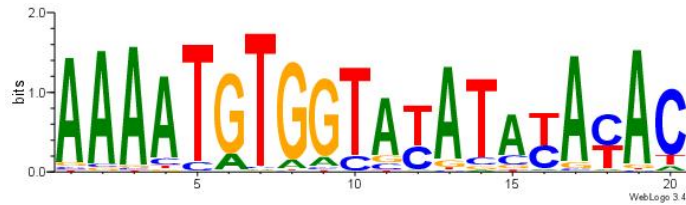
**Best Matches for Motif ID 225 (Highest to Lowest)**

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

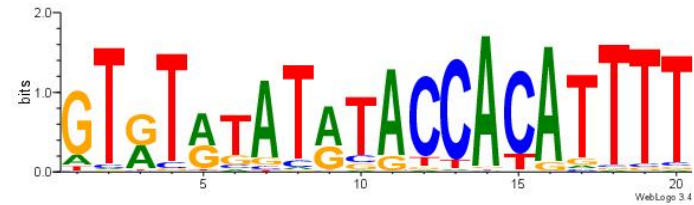
Alignment:

AAAATGTGGTAYATAYAYAC  
AAGTTCTKGGKTACATGTGC

Original motif      Consensus sequence: AAAATGTGGTAYATAYAYAC



Reverse complement motif      Consensus sequence:  
GTKTMTATMTACCACATTTT



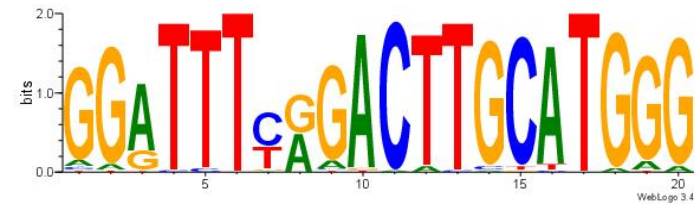
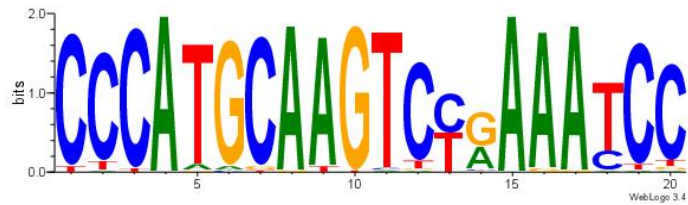
Dataset #: 1  
Motif ID: 310  
Motif name: Motif 310  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Reverse Complement  
Direction: Forward  
Position number: 2  
Number of overlap: 19  
Similarity score: 0.591599

Alignment:

GGATTTMKGACTTGCATGGG-  
-AAGTTCTKGGKTACATGTGC

Original motif      Consensus sequence: CCCATGCAAGTCYRAAATCC

Reverse complement motif      Consensus sequence:  
GGATTTMKGACTTGCATGGG

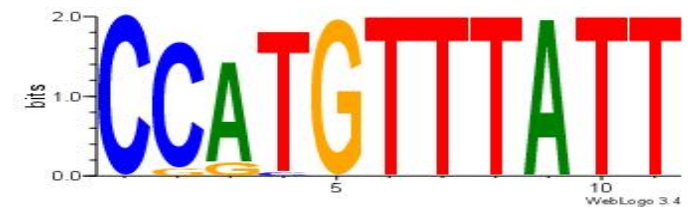


**Dataset #: 1      Motif ID: 226      Motif name: Motif 226**

Original motif      Consensus sequence: AATAACATGG



Reverse complement motif      Consensus sequence: CCATGTTTATT

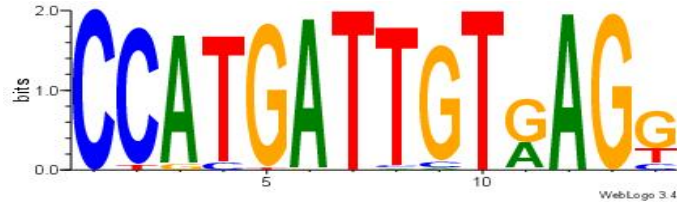


**Best Matches for Motif ID 226 (Highest to Lowest)**

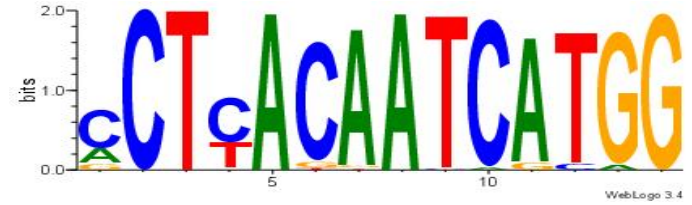
Dataset #:	1
Motif ID:	270
Motif name:	Motif 270
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	11
Similarity score:	0.0612696

Alignment:  
 CCTMACAATCATGG  
 ---AATAACATGG

Original motif      Consensus sequence: CCATGATTGTRAGG



Reverse complement motif      Consensus sequence: CCTMACAATCATG



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

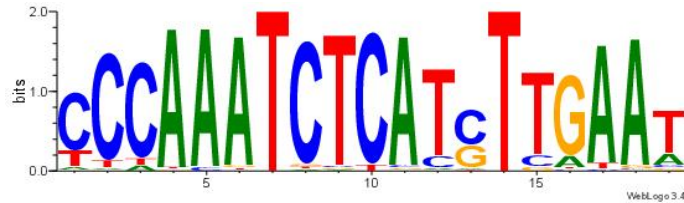


Reverse complement motif      Consensus sequence: CCMKGCTAATT

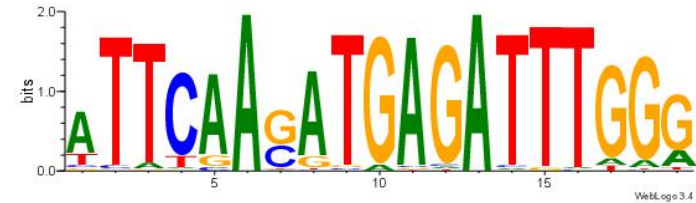


**Dataset #: 1      Motif ID: 227      Motif name: Motif 227**

Original motif      Consensus sequence: CCCAAATCTCATSTTGAAT



Reverse complement motif      Consensus sequence: ATTCAASATGAGATTTGGG



### 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

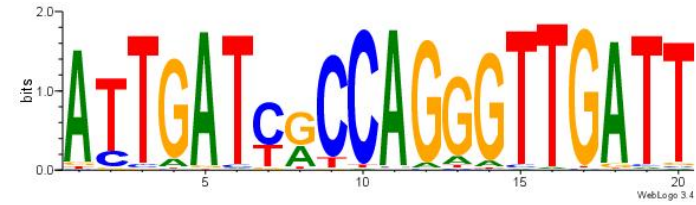
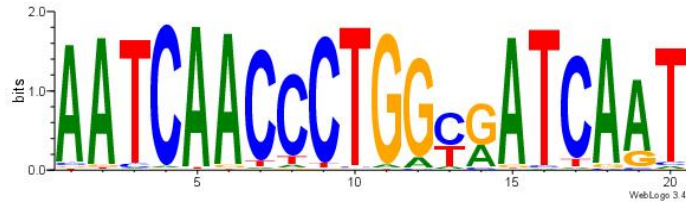
#### Alignment:

```
AATCAACCCTGGYRATCAAT  
-CCCAAATCTCATSTTGAAT
```

Original motif      Consensus sequence: AATCAACCCTGGYRATCAAT

Reverse complement motif      Consensus sequence: ATTGATMKCCAGGGTTGATT

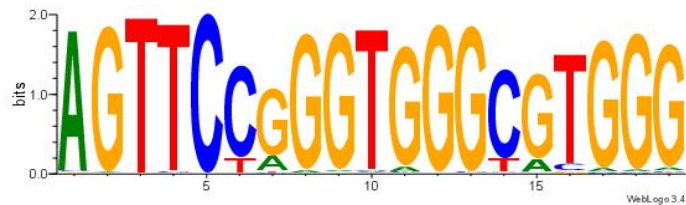




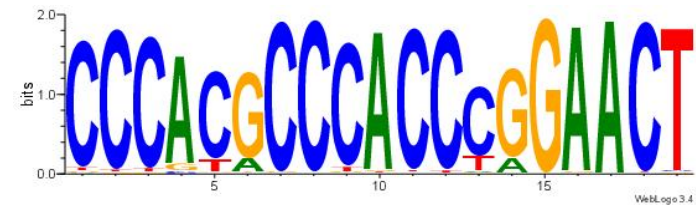
Dataset #: 1  
 Motif ID: 98  
 Motif name: Motif 98  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 2  
 Number of overlap: 18  
 Similarity score: 0.595387

Alignment:  
 -AGTTCCGGGTGGGCGTGGG  
 ATTCAASATGAGATTTGGG-

Original motif      Consensus sequence: AGTTCCGGGTGGGCGTGGG

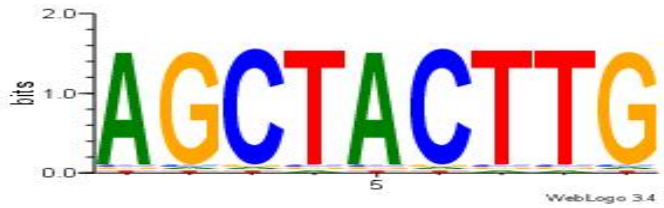


Reverse complement motif      Consensus sequence: CCCACGCCACCCGGAAT



**Dataset #: 1      Motif ID: 228      Motif name: Motif 228**

Original motif    Consensus sequence: AGCTACTTG



Reverse complement motif    Consensus sequence: CAAGTAGCT



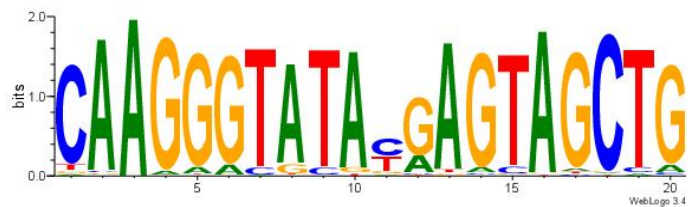
### Best Matches for Motif ID 228 (Highest to Lowest)

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

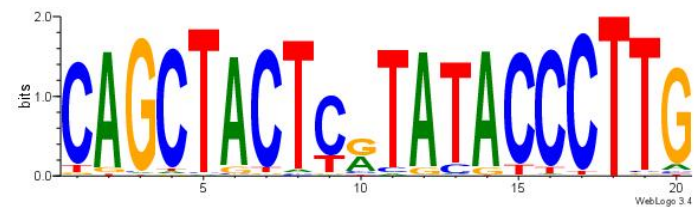
Alignment:

```
CAGCTACTCKTATACCCTTG
-----AGCTACTTG--
```

Original motif    Consensus sequence: CAAGGGTATAYGAGTAGCTG



Reverse complement motif    Consensus sequence: CAGCTACTCKTATACCCTTG

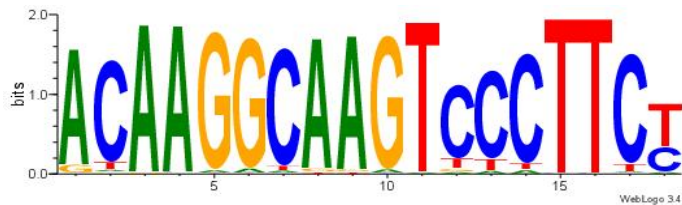


Dataset #: 1  
 Motif ID: 231  
 Motif name: Motif 231  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 4  
 Number of overlap: 9  
 Similarity score: 0.0563554

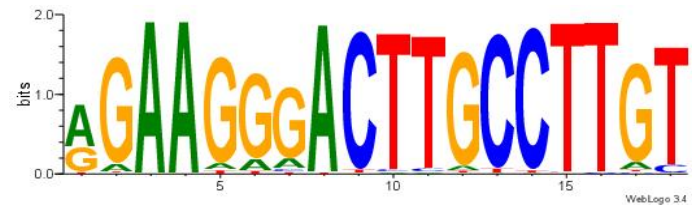
Alignment:

MGAAGGGACTTGCCTTGT  
 ---AGCTACTTG-----

Original motif      Consensus sequence: ACAAGGCAAGTCCCTTCY



Reverse complement motif      Consensus sequence: MGAAGGGACTTGCCTTGT

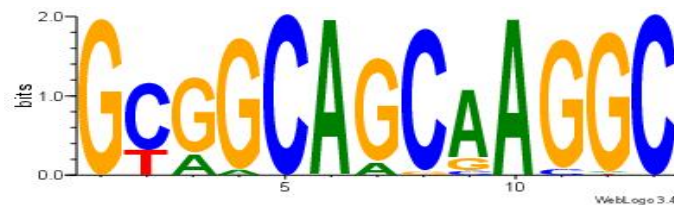
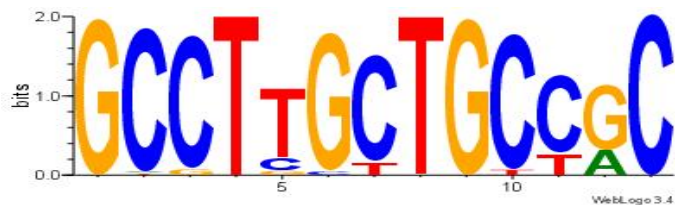



---

**Dataset #: 1      Motif ID: 229      Motif name: Motif 229**

Original motif      Consensus sequence: GCCTTGCTGCCGC

Reverse complement motif      Consensus sequence: GCGGCAGCAAGG



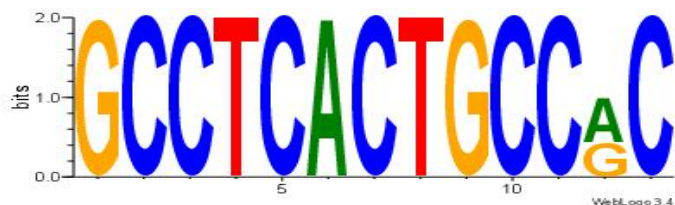
### Best Matches for Motif ID 229 (Highest to Lowest)

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

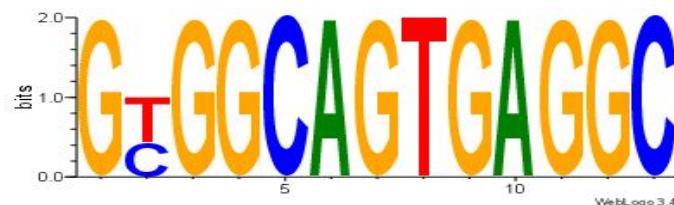
#### Alignment:

GCCTCACTGCCRC  
 GCCTTGCTGCCGC

Original motif      Consensus sequence: GCCTCACTGCCRC



Reverse complement motif      Consensus sequence: GKGGCAGTGAGGC



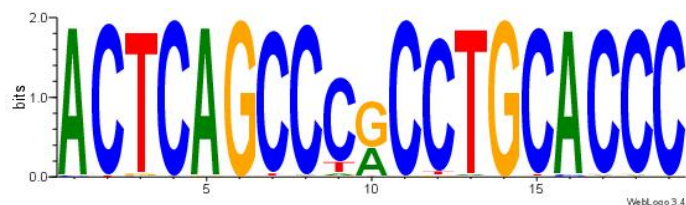
Dataset #: 1

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

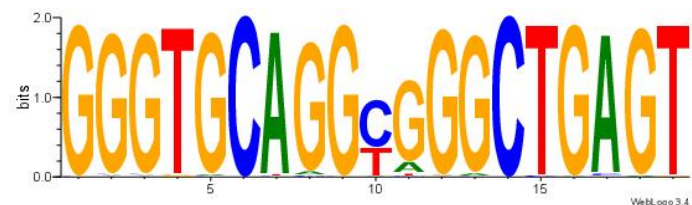
**Alignment:**

GGGTGCAGGMGGGCTGAGT  
 -GCGGCAGCAAGGC-----

Original motif      Consensus sequence: ACTCAGCCRCCTGCACCC

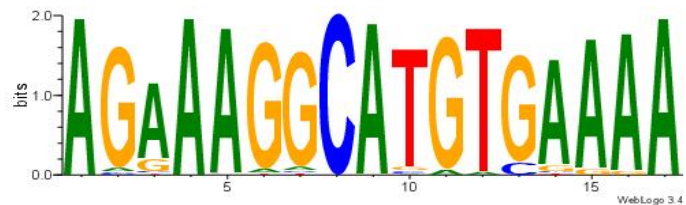


Reverse complement motif      Consensus sequence: GGGTGCAGGMGGGCTGAGT

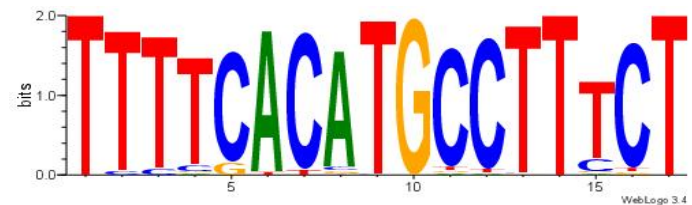


**Dataset #: 1      Motif ID: 230      Motif name: Motif 230**

Original motif      Consensus sequence: AGAAAGGCATGTGAAAA



Reverse complement motif      Consensus sequence: TTTTACATGCCTTTCT



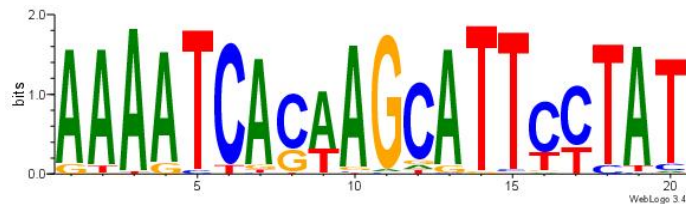
## Best Matches for Motif ID 230 (Highest to Lowest)

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

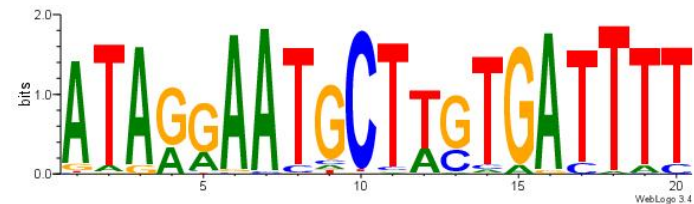
### Alignment:

```
AAAATCACAAGCATTCTAT  
-TTTTACATGCCTTTCT--
```

Original motif      Consensus sequence: AAAATCACAAGCATTCTAT



Reverse complement motif      Consensus sequence: ATAGGAATGCTTGTGATTTT



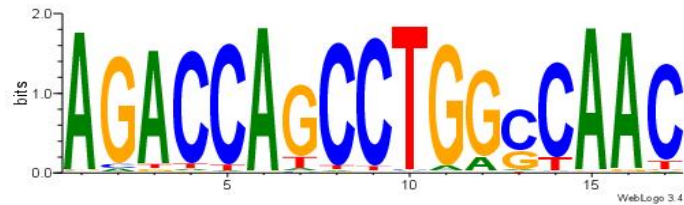
---

Dataset #: 1  
Motif ID: 12  
Motif name: Motif 12  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Reverse Complement

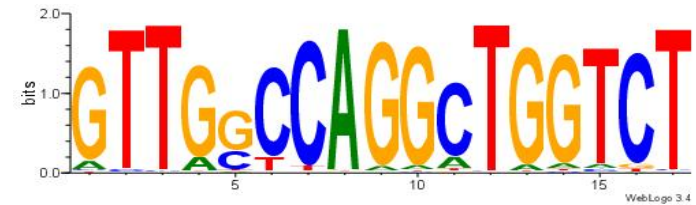
Direction: Forward  
 Position number: 1  
 Number of overlap: 17  
 Similarity score: 0.102426

Alignment:  
 GTTGGCCAGGCTGGTCT  
 TTTTCACATGCCTTTCT

Original motif    Consensus sequence: AGACCAGCCTGGCCAAC

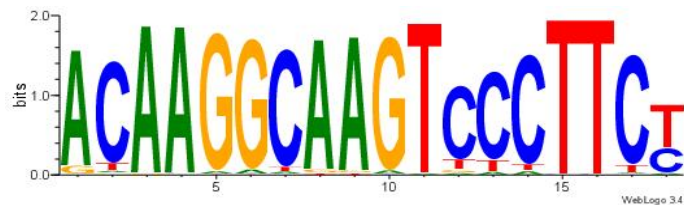


Reverse complement motif    Consensus sequence: GTTGGCCAGGCTGGTCT

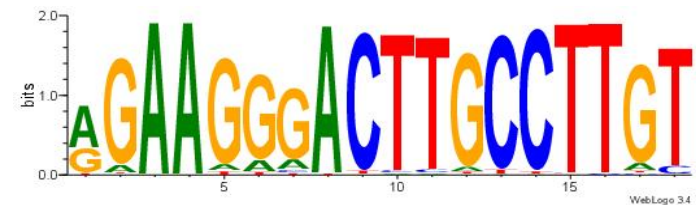


**Dataset #: 1      Motif ID: 231      Motif name: Motif 231**

Original motif    Consensus sequence: ACAAGGCAAGTCCCCTTC



Reverse complement motif    Consensus sequence: MGAAGGACTTGCCTTGT



**Best Matches for Motif ID 231 (Highest to Lowest)**

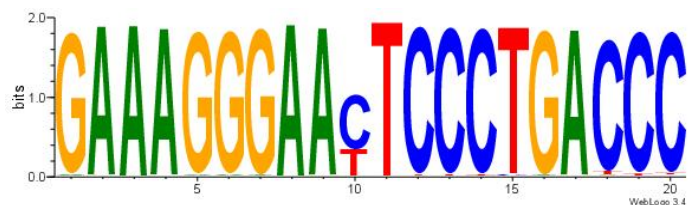
Dataset #: 1

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

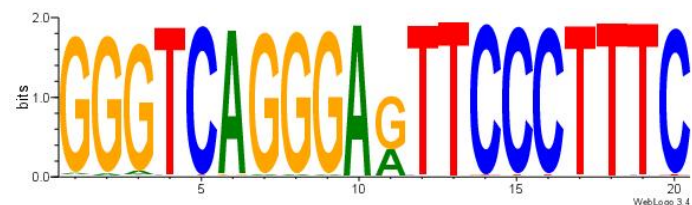
**Alignment:**

GAAAGGGA ACTCCCTGACCC  
 ACAAGGCAAGTCCCTTCY--

Original motif    Consensus sequence: GAAAGGGA ACTCCCTGACCC



Reverse complement motif    Consensus sequence: GGGTCAGG GAGTTCCCTTTC



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

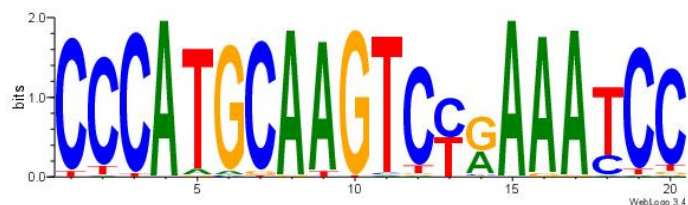


Similarity score: 0.0932717

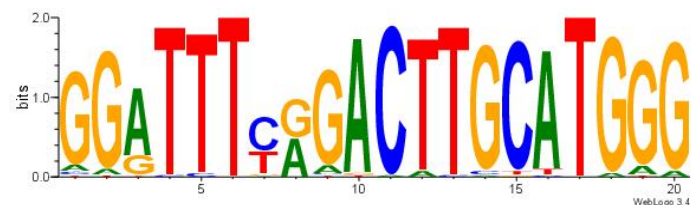
Alignment:

GGATTTMKGACTTGCATGGG  
--MGAAGGGACTTGCCTTGT

Original motif      Consensus sequence: CCCATGCAAGTCYRAAATCC

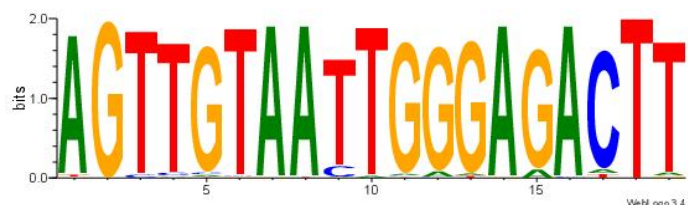


Reverse complement motif      Consensus sequence: GGATTTMKGACTTGCATGGG

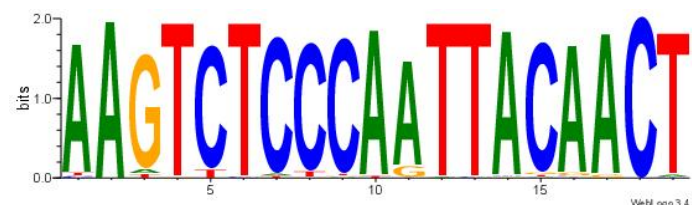


**Dataset #: 1      Motif ID: 232      Motif name: Motif 232**

Original motif      Consensus sequence: AGTTGTAATTGGGAGACTT



Reverse complement motif      Consensus sequence: AAGTCTCCAATTACAAC



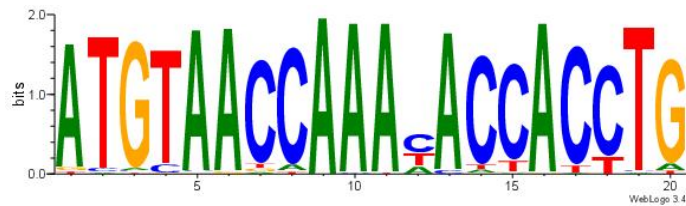
**Best Matches for Motif ID 232 (Highest to Lowest)**

Dataset #:	1
Motif ID:	336
Motif name:	Motif 336
Matching format of first motif:	Reverse Complement

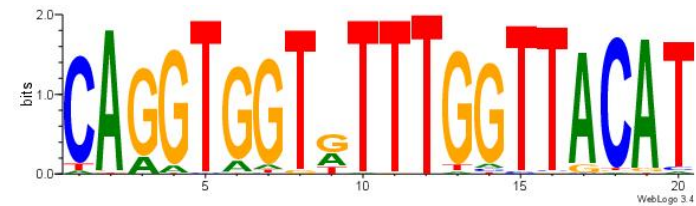
Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 19  
 Similarity score: 0.0998938

Alignment:  
 ATGTAACCAAAYACCACCTG  
 AAGTCTCCAATTACA ACT-

Original motif      Consensus sequence: ATGTAACCAAAYACCACCTG



Reverse complement motif      Consensus sequence:  
 CAGGTGGTKTTTGGTTACAT

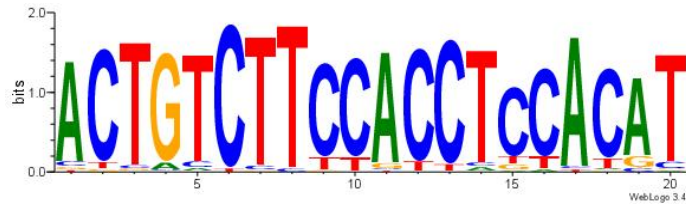


Dataset #: 1  
 Motif ID: 178  
 Motif name: Motif 178  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 19  
 Similarity score: 0.102119

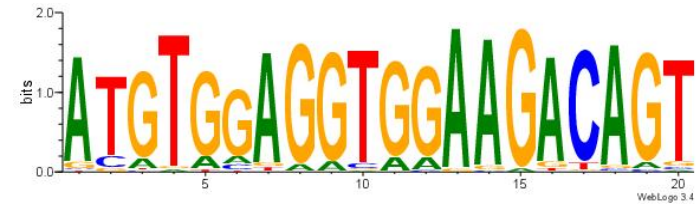
Alignment:

ACTGTCTTCCACCTCCACAT  
AAGTCTCCCAATTACAAC-

Original motif      Consensus sequence: ACTGTCTTCCACCTCCACAT

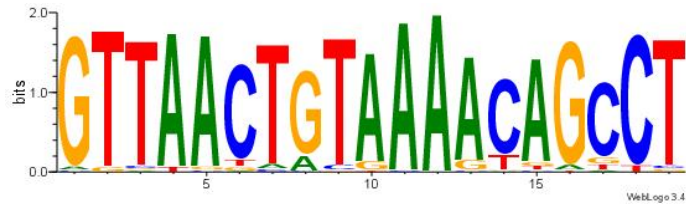


Reverse complement motif      Consensus sequence:  
ATGTGGAGGTGGAAGACAGT

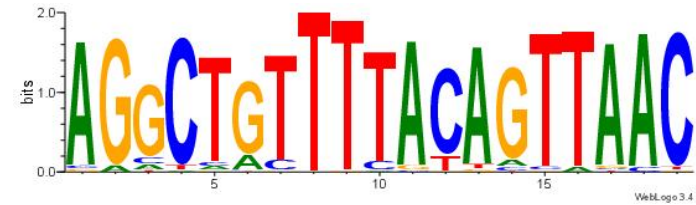


**Dataset #: 1      Motif ID: 233      Motif name: Motif 233**

Original motif      Consensus sequence: GTTAACTGTAAAACAGCCT



Reverse complement motif      Consensus sequence:  
AGGCTGTTTACAGTTAAC



### Best Matches for Motif ID 233 (Highest to Lowest)

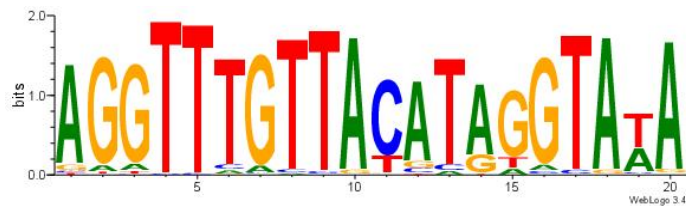
Dataset #:	1
Motif ID:	137
Motif name:	Motif 137
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1

Number of overlap: 19  
Similarity score: 0.105595

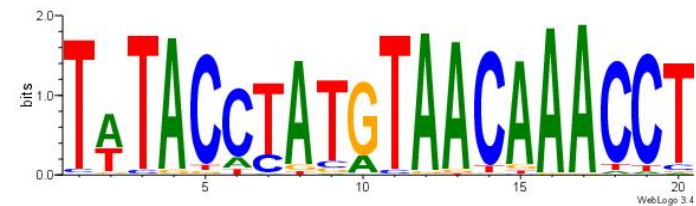
Alignment:

TWTACCTATGTAACAAACCT  
-GTTAACTGTAAAACAGCCT

Original motif    Consensus sequence: AGGTTTGTACATAGGTAWA



Reverse complement motif    Consensus sequence: TWTACCTATGTAACAAACCT

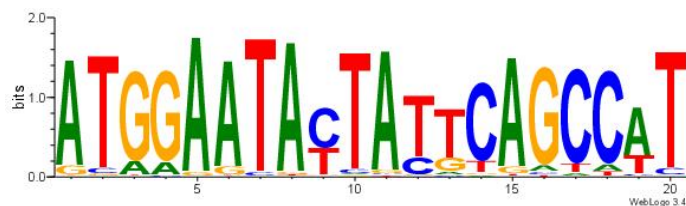


Dataset #: 1  
Motif ID: 55  
Motif name: Motif 55  
Matching format of first motif: Original Motif  
Matching format of second motif: Original Motif  
Direction: Backward  
Position number: 2  
Number of overlap: 19  
Similarity score: 0.106073

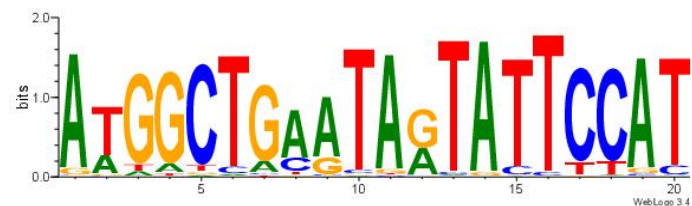
Alignment:

ATGGAATAYTATTCAGCCAT  
GTTAACTGTAAAACAGCCT-

Original motif      Consensus sequence: ATGGAATAYTATTCAGCCAT

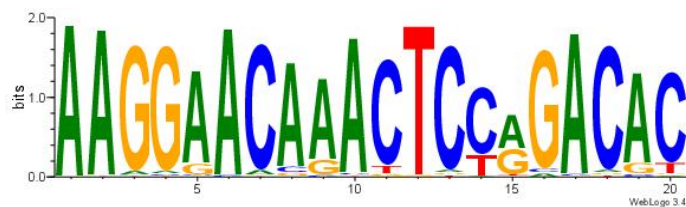


Reverse complement motif      Consensus sequence: ATGGCTGAATAKTATTCCAT

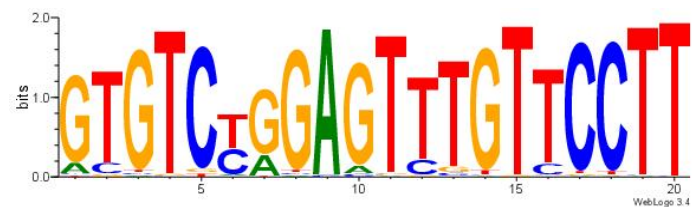


**Dataset #: 1      Motif ID: 234      Motif name: Motif 234**

Original motif      Consensus sequence: AAGGAACAACTCCRGACAC



Reverse complement motif      Consensus sequence: GTGCKGGAGTTTGTTCTT



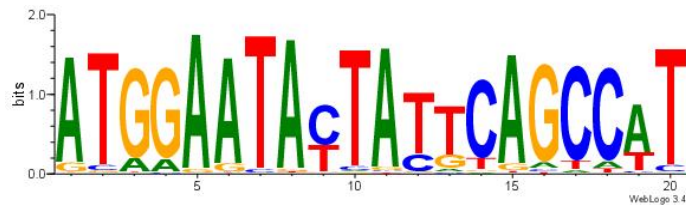
**Best Matches for Motif ID 234 (Highest to Lowest)**

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

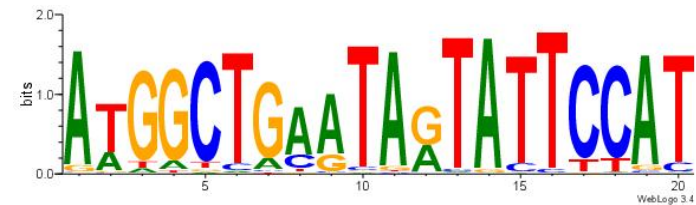
Alignment:

ATGGCTGAATAKTATTCCAT  
GTGTCKGGAGTTTGTTCCTT

Original motif      Consensus sequence: ATGGAATAYTATTCAGCCAT



Reverse complement motif      Consensus sequence:  
ATGGCTGAATAKTATTCCAT



---

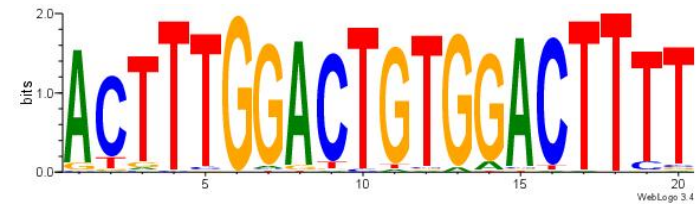
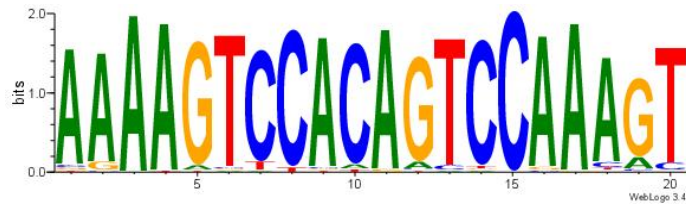
Dataset #:	1
Motif ID:	171
Motif name:	Motif 171
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	2
Number of overlap:	19
Similarity score:	0.600364

Alignment:

-ACTTTGGACTGTGGACTTTT  
GTGTCKGGAGTTTGTTCCTT-

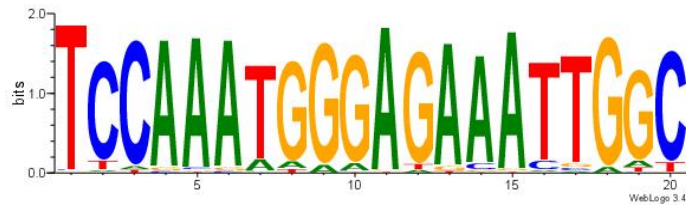
Original motif      Consensus sequence: AAAAGTCCACAGTCCAAAGT

Reverse complement motif      Consensus sequence:  
ACTTTGGACTGTGGACTTTT

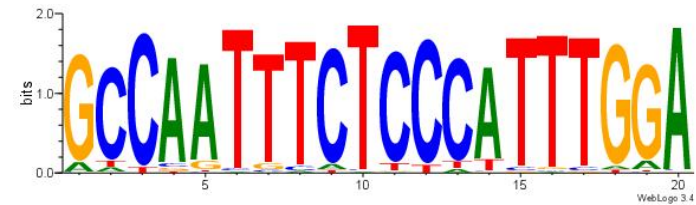


**Dataset #: 1      Motif ID: 235      Motif name: Motif 235**

Original motif      Consensus sequence: TCCAATGGGAGAAATTGGC



Reverse complement motif      Consensus sequence: GCCAATTTCTCCCATTTGGA



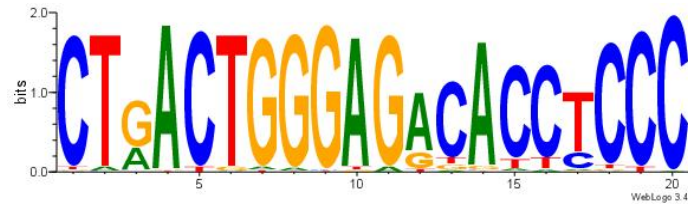
**Best Matches for Motif ID 235 (Highest to Lowest)**

Dataset #:	1
Motif ID:	293
Motif name:	Motif 293
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:	0.0906025

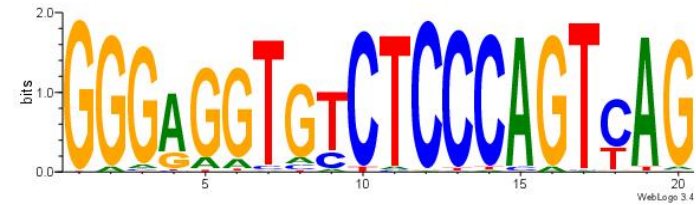
Alignment:

-CTGACTGGGAGACACCTCCC  
TCCAAATGGGAGAAATTGGC-

Original motif      Consensus sequence: CTGACTGGGAGACACCTCCC



Reverse complement motif      Consensus sequence:  
GGGAGGTGTCTCCCAGTCAG



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:	19
Similarity score:	0.0911292

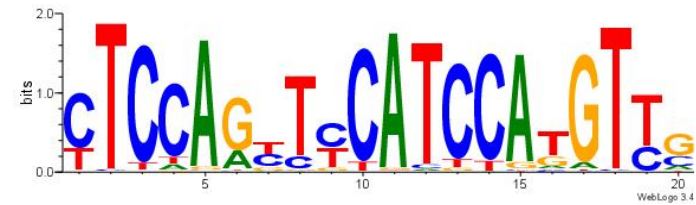
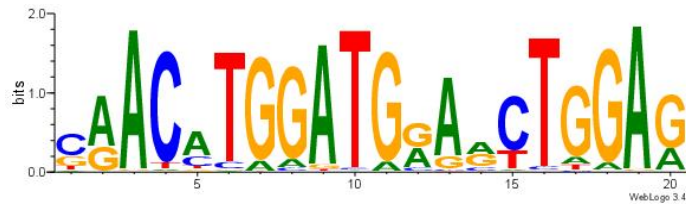
Alignment:

-CAACATGGATGRARCTGGAG  
TCCAAATGGGAGAAATTGGC-

Original motif      Consensus sequence: CAACATGGATGRARCTGGAG

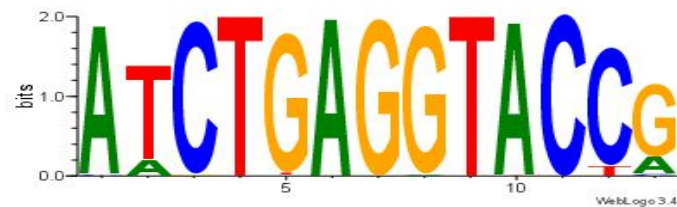
Reverse complement motif      Consensus sequence:  
CTCCAGKTMCATCCATGTTG



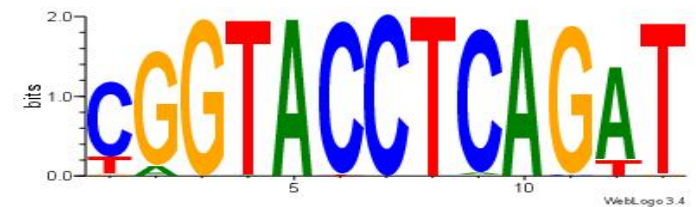


**Dataset #: 1      Motif ID: 236      Motif name: Motif 236**

Original motif      Consensus sequence: ATCTGAGGTACCG



Reverse complement motif      Consensus sequence: CGGTACCTCAGAT

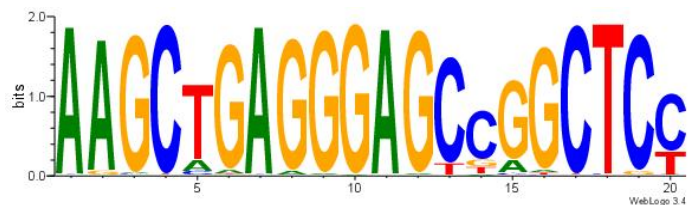


**Best Matches for Motif ID 236 (Highest to Lowest)**

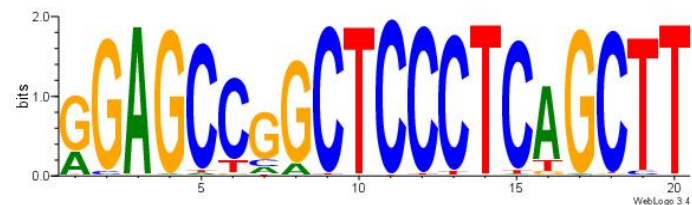
Dataset #:	1
Motif ID:	96
Motif name:	Motif 96
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	7
Number of overlap:	13
Similarity score:	0.072129

Alignment:  
GGAGCCGGCTCCCTCAGCTT  
-----CGGTACCTCAGAT-

Original motif      Consensus sequence: AAGCTGAGGGAGCCGGCTCC



Reverse complement motif      Consensus sequence: GGAGCCGGCTCCCTCAGCTT

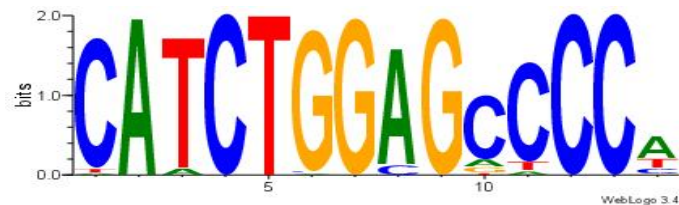


Dataset #: 1  
Motif ID: 320  
Motif name: Motif 320  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Reverse Complement  
Direction: Backward  
Position number: 2  
Number of overlap: 13  
Similarity score: 0.0813404

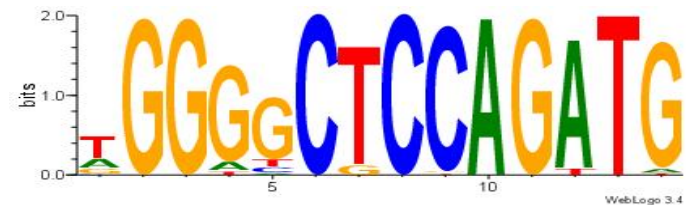
Alignment:

TGGGGCTCCAGATG  
CGGTACCTCAGAT-

Original motif      Consensus sequence: CATCTGGAGCCCCA



Reverse complement motif      Consensus sequence: TGGGGCTCCAGATG

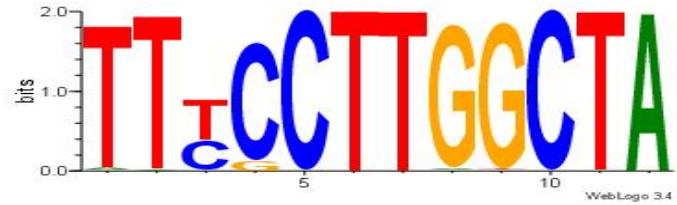


**Dataset #: 1      Motif ID: 237      Motif name: Motif 237**

Original motif      Consensus sequence: TAGCCAAGG<sub>A</sub>AA



Reverse complement motif      Consensus sequence: TTKCCTTGGCTA



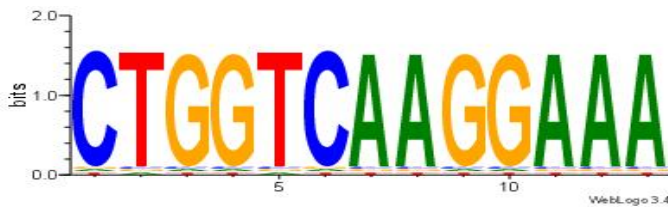
**Best Matches for Motif ID 237 (Highest to Lowest)**

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

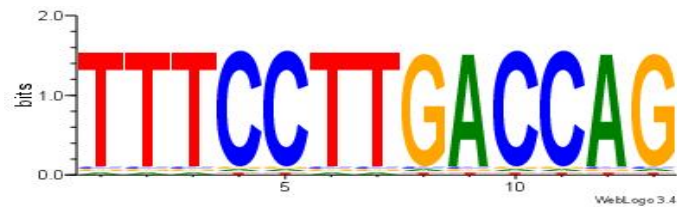
**Alignment:**

CTGGTCAAGGAAA  
-TAGCCAAGG<sub>A</sub>AA

Original motif      Consensus sequence: CTGGTCAAGGAAA



Reverse complement motif      Consensus sequence: TTTCCCTTGGACCAG

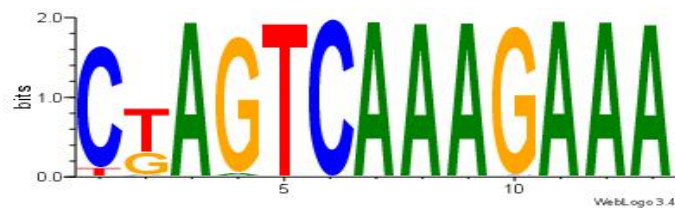


Dataset #: 1  
 Motif ID: 24  
 Motif name: Motif 24  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 12  
 Similarity score: 0.0581846

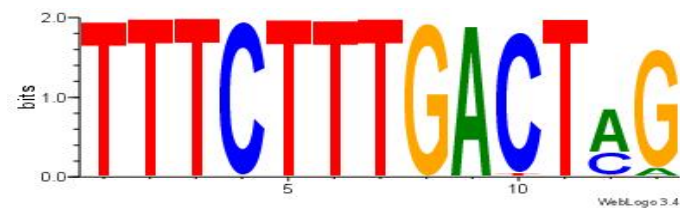
Alignment:

TTTCTTTGACTRG  
 TTKCCTTGGCTA-

Original motif      Consensus sequence: CKAGTCAAAGAAA



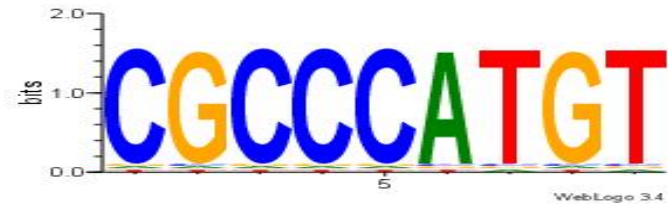
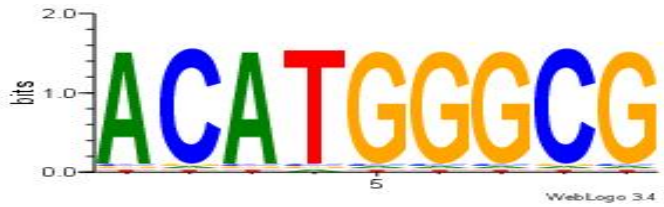
Reverse complement motif      Consensus sequence: TTTCTTTGACTRG



**Dataset #: 1      Motif ID: 238      Motif name: Motif 238**

Original motif      Consensus sequence: ACATGGGCG

Reverse complement motif      Consensus sequence: CGCCCATGT

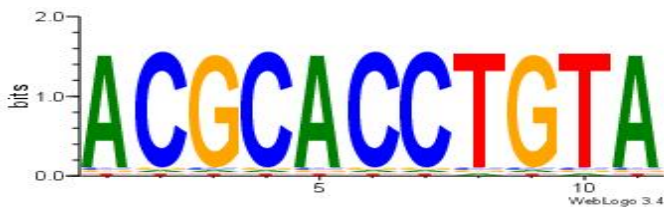


### Best Matches for Motif ID 238 (Highest to Lowest)

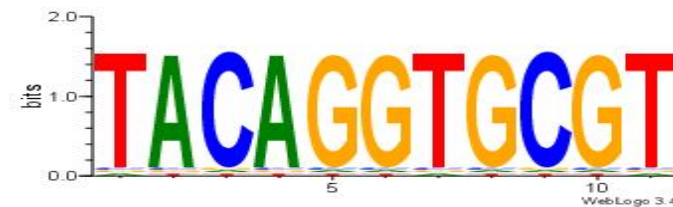
Dataset #: 1  
 Motif ID: 324  
 Motif name: Motif 324  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 2  
 Number of overlap: 9  
 Similarity score: 0.0421539

Alignment:  
 TACAGGTGCGT  
 -ACATGGGCG-

Original motif    Consensus sequence: ACGCACCTGTA



Reverse complement motif    Consensus sequence: TACAGGTGCGT

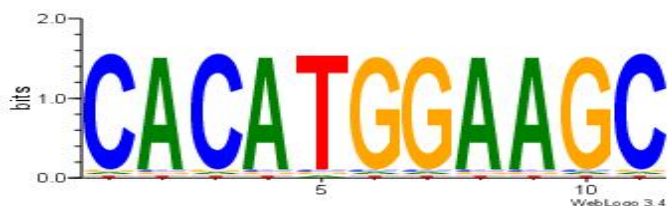


Dataset #: 1

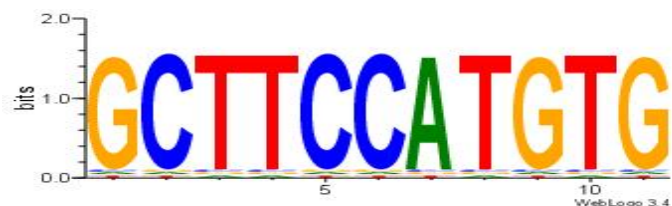
Motif ID: 353  
 Motif name: Motif 353  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 2  
 Number of overlap: 9  
 Similarity score: 0.0421539

Alignment:  
 CACATGGAAGC  
 -ACATGGGCG-

Original motif    Consensus sequence: CACATGGAAGC

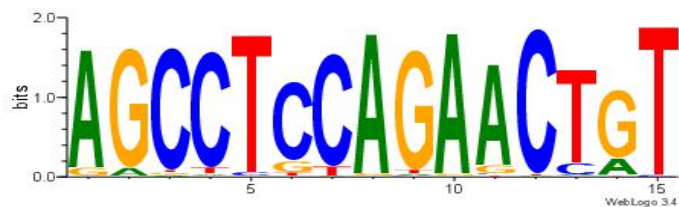


Reverse complement motif    Consensus sequence: GCTTCCATGTG

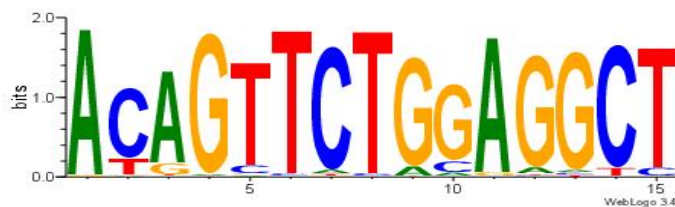


**Dataset #: 1      Motif ID: 239      Motif name: Motif 239**

Original motif    Consensus sequence: AGCCTCCAGAACTGT



Reverse complement motif    Consensus sequence: ACAGTTCTGGAGGCT



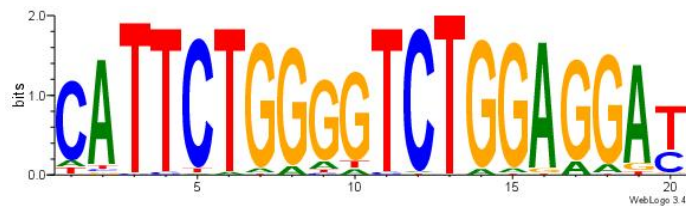
## Best Matches for Motif ID 239 (Highest to Lowest)

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

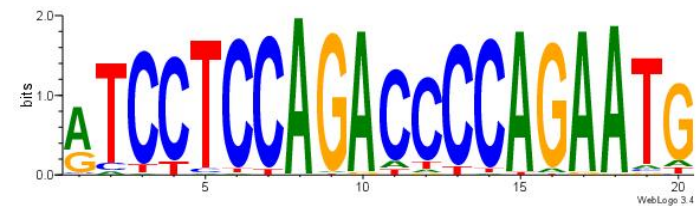
### Alignment:

```
MTCCTCCAGACCCCAGAATG  
AGCCTCCAGAACTGT-----
```

Original motif      Consensus sequence: CATTCTGGGGTCTGGAGGAY



Reverse complement motif      Consensus sequence:  
MTCCTCCAGACCCCAGAATG

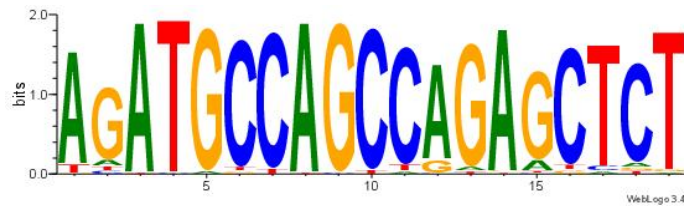


Dataset #: 1  
Motif ID: 307  
Motif name: Motif 307  
Matching format of first motif: Original Motif  
Matching format of second motif: Original Motif

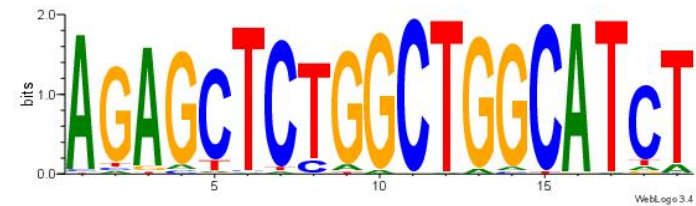
Direction: Backward  
 Position number: 1  
 Number of overlap: 15  
 Similarity score: 0.0931523

Alignment:  
 AGATGCCAGCCAGAGCTCT  
 ----AGCCTCCAGAACTGT

Original motif      Consensus sequence: AGATGCCAGCCAGAGCTCT

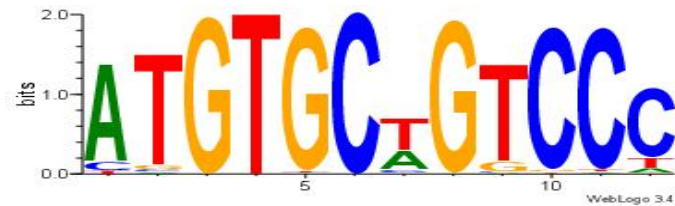


Reverse complement motif      Consensus sequence: AGAGCTCTGGCTGGCATCT



**Dataset #: 1      Motif ID: 240      Motif name: Motif 240**

Original motif      Consensus sequence: ATGTGCWGTC



Reverse complement motif      Consensus sequence: GGGACWGCACAT



**Best Matches for Motif ID 240 (Highest to Lowest)**

Dataset #: 1  
 Motif ID: 279

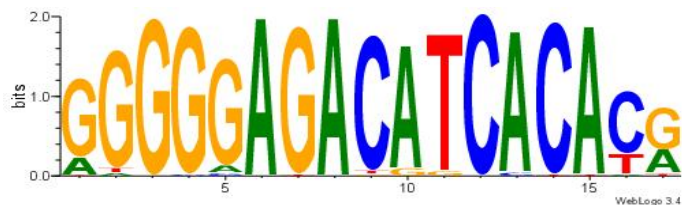


Motif name: Motif 279  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 5  
 Number of overlap: 12  
 Similarity score: 0.0578868

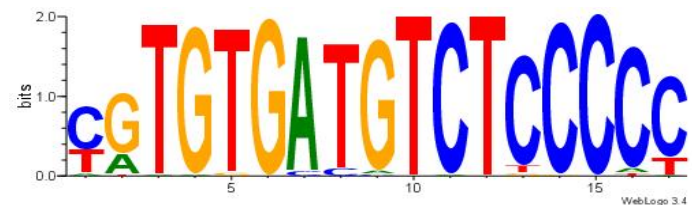
**Alignment:**

GGGGGAGACATCACACR  
 ----GGGACWGCACAT-

Original motif    Consensus sequence: GGGGGAGACATCACACR



Reverse complement motif    Consensus sequence: MGTGTGATGTCTCCCC

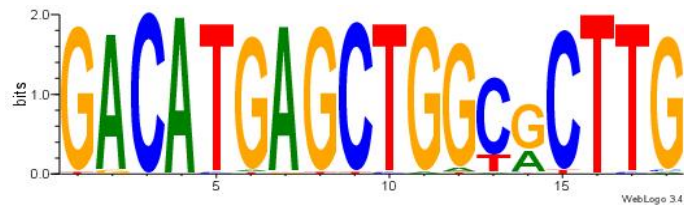


Dataset #: 1  
 Motif ID: 306  
 Motif name: Motif 306  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 4  
 Number of overlap: 12  
 Similarity score: 0.0660844

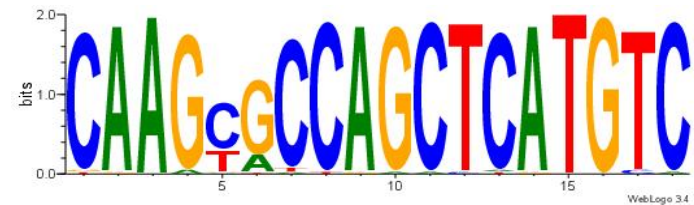
Alignment:

GACATGAGCTGGCGCTTG  
---ATGTGCWGTCCC---

Original motif      Consensus sequence: GACATGAGCTGGCGCTTG

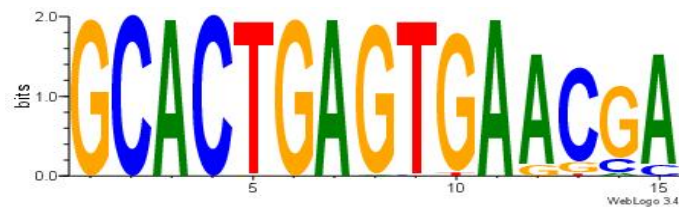


Reverse complement motif      Consensus sequence:  
CAAGCGCCAGCTCATGTC

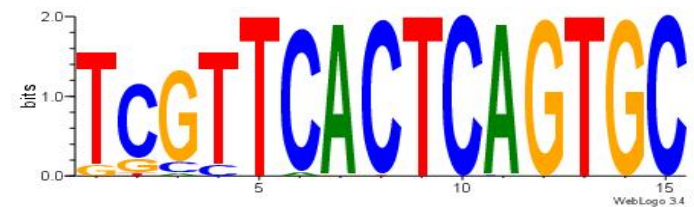


**Dataset #: 1      Motif ID: 241      Motif name: Motif 241**

Original motif      Consensus sequence: GCACTGAGTGAACGA



Reverse complement motif      Consensus sequence: TCGTTCAGTGC



**Best Matches for Motif ID 241 (Highest to Lowest)**

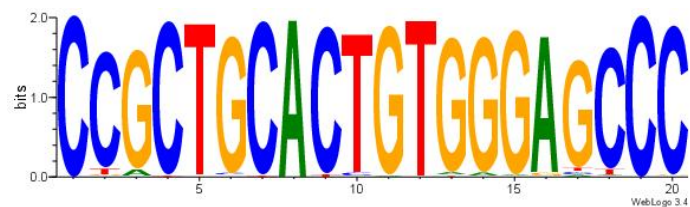
Dataset #:	1
Motif ID:	144
Motif name:	Motif 144
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward

Position number: 6  
Number of overlap: 15  
Similarity score: 0.0442756

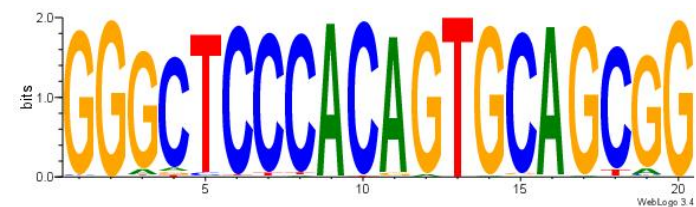
Alignment:

CCGCTGCACTGTGGGAGCCC  
-----GCACTGAGTGAACGA

Original motif    Consensus sequence: CCGCTGCACTGTGGGAGCCC



Reverse complement motif    Consensus sequence: GGGCTCCCACAGTGCAGCGG

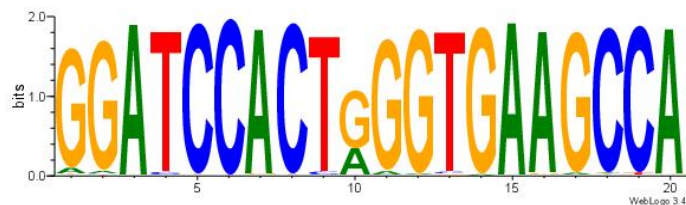


Dataset #: 1  
Motif ID: 61  
Motif name: Motif 61  
Matching format of first motif: Original Motif  
Matching format of second motif: Original Motif  
Direction: Forward  
Position number: 5  
Number of overlap: 15  
Similarity score: 0.0478162

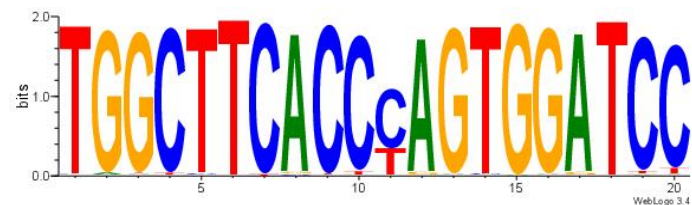
Alignment:

GGATCCACTGGGTGAAGCCA  
-----GCACTGAGTGAACGA-

Original motif      Consensus sequence: GGATCCACTGGGTGAAGCCA

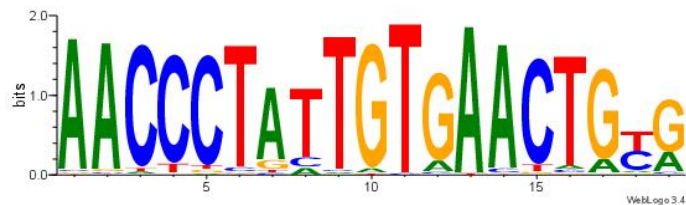


Reverse complement motif      Consensus sequence: TGGCTTCACCCAGTGGATCC

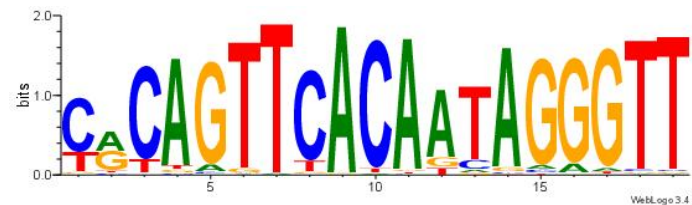


**Dataset #: 1      Motif ID: 242      Motif name: Motif 242**

Original motif      Consensus sequence: AACCTATTGTGAACTGYG



Reverse complement motif      Consensus sequence: CMCAGTTCACAATAGGGTT



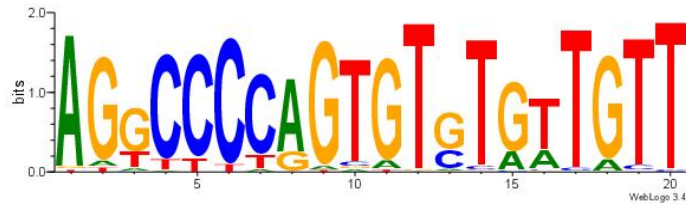
### Best Matches for Motif ID 242 (Highest to Lowest)

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

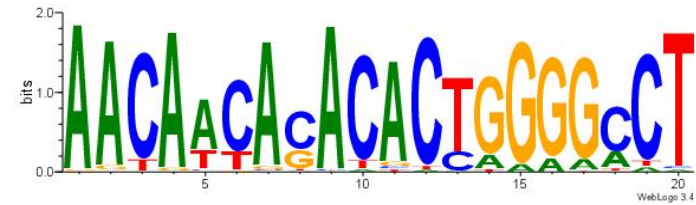
Alignment:

