



MOTIFSIM - MOTIF SIMilarity Detection Tool

Version 2.1

INPUT

Input Parameters

Number of files:	4
Number of top significant motifs:	10
Number of best matches:	5
Similarity cutoff >=	0.75
Matching motif database:	UniProbe Mus Musculus
Phylogenetic tree:	Yes
Combined similar motifs:	Yes
Output file type:	All
Output file format:	All

Input files and motif counts

File name	Count of motifs	Dataset number
DREME_DM254.txt	45	1
MEME-CHIP_DM254.txt	24	2
PScanChIP_DM254.txt	63	3
RSAT_peak-motifs_DM254.txt	39	4

RESULTS

Top 10 Significant Motifs - Global Matching (Highest to Lowest)

Dataset #: 2 Motif ID: 46 Motif name: Motif 46

Original motif Consensus sequence: AGRKGGCR



Reverse complement motif Consensus sequence: KGCCYKCT



Best Matches for Top Significant Motif ID 46 (Highest to Lowest)

Dataset #:	1
Motif ID:	1
Motif name:	Motif 1
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	8
Similarity score:	0

Alignment:
AGRKGGCR
AGRKGGCR

Original motif Consensus sequence: AGRKGGCR

Reverse complement motif Consensus sequence: KGCCYKCT



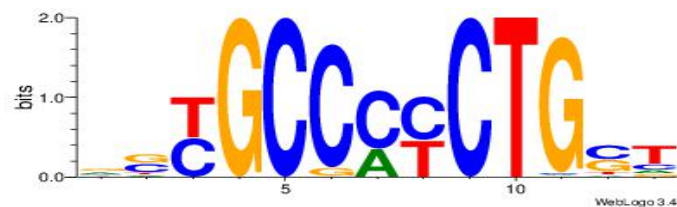
Dataset #: 4
 Motif ID: 147
 Motif name: asCAGrkGGCrSy
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 8
 Similarity score: 0.00651548

Alignment:
 ASCAGRGGGCRSB
 ---AGRKGCCR--

Original motif Consensus sequence: ASCAGRGGGCRSB



Reverse complement motif Consensus sequence: BSKGCCCMCTGST



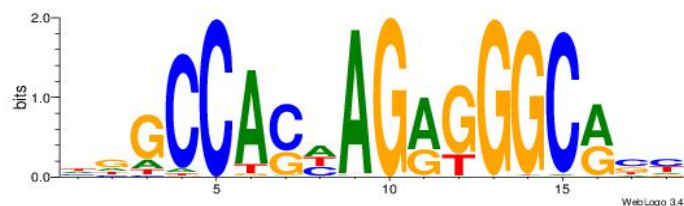
Dataset #: 4
 Motif ID: 165

Motif name: wgGCCAshAGrGGGCrSy
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 9
 Number of overlap: 8
 Similarity score: 0.0102443

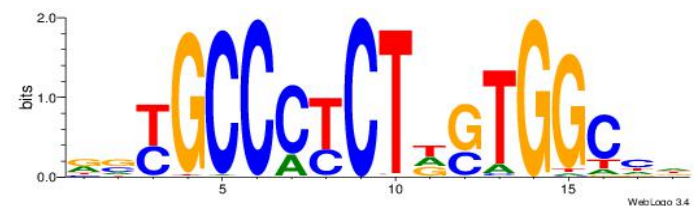
Alignment:

KBKGCCCKCTHGTGGCHH
 --KGCCYKCT-----

Original motif Consensus sequence: HDGCCACHAGRGGGCRBY



Reverse complement motif Consensus sequence: KBKGCCCKCTHGTGGCHH



Dataset #: 4
 Motif ID: 166
 Motif name: CasCAGrGGGCrSy
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3
 Number of overlap: 8
 Similarity score: 0.0104954

Alignment:

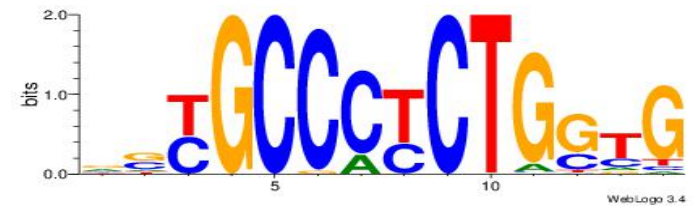
BSKGCCCKCTGGTG

--KGCCYKCT----

Original motif Consensus sequence: CACCAGRGGGCRSB



Reverse complement motif Consensus sequence: BSKGCCCKCTGGT



Dataset #:	4
Motif ID:	163
Motif name:	gwGGCCAGmAGAGGGCrby
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	3
Number of overlap:	8
Similarity score:	0.0165822

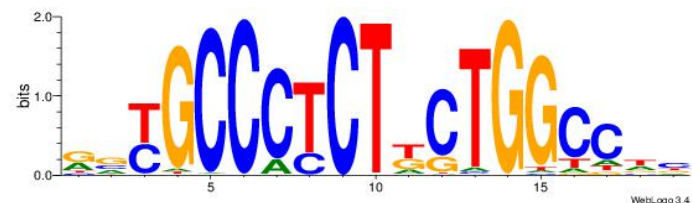
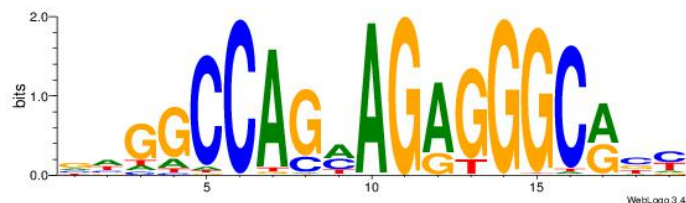
Alignment:

KBKGCCCTCTYCTGGCCHV

--KGCCYKCT-----

Original motif Consensus sequence: VHGGCCAGMAGAGGGCRBY

Reverse complement motif Consensus sequence:
KBKGCCCTCTYCTGGCCHV



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

Original motif Consensus sequence: AAATAH



Reverse complement motif Consensus sequence: DTATTT



Best Matches for Top Significant Motif ID 8 (Highest to Lowest)

Dataset #:	4
Motif ID:	150
Motif name:	waATwAAAATAww
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2
Number of overlap:	6
Similarity score:	0.00224204

Alignment:
 DHATWAAAATAHD
 -----AAATAH-

bits

2.0

1.0

0.0

5 10 15

Webb 2003.4

Alignment:

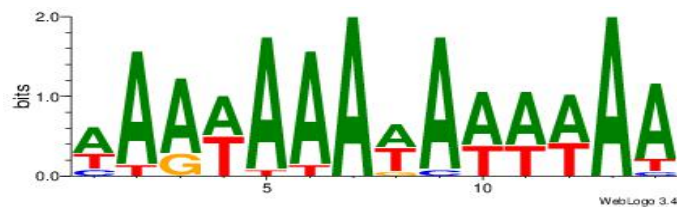
```
WWTAAAAATAD
-----AAATAH
```

Dataset #: 2
 Motif ID: 68
 Motif name: Motif 68
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 5
 Number of overlap: 6
 Similarity score: 0.0128826

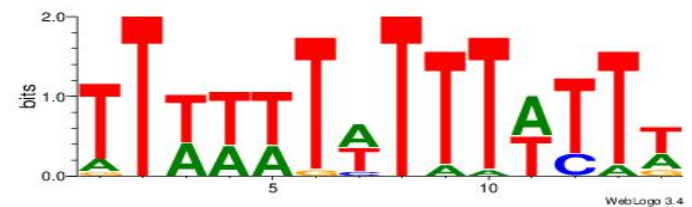
Alignment:

WAAWAAAWAWWWAA
 ----AAATAH-----

Original motif Consensus sequence: WAAWAAAWAWWWAA



Reverse complement motif Consensus sequence: TTWWWTWTTTWTTW



Dataset #: 2
 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: 1

Number of overlap: 6
Similarity score: 0.0167304

Alignment:
AAATAAAW
AAATAH--

Original motif Consensus sequence: AAATAAAW



Reverse complement motif Consensus sequence: WTTTATTT

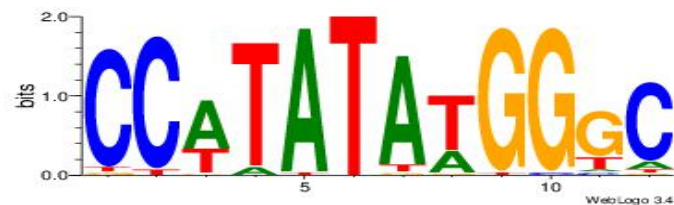
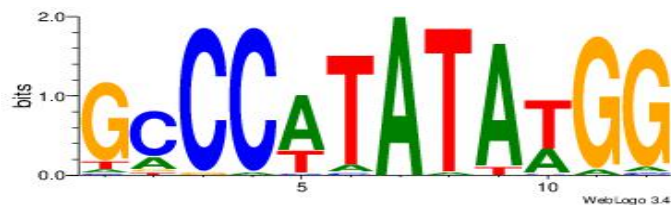


Dataset #: 3
Motif ID: 118
Motif name: SRF
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 3
Number of overlap: 6
Similarity score: 0.0210491

Alignment:
GCCCATATATGG
----AAATAH--

Original motif Consensus sequence: GCCCATATATGG

Reverse complement motif Consensus sequence: CCATATATGGGC



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

Original motif Consensus sequence: CACGTR



Reverse complement motif Consensus sequence: MACGTG



Best Matches for Top Significant Motif ID 20 (Highest to Lowest)

Dataset #:	3
Motif ID:	71
Motif name:	Arnt
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	6
Similarity score:	0

Alignment:

CACGTG

CACGTR

Original motif Consensus sequence: CACGTG



Reverse complement motif Consensus sequence: CACGTG



Dataset #: 3
Motif ID: 95
Motif name: MYCMAX
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 3
Number of overlap: 6
Similarity score: 0.0102183

Alignment:

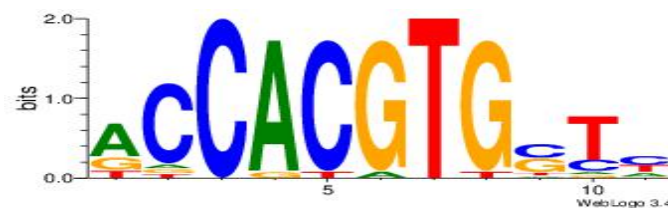
RASCACGTGGT

---MACGTG---

Original motif Consensus sequence: RASCACGTGGT



Reverse complement motif Consensus sequence: ACCACGTGSTM



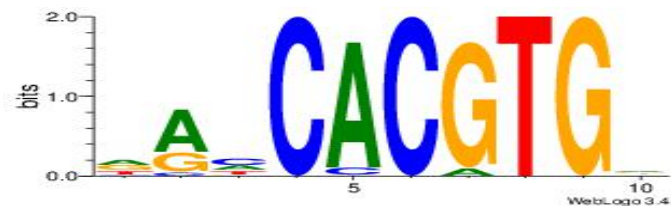
Dataset #: 3
 Motif ID: 91
 Motif name: MAX
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 4
 Number of overlap: 6
 Similarity score: 0.011152

Alignment:

BCACGTGDTD

-CACGTR---

Original motif Consensus sequence: DAHCACGTGD



Reverse complement motif Consensus sequence: BCACGTGDTD



Dataset #: 3
 Motif ID: 126
 Motif name: USF1
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 6

Similarity score: 0.0131944

Alignment:

MCACGTG

-CACGTR

Original motif Consensus sequence: CACGTGR



Reverse complement motif Consensus sequence: MCACGTG



Dataset #:	3
Motif ID:	94
Motif name:	Myc
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	3
Number of overlap:	6
Similarity score:	0.0253396

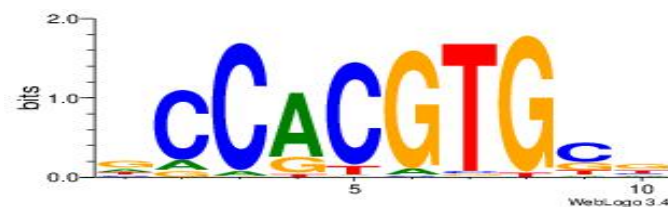
Alignment:

DCCACGTGCV

--CACGTR--

Original motif Consensus sequence: VGCACGTGGH

Reverse complement motif Consensus sequence: DCCACGTGCV



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

Original motif Consensus sequence: AGRKGGCR



Reverse complement motif Consensus sequence: KGCCYKCT



Best Matches for Top Significant Motif ID 1 (Highest to Lowest)

Dataset #:	2
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:	8
Similarity score:	0

Alignment:
 AGRKGGCR
 AGRKGGCR

Original motif Consensus sequence: AGRKGGCR



Reverse complement motif Consensus sequence: KGCCYKCT



Dataset #: 4
Motif ID: 147
Motif name: asCAGrkGGCrSy
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: 0.00628523

Alignment:

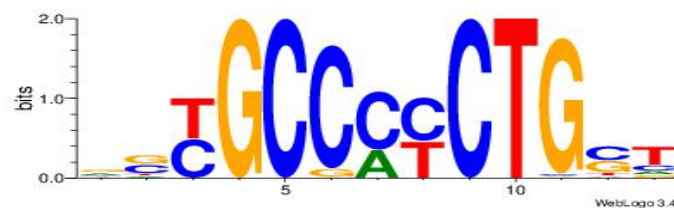
ASCAGRGGGCRSB

---AGRKGGCR---

Original motif Consensus sequence: ASCAGRGGGCRSB



Reverse complement motif Consensus sequence: BSKGCCCCMCTGST

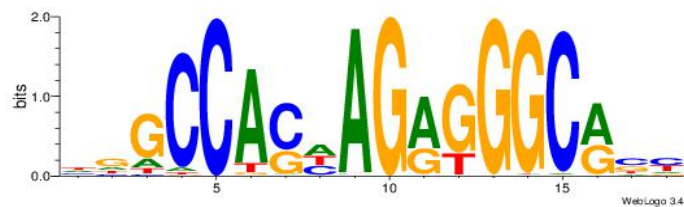


Dataset #: 4
 Motif ID: 165
 Motif name: wgGCCAshAGrGGGCrSy
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3
 Number of overlap: 8
 Similarity score: 0.0102152

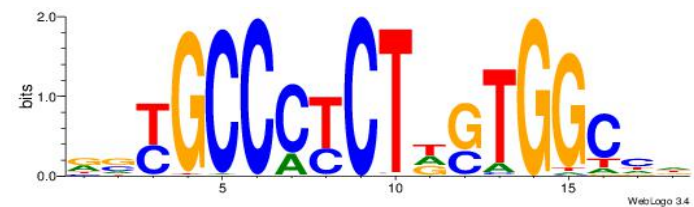
Alignment:

KBKGCCCKCTHGTGGCHH
 --KGCCYKCT-----

Original motif Consensus sequence: HDGCCACHAGRGGGCRBY



Reverse complement motif Consensus sequence: KBKGCCCKCTHGTGGCHH



Dataset #: 4
 Motif ID: 166
 Motif name: CasCAGrGGGCrSy
 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: 0.0106761

Alignment:
CACCAGRGGGCRSB
----AGRKGCCR--

Original motif Consensus sequence: CACCAGRGGGCRSB



Reverse complement motif Consensus sequence: BSKGCCCKCTGGT

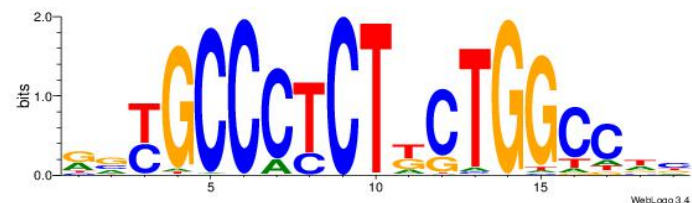
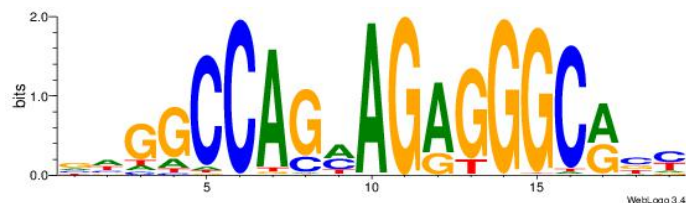


Dataset #: 4
Motif ID: 163
Motif name: gwGGCCAGmAGAGGGCrby
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 3
Number of overlap: 8
Similarity score: 0.016658

Alignment:
KBKGCCCTCTYCTGGCCHV
--KGCCYKCT-----

Original motif Consensus sequence: VHGGCCAGMAGAGGGCRBY

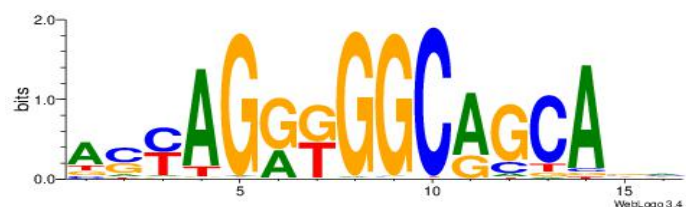
Reverse complement motif Consensus sequence:
KBKGCCCTCTYCTGGCCHV



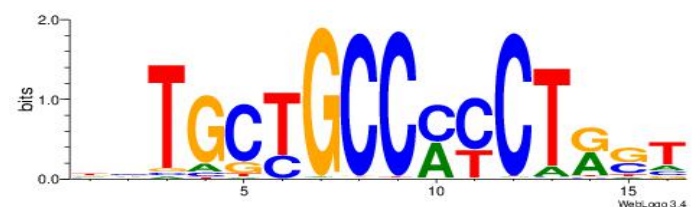
Dataset #: 4
 Motif ID: 164
 Motif name: asyAGrkGGCRGCAGa
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 8
 Similarity score: 0.0201849

Alignment:
 ASYAGRKGGCAGCABH
 ---AGRKGGCR-----

Original motif Consensus sequence: ASYAGRKGGCAGCABH



Reverse complement motif Consensus sequence: HBTGCTGCCYMCTKST



Dataset #: 3 Motif ID: 127 Motif name: YY1

Original motif Consensus sequence: RCCATB



Reverse complement motif Consensus sequence: BATGGM



Best Matches for Top Significant Motif ID 127 (Highest to Lowest)

Dataset #:	2
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:	2
Number of overlap:	6
Similarity score:	0.00122549

Alignment:
AGATGGY
BATGGM-

Original motif Consensus sequence: AGATGGY



Reverse complement motif Consensus sequence: KCCATCT



Dataset #: 1
 Motif ID: 12
 Motif name: Motif 12
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 6
 Similarity score: 0.00857843

Alignment:
 GAGCCATC
 RCCATB--

Original motif Consensus sequence: GATGGCTC



Reverse complement motif Consensus sequence: GAGCCATC

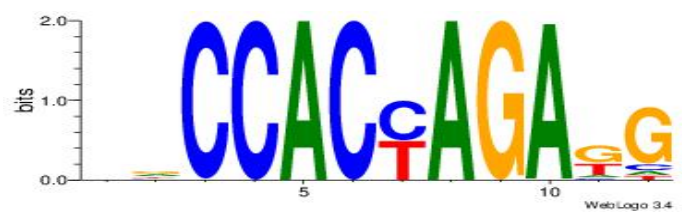


Dataset #: 4
 Motif ID: 145
 Motif name: grCCACyAGAkG
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 6

Similarity score: 0.022036

Alignment:
CYTCTKGTGGHH
-----BATGGM-

Original motif Consensus sequence: DDCCACYAGAKG



Reverse complement motif Consensus sequence: CYTCTKGTGGHH

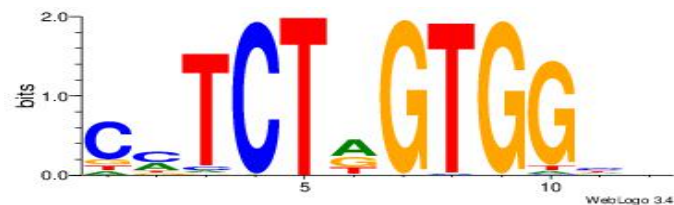
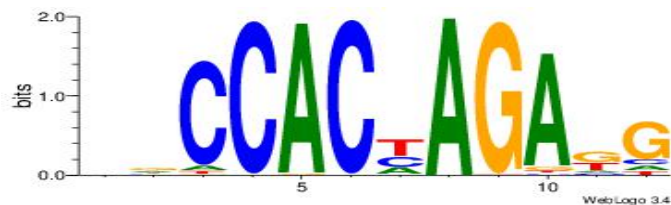


Dataset #: 4
Motif ID: 138
Motif name: grCCACyAGAkG
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 2
Number of overlap: 6
Similarity score: 0.0223679

Alignment:
DDCCACYAGAKG
-RCCATB-----

Original motif Consensus sequence: DDCCACYAGAKG

Reverse complement motif Consensus sequence: CYTCTMGTGGHH

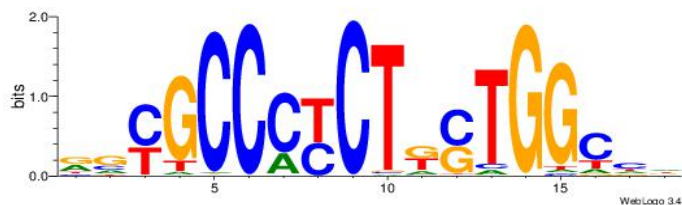


Dataset #: 4
 Motif ID: 156
 Motif name: rgyGCCMyCTksTGGccd
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3
 Number of overlap: 6
 Similarity score: 0.0275501

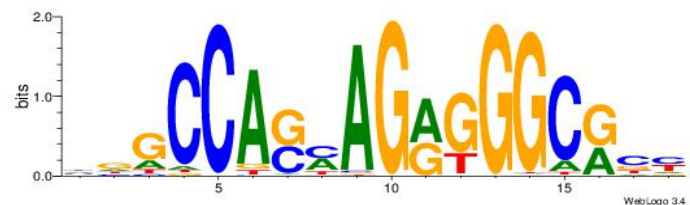
Alignment:

DDGCCASYAGMGGGCKVM
 --RCCATB-----

Original motif Consensus sequence: RYVGCCCYCTKSTGGCHD

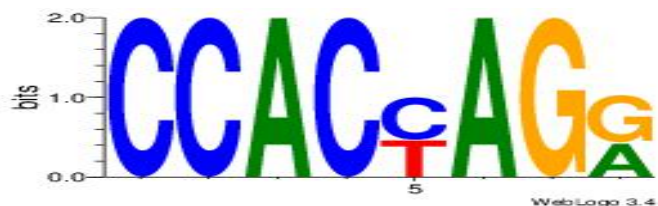


Reverse complement motif Consensus sequence: DDGCCASYAGMGGGCKVM



Dataset #: 2 Motif ID: 48 Motif name: Motif 48

Original motif Consensus sequence: CCACYAGR



Reverse complement motif Consensus sequence: MCTKGTGG

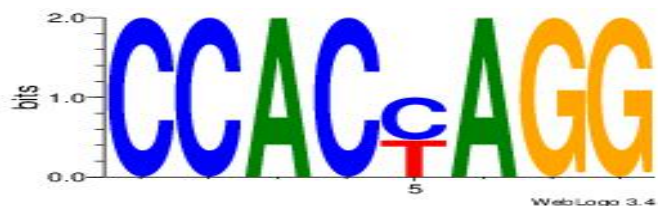


Best Matches for Top Significant Motif ID 48 (Highest to Lowest)

Dataset #: 1
Motif ID: 21
Motif name: Motif 21
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: 0.00903109

Alignment:
CCACYAGG
CCACYAGR

Original motif Consensus sequence: CCACYAGG



Reverse complement motif Consensus sequence: CCTKGTGG

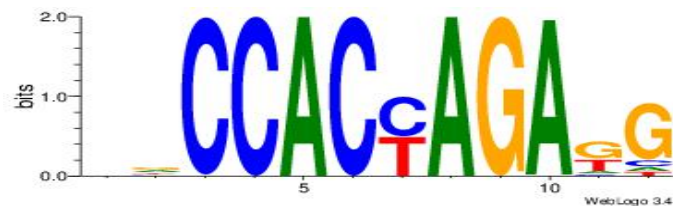


Dataset #: 4
 Motif ID: 145
 Motif name: grCCACyAGAkG
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 8
 Similarity score: 0.0155354

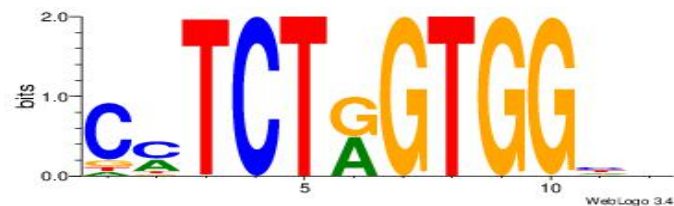
Alignment:

DDCCACYAGAKG
 --CCACYAGR--

Original motif Consensus sequence: DDCCACYAGAKG



Reverse complement motif Consensus sequence: CYTCTKGTGGHH



Dataset #: 4
 Motif ID: 158
 Motif name: grCCACwAGrk
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 8

Similarity score: 0.0192652

Alignment:
DDCCACWAGRK
--CCACYAGR--

Original motif Consensus sequence: DDCCACWAGRK



Reverse complement motif Consensus sequence: YMCTWGTGGHH

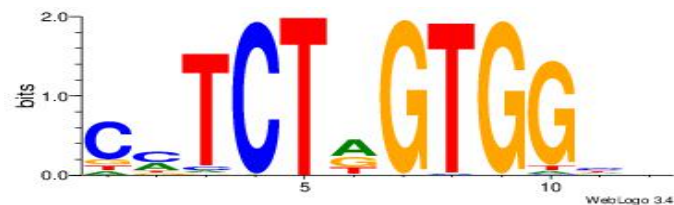
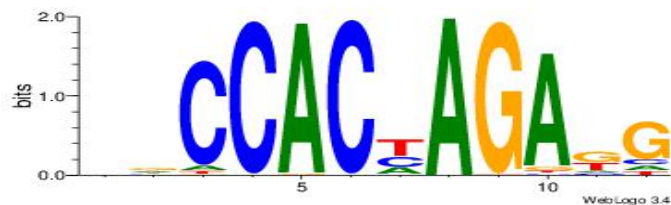


Dataset #: 4
Motif ID: 138
Motif name: grCCACyAGAkG
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 3
Number of overlap: 8
Similarity score: 0.0244381

Alignment:
DDCCACYAGAKG
--CCACYAGR--

Original motif Consensus sequence: DDCCACYAGAKG

Reverse complement motif Consensus sequence: CYTCTMGTGGHH

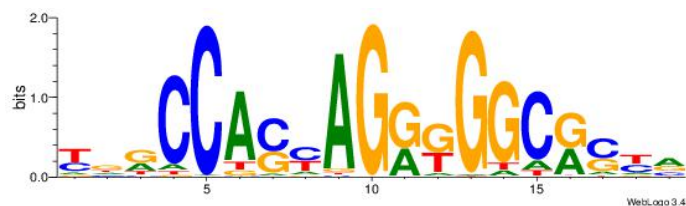


Dataset #: 3
 Motif ID: 74
 Motif name: CTCF
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 9
 Number of overlap: 8
 Similarity score: 0.0284404

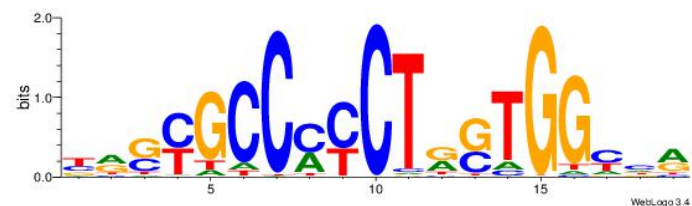
Alignment:

BSMGCCYMCTKSTGGMHM
 -----MCTKGTGG---

Original motif Consensus sequence: YDRCCASYAGRKGGCRSYV



Reverse complement motif Consensus sequence: BSMGCCYMCTKSTGGMHM



Dataset #: 2 Motif ID: 65 Motif name: Motif 65

Original motif Consensus sequence: ARAACA



Reverse complement motif Consensus sequence: TGTTMT



Best Matches for Top Significant Motif ID 65 (Highest to Lowest)

Dataset #:	4
Motif ID:	141
Motif name:	raCAAAACam
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	4
Number of overlap:	6
Similarity score:	0.00122368

Alignment:

DACAAAACAH

---ARAACA-

Original motif Consensus sequence: DACAAAACAH



Reverse complement motif Consensus sequence: HTGTTTTGTD



Dataset #: 1
 Motif ID: 44
 Motif name: Motif 44
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 6
 Similarity score: 0.0101983

Alignment:
 GDAAACA
 -ARAACA

Original motif Consensus sequence: GDAAACA



Reverse complement motif Consensus sequence: TGTTTDC



Dataset #: 4
 Motif ID: 159
 Motif name: kkAAGAGCAsy
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 6

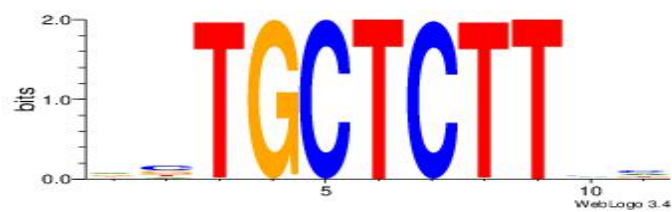
Similarity score: 0.0232212

Alignment:
DBAAGAGCAVH
---ARAACA--

Original motif Consensus sequence: DBAAGAGCAVH



Reverse complement motif Consensus sequence: HVTGCTCTTBH

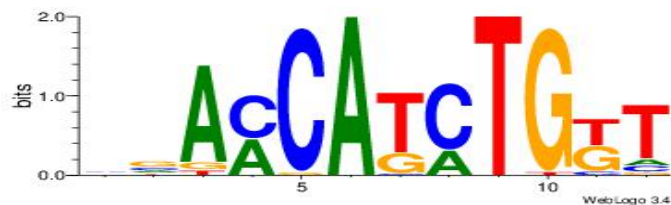


Dataset #: 3
Motif ID: 121
Motif name: TAL1TCF3
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 7
Number of overlap: 6
Similarity score: 0.0330056

Alignment:
HVAMCATCTGKT
ARAACA-----

Original motif Consensus sequence: HVAMCATCTGKT

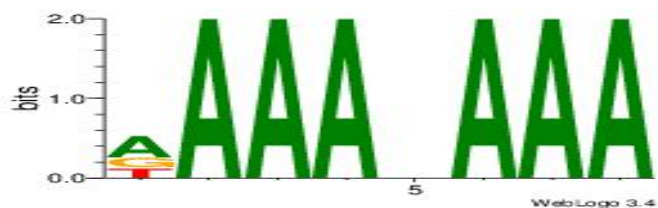
Reverse complement motif Consensus sequence: ARCAGATGRTVD



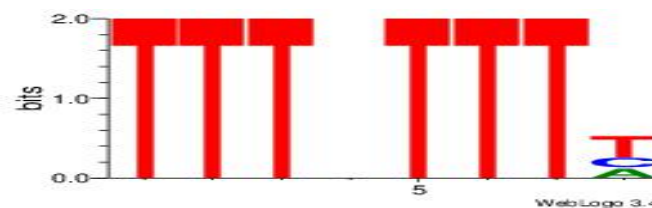
Dataset #: 1
 Motif ID: 2
 Motif name: Motif 2
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 6
 Similarity score: 0.0333069

Alignment:
 AAAAHAAA
 ARAACA--

Original motif Consensus sequence: AAAAHAAA



Reverse complement motif Consensus sequence: TTTDTTTT



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

Original motif Consensus sequence: CCCCDCCC



Reverse complement motif Consensus sequence: GGGDGGGG



Best Matches for Top Significant Motif ID 5 (Highest to Lowest)

Dataset #:	2
Motif ID:	59
Motif name:	Motif 59
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	8
Similarity score:	0.00363191

Alignment:
 CCCCRCRCC
 CCCCDCCC

Original motif Consensus sequence: CCCCRCRCC



Reverse complement motif Consensus sequence: GGGKGGGG

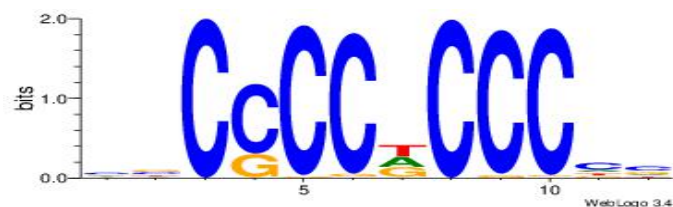


Dataset #: 4
 Motif ID: 155
 Motif name: csCSCCdCCCcs
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 8
 Similarity score: 0.00464015

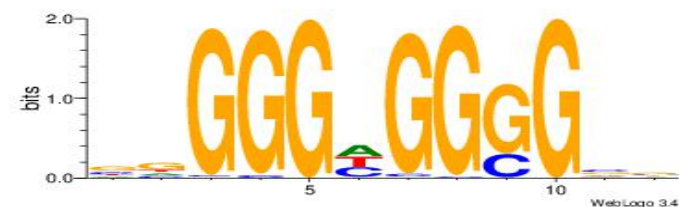
Alignment:

VBCCCCDCCCHV
 --CCCCDCCC--

Original motif Consensus sequence: VBCCCCDCCCHV



Reverse complement motif Consensus sequence: VDGGGDGGGGBV

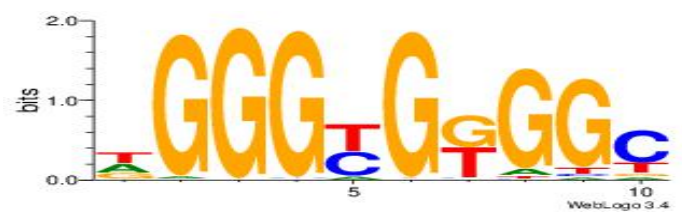


Dataset #: 3
 Motif ID: 89
 Motif name: Klf4
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 8

Similarity score: 0.0352587

Alignment:
GCCYCMCCCD
-CCCCDCCC-

Original motif Consensus sequence: DGGYGKGGC



Reverse complement motif Consensus sequence: GCCYCMCCCD



Dataset #: 4
Motif ID: 154
Motif name: csCsCCTCCcc
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: 0.0361349

Alignment:
VBCCCCTCCHB
--CCCCDCCC-

Original motif Consensus sequence: VBCCCCTCCHB

Reverse complement motif Consensus sequence: BDGGAGGGGBV



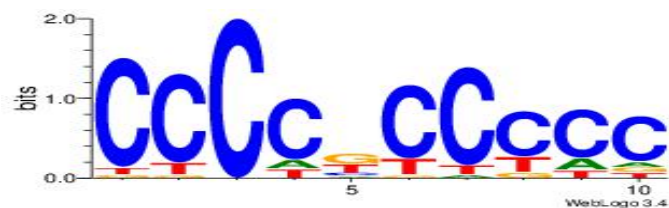
Dataset #: 3
 Motif ID: 116
 Motif name: SP1
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 8
 Similarity score: 0.0368066

Alignment:

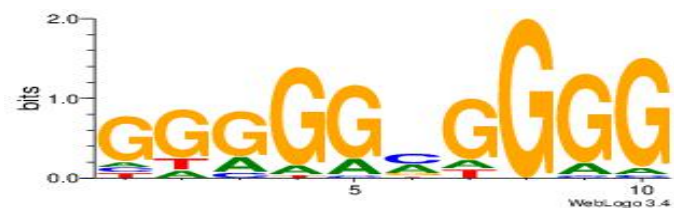
CCCCKCCCCC

CCCDCCC--

Original motif Consensus sequence: CCCCKCCCCC



Reverse complement motif Consensus sequence: GGGGYGGGG



Dataset #: 3 Motif ID: 72 Motif name: ArntAhr

Original motif Consensus sequence: YGCGTG



Reverse complement motif Consensus sequence: CACGCM



Best Matches for Top Significant Motif ID 72 (Highest to Lowest)

Dataset #: 4
 Motif ID: 134
 Motif name: ssCGwGCGss
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 5
 Number of overlap: 6
 Similarity score: 0.0128947

Alignment:

BSCGWGCGBV
 YGCGTG----

Original motif Consensus sequence: BSCGWGCGBV



Reverse complement motif Consensus sequence: VBCGWCGBS



Dataset #: 1
 Motif ID: 20
 Motif name: Motif 20
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 6
 Similarity score: 0.0206428

Alignment:

MACGTG

YGCGTG

Original motif Consensus sequence: CACGTR



Reverse complement motif Consensus sequence: MACGTG



Dataset #: 1
 Motif ID: 42
 Motif name: Motif 42
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 6

Similarity score: 0.0259081

Alignment:
CSGCGCG
YGCGTG-

Original motif Consensus sequence: CGCGCSG



Reverse complement motif Consensus sequence: CSGCGCG



Dataset #: 4
Motif ID: 152
Motif name: yrCATGCAyr
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 3
Number of overlap: 6
Similarity score: 0.0279287

Alignment:
BRCATGCABD
--CACGCM--

Original motif Consensus sequence: BRCATGCABD

Reverse complement motif Consensus sequence: HVTGCATGKV



Dataset #: 2
 Motif ID: 57
 Motif name: Motif 57
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 6
 Similarity score: 0.0315171

Alignment:
 ACACACAY
 -CACGCM-

Original motif Consensus sequence: ACACACAY



Reverse complement motif Consensus sequence: KTGTGTGT



Dataset #: 3 Motif ID: 101 Motif name: NFIC

Original motif Consensus sequence: TTGGCD



Reverse complement motif Consensus sequence: DGCCAA



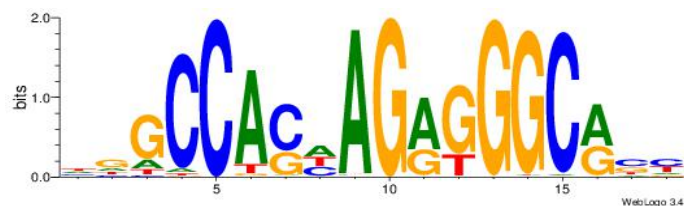
Best Matches for Top Significant Motif ID 101 (Highest to Lowest)

Dataset #: 4
 Motif ID: 165
 Motif name: wgGCCAshAGrGGGCrSy
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 12
 Number of overlap: 6
 Similarity score: 0.0215379

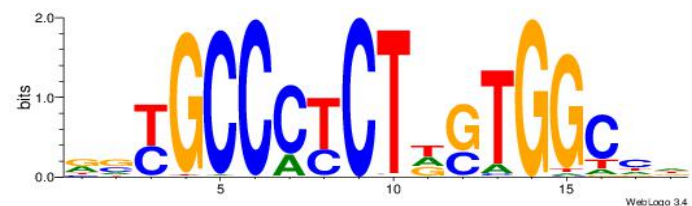
Alignment:

HDGCCACHAGRGGGCRBY
 -DGCCAA-----

Original motif Consensus sequence: HDGCCACHAGRGGGCRBY



Reverse complement motif Consensus sequence: KBKGCCCKCTHGTGGCHH

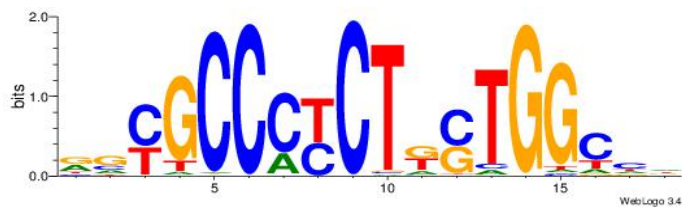


Dataset #: 4
 Motif ID: 156
 Motif name: rgyGCCMyCTksTGGccd
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 6
 Similarity score: 0.026631

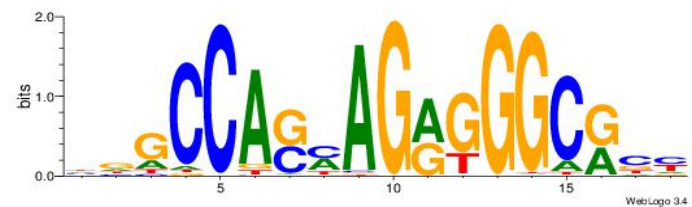
Alignment:

DDGCCASYAGMGGGCKVM
 -DGCCAA-----

Original motif Consensus sequence: RYVGCCCYCTKSTGGCHD



Reverse complement motif Consensus sequence: DDGCCASYAGMGGGCKVM



Dataset #: 4
 Motif ID: 151
 Motif name: agrCCAGmAGrg
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2

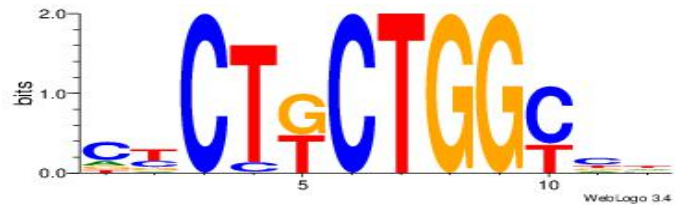
Number of overlap: 6
Similarity score: 0.0273632

Alignment:
CKCTRCTGGCVH
-----TTGGCD-

Original motif Consensus sequence: HVGCCAGMAGRG



Reverse complement motif Consensus sequence: CKCTRCTGGCVH



Dataset #: 1
Motif ID: 9
Motif name: Motif 9
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 2
Number of overlap: 6
Similarity score: 0.0280507

Alignment:
SWGCCACC
-DGCCAA-

Original motif Consensus sequence: GGTGGCWS

Reverse complement motif Consensus sequence: SWGCCACC

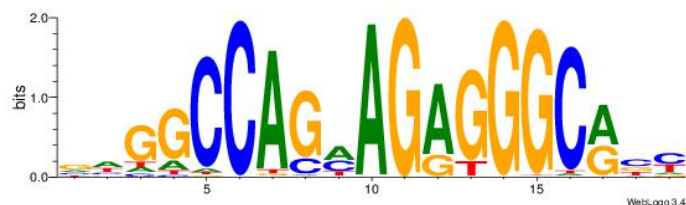


Dataset #: 4
 Motif ID: 163
 Motif name: gwGGCCAGmAGAGGGCrby
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 6
 Similarity score: 0.0280858

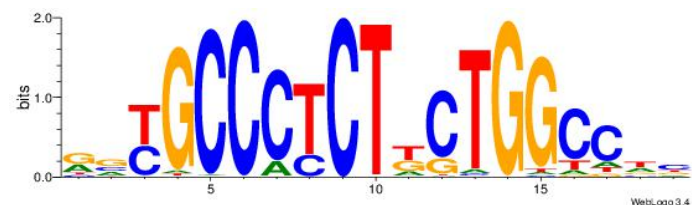
Alignment:

KBKGCCCTCTYCTGGCCHV
 -----TTGGCD--

Original motif Consensus sequence: VHGGCCAGMAGAGGGCRBY



Reverse complement motif Consensus sequence: KBKGCCCTCTYCTGGCCHV



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

Dataset #: 3 **Motif ID: 71** **Motif name: Arnt**

Original motif Consensus sequence: CACGTG



Reverse complement motif Consensus sequence: CACGTG



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

Dataset #:	1
Motif ID:	20
Motif name:	Motif 20
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	6
Similarity score:	0

Alignment:

MACGTG

CACGTG

Original motif Consensus sequence: CACGTR

Reverse complement motif Consensus sequence: MACGTG



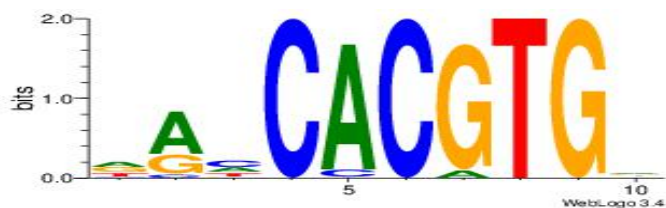
Dataset #: 3
 Motif ID: 91
 Motif name: MAX
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 6
 Similarity score: 0.00380329

Alignment:

BCACGTGDTD

-CACGTG---

Original motif Consensus sequence: DAHCACGTGD



Reverse complement motif Consensus sequence: BCACGTGDTD



Dataset #: 3
 Motif ID: 126

Motif name:	USF1
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	6
Similarity score:	0.00445689

Alignment:
MCACGTG
-CACGTG

Original motif Consensus sequence: CACGTGR



Reverse complement motif Consensus sequence: MCACGTG



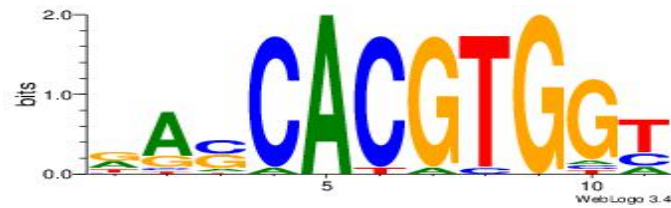
Dataset #:	3
Motif ID:	95
Motif name:	MYCMAX
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	3
Number of overlap:	6
Similarity score:	0.00495292

Alignment:

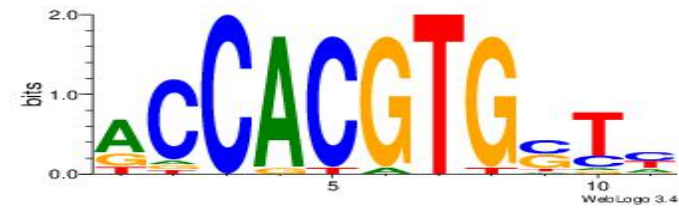
RASCACGTGGT

---CACGTG---

Original motif Consensus sequence: RASCACGTGGT



Reverse complement motif Consensus sequence: ACCACGTGSTM



Dataset #:	3
Motif ID:	94
Motif name:	Myc
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	3
Number of overlap:	6
Similarity score:	0.0173209

Alignment:

DCCACGTGCV

--CACGTG--

Original motif Consensus sequence: VGCACGTGGH

Reverse complement motif Consensus sequence: DCCACGTGCV



Dataset #: 2 Motif ID: 46 Motif name: Motif 46

Original motif Consensus sequence: AGRKGGCR



Reverse complement motif Consensus sequence: KGCCYKCT



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

Dataset #:	1
Motif ID:	1
Motif name:	Motif 1
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	8
Similarity score:	0

Alignment:
 AGRKGGCR
 AGRKGGCR

Original motif Consensus sequence: AGRKGGCR



Reverse complement motif Consensus sequence: KGCCYKCT



Dataset #: 4
Motif ID: 147
Motif name: asCAGrkGGCrSy
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 4
Number of overlap: 8
Similarity score: 0.00651548

Alignment:

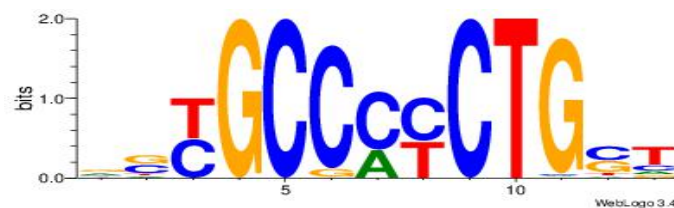
ASCAGRGGGCRSB

---AGRKGGCR---

Original motif Consensus sequence: ASCAGRGGGCRSB



Reverse complement motif Consensus sequence: BSKGCCCCMCTGST

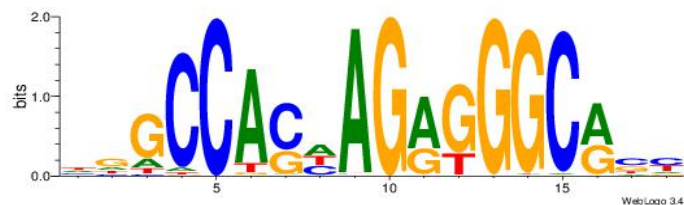


Dataset #: 4
 Motif ID: 165
 Motif name: wgGCCAshAGrGGGCrSy
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 9
 Number of overlap: 8
 Similarity score: 0.0102443

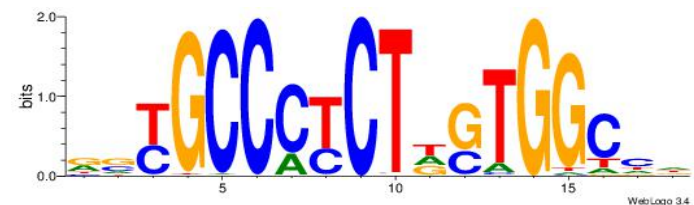
Alignment:

KBKGCCCKCTHGTGGCHH
 --KGCCYKCT-----

Original motif Consensus sequence: HDGCCACHAGRGGGCRBY



Reverse complement motif Consensus sequence: KBKGCCCKCTHGTGGCHH



Dataset #: 4
 Motif ID: 166
 Motif name: CasCAGrGGGCrSy
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3

Number of overlap: 8
Similarity score: 0.0104954

Alignment:
BSKGCCCKCTGGTG
--KGCCYKCT-----

Original motif Consensus sequence: CACCAGRGGGCRSB



Reverse complement motif Consensus sequence: BSKGCCCKCTGGT

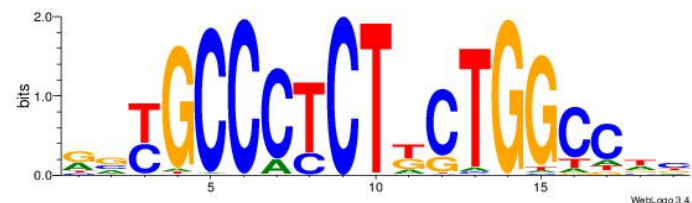
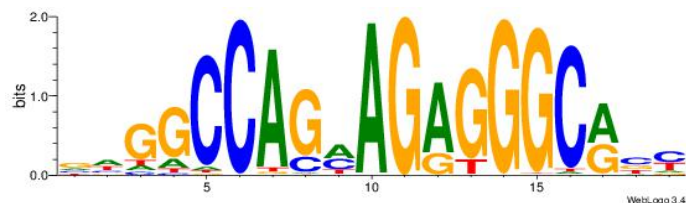


Dataset #: 4
Motif ID: 163
Motif name: gwGGCCAGmAGAGGGCrby
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 3
Number of overlap: 8
Similarity score: 0.0165822

Alignment:
KBKGCCCTCTYCTGGCCHV
--KGCCYKCT-----

Original motif Consensus sequence: VHGGCCAGMAGAGGGCRBY

Reverse complement motif Consensus sequence:
KBKGCCCTCTYCTGGCCHV

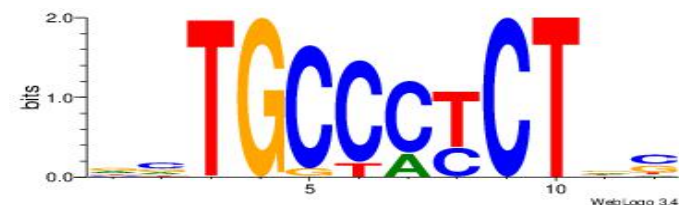


Dataset #: 4 Motif ID: 133 Motif name: shAGrGGGCAGy

Original motif Consensus sequence: SHAGRGGGCABH



Reverse complement motif Consensus sequence: DBTGCCCKCTDS



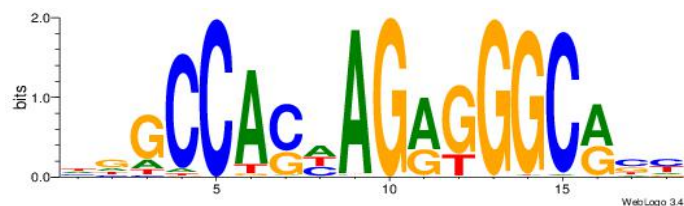
Best Matches for Significant Motif ID 133 (Highest to Lowest)

Dataset #:	4
Motif ID:	165
Motif name:	wgGCCAshAGrGGGCrsy
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	7
Number of overlap:	12
Similarity score:	0.00159897

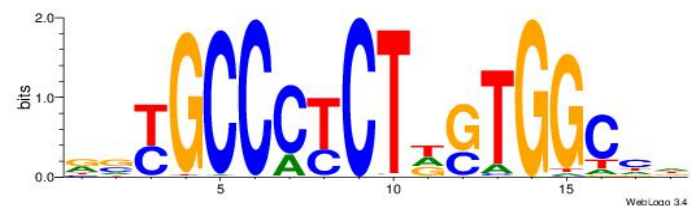
Alignment:

```
HDGCCACHAGRGGGCRBY
-----SHAGRGGGCABH
```

Original motif Consensus sequence: HDGCCACHAGRGGGCRBY



Reverse complement motif Consensus sequence: KBKGGCCCKCTHGTGGCHH

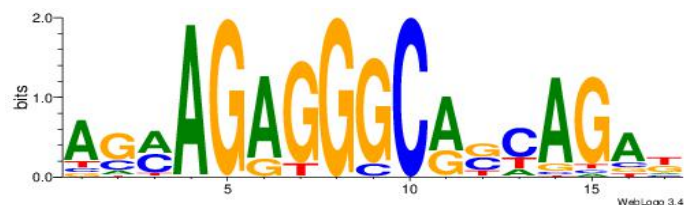


Dataset #: 4
Motif ID: 143
Motif name: AgmAGAGGGCrscAGak
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 5
Number of overlap: 12
Similarity score: 0.00815796

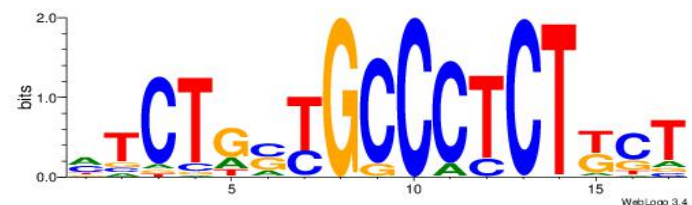
Alignment:

AGMAGAGGGCASCAGAK
-SHAGRGGGCABH----

Original motif Consensus sequence: AGMAGAGGGCASCAGAK



Reverse complement motif Consensus sequence: RTCTGSTGCCCTCTYCT



Dataset #: 4
 Motif ID: 163
 Motif name: gwGGCCAGmAGAGGGCrby
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 8
 Number of overlap: 12
 Similarity score: 0.0109424

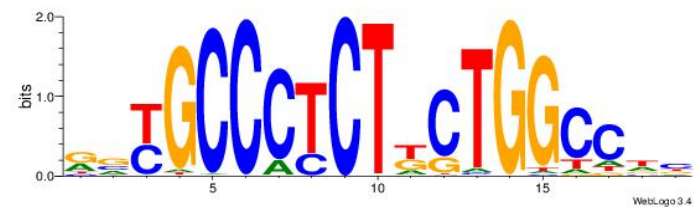
Alignment:

VHGGCCAGMAGAGGGCRBY
 -----SHAGRGGGCABH

Original motif Consensus sequence: VHGGCCAGMAGAGGGCRBY



Reverse complement motif Consensus sequence: KBKGCCCTCTYCTGGCCHV



Dataset #: 4
 Motif ID: 166
 Motif name: CasCAGrGGGCrSy
 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: 0.0124424

Alignment:
BSKGCCCKCTGGTG
DBTGCCCKCTDS--

Original motif Consensus sequence: CACCAGRGGGCRSB



Reverse complement motif Consensus sequence: BSKGCCCKCTGGT

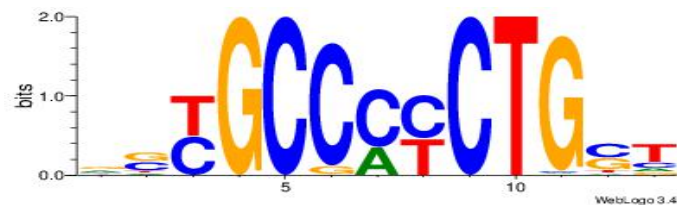


Dataset #: 4
Motif ID: 147
Motif name: asCAGrkGGCrSy
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 2
Number of overlap: 12
Similarity score: 0.0128393

Alignment:
ASCAGRGGGCRSB
-SHAGRGGGCABH

Original motif Consensus sequence: ASCAGRGGGCRSB

Reverse complement motif Consensus sequence: BSKGCCCMCTGST



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

Original motif Consensus sequence: AAATAH



Reverse complement motif Consensus sequence: DTATTT

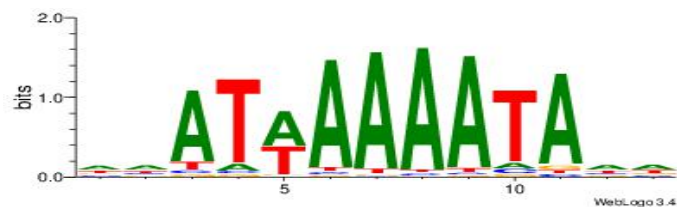


Best Matches for Significant Motif ID 8 (Highest to Lowest)

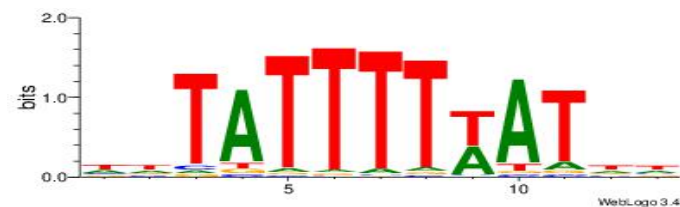
Dataset #:	4
Motif ID:	150
Motif name:	waATwAAAATAww
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2
Number of overlap:	6
Similarity score:	0.00224204

Alignment:
 DHATWAAAATAHD
 -----AAATAH-

Original motif Consensus sequence: DHATWAAAATAHD



Reverse complement motif Consensus sequence: DHTATTTTWATHD



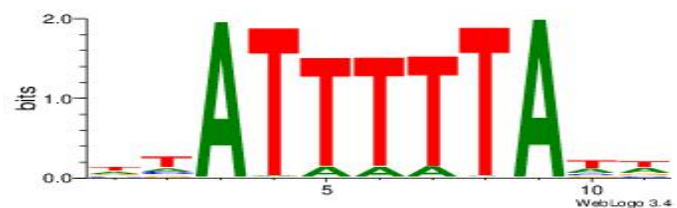
Dataset #: 4
Motif ID: 157
Motif name: wtATTTTAAww
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 6
Similarity score: 0.00556446

Alignment:

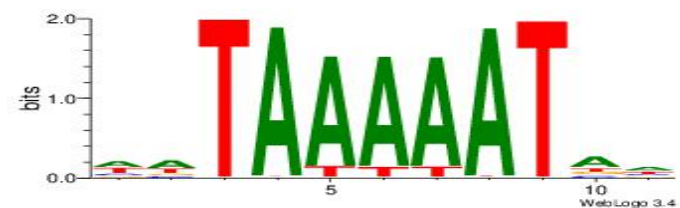
WWTAAAAATAD

-----AAATAH

Original motif Consensus sequence: DTATTTTAAWW



Reverse complement motif Consensus sequence: WWTAAAAATAD

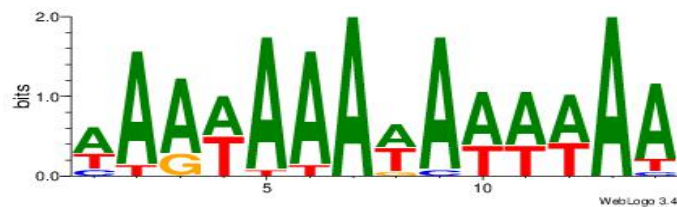


Dataset #: 2
 Motif ID: 68
 Motif name: Motif 68
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 5
 Number of overlap: 6
 Similarity score: 0.0128826

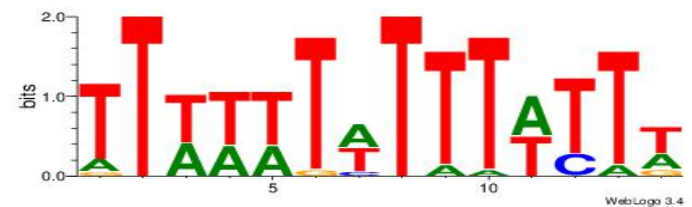
Alignment:

TTWWWTWTTTWTW
 ----DTATTT----

Original motif Consensus sequence: WAAWAAWAWWWAA



Reverse complement motif Consensus sequence: TTWWWTWTTTWTW



Dataset #: 2
 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: 1

Number of overlap: 6
Similarity score: 0.0167304

Alignment:
AAATAAAW
AAATAH--

Original motif Consensus sequence: AAATAAAW



Reverse complement motif Consensus sequence: WTTTATTT

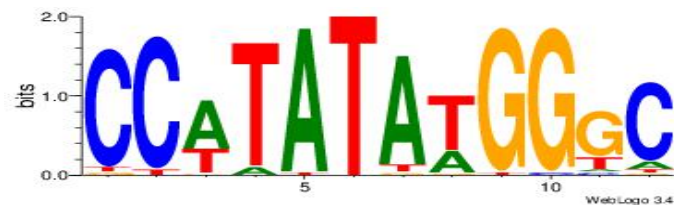
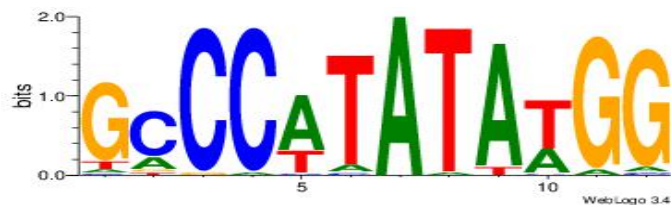


Dataset #: 3
Motif ID: 118
Motif name: SRF
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 3
Number of overlap: 6
Similarity score: 0.0210491

Alignment:
GCCCATATATGG
----AAATAH--

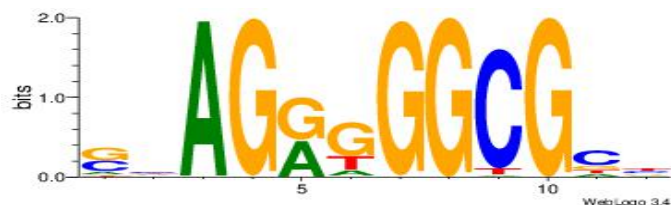
Original motif Consensus sequence: GCCCATATATGG

Reverse complement motif Consensus sequence: CCATATATGGGC

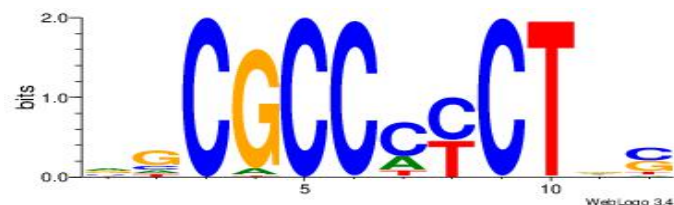


Dataset #: 4 **Motif ID: 153** **Motif name: scAGrkGGCGcy**

Original motif Consensus sequence: SHAGRGGGCGCB



Reverse complement motif Consensus sequence: VCGCCCMCTDS

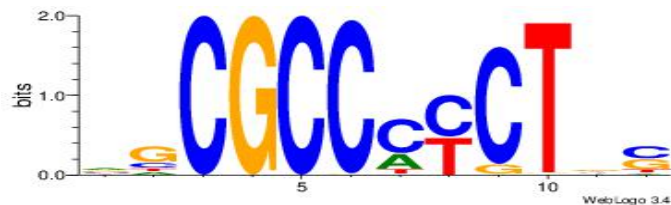


Best Matches for Significant Motif ID 153 (Highest to Lowest)

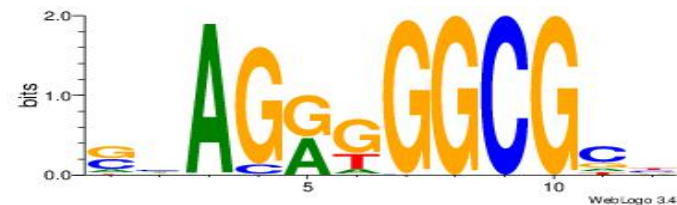
Dataset #:	4
Motif ID:	137
Motif name:	rgCGCCmyCTgs
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	12
Similarity score:	0

Alignment:
SHAGKGGGCGCB
SHAGRGGGCGCB

Original motif Consensus sequence: VGCGCCCYCTDS



Reverse complement motif Consensus sequence: SHAGKGGGCGCB



Dataset #: 4
 Motif ID: 147
 Motif name: asCAGrkGGCrSy
 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: 0.0112071

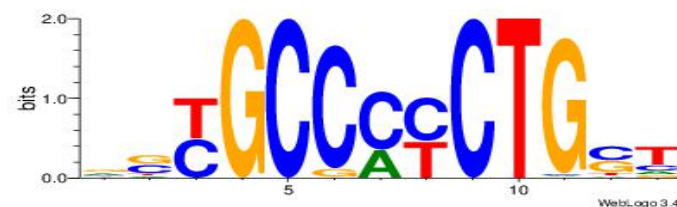
Alignment:

ASCAGRGGGCRSB
 -SHAGRGGGCGCB

Original motif Consensus sequence: ASCAGRGGGCRSB



Reverse complement motif Consensus sequence: BSKGCCCCMCTGST

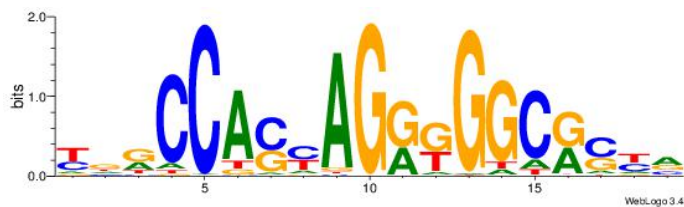


Dataset #: 3
 Motif ID: 74
 Motif name: CTCF
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 7
 Number of overlap: 12
 Similarity score: 0.0133899

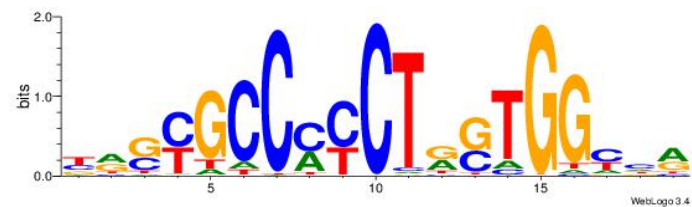
Alignment:

YDRCCASYAGRKGGRSYV
 -----SHAGRGGGCGCB-

Original motif Consensus sequence: YDRCCASYAGRKGGRSYV



Reverse complement motif Consensus sequence: BMSMGCCYMCTKSTGGMHM

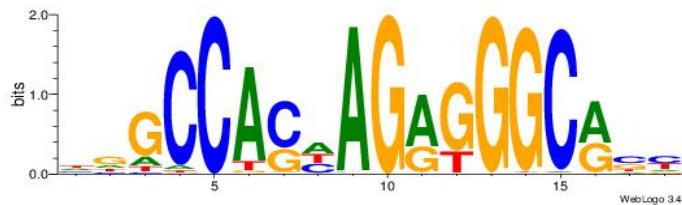


Dataset #: 4
 Motif ID: 165
 Motif name: wgGCCAshAGrGGGCrSy
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1

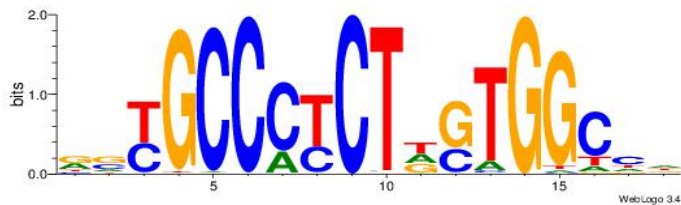
Number of overlap: 12
Similarity score: 0.0146442

Alignment:
HDGCCACHAGRGGGCRBY
-----SHAGRGGGCGCB

Original motif Consensus sequence: HDGCCACHAGRGGGCRBY



Reverse complement motif Consensus sequence:
KBKGCCCKCTHGTGGCHH

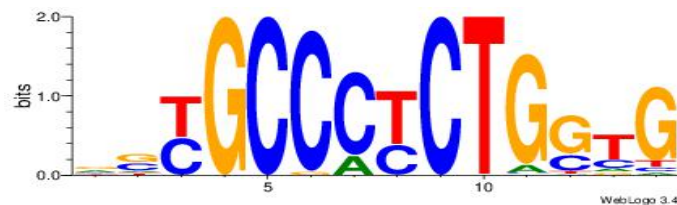


Dataset #: 4
Motif ID: 166
Motif name: CasCAGrGGGCrSy
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 3
Number of overlap: 12
Similarity score: 0.0200811

Alignment:
CACCAGRGGGCRSB
--SHAGRGGGCGCB

Original motif Consensus sequence: CACCAGRGGGCRSB

Reverse complement motif Consensus sequence: BSKGCCCKCTGGT



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

Original motif Consensus sequence: CACGTR



Reverse complement motif Consensus sequence: MACGTG



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

Dataset #:	3
Motif ID:	71
Motif name:	Arnt
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	6
Similarity score:	0

Alignment:

CACGTG

CACGTR

Original motif Consensus sequence: CACGTG



Reverse complement motif Consensus sequence: CACGTG



Dataset #: 3
Motif ID: 95
Motif name: MYCMAX
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 3
Number of overlap: 6
Similarity score: 0.0102183

Alignment:

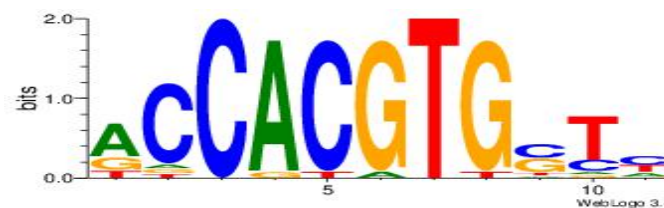
ACCACGTGSTM

--CACGTR---

Original motif Consensus sequence: RASCACGTGGT



Reverse complement motif Consensus sequence: ACCACGTGSTM



Dataset #: 3
 Motif ID: 91
 Motif name: MAX
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 6
 Similarity score: 0.011152

Alignment:

BCACGTGDTD

-CACGTR---

Original motif Consensus sequence: DAHCACGTGD



Reverse complement motif Consensus sequence: BCACGTGDTD



Dataset #: 3
 Motif ID: 126
 Motif name: USF1
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 6

Similarity score: 0.0131944

Alignment:

MCACGTG

-CACGTR

Original motif Consensus sequence: CACGTGR



Reverse complement motif Consensus sequence: MCACGTG



Dataset #:	3
Motif ID:	94
Motif name:	Myc
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	3
Number of overlap:	6
Similarity score:	0.0253396

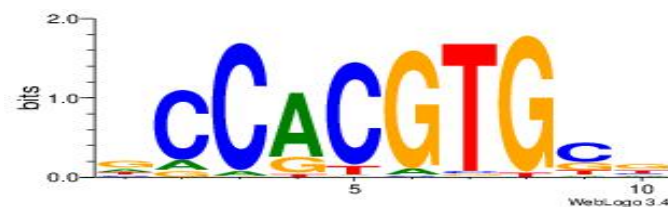
Alignment:

DCCACGTGCV

--CACGTR--

Original motif Consensus sequence: VGCACGTGGH

Reverse complement motif Consensus sequence: DCCACGTGCV



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

Original motif Consensus sequence: AGRKGGCR



Reverse complement motif Consensus sequence: KGCCYKCT



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

Dataset #:	2
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:	8
Similarity score:	0

Alignment:
 AGRKGGCR
 AGRKGGCR

Original motif Consensus sequence: AGRKGGCR



Reverse complement motif Consensus sequence: KGCCYKCT



Dataset #: 4
Motif ID: 147
Motif name: asCAGrkGGCrSy
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: 0.00628523

Alignment:

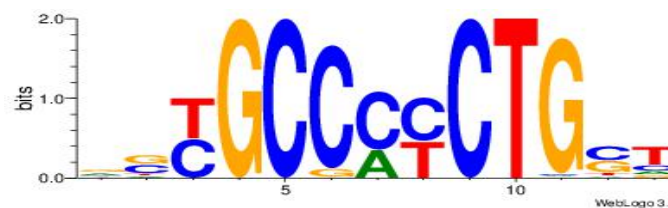
ASCAGRGGGCRSB

---AGRKGGCR---

Original motif Consensus sequence: ASCAGRGGGCRSB



Reverse complement motif Consensus sequence: BSKGCCCCMCTGST

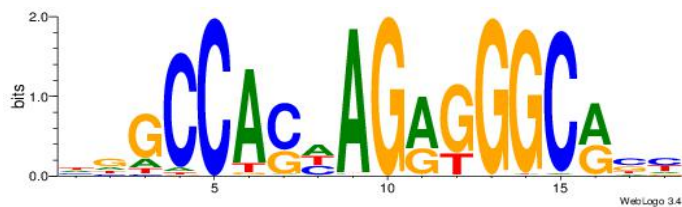


Dataset #: 4
 Motif ID: 165
 Motif name: wgGCCAshAGrGGGCrSy
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 8
 Similarity score: 0.0102152

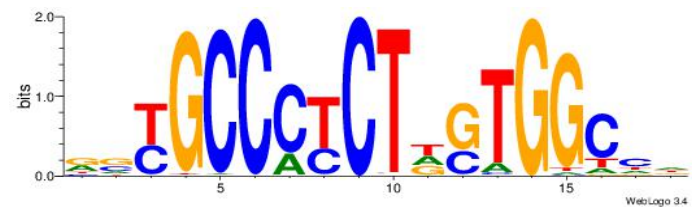
Alignment:

HDGCCACHAGRGGGCRBY
 -----AGRKGCCR--

Original motif Consensus sequence: HDGCCACHAGRGGGCRBY



Reverse complement motif Consensus sequence: KBKGCCCKCTHGTGGCHH



Dataset #: 4
 Motif ID: 166
 Motif name: CasCAGrGGGCrSy
 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: 0.0106761

Alignment:
CACCAGRGGGCRSB
----AGRKGCCR--

Original motif Consensus sequence: CACCAGRGGGCRSB



Reverse complement motif Consensus sequence: BSKGCCCKCTGGT

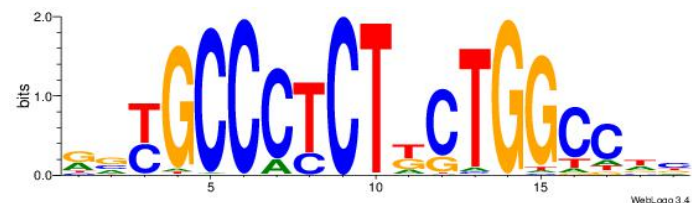
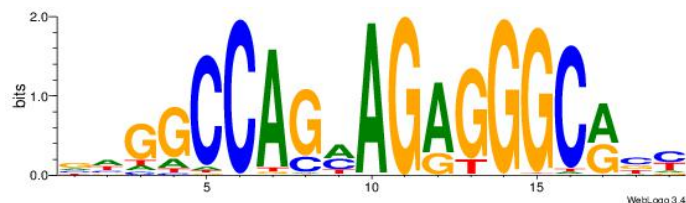


Dataset #: 4
Motif ID: 163
Motif name: gwGGCCAGmAGAGGGCrby
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 3
Number of overlap: 8
Similarity score: 0.016658