AACAACASACTGGGGCCT  
CMCAGTTCACAATAGGGTT-

Original motif      Consensus sequence: AGGCCCCAGTGTSTGTTGTT



Reverse complement motif      Consensus sequence:  
AACAACASACTGGGGCCT



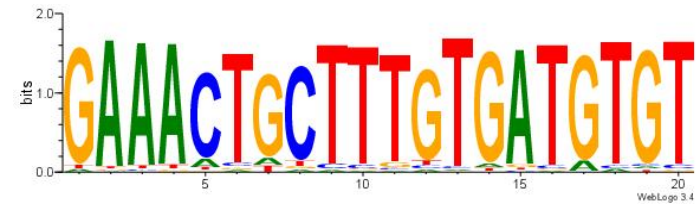
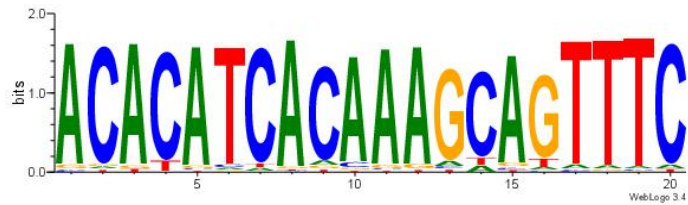
Dataset #: 1  
Motif ID: 202  
Motif name: Motif 202  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Original Motif  
Direction: Backward  
Position number: 2  
Number of overlap: 19  
Similarity score: 0.11357

Alignment:

ACACATCACAAAGCAGTTTC  
CMCAGTTCACAATAGGGTT-

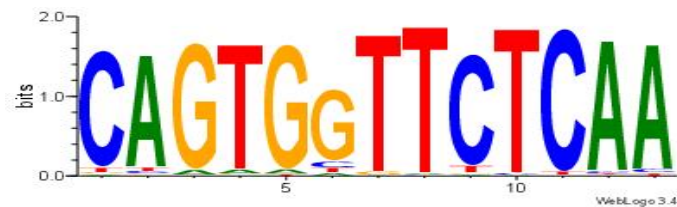
Original motif      Consensus sequence: ACACATCACAAAGCAGTTTC

Reverse complement motif      Consensus sequence:  
GAAACTGCTTTGTGATGTGT



**Dataset #: 1      Motif ID: 243      Motif name: Motif 243**

Original motif      Consensus sequence: CAGTGGTTCTCAA



Reverse complement motif      Consensus sequence: TTGAGAAcCACTG

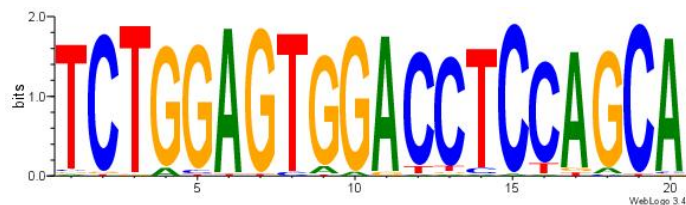


**Best Matches for Motif ID 243 (Highest to Lowest)**

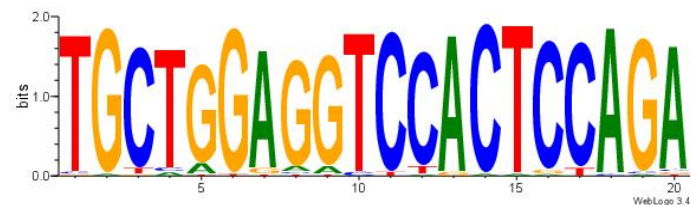
Dataset #:	1
Motif ID:	350
Motif name:	Motif 350
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	5
Number of overlap:	13
Similarity score:	0.0720775

Alignment:  
 TGCTGGAGGTCCACTCCAGA  
 ---TTGAGAACCACTG----

Original motif      Consensus sequence: TCTGGAGTGGACCTCCAGCA



Reverse complement motif      Consensus sequence: TGCTGGAGGTCCACTCCAGA

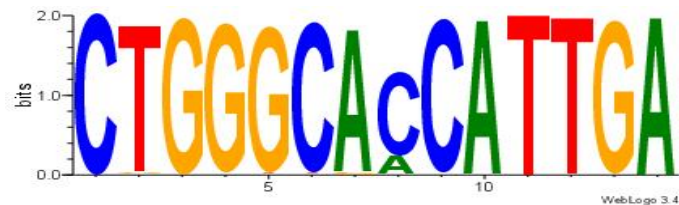


Dataset #: 1  
Motif ID: 147  
Motif name: Motif 147  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Original Motif  
Direction: Backward  
Position number: 1  
Number of overlap: 13  
Similarity score: 0.0768151

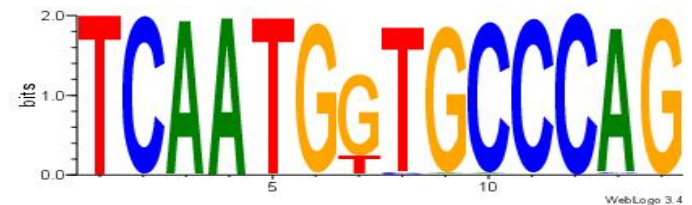
Alignment:

CTGGGCACCATTGA  
-TTGAGAACCACTG

Original motif      Consensus sequence: CTGGGCACCATTGA

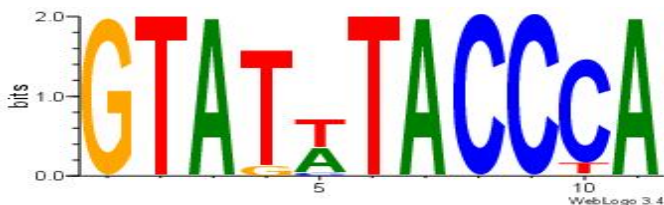


Reverse complement motif      Consensus sequence: TCAATGGTGCCCAAG



**Dataset #: 1      Motif ID: 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

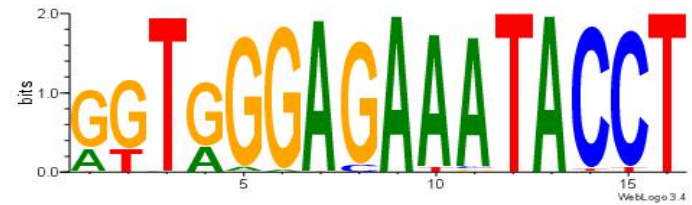
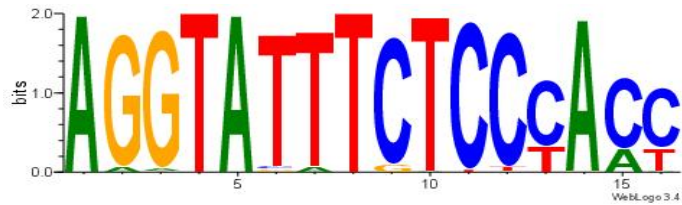
Alignment:

```
GGTGGGAGAAATACCT  
---TGGGTAWATAC--
```

Original motif      Consensus sequence: AGGTATTTCTCCCACC

Reverse complement motif      Consensus sequence:  
GGTGGGAGAAATACCT

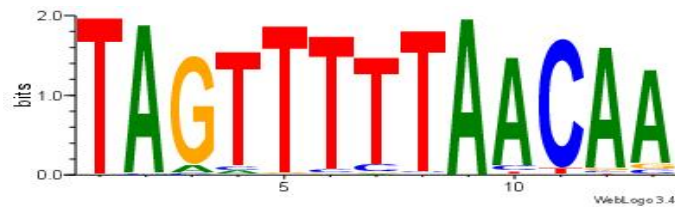




Dataset #: 1  
 Motif ID: 319  
 Motif name: Motif 319  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 11  
 Similarity score: 0.0769317

Alignment:  
 TTGTTAAAACTA  
 TGGTAWATACT--

Original motif      Consensus sequence: TAGTTTTTAACAA

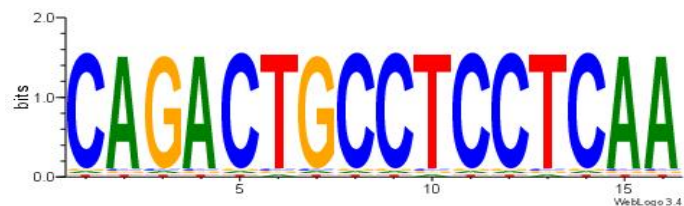


Reverse complement motif      Consensus sequence: TTGTTAAAACTA

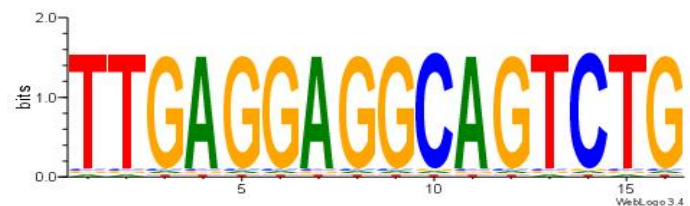


**Dataset #: 1      Motif ID: 245      Motif name: Motif 245**

Original motif    Consensus sequence: CAGACTGCCTCCTCAA



Reverse complement motif    Consensus sequence: TTGAGGAGGCAGTCTG



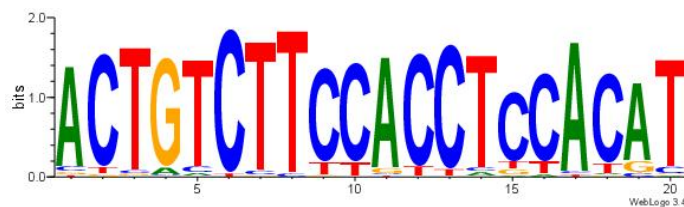
### Best Matches for Motif ID 245 (Highest to Lowest)

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

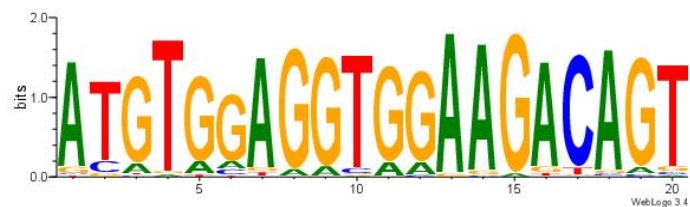
#### Alignment:

```
ATGTGGAGGTGGAAGACAGT
---TTGAGGAGGCAGTCTG---
```

Original motif    Consensus sequence: ACTGTCTTCCACCTCCACAT



Reverse complement motif    Consensus sequence: ATGTGGAGGTGGAAGACAGT

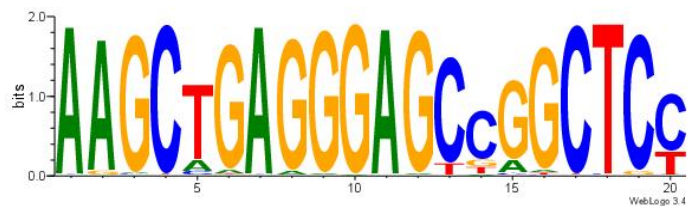


Dataset #: 1  
 Motif ID: 96  
 Motif name: Motif 96  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 4  
 Number of overlap: 16  
 Similarity score: 0.0972589

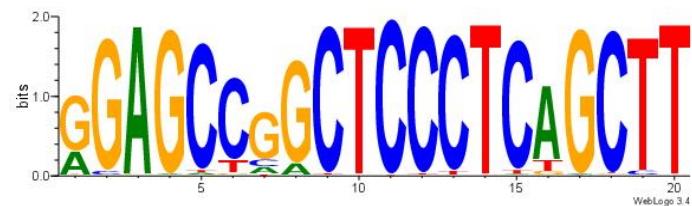
Alignment:

AAGCTGAGGGAGCCGGCTCC  
 -TTGAGGAGGCAGTCTG---

Original motif      Consensus sequence: AAGCTGAGGGAGCCGGCTCC



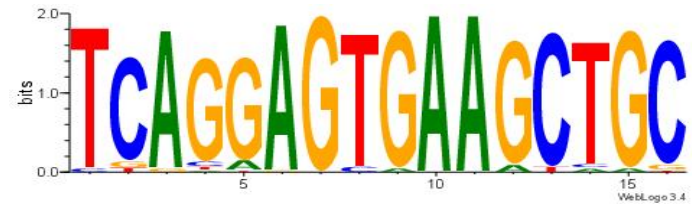
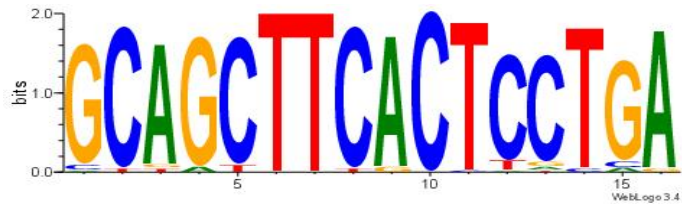
Reverse complement motif      Consensus sequence: GGAGCCGGCTCCCTCAGCTT



**Dataset #: 1      Motif ID: 246      Motif name: Motif 246**

Original motif      Consensus sequence: GCAGCTTCACTCCTGA

Reverse complement motif      Consensus sequence: TCAGGAGTGAAGCTGC

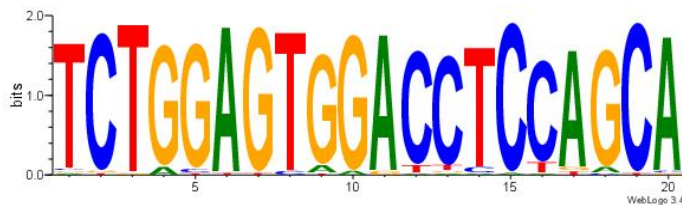


**Best Matches for Motif ID 246 (Highest to Lowest)**

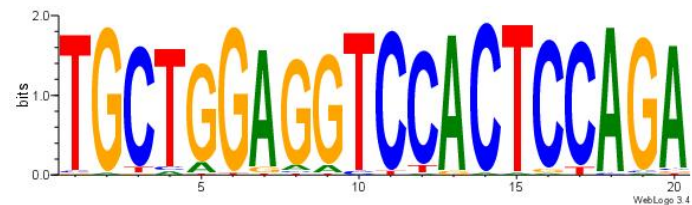
Dataset #: 1  
 Motif ID: 350  
 Motif name: Motif 350  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 16  
 Similarity score: 0.0626054

Alignment:  
 TCTGGAGTGGACCTCCAGCA  
 TCAGGAGTGAAGCTGC-----

Original motif      Consensus sequence: TCTGGAGTGGACCTCCAGCA



Reverse complement motif      Consensus sequence: TGCTGGAGGTCCACTCCAGA

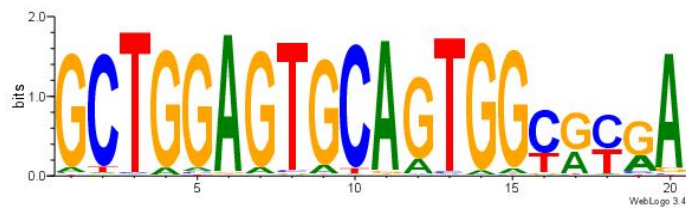


Dataset #: 1  
 Motif ID: 3  
 Motif name: Motif 3  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 16  
 Similarity score: 0.0810673

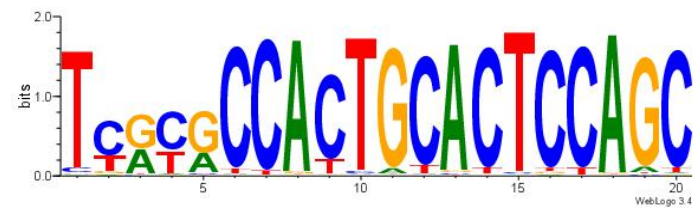
Alignment:

GCTGGAGTGCAGTGGCRYGA  
 ----TCAGGAGTGAAGCTGC

Original motif      Consensus sequence: GCTGGAGTGCAGTGGCRYGA



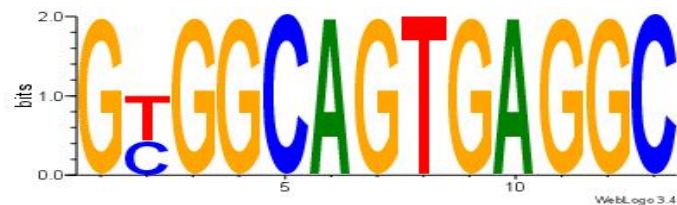
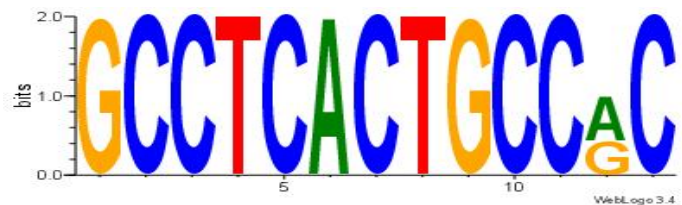
Reverse complement motif      Consensus sequence: TCKMGCCACTGCACTCCAGC



**Dataset #: 1      Motif ID: 247      Motif name: Motif 247**

Original motif      Consensus sequence: GCCTCACTGCCRC

Reverse complement motif      Consensus sequence: GKGGCAGTGAGG

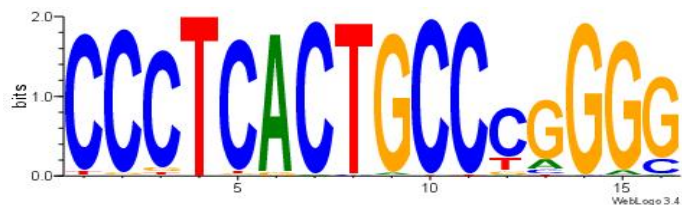


**Best Matches for Motif ID 247 (Highest to Lowest)**

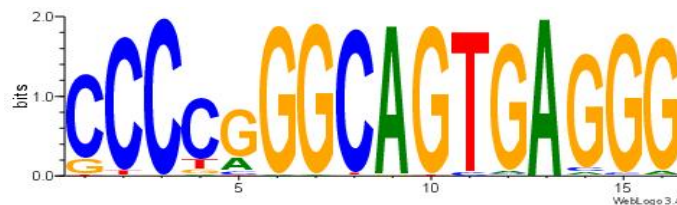
Dataset #: 1  
 Motif ID: 136  
 Motif name: Motif 136  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 13  
 Similarity score: 0.0407776

Alignment:  
 CCCCggGCAGTGAGGG  
 ---GKGGCAGTGAGGC

Original motif      Consensus sequence: CCCTCACTGCCGGGG



Reverse complement motif      Consensus sequence: CCCCggGCAGTGAGGG

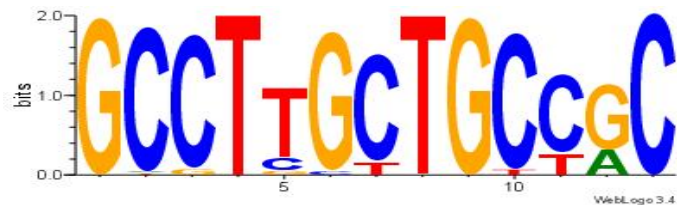


Dataset #: 1  
 Motif ID: 229  
 Motif name: Motif 229  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 13  
 Similarity score: 0.0419595

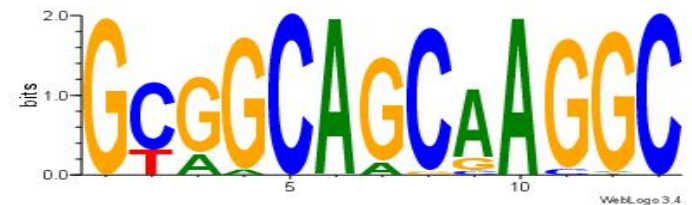
Alignment:

GCCTTGCTGCCGC  
 GCCTCACTGCCRC

Original motif    Consensus sequence: GCCTTGCTGCCGC

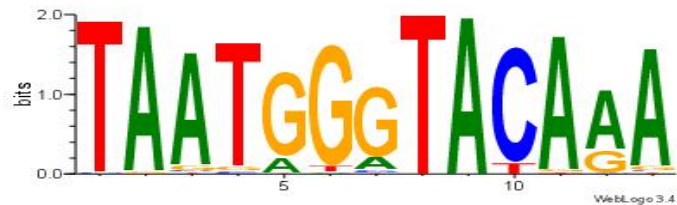


Reverse complement motif    Consensus sequence: GCGGCAGCAAGGC

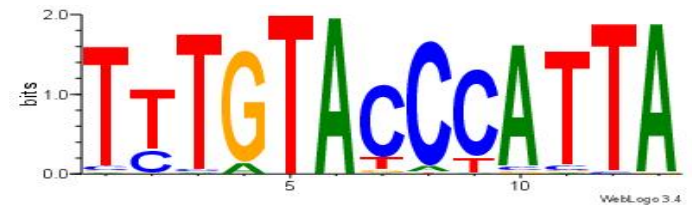


**Dataset #: 1      Motif ID: 248      Motif name: Motif 248**

Original motif    Consensus sequence: TAATGGGTACAAA



Reverse complement motif    Consensus sequence: TTTGTACCCATTA



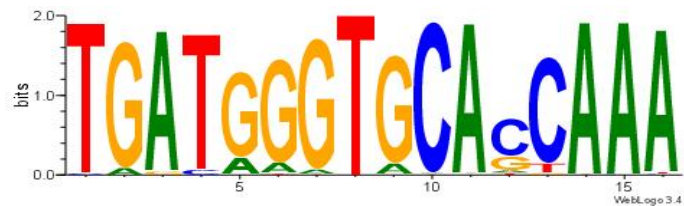
## Best Matches for Motif ID 248 (Highest to Lowest)

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

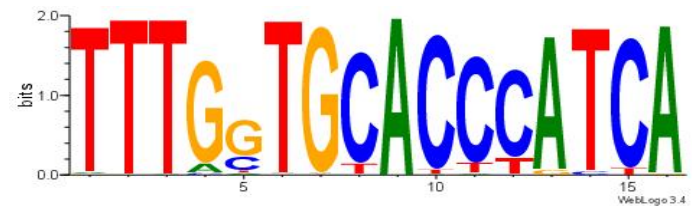
### Alignment:

```
TGATGGGTGCACCAA  
TAATGGGTACAAA---
```

Original motif      Consensus sequence: TGATGGGTGCACCAA



Reverse complement motif      Consensus sequence:  
TTTGGTGCACCCATCA



---

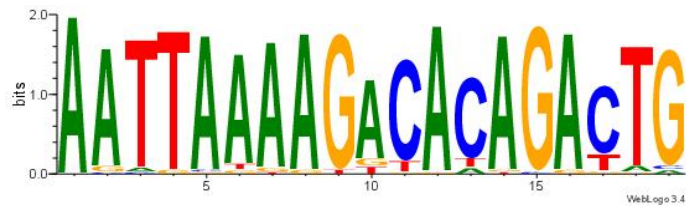
Dataset #: 1  
Motif ID: 356  
Motif name: Motif 356  
Matching format of first motif: Original Motif  
Matching format of second motif: Original Motif



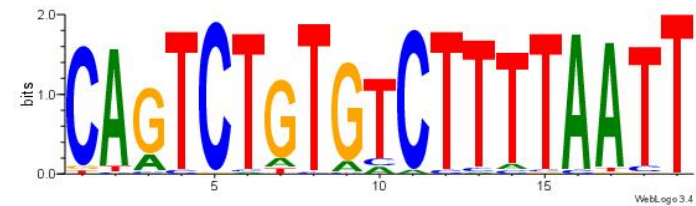
Direction: Backward  
 Position number: 4  
 Number of overlap: 13  
 Similarity score: 0.0698241

Alignment:  
 AATTAAAAGACACAGACTG  
 ---TAATGGGTACAAA---

Original motif      Consensus sequence: AATTAAAAGACACAGACTG

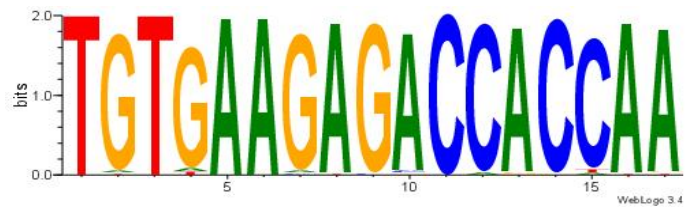


Reverse complement motif      Consensus sequence: CAGTCTGTCTTTTAATT

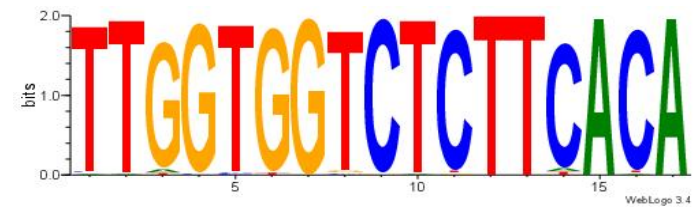


**Dataset #: 1      Motif ID: 249      Motif name: Motif 249**

Original motif      Consensus sequence: TGTGAAGAGACCACCA



Reverse complement motif      Consensus sequence: TTGGTGGTCTCTTCACA



**Best Matches for Motif ID 249 (Highest to Lowest)**

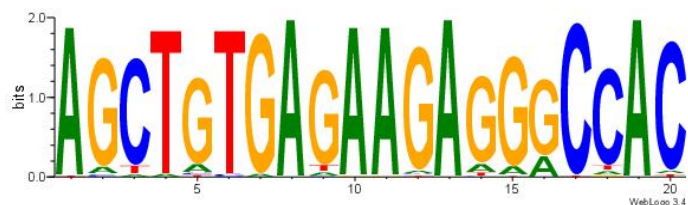
Dataset #: 1

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

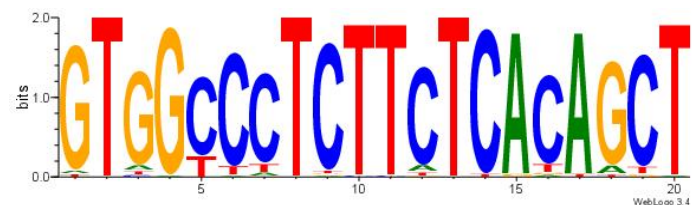
**Alignment:**

AGCTGTGAGAAGAGGGCCAC  
 ---TGTGAAGAGACCACCAA

Original motif    Consensus sequence: AGCTGTGAGAAGAGGGCCAC



Reverse complement motif    Consensus sequence: GTGGCCCTCTTCTCACAGCT



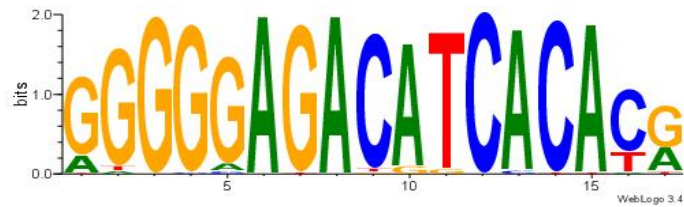
Dataset #: 1  
 Motif ID: 279  
 Motif name: Motif 279  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 17

Similarity score: 0.106605

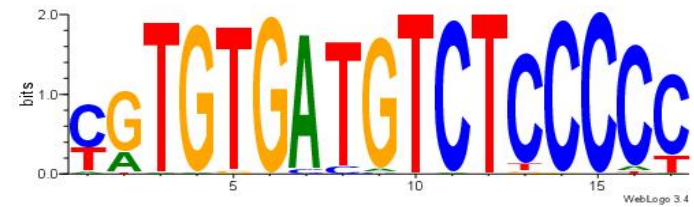
Alignment:

MGTGTGATGTCTCCCC  
TTGGTGGTCTCTCACA

Original motif      Consensus sequence: GGGGGAGACATCACACR

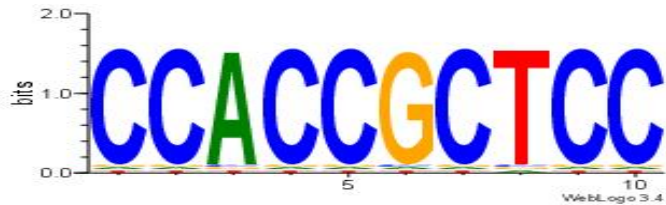


Reverse complement motif      Consensus sequence: MGTGTGATGTCTCCCC

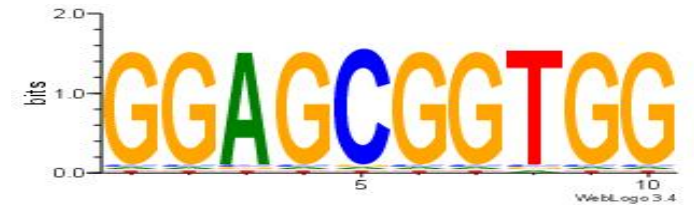


**Dataset #: 1      Motif ID: 250      Motif name: Motif 250**

Original motif      Consensus sequence: CCACCGCTCC



Reverse complement motif      Consensus sequence: GGAGCGGTGG



**Best Matches for Motif ID 250 (Highest to Lowest)**

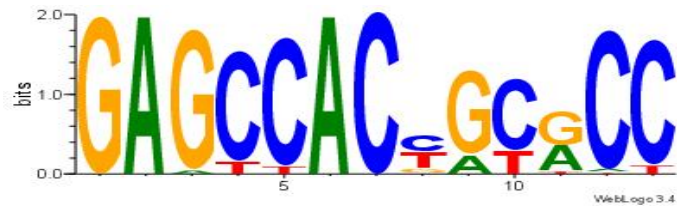
Dataset #:	1
Motif ID:	107
Motif name:	Motif 107
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement

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

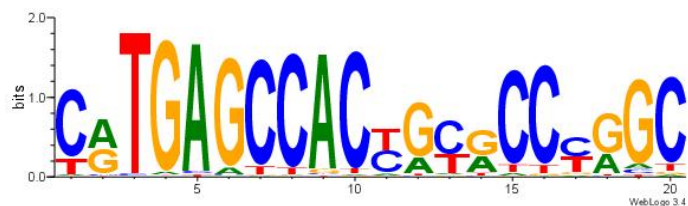


Dataset #: 1  
 Motif ID: 56  
 Motif name: Motif 56  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 7  
 Number of overlap: 10  
 Similarity score: 0.0459856

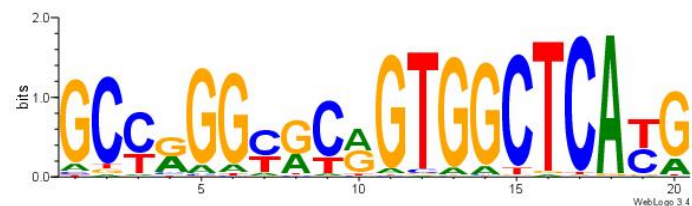
**Alignment:**

CRTGAGCCACYGYRCCYGGC  
 -----CCACCGCTCC-----

Original motif      Consensus sequence: CRTGAGCCACYGYRCCYGGC

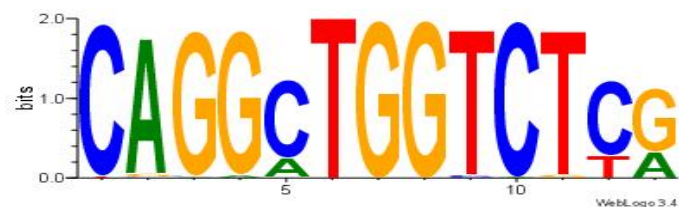


Reverse complement motif      Consensus sequence: GCCKGGMKCMGTGGCTCAKG



**Dataset #: 1      Motif ID: 251      Motif name: Motif 251**

Original motif      Consensus sequence: CAGGCTGGTCTCG



Reverse complement motif      Consensus sequence: CGAGACCAGCCTG



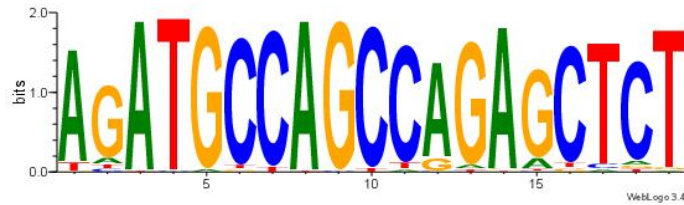
### Best Matches for Motif ID 251 (Highest to Lowest)

Dataset #:	1
Motif ID:	307
Motif name:	Motif 307
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	7
Number of overlap:	13
Similarity score:	0.0730434

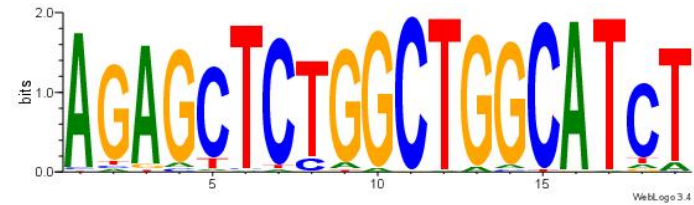
Alignment:

AGATGCCAGCCAGAGCTCT  
CGAGACCAGCCTG-----

Original motif      Consensus sequence: AGATGCCAGCCAGAGCTCT



Reverse complement motif      Consensus sequence:  
AGAGCTCTGGCTGGCATCT

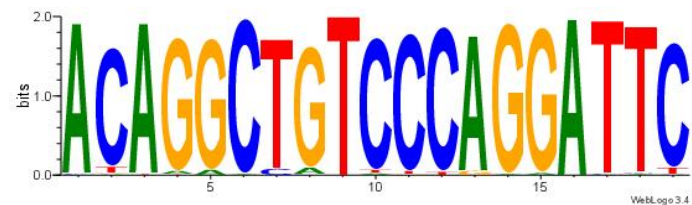
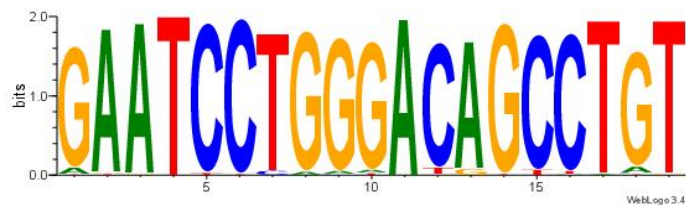


Dataset #: 1  
Motif ID: 192  
Motif name: Motif 192  
Matching format of first motif: Original Motif  
Matching format of second motif: Reverse Complement  
Direction: Forward  
Position number: 6  
Number of overlap: 13  
Similarity score: 0.0761402

Alignment:  
ACAGGCTGTCCCAGGATTC  
-----CAGGCTGGTCTCG-

Original motif      Consensus sequence: GAATCCTGGGACAGCCTGT

Reverse complement motif      Consensus sequence:  
ACAGGCTGTCCCAGGATTC



**Dataset #: 1      Motif ID: 252      Motif name: Motif 252**

Original motif      Consensus sequence: AATTAGCYRGG



Reverse complement motif      Consensus sequence: CCMKGCTAATT

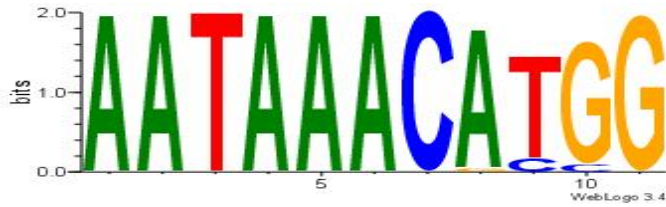


**Best Matches for Motif ID 252 (Highest to Lowest)**

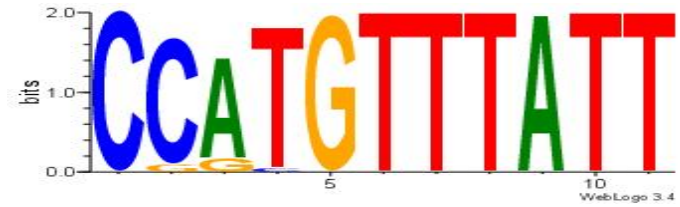
Dataset #:	1
Motif ID:	226
Motif name:	Motif 226
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	11
Similarity score:	0.0630561

Alignment:  
 CCATGTTTATT  
 CCMKGCTAATT

Original motif      Consensus sequence: AATAACATGG



Reverse complement motif      Consensus sequence: CCATGTTTATT

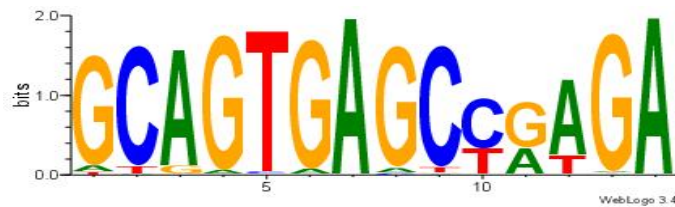


Dataset #: 1  
Motif ID: 38  
Motif name: Motif 38  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Reverse Complement  
Direction: Backward  
Position number: 3  
Number of overlap: 11  
Similarity score: 0.0649059

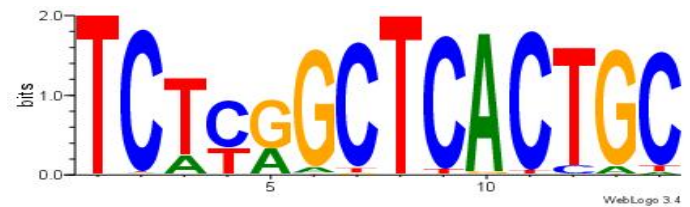
Alignment:

TCTMKGCTCACTGC  
-CCMKGCTAATT--

Original motif      Consensus sequence: GCAGTGAGCCGAGA



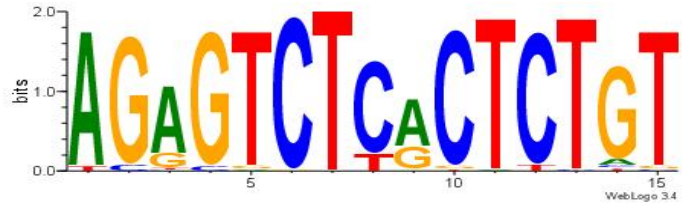
Reverse complement motif      Consensus sequence: TCTMKGCTCACTGC



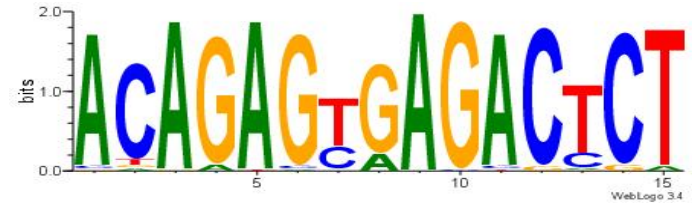


**Dataset #: 1      Motif ID: 253      Motif name: Motif 253**

Original motif      Consensus sequence: AGAGTCTCACTCTGT



Reverse complement motif      Consensus sequence: ACAGAGTGAGACTCT



**Best Matches for Motif ID 253 (Highest to Lowest)**

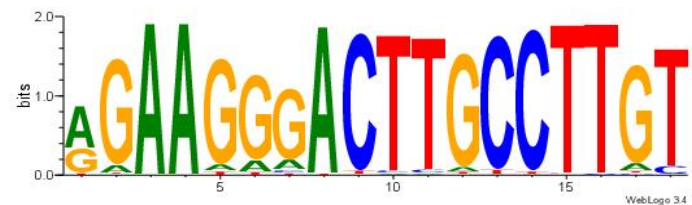
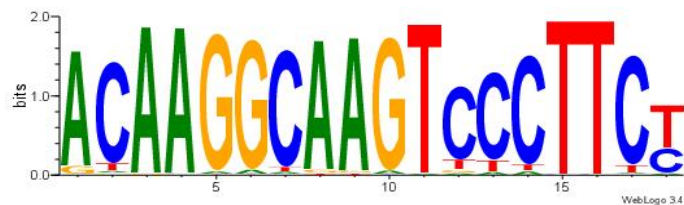
Dataset #:	1
Motif ID:	231
Motif name:	Motif 231
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	15
Similarity score:	0.0826494

**Alignment:**

```
ACAAGGCAAGTCCCTTCY
---ACAGAGTGAGACTCT
```

Original motif      Consensus sequence: ACAAGGCAAGTCCCTTCY

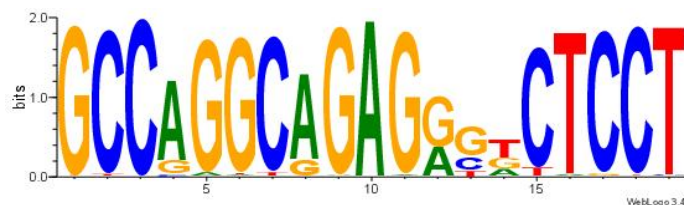
Reverse complement motif      Consensus sequence: MGAAGGACTTGCCTTGT



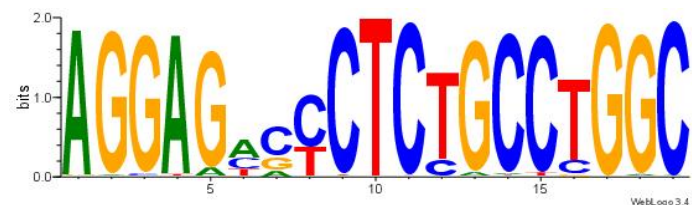
Dataset #: 1  
 Motif ID: 43  
 Motif name: Motif 43  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 4  
 Number of overlap: 15  
 Similarity score: 0.0874293

Alignment:  
 AGGAGRCMCTCTGCCTGGC  
 -AGAGTCTCACTCTGT---

Original motif      Consensus sequence: GCCAGGCAGAGRGKCTCCT

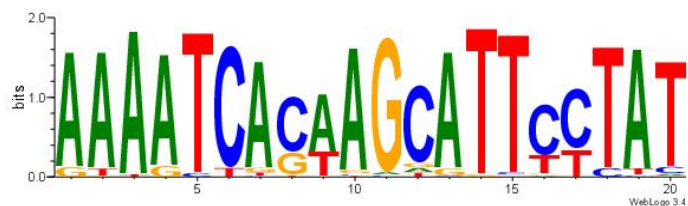


Reverse complement motif      Consensus sequence: AGGAGRCMCTCTGCCTGGC

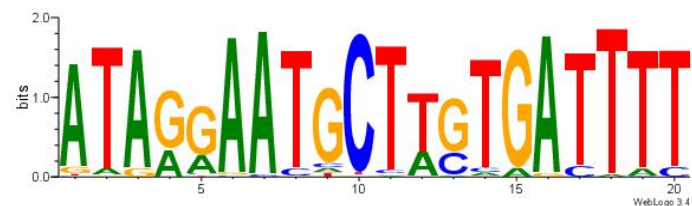


**Dataset #: 1      Motif ID: 254      Motif name: Motif 254**

Original motif      Consensus sequence: AAAATCACAAGCATTCTAT



Reverse complement motif      Consensus sequence: ATAGGAATGCTTGTGATTTT



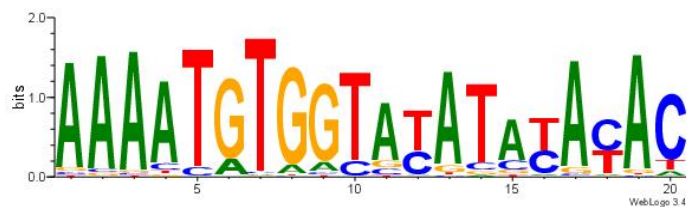
### Best Matches for Motif ID 254 (Highest to Lowest)

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

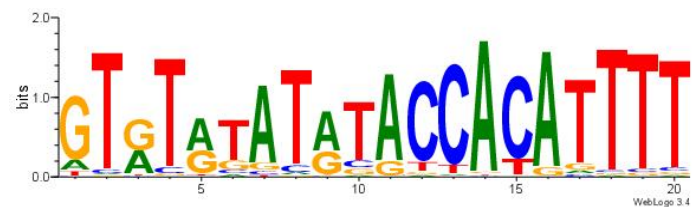
#### Alignment:

```
AAAATGTGGTAYATAYAYAC
AAAATCACAAGCATTCTAT
```

Original motif      Consensus sequence: AAAATGTGGTAYATAYAYAC



Reverse complement motif      Consensus sequence: GTKTMTATMTACCACATTTT

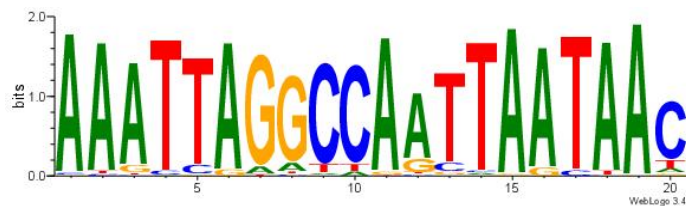


Dataset #: 1  
 Motif ID: 308  
 Motif name: Motif 308  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 2  
 Number of overlap: 19  
 Similarity score: 0.596633

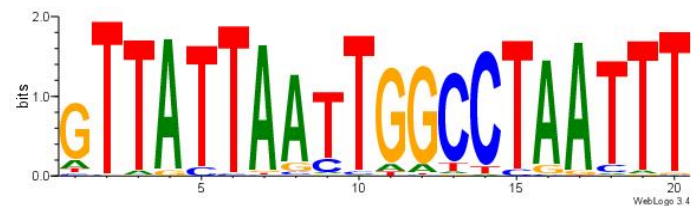
Alignment:

GTTATTAATTGGCCTAATTT-  
 -ATAGGAATGCTTGTGATTTT

Original motif      Consensus sequence: AAATTAGGCCAATTAATAAC



Reverse complement motif      Consensus sequence:  
 GTTATTAATTGGCCTAATTT



**Dataset #: 1      Motif ID: 255      Motif name: Motif 255**

Original motif      Consensus sequence: CTGCTATAACAAA

Reverse complement motif      Consensus sequence: TTTGTTATAGCAG

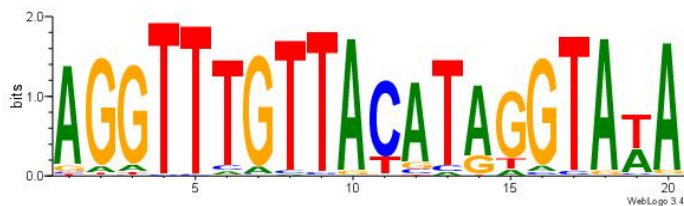


**Best Matches for Motif ID 255 (Highest to Lowest)**

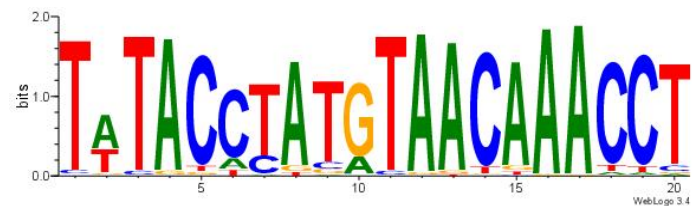
Dataset #: 1  
 Motif ID: 137  
 Motif name: Motif 137  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 5  
 Number of overlap: 13  
 Similarity score: 0.0686391

Alignment:  
 AGGTTTGTTACATAGGTAWA  
 ----TTTGTATATAGCAG----

Original motif      Consensus sequence: AGGTTTGTTACATAGGTAWA



Reverse complement motif      Consensus sequence: TWTACCTATGTAACAAACCT

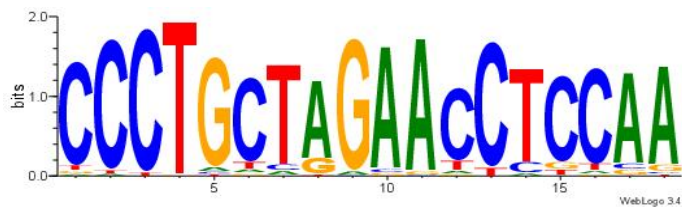


Dataset #: 1  
 Motif ID: 299  
 Motif name: Motif 299  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 3  
 Number of overlap: 13  
 Similarity score: 0.0785239

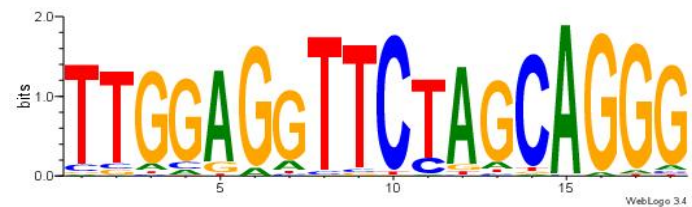
Alignment:

TTGGAGGTTCTAGCAGGG  
 ---TTTGTTATAGCAG--

Original motif      Consensus sequence: CCCTGCTAGAACCTCCAA



Reverse complement motif      Consensus sequence: TTGGAGGTTCTAGCAGGG

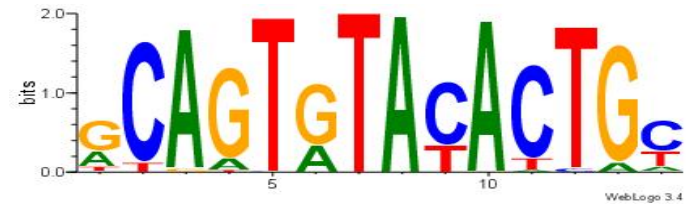
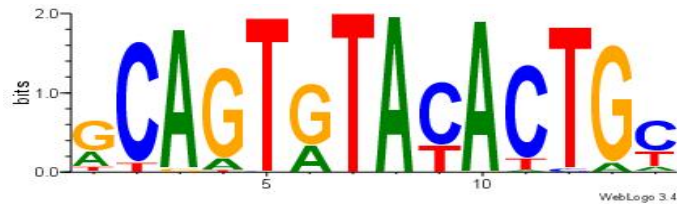



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**Dataset #: 1      Motif ID: 256      Motif name: Motif 256**

Original motif      Consensus sequence: RCAGTGTACTGY

Reverse complement motif      Consensus sequence: KCAGTGTACTGY

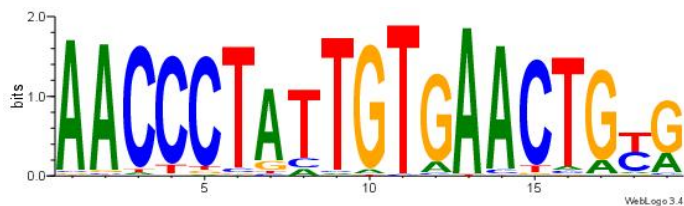


**Best Matches for Motif ID 256 (Highest to Lowest)**

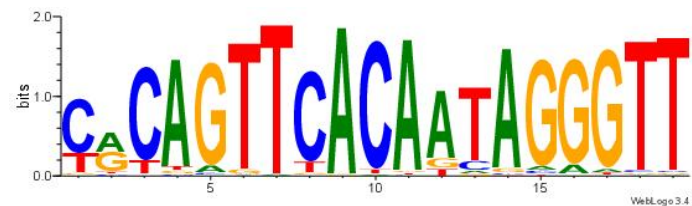
Dataset #: 1  
 Motif ID: 242  
 Motif name: Motif 242  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 5  
 Number of overlap: 14  
 Similarity score: 0.0643389

Alignment:  
 AACCTATTGTGAACTGYG  
 ----RCAGTGTACTACTGY-

Original motif      Consensus sequence: AACCTATTGTGAACTGYG



Reverse complement motif      Consensus sequence: CMCAGTTCACAATAGGGTT

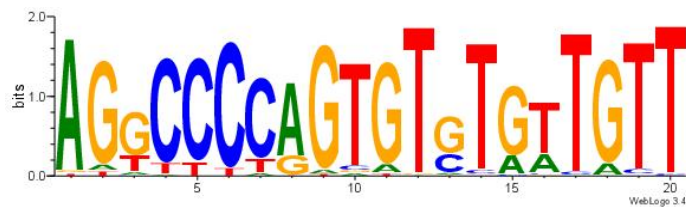


Dataset #: 1  
 Motif ID: 176  
 Motif name: Motif 176  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 2  
 Number of overlap: 14  
 Similarity score: 0.0671024

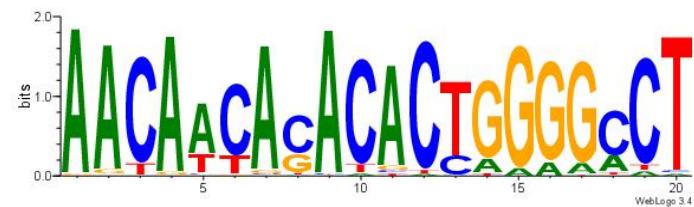
Alignment:

AGGCCCCAGTGTSTGTTGTT  
 -----RCAGTGTACTGY-

Original motif      Consensus sequence: AGGCCCCAGTGTSTGTTGTT



Reverse complement motif      Consensus sequence: AACACASACTGGGGCCT

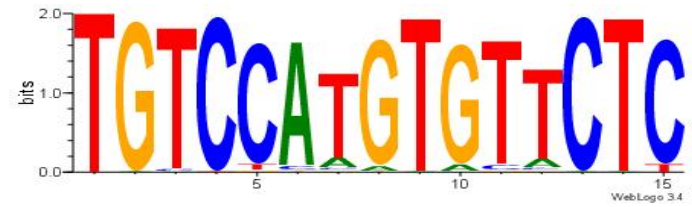
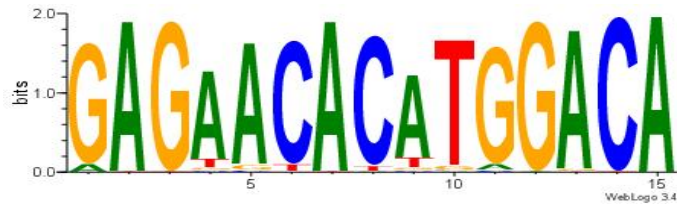


**Dataset #: 1      Motif ID: 257      Motif name: Motif 257**

Original motif      Consensus sequence: GAGAACACATGGACA

Reverse complement motif      Consensus sequence: TGTCCATGTGTTCT



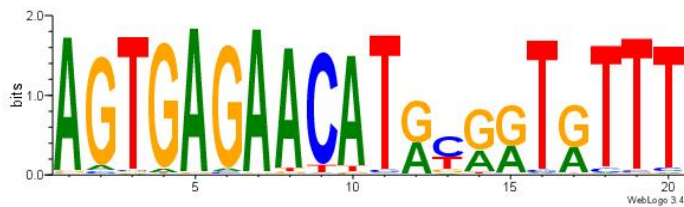


**Best Matches for Motif ID 257 (Highest to Lowest)**

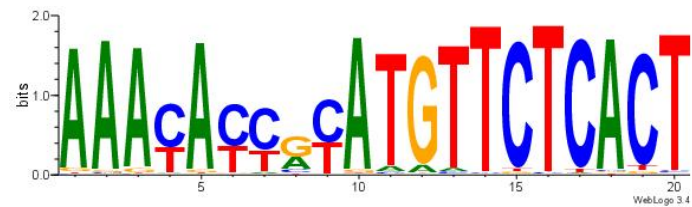
Dataset #: 1  
 Motif ID: 63  
 Motif name: Motif 63  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 3  
 Number of overlap: 15  
 Similarity score: 0.0985209

Alignment:  
 AGTGAGAACATRYRRTRTTT  
 ---GAGAACACATGGACA---

Original motif    Consensus sequence: AGTGAGAACATRYRRTRTTT



Reverse complement motif    Consensus sequence: AAAMAMMKMATGTTCTCACT

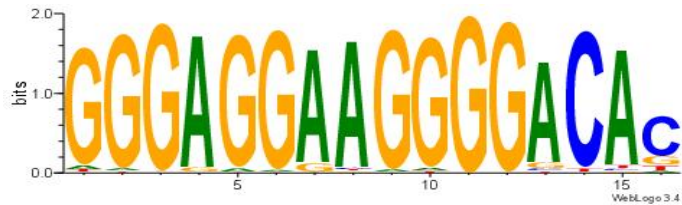


Dataset #: 1  
 Motif ID: 221  
 Motif name: Motif 221  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 2  
 Number of overlap: 15  
 Similarity score: 0.10032

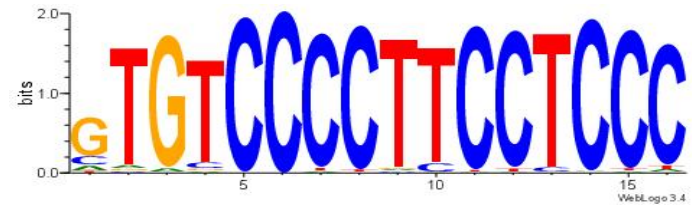
Alignment:

GGGAGGAAGGGGACAC  
 GAGAACACATGGACA-

Original motif    Consensus sequence: GGGAGGAAGGGGACAC



Reverse complement motif    Consensus sequence: GTGTCCCCTTCCTCCC

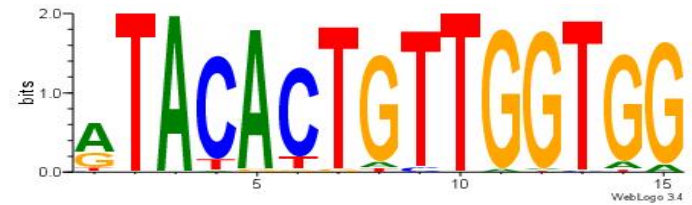
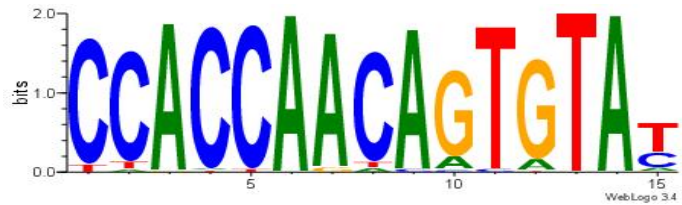



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**Dataset #: 1      Motif ID: 258      Motif name: Motif 258**

Original motif    Consensus sequence: CCACCAACAGTGTAY

Reverse complement motif    Consensus sequence: MTACACTGTTGGT

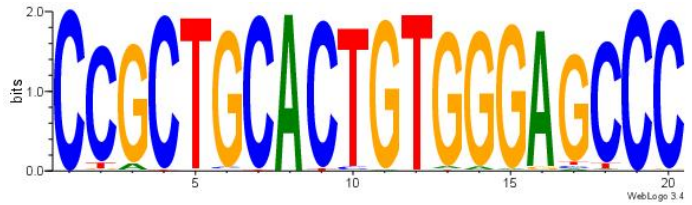


**Best Matches for Motif ID 258 (Highest to Lowest)**

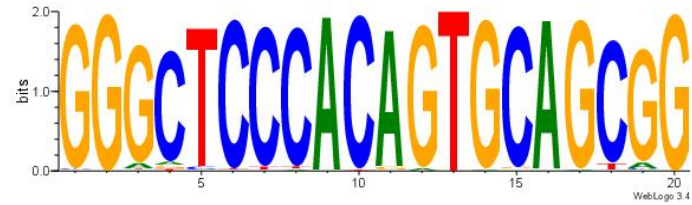
Dataset #: 1  
 Motif ID: 144  
 Motif name: Motif 144  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 3  
 Number of overlap: 15  
 Similarity score: 0.0771788

Alignment:  
 GGGCTCCCACAGTGCAGCGG  
 ---CCACCAACAGTGTAY--

Original motif      Consensus sequence: CCGCTGCACTGTGGGAGCCC



Reverse complement motif      Consensus sequence: GGGCTCCCACAGTGCAGCGG

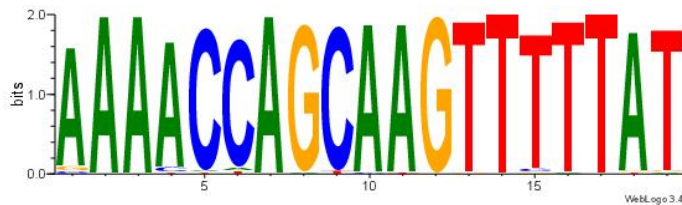


Dataset #: 1  
 Motif ID: 330  
 Motif name: Motif 330  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 5  
 Number of overlap: 15  
 Similarity score: 0.0810042

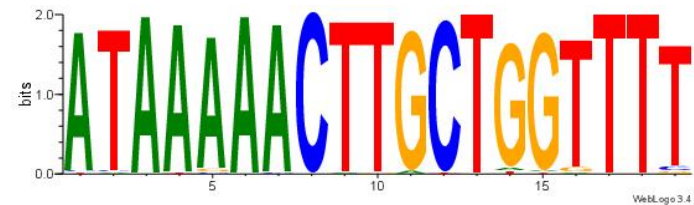
Alignment:

ATAAAACTTGCTGGTTTT  
 MTACACTGTTGGTGG----

Original motif      Consensus sequence: AAAACCAGCAAGTTTTTAT



Reverse complement motif      Consensus sequence: ATAAAACTTGCTGGTTTT

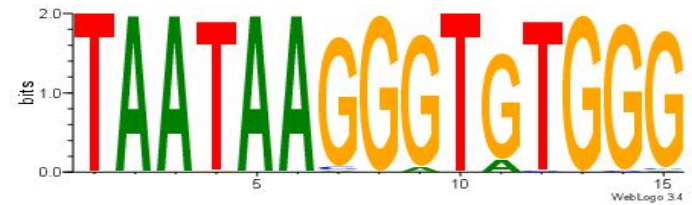
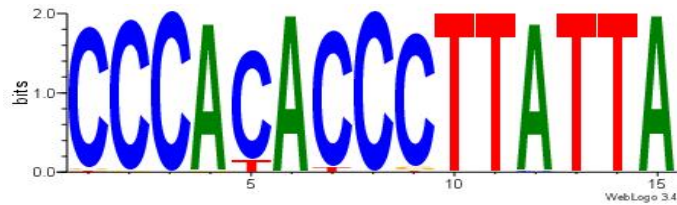



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**Dataset #: 1      Motif ID: 259      Motif name: Motif 259**

Original motif      Consensus sequence: CCCACACCCTTATTA

Reverse complement motif      Consensus sequence: TAATAAGGGTGTG

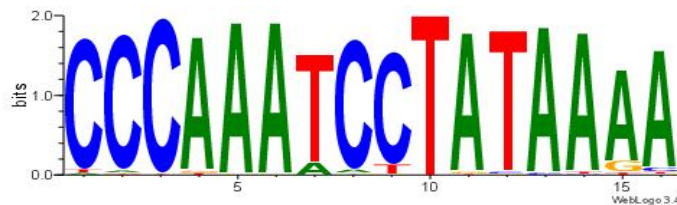


**Best Matches for Motif ID 259 (Highest to Lowest)**

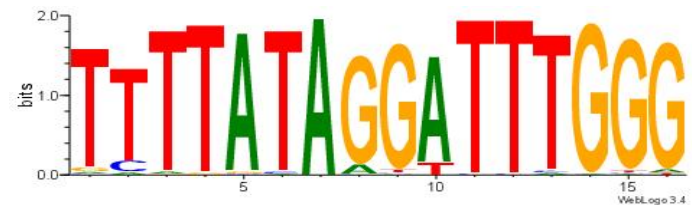
Dataset #: 1  
 Motif ID: 169  
 Motif name: Motif 169  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 15  
 Similarity score: 0.0922705

Alignment:  
 TTTTATAGGATTTGGG  
 -TAATAAGGGTGTGGG

Original motif      Consensus sequence: CCCAATCCTATAAAA



Reverse complement motif      Consensus sequence: TTTTATAGGATTTGGG

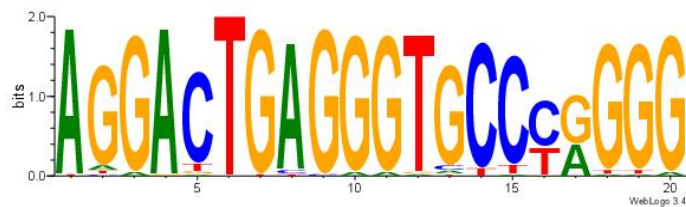


Dataset #: 1  
 Motif ID: 312  
 Motif name: Motif 312  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 4  
 Number of overlap: 15  
 Similarity score: 0.0982406

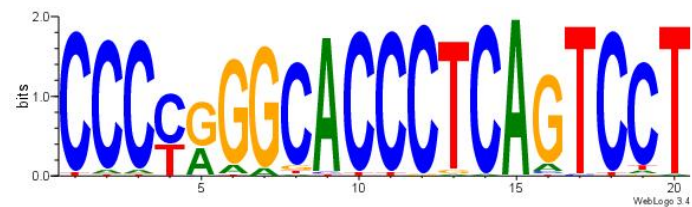
Alignment:

CCCMKGGCACCCCTCAGTCCT  
 ---CCCACACCCTTATTA--

Original motif      Consensus sequence: AGGACTGAGGGTGCCYRGGG



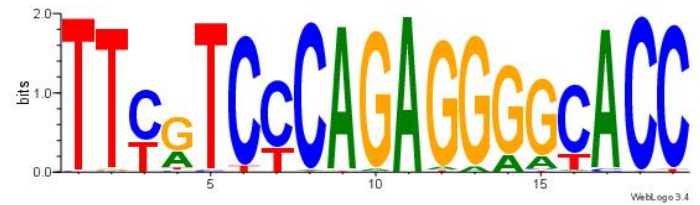
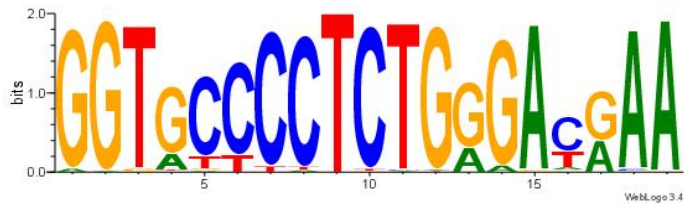
Reverse complement motif      Consensus sequence: CCCMKGGCACCCCTCAGTCCT



**Dataset #: 1      Motif ID: 260      Motif name: Motif 260**

Original motif      Consensus sequence: GGTGCCCTCTGGGACRAA

Reverse complement motif      Consensus sequence: TTMGTCCCAGAGGGGCACC

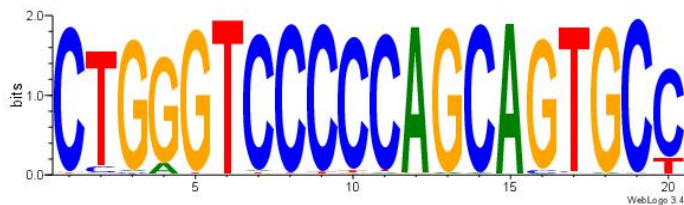


**Best Matches for Motif ID 260 (Highest to Lowest)**

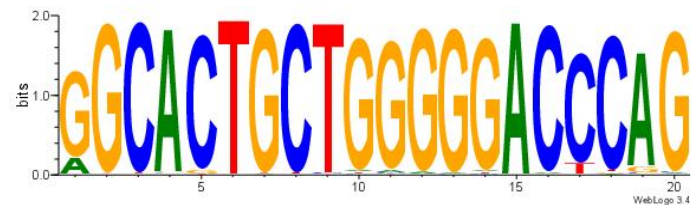
Dataset #: 1  
 Motif ID: 84  
 Motif name: Motif 84  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 19  
 Similarity score: 0.0961044

Alignment:  
 CTGGGTCCCCCAGCAGTGCC  
 TTMGTCCCAGAGGGGCACC-

Original motif      Consensus sequence: CTGGGTCCCCCAGCAGTGCC



Reverse complement motif      Consensus sequence: GGCAGTCTGGGGGACCCAG

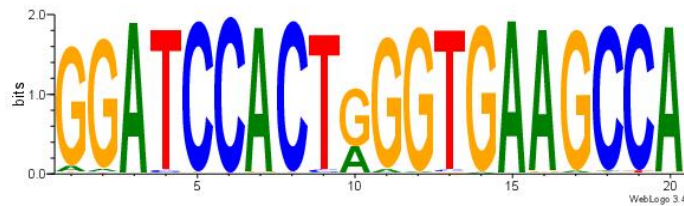


Dataset #: 1  
 Motif ID: 61  
 Motif name: Motif 61  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 2  
 Number of overlap: 19  
 Similarity score: 0.100972

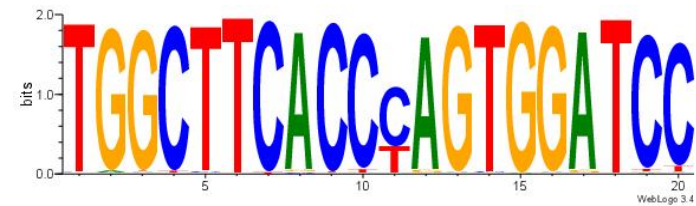
Alignment:

TGGCTTCACCCAGTGGATCC  
 -TTMGTCCCAGAGGGGCACC

Original motif      Consensus sequence: GGATCCACTGGGTGAAGCCA



Reverse complement motif      Consensus sequence: TGGCTTCACCCAGTGGATCC



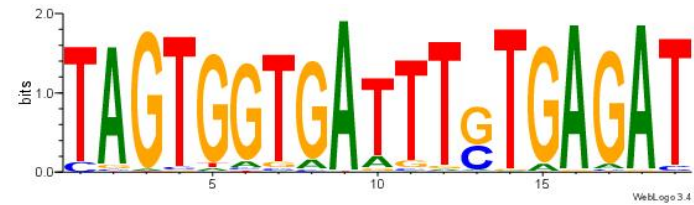
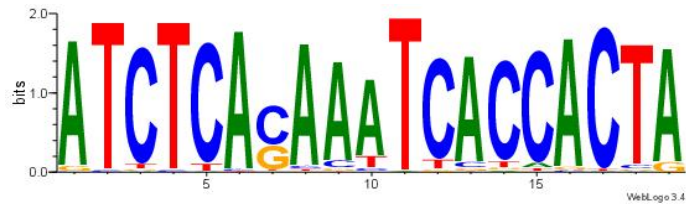

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**Dataset #: 1      Motif ID: 261      Motif name: Motif 261**

Original motif      Consensus sequence: ATCTCASAAATCACCACTA

Reverse complement motif      Consensus sequence: TAGTGGTGATTTSTGAGAT



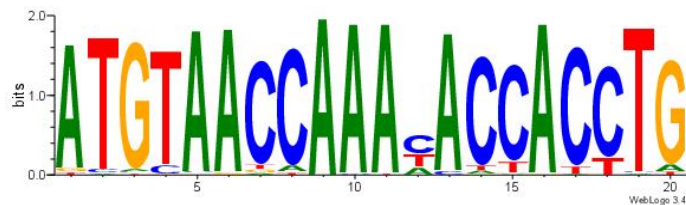


**Best Matches for Motif ID 261 (Highest to Lowest)**

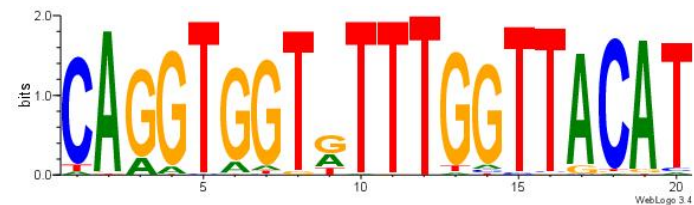
Dataset #: 1  
 Motif ID: 336  
 Motif name: Motif 336  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 19  
 Similarity score: 0.0782433

Alignment:  
 ATGTAACCAAAYACCACCTG  
 ATCTCASAAATCACC ACTA-

Original motif      Consensus sequence: ATGTAACCAAAYACCACCTG



Reverse complement motif      Consensus sequence: CAGGTGGTKTTTGGTTACAT

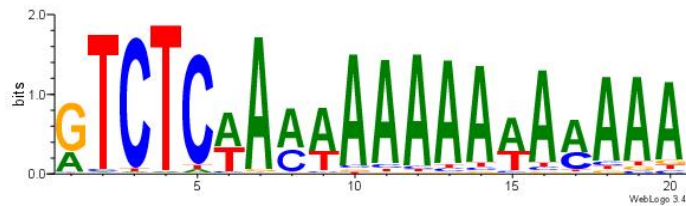


Dataset #: 1  
 Motif ID: 7  
 Motif name: Motif 7  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 19  
 Similarity score: 0.0942998

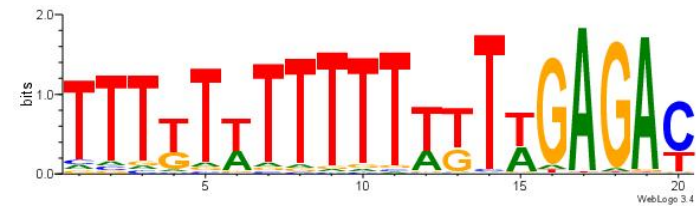
Alignment:

GTCTCWAMAAAAAWAMAAA  
 ATCTCASAAATCACCCTA-

Original motif      Consensus sequence: GTCTCWAMAAAAAWAMAAA



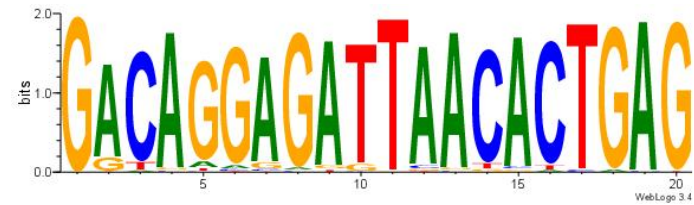
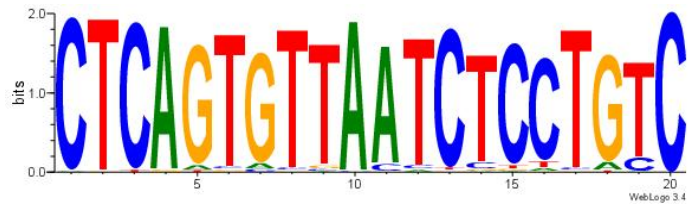
Reverse complement motif      Consensus sequence: TTTYTWTTTTTWTGAGAC



**Dataset #: 1      Motif ID: 262      Motif name: Motif 262**

Original motif      Consensus sequence: CTCAGTGTTAATCTCCTGTC

Reverse complement motif      Consensus sequence: GACAGGAGATTAACACTGAG

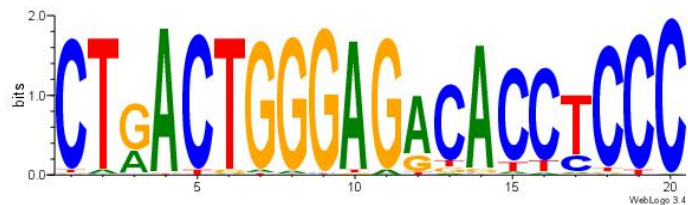


**Best Matches for Motif ID 262 (Highest to Lowest)**

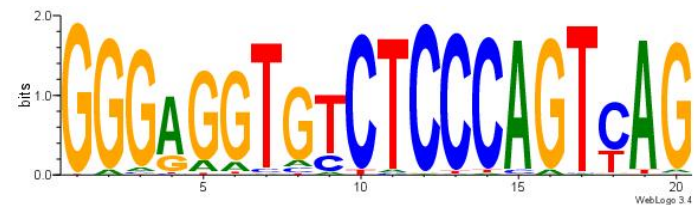
Dataset #: 1  
 Motif ID: 293  
 Motif name: Motif 293  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 20  
 Similarity score: 0.108944

Alignment:  
 CTGACTGGGAGACACCTCCC  
 CTCAGTGTTAATCTCCTGTC

Original motif    Consensus sequence: CTGACTGGGAGACACCTCCC



Reverse complement motif    Consensus sequence: GGGAGGTGTCTCCAGTCAG

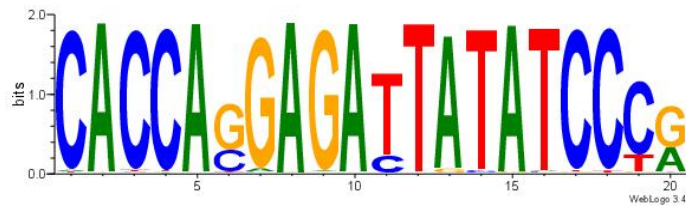


Dataset #: 1  
 Motif ID: 19  
 Motif name: Motif 19  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 2  
 Number of overlap: 19  
 Similarity score: 0.600148

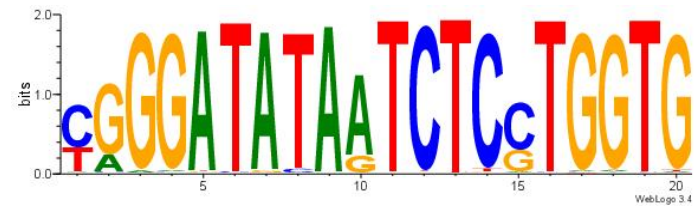
Alignment:

MGGGATATAATCTCCTGGTG-  
 -CTCAGTGTTAATCTCCTGTC

Original motif      Consensus sequence: CACCAGGAGATTATATCCCR



Reverse complement motif      Consensus sequence: MGGGATATAATCTCCTGGTG

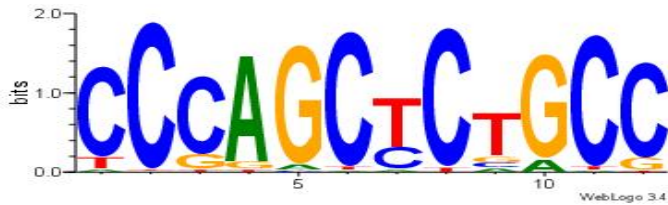



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**Dataset #: 1      Motif ID: 263      Motif name: Motif 263**

Original motif      Consensus sequence: CCCAGCTCTGCC

Reverse complement motif      Consensus sequence: GGCAGAGCTGGG

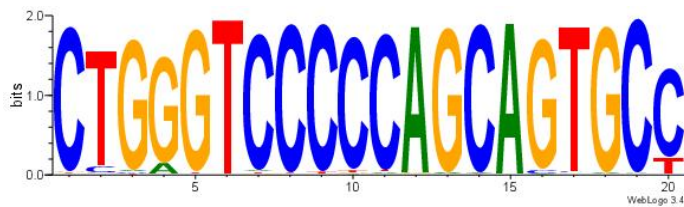


**Best Matches for Motif ID 263 (Highest to Lowest)**

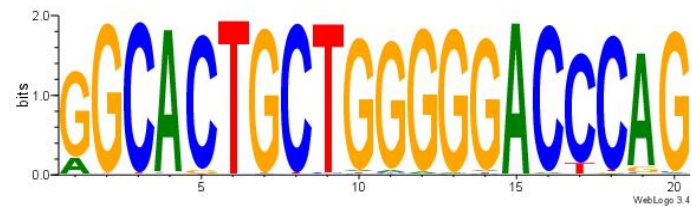
Dataset #: 1  
 Motif ID: 84  
 Motif name: Motif 84  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 12  
 Similarity score: 0.0427579

Alignment:  
 GGC ACTGCTGGGGGACCCAG  
 GGCAGAGCTGGG-----

Original motif      Consensus sequence: CTGGGTCCCCCAGCAGTGCC



Reverse complement motif      Consensus sequence: GGC ACTGCTGGGGGACCCAG

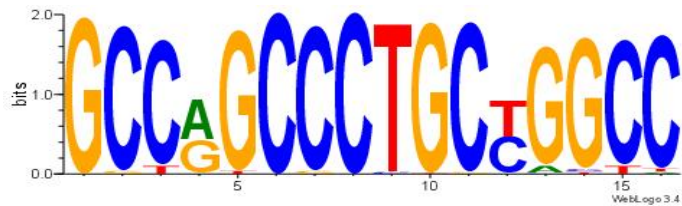


Dataset #: 1  
 Motif ID: 183  
 Motif name: Motif 183  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 12  
 Similarity score: 0.0507335

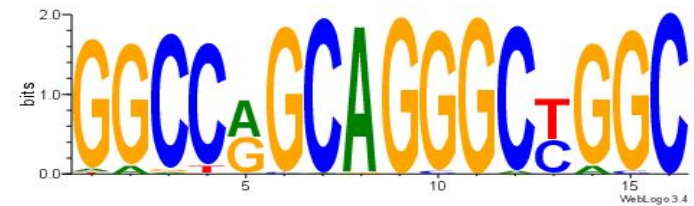
Alignment:

GCCRGCCCTGCYGGCC  
 CCCAGCTCTGCC-----

Original motif      Consensus sequence: GCCRGCCCTGCYGGCC



Reverse complement motif      Consensus sequence: GGCCMGCAGGGCKGGC

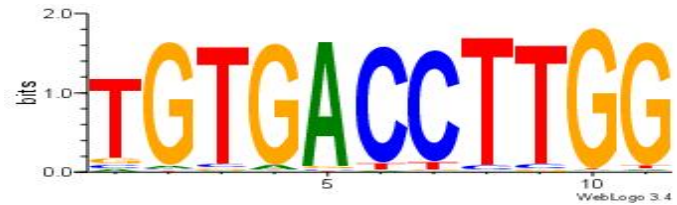
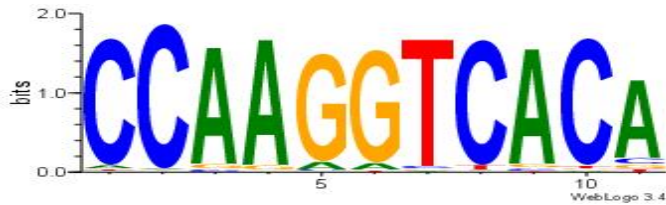



---

**Dataset #: 1      Motif ID: 264      Motif name: Motif 264**

Original motif      Consensus sequence: CCAAGGTCACA

Reverse complement motif      Consensus sequence: TGTGACCTTGG

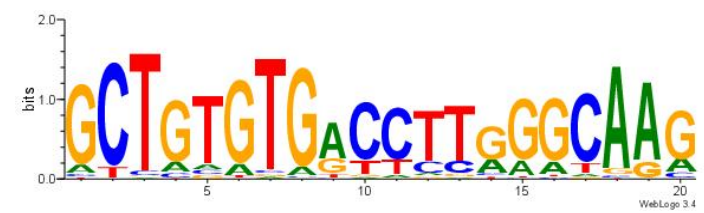


**Best Matches for Motif ID 264 (Highest to Lowest)**

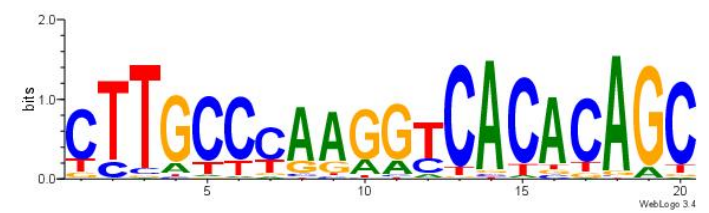
Dataset #: 1  
 Motif ID: 112  
 Motif name: Motif 112  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 5  
 Number of overlap: 11  
 Similarity score: 0.0343671

Alignment:  
 CTTGCCCAAGGTCACACAGC  
 ----CCAAGGTCACA-----

Original motif      Consensus sequence: GCTGTGTGACCTTGGGCAAG



Reverse complement motif      Consensus sequence: CTTGCCCAAGGTCACACAGC

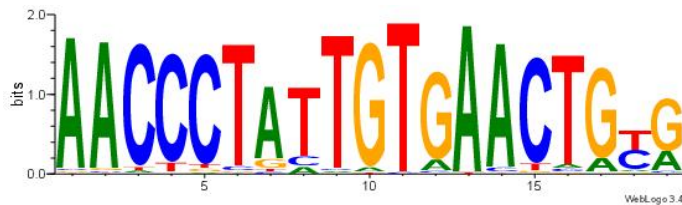


Dataset #: 1  
 Motif ID: 242  
 Motif name: Motif 242  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 11  
 Similarity score: 0.0609262

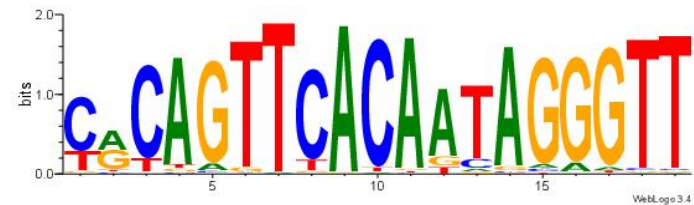
Alignment:

AACCTATTGTGAACTGYG  
 TGTGACCTTGG-----

Original motif      Consensus sequence: AACCTATTGTGAACTGYG



Reverse complement motif      Consensus sequence: CMCAGTTCACAATAGGGTT



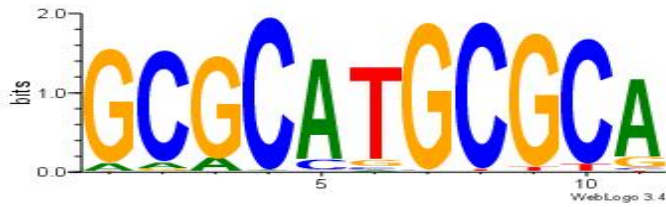

---

**Dataset #: 1      Motif ID: 265      Motif name: Motif 265**

Original motif      Consensus sequence: GCGCATGCGCA

Reverse complement motif      Consensus sequence: TGCGCATGCGC



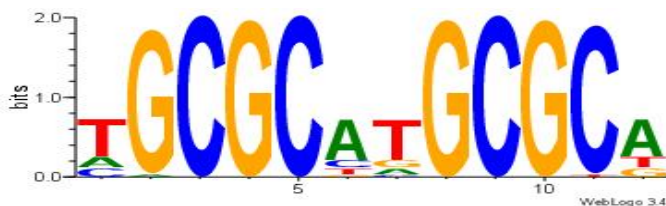


**Best Matches for Motif ID 265 (Highest to Lowest)**

Dataset #: 1  
 Motif ID: 180  
 Motif name: Motif 180  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 2  
 Number of overlap: 11  
 Similarity score: 0.00596496

Alignment:  
 TGCATGCGC  
 -GCGCATGCGC

Original motif      Consensus sequence: TGCATGCGC



Reverse complement motif      Consensus sequence: TGCATGCGC



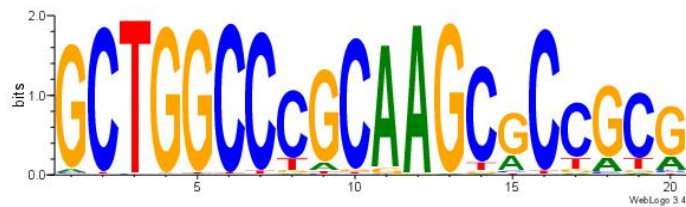
Dataset #: 1

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

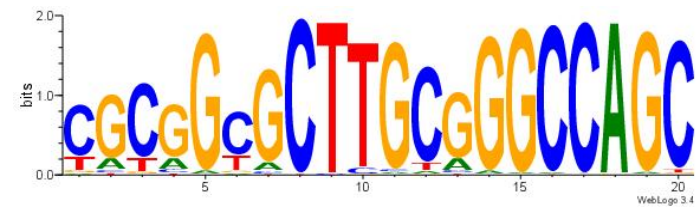
**Alignment:**

CGCGGCGCTTGC GGGCCAGC  
 ---TGC GCATGCGC-----

Original motif      Consensus sequence: GCTGGCCCGCAAGCGCCGCG

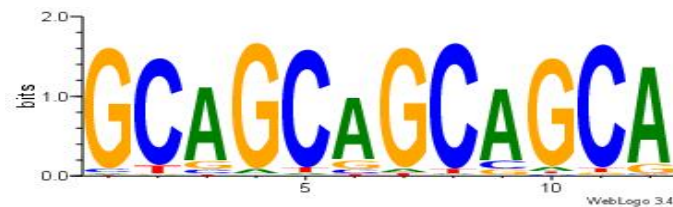


Reverse complement motif      Consensus sequence: CGCGGCGCTTGC GGGCCAGC

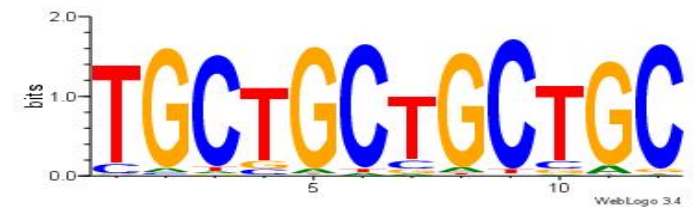


**Dataset #: 1      Motif ID: 266      Motif name: Motif 266**

Original motif      Consensus sequence: GCAGCAGCAGCA



Reverse complement motif      Consensus sequence: TGCTGCTGCTGC



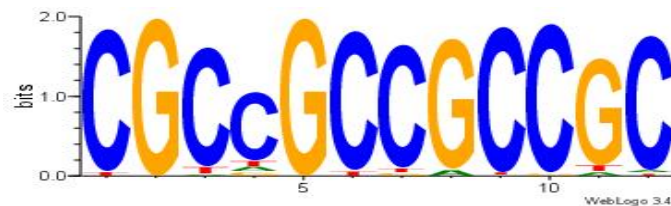
## Best Matches for Motif ID 266 (Highest to Lowest)

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

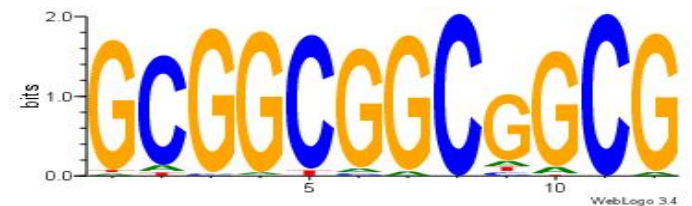
### Alignment:

CGCCGCCGCCGC  
TGCTGCTGCTGC

Original motif      Consensus sequence: CGCCGCCGCCGC



Reverse complement motif      Consensus sequence: GCGGCGGCGGCG

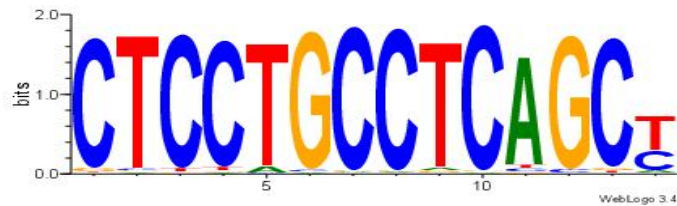


Dataset #: 1  
Motif ID: 313  
Motif name: Motif 313  
Matching format of first motif: Original Motif  
Matching format of second motif: Reverse Complement

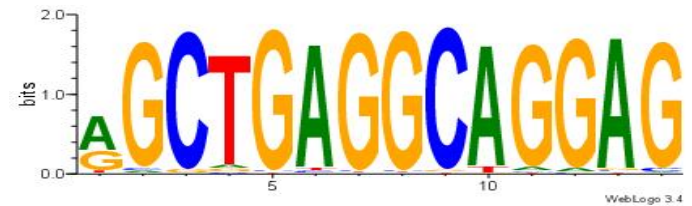
Direction: Backward  
 Position number: 2  
 Number of overlap: 12  
 Similarity score: 0.0732114

Alignment:  
 MGCTGAGGCAGGAG  
 -GCAGCAGCAGCA-

Original motif    Consensus sequence: CTCCTGCCTCAGCY



Reverse complement motif    Consensus sequence: MGCTGAGGCAGGAG



**Dataset #: 1      Motif ID: 267      Motif name: Motif 267**

Original motif    Consensus sequence: ATGGA<sub>A</sub>CTTGAGA



Reverse complement motif    Consensus sequence: TCTCAAG<sub>G</sub>TCCAT



**Best Matches for Motif ID 267 (Highest to Lowest)**

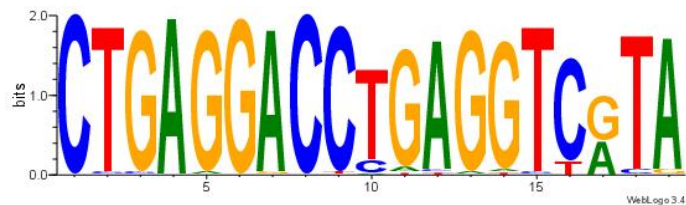
Dataset #: 1  
 Motif ID: 291  
 Motif name: Motif 291

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

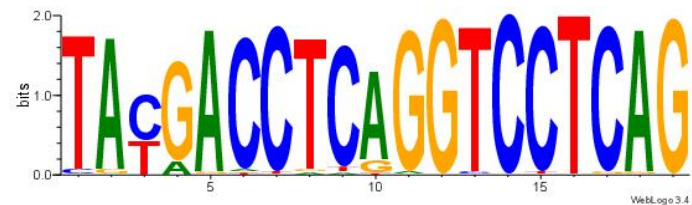
Alignment:

```
CTGAGGACCTGAGGTCRТА
--ATGGACTTGAGA-----
```

Original motif      Consensus sequence: CTGAGGACCTGAGGTCRТА



Reverse complement motif      Consensus sequence: TAMGACCTCAGGTCCTCAG

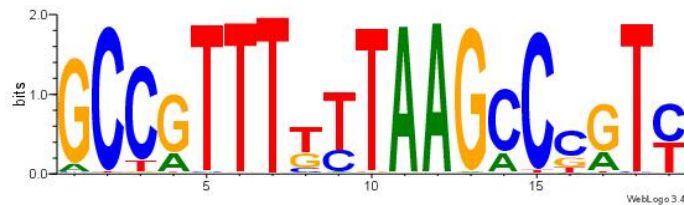


Dataset #:	1
Motif ID:	21
Motif name:	Motif 21
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	2
Number of overlap:	12
Similarity score:	0.0832965

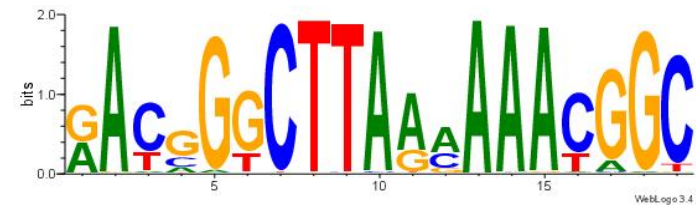
Alignment:

```
KACGGGCTTAARAAACGGC  
-----ATGGACTTGAGA-
```

Original motif      Consensus sequence: GCCGTTTKTTAAGCCCGTY

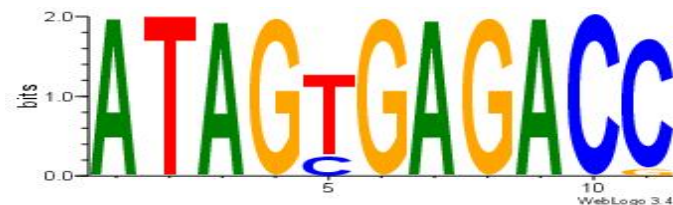


Reverse complement motif      Consensus sequence:  
KACGGGCTTAARAAACGGC

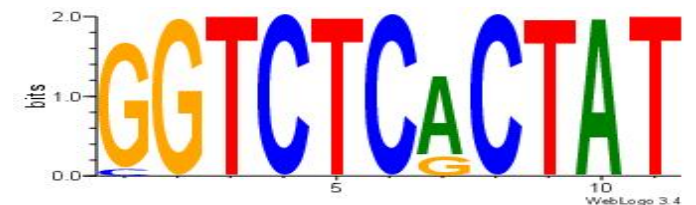


**Dataset #: 1      Motif ID: 268      Motif name: Motif 268**

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

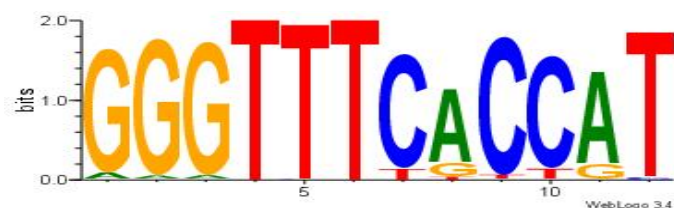
Position number: 1  
Number of overlap: 11  
Similarity score: 0.0513709

Alignment:  
ATGGTGAAACCC  
ATAGTGAGACC-

Original motif      Consensus sequence: ATGGTGAAACCC



Reverse complement motif      Consensus sequence: GGGTTTCACCAT



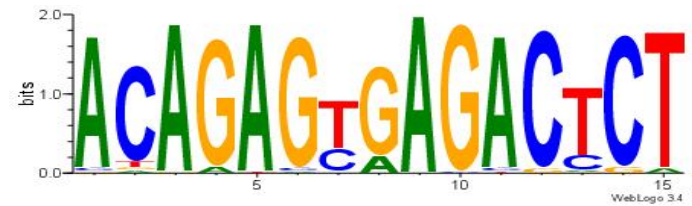
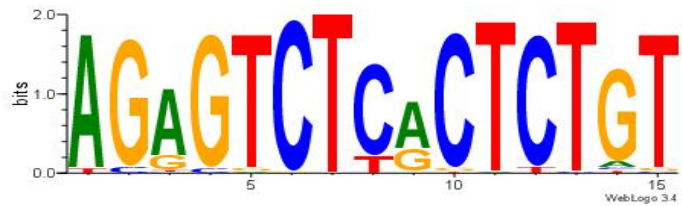
---

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--

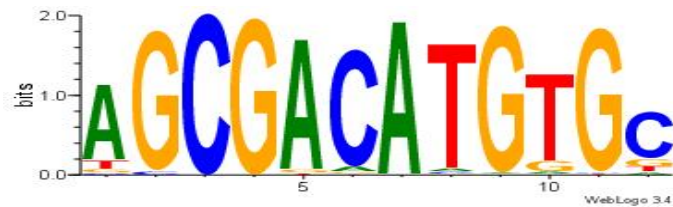
Original motif      Consensus sequence: AGAGTCTCACTCTGT

Reverse complement motif      Consensus sequence: ACAGAGTGAGACTCT

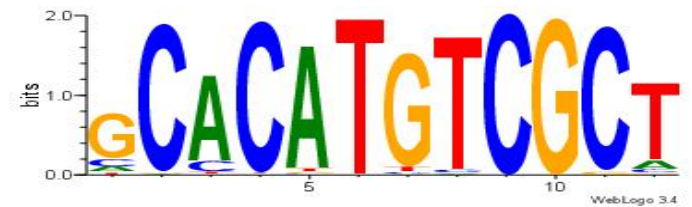


**Dataset #: 1      Motif ID: 269      Motif name: Motif 269**

Original motif      Consensus sequence: AGCGACATGTGC



Reverse complement motif      Consensus sequence: GCACATGTCGCT



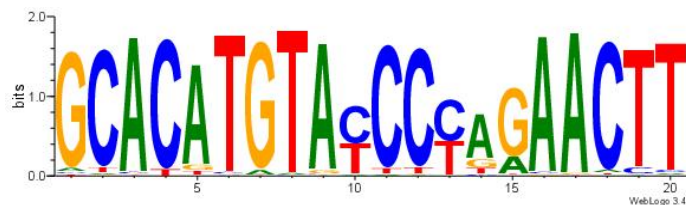
**Best Matches for Motif ID 269 (Highest to Lowest)**

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

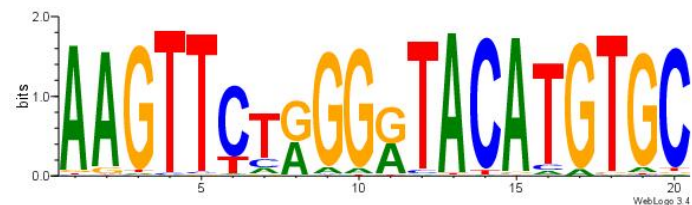
Alignment:  
 GCACATGTAYCCYAGAACTT  
 -----GCACATGTCGCT



Original motif      Consensus sequence: GCACATGTAYCCYAGAACTT



Reverse complement motif      Consensus sequence: AAGTTCTKGGKTACATGTGC

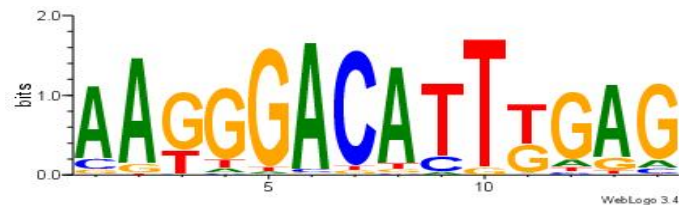


Dataset #: 1  
Motif ID: 166  
Motif name: Motif 166  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Reverse Complement  
Direction: Backward  
Position number: 2  
Number of overlap: 12  
Similarity score: 0.0581181

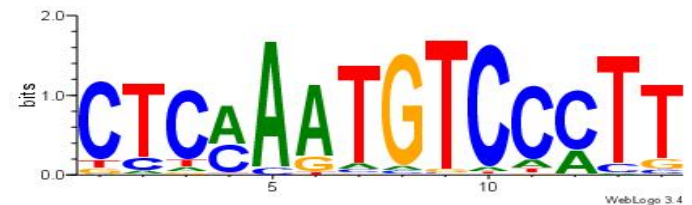
Alignment:

CTCRAATGTCCCTT  
-GCACATGTGCT-

Original motif      Consensus sequence: AAGGGACATTKGAG

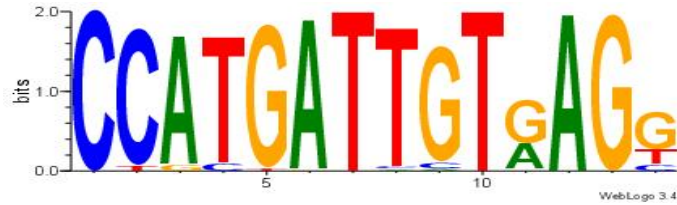


Reverse complement motif      Consensus sequence: CTCRAATGTCCCTT

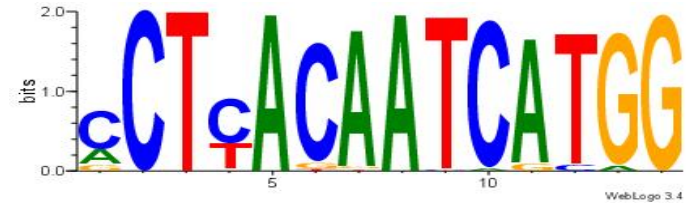


**Dataset #: 1      Motif ID: 270      Motif name: Motif 270**

Original motif      Consensus sequence: CCATGATTGTRAGG



Reverse complement motif      Consensus sequence: CCTMACAATCATGG



**Best Matches for Motif ID 270 (Highest to Lowest)**

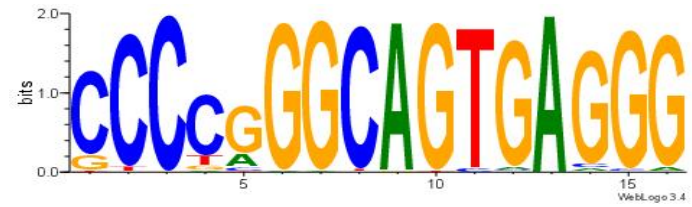
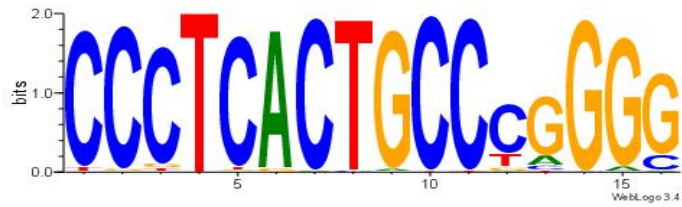
Dataset #:	1
Motif ID:	136
Motif name:	Motif 136
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2
Number of overlap:	14
Similarity score:	0.0904714

**Alignment:**

```
CCCTCACTGCCCGGGG  
-CCTMACAATCATGG-
```

Original motif      Consensus sequence: CCCTCACTGCCCGGGG

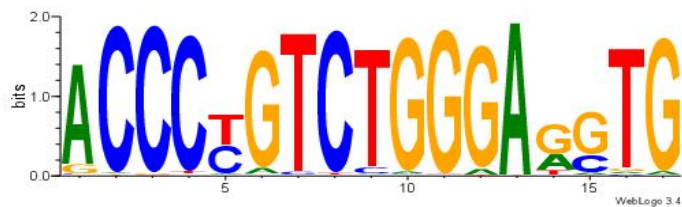
Reverse complement motif      Consensus sequence: CCCCAGGTCAGTGGG



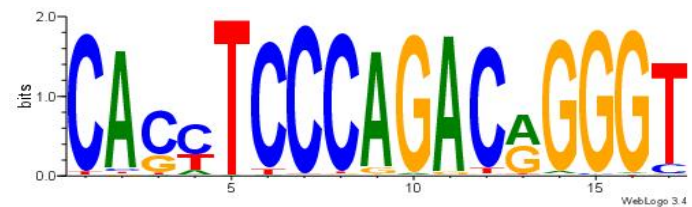
Dataset #: 1  
 Motif ID: 95  
 Motif name: Motif 95  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 2  
 Number of overlap: 14  
 Similarity score: 0.091519

Alignment:  
 CACCTCCCAGACMGGGT  
 --CCTMACAATCATGG-

Original motif      Consensus sequence: ACCCYGTCTGGGAGGTG

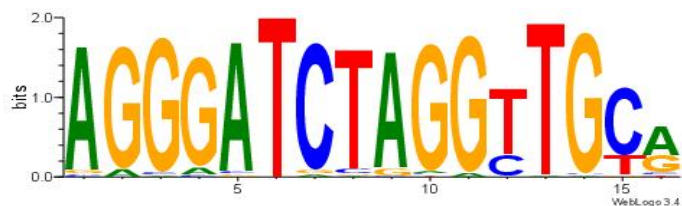


Reverse complement motif      Consensus sequence: CACCTCCCAGACMGGGT

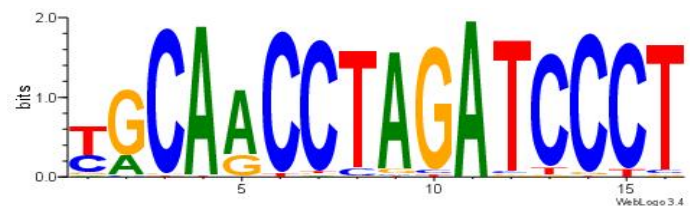


**Dataset #: 1      Motif ID: 271      Motif name: Motif 271**

Original motif      Consensus sequence: AGGGATCTAGGTTGCR



Reverse complement motif      Consensus sequence: KGCAACCTAGATCCCT



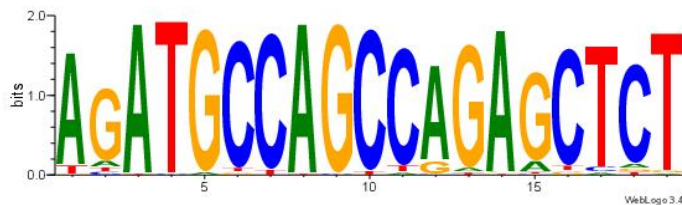
### Best Matches for Motif ID 271 (Highest to Lowest)

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

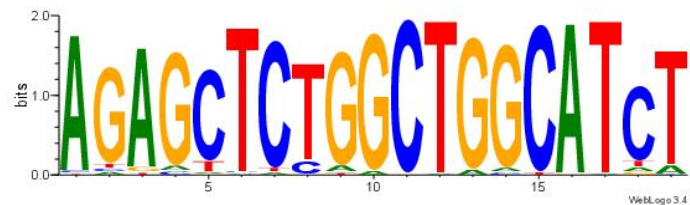
#### Alignment:

```
AGAGCTCTGGCTGGCATCT  
AGGGATCTAGGTTGCR---
```

Original motif      Consensus sequence: AGATGCCAGCCAGAGCTCT



Reverse complement motif      Consensus sequence: AGAGCTCTGGCTGGCATCT

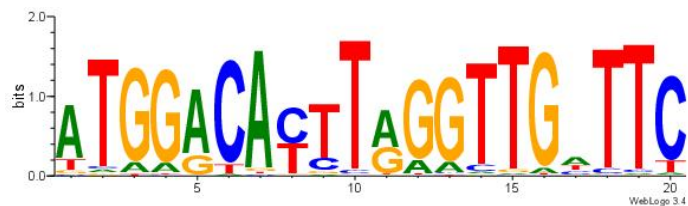


Dataset #: 1  
 Motif ID: 58  
 Motif name: Motif 58  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 3  
 Number of overlap: 16  
 Similarity score: 0.0869615

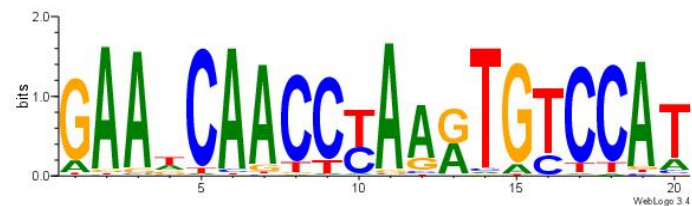
Alignment:

ATGGACAYTTRGGTTGHTTC  
 --AGGGATCTAGGTTGCR--

Original motif    Consensus sequence: ATGGACAYTTRGGTTGHTTC



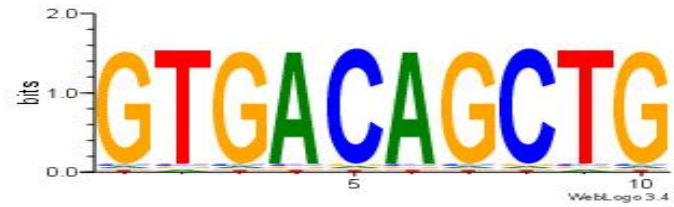
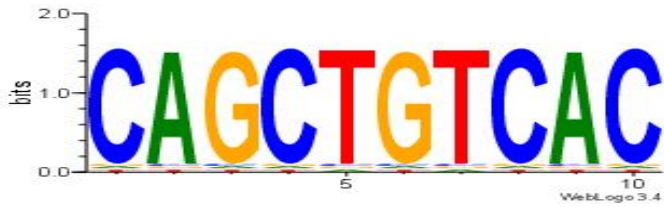
Reverse complement motif    Consensus sequence: GAAHCAACCKAAKTGTCCAT



**Dataset #: 1      Motif ID: 272      Motif name: Motif 272**

Original motif    Consensus sequence: CAGCTGTCAC

Reverse complement motif    Consensus sequence: GTGACAGCTG



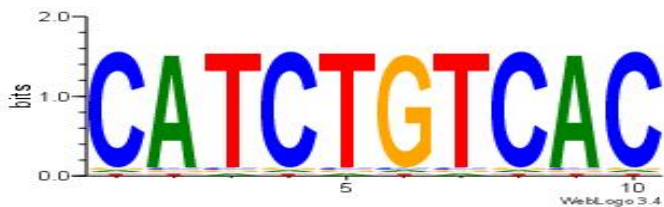
### Best Matches for Motif ID 272 (Highest to Lowest)

Dataset #: 1  
 Motif ID: 334  
 Motif name: Motif 334  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 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



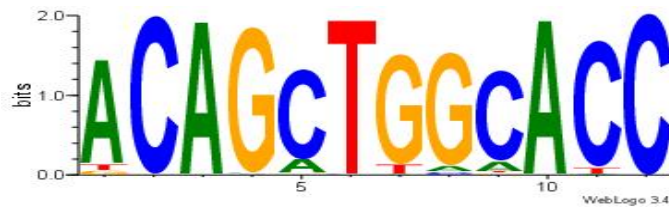

---

Dataset #: 1

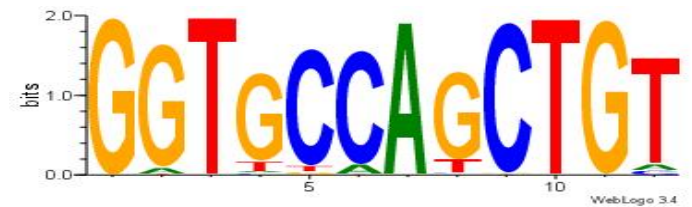
Motif ID: 199  
 Motif name: Motif 199  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 2  
 Number of overlap: 10  
 Similarity score: 0.037149

Alignment:  
 GGTGCCAGCTGT  
 -GTGACAGCTG-

Original motif      Consensus sequence: ACAGCTGGCACC

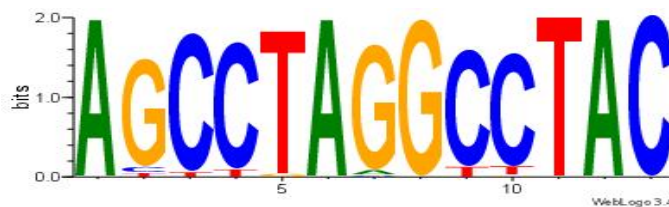


Reverse complement motif      Consensus sequence: GGTGCCAGCTGT

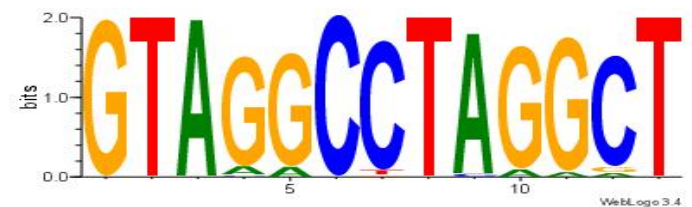


**Dataset #: 1      Motif ID: 273      Motif name: Motif 273**

Original motif      Consensus sequence: AGCCTAGGCCTAC



Reverse complement motif      Consensus sequence: GTAGGCCTAGGCT



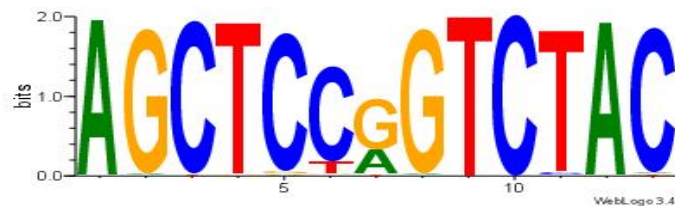
## Best Matches for Motif ID 273 (Highest to Lowest)

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

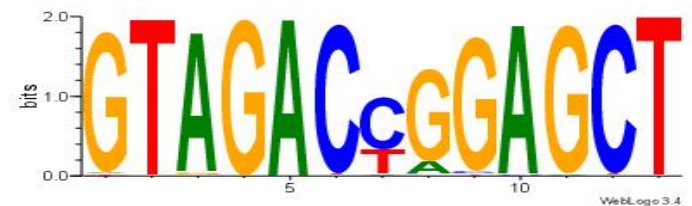
### Alignment:

AGCTCCGGTCTAC  
AGCCTAGGCCTAC

Original motif    Consensus sequence: AGCTCCGGTCTAC



Reverse complement motif    Consensus sequence: GTAGACCGGAGCT



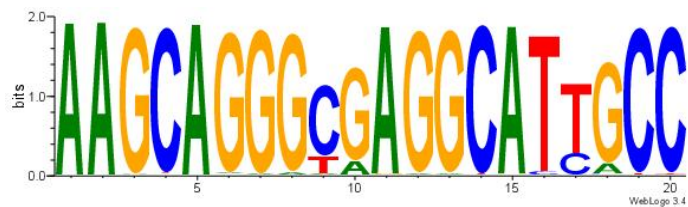
Dataset #: 1  
Motif ID: 13  
Motif name: Motif 13  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Original Motif



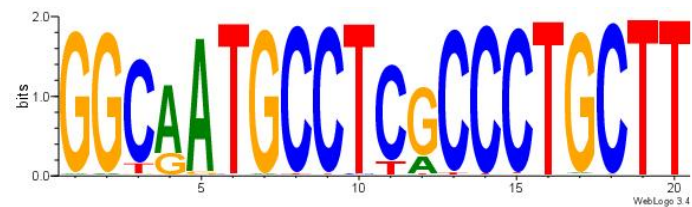
Direction: Backward  
 Position number: 3  
 Number of overlap: 13  
 Similarity score: 0.0735654

Alignment:  
 AAGCAGGGCGAGGCATTGCC  
 -----GTAGGCCTAGGCT--

Original motif      Consensus sequence: AAGCAGGGCGAGGCATTGCC

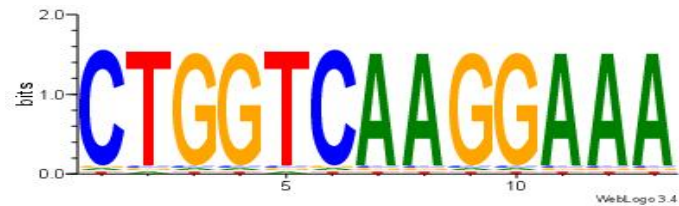


Reverse complement motif      Consensus sequence: GGCAATGCCTCGCCCTGCTT

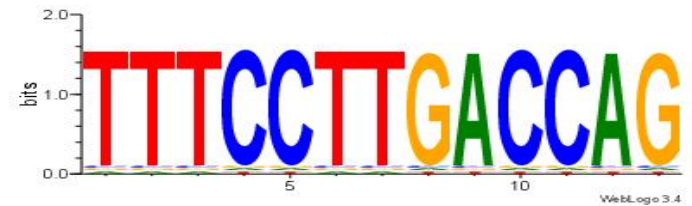


**Dataset #: 1      Motif ID: 274      Motif name: Motif 274**

Original motif      Consensus sequence: CTGGTCAAGGAAA



Reverse complement motif      Consensus sequence: TTTCTTGACCAG



**Best Matches for Motif ID 274 (Highest to Lowest)**

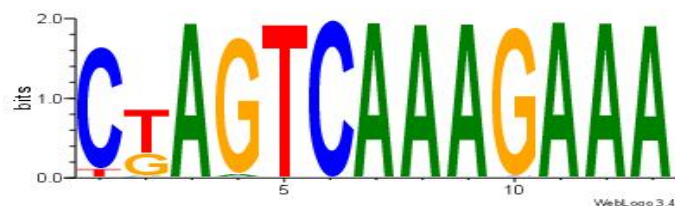
Dataset #: 1  
 Motif ID: 24

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

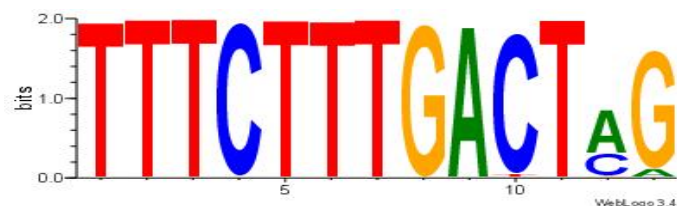
Alignment:

```
CKAGTCAAAGAAA
CTGGTCAAGGAAA
```

Original motif    Consensus sequence: CKAGTCAAAGAAA



Reverse complement motif    Consensus sequence: TTTCTTTGACTRG

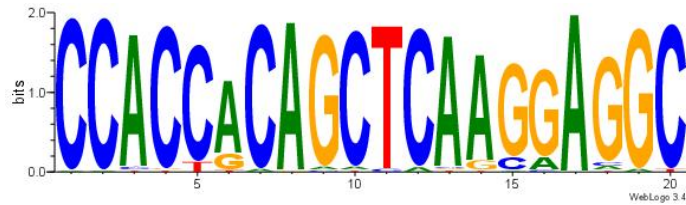


Dataset #:	1
Motif ID:	331
Motif name:	Motif 331
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2
Number of overlap:	13
Similarity score:	0.0763683

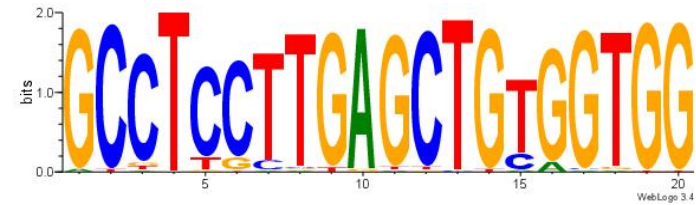
Alignment:

```
CCACCACAGCTCAAGGAGGC
-----CTGGTCAAGGAAA-
```

Original motif      Consensus sequence: CCACCACAGCTCAAGGAGGC



Reverse complement motif      Consensus sequence: GCCTCCTTGAGCTGTGGTGG

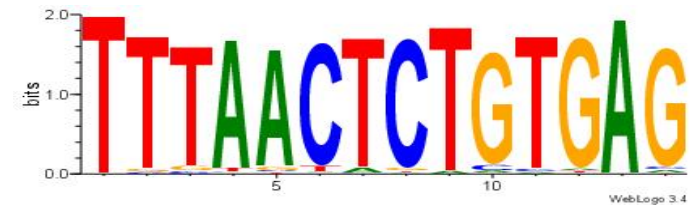


**Dataset #: 1      Motif ID: 275      Motif name: Motif 275**

Original motif      Consensus sequence: CTCACAGAGTTAAA



Reverse complement motif      Consensus sequence: TTTAACTCTGTGAG



**Best Matches for Motif ID 275 (Highest to Lowest)**

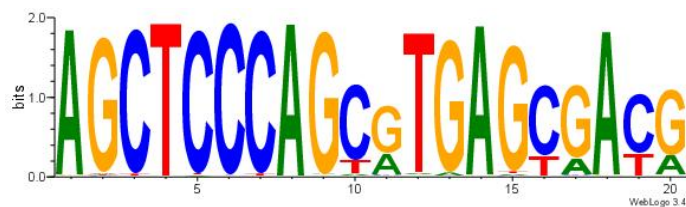
Dataset #:	1
Motif ID:	48
Motif name:	Motif 48
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward

Position number: 3  
Number of overlap: 14  
Similarity score: 0.0799887

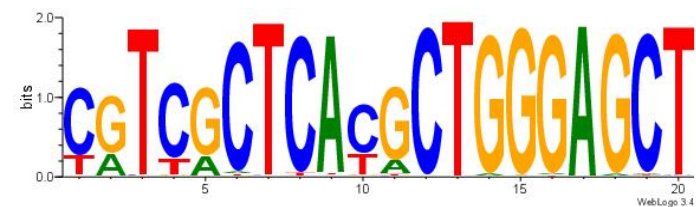
Alignment:

CGTCGCTCACGCTGGGAGCT  
----TTTAACTCTGTGAG--

Original motif      Consensus sequence: AGCTCCAGCGTGAGCGACG



Reverse complement motif      Consensus sequence: CGTCGCTCACGCTGGGAGCT

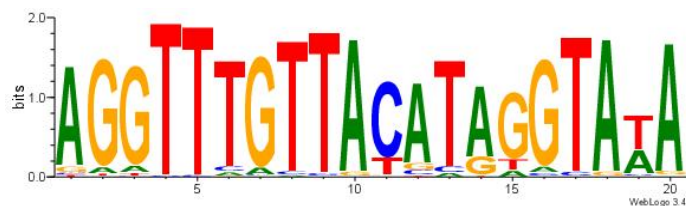


Dataset #: 1  
Motif ID: 137  
Motif name: Motif 137  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Reverse Complement  
Direction: Backward  
Position number: 7  
Number of overlap: 14  
Similarity score: 0.0822742

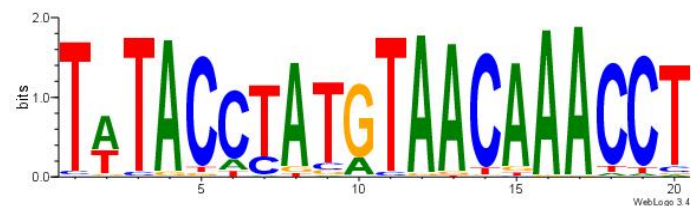
Alignment:

TWTACCTATGTAACAAACCT  
TTTAACTCTGTGAG-----

Original motif      Consensus sequence: AGGTTTGTTACATAGGTAWA

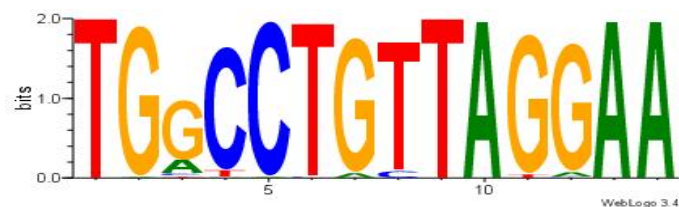


Reverse complement motif      Consensus sequence: TWTACCTATGTAACAAACCT



**Dataset #: 1      Motif ID: 276      Motif name: Motif 276**

Original motif      Consensus sequence: TGGCCTGTTAGGAA



Reverse complement motif      Consensus sequence: TTCCTAACAGGCC



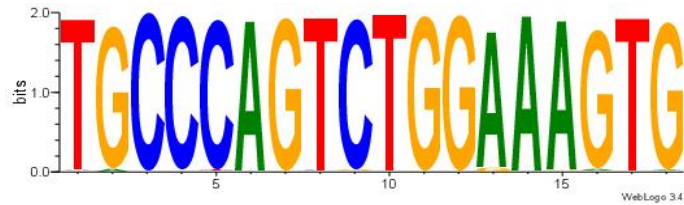
### Best Matches for Motif ID 276 (Highest to Lowest)

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

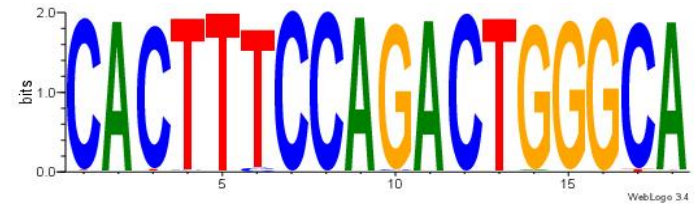
Alignment:

TGCCCAGTCTGGAAAGTG  
TGCCTGTTAGGAA-----

Original motif      Consensus sequence: TGCCCAGTCTGGAAAGTG



Reverse complement motif      Consensus sequence:  
CACTTTCCAGACTGGGCA

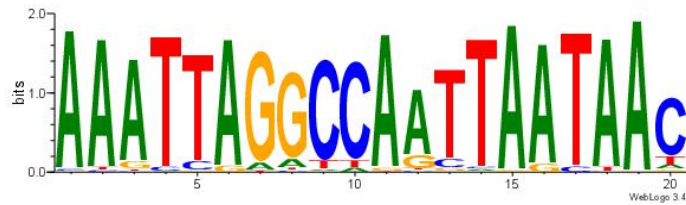


Dataset #: 1  
Motif ID: 308  
Motif name: Motif 308  
Matching format of first motif: Original Motif  
Matching format of second motif: Original Motif  
Direction: Backward  
Position number: 2  
Number of overlap: 14  
Similarity score: 0.0893293

Alignment:  
AAATTAGGCCAATTAATAAC  
-----TGCCTGTTAGGAA-

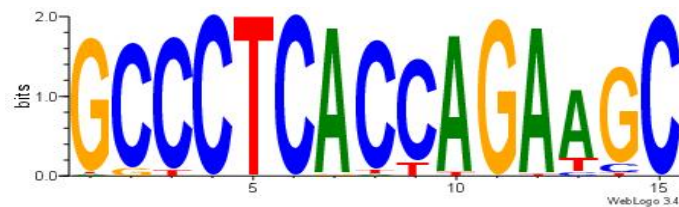
Original motif      Consensus sequence: AAATTAGGCCAATTAATAAC

Reverse complement motif      Consensus sequence:  
GTTATTAATTGGCCTAATT

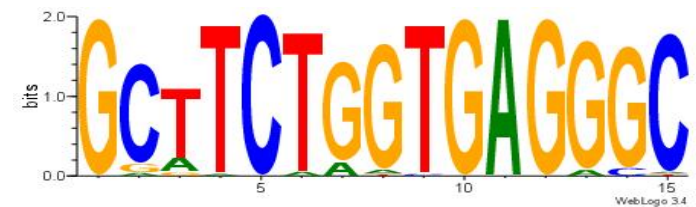


**Dataset #: 1      Motif ID: 277      Motif name: Motif 277**

Original motif      Consensus sequence: GCCCTCACCAGAAGC



Reverse complement motif      Consensus sequence: GCTTCTGGTGAGGC

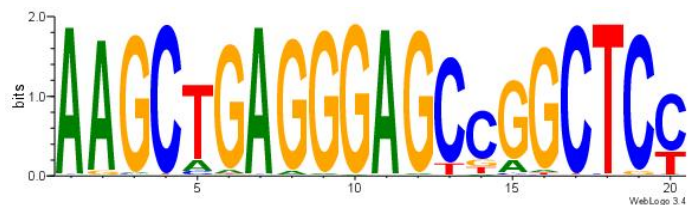


**Best Matches for Motif ID 277 (Highest to Lowest)**

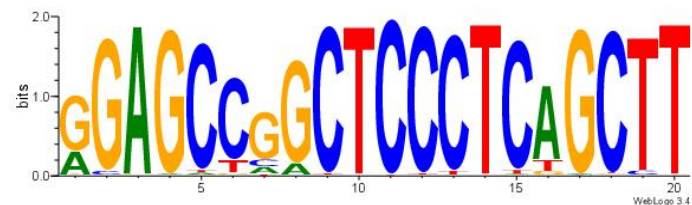
Dataset #:	1
Motif ID:	96
Motif name:	Motif 96
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	4
Number of overlap:	15
Similarity score:	0.0937412

Alignment:  
AAGCTGAGGGAGCCGGCTCC  
---GCTTCTGGTGAGGGC--

Original motif      Consensus sequence: AAGCTGAGGGAGCCGGCTCC



Reverse complement motif      Consensus sequence: GGAGCCGGCTCCCTCAGCTT

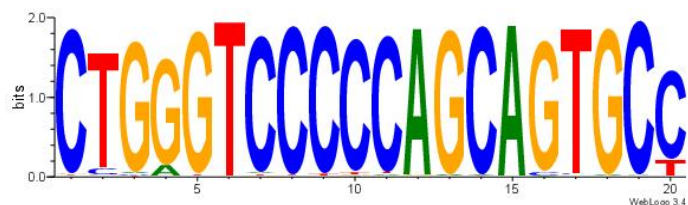


Dataset #: 1  
Motif ID: 84  
Motif name: Motif 84  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Reverse Complement  
Direction: Forward  
Position number: 1  
Number of overlap: 15  
Similarity score: 0.094292

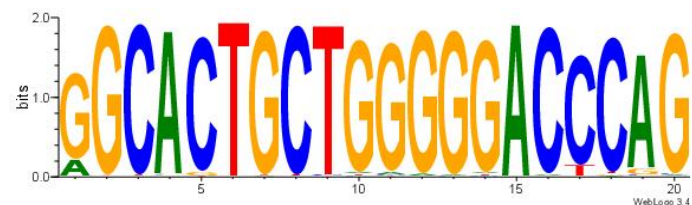
Alignment:

GGCACTGCTGGGGGACCCAG  
GCTTCTGGTGAGGGC-----

Original motif      Consensus sequence: CTGGGTCCCCCAGCAGTGCC



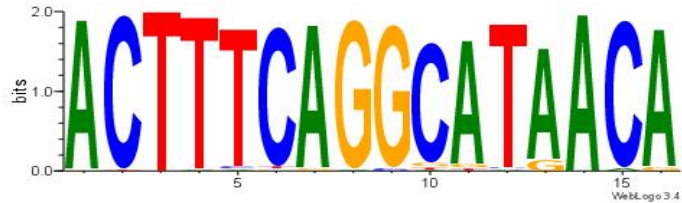
Reverse complement motif      Consensus sequence: GGCACTGCTGGGGGACCCAG