Alignment:
KBKGCCCTCTYCTGGCCHV
--KGCCYKCT-----

Original motif Consensus sequence: VHGGCCAGMAGAGGGCRBY

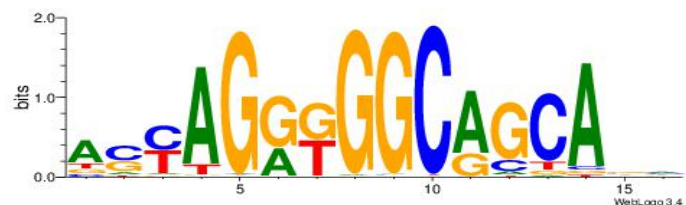
Reverse complement motif Consensus sequence:
KBKGCCCTCTYCTGGCCHV



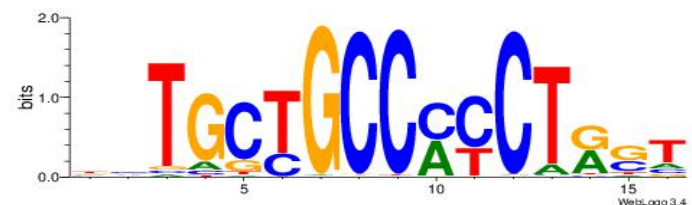
Dataset #: 4
 Motif ID: 164
 Motif name: asyAGrkGGCRGCAGa
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 8
 Similarity score: 0.0201849

Alignment:
 ASYAGRKGGCAGCABH
 ---AGRKGGCR-----

Original motif Consensus sequence: ASYAGRKGGCAGCABH



Reverse complement motif Consensus sequence: HBTGCTGCCYMCTKST

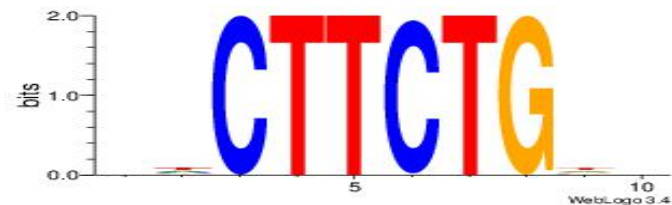


Dataset #: 4 Motif ID: 136 Motif name: dwCAGAAGwh

Original motif Consensus sequence: DHCAGAAAGDH



Reverse complement motif Consensus sequence: HDCTTCTGHD



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

Dataset #:	4
Motif ID:	151
Motif name:	agrCCAGmAGrg
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	3
Number of overlap:	10
Similarity score:	0.00562474

Alignment:

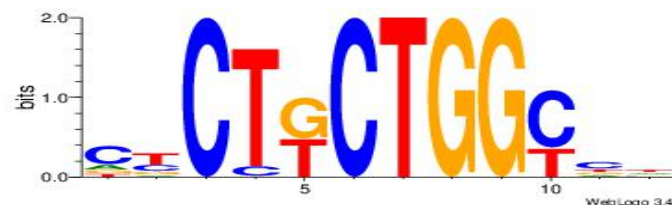
HVGCCAGMAGRG

--DHCAGAAAGDH

Original motif Consensus sequence: HVGCCAGMAGRG



Reverse complement motif Consensus sequence: CKCTRCTGGCVH



Dataset #: 4
 Motif ID: 141
 Motif name: raCAAAACam
 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: 0.0107169

Alignment:

DACAAAACAH

DHCAGAAGDH

Original motif Consensus sequence: DACAAAACAH



Reverse complement motif Consensus sequence: HTGTTTTGTD



Dataset #: 4
 Motif ID: 158
 Motif name: grCCACwAGrk
 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: 0.0167426

Alignment:
DDCCACWAGRK
-DHCAGAAGDH

Original motif Consensus sequence: DDCCACWAGRK



Reverse complement motif Consensus sequence: YMCTWGTGGHH

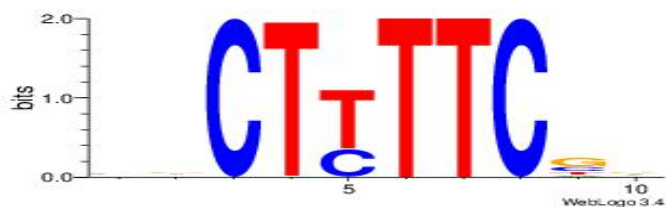


Dataset #: 4
Motif ID: 139
Motif name: mkCTyTTCsg
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 10
Similarity score: 0.0207259

Alignment:
HBCTTTTCBD
HDCTTCTGHD

Original motif Consensus sequence: HBCTTTTCBD

Reverse complement motif Consensus sequence: HBGAAAAGBD

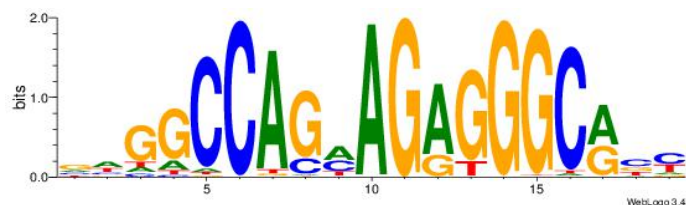


Dataset #: 4
 Motif ID: 163
 Motif name: gwGGCCAGmAGAGGGCrby
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 10
 Similarity score: 0.0212719

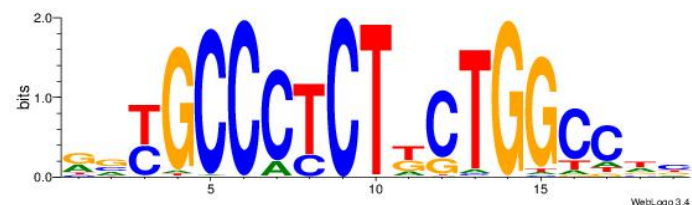
Alignment:

VHGGCCAGMAGAGGGCRBY
 ---DHCAGAAGDH-----

Original motif Consensus sequence: VHGGCCAGMAGAGGGCRBY



Reverse complement motif Consensus sequence: KBKGCCCTCTYCTGGCCHV



Dataset #: 3 Motif ID: 127 Motif name: YY1

Original motif Consensus sequence: RCCATB



Reverse complement motif Consensus sequence: BATGGM



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

Dataset #: 2
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: 2
Number of overlap: 6
Similarity score: 0.00122549

Alignment:
KCCATCT
-RCCATB

Original motif Consensus sequence: AGATGGY



Reverse complement motif Consensus sequence: KCCATCT



Dataset #: 1
 Motif ID: 12
 Motif name: Motif 12
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 6
 Similarity score: 0.00857843

Alignment:
 GAGCCATC
 RCCATB--

Original motif Consensus sequence: GATGGCTC



Reverse complement motif Consensus sequence: GAGCCATC

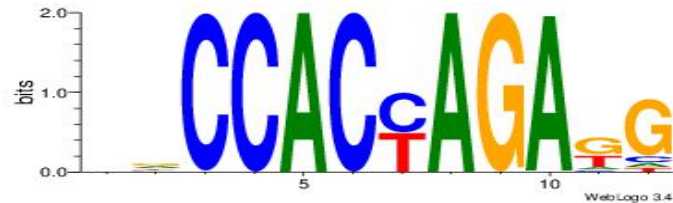


Dataset #: 4
 Motif ID: 145
 Motif name: grCCACyAGAkG
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 6

Similarity score: 0.022036

Alignment:
CYTCTKGTGGHH
-----BATGGM-

Original motif Consensus sequence: DDCCACYAGAKG



Reverse complement motif Consensus sequence: CYTCTKGTGGHH

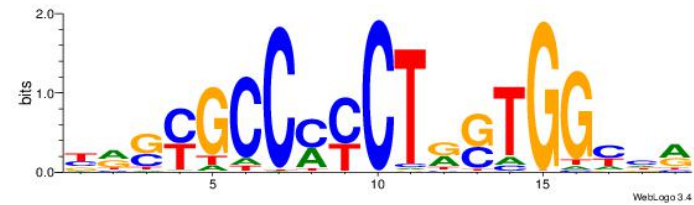
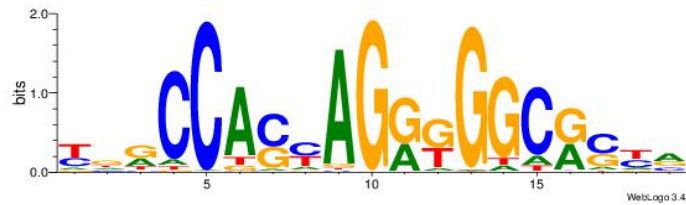


Dataset #: 3
Motif ID: 74
Motif name: CTCF
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 3
Number of overlap: 6
Similarity score: 0.0220417

Alignment:
BMSMGCCYMCTKSTGGMHM
-----BATGGM--

Original motif Consensus sequence: YDRCCASYAGRKGGRSYV

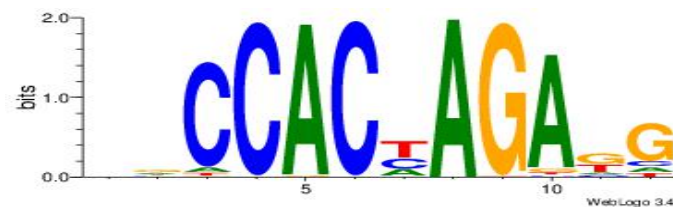
Reverse complement motif Consensus sequence:
BMSMGCCYMCTKSTGGMHM



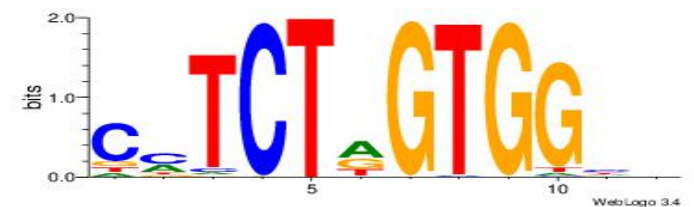
Dataset #: 4
 Motif ID: 138
 Motif name: grCCACyAGAkG
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 6
 Similarity score: 0.0223679

Alignment:
 DDCCACYAGAKG
 -RCCATB-----

Original motif Consensus sequence: DDCCACYAGAKG



Reverse complement motif Consensus sequence: CYTCTMGTGGHH



Dataset #: 3 Motif ID: 72 Motif name: ArntAhr

Original motif Consensus sequence: YGCGTG



Reverse complement motif Consensus sequence: CACGCM



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

Dataset #: 3
 Motif ID: 86
 Motif name: HIF1AARNT
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 6
 Similarity score: 0

Alignment:
 VBACGTGV
 -YGCGTG-

Original motif Consensus sequence: VBACGTGV



Reverse complement motif Consensus sequence: VCACGTBV

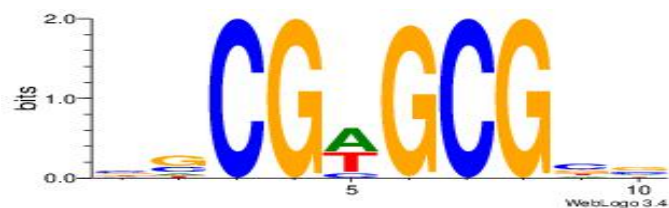


Dataset #: 4
 Motif ID: 134
 Motif name: ssCGwGCGss
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 5
 Number of overlap: 6
 Similarity score: 0.0128947

Alignment:

BSCGWGCGBV
 YGCGTG----

Original motif Consensus sequence: BSCGWGCGBV



Reverse complement motif Consensus sequence: VBCGCWCGSB



Dataset #: 3
 Motif ID: 71
 Motif name: Arnt
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 6

Similarity score: 0.0203526

Alignment:
CACGTG
YGCGTG

Original motif Consensus sequence: CACGTG



Reverse complement motif Consensus sequence: CACGTG



Dataset #: 1
Motif ID: 20
Motif name: Motif 20
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 6
Similarity score: 0.0206428

Alignment:
MACGTG
YGCGTG

Original motif Consensus sequence: CACGTR

Reverse complement motif Consensus sequence: MACGTG



Dataset #: 3
 Motif ID: 126
 Motif name: USF1
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 6
 Similarity score: 0.0255609

Alignment:
 MCACGTG
 -YGCGTG

Original motif Consensus sequence: CACGTGR



Reverse complement motif Consensus sequence: MCACGTG



Best Matches for Each Motif (Highest to Lowest)

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

Original motif Consensus sequence: AGRKGGCR



Reverse complement motif Consensus sequence: KGCCYKCT



Best Matches for Motif ID 1 (Highest to Lowest)

Dataset #:	2
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:	8
Similarity score:	0

Alignment:
AGRKGGCR
AGRKGGCR

Original motif Consensus sequence: AGRKGGCR

Reverse complement motif Consensus sequence: KGCCYKCT



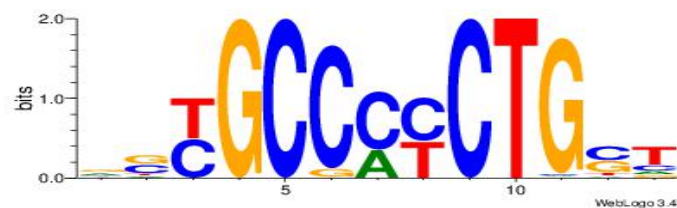
Dataset #: 4
 Motif ID: 147
 Motif name: asCAGrkGGCrSy
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 8
 Similarity score: 0.00628523

Alignment:
 ASCAGRGGGCRSB
 ---AGRKGCCR--

Original motif Consensus sequence: ASCAGRGGGCRSB



Reverse complement motif Consensus sequence: BSKGCCCMCTGST



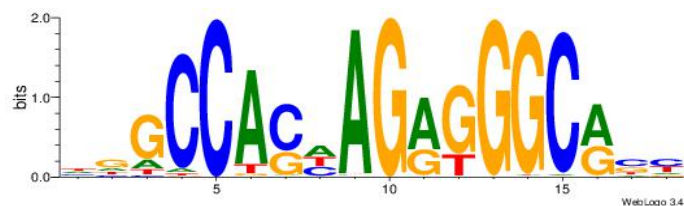
Dataset #: 4
 Motif ID: 165

Motif name: wgGCCAshAGrGGGCrSy
 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: 0.0102152

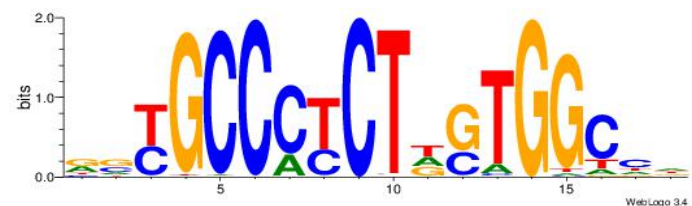
Alignment:

HDGCCACHAGRGGGCRBY
 -----AGRKGGR--

Original motif Consensus sequence: HDGCCACHAGRGGGCRBY



Reverse complement motif Consensus sequence: KBKGCCCKCTHGTGGCHH



Dataset #: 4
 Motif ID: 166
 Motif name: CasCAGrGGGCrSy
 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: 0.0106761

Alignment:

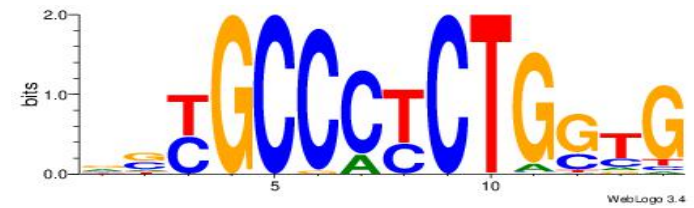
CACCAGRGGGCRSB

----AGRKGCCR--

Original motif Consensus sequence: CACCAGRGGGCRSB



Reverse complement motif Consensus sequence: BSKGCCCKCTGGT



Dataset #:	4
Motif ID:	163
Motif name:	gwGGCCAGmAGAGGGCrby
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	3
Number of overlap:	8
Similarity score:	0.016658

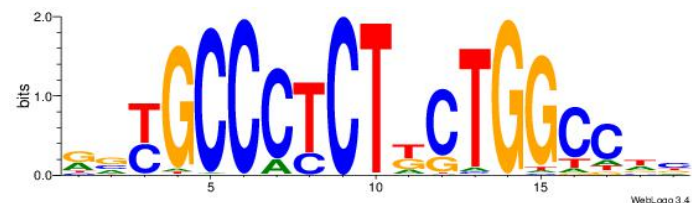
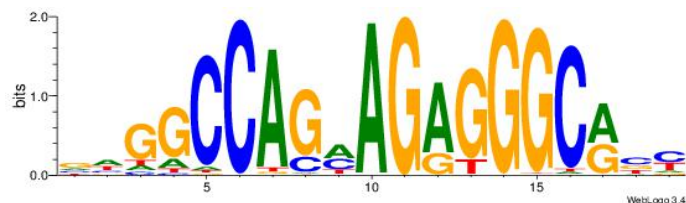
Alignment:

KBKGCCCTCTYCTGGCCHV

--KGCCYKCT-----

Original motif Consensus sequence: VHGGCCAGMAGAGGGCRBY

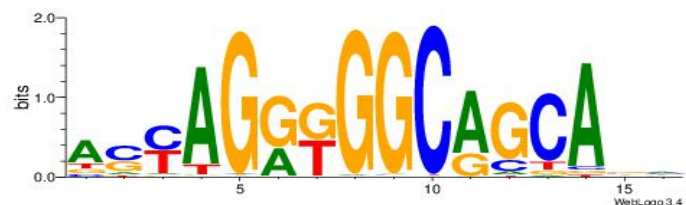
Reverse complement motif Consensus sequence:
KBKGCCCTCTYCTGGCCHV



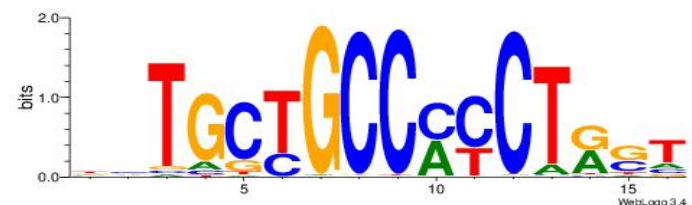
Dataset #: 4
 Motif ID: 164
 Motif name: asyAGrkGGCRGCAGa
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 8
 Similarity score: 0.0201849

Alignment:
 ASYAGRKGGCAGCABH
 ---AGRKGGCR-----

Original motif Consensus sequence: ASYAGRKGGCAGCABH

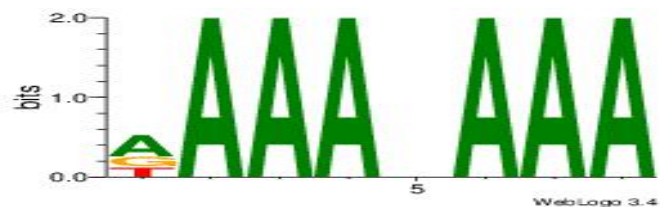


Reverse complement motif Consensus sequence: HBTGCTGCCYMCTKST

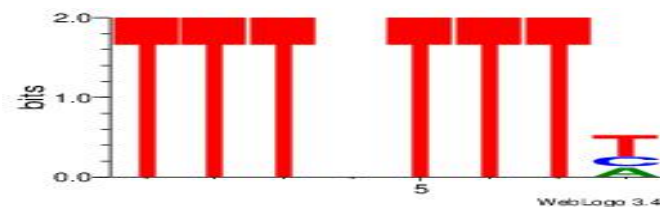


Dataset #: 1 Motif ID: 2 Motif name: Motif 2

Original motif Consensus sequence: AAAAHAAA



Reverse complement motif Consensus sequence: TTTDTTTT



Best Matches for Motif ID 2 (Highest to Lowest)

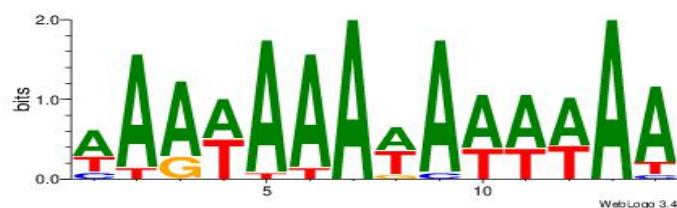
Dataset #:	2
Motif ID:	68
Motif name:	Motif 68
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	4
Number of overlap:	8
Similarity score:	0.034263

Alignment:

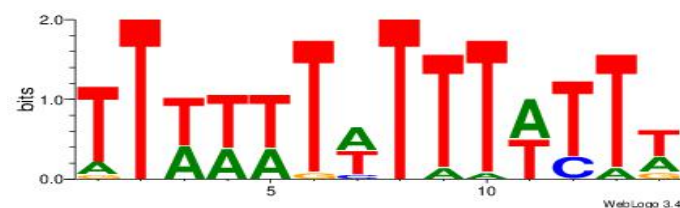
WAAWAAWAWWWAA

---AAAHAAA---

Original motif Consensus sequence: WAAWAAWAWWWAA



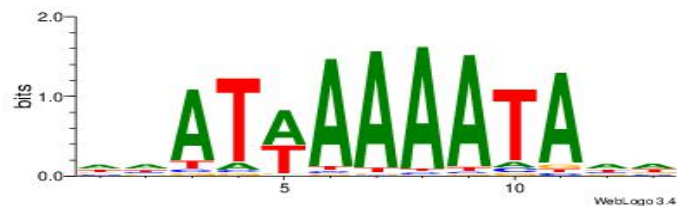
Reverse complement motif Consensus sequence: TTWWWTWTTTWTTW



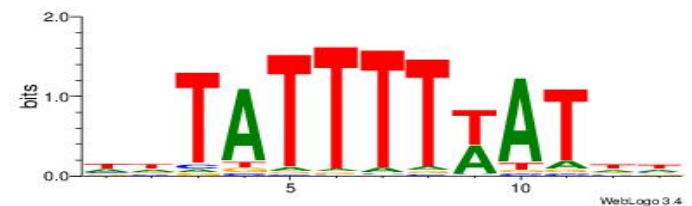
Dataset #: 4
 Motif ID: 150
 Motif name: waATwAAAATAww
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 8
 Similarity score: 0.061025

Alignment:
 DHTATTTTWATHD
 TTTDTTTT-----

Original motif Consensus sequence: DHATWAAAATAHD



Reverse complement motif Consensus sequence: DHTATTTTWATHD



Dataset #: 2
 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: 1
 Number of overlap: 8

Similarity score: 0.0613251

Alignment:
AAATAAAW
AAAAHAAA

Original motif Consensus sequence: AAATAAAW



Reverse complement motif Consensus sequence: WTTTATTT

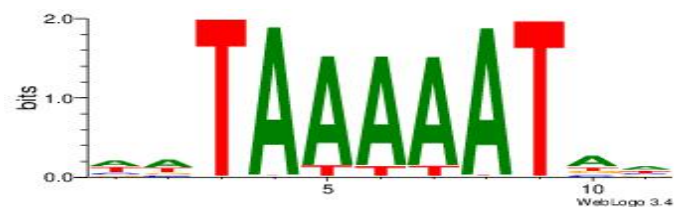
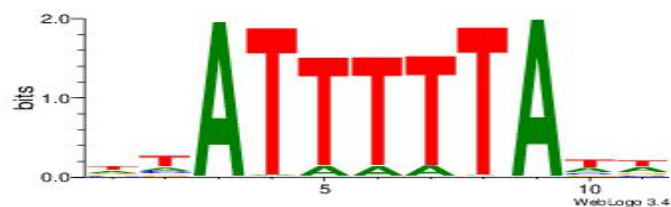


Dataset #: 4
Motif ID: 157
Motif name: wtATTTTAAWw
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 4
Number of overlap: 8
Similarity score: 0.0669479

Alignment:
WWTAAAAATAD
AAAAHAAA---

Original motif Consensus sequence: DTATTTTAAW

Reverse complement motif Consensus sequence: WWTAAAAATAD



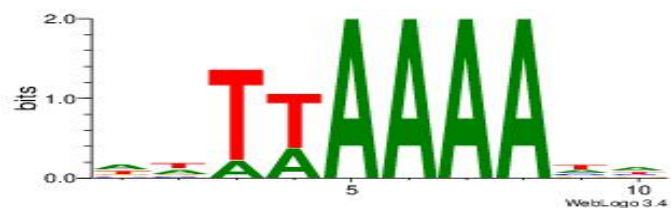
Dataset #: 4
 Motif ID: 148
 Motif name: wwTwAAAAww
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 8
 Similarity score: 0.0808845

Alignment:

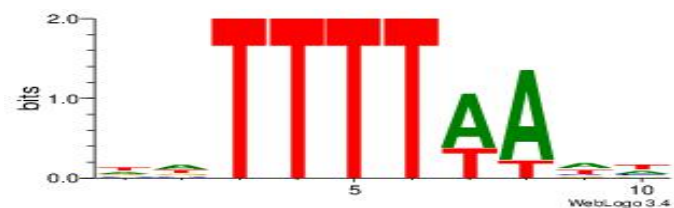
DDTWAAAAHH

AAAAHAAA--

Original motif Consensus sequence: DDTWAAAAHH



Reverse complement motif Consensus sequence: HHTTTTWADD



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

Original motif Consensus sequence: CACACACA



Reverse complement motif Consensus sequence: TGTGTGTG



Best Matches for Motif ID 3 (Highest to Lowest)

Dataset #:	1
Motif ID:	24
Motif name:	Motif 24
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:	0.0443933

Alignment:

CACCCACA

CACACACA

Original motif Consensus sequence: TGTGGGTG



Reverse complement motif Consensus sequence: CACCCACA



Dataset #: 1
 Motif ID: 31
 Motif name: Motif 31
 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: 0.0599548

Alignment:
 CATGYACA
 CACACACA

Original motif Consensus sequence: CATGYACA



Reverse complement motif Consensus sequence: TGTKCATG



Dataset #: 3
 Motif ID: 120
 Motif name: T
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3
 Number of overlap: 8

Alignment:

```
TTCACACCTAG
--CACACACA--
```

Alignment:
CATATRCA
CACACACA

Reverse complement motif Consensus sequence: TGMATATG

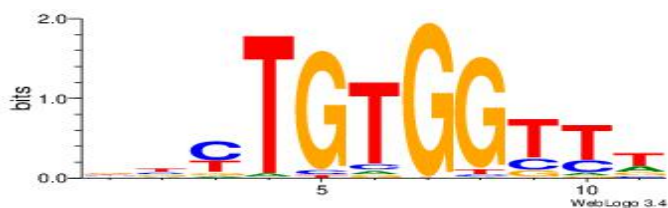


Dataset #: 3
 Motif ID: 114
 Motif name: RUNX1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 8
 Similarity score: 0.0795385

Alignment:

BBTGTGGTTT
 ---TGTGTGTG

Original motif Consensus sequence: BBTGTGGTTT



Reverse complement motif Consensus sequence: AAACCAKVB



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

Original motif Consensus sequence: TTTWWAW



Reverse complement motif Consensus sequence: WTTWWAAA



Best Matches for Motif ID 4 (Highest to Lowest)

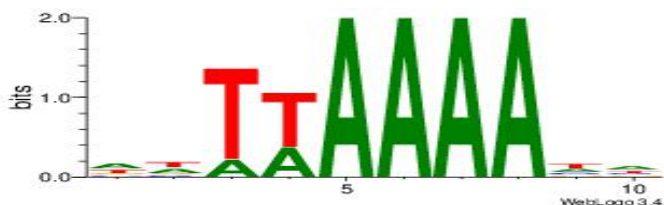
Dataset #:	4
Motif ID:	148
Motif name:	wwTwAAAAww
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	3
Number of overlap:	7
Similarity score:	0.0204013

Alignment:

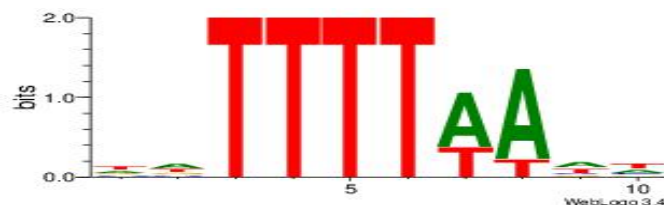
DDTWAAAAHH

-WTTWAAA--

Original motif Consensus sequence: DDTWAAAAHH



Reverse complement motif Consensus sequence: HHTTTTWADD



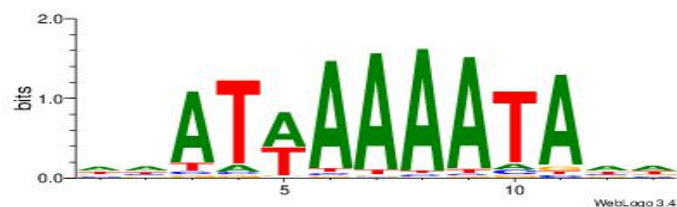
Dataset #: 4
 Motif ID: 150
 Motif name: waATwAAAATAww
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 7
 Similarity score: 0.0245609

Alignment:

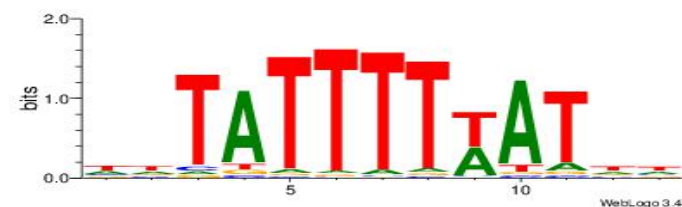
DHATWAAAATAHD

--WTWWAAA----

Original motif Consensus sequence: DHATWAAAATAHD



Reverse complement motif Consensus sequence: DHTATTTTWATHD

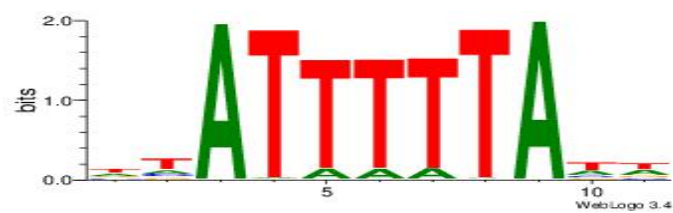


Dataset #: 4
 Motif ID: 157
 Motif name: wtATTTTAAww
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 7

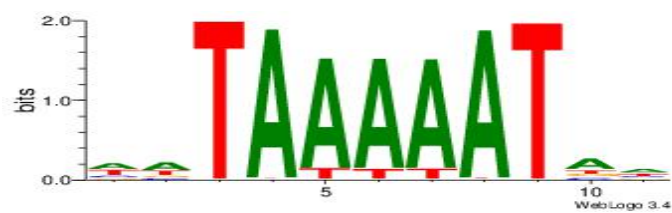
Similarity score: 0.028753

Alignment:
WWTAAAAATAD
-WTWWAAA---

Original motif Consensus sequence: DTATTTTAAWW



Reverse complement motif Consensus sequence: WWTAAAAATAD

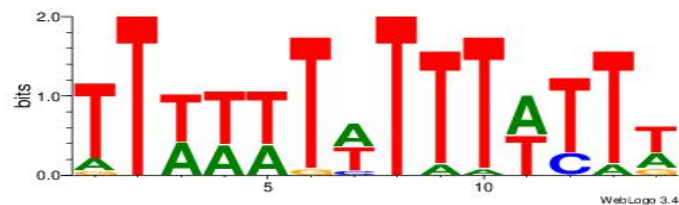
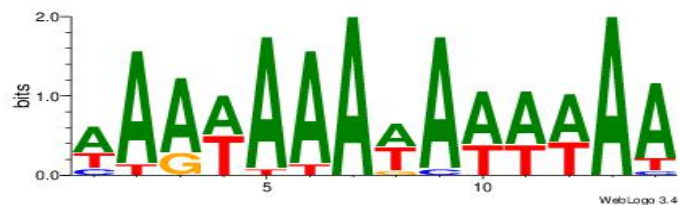


Dataset #: 2
Motif ID: 68
Motif name: Motif 68
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 7
Similarity score: 0.048084

Alignment:
TTWWWTWTTTWTTW
-----TTTWWAW

Original motif Consensus sequence: WAAWAAWAWWWAA

Reverse complement motif Consensus sequence:
TTWWWTWTTTWTTW



Dataset #: 2
 Motif ID: 52
 Motif name: Motif 52
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 7
 Similarity score: 0.0637767

Alignment:
 WTTTATTT
 -TTTWWAW

Original motif Consensus sequence: AAATAAAW



Reverse complement motif Consensus sequence: WTTTATTT



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

Original motif Consensus sequence: CCCCDCCC



Reverse complement motif Consensus sequence: GGGDGGGG



Best Matches for Motif ID 5 (Highest to Lowest)

Dataset #:	2
Motif ID:	59
Motif name:	Motif 59
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	8
Similarity score:	0.00363191

Alignment:
 CCCCRCRCC
 CCCCDCCC

Original motif Consensus sequence: CCCCRCRCC



Reverse complement motif Consensus sequence: GGGKGGGG

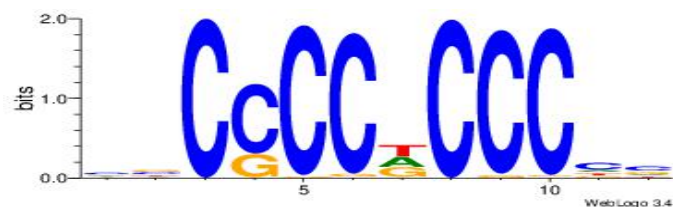


Dataset #: 4
 Motif ID: 155
 Motif name: csCSCCdCCCcs
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 8
 Similarity score: 0.00464015

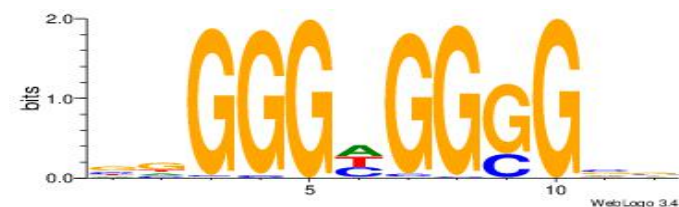
Alignment:

VBCCCCDCCCHV
 --CCCCDCCC--

Original motif Consensus sequence: VBCCCCDCCCHV



Reverse complement motif Consensus sequence: VDGGGDGGGGBV

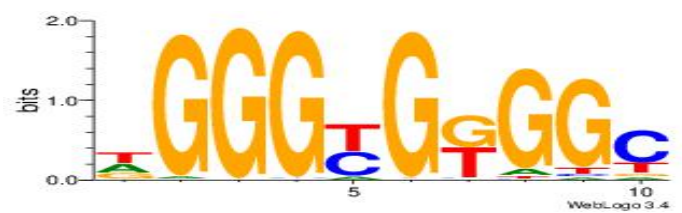


Dataset #: 3
 Motif ID: 89
 Motif name: Klf4
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 8

Similarity score: 0.0352587

Alignment:
GCCYCMCCCD
-CCCCDCCC-

Original motif Consensus sequence: DGGYGKGGC



Reverse complement motif Consensus sequence: GCCYCMCCCD



Dataset #: 4
Motif ID: 154
Motif name: csCsCCTCCcc
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 2
Number of overlap: 8
Similarity score: 0.0361349

Alignment:
BDGGAGGGGBV
-GGGDGGGG--

Original motif Consensus sequence: VBCCCCTCCHB

Reverse complement motif Consensus sequence: BDGGAGGGGBV



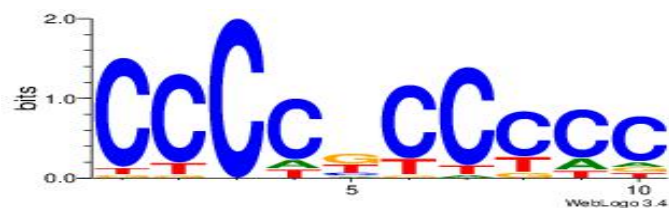
Dataset #: 3
 Motif ID: 116
 Motif name: SP1
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 8
 Similarity score: 0.0368066

Alignment:

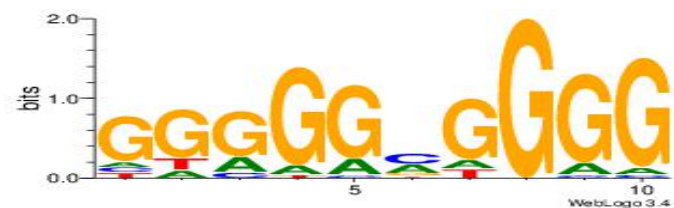
CCCCKCCCCC

CCCDCCC--

Original motif Consensus sequence: CCCCKCCCCC



Reverse complement motif Consensus sequence: GGGGYGGGG



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

Original motif Consensus sequence: CTGGRRA



Reverse complement motif Consensus sequence: TMMCCAG



Best Matches for Motif ID 6 (Highest to Lowest)

Dataset #:	1
Motif ID:	40
Motif name:	Motif 40
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	7
Similarity score:	0.0326828

Alignment:
CTGGGAMT
CTGGRRA-

Original motif Consensus sequence: ARTCCCAG



Reverse complement motif Consensus sequence: CTGGGAMT

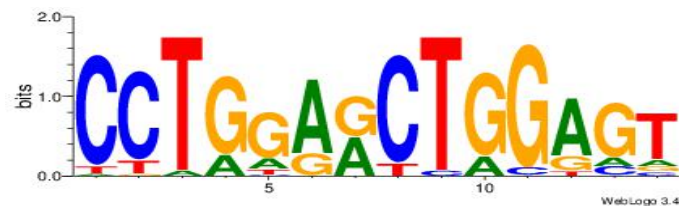


Dataset #: 2
 Motif ID: 69
 Motif name: Motif 69
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 7
 Number of overlap: 7
 Similarity score: 0.0472643

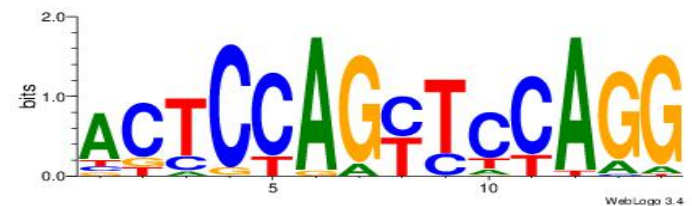
Alignment:

CCTGGARCTGGAGT
 -CTGGRRA-----

Original motif Consensus sequence: CCTGGARCTGGAGT



Reverse complement motif Consensus sequence: ACTCCAGMTCCAG

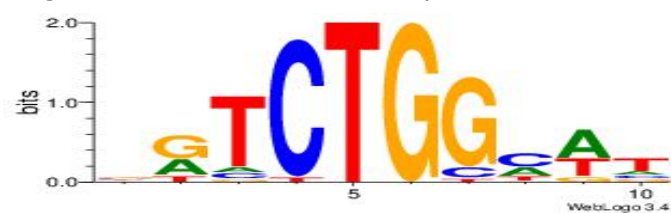


Dataset #: 3
 Motif ID: 85
 Motif name: Hand1Tcfe2a
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 7

Similarity score: 0.0513687

Alignment:
BRTCTGGMWT
---CTGGRRA

Original motif Consensus sequence: BRTCTGGMWT



Reverse complement motif Consensus sequence: AWRCCAGAMB

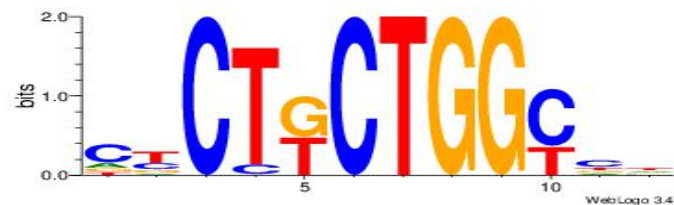


Dataset #: 4
Motif ID: 151
Motif name: agrCCAGmAGrg
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 6
Number of overlap: 7
Similarity score: 0.0514331

Alignment:
HVGCCAGMAGRG
TMMCCAG-----

Original motif Consensus sequence: HVGCCAGMAGRG

Reverse complement motif Consensus sequence: CKCTRCTGGCVH



Dataset #: 1
 Motif ID: 33
 Motif name: Motif 33
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 7
 Similarity score: 0.0553656

Alignment:
 GWAGCCAG
 -TMMCCAG

Original motif Consensus sequence: CTGGCTWC



Reverse complement motif Consensus sequence: GWAGCCAG



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

Original motif Consensus sequence: AGRAAA



Reverse complement motif Consensus sequence: TTTMCT

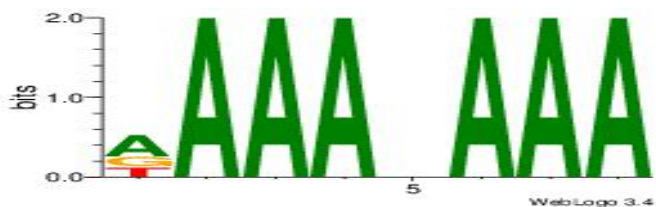


Best Matches for Motif ID 7 (Highest to Lowest)

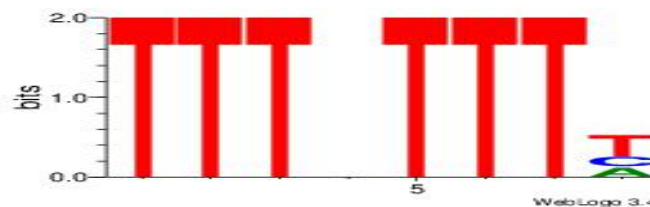
Dataset #:	1
Motif ID:	2
Motif name:	Motif 2
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	6
Similarity score:	0.0617932

Alignment:
TTTDTTTT
TTTMCT--

Original motif Consensus sequence: AAAHAAA



Reverse complement motif Consensus sequence: TTTDTTTT



Dataset #: 1
 Motif ID: 32
 Motif name: Motif 32
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 6
 Similarity score: 0.0627423

Alignment:
 TTTATTY
 TTTMCT-

Original motif Consensus sequence: KAATAAA



Reverse complement motif Consensus sequence: TTTATTY



Dataset #: 2
 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: 6

Similarity score: 0.0627423

Alignment:
WTTTATTT
-TTTMCT-

Original motif Consensus sequence: AAATAAAW



Reverse complement motif Consensus sequence: WTTTATTT

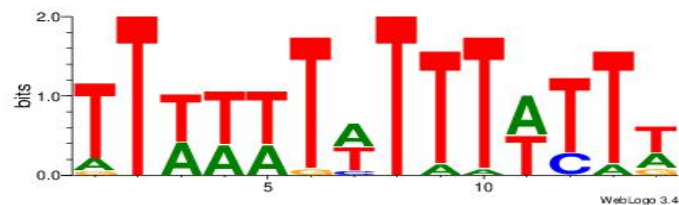
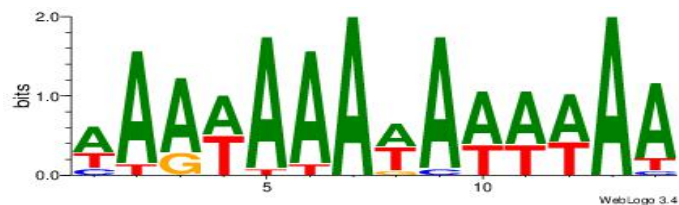


Dataset #: 2
Motif ID: 68
Motif name: Motif 68
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 8
Number of overlap: 6
Similarity score: 0.0627423

Alignment:
WAAWAAAWAWWWAA
-AGRAAA-----

Original motif Consensus sequence: WAAWAAAWAWWWAA

Reverse complement motif Consensus sequence:
TTWWWTWTTTWTTW



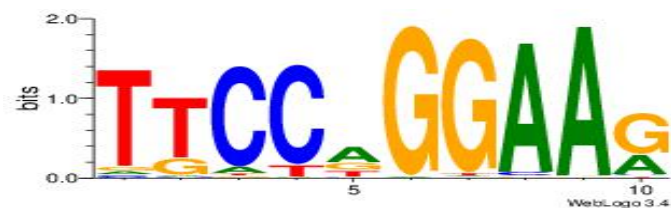
Dataset #: 3
 Motif ID: 119
 Motif name: Stat3
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 6
 Similarity score: 0.069443

Alignment:

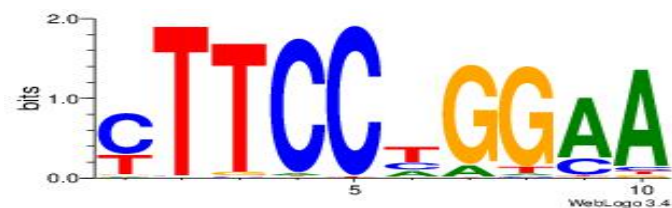
TTCCAGGAAG

----AGRAAA

Original motif Consensus sequence: TTCCAGGAAG



Reverse complement motif Consensus sequence: CTTCTGGAA



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

Original motif Consensus sequence: AAATAH



Reverse complement motif Consensus sequence: DTATTT



Best Matches for Motif ID 8 (Highest to Lowest)

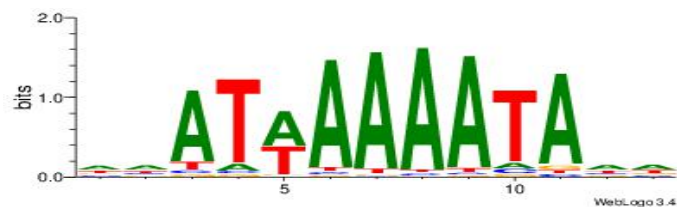
Dataset #:	4
Motif ID:	150
Motif name:	waATwAAAATAww
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2
Number of overlap:	6
Similarity score:	0.00224204

Alignment:

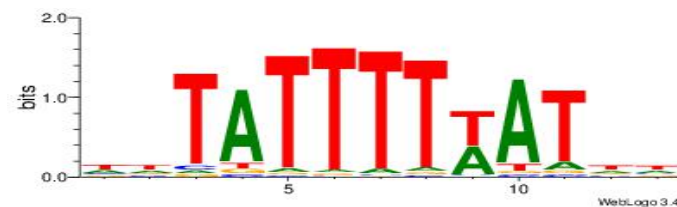
DHATWAAAATAHD

-----AAATAH-

Original motif Consensus sequence: DHATWAAAATAHD



Reverse complement motif Consensus sequence: DHTATTTTWATHD

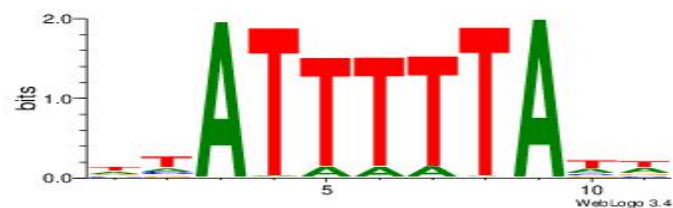


Dataset #: 4
 Motif ID: 157
 Motif name: wtATTTTAAww
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 6
 Similarity score: 0.00556446

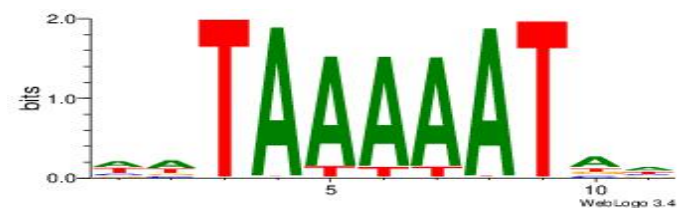
Alignment:

WWTAAAAATAD
 -----AAATAH

Original motif Consensus sequence: DTATTTTAAWW



Reverse complement motif Consensus sequence: WWTAAAAATAD

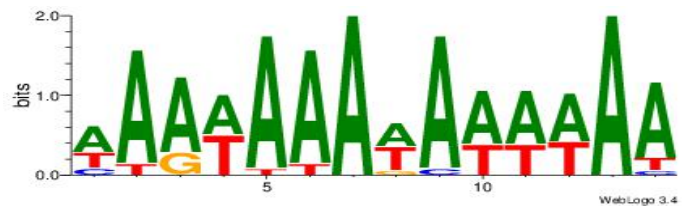


Dataset #: 2
 Motif ID: 68
 Motif name: Motif 68
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 5
 Number of overlap: 6

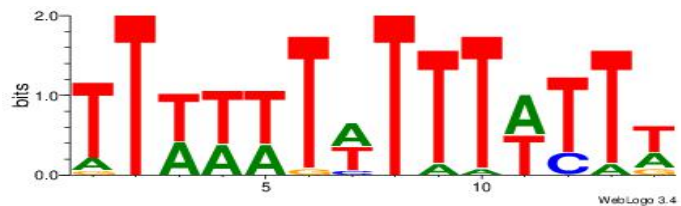
Similarity score: 0.0128826

Alignment:
TTWWWTWTTTWTTW
----DTATTT----

Original motif Consensus sequence: WAAWAAAWAWWWAA



Reverse complement motif Consensus sequence: TTWWWTWTTTWTTW



Dataset #: 2
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: 1
Number of overlap: 6
Similarity score: 0.0167304

Alignment:
AAATAAAW
AAATAH--

Original motif Consensus sequence: AAATAAAW

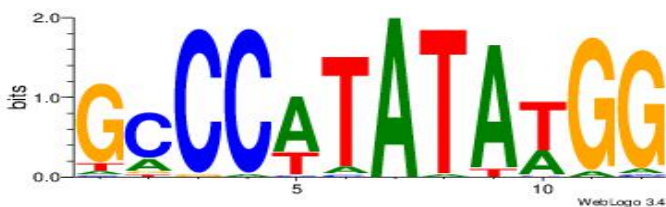
Reverse complement motif Consensus sequence: WTTTATTT



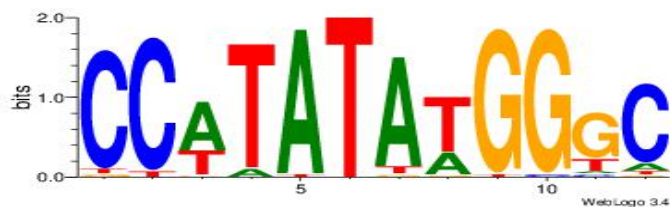
Dataset #: 3
 Motif ID: 118
 Motif name: SRF
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 6
 Similarity score: 0.0210491

Alignment:
 GCCCATATATGG
 ----AAATAH--

Original motif Consensus sequence: GCCCATATATGG



Reverse complement motif Consensus sequence: CCATATATGGGC



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

Original motif Consensus sequence: GGTGGCWS



Reverse complement motif Consensus sequence: SWGCCACC



Best Matches for Motif ID 9 (Highest to Lowest)

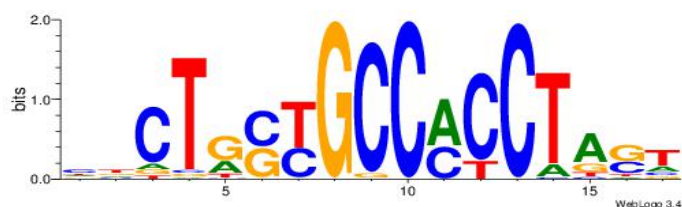
Dataset #:	4
Motif ID:	144
Motif name:	ctCTrsyGCCmCCTast
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	5
Number of overlap:	8
Similarity score:	0.0240374

Alignment:

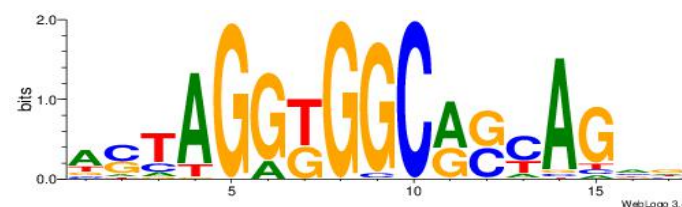
ASTAGGYGGCMSCAGDD

-----GGTGGCWS-----

Original motif Consensus sequence: HDCTGSYGCCMCCTAST



Reverse complement motif Consensus sequence: ASTAGGYGGCMSCAGDD

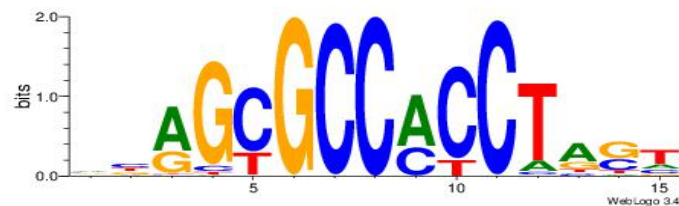


Dataset #: 4
 Motif ID: 146
 Motif name: myrGYGCCmCCTast
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 5
 Number of overlap: 8
 Similarity score: 0.0280157

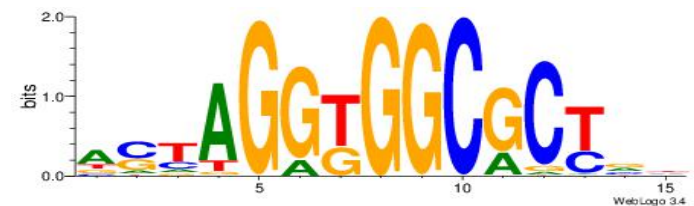
Alignment:

ASTAGGYGGCGCTBB
 ----GGTGGCWS----

Original motif Consensus sequence: VBAGCGCCMCCTAST



Reverse complement motif Consensus sequence: ASTAGGYGGCGCTBB

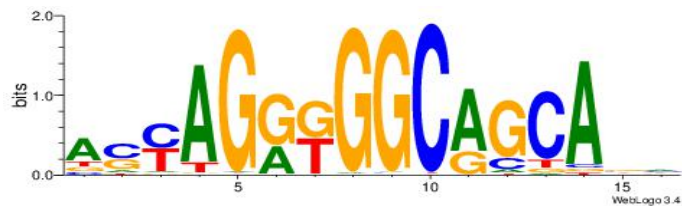


Dataset #: 4
 Motif ID: 164
 Motif name: asyAGrkGGCRGCaga
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 5
 Number of overlap: 8

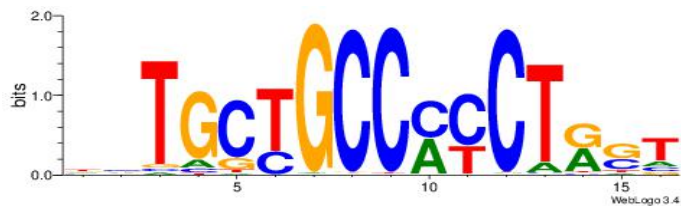
Similarity score: 0.0360935

Alignment:
ASYAGRKGGCAGCABH
----GGTGGCWS----

Original motif Consensus sequence: ASYAGRKGGCAGCABH



Reverse complement motif Consensus sequence:
HBTGCTGCCYMCTKST

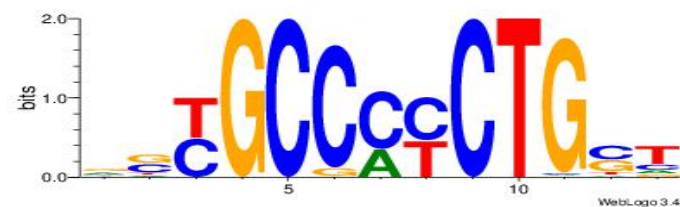


Dataset #: 4
Motif ID: 147
Motif name: asCAGrkGGCrsy
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2
Number of overlap: 8
Similarity score: 0.0392839

Alignment:
ASCAGRGGGCRSB
----GGTGGCWS-

Original motif Consensus sequence: ASCAGRGGGCRSB

Reverse complement motif Consensus sequence: BSKGCCMCTGST

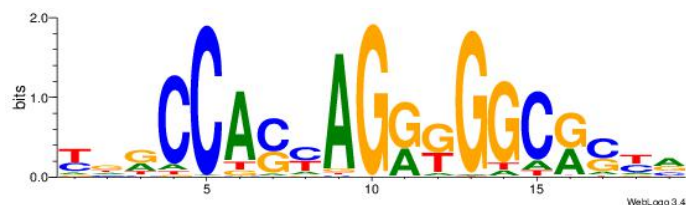


Dataset #: 3
 Motif ID: 74
 Motif name: CTCF
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 10
 Number of overlap: 8
 Similarity score: 0.0429881

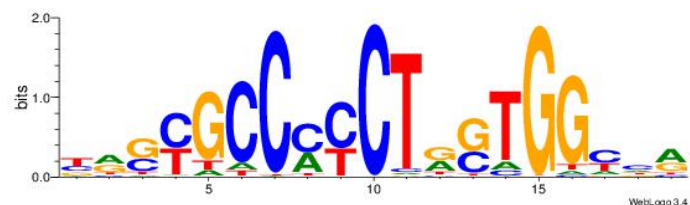
Alignment:

YDRCCASYAGRKGGRSYV
 -----GGTGGCWS--

Original motif Consensus sequence: YDRCCASYAGRKGGRSYV



Reverse complement motif Consensus sequence: BMSMGCCYMCTKSTGGMHM



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

Original motif Consensus sequence: CTGGCCTC



Reverse complement motif Consensus sequence: GAGGCCAG



Best Matches for Motif ID 10 (Highest to Lowest)

Dataset #:	2
Motif ID:	49
Motif name:	Motif 49
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

Alignment:

GAGGCCAG

GAGGCCAG

Original motif Consensus sequence: CTGGCCTC



Reverse complement motif Consensus sequence: GAGGCCAG



Dataset #: 1
 Motif ID: 33
 Motif name: Motif 33
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 8
 Similarity score: 0.0326888

Alignment:
 CTGGCTWC
 CTGGCCTC

Original motif Consensus sequence: CTGGCTWC



Reverse complement motif Consensus sequence: GWAGCCAG

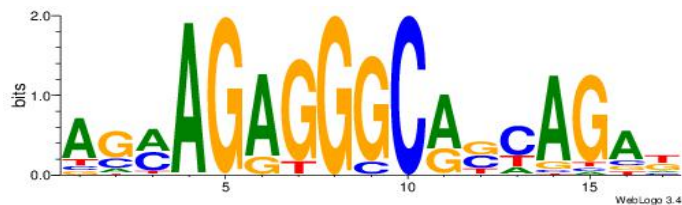


Dataset #: 4
 Motif ID: 143
 Motif name: AgmAGAGGGCrscAGak
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 5
 Number of overlap: 8

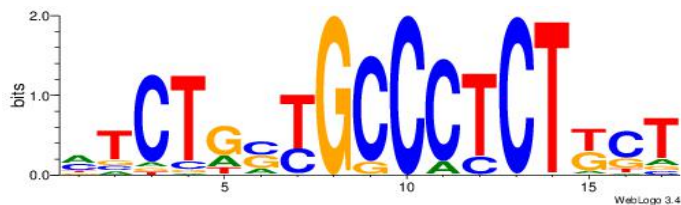
Similarity score: 0.047812

Alignment:
AGMAGAGGGCASCAGAK
-----GAGGCCAG-----

Original motif Consensus sequence: AGMAGAGGGCASCAGAK



Reverse complement motif Consensus sequence:
RTCTGSTGCCCTCTYCT

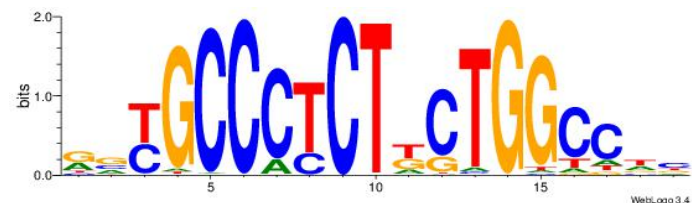
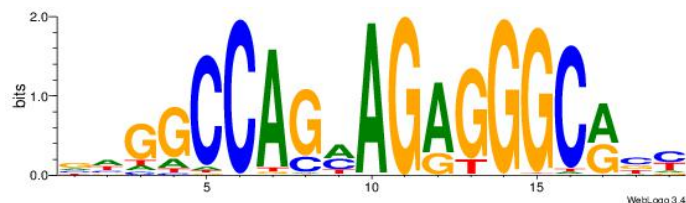


Dataset #: 4
Motif ID: 163
Motif name: gwGGCCAGmAGAGGGCrby
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 8
Similarity score: 0.0506629

Alignment:
VHGGCCAGMAGAGGGCRBY
GAGGCCAG-----

Original motif Consensus sequence: VHGGCCAGMAGAGGGCRBY

Reverse complement motif Consensus sequence:
KBKGCCCTCTYCTGGCCHV



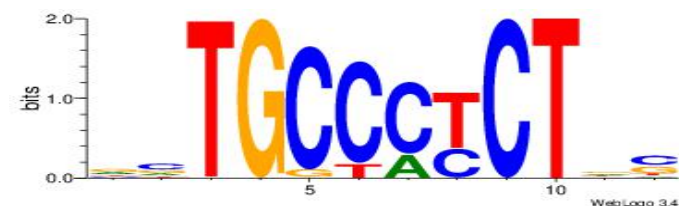
Dataset #: 4
 Motif ID: 133
 Motif name: shAGrGGGCAGy
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 8
 Similarity score: 0.0509007

Alignment:
 SHAGRGGGCABH
 ---GAGGCCAG--

Original motif Consensus sequence: SHAGRGGGCABH

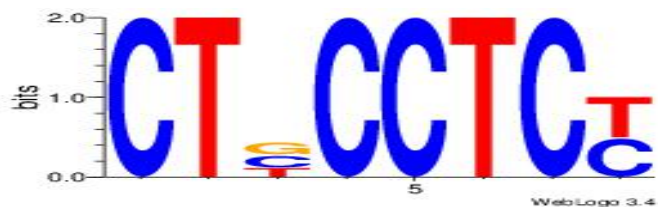


Reverse complement motif Consensus sequence: DBTGCCCKCTDS



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

Original motif Consensus sequence: CTBCCTCY



Reverse complement motif Consensus sequence: MGAGGBAG



Best Matches for Motif ID 11 (Highest to Lowest)

Dataset #:	2
Motif ID:	63
Motif name:	Motif 63
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:	0.0297241

Alignment:
CWCCCTCT
CTBCCTCY

Original motif Consensus sequence: AGAGGGWG



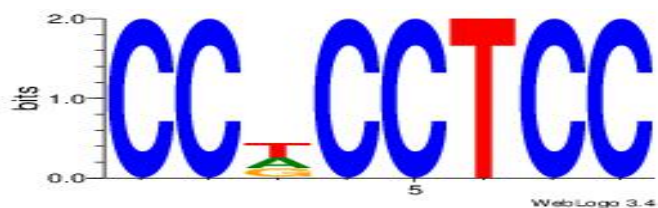
Reverse complement motif Consensus sequence: CWCCCTCT



Dataset #: 1
 Motif ID: 17
 Motif name: Motif 17
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 8
 Similarity score: 0.0448422

Alignment:
 CCDCCTCC
 CTBCCTCY

Original motif Consensus sequence: CCDCCTCC



Reverse complement motif Consensus sequence: GGAGGDGG

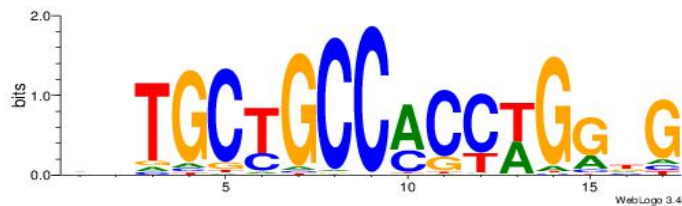


Dataset #: 4
 Motif ID: 169
 Motif name: yvTGCyGCCmCCwGgtG
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 6
 Number of overlap: 8

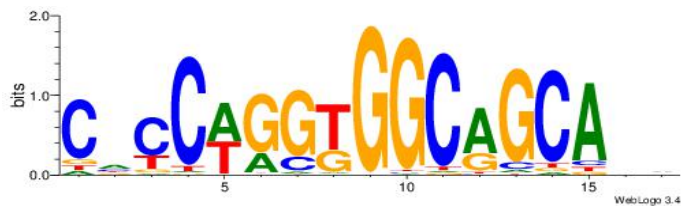
Similarity score: 0.0620322

Alignment:
BVTGCTGCCACCWGGDG
-----CTBCCTCY-----

Original motif Consensus sequence: BVTGCTGCCACCWGGDG



Reverse complement motif Consensus sequence:
CDCCWGGTGGCAGCAVV

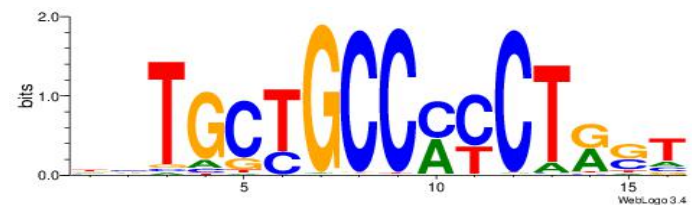
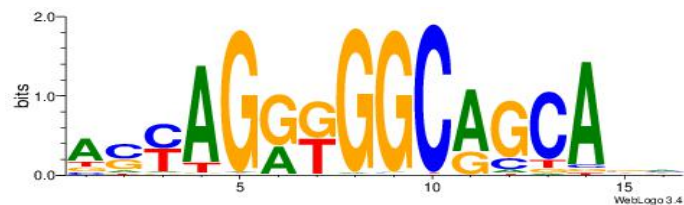


Dataset #: 4
Motif ID: 164
Motif name: asyAGrkGGCRGCa
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 5
Number of overlap: 8
Similarity score: 0.0623054

Alignment:
HBTGCTGCCYMCTKST
-----CTBCCTCY-----

Original motif Consensus sequence: ASYAGRKGGCAGCABH

Reverse complement motif Consensus sequence:
HBTGCTGCCYMCTKST



Dataset #: 4
 Motif ID: 154
 Motif name: csCsCCTCCcc
 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: 0.067516

Alignment:
 VBCCCCTCCHB
 -CTBCCTCY--

Original motif Consensus sequence: VBCCCCTCCHB



Reverse complement motif Consensus sequence: BDGGAGGGGBV



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

Original motif Consensus sequence: GATGGCTC



Reverse complement motif Consensus sequence: GAGCCATC



Best Matches for Motif ID 12 (Highest to Lowest)

Dataset #:	1
Motif ID:	9
Motif name:	Motif 9
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:	0.0446318

Alignment:
SWGCCACC
GAGCCATC

Original motif Consensus sequence: GGTGGCWS



Reverse complement motif Consensus sequence: SWGCCACC

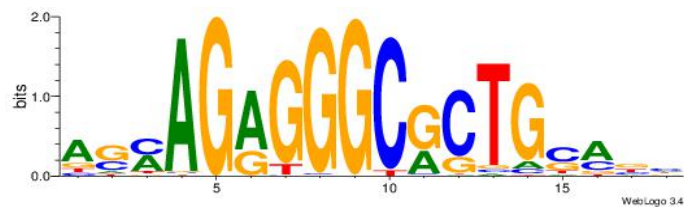


Dataset #: 4
 Motif ID: 149
 Motif name: asmAGRGGGCrCTGsmkc
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 5
 Number of overlap: 8
 Similarity score: 0.053856

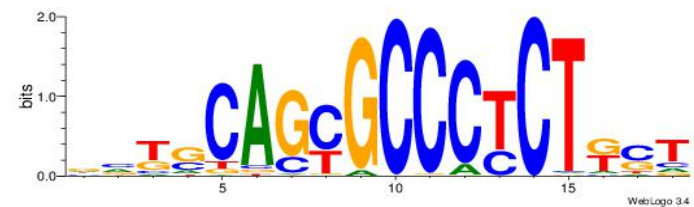
Alignment:

DBTSCAGMGCCCTCTRST
 -----GAGCCATC-----

Original motif Consensus sequence: ASMAGAGGGCRCTGSABH



Reverse complement motif Consensus sequence: DBTSCAGMGCCCTCTRST

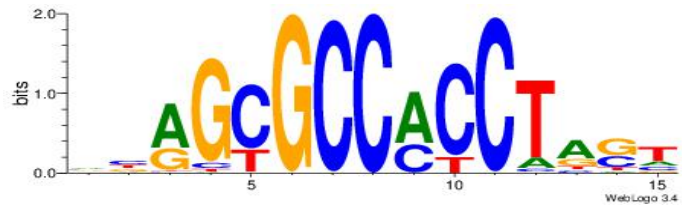


Dataset #: 4
 Motif ID: 146
 Motif name: myrGYGCCmCCTast
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 5

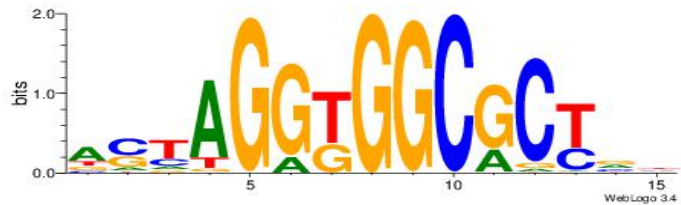
Number of overlap: 8
Similarity score: 0.0558657

Alignment:
ASTAGGYGGCGCTBB
-----GATGGCTC---

Original motif Consensus sequence: V BAGCGCCMCCTAST



Reverse complement motif Consensus sequence: ASTAGGYGGCGCT

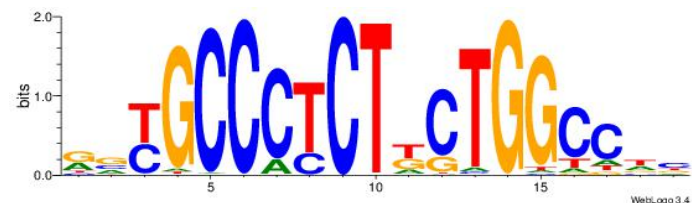
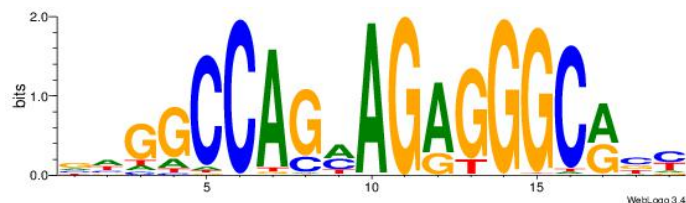


Dataset #: 4
Motif ID: 163
Motif name: gwGGCCAGmAGAGGGCrby
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 11
Number of overlap: 8
Similarity score: 0.0592323

Alignment:
VHGGCCAGMAGAGGGCRBY
-----GATGGCTC-

Original motif Consensus sequence: VHGGCCAGMAGAGGGCRBY

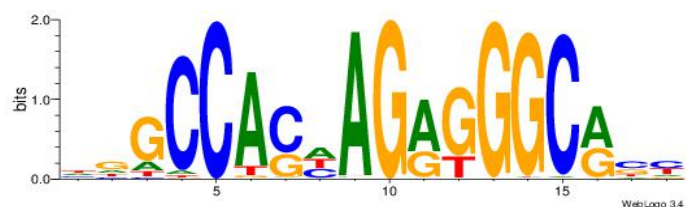
Reverse complement motif Consensus sequence:
KBKGCCCTCTYCTGGCCHV



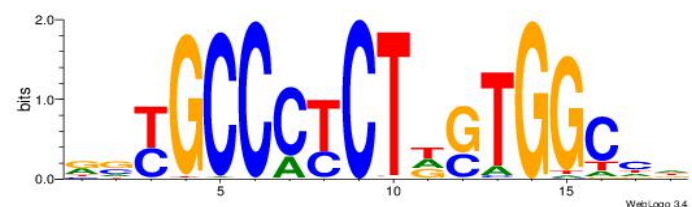
Dataset #: 4
 Motif ID: 165
 Motif name: wgGCCAshAGrGGGCrSy
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 8
 Similarity score: 0.0607886

Alignment:
 HDGCCACHAGRGGGCRBY
 -----GATGGCTC-

Original motif Consensus sequence: HDGCCACHAGRGGGCRBY



Reverse complement motif Consensus sequence: KBKGCCCKCTHGTGGCHH



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

Original motif Consensus sequence: CAGYDCC



Reverse complement motif Consensus sequence: GGDKCTG



Best Matches for Motif ID 13 (Highest to Lowest)

Dataset #:	2
Motif ID:	47
Motif name:	Motif 47
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	7
Similarity score:	0

Alignment:

GGDKCTG

GGDKCTG

Original motif Consensus sequence: CAGYDCC



Reverse complement motif Consensus sequence: GGDKCTG



Dataset #: 2
 Motif ID: 53
 Motif name: Motif 53
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 7
 Similarity score: 0.0294104

Alignment:
 GGGATCTG
 -GGDKCTG

Original motif Consensus sequence: CAGATCCC



Reverse complement motif Consensus sequence: GGGATCTG

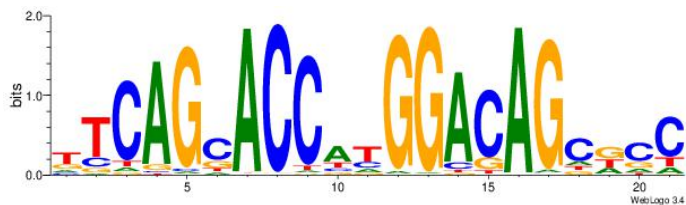


Dataset #: 3
 Motif ID: 113
 Motif name: REST
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 13
 Number of overlap: 7

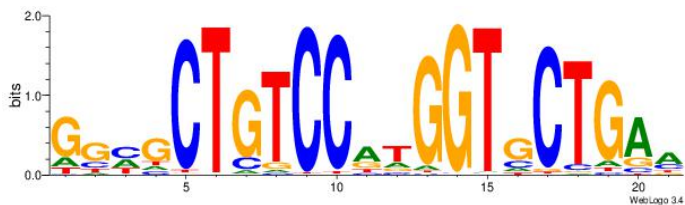
Similarity score: 0.0500473

Alignment:
TTCAGCACCATGGACAGCKCC
--CAGYDCC-----

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC



Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA



Dataset #: 1
Motif ID: 22
Motif name: Motif 22
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 2
Number of overlap: 7
Similarity score: 0.0533516

Alignment:
GGKATCTG
-GGDKCTG

Original motif Consensus sequence: CAGATYCC

Reverse complement motif Consensus sequence: GGKATCTG

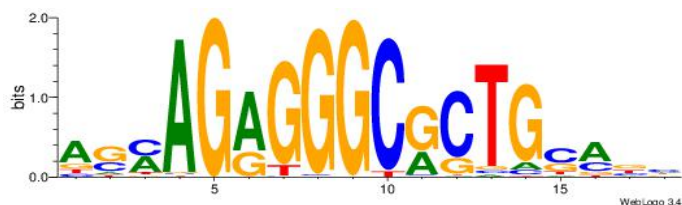


Dataset #: 4
 Motif ID: 149
 Motif name: asmAGRGGGCrCTGsmkc
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 8
 Number of overlap: 7
 Similarity score: 0.0558573

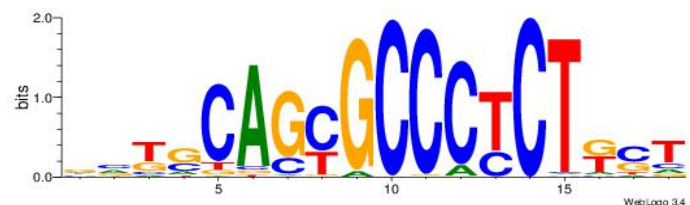
Alignment:

DBTSCAGMGCCCTCTRST
 ----CAGYDCC-----

Original motif Consensus sequence: ASMAGAGGGCRCTGSABH



Reverse complement motif Consensus sequence: DBTSCAGMGCCCTCTRST



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

Original motif Consensus sequence: TSTGTR



Reverse complement motif Consensus sequence: MACASA



Best Matches for Motif ID 14 (Highest to Lowest)

Dataset #:	2
Motif ID:	57
Motif name:	Motif 57
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	2
Number of overlap:	6
Similarity score:	0.0165773

Alignment:

KTGTGTGT

-TSTGTR-

Original motif Consensus sequence: ACACACAY



Reverse complement motif Consensus sequence: KTGTGTGT



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: 3
 Number of overlap: 6
 Similarity score: 0.0165773

Alignment:
 CACACACA
 MACASA--

Original motif Consensus sequence: CACACACA



Reverse complement motif Consensus sequence: TGTGTGTG



Dataset #: 4
 Motif ID: 136
 Motif name: dwCAGAAGwh
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 6

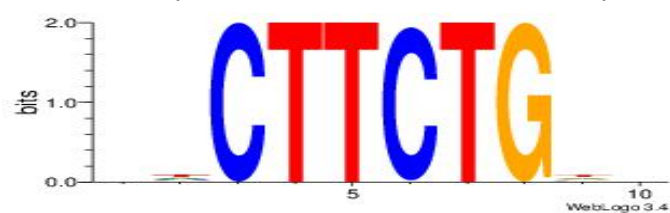
Similarity score: 0.0401476

Alignment:
HDCTTCTGHD
----TSTGTR

Original motif Consensus sequence: DHCAGAAGDH



Reverse complement motif Consensus sequence: HDCTTCTGHD

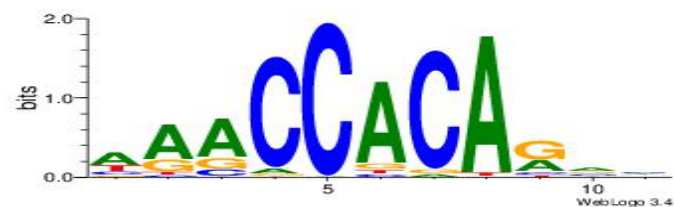
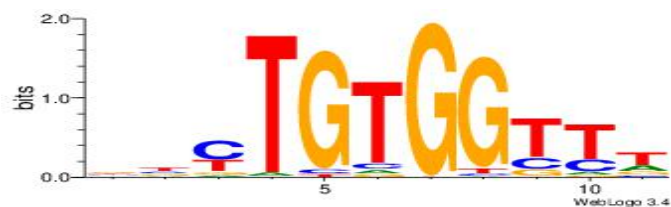


Dataset #: 3
Motif ID: 114
Motif name: RUNX1
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 2
Number of overlap: 6
Similarity score: 0.0445836

Alignment:
BBYTGTGGTTT
-TSTGTR----

Original motif Consensus sequence: BBTGTGGTTT

Reverse complement motif Consensus sequence: AAACCACAKVB



Dataset #: 1
 Motif ID: 24
 Motif name: Motif 24
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 6
 Similarity score: 0.0456841

Alignment:
 TGTGGGTG
 --TSTGTR

Original motif Consensus sequence: TGTGGGTG

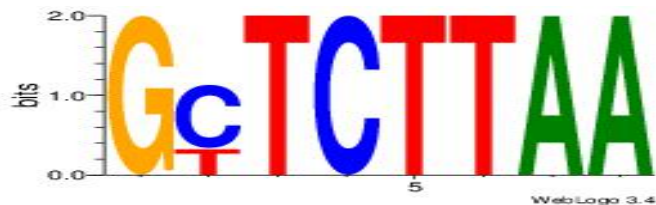


Reverse complement motif Consensus sequence: CACCCACA



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

Original motif Consensus sequence: GCTCTTAA



Reverse complement motif Consensus sequence: TTAAGAGC



Best Matches for Motif ID 15 (Highest to Lowest)

Dataset #: 4
Motif ID: 159
Motif name: kkAAGAGCAsy
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 8
Similarity score: 0.0216416

Alignment:

DBAAGAGCAVH

TTAAGAGC---

Original motif Consensus sequence: DBAAGAGCAVH



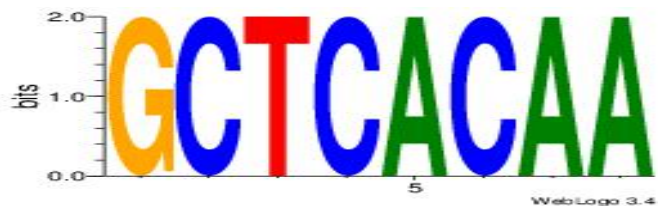
Reverse complement motif Consensus sequence: HVTGCTCTTBH



Dataset #: 2
 Motif ID: 55
 Motif name: Motif 55
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 8
 Similarity score: 0.0390835

Alignment:
 GCTCACAA
 GCTCTTAA

Original motif Consensus sequence: GCTCACAA



Reverse complement motif Consensus sequence: TTGTGAGC



Dataset #: 4
 Motif ID: 148
 Motif name: wwTwAAAAww
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 8

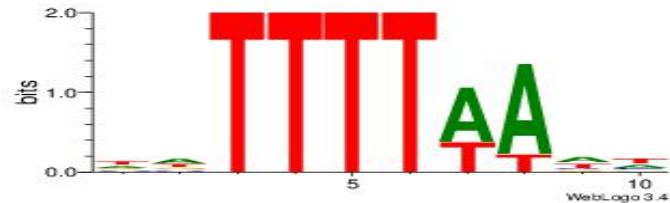
Similarity score: 0.0584188

Alignment:
HHTTTTWADD
GCTCTTAA--

Original motif Consensus sequence: DDTWAAAHH



Reverse complement motif Consensus sequence: HHTTTTWADD



Dataset #: 3
Motif ID: 120
Motif name: T
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 4
Number of overlap: 8
Similarity score: 0.0666592

Alignment:
CTAGGTGTGAA
---GCTCTTAA

Original motif Consensus sequence: CTAGGTGTGAA

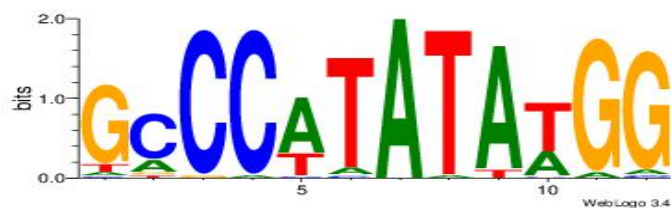
Reverse complement motif Consensus sequence: TTCACACCTAG



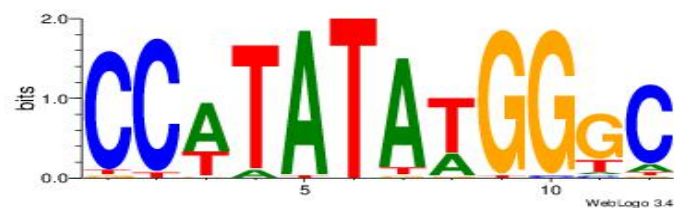
Dataset #: 3
 Motif ID: 118
 Motif name: SRF
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 5
 Number of overlap: 8
 Similarity score: 0.0676161

Alignment:
 CCATATATGGGC
 ----TTAAGAGC

Original motif Consensus sequence: GCCCATATATGG



Reverse complement motif Consensus sequence: CCATATATGGGC



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

Original motif Consensus sequence: GGAAGRR



Reverse complement motif Consensus sequence: MMCTTCC



Best Matches for Motif ID 16 (Highest to Lowest)

Dataset #:	3
Motif ID:	84
Motif name:	GABPA
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	3
Number of overlap:	7
Similarity score:	0.0238137

Alignment:

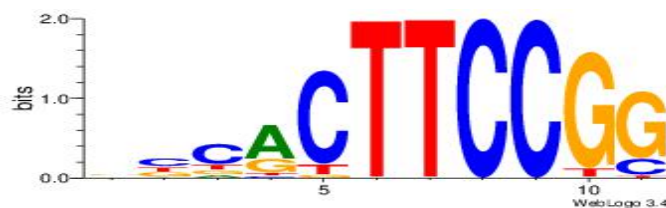
VVCACTTCCGG

--MMCTTCC--

Original motif Consensus sequence: CCGGAAGTGVV



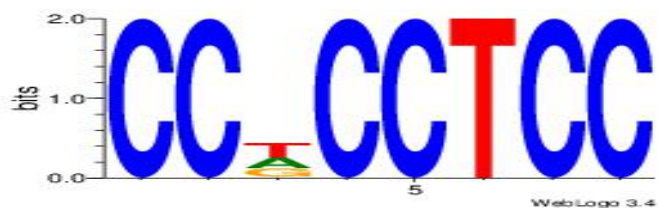
Reverse complement motif Consensus sequence: VVCACTTCCGG



Dataset #: 1
 Motif ID: 17
 Motif name: Motif 17
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 7
 Similarity score: 0.0632856

Alignment:
 GGAGGDGG
 GGAAGR-

Original motif Consensus sequence: CCDCCTCC



Reverse complement motif Consensus sequence: GGAGGDGG



Dataset #: 4
 Motif ID: 136
 Motif name: dwCAGAAGwh
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 7

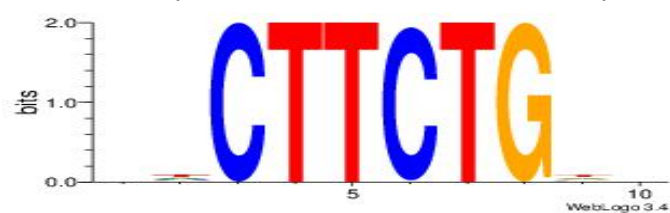
Similarity score: 0.0705782

Alignment:
HDCTTCTGHD
MMCTTCC---

Original motif Consensus sequence: DHCAGAAGDH



Reverse complement motif Consensus sequence: HDCTTCTGHD

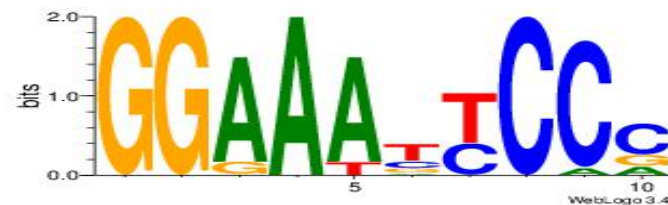


Dataset #: 3
Motif ID: 112
Motif name: RELA
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 7
Similarity score: 0.0712379

Alignment:
GGGRATTTC
---MMCTTCC

Original motif Consensus sequence: GGGRATTTC

Reverse complement motif Consensus sequence: GGAAATKCCC



Dataset #: 4
 Motif ID: 154
 Motif name: csCsCCTCCcc
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 7
 Similarity score: 0.0768131

Alignment:

BDGGAGGGGBV

--GGAAGRR--

Original motif Consensus sequence: VBCCCCTCCHB



Reverse complement motif Consensus sequence: BDGGAGGGGBV



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

Original motif Consensus sequence: CCDCCTCC



Reverse complement motif Consensus sequence: GGAGGDGG



Best Matches for Motif ID 17 (Highest to Lowest)

Dataset #:	4
Motif ID:	154
Motif name:	csCsCCTCCcc
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	2
Number of overlap:	8
Similarity score:	0.0325807

Alignment:

BDGGAGGGGBV

--GGAGGDGG--

Original motif Consensus sequence: VBCCCTCCHB



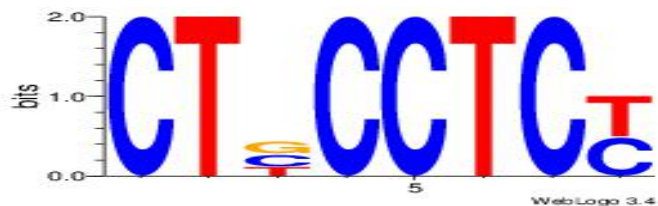
Reverse complement motif Consensus sequence: BDGGAGGGGBV



Dataset #: 1
 Motif ID: 11
 Motif name: Motif 11
 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: 0.0441606

Alignment:
 CTBCCTCY
 CCDCCTCC

Original motif Consensus sequence: CTBCCTCY



Reverse complement motif Consensus sequence: MGAGGBAG

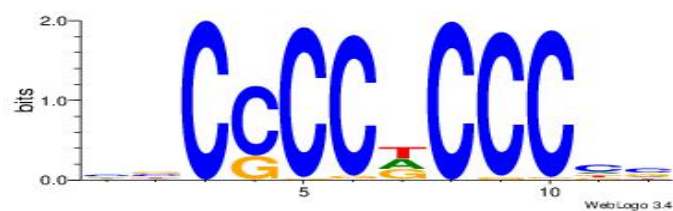


Dataset #: 4
 Motif ID: 155
 Motif name: csCSCCdCCCcs
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 4
 Number of overlap: 8

Similarity score: 0.0485525

Alignment:
VDGGGDGGGGBV
---GGAGGDGG--

Original motif Consensus sequence: VBCCCCDCCCHV



Reverse complement motif Consensus sequence: VDGGGDGGGGBV



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: 8
Similarity score: 0.0499486

Alignment:
CSGCCGCC
CCDCCTCC

Original motif Consensus sequence: CSGCCGCC

Reverse complement motif Consensus sequence: GCGGCSG



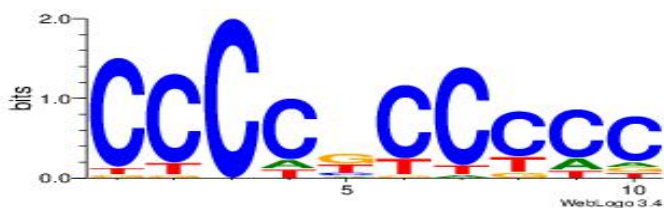
Dataset #: 3
 Motif ID: 116
 Motif name: SP1
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 8
 Similarity score: 0.0500496

Alignment:

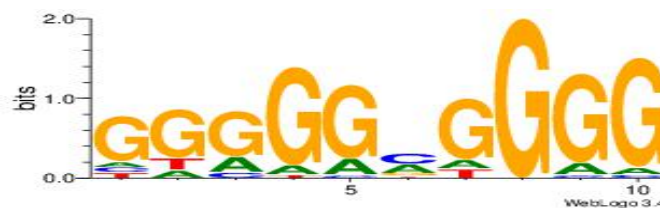
CCCCKCCCCC

--CCDCCTCC

Original motif Consensus sequence: CCCCKCCCCC



Reverse complement motif Consensus sequence: GGGGYGGGG



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

Original motif Consensus sequence: CATGYATG



Reverse complement motif Consensus sequence: CATKCATG



Best Matches for Motif ID 18 (Highest to Lowest)

Dataset #:	4
Motif ID:	152
Motif name:	yrCATGCAyr
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:	0.058327

Alignment:

HVTGCATGKV

CATGYATG--

Original motif Consensus sequence: BRCATGCABD



Reverse complement motif Consensus sequence: HVTGCATGKV



Dataset #: 1
 Motif ID: 31
 Motif name: Motif 31
 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: 0.0666244

Alignment:
 CATGYACA
 CATGYATG

Original motif Consensus sequence: CATGYACA



Reverse complement motif Consensus sequence: TGTKCATG



Dataset #: 3
 Motif ID: 125
 Motif name: TP53
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 8
 Number of overlap: 8

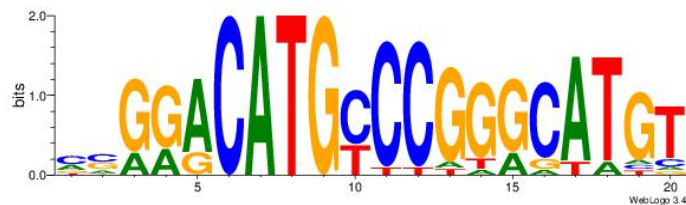
Similarity score: 0.068413

Alignment:

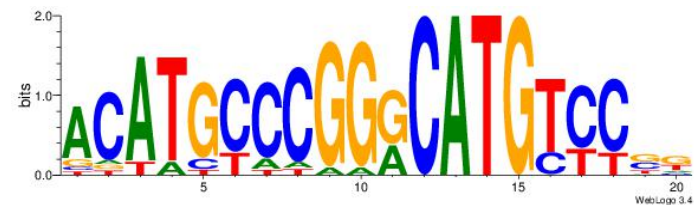
ACATGCCCGGKCATGTCCSR

-----CATKCATG-----

Original motif Consensus sequence: MSGGACATGYCCGGGCATGT



Reverse complement motif Consensus sequence: ACATGCCCGGKCATGTCCSR



Dataset #: 3
Motif ID: 118
Motif name: SRF
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: 0.0745698

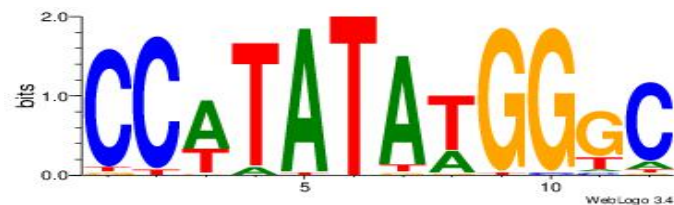
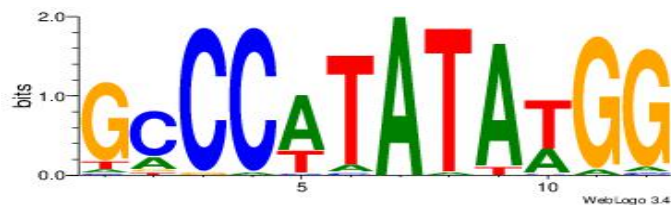
Alignment:

CCATATATGGGC

-CATGYATG---

Original motif Consensus sequence: GCCCATATATGG

Reverse complement motif Consensus sequence: CCATATATGGGC

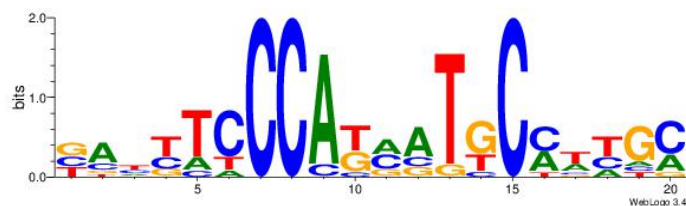


Dataset #: 3
 Motif ID: 131
 Motif name: znf143
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 8
 Similarity score: 0.105729

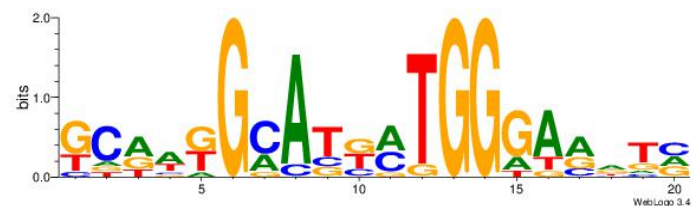
Alignment:

BAHYTCCCAKMATGCMWYGC
 -----CATKCATG--

Original motif Consensus sequence: BAHYTCCCAKMATGCMWYGC



Reverse complement motif Consensus sequence: GCMWRGCATYRTGGGAMHTB



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

Original motif Consensus sequence: CAGSCAG



Reverse complement motif Consensus sequence: CTGSCCTG



Best Matches for Motif ID 19 (Highest to Lowest)

Dataset #:	1
Motif ID:	33
Motif name:	Motif 33
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	7
Similarity score:	0.0196488

Alignment:
 GWAGCCAG
 -CAGSCAG

Original motif Consensus sequence: CTGGCTWC



Reverse complement motif Consensus sequence: GWAGCCAG



Dataset #: 1
 Motif ID: 28
 Motif name: Motif 28
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 7
 Similarity score: 0.0338273

Alignment:
 CTCCTG
 CTGCTG

Original motif Consensus sequence: CTCCTG



Reverse complement motif Consensus sequence: CAGGAAG



Dataset #: 1
 Motif ID: 11
 Motif name: Motif 11
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 7

Similarity score: 0.0430055

Alignment:
MGAGGBAG
CAGSCAG-

Original motif Consensus sequence: CTBCCTCY



Reverse complement motif Consensus sequence: MGAGGBAG



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: 1
Number of overlap: 7
Similarity score: 0.0473229

Alignment:
GAGGCCAG
CAGSCAG-

Original motif Consensus sequence: CTGGCCTC

Reverse complement motif Consensus sequence: GAGGCCAG



Dataset #: 1
 Motif ID: 25
 Motif name: Motif 25
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 7
 Similarity score: 0.0479304

Alignment:
 CTGRGTTC
 CTGSCTG-

Original motif Consensus sequence: CTGRGTTC



Reverse complement motif Consensus sequence: GAACKCAG



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

Original motif Consensus sequence: CACGTR



Reverse complement motif Consensus sequence: MACGTG



Best Matches for Motif ID 20 (Highest to Lowest)

Dataset #:	3
Motif ID:	71
Motif name:	Arnt
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	6
Similarity score:	0

Alignment:

CACGTG

CACGTR

Original motif Consensus sequence: CACGTG



Reverse complement motif Consensus sequence: CACGTG



Dataset #: 3
 Motif ID: 95
 Motif name: MYCMAX
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3
 Number of overlap: 6
 Similarity score: 0.0102183

Alignment:

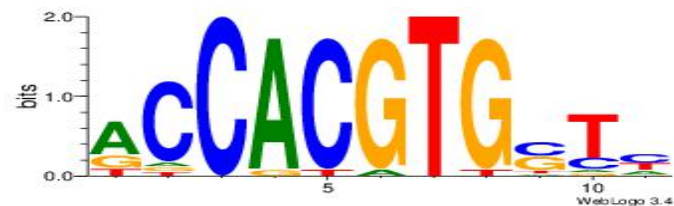
ACCACGTGSTM

--CACGTR---

Original motif Consensus sequence: RASCACGTGGT



Reverse complement motif Consensus sequence: ACCACGTGSTM



Dataset #: 3
 Motif ID: 91
 Motif name: MAX
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 6

Similarity score: 0.011152

Alignment:

BCACGTGDTD

-CACGTR---

Original motif Consensus sequence: DAHCACGTGD



Reverse complement motif Consensus sequence: BCACGTGDTD



Dataset #: 3
Motif ID: 126
Motif name: USF1
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 2
Number of overlap: 6
Similarity score: 0.0131944

Alignment:

MCACGTG

-CACGTR

Original motif Consensus sequence: CACGTGR

Reverse complement motif Consensus sequence: MCACGTG



Dataset #: 3
 Motif ID: 94
 Motif name: Myc
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 6
 Similarity score: 0.0253396

Alignment:

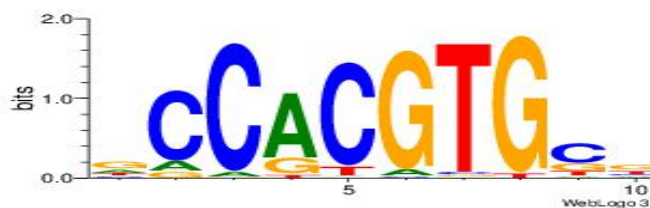
DCCACGTGCV

--CACGTR--

Original motif Consensus sequence: VGCACGTGGH

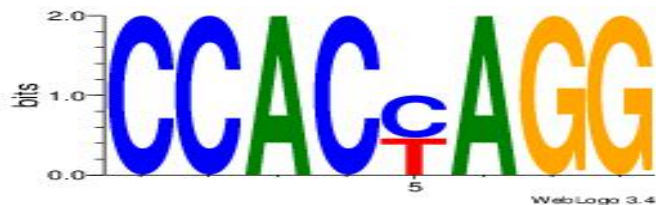


Reverse complement motif Consensus sequence: DCCACGTGCV



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

Original motif Consensus sequence: CCACYAGG



Reverse complement motif Consensus sequence: CCTKGTGG



Best Matches for Motif ID 21 (Highest to Lowest)

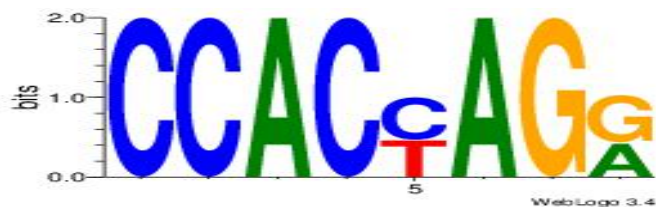
Dataset #:	2
Motif ID:	48
Motif name:	Motif 48
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	8
Similarity score:	0.00903109

Alignment:

CCACYAGR

CCACYAGG

Original motif Consensus sequence: CCACYAGR



Reverse complement motif Consensus sequence: MCTKGTGG

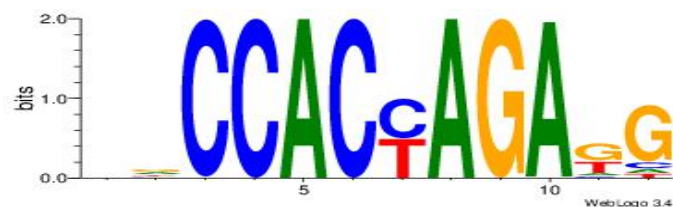


Dataset #: 4
 Motif ID: 145
 Motif name: grCCACyAGAkG
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3
 Number of overlap: 8
 Similarity score: 0.028408

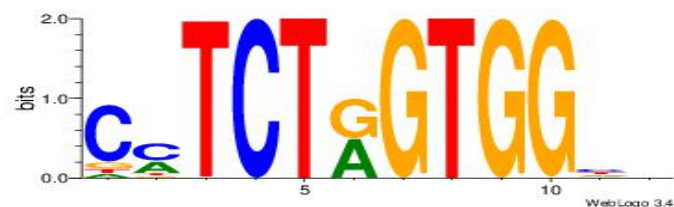
Alignment:

CYTCTKGTGGHH
 --CCTKGTGG--

Original motif Consensus sequence: DDCCACYAGAKG



Reverse complement motif Consensus sequence: CYTCTKGTGGHH



Dataset #: 4
 Motif ID: 158
 Motif name: grCCACwAGrk
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 8

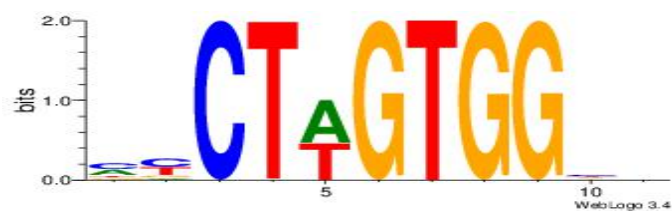
Similarity score: 0.0314791

Alignment:
DDCCACWAGRK
--CCACYAGG--

Original motif Consensus sequence: DDCCACWAGRK



Reverse complement motif Consensus sequence: YMCTWGTGGHH

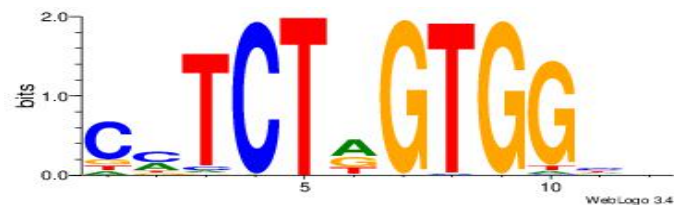
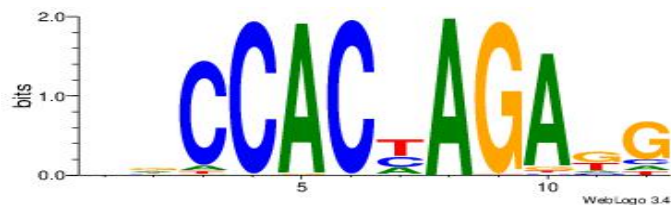


Dataset #: 4
Motif ID: 138
Motif name: grCCACyAGAkG
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 3
Number of overlap: 8
Similarity score: 0.0373754

Alignment:
DDCCACYAGAKG
--CCACYAGG--

Original motif Consensus sequence: DDCCACYAGAKG

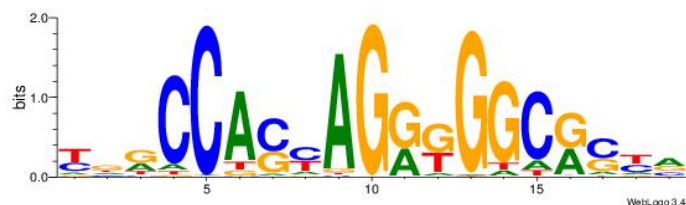
Reverse complement motif Consensus sequence: CYTCTMGTGGHH



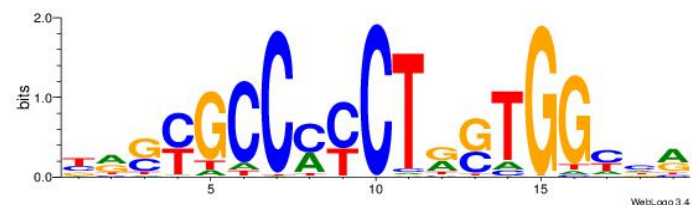
Dataset #: 3
 Motif ID: 74
 Motif name: CTCF
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 9
 Number of overlap: 8
 Similarity score: 0.0387762

Alignment:
 BSMGCCYMCTKSTGGMHM
 -----CCTKGTGG---

Original motif Consensus sequence: YDRCCASYAGRKGGRSYV



Reverse complement motif Consensus sequence: BSMGCCYMCTKSTGGMHM



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

Original motif Consensus sequence: CAGATYCC



Reverse complement motif Consensus sequence: GGKATCTG



Best Matches for Motif ID 22 (Highest to Lowest)

Dataset #:	2
Motif ID:	53
Motif name:	Motif 53
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	8
Similarity score:	0

Alignment:

GGGATCTG

GGKATCTG

Original motif Consensus sequence: CAGATCCC



Reverse complement motif Consensus sequence: GGGATCTG

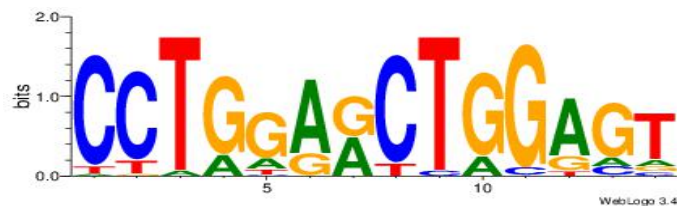


Dataset #: 2
 Motif ID: 69
 Motif name: Motif 69
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 5
 Number of overlap: 8
 Similarity score: 0.060058

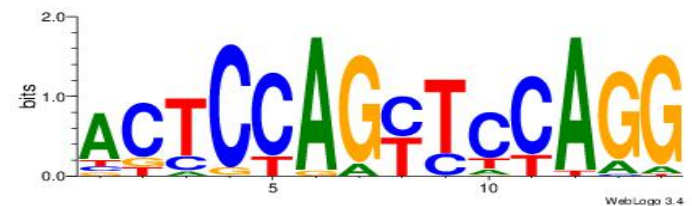
Alignment:

ACTCCAGMTCCAGG
 ----CAGATYCC--

Original motif Consensus sequence: CCTGGARCTGGAGT



Reverse complement motif Consensus sequence: ACTCCAGMTCCAGG

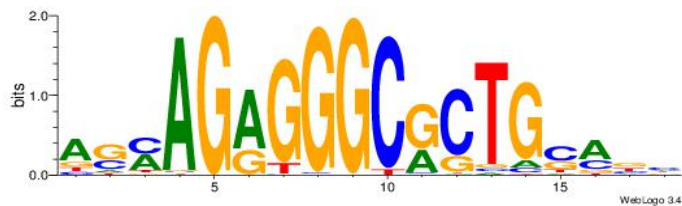


Dataset #: 4
 Motif ID: 149
 Motif name: asmAGRGGGCrCTGsmkc
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 7
 Number of overlap: 8

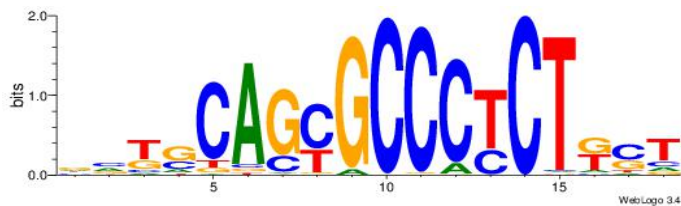
Similarity score: 0.0603056

Alignment:
DBTSCAGMGCCCTCTRST
-----CAGATYCC-----

Original motif Consensus sequence: ASMAGAGGGCRCTGSABH



Reverse complement motif Consensus sequence:
DBTSCAGMGCCCTCTRST



Dataset #: 2
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: 8
Similarity score: 0.0721296

Alignment:
CATATRCA
CAGATYCC

Original motif Consensus sequence: CATATRCA

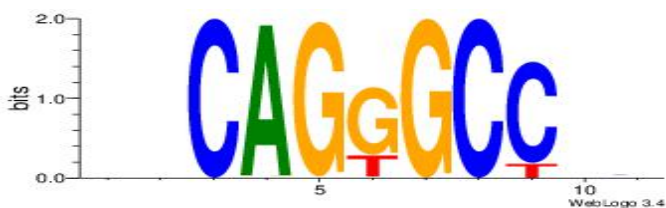
Reverse complement motif Consensus sequence: TGMATATG



Dataset #: 4
 Motif ID: 160
 Motif name: brCAGGGCCrs
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 8
 Similarity score: 0.0730966

Alignment:
 BBGGCCCTGBB
 -GGKATCTG--

Original motif Consensus sequence: BVCAGGGCCVB



Reverse complement motif Consensus sequence: BBGGCCCTGBB

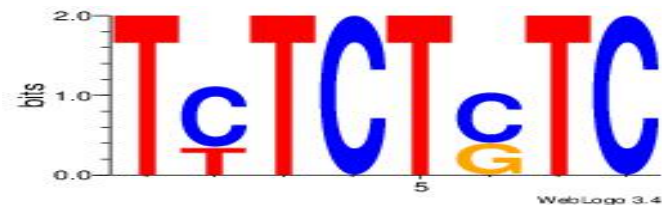


Dataset #: 1 Motif ID: 23 Motif name: Motif 23

Original motif Consensus sequence: GASAGAGA



Reverse complement motif Consensus sequence: TCTCTSTC



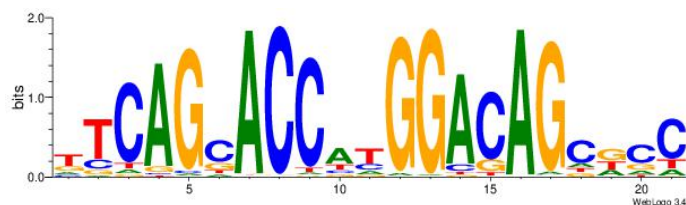
Best Matches for Motif ID 23 (Highest to Lowest)

Dataset #:	3
Motif ID:	113
Motif name:	REST
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	13
Number of overlap:	8
Similarity score:	0.0614501

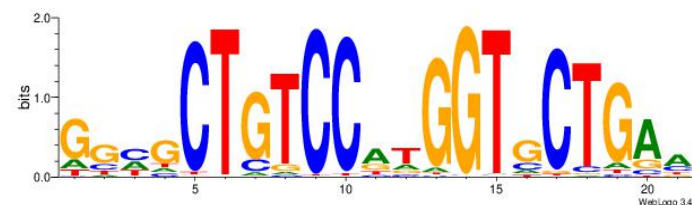
Alignment:

```
TTCAGCACCATGGACAGCKCC
-----GASAGAGA-----
```

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC



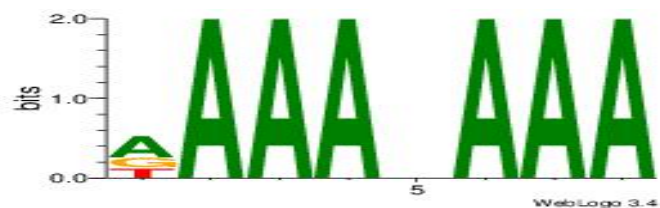
Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA



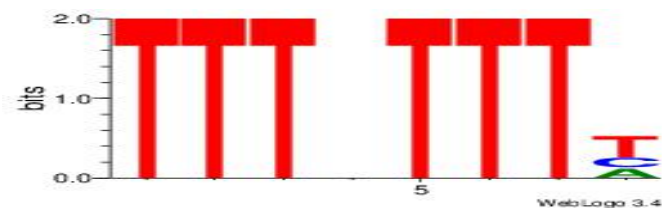
Dataset #: 1
 Motif ID: 2
 Motif name: Motif 2
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 8
 Similarity score: 0.0761109

Alignment:
 AAAAHAAA
 GASAGAGA

Original motif Consensus sequence: AAAAHAAA



Reverse complement motif Consensus sequence: TTTDTTTT



Dataset #: 1
 Motif ID: 38
 Motif name: Motif 38
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 8

Similarity score: 0.081673

Alignment:
GAGTTACA
GASAGAGA

Original motif Consensus sequence: GAGTTACA



Reverse complement motif Consensus sequence: TGTAAGTC



Dataset #: 2
Motif ID: 51
Motif name: Motif 51
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 8
Similarity score: 0.081673

Alignment:
GAGTTACA
GASAGAGA

Original motif Consensus sequence: GAGTTACA

Reverse complement motif Consensus sequence: TGTAAGTC



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: 8
 Similarity score: 0.0826138

Alignment:
 CACACACA
 GASAGAGA

Original motif Consensus sequence: CACACACA



Reverse complement motif Consensus sequence: TGTGTGTG



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

Original motif Consensus sequence: TGTGGGTG



Reverse complement motif Consensus sequence: CACCCACA



Best Matches for Motif ID 24 (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:	8
Similarity score:	0.0589779

Alignment:

CACACACA

CACCCACA

Original motif Consensus sequence: CACACACA



Reverse complement motif Consensus sequence: TGTGTGTG



Dataset #: 4
 Motif ID: 162
 Motif name: ccAsCCCCAcc
 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: 0.060611

Alignment:

HVASCCCCABH
 -CACCCACA--

Original motif Consensus sequence: HVASCCCCABH



Reverse complement motif Consensus sequence: DBTGGGGSTVD

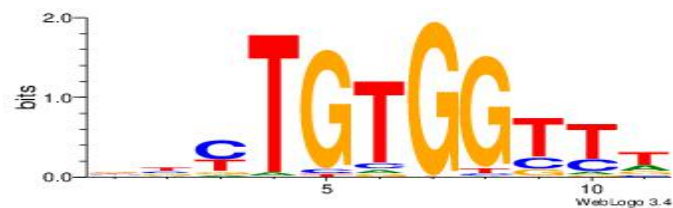


Dataset #: 3
 Motif ID: 114
 Motif name: RUNX1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 4
 Number of overlap: 8

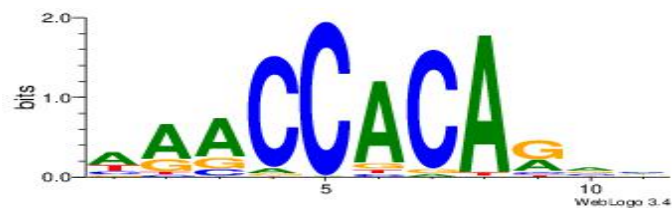
Similarity score: 0.0649239

Alignment:
AAACCACAKVB
CACCCACA---

Original motif Consensus sequence: BBYTGTGGTTT



Reverse complement motif Consensus sequence: AAACCACAKVB



Dataset #: 1
Motif ID: 31
Motif name: Motif 31
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: 0.0828996

Alignment:
TGTKCATG
TGTGGGTG

Original motif Consensus sequence: CATGYACA

Reverse complement motif Consensus sequence: TGTKCATG



Dataset #: 1
 Motif ID: 34
 Motif name: Motif 34
 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: 0.0843302

Alignment:
 TGTGGYCA
 TGTGGGTG

Original motif Consensus sequence: TGKCCACA



Reverse complement motif Consensus sequence: TGTGGYCA



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

Original motif Consensus sequence: CTGRGTTTC



Reverse complement motif Consensus sequence: GAACKCAG



Best Matches for Motif ID 25 (Highest to Lowest)

Dataset #:	1
Motif ID:	33
Motif name:	Motif 33
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	8
Similarity score:	0.0224867

Alignment:

CTGGCTWC

CTGRGTTTC

Original motif Consensus sequence: CTGGCTWC



Reverse complement motif Consensus sequence: GWAGCCAG



Dataset #: 1
 Motif ID: 10
 Motif name: Motif 10
 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: 0.034485

Alignment:
 CTGGCCTC
 CTGRGTTC

Original motif Consensus sequence: CTGGCCTC



Reverse complement motif Consensus sequence: GAGGCCAG



Dataset #: 2
 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: 8

Similarity score: 0.052298

Alignment:
CTGGCCTC
CTGRGTTC

Original motif Consensus sequence: CTGGCCTC



Reverse complement motif Consensus sequence: GAGGCCAG

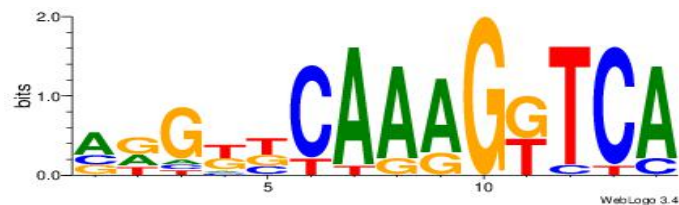


Dataset #: 3
Motif ID: 107
Motif name: NR2F1
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 6
Number of overlap: 8
Similarity score: 0.0551569

Alignment:
TGAMCTTTGMMCYT
-GAACKCAG-----

Original motif Consensus sequence: TGAMCTTTGMMCYT

Reverse complement motif Consensus sequence: AKGYCAAAGRTC



Dataset #: 1
 Motif ID: 37
 Motif name: Motif 37
 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: 0.0560348

Alignment:
 CTGAGCYA
 CTGRGTTC

Original motif Consensus sequence: CTGAGCYA



Reverse complement motif Consensus sequence: TKGCTCAG



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

Original motif Consensus sequence: CAGAGGAY



Reverse complement motif Consensus sequence: KTCCTCTG



Best Matches for Motif ID 26 (Highest to Lowest)

Dataset #:	4
Motif ID:	136
Motif name:	dwCAGAAGwh
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:	0.0359628

Alignment:

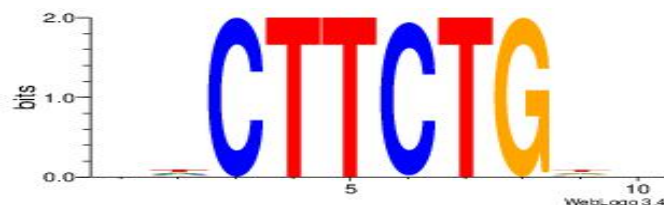
DHCAGAAGDH

--CAGAGGAY

Original motif Consensus sequence: DHCAGAAGDH



Reverse complement motif Consensus sequence: HDCTTCTGHD



Dataset #: 4
 Motif ID: 166
 Motif name: CasCAGrGGGCrSy
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 4
 Number of overlap: 8
 Similarity score: 0.036576

Alignment:

CACCAGRGGGCRSB
 ---CAGAGGAY---

Original motif Consensus sequence: CACCAGRGGGCRSB



Reverse complement motif Consensus sequence: BSKGCCCKCTGGT

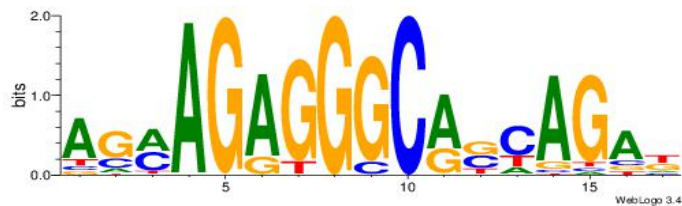


Dataset #: 4
 Motif ID: 143
 Motif name: AgmAGAGGGCrscAGak
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 8
 Number of overlap: 8

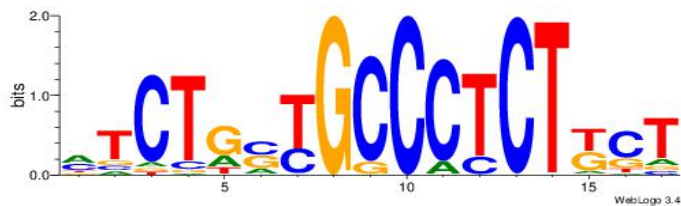
Similarity score: 0.0438271

Alignment:
AGMAGAGGGCASCAGAK
--CAGAGGAY-----

Original motif Consensus sequence: AGMAGAGGGCASCAGAK



Reverse complement motif Consensus sequence:
RTCTGSTGCCCTCTYCT

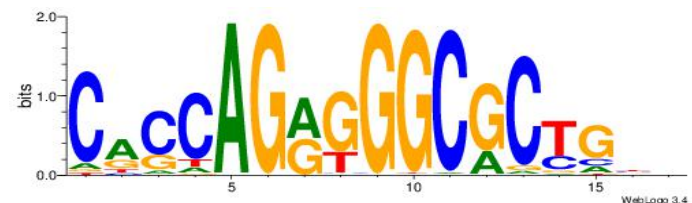
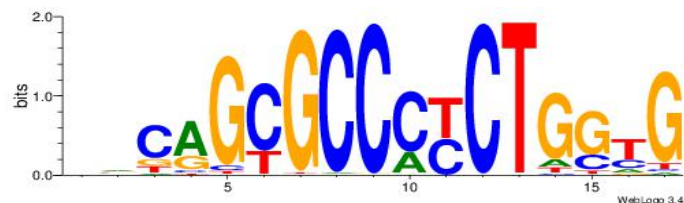


Dataset #: 4
Motif ID: 168
Motif name: yrcrYGCCMyCTGGtG
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 7
Number of overlap: 8
Similarity score: 0.0450811

Alignment:
CACCAGMGGGCGCTGBD
---CAGAGGAY-----

Original motif Consensus sequence: HVCAGCGCCCYCTGGTG

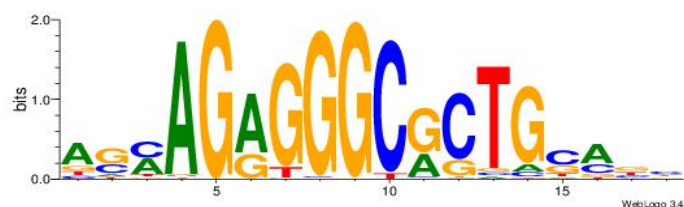
Reverse complement motif Consensus sequence:
CACCAGMGGGCGCTGBD



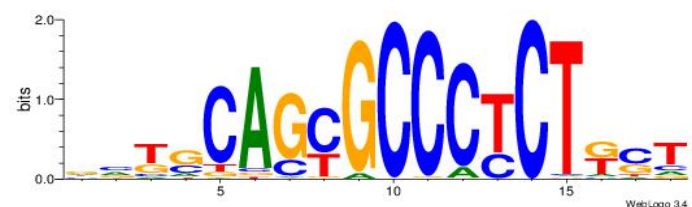
Dataset #: 4
 Motif ID: 149
 Motif name: asmAGRGGGCrCTGsmkc
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 9
 Number of overlap: 8
 Similarity score: 0.0460269

Alignment:
 DBTSCAGMGCCCTCTRST
 -----KTCCTCTG--

Original motif Consensus sequence: ASMAGAGGGCRCTGSABH



Reverse complement motif Consensus sequence: DBTSCAGMGCCCTCTRST



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

Original motif Consensus sequence: CSGCCGCC



Reverse complement motif Consensus sequence: GGCGGCSG



Best Matches for Motif ID 27 (Highest to Lowest)

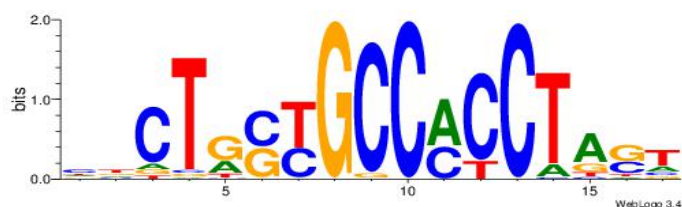
Dataset #:	4
Motif ID:	144
Motif name:	ctCTrsyGCCmCCTast
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	5
Number of overlap:	8
Similarity score:	0.0594103

Alignment:

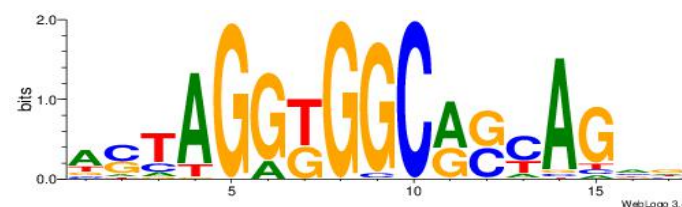
ASTAGGYGGCMSCAGDD

-----GGCGGCSG-----

Original motif Consensus sequence: HDCTGSYGCCMCCTAST



Reverse complement motif Consensus sequence: ASTAGGYGGCMSCAGDD

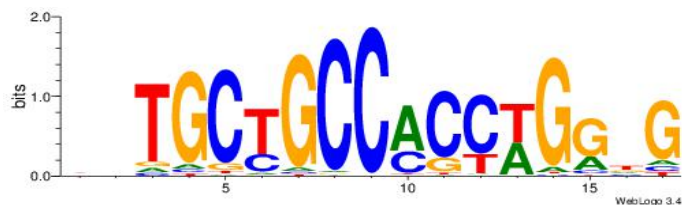


Dataset #: 4
 Motif ID: 169
 Motif name: yvTGCyGCCmCCwGgtG
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 6
 Number of overlap: 8
 Similarity score: 0.0661709

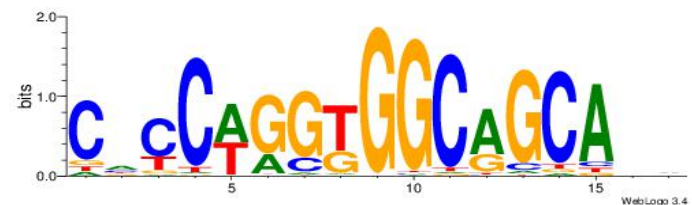
Alignment:

CDCCWGGTGGCAGCAVV
 -----GGCGGCSG-----

Original motif Consensus sequence: BVTGCTGCCACCWGGDG



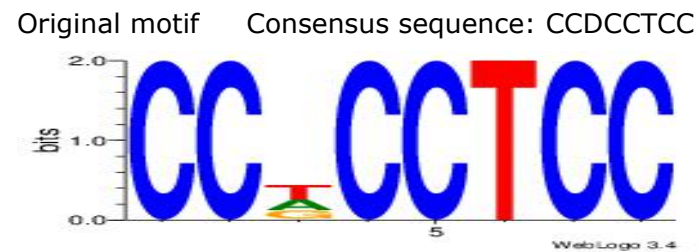
Reverse complement motif Consensus sequence: CDCCWGGTGGCAGCAVV



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: 1

Alignment:

```
CCDCCTCC
CSGCCGCC
```



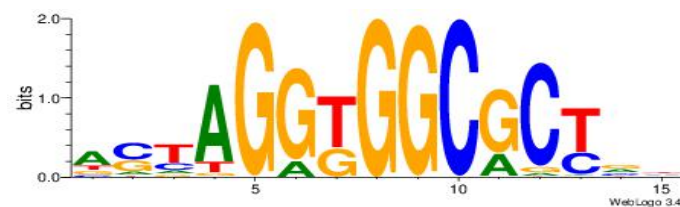
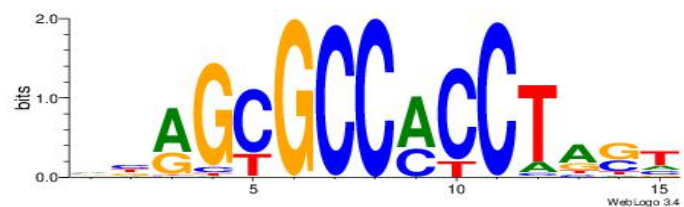
Dataset #:	4
Motif ID:	146
Motif name:	myrGYGCCmCCTast
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	4
Number of overlap:	8
Similarity score:	0.0682918

Alignment:

```
ASTAGGYGGCGCTBB
-----GGCGGCSG----
```

Original motif Consensus sequence: VBAGCGCCMCCTAST

Reverse complement motif Consensus sequence: ASTAGGYGGCGCT



Dataset #: 4
 Motif ID: 135
 Motif name: ssCGGCCGss
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 8
 Similarity score: 0.0688339

Alignment:

BSCGGCCGSV

GGCGGCSG--

Original motif Consensus sequence: BSCGGCCGSV



Reverse complement motif Consensus sequence: VSCGGCCGSB



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

Original motif Consensus sequence: CTCCTG



Reverse complement motif Consensus sequence: CAGGAAG



Best Matches for Motif ID 28 (Highest to Lowest)

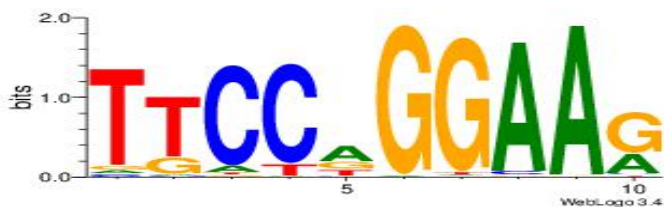
Dataset #:	3
Motif ID:	119
Motif name:	Stat3
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	4
Number of overlap:	7
Similarity score:	0.0301014

Alignment:

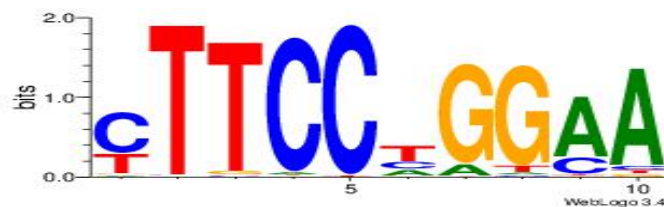
TTCCAGGAAG

---CAGGAAG

Original motif Consensus sequence: TTCCAGGAAG



Reverse complement motif Consensus sequence: CTCCTGGAA



Dataset #: 3
 Motif ID: 84
 Motif name: GABPA
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 7
 Similarity score: 0.0389741

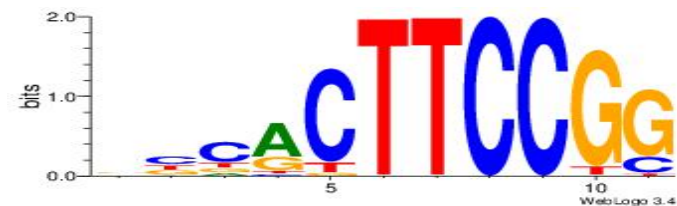
Alignment:

CCGGAAGTGVV
 CAGGAAG----

Original motif Consensus sequence: CCGGAAGTGVV



Reverse complement motif Consensus sequence: VVCACTTCGG



Dataset #: 3
 Motif ID: 80
 Motif name: ELK4
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 7

Similarity score: 0.044949

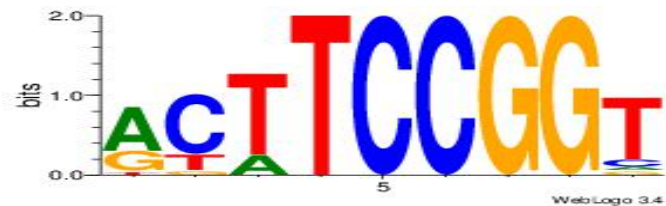
Alignment:

ACCGGAAGT
-CAGGAAG-

Original motif Consensus sequence: ACCGGAAGT



Reverse complement motif Consensus sequence: ACTTCGGT



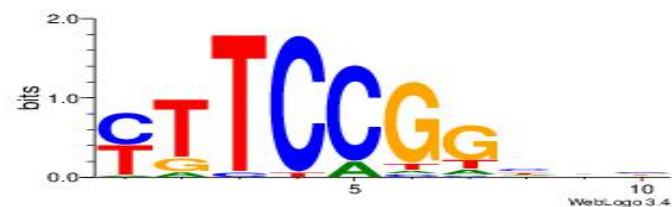
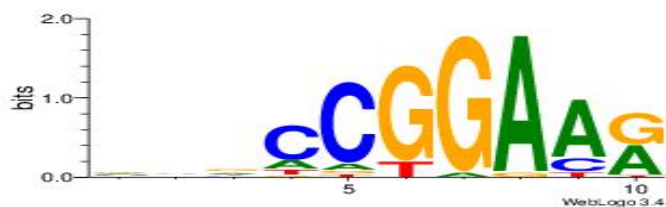
Dataset #: 3
Motif ID: 79
Motif name: ELK1
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 7
Similarity score: 0.0709694

Alignment:

VDDCCGGAAR
---CAGGAAG

Original motif Consensus sequence: VDDCCGGAAR

Reverse complement motif Consensus sequence: MTTCCGGHBV



Dataset #: 1
 Motif ID: 19
 Motif name: Motif 19
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 7
 Similarity score: 0.0713134

Alignment:
 CAGSCAG
 CAGGAAG

Original motif Consensus sequence: CAGSCAG



Reverse complement motif Consensus sequence: CTGSCCTG



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

Original motif Consensus sequence: CATTTCY



Reverse complement motif Consensus sequence: MGAAATG



Best Matches for Motif ID 29 (Highest to Lowest)

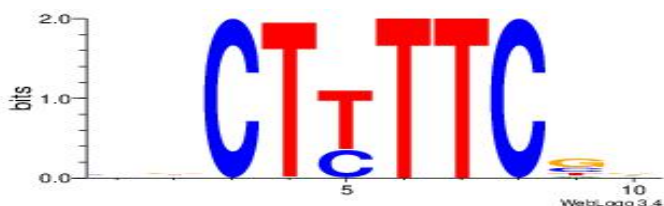
Dataset #:	4
Motif ID:	139
Motif name:	mkCTyTTCsg
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	3
Number of overlap:	7
Similarity score:	0.0479916

Alignment:

HBGAAAAGBD

-MGAAATG--

Original motif Consensus sequence: HBCTTTTCBD



Reverse complement motif Consensus sequence: HBGAAAAGBD



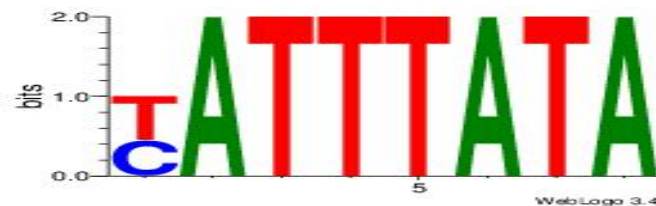
Dataset #: 2
 Motif ID: 66
 Motif name: Motif 66
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 7
 Similarity score: 0.050303

Alignment:
 TATAAATR
 -MGAAATG

Original motif Consensus sequence: TATAAATR



Reverse complement motif Consensus sequence: KATTTATA



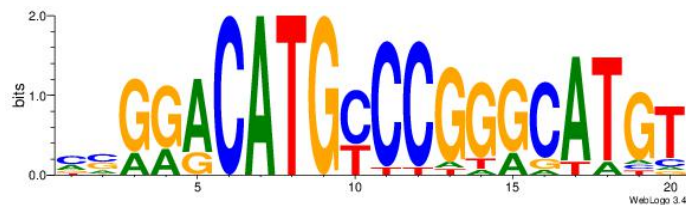
Dataset #: 3
 Motif ID: 125
 Motif name: TP53
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 12
 Number of overlap: 7

Similarity score: 0.058821

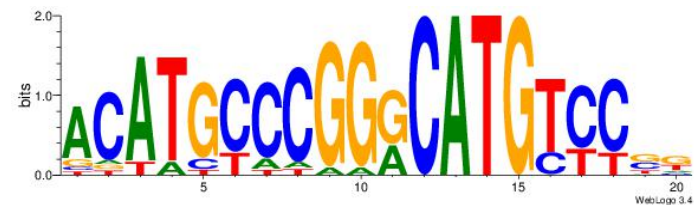
Alignment:

ACATGCCCGGKCATGTCCSR
-----CATTTCY--

Original motif Consensus sequence: MSGGACATGYCCGGGCATGT



Reverse complement motif Consensus sequence:
ACATGCCCGGKCATGTCCSR



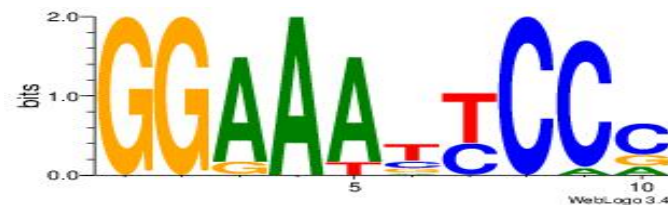
Dataset #: 3
Motif ID: 112
Motif name: RELA
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 7
Similarity score: 0.0629654

Alignment:

GGAAATKCCC
MGAAATG---

Original motif Consensus sequence: GGGRATTTCC

Reverse complement motif Consensus sequence: GGAAATKCCC



Dataset #: 3
 Motif ID: 84
 Motif name: GABPA
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3
 Number of overlap: 7
 Similarity score: 0.0668119

Alignment:

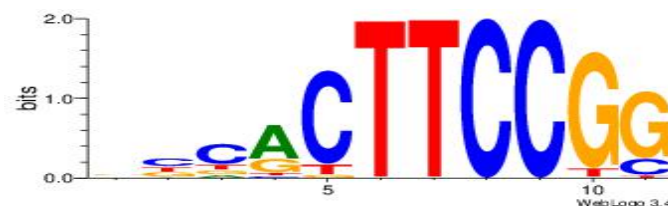
VVCACTTCCGG

--CATTTTCY--

Original motif Consensus sequence: CCGGAAGTG



Reverse complement motif Consensus sequence: VVCACTTCCGG



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

Original motif Consensus sequence: CWGCAGC



Reverse complement motif Consensus sequence: GCTGCWG



Best Matches for Motif ID 30 (Highest to Lowest)

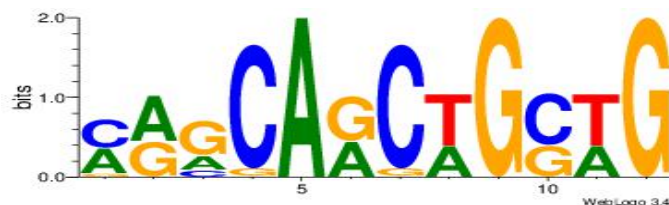
Dataset #:	3
Motif ID:	97
Motif name:	Myf
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	7
Similarity score:	0.0232337

Alignment:

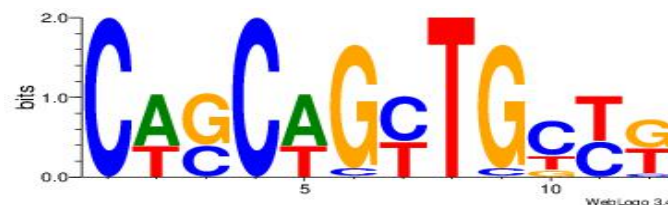
MRGCARCWGSWG

-----GCTGCWG

Original motif Consensus sequence: MRGCARCWGSWG



Reverse complement motif Consensus sequence: CWSCWGMTGCKR



Dataset #: 1
 Motif ID: 41
 Motif name: Motif 41
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 7
 Similarity score: 0.027698

Alignment:
 CCTGCTGK
 GCTGCWG-

Original motif Consensus sequence: CCTGCTGK



Reverse complement motif Consensus sequence: YCAGCAGG

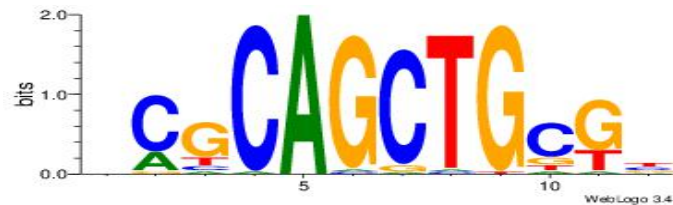


Dataset #: 3
 Motif ID: 105
 Motif name: NHLH1
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 7

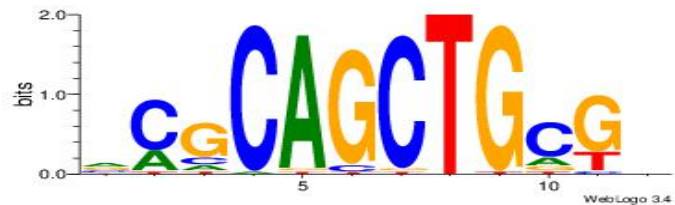
Similarity score: 0.032311

Alignment:
VCGCAGCTGCGV
CWGCAGC-----

Original motif Consensus sequence: VCGCAGCTGCGB



Reverse complement motif Consensus sequence: VCGCAGCTGCGV



Dataset #: 1
Motif ID: 27
Motif name: Motif 27
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 2
Number of overlap: 7
Similarity score: 0.037602

Alignment:
GGCGGCSG
-GCTGCWG

Original motif Consensus sequence: CSGCCGCC

Reverse complement motif Consensus sequence: GGCGGCSG



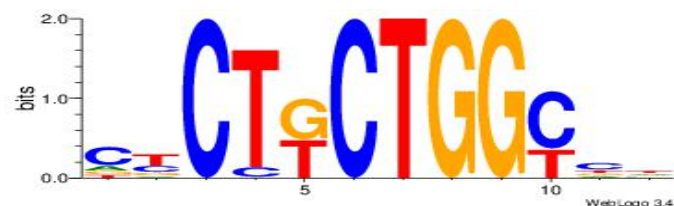
Dataset #: 4
 Motif ID: 151
 Motif name: agrCCAGmAGrg
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 5
 Number of overlap: 7
 Similarity score: 0.0377961

Alignment:
 CKCTRCTGGCVH
 -GCTGCWG----

Original motif Consensus sequence: HVGCCAGMAGRG



Reverse complement motif Consensus sequence: CKCTRCTGGCVH



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

Original motif Consensus sequence: CATGYACA



Reverse complement motif Consensus sequence: TGTKCATG



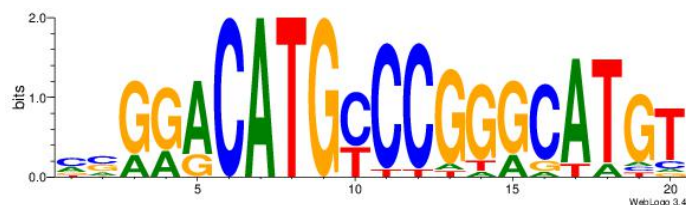
Best Matches for Motif ID 31 (Highest to Lowest)

Dataset #: 3
Motif ID: 125
Motif name: TP53
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: 0.0607115

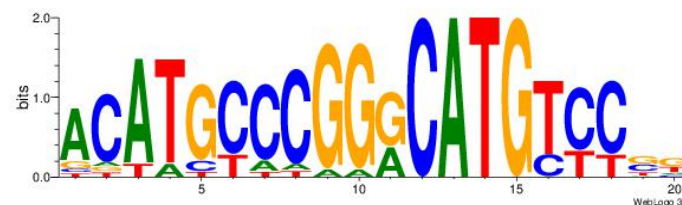
Alignment:

```
ACATGCCCGGKCATGTCCSR  
-----TGTKCATG-----
```

Original motif Consensus sequence: MSGGACATGYCCGGGCATGT



Reverse complement motif Consensus sequence:
ACATGCCCGGKCATGTCCSR



Dataset #: 4
 Motif ID: 152
 Motif name: yrCATGCAyr
 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: 0.0609044

Alignment:

BRCATGCABD

--CATGYACA

Original motif Consensus sequence: BRCATGCABD



Reverse complement motif Consensus sequence: HVTGCATGKV



Dataset #: 1
 Motif ID: 18
 Motif name: Motif 18
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 8

Similarity score: 0.0666244

Alignment:

CATGYATG

CATGYACA

Original motif Consensus sequence: CATGYATG



Reverse complement motif Consensus sequence: CATKCATG



Dataset #: 2
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: 8
Similarity score: 0.0706964

Alignment:

CATATRCA

CATGYACA

Original motif Consensus sequence: CATATRCA

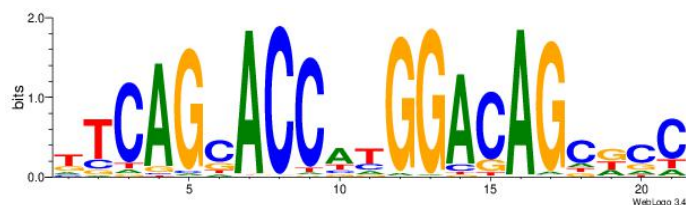
Reverse complement motif Consensus sequence: TGMATATG



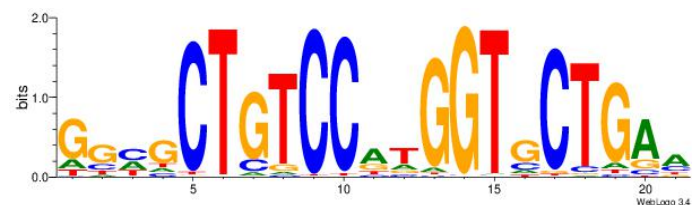
Dataset #: 3
 Motif ID: 113
 Motif name: REST
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 6
 Number of overlap: 8
 Similarity score: 0.0726387

Alignment:
 GYGCTGTCCATGGTGCTGAA
 -----TGTKCATG-----

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC



Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA



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

Original motif Consensus sequence: KAATAAA



Reverse complement motif Consensus sequence: TTTATTY



Best Matches for Motif ID 32 (Highest to Lowest)

Dataset #: 2
 Motif ID: 52
 Motif name: Motif 52
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 7
 Similarity score: 0.017829

Alignment:
 WTTTATTT
 -TTTATTY

Original motif Consensus sequence: AAATAAAW



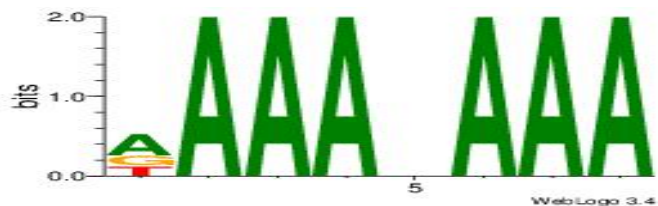
Reverse complement motif Consensus sequence: WTTTATTT



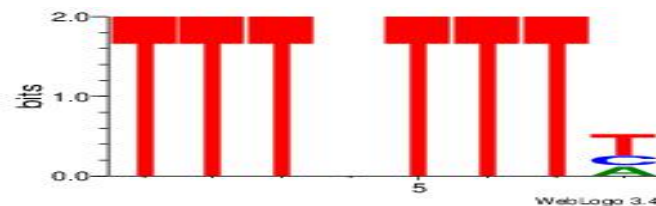
Dataset #: 1
 Motif ID: 2
 Motif name: Motif 2
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 7
 Similarity score: 0.0445453

Alignment:
 TTTDTTTT
 TTTATTY-

Original motif Consensus sequence: AAAAHAAA



Reverse complement motif Consensus sequence: TTTDTTTT

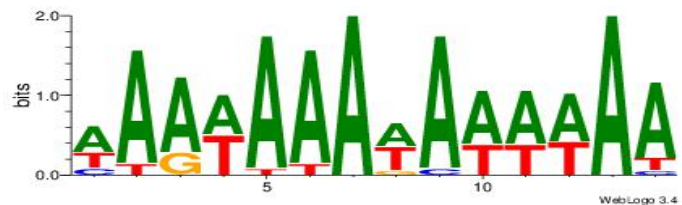


Dataset #: 2
 Motif ID: 68
 Motif name: Motif 68
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 8
 Number of overlap: 7

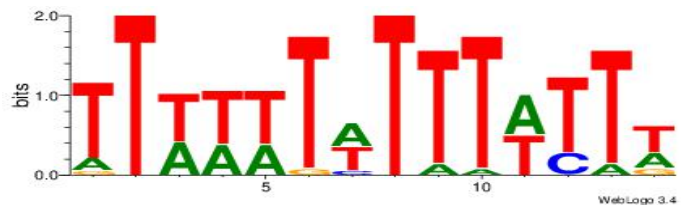
Similarity score: 0.0470498

Alignment:
TTWWWTWTTTWTTW
-----TTTATTY

Original motif Consensus sequence: WAAWAAAWAWWWAA



Reverse complement motif Consensus sequence: TTWWWTWTTTWTTW

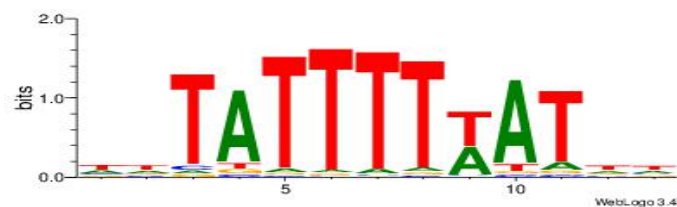
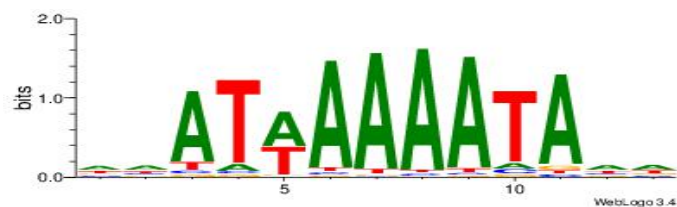


Dataset #: 4
Motif ID: 150
Motif name: waATwAAAATAww
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 7
Similarity score: 0.0674341

Alignment:
DHTATTTTWATHD
-----TTTATTY

Original motif Consensus sequence: DHATWAAAATAHD

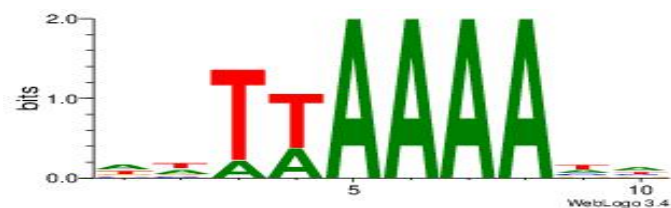
Reverse complement motif Consensus sequence: DHTATTTTWATHD



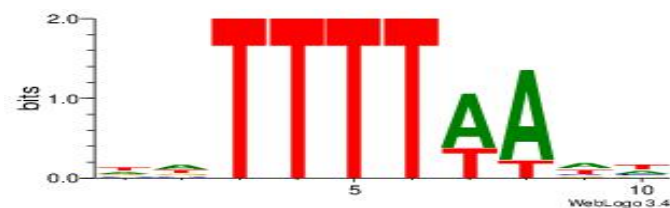
Dataset #: 4
 Motif ID: 148
 Motif name: wwTwAAAAww
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 7
 Similarity score: 0.0811175

Alignment:
 HHTTTTWADD
 ---TTTATTY

Original motif Consensus sequence: DDTWAAAAHH



Reverse complement motif Consensus sequence: HHTTTTWADD



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

Original motif Consensus sequence: CTGGCTWC



Reverse complement motif Consensus sequence: GWAGCCAG



Best Matches for Motif ID 33 (Highest to Lowest)

Dataset #:	2
Motif ID:	49
Motif name:	Motif 49
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:	0.011666

Alignment:

CTGGCCTC

CTGGCTWC

Original motif Consensus sequence: CTGGCCTC



Reverse complement motif Consensus sequence: GAGGCCAG



Dataset #: 1
 Motif ID: 10
 Motif name: Motif 10
 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: 0.029479