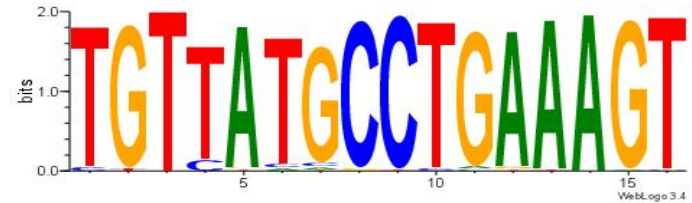


**Dataset #: 1      Motif ID: 278      Motif name: Motif 278**

Original motif      Consensus sequence: ACTTTCAGGCATAACA



Reverse complement motif      Consensus sequence: TGTTATGCCTGAAAGT



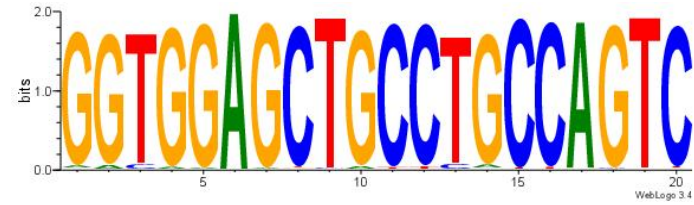
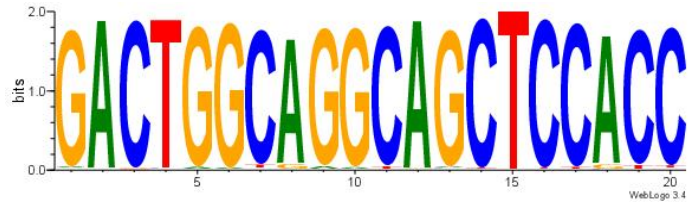
**Best Matches for Motif ID 278 (Highest to Lowest)**

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

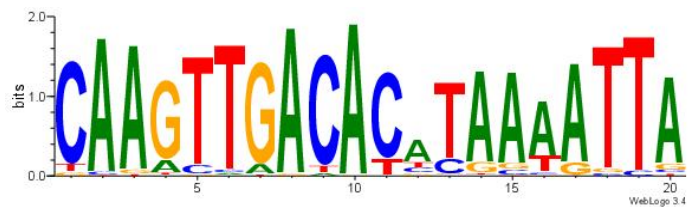


Dataset #: 1  
 Motif ID: 357  
 Motif name: Motif 357  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 4  
 Number of overlap: 16  
 Similarity score: 0.101075

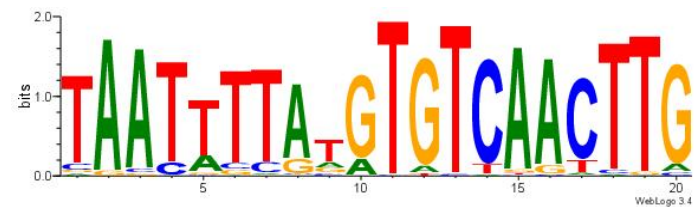
Alignment:

TAATTTTATGTGTCAACTTG  
 ---TGTTATGCCTGAAAGT-

Original motif      Consensus sequence: CAAGTTGACACATAAAATTA

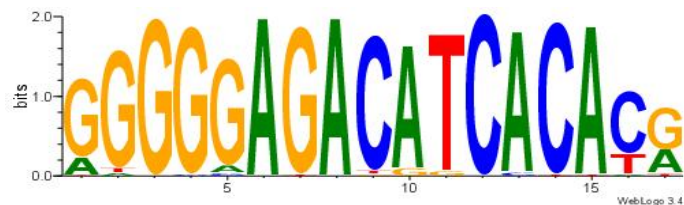


Reverse complement motif      Consensus sequence: TAATTTTATGTGTCAACTTG

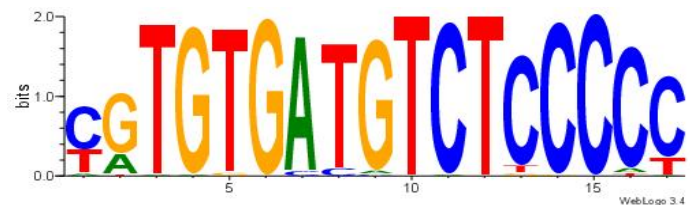


**Dataset #: 1      Motif ID: 279      Motif name: Motif 279**

Original motif      Consensus sequence: GGGGGAGACATCACACR



Reverse complement motif      Consensus sequence: MGTGTGATGTCTCCCC



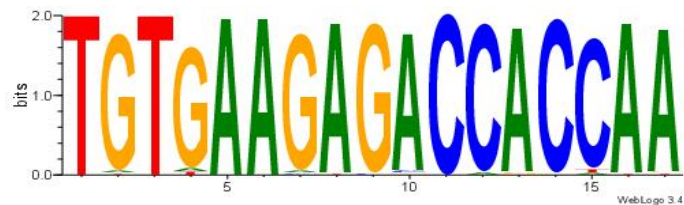
### Best Matches for Motif ID 279 (Highest to Lowest)

Dataset #:	1
Motif ID:	249
Motif name:	Motif 249
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	17
Similarity score:	0.10127

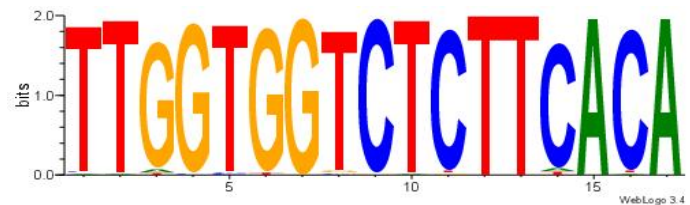
#### Alignment:

```
TTGGTGGTCTCTTCACA  
MGTGTGATGTCTCCCC
```

Original motif      Consensus sequence: TGTGAAGAGACCACCAA



Reverse complement motif      Consensus sequence: TTGGTGGTCTCTTCACA

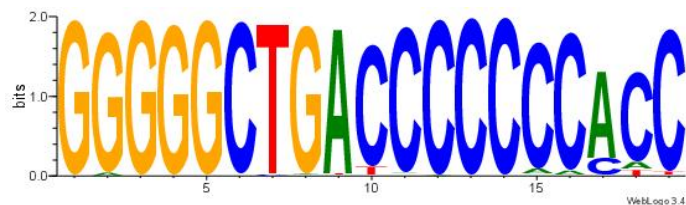


Dataset #: 1  
 Motif ID: 92  
 Motif name: Motif 92  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 2  
 Number of overlap: 17  
 Similarity score: 0.103877

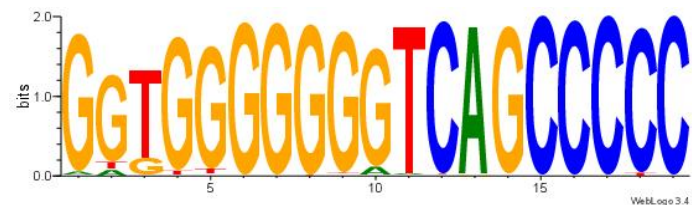
Alignment:

GGTGGGGGGGTCAGCCCC  
 -MGTGTGATGTCTCCCC-

Original motif      Consensus sequence: GGGGCTGACCCCCCACC



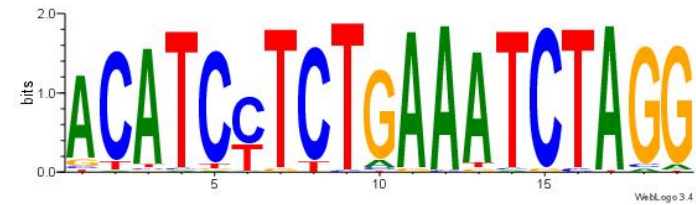
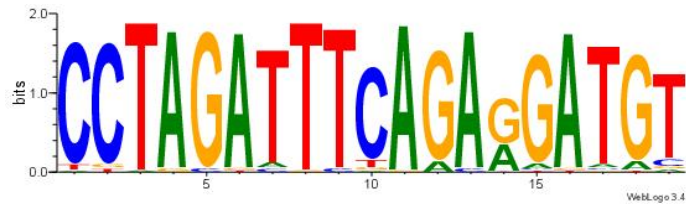
Reverse complement motif      Consensus sequence: GGTGGGGGGGTCAGCCCC



**Dataset #: 1      Motif ID: 280      Motif name: Motif 280**

Original motif      Consensus sequence: CCTAGATTTTCAGARGATGT

Reverse complement motif      Consensus sequence: ACATCMTCTGAAATCTAGG

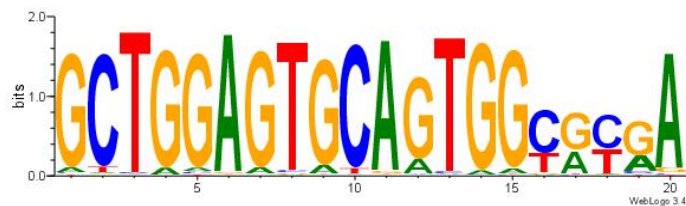


**Best Matches for Motif ID 280 (Highest to Lowest)**

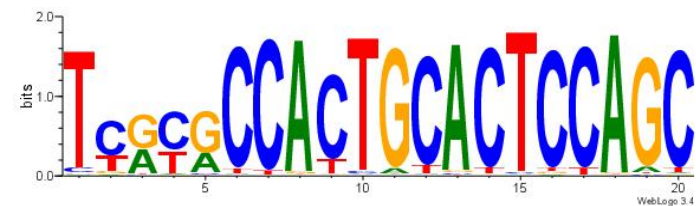
Dataset #: 1  
 Motif ID: 3  
 Motif name: Motif 3  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 2  
 Number of overlap: 19  
 Similarity score: 0.098089

Alignment:  
 TCKMGCCACTGCACTCCAGC  
 -ACATCMTCTGAAATCTAGG

Original motif      Consensus sequence: GCTGGAGTGCAGTGGCRYGA



Reverse complement motif      Consensus sequence: TCKMGCCACTGCACTCCAGC

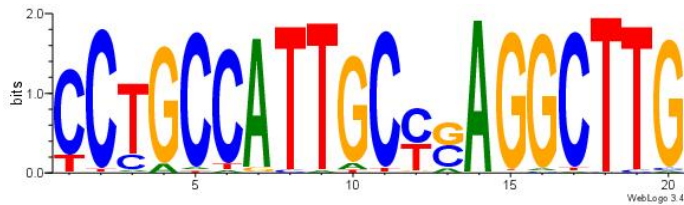


Dataset #: 1  
 Motif ID: 196  
 Motif name: Motif 196  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 2  
 Number of overlap: 19  
 Similarity score: 0.110835

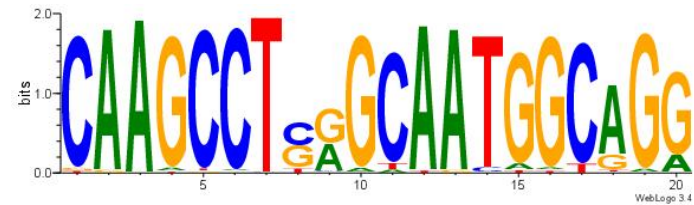
Alignment:

CAAGCCTSKGCAATGGCAGG  
 ACATCMTCTGAAATCTAGG-

Original motif      Consensus sequence: CCTGCCATTGCYSAGGCTTG



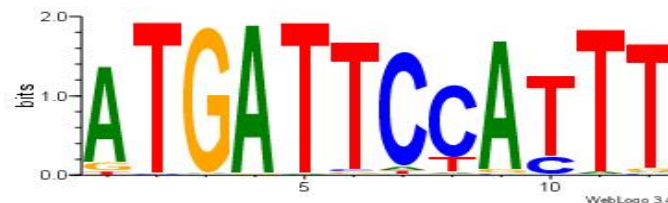
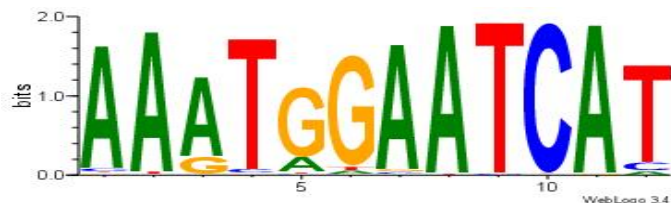
Reverse complement motif      Consensus sequence: CAAGCCTSKGCAATGGCAGG



**Dataset #: 1      Motif ID: 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)

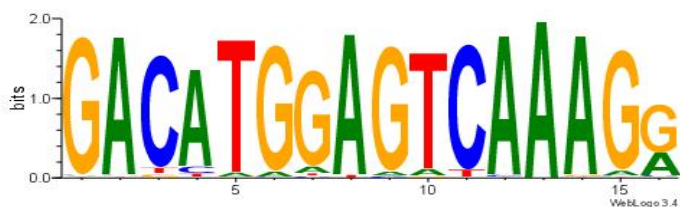
Dataset #: 1  
 Motif ID: 326  
 Motif name: Motif 326  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 4  
 Number of overlap: 12  
 Similarity score: 0.0598156

#### Alignment:

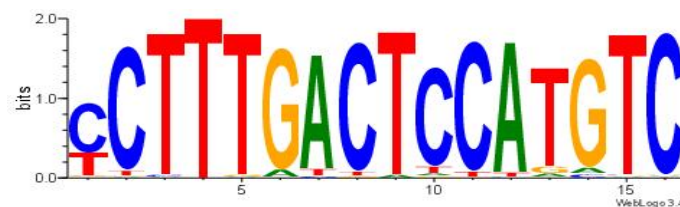
```

CCTTTGACTCCATGTC
---ATGATTCCATTT-
  
```

Original motif      Consensus sequence: GACATGGAGTCAAAGG



Reverse complement motif      Consensus sequence: CCTTTGACTCCATGTC

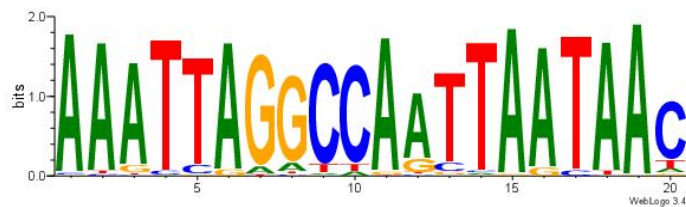


Dataset #: 1  
 Motif ID: 308  
 Motif name: Motif 308  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 7  
 Number of overlap: 12  
 Similarity score: 0.0709771

Alignment:

GTTATTAATTGGCCTAATTT  
 -----AAATGGAATCAT--

Original motif      Consensus sequence: AAATTAGGCCAATTAATAAC



Reverse complement motif      Consensus sequence: GTTATTAATTGGCCTAATTT

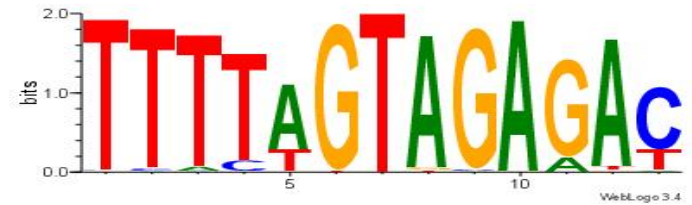
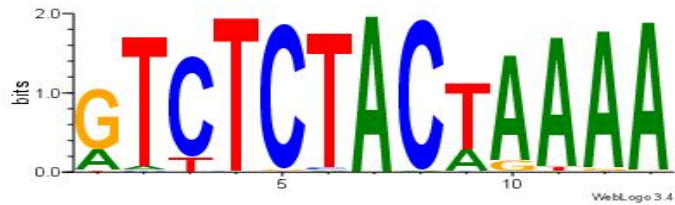


**Dataset #: 1      Motif ID: 282      Motif name: Motif 282**

Original motif      Consensus sequence: GTCTCTACTAAAA

Reverse complement motif      Consensus sequence: TTTTAGTAGAGAC



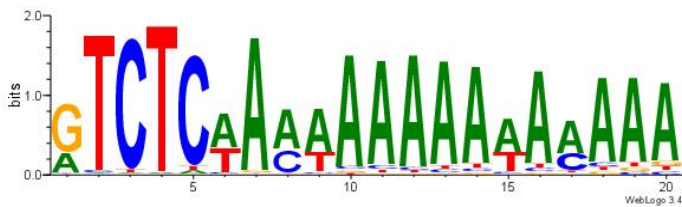


**Best Matches for Motif ID 282 (Highest to Lowest)**

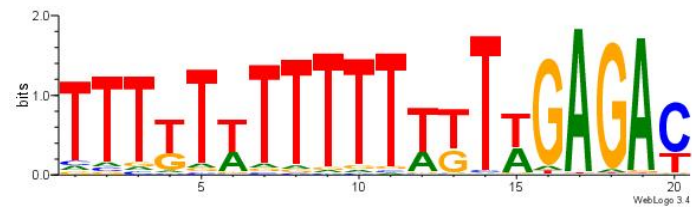
Dataset #: 1  
 Motif ID: 7  
 Motif name: Motif 7  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 13  
 Similarity score: 0.033043

Alignment:  
 GTCTCWAMAAAAAAWAMAAA  
 GTCTCTACTAAAA-----

Original motif      Consensus sequence: GTCTCWAMAAAAAAWAMAAA



Reverse complement motif      Consensus sequence: TTTTWTAGTAGAGAC

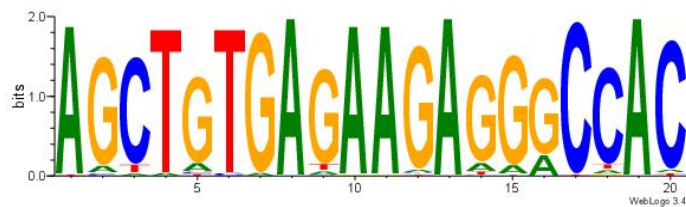


Dataset #: 1  
 Motif ID: 294  
 Motif name: Motif 294  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 5  
 Number of overlap: 13  
 Similarity score: 0.0894973

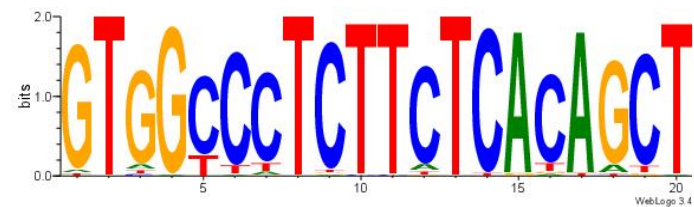
Alignment:

AGCTGTGAGAAGAGGGCCAC  
 ---TTTTAGTAGAGAC----

Original motif      Consensus sequence: AGCTGTGAGAAGAGGGCCAC



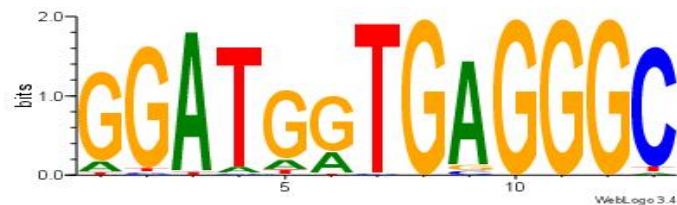
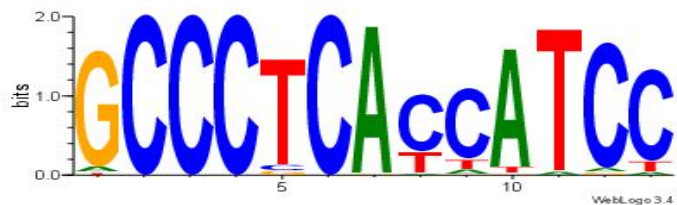
Reverse complement motif      Consensus sequence: GTGGCCCTCTTCTCACAGCT



**Dataset #: 1      Motif ID: 283      Motif name: Motif 283**

Original motif      Consensus sequence: GCCCTACCATCC

Reverse complement motif      Consensus sequence: GGATGGTGAGGG



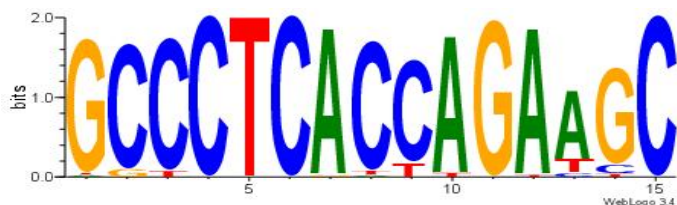
**Best Matches for Motif ID 283 (Highest to Lowest)**

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

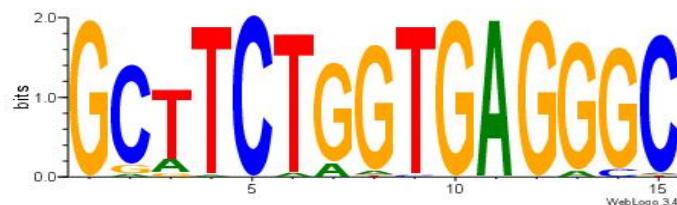
**Alignment:**

GCCCTCACCAGAAGC  
 GCCCTCACCATCC--

Original motif      Consensus sequence: GCCCTCACCAGAAGC



Reverse complement motif      Consensus sequence: GCTTCTGGTGAGGGC



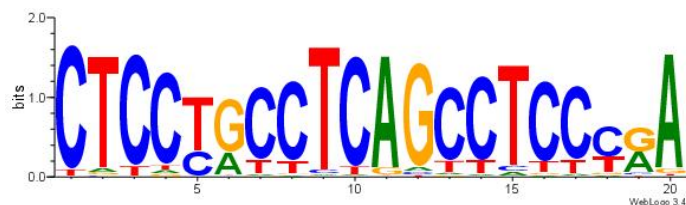
Dataset #: 1

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

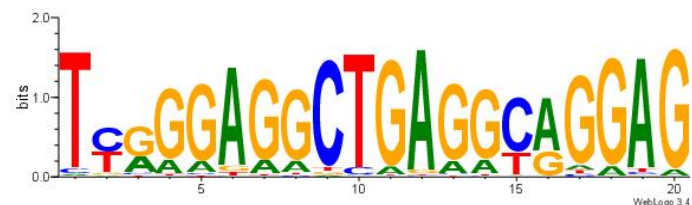
Alignment:

TMGGGAGGCTGAGGCAGGAG  
 ---GGATGGTGAGGGC----

Original motif    Consensus sequence: CTCCTGCCTCAGCCTCCRA

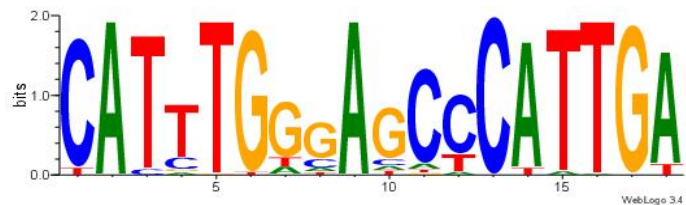


Reverse complement motif    Consensus sequence: TMGGGAGGCTGAGGCAGGAG

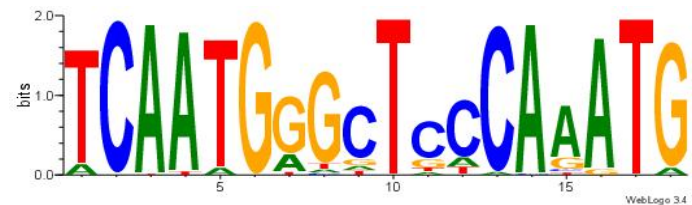


**Dataset #: 1      Motif ID: 284      Motif name: Motif 284**

Original motif    Consensus sequence: CATTGGGAGCCATTGA



Reverse complement motif    Consensus sequence: TCAATGGGCTCCCAAATG



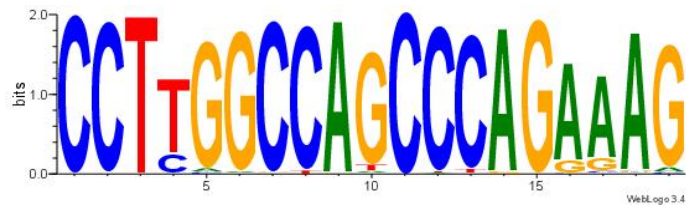
## Best Matches for Motif ID 284 (Highest to Lowest)

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

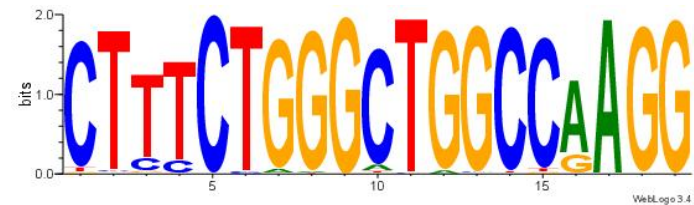
### Alignment:

```
CCTTGGCCAGCCCAGAAAG  
CATTGGGAGCCCATTGA-
```

Original motif      Consensus sequence: CCTTGGCCAGCCCAGAAAG



Reverse complement motif      Consensus sequence: CTTTCTGGGCTGGCCAAGG



---

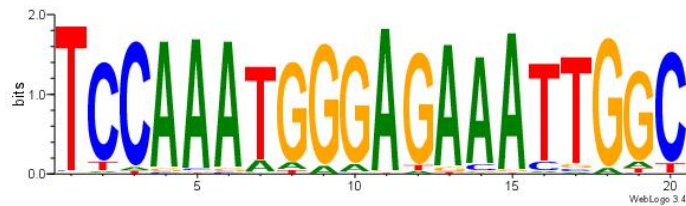
Dataset #: 1  
Motif ID: 235  
Motif name: Motif 235  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Reverse Complement

Direction: Backward  
 Position number: 3  
 Number of overlap: 18  
 Similarity score: 0.105262

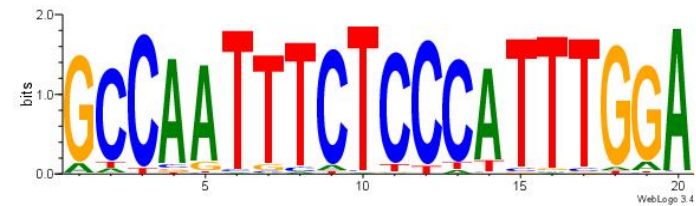
**Alignment:**

GCCAATTTCTCCCATTGGA  
 TCAATGGGCTCCCAAATG--

Original motif      Consensus sequence: TCCAATGGGAGAAATTGGC

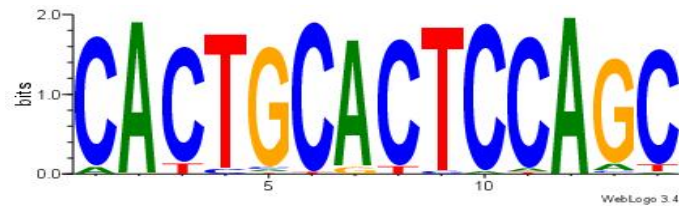


Reverse complement motif      Consensus sequence: GCCAATTTCTCCCATTGGA

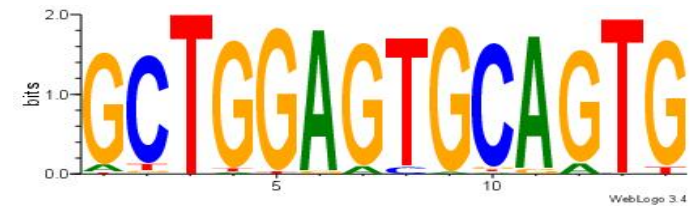


**Dataset #: 1      Motif ID: 285      Motif name: Motif 285**

Original motif      Consensus sequence: CACTGCACTCCAGC



Reverse complement motif      Consensus sequence: GCTGGAGTGCAGTG



**Best Matches for Motif ID 285 (Highest to Lowest)**

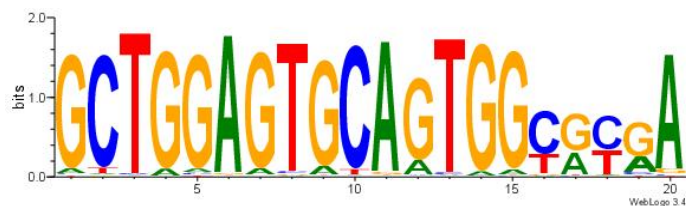
Dataset #: 1  
 Motif ID: 3

Motif name: Motif 3  
 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: 0.00211425

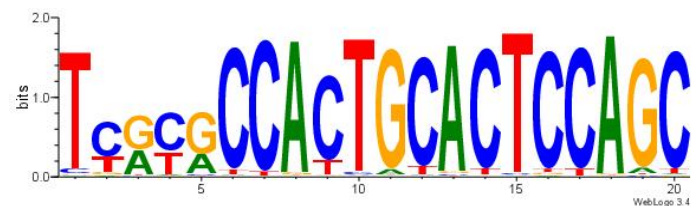
Alignment:

GCTGGAGTGCAGTGGCRYGA  
 -----GCTGGAGTGCAGTG

Original motif      Consensus sequence: GCTGGAGTGCAGTGGCRYGA



Reverse complement motif      Consensus sequence: TCKMGCCACTGCACTCCAGC

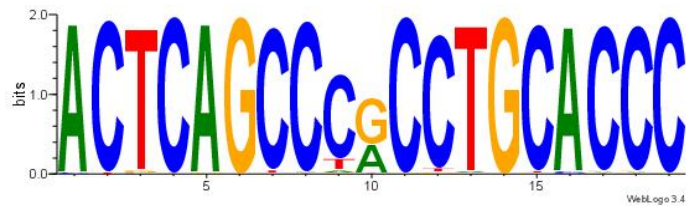


Dataset #: 1  
 Motif ID: 149  
 Motif name: Motif 149  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 5  
 Number of overlap: 14  
 Similarity score: 0.0792554

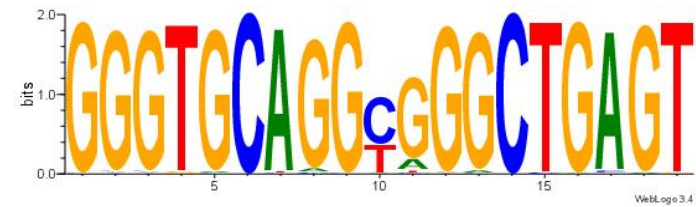
Alignment:

```
GGGTGCAGGMGGGCTGAGT  
----GCTGGAGTGCAGTG--
```

Original motif      Consensus sequence: ACTCAGCCRCCTGCACCC

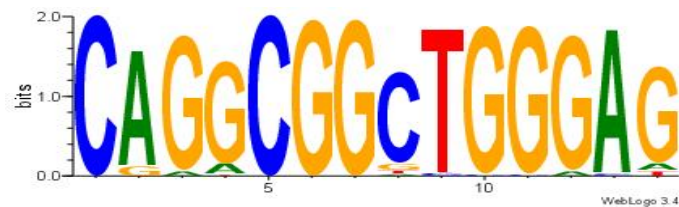


Reverse complement motif      Consensus sequence:  
GGGTGCAGGMGGGCTGAGT

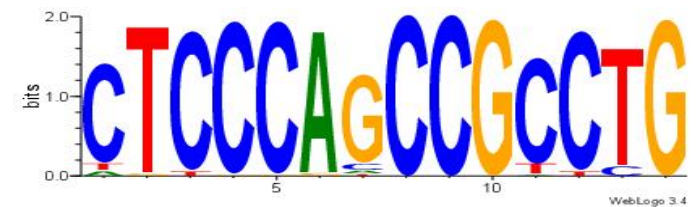


**Dataset #: 1      Motif ID: 286      Motif name: Motif 286**

Original motif      Consensus sequence: CAGGCGGCTGGGAG



Reverse complement motif      Consensus sequence: CTCCCAGCCGCTG



**Best Matches for Motif ID 286 (Highest to Lowest)**

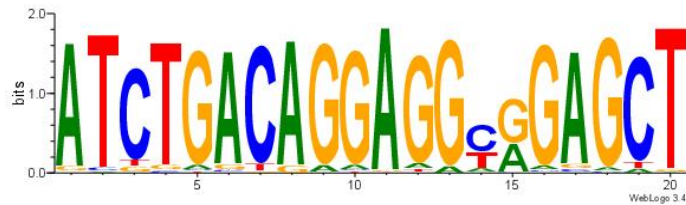
Dataset #:	1
Motif ID:	165
Motif name:	Motif 165
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward



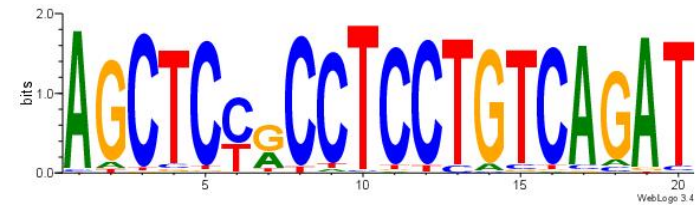
Position number: 7  
 Number of overlap: 14  
 Similarity score: 0.0824568

Alignment:  
 AGCTCMKCCTCCTGTCAGAT  
 CTCCCAGCCGCTG-----

Original motif      Consensus sequence: ATCTGACAGGAGGYRGAGCT



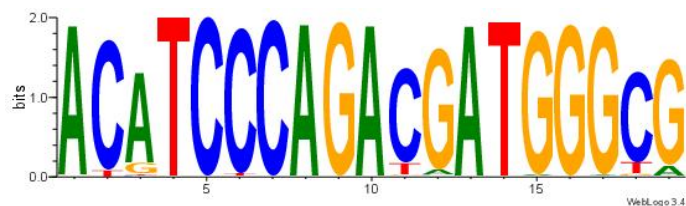
Reverse complement motif      Consensus sequence: AGCTCMKCCTCCTGTCAGAT



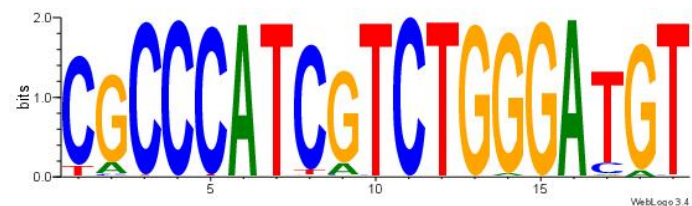
Dataset #: 1  
 Motif ID: 36  
 Motif name: Motif 36  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 4  
 Number of overlap: 14  
 Similarity score: 0.0825275

Alignment:  
 CGCCCATCGTCTGGGATGT  
 --CAGGCGGCTGGGAG---

Original motif      Consensus sequence: ACATCCCAGACGATGGGCG

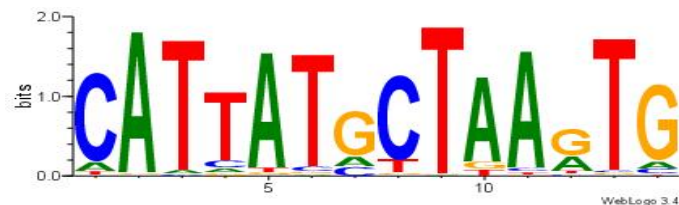


Reverse complement motif      Consensus sequence: CGCCCATCGTCTGGGATGT

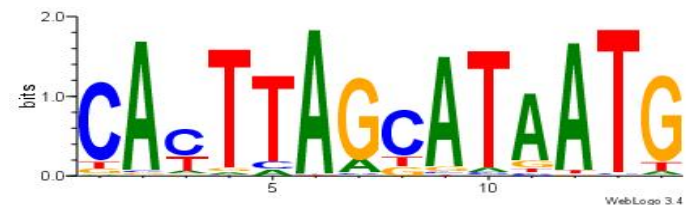


**Dataset #: 1      Motif ID: 287      Motif name: Motif 287**

Original motif      Consensus sequence: CATTATGCTAARTG



Reverse complement motif      Consensus sequence: CAMTTAGCATAATG



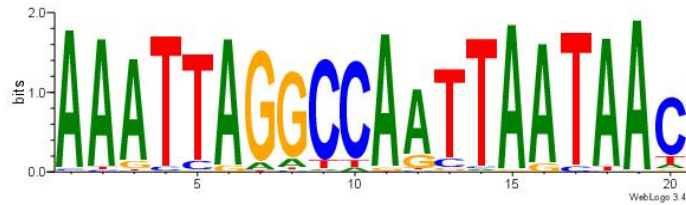
### Best Matches for Motif ID 287 (Highest to Lowest)

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

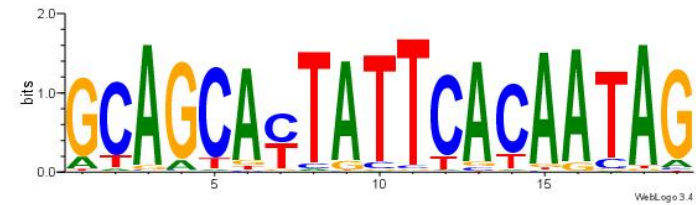
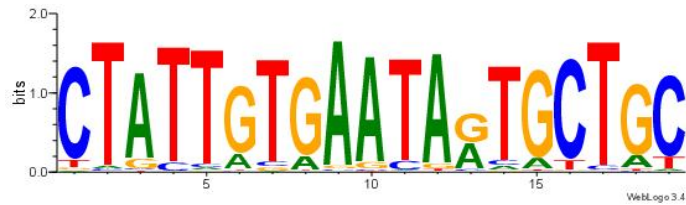


Dataset #: 1  
Motif ID: 70  
Motif name: Motif 70  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Reverse Complement  
Direction: Backward  
Position number: 2  
Number of overlap: 14  
Similarity score: 0.0796028

Alignment:  
GCAGCAMTATTCACAATAG  
-----CAMTTAGCATAATG--

Original motif      Consensus sequence: CTATTGTGAATARTGCTGC

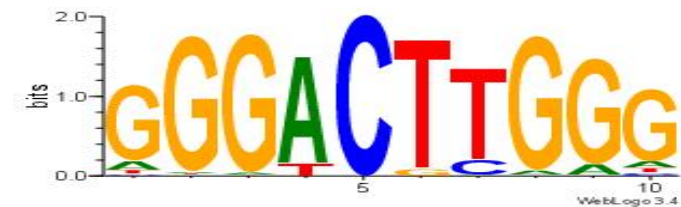
Reverse complement motif      Consensus sequence:  
GCAGCAMTATTCACAATAG



**Dataset #: 1      Motif ID: 288      Motif name: Motif 288**

Original motif      Consensus sequence: CCAAGTCCC

Reverse complement motif      Consensus sequence: GGGACTTGGG

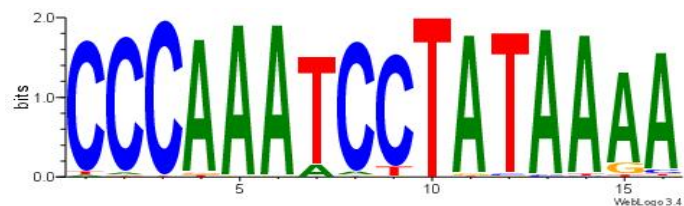


**Best Matches for Motif ID 288 (Highest to Lowest)**

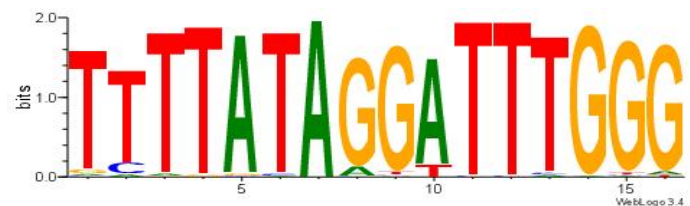
Dataset #:	1
Motif ID:	169
Motif name:	Motif 169
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	7
Number of overlap:	10
Similarity score:	0.0450065

Alignment:  
 CCCAAATCCTATAAAA  
 CCAAGTCCC-----

Original motif      Consensus sequence: CCCAAATCCTATAAAA



Reverse complement motif      Consensus sequence: TTTTATAGGATTTGGG

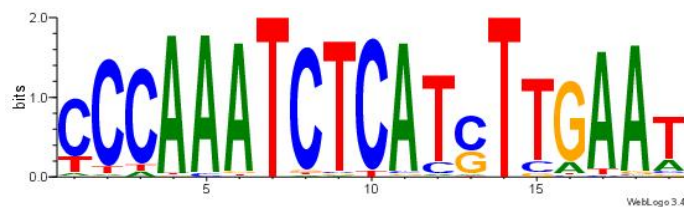


Dataset #: 1  
Motif ID: 227  
Motif name: Motif 227  
Matching format of first motif: Original Motif  
Matching format of second motif: Original Motif  
Direction: Backward  
Position number: 10  
Number of overlap: 10  
Similarity score: 0.0494747

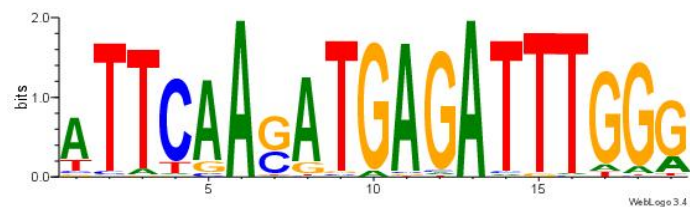
Alignment:

CCCAAATCTCATSTTGAAT  
CCCAAGTCCC-----

Original motif      Consensus sequence: CCCAAATCTCATSTTGAAT

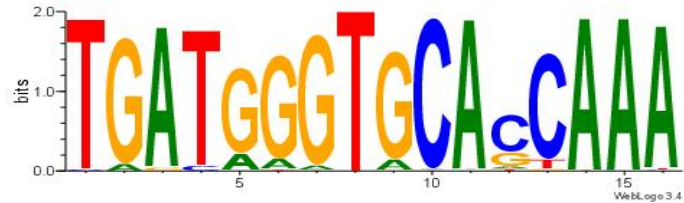


Reverse complement motif      Consensus sequence: ATTCAASATGAGATTTGGG

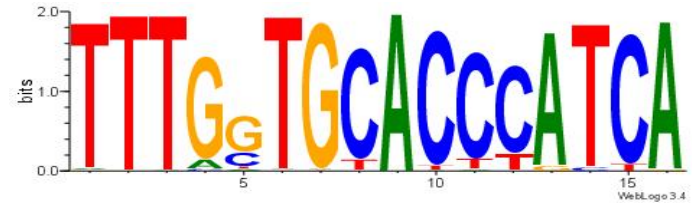


**Dataset #: 1      Motif ID: 289      Motif name: Motif 289**

Original motif      Consensus sequence: TGATGGGTGCACCAA



Reverse complement motif      Consensus sequence: TTTGGTGCACCCATCA



### Best Matches for Motif ID 289 (Highest to Lowest)

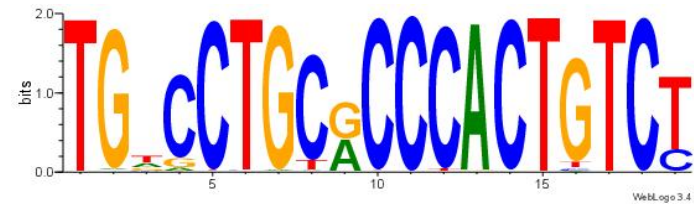
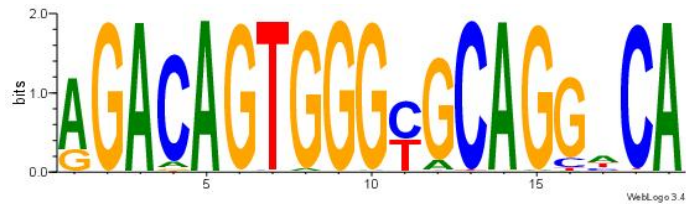
Dataset #:	1
Motif ID:	17
Motif name:	Motif 17
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	4
Number of overlap:	16
Similarity score:	0.100149

#### Alignment:

```
AGACAGTGGGYGCAGGHCA  
---TGATGGGTGCACCAA
```

Original motif      Consensus sequence: AGACAGTGGGYGCAGGHCA

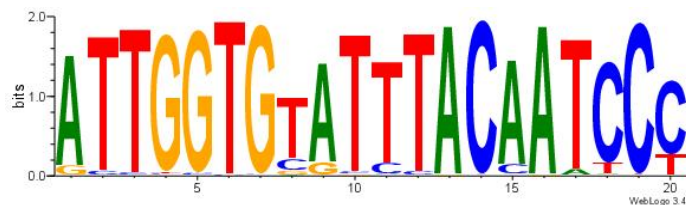
Reverse complement motif      Consensus sequence: TGHCTGCKCCCACTGTCT



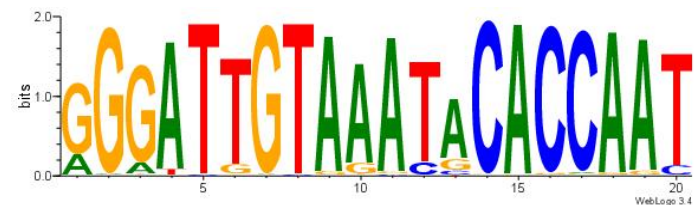
Dataset #: 1  
 Motif ID: 106  
 Motif name: Motif 106  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 5  
 Number of overlap: 16  
 Similarity score: 0.103791

Alignment:  
 ATTGGTGTATTTACAATCCC  
 ----TTTGGTGCACCCATCA

Original motif      Consensus sequence: ATTGGTGTATTTACAATCCC

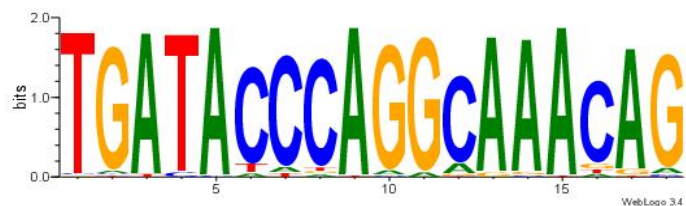


Reverse complement motif      Consensus sequence: GGGATTGTAAATACACCAAT

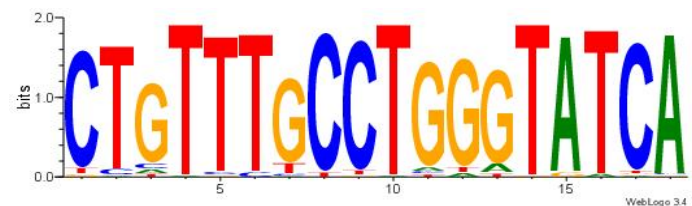


**Dataset #: 1      Motif ID: 290      Motif name: Motif 290**

Original motif      Consensus sequence: TGATACCCAGGCAAACAG



Reverse complement motif      Consensus sequence: CTGTTTGCCTGGGTATCA



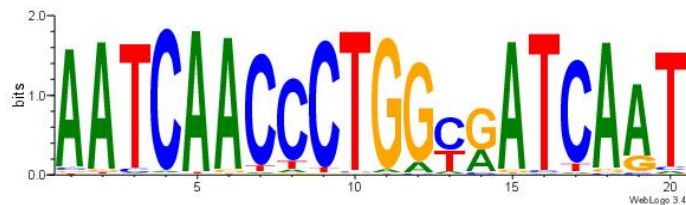
### Best Matches for Motif ID 290 (Highest to Lowest)

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

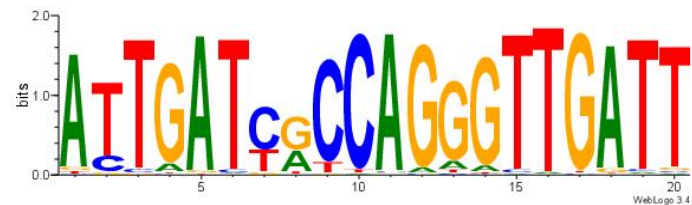
#### Alignment:

```
AATCAACCCTGGYRATCAAT  
-TGATACCCAGGCAAACAG-
```

Original motif      Consensus sequence: AATCAACCCTGGYRATCAAT



Reverse complement motif      Consensus sequence: ATTGATMKCCAGGGTTGATT



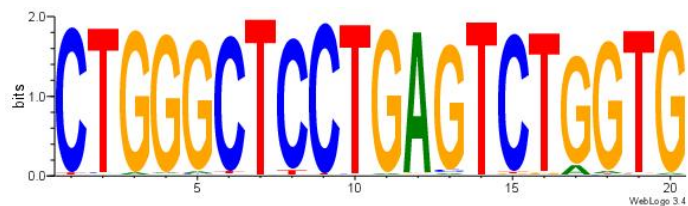


Dataset #: 1  
 Motif ID: 67  
 Motif name: Motif 67  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 18  
 Similarity score: 0.0999158

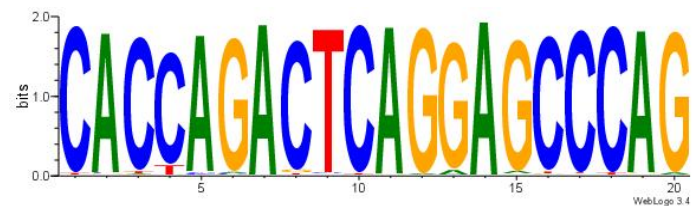
Alignment:

CTGGGCTCCTGAGTCTGGTG  
 --CTGTTTGCCTGGGTATCA

Original motif    Consensus sequence: CTGGGCTCCTGAGTCTGGTG



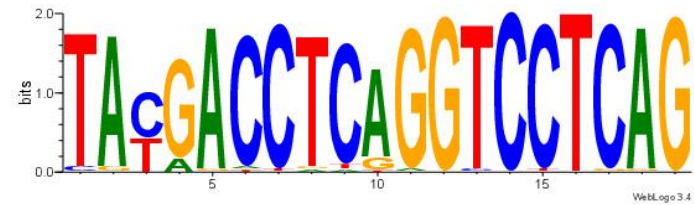
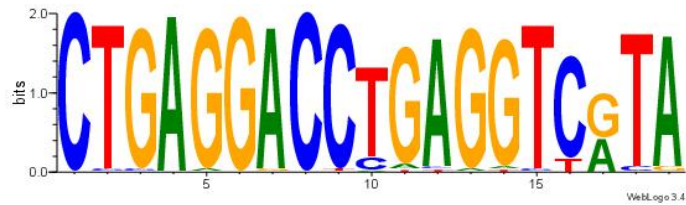
Reverse complement motif    Consensus sequence:  
 CACCAGACTCAGGAGCCCAG



**Dataset #: 1      Motif ID: 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)

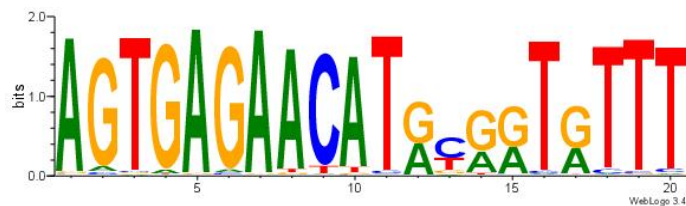
Dataset #: 1  
 Motif ID: 63  
 Motif name: Motif 63  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 2  
 Number of overlap: 19  
 Similarity score: 0.0928513

#### Alignment:

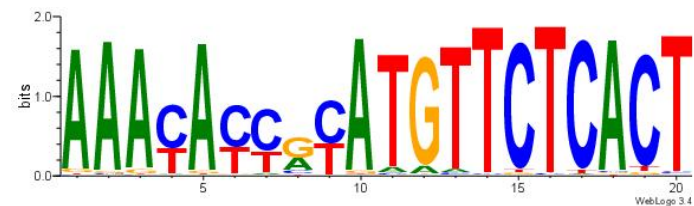
```

AAAMAMMKMATGTTCTCACT
TAMGACCTCAGGTCCTCAG-
  
```

Original motif      Consensus sequence: AGTGAGAACATRYRRRTTTT



Reverse complement motif      Consensus sequence: AAAMAMMKMATGTTCTCACT

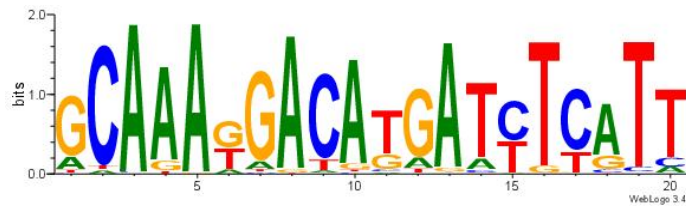


Dataset #: 1  
 Motif ID: 99  
 Motif name: Motif 99  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 2  
 Number of overlap: 19  
 Similarity score: 0.0929924

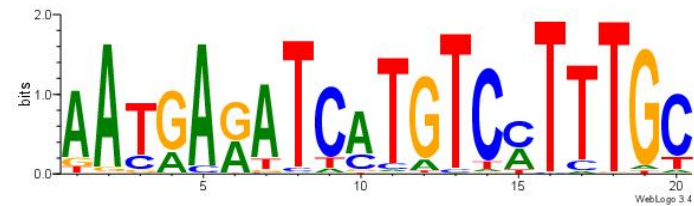
Alignment:

GCAAAGACATGATYTCATT  
 -CTGAGGACCTGAGGTCRTA

Original motif      Consensus sequence: GCAAAGACATGATYTCATT



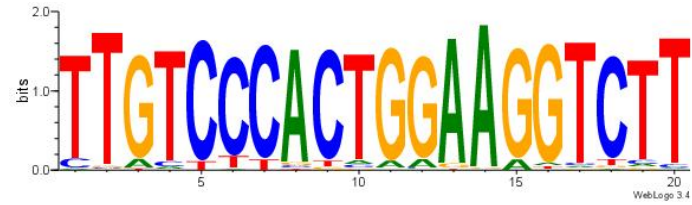
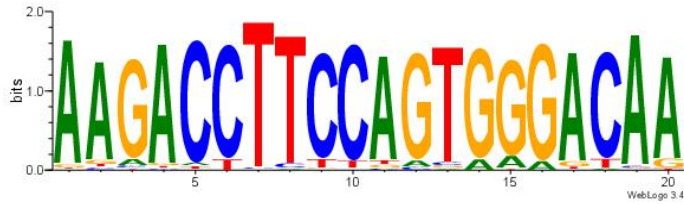
Reverse complement motif      Consensus sequence: AATGAKATCATGTCYTTTGC



**Dataset #: 1      Motif ID: 292      Motif name: Motif 292**

Original motif      Consensus sequence: AAGACCTTCCAGTGGGACAA

Reverse complement motif      Consensus sequence: TTGTCCCACTGGAAGGTCTT

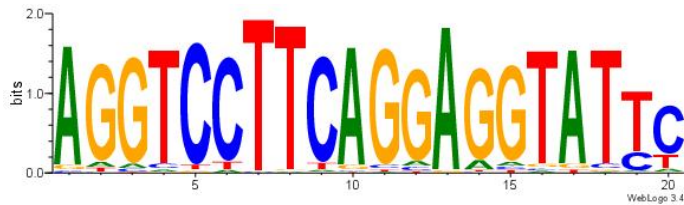


**Best Matches for Motif ID 292 (Highest to Lowest)**

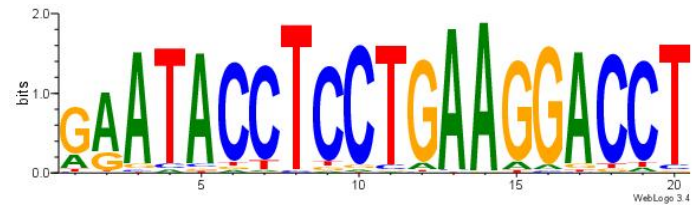
Dataset #: 1  
 Motif ID: 179  
 Motif name: Motif 179  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 20  
 Similarity score: 0.094932

Alignment:  
 GAATACCTCCTGAAGGACCT  
 TTGTCCCAGTGGAGGTCTT

Original motif      Consensus sequence: AGGTCCTCAGGAGGTATTC



Reverse complement motif      Consensus sequence: GAATACCTCCTGAAGGACCT

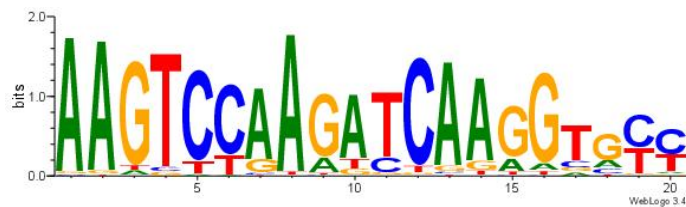


Dataset #: 1  
 Motif ID: 119  
 Motif name: Motif 119  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 20  
 Similarity score: 0.106872

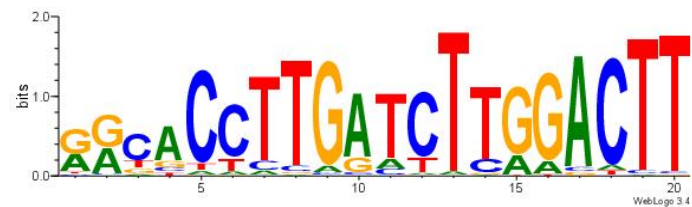
Alignment:

KKCACCTTGATCTTGGACTT  
 AAGACCTTCCAGTGGGACAA

Original motif    Consensus sequence: AAGTCCAAGATCAAGGTGYY



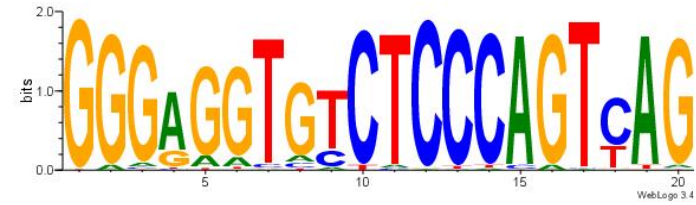
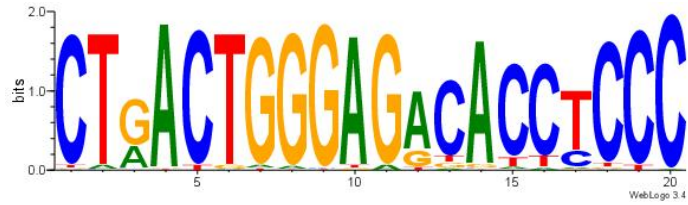
Reverse complement motif    Consensus sequence: KKCACCTTGATCTTGGACTT



**Dataset #: 1      Motif ID: 293      Motif name: Motif 293**

Original motif    Consensus sequence: CTGACTGGGAGACACCTCCC

Reverse complement motif    Consensus sequence: GGGAGGTGTCTCCCAGTCAG



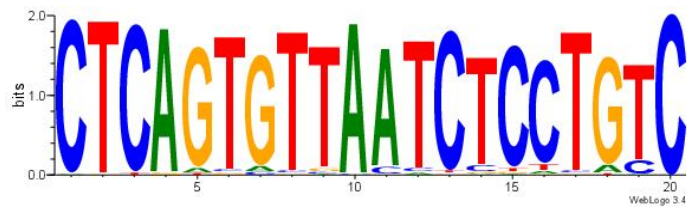
### Best Matches for Motif ID 293 (Highest to Lowest)

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

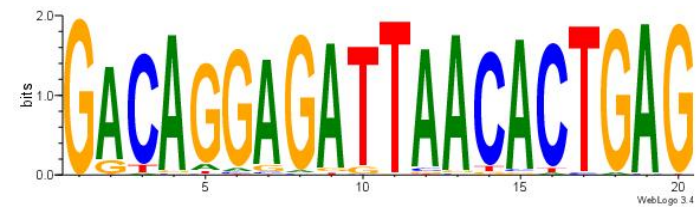
#### Alignment:

CTCAGTGTTAATCTCCTGTC  
 CTGACTGGGAGACACCTCCC

Original motif      Consensus sequence: CTCAGTGTTAATCTCCTGTC



Reverse complement motif      Consensus sequence: GACAGGAGATTAACACTGAG

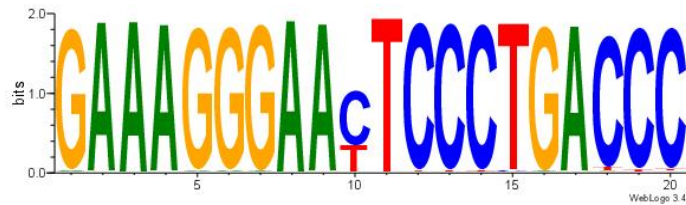


Dataset #: 1  
 Motif ID: 16  
 Motif name: Motif 16  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 20  
 Similarity score: 0.115344

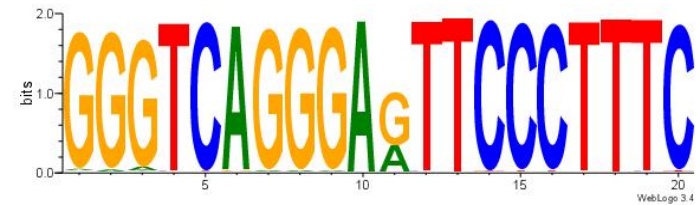
Alignment:

GAAAGGGA ACTCCCTGACCC  
 GGGAGGTGTCTCC CAGTCAG

Original motif      Consensus sequence: GAAAGGGA ACTCCCTGACCC



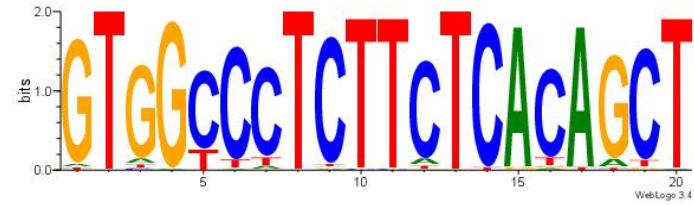
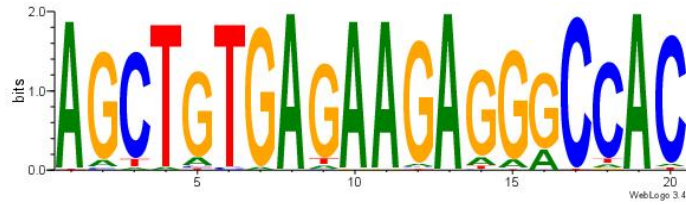
Reverse complement motif      Consensus sequence: GGGTCAGG GAGTTCCCTTTC



**Dataset #: 1      Motif ID: 294      Motif name: Motif 294**

Original motif      Consensus sequence: AGCTGTGAGAAGAGGGCCAC

Reverse complement motif      Consensus sequence: GTGGCCCTCTTCTCACAGCT



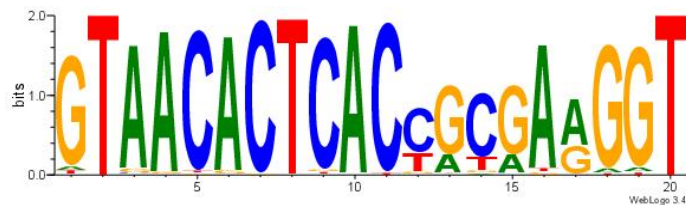
### Best Matches for Motif ID 294 (Highest to Lowest)

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

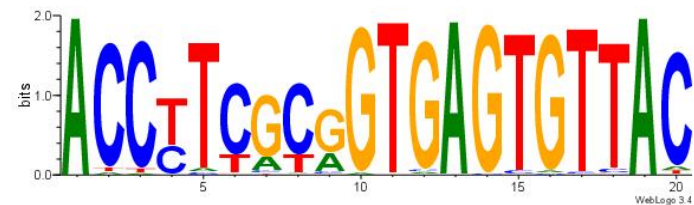
#### Alignment:

ACCKTCGCGGTGAGTGTTAC  
 AGCTGTGAGAAGAGGGCCAC

Original motif      Consensus sequence: GTAACACTCACCGCGARGGT



Reverse complement motif      Consensus sequence: ACCKTCGCGGTGAGTGTTAC



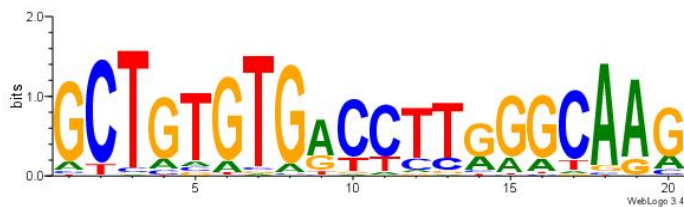


Dataset #: 1  
 Motif ID: 112  
 Motif name: Motif 112  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 2  
 Number of overlap: 19  
 Similarity score: 0.591581

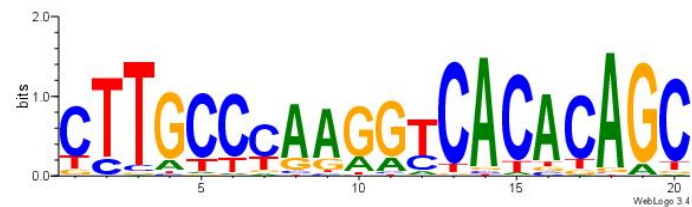
Alignment:

CTTGCCCAAGGTCACACAGC-  
 -GTGGCCCTCTTCTCACAGCT

Original motif      Consensus sequence: GCTGTGTGACCTTGGGCAAG



Reverse complement motif      Consensus sequence: CTTGCCCAAGGTCACACAGC

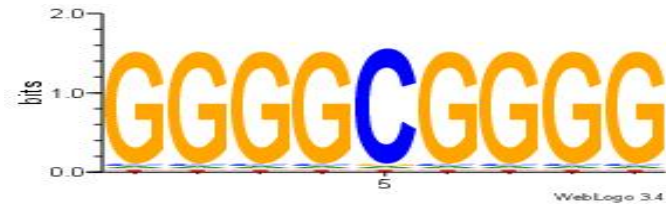
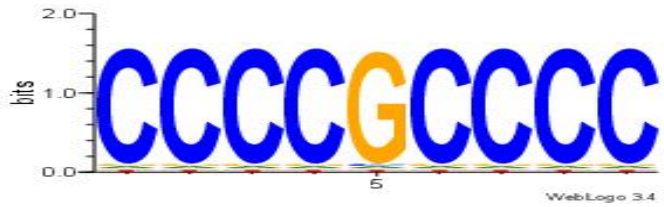



---

**Dataset #: 1      Motif ID: 295      Motif name: Motif 295**

Original motif      Consensus sequence: CCCC GCCC

Reverse complement motif      Consensus sequence: GGGC GGGG



### Best Matches for Motif ID 295 (Highest to Lowest)

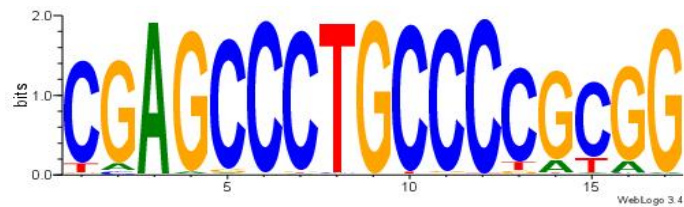
Dataset #: 1  
 Motif ID: 78  
 Motif name: Motif 78  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 5  
 Number of overlap: 9  
 Similarity score: 0.02574