Alignment:
 CTGGCCTC
 CTGGCTWC

Original motif Consensus sequence: CTGGCCTC



Reverse complement motif Consensus sequence: GAGGCCAG



Dataset #: 1
 Motif ID: 25
 Motif name: Motif 25
 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: 0.0400133

Alignment:

CTGRGTTC

CTGGCTWC

Original motif Consensus sequence: CTGRGTTC



Reverse complement motif Consensus sequence: GAACKCAG



Dataset #: 4
Motif ID: 163
Motif name: gwGGCCAGmAGAGGGCrby
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: 0.050611

Alignment:

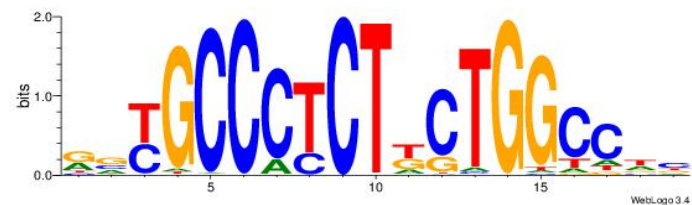
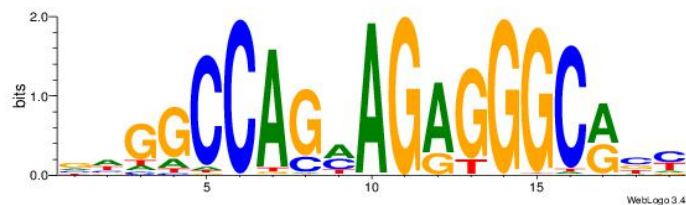
KBKGCCCTCTYCTGGCCHV

-----CTGGCTWC

Original motif Consensus sequence: VHGGCCAGMAGAGGGCRBY

Reverse complement motif
KBKGCCCTCTYCTGGCCHV

Consensus sequence:



Dataset #: 4
 Motif ID: 133
 Motif name: shAGrGGGCAGy
 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: 0.0636793

Alignment:
 DBTGCCCKCTDS
 -CTGGCTWC---

Original motif Consensus sequence: SHAGRGGGCABH



Reverse complement motif Consensus sequence: DBTGCCCKCTDS



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

Original motif Consensus sequence: TGKCCACA



Reverse complement motif Consensus sequence: TGTGGYCA



Best Matches for Motif ID 34 (Highest to Lowest)

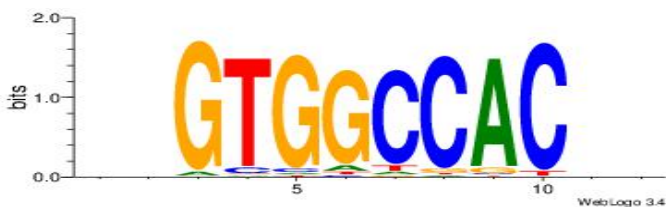
Dataset #:	4
Motif ID:	171
Motif name:	ysGTGGCCACsr
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	2
Number of overlap:	8
Similarity score:	0.0504663

Alignment:

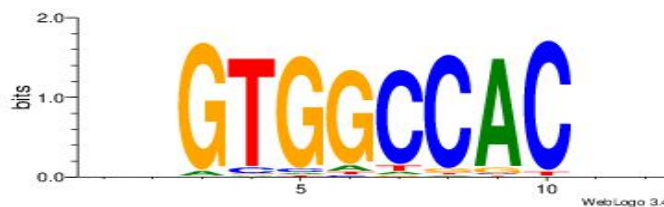
VBGTGGCCACVB

---TGKCCACA-

Original motif Consensus sequence: BVGTGGCCACBV



Reverse complement motif Consensus sequence: VBGTGGCCACVB

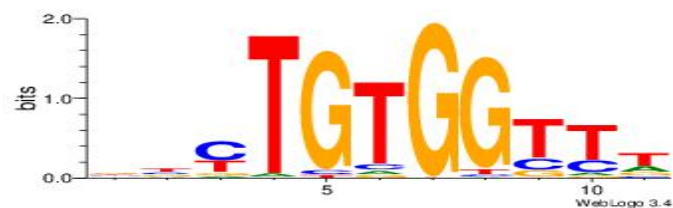


Dataset #: 3
 Motif ID: 114
 Motif name: RUNX1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 8
 Similarity score: 0.0690177

Alignment:

BBYTGTGGTTT
 ---TGTGGYCA

Original motif Consensus sequence: BBYTGTGGTTT



Reverse complement motif Consensus sequence: AAACCACAKVB

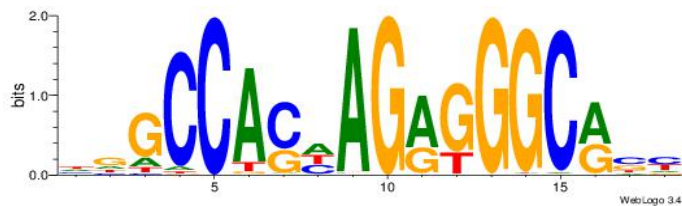


Dataset #: 4
 Motif ID: 165
 Motif name: wgGCCAshAGrGGGCrSy
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 11
 Number of overlap: 8

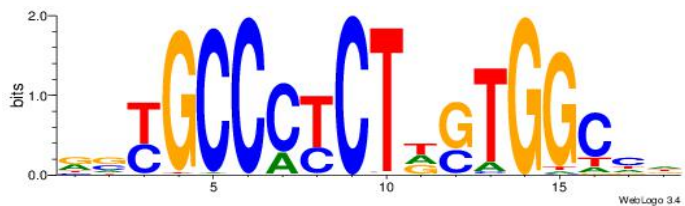
Similarity score: 0.083395

Alignment:
KBKGCCCKCTHGTGGCHH
-----TGTGGYCA

Original motif Consensus sequence: HDGCCACHAGRGGGCRBY



Reverse complement motif Consensus sequence:
KBKGCCCKCTHGTGGCHH



Dataset #: 1
Motif ID: 24
Motif name: Motif 24
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: 0.0843302

Alignment:
CACCCACA
TGKCCACA

Original motif Consensus sequence: TGTGGGTG

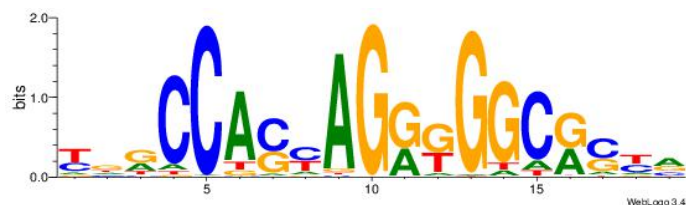
Reverse complement motif Consensus sequence: CACCCACA



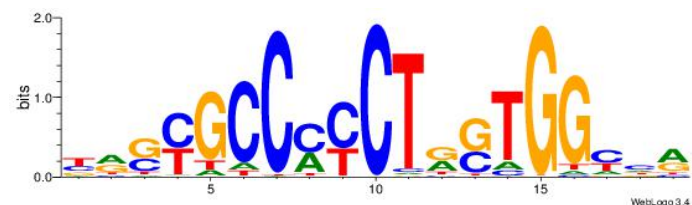
Dataset #: 3
 Motif ID: 74
 Motif name: CTCF
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 12
 Number of overlap: 8
 Similarity score: 0.0872346

Alignment:
 BSMGCCYMCTKSTGGMHM
 -----TGTGGYCA

Original motif Consensus sequence: YDRCCASYAGRKGGRSYV



Reverse complement motif Consensus sequence: BSMGCCYMCTKSTGGMHM



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

Original motif Consensus sequence: ACAACCA_Y



Reverse complement motif Consensus sequence: KTGGTTGT



Best Matches for Motif ID 35 (Highest to Lowest)

Dataset #:	2
Motif ID:	57
Motif name:	Motif 57
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:	0.0737654

Alignment:

ACACACAY

ACAACCA_Y

Original motif Consensus sequence: ACACACAY



Reverse complement motif Consensus sequence: KTGTGTGT

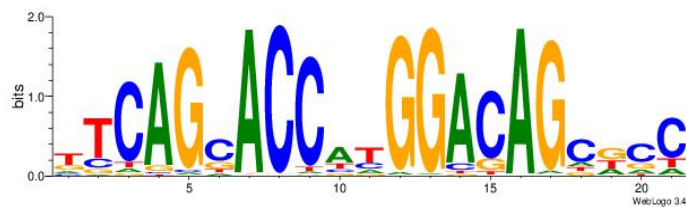


Dataset #: 3
 Motif ID: 113
 Motif name: REST
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 8
 Similarity score: 0.0887654

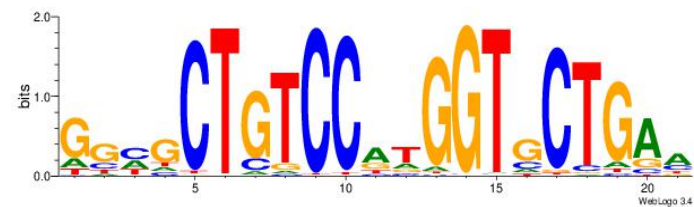
Alignment:

TTCAGCACCATGGACAGCKCC
 ---ACAACCAY-----

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC



Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA



Dataset #: 3
 Motif ID: 120
 Motif name: T
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 4

Number of overlap: 8
Similarity score: 0.0890625

Alignment:
CTAGGTGTGAA
KTGGTTGT---

Original motif Consensus sequence: CTAGGTGTGAA



Reverse complement motif Consensus sequence: TTCACACCTAG



Dataset #: 4
Motif ID: 162
Motif name: ccAsCCCCAcc
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2
Number of overlap: 8
Similarity score: 0.0921848

Alignment:
HVASCCCCABH
--ACAACCAY-

Original motif Consensus sequence: HVASCCCCABH

Reverse complement motif Consensus sequence: DBTGGGGSTVD



Dataset #: 4
 Motif ID: 152
 Motif name: yrCATGCAYr
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 8
 Similarity score: 0.0932982

Alignment:

BRCATGCABD

-ACAACCAY-

Original motif Consensus sequence: BRCATGCABD



Reverse complement motif Consensus sequence: HVTGCATGKV



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

Original motif Consensus sequence: TCCTGGRA



Reverse complement motif Consensus sequence: TMCCAGGA



Best Matches for Motif ID 36 (Highest to Lowest)

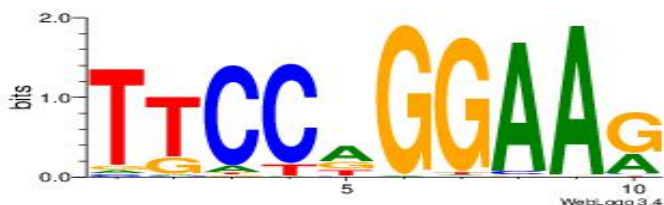
Dataset #:	3
Motif ID:	119
Motif name:	Stat3
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	3
Number of overlap:	8
Similarity score:	0.0190833

Alignment:

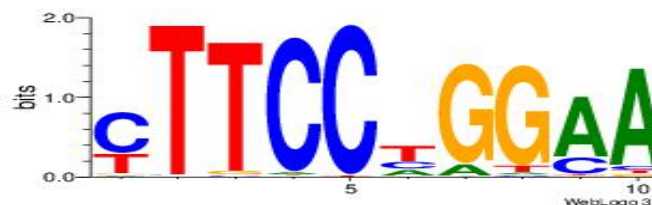
CTTCCTGGAA

--TCCTGGRA

Original motif Consensus sequence: TTCCAGGAAG



Reverse complement motif Consensus sequence: CTTCTGGAA



Dataset #: 4
 Motif ID: 151
 Motif name: agrCCAGmAGrg
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 8
 Similarity score: 0.0609014

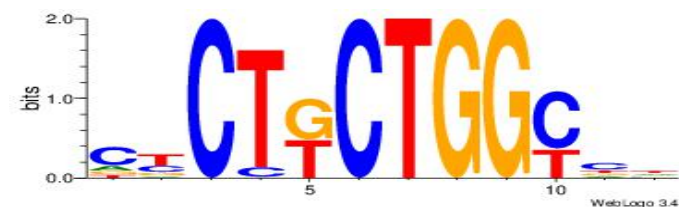
Alignment:

CKCTRCTGGCVH
 ---TCCTGGRA-

Original motif Consensus sequence: HVGCCAGMAGRG



Reverse complement motif Consensus sequence: CKCTRCTGGCVH

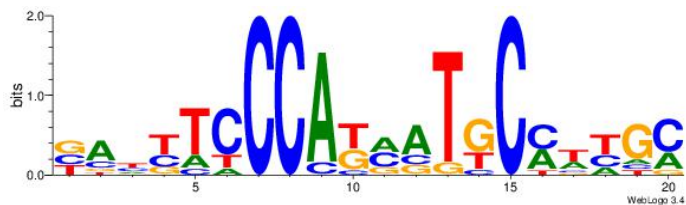


Dataset #: 3
 Motif ID: 131
 Motif name: znf143
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 9
 Number of overlap: 8

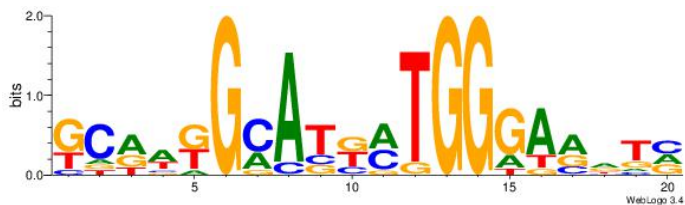
Similarity score: 0.061907

Alignment:
BAHYTCCCAKMATGCMWYGC
-----TMCCAGGA-----

Original motif Consensus sequence: BAHYTCCCAKMATGCMWYGC



Reverse complement motif Consensus sequence: GCMWRGCATYRTGGGAMHTB

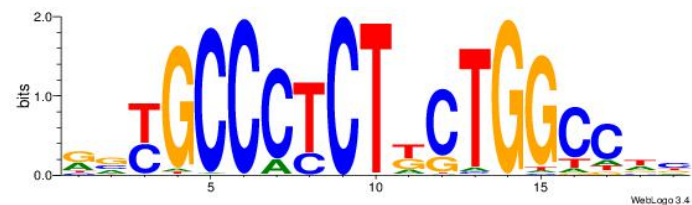
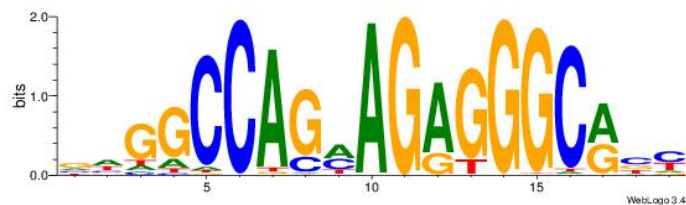


Dataset #: 4
Motif ID: 163
Motif name: gwGGCCAGmAGAGGGCrby
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 3
Number of overlap: 8
Similarity score: 0.0667495

Alignment:
KBKGCCCTCTYCTGGCCHV
-----TCCTGGRA--

Original motif Consensus sequence: VHGGCCAGMAGAGGGCRBY

Reverse complement motif Consensus sequence: KBKGCCCTCTYCTGGCCHV



Dataset #: 3
 Motif ID: 85
 Motif name: Hand1Tcfe2a
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 8
 Similarity score: 0.0719458

Alignment:

AWRCCAGAMB

-TMCCAGGA-

Original motif Consensus sequence: BRTCTGGMWT



Reverse complement motif Consensus sequence: AWRCCAGAMB



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

Original motif Consensus sequence: CTGAGCYA



Reverse complement motif Consensus sequence: TKGCTCAG



Best Matches for Motif ID 37 (Highest to Lowest)

Dataset #:	3
Motif ID:	100
Motif name:	NFE2L2
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:	0.0542114

Alignment:

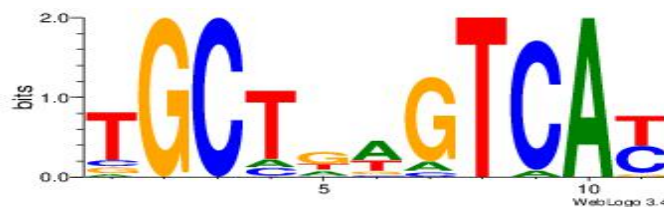
RTGACWHAGCA

-TKGCTCAG--

Original motif Consensus sequence: RTGACWHAGCA



Reverse complement motif Consensus sequence: TGCTDWGTCAG



Dataset #: 4
 Motif ID: 160
 Motif name: brCAGGGCCrs
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 8
 Similarity score: 0.0573364

Alignment:

BBGGCCCTGBB

-TKGCTCAG--

Original motif Consensus sequence: BVCAGGGCCVB



Reverse complement motif Consensus sequence: BBGGCCCTGBB

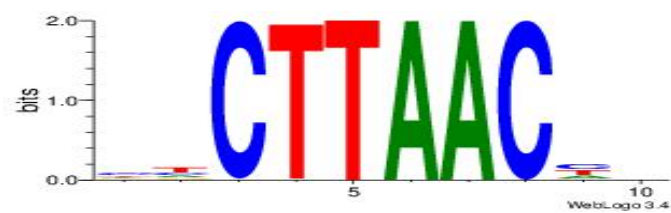


Dataset #: 4
 Motif ID: 142
 Motif name: ctCTTAACyw
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 8

Similarity score: 0.0660909

Alignment:
HHCTTAACHD
--CTGAGCYA

Original motif Consensus sequence: HHCTTAACHD



Reverse complement motif Consensus sequence: DDGTTAAGHD

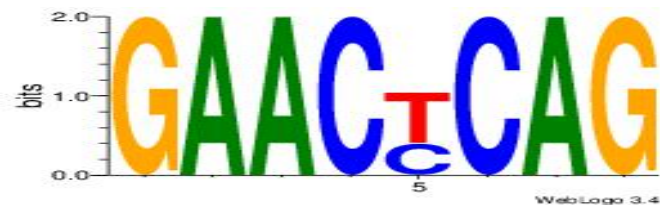


Dataset #: 1
Motif ID: 25
Motif name: Motif 25
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 8
Similarity score: 0.0673416

Alignment:
CTGRGTTC
CTGAGCYA

Original motif Consensus sequence: CTGRGTTC

Reverse complement motif Consensus sequence: GAACKCAG

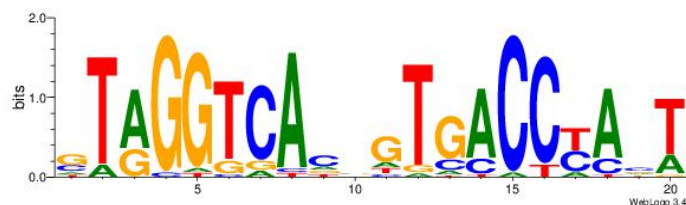


Dataset #: 3
 Motif ID: 111
 Motif name: PPARG
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 11
 Number of overlap: 8
 Similarity score: 0.0687591

Alignment:

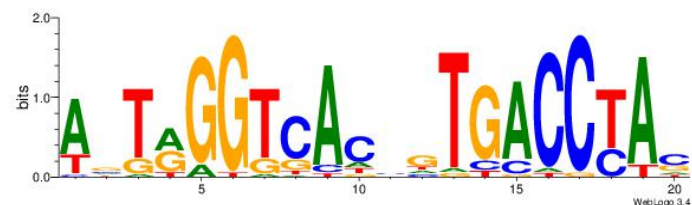
STAGGTCACBG TGACCYABT
 -----CTGAGCYA--

Original motif Consensus sequence: STAGGTCACBG TGACCYABT



Reverse complement motif
ABTMGGTCACBG TGACCTAS

Consensus sequence:



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

Original motif Consensus sequence: GAGTTACA



Reverse complement motif Consensus sequence: TGTAAGTC



Best Matches for Motif ID 38 (Highest to Lowest)

Dataset #:	2
Motif ID:	51
Motif name:	Motif 51
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

Alignment:

GAGTTACA

GAGTTACA

Original motif Consensus sequence: GAGTTACA



Reverse complement motif Consensus sequence: TGTAAGTC



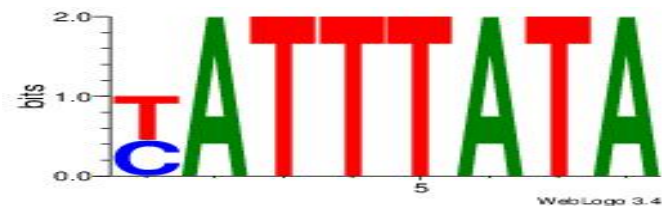
Dataset #: 2
 Motif ID: 66
 Motif name: Motif 66
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 8
 Similarity score: 0.0742432

Alignment:
 KATTTATA
 GAGTTACA

Original motif Consensus sequence: TATAAATR



Reverse complement motif Consensus sequence: KATTTATA



Dataset #: 3
 Motif ID: 117
 Motif name: Spz1
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 8

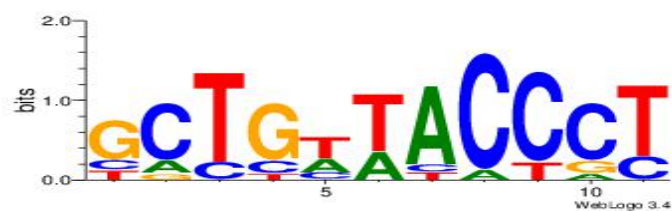
Similarity score: 0.0855279

Alignment:
AGGGTAWCAGC
-GAGTTACA--

Original motif Consensus sequence: AGGGTAWCAGC



Reverse complement motif Consensus sequence: GCTGWTACCCT

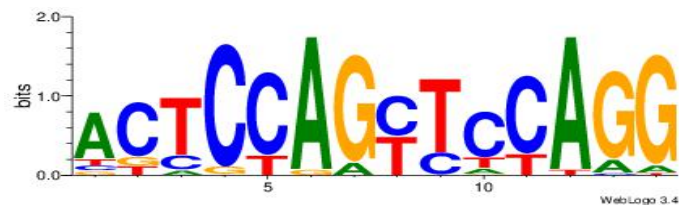
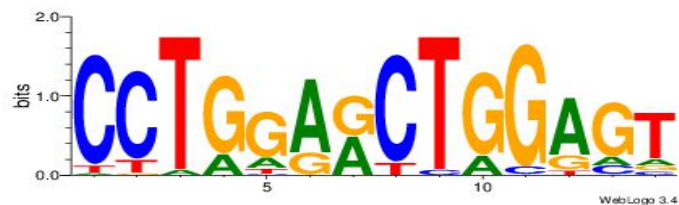


Dataset #: 2
Motif ID: 69
Motif name: Motif 69
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 5
Number of overlap: 8
Similarity score: 0.0901267

Alignment:
CCTGGARCTGGAGT
--TGTAAGTC----

Original motif Consensus sequence: CCTGGARCTGGAGT

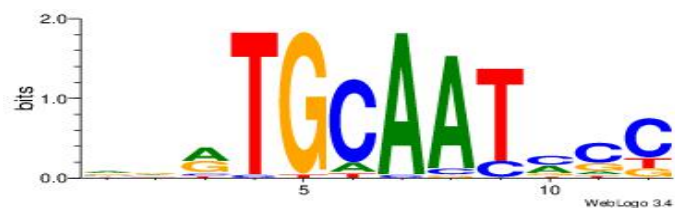
Reverse complement motif Consensus sequence: ACTCCAGMTCCAG



Dataset #: 3
 Motif ID: 75
 Motif name: Ddit3Cebpa
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 4
 Number of overlap: 8
 Similarity score: 0.0913372

Alignment:
 GGRATTGCAKHB
 -GAGTTACA---

Original motif Consensus sequence: VDRTGCAATMCC



Reverse complement motif Consensus sequence: GGRATTGCAKHB



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

Original motif Consensus sequence: BAGAAA



Reverse complement motif Consensus sequence: TTTCTB



Best Matches for Motif ID 39 (Highest to Lowest)

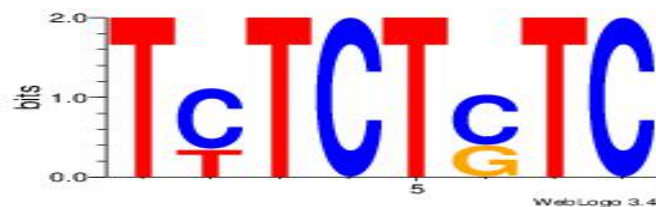
Dataset #:	1
Motif ID:	23
Motif name:	Motif 23
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	3
Number of overlap:	6
Similarity score:	0.0215381

Alignment:
 GASAGAGA
 --BAGAAA

Original motif Consensus sequence: GASAGAGA



Reverse complement motif Consensus sequence: TCTCTSTC



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: 2
 Number of overlap: 6
 Similarity score: 0.0344566

Alignment:
 GSAGAGA
 -BAGAAA

Original motif Consensus sequence: GSAGAGA



Reverse complement motif Consensus sequence: TCTCTSC

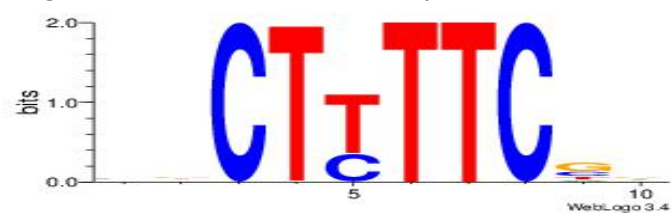


Dataset #: 4
 Motif ID: 139
 Motif name: mkCTyTTCsg
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 5
 Number of overlap: 6

Similarity score: 0.0384118

Alignment:
HBCTTTTCBD
----TTTCTB

Original motif Consensus sequence: HBCTTTTCBD



Reverse complement motif Consensus sequence: HBGAAAAGBD

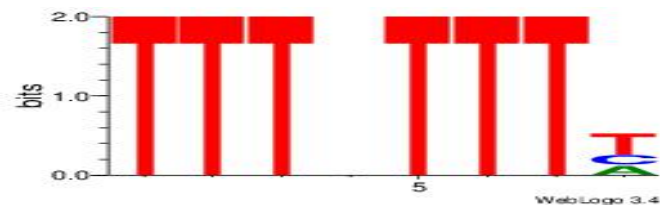
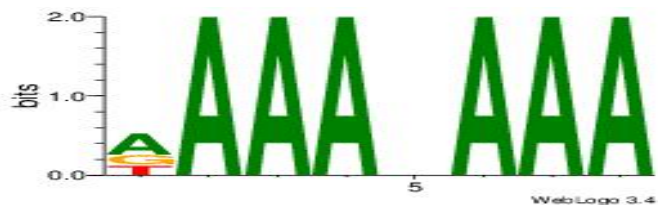


Dataset #: 1
Motif ID: 2
Motif name: Motif 2
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 6
Similarity score: 0.0438306

Alignment:
TTTDTTTT
TTTCTB--

Original motif Consensus sequence: AAAAHAAA

Reverse complement motif Consensus sequence: TTTDTTTT



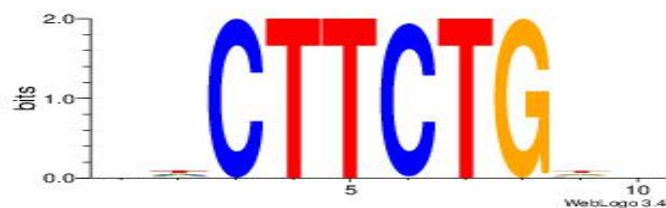
Dataset #: 4
 Motif ID: 136
 Motif name: dwCAGAAGwh
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 6
 Similarity score: 0.0496185

Alignment:
 DHCAGAAGDH
 --BAGAAA--

Original motif Consensus sequence: DHCAGAAGDH



Reverse complement motif Consensus sequence: HDCTTCTGHD



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

Original motif Consensus sequence: ARTCCCAG



Reverse complement motif Consensus sequence: CTGGGAMT



Best Matches for Motif ID 40 (Highest to Lowest)

Dataset #: 4
Motif ID: 162
Motif name: ccAsCCCCAcc
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 3
Number of overlap: 8
Similarity score: 0.0511488

Alignment:

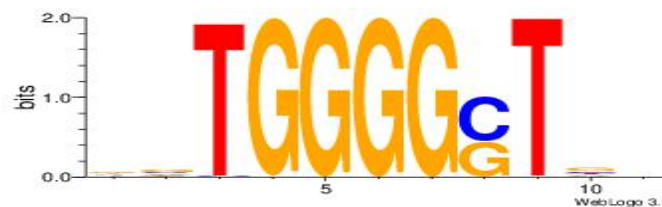
DBTGGGGSTVD

-CTGGGAMT--

Original motif Consensus sequence: HVASCCCCABH



Reverse complement motif Consensus sequence: DBTGGGGSTVD

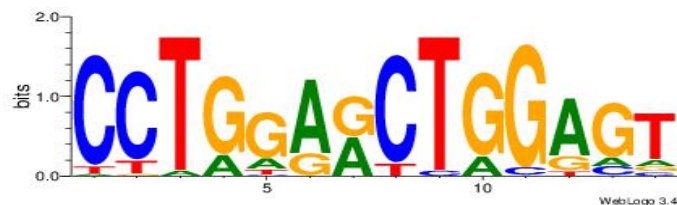


Dataset #: 2
 Motif ID: 69
 Motif name: Motif 69
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 8
 Similarity score: 0.0574096

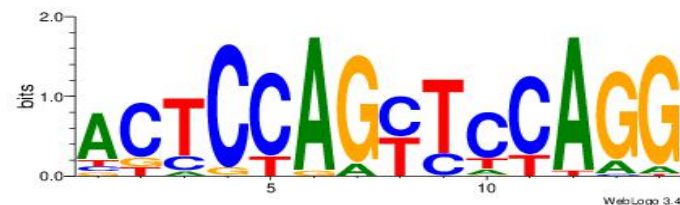
Alignment:

CCTGGARCTGGAGT
 -CTGGGAMT-----

Original motif Consensus sequence: CCTGGARCTGGAGT



Reverse complement motif Consensus sequence: ACTCCAGMTCCAG

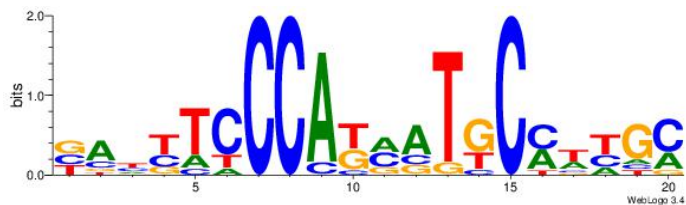


Dataset #: 3
 Motif ID: 131
 Motif name: znf143
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 11
 Number of overlap: 8

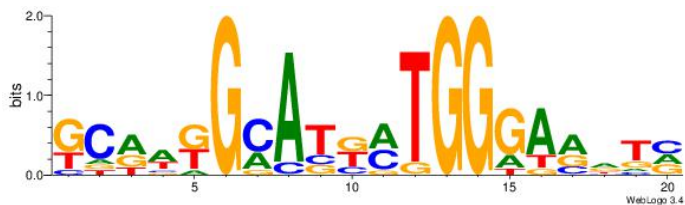
Similarity score: 0.0623563

Alignment:
GCMWRGCATYRTGGGAMHTB
-----CTGGGAMT--

Original motif Consensus sequence: BAHYTCCCAKMATGCMWYGC



Reverse complement motif Consensus sequence: GCMWRGCATYRTGGGAMHTB

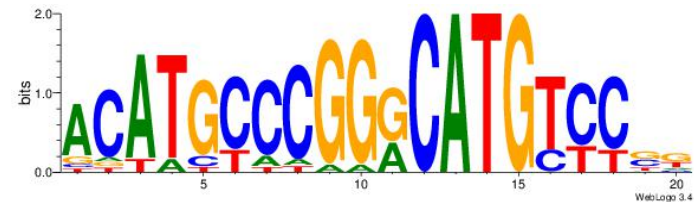
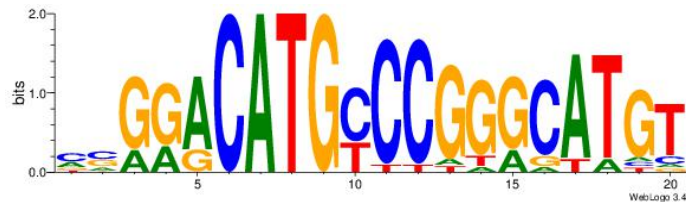


Dataset #: 3
Motif ID: 125
Motif name: TP53
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 11
Number of overlap: 8
Similarity score: 0.0776137

Alignment:
MSGGACATGYCCGGGCATGT
-----CTGGGAMT--

Original motif Consensus sequence: MSGGACATGYCCGGGCATGT

Reverse complement motif Consensus sequence: ACATGCCCGGKCATGTCCSR



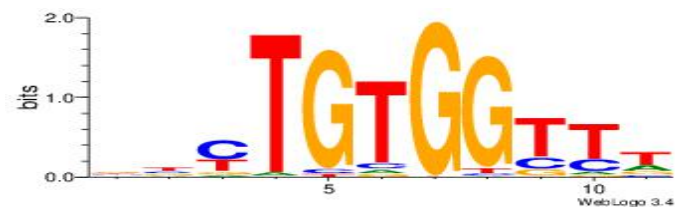
Dataset #: 3
 Motif ID: 114
 Motif name: RUNX1
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 8
 Similarity score: 0.080122

Alignment:

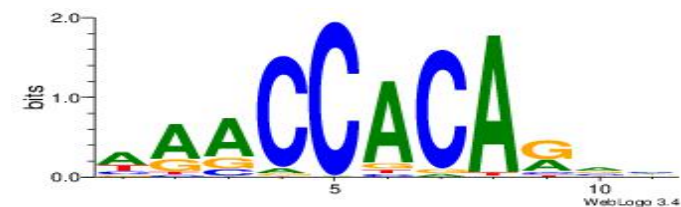
AAACCACAKVB

-ARTCCCAG--

Original motif Consensus sequence: BBTGTGGTTT



Reverse complement motif Consensus sequence: AAACCACAKVB



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

Original motif Consensus sequence: CCTGCTGK



Reverse complement motif Consensus sequence: YCAGCAGG



Best Matches for Motif ID 41 (Highest to Lowest)

Dataset #:	4
Motif ID:	151
Motif name:	agrCCAGmAGrg
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:	0.028602

Alignment:

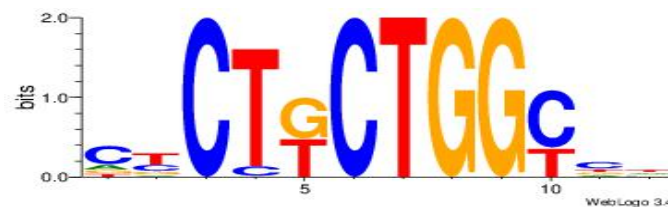
HVGCCAGMAGRG

---YCAGCAGG-

Original motif Consensus sequence: HVGCCAGMAGRG



Reverse complement motif Consensus sequence: CKCTRCTGGCVH

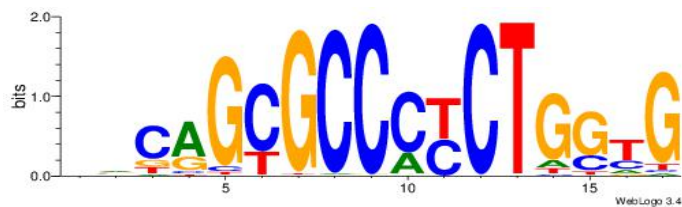


Dataset #: 4
 Motif ID: 168
 Motif name: yrcrGYGCCMyCTGGtG
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3
 Number of overlap: 8
 Similarity score: 0.0340048

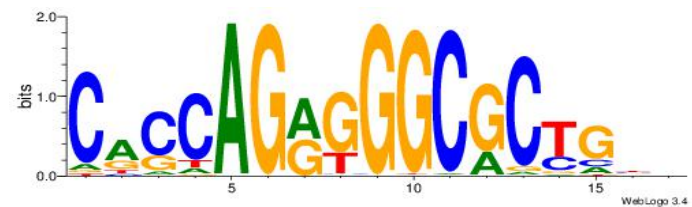
Alignment:

CACCAGMGGGCGCTGBD
 --YCAGCAGG-----

Original motif Consensus sequence: HVCAGCGCCCYCTGGTG



Reverse complement motif Consensus sequence: CACCAGMGGGCGCTGBD



Dataset #: 1
 Motif ID: 21
 Motif name: Motif 21
 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: 0.0342298

Alignment:
CCTKGTGG
CCTGCTGK

Original motif Consensus sequence: CCACYAGG



Reverse complement motif Consensus sequence: CCTKGTGG

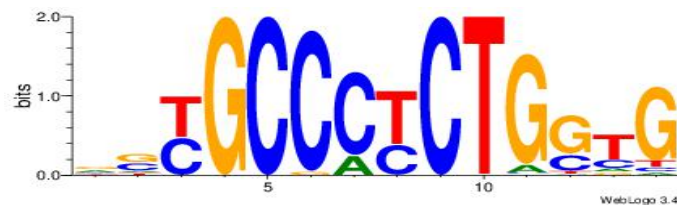


Dataset #: 4
Motif ID: 166
Motif name: CasCAGrGGGCrSy
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 5
Number of overlap: 8
Similarity score: 0.0366705

Alignment:
BSKGCCCKCTGGTG
----CCTGCTGK--

Original motif Consensus sequence: CACCAGRGGGCRSB

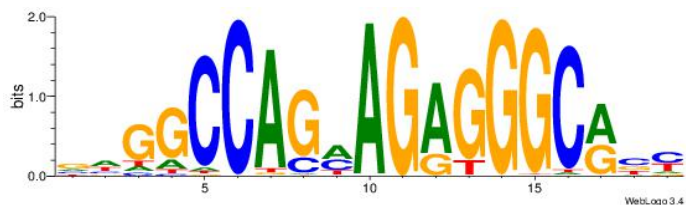
Reverse complement motif Consensus sequence: BSKGCCCKCTGGT



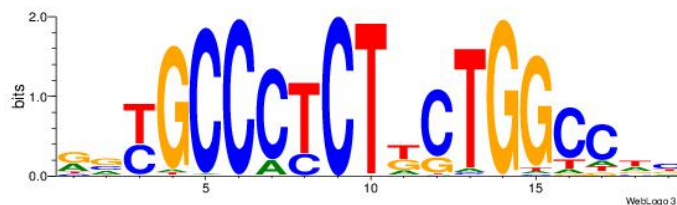
Dataset #: 4
 Motif ID: 163
 Motif name: gwGGCCAGmAGAGGGCrby
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 5
 Number of overlap: 8
 Similarity score: 0.0407982

Alignment:
 VHGGCCAGMAGAGGGCRBY
 ----YCAGCAGG-----

Original motif Consensus sequence: VHGGCCAGMAGAGGGCRBY



Reverse complement motif Consensus sequence: KBKGCCCTCTYCTGGCCHV



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

Original motif Consensus sequence: CGCGCSG



Reverse complement motif Consensus sequence: CSGCGCG



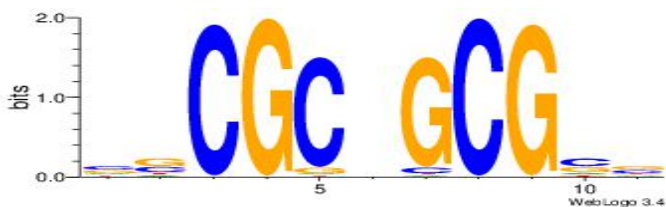
Best Matches for Motif ID 42 (Highest to Lowest)

Dataset #: 4
 Motif ID: 161
 Motif name: ssCGCwGCGss
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 5
 Number of overlap: 7
 Similarity score: 0.0226692

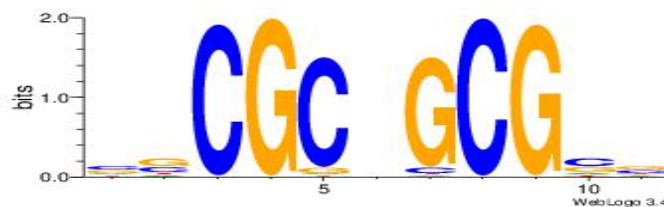
Alignment:

VSCGCDGCGSB
 ----CSGCGCG

Original motif Consensus sequence: VSCGCDGCGSB



Reverse complement motif Consensus sequence: BSCGCDGCGSV



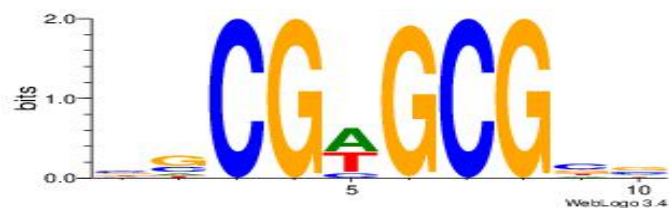
Dataset #: 4
 Motif ID: 134
 Motif name: ssCGwGCGss
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 7
 Similarity score: 0.0315768

Alignment:

BSCGWGCGBV

-CSGCGCG--

Original motif Consensus sequence: BSCGWGCGBV



Reverse complement motif Consensus sequence: VBCGWCGBS

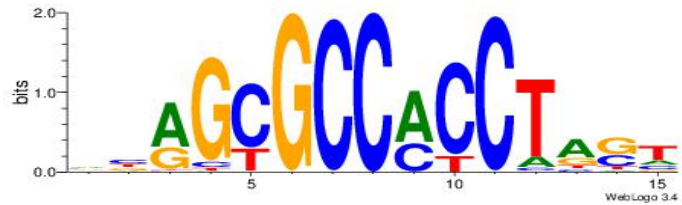


Dataset #: 4
 Motif ID: 146
 Motif name: myrYGCCmCCTast
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 7

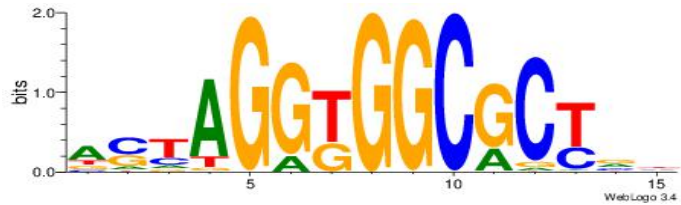
Similarity score: 0.0331622

Alignment:
ASTAGGYGGCGCTBB
-----CSGCGCG--

Original motif Consensus sequence: VBAGCGCCMCCTAST



Reverse complement motif Consensus sequence: ASTAGGYGGCGCT

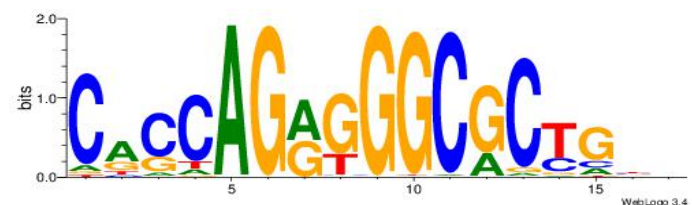
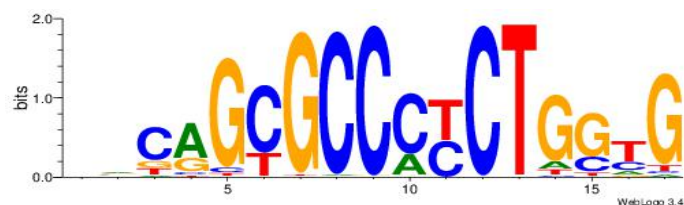


Dataset #: 4
Motif ID: 168
Motif name: yrcrYGCCMyCTGGtG
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 3
Number of overlap: 7
Similarity score: 0.0399606

Alignment:
CACCAGMGGGCGCTGBD
-----CGCGCSG--

Original motif Consensus sequence: HVCAGCGCCCYCTGGTG

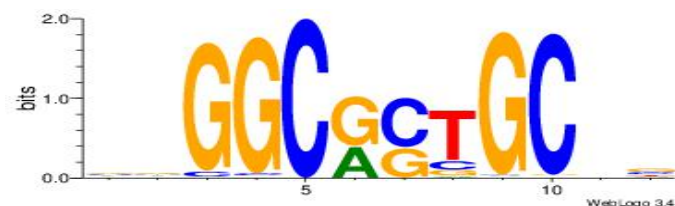
Reverse complement motif Consensus sequence:
CACCAGMGGGCGCTGBD



Dataset #: 4
 Motif ID: 170
 Motif name: ssGGCrSTGCrS
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 4
 Number of overlap: 7
 Similarity score: 0.0456255

Alignment:
 VVGGRSTGCVB
 --CGCGCSG---

Original motif Consensus sequence: VVGGRSTGCVB



Reverse complement motif Consensus sequence: BVGCASMGCCVV



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

Original motif Consensus sequence: ACATYTA



Reverse complement motif Consensus sequence: TAMATGT



Best Matches for Motif ID 43 (Highest to Lowest)

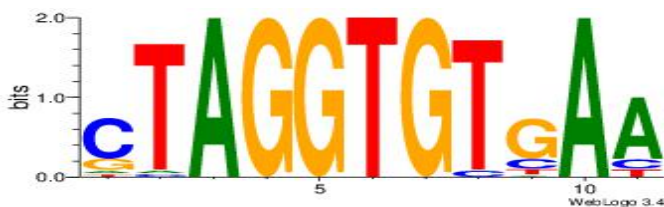
Dataset #:	3
Motif ID:	120
Motif name:	T
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	4
Number of overlap:	7
Similarity score:	0.0260628

Alignment:

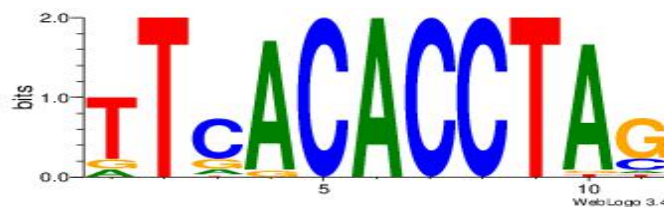
TTCACACCTAG

---ACATYTA-

Original motif Consensus sequence: CTAGGTGTGAA



Reverse complement motif Consensus sequence: TTCACACCTAG



Dataset #: 2
 Motif ID: 58
 Motif name: Motif 58
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 7
 Similarity score: 0.0342454

Alignment:
 TACATGCA
 TAMATGT-

Original motif Consensus sequence: TACATGCA



Reverse complement motif Consensus sequence: TGCATGTA



Dataset #: 2
 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: 2
 Number of overlap: 7

Similarity score: 0.0444069

Alignment:

TGMATATG

TAMATGT-

Original motif Consensus sequence: CATATRCA



Reverse complement motif Consensus sequence: TGMATATG



Dataset #: 4
Motif ID: 152
Motif name: yrCATGCAyr
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 3
Number of overlap: 7
Similarity score: 0.0458993

Alignment:

HVTGCATGKV

--TAMATGT-

Original motif Consensus sequence: BRCATGCABD

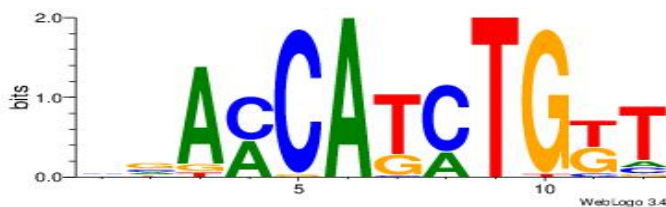
Reverse complement motif Consensus sequence: HVTGCATGKV



Dataset #: 3
 Motif ID: 121
 Motif name: TAL1TCF3
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 7
 Similarity score: 0.0525238

Alignment:
 HVAMCATCTGKT
 ---ACATYTA--

Original motif Consensus sequence: HVAMCATCTGKT



Reverse complement motif Consensus sequence: ARCAGATGRTVD



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

Original motif Consensus sequence: GDAAACA



Reverse complement motif Consensus sequence: TGTTTDC



Best Matches for Motif ID 44 (Highest to Lowest)

Dataset #: 4
 Motif ID: 141
 Motif name: raCAAAACam
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 7
 Similarity score: 0.0588603

Alignment:

HTGTTTTGTD

-TGTTTDC--

Original motif Consensus sequence: DACAAAACAH



Reverse complement motif Consensus sequence: HTGTTTTGTD

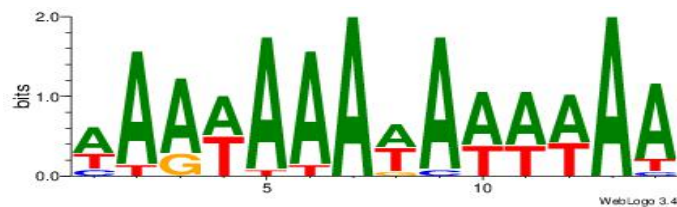


Dataset #: 2
 Motif ID: 68
 Motif name: Motif 68
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 6
 Number of overlap: 7
 Similarity score: 0.0651624

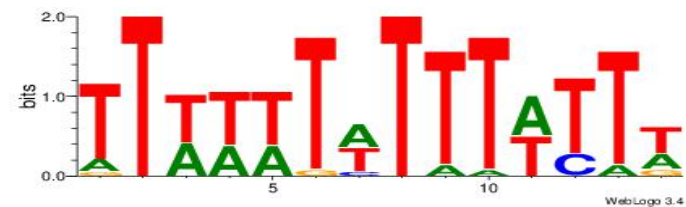
Alignment:

WAAWAAAWAWWWAA
 --GDAAACA-----

Original motif Consensus sequence: WAAWAAAWAWWWAA



Reverse complement motif Consensus sequence: TTWWWTWTTTWTTW



Dataset #: 1
 Motif ID: 33
 Motif name: Motif 33
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2

Number of overlap: 7
Similarity score: 0.0667857

Alignment:
CTGGCTWC
TGT TDC-

Original motif Consensus sequence: CTGGCTWC



Reverse complement motif Consensus sequence: GWAGCCAG



Dataset #: 1
Motif ID: 34
Motif name: Motif 34
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 2
Number of overlap: 7
Similarity score: 0.066941

Alignment:
TGKCCACA
-GDAAACA

Original motif Consensus sequence: TGKCCACA

Reverse complement motif Consensus sequence: TGTGGYCA



Dataset #: 2
 Motif ID: 57
 Motif name: Motif 57
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 7
 Similarity score: 0.0694703

Alignment:
 KTGTGTGT
 -TGTTTDC

Original motif Consensus sequence: ACACACAY



Reverse complement motif Consensus sequence: KTGTGTGT



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

Original motif Consensus sequence: GSAGAGA



Reverse complement motif Consensus sequence: TCTCTSC



Best Matches for Motif ID 45 (Highest to Lowest)

Dataset #:	4
Motif ID:	140
Motif name:	vkCKCTkCGk
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	2
Number of overlap:	7
Similarity score:	0.0315852

Alignment:

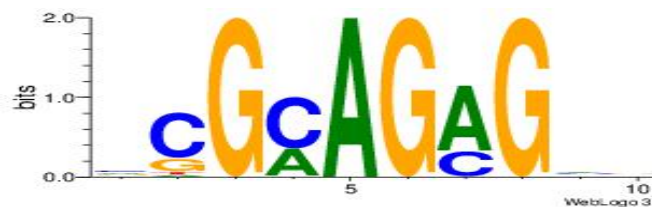
BCGYAGAGDV

--GSAGAGA--

Original motif Consensus sequence: VDCTCTKCGB



Reverse complement motif Consensus sequence: BCGYAGAGDV



Dataset #: 1
 Motif ID: 23
 Motif name: Motif 23
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 7
 Similarity score: 0.0364931

Alignment:
 GASAGAGA
 -GSAGAGA

Original motif Consensus sequence: GASAGAGA



Reverse complement motif Consensus sequence: TCTCTSTC

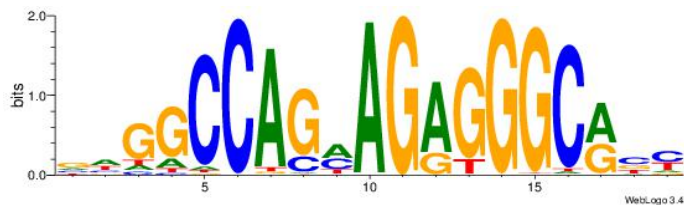


Dataset #: 4
 Motif ID: 163
 Motif name: gwGGCCAGmAGAGGGCrby
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 6
 Number of overlap: 7

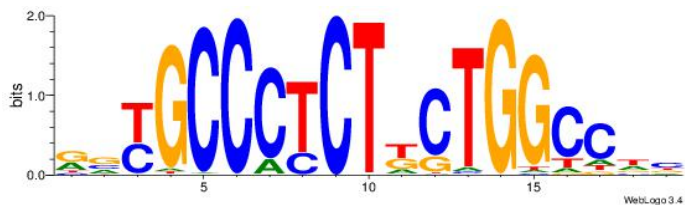
Similarity score: 0.0625376

Alignment:
VHGGCCAGMAGAGGGCRBY
-----GSAGAGA-----

Original motif Consensus sequence: VHGGCCAGMAGAGGGCRBY



Reverse complement motif Consensus sequence: KBKGCCCTCTYCTGGCCHV

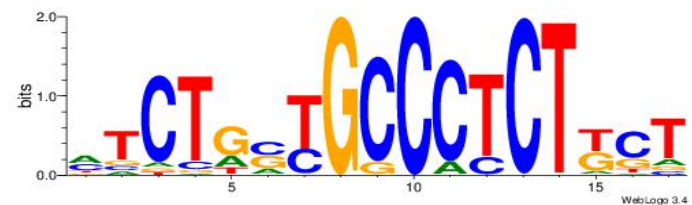
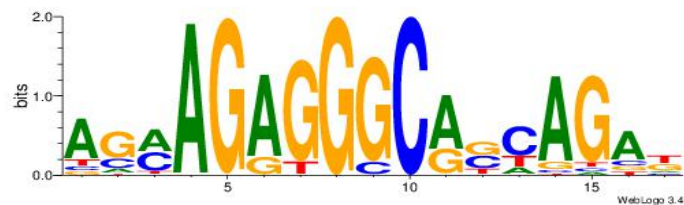


Dataset #: 4
Motif ID: 143
Motif name: AgmAGAGGGCrscAGak
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 10
Number of overlap: 7
Similarity score: 0.0633827

Alignment:
RTCTGSTGCCCTCTYCT
-----TCTCTSC--

Original motif Consensus sequence: AGMAGAGGGCASCAGAK

Reverse complement motif Consensus sequence: RTCTGSTGCCCTCTYCT



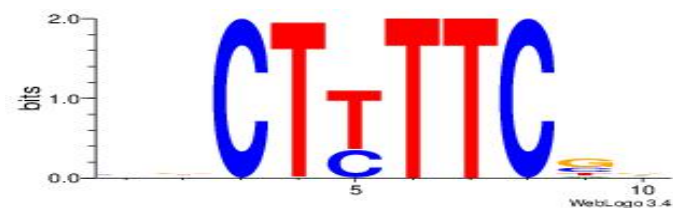
Dataset #: 4
 Motif ID: 139
 Motif name: mkCTyTTCsg
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 7
 Similarity score: 0.0693299

Alignment:

HBCTTTTCBD

-TCTCTSC--

Original motif Consensus sequence: HBCTTTTCBD



Reverse complement motif Consensus sequence: HBGAAAAGBD



Dataset #: 2 Motif ID: 46 Motif name: Motif 46

Original motif Consensus sequence: AGRKGGCR



Reverse complement motif Consensus sequence: KGCCYKCT



Best Matches for Motif ID 46 (Highest to Lowest)

Dataset #: 1
Motif ID: 1
Motif name: Motif 1
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 8
Similarity score: 0

Alignment:

AGRKGGCR

AGRKGGCR

Original motif Consensus sequence: AGRKGGCR



Reverse complement motif Consensus sequence: KGCCYKCT



Dataset #: 4
 Motif ID: 147
 Motif name: asCAGrkGGCrSy
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 8
 Similarity score: 0.00651548

Alignment:

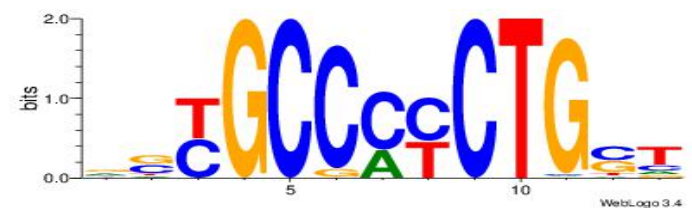
ASCAGRGGGCRSB

---AGRKGCCR--

Original motif Consensus sequence: ASCAGRGGGCRSB



Reverse complement motif Consensus sequence: BSKGCCCMCTGST

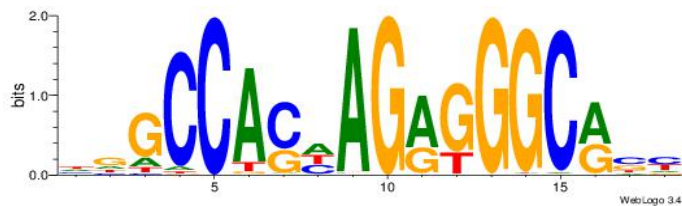


Dataset #: 4
 Motif ID: 165
 Motif name: wgGCCAshAGrGGGCrSy
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 9
 Number of overlap: 8

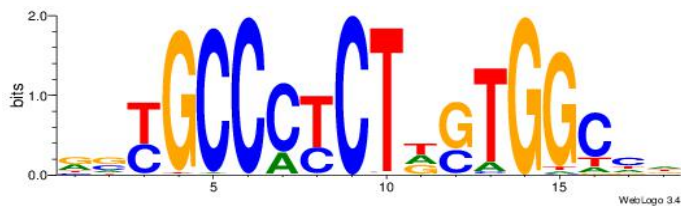
Similarity score: 0.0102443

Alignment:
KBKGCCCKCTHGTGGCHH
--KGCCYKCT-----

Original motif Consensus sequence: HDGCCACHAGRGGGCRBY



Reverse complement motif Consensus sequence: KBKGCCCKCTHGTGGCHH

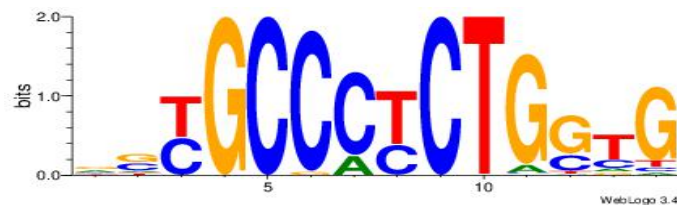


Dataset #: 4
Motif ID: 166
Motif name: CasCAGrGGGCrSy
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 3
Number of overlap: 8
Similarity score: 0.0104954

Alignment:
BSKGCCCKCTGGTG
--KGCCYKCT-----

Original motif Consensus sequence: CACCAGRGGGCRSB

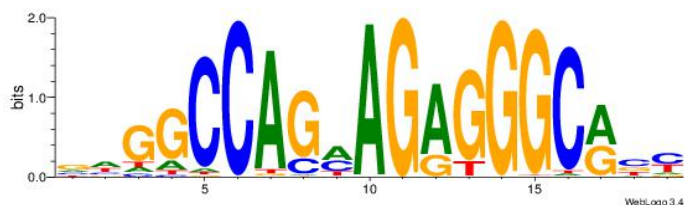
Reverse complement motif Consensus sequence: BSKGCCCKCTGGT



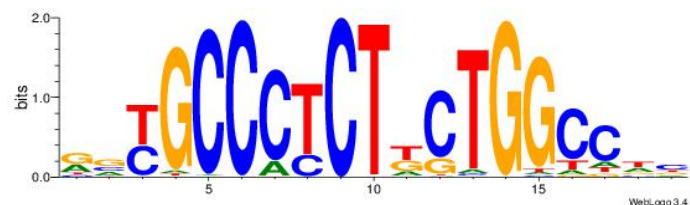
Dataset #: 4
 Motif ID: 163
 Motif name: gwGGCCAGmAGAGGGCrby
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3
 Number of overlap: 8
 Similarity score: 0.0165822

Alignment:
 KBKGCCCTCTYCTGGCCHV
 --KGCCYKCT-----

Original motif Consensus sequence: VHGGCCAGMAGAGGGCRBY



Reverse complement motif Consensus sequence: KBKGCCCTCTYCTGGCCHV



Dataset #: 2 Motif ID: 47 Motif name: Motif 47

Original motif Consensus sequence: CAGYDCC



Reverse complement motif Consensus sequence: GGDKCTG



Best Matches for Motif ID 47 (Highest to Lowest)

Dataset #:	1
Motif ID:	13
Motif name:	Motif 13
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	7
Similarity score:	0

Alignment:

GGDKCTG

GGDKCTG

Original motif Consensus sequence: CAGYDCC



Reverse complement motif Consensus sequence: GGDKCTG



Dataset #: 2
 Motif ID: 53
 Motif name: Motif 53
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 7
 Similarity score: 0.0288002

Alignment:
 GGGATCTG
 -GGDKCTG

Original motif Consensus sequence: CAGATCCC



Reverse complement motif Consensus sequence: GGGATCTG

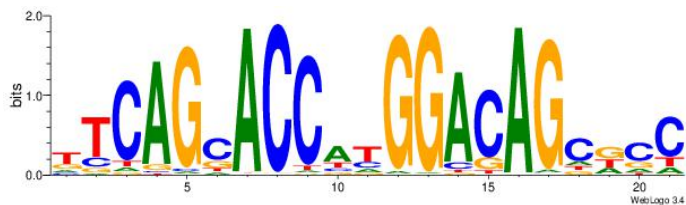


Dataset #: 3
 Motif ID: 113
 Motif name: REST
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 13
 Number of overlap: 7

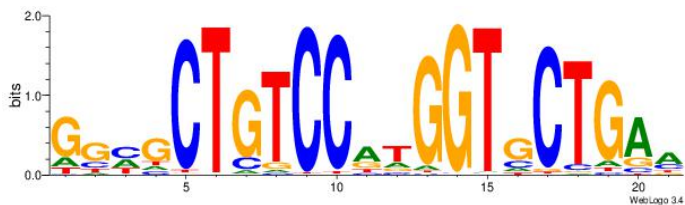
Similarity score: 0.0502666

Alignment:
GGYGCTGTCCATGGTGCTGAA
-----GGDKCTG--

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC



Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA



Dataset #: 1
Motif ID: 22
Motif name: Motif 22
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 2
Number of overlap: 7
Similarity score: 0.0531399

Alignment:
GGKATCTG
-GGDKCTG

Original motif Consensus sequence: CAGATYCC

Reverse complement motif Consensus sequence: GGKATCTG



Dataset #: 4
 Motif ID: 160
 Motif name: brCAGGGCCrs
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 7
 Similarity score: 0.0559697

Alignment:

BVCAGGGCCVB

--CAGYDCC--

Original motif Consensus sequence: BVCAGGGCCVB

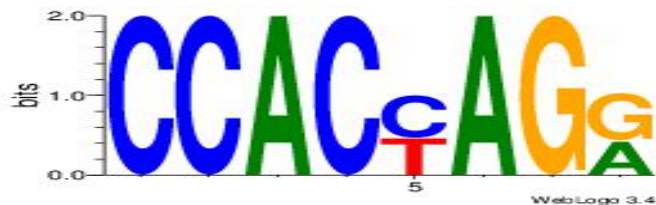


Reverse complement motif Consensus sequence: BBGGCCCTGBB



Dataset #: 2 Motif ID: 48 Motif name: Motif 48

Original motif Consensus sequence: CCACYAGR



Reverse complement motif Consensus sequence: MCTKGTGG



Best Matches for Motif ID 48 (Highest to Lowest)

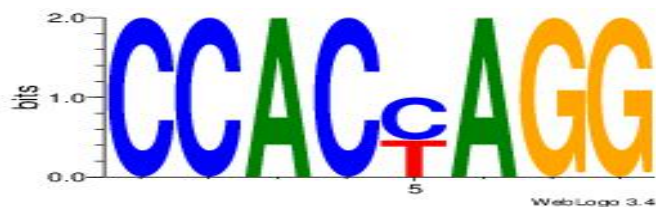
Dataset #:	1
Motif ID:	21
Motif name:	Motif 21
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	8
Similarity score:	0.00903109

Alignment:

CCACYAGG

CCACYAGR

Original motif Consensus sequence: CCACYAGG



Reverse complement motif Consensus sequence: CCTKGTGG

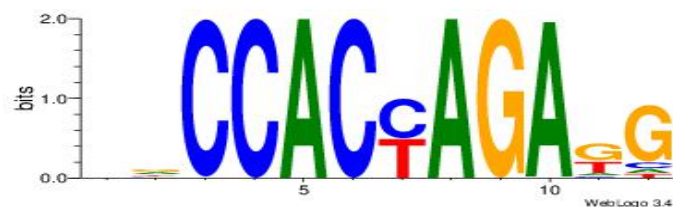


Dataset #: 4
 Motif ID: 145
 Motif name: grCCACyAGAkG
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 8
 Similarity score: 0.0155354

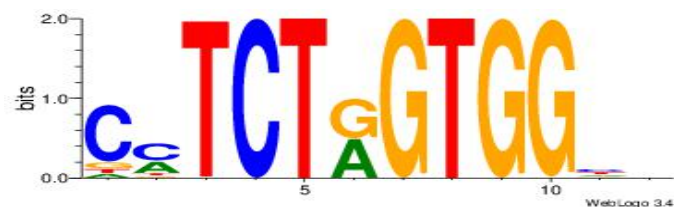
Alignment:

DDCCACYAGAKG
 --CCACYAGR--

Original motif Consensus sequence: DDCCACYAGAKG



Reverse complement motif Consensus sequence: CYTCTKGTGGHH



Dataset #: 4
 Motif ID: 158
 Motif name: grCCACwAGrk
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 8

Similarity score: 0.0192652

Alignment:
DDCCACWAGRK
--CCACYAGR--

Original motif Consensus sequence: DDCCACWAGRK



Reverse complement motif Consensus sequence: YMCTWGTGGHH

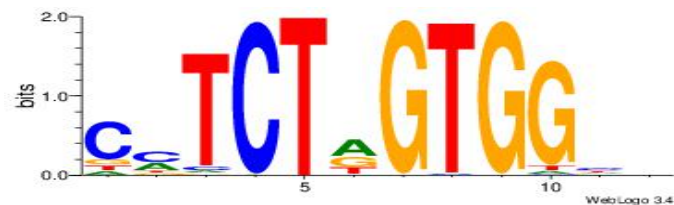
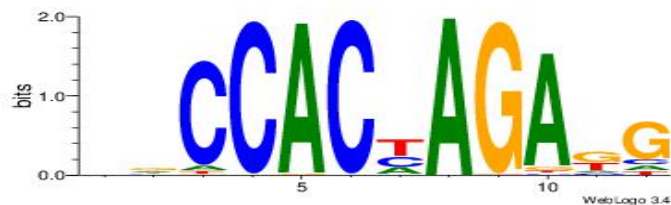


Dataset #: 4
Motif ID: 138
Motif name: grCCACyAGAkG
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 3
Number of overlap: 8
Similarity score: 0.0244381

Alignment:
DDCCACYAGAKG
--CCACYAGR--

Original motif Consensus sequence: DDCCACYAGAKG

Reverse complement motif Consensus sequence: CYTCTMGTGGHH

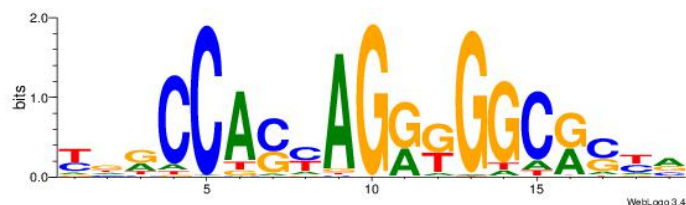


Dataset #: 3
 Motif ID: 74
 Motif name: CTCF
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 9
 Number of overlap: 8
 Similarity score: 0.0284404

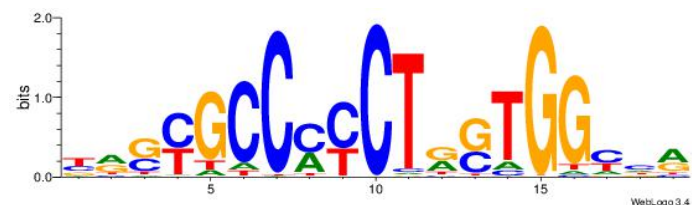
Alignment:

YDRCCASYAGRKGGRSYV
 ---CCACYAGR-----

Original motif Consensus sequence: YDRCCASYAGRKGGRSYV



Reverse complement motif Consensus sequence: BMSMGCCYMCTKSTGGMHM



Dataset #: 2 Motif ID: 49 Motif name: Motif 49

Original motif Consensus sequence: CTGGCCTC



Reverse complement motif Consensus sequence: GAGGCCAG



Best Matches for Motif ID 49 (Highest to Lowest)

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

Alignment:

CTGGCCTC

CTGGCCTC

Original motif Consensus sequence: CTGGCCTC



Reverse complement motif Consensus sequence: GAGGCCAG



Dataset #: 1
 Motif ID: 33
 Motif name: Motif 33
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 8
 Similarity score: 0.0148758

Alignment:
 CTGGCTWC
 CTGGCCTC

Original motif Consensus sequence: CTGGCTWC



Reverse complement motif Consensus sequence: GWAGCCAG



Dataset #: 4
 Motif ID: 163
 Motif name: gwGGCCAGmAGAGGGCrby
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 12
 Number of overlap: 8

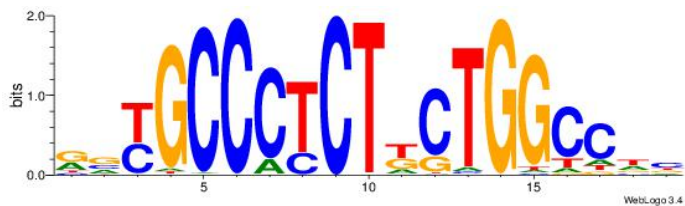
Similarity score: 0.0362649

Alignment:
KBKGCCCTCTYCTGGCCHV
-----CTGGCCTC

Original motif Consensus sequence: VHGGCCAGMAGAGGGCRBY



Reverse complement motif Consensus sequence: KBKGCCCTCTYCTGGCCHV

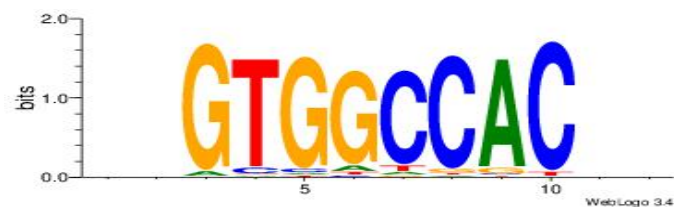
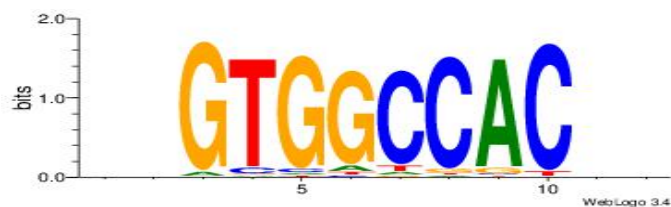


Dataset #: 4
Motif ID: 171
Motif name: ysGTGGCCACsr
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 3
Number of overlap: 8
Similarity score: 0.0504205

Alignment:
VBGTGGCCACVB
--CTGGCCTC--

Original motif Consensus sequence: BVGTGGCCACBV

Reverse complement motif Consensus sequence: VBGTGGCCACVB



Dataset #: 4
 Motif ID: 133
 Motif name: shAGrGGGCAGy
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 8
 Similarity score: 0.0509007

Alignment:
 SHAGRGGGCABH
 ---GAGGCCAG--

Original motif Consensus sequence: SHAGRGGGCABH



Reverse complement motif Consensus sequence: DBTGCCCKCTDS



Dataset #: 2 Motif ID: 50 Motif name: Motif 50

Original motif Consensus sequence: AGRAA



Reverse complement motif Consensus sequence: TTMCT



Best Matches for Motif ID 50 (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:	Backward
Position number:	1
Number of overlap:	5
Similarity score:	0

Alignment:

TTMCT

-TTMCT

Original motif Consensus sequence: AGRAAA



Reverse complement motif Consensus sequence: TTTMCT



Dataset #: 1
 Motif ID: 39
 Motif name: Motif 39
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 5
 Similarity score: 0.0244128

Alignment:

BAGAAA

-AGRAA

Original motif Consensus sequence: BAGAAA



Reverse complement motif Consensus sequence: TTTCTB



Dataset #: 1
 Motif ID: 28
 Motif name: Motif 28
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 5

Similarity score: 0.0419638

Alignment:
CAGGAAG
-AGRAA-

Original motif Consensus sequence: CTCCTG



Reverse complement motif Consensus sequence: CAGGAAG



Dataset #:	1
Motif ID:	29
Motif name:	Motif 29
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	5
Similarity score:	0.0427966

Alignment:
CATTCY
TTMCT--

Original motif Consensus sequence: CATTCY

Reverse complement motif Consensus sequence: MGAAATG



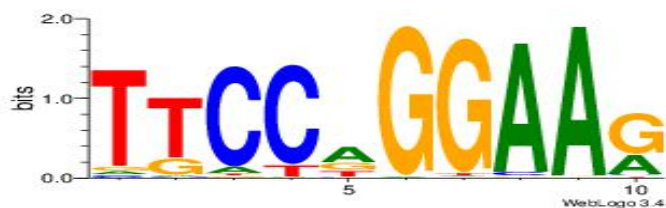
Dataset #: 3
 Motif ID: 119
 Motif name: Stat3
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 5
 Similarity score: 0.0502276

Alignment:

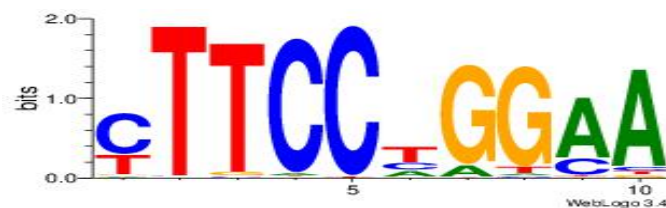
TTCCAGGAAG

----AGRAA--

Original motif Consensus sequence: TTCCAGGAAG



Reverse complement motif Consensus sequence: CTTCTGGAA



Dataset #: 2 Motif ID: 51 Motif name: Motif 51

Original motif Consensus sequence: GAGTTACA



Reverse complement motif Consensus sequence: TGTAAC^cTC



Best Matches for Motif ID 51 (Highest to Lowest)

Dataset #:	1
Motif ID:	38
Motif name:	Motif 38
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	8
Similarity score:	0

Alignment:
GAGTTACA
GAGTTACA

Original motif Consensus sequence: GAGTTACA



Reverse complement motif Consensus sequence: TGTAAC^cTC



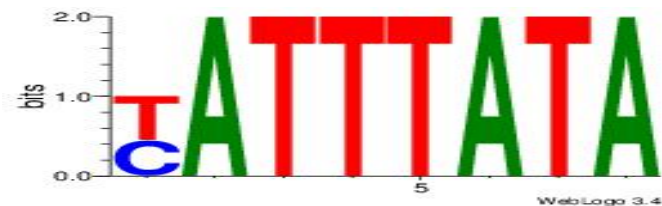
Dataset #: 2
 Motif ID: 66
 Motif name: Motif 66
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 8
 Similarity score: 0.0742432

Alignment:
 KATTTATA
 GAGTTACA

Original motif Consensus sequence: TATAAATR



Reverse complement motif Consensus sequence: KATTTATA

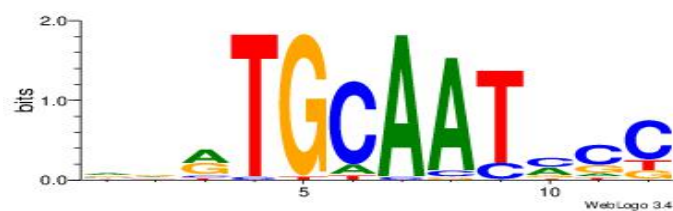


Dataset #: 3
 Motif ID: 75
 Motif name: Ddit3Cebpa
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 4
 Number of overlap: 8

Similarity score: 0.0857192

Alignment:
GGRATTGCAKHB
-GAGTTACA---

Original motif Consensus sequence: VDRTGCAATMCC



Reverse complement motif Consensus sequence: GGRATTGCAKHB

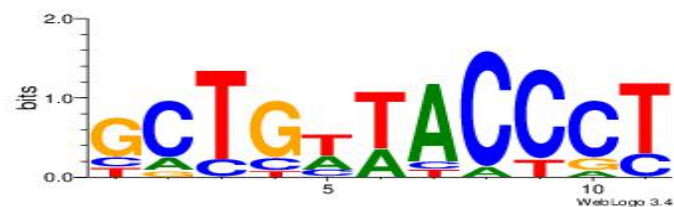


Dataset #: 3
Motif ID: 117
Motif name: Spz1
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 3
Number of overlap: 8
Similarity score: 0.0885417

Alignment:
AGGGTAWCAGC
-GAGTTACA--

Original motif Consensus sequence: AGGGTAWCAGC

Reverse complement motif Consensus sequence: GCTGWTACCCT



Dataset #: 3
 Motif ID: 112
 Motif name: RELA
 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: 0.0911946

Alignment:

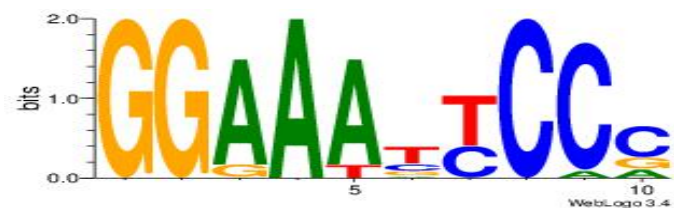
GGGRATTTC

--GAGTTACA

Original motif Consensus sequence: GGGRATTTC



Reverse complement motif Consensus sequence: GGAAATKCCC



Dataset #: 2 **Motif ID: 52** **Motif name: Motif 52**

Original motif Consensus sequence: AAATAAAW



Reverse complement motif Consensus sequence: WTTTATTT



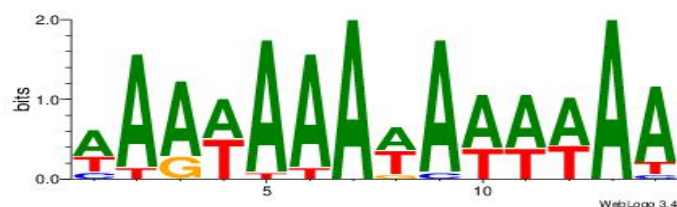
Best Matches for Motif ID 52 (Highest to Lowest)

Dataset #:	2
Motif ID:	68
Motif name:	Motif 68
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:	0.0178205

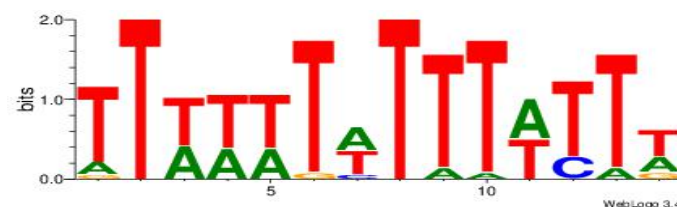
Alignment:

```
TTWWWTWTTTWTTW
-----WTTTATTT
```

Original motif Consensus sequence: WAAWAAAWWWAA



Reverse complement motif Consensus sequence: TTWWWTWTTTWTTW

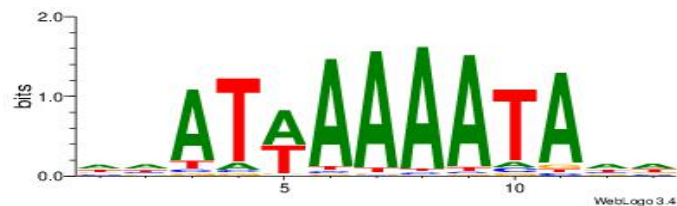


Dataset #: 4
 Motif ID: 150
 Motif name: waATwAAAATAww
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 8
 Similarity score: 0.0502803

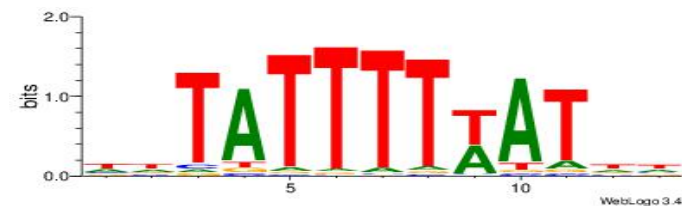
Alignment:

DHTATTTTWATHD
 -----WTTTATTT

Original motif Consensus sequence: DHATWAAAATAHD



Reverse complement motif Consensus sequence: DHTATTTTWATHD



Dataset #: 1
 Motif ID: 2
 Motif name: Motif 2
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 8

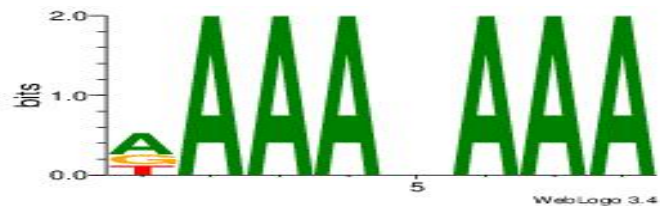
Similarity score: 0.0573886

Alignment:

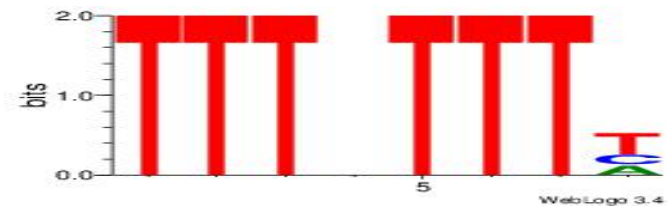
AAAAHAAA

AAATAAAW

Original motif Consensus sequence: AAAAHAAA



Reverse complement motif Consensus sequence: TTTDTTTT



Dataset #: 4
Motif ID: 148
Motif name: wwTwAAAAww
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: 0.0617903

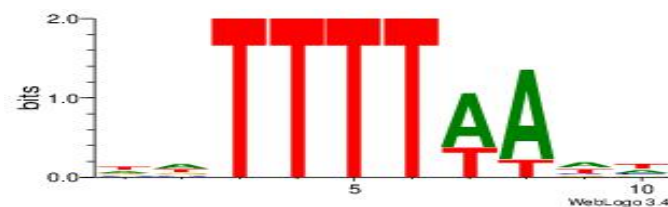
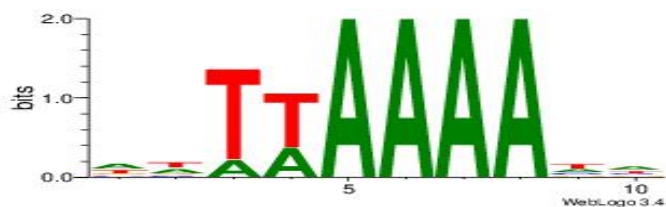
Alignment:

HHTTTTWADD

--WTTTATTT

Original motif Consensus sequence: DDTWAAAAHH

Reverse complement motif Consensus sequence: HHTTTTWADD



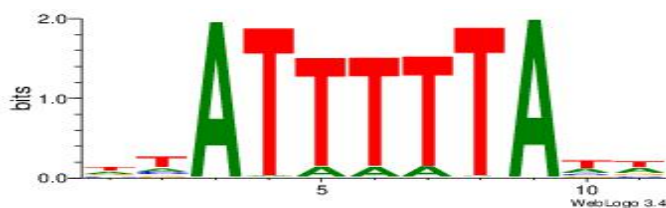
Dataset #: 4
 Motif ID: 157
 Motif name: wtATTTTAAww
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 8
 Similarity score: 0.0718936

Alignment:

DTATTTTAAWW

--WTTTATTT--

Original motif Consensus sequence: DTATTTTAAWW



Reverse complement motif Consensus sequence: WWTAAAAATAD



Dataset #: 2 Motif ID: 53 Motif name: Motif 53

Original motif Consensus sequence: CAGATCCC



Reverse complement motif Consensus sequence: GGGATCTG



Best Matches for Motif ID 53 (Highest to Lowest)

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

Alignment:
CAGATYCC
CAGATCCC

Original motif Consensus sequence: CAGATYCC



Reverse complement motif Consensus sequence: GGKATCTG

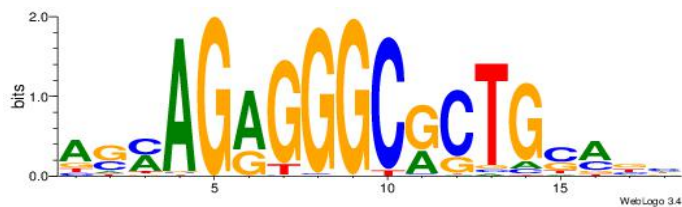


Dataset #: 4
 Motif ID: 149
 Motif name: asmAGRGGGCrCTGsmkc
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 7
 Number of overlap: 8
 Similarity score: 0.0479917

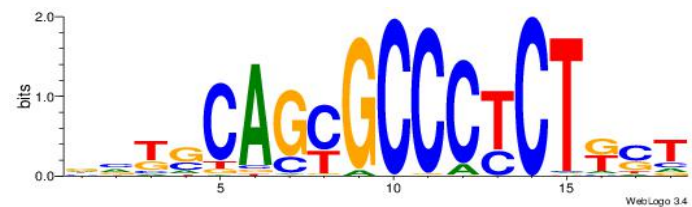
Alignment:

DBTSCAGMGCCCTCTRST
 ----CAGATCCC-----

Original motif Consensus sequence: ASMAGAGGGCRCTGSABH



Reverse complement motif Consensus sequence: DBTSCAGMGCCCTCTRST



Dataset #: 4
 Motif ID: 160
 Motif name: brCAGGGCCrs
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3

Number of overlap: 8
Similarity score: 0.0605671

Alignment:
BBGGCCCTGBB
-GGGATCTG--

Original motif Consensus sequence: BVCAGGGCCVB



Reverse complement motif Consensus sequence: BBGGCCCTGBB

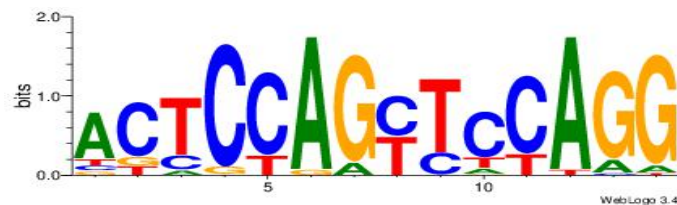
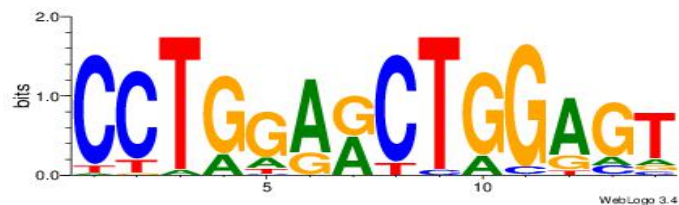


Dataset #: 2
Motif ID: 69
Motif name: Motif 69
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 5
Number of overlap: 8
Similarity score: 0.0606088

Alignment:
ACTCCAGMTCCAGG
----CAGATCCC--

Original motif Consensus sequence: CCTGGARCTGGAGT

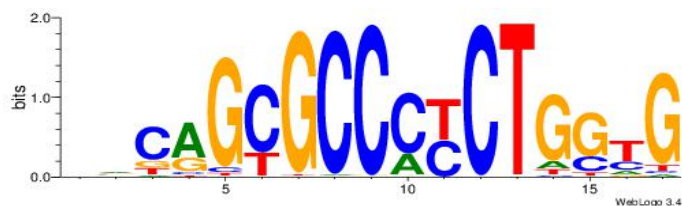
Reverse complement motif Consensus sequence: ACTCCAGMTCCAGG



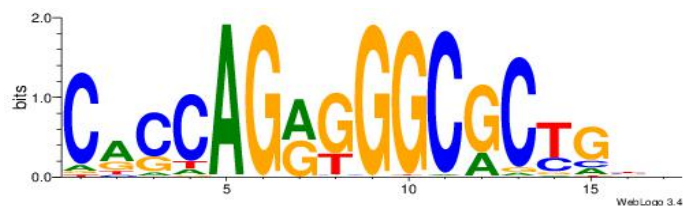
Dataset #: 4
 Motif ID: 168
 Motif name: yrcrYGCCMyCTGGtG
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 8
 Similarity score: 0.065385

Alignment:
 CACCAGMGGGCGCTGBD
 -----GGGATCTG--

Original motif Consensus sequence: HVCAGCGCCCYCTGGTG



Reverse complement motif Consensus sequence: CACCAGMGGGCGCTGBD



Dataset #: 2 Motif ID: 54 Motif name: Motif 54

Original motif Consensus sequence: ATTY



Reverse complement motif Consensus sequence: MKAAT



Best Matches for Motif ID 54 (Highest to Lowest)

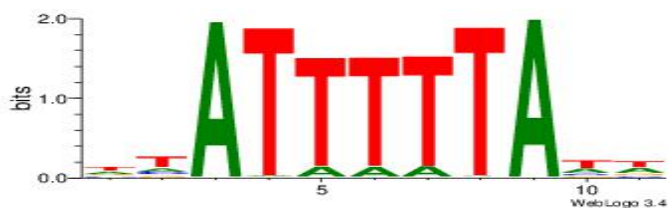
Dataset #:	4
Motif ID:	157
Motif name:	wtATTTTAAw
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	3
Number of overlap:	5
Similarity score:	0.0491344

Alignment:

DTATTTTAAW

--ATTY----

Original motif Consensus sequence: DTATTTTAAW



Reverse complement motif Consensus sequence: WWTAAAAATAD



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: 2
 Number of overlap: 5
 Similarity score: 0.0551561

Alignment:
 CATTCY
 -ATYY-

Original motif Consensus sequence: CATTCY



Reverse complement motif Consensus sequence: MGAAATG



Dataset #: 4
 Motif ID: 150
 Motif name: waATwAAAATAww
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 6
 Number of overlap: 5

Similarity score: 0.0567288

Alignment:

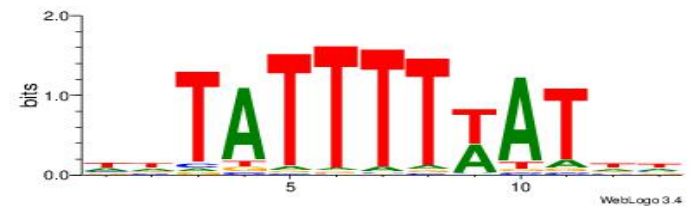
DHTATTTTWATHD

---ATTYY-----

Original motif Consensus sequence: DHATWAAAATAHD



Reverse complement motif Consensus sequence: DHTATTTTWATHD



Dataset #: 4
Motif ID: 148
Motif name: wwTwAAAAww
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 5
Number of overlap: 5
Similarity score: 0.0727457

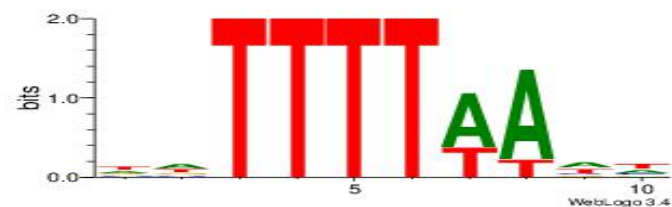
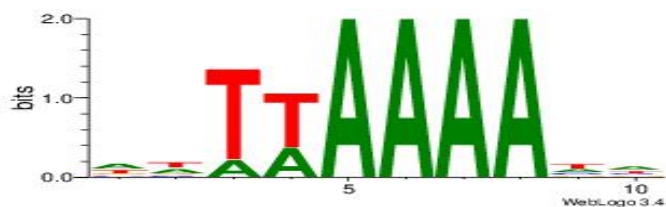
Alignment:

HHTTTTWADD

-ATTYY-----

Original motif Consensus sequence: DDTWAAAHH

Reverse complement motif Consensus sequence: HHTTTTWADD

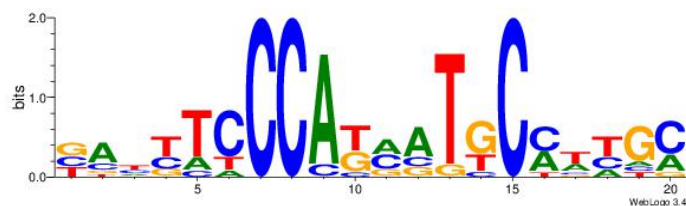


Dataset #: 3
 Motif ID: 131
 Motif name: znf143
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 8
 Number of overlap: 5
 Similarity score: 0.0737392

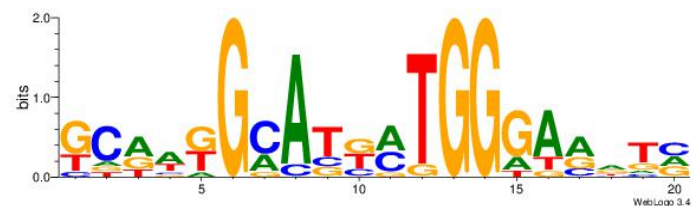
Alignment:

BAHYTCCCAKMATGCMWYGC
 -----MKAAT-----

Original motif Consensus sequence: BAHYTCCCAKMATGCMWYGC

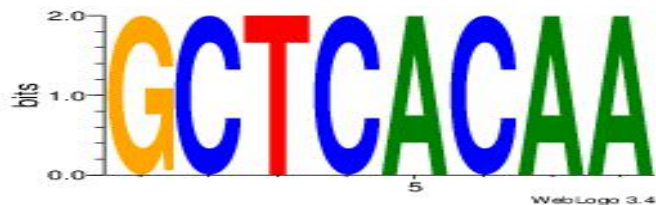


Reverse complement motif Consensus sequence: GCMWRGCATYRTGGGAMHTB



Dataset #: 2 Motif ID: 55 Motif name: Motif 55

Original motif Consensus sequence: GCTCACAA



Reverse complement motif Consensus sequence: TTGTGAGC

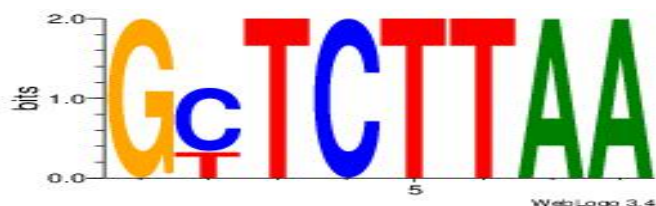


Best Matches for Motif ID 55 (Highest to Lowest)

Dataset #:	1
Motif ID:	15
Motif name:	Motif 15
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	8
Similarity score:	0.071643

Alignment:
GCTCTTAA
GCTCACAA

Original motif Consensus sequence: GCTCTTAA



Reverse complement motif Consensus sequence: TTAAGAGC



Dataset #: 2
 Motif ID: 57
 Motif name: Motif 57
 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: 0.0907452

Alignment:
 KTGTGTGT
 TTGTGAGC

Original motif Consensus sequence: ACACACAY



Reverse complement motif Consensus sequence: KTGTGTGT



Dataset #: 4
 Motif ID: 145
 Motif name: grCCACyAGAkG
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 5
 Number of overlap: 8

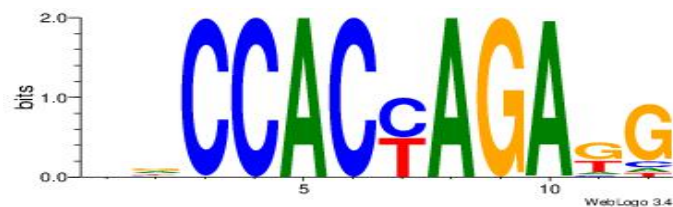
Similarity score: 0.0949146

Alignment:

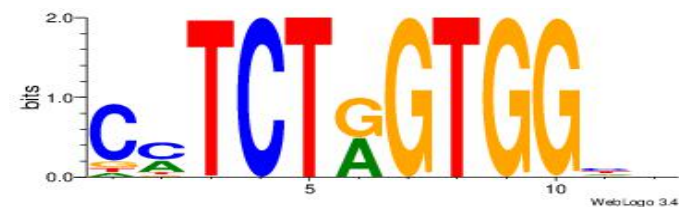
CYTCTKGTGGHH

----TTGTGAGC

Original motif Consensus sequence: DDCCACYAGAKG



Reverse complement motif Consensus sequence: CYTCTKGTGGHH



Dataset #: 4
Motif ID: 158
Motif name: grCCACwAGrk
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 4
Number of overlap: 8
Similarity score: 0.0951691

Alignment:

YMCTWGTGGHH

---TTGTGAGC

Original motif Consensus sequence: DDCCACWAGRK

Reverse complement motif Consensus sequence: YMCTWGTGGHH



Dataset #: 3
 Motif ID: 78
 Motif name: Egr1
 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: 0.103125

Alignment:
 GCGCSAAA
 GCTCACAA

Original motif Consensus sequence: TTTSGCGC



Reverse complement motif Consensus sequence: GCGCSAAA



Dataset #: 2 Motif ID: 56 Motif name: Motif 56

Original motif Consensus sequence: CCACATGG



Reverse complement motif Consensus sequence: CCATGTGG



Best Matches for Motif ID 56 (Highest to Lowest)

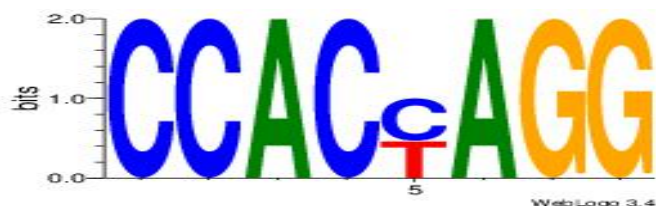
Dataset #:	1
Motif ID:	21
Motif name:	Motif 21
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	8
Similarity score:	0.0480363

Alignment:

CCTKGTGG

CCATGTGG

Original motif Consensus sequence: CCACYAGG



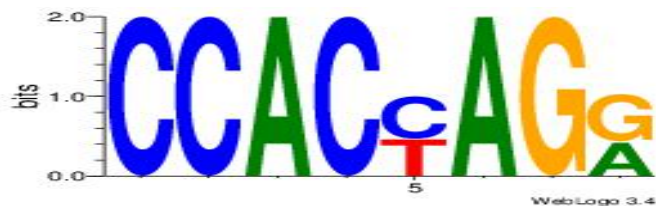
Reverse complement motif Consensus sequence: CCTKGTGG



Dataset #: 2
 Motif ID: 48
 Motif name: Motif 48
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 8
 Similarity score: 0.0609421

Alignment:
 MCTKGTGG
 CCATGTGG

Original motif Consensus sequence: CCACYAGR



Reverse complement motif Consensus sequence: MCTKGTGG

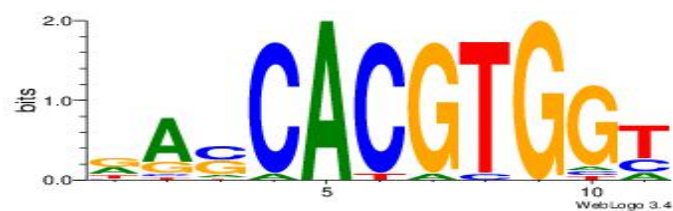


Dataset #: 3
 Motif ID: 95
 Motif name: MYCMAX
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 8

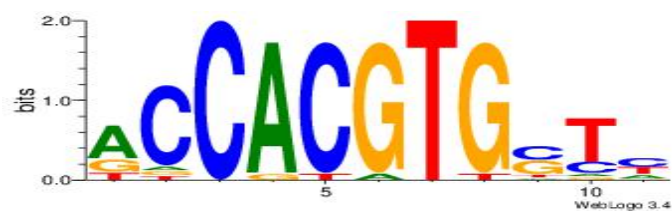
Similarity score: 0.0616071

Alignment:
RASCACGTGGT
--CCACATGG--

Original motif Consensus sequence: RASCACGTGGT



Reverse complement motif Consensus sequence: ACCACGTGSTM

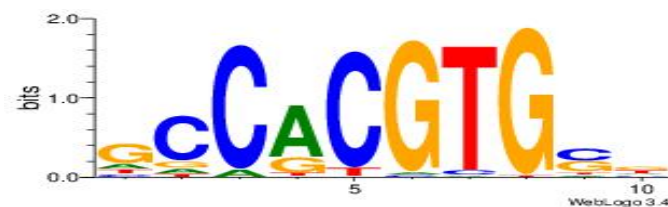


Dataset #: 3
Motif ID: 96
Motif name: Mycn
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2
Number of overlap: 8
Similarity score: 0.0634989

Alignment:
HSCACGTGGC
-CCACATGG-

Original motif Consensus sequence: HSCACGTGGC

Reverse complement motif Consensus sequence: GCCACGTGSD



Dataset #: 4
 Motif ID: 158
 Motif name: grCCACwAGrk
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 8
 Similarity score: 0.0666667

Alignment:

DDCCACWAGRK

--CCACATGG--

Original motif Consensus sequence: DDCCACWAGRK



Reverse complement motif Consensus sequence: YMCTWGTGGHH



Dataset #: 2 Motif ID: 57 Motif name: Motif 57

Original motif Consensus sequence: ACACACAY



Reverse complement motif Consensus sequence: KTGTGTGT



Best Matches for Motif ID 57 (Highest to Lowest)

Dataset #:	1
Motif ID:	35
Motif name:	Motif 35
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	8
Similarity score:	0.0591808

Alignment:
KTGGTTGT
KTGTGTGT

Original motif Consensus sequence: ACAACCAAY



Reverse complement motif Consensus sequence: KTGGTTGT

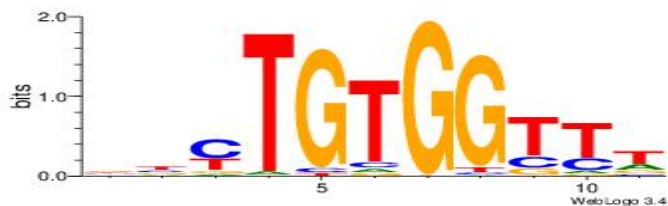


Dataset #: 3
 Motif ID: 114
 Motif name: RUNX1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 8
 Similarity score: 0.0712868

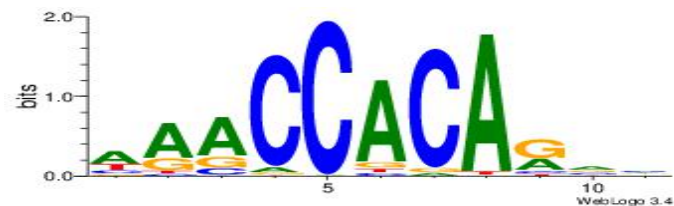
Alignment:

BBYTGTGGTTT
 --KTGTGTGT--

Original motif Consensus sequence: BBYTGTGGTTT



Reverse complement motif Consensus sequence: AAACCACAKVB

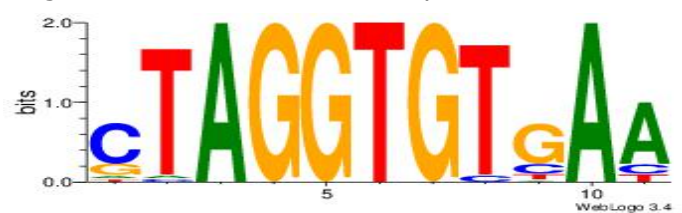


Dataset #: 3
 Motif ID: 120
 Motif name: T
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 8

Similarity score: 0.0758601

Alignment:
TTCACACCTAG
-ACACACAY--

Original motif Consensus sequence: CTAGGTGTGAA



Reverse complement motif Consensus sequence: TTCACACCTAG



Dataset #: 2
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: 8
Similarity score: 0.0761605

Alignment:
TTGTGAGC
KTGTGTGT

Original motif Consensus sequence: GCTCACAA

Reverse complement motif Consensus sequence: TTGTGAGC



Dataset #: 4
 Motif ID: 162
 Motif name: ccAsCCCCAcc
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 8
 Similarity score: 0.0776002

Alignment:
 DBTGGGGSTVD
 -KTGTGTGT--

Original motif Consensus sequence: HVASCCCCABH



Reverse complement motif Consensus sequence: DBTGGGGSTVD



Dataset #: 2 Motif ID: 58 Motif name: Motif 58

Original motif Consensus sequence: TACATGCA



Reverse complement motif Consensus sequence: TGCATGTA



Best Matches for Motif ID 58 (Highest to Lowest)

Dataset #:	4
Motif ID:	152
Motif name:	yrCATGCAyr
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:	0.0160706

Alignment:

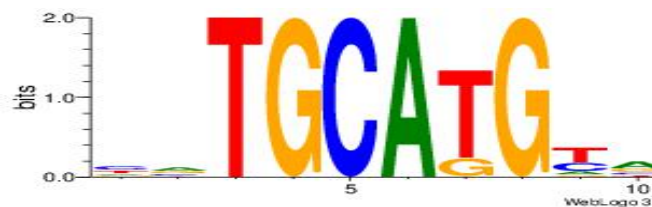
BRCATGCABD

TACATGCA--

Original motif Consensus sequence: BRCATGCABD



Reverse complement motif Consensus sequence: HVTGCATGKV

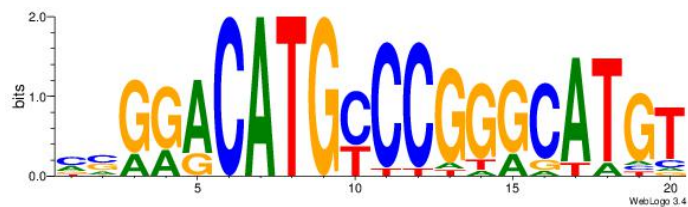


Dataset #: 3
 Motif ID: 125
 Motif name: TP53
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 4
 Number of overlap: 8
 Similarity score: 0.0595681

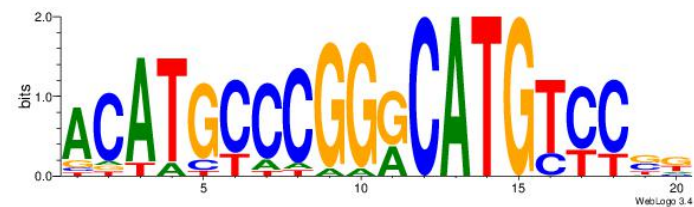
Alignment:

ACATGCCCGGKCATGTCCSR
 -----TGCATGTA----

Original motif Consensus sequence: MSGGACATGYCCGGGCATGT



Reverse complement motif Consensus sequence: ACATGCCCGGKCATGTCCSR



Dataset #: 2
 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: 8
Similarity score: 0.0642891

Alignment:
CATATRCA
TACATGCA

Original motif Consensus sequence: CATATRCA



Reverse complement motif Consensus sequence: TGMATATG



Dataset #: 1
Motif ID: 36
Motif name: Motif 36
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 8
Similarity score: 0.0792922

Alignment:
TCCTGGRA
TGCATGTA

Original motif Consensus sequence: TCCTGGRA

Reverse complement motif Consensus sequence: TMCCAGGA



Dataset #: 3
 Motif ID: 95
 Motif name: MYCMAX
 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: 0.0822408

Alignment:

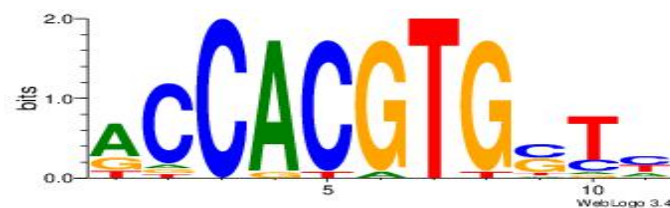
RASCACGTGGT

-TGCATGTA--

Original motif Consensus sequence: RASCACGTGGT



Reverse complement motif Consensus sequence: ACCACGTGSTM



Dataset #: 2 Motif ID: 59 Motif name: Motif 59

Original motif Consensus sequence: CCCCRCCC



Reverse complement motif Consensus sequence: GGGKGGGG



Best Matches for Motif ID 59 (Highest to Lowest)

Dataset #:	1
Motif ID:	5
Motif name:	Motif 5
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:	0.00363191

Alignment:

GGGDGGGG

GGGKGGGG

Original motif Consensus sequence: CCCDCCC



Reverse complement motif Consensus sequence: GGGDGGGG

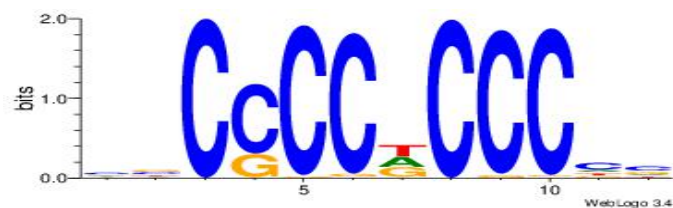


Dataset #: 4
 Motif ID: 155
 Motif name: csCSCCdCCCcs
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3
 Number of overlap: 8
 Similarity score: 0.0143924

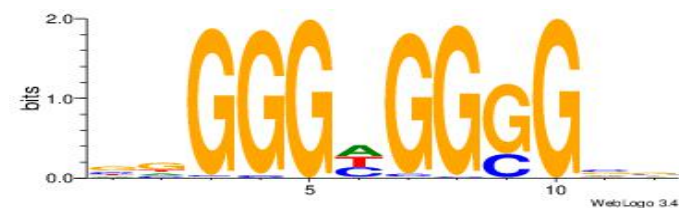
Alignment:

VDGGGDGGGGBV
 --GGGKGGGG--

Original motif Consensus sequence: VBCCCCDCCCHV



Reverse complement motif Consensus sequence: VDGGGDGGGGBV

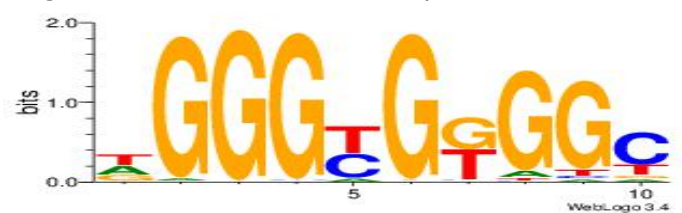


Dataset #: 3
 Motif ID: 89
 Motif name: Klf4
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 8

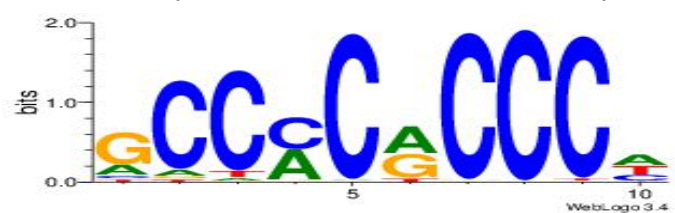
Similarity score: 0.0334874

Alignment:
GCCYCMCCCD
-CCCCRCCC-

Original motif Consensus sequence: DGGGYGKGGC



Reverse complement motif Consensus sequence: GCCYCMCCCD

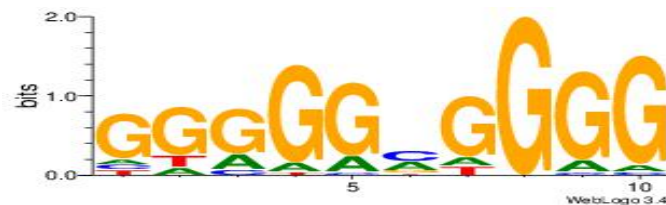
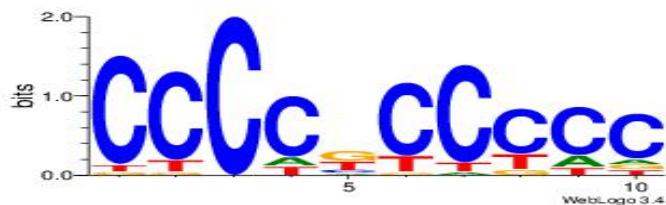


Dataset #: 3
Motif ID: 116
Motif name: SP1
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 8
Similarity score: 0.0421627

Alignment:
GGGGGYGGGG
--GGGKGGGG

Original motif Consensus sequence: CCCCKCCCCC

Reverse complement motif Consensus sequence: GGGGGYGGGG



Dataset #: 4
 Motif ID: 154
 Motif name: csCsCCTCCcc
 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: 0.0467112

Alignment:

VBCCCCTCCHB

--CCCCRCCC--

Original motif Consensus sequence: VBCCCCTCCHB



Reverse complement motif Consensus sequence: BDGGAGGGGBV



Dataset #: 2 Motif ID: 60 Motif name: Motif 60

Original motif Consensus sequence: CTGGAR



Reverse complement motif Consensus sequence: MTCCAG



Best Matches for Motif ID 60 (Highest to Lowest)

Dataset #:	1
Motif ID:	6
Motif name:	Motif 6
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2
Number of overlap:	6
Similarity score:	0.00500479

Alignment:

CTGGRRA

CTGGAR-

Original motif Consensus sequence: CTGGRRA



Reverse complement motif Consensus sequence: TMMCCAG

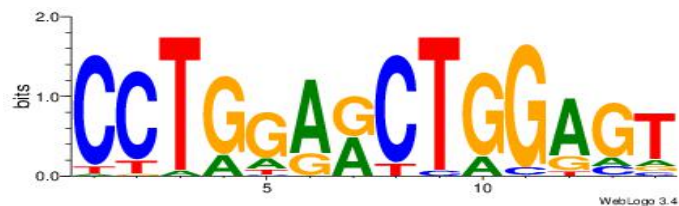


Dataset #: 2
 Motif ID: 69
 Motif name: Motif 69
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 8
 Number of overlap: 6
 Similarity score: 0.0149252

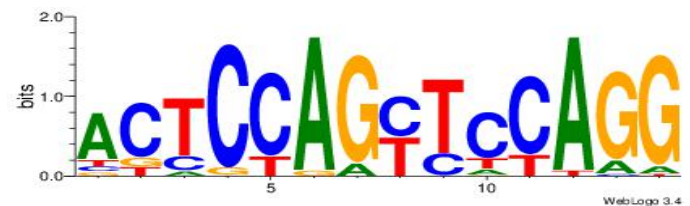
Alignment:

CCTGGARCTGGAGT
 -----CTGGAR-

Original motif Consensus sequence: CCTGGARCTGGAGT



Reverse complement motif Consensus sequence: ACTCCAGMTCCAG



Dataset #: 1
 Motif ID: 36
 Motif name: Motif 36
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 6

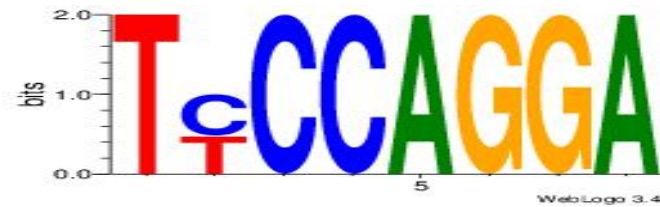
Similarity score: 0.0273394

Alignment:
TCCTGGRA
--CTGGAR

Original motif Consensus sequence: TCCTGGRA



Reverse complement motif Consensus sequence: TMCCAGGA

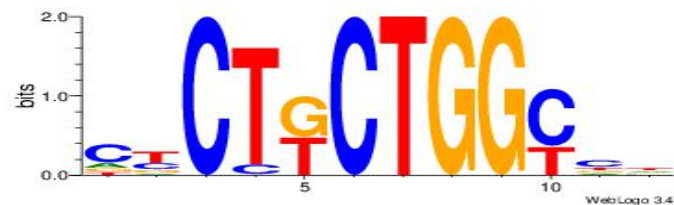


Dataset #: 4
Motif ID: 151
Motif name: agrCCAGmAGrg
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 6
Number of overlap: 6
Similarity score: 0.0324331

Alignment:
CKCTRCTGGCVH
-----CTGGAR-

Original motif Consensus sequence: HVGCCAGMAGRG

Reverse complement motif Consensus sequence: CKCTRCTGGCVH



Dataset #: 3
 Motif ID: 85
 Motif name: Hand1Tcfe2a
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 6
 Similarity score: 0.0370865

Alignment:
 BRTCTGGMWT
 ---CTGGAR-

Original motif Consensus sequence: BRTCTGGMWT



Reverse complement motif Consensus sequence: AWRCCAGAMB



Dataset #: 2 Motif ID: 61 Motif name: Motif 61

Original motif Consensus sequence: AGATGGY



Reverse complement motif Consensus sequence: KCCATCT



Best Matches for Motif ID 61 (Highest to Lowest)

Dataset #:	2
Motif ID:	63
Motif name:	Motif 63
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	2
Number of overlap:	7
Similarity score:	0.0339703

Alignment:
CWCCCTCT
-KCCATCT

Original motif Consensus sequence: AGAGGGWG



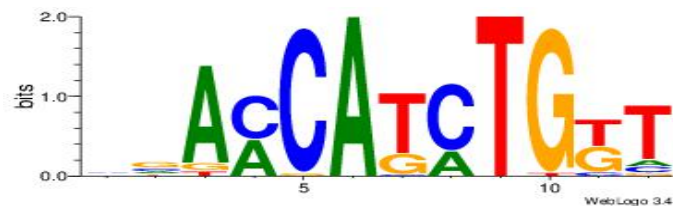
Reverse complement motif Consensus sequence: CWCCCTCT



Dataset #: 3
 Motif ID: 121
 Motif name: TAL1TCF3
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 4
 Number of overlap: 7
 Similarity score: 0.034782

Alignment:
 ARCAGATGRTVD
 ---AGATGGY--

Original motif Consensus sequence: HVAMCATCTGKT



Reverse complement motif Consensus sequence: ARCAGATGRTVD



Dataset #: 4
 Motif ID: 163
 Motif name: gwGGCCAGmAGAGGGCrby
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 4
 Number of overlap: 7

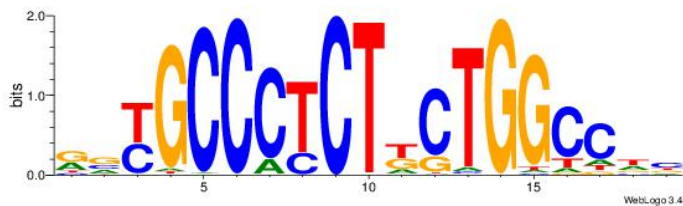
Similarity score: 0.0365189

Alignment:
VHGGCCAGMAGAGGGCRBY
-----AGATGGY---

Original motif Consensus sequence: VHGGCCAGMAGAGGGCRBY



Reverse complement motif Consensus sequence: KBKGCCCTCTYCTGGCCHV



Dataset #: 2
Motif ID: 46
Motif name: Motif 46
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2
Number of overlap: 7
Similarity score: 0.0371728

Alignment:
AGRKGGCR
AGATGGY-

Original motif Consensus sequence: AGRKGGCR

Reverse complement motif Consensus sequence: KGCCYKCT



Dataset #: 1
 Motif ID: 1
 Motif name: Motif 1
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 7
 Similarity score: 0.0375558

Alignment:
 AGRKGGCR
 AGATGGY-

Original motif Consensus sequence: AGRKGGCR



Reverse complement motif Consensus sequence: KGCCYKCT



Dataset #: 2 Motif ID: 62 Motif name: Motif 62

Original motif Consensus sequence: CGCCVCC



Reverse complement motif Consensus sequence: GGVGGCG



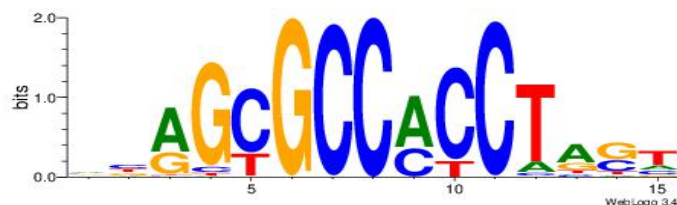
Best Matches for Motif ID 62 (Highest to Lowest)

Dataset #:	4
Motif ID:	146
Motif name:	myrGYGCCmCCTast
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	5
Number of overlap:	7
Similarity score:	0.0315476

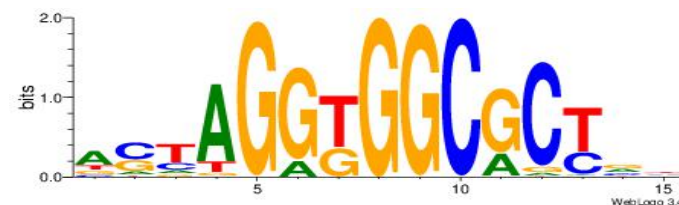
Alignment:

```
VBAGCGCCMCCTAST
-----CGCCVCC-----
```

Original motif Consensus sequence: VBAGCGCCMCCTAST



Reverse complement motif Consensus sequence: ASTAGGYGGCGCT



Dataset #: 1
 Motif ID: 27
 Motif name: Motif 27
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 7
 Similarity score: 0.0348335

Alignment:
 GGCGGCSG
 GGVGGCG-

Original motif Consensus sequence: CSGCCGCC



Reverse complement motif Consensus sequence: GGCGGCSG

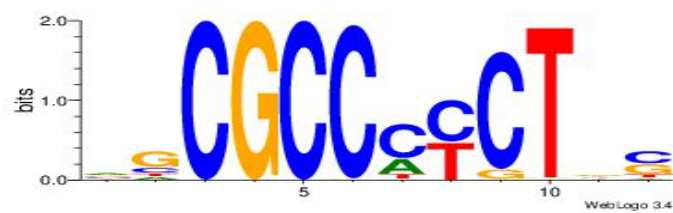


Dataset #: 4
 Motif ID: 137
 Motif name: rgCGCCmyCTgs
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 4
 Number of overlap: 7

Similarity score: 0.0357527

Alignment:
SHAGKGGGCGCB
---GGVGGCG---

Original motif Consensus sequence: VCGCCCYCTDS



Reverse complement motif Consensus sequence: SHAGKGGGCGCB

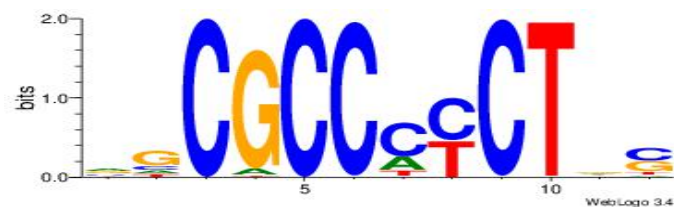
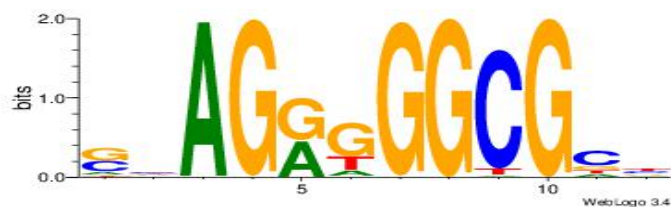


Dataset #: 4
Motif ID: 153
Motif name: scAGrkGGCGcy
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 3
Number of overlap: 7
Similarity score: 0.0403279

Alignment:
VCGCCCMCTDS
--CGCCVCC---

Original motif Consensus sequence: SHAGRGGGCGCB

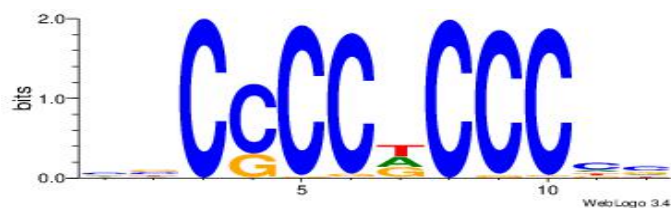
Reverse complement motif Consensus sequence: VCGCCCMCTDS



Dataset #: 4
 Motif ID: 155
 Motif name: csCSCCdCCCcs
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 7
 Similarity score: 0.0439081

Alignment:
 VBCCCCDCCCHV
 --CGCCVCC---

Original motif Consensus sequence: VBCCCCDCCCHV



Reverse complement motif Consensus sequence: VDGGGDGGGGBV



Dataset #: 2 Motif ID: 63 Motif name: Motif 63

Original motif Consensus sequence: AGAGGGWG



Reverse complement motif Consensus sequence: CWCCCTCT



Best Matches for Motif ID 63 (Highest to Lowest)

Dataset #:	1
Motif ID:	11
Motif name:	Motif 11
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	8
Similarity score:	0.0323316

Alignment:
MGAGGBAG
AGAGGGWG

Original motif Consensus sequence: CTBCCTCY



Reverse complement motif Consensus sequence: MGAGGBAG

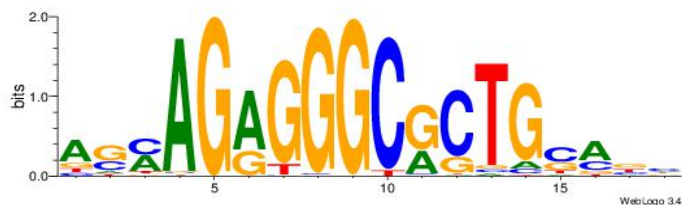


Dataset #: 4
 Motif ID: 149
 Motif name: asmAGRGGGCrCTGsmkc
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 8
 Number of overlap: 8
 Similarity score: 0.040911

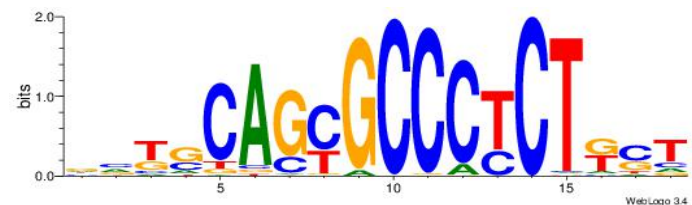
Alignment:

DBTSCAGMGCCCTCTRST
 -----CWCCCTCT---

Original motif Consensus sequence: ASMAGAGGGCRCTGSABH



Reverse complement motif Consensus sequence: DBTSCAGMGCCCTCTRST



Dataset #: 4
 Motif ID: 153
 Motif name: scAGrkGGCGcy
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3

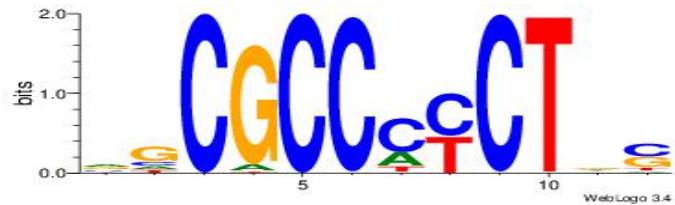
Number of overlap: 8
Similarity score: 0.0435349

Alignment:
SHAGRGGGCGCB
--AGAGGGWG--

Original motif Consensus sequence: SHAGRGGGCGCB



Reverse complement motif Consensus sequence: VGCGCCCMCTDS

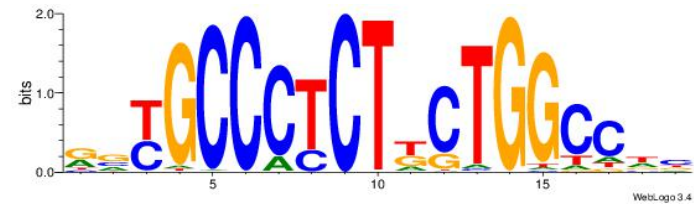
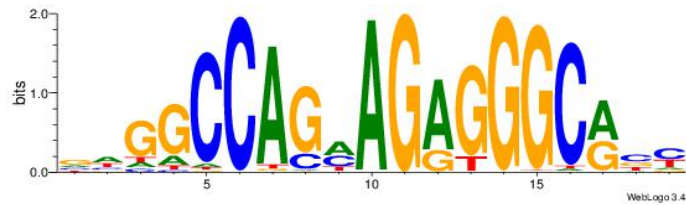


Dataset #: 4
Motif ID: 163
Motif name: gwGGCCAGmAGAGGGCrby
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 3
Number of overlap: 8
Similarity score: 0.0462891

Alignment:
VHGGCCAGMAGAGGGCRBY
-----AGAGGGWG--

Original motif Consensus sequence: VHGGCCAGMAGAGGGCRBY

Reverse complement motif Consensus sequence:
KBKGCCCTCTYCTGGCCHV



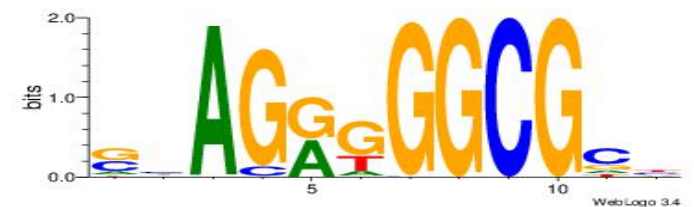
Dataset #: 4
 Motif ID: 137
 Motif name: rgCGCCmyCTgs
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 8
 Similarity score: 0.0481673

Alignment:
 VCGCCCYCTDS
 --CWCCCTCT--

Original motif Consensus sequence: VCGCCCYCTDS



Reverse complement motif Consensus sequence: SHAGKGGGCGCB



Dataset #: 2 Motif ID: 64 Motif name: Motif 64

Original motif Consensus sequence: CATATRCA



Reverse complement motif Consensus sequence: TGMATATG



Best Matches for Motif ID 64 (Highest to Lowest)

Dataset #:	1
Motif ID:	31
Motif name:	Motif 31
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	8
Similarity score:	0.0465487

Alignment:
CATGYACA
CATATRCA

Original motif Consensus sequence: CATGYACA



Reverse complement motif Consensus sequence: TGTKCATG



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: 8
 Similarity score: 0.0585881

Alignment:
 CACACACA
 CATATRCA

Original motif Consensus sequence: CACACACA



Reverse complement motif Consensus sequence: TGTGTGTG



Dataset #: 2
 Motif ID: 58
 Motif name: Motif 58
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 8

Similarity score: 0.0607109

Alignment:
TACATGCA
CATATRCA

Original motif Consensus sequence: TACATGCA



Reverse complement motif Consensus sequence: TGCATGTA



Dataset #: 4
Motif ID: 152
Motif name: yrCATGCAyr
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 8
Similarity score: 0.0626249

Alignment:
BRCATGCABD
CATATRCA--

Original motif Consensus sequence: BRCATGCABD

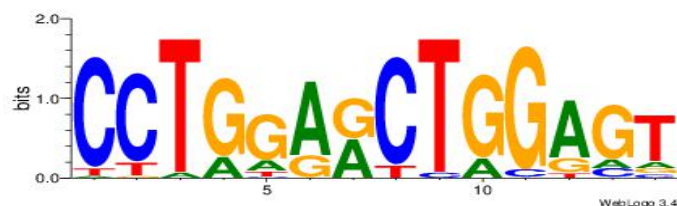
Reverse complement motif Consensus sequence: HVTGCATGKV



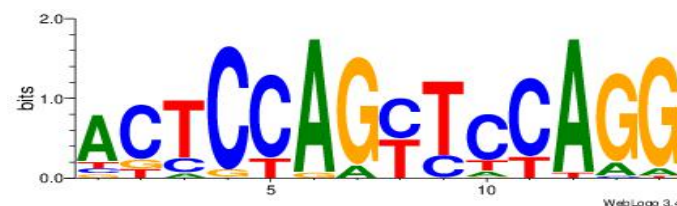
Dataset #: 2
 Motif ID: 69
 Motif name: Motif 69
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 5
 Number of overlap: 8
 Similarity score: 0.0676075

Alignment:
 ACTCCAGMTCCAGG
 ----CATATRCA--

Original motif Consensus sequence: CCTGGARCTGGAGT



Reverse complement motif Consensus sequence: ACTCCAGMTCCAGG



Dataset #: 2 Motif ID: 65 Motif name: Motif 65

Original motif Consensus sequence: ARAACA



Reverse complement motif Consensus sequence: TGTTMT



Best Matches for Motif ID 65 (Highest to Lowest)

Dataset #:	4
Motif ID:	141
Motif name:	raCAAAACam
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2
Number of overlap:	6
Similarity score:	0.00122368

Alignment:

DACAAAACAH

---ARAACA-

Original motif Consensus sequence: DACAAAACAH



Reverse complement motif Consensus sequence: HTGTTTGTG



Dataset #: 1
 Motif ID: 44
 Motif name: Motif 44
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 6
 Similarity score: 0.0101983

Alignment:
 GDAAACA
 -ARAACA

Original motif Consensus sequence: GDAAACA



Reverse complement motif Consensus sequence: TGTTTDC



Dataset #: 4
 Motif ID: 159
 Motif name: kkAAGAGCAsy
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3
 Number of overlap: 6

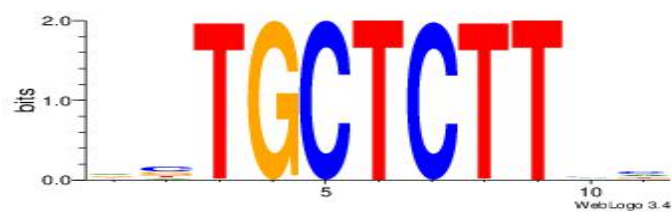
Similarity score: 0.0232212

Alignment:
HVTGCTCTTBH
--TGTMT---

Original motif Consensus sequence: DBAAGAGCAVH



Reverse complement motif Consensus sequence: HVTGCTCTTBH

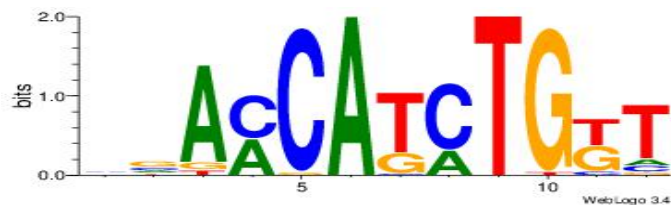


Dataset #: 3
Motif ID: 121
Motif name: TAL1TCF3
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 7
Number of overlap: 6
Similarity score: 0.0330056

Alignment:
HVAMCATCTGKT
ARAACA-----

Original motif Consensus sequence: HVAMCATCTGKT

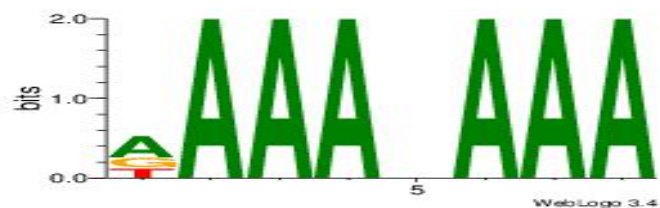
Reverse complement motif Consensus sequence: ARCAGATGRTVD



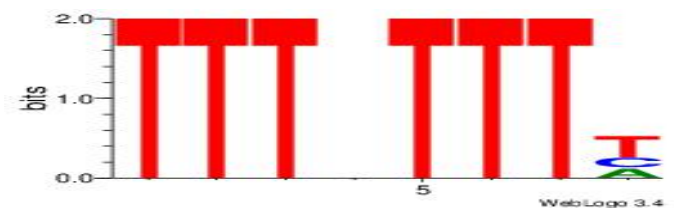
Dataset #: 1
 Motif ID: 2
 Motif name: Motif 2
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 6
 Similarity score: 0.0333069

Alignment:
 AAAAHAAA
 ARAACA--

Original motif Consensus sequence: AAAAHAAA



Reverse complement motif Consensus sequence: TTTDTTTT



Dataset #: 2 Motif ID: 66 Motif name: Motif 66

Original motif Consensus sequence: TATAAATR



Reverse complement motif Consensus sequence: KATTTATA



Best Matches for Motif ID 66 (Highest to Lowest)

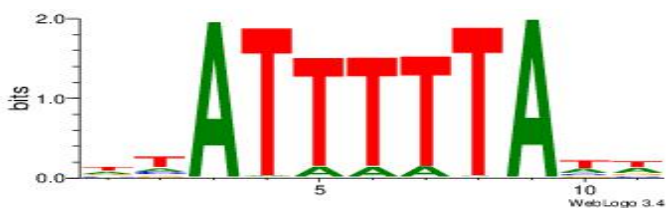
Dataset #:	4
Motif ID:	157
Motif name:	wtATTTTAAww
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	2
Number of overlap:	8
Similarity score:	0.00950221

Alignment:

WWTAAAAATAD

--TATAAATR--

Original motif Consensus sequence: DTATTTTAAWW



Reverse complement motif Consensus sequence: WWTAAAAATAD



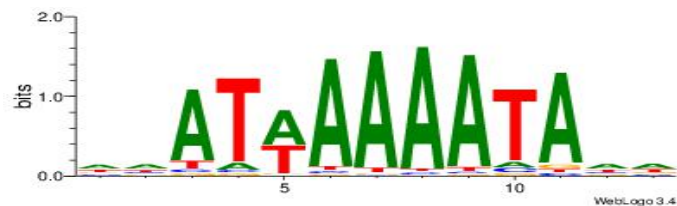
Dataset #: 4
 Motif ID: 150
 Motif name: waATwAAAATAww
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 4
 Number of overlap: 8
 Similarity score: 0.0358566

Alignment:

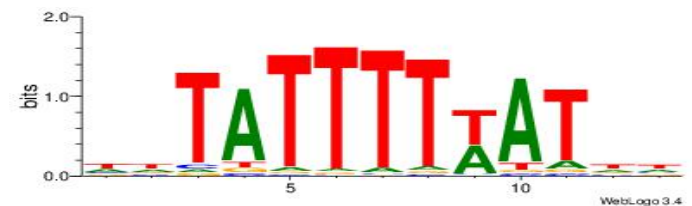
DHTATTTTWATHD

--KATTTATA---

Original motif Consensus sequence: DHATWAAAATAHD



Reverse complement motif Consensus sequence: DHTATTTTWATHD



Dataset #: 1
 Motif ID: 38
 Motif name: Motif 38
 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: 0.0432007

Alignment:
TGTAAGTC
TATAAATR

Original motif Consensus sequence: GAGTTACA



Reverse complement motif Consensus sequence: TGTAAGTC



Dataset #: 2
Motif ID: 51
Motif name: Motif 51
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 8
Similarity score: 0.0432007

Alignment:
TGTAAGTC
TATAAATR

Original motif Consensus sequence: GAGTTACA

Reverse complement motif Consensus sequence: TGTAAGTC



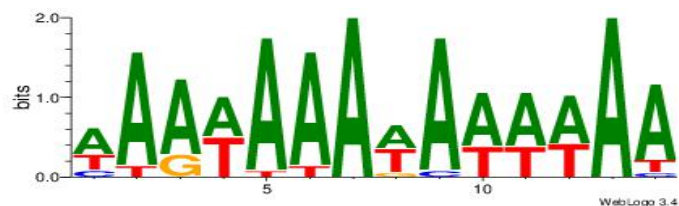
Dataset #: 2
 Motif ID: 68
 Motif name: Motif 68
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 8
 Similarity score: 0.0496717

Alignment:

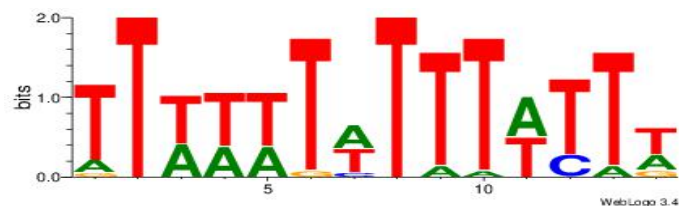
WAAWAAAWAWWWAA

-TATAATR-----

Original motif Consensus sequence: WAAWAAAWAWWWAA

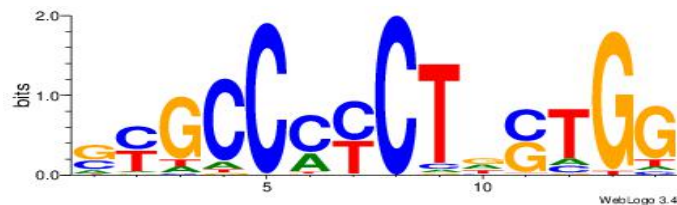


Reverse complement motif Consensus sequence: TTWWWTWTTTWTTW

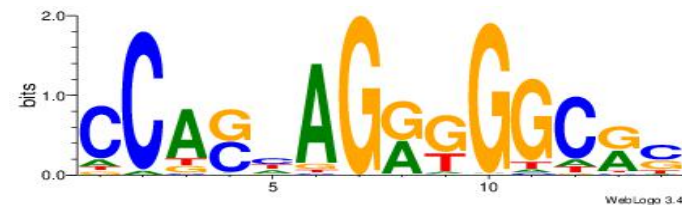


Dataset #: 2 Motif ID: 67 Motif name: Motif 67

Original motif Consensus sequence: SYGCCCCTDSTGG



Reverse complement motif Consensus sequence: CCASHAGKGGGCK



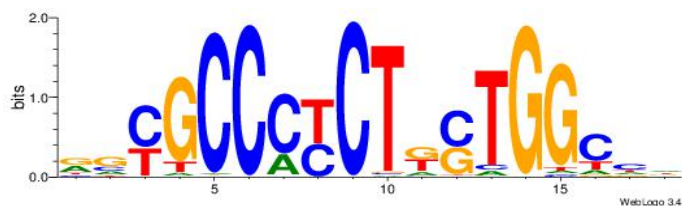
Best Matches for Motif ID 67 (Highest to Lowest)

Dataset #:	4
Motif ID:	156
Motif name:	rgyGCCMyCTksTGGccd
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

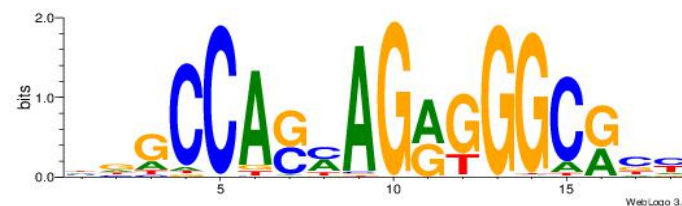
Alignment:

```
RVYGCCCYCTKSTGGCHD  
-SYGCCCCTDSTGG---
```

Original motif Consensus sequence: RVYGCCCYCTKSTGGCHD



Reverse complement motif Consensus sequence:
DDGCCASYAGMGGGCKVM

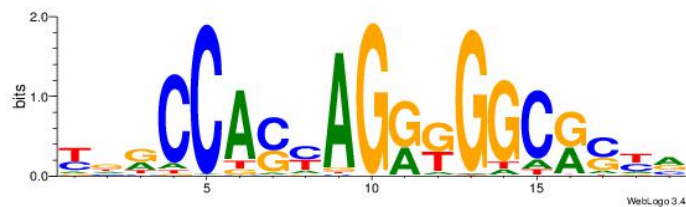


Dataset #: 3
 Motif ID: 74
 Motif name: CTCF
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3
 Number of overlap: 14
 Similarity score: 0.0137353

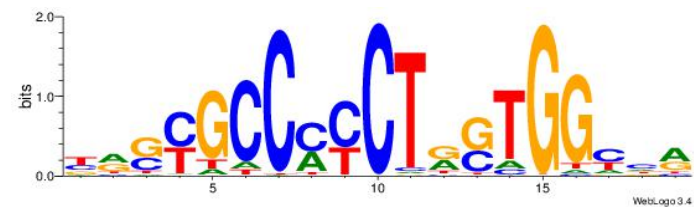
Alignment:

BSMGCCYMCTKSTGGMHM
 --SYGCCCYCTDSTGG---

Original motif Consensus sequence: YDRCCASYAGRKGGRSYV



Reverse complement motif Consensus sequence: BSMGCCYMCTKSTGGMHM



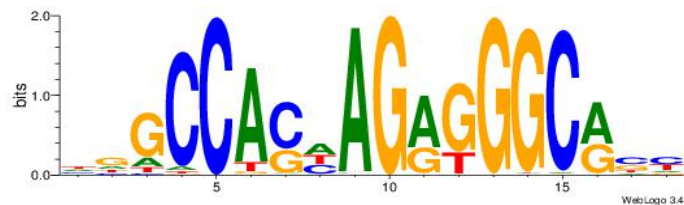
Dataset #: 4
 Motif ID: 165
 Motif name: wgGCCAshAGrGGGCrSy
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4

Number of overlap: 14
Similarity score: 0.0259772

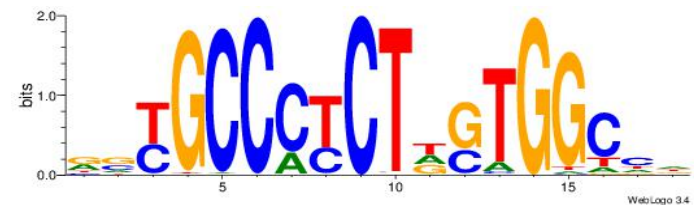
Alignment:

HDGCCACHAGRGGGCRBY
---CCASHAGKGGGCKS-

Original motif Consensus sequence: HDGCCACHAGRGGGCRBY



Reverse complement motif Consensus sequence: KBKGCCCKCTHGTGGCHH

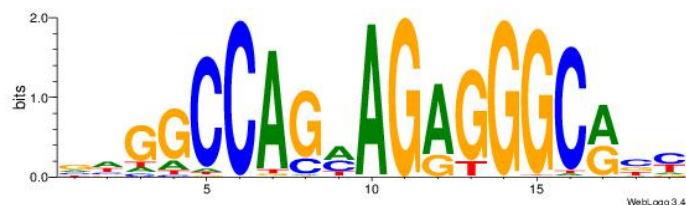


Dataset #: 4
Motif ID: 163
Motif name: gwGGCCAGmAGAGGGCrby
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2
Number of overlap: 14
Similarity score: 0.0316372

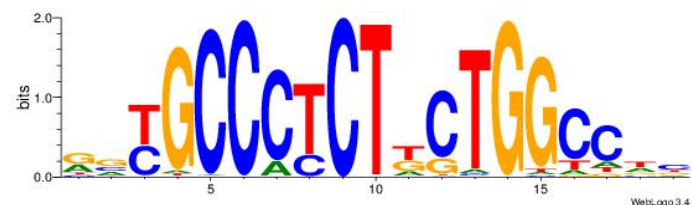
Alignment:

VHGGCCAGMAGAGGGCRBY
----CCASHAGKGGGCKS-

Original motif Consensus sequence: VHGGCCAGMAGAGGGCRBY



Reverse complement motif Consensus sequence: KBKGCCCTCTYCTGGCCHV

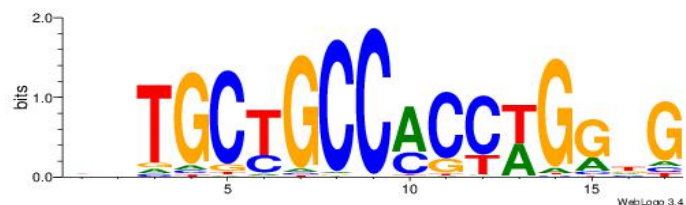


Dataset #: 4
Motif ID: 169
Motif name: yvTGCyGCCmCCwGgtG
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 3
Number of overlap: 14
Similarity score: 0.0786902

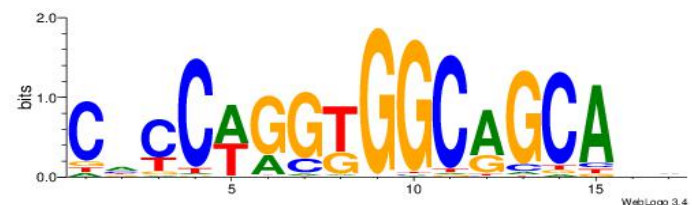
Alignment:

BVTGCTGCCACCWGGDG
-SYGCCCYCTDSTGG--

Original motif Consensus sequence: BVTGCTGCCACCWGGDG

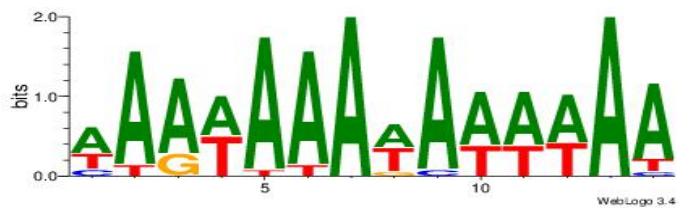


Reverse complement motif Consensus sequence: CDCCWGGTGGCAGCAVV

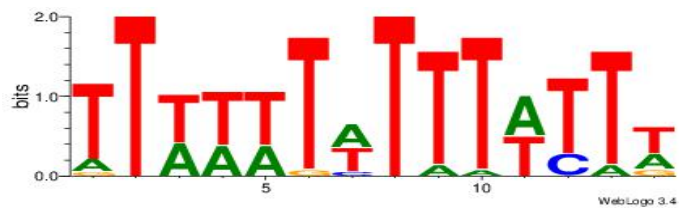


Dataset #: 2 Motif ID: 68 Motif name: Motif 68

Original motif Consensus sequence: WAAWAAWAWWWAA



Reverse complement motif Consensus sequence: TTWWWTWTTTWTTW



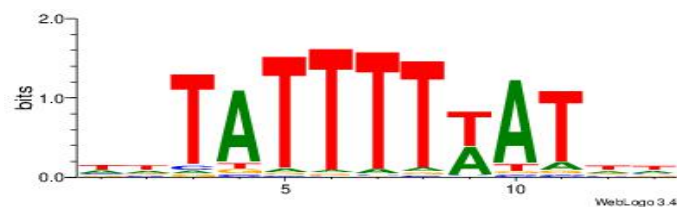
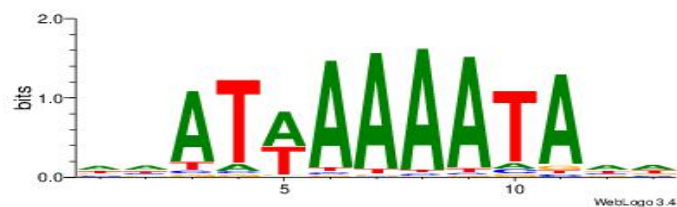
Best Matches for Motif ID 68 (Highest to Lowest)

Dataset #:	4
Motif ID:	150
Motif name:	waATwAAAATAww
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:	0.0423083