#### Alignment:

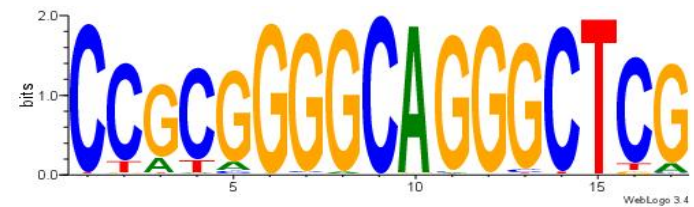
```

CGAGCCCTGCCCGCGG
----CCCCGCCCC----
  
```

Original motif      Consensus sequence: CGAGCCCTGCCCGCGG



Reverse complement motif      Consensus sequence: CCGCGGGGCAGGGCTCG



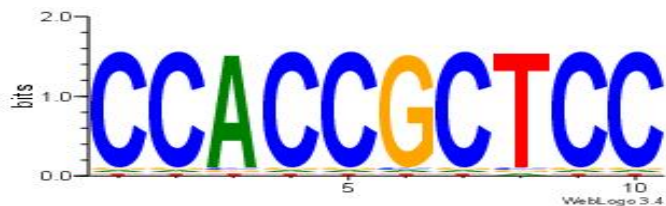
Dataset #: 1  
 Motif ID: 250  
 Motif name: Motif 250  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 2  
 Number of overlap: 9  
 Similarity score: 0.0380756

Alignment:

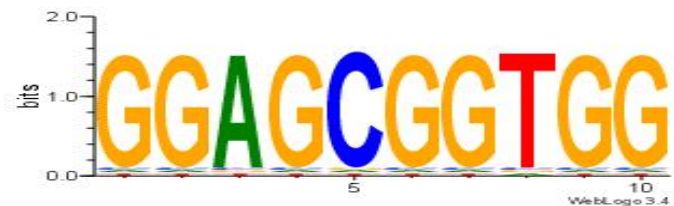
GGAGCGGTGG

GGGCGGGG-

Original motif      Consensus sequence: CCACCGCTCC



Reverse complement motif      Consensus sequence: GGAGCGGTGG



**Dataset #: 1      Motif ID: 296      Motif name: Motif 296**

Original motif      Consensus sequence: CCACGTGG



Reverse complement motif      Consensus sequence: CCACGTGG



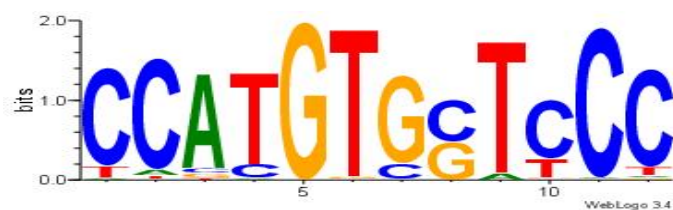
## Best Matches for Motif ID 296 (Highest to Lowest)

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

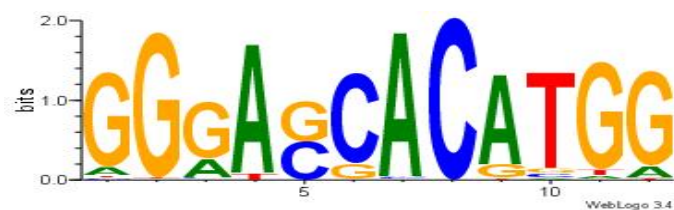
### Alignment:

```
CCATGTGSTCCC  
CCACGTGG-----
```

Original motif      Consensus sequence: CCATGTGSTCCC



Reverse complement motif      Consensus sequence: GGGASCACATGG



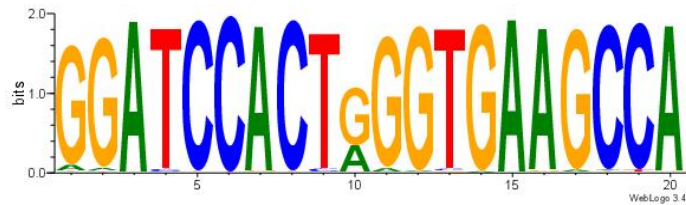
---

Dataset #: 1  
Motif ID: 61  
Motif name: Motif 61  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Original Motif

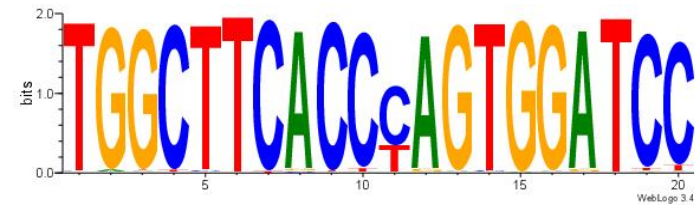
Direction: Backward  
 Position number: 5  
 Number of overlap: 8  
 Similarity score: 0.0551535

Alignment:  
 GGATCCACTGGGTGAAGCCA  
 -----CCACGTGG-----

Original motif Consensus sequence: GGATCCACTGGGTGAAGCCA

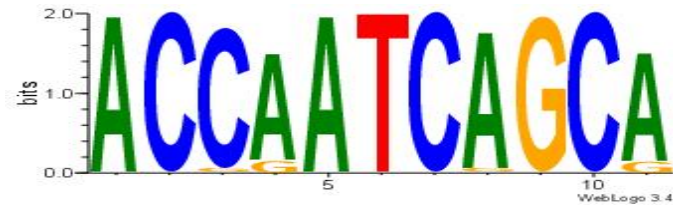


Reverse complement motif Consensus sequence: TGGCTTCACCCAGTGGATCC

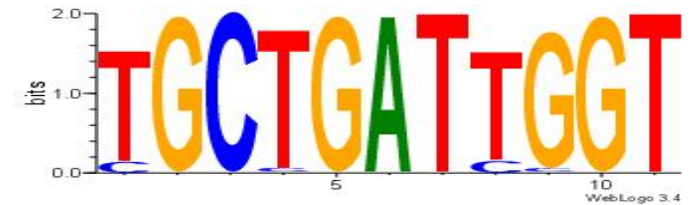


**Dataset #: 1 Motif ID: 297 Motif name: Motif 297**

Original motif Consensus sequence: ACCAATCAGCA



Reverse complement motif Consensus sequence: TGCTGATTGGT



**Best Matches for Motif ID 297 (Highest to Lowest)**

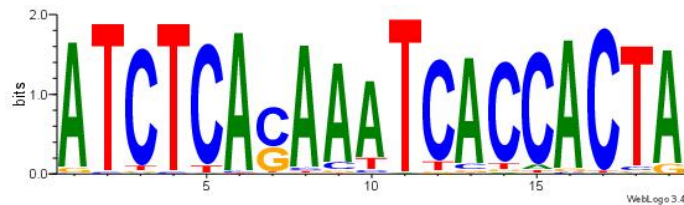
Dataset #: 1  
 Motif ID: 261

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

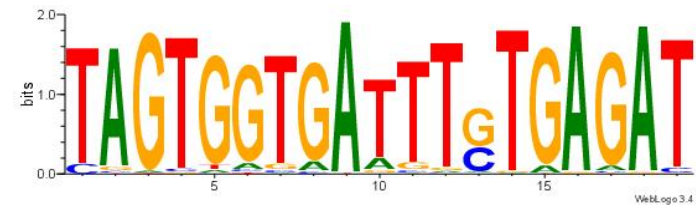
**Alignment:**

TAGTGGTGATTTSTGAGAT  
 ---TGCTGATTGGT-----

Original motif    Consensus sequence: ATCTCASAAATCACCCTA



Reverse complement motif    Consensus sequence: TAGTGGTGATTTSTGAGAT

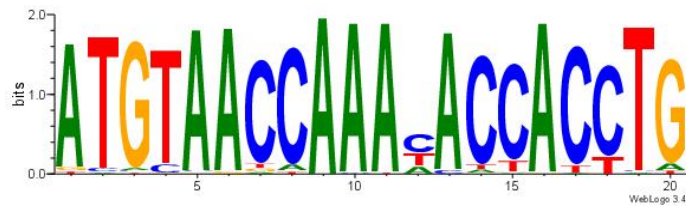


Dataset #: 1  
 Motif ID: 336  
 Motif name: Motif 336  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 5  
 Number of overlap: 11  
 Similarity score: 0.0632904

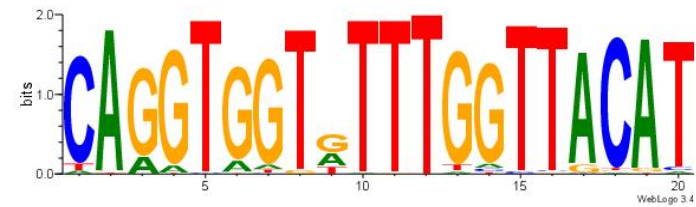
Alignment:

```
CAGGTGGTKTTTGGTTACAT
----TGCTGATTGGT-----
```

Original motif      Consensus sequence: ATGTAACCAAAYACCACCTG

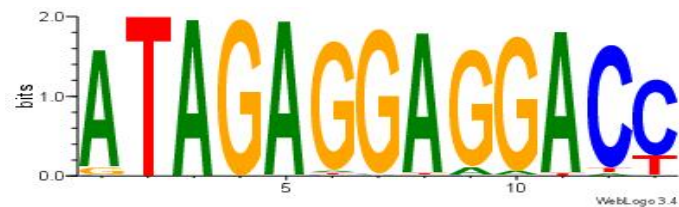


Reverse complement motif      Consensus sequence: CAGGTGGTKTTTGGTTACAT

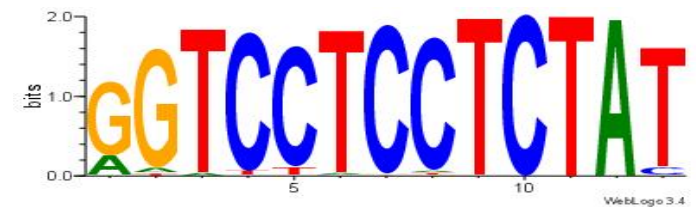


**Dataset #: 1      Motif ID: 298      Motif name: Motif 298**

Original motif      Consensus sequence: ATAGAGGAGGACC



Reverse complement motif      Consensus sequence: GTCCTCCTCTAT



**Best Matches for Motif ID 298 (Highest to Lowest)**

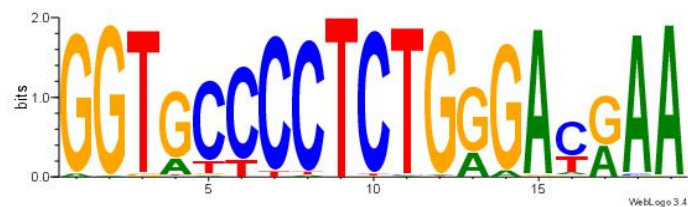
Dataset #:	1
Motif ID:	260
Motif name:	Motif 260
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward

Position number: 1  
Number of overlap: 13  
Similarity score: 0.0631665

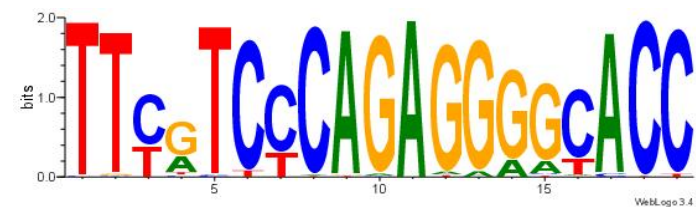
Alignment:

GGTGCCCTCTGGGACRAA  
-----GGTCCTCCTCTAT

Original motif      Consensus sequence: GGTGCCCTCTGGGACRAA



Reverse complement motif      Consensus sequence: TTMGTCCCAGAGGGGCACC



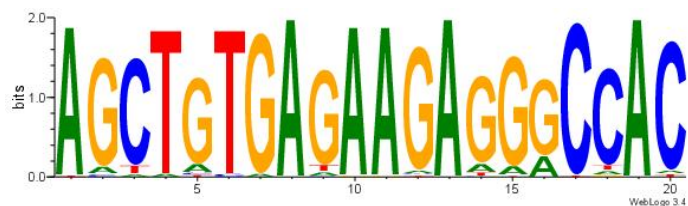
Dataset #: 1  
Motif ID: 294  
Motif name: Motif 294  
Matching format of first motif: Original Motif  
Matching format of second motif: Original Motif  
Direction: Forward  
Position number: 6  
Number of overlap: 13  
Similarity score: 0.0642679

Alignment:

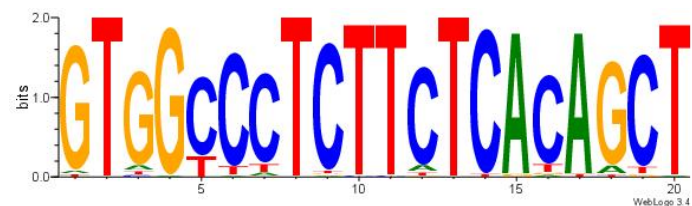
AGCTGTGAGAAGAGGGCCAC  
-----ATAGAGGAGGACC--



Original motif      Consensus sequence: AGCTGTGAGAAGAGGGCCAC

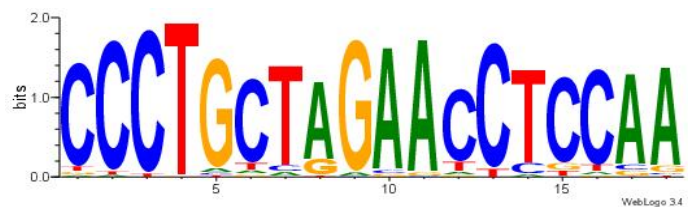


Reverse complement motif      Consensus sequence: GTGGCCCTCTTCTCACAGCT

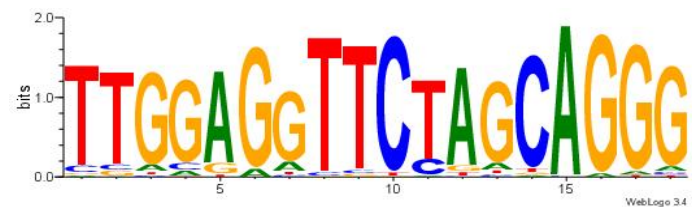


**Dataset #: 1      Motif ID: 299      Motif name: Motif 299**

Original motif      Consensus sequence: CCCTGCTAGAACCTCCAA



Reverse complement motif      Consensus sequence: TTGGAGTTCTAGCAGGG



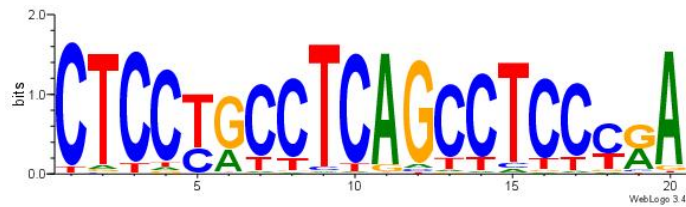
### Best Matches for Motif ID 299 (Highest to Lowest)

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

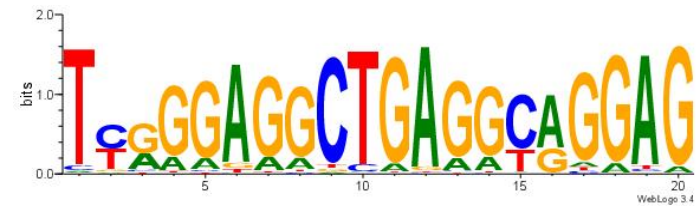
Alignment:

CTCCTGCCTCAGCCTCCCRA  
-CCCTGCTAGAACCTCCAA-

Original motif      Consensus sequence: CTCCTGCCTCAGCCTCCCRA



Reverse complement motif      Consensus sequence:  
TMGGGAGGCTGAGGCAGGAG



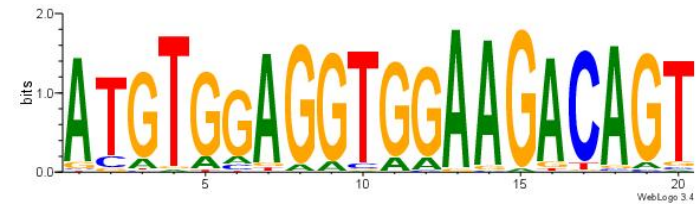
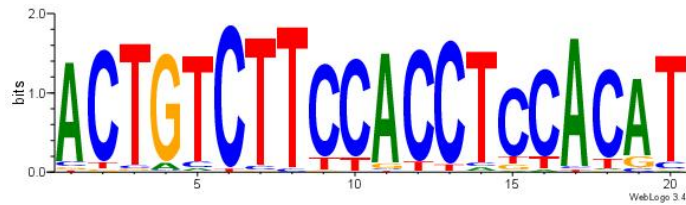
Dataset #: 1  
Motif ID: 178  
Motif name: Motif 178  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Reverse Complement  
Direction: Backward  
Position number: 1  
Number of overlap: 18  
Similarity score: 0.097377

Alignment:

ATGTGGAGGTGGAAGACAGT  
--TTGGAGGTTCTAGCAGGG

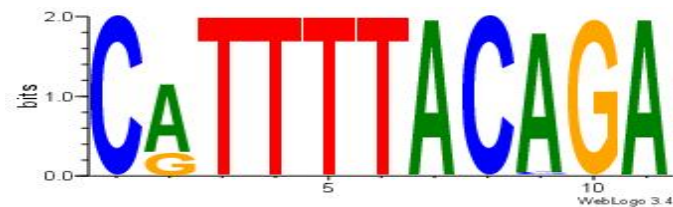
Original motif      Consensus sequence: ACTGTCTTCCACCTCCACAT

Reverse complement motif      Consensus sequence:  
ATGTGGAGGTGGAAGACAGT

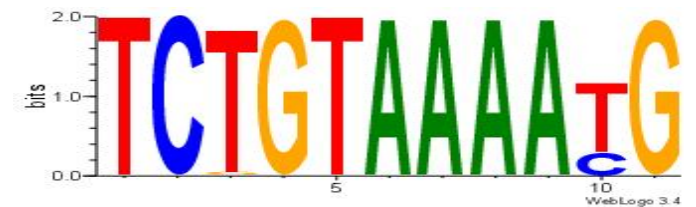


**Dataset #: 1      Motif ID: 300      Motif name: Motif 300**

Original motif      Consensus sequence: CATTTTACAGA



Reverse complement motif      Consensus sequence: TCTGTAAAATG

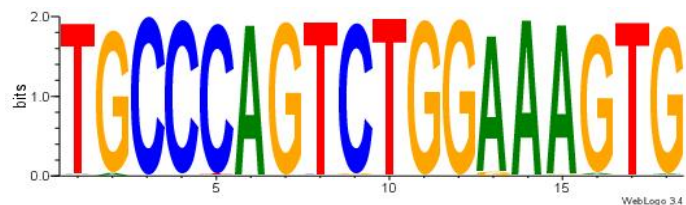


**Best Matches for Motif ID 300 (Highest to Lowest)**

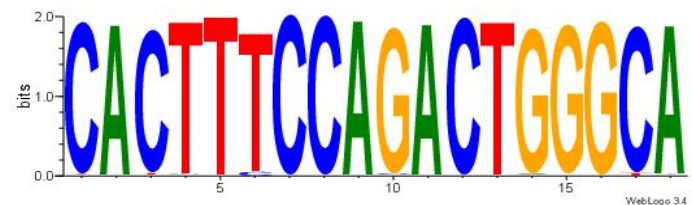
Dataset #:	1
Motif ID:	45
Motif name:	Motif 45
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	11
Similarity score:	0.0501861

Alignment:  
 CACTTTCCAGACTGGGCA  
 -----CATTTTACAGA

Original motif      Consensus sequence: TGCCCAAGTCTGGAAAGTG



Reverse complement motif      Consensus sequence: CACTTTCAGACTGGGCA

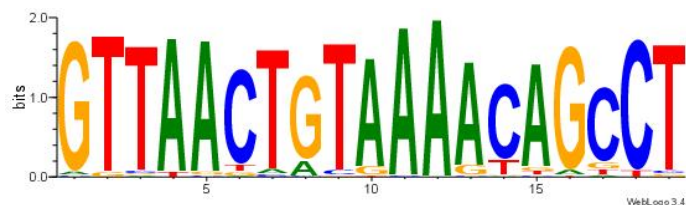


Dataset #: 1  
Motif ID: 233  
Motif name: Motif 233  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Original Motif  
Direction: Forward  
Position number: 5  
Number of overlap: 11  
Similarity score: 0.071946

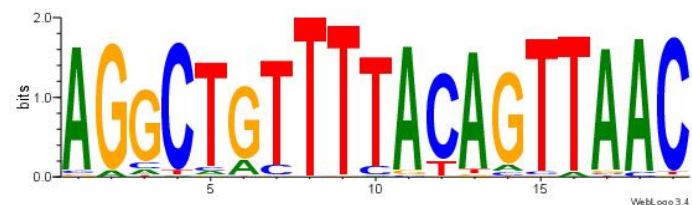
Alignment:

GTAACTGTAAAACAGCCT  
----TCTGTAAAATG----

Original motif      Consensus sequence: GTAACTGTAAAACAGCCT

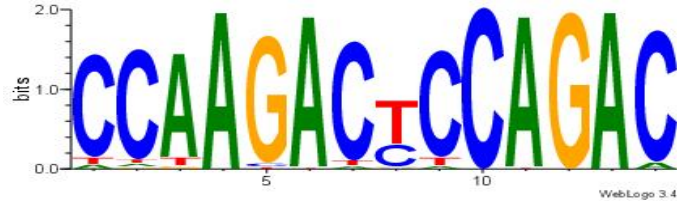


Reverse complement motif      Consensus sequence: AGGCTTTTACAGTTAAC

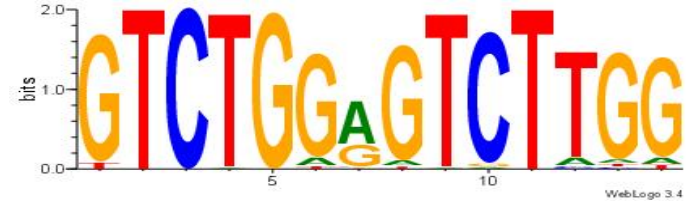


**Dataset #: 1      Motif ID: 301      Motif name: Motif 301**

Original motif      Consensus sequence: CCAAGACYCCAGAC



Reverse complement motif      Consensus sequence: GTCTGGMGTCCTTG



**Best Matches for Motif ID 301 (Highest to Lowest)**

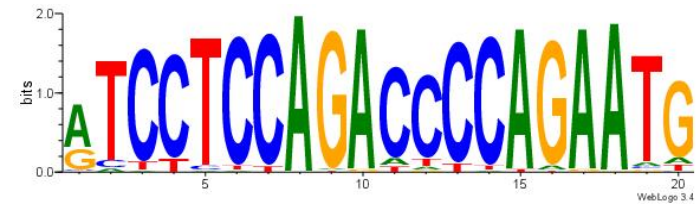
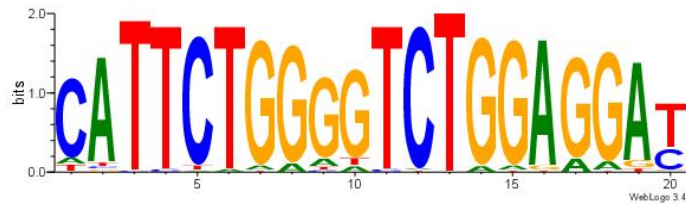
Dataset #:	1
Motif ID:	309
Motif name:	Motif 309
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	3
Number of overlap:	14
Similarity score:	0.0547706

**Alignment:**

```
MTCCTCCAGACCCCAGAATG
----CCAAGACYCCAGAC--
```

Original motif      Consensus sequence: CATTCTGGGGTCTGGAGGAY

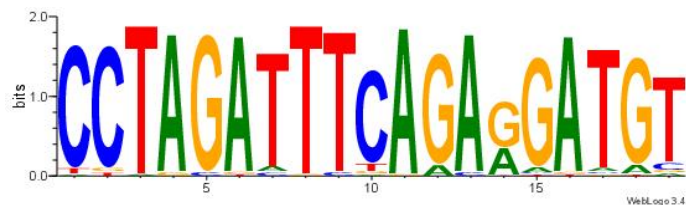
Reverse complement motif      Consensus sequence: MTCCTCCAGACCCCAGAATG



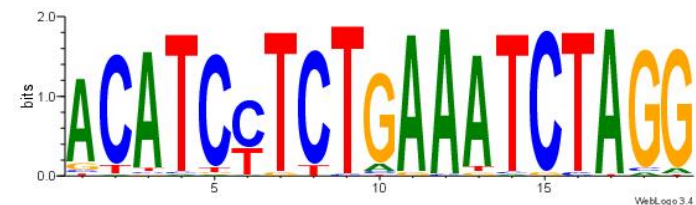
Dataset #: 1  
 Motif ID: 280  
 Motif name: Motif 280  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 14  
 Similarity score: 0.0659934

Alignment:  
 CCTAGATTTTCAGARGATGT  
 CCAAGACYCCAGAC-----

Original motif      Consensus sequence: CCTAGATTTTCAGARGATGT



Reverse complement motif      Consensus sequence: ACATCMTCTGAAATCTAGG

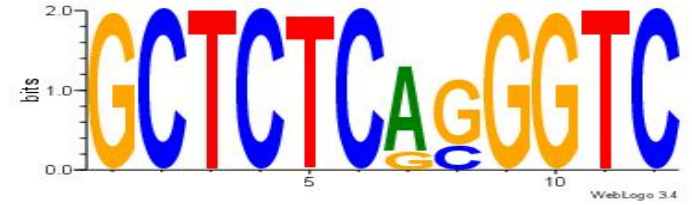


**Dataset #: 1      Motif ID: 302      Motif name: Motif 302**

Original motif    Consensus sequence: GACCCTGAGAGC



Reverse complement motif    Consensus sequence: GCTCTCAGGGTC



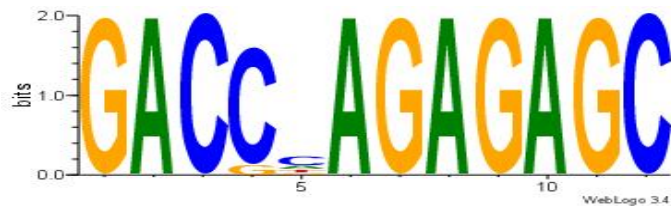
### Best Matches for Motif ID 302 (Highest to Lowest)

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

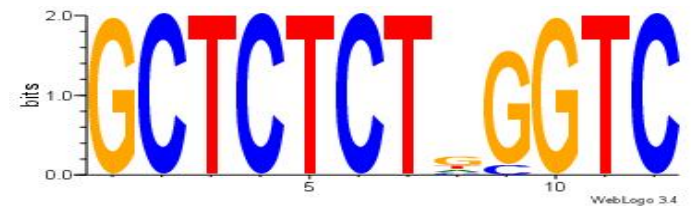
Alignment:

GACCCAGAGAGC  
GACCCTGAGAGC

Original motif    Consensus sequence: GACCCAGAGAGC



Reverse complement motif    Consensus sequence: GCTCTCTGGGTC

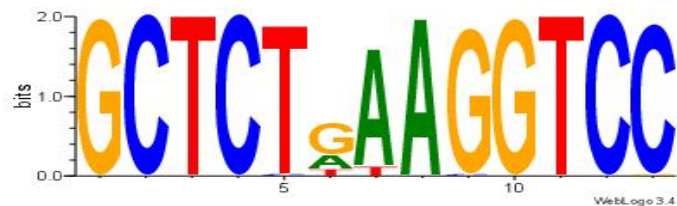


Dataset #: 1  
 Motif ID: 362  
 Motif name: Motif 362  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 12  
 Similarity score: 0.0423209

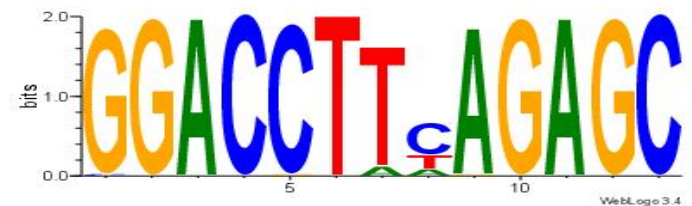
Alignment:

GGACCTTCAGAGC  
 -GACCCTGAGAGC

Original motif      Consensus sequence: GCTCTGAAGGTCC



Reverse complement motif      Consensus sequence: GGACCTTCAGAGC



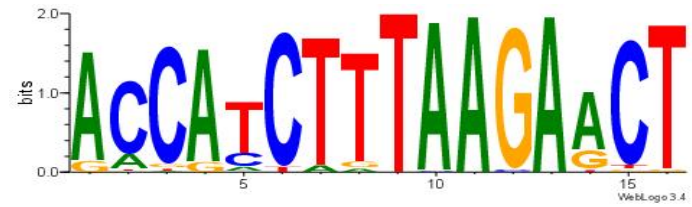
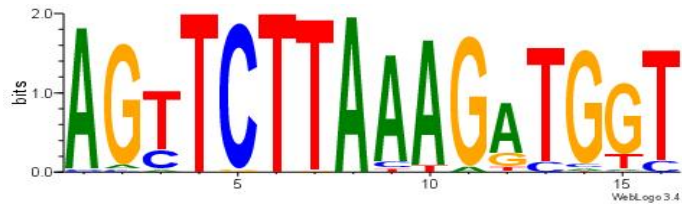

---

**Dataset #: 1      Motif ID: 303      Motif name: Motif 303**

Original motif      Consensus sequence: AGTTCTTAAAGATGGT

Reverse complement motif      Consensus sequence:  
ACCATCTTTAAGAACT



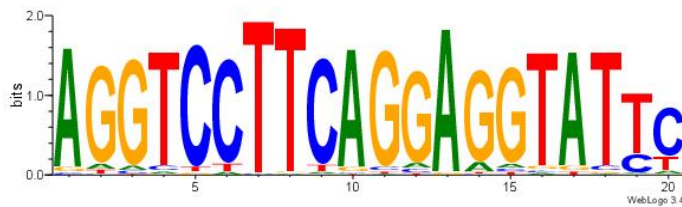


**Best Matches for Motif ID 303 (Highest to Lowest)**

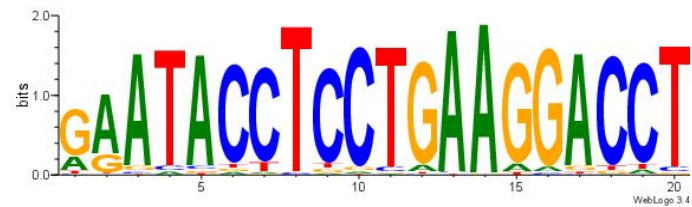
Dataset #: 1  
 Motif ID: 179  
 Motif name: Motif 179  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 5  
 Number of overlap: 16  
 Similarity score: 0.0731282

Alignment:  
 GAATACCTCCTGAAGGACCT  
 ----ACCATCTTTAAGAACT

Original motif      Consensus sequence: AGGTCCTCAGGAGGTATTC



Reverse complement motif      Consensus sequence: GAATACCTCCTGAAGGACCT

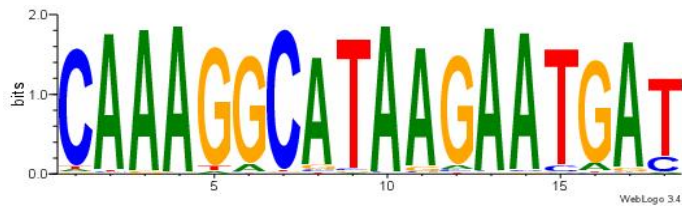


Dataset #: 1  
 Motif ID: 190  
 Motif name: Motif 190  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 3  
 Number of overlap: 16  
 Similarity score: 0.0867922

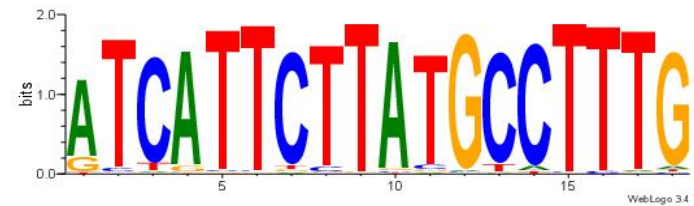
Alignment:

ATCATTCTTATGCCTTTG  
 ACCATCTTTAAGAACT--

Original motif      Consensus sequence: CAAAGGCATAAGAATGAT



Reverse complement motif      Consensus sequence: ATCATTCTTATGCCTTTG

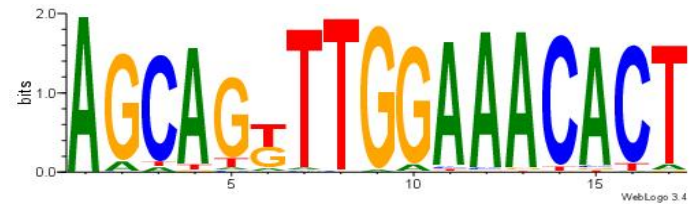
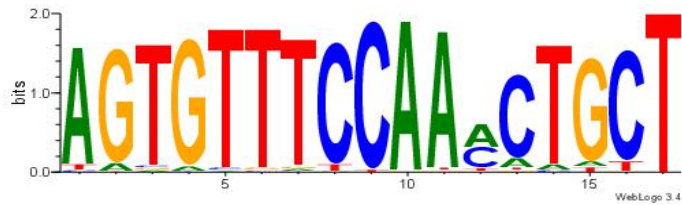



---

**Dataset #: 1      Motif ID: 304      Motif name: Motif 304**

Original motif      Consensus sequence: AGTGTTC CAAMCTGCT

Reverse complement motif      Consensus sequence: AGCAGYTTGGAAACT

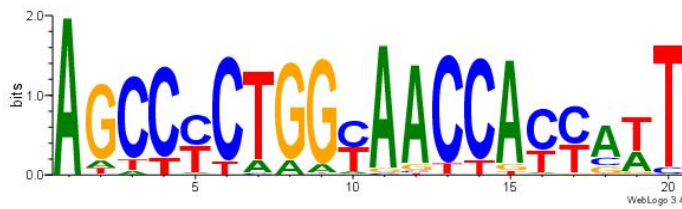


**Best Matches for Motif ID 304 (Highest to Lowest)**

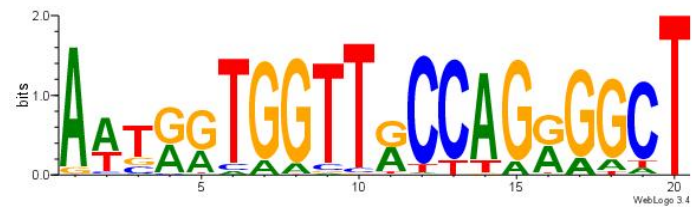
Dataset #: 1  
 Motif ID: 139  
 Motif name: Motif 139  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 17  
 Similarity score: 0.0916595

Alignment:  
 AWTKKTGGTTKCCAGKGGCT  
 AGTGTTTCCAAMCTGCT---

Original motif      Consensus sequence: AGCCYCTGGYAACCAYYAWT



Reverse complement motif      Consensus sequence: AWTKKTGGTTKCCAGKGGCT

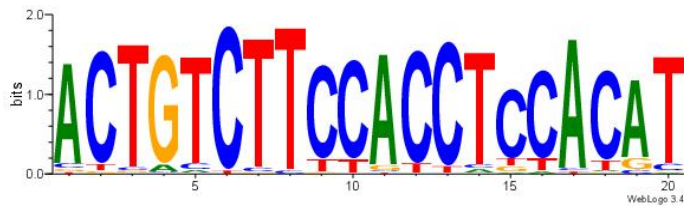


Dataset #: 1  
 Motif ID: 178  
 Motif name: Motif 178  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 4  
 Number of overlap: 17  
 Similarity score: 0.0916702

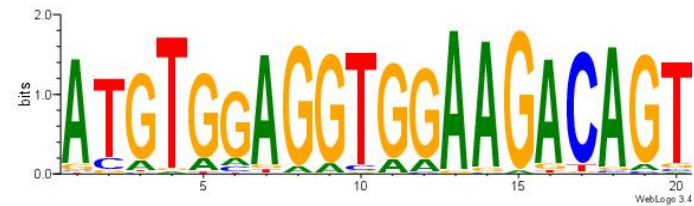
Alignment:

ACTGTCTTCCACCTCCACAT  
 AGTGTTCCTCAAMCTGCT---

Original motif      Consensus sequence: ACTGTCTTCCACCTCCACAT



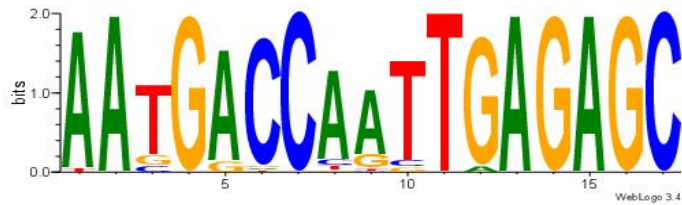
Reverse complement motif      Consensus sequence: ATGTGGAGGTGGAAGACAGT



**Dataset #: 1      Motif ID: 305      Motif name: Motif 305**

Original motif      Consensus sequence: AATGACCAATTGAGAGC

Reverse complement motif      Consensus sequence: GCTCTCAATTGGTCATT

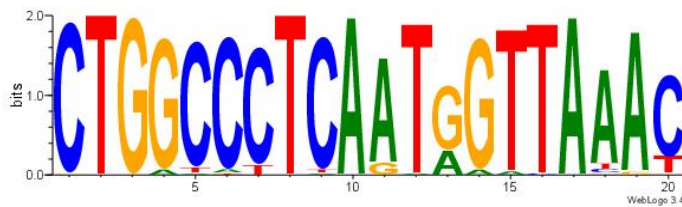


**Best Matches for Motif ID 305 (Highest to Lowest)**

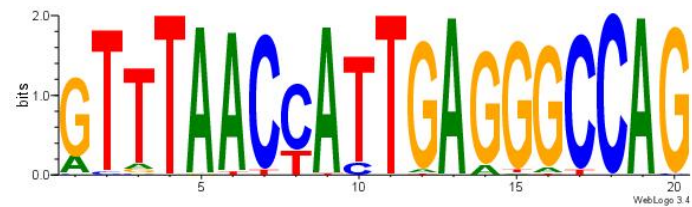
Dataset #: 1  
 Motif ID: 332  
 Motif name: Motif 332  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 17  
 Similarity score: 0.0848872

Alignment:  
 GTTTAACCATTGAGGGCCAG  
 AATGACCAATTGAGAGC---

Original motif      Consensus sequence: CTGGCCCTCAATGGTTAAAC



Reverse complement motif      Consensus sequence: GTTTAACCATTGAGGGCCAG

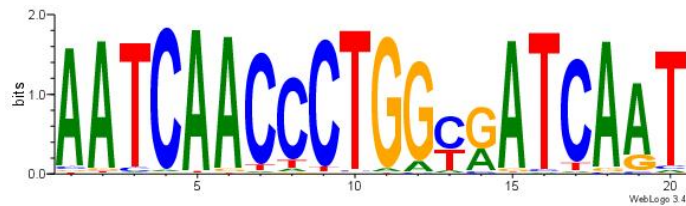


Dataset #: 1  
 Motif ID: 170  
 Motif name: Motif 170  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 17  
 Similarity score: 0.0979755

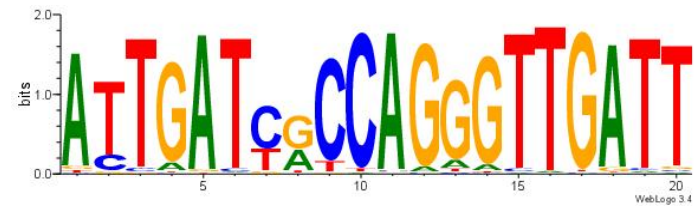
Alignment:

ATTGATMKCCAGGGTTGATT  
 ---GCTCTCAATTGGTCATT

Original motif      Consensus sequence: AATCAACCCTGGYRATCAAT



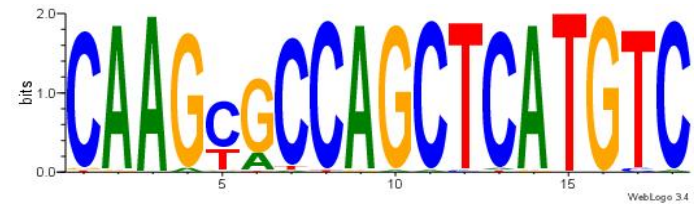
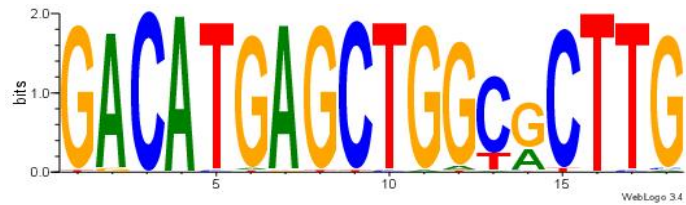
Reverse complement motif      Consensus sequence: ATTGATMKCCAGGGTTGATT



**Dataset #: 1      Motif ID: 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)

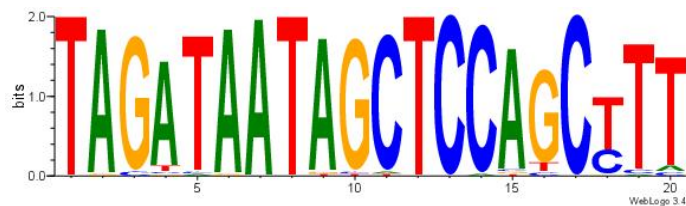
Dataset #: 1  
 Motif ID: 333  
 Motif name: Motif 333  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 18  
 Similarity score: 0.102628

#### Alignment:

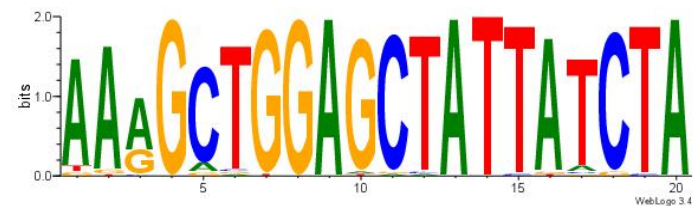
```

AAAGCTGGAGCTATTATCTA
CAAGCGCCAGCTCATGTC--
  
```

Original motif      Consensus sequence: TAGATAATAGCTCCAGCTTT



Reverse complement motif      Consensus sequence: AAAGCTGGAGCTATTATCTA

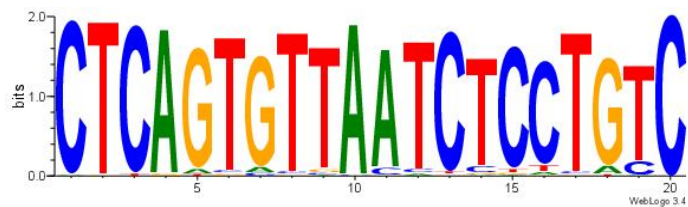


Dataset #: 1  
 Motif ID: 262  
 Motif name: Motif 262  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 3  
 Number of overlap: 18  
 Similarity score: 0.107908

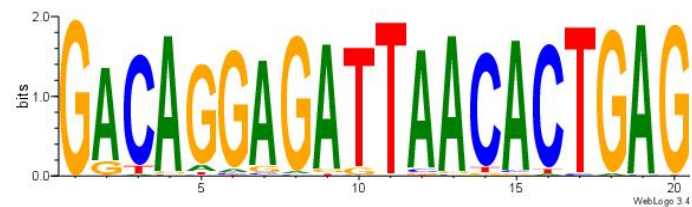
Alignment:

GACAGGAGATTAACACTGAG  
 --GACATGAGCTGGCGCTTG

Original motif      Consensus sequence: CTCAGTGTTAATCTCCTGTC



Reverse complement motif      Consensus sequence: GACAGGAGATTAACACTGAG

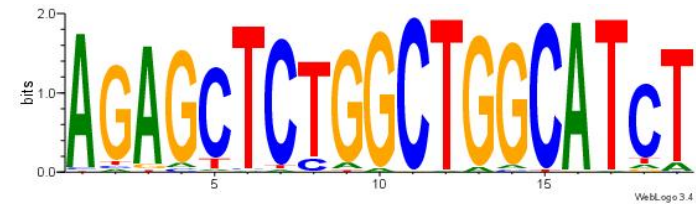
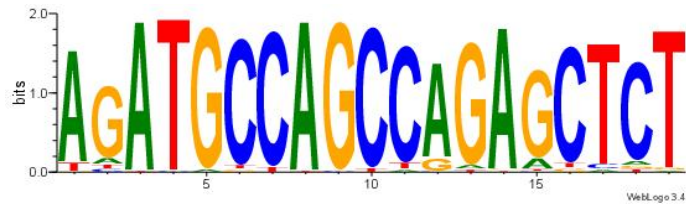


**Dataset #: 1      Motif ID: 307      Motif name: Motif 307**

Original motif      Consensus sequence: AGATGCCAGCCAGAGCTCT

Reverse complement motif      Consensus sequence: AGAGCTCTGGCTGGCATCT



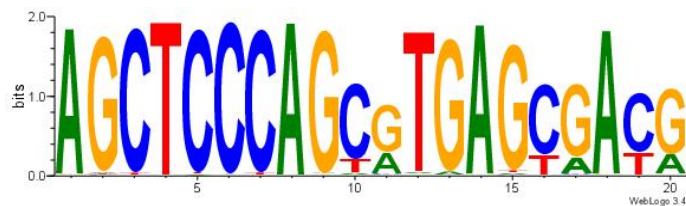


**Best Matches for Motif ID 307 (Highest to Lowest)**

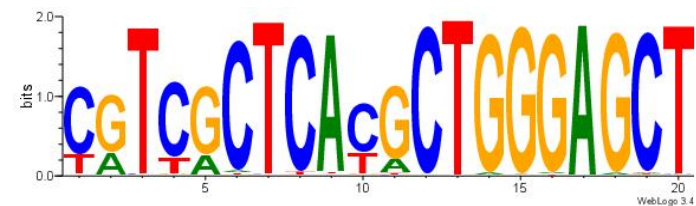
Dataset #: 1  
 Motif ID: 48  
 Motif name: Motif 48  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 2  
 Number of overlap: 19  
 Similarity score: 0.0871974

Alignment:  
 AGCTCCCAGCGTGAGCGACG  
 AGATGCCAGCCAGAGCTCT-

Original motif      Consensus sequence: AGCTCCCAGCGTGAGCGACG



Reverse complement motif      Consensus sequence: CGTCGCTCAGCTGGGAGCT

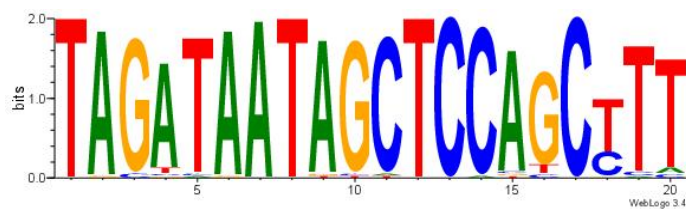


Dataset #: 1  
 Motif ID: 333  
 Motif name: Motif 333  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 19  
 Similarity score: 0.0921664

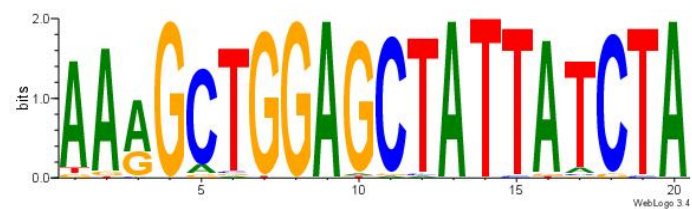
Alignment:

AAAGCTGGAGCTATTATCTA  
 AGAGCTCTGGCTGGCATCT-

Original motif      Consensus sequence: TAGATAATAGCTCCAGCTTT



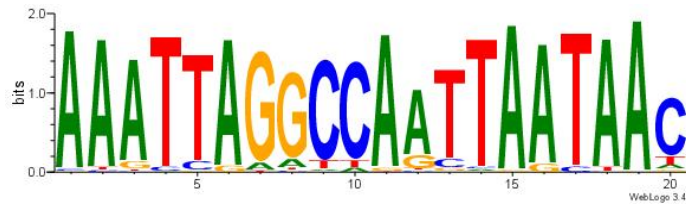
Reverse complement motif      Consensus sequence: AAAGCTGGAGCTATTATCTA



**Dataset #: 1      Motif ID: 308      Motif name: Motif 308**

Original motif      Consensus sequence: AAATTAGGCCAATTAATAAC

Reverse complement motif      Consensus sequence: GTTATTAATTGGCCTAATTT

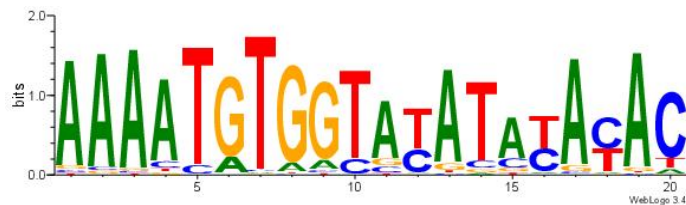


### Best Matches for Motif ID 308 (Highest to Lowest)

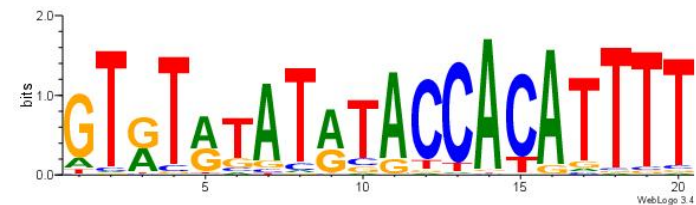
Dataset #: 1  
 Motif ID: 83  
 Motif name: Motif 83  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 20  
 Similarity score: 0.109629

Alignment:  
 GTKTMTATMTACCACATTTT  
 GTTATTAATTGGCCTAATTT

Original motif      Consensus sequence: AAAATGTGGTAYATAYAYAC



Reverse complement motif      Consensus sequence: GTKTMTATMTACCACATTTT

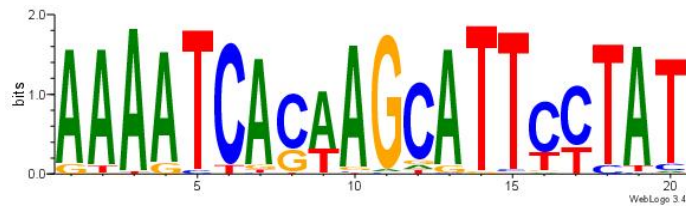


Dataset #: 1  
 Motif ID: 254  
 Motif name: Motif 254  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 2  
 Number of overlap: 19  
 Similarity score: 0.593176

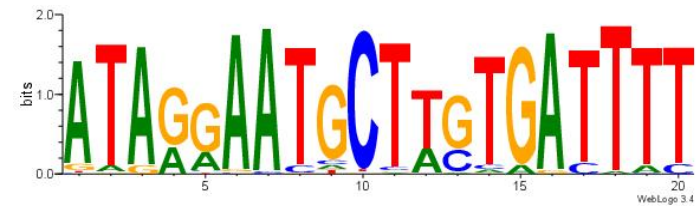
Alignment:

-ATAGGAATGCTTGTGATTTT  
 GTTATTAATTGGCCTAATTT-

Original motif      Consensus sequence: AAAATCACAGCATTCTAT



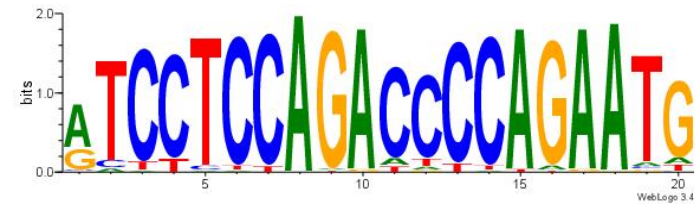
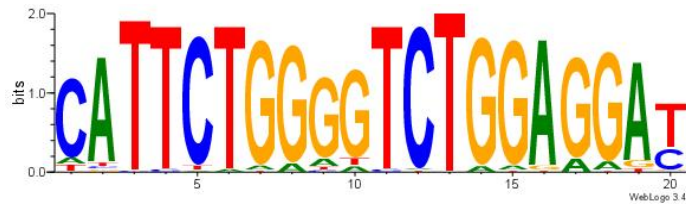
Reverse complement motif      Consensus sequence: ATAGGAATGCTTGTGATTTT



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

Original motif      Consensus sequence: CATTCTGGGGTCTGGAGGAY

Reverse complement motif      Consensus sequence: MTCCTCCAGACCCCAGAATG

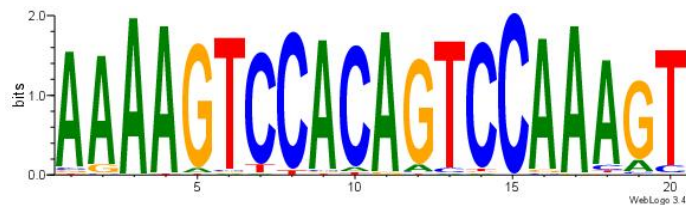


**Best Matches for Motif ID 309 (Highest to Lowest)**

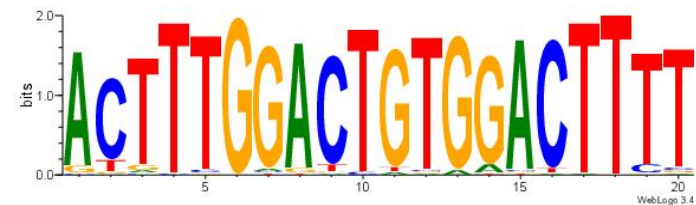
Dataset #: 1  
 Motif ID: 171  
 Motif name: Motif 171  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 2  
 Number of overlap: 19  
 Similarity score: 0.0981972

Alignment:  
 ACTTTGGACTGTGGACTTTT-  
 -CATTCTGGGGTCTGGAGGAY

Original motif      Consensus sequence: AAAAGTCCACAGTCCAAAGT



Reverse complement motif      Consensus sequence: ACTTTGGACTGTGGACTTTT

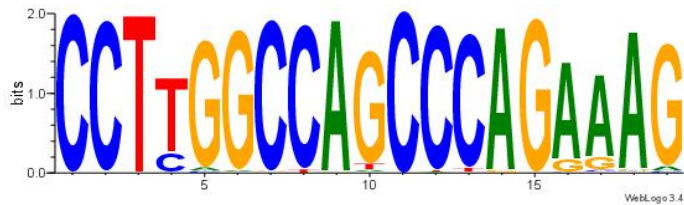


Dataset #: 1  
 Motif ID: 122  
 Motif name: Motif 122  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 19  
 Similarity score: 0.102502

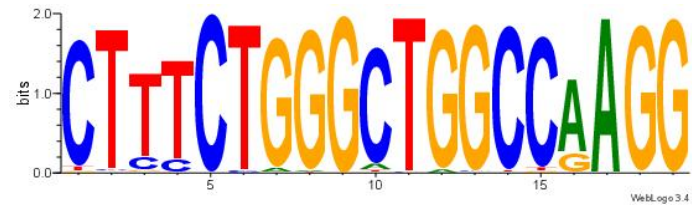
Alignment:

CCTTGGCCAGCCCAGAAAG-  
 MTCCTCCAGACCCCAGAATG

Original motif      Consensus sequence: CCTTGGCCAGCCCAGAAAG



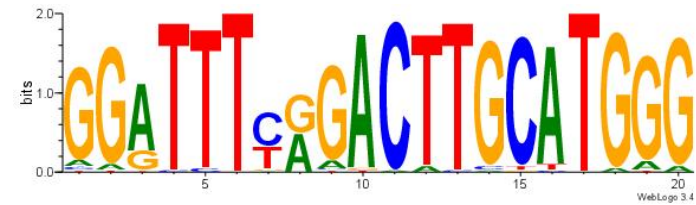
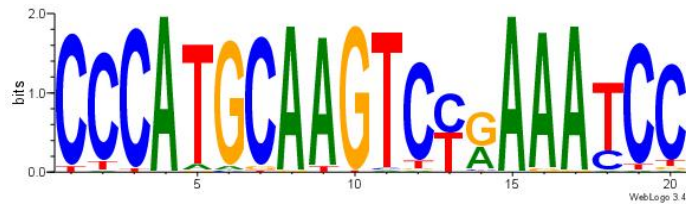
Reverse complement motif      Consensus sequence: CTTTCTGGGCTGGCCAAGG



**Dataset #: 1      Motif ID: 310      Motif name: Motif 310**

Original motif      Consensus sequence: CCCATGCAAGTCYRAAATCC

Reverse complement motif      Consensus sequence: GGATTTMKGACTTGCATGGG

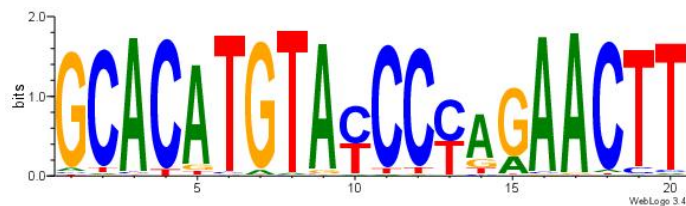


**Best Matches for Motif ID 310 (Highest to Lowest)**

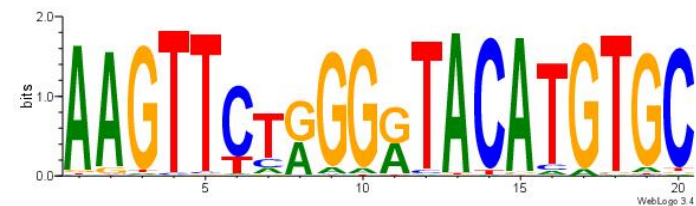
Dataset #: 1  
 Motif ID: 225  
 Motif name: Motif 225  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 2  
 Number of overlap: 19  
 Similarity score: 0.0916027

Alignment:  
 -AAGTTCTKGGKTACATGTGC  
 GGATTTMKGACTTGCATGGG-

Original motif      Consensus sequence: GCACATGTAYCCYAGAACTT



Reverse complement motif      Consensus sequence: AAGTTCTKGGKTACATGTGC

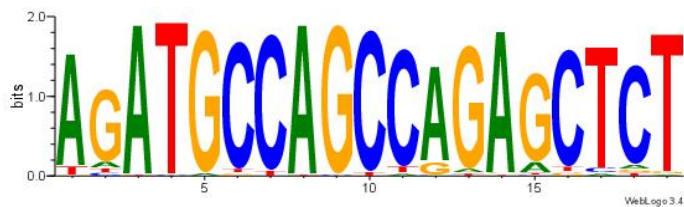


Dataset #: 1  
 Motif ID: 307  
 Motif name: Motif 307  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 19  
 Similarity score: 0.0934682

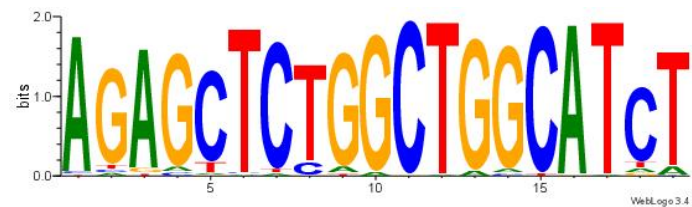
Alignment:

AGAGCTCTGGCTGGCATCT-  
 GGATTTMKGACTTGCATGGG

Original motif      Consensus sequence: AGATGCCAGCCAGAGCTCT



Reverse complement motif      Consensus sequence: AGAGCTCTGGCTGGCATCT

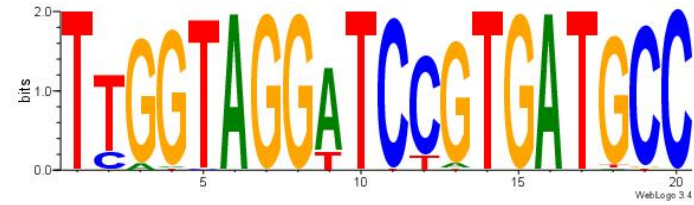
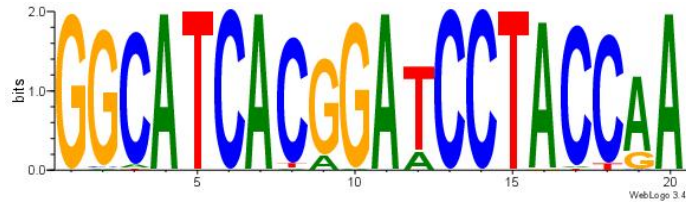


**Dataset #: 1      Motif ID: 311      Motif name: Motif 311**

Original motif      Consensus sequence: GGCATCACGGATCCTACCAA

Reverse complement motif      Consensus sequence: TTGGTAGGATCCGTGATGCC



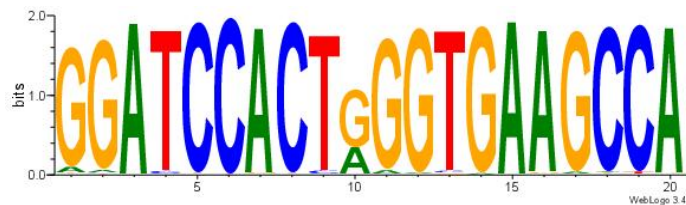


**Best Matches for Motif ID 311 (Highest to Lowest)**

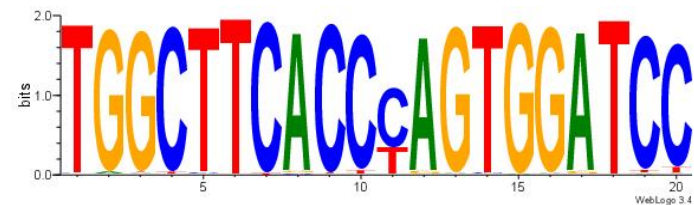
Dataset #: 1  
 Motif ID: 61  
 Motif name: Motif 61  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 2  
 Number of overlap: 19  
 Similarity score: 0.113575

Alignment:  
 -TGGCTTCACCCAGTGGATCC  
 GGCATCACGGATCCTACCAA-

Original motif    Consensus sequence: GGATCCACTGGGTGAAGCCA



Reverse complement motif    Consensus sequence: TGGCTTCACCCAGTGGATCC



Dataset #: 1  
 Motif ID: 211  
 Motif name: Motif 211  
 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: 0.118597

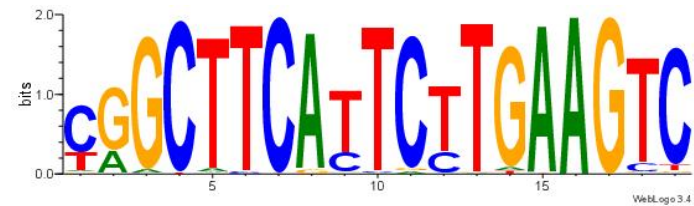
Alignment:

GACTTCAAGAATGAAGCCG-  
 GGCATCACGGATCCTACCAA

Original motif      Consensus sequence: GACTTCAAGAATGAAGCCG



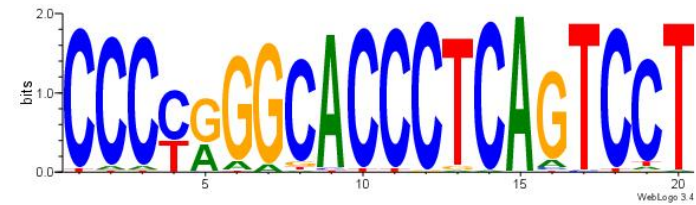
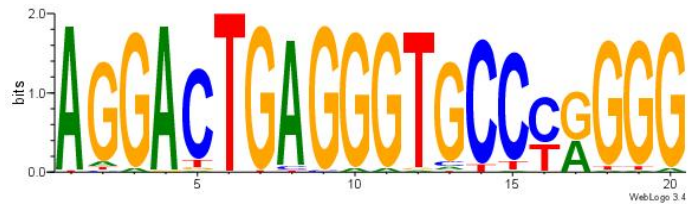
Reverse complement motif      Consensus sequence: CGGCTTCATTCTTGAAGTC



**Dataset #: 1      Motif ID: 312      Motif name: Motif 312**

Original motif      Consensus sequence: AGGACTGAGGGTGCCYRGGG

Reverse complement motif      Consensus sequence: CCCMKGGCACCCCTCAGTCCT

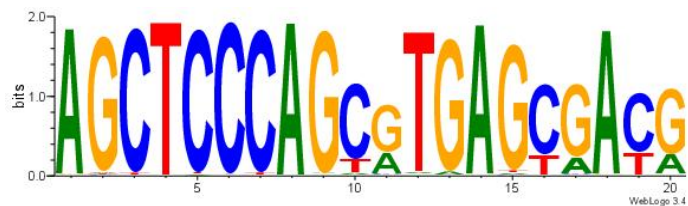


**Best Matches for Motif ID 312 (Highest to Lowest)**

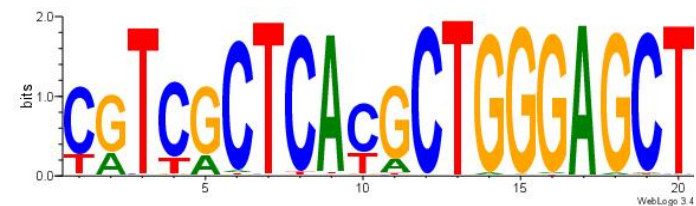
Dataset #: 1  
 Motif ID: 48  
 Motif name: Motif 48  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 20  
 Similarity score: 0.104551