Alignment:
-DHTATTTTWATHD
TTWWWTWTTTWTTW

Original motif Consensus sequence: DHATWAAAATAHD

Reverse complement motif Consensus sequence: DHTATTTTWATHD

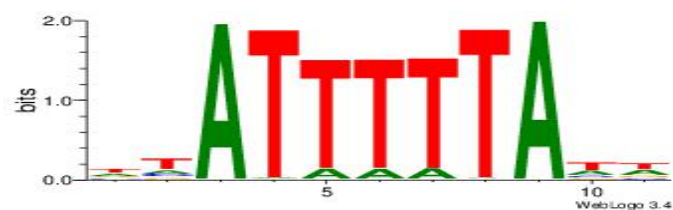


Dataset #: 4
 Motif ID: 157
 Motif name: wtATTTTAAww
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 11
 Similarity score: 1.06057

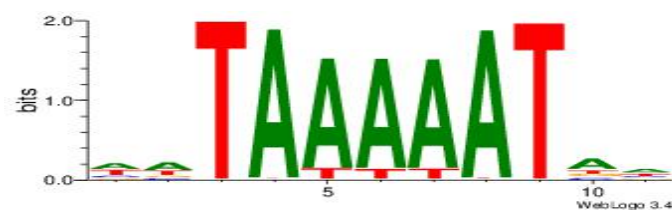
Alignment:

---WWTAAAAATAD
 WAAWAAWAWWWAA

Original motif Consensus sequence: DTATTTTAAWW



Reverse complement motif Consensus sequence: WWTAAAAATAD



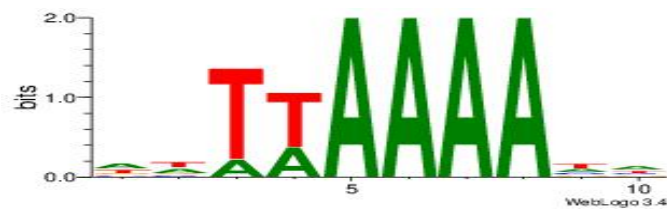
Dataset #: 4
 Motif ID: 148

Motif name: wwTwAAAAww
 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: 1.54726

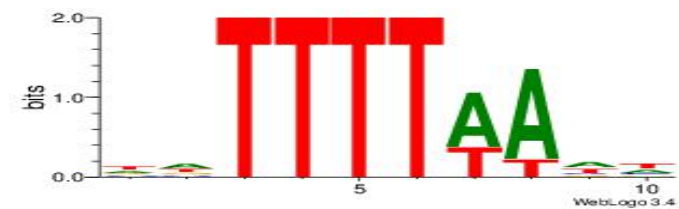
Alignment:

DDTWAAAAHH-----
 WAAWAAAWAWWWAA

Original motif Consensus sequence: DDTWAAAAHH



Reverse complement motif Consensus sequence: HHTTTTWADD



Dataset #: 4
 Motif ID: 141
 Motif name: raCAAAACam
 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: 1.55678

Alignment:

----HTGTTTTGTD
TTWWWTWTTTWTTW

Original motif Consensus sequence: DACAAAACAH



Reverse complement motif Consensus sequence: HTGTTTTGTD



Dataset #:	2
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:	1
Number of overlap:	8
Similarity score:	2.5

Alignment:

AAATAAAW-----
WAAWAAAWAWWWAA

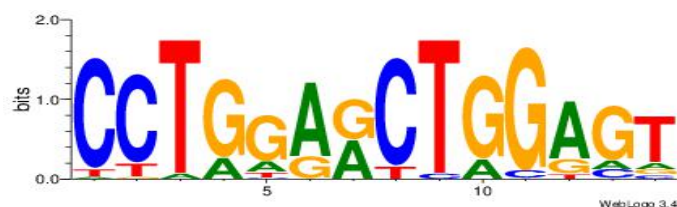
Original motif Consensus sequence: AAATAAAW

Reverse complement motif Consensus sequence: WTTTATTT

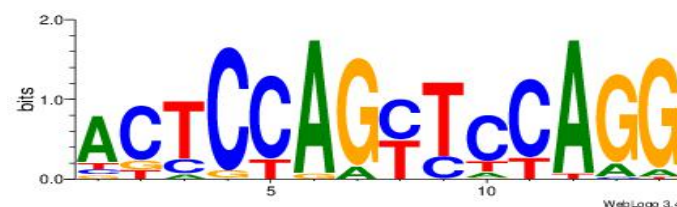


Dataset #: 2 Motif ID: 69 Motif name: Motif 69

Original motif Consensus sequence: CCTGGARCTGGAGT



Reverse complement motif Consensus sequence: ACTCCAGMTCCAGG



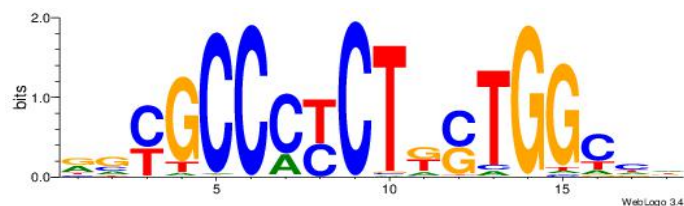
Best Matches for Motif ID 69 (Highest to Lowest)

Dataset #:	4
Motif ID:	156
Motif name:	rgyGCCMyCTksTGGccd
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	14
Similarity score:	0.070946

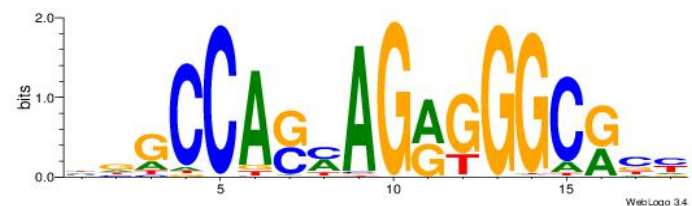
Alignment:

```
DDGCCASYAGMGGGCKVM
ACTCCAGMTCCAGG----
```

Original motif Consensus sequence: RVYGCCYCTKSTGGCHD



Reverse complement motif Consensus sequence: DDGCCASYAGMGGGCKVM

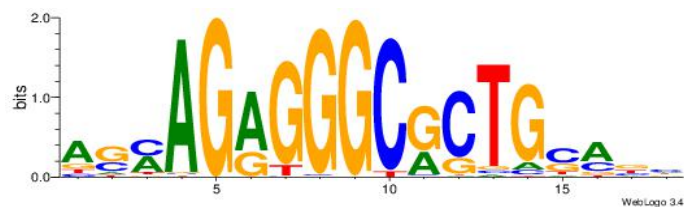


Dataset #: 4
Motif ID: 149
Motif name: asmAGRGGGCrCTGsmkc
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 5
Number of overlap: 14
Similarity score: 0.073647

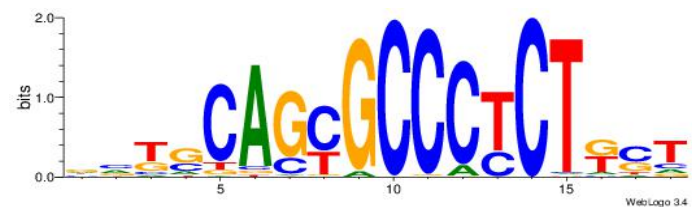
Alignment:

DBTSCAGMGCCCTCTRST
ACTCCAGMTCCAGG----

Original motif Consensus sequence: ASMAGAGGGCRCTGSABH



Reverse complement motif Consensus sequence: DBTSCAGMGCCCTCTRST



Dataset #: 4
 Motif ID: 163
 Motif name: gwGGCCAGmAGAGGGCrby
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 14
 Similarity score: 0.0761843

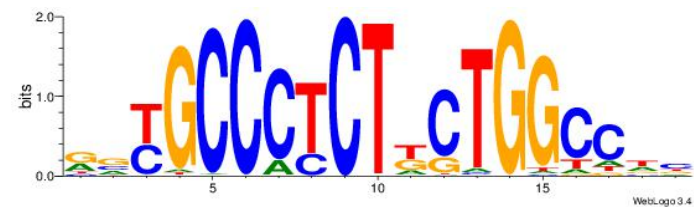
Alignment:

VHGGCCAGMAGAGGGCRBY
 -ACTCCAGMTCCAGG-----

Original motif Consensus sequence: VHGGCCAGMAGAGGGCRBY



Reverse complement motif Consensus sequence: KBKGCCCTCTYCTGGCCHV



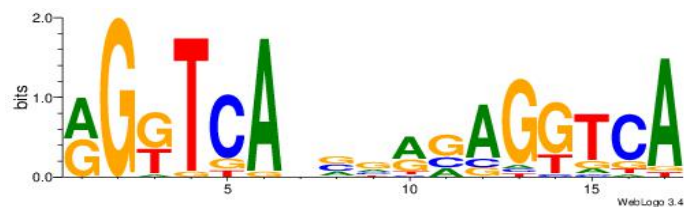
Dataset #: 3
 Motif ID: 115
 Motif name: RXRRAR_DR5
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1

Number of overlap: 14
Similarity score: 0.0775577

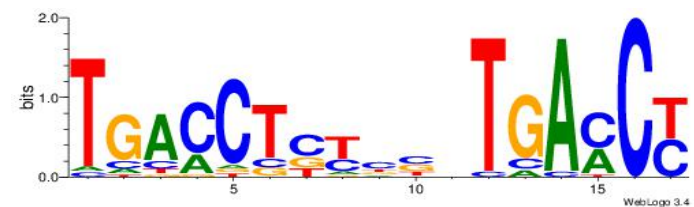
Alignment:

RGKTCABVVRGAGGTCA
ACTCCAGMTCCAGG---

Original motif Consensus sequence: RGKTCABVVRGAGGTCA



Reverse complement motif Consensus sequence:
TGACCTCKVVB TGAYCK



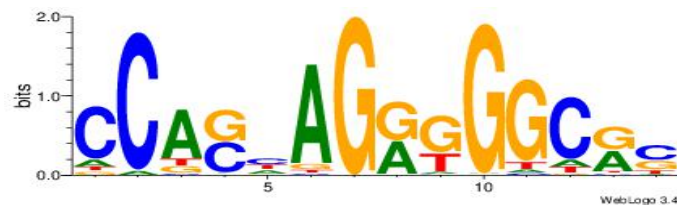
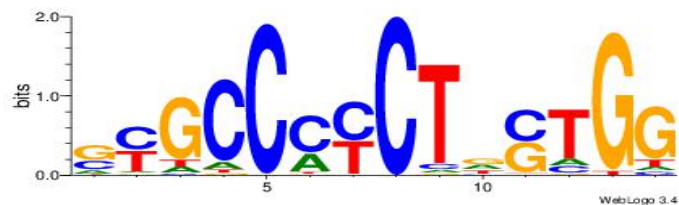
Dataset #: 2
Motif ID: 67
Motif name: Motif 67
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 14
Similarity score: 0.0806144

Alignment:

CCASHAGKGGGCKS
CCTGGARCTGGAGT

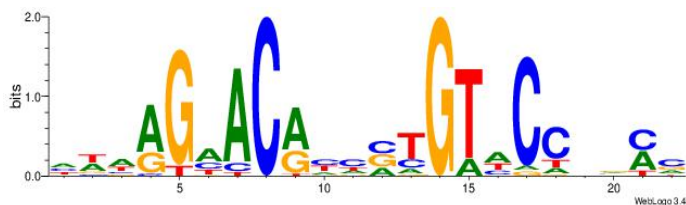
Original motif Consensus sequence: SYGCCCYCTDSTGG

Reverse complement motif Consensus sequence: CCASHAGKGGGCKS

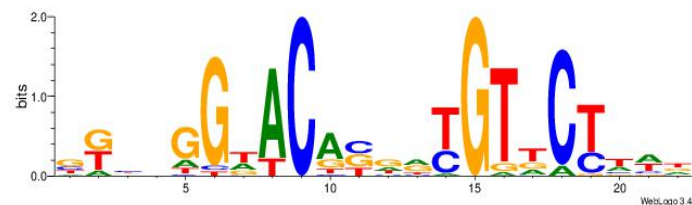


Dataset #: 3 Motif ID: 70 Motif name: Ar

Original motif Consensus sequence: HWDAGHACRHHVTGTHCCHVMV



Reverse complement motif Consensus sequence: VRVDGGHACAVDDKGTHCTDWH



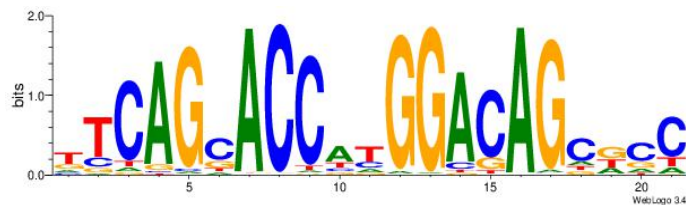
Best Matches for Motif ID 70 (Highest to Lowest)

Dataset #:	3
Motif ID:	113
Motif name:	REST
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	21
Similarity score:	0.0696331

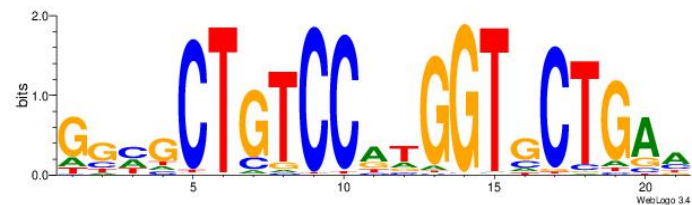
Alignment:

-GGYGCTGTCCATGGTGCTGAA
VRVDGGHACAVDDKGTHTDWH

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC



Reverse complement motif Consensus sequence:
GGYGCTGTCCATGGTGCTGAA



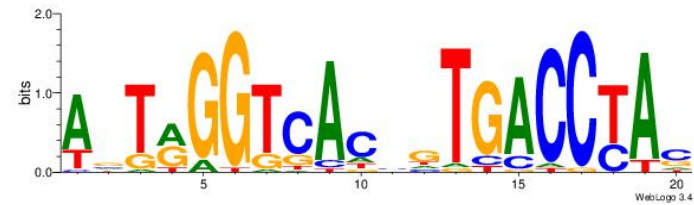
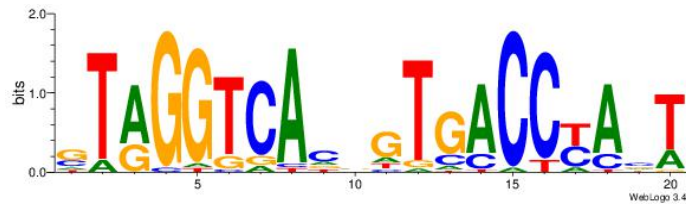
Dataset #:	3
Motif ID:	111
Motif name:	PPARG
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	20
Similarity score:	0.55978

Alignment:

--STAGGTCACBGTGACCYABT
VRVDGGHACAVDDKGTHTDWH

Original motif Consensus sequence: STAGGTCACBGTGACCYABT

Reverse complement motif Consensus sequence:
ABTMGGTCACBGTGACCTAS

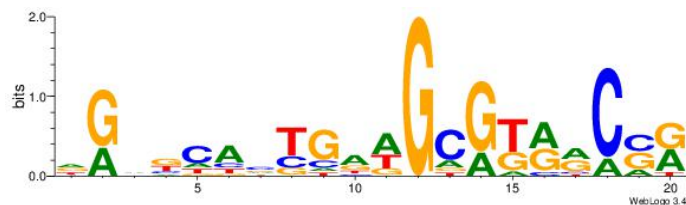


Dataset #: 3
 Motif ID: 109
 Motif name: Pax5
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.564914

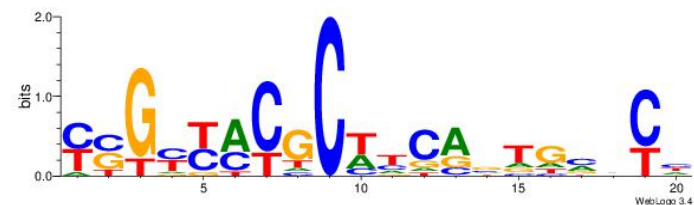
Alignment:

--MSGKKRCGCWDCABTGBBCD
 VRVDGGHACAVDDKGTHTDWH

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD



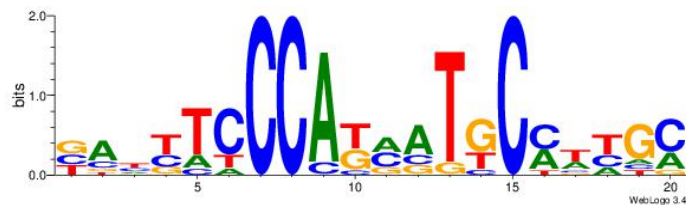
Dataset #: 3

Motif ID: 131
 Motif name: znf143
 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: 0.566373

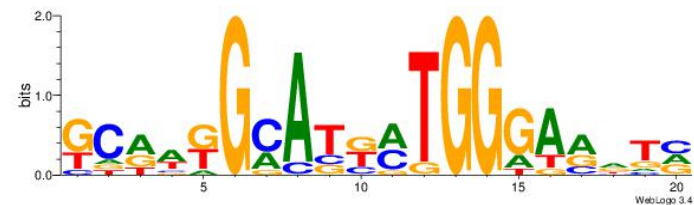
Alignment:

GCMWRGCATYRTGGGAMHTB--
 VRVDGGHACAVDDKGTHCTDWH

Original motif Consensus sequence: BAHYTCCCAKMATGCMWYGC



Reverse complement motif Consensus sequence: GCMWRGCATYRTGGGAMHTB



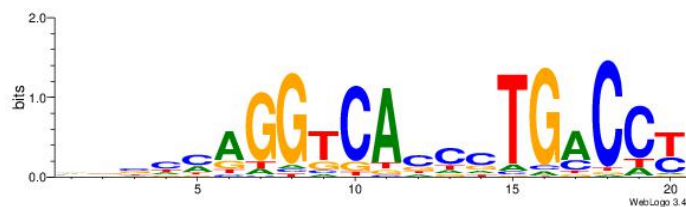
Dataset #: 3
 Motif ID: 81
 Motif name: ESR1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 19

Similarity score: 1.05195

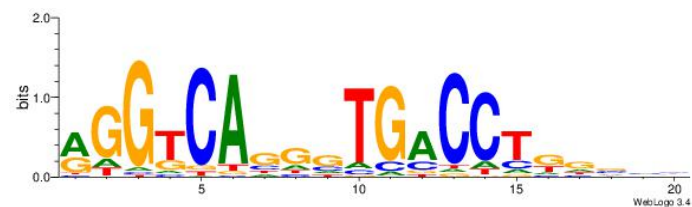
Alignment:

VDBHMAGGTCACCCTGACCY---
-VRVDGGHACAVDDKGTHCTDWH

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV



Dataset #: 3 Motif ID: 71 Motif name: Arnt

Original motif Consensus sequence: CACGTG



Reverse complement motif Consensus sequence: CACGTG



Best Matches for Motif ID 71 (Highest to Lowest)

Dataset #:	1
Motif ID:	20
Motif name:	Motif 20
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement

Direction: Forward
 Position number: 1
 Number of overlap: 6
 Similarity score: 0

Alignment:

MACGTG

CACGTG

Original motif Consensus sequence: CACGTR



Reverse complement motif Consensus sequence: MACGTG



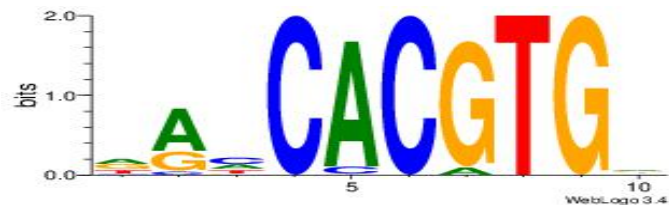
Dataset #: 3
 Motif ID: 91
 Motif name: MAX
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 6
 Similarity score: 0.00380329

Alignment:

BCACGTGDTD

-CACGTG---

Original motif Consensus sequence: DAHCACGTGD



Reverse complement motif Consensus sequence: BCACGTGDTD



Dataset #: 3
Motif ID: 126
Motif name: USF1
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 6
Similarity score: 0.00445689

Alignment:
MCACGTG
-CACGTG

Original motif Consensus sequence: CACGTGR



Reverse complement motif Consensus sequence: MCACGTG

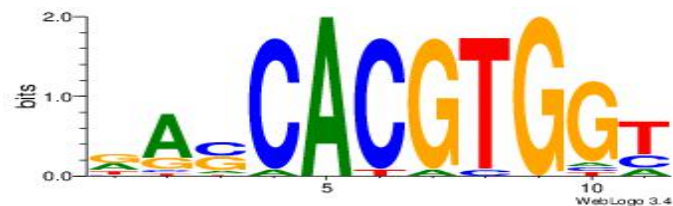


Dataset #: 3
 Motif ID: 95
 Motif name: MYCMAX
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 6
 Similarity score: 0.00495292

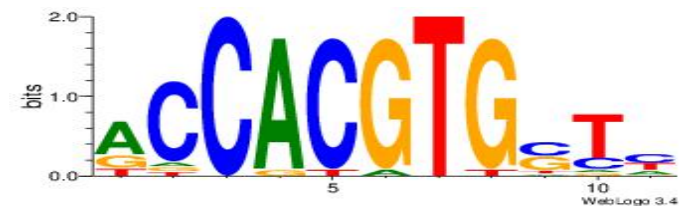
Alignment:

RASCACGTGGT
 ---CACGTG--

Original motif Consensus sequence: RASCACGTGGT



Reverse complement motif Consensus sequence: ACCACGTGSTM



Dataset #: 3
 Motif ID: 94
 Motif name: Myc
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 6

Similarity score: 0.0173209

Alignment:
DCCACGTGCV
--CACGTG--

Original motif Consensus sequence: VGCACGTGGH



Reverse complement motif Consensus sequence: DCCACGTGCV



Dataset #: 3 Motif ID: 72 Motif name: ArntAhr

Original motif Consensus sequence: YGCGTG



Reverse complement motif Consensus sequence: CACGCM



Best Matches for Motif ID 72 (Highest to Lowest)

Dataset #:	3
Motif ID:	86
Motif name:	HIF1AARNT
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward

Position number: 2
Number of overlap: 6
Similarity score: 0

Alignment:
VBACGTGV
-YGCGTG-

Original motif Consensus sequence: VBACGTGV



Reverse complement motif Consensus sequence: VCACGTBV



Dataset #: 4
Motif ID: 134
Motif name: ssCGwGCGss
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 5
Number of overlap: 6
Similarity score: 0.0128947

Alignment:
BSCGWGCGBV
YGCGTG----

Original motif Consensus sequence: BSCGWGCGBV

Reverse complement motif Consensus sequence: VBCGWCGBS



Dataset #: 3
 Motif ID: 71
 Motif name: Arnt
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 6
 Similarity score: 0.0203526

Alignment:
 CACGTG
 YGCGTG

Original motif Consensus sequence: CACGTG



Reverse complement motif Consensus sequence: CACGTG



Dataset #: 1

Motif ID:	20
Motif name:	Motif 20
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	6
Similarity score:	0.0206428

Alignment:
MACGTG
YGCGTG

Original motif Consensus sequence: CACGTR



Reverse complement motif Consensus sequence: MACGTG



Dataset #:	3
Motif ID:	126
Motif name:	USF1
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	2
Number of overlap:	6
Similarity score:	0.0255609

Alignment:
MCACGTG
-YGCGTG

Original motif Consensus sequence: CACGTGR



Reverse complement motif Consensus sequence: MCACGTG



Dataset #: 3 Motif ID: 73 Motif name: CREB1

Original motif Consensus sequence: TGACGTCA



Reverse complement motif Consensus sequence: TGACGTCA



Best Matches for Motif ID 73 (Highest to Lowest)

Dataset #:	3
Motif ID:	92
Motif name:	MIZF
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: 0.00956439

Alignment:

GCGGACGTTV
--TGACGTCA

Original motif Consensus sequence: BAACGTCCGC



Reverse complement motif Consensus sequence: GCGGACGTTV



Dataset #: 3
Motif ID: 115
Motif name: RXRRAR_DR5
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 10
Number of overlap: 8
Similarity score: 0.0133811

Alignment:

RGKTCABVVRGAGGTCA
-----TGACGTCA

Original motif Consensus sequence: RGKTCABVVRGAGGTCA

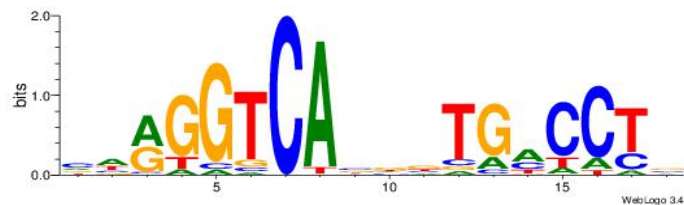
Reverse complement motif Consensus sequence:
TGACCTCKVVBGTGAYCK

Motif ID: 82
 Motif name: ESR2
 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: 0.0208174

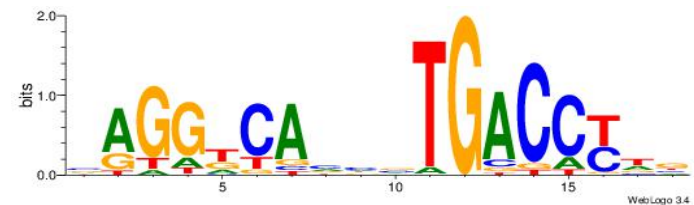
Alignment:

BAGGYCABHBTGACCKHV
 -----TGACGTCA

Original motif Consensus sequence: VHRGGTCABDBTGMCTB



Reverse complement motif Consensus sequence: BAGGYCABHBTGACCKHV



Dataset #: 1
 Motif ID: 34
 Motif name: Motif 34
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 8

Similarity score: 0.0253747

Alignment:
TGKCCACA
TGACGTCA

Original motif Consensus sequence: TGKCCACA

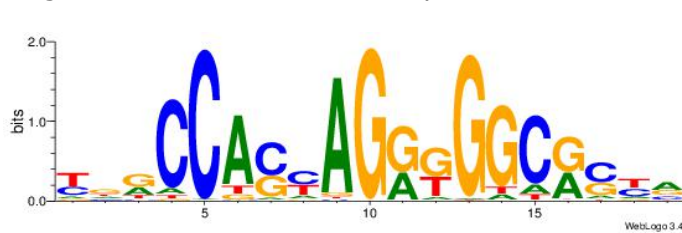


Reverse complement motif Consensus sequence: TGTGGYCA

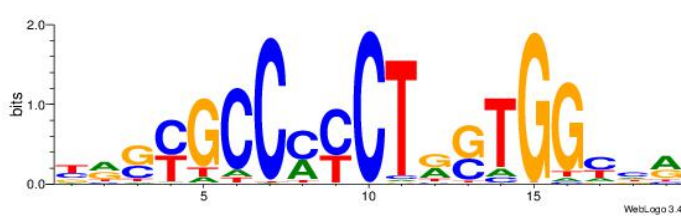


Dataset #: 3 Motif ID: 74 Motif name: CTCF

Original motif Consensus sequence: YDRCCASYAGRKGGRSYV



Reverse complement motif Consensus sequence: BMSMGCCYMCTKSTGGMHM



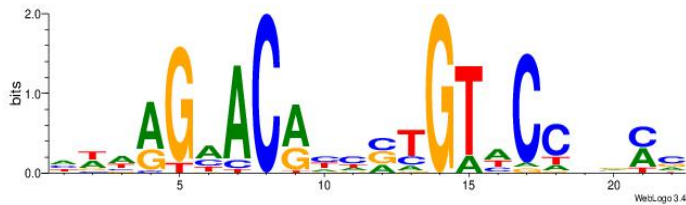
Best Matches for Motif ID 74 (Highest to Lowest)

Dataset #:	3
Motif ID:	70
Motif name:	Ar
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif

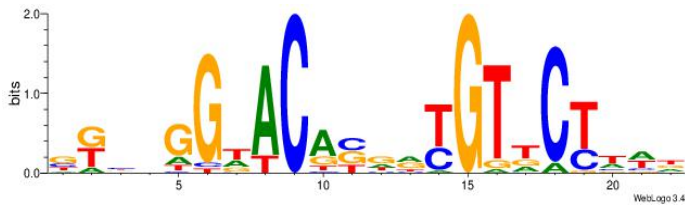
Direction: Forward
Position number: 3
Number of overlap: 19
Similarity score: 0.0903626

Alignment:
HWDAGHACRHHVTGTHCCHVMV
--BSMGCCYMCTKSTGGMHM--

Original motif Consensus sequence: HWDAGHACRHHVTGTHCCHVMV



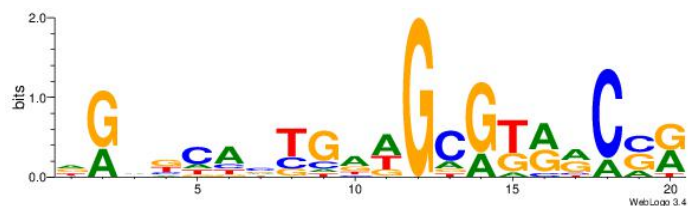
Reverse complement motif Consensus sequence: VRVDGGHACAVDDKGTHCTDWH



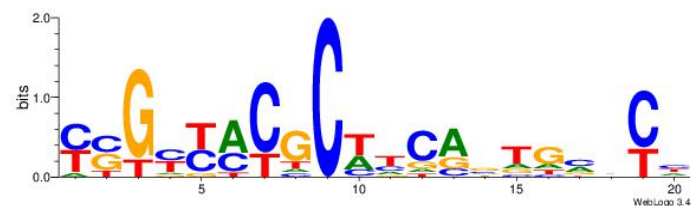
Dataset #: 3
Motif ID: 109
Motif name: Pax5
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 19
Similarity score: 0.0909586

Alignment:
DGVBCABTGDWGCGRRCR
YDRCCASYAGRKGGRSYV--

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBB

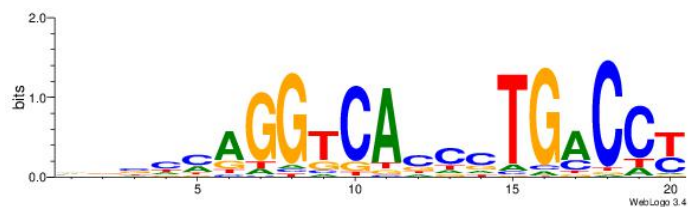


Dataset #: 3
Motif ID: 81
Motif name: ESR1
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 2
Number of overlap: 19
Similarity score: 0.0943322

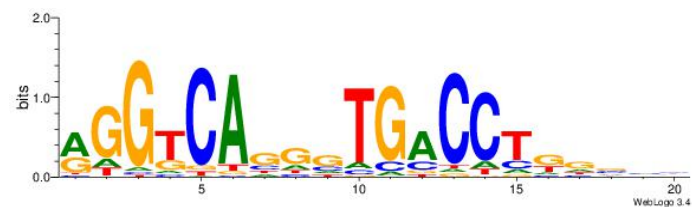
Alignment:

VDBHMAGGTCACCCTGACCY
-BMSMGCCYMCTKSTGGMHM

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRD

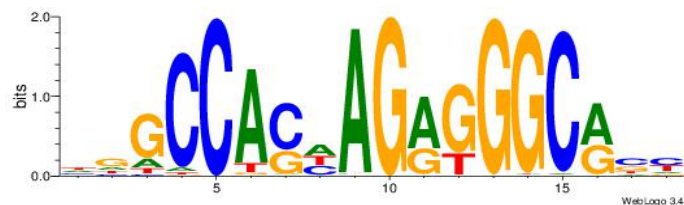


Dataset #: 4
 Motif ID: 165
 Motif name: wgGCCAshAGrGGGCrSy
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 18
 Similarity score: 0.504548

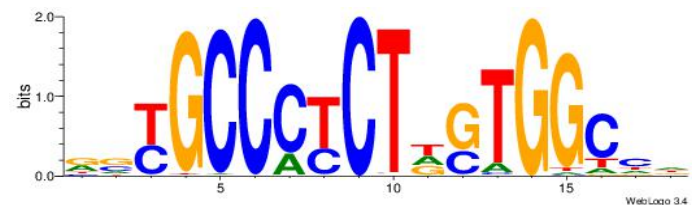
Alignment:

HDGCCACHAGRGGGCRBY-
 YDRCCASYAGRKGGRSYV

Original motif Consensus sequence: HDGCCACHAGRGGGCRBY



Reverse complement motif Consensus sequence: KBKGCCCKCTHGTGGCHH



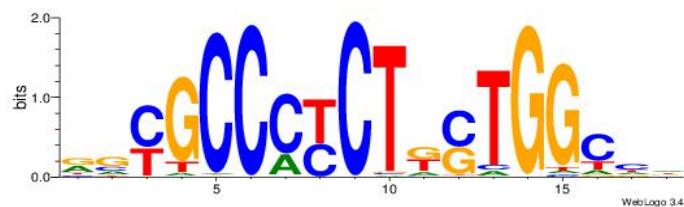
Dataset #: 4
 Motif ID: 156
 Motif name: rgyGCCMyCTksTGGccd
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1

Number of overlap: 18
Similarity score: 0.515938

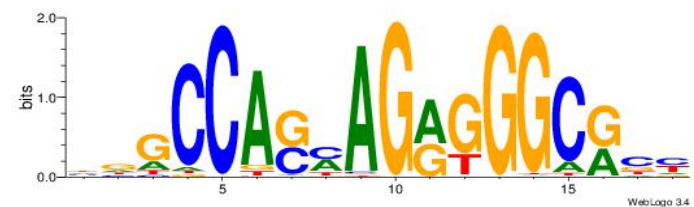
Alignment:

-RVYGCCCYCTKSTGGCHD
BMSGCCYMCTKSTGGMHM

Original motif Consensus sequence: RVYGCCCYCTKSTGGCHD

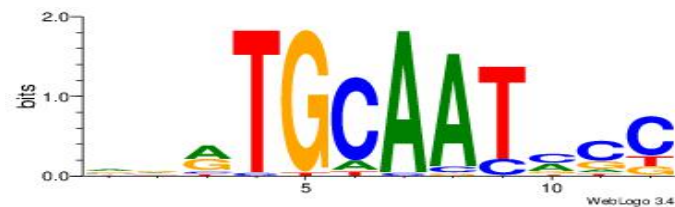


Reverse complement motif Consensus sequence: DDGCCASYAGMGGGCKVM



Dataset #: 3 Motif ID: 75 Motif name: Ddit3Cebpa

Original motif Consensus sequence: VDRTGCAATMCC



Reverse complement motif Consensus sequence: GGRATTGCAKHB



Best Matches for Motif ID 75 (Highest to Lowest)

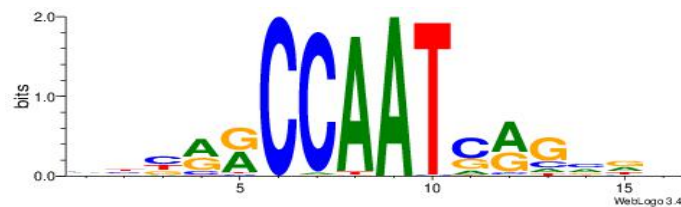
Dataset #: 3
Motif ID: 104
Motif name: NFYA
Matching format of first motif: Reverse Complement

Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	2
Number of overlap:	12
Similarity score:	0.018401

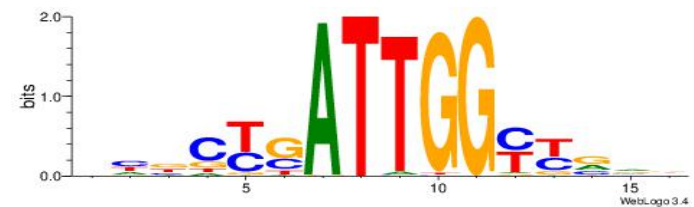
Alignment:

```
BHVCKSATTTGGMKBVV
---GGRATTGCAKHB--
```

Original motif Consensus sequence: VBBRCCAATSRGVDB



Reverse complement motif Consensus sequence: BHVCKSATTTGGMKBVV

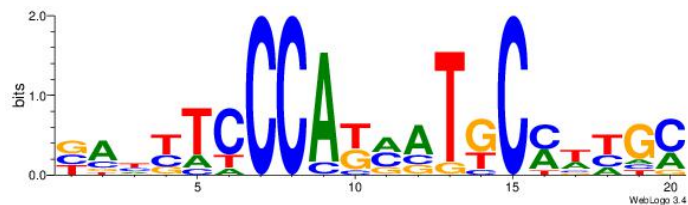


Dataset #:	3
Motif ID:	131
Motif name:	znf143
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	9
Number of overlap:	12
Similarity score:	0.037862

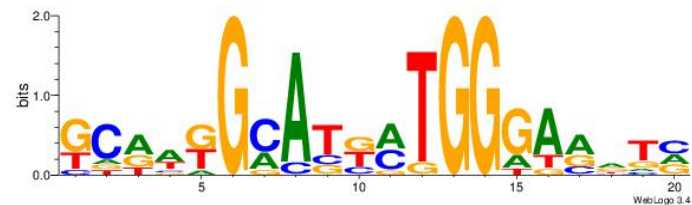
Alignment:

BAHYTCCCAKMATGCMWYGC
GGRATTGCAKHB-----

Original motif Consensus sequence: BAHYTCCCAKMATGCMWYGC



Reverse complement motif Consensus sequence: GCMWRGCATYRTGGGAMHTB

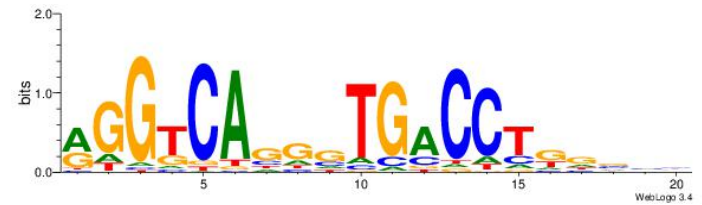
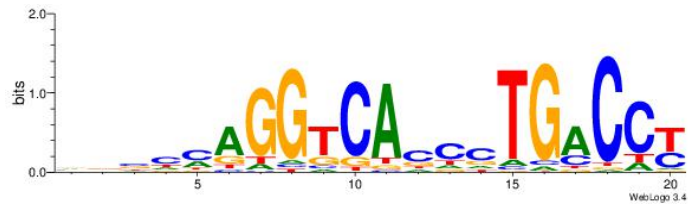


Dataset #:	3
Motif ID:	81
Motif name:	ESR1
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	3
Number of overlap:	12
Similarity score:	0.0416577

Alignment:
MGGTCAGGGTGACCTRDBHV
-----VDRTGCAATMCC--

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY

Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV

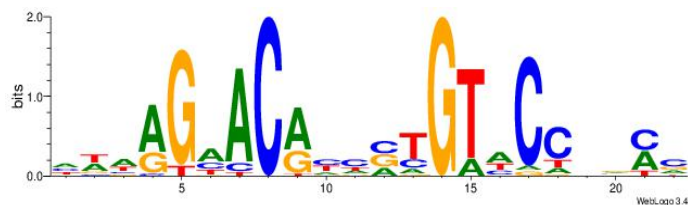


Dataset #: 3
 Motif ID: 70
 Motif name: Ar
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 12
 Similarity score: 0.0468764

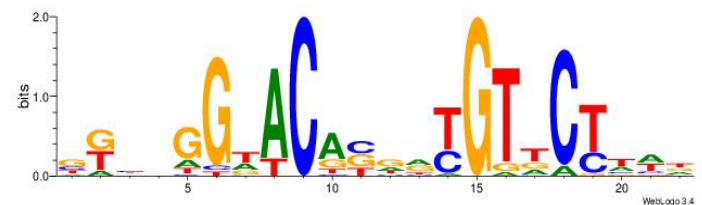
Alignment:

HWDAGHACRHHVTGTHCCHVMV
 -----GGRATTGCAKHB

Original motif Consensus sequence: HWDAGHACRHHVTGTHCCHVMV



Reverse complement motif Consensus sequence: VRVDGGHACAVDDKGTHCTDWH



Dataset #: 3

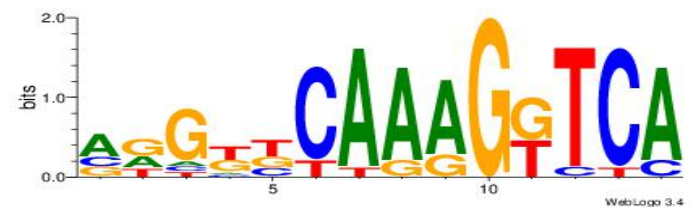
Motif ID: 107
 Motif name: NR2F1
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 12
 Similarity score: 0.0480116

Alignment:
 AKGYCAAAGRTCA
 VDRTGCAATMCC--

Original motif Consensus sequence: TGAMCTTTGMMCYT



Reverse complement motif Consensus sequence: AKGYCAAAGRTCA



Dataset #: 3 Motif ID: 76 Motif name: E2F1

Original motif Consensus sequence: TTTSGCGC



Reverse complement motif Consensus sequence: GCGCSAAA



Best Matches for Motif ID 76 (Highest to Lowest)

Dataset #: 3
Motif ID: 78
Motif name: Egr1
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 8
Similarity score: 0

Alignment:

TTTSGCGC

TTTSGCGC

Original motif Consensus sequence: TTTSGCGC



Reverse complement motif Consensus sequence: GCGCSAAA

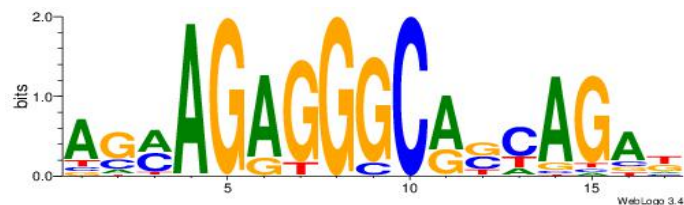


Dataset #: 4
Motif ID: 143
Motif name: AgmAGAGGGCrscAGak
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif

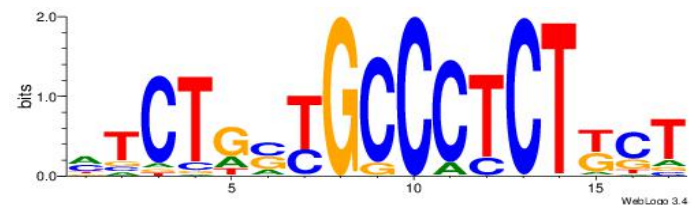
Direction: Backward
 Position number: 2
 Number of overlap: 8
 Similarity score: 0.0915396

Alignment:
 AGMAGAGGGCASCAGAK
 -----GCGCSAAA--

Original motif Consensus sequence: AGMAGAGGGCASCAGAK



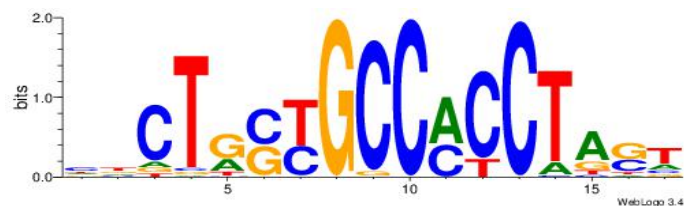
Reverse complement motif Consensus sequence: RTCTGSTGCCCTCTYCT



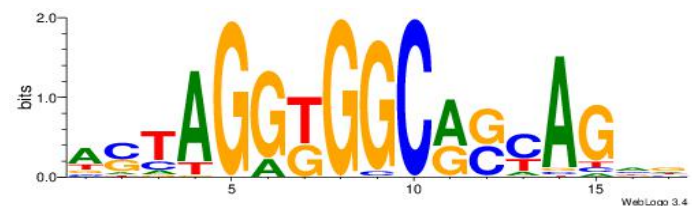
Dataset #: 4
 Motif ID: 144
 Motif name: ctCTrsyGCCmCCTast
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 8
 Similarity score: 0.0943326

Alignment:
 HDCTGSYGCCMCCTAST
 -TTTSGCGC-----

Original motif Consensus sequence: HDCTGSYGCCMCCTAST



Reverse complement motif Consensus sequence: ASTAGGYGGCMSCAGDD

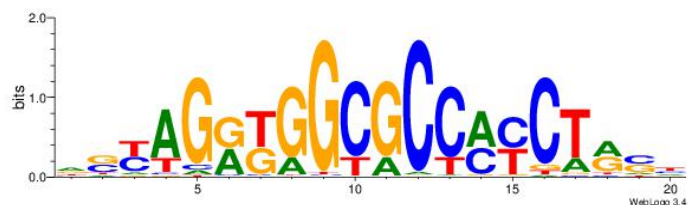


Dataset #: 4
Motif ID: 167
Motif name: rsyAGrkGGCGCCmyCTrsy
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 5
Number of overlap: 8
Similarity score: 0.0955357

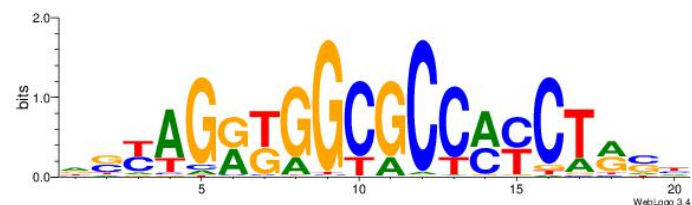
Alignment:

HSKAGKYGGCGCCRMCTMSD
-----GCGCSAAA-----

Original motif Consensus sequence: DSYAGRKGGCGCCMYCTRSH



Reverse complement motif Consensus sequence: HSKAGKYGGCGCCRMCTMSD



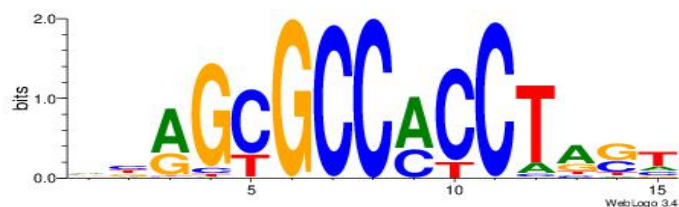
Dataset #: 4
 Motif ID: 146
 Motif name: myrGYGCCmCCTast
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 4
 Number of overlap: 8
 Similarity score: 0.0975521

Alignment:

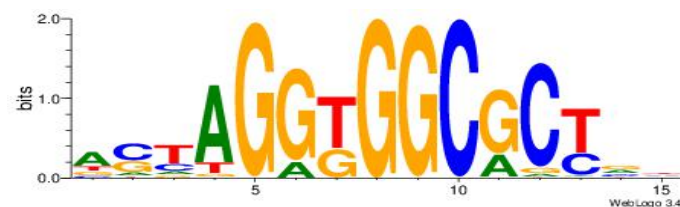
ASTAGGYGGCGCTBB

----TTTSGCGC----

Original motif Consensus sequence: VBAGCGCCMCCTAST



Reverse complement motif Consensus sequence: ASTAGGYGGCGCTBB

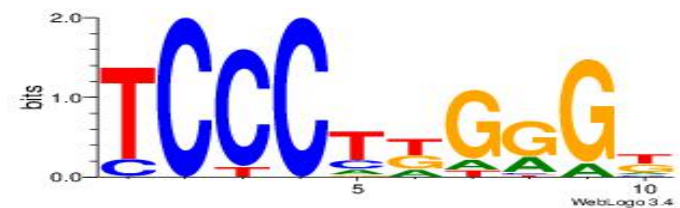


Dataset #: 3 Motif ID: 77 Motif name: EBF1

Original motif Consensus sequence: MCCCAGGGA



Reverse complement motif Consensus sequence: TCCCTYGGGY



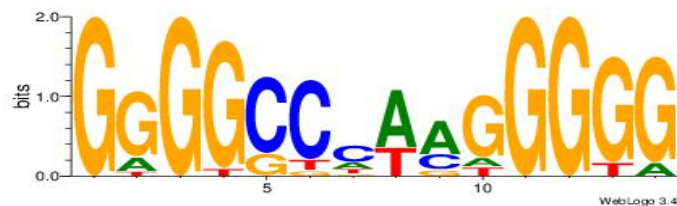
Best Matches for Motif ID 77 (Highest to Lowest)

Dataset #: 3
 Motif ID: 110
 Motif name: PLAG1
 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: 0.0581959

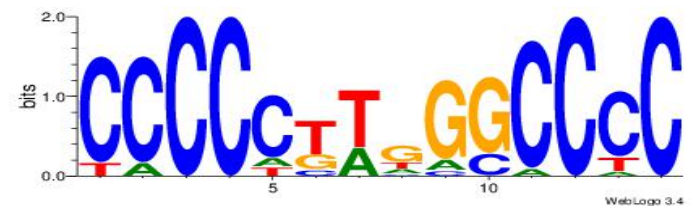
Alignment:

CCCCCTTGGGCCCC
 -TCCCTYGGGY---

Original motif Consensus sequence: GGGGCCCAAGGGGG



Reverse complement motif Consensus sequence: CCCCCTTGGGCCCC

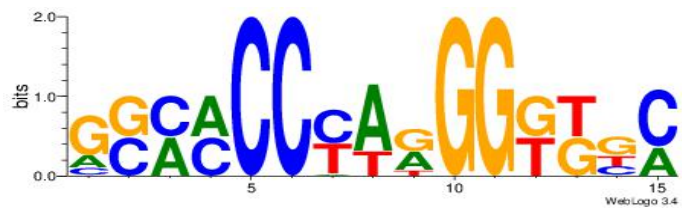


Dataset #: 3
 Motif ID: 129
 Motif name: Zfp423
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif

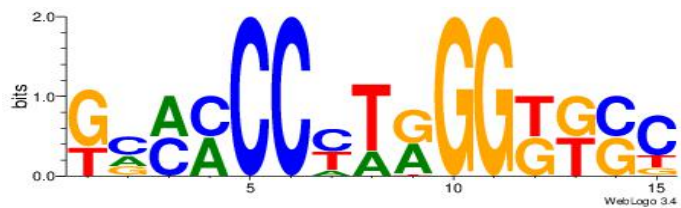
Direction: Forward
Position number: 4
Number of overlap: 10
Similarity score: 0.05861

Alignment:
GSMCCYARGGKKKC
---MCCCMAGGGA--

Original motif Consensus sequence: GSMCCYARGGKKKC



Reverse complement motif Consensus sequence: GYRYCCMTKGGYR



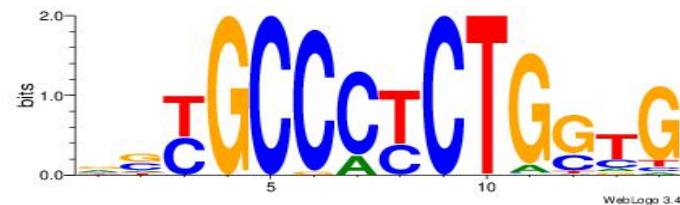
Dataset #: 4
Motif ID: 166
Motif name: CasCAGrGGGCrSy
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 4
Number of overlap: 10
Similarity score: 0.0747791

Alignment:
BSKGCCCKCTGGTG
---TCCCTYGGGY-

Original motif Consensus sequence: CACCAGRGGGCRSB



Reverse complement motif Consensus sequence: BSKGCCCKCTGGT

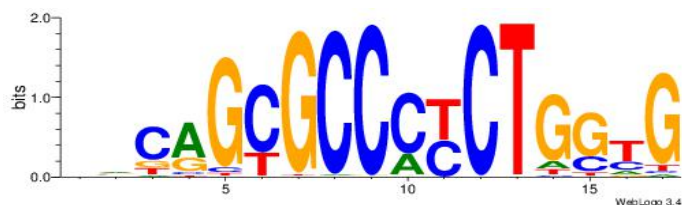


Dataset #: 4
Motif ID: 168
Motif name: yrcrYGCCMyCTGGtG
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2
Number of overlap: 10
Similarity score: 0.076024

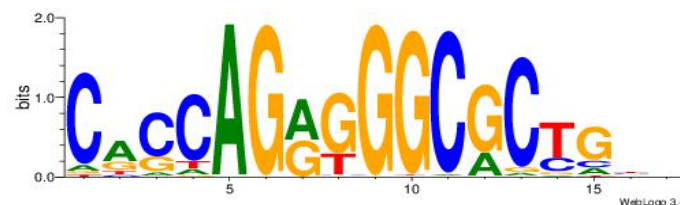
Alignment:

HVCAGCGCCCYCTGGTG
-----TCCCTYGGGY-

Original motif Consensus sequence: HVCAGCGCCCYCTGGTG



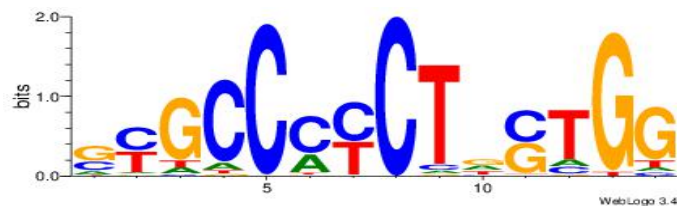
Reverse complement motif Consensus sequence: CACCAGMGGGCGCTGBD



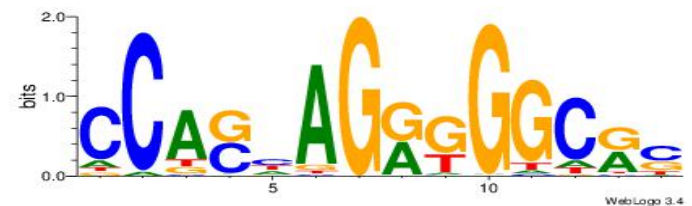
Dataset #: 2
 Motif ID: 67
 Motif name: Motif 67
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 10
 Similarity score: 0.076343

Alignment:
 SYGCCCCTDSTGG
 TCCCTYGGGY----

Original motif Consensus sequence: SYGCCCCTDSTGG



Reverse complement motif Consensus sequence: CCASHAGKGGGCK



Dataset #: 3 Motif ID: 78 Motif name: Egr1

Original motif Consensus sequence: TTTSGCGC



Reverse complement motif Consensus sequence: GCGSAAA



Best Matches for Motif ID 78 (Highest to Lowest)

Dataset #: 3
Motif ID: 76
Motif name: E2F1
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

Alignment:

TTTSGCGC

TTTSGCGC

Original motif Consensus sequence: TTTSGCGC



Reverse complement motif Consensus sequence: GCGCSAAA

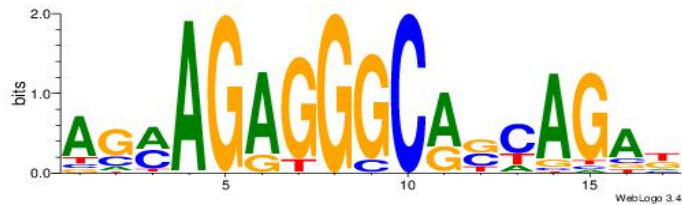


Dataset #: 4
Motif ID: 143
Motif name: AgmAGAGGGCrscAGak
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif

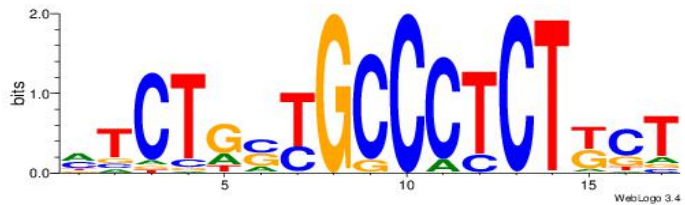
Direction: Forward
Position number: 9
Number of overlap: 8
Similarity score: 0.0915396

Alignment:
AGMAGAGGGCASCAGAK
-----GCGCSAAA--

Original motif Consensus sequence: AGMAGAGGGCASCAGAK



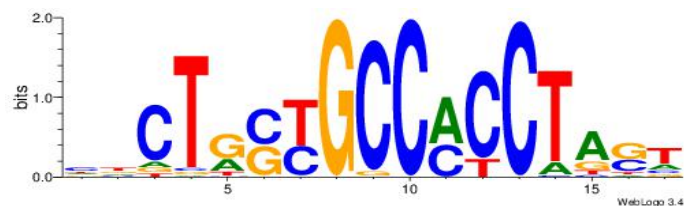
Reverse complement motif Consensus sequence: RTCTGSTGCCCTCTYCT



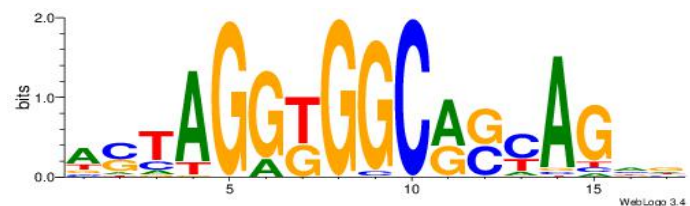
Dataset #: 4
Motif ID: 144
Motif name: ctCTrsyGCCmCCTast
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 2
Number of overlap: 8
Similarity score: 0.0943326

Alignment:
HDCTGSYGCCMCCTAST
-TTTSGCGC-----

Original motif Consensus sequence: HDCTGSYGCCMCCTAST



Reverse complement motif Consensus sequence: ASTAGGYGGCMSCAGDD

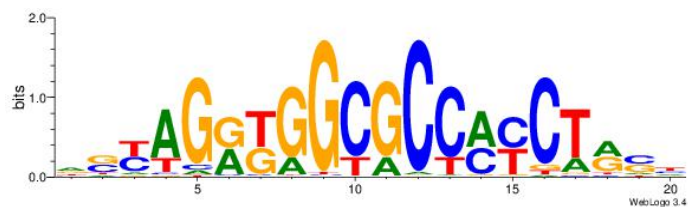


Dataset #: 4
Motif ID: 167
Motif name: rsyAGrkGGCGCCmyCTrsy
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 9
Number of overlap: 8
Similarity score: 0.0955357

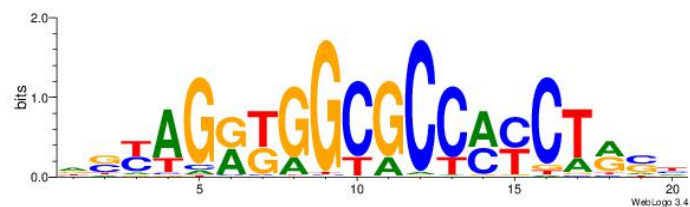
Alignment:

HSKAGKYGGCGCCRMCTMSD
-----GCGCSAAA-----

Original motif Consensus sequence: DSYAGRKGGCGCCMYCTRSH



Reverse complement motif Consensus sequence: HSKAGKYGGCGCCRMCTMSD



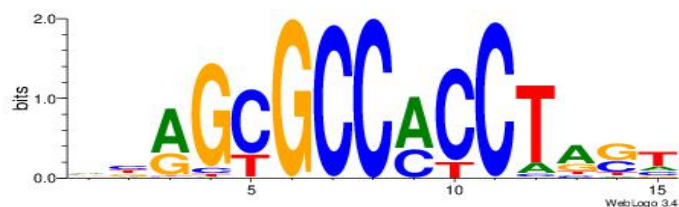
Dataset #: 4
 Motif ID: 146
 Motif name: myrGYGCCmCCTast
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 5
 Number of overlap: 8
 Similarity score: 0.0975521

Alignment:

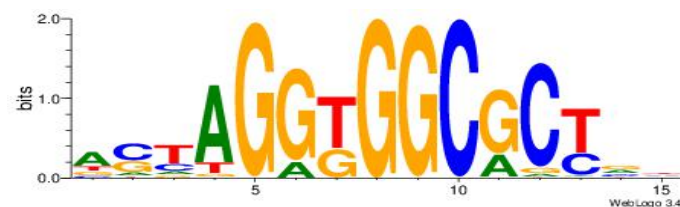
ASTAGGYGGCGCTBB

----TTTSGCGC----

Original motif Consensus sequence: VBAGCGCCMCCTAST

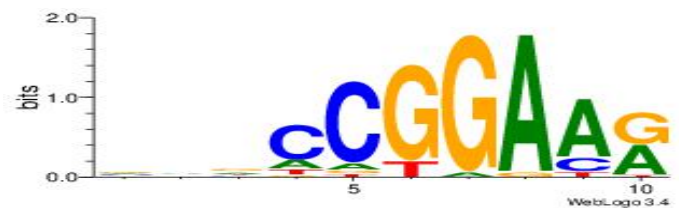


Reverse complement motif Consensus sequence: ASTAGGYGGCGCTBB

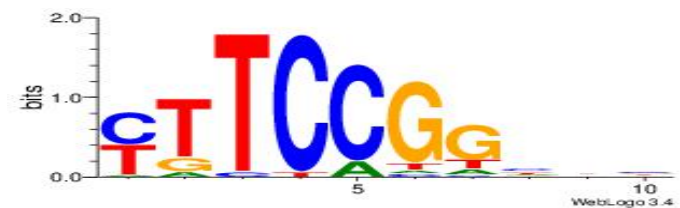


Dataset #: 3 Motif ID: 79 Motif name: ELK1

Original motif Consensus sequence: VDDCCGGAAR



Reverse complement motif Consensus sequence: MTTCCGGHBV



Best Matches for Motif ID 79 (Highest to Lowest)

Dataset #: 3
Motif ID: 85
Motif name: Hand1Tcfe2a
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: 0.0406986

Alignment:

AWRCCAGAMB

VDDCCGGAAR

Original motif Consensus sequence: BRTCTGGMWT



Reverse complement motif Consensus sequence: AWRCCAGAMB



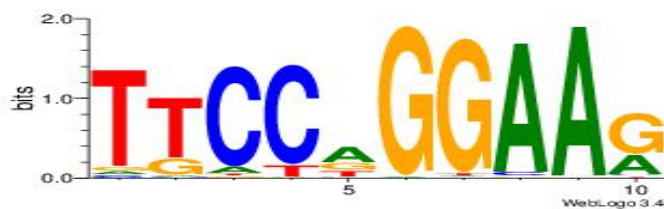
Dataset #: 3
Motif ID: 119
Motif name: Stat3
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement

Direction: Backward
 Position number: 1
 Number of overlap: 10
 Similarity score: 0.0421921

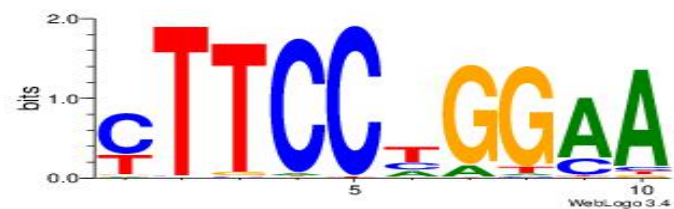
Alignment:

CTTCCTGGAA
 MTTCCGGHBV

Original motif Consensus sequence: TTCCAGGAAG



Reverse complement motif Consensus sequence: CTTCCTGGAA



Dataset #: 4
 Motif ID: 151
 Motif name: agrCCAGmAGrg
 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: 0.0478168

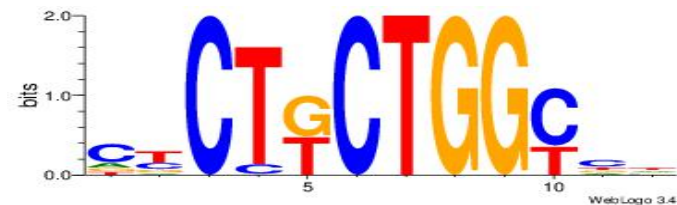
Alignment:

HVGCCAGMAGRG
 VDDCCGGAAR--

Original motif Consensus sequence: HVGCCAGMAGRG



Reverse complement motif Consensus sequence: CKCTRCTGGCVH

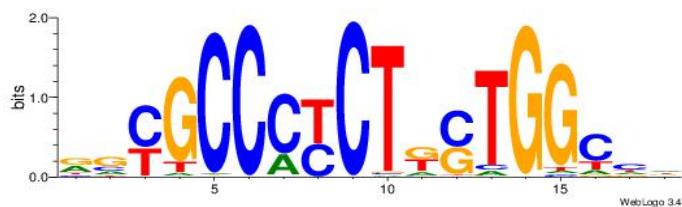


Dataset #: 4
Motif ID: 156
Motif name: rgyGCCMyCTksTGGccd
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 9
Number of overlap: 10
Similarity score: 0.0493569

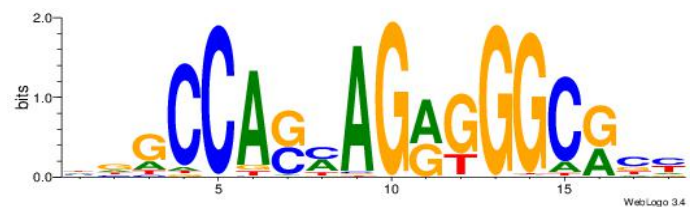
Alignment:

RVYGCCCYCTKSTGGCHD
-----MTTCCGGBHV

Original motif Consensus sequence: RVYGCCCYCTKSTGGCHD



Reverse complement motif Consensus sequence: DDGCCASYAGMGGGCKVM

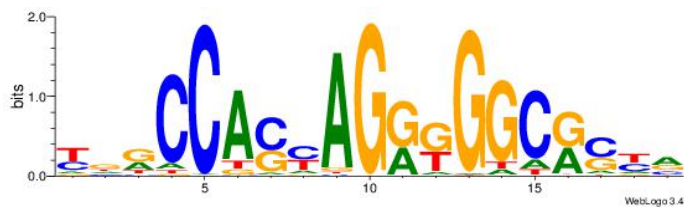


Dataset #: 3
 Motif ID: 74
 Motif name: CTCF
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 10
 Number of overlap: 10
 Similarity score: 0.0506531

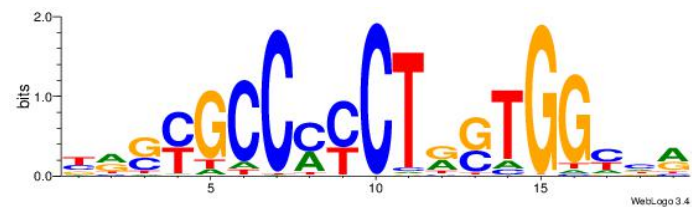
Alignment:

BSMGCCYMCTKSTGGMHM
 -----MTTCCGGBV

Original motif Consensus sequence: YDRCCASYAGRKGGRSYV



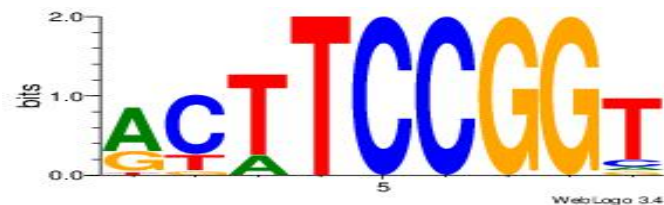
Reverse complement motif Consensus sequence: BSMGCCYMCTKSTGGMHM



Dataset #: 3 Motif ID: 80 Motif name: ELK4

Original motif Consensus sequence: ACCGGAAGT

Reverse complement motif Consensus sequence: ACTTCGGT



Best Matches for Motif ID 80 (Highest to Lowest)

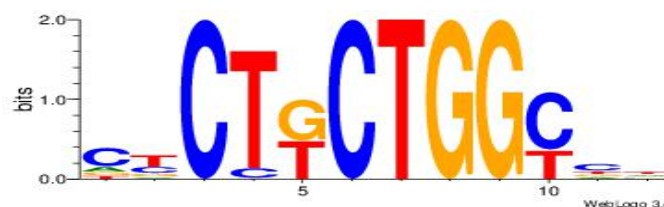
Dataset #: 4
 Motif ID: 151
 Motif name: agrCCAGmAGrg
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 9
 Similarity score: 0.0699758

Alignment:
 HVGCCAGMAGRG
 --ACCGGAAGT-

Original motif Consensus sequence: HVGCCAGMAGRG



Reverse complement motif Consensus sequence: CKCTRCTGGCVH



Dataset #: 4

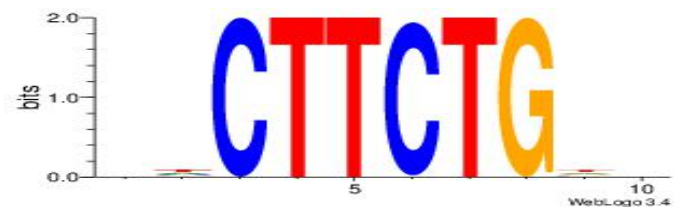
Motif ID: 136
 Motif name: dwCAGAAGwh
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 9
 Similarity score: 0.0710473

Alignment:
 DHCAGAAGDH
 ACCGGAAGT-

Original motif Consensus sequence: DHCAGAAGDH



Reverse complement motif Consensus sequence: HDCTTCTGHD



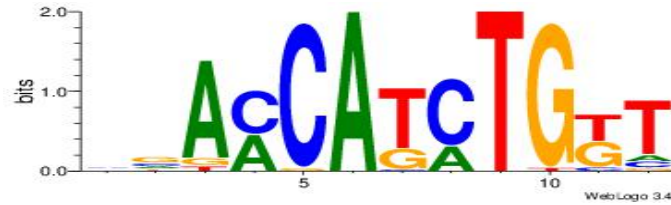
Dataset #: 3
 Motif ID: 121
 Motif name: TAL1TCF3
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 9
 Similarity score: 0.0754906

Alignment:

HVAMCATCTGKT

---ACTTCCGGT

Original motif Consensus sequence: HVAMCATCTGKT



Reverse complement motif Consensus sequence: ARCAGATGRTVD



Dataset #:	4
Motif ID:	166
Motif name:	CasCAGrGGGCrSy
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:	0.0818647

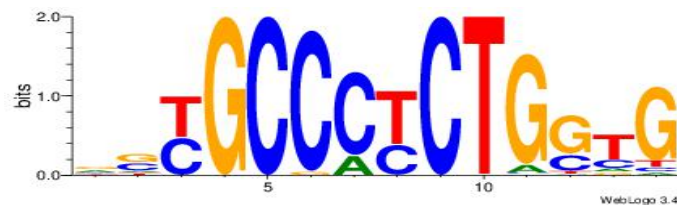
Alignment:

BSKGCCCKCTGGTG

----ACTTCCGGT-

Original motif Consensus sequence: CACCAGRGGGCRSB

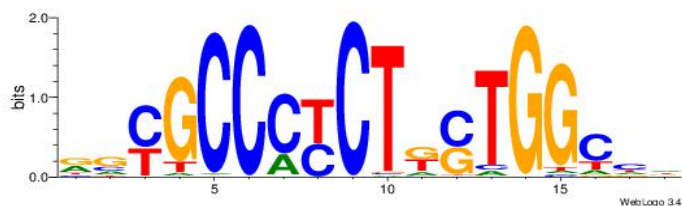
Reverse complement motif Consensus sequence: BSKGCCCKCTGGT



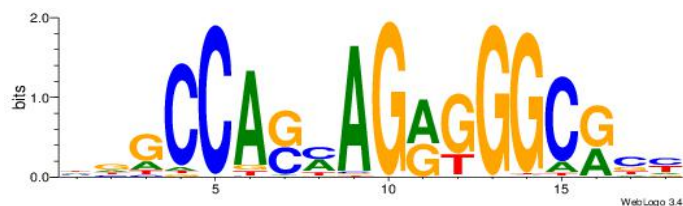
Dataset #: 4
 Motif ID: 156
 Motif name: rgyGCCMyCTksTGGccd
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 9
 Similarity score: 0.0852431

Alignment:
 RYVGCCCYCTKSTGGCHD
 -----ACTTCCGGT--

Original motif Consensus sequence: RYVGCCCYCTKSTGGCHD

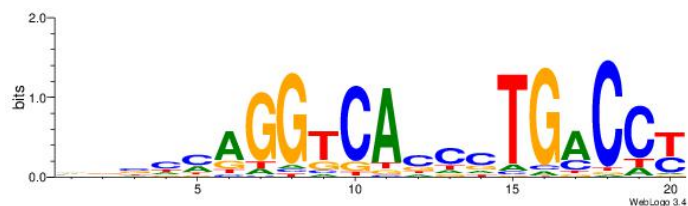


Reverse complement motif Consensus sequence: DDGCCASYAGMGGGCKVM

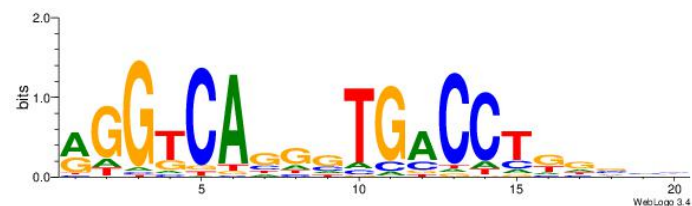


Dataset #: 3 Motif ID: 81 Motif name: ESR1

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV



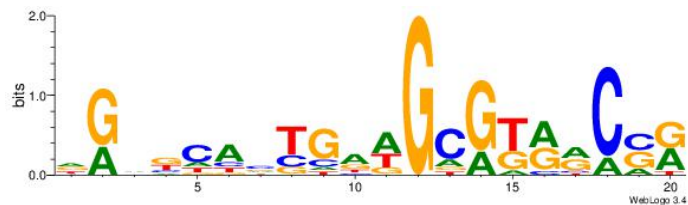
Best Matches for Motif ID 81 (Highest to Lowest)

Dataset #:	3
Motif ID:	109
Motif name:	Pax5
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:	0.0624908

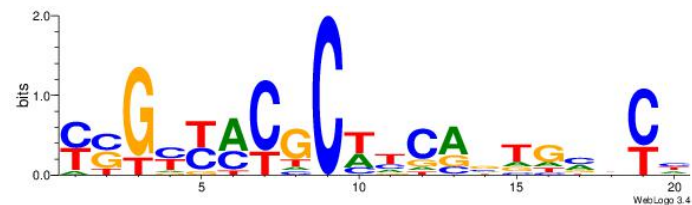
Alignment:

MSGKKRCGCWDCABTGBBCD
MGGTCAGGGTGACCTRDBHV

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD

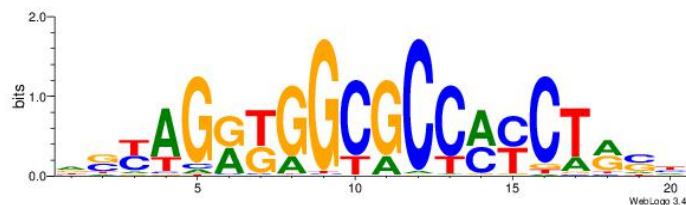


Dataset #: 4
 Motif ID: 167
 Motif name: rsyAGrkGGCGCCmyCTrsy
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.0752066

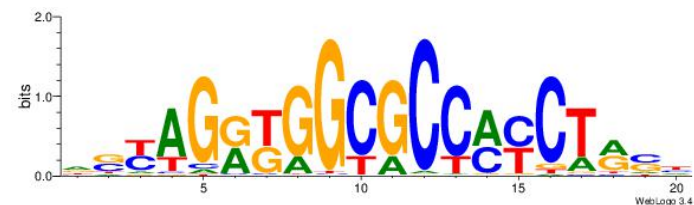
Alignment:

DSYAGRKGGCGCCMYCTRSH
 VDBHMAGGTCACCCTGACCY

Original motif Consensus sequence: DSYAGRKGGCGCCMYCTRSH



Reverse complement motif Consensus sequence: HSKAGKYGGCGCCRMCTMSD



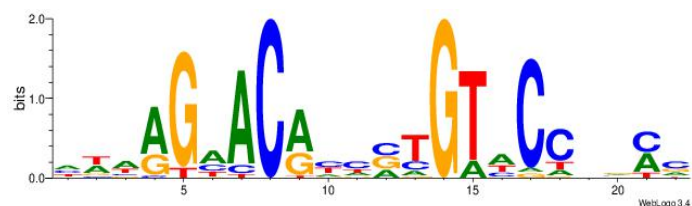
Dataset #: 3
 Motif ID: 70
 Motif name: Ar
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward

Position number: 4
Number of overlap: 19
Similarity score: 0.556363

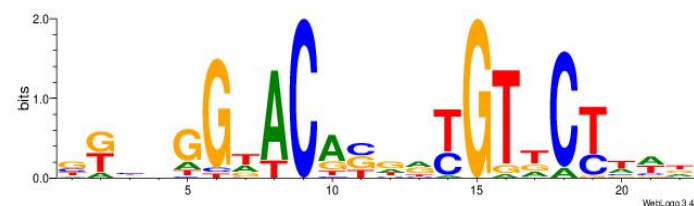
Alignment:

-HWDAGHACRHHVTGTHCCHVMV
MGGTCAGGGTGACCTRDBHV---

Original motif Consensus sequence: HWDAGHACRHHVTGTHCCHVMV



Reverse complement motif Consensus sequence: VRVDGGHACAVDDKGTHCTDWH

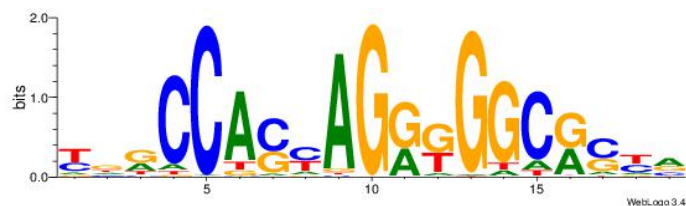


Dataset #: 3
Motif ID: 74
Motif name: CTCF
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 19
Similarity score: 0.579928

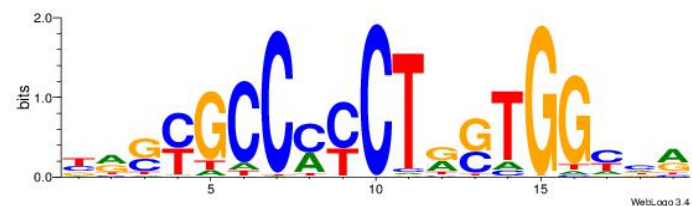
Alignment:

-YDRCCASYAGRKGGCRSYV
MGGTCAGGGTGACCTRDBHV

Original motif Consensus sequence: YDRCCASYAGRKGGCRSYV



Reverse complement motif Consensus sequence: BMSMGCCYMCTKSTGGMHM

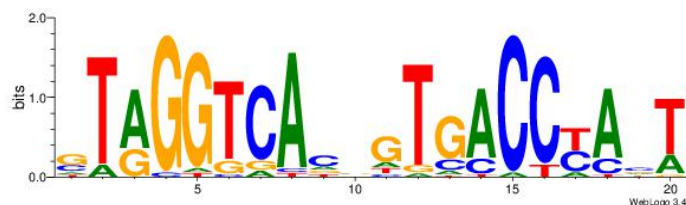


Dataset #: 3
Motif ID: 111
Motif name: PPARG
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 3
Number of overlap: 18
Similarity score: 1.01936

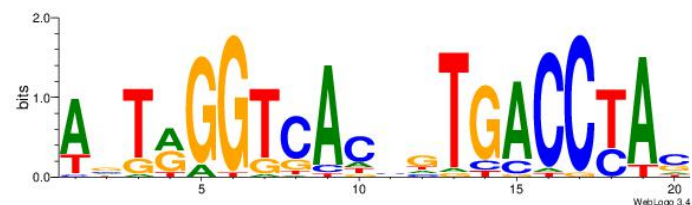
Alignment:

STAGGTCACBG TGACCYABT--
--MGGTCAGGGT GACCTRDBHV

Original motif Consensus sequence: STAGGTCACBG TGACCYABT

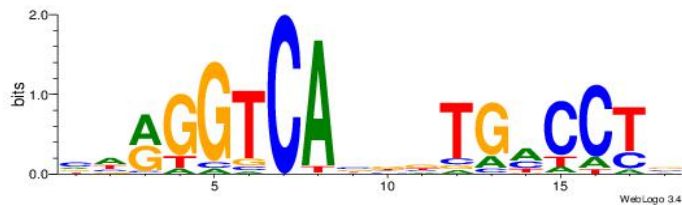


Reverse complement motif Consensus sequence: ABTMGGTCACBG TGACCTAS

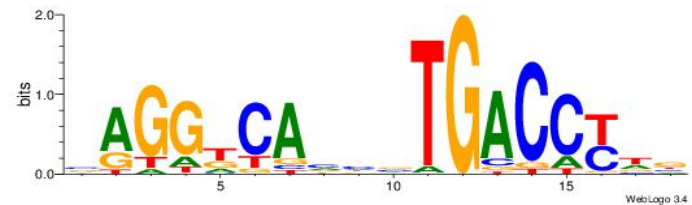


Dataset #: 3 **Motif ID: 82** **Motif name: ESR2**

Original motif Consensus sequence: VHRGGTCABDBTGMCTB



Reverse complement motif Consensus sequence:
BAGGYCABHBTGACCKHV



Best Matches for Motif ID 82 (Highest to Lowest)

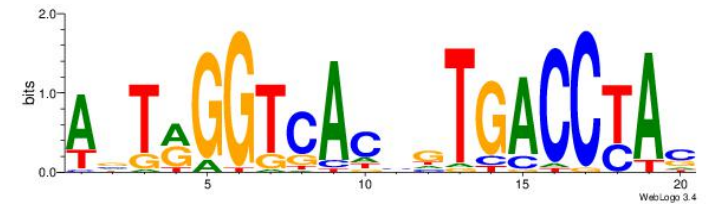
Dataset #:	3
Motif ID:	111
Motif name:	PPARG
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	18
Similarity score:	0.0125377

Alignment:

```
ABTMGGTCACBG TGACCTAS
--BAGGYCABHBTGACCKHV
```

Original motif Consensus sequence: STAGGTCACBG TGACCTAS

Reverse complement motif Consensus sequence:
ABTMGGTCACBG TGACCTAS



Alignment:

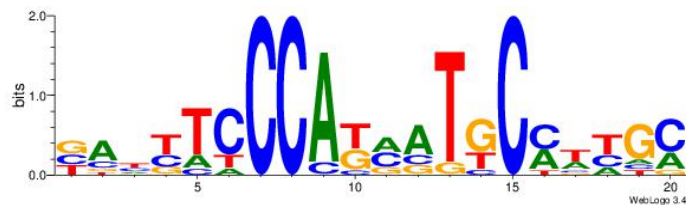
```
HWDAGHACRHHVTGTHCCHVMV
--BAGGYCABHBTGACCKHV--
```

Motif ID: 131
 Motif name: znf143
 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: 0.0692215

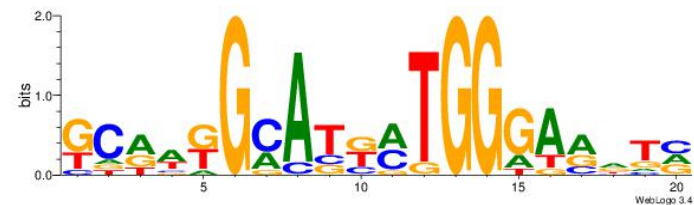
Alignment:

GCMWRGCATYRTGGGAMHTB
 -BAGGYCABHBTGACCKHV-

Original motif Consensus sequence: BAHYTCCCAKMATGCMWYGC



Reverse complement motif Consensus sequence: GCMWRGCATYRTGGGAMHTB

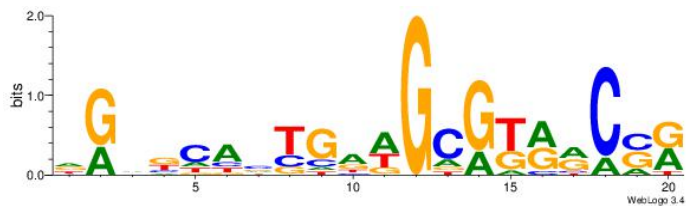


Dataset #: 3
 Motif ID: 109
 Motif name: Pax5
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 18

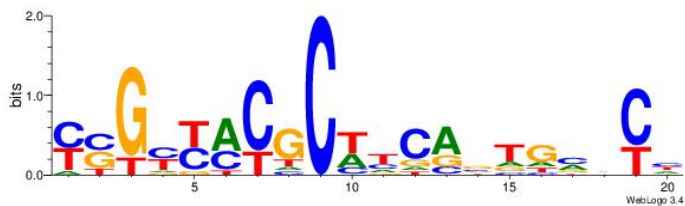
Similarity score: 0.0761757

Alignment:
MSGKKRCGCWDCABTGBB
BAGGYCABHBTGACCKHV--

Original motif Consensus sequence: DGVBCABTGDWGCGRRC



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBB

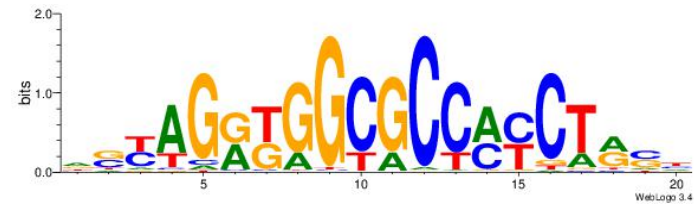
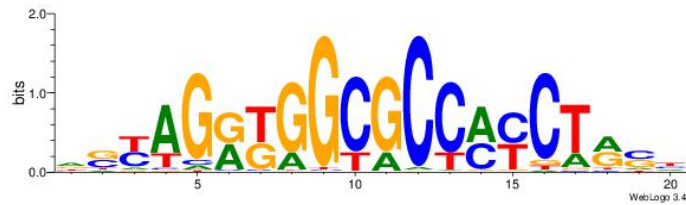


Dataset #: 4
Motif ID: 167
Motif name: rsyAGrkGGCGCCmyCTrsy
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 18
Similarity score: 0.0808384

Alignment:
HSKAGKYGGCGCCRMCTMSD
VHRGGTCABDBTGMCTB--

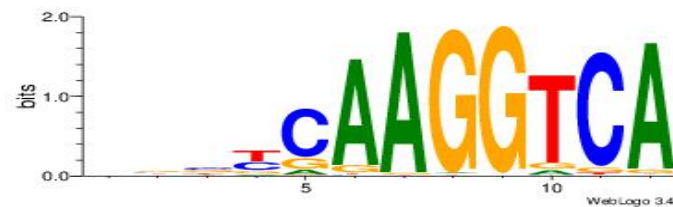
Original motif Consensus sequence: DSYAGRKGCGCCMYCTRSH

Reverse complement motif Consensus sequence: HSKAGKYGGCGCCRMCTMSD

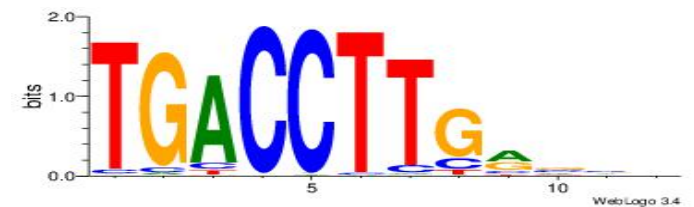


Dataset #: 3 **Motif ID: 83** **Motif name: Esrrb**

Original motif Consensus sequence: VBBYCAAGGTCA



Reverse complement motif Consensus sequence: TGACCTTGMBBB



Best Matches for Motif ID 83 (Highest to Lowest)

Dataset #:	3
Motif ID:	107
Motif name:	NR2F1
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:	0.0442611

Alignment:

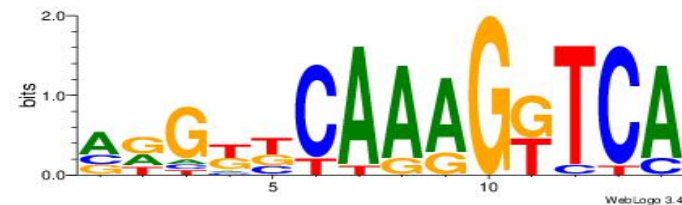
AKGYCAAAGRTCA

--VBBYCAAGGTCA

Original motif Consensus sequence: TGAMCTTTGMMCYT



Reverse complement motif Consensus sequence: AKGYCAAAGRTCA

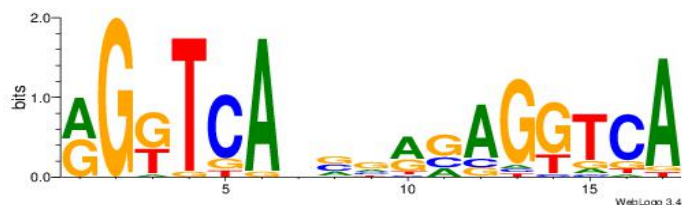


Dataset #: 3
Motif ID: 115
Motif name: RXRRAR_DR5
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 12
Similarity score: 0.0442659

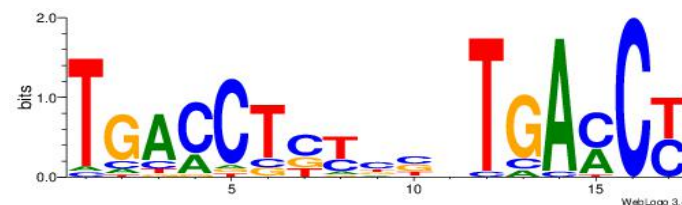
Alignment:

TGACCTCKVVBTGAYCK
TGACCTTGMBBB-----

Original motif Consensus sequence: RGKTCABVVRGAGGTCA



Reverse complement motif Consensus sequence:
TGACCTCKVVBTGAYCK

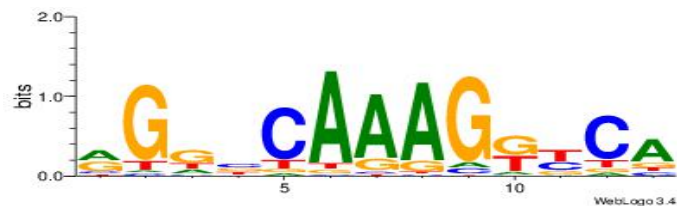


Dataset #: 3
 Motif ID: 87
 Motif name: HNF4A
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 12
 Similarity score: 0.0470808

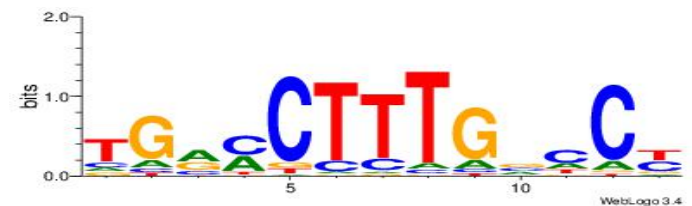
Alignment:

RGGBCAAAGKYCA
 -VBBYCAAGGTCA

Original motif Consensus sequence: RGGBCAAAGKYCA



Reverse complement motif Consensus sequence: TGMYYCTTTGBCCK

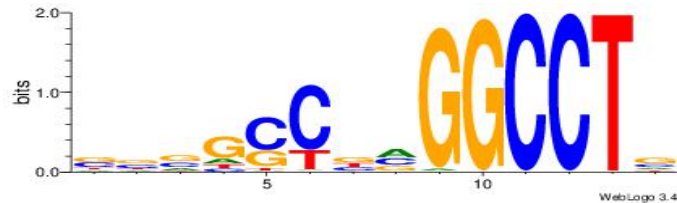


Dataset #: 3
 Motif ID: 130
 Motif name: Zfx
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 12

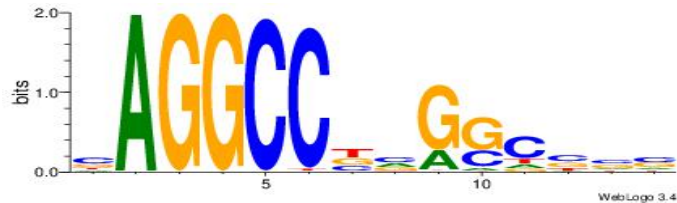
Similarity score: 0.0625961

Alignment:
VAGGCCBBGGCVBB
-TGACCTTGMBBB-

Original motif Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif Consensus sequence: VAGGCCBBGGCVBB

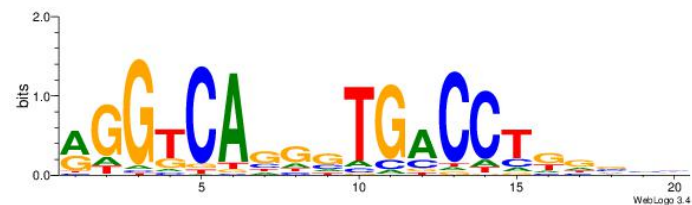
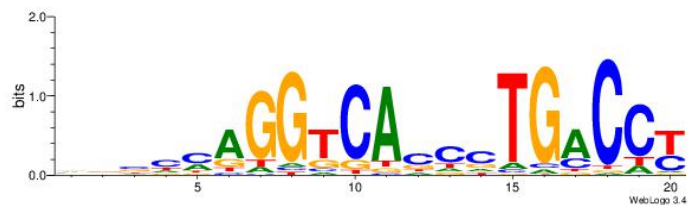


Dataset #: 3
Motif ID: 81
Motif name: ESR1
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 9
Number of overlap: 12
Similarity score: 0.0628484

Alignment:
VDBHMAGGTCACCCTGACCY
TGACCTTGMBBB-----

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY

Reverse complement motif Consensus sequence:
MGGTCAGGGTGACCTRDBHV

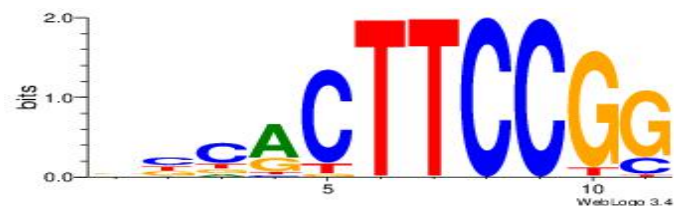


Dataset #: 3 Motif ID: 84 Motif name: GABPA

Original motif Consensus sequence: CCGGAAGTGVV



Reverse complement motif Consensus sequence: VVCACTTCCGG



Best Matches for Motif ID 84 (Highest to Lowest)

Dataset #:	4
Motif ID:	154
Motif name:	csCsCCTCCcc
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:	0.0708637

Alignment:
VBCCCCTCCHB
VVCACTTCCGG

Original motif Consensus sequence: VBCCCTCCHB



Reverse complement motif Consensus sequence: BDGGAGGGGBV

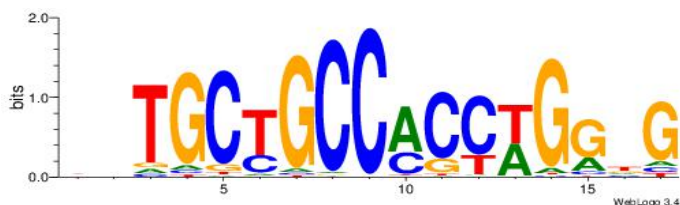


Dataset #: 4
Motif ID: 169
Motif name: yvTGCyGCCmCCwGgtG
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 7
Number of overlap: 11
Similarity score: 0.0756694

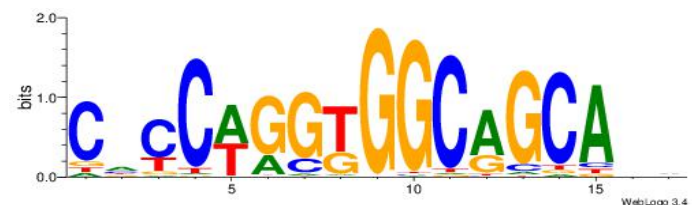
Alignment:

CDCCWGGTGGCAGCAVV
-----CCGGAAGTGVV

Original motif Consensus sequence: BVTGCTGCCACCWGGDG



Reverse complement motif Consensus sequence: CDCCWGGTGGCAGCAVV

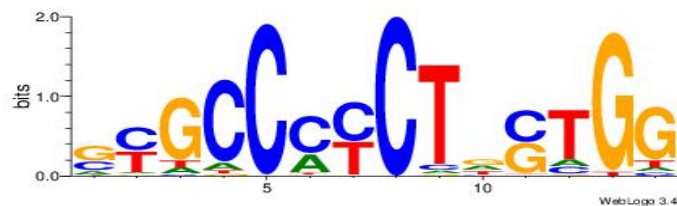


Dataset #: 2
 Motif ID: 67
 Motif name: Motif 67
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 4
 Number of overlap: 11
 Similarity score: 0.0810917

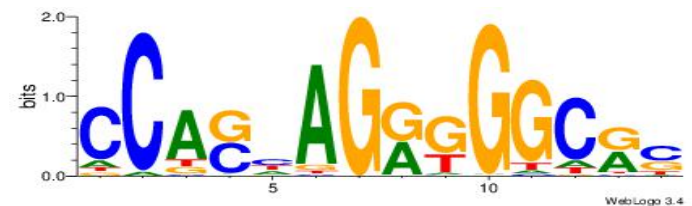
Alignment:

SYGCCCCTDSTGG
 VVCACTTCCGG---

Original motif Consensus sequence: SYGCCCCTDSTGG



Reverse complement motif Consensus sequence: CCASHAGKGGGCK

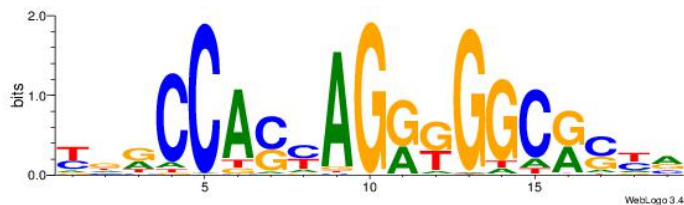


Dataset #: 3
 Motif ID: 74
 Motif name: CTCF
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 4
 Number of overlap: 11

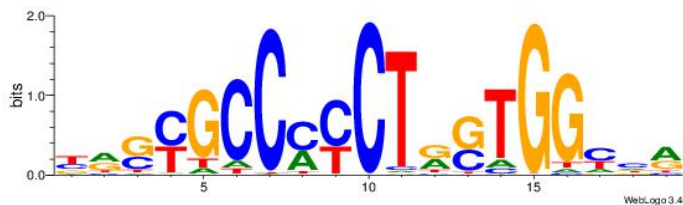
Similarity score: 0.0813947

Alignment:
BMSMGCCYMCTKSTGGMHM
-----VVCACTTCCGG----

Original motif Consensus sequence: YDRCCASYAGRKGGCRSYV



Reverse complement motif Consensus sequence:
BMSMGCCYMCTKSTGGMHM

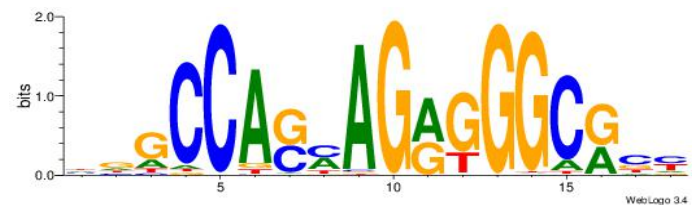
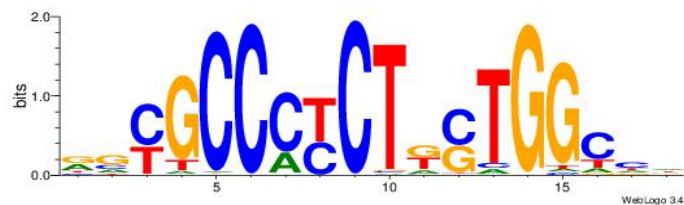


Dataset #: 4
Motif ID: 156
Motif name: rgyGCCMyCTksTGGccd
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 5
Number of overlap: 11
Similarity score: 0.0837237

Alignment:
RVYGCCCYCTKSTGGCHD
-----VVCACTTCCGG----

Original motif Consensus sequence: RVYGCCCYCTKSTGGCHD

Reverse complement motif Consensus sequence:
DDGCCASYAGMGGGCKVM



Dataset #: 3 Motif ID: 85 Motif name: Hand1Tcfe2a

Original motif Consensus sequence: BRTCTGGMWT



Reverse complement motif Consensus sequence: AWRCCAGAMB



Best Matches for Motif ID 85 (Highest to Lowest)

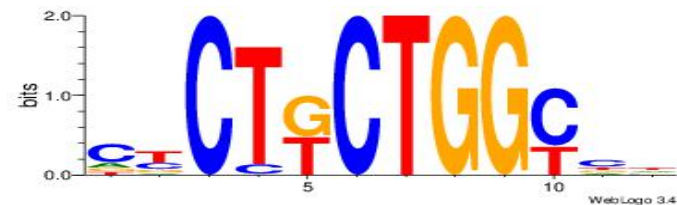
Dataset #:	4
Motif ID:	151
Motif name:	agrCCAGmAGrg
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	3
Number of overlap:	10
Similarity score:	0.0194367

Alignment:
 HVGCCAGMAGRG
 AWRCCAGAMB--

Original motif Consensus sequence: HVGCCAGMAGRG



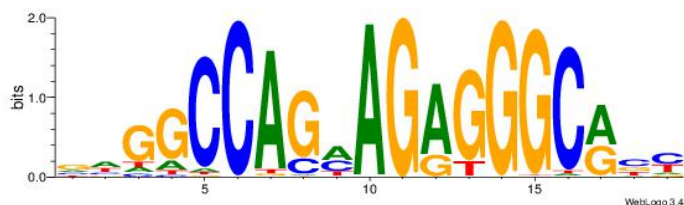
Reverse complement motif Consensus sequence: CKCTRCTGGCVH



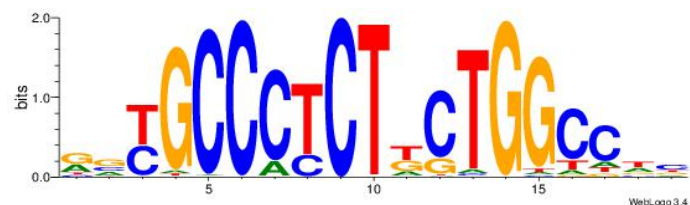
Dataset #: 4
 Motif ID: 163
 Motif name: gwGGCCAGmAGAGGGCrby
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 10
 Similarity score: 0.027647

Alignment:
 VHGGCCAGMAGAGGGCRBY
 -AWRCCAGAMB-----

Original motif Consensus sequence: VHGGCCAGMAGAGGGCRBY



Reverse complement motif Consensus sequence: KBKGCCCTCTYCTGGCCHV



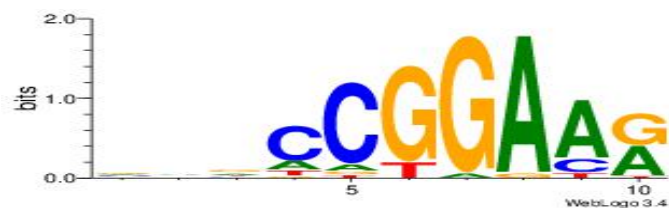
Dataset #: 3
 Motif ID: 79
 Motif name: ELK1
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 10
 Similarity score: 0.0297824

Alignment:

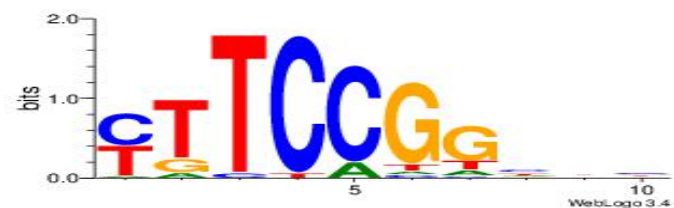
MTTCCGGHBV

BRTCTGGMWT

Original motif Consensus sequence: VDDCCGGAAR



Reverse complement motif Consensus sequence: MTTCCGGHBV

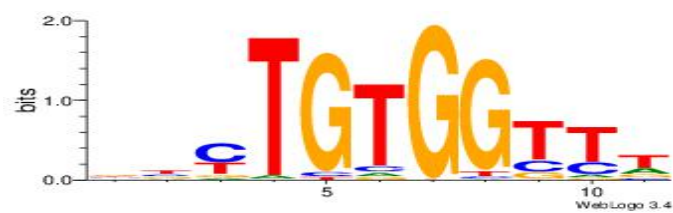


Dataset #: 3
 Motif ID: 114
 Motif name: RUNX1
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 10

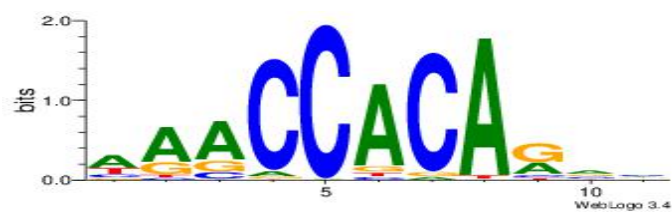
Similarity score: 0.0323511

Alignment:
BBYTGTGGTTT
-BRTCTGGMWT

Original motif Consensus sequence: BBYTGTGGTTT



Reverse complement motif Consensus sequence: AAACCACAKVB

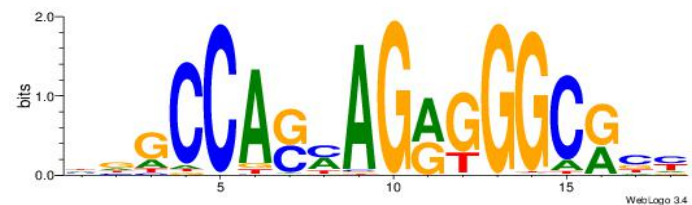
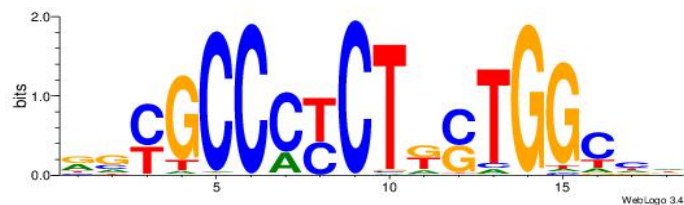


Dataset #: 4
Motif ID: 156
Motif name: rgyGCCMyCTksTGGccd
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 9
Number of overlap: 10
Similarity score: 0.0371584

Alignment:
RVYGCCCYCTKSTGGCHD
-----BRTCTGGMWT

Original motif Consensus sequence: RVYGCCCYCTKSTGGCHD

Reverse complement motif Consensus sequence:
DDGCCASYAGMGGGCKVM



Dataset #: 3 Motif ID: 86 Motif name: HIF1AARNT

Original motif Consensus sequence: VBACGTGV



Reverse complement motif Consensus sequence: VCACGTBV



Best Matches for Motif ID 86 (Highest to Lowest)

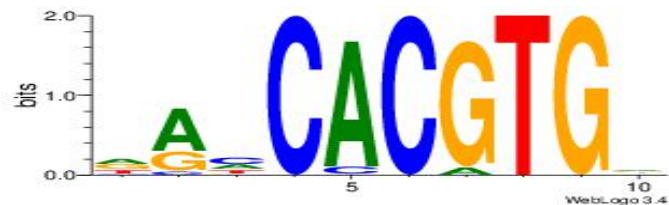
Dataset #:	3
Motif ID:	91
Motif name:	MAX
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	3
Number of overlap:	8
Similarity score:	0.0166242

Alignment:

BCACGTGDTD

VCACGTBV--

Original motif Consensus sequence: DAHCACGTGD



Reverse complement motif Consensus sequence: BCACGTGDTD



Dataset #: 3
Motif ID: 96
Motif name: Mycn
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: 0.0228069

Alignment:

GCCACGTGSD

-VBACGTGV-

Original motif Consensus sequence: HSCACGTGGC



Reverse complement motif Consensus sequence: GCCACGTGSD



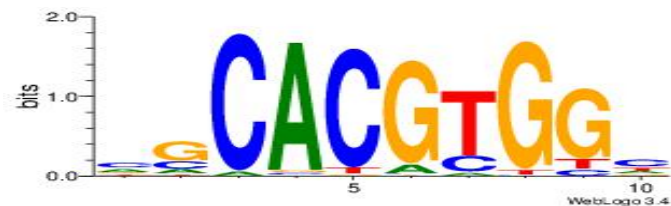
Dataset #: 3
 Motif ID: 94
 Motif name: Myc
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 8
 Similarity score: 0.0249459

Alignment:

DCCACGTGCV

-VBACGTGV-

Original motif Consensus sequence: VGCACGTGGH



Reverse complement motif Consensus sequence: DCCACGTGCV

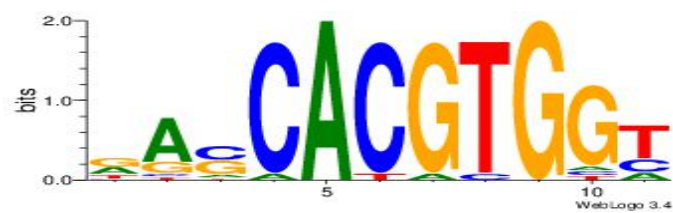


Dataset #: 3
 Motif ID: 95
 Motif name: MYCMAX
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 8

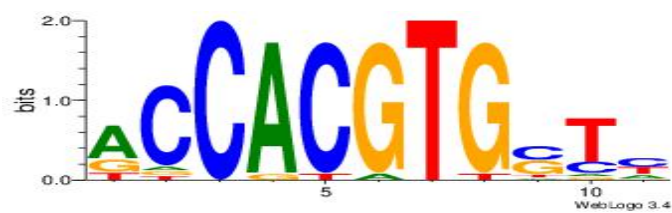
Similarity score: 0.0254922

Alignment:
ACCACGTGSTM
-VCACGTBV--

Original motif Consensus sequence: RASCACGTGGT



Reverse complement motif Consensus sequence: ACCACGTGSTM

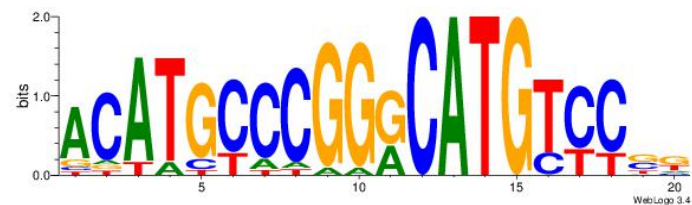
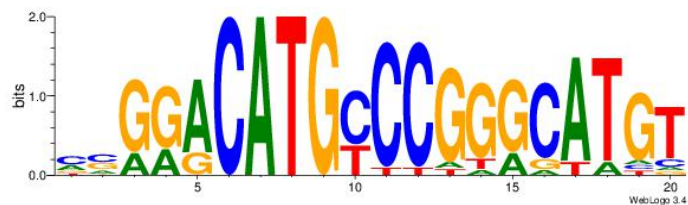


Dataset #: 3
Motif ID: 125
Motif name: TP53
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 11
Number of overlap: 8
Similarity score: 0.0362969

Alignment:
MSGGACATGYCCGGGCATGT
--VBACGTGV-----

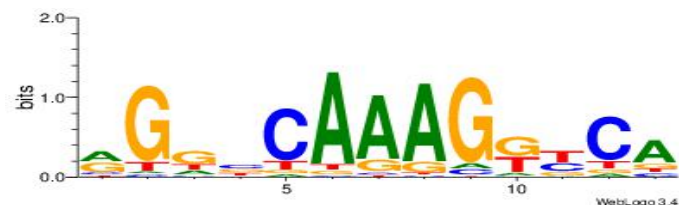
Original motif Consensus sequence: MSGGACATGYCCGGGCATGT

Reverse complement motif Consensus sequence:
ACATGCCCGGKCATGTCCSR

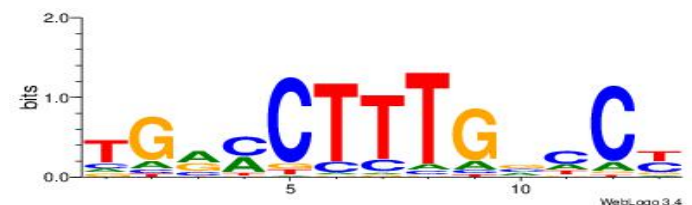


Dataset #: 3 Motif ID: 87 Motif name: HNF4A

Original motif Consensus sequence: RGGBCAAAGKYCA



Reverse complement motif Consensus sequence: TGM YCTTTGBCCK



Best Matches for Motif ID 87 (Highest to Lowest)

Dataset #:	3
Motif ID:	107
Motif name:	NR2F1
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:	0.0127044

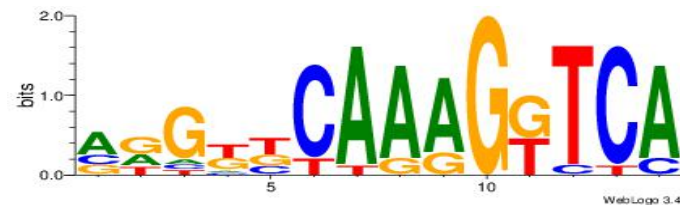
Alignment:

```
AKGY YCAAAGRTCA
-RGGBCAAAGKYCA
```

Original motif Consensus sequence: TGAMCTTTGMMCYT



Reverse complement motif Consensus sequence: AKGYCAAAGRTCA

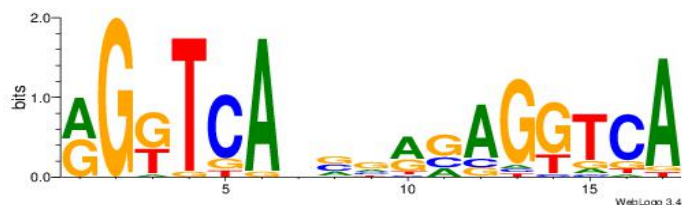


Dataset #: 3
Motif ID: 115
Motif name: RXRRAR_DR5
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 13
Similarity score: 0.0388151

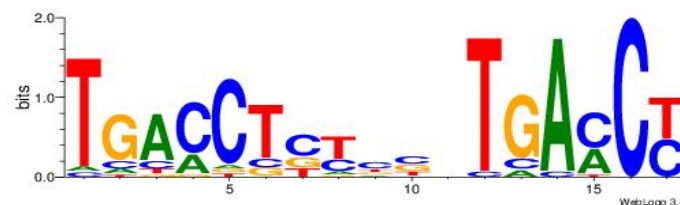
Alignment:

TGACCTCKVVB TGAYCK
TGM YCTTTGB CCK----

Original motif Consensus sequence: RGKTCABVVRGAGGTCA



Reverse complement motif Consensus sequence:
TGACCTCKVVB TGAYCK

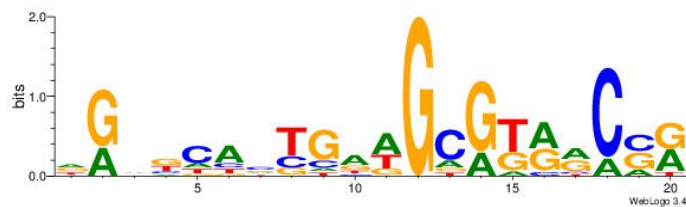


Dataset #: 3
 Motif ID: 109
 Motif name: Pax5
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 8
 Number of overlap: 13
 Similarity score: 0.0538871

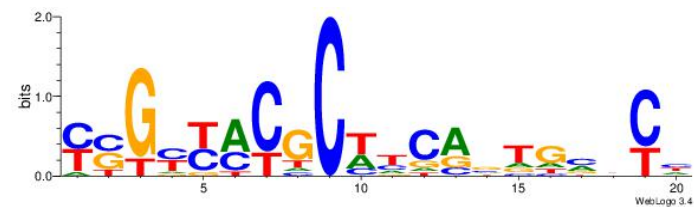
Alignment:

MSGKKRCGCWDCABTGGBCD
 -----RGGBCAAAGKYCA

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGGBCD



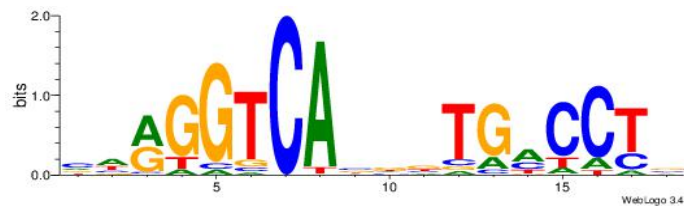
Dataset #: 3
 Motif ID: 82
 Motif name: ESR2
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3

Number of overlap: 13
Similarity score: 0.0571246

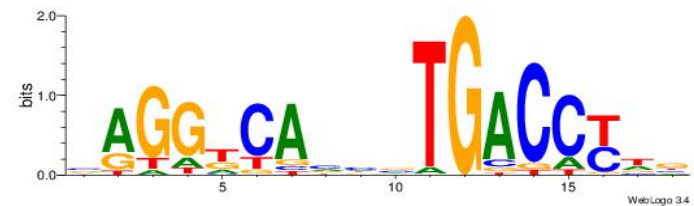
Alignment:

VHRGGTCABDBTGMCTB
--RGGBCAAAGKYCA---

Original motif Consensus sequence: VHRGGTCABDBTGMCTB



Reverse complement motif Consensus sequence: BAGGYCABHBTGACCKHV

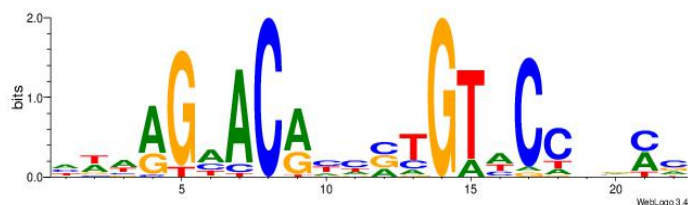


Dataset #: 3
Motif ID: 70
Motif name: Ar
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 4
Number of overlap: 13
Similarity score: 0.0577381

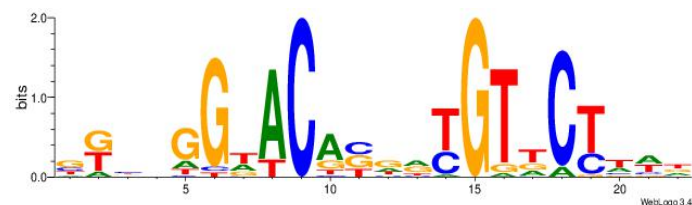
Alignment:

VRVDGGHACAVDDKGTHTDWH
-----TGMCTTTGBCK---

Original motif Consensus sequence: HWDAGHACRHHVTGTHCCHVMV

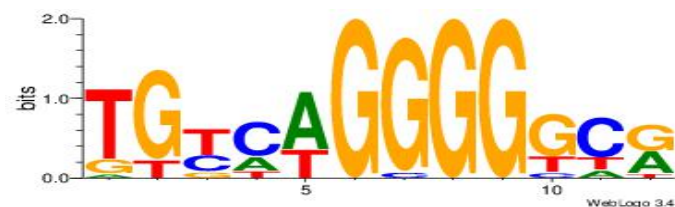


Reverse complement motif Consensus sequence: VRVDGGHACAVDDKGTHCTDWH

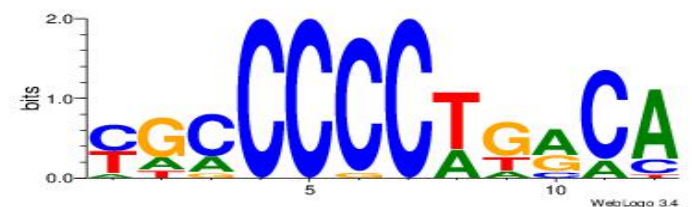


Dataset #: 3 Motif ID: 88 Motif name: INSM1

Original motif Consensus sequence: TGYCAGGGGGCR



Reverse complement motif Consensus sequence: MGCCCCCTGMCA



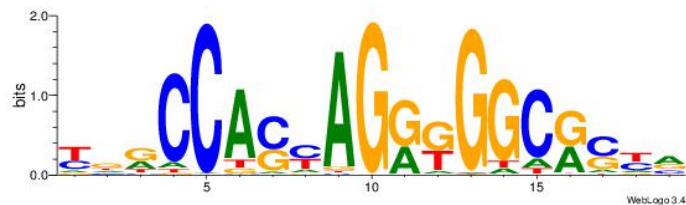
Best Matches for Motif ID 88 (Highest to Lowest)

Dataset #:	3
Motif ID:	74
Motif name:	CTCF
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	5
Number of overlap:	12
Similarity score:	0.0323447

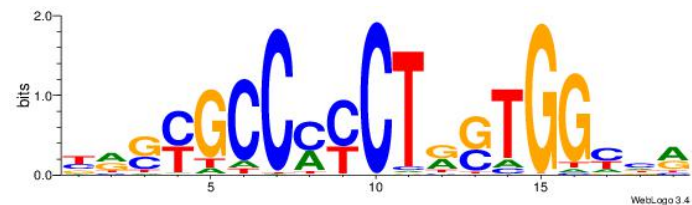
Alignment:

BMSMGCCYMCTKSTGGMHM
 ---MGCCCCCTGMCA----

Original motif Consensus sequence: YDRCCASYAGRKGGCRSYV



Reverse complement motif Consensus sequence:
 BMSMGCCYMCTKSTGGMHM

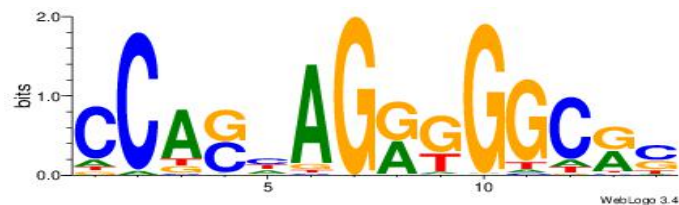
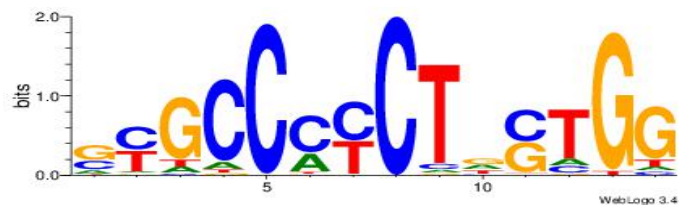


Dataset #:	2
Motif ID:	67
Motif name:	Motif 67
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	2
Number of overlap:	12
Similarity score:	0.0361443

Alignment:
 CCASHAGKGGGCKS
 -TGYCAGGGGGCR-

Original motif Consensus sequence: SYGCCCYCTDSTGG

Reverse complement motif Consensus sequence: CCASHAGKGGGCKS



Dataset #: 4
 Motif ID: 166
 Motif name: CasCAGrGGGCrSy
 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: 0.0386733

Alignment:

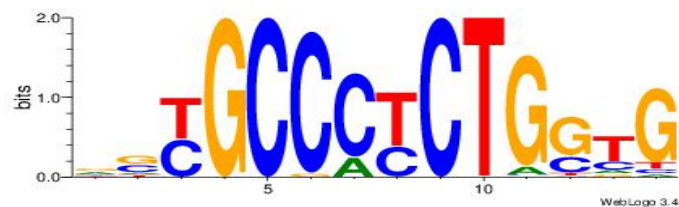
CACCAGRGGGCRSB

TGYCAGGGGGCR--

Original motif Consensus sequence: CACCAGRGGGCRSB



Reverse complement motif Consensus sequence: BSKGCCCKCTGGT



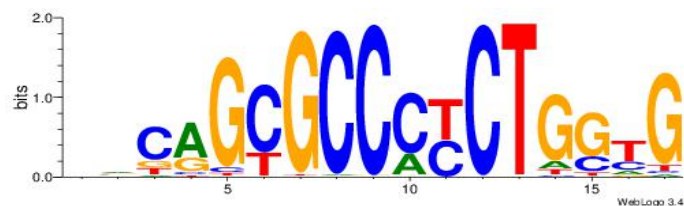
Dataset #: 4
 Motif ID: 168

Motif name: yrcrGYGCCMyCTGGtG
 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: 0.0393748

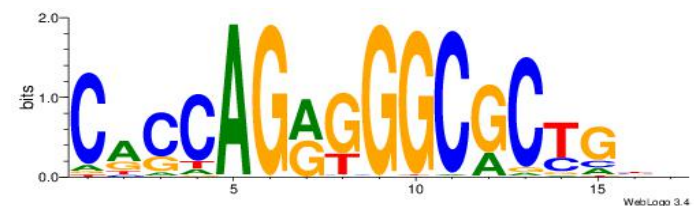
Alignment:

HVCAGCGCCCYCTGGTG
 -----MGCCCCCTGMCA

Original motif Consensus sequence: HVCAGCGCCCYCTGGTG



Reverse complement motif Consensus sequence: CACCAGMGGGCGCTGBD



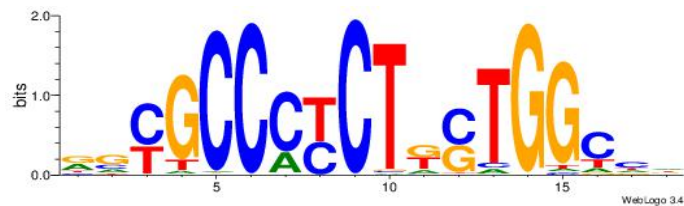
Dataset #: 4
 Motif ID: 156
 Motif name: rgyGCCMyCTksTGGccd
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 5
 Number of overlap: 12
 Similarity score: 0.0427424

Alignment:

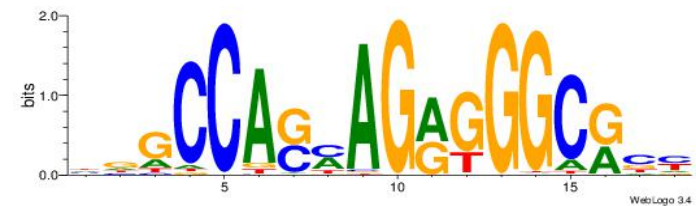
RVYGCCCYCTKSTGGCHD

--MGCCCCCTGMCA----

Original motif Consensus sequence: RVYGCCCYCTKSTGGCHD



Reverse complement motif Consensus sequence: DDGCCASYAGMGGGCKVM

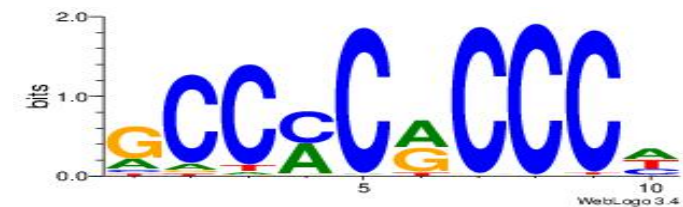


Dataset #: 3 Motif ID: 89 Motif name: Klf4

Original motif Consensus sequence: DGGGYGKGGC



Reverse complement motif Consensus sequence: GCCYCMCCCD



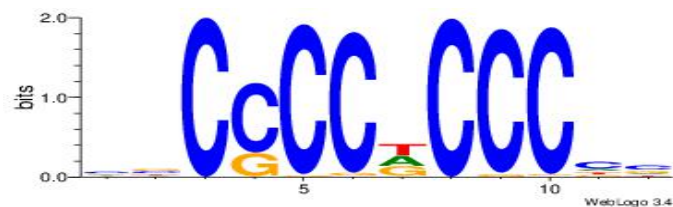
Best Matches for Motif ID 89 (Highest to Lowest)

Dataset #:	4
Motif ID:	155
Motif name:	csCSCCdCCCcs
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward

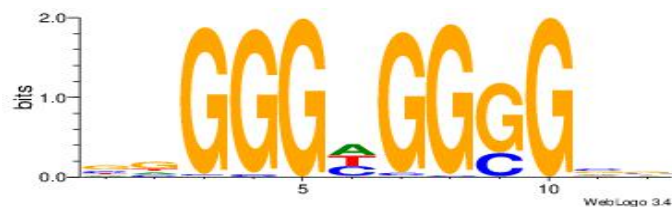
Position number: 2
Number of overlap: 10
Similarity score: 0.0234217

Alignment:
VDGGGDGGGGBV
-DGGGYGKGGC-

Original motif Consensus sequence: VBCCCCDCCCHV



Reverse complement motif Consensus sequence: VDGGGDGGGGBV



Dataset #: 4
Motif ID: 154
Motif name: csCsCCTCCcc
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 10
Similarity score: 0.0429499

Alignment:
VBCCCCTCCHB
-GCCYCMCCCD

Original motif Consensus sequence: VBCCCCTCCHB

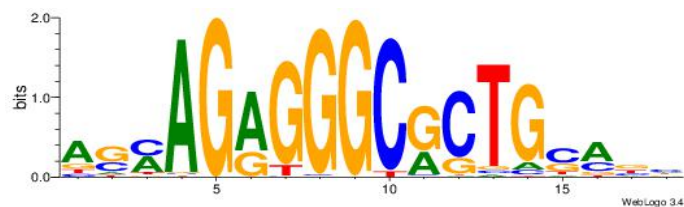
Reverse complement motif Consensus sequence: BDGGAGGGGBV



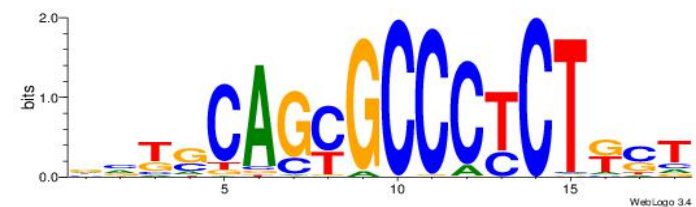
Dataset #: 4
 Motif ID: 149
 Motif name: asmAGRGGGCrCTGsmkc
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 4
 Number of overlap: 10
 Similarity score: 0.0512984

Alignment:
 ASMAGAGGGCRCTGSABH
 -----DGGGYGKGGC----

Original motif Consensus sequence: ASMAGAGGGCRCTGSABH



Reverse complement motif Consensus sequence: DBTSCAGMGCCCTCTRST



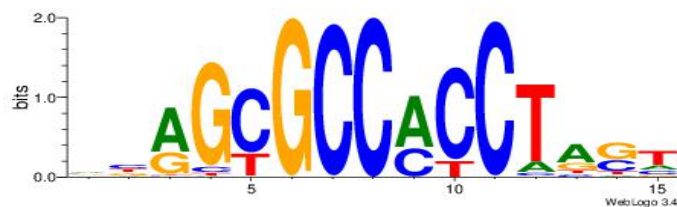
Dataset #: 4

Motif ID: 146
 Motif name: myrGYGCCmCCTast
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 10
 Similarity score: 0.0522764

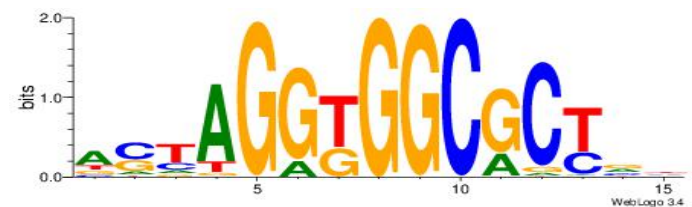
Alignment:

VBAGCGCCMCCTAST
 ---GCCYCMCCCD--

Original motif Consensus sequence: VBAGCGCCMCCTAST



Reverse complement motif Consensus sequence: ASTAGGYGGCGCT



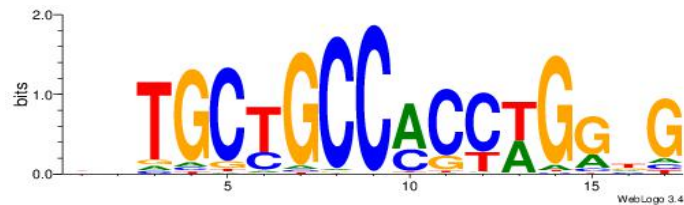
Dataset #: 4
 Motif ID: 169
 Motif name: yvTGCyGCCmCCwGgtG
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 10
 Similarity score: 0.0619219

Alignment:

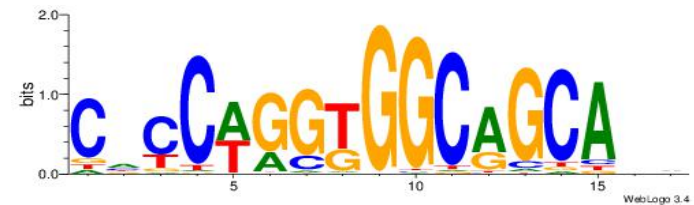
BVTGCTGCCACCWGGDG

---GCCYCMCCCD----

Original motif Consensus sequence: BVTGCTGCCACCWGGDG



Reverse complement motif Consensus sequence: CDCCWGGTGGCAGCAVV

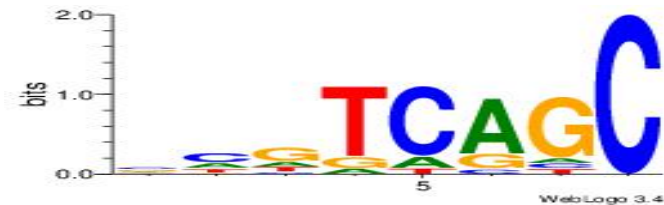


Dataset #: 3 Motif ID: 90 Motif name: Mafb

Original motif Consensus sequence: GCTGACDB



Reverse complement motif Consensus sequence: BHGTCAGC



Best Matches for Motif ID 90 (Highest to Lowest)

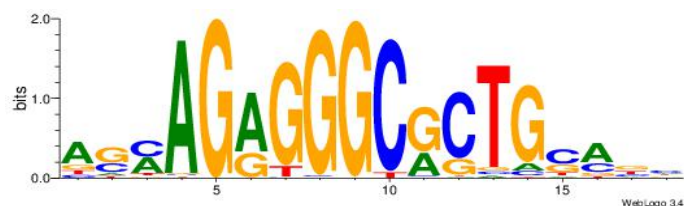
Dataset #:	4
Motif ID:	149
Motif name:	asmAGRGGGCrCTGsmkc
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward

Position number: 1
Number of overlap: 8
Similarity score: 0.0232655

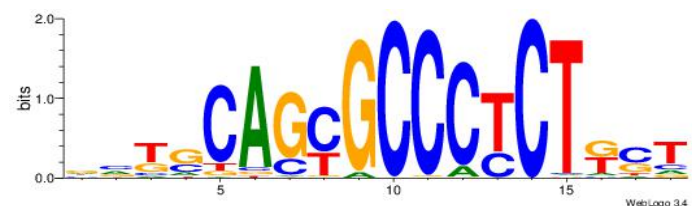
Alignment:

ASMAGAGGGCRCTGSABH
-----GCTGACDB

Original motif Consensus sequence: ASMAGAGGGCRCTGSABH



Reverse complement motif Consensus sequence: DBTSCAGMGCCCTCTRST

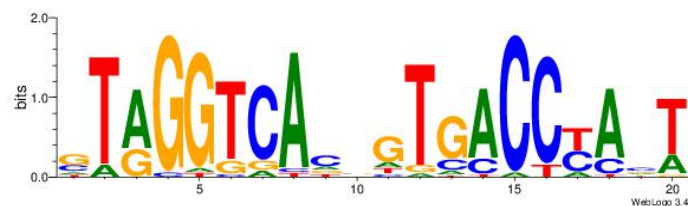


Dataset #: 3
Motif ID: 111
Motif name: PPARG
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 10
Number of overlap: 8
Similarity score: 0.0322069

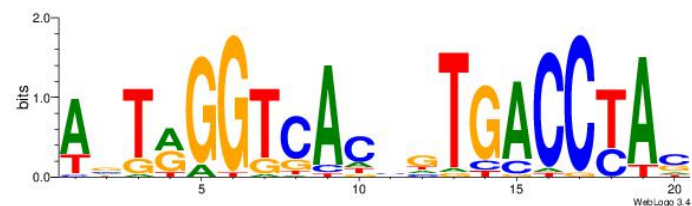
Alignment:

STAGGTCACBG TGACCYABT
---GCTGACDB-----

Original motif Consensus sequence: STAGGTCACBG TGACCYABT



Reverse complement motif Consensus sequence: ABTMGGTCACBG TGACCTAS

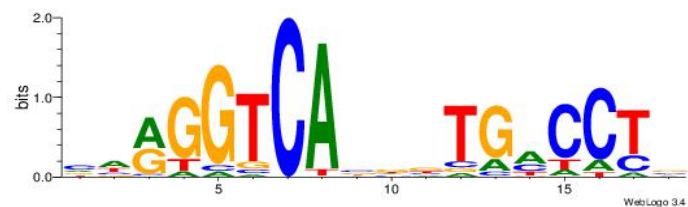


Dataset #: 3
Motif ID: 82
Motif name: ESR2
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 9
Number of overlap: 8
Similarity score: 0.035275

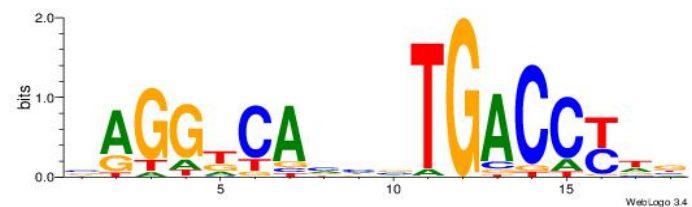
Alignment:

BAGGYCABHBTGACCKHV
-----GCTGACDB--

Original motif Consensus sequence: VHRGGTCABDBTGM CCTB



Reverse complement motif Consensus sequence: BAGGYCABHBTGACCKHV

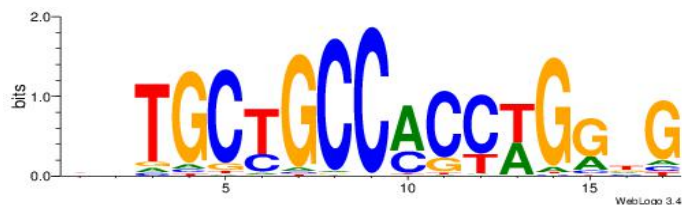


Dataset #: 4
 Motif ID: 169
 Motif name: yvTGCyGCCmCCwGgtG
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 7
 Number of overlap: 8
 Similarity score: 0.0358393

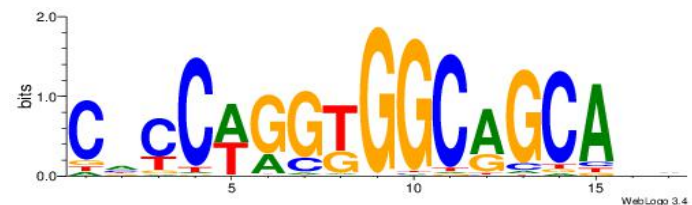
Alignment:

CDCCWGGTGGCAGCAVV
 -----BHGTCAGC----

Original motif Consensus sequence: BVTGCTGCCACCWGGDG



Reverse complement motif Consensus sequence: CDCCWGGTGGCAGCAVV



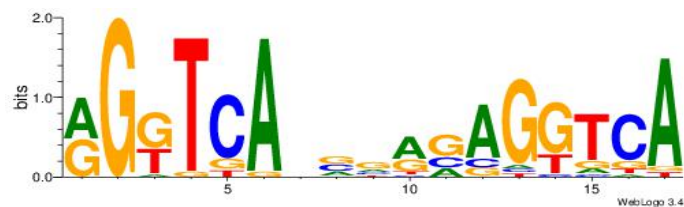
Dataset #: 3
 Motif ID: 115
 Motif name: RXRRAR_DR5
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2

Number of overlap: 8
Similarity score: 0.0388936

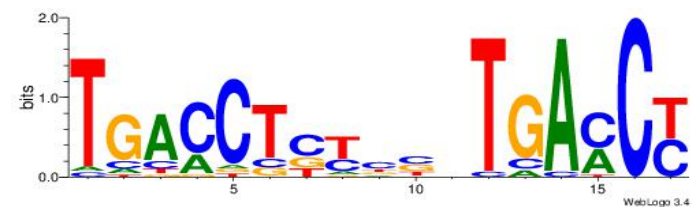
Alignment:

RGKTCABVVRGAGGTCA
-GCTGACDB-----

Original motif Consensus sequence: RGKTCABVVRGAGGTCA



Reverse complement motif Consensus sequence: TGACCTCKVVBGTGAYCK



Dataset #: 3 Motif ID: 91 Motif name: MAX

Original motif Consensus sequence: DAHCACGTGD



Reverse complement motif Consensus sequence: BCACGTGDTD



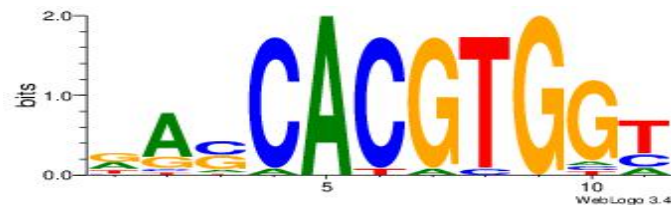
Best Matches for Motif ID 91 (Highest to Lowest)

Dataset #: 3
Motif ID: 95
Motif name: MYCMAX
Matching format of first motif: Original Motif

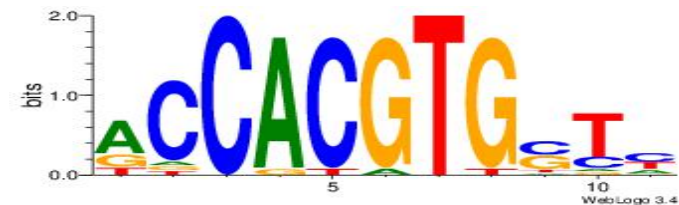
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	10
Similarity score:	0.0266106

Alignment:
RASCACGTGGT
DAHCACGTGD-

Original motif Consensus sequence: RASCACGTGGT



Reverse complement motif Consensus sequence: ACCACGTGSTM



Dataset #:	3
Motif ID:	121
Motif name:	TAL1TCF3
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:	0.0735692

Alignment:

ARCAGATGRTVD
-BCACGTGDTD-

Original motif Consensus sequence: HVAMCATCTGKT



Reverse complement motif Consensus sequence: ARCAGATGRTVD



Dataset #: 4
Motif ID: 158
Motif name: grCCACwAGrk
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2
Number of overlap: 10
Similarity score: 0.0740659

Alignment:
DDCCACWAGRK
DAHACGTGTD-

Original motif Consensus sequence: DDCCACWAGRK



Reverse complement motif Consensus sequence: YMCTWGTGGHH



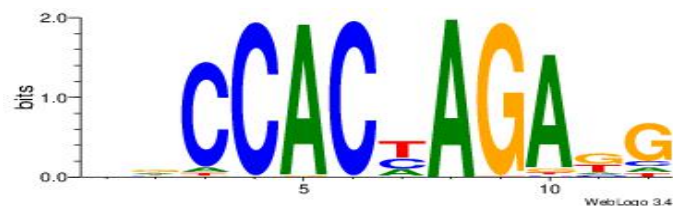
Dataset #: 4
Motif ID: 138
Motif name: grCCACyAGAkG
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 10
Similarity score: 0.0824309

Alignment:

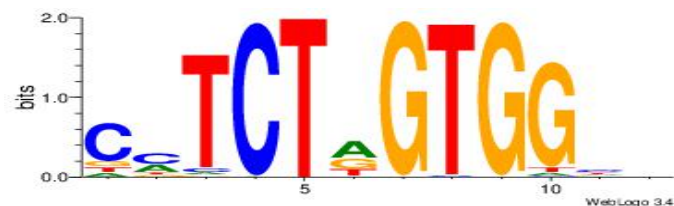
DDCCACYAGAKG

DAHCACTGD--

Original motif Consensus sequence: DDCCACYAGAKG



Reverse complement motif Consensus sequence: CYTCTMGTGGHH

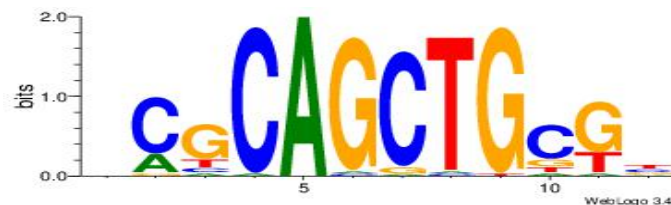


Dataset #: 3
Motif ID: 105
Motif name: NHLH1
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 3

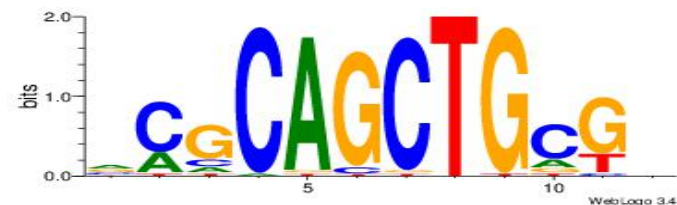
Number of overlap: 10
Similarity score: 0.0853797

Alignment:
VCGCAGCTGCGB
--BCACGTGDTD

Original motif Consensus sequence: VCGCAGCTGCGB

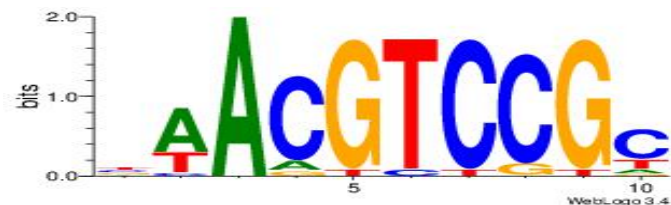


Reverse complement motif Consensus sequence: VCGCAGCTGCGV



Dataset #: 3 Motif ID: 92 Motif name: MIZF

Original motif Consensus sequence: BAACGTCCGC



Reverse complement motif Consensus sequence: GCGGACGTTV



Best Matches for Motif ID 92 (Highest to Lowest)

Dataset #: 3
Motif ID: 84
Motif name: GABPA
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement

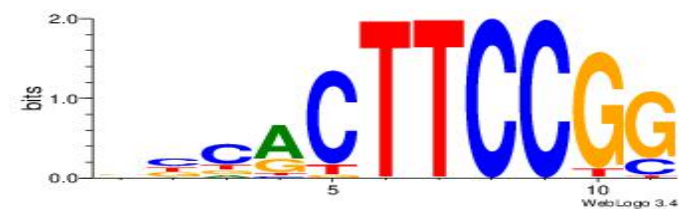
Direction: Backward
 Position number: 2
 Number of overlap: 10
 Similarity score: 0.0326212

Alignment:
 VVCACTTCCGG
 BAACGTCCGC-

Original motif Consensus sequence: CCGGAAGTVV



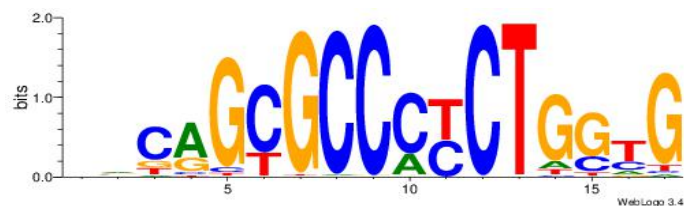
Reverse complement motif Consensus sequence: VVCACTTCCGG



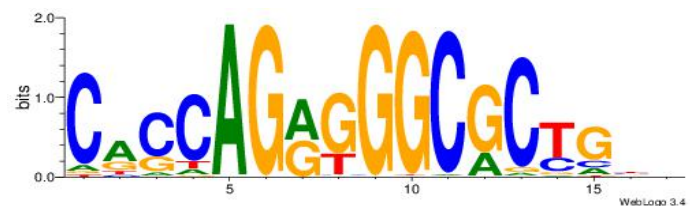
Dataset #: 4
 Motif ID: 168
 Motif name: yrcrGYGCCMyCTGGtG
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 6
 Number of overlap: 10
 Similarity score: 0.0553693

Alignment:
 CACCAGMGGGCGCTGBD
 -----GCGGACGTTV--

Original motif Consensus sequence: HVCAGCGCCCYCTGGTG



Reverse complement motif Consensus sequence: CACCAGMGGGCGCTGBD

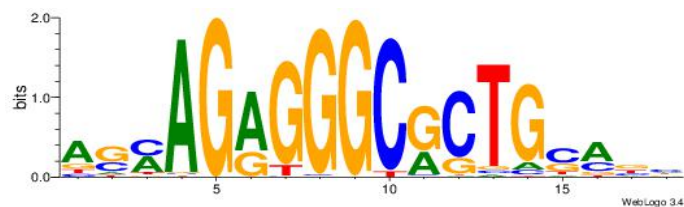


Dataset #: 4
Motif ID: 149
Motif name: asmAGRGGGCrCTGsmkc
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 5
Number of overlap: 10
Similarity score: 0.0554206

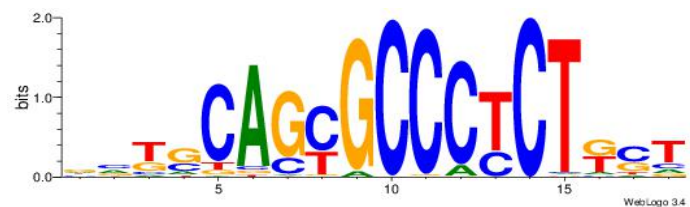
Alignment:

DBTSCAGMGCCCTCTRST
-----BAACGTCCGC-----

Original motif Consensus sequence: ASMAGAGGGCRCTGSABH



Reverse complement motif Consensus sequence: DBTSCAGMGCCCTCTRST

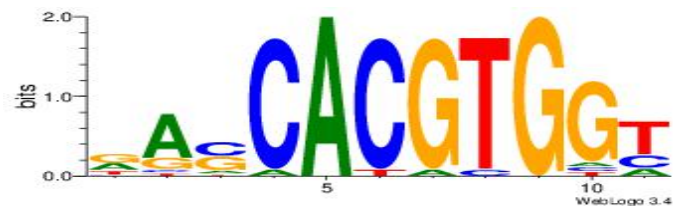


Dataset #: 3
 Motif ID: 95
 Motif name: MYCMAX
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 10
 Similarity score: 0.0558866

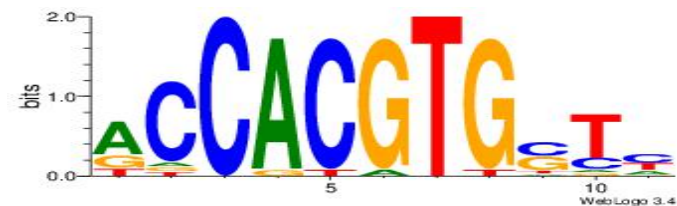
Alignment:

ACCACGTGSTM
 -BAACGTCCGC

Original motif Consensus sequence: RASCACGTGGT



Reverse complement motif Consensus sequence: ACCACGTGSTM

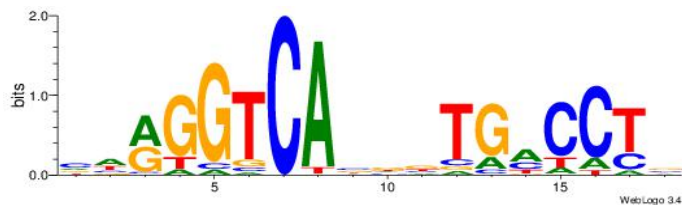


Dataset #: 3
 Motif ID: 82
 Motif name: ESR2
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 10