Alignment:  
 CGTCGCTCACGCTGGGAGCT  
 CCCMKGGCACCCCTCAGTCCT

Original motif      Consensus sequence: AGCTCCCAGCGTGAGCGACG



Reverse complement motif      Consensus sequence: CGTCGCTCACGCTGGGAGCT

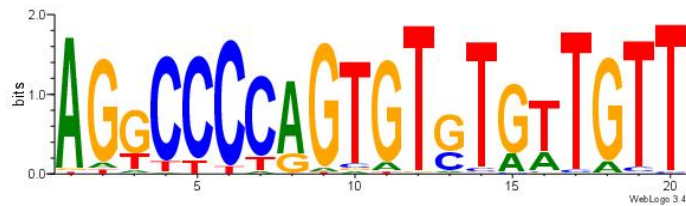


Dataset #: 1  
 Motif ID: 176  
 Motif name: Motif 176  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 20  
 Similarity score: 0.105418

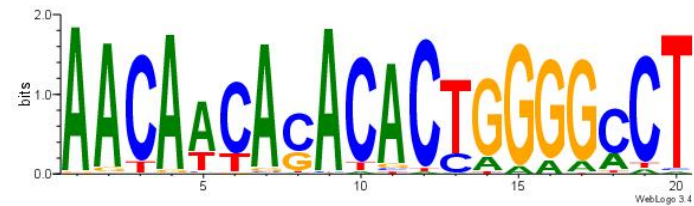
Alignment:

AAC AACASACTGGGGCCT  
 CCCMKGGCACCCCTCAGTCCT

Original motif      Consensus sequence: AGGCCCCAGTGTSTGTTGTT



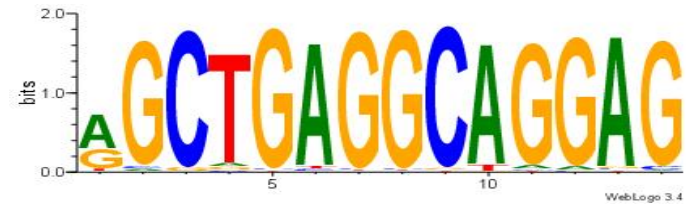
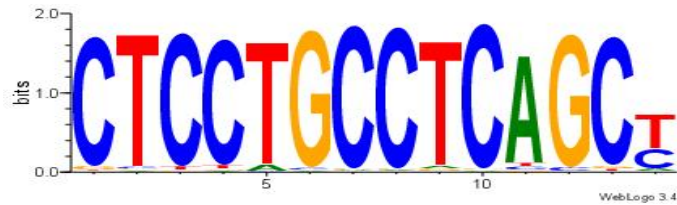
Reverse complement motif      Consensus sequence: AAC AACASACTGGGGCCT



**Dataset #: 1      Motif ID: 313      Motif name: Motif 313**

Original motif      Consensus sequence: CTCCTGCCTCAGCY

Reverse complement motif      Consensus sequence: MGCTGAGGCAGG

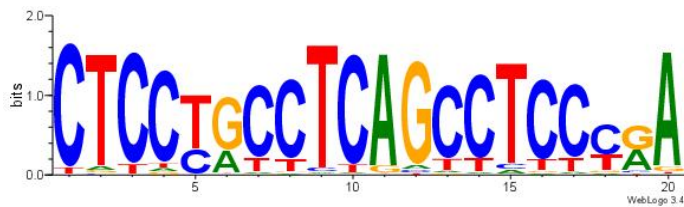


**Best Matches for Motif ID 313 (Highest to Lowest)**

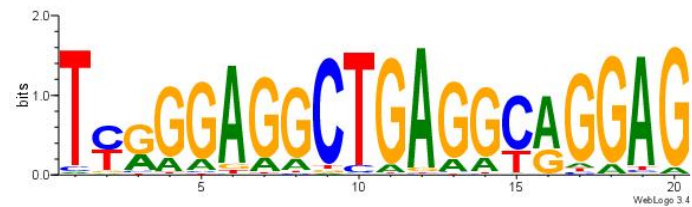
Dataset #: 1  
 Motif ID: 26  
 Motif name: Motif 26  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 7  
 Number of overlap: 14  
 Similarity score: 0.0298178

Alignment:  
 CTCCTGCCTCAGCCTCCRA  
 CTCCTGCCTCAGCY-----

Original motif      Consensus sequence: CTCCTGCCTCAGCCTCCRA



Reverse complement motif      Consensus sequence: TMGGGAGGCTGAGGCAGGAG

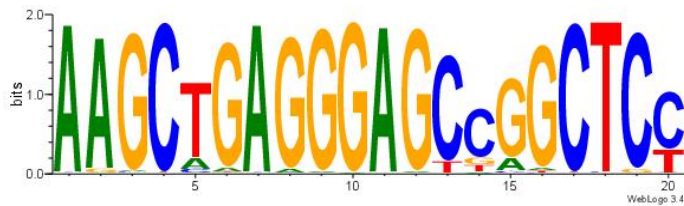


Dataset #: 1  
 Motif ID: 96  
 Motif name: Motif 96  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 2  
 Number of overlap: 14  
 Similarity score: 0.0599095

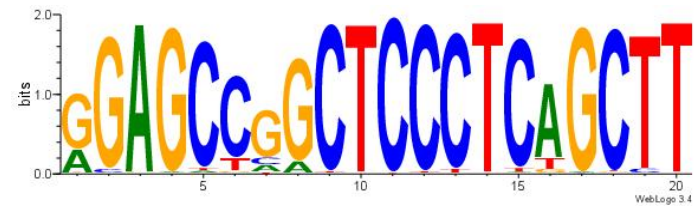
Alignment:

AAGCTGAGGGAGCCGGCTCC  
 -----MGCTGAGGCAGGAG-

Original motif      Consensus sequence: AAGCTGAGGGAGCCGGCTCC



Reverse complement motif      Consensus sequence: GGAGCCGGCTCCCTCAGCTT

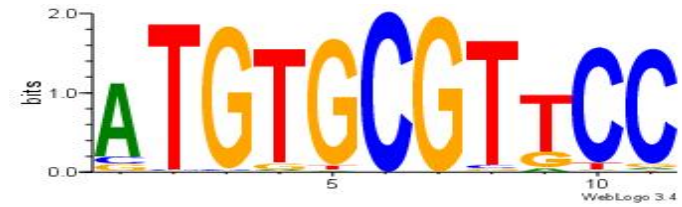
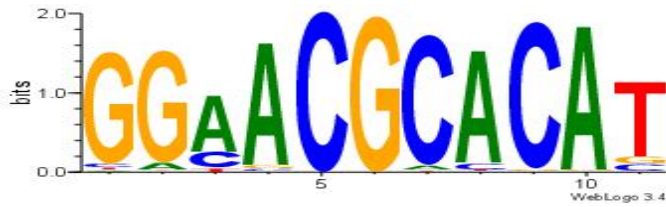



---

**Dataset #: 1      Motif ID: 314      Motif name: Motif 314**

Original motif      Consensus sequence: GGAACGCACAT

Reverse complement motif      Consensus sequence: ATGTGCGTTCC

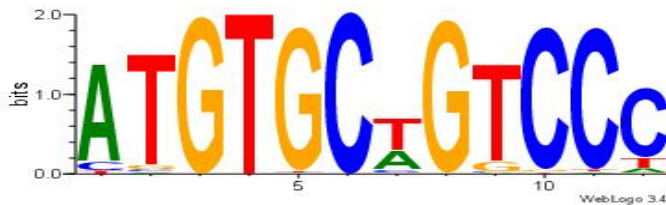


**Best Matches for Motif ID 314 (Highest to Lowest)**

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

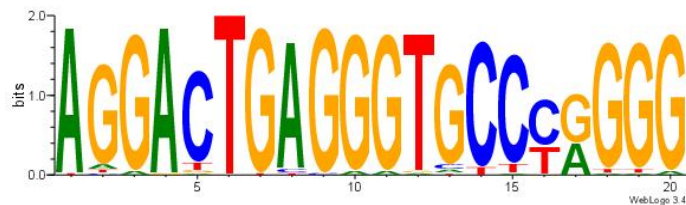


Dataset #: 1

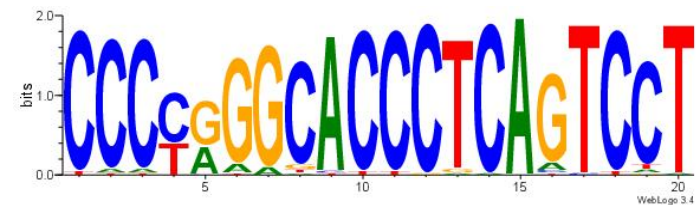
Motif ID: 312  
 Motif name: Motif 312  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 6  
 Number of overlap: 11  
 Similarity score: 0.0705974

Alignment:  
 AGGACTGAGGGTGCCYRGGG  
 -----ATGTGCGTTCC-----

Original motif      Consensus sequence: AGGACTGAGGGTGCCYRGGG

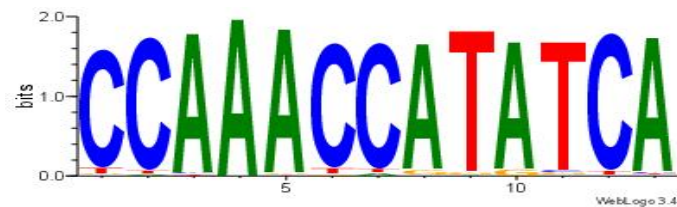


Reverse complement motif      Consensus sequence: CCCMKGGCACCCTCAGTCCT

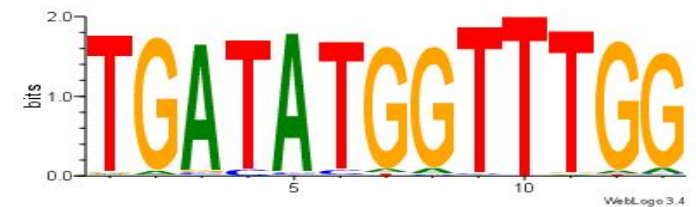


**Dataset #: 1      Motif ID: 315      Motif name: Motif 315**

Original motif      Consensus sequence: CCAAACCATATCA



Reverse complement motif      Consensus sequence: TGATATGGTTTGG





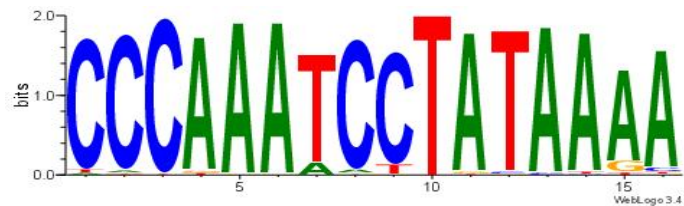
## Best Matches for Motif ID 315 (Highest to Lowest)

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

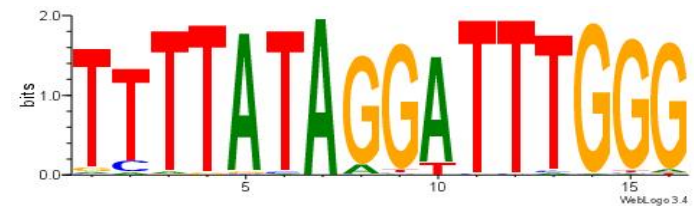
### Alignment:

```
TTTTATAGGATTTGGG  
--TGATATGGTTTGG--
```

Original motif      Consensus sequence: CCCAATCCTATAAAA



Reverse complement motif      Consensus sequence: TTTTATAGGATTTGGG



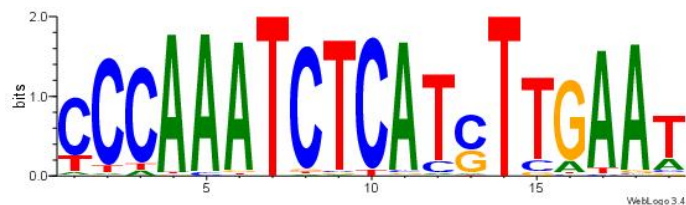
---

Dataset #: 1  
Motif ID: 227  
Motif name: Motif 227  
Matching format of first motif: Original Motif  
Matching format of second motif: Original Motif

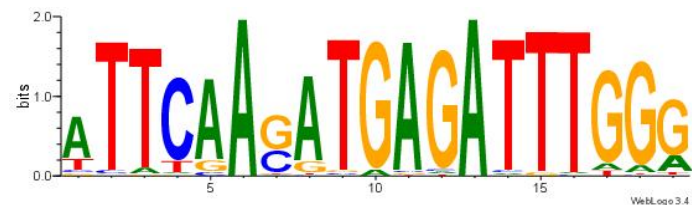
Direction: Forward  
 Position number: 2  
 Number of overlap: 13  
 Similarity score: 0.0822582

Alignment:  
 CCCAAATCTCATSTTGAAT  
 -CCAAACCATATCA-----

Original motif      Consensus sequence: CCCAAATCTCATSTTGAAT



Reverse complement motif      Consensus sequence: ATTCAASATGAGATTTGGG

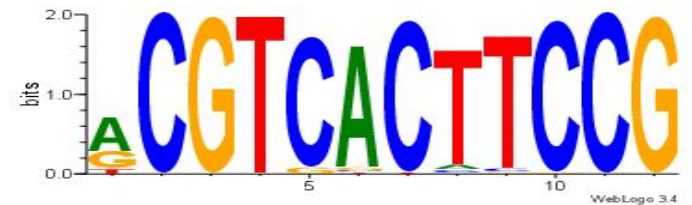


**Dataset #: 1      Motif ID: 316      Motif name: Motif 316**

Original motif      Consensus sequence: CGGAAGTGACGT



Reverse complement motif      Consensus sequence: ACGTCACTTCCG



**Best Matches for Motif ID 316 (Highest to Lowest)**

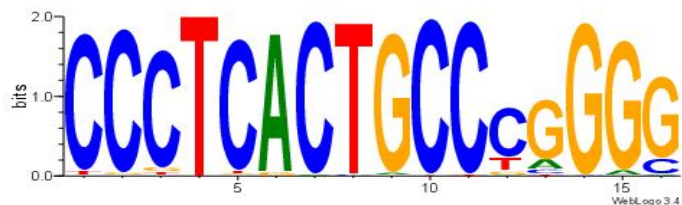
Dataset #: 1  
 Motif ID: 136

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

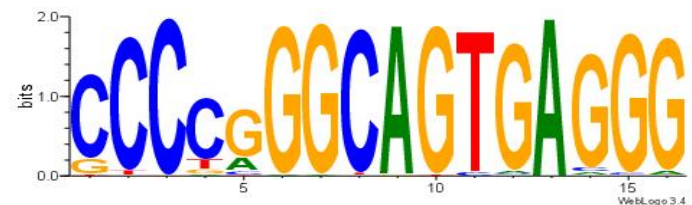
**Alignment:**

CCCCAGGCAGTGAGGG  
 CGGAAGTGACGT-----

Original motif    Consensus sequence: CCCTCACTGCCCGGGG



Reverse complement motif    Consensus sequence: CCCCAGGCAGTGAGGG

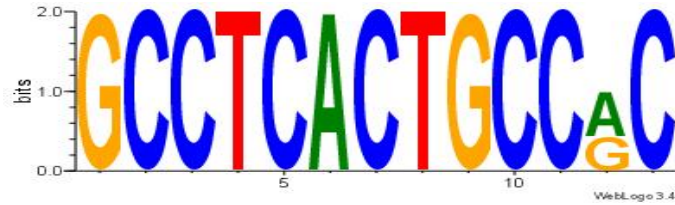


Dataset #: 1  
 Motif ID: 247  
 Motif name: Motif 247  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 12  
 Similarity score: 0.0581297

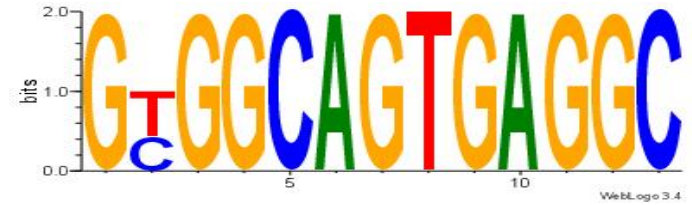
Alignment:

GKGGCAGTGAGGC  
CGGAAGTGACGT-

Original motif      Consensus sequence: GCCTCACTGCC C

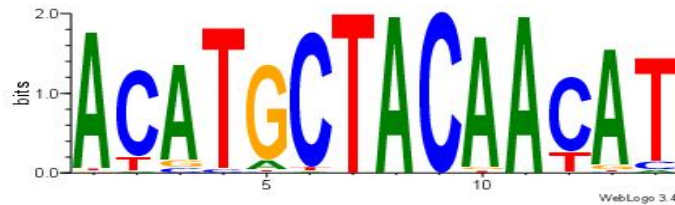


Reverse complement motif      Consensus sequence: GKGGCAGTGAGGC

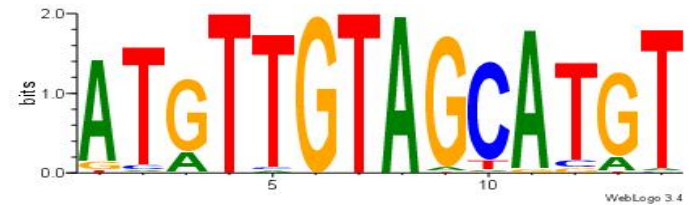


**Dataset #: 1      Motif ID: 317      Motif name: Motif 317**

Original motif      Consensus sequence: ACATGCTACAACAT



Reverse complement motif      Consensus sequence: ATGTTGTAGCATGT



**Best Matches for Motif ID 317 (Highest to Lowest)**

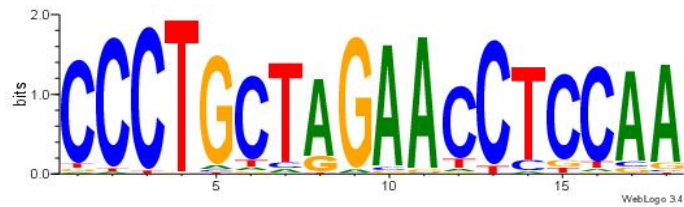
Dataset #:	1
Motif ID:	299
Motif name:	Motif 299
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	5

Number of overlap: 14  
Similarity score: 0.0691153

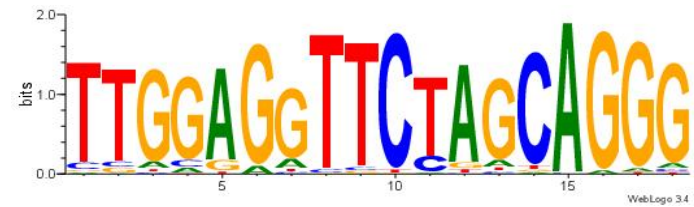
Alignment:

TTGGAGGTTCTAGCAGGG  
----ATGTTGTAGCATGT

Original motif    Consensus sequence: CCCTGCTAGAACCTCCAA



Reverse complement motif    Consensus sequence:  
TTGGAGGTTCTAGCAGGG

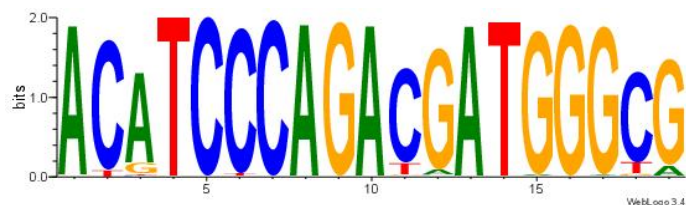


Dataset #: 1  
Motif ID: 36  
Motif name: Motif 36  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Reverse Complement  
Direction: Backward  
Position number: 1  
Number of overlap: 14  
Similarity score: 0.0828209

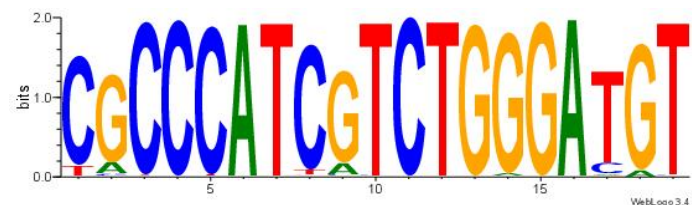
Alignment:

CGCCCATCGTCTGGGATGT  
-----ATGTTGTAGCATGT

Original motif      Consensus sequence: ACATCCCAGACGATGGGCG



Reverse complement motif      Consensus sequence: CGCCCATCGTCTGGGATGT



**Dataset #: 1      Motif ID: 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

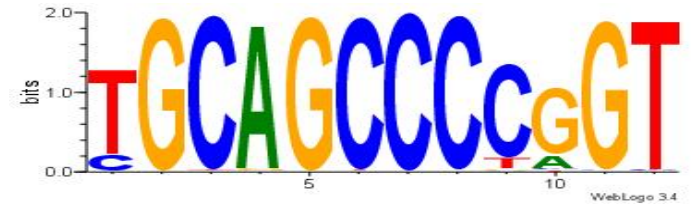
Alignment:

ACCGGGGCTGCA  
--CGGGGCTG--

Original motif      Consensus sequence: ACCGGGGCTGCA



Reverse complement motif      Consensus sequence: TGCAGCCCCGGT

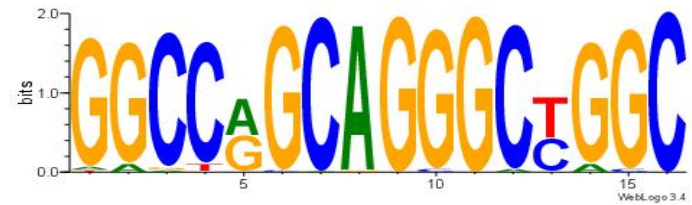
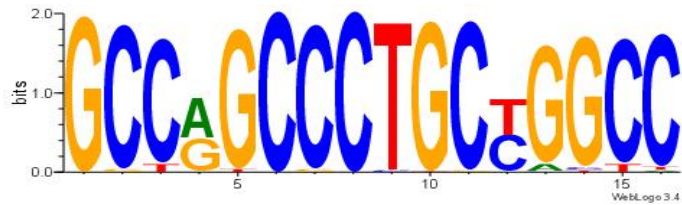


Dataset #: 1  
Motif ID: 183  
Motif name: Motif 183  
Matching format of first motif: Original Motif  
Matching format of second motif: Original Motif  
Direction: Forward  
Position number: 3  
Number of overlap: 8  
Similarity score: 0.0248687

Alignment:  
GCCRGCCCTGCGYGGCC  
--CAGCCCCG-----

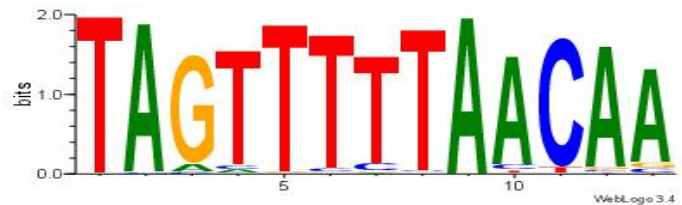
Original motif      Consensus sequence: GCCRGCCCTGCGYGGCC

Reverse complement motif      Consensus sequence:  
GGCCMGCAGGGCKGGC



**Dataset #: 1      Motif ID: 319      Motif name: Motif 319**

Original motif      Consensus sequence: TAGTTTTTAACAA



Reverse complement motif      Consensus sequence: TTGTTAAAACTA



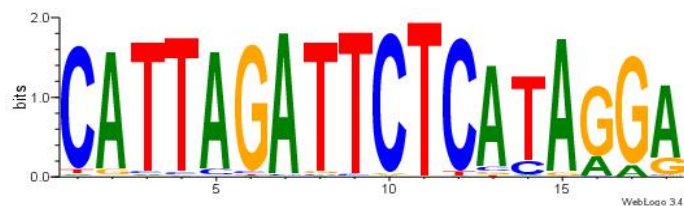
**Best Matches for Motif ID 319 (Highest to Lowest)**

Dataset #:	1
Motif ID:	154
Motif name:	Motif 154
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	3
Number of overlap:	13
Similarity score:	0.0753436

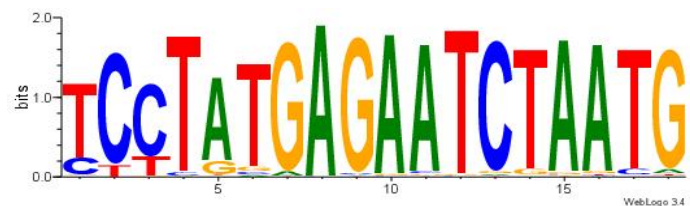
Alignment:  
 CATTAGATTCTCATAGGA  
 ---TAGTTTTTAACAA---



Original motif      Consensus sequence: CATTAGATTCTCATAGGA



Reverse complement motif      Consensus sequence: TCCTATGAGAATCTAATG

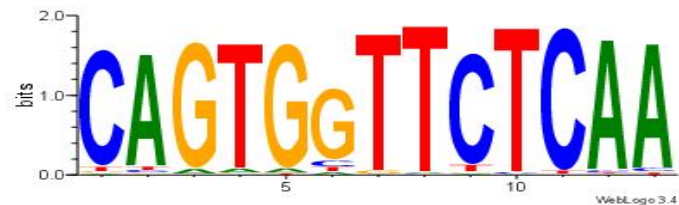


Dataset #: 1  
Motif ID: 243  
Motif name: Motif 243  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Reverse Complement  
Direction: Backward  
Position number: 1  
Number of overlap: 13  
Similarity score: 0.0843202

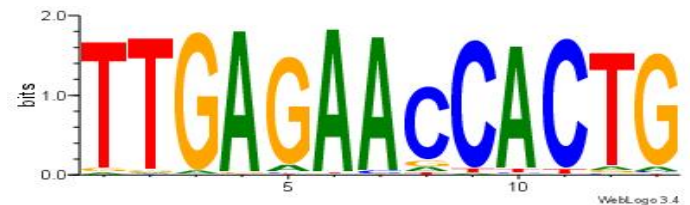
Alignment:

TTGAGAACCACTG  
TTGTTAAAACTA

Original motif      Consensus sequence: CAGTGgTTcTCAA

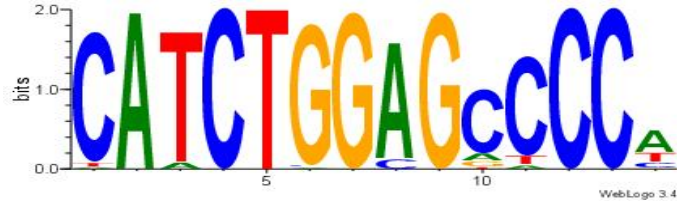


Reverse complement motif      Consensus sequence: TTGAGAACCACTG

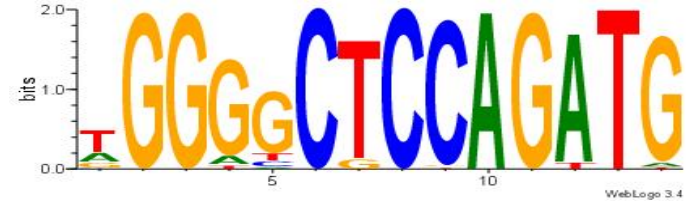


**Dataset #: 1      Motif ID: 320      Motif name: Motif 320**

Original motif      Consensus sequence: CATCTGGAGCCCCA



Reverse complement motif      Consensus sequence: TGGGGCTCCAGATG



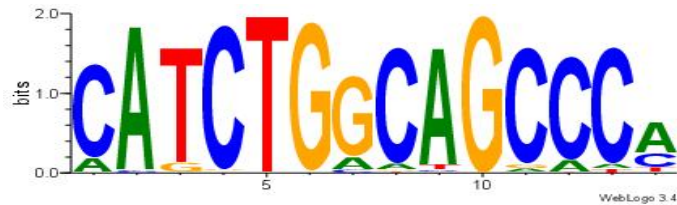
**Best Matches for Motif ID 320 (Highest to Lowest)**

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

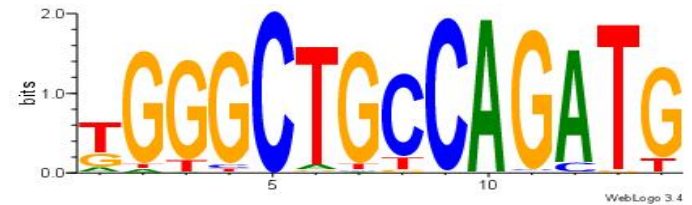
**Alignment:**

CATCTGGCAGCCCCA  
 CATCTGGAGCCCCA

Original motif      Consensus sequence: CATCTGGCAGCCCCA



Reverse complement motif      Consensus sequence: TGGGCTGCCAGATG

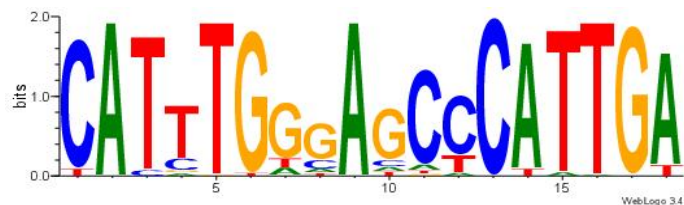


Dataset #: 1  
 Motif ID: 284  
 Motif name: Motif 284  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 14  
 Similarity score: 0.071304

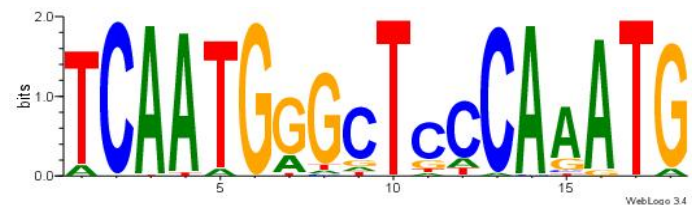
Alignment:

CATTGGGAGCCCATTGA  
 CATCTGGAGCCCCA-----

Original motif    Consensus sequence: CATTGGGAGCCCATTGA



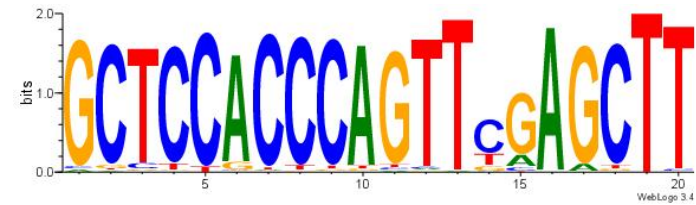
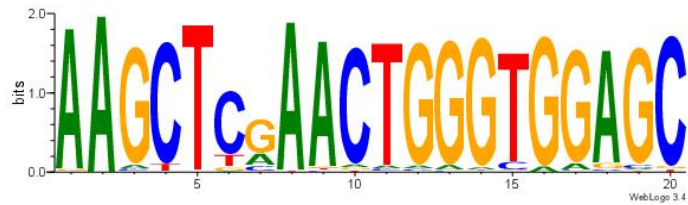
Reverse complement motif    Consensus sequence:  
TCAATGGGCTCCCAAATG



**Dataset #: 1      Motif ID: 321      Motif name: Motif 321**

Original motif    Consensus sequence: AAGCTCGAACTGGGTGGAGC

Reverse complement motif    Consensus sequence:  
GCTCCACCCAGTTCGAGCTT



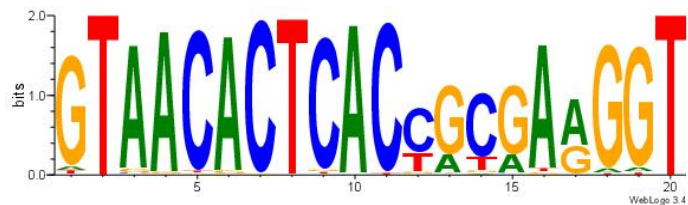
### Best Matches for Motif ID 321 (Highest to Lowest)

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

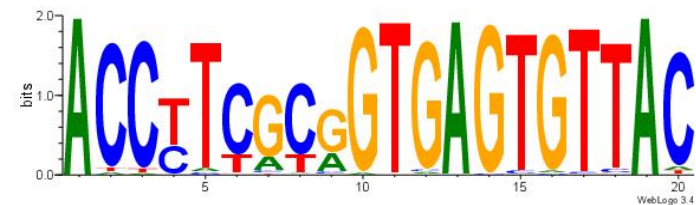
#### Alignment:

ACCKTCGCGGTGAGTGTTAC  
 AAGCTCGAACTGGGTGGAGC

Original motif      Consensus sequence: GTAACACTCACCGCGARGGT



Reverse complement motif      Consensus sequence: ACCKTCGCGGTGAGTGTTAC

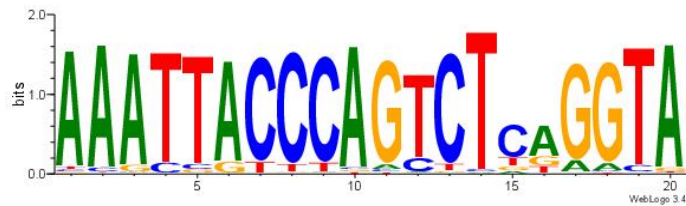


Dataset #: 1  
 Motif ID: 160  
 Motif name: Motif 160  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 20  
 Similarity score: 0.117485

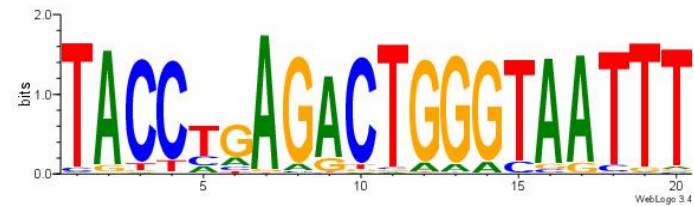
Alignment:

AAATTACCCAGTCTCAGGTA  
 GCTCCACCCAGTTCGAGCTT

Original motif    Consensus sequence: AAATTACCCAGTCTCAGGTA



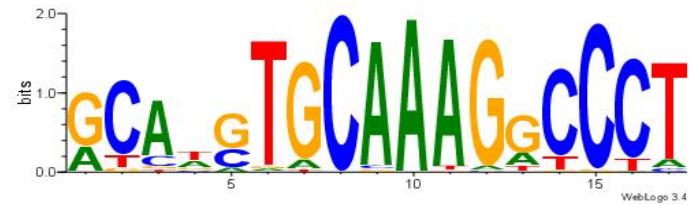
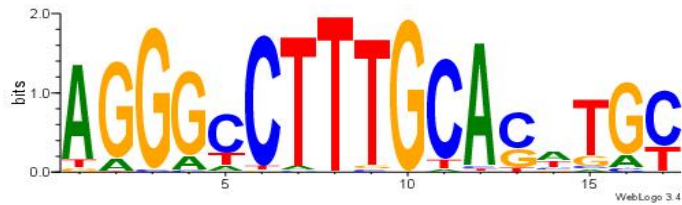
Reverse complement motif    Consensus sequence: TACCTGAGACTGGGTAATTT



**Dataset #: 1      Motif ID: 322      Motif name: Motif 322**

Original motif    Consensus sequence: AGGCCTTTGCASWTGC

Reverse complement motif    Consensus sequence: GCAWSTGCAAAGGCCCT

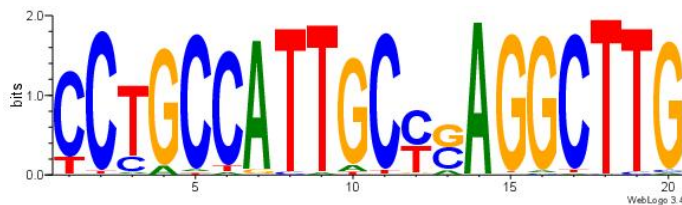


**Best Matches for Motif ID 322 (Highest to Lowest)**

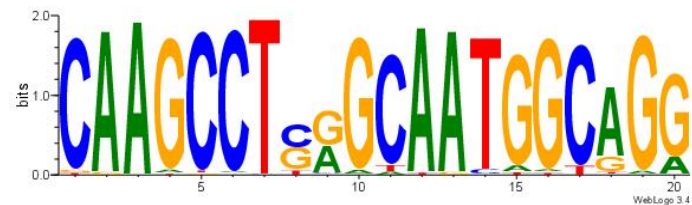
Dataset #: 1  
 Motif ID: 196  
 Motif name: Motif 196  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 17  
 Similarity score: 0.0779611

Alignment:  
 CAAGCCTSKGCAATGGCAGG  
 ---GCAWSTGCAAAGGCCCT

Original motif      Consensus sequence: CCTGCCATTGCYSAGGCTTG



Reverse complement motif      Consensus sequence: CAAGCCTSKGCAATGGCAGG

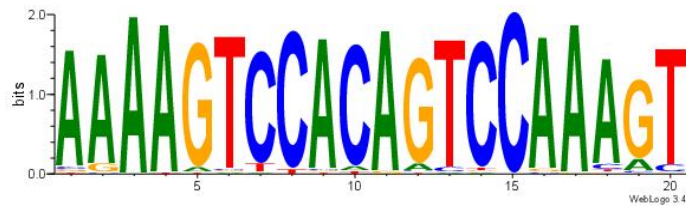


Dataset #: 1  
 Motif ID: 171  
 Motif name: Motif 171  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 17  
 Similarity score: 0.0904024

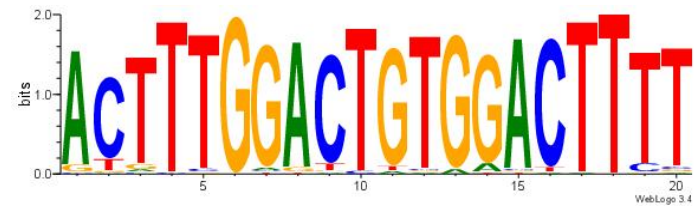
Alignment:

ACTTTGGACTGTGGACTTTT  
 AGGGCCTTTCASWTGC---

Original motif      Consensus sequence: AAAAGTCCACAGTCCAAAGT



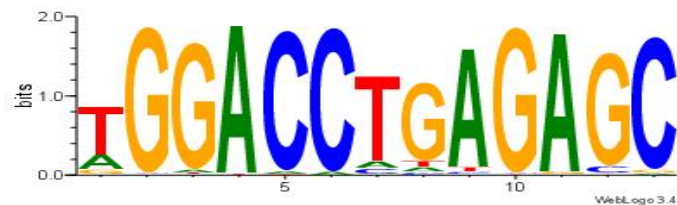
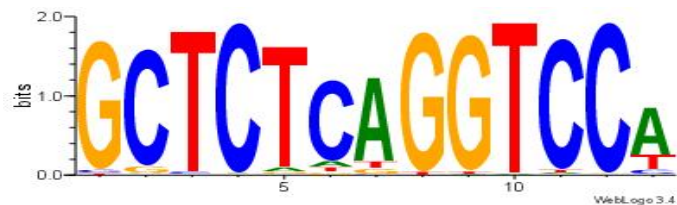
Reverse complement motif      Consensus sequence: ACTTTGGACTGTGGACTTTT



**Dataset #: 1      Motif ID: 323      Motif name: Motif 323**

Original motif      Consensus sequence: GCTCTCAGGTCCA

Reverse complement motif      Consensus sequence: TGGACCTGAGAGC

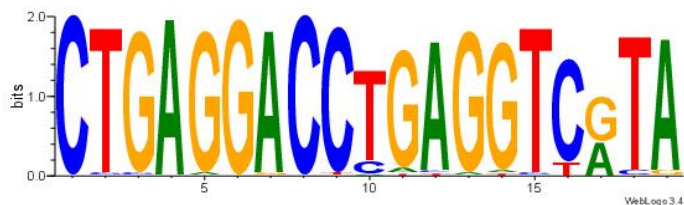


**Best Matches for Motif ID 323 (Highest to Lowest)**

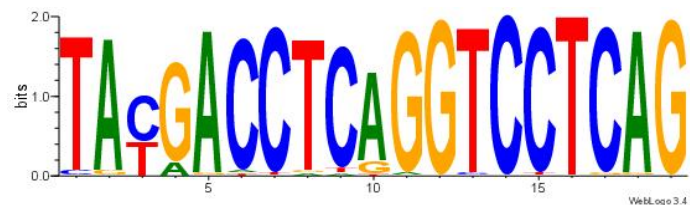
Dataset #: 1  
 Motif ID: 291  
 Motif name: Motif 291  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 4  
 Number of overlap: 13  
 Similarity score: 0.0533584

Alignment:  
 CTGAGGACCTGAGGTCRTA  
 ---TGGACCTGAGAGC---

Original motif      Consensus sequence: CTGAGGACCTGAGGTCRTA



Reverse complement motif      Consensus sequence: TAMGACCTCAGGTCCTCAG



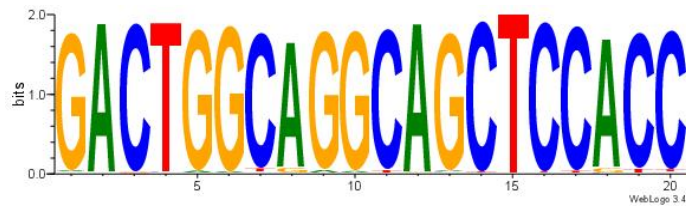


Dataset #: 1  
 Motif ID: 52  
 Motif name: Motif 52  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 6  
 Number of overlap: 13  
 Similarity score: 0.0809407

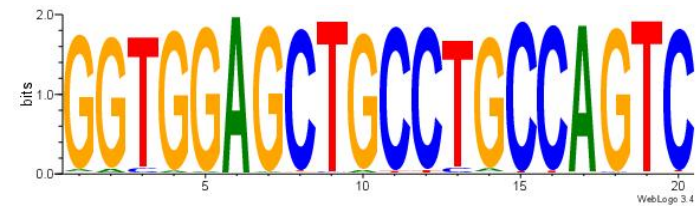
Alignment:

GACTGGCAGGCAGCTCCACC  
 -----GCTCTCAGGTCCA--

Original motif      Consensus sequence: GACTGGCAGGCAGCTCCACC



Reverse complement motif      Consensus sequence: GGTGGAGCTGCCTGCCAGTC

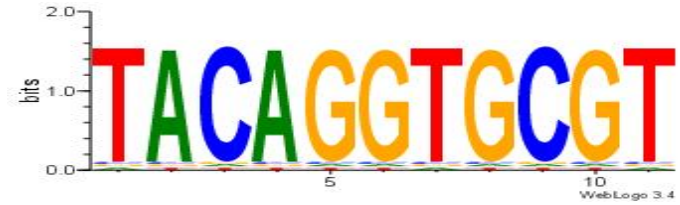
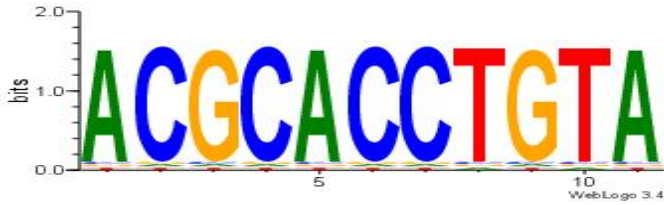



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**Dataset #: 1      Motif ID: 324      Motif name: Motif 324**

Original motif      Consensus sequence: ACGCACCTGTA

Reverse complement motif      Consensus sequence: TACAGGTGCGT

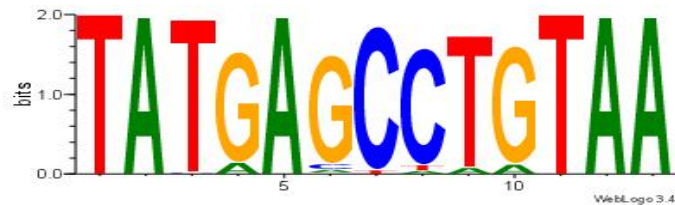


**Best Matches for Motif ID 324 (Highest to Lowest)**

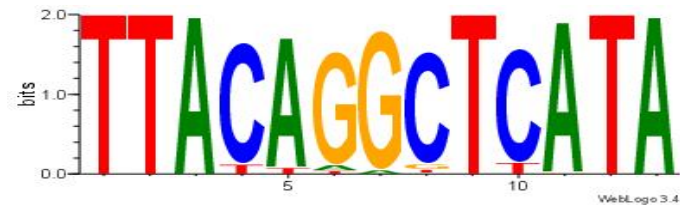
Dataset #: 1  
 Motif ID: 355  
 Motif name: Motif 355  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 2  
 Number of overlap: 11  
 Similarity score: 0.0752538

Alignment:  
 TATGAGCCTGTAA  
 -ACGCACCTGTA-

Original motif      Consensus sequence: TATGAGCCTGTAA



Reverse complement motif      Consensus sequence: TTACAGGCTCATA

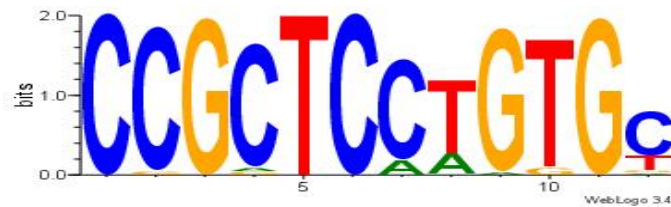


Dataset #: 1

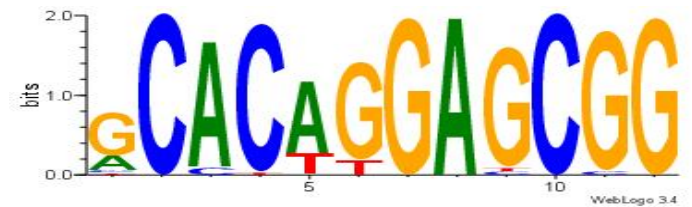
Motif ID: 167  
 Motif name: Motif 167  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 11  
 Similarity score: 0.0802613

Alignment:  
 CCGCTCCTGTGC  
 ACGCACCTGTA-

Original motif    Consensus sequence: CCGCTCCTGTGC

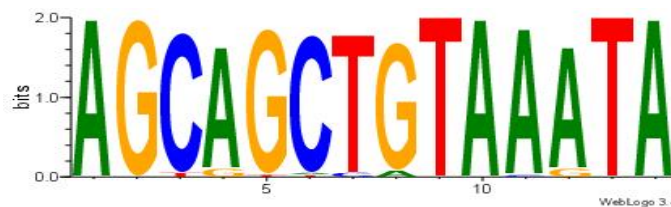


Reverse complement motif    Consensus sequence: GCACAGGAGCGG

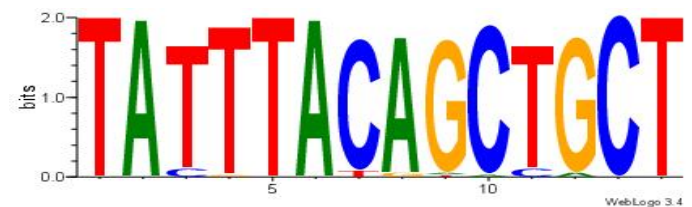


**Dataset #: 1      Motif ID: 325      Motif name: Motif 325**

Original motif    Consensus sequence: AGCAGCTGTAAATA



Reverse complement motif    Consensus sequence: TATTTACAGCTGCT



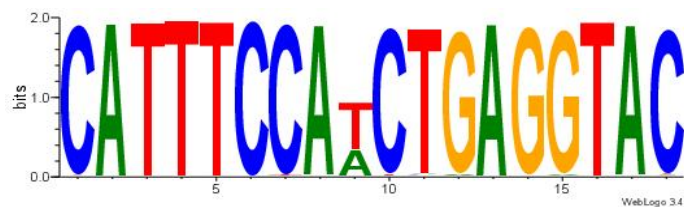
## Best Matches for Motif ID 325 (Highest to Lowest)

Dataset #: 1  
Motif ID: 25  
Motif name: Motif 25  
Matching format of first motif: Original Motif  
Matching format of second motif: Reverse Complement  
Direction: Forward  
Position number: 1  
Number of overlap: 14  
Similarity score: 0.087674

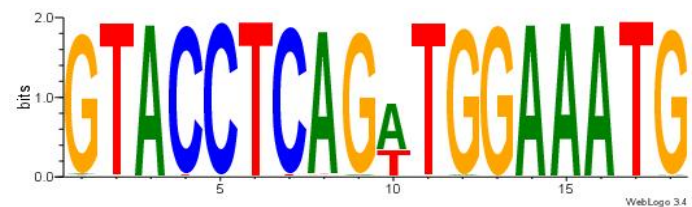
### Alignment:

```
GTACCTCAGWTGGAAATG  
AGCAGCTGTAAATA-----
```

Original motif      Consensus sequence: CATTCCA WCTGAGGTAC



Reverse complement motif      Consensus sequence:  
GTACCTCAGWTGGAAATG



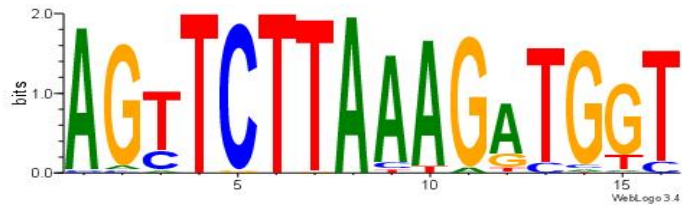
---

Dataset #: 1  
Motif ID: 303  
Motif name: Motif 303  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Original Motif

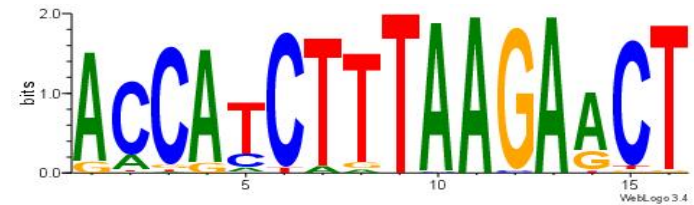
Direction: Forward  
 Position number: 1  
 Number of overlap: 14  
 Similarity score: 0.0891021

Alignment:  
 AGTTCTTAAAGATGGT  
 TATTTACAGCTGCT--

Original motif    Consensus sequence: AGTTCTTAAAGATGGT

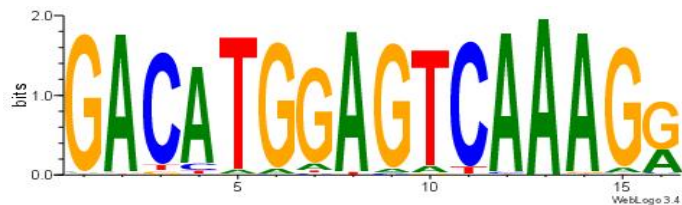


Reverse complement motif    Consensus sequence: ACCATCTTAAAGAACT

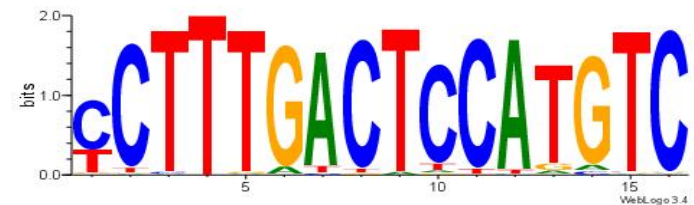


**Dataset #: 1      Motif ID: 326      Motif name: Motif 326**

Original motif    Consensus sequence: GACATGGAGTCAAAGG



Reverse complement motif    Consensus sequence: CCTTGACTCCATGTC



**Best Matches for Motif ID 326 (Highest to Lowest)**

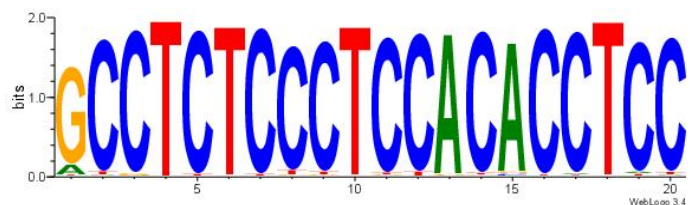
Dataset #: 1

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

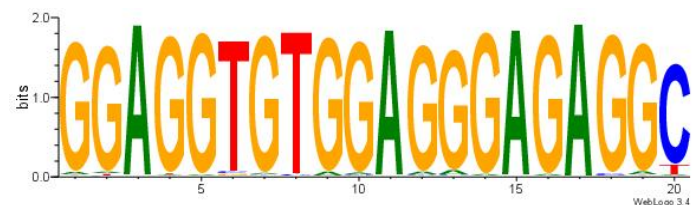
**Alignment:**

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:

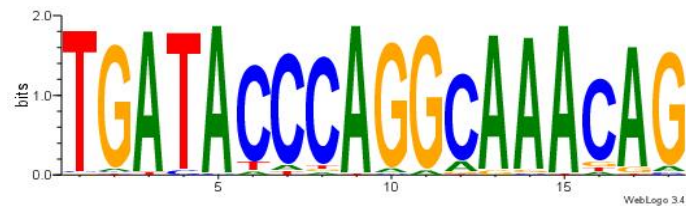
0.0886417

Alignment:

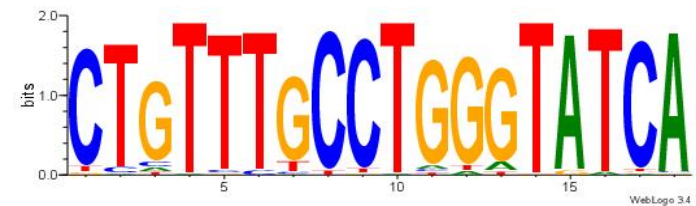
TGATACCCAGGCAAACAG

-GACATGGAGTCAAAGG-

Original motif      Consensus sequence: TGATACCCAGGCAAACAG

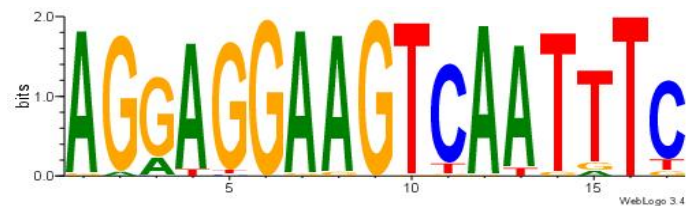


Reverse complement motif      Consensus sequence: CTGTTGCCTGGGTATCA

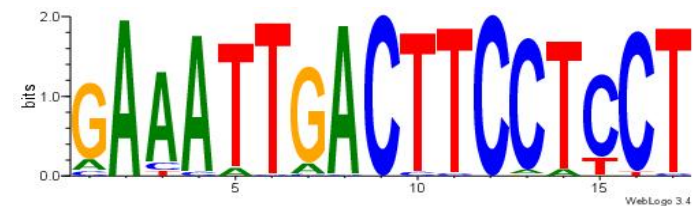


**Dataset #: 1      Motif ID: 327      Motif name: Motif 327**

Original motif      Consensus sequence: AGGAGGAAGTCAATTC



Reverse complement motif      Consensus sequence: GAAATTGACTTCCTCCT



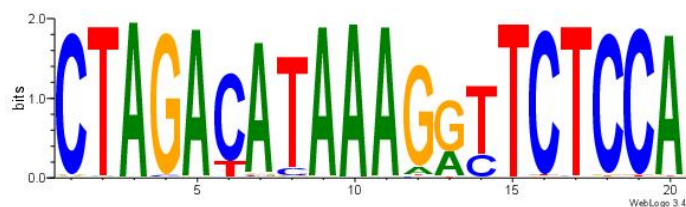
**Best Matches for Motif ID 327 (Highest to Lowest)**

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

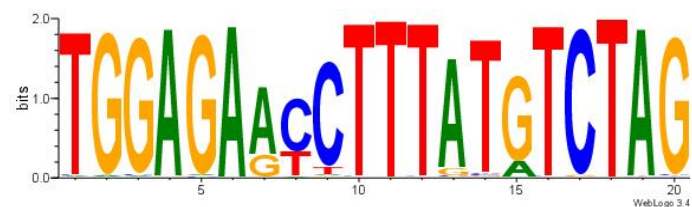
Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 4  
 Number of overlap: 17  
 Similarity score: 0.087633

Alignment:  
 CTAGACATAAAGGTTCTCCA  
 GAAATTGACTTCCTCCT---

Original motif      Consensus sequence: CTAGACATAAAGGTTCTCCA



Reverse complement motif      Consensus sequence:  
 TGGAGAACCTTTATGTCTAG



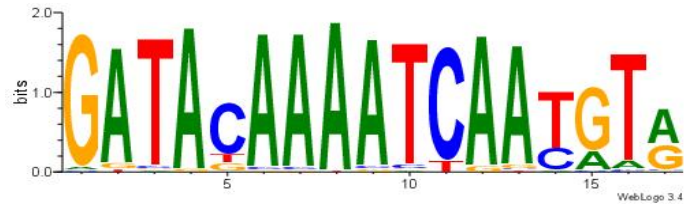
Dataset #: 1  
 Motif ID: 328  
 Motif name: Motif 328  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 17  
 Similarity score: 0.0921863

Alignment:

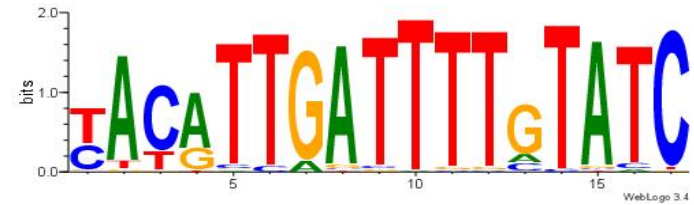


KACATTGATTTTGTATC  
GAAATTGACTTCCTCCT

Original motif    Consensus sequence: GATACAAAATCAATGTR

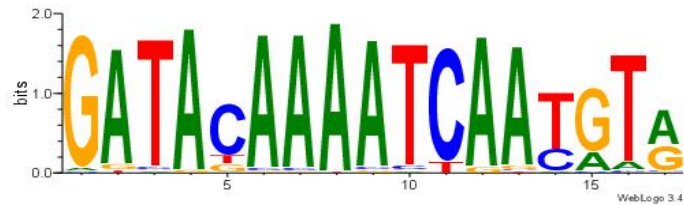


Reverse complement motif    Consensus sequence:  
KACATTGATTTTGTATC

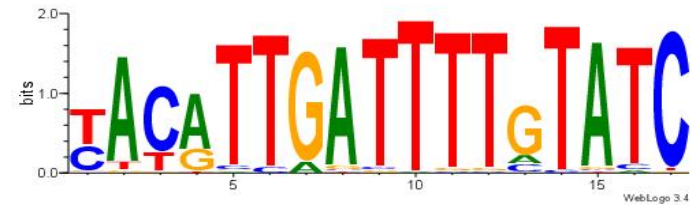


**Dataset #: 1      Motif ID: 328      Motif name: Motif 328**

Original motif    Consensus sequence: GATACAAAATCAATGTR



Reverse complement motif    Consensus sequence:  
KACATTGATTTTGTATC



**Best Matches for Motif ID 328 (Highest to Lowest)**

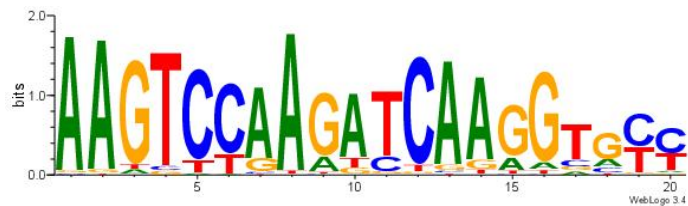
Dataset #:	1
Motif ID:	119
Motif name:	Motif 119
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2

Number of overlap: 17  
Similarity score: 0.0460385

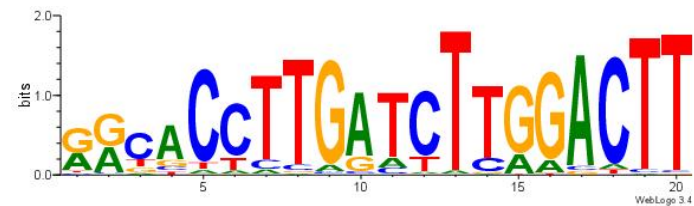
Alignment:

AAGTCCAAGATCAAGGTGYY  
-GATACAAAATCAATGTR--

Original motif      Consensus sequence: AAGTCCAAGATCAAGGTGYY



Reverse complement motif      Consensus sequence:  
KKCACCTTGATCTTGGACTT

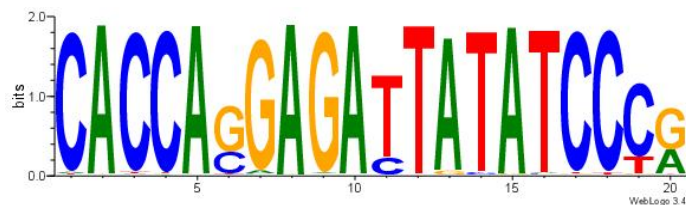


Dataset #: 1  
Motif ID: 19  
Motif name: Motif 19  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Original Motif  
Direction: Forward  
Position number: 4  
Number of overlap: 17  
Similarity score: 0.0587823

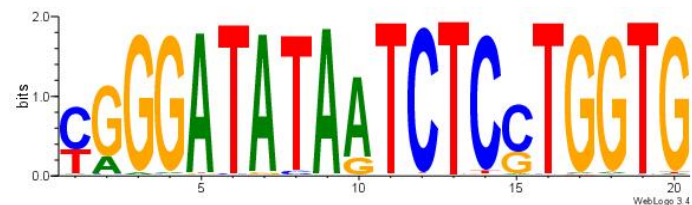
Alignment:

CACCAGGAGATTATATCCCR  
---KACATTGATTTTGTATC

Original motif      Consensus sequence: CACCAGGAGATTATATCCCR

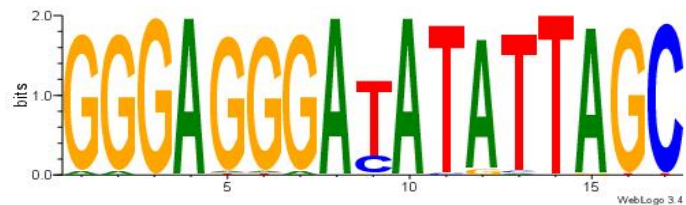


Reverse complement motif      Consensus sequence: MGGGATATAATCTCCTGGTG

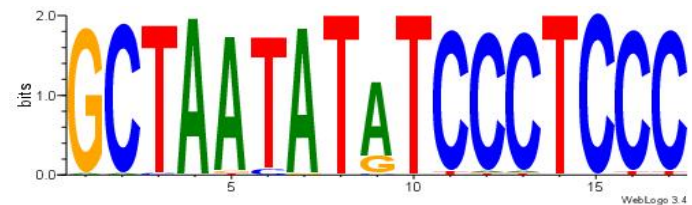


**Dataset #: 1      Motif ID: 329      Motif name: Motif 329**

Original motif      Consensus sequence: GGGAGGGATATATTAGC



Reverse complement motif      Consensus sequence: GCTAATATCCCTCCC



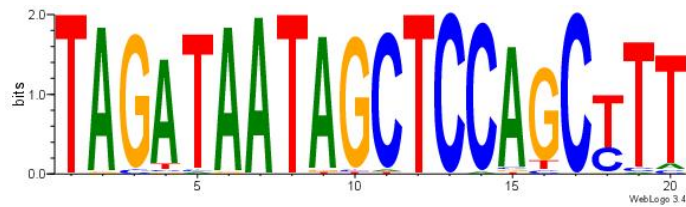
### Best Matches for Motif ID 329 (Highest to Lowest)

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

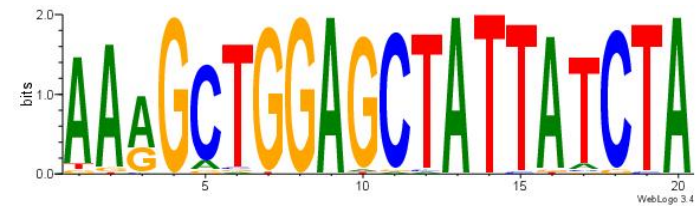
Alignment:

TAGATAATAGCTCCAGCTTT  
--GCTAATATATCCCTCCC-

Original motif      Consensus sequence: TAGATAATAGCTCCAGCTTT



Reverse complement motif      Consensus sequence:  
AAAGCTGGAGCTATTATCTA



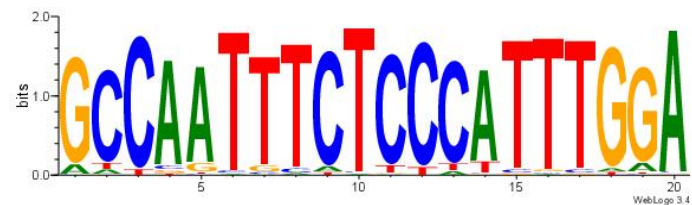
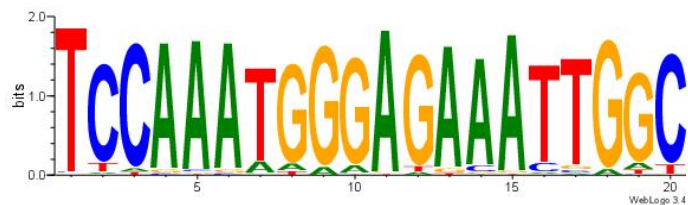
Dataset #: 1  
Motif ID: 235  
Motif name: Motif 235  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Reverse Complement  
Direction: Forward  
Position number: 1  
Number of overlap: 17  
Similarity score: 0.102804

Alignment:

GCCAATTTCTCCATTGGA  
GCTAATATATCCCTCCC---

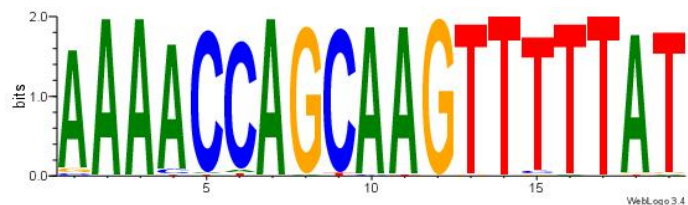
Original motif      Consensus sequence: TCCAATGGGAGAAATTGGC

Reverse complement motif      Consensus sequence:  
GCCAATTTCTCCATTGGA

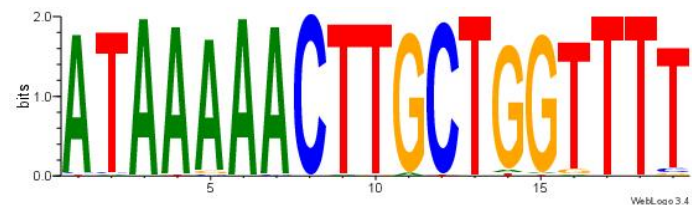


**Dataset #: 1      Motif ID: 330      Motif name: Motif 330**

Original motif      Consensus sequence: AAAACCAGCAAGTTTTTAT



Reverse complement motif      Consensus sequence: ATAAAACTTGCTGGTTTT



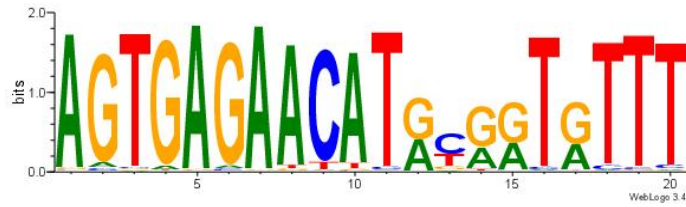
**Best Matches for Motif ID 330 (Highest to Lowest)**

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

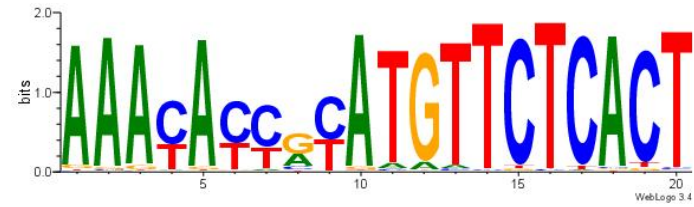
Alignment:

AGTGAGAACATRYRRTRTTT  
ATAAAAACCTTGCTGGTTTT-

Original motif      Consensus sequence: AGTGAGAACATRYRRTRTTT



Reverse complement motif      Consensus sequence:  
AAAMAMMKMATGTTCTCACT

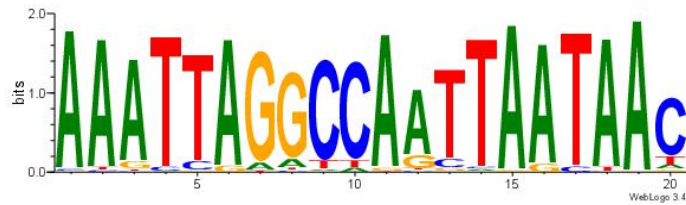


Dataset #: 1  
Motif ID: 308  
Motif name: Motif 308  
Matching format of first motif: Original Motif  
Matching format of second motif: Original Motif  
Direction: Forward  
Position number: 1  
Number of overlap: 19  
Similarity score: 0.112206

Alignment:  
AAATTAGGCCAATTAATAAC  
AAAACCAGCAAGTTTTTAT-

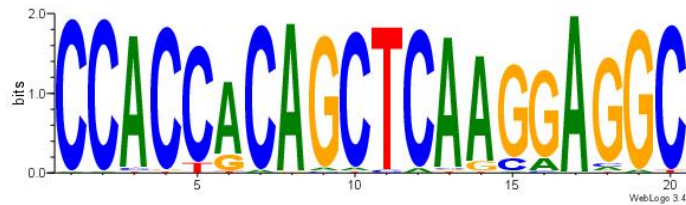
Original motif      Consensus sequence: AAATTAGGCCAATTAATAAC

Reverse complement motif      Consensus sequence:  
GTTATTAATTGGCCTAATT

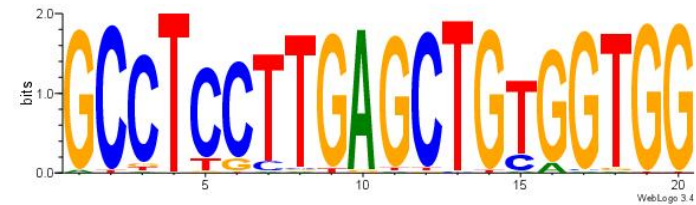


**Dataset #: 1      Motif ID: 331      Motif name: Motif 331**

Original motif      Consensus sequence: CCACCACAGCTCAAGGAGGC



Reverse complement motif      Consensus sequence: GCCTCCTTGAGCTGTGGTGG



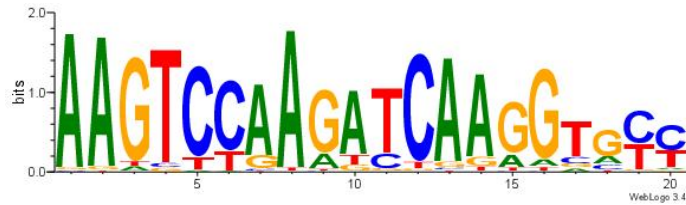
**Best Matches for Motif ID 331 (Highest to Lowest)**

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

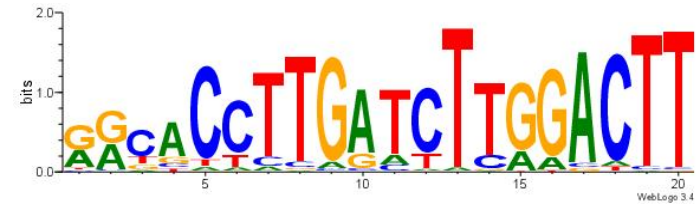
Alignment:

KKCACCTTGATCTTGGACTT  
GCCTCCTTGAGCTGTGGTGG

Original motif      Consensus sequence: AAGTCCAAGATCAAGGTGY



Reverse complement motif      Consensus sequence:  
KKCACCTTGATCTTGGACTT



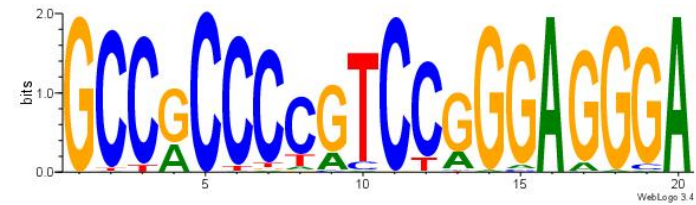
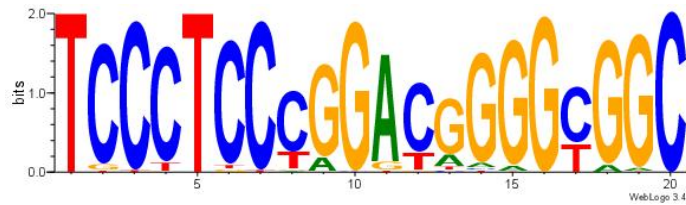
Dataset #: 1  
Motif ID: 155  
Motif name: Motif 155  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Reverse Complement  
Direction: Forward  
Position number: 1  
Number of overlap: 20  
Similarity score: 0.115101

Alignment:  
GCCKCCCCGTCCGGGAGGGA  
GCCTCCTTGAGCTGTGGTGG

Original motif      Consensus sequence: TCCCTCCCGGACGGGGYGGC

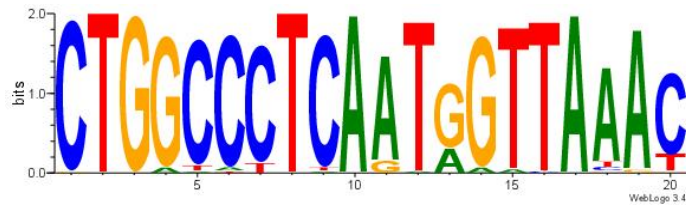
Reverse complement motif      Consensus sequence:  
GCCKCCCCGTCCGGGAGGGA



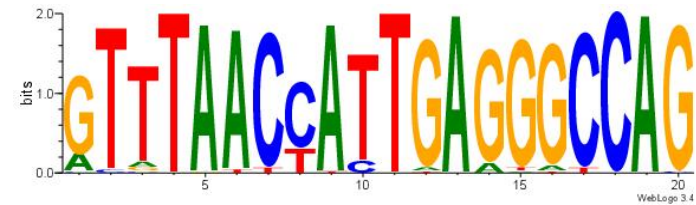


**Dataset #: 1      Motif ID: 332      Motif name: Motif 332**

Original motif      Consensus sequence: CTGGCCCTCAATGGTTAAAC



Reverse complement motif      Consensus sequence: GTTTAACCATTGAGGGCCAG



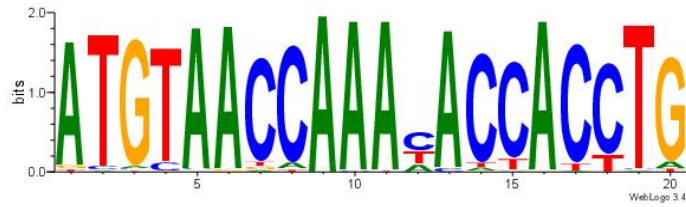
**Best Matches for Motif ID 332 (Highest to Lowest)**

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

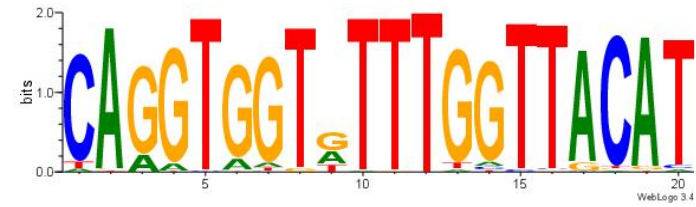
Alignment:

CAGGTGGTKTTTGGTTACAT  
CTGGCCCTCAATGGTTAAAC

Original motif      Consensus sequence: ATGTAACCAAAYACCACCTG



Reverse complement motif      Consensus sequence:  
CAGGTGGTKTTTGGTTACAT



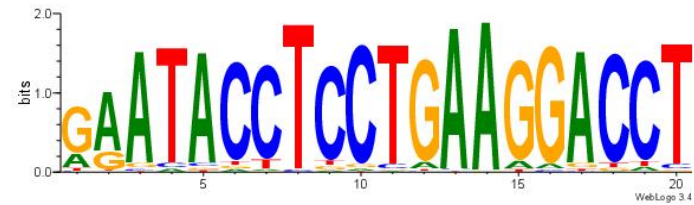
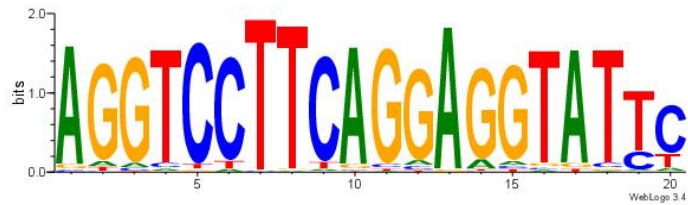
Dataset #: 1  
Motif ID: 179  
Motif name: Motif 179  
Matching format of first motif: Original Motif  
Matching format of second motif: Original Motif  
Direction: Backward  
Position number: 1  
Number of overlap: 20  
Similarity score: 0.106854

Alignment:

AGGTCCTTCAGGAGGTATTC  
CTGGCCCTCAATGGTTAAAC

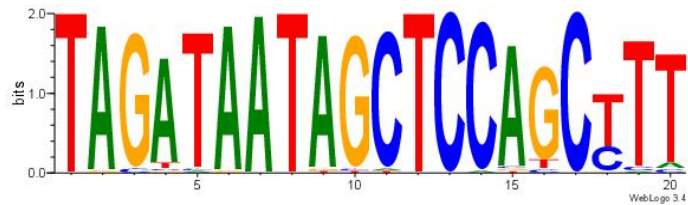
Original motif      Consensus sequence: AGGTCCTTCAGGAGGTATTC

Reverse complement motif      Consensus sequence:  
GAATACCTCCTGAAGGACCT

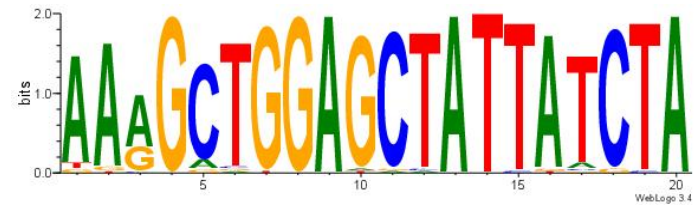


**Dataset #: 1      Motif ID: 333      Motif name: Motif 333**

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

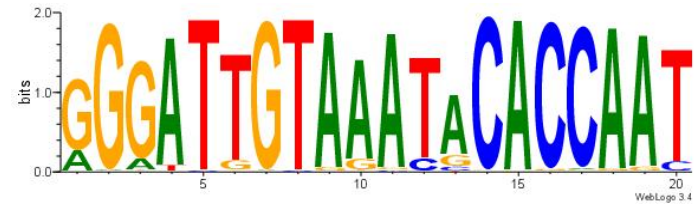
Alignment:

ATTGGTGTATTTACAATCCC  
AAAGCTGGAGCTATTATCTA

Original motif      Consensus sequence: ATTGGTGTATTTACAATCCC



Reverse complement motif      Consensus sequence:  
GGGATTGTAAATACACCAAT

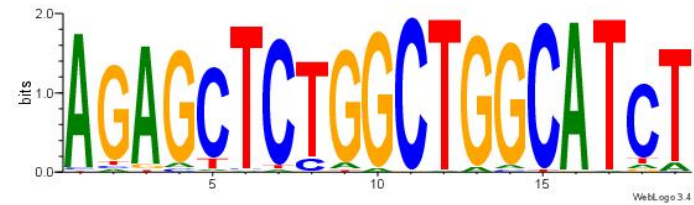
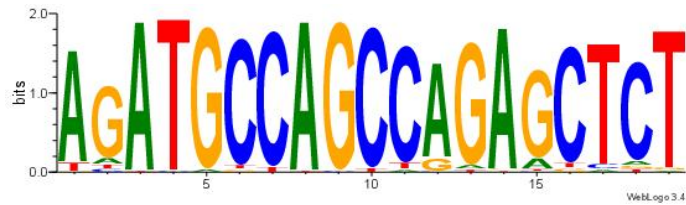


Dataset #: 1  
Motif ID: 307  
Motif name: Motif 307  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Reverse Complement  
Direction: Forward  
Position number: 1  
Number of overlap: 19  
Similarity score: 0.562386

Alignment:  
AGAGCTCTGGCTGGCATCT-  
AAAGCTGGAGCTATTATCTA

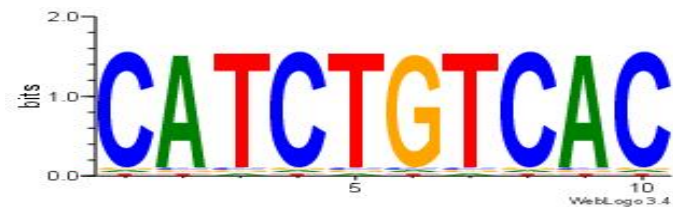
Original motif      Consensus sequence: AGATGCCAGCCAGAGCTCT

Reverse complement motif      Consensus sequence:  
AGAGCTCTGGCTGGCATCT



**Dataset #: 1      Motif ID: 334      Motif name: Motif 334**

Original motif      Consensus sequence: CATCTGTCAC



Reverse complement motif      Consensus sequence: GTGACAGATG

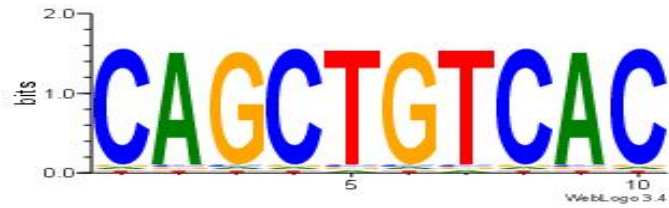


**Best Matches for Motif ID 334 (Highest to Lowest)**

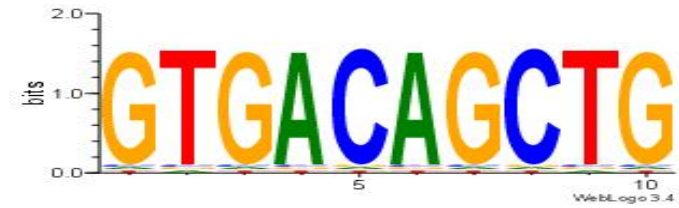
Dataset #:	1
Motif ID:	272
Motif name:	Motif 272
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	10
Similarity score:	0.0227273

Alignment:  
 CAGCTGTCAC  
 CATCTGTCAC

Original motif    Consensus sequence: CAGCTGTCAC



Reverse complement motif    Consensus sequence: GTGACAGCTG

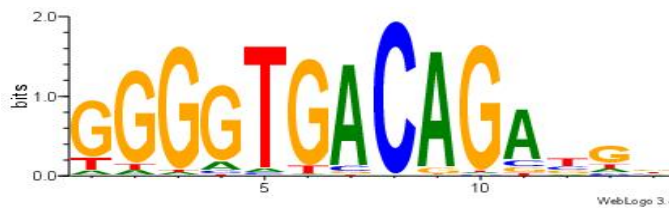


Dataset #: 1  
Motif ID: 1  
Motif name: Motif 1  
Matching format of first motif: Original Motif  
Matching format of second motif: Reverse Complement  
Direction: Backward  
Position number: 2  
Number of overlap: 10  
Similarity score: 0.0317788

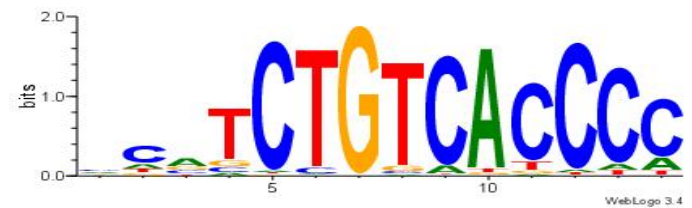
Alignment:

```
BCVTCTGTCACCCC  
---CATCTGTCAC--
```

Original motif    Consensus sequence: GGGGTGACAGABGB

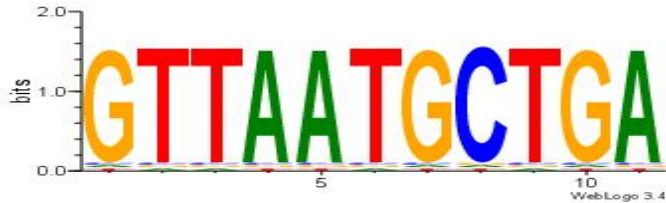


Reverse complement motif    Consensus sequence: BCVTCTGTCACCCC

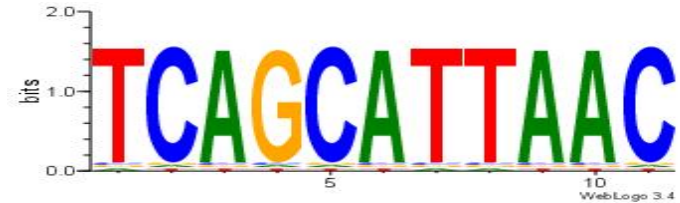


**Dataset #: 1      Motif ID: 335      Motif name: Motif 335**

Original motif      Consensus sequence: GTTAATGCTGA



Reverse complement motif      Consensus sequence: TCAGCATTAAC



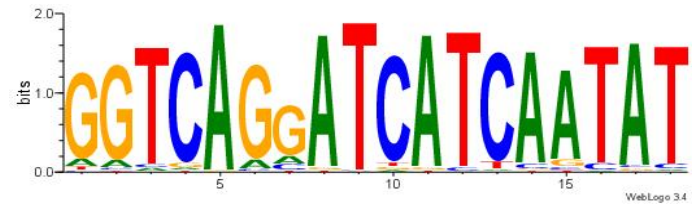
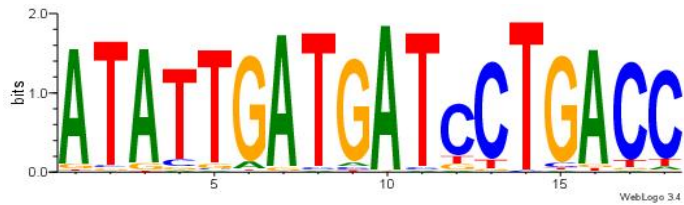
**Best Matches for Motif ID 335 (Highest to Lowest)**

Dataset #:	1
Motif ID:	184
Motif name:	Motif 184
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	3
Number of overlap:	11
Similarity score:	0.054088

Alignment:  
 ATATTGATGATCCTGACC  
 -----GTTAATGCTGA--

Original motif      Consensus sequence: ATATTGATGATCCTGACC

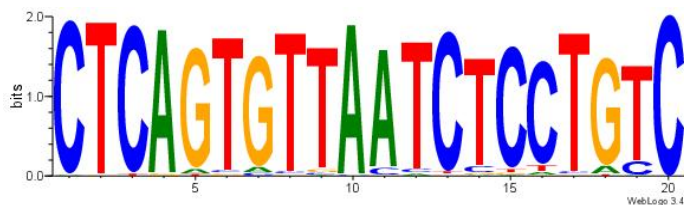
Reverse complement motif      Consensus sequence:  
 GGTCAGGATCATCAATAT



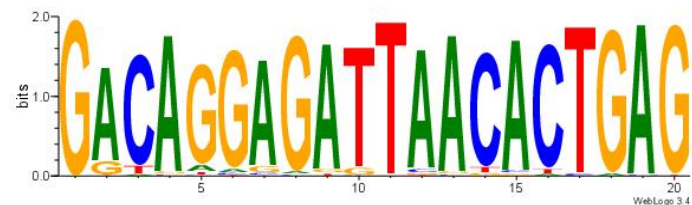
Dataset #: 1  
 Motif ID: 262  
 Motif name: Motif 262  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 9  
 Number of overlap: 11  
 Similarity score: 0.0564195

Alignment:  
 GACAGGAGATTAACACTGAG  
 -GTTAATGCTGA-----

Original motif      Consensus sequence: CTCAGTGTTAATCTCCCTGTC



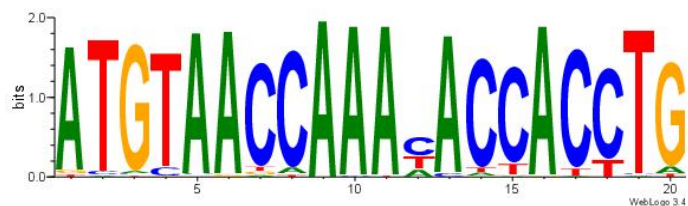
Reverse complement motif      Consensus sequence: GACAGGAGATTAACACTGAG



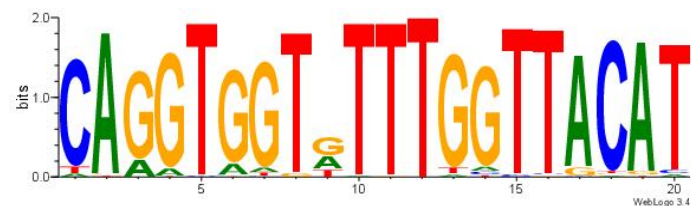
**Dataset #: 1      Motif ID: 336      Motif name: Motif 336**



Original motif      Consensus sequence: ATGTAACCAAAYACCACCTG



Reverse complement motif      Consensus sequence: CAGGTGGTKTTTGGTTACAT



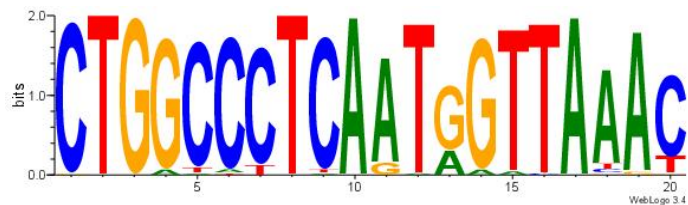
### Best Matches for Motif ID 336 (Highest to Lowest)

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

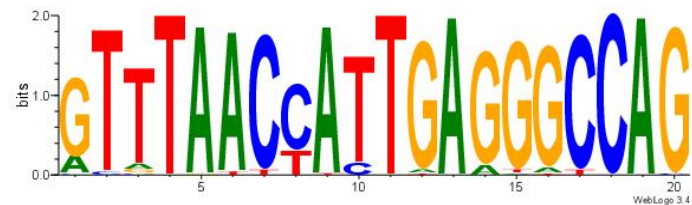
#### Alignment:

```
GTTTAACCATTGAGGGCCAG  
ATGTAACCAAAYACCACCTG
```

Original motif      Consensus sequence: CTGGCCCTCAATGGTTAAAC



Reverse complement motif      Consensus sequence: GTTTAACCATTGAGGGCCAG

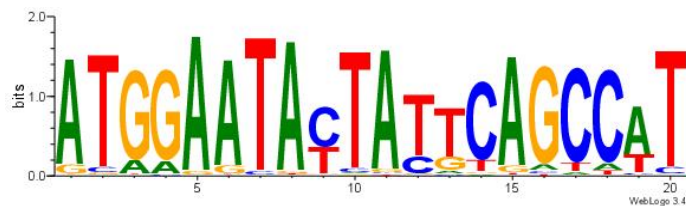


Dataset #: 1  
 Motif ID: 55  
 Motif name: Motif 55  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 20  
 Similarity score: 0.115891

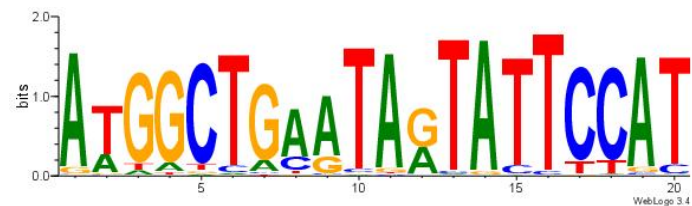
Alignment:

ATGGCTGAATAKTATTCCAT  
 CAGGTGGTKTTTGGTTACAT

Original motif    Consensus sequence: ATGGAATAYTATTCAGCCAT



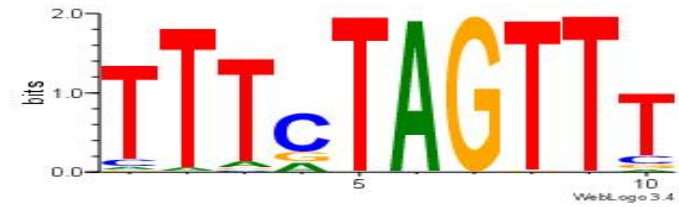
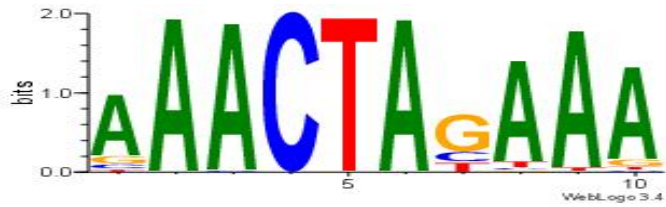
Reverse complement motif    Consensus sequence:  
ATGGCTGAATAKTATTCCAT



**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)

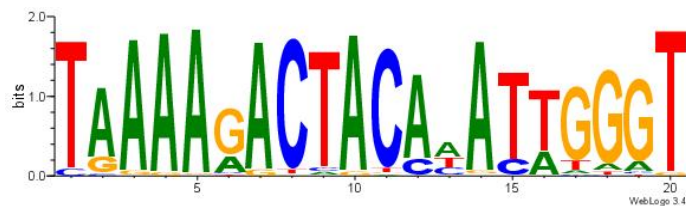
Dataset #: 1  
 Motif ID: 195  
 Motif name: Motif 195  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 7  
 Number of overlap: 10  
 Similarity score: 0.0563059

#### Alignment:

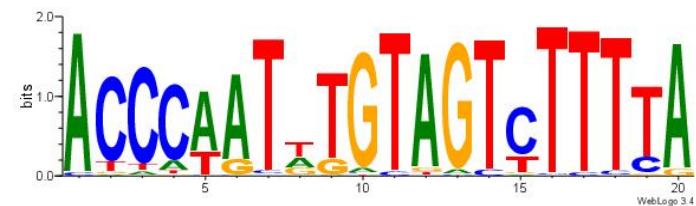
```

TAAAAGACTACAWATTGGGT
----AAACTAGAAA-----
  
```

Original motif      Consensus sequence: TAAAAGACTACAWATTGGGT



Reverse complement motif      Consensus sequence: ACCCAATWTGTAGTCTTTTA

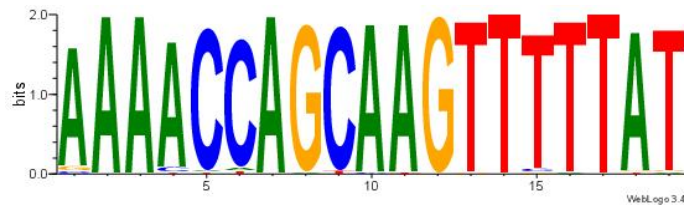


Dataset #: 1  
 Motif ID: 330  
 Motif name: Motif 330  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 2  
 Number of overlap: 10  
 Similarity score: 0.0573722

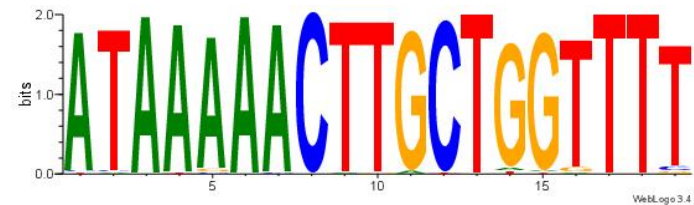
Alignment:

ATAAAACTTGCTGGTTTT  
 -----TTTCTAGTTT-

Original motif      Consensus sequence: AAAACCAGCAAGTTTTTAT



Reverse complement motif      Consensus sequence: ATAAAACTTGCTGGTTTT

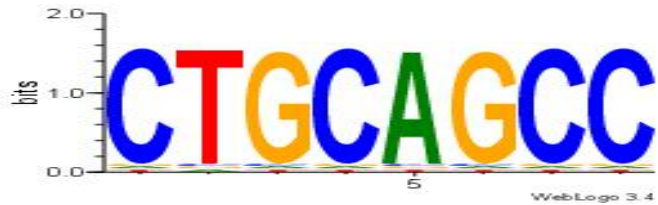



---

**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)

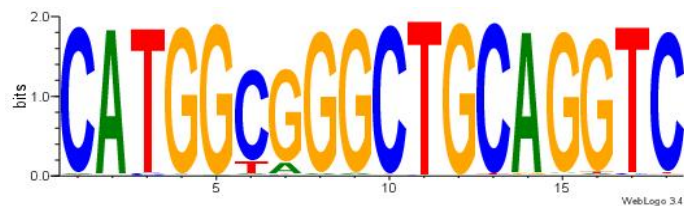
Dataset #: 1  
 Motif ID: 68  
 Motif name: Motif 68  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 4  
 Number of overlap: 8  
 Similarity score: 0.0130204

#### Alignment:

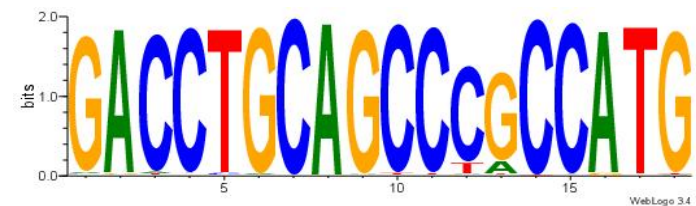
```

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: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 8  
 Similarity score: 0.0154581

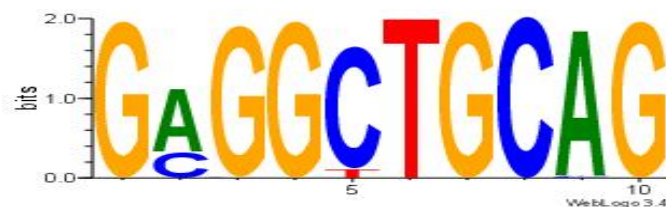
Alignment:

GAGGCTGCAG  
 --GGCTGCAG

Original motif      Consensus sequence: CTGCAGCCTC

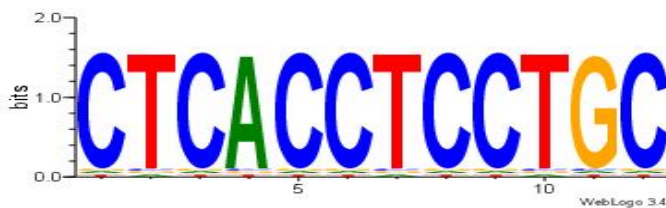


Reverse complement motif      Consensus sequence: GAGGCTGCAG

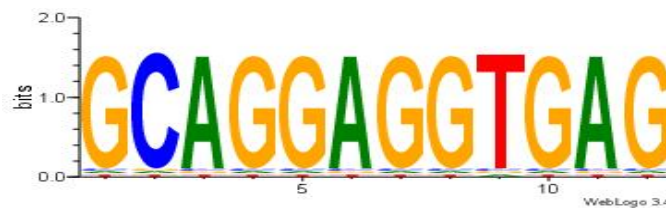


**Dataset #: 1      Motif ID: 339      Motif name: Motif 339**

Original motif      Consensus sequence: CTCACCTCCTGC



Reverse complement motif      Consensus sequence: GCAGGAGGTGAG



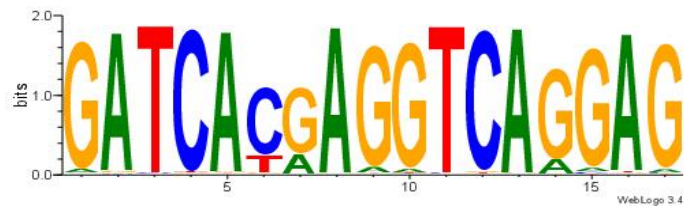
## Best Matches for Motif ID 339 (Highest to Lowest)

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

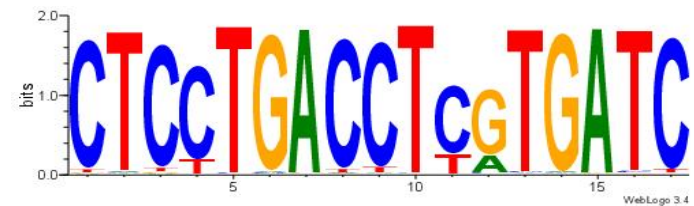
### Alignment:

```
CTCCTGACCTCGTGATC  
--CTCACCTCCTGC---
```

Original motif      Consensus sequence: GATCAGAGGTCAGGAG



Reverse complement motif      Consensus sequence:  
CTCCTGACCTCGTGATC



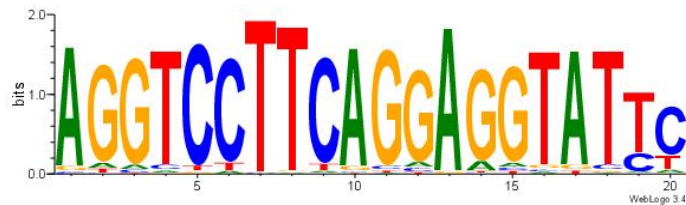
---

Dataset #: 1  
Motif ID: 179  
Motif name: Motif 179  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Original Motif

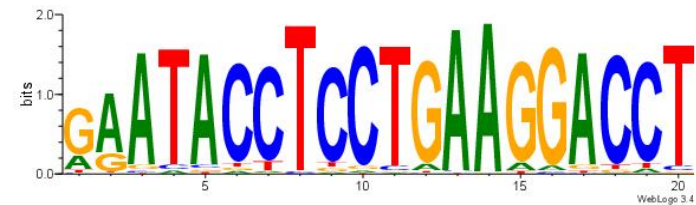
Direction: Forward  
 Position number: 2  
 Number of overlap: 12  
 Similarity score: 0.0795057

Alignment:  
 AGGTCCTTCAGGAGGTATTC  
 -GCAGGAGGTGAG-----

Original motif      Consensus sequence: AGGTCCTTCAGGAGGTATTC

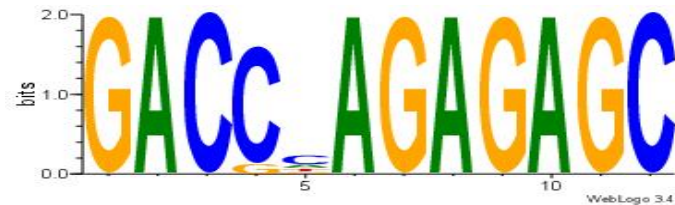


Reverse complement motif      Consensus sequence: GAATACCTCTGAAGGACCT

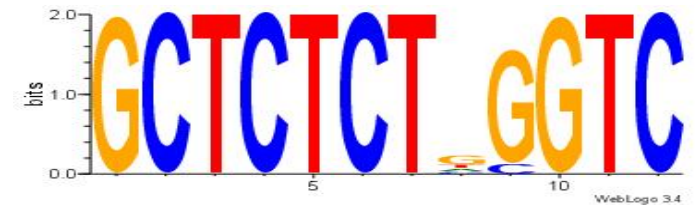


**Dataset #: 1      Motif ID: 340      Motif name: Motif 340**

Original motif      Consensus sequence: GACCCAGAGAGC



Reverse complement motif      Consensus sequence: GCTCTCTGGTC



**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

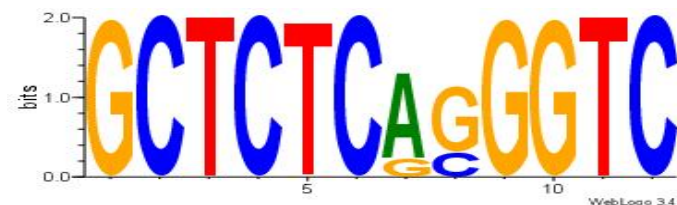
Alignment:

GACCCTGAGAGC  
 GACCCAGAGAGC

Original motif    Consensus sequence: GACCCTGAGAGC



Reverse complement motif    Consensus sequence: GCTCTCAGGGTC



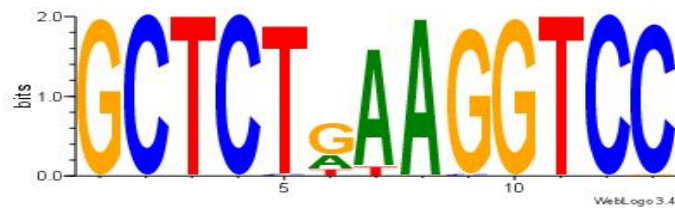
Dataset #: 1  
 Motif ID: 362  
 Motif name: Motif 362  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 2  
 Number of overlap: 12  
 Similarity score: 0.0566001

Alignment:

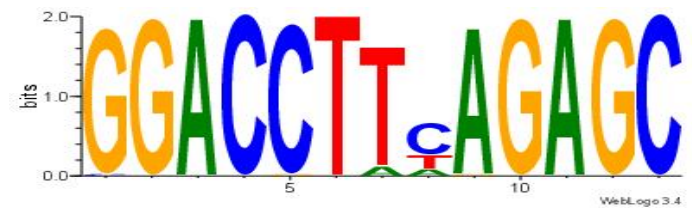
GCTCTGAAGGTCC

GCTCTCTGGGTC-

Original motif      Consensus sequence: GCTCTGAAGGTCC

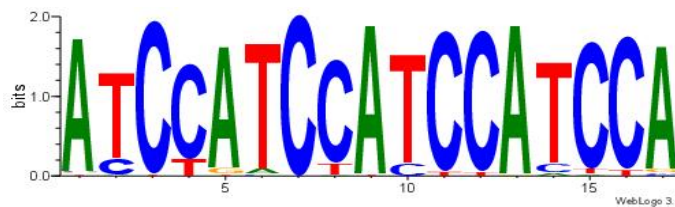


Reverse complement motif      Consensus sequence: GGACCTTCAGAGC

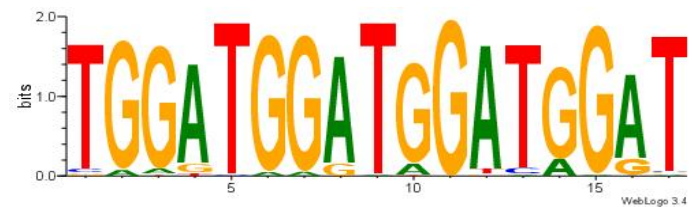


**Dataset #: 1      Motif ID: 341      Motif name: Motif 341**

Original motif      Consensus sequence: ATCCATCCATCCATCCA



Reverse complement motif      Consensus sequence:  
TGGATGGATGGATGGAT



**Best Matches for Motif ID 341 (Highest to Lowest)**

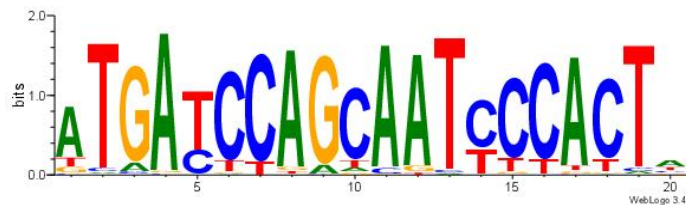
Dataset #:	1
Motif ID:	115
Motif name:	Motif 115
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward

Position number: 1  
Number of overlap: 17  
Similarity score: 0.0809092

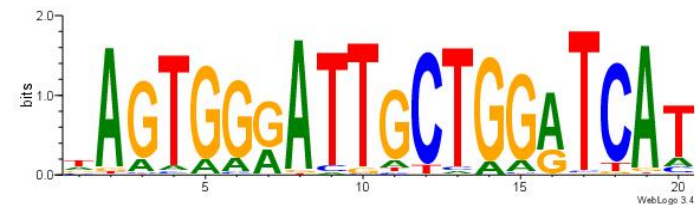
Alignment:

HAGTGGKATTGCTGGATCAT  
TGGATGGATGGATGGAT---

Original motif      Consensus sequence: ATGATCCAGCAATYCCACTH



Reverse complement motif      Consensus sequence:  
HAGTGGKATTGCTGGATCAT



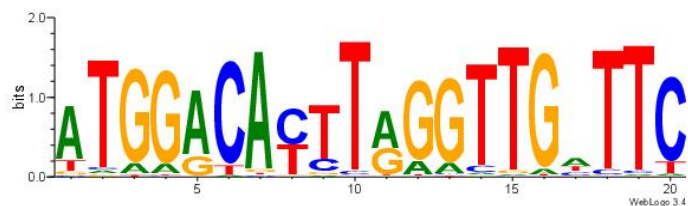
---

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

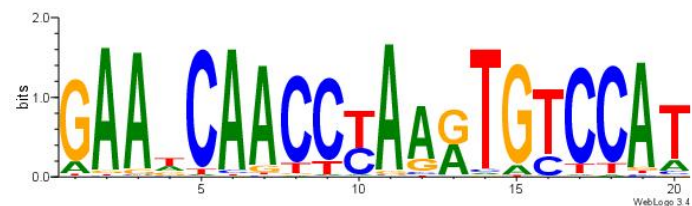
Alignment:

GAAHCAACCKAAKTGTCCAT  
-ATCCATCCATCCATCCA--

Original motif      Consensus sequence: ATGGACAYTTRGGTTGHTTC

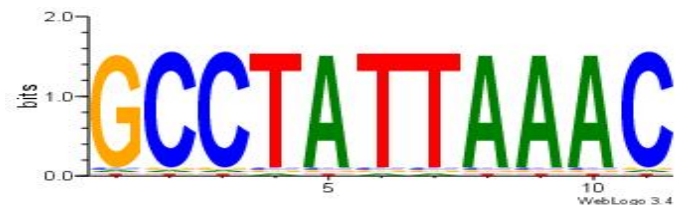


Reverse complement motif      Consensus sequence: GAAHCAACCKAAKTGTCCAT

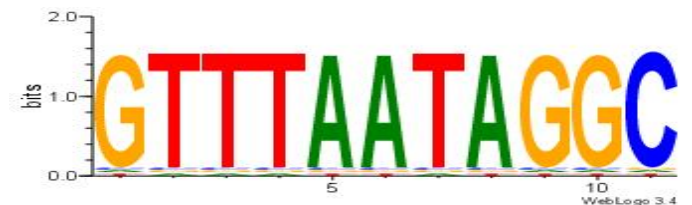


**Dataset #: 1      Motif ID: 342      Motif name: Motif 342**

Original motif      Consensus sequence: GCCTATTA AAC



Reverse complement motif      Consensus sequence: GTTTAATAGGC



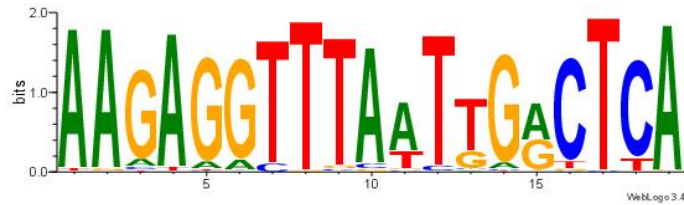
**Best Matches for Motif ID 342 (Highest to Lowest)**

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

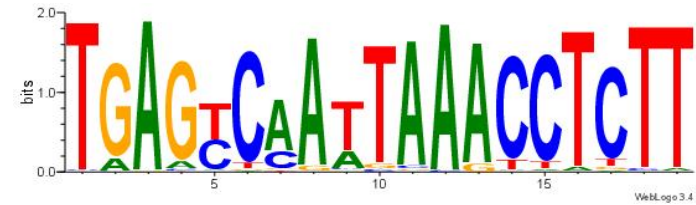
Alignment:

TGAGKCAATTAAACCTCTT  
 -----GCCTATTAAAC----

Original motif      Consensus sequence: AAGAGGTTTAATTGRCTCA



Reverse complement motif      Consensus sequence:  
 TGAGKCAATTAAACCTCTT

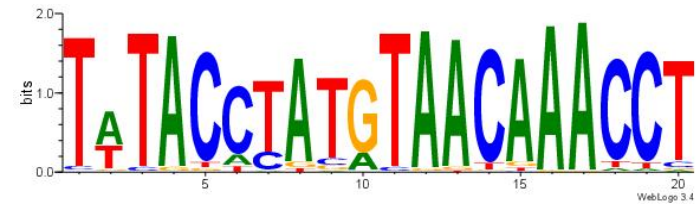
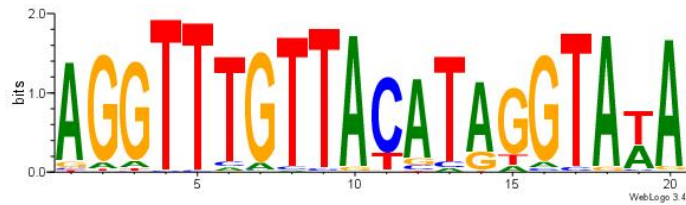


Dataset #:	1
Motif ID:	137
Motif name:	Motif 137
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	7
Number of overlap:	11
Similarity score:	0.0624203

Alignment:  
 AGGTTTGTTACATAGGTAWA  
 ---GTTTAATAGGC-----

Original motif      Consensus sequence: AGGTTTGTTACATAGGTAWA

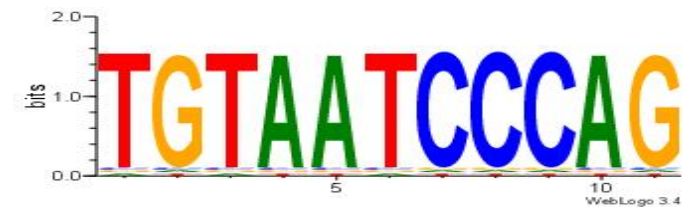
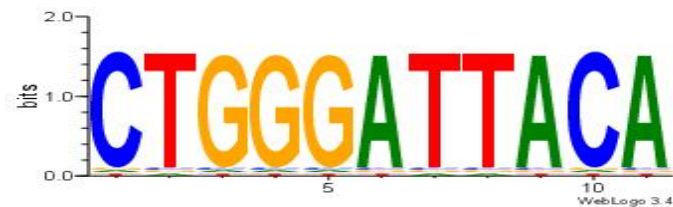
Reverse complement motif      Consensus sequence:  
 TWTACCTATGTAACAAACCT



**Dataset #: 1      Motif ID: 343      Motif name: Motif 343**

Original motif      Consensus sequence: CTGGGATTACA

Reverse complement motif      Consensus sequence: TGTAATCCCAG

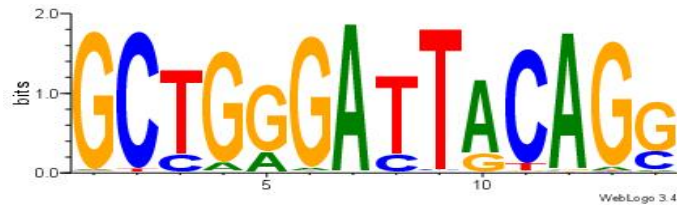


**Best Matches for Motif ID 343 (Highest to Lowest)**

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: GCTGGATTACAGG



Reverse complement motif    Consensus sequence: CCTGTAATCCCAGG

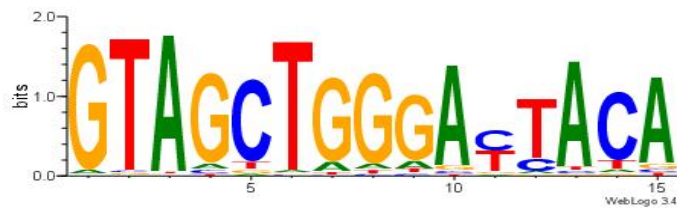


Dataset #: 1  
Motif ID: 69  
Motif name: Motif 69  
Matching format of first motif: Original Motif  
Matching format of second motif: Original Motif  
Direction: Forward  
Position number: 5  
Number of overlap: 11  
Similarity score: 0.0277108

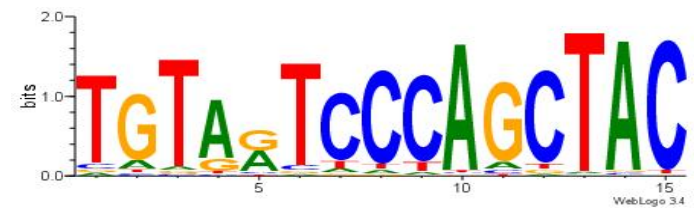
Alignment:

GTAGCTGGGAYTACA  
----CTGGGATTACA

Original motif    Consensus sequence: GTAGCTGGGAYTACA



Reverse complement motif    Consensus sequence: TGTAKTCCCAGCT

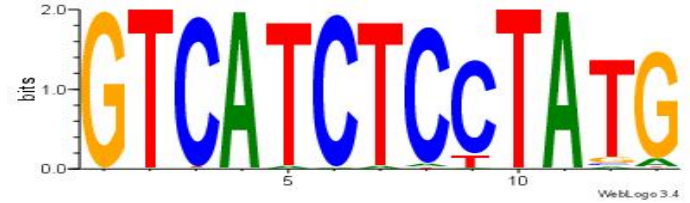


**Dataset #: 1      Motif ID: 344      Motif name: Motif 344**

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

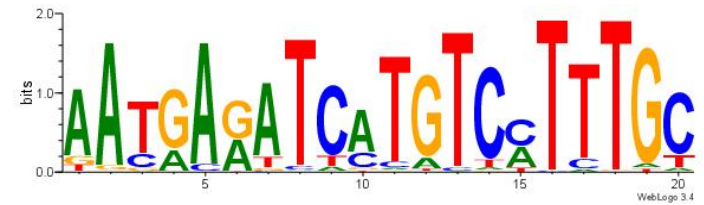
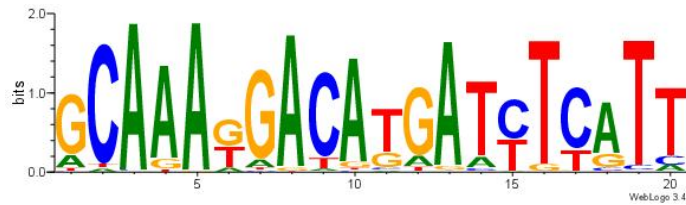
**Alignment:**

```
GCAAAGKACATGATYTCATT
-CATAGGAGATGAC-----
```

Original motif      Consensus sequence: GCAAAGKACATGATYTCATT

Reverse complement motif      Consensus sequence:  
AATGAKATCATGTCYTTTGC

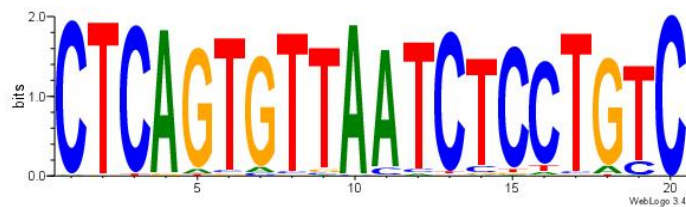




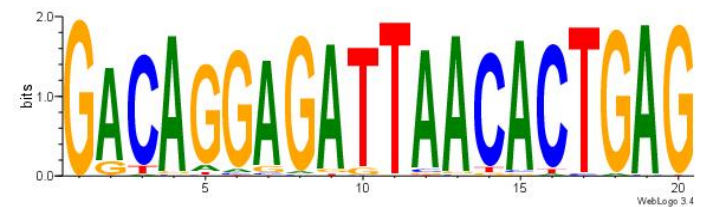
Dataset #: 1  
 Motif ID: 262  
 Motif name: Motif 262  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 8  
 Number of overlap: 13  
 Similarity score: 0.0805293

Alignment:  
 GACAGGAGATTAACACTGAG  
 -----CATAGGAGATGAC

Original motif      Consensus sequence: CTCAGTGTTAATCTCCCTGTC



Reverse complement motif      Consensus sequence: GACAGGAGATTAACACTGAG

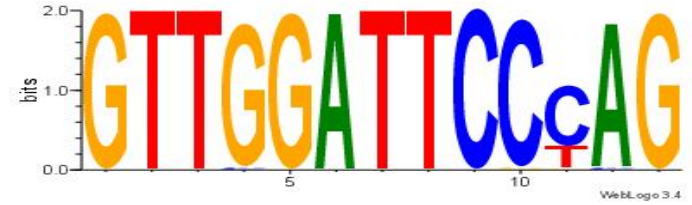


**Dataset #: 1      Motif ID: 345      Motif name: Motif 345**

Original motif      Consensus sequence: CTGGGAATCCAAC



Reverse complement motif      Consensus sequence: GTTGGATTCCcAG



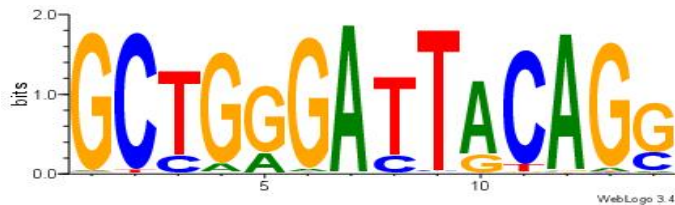
### Best Matches for Motif ID 345 (Highest to Lowest)

Dataset #:	1
Motif ID:	4
Motif name:	Motif 4
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	13
Similarity score:	0.0624846

#### Alignment:

```
CCTGTAATCCCAGC  
GTTGGATTCCCAG-
```

Original motif      Consensus sequence: GCTGGGATTACAGG



Reverse complement motif      Consensus sequence: CCTGTAATCCCAG

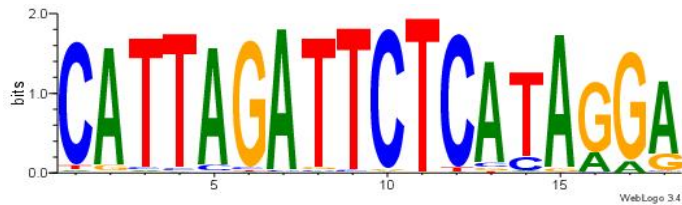


Dataset #: 1  
 Motif ID: 154  
 Motif name: Motif 154  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 2  
 Number of overlap: 13  
 Similarity score: 0.0631163

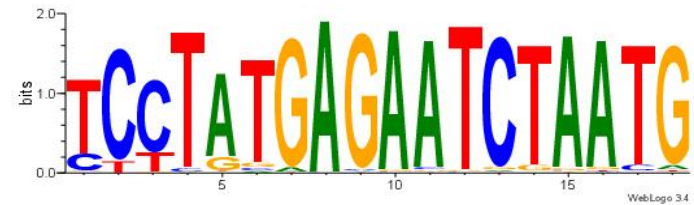
Alignment:

CATTAGATTCTCATAGGA  
 ----GTTGGATTCCCAG-

Original motif      Consensus sequence: CATTAGATTCTCATAGGA



Reverse complement motif      Consensus sequence: TCCTATGAGAATCTAATG

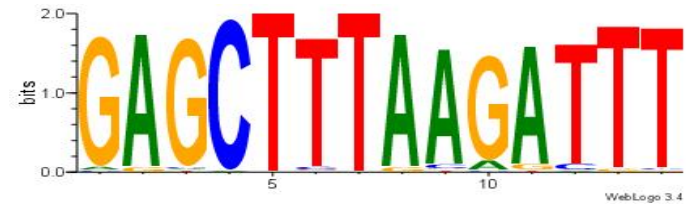
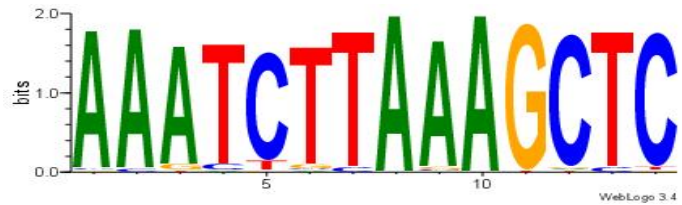



---

**Dataset #: 1      Motif ID: 346      Motif name: Motif 346**

Original motif      Consensus sequence: AAATCTTAAAGCTC

Reverse complement motif      Consensus sequence: GAGCTTTAAGATT

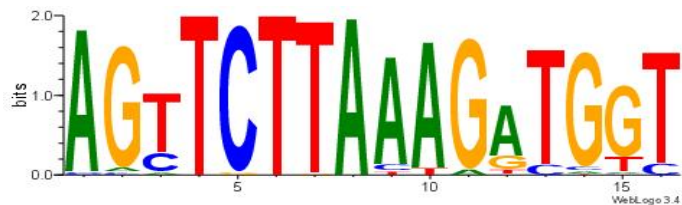


**Best Matches for Motif ID 346 (Highest to Lowest)**

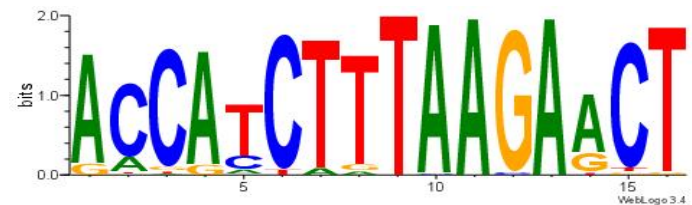
Dataset #: 1  
 Motif ID: 303  
 Motif name: Motif 303  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 14  
 Similarity score: 0.0682748

Alignment:  
 ACCATCTTTAAGAACT  
 --GAGCTTTAAGATTT

Original motif    Consensus sequence: AGTTCTTAAAGATGGT



Reverse complement motif    Consensus sequence: ACCATCTTTAAGAACT

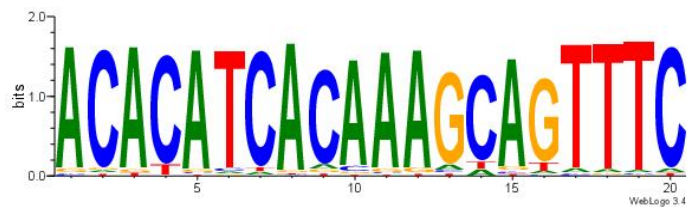


Dataset #: 1  
 Motif ID: 202  
 Motif name: Motif 202  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 3  
 Number of overlap: 14  
 Similarity score: 0.0876662

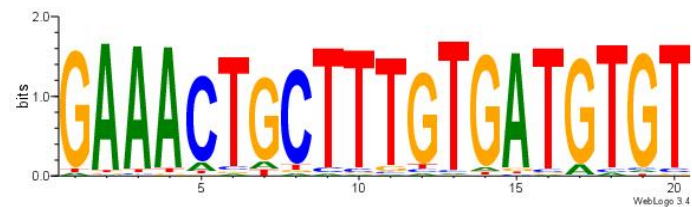
Alignment:

GAAACTGCTTTGTGATGTGT  
 ----GAGCTTTAAGATTT--

Original motif      Consensus sequence: ACACATCACAAAGCAGTTTC



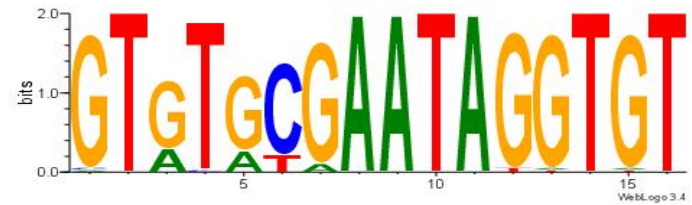
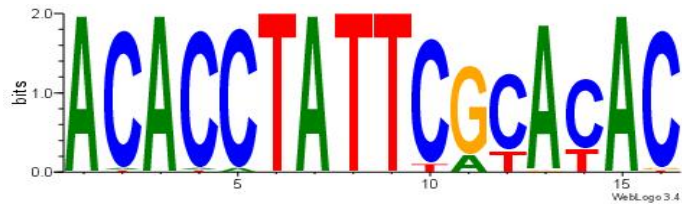
Reverse complement motif      Consensus sequence: GAAACTGCTTTGTGATGTGT



**Dataset #: 1      Motif ID: 347      Motif name: Motif 347**

Original motif      Consensus sequence: ACACCTATTCGCACAC

Reverse complement motif      Consensus sequence: GTGTGCGAATAGGTGT

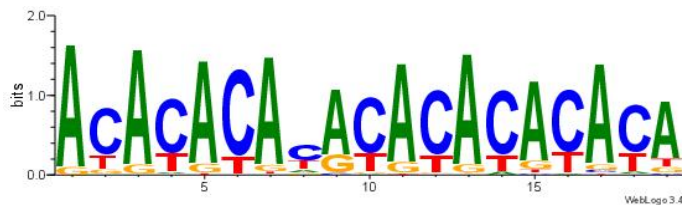


**Best Matches for Motif ID 347 (Highest to Lowest)**

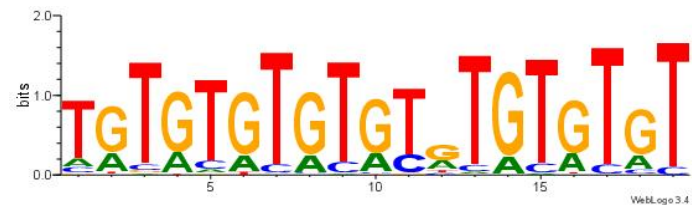
Dataset #: 1  
 Motif ID: 66  
 Motif name: Motif 66  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 16  
 Similarity score: 0.0719682

Alignment:  
 ACACACAYACACACACACA  
 ACACCTATTTCGCACAC---

Original motif      Consensus sequence: ACACACAYACACACACACA



Reverse complement motif      Consensus sequence: TGTGTGTGTGKTGTGTGT

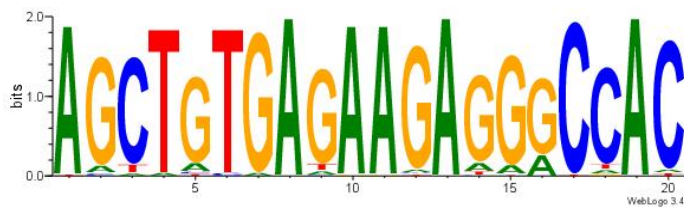


Dataset #: 1  
 Motif ID: 294  
 Motif name: Motif 294  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 3  
 Number of overlap: 16  
 Similarity score: 0.0824744

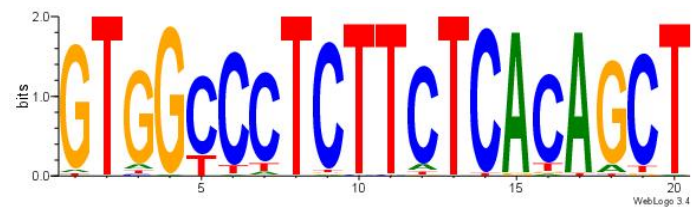
Alignment:

AGCTGTGAGAAGAGGGCCAC  
 --GTGTGCGAATAGGTGT--

Original motif      Consensus sequence: AGCTGTGAGAAGAGGGCCAC



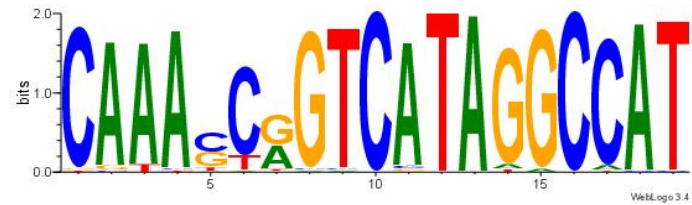
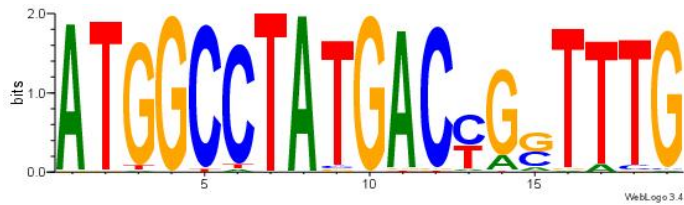
Reverse complement motif      Consensus sequence: GTGGCCCTCTTCTCACAGCT



**Dataset #: 1      Motif ID: 348      Motif name: Motif 348**

Original motif      Consensus sequence: ATGGCCTATGACYGSTTTG

Reverse complement motif      Consensus sequence: CAAASCKGTCATAGGCCAT

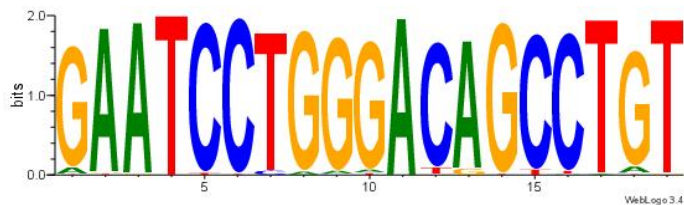


**Best Matches for Motif ID 348 (Highest to Lowest)**

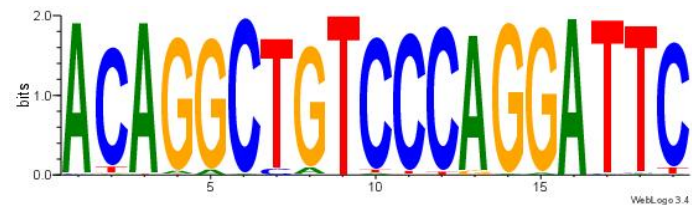
Dataset #: 1  
 Motif ID: 192  
 Motif name: Motif 192  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 19  
 Similarity score: 0.115392

Alignment:  
 ACAGGCTGTCCCAGGATTC  
 ATGGCCTATGACYGSTTTG

Original motif      Consensus sequence: GAATCCTGGGACAGCCTGT



Reverse complement motif      Consensus sequence: ACAGGCTGTCCCAGGATTC



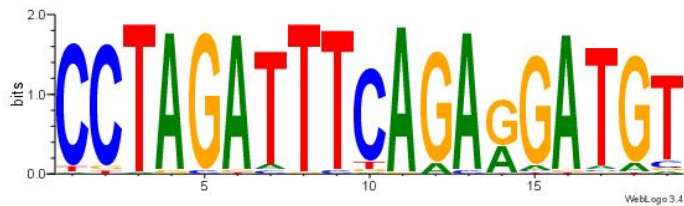


Dataset #: 1  
 Motif ID: 280  
 Motif name: Motif 280  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 19  
 Similarity score: 0.117513

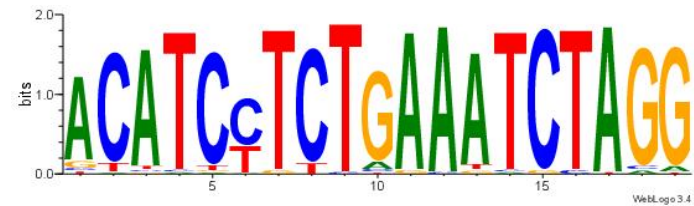
Alignment:

ACATCMTCTGAAATCTAGG  
 ATGGCCTATGACYGSTTTG

Original motif      Consensus sequence: CCTAGATTTcAGAGGATGT



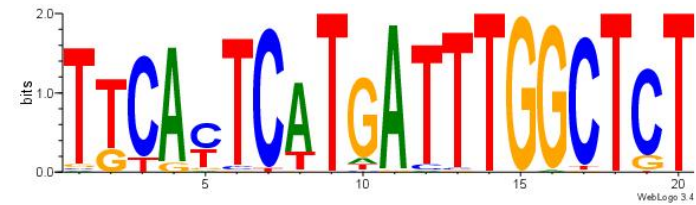
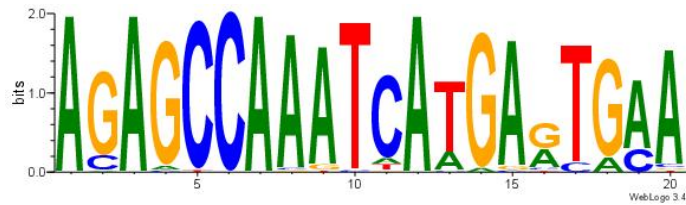
Reverse complement motif      Consensus sequence: ACATCMTCTGAAATCTAGG



**Dataset #: 1      Motif ID: 349      Motif name: Motif 349**

Original motif      Consensus sequence: AGAGCCAAATCATGARTGAA

Reverse complement motif      Consensus sequence: TTCAMTCATGATTTGGCTCT

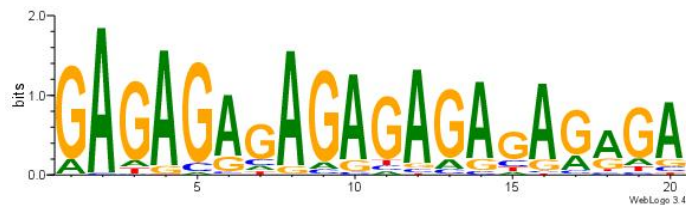


**Best Matches for Motif ID 349 (Highest to Lowest)**

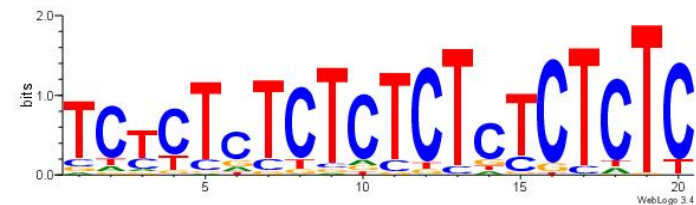
Dataset #: 1  
 Motif ID: 109  
 Motif name: Motif 109  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 2  
 Number of overlap: 19  
 Similarity score: 0.0991551

Alignment:  
 GAGAGAGAGAGAGAGAGAGA-  
 -AGAGCCAAATCATGARTGAA

Original motif      Consensus sequence: GAGAGAGAGAGAGAGAGAGA



Reverse complement motif      Consensus sequence: TCTCTCTCTCTCTCTCTCTCT

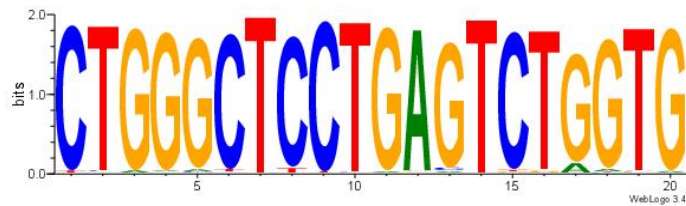


Dataset #: 1  
 Motif ID: 67  
 Motif name: Motif 67  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 2  
 Number of overlap: 19  
 Similarity score: 0.110012

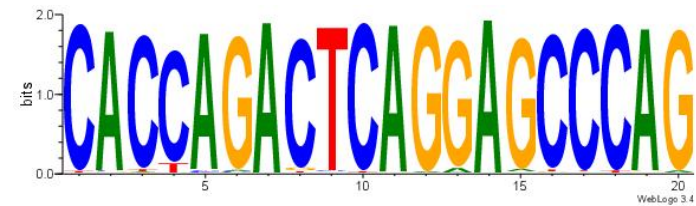
Alignment:

-CTGGGCTCCTGAGTCTGGTG  
 TTCAMTCATGATTTGGCTCT-

Original motif      Consensus sequence: CTGGGCTCCTGAGTCTGGTG



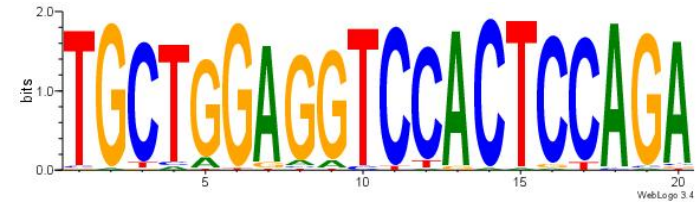
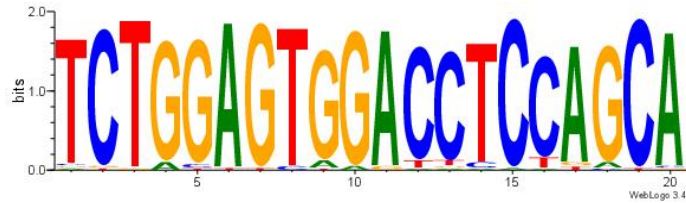
Reverse complement motif      Consensus sequence: CACCAGACTCAGGAGCCCAG



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

Original motif      Consensus sequence: TCTGGAGTGGACCTCCAGCA

Reverse complement motif      Consensus sequence: TGCTGGAGGTCCACTCCAGA

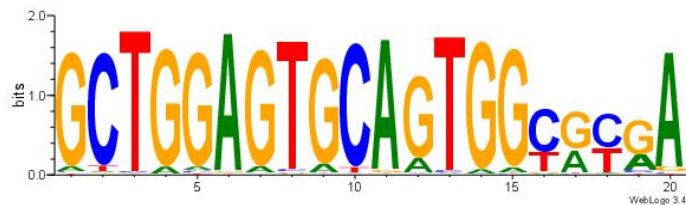


**Best Matches for Motif ID 350 (Highest to Lowest)**

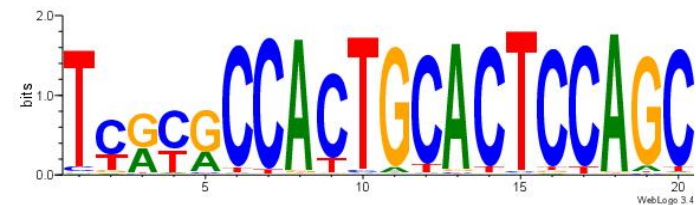
Dataset #: 1  
 Motif ID: 3  
 Motif name: Motif 3  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 20  
 Similarity score: 0.100512

Alignment:  
 GCTGGAGTGCAGTGGCRYGA  
 TCTGGAGTGGACCTCCAGCA

Original motif      Consensus sequence: GCTGGAGTGCAGTGGCRYGA



Reverse complement motif      Consensus sequence: TCKMGCCACTGCACTCCAGC

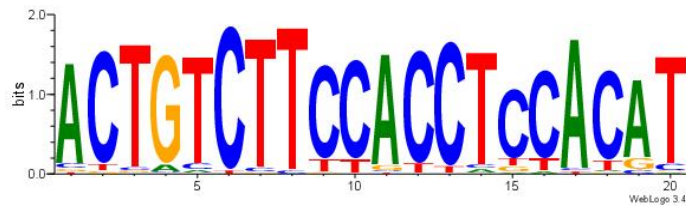


Dataset #: 1  
 Motif ID: 178  
 Motif name: Motif 178  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 20  
 Similarity score: 0.103785

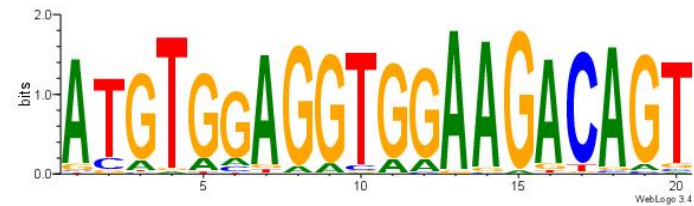
Alignment:

ATGTGGAGGTGGAAGACAGT  
 TGCTGGAGGTCCACTCCAGA

Original motif    Consensus sequence: ACTGTCTTCCACCTCCACAT



Reverse complement motif    Consensus sequence: ATGTGGAGGTGGAAGACAGT



**Dataset #: 1      Motif ID: 351      Motif name: Motif 351**

Original motif    Consensus sequence: ATTMGGGTGGG

Reverse complement motif    Consensus sequence: CCCACCCYAAT

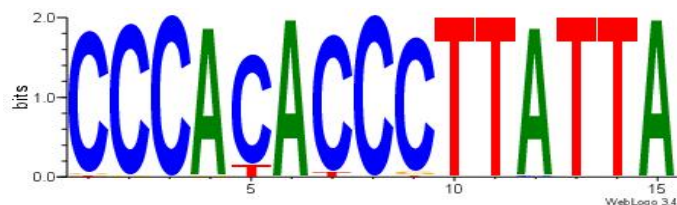


**Best Matches for Motif ID 351 (Highest to Lowest)**

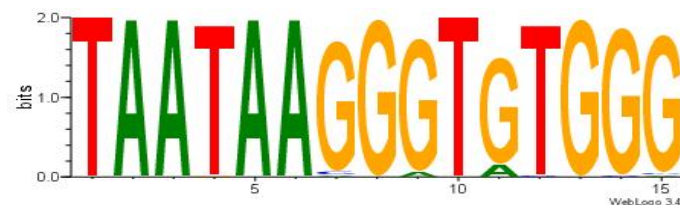
Dataset #: 1  
 Motif ID: 259  
 Motif name: Motif 259  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 3  
 Number of overlap: 11  
 Similarity score: 0.0511125

Alignment:  
 CCCACACCCTTATTA  
 --CCCACCCYAAT--

Original motif      Consensus sequence: CCCACACCCTTATTA



Reverse complement motif      Consensus sequence: TAATAAGGGTGTGGG



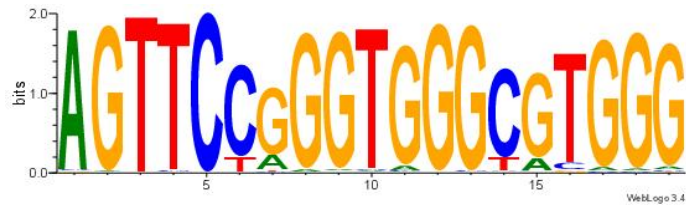
Dataset #: 1

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

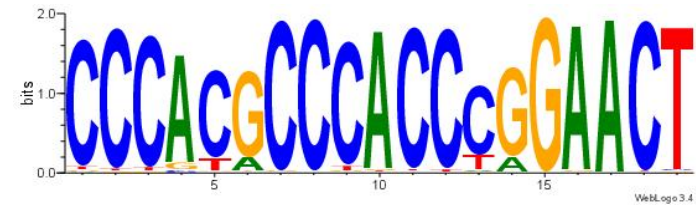
**Alignment:**

AGTTCCGGGTGGGCGTGGG  
 --ATTMGGGTGGG-----

Original motif    Consensus sequence: AGTTCCGGGTGGGCGTGGG

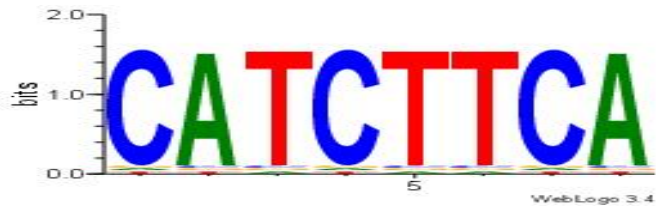


Reverse complement motif    Consensus sequence: CCCACGCCACCCGGAAC



**Dataset #: 1      Motif ID: 352      Motif name: Motif 352**

Original motif    Consensus sequence: CATCTTCA



Reverse complement motif    Consensus sequence: TGAAGATG



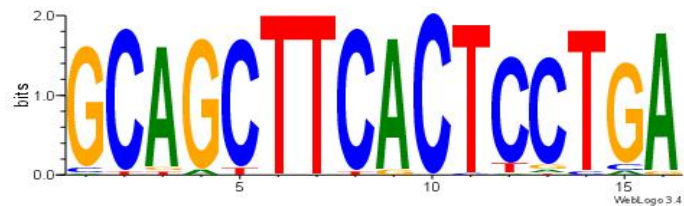
## Best Matches for Motif ID 352 (Highest to Lowest)

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

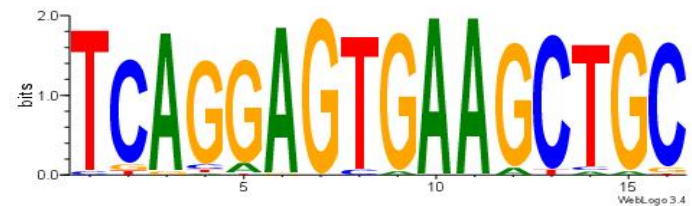
### Alignment:

```
TCAGGAGTGAAGCTGC  
-----TGAAGATG--
```

Original motif      Consensus sequence: GCAGCTTCACTCCCTGA



Reverse complement motif      Consensus sequence: TCAGGAGTGAAGCTGC



---

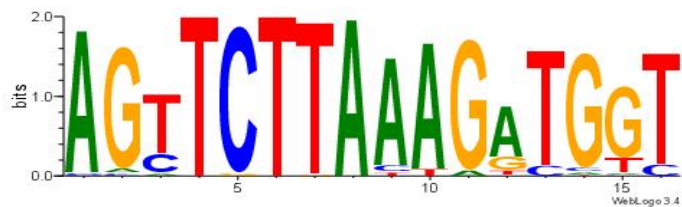
Dataset #: 1  
Motif ID: 303  
Motif name: Motif 303  
Matching format of first motif: Original Motif  
Matching format of second motif: Reverse Complement



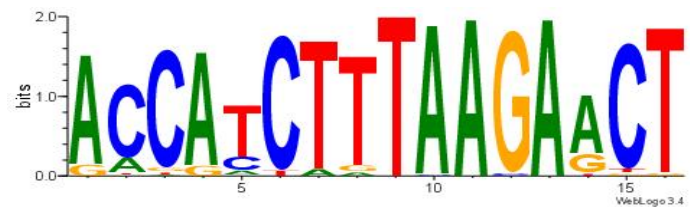
Direction: Backward  
 Position number: 3  
 Number of overlap: 8  
 Similarity score: 0.0334876

Alignment:  
 ACCATCTTTAAGAACT  
 -----CATCTTCA--

Original motif    Consensus sequence: AGTTCTTAAAGATGGT

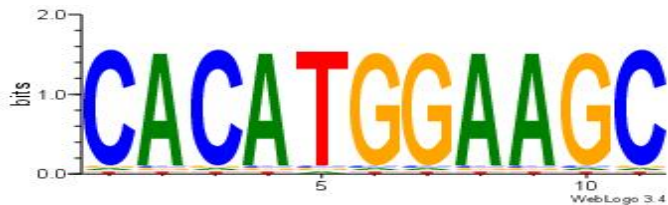


Reverse complement motif    Consensus sequence: ACCATCTTTAAGAACT

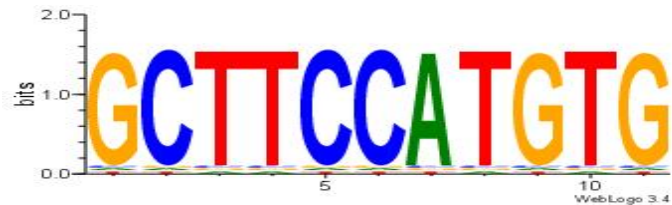


**Dataset #: 1      Motif ID: 353      Motif name: Motif 353**

Original motif    Consensus sequence: CACATGGAAGC



Reverse complement motif    Consensus sequence: GCTTCCATGTG



**Best Matches for Motif ID 353 (Highest to Lowest)**

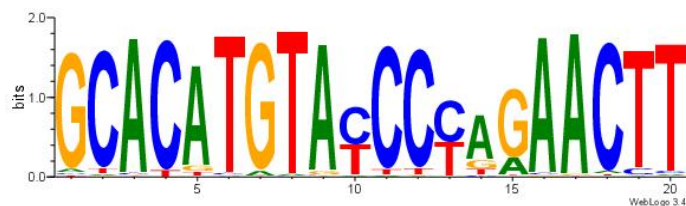
Dataset #: 1  
 Motif ID: 225

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

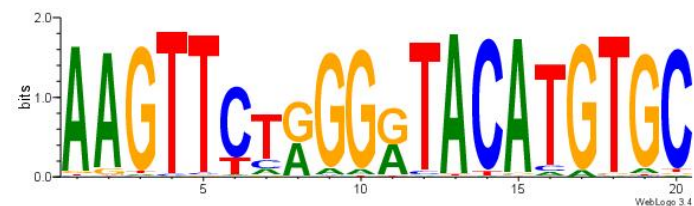
Alignment:

AAGTTCTKGGKTACATGTGC  
 -----GCTTCCATGTG-

Original motif      Consensus sequence: GCACATGTAYCCYAGAACTT



Reverse complement motif      Consensus sequence: AAGTTCTKGGKTACATGTGC

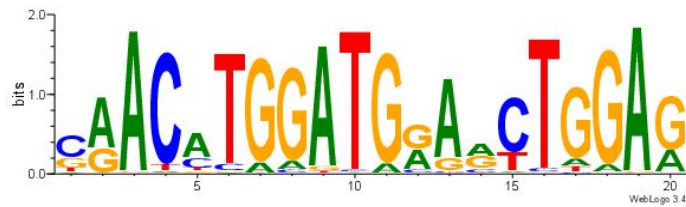


Dataset #: 1  
 Motif ID: 104  
 Motif name: Motif 104  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 2  
 Number of overlap: 11  
 Similarity score: 0.0616894

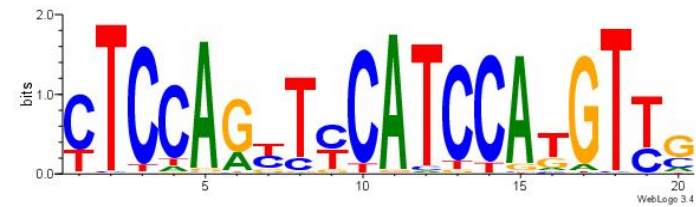
Alignment:

```
CTCCAGKTMCATCCATGTTG
-----GCTTCCATGTG-
```

Original motif      Consensus sequence: CAACATGGATGRARCTGGAG



Reverse complement motif      Consensus sequence: CTCCAGKTMCATCCATGTTG

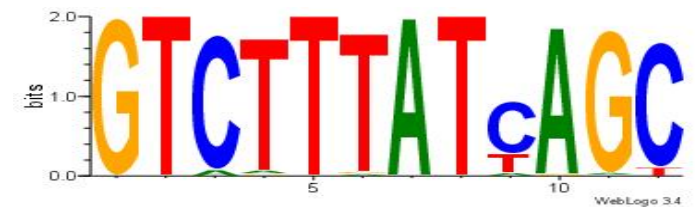


**Dataset #: 1      Motif ID: 354      Motif name: Motif 354**

Original motif      Consensus sequence: GCTGATAAAGAC



Reverse complement motif      Consensus sequence: GTCTTTATCAGC



**Best Matches for Motif ID 354 (Highest to Lowest)**

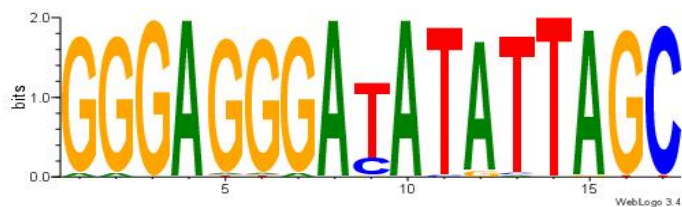
Dataset #:	1
Motif ID:	329
Motif name:	Motif 329
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward

Position number: 6  
Number of overlap: 12  
Similarity score: 0.0760989

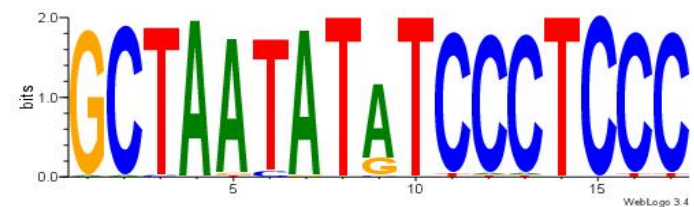
Alignment:

GGGAGGGATATATTAGC  
GTCTTTATCAGC-----

Original motif      Consensus sequence: GGGAGGGATATATTAGC



Reverse complement motif      Consensus sequence: GCTAATATATCCCTCCC

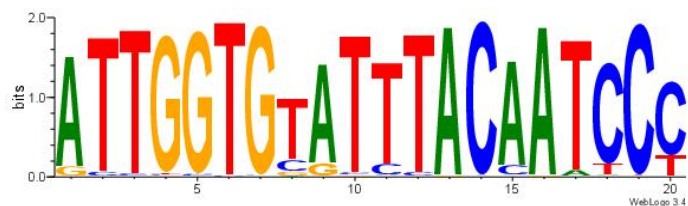


Dataset #: 1  
Motif ID: 106  
Motif name: Motif 106  
Matching format of first motif: Original Motif  
Matching format of second motif: Reverse Complement  
Direction: Forward  
Position number: 7  
Number of overlap: 12  
Similarity score: 0.0776121

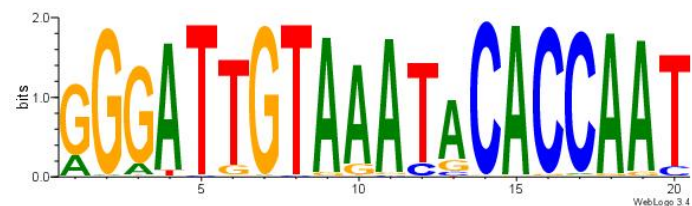
Alignment:

GGGATTGTAAATACACCAAT  
-----GCTGATAAAGAC--

Original motif      Consensus sequence: ATTGGTGTATTACAATCCC

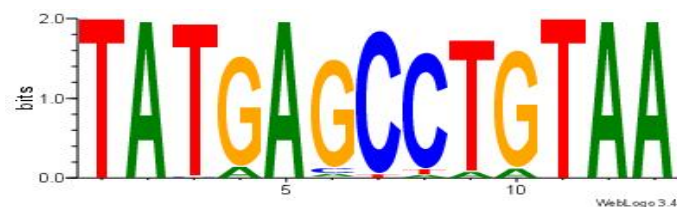


Reverse complement motif      Consensus sequence: GGGATTGTAAATACACCAAT

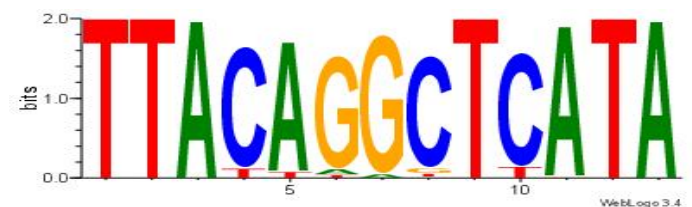


**Dataset #: 1      Motif ID: 355      Motif name: Motif 355**

Original motif      Consensus sequence: TATGAGCCTGTAA



Reverse complement motif      Consensus sequence: TTACAGGCTCATA



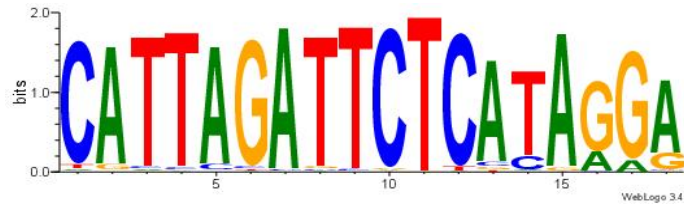
### Best Matches for Motif ID 355 (Highest to Lowest)

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

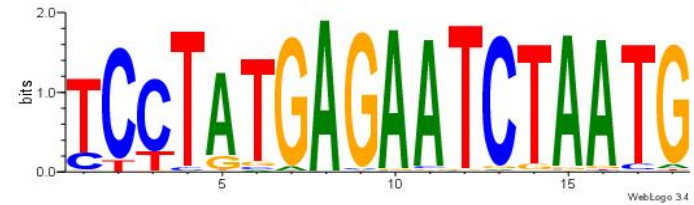
Alignment:

TCCTATGAGAATCTAATG  
--TATGAGCCTGTAA---

Original motif      Consensus sequence: CATTAGATTCTCATAGGA



Reverse complement motif      Consensus sequence: TCCTATGAGAATCTAATG

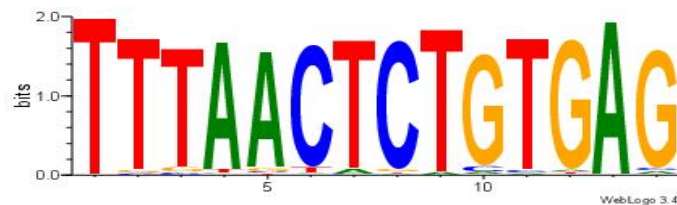
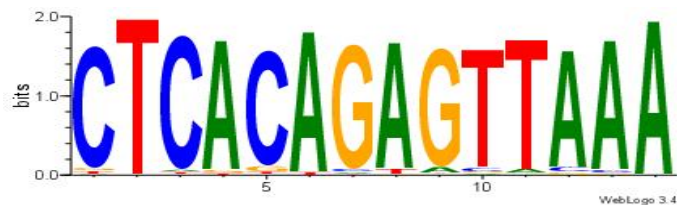


Dataset #: 1  
Motif ID: 275  
Motif name: Motif 275  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Original Motif  
Direction: Forward  
Position number: 1  
Number of overlap: 13  
Similarity score: 0.0903624

Alignment:  
CTCACAGAGTTAAA  
TTACAGGCTCATA-

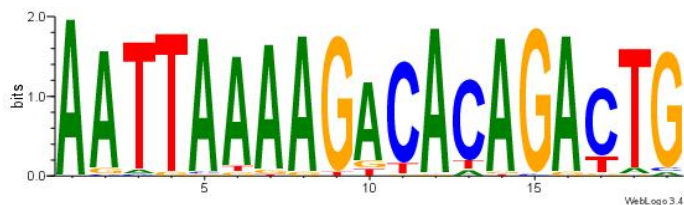
Original motif      Consensus sequence: CTCACAGAGTTAAA

Reverse complement motif      Consensus sequence: TTTAACTCTGTGAA

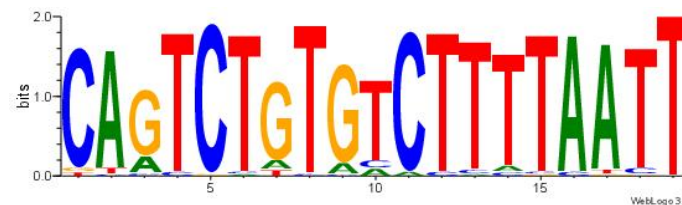


**Dataset #: 1      Motif ID: 356      Motif name: Motif 356**

Original motif      Consensus sequence: AATTAAAGACACAGACTG



Reverse complement motif      Consensus sequence: CAGTCTGTCTTTTAATT



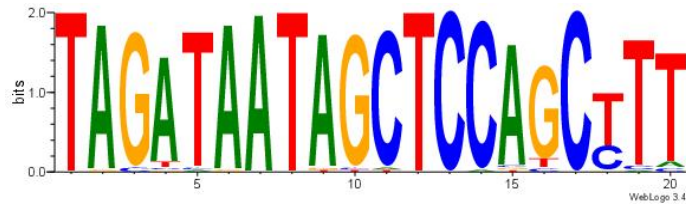
**Best Matches for Motif ID 356 (Highest to Lowest)**

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

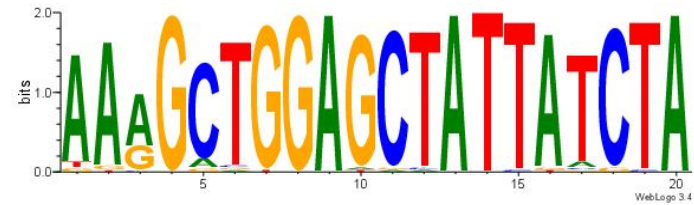
Alignment:

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

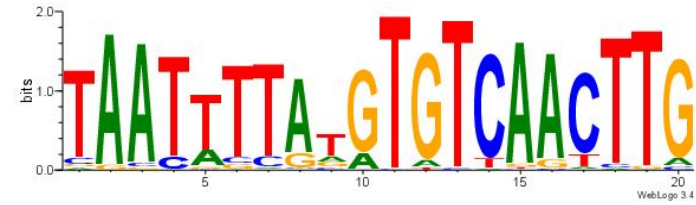
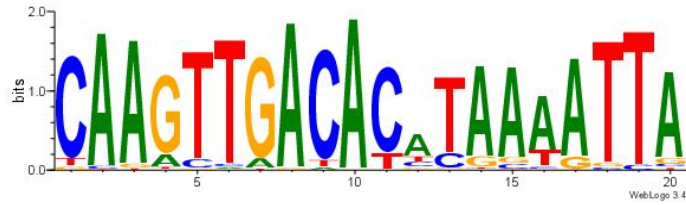
Alignment:

TAATTTTATGTGTCAACTTG  
-AATTAAAAGACACAGACTG

Original motif      Consensus sequence: CAAGTTGACACATAAAATTA

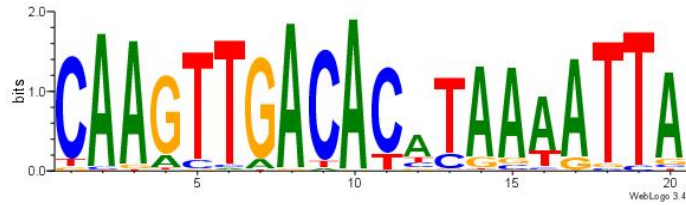
Reverse complement motif      Consensus sequence:  
TAATTTTATGTGTCAACTTG



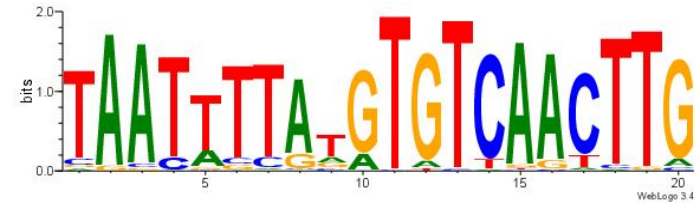


**Dataset #: 1      Motif ID: 357      Motif name: Motif 357**

Original motif      Consensus sequence: CAAGTTGACACATAAAAATTA



Reverse complement motif      Consensus sequence: TAATTTATGTGTCAACTTG



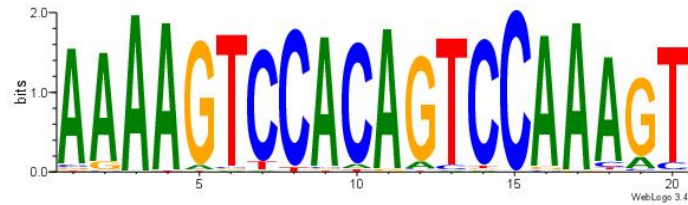
**Best Matches for Motif ID 357 (Highest to Lowest)**

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:	0.0907717

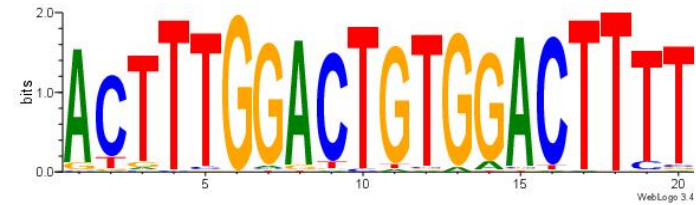
Alignment:

-ACTTTGGACTGTGGACTTTT  
TAATTTTATGTGTCAACTTG-

Original motif      Consensus sequence: AAAAGTCCACAGTCCAAAGT



Reverse complement motif      Consensus sequence:  
ACTTTGGACTGTGGACTTTT



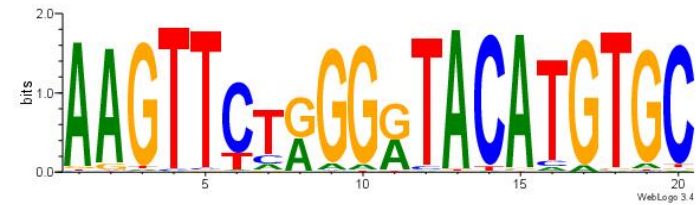
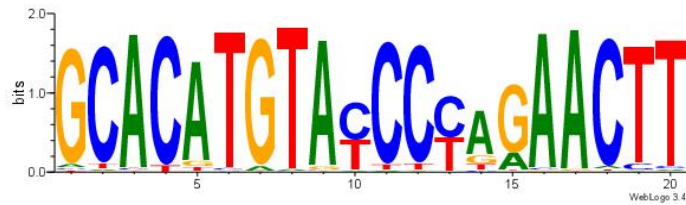
Dataset #: 1  
Motif ID: 225  
Motif name: Motif 225  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Reverse Complement  
Direction: Backward  
Position number: 2  
Number of overlap: 19  
Similarity score: 0.100576

Alignment:

-AAGTTCTKGGKTACATGTGC  
TAATTTTATGTGTCAACTTG-

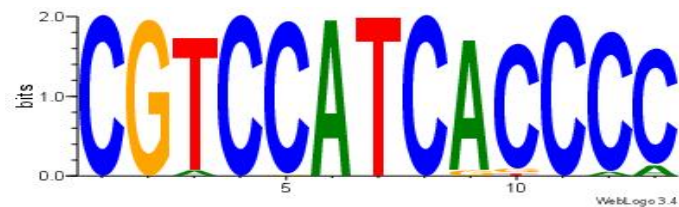
Original motif      Consensus sequence: GCACATGTAYCCYAGAACTT

Reverse complement motif      Consensus sequence:  
AAGTTCTKGGKTACATGTGC

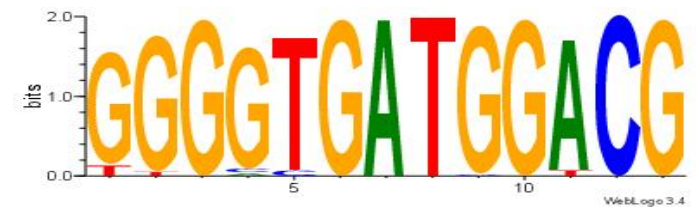


**Dataset #: 1      Motif ID: 358      Motif name: Motif 358**

Original motif      Consensus sequence: CGTCCATCACCCC



Reverse complement motif      Consensus sequence: GGGGTGATGGACCG

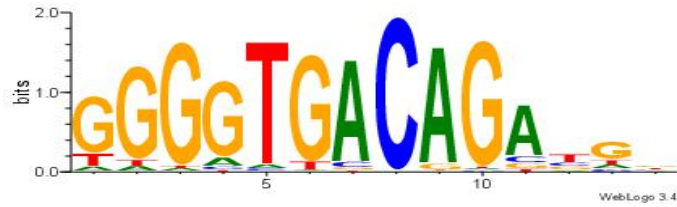


**Best Matches for Motif ID 358 (Highest to Lowest)**

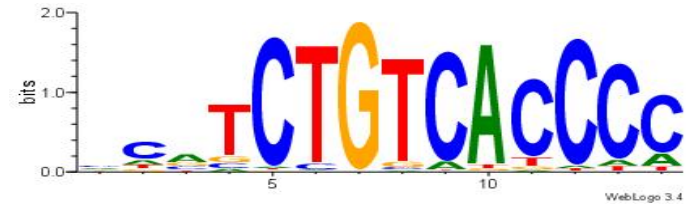
Dataset #:	1
Motif ID:	1
Motif name:	Motif 1
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	13
Similarity score:	0.0685601

Alignment:  
 BCVTCTGTCACCCC  
 CGTCCATCACCCC-

Original motif      Consensus sequence: GGGGTGACAGABGB



Reverse complement motif      Consensus sequence: BCVTCTGTCACCC

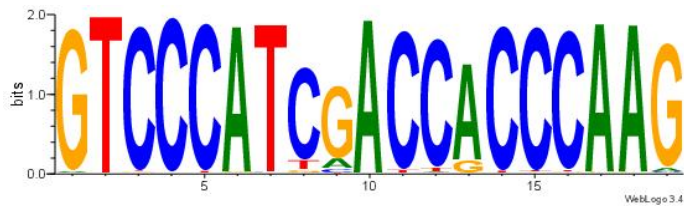


Dataset #: 1  
 Motif ID: 53  
 Motif name: Motif 53  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 5  
 Number of overlap: 13  
 Similarity score: 0.0721847

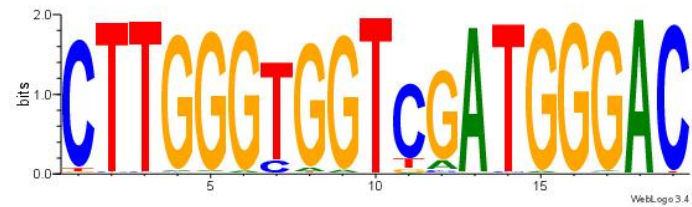
Alignment:

```
GTCCCATCGACCACCCAAG
----CGTCCATCACCC--
```

Original motif      Consensus sequence: GTCCCATCGACCACCCAAG



Reverse complement motif      Consensus sequence: CTTGGGTGGTTCGATGGGAC



**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)

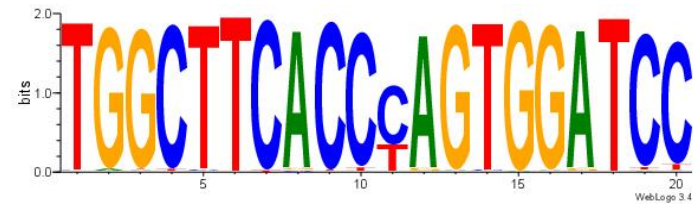
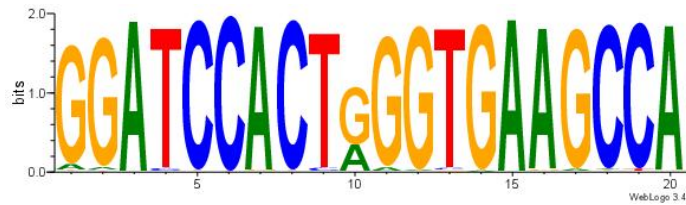
Dataset #:	1
Motif ID:	61
Motif name:	Motif 61
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	10
Similarity score:	0.0622858

#### Alignment:

```
GGATCCACTGGGTGAAGCCA  
SGTGACGTCA-----
```

Original motif      Consensus sequence: GGATCCACTGGGTGAAGCCA

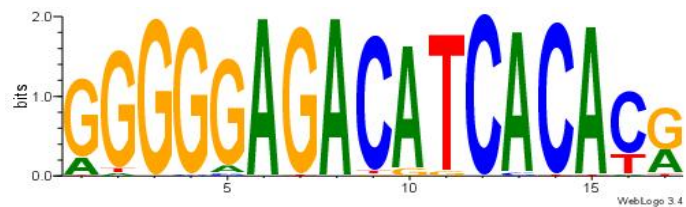
Reverse complement motif      Consensus sequence:  
TGGCTTCACCCAGTGGATCC



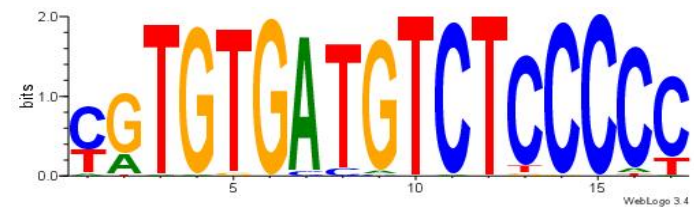
Dataset #: 1  
 Motif ID: 279  
 Motif name: Motif 279  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 4  
 Number of overlap: 10  
 Similarity score: 0.0624843

Alignment:  
 MGTGTGATGTCTCCCCC  
 ---TGACGTCACS-----

Original motif      Consensus sequence: GGGGGAGACATCACACR

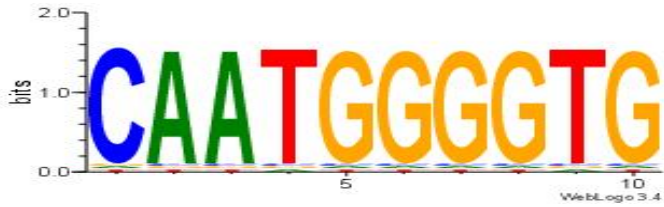


Reverse complement motif      Consensus sequence: MGTGTGATGTCTCCCCC

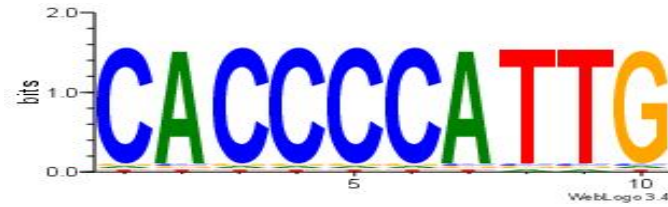


**Dataset #: 1      Motif ID: 360      Motif name: Motif 360**

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

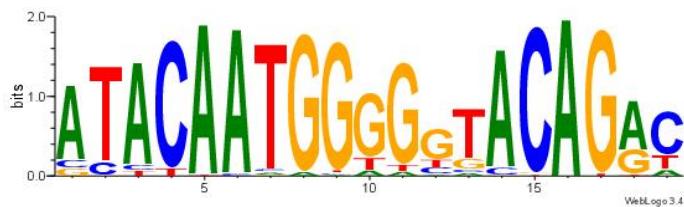
Alignment:

```

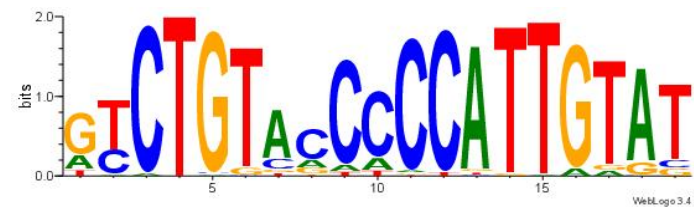
ATACAATGGGGGTACAGRC
---CAATGGGGTG-----

```

Original motif    Consensus sequence: ATACAATGGGGGTACAGRC



Reverse complement motif    Consensus sequence: GKCTGTACCCCATTTGTAT

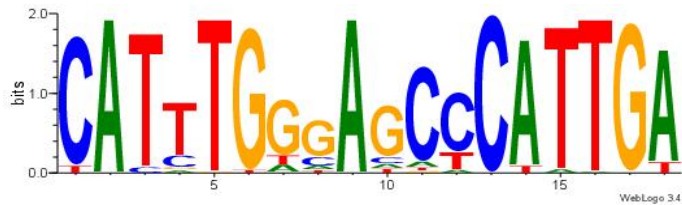


Dataset #: 1  
 Motif ID: 284  
 Motif name: Motif 284  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 2  
 Number of overlap: 10  
 Similarity score: 0.0546882

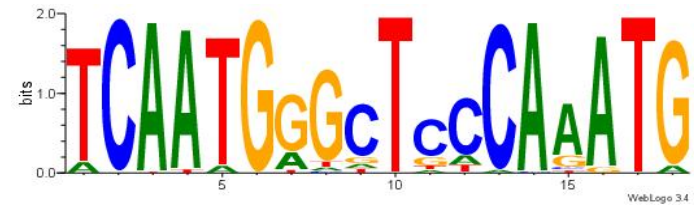
Alignment:

TCAATGGGCTCCCAAATG  
 -----CAATGGGGTG--

Original motif      Consensus sequence: CATTGGGAGCCCATTGA



Reverse complement motif      Consensus sequence: TCAATGGGCTCCCAAATG



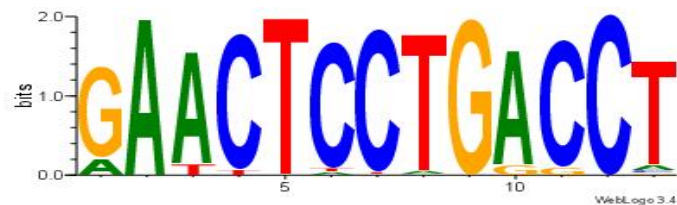
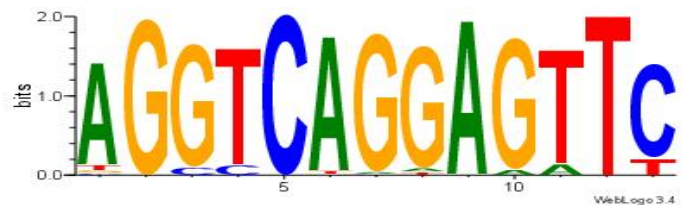

---

**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)

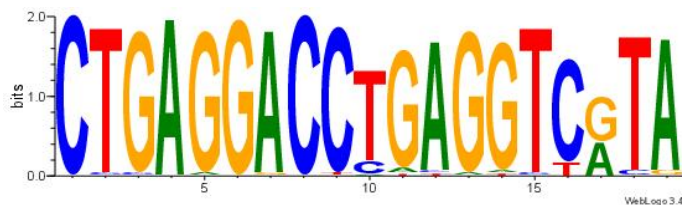
Dataset #: 1  
 Motif ID: 291  
 Motif name: Motif 291  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 4  
 Number of overlap: 13  
 Similarity score: 0.0663108

#### Alignment:

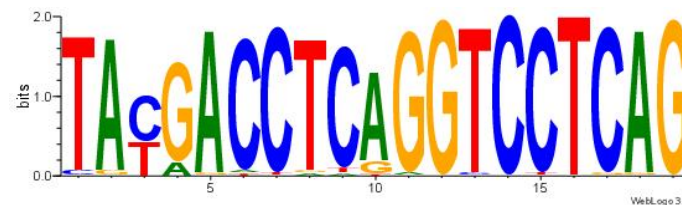
```

TAMGACCTCAGGTCCTCAG
---GAACTCCTGACCT---
  
```

Original motif      Consensus sequence: CTGAGGACCTGAGGTCRTA



Reverse complement motif      Consensus sequence: TAMGACCTCAGGTCCTCAG

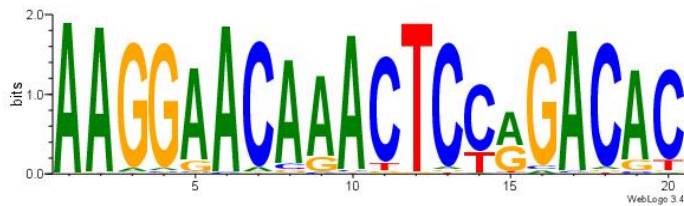


Dataset #: 1  
 Motif ID: 234  
 Motif name: Motif 234  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 8  
 Number of overlap: 13  
 Similarity score: 0.0705628

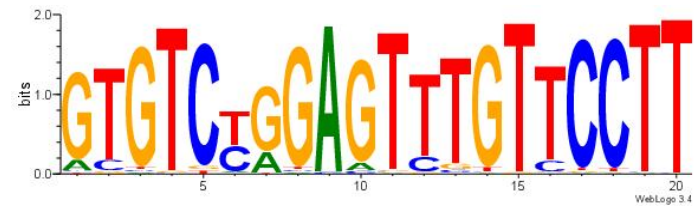
Alignment:

AAGGAACAACTCCRGACAC  
 GAACTCCTGACCT-----

Original motif      Consensus sequence: AAGGAACAACTCCRGACAC



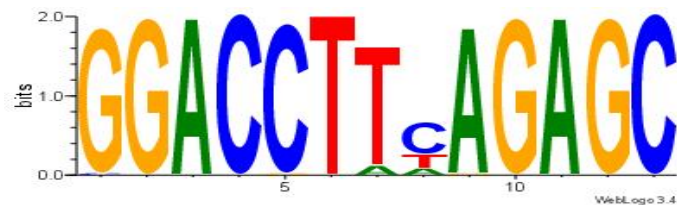
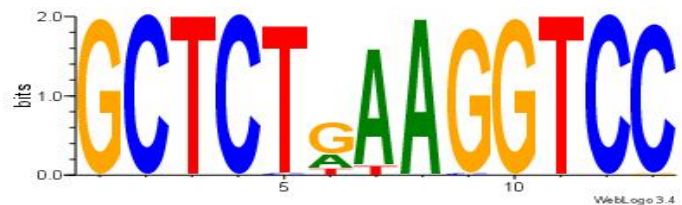
Reverse complement motif      Consensus sequence: GTGTCKGGAGTTTGTTCCTT



**Dataset #: 1      Motif ID: 362      Motif name: Motif 362**

Original motif      Consensus sequence: GCTCTGAAGGTCC

Reverse complement motif      Consensus sequence: GGACCTTCAGAGC

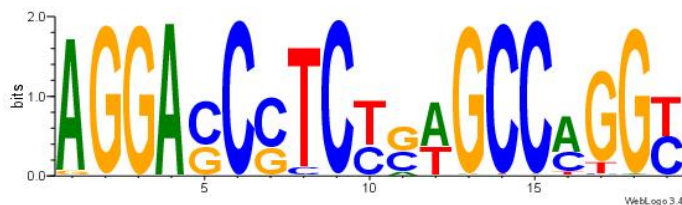


**Best Matches for Motif ID 362 (Highest to Lowest)**

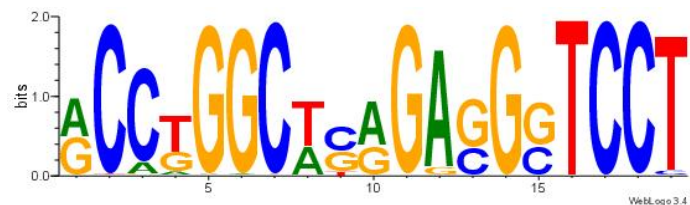
Dataset #: 1  
 Motif ID: 10  
 Motif name: Motif 10  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 2  
 Number of overlap: 13  
 Similarity score: 0.0695238

Alignment:  
 MCCYGGCWSMGASGSTCCT  
 -GCTCTGAAGGTCC-----

Original motif      Consensus sequence: AGGASCSTCYSWGCCMGY



Reverse complement motif      Consensus sequence: MCCYGGCWSMGASGSTCCT

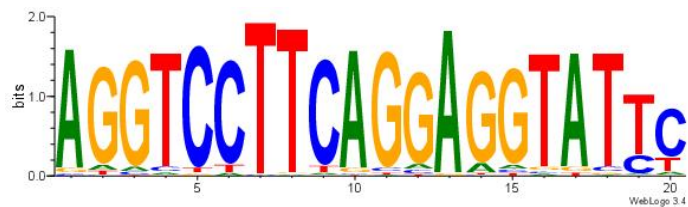


Dataset #: 1  
 Motif ID: 179  
 Motif name: Motif 179  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 2  
 Number of overlap: 13  
 Similarity score: 0.0873004

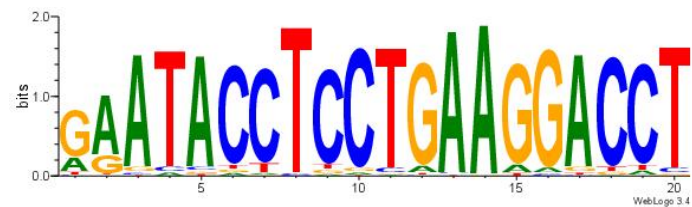
Alignment:

GAATACCTCCTGAAGGACCT  
 -GCTCTGAAGGTCC-----

Original motif      Consensus sequence: AGGTCCTCAGGAGGTATTC



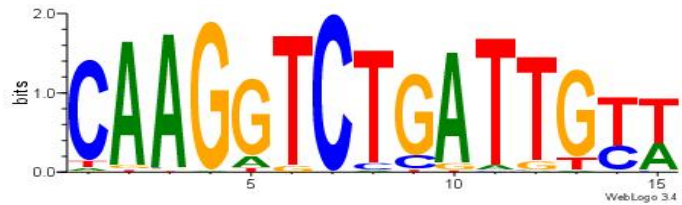
Reverse complement motif      Consensus sequence: GAATACCTCCTGAAGGACCT



**Dataset #: 1      Motif ID: 363      Motif name: Motif 363**

Original motif      Consensus sequence: CAAGTCTGATTGTW

Reverse complement motif      Consensus sequence: WACAATCAGACCT

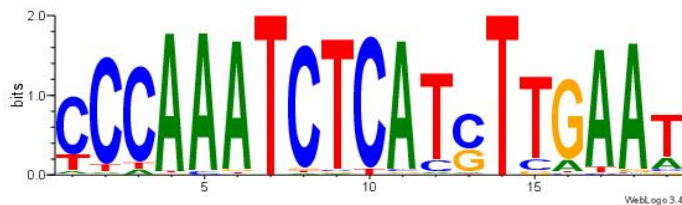


**Best Matches for Motif ID 363 (Highest to Lowest)**

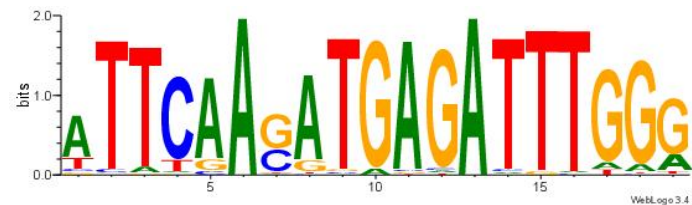
Dataset #: 1  
 Motif ID: 227  
 Motif name: Motif 227  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 4  
 Number of overlap: 15  
 Similarity score: 0.0937179

Alignment:  
 ATTCAASATGAGATTTGGG  
 -CAAGGTCTGATTGTW---

Original motif      Consensus sequence: CCCAAATCTCATSTTGAAT



Reverse complement motif      Consensus sequence: ATTCAASATGAGATTTGGG

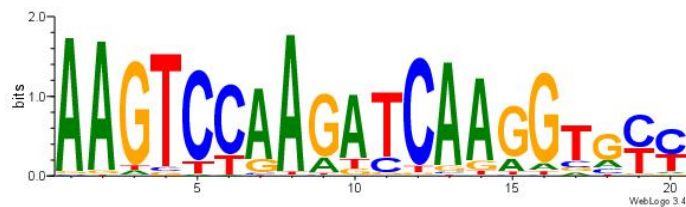


Dataset #: 1  
 Motif ID: 119  
 Motif name: Motif 119  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 15  
 Similarity score: 0.0941068

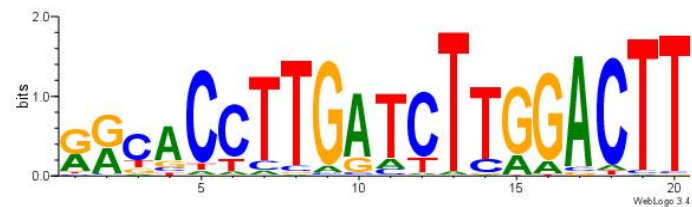
Alignment:

AAGTCCAAGATCAAGGTGY  
 -----CAAGGTCTGATTGTW

Original motif      Consensus sequence: AAGTCCAAGATCAAGGTGY



Reverse complement motif      Consensus sequence: KKCACCTTGATCTTGGACTT

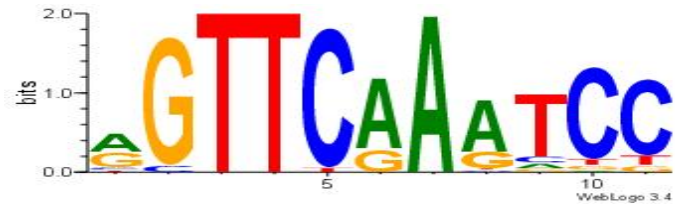
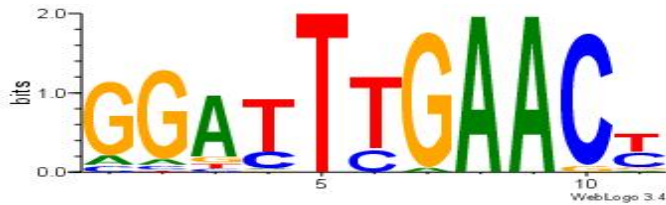



---

**Dataset #: 1      Motif ID: 364      Motif name: Motif 364**

Original motif      Consensus sequence: GGATTTGAACY

Reverse complement motif      Consensus sequence: MGTTCAAATCC

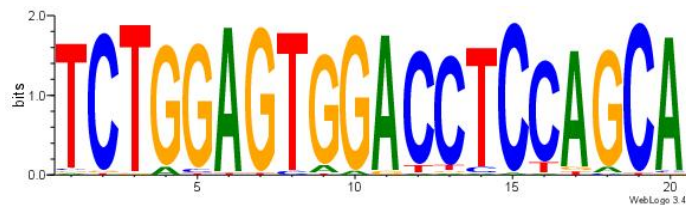


**Best Matches for Motif ID 364 (Highest to Lowest)**

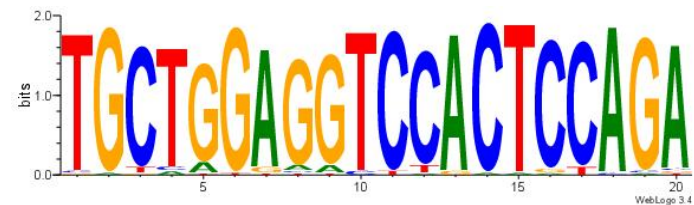
Dataset #: 1  
 Motif ID: 350  
 Motif name: Motif 350  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 7  
 Number of overlap: 11  
 Similarity score: 0.0565307

Alignment:  
 TGCTGGAGGTCCACTCCAGA  
 -----MGTTCAAATCC----

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

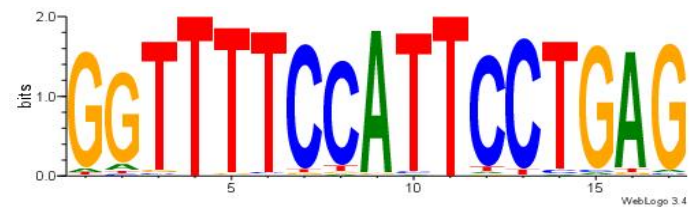
Alignment:

GGTTTTCCATTCCCTGAG  
 --MGTTCAAATCC-----

Original motif    Consensus sequence: CTCAGGAATGGAAAACC



Reverse complement motif    Consensus sequence: GGTTTTCCATTCCCTGAG



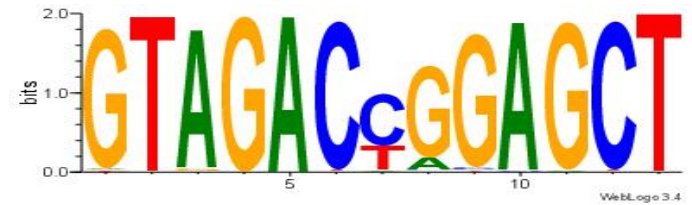
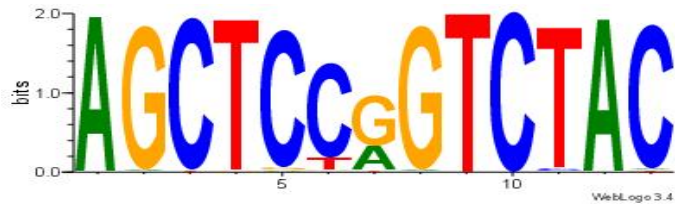

---

**Dataset #: 1      Motif ID: 365      Motif name: Motif 365**

Original motif    Consensus sequence: AGCTCCGGTCTAC

Reverse complement motif    Consensus sequence: GTAGACCGGAGCT



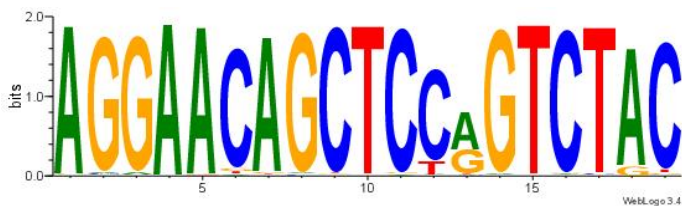


**Best Matches for Motif ID 365 (Highest to Lowest)**

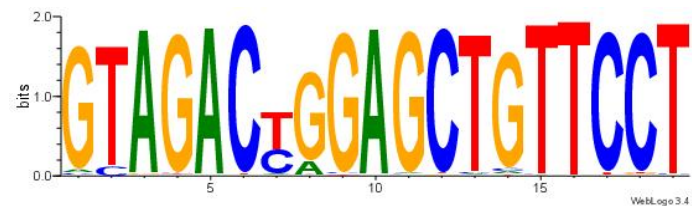
Dataset #: 1  
 Motif ID: 62  
 Motif name: Motif 62  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 7  
 Number of overlap: 13  
 Similarity score: 0.00780309

Alignment:  
 AGGAACAGCTCCRGCTCTAC  
 -----AGCTCCGGTCTAC

Original motif      Consensus sequence: AGGAACAGCTCCRGCTCTAC



Reverse complement motif      Consensus sequence: GTAGACKGGAGCTGTTCCCT

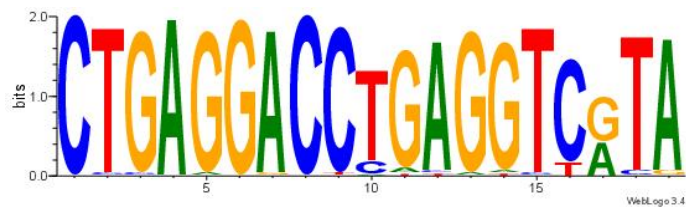


Dataset #: 1  
 Motif ID: 291  
 Motif name: Motif 291  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 3  
 Number of overlap: 13  
 Similarity score: 0.0802174

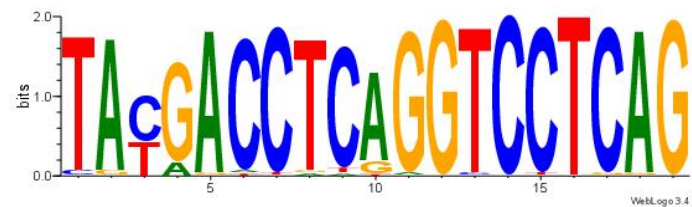
Alignment:

CTGAGGACCTGAGGTCRТА  
 ----GTAGACCGGAGCT--

Original motif      Consensus sequence: CTGAGGACCTGAGGTCRТА



Reverse complement motif      Consensus sequence: TAMGACCTCAGGTCCTCAG



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 Runtime: 460.96 seconds

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