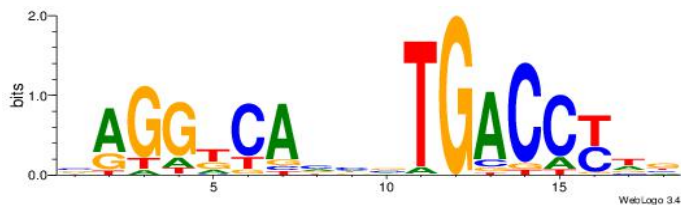
Similarity score: 0.0567619

Alignment:
BAGGYCABHBTGACCKHV
-----GCGGACGTTV

Original motif Consensus sequence: VHRGGTCABDBTGMCTB



Reverse complement motif Consensus sequence: BAGGYCABHBTGACCKHV

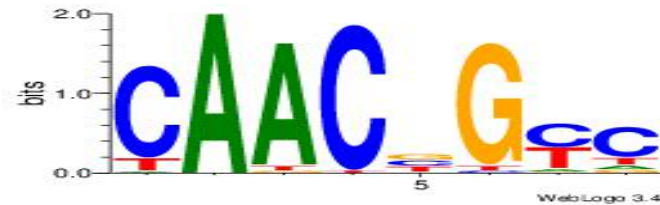


Dataset #: 3 Motif ID: 93 Motif name: Myb

Original motif Consensus sequence: GRCVGTTG



Reverse complement motif Consensus sequence: CAACVGMC



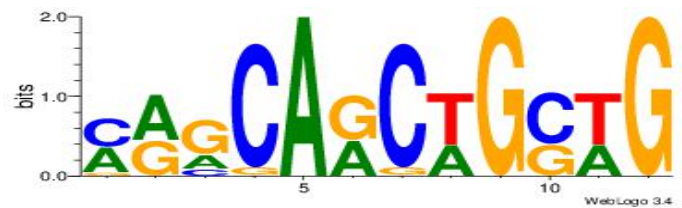
Best Matches for Motif ID 93 (Highest to Lowest)

Dataset #:	3
Motif ID:	97
Motif name:	Myf
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif

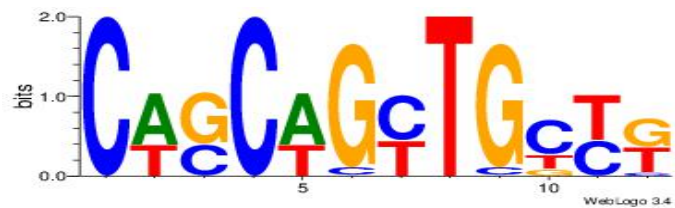
Direction: Forward
Position number: 4
Number of overlap: 8
Similarity score: 0.0229626

Alignment:
MRGCARCWGSWG
---CAACVGMC-

Original motif Consensus sequence: MRGCARCWGSWG



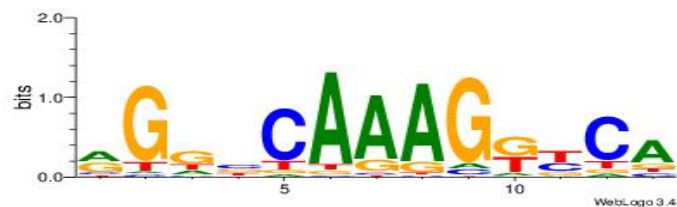
Reverse complement motif Consensus sequence: CWSCWGMTGCKR



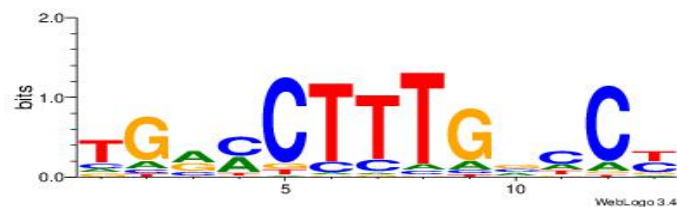
Dataset #: 3
Motif ID: 87
Motif name: HNF4A
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 5
Number of overlap: 8
Similarity score: 0.0239903

Alignment:
RGGBCAAAGKYCA
-CAACVGMC----

Original motif Consensus sequence: RGGBCAAAGKYCA



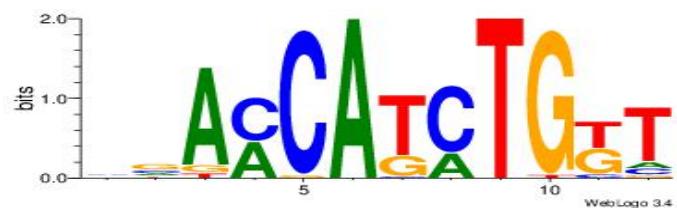
Reverse complement motif Consensus sequence: TGMVCTTTGBCCK



Dataset #: 3
Motif ID: 121
Motif name: TAL1TCF3
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: 0.0259637

Alignment:
ARCAGATGRTVD
GRCVGTG-----

Original motif Consensus sequence: HVAMCATCTGKT



Reverse complement motif Consensus sequence: ARCAGATGRTVD



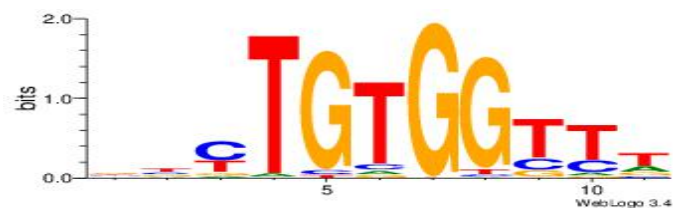
Dataset #: 3
 Motif ID: 114
 Motif name: RUNX1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 4
 Number of overlap: 8
 Similarity score: 0.0297264

Alignment:

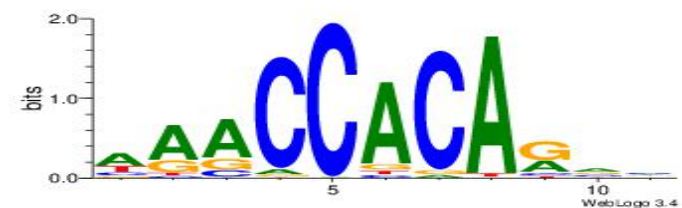
AAACCACAKVB

---CAACVGMC

Original motif Consensus sequence: BBTGTGGTTT



Reverse complement motif Consensus sequence: AAACCACAKVB

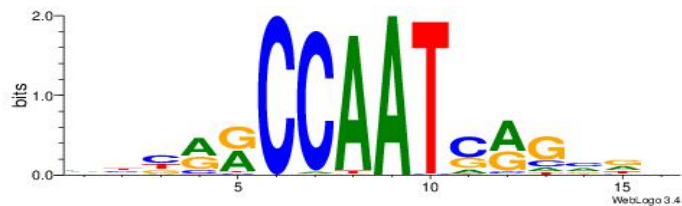


Dataset #: 3
 Motif ID: 104
 Motif name: NFYA
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 8

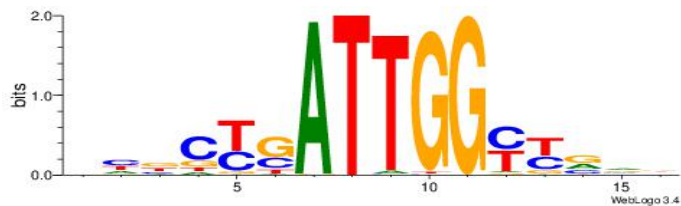
Similarity score: 0.0310894

Alignment:
VBBRRCCAATSRGVDB
-----CAACVGMC--

Original motif Consensus sequence: VBBRRCCAATSRGVDB



Reverse complement motif Consensus sequence: BHVCKSATTGGMKBVV

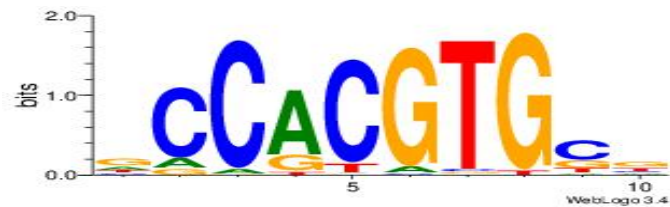


Dataset #: 3 Motif ID: 94 Motif name: Myc

Original motif Consensus sequence: VGCACGTGGH



Reverse complement motif Consensus sequence: DCCACGTGCV



Best Matches for Motif ID 94 (Highest to Lowest)

Dataset #:	3
Motif ID:	96
Motif name:	Mycn
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

Alignment:

HSCACGTGGC

VGCACGTGGH

Original motif Consensus sequence: HSCACGTGGC



Reverse complement motif Consensus sequence: GCCACGTGSD



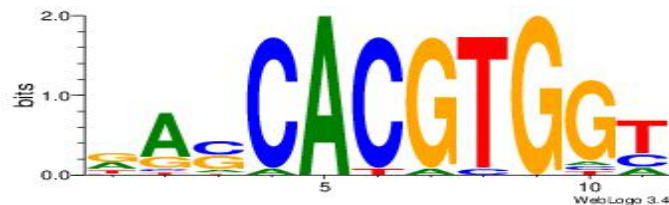
Dataset #: 3
 Motif ID: 95
 Motif name: MYCMAX
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 10
 Similarity score: 0.0209359

Alignment:

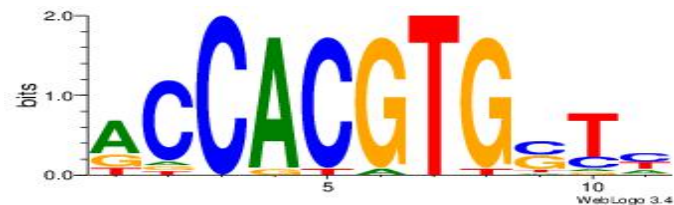
RASCACGTGGT

-VGCACGTGGH

Original motif Consensus sequence: RASCACGTGGT



Reverse complement motif Consensus sequence: ACCACGTGSTM

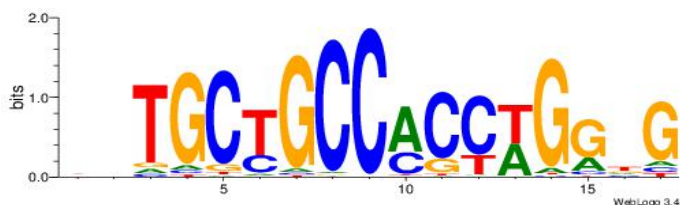


Dataset #: 4
 Motif ID: 169
 Motif name: yvTGCyGCCmCCwGgtG
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 7
 Number of overlap: 10
 Similarity score: 0.0628757

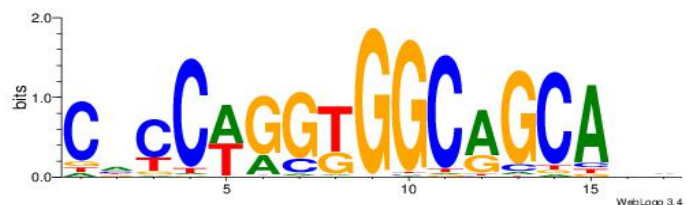
Alignment:

CDCCWGGTGGCAGCAVV
 -VGCACGTGGH-----

Original motif Consensus sequence: BVTGCTGCCACCWGGDG



Reverse complement motif Consensus sequence: CDCCWGGTGGCAGCAVV



Dataset #: 4
 Motif ID: 147
 Motif name: asCAGrkGGCrSy
 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: 0.0675017

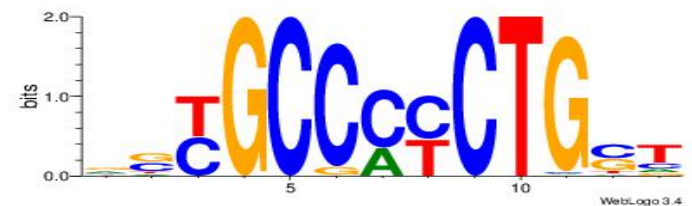
Alignment:

ASCAGRGGGCRSB
 VGCACGTGGH---

Original motif Consensus sequence: ASCAGRGGGCRSB



Reverse complement motif Consensus sequence: BSKGCCCMCTGST

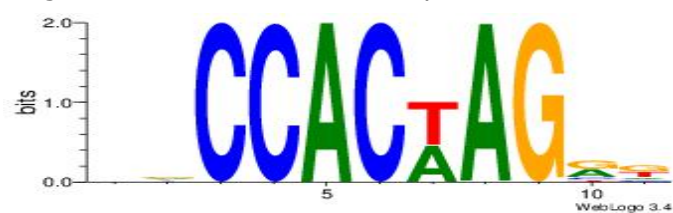


Dataset #: 4
 Motif ID: 158
 Motif name: grCCACwAGrk
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 10

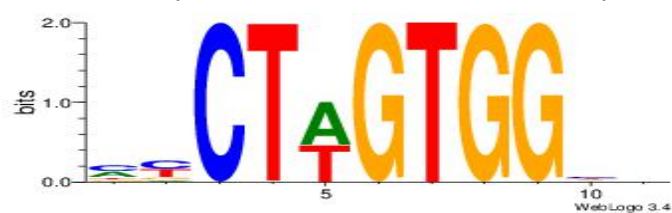
Similarity score: 0.0682475

Alignment:
DDCCACWAGRK
-DCCACGTGCV

Original motif Consensus sequence: DDCCACWAGRK

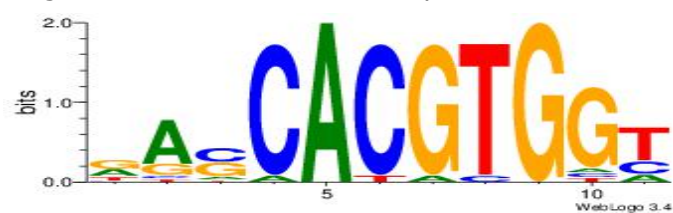


Reverse complement motif Consensus sequence: YMCTWGTGGHH

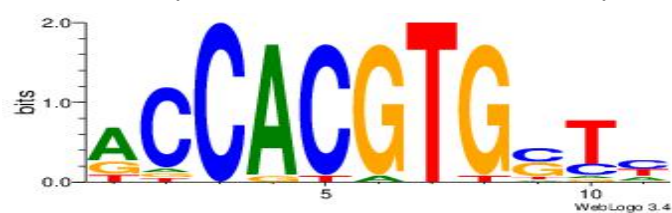


Dataset #: 3 Motif ID: 95 Motif name: MYCMAX

Original motif Consensus sequence: RASCACGTGGT



Reverse complement motif Consensus sequence: ACCACGTGSTM



Best Matches for Motif ID 95 (Highest to Lowest)

Dataset #:	3
Motif ID:	121
Motif name:	TAL1TCF3
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: 0.0652343

Alignment:
HVAMCATCTGKT
-RASCACGTGGT

Original motif Consensus sequence: HVAMCATCTGKT



Reverse complement motif Consensus sequence: ARCAGATGRTVD



Dataset #: 4
Motif ID: 158
Motif name: grCCACwAGrk
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: 0.0786918

Alignment:
DDCCACWAGRK
RASCACGTGGT

Original motif Consensus sequence: DDCCACWAGRK

Reverse complement motif Consensus sequence: YMCTWGTGGHH

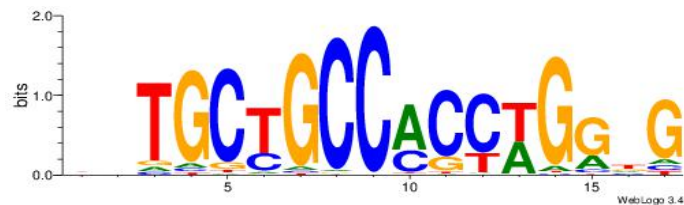


Dataset #: 4
 Motif ID: 169
 Motif name: yvTGCyGCCmCCwGgtG
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 7
 Number of overlap: 11
 Similarity score: 0.0804522

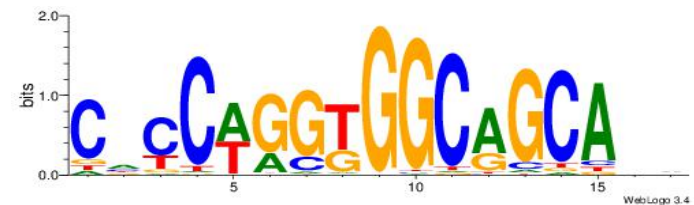
Alignment:

CDCCWGGTGGCAGCAVV
 RASCACGTGGT-----

Original motif Consensus sequence: BVTGCTGCCACCWGGDG



Reverse complement motif Consensus sequence: CDCCWGGTGGCAGCAVV



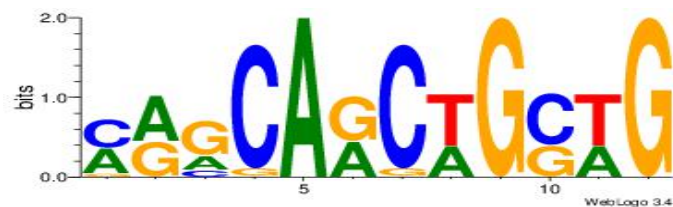
Dataset #: 3

Motif ID: 97
 Motif name: Myf
 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: 0.0843705

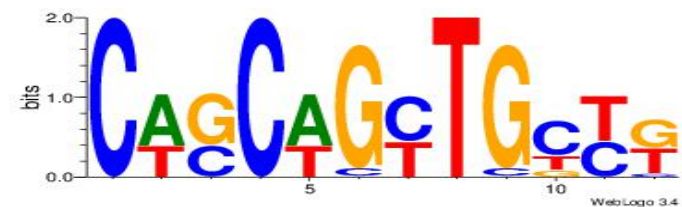
Alignment:

CWSCWGMTGCKR
 -ACCACGTGSTM

Original motif Consensus sequence: MRGCARCWGSWG



Reverse complement motif Consensus sequence: CWSCWGMTGCKR



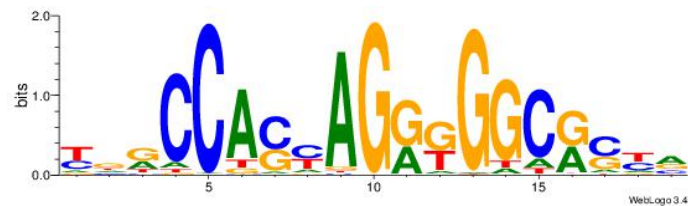
Dataset #: 3
 Motif ID: 74
 Motif name: CTCF
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 5
 Number of overlap: 11
 Similarity score: 0.084904

Alignment:

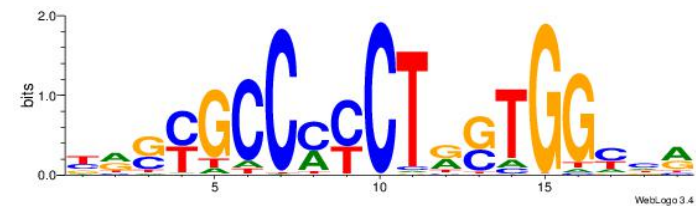
YDRCCASYAGRKGGCRSYV

-----RASCACGTGGT-----

Original motif Consensus sequence: YDRCCASYAGRKGGCRSYV



Reverse complement motif Consensus sequence: BMSMGCCYMCTKSTGGMHM



Dataset #: 3 Motif ID: 96 Motif name: Mycn

Original motif Consensus sequence: HSCACGTGGC



Reverse complement motif Consensus sequence: GCCACGTGSD



Best Matches for Motif ID 96 (Highest to Lowest)

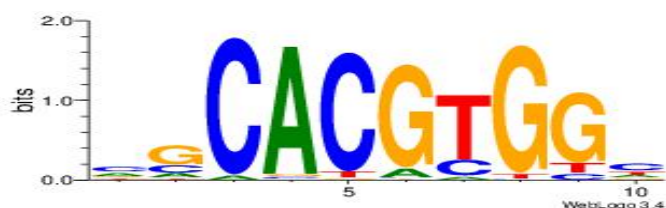
Dataset #:	3
Motif ID:	94
Motif name:	Myc
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward

Position number: 1
Number of overlap: 10
Similarity score: 0

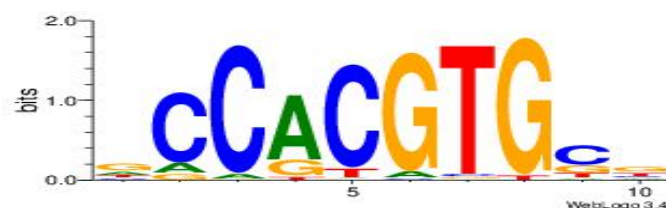
Alignment:

DCCACGTGCV
GCCACGTGSD

Original motif Consensus sequence: VGCACGTGGH



Reverse complement motif Consensus sequence: DCCACGTGCV



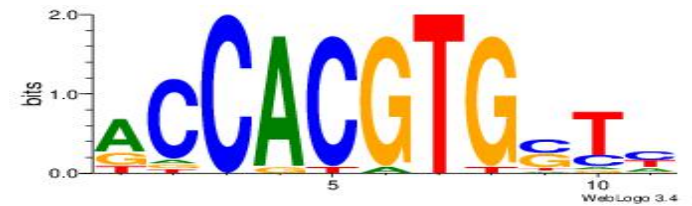
Dataset #: 3
Motif ID: 95
Motif name: MYCMAX
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 2
Number of overlap: 10
Similarity score: 0.0200467

Alignment:

RASCACGTGGT
-HSCACGTGGC

Original motif Consensus sequence: RASCACGTGGT

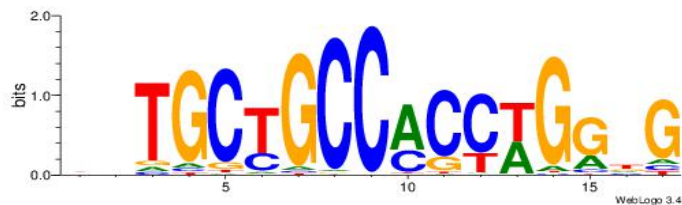
Reverse complement motif Consensus sequence: ACCACGTGSTM



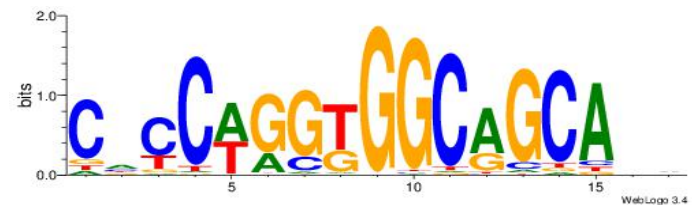
Dataset #: 4
 Motif ID: 169
 Motif name: yvTGCyGCCmCCwGgtG
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 10
 Similarity score: 0.0581322

Alignment:
 CDCCWGGTGGCAGCAVV
 -HSCACGTGGC-----

Original motif Consensus sequence: BVTGCTGCCACCWGGDG



Reverse complement motif Consensus sequence: CDCCWGGTGGCAGCAVV



Dataset #: 4

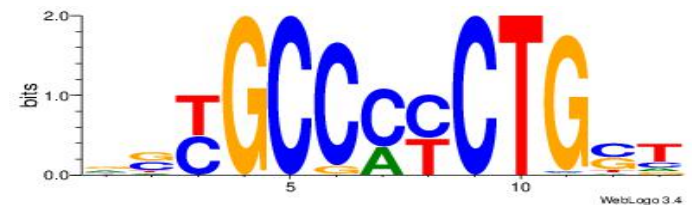
Motif ID: 147
 Motif name: asCAGrkGGCrSy
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 10
 Similarity score: 0.0621075

Alignment:
 ASCAGRGGGCRSB
 HSCACGTGGC---

Original motif Consensus sequence: ASCAGRGGGCRSB



Reverse complement motif Consensus sequence: BSKGCCCMCTGST



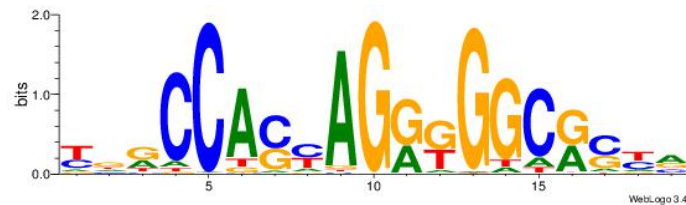
Dataset #: 3
 Motif ID: 74
 Motif name: CTCF
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 6
 Number of overlap: 10
 Similarity score: 0.0679017

Alignment:

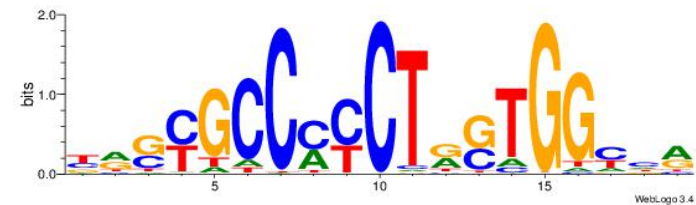
YDRCCASYAGRKGGCRSYV

-----HSCACGTGGC-----

Original motif Consensus sequence: YDRCCASYAGRKGGCRSYV

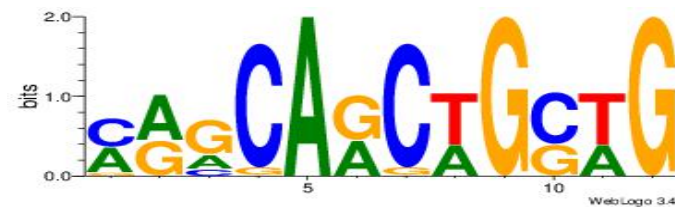


Reverse complement motif Consensus sequence: BMSMGCCYMCTKSTGGMHM

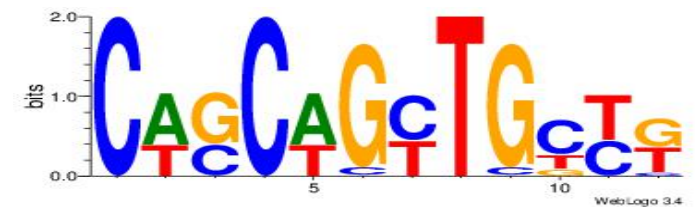


Dataset #: 3 Motif ID: 97 Motif name: Myf

Original motif Consensus sequence: MRGCARCWGSWG



Reverse complement motif Consensus sequence: CWSCWGMTGCKR



Best Matches for Motif ID 97 (Highest to Lowest)

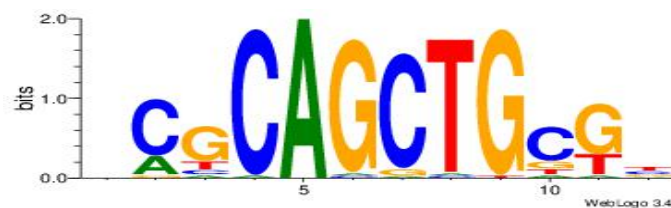
Dataset #:	3
Motif ID:	105
Motif name:	NHLH1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward

Position number: 1
Number of overlap: 12
Similarity score: 0.0355504

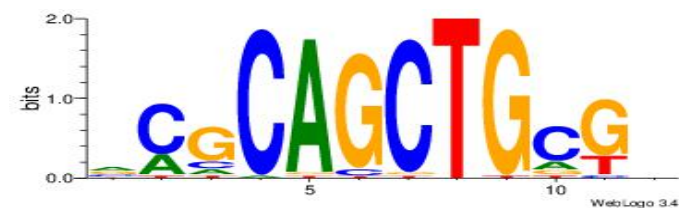
Alignment:

VCGCAGCTGCGV
CWSCWGMTGCKR

Original motif Consensus sequence: VCGCAGCTGCGB



Reverse complement motif Consensus sequence: VCGCAGCTGCGV

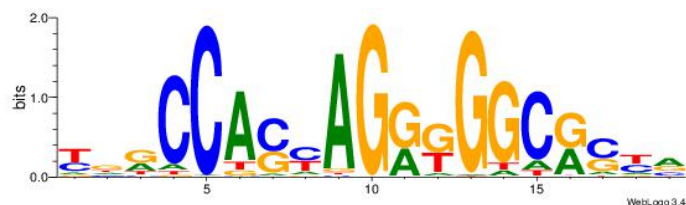


Dataset #: 3
Motif ID: 74
Motif name: CTCF
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 4
Number of overlap: 12
Similarity score: 0.0508517

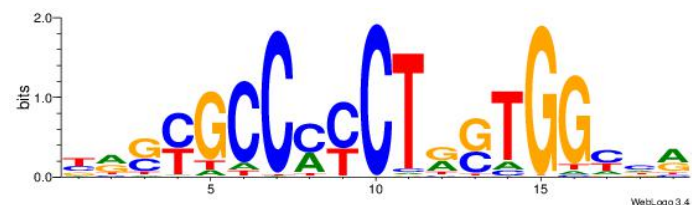
Alignment:

YDRCCASYAGRKGGCRSYV
---CWSCWGMTGCKR----

Original motif Consensus sequence: YDRCCASYAGRKGGRSYV



Reverse complement motif Consensus sequence: BMSMGCCYMCTKSTGGMHM



Dataset #: 4
Motif ID: 166
Motif name: CasCAGrGGGCrSy
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: 0.055783

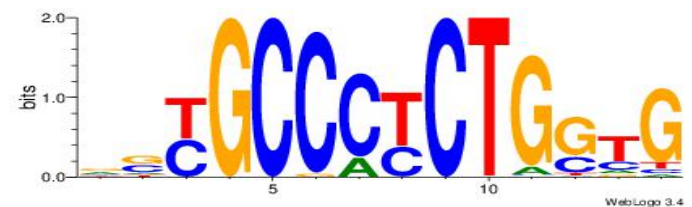
Alignment:

CACCAGRGGGCRSB
CWSCWGMTGCKR--

Original motif Consensus sequence: CACCAGRGGGCRSB



Reverse complement motif Consensus sequence: BSKGCCCKCTGGT

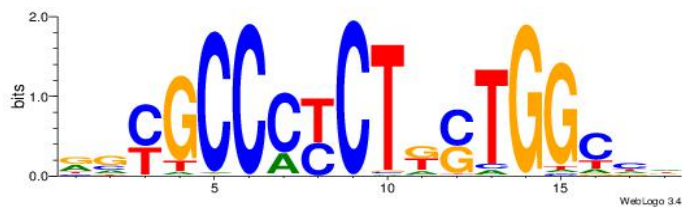


Dataset #: 4
 Motif ID: 156
 Motif name: rgyGCCMyCTksTGGccd
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 12
 Similarity score: 0.058463

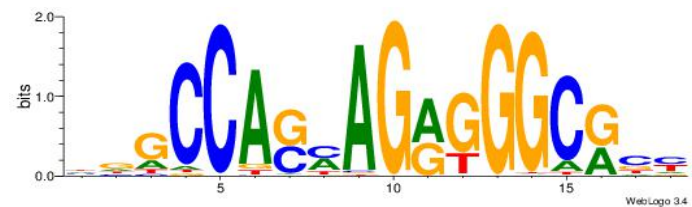
Alignment:

DDGCCASYAGMGGGCKVM
 ----CWSCWGMTGCKR--

Original motif Consensus sequence: RYVGCCCYCTKSTGGCHD



Reverse complement motif Consensus sequence: DDGCCASYAGMGGGCKVM

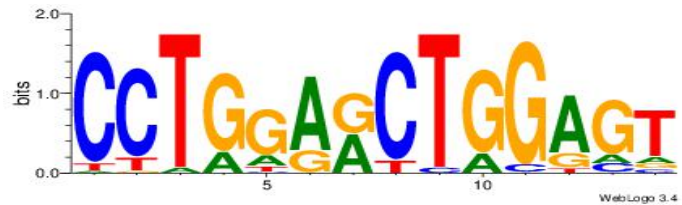


Dataset #: 2
 Motif ID: 69
 Motif name: Motif 69
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2

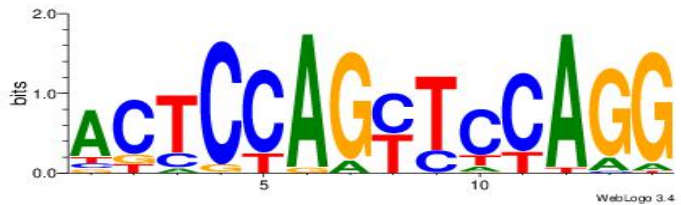
Number of overlap: 12
Similarity score: 0.0591644

Alignment:
ACTCCAGMTCCAGG
-CWSCWGMTGCKR-

Original motif Consensus sequence: CCTGGARCTGGAGT



Reverse complement motif Consensus sequence: ACTCCAGMTCCAGG



Dataset #: 3 Motif ID: 98 Motif name: MZF1_1-4

Original motif Consensus sequence: BGGGGA



Reverse complement motif Consensus sequence: TCCCCV



Best Matches for Motif ID 98 (Highest to Lowest)

Dataset #: 3
Motif ID: 88
Motif name: INSM1
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement

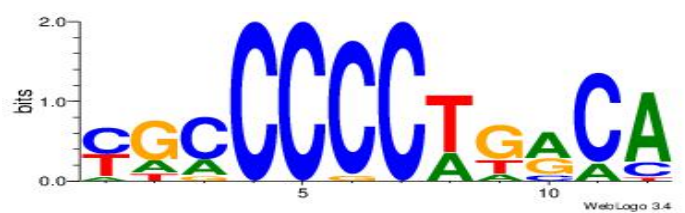
Direction: Forward
Position number: 3
Number of overlap: 6
Similarity score: 0.033712

Alignment:
MGCCCCCTGMCA
--TCCCCV----

Original motif Consensus sequence: TGYCAGGGGGCR



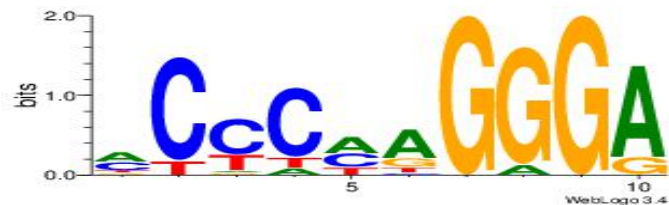
Reverse complement motif Consensus sequence: MGCCCCCTGMCA



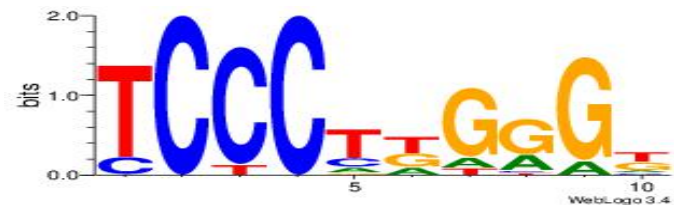
Dataset #: 3
Motif ID: 77
Motif name: EBF1
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 5
Number of overlap: 6
Similarity score: 0.0339898

Alignment:
MCCCMAGGGA
----BGGGGA

Original motif Consensus sequence: MCCCMAAGGA



Reverse complement motif Consensus sequence: TCCCTYGGGY

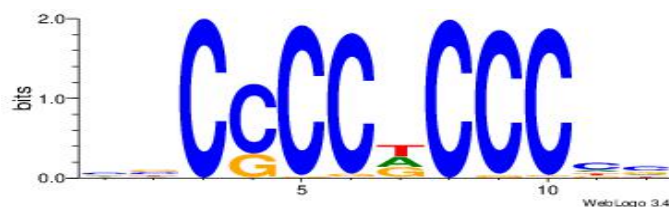


Dataset #: 4
Motif ID: 155
Motif name: csCSCCdCCCcs
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 6
Similarity score: 0.0344568

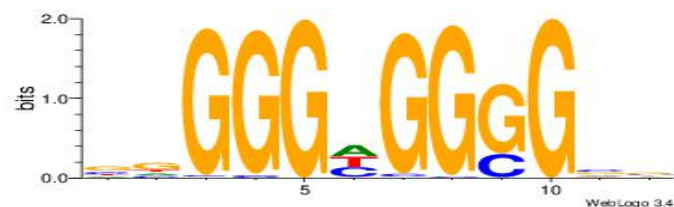
Alignment:

VBCCCCDCCCHV
-----TCCCCV

Original motif Consensus sequence: VBCCCCDCCCHV



Reverse complement motif Consensus sequence: VDGGGDGGGGBV



Dataset #: 3
 Motif ID: 99
 Motif name: MZF1_5-13
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 6
 Similarity score: 0.0375315

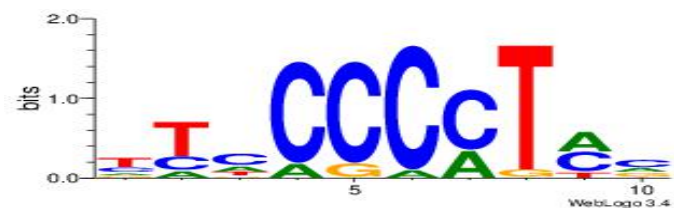
Alignment:

BKAGGGGDAD
 ---BGGGA-

Original motif Consensus sequence: BKAGGGGDAD



Reverse complement motif Consensus sequence: BTHCCCTYB

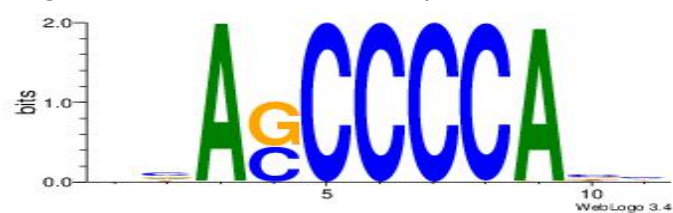


Dataset #: 4
 Motif ID: 162
 Motif name: ccAsCCCCAcc
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 6

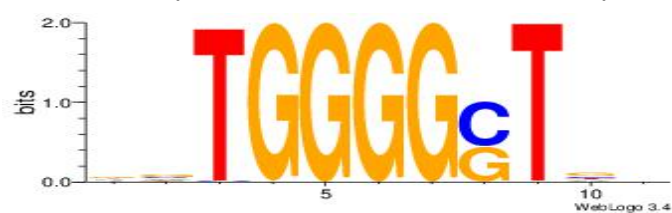
Similarity score: 0.0465466

Alignment:
HVASCCCCABH
---TCCCCV--

Original motif Consensus sequence: HVASCCCCABH



Reverse complement motif Consensus sequence: DBTGGGGSTVD

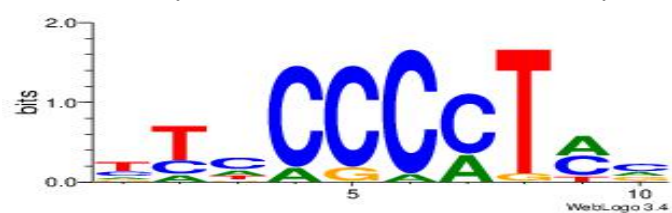


Dataset #: 3 Motif ID: 99 Motif name: MZF1_5-13

Original motif Consensus sequence: BKAGGGGDAD



Reverse complement motif Consensus sequence: BTHCCCTYB



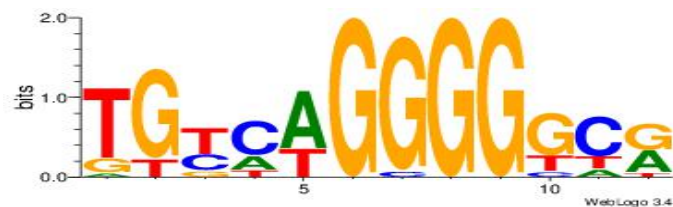
Best Matches for Motif ID 99 (Highest to Lowest)

Dataset #:	3
Motif ID:	88
Motif name:	INSM1
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward

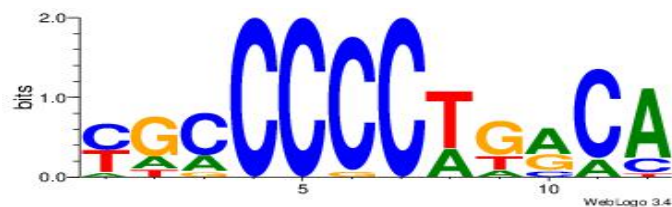
Position number: 1
Number of overlap: 10
Similarity score: 0.0360532

Alignment:
TGYCAGGGGGCR
--BKAGGGGDAD

Original motif Consensus sequence: TGYCAGGGGGCR



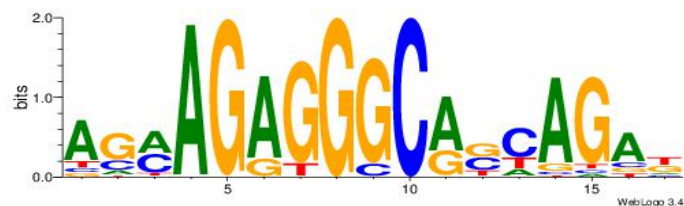
Reverse complement motif Consensus sequence: MGCCCCCTGMCA



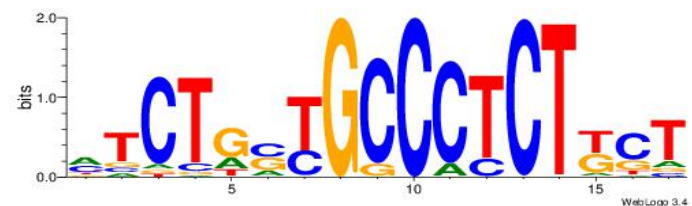
Dataset #: 4
Motif ID: 143
Motif name: AgmAGAGGGCrscAGak
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 7
Number of overlap: 10
Similarity score: 0.0361803

Alignment:
RTCTGSTGCCCTCTYCT
-----BTHCCCCTYB-

Original motif Consensus sequence: AGMAGAGGGCASCAGAK



Reverse complement motif Consensus sequence: RTCTGSTGCCCTCTYCT

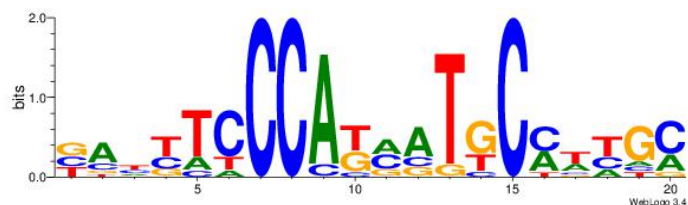


Dataset #: 3
Motif ID: 131
Motif name: znf143
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 3
Number of overlap: 10
Similarity score: 0.0377199

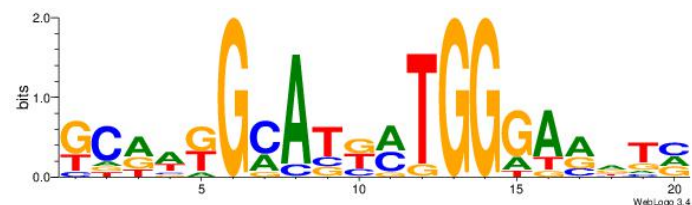
Alignment:

GCMWRGCATYRTGGGAMHTB
-----BKAGGGGDAD--

Original motif Consensus sequence: BAHYTCCCAKMATGCMWYGC



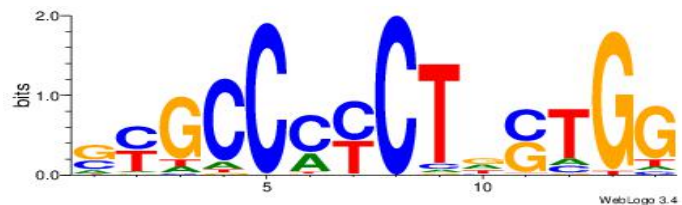
Reverse complement motif Consensus sequence: GCMWRGCATYRTGGGAMHTB



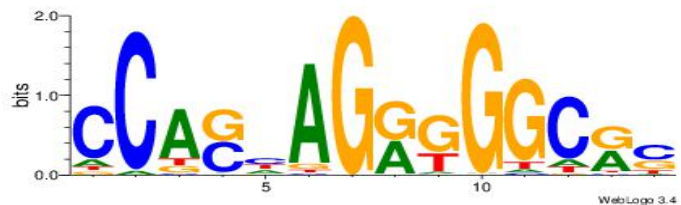
Dataset #: 2
Motif ID: 67
Motif name: Motif 67
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 4
Number of overlap: 10
Similarity score: 0.0386182

Alignment:
CCASHAGKGGGCKS
-BKAGGGGDAD---

Original motif Consensus sequence: SYGCCCCTDSTGG



Reverse complement motif Consensus sequence: CCASHAGKGGGCKS

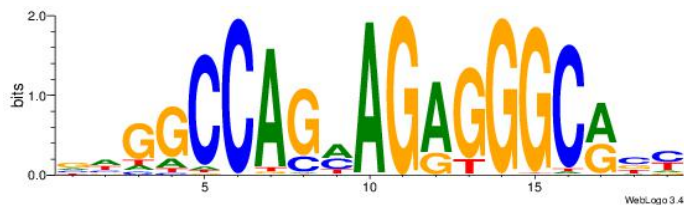


Dataset #: 4
Motif ID: 163
Motif name: gwGGCCAGmAGAGGGCrby
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 3
Number of overlap: 10

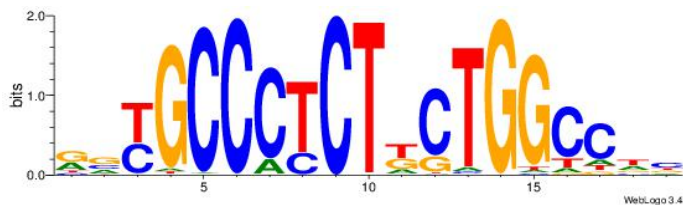
Similarity score: 0.0397537

Alignment:
KBKGCCCTCTYCTGGCCHV
--BTHCCCCTYB-----

Original motif Consensus sequence: VHGGCCAGMAGAGGGCRBY



Reverse complement motif Consensus sequence: KBKGCCCTCTYCTGGCCHV



Dataset #: 3 Motif ID: 100 Motif name: NFE2L2

Original motif Consensus sequence: RTGACWHAGCA



Reverse complement motif Consensus sequence: TGCTDWGTCAK



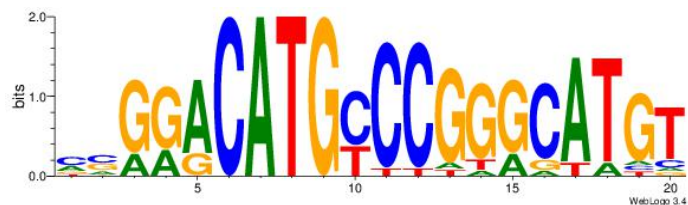
Best Matches for Motif ID 100 (Highest to Lowest)

Dataset #:	3
Motif ID:	125
Motif name:	TP53
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement

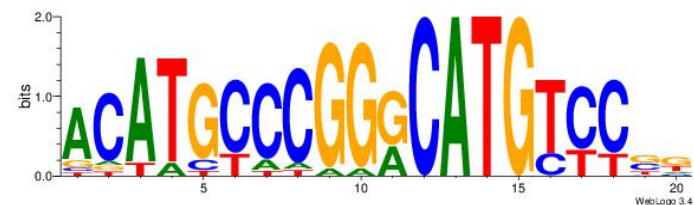
Direction: Forward
 Position number: 4
 Number of overlap: 11
 Similarity score: 0.0588881

Alignment:
 ACATGCCCGGKCATGTCCSR
 ---TGCTDWGTCAK-----

Original motif Consensus sequence: MSGGACATGYCCGGGCATGT



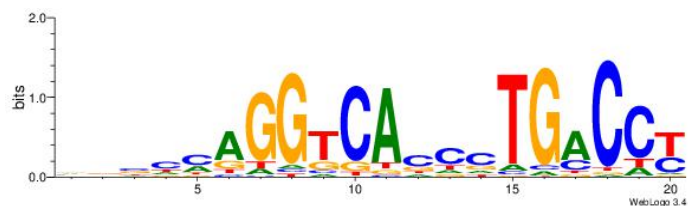
Reverse complement motif Consensus sequence: ACATGCCCGGKCATGTCCSR



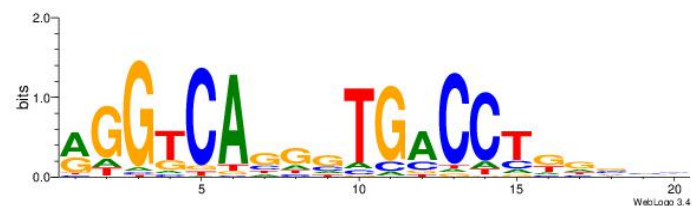
Dataset #: 3
 Motif ID: 81
 Motif name: ESR1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 11
 Similarity score: 0.0627853

Alignment:
 VDBHMAGGTCACCCTGACCY
 -----TGCTDWGTCAK-

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



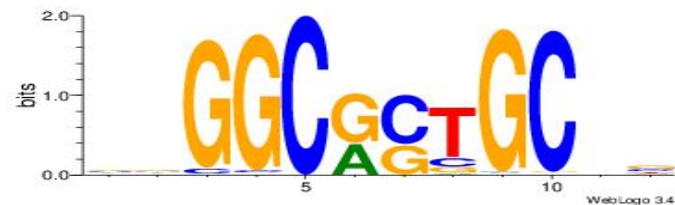
Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV



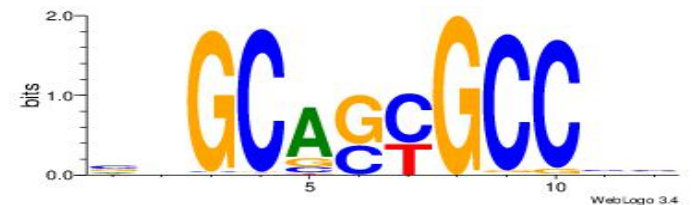
Dataset #: 4
Motif ID: 170
Motif name: ssGGCrSTGCrs
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 11
Similarity score: 0.0672435

Alignment:
VVGGRSTGCVB
RTGACWHAGCA-

Original motif Consensus sequence: VVGGRSTGCVB



Reverse complement motif Consensus sequence: BVGCASMGCCVV

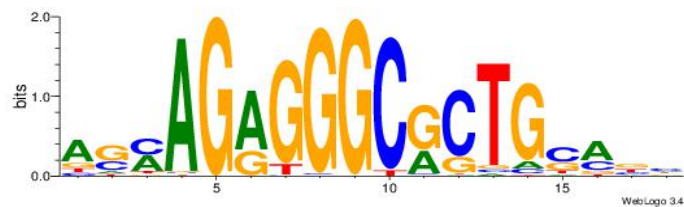


Dataset #: 4
 Motif ID: 149
 Motif name: asmAGRGGGCrCTGsmkc
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 6
 Number of overlap: 11
 Similarity score: 0.070397

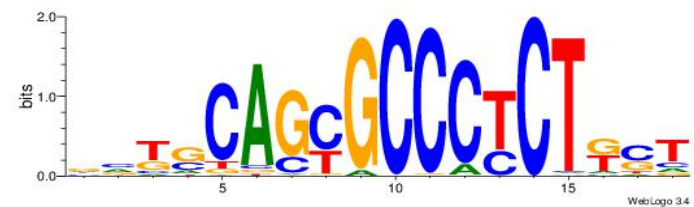
Alignment:

ASMAGAGGGCRCTGSABH
 -----RTGACWHAGCA--

Original motif Consensus sequence: ASMAGAGGGCRCTGSABH



Reverse complement motif Consensus sequence: DBTSCAGMGCCCTCTRST

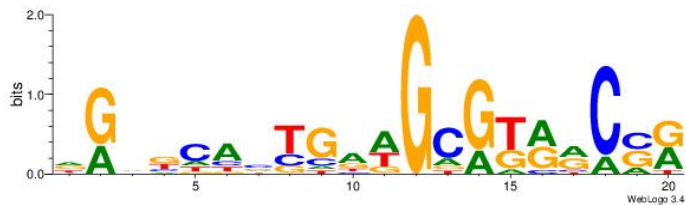


Dataset #: 3
 Motif ID: 109
 Motif name: Pax5
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 8

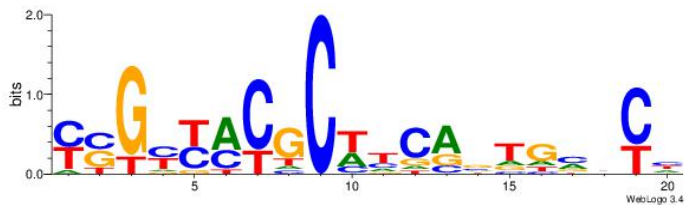
Number of overlap: 11
Similarity score: 0.0725913

Alignment:
MSGKKRCGCWDCABTGGBCD
--RTGACWHAGCA-----

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGGBCD



Dataset #: 3 Motif ID: 101 Motif name: NFIC

Original motif Consensus sequence: TTGGCD



Reverse complement motif Consensus sequence: DGCCAA



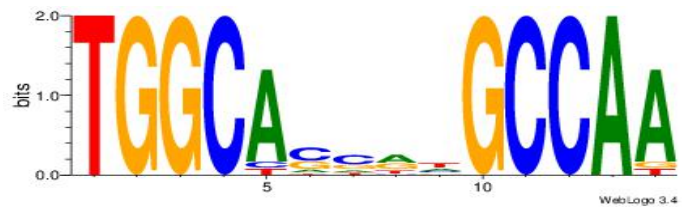
Best Matches for Motif ID 101 (Highest to Lowest)

Dataset #: 3
Motif ID: 124
Motif name: TLX1NFIC
Matching format of first motif: Original Motif

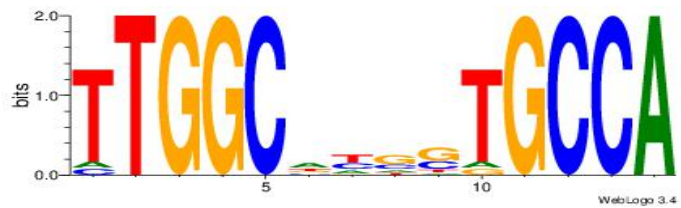
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 6
Similarity score: 0

Alignment:
TTGGCHDBSTGCCA
TTGGCD-----

Original motif Consensus sequence: TGGCASBDHGCCAA



Reverse complement motif Consensus sequence: TTGGCHDBSTGCCA



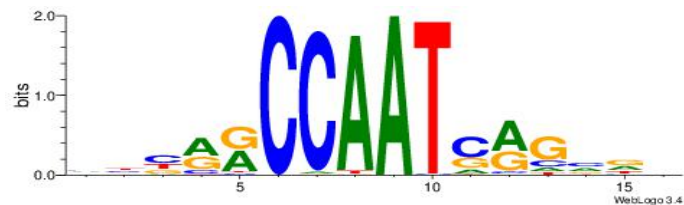
Dataset #: 3
Motif ID: 104
Motif name: NFYA
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 4
Number of overlap: 6
Similarity score: 0.020508

Alignment:

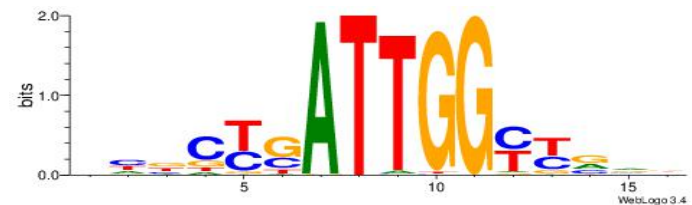
VBBRRCCAATSRGVDB

---DGCCAA-----

Original motif Consensus sequence: VBBRRCCAATSRGVDB



Reverse complement motif Consensus sequence: BHVCKSATTGGMKBVV



Dataset #:	4
Motif ID:	165
Motif name:	wgGCCAshAGrGGGCrSy
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	12
Number of overlap:	6
Similarity score:	0.0215379

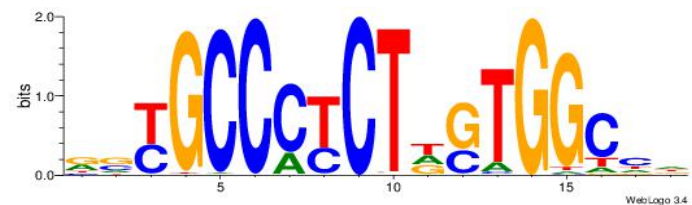
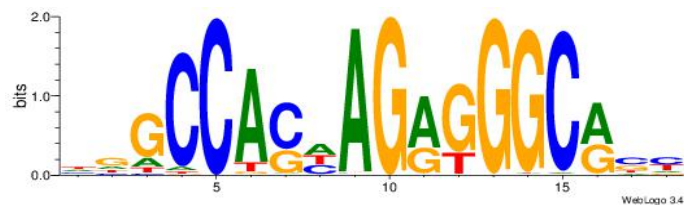
Alignment:

HDGCCACHAGRGGGCRBY

---DGCCAA-----

Original motif Consensus sequence: HDGCCACHAGRGGGCRBY

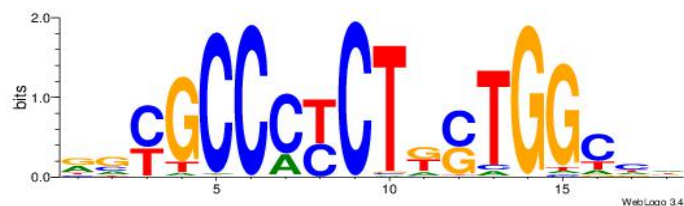
Reverse complement motif Consensus sequence: KBKGCCCKCTHGTGGCHH



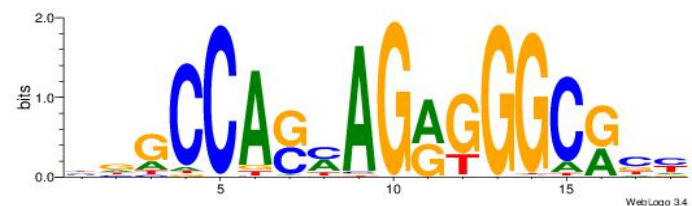
Dataset #: 4
 Motif ID: 156
 Motif name: rgyGCCMyCTksTGGccd
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 12
 Number of overlap: 6
 Similarity score: 0.026631

Alignment:
 DDGCCASYAGMGGGCKVM
 -DGCCAA-----

Original motif Consensus sequence: RVYGCCCYCTKSTGGCHD



Reverse complement motif Consensus sequence: DDGCCASYAGMGGGCKVM



Dataset #: 4

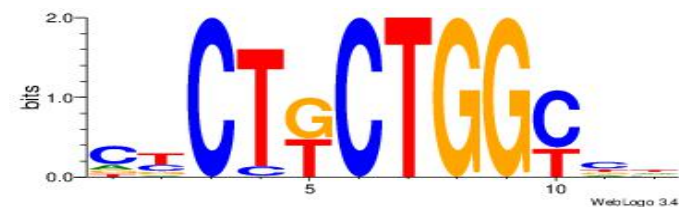
Motif ID: 151
 Motif name: agrCCAGmAGrg
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 6
 Similarity score: 0.0273632

Alignment:
 CKCTRCTGGCVH
 -----TTGGCD-

Original motif Consensus sequence: HVGCCAGMAGRG



Reverse complement motif Consensus sequence: CKCTRCTGGCVH



Dataset #: 3 Motif ID: 102 Motif name: NF-kappaB

Original motif Consensus sequence: GGGRMTTYCC



Reverse complement motif Consensus sequence: GGMAAYKCCC



Best Matches for Motif ID 102 (Highest to Lowest)

Dataset #: 3
Motif ID: 112
Motif name: RELA
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: 0.0219591

Alignment:

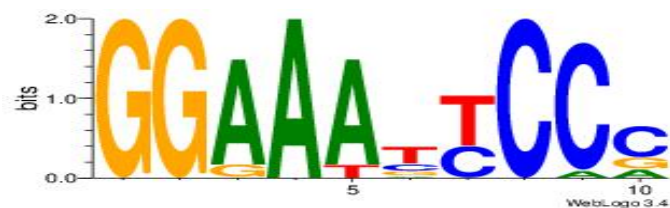
GGGRATTTC

GGGRMTTYCC

Original motif Consensus sequence: GGGRATTTC



Reverse complement motif Consensus sequence: GGAAATKCCC



Dataset #: 3
Motif ID: 103
Motif name: NFKB1
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: 0.0264912

Alignment:
GGGGRTTCCCC
GGRMTTYCC-

Original motif Consensus sequence: GGGGRTTCCCC



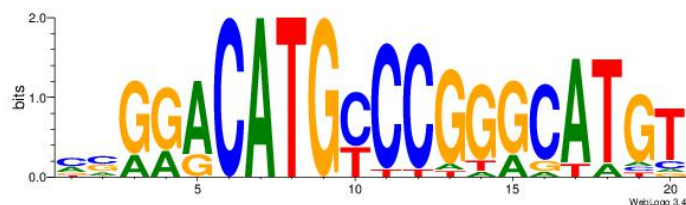
Reverse complement motif Consensus sequence: GGGGAATCCCC



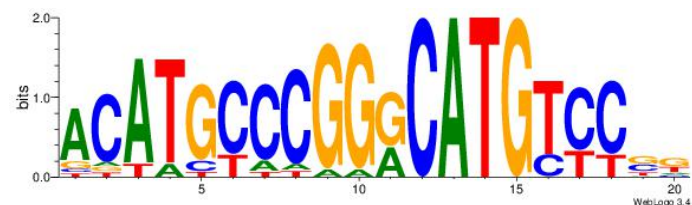
Dataset #: 3
Motif ID: 125
Motif name: TP53
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 9
Number of overlap: 10
Similarity score: 0.0780263

Alignment:
MSGGACATGYCCGGGCATGT
--GGMAAYKCCC-----

Original motif Consensus sequence: MSGGACATGYCCGGGCATGT



Reverse complement motif Consensus sequence:
ACATGCCCCGKCATGTCCSR

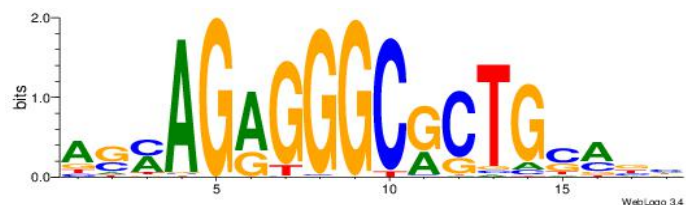


Dataset #: 4
Motif ID: 149
Motif name: asmAGRGGGCrCTGsmkc
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 7
Number of overlap: 10
Similarity score: 0.078539

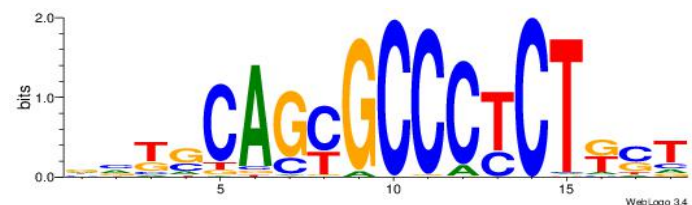
Alignment:

DBTSCAGMGCCCTCTRST
--GGMAAYKCCC-----

Original motif Consensus sequence: ASMAGAGGGCRCTGSABH



Reverse complement motif Consensus sequence:
DBTSCAGMGCCCTCTRST

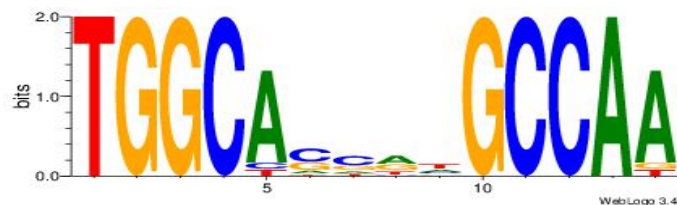


Dataset #: 3
 Motif ID: 124
 Motif name: TLX1NFIC
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 10
 Similarity score: 0.0847697

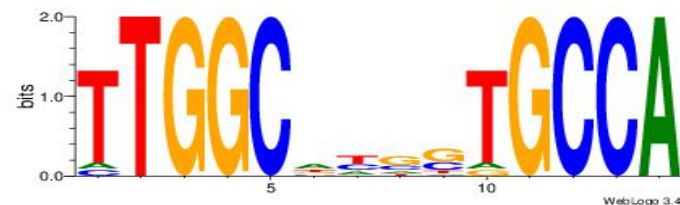
Alignment:

TGGCASBDHGCCAA
 -GGMAAYKCCC---

Original motif Consensus sequence: TGGCASBDHGCCAA



Reverse complement motif Consensus sequence: TTGGCHDBSTGCC



Dataset #: 3 Motif ID: 103 Motif name: NFKB1

Original motif Consensus sequence: GGGGRTTCCC



Reverse complement motif Consensus sequence: GGGGAATCCC



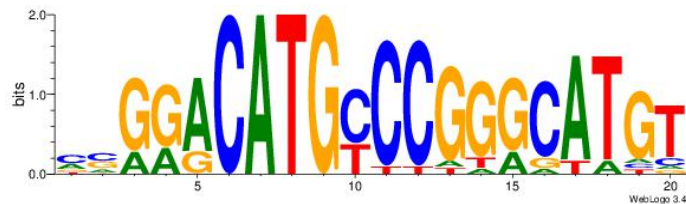
Best Matches for Motif ID 103 (Highest to Lowest)

Dataset #: 3
Motif ID: 125
Motif name: TP53
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: 0.100899

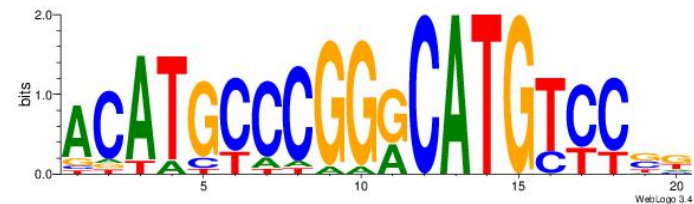
Alignment:

MSGGACATGYCCGGGCATGT
-GGGGAACKCCCC-----

Original motif Consensus sequence: MSGGACATGYCCGGGCATGT



Reverse complement motif Consensus sequence:
ACATGCCCGGKCATGTCCSR

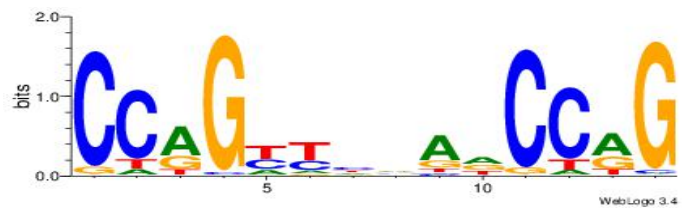


Dataset #: 3
Motif ID: 122
Motif name: Tcfcp2l1
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement

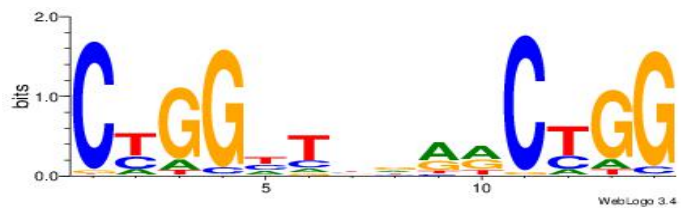
Direction: Backward
Position number: 4
Number of overlap: 11
Similarity score: 0.103405

Alignment:
CKGGDTBDMMCTGG
GGGGRTTCCCC---

Original motif Consensus sequence: CCAGYYHVADCCRG



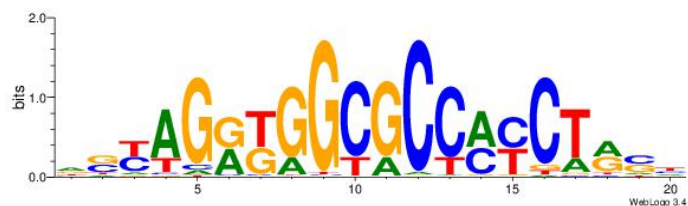
Reverse complement motif Consensus sequence: CKGGDTBDMMCTGG



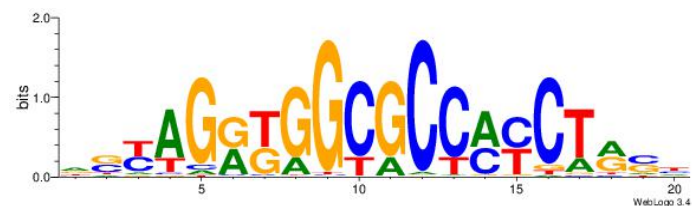
Dataset #: 4
Motif ID: 167
Motif name: rsyAGrkGGCGCCmyCTrsy
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 5
Number of overlap: 11
Similarity score: 0.104275

Alignment:
DSYAGRKGGCGCCMYCTRSH
-----GGGGRTTCCCC-----

Original motif Consensus sequence: DSYAGRKGCGCCMYCTRSH



Reverse complement motif Consensus sequence: HSKAGKYGGCGCCRMCTMSD

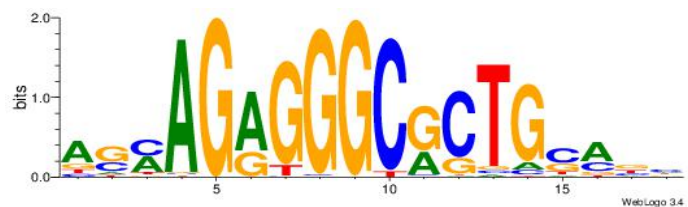


Dataset #: 4
Motif ID: 149
Motif name: asmAGRGGGCrCTGsmkc
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 11
Similarity score: 0.109809

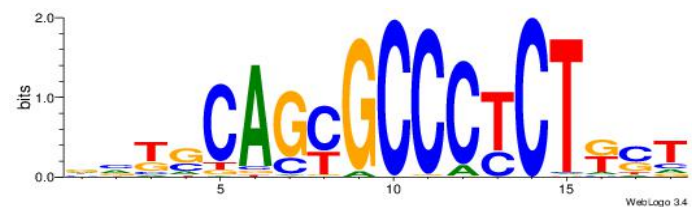
Alignment:

DBTSCAGMGCCCTCTRST
GGGGA AKCCCC-----

Original motif Consensus sequence: ASMAGAGGGCRCTGSABH



Reverse complement motif Consensus sequence: DBTSCAGMGCCCTCTRST



Dataset #: 3
 Motif ID: 117
 Motif name: Spz1
 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: 0.11048

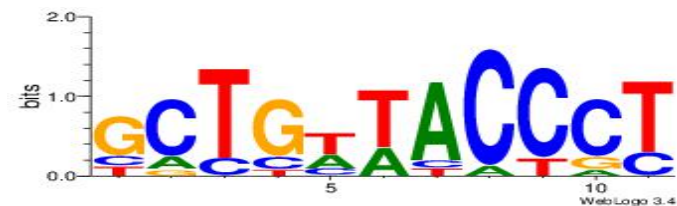
Alignment:

AGGGTAWCAGC
 GGGGAACCCCC

Original motif Consensus sequence: AGGGTAWCAGC



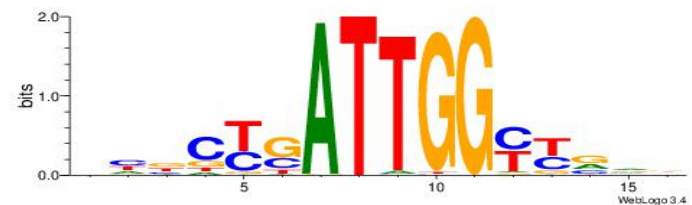
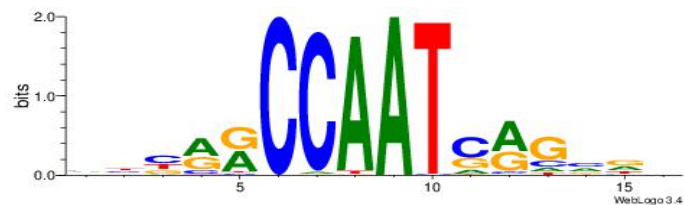
Reverse complement motif Consensus sequence: GCTGWTACCCT



Dataset #: 3 Motif ID: 104 Motif name: NFYA

Original motif Consensus sequence: VBBRCCAATSRGVDB

Reverse complement motif Consensus sequence:
BHVCKSATTGGMKBVV



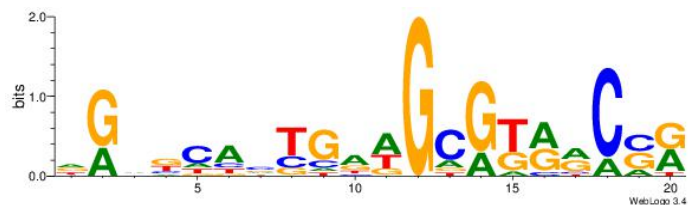
Best Matches for Motif ID 104 (Highest to Lowest)

Dataset #: 3
 Motif ID: 109
 Motif name: Pax5
 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: 0.0555608

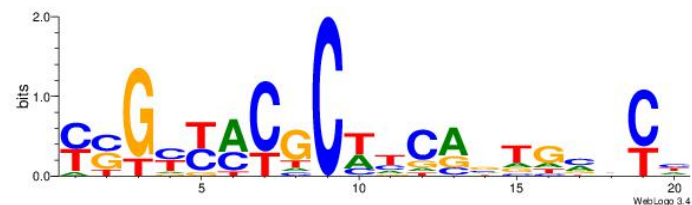
Alignment:

MSGKKRCGCWDCABTGBBCD
 -VBBRCCAATSRGVDB---

Original motif Consensus sequence: DGVBCABTGDWCGKRRCSR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD

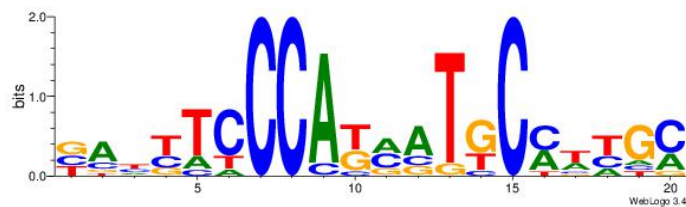


Dataset #: 3
 Motif ID: 131
 Motif name: znf143
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 16
 Similarity score: 0.0645227

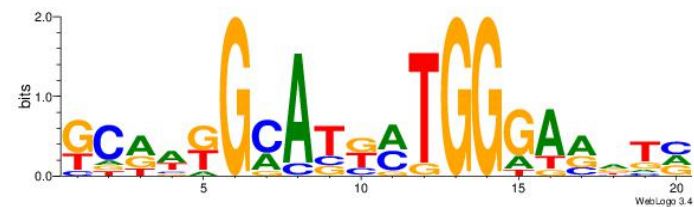
Alignment:

BAHYTCCCAKMATGCMWYGC
 -VBBRRCCAATSRGVDB---

Original motif Consensus sequence: BAHYTCCCAKMATGCMWYGC



Reverse complement motif Consensus sequence: GCMWRGCATYRTGGGAMHTB



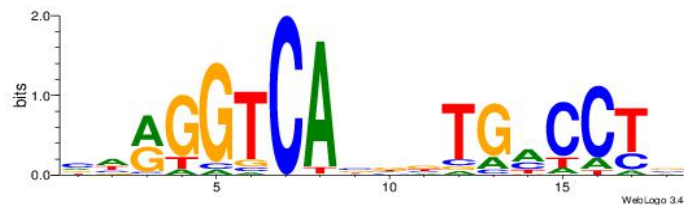
Dataset #: 3
 Motif ID: 82
 Motif name: ESR2
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3

Number of overlap: 16
Similarity score: 0.0658537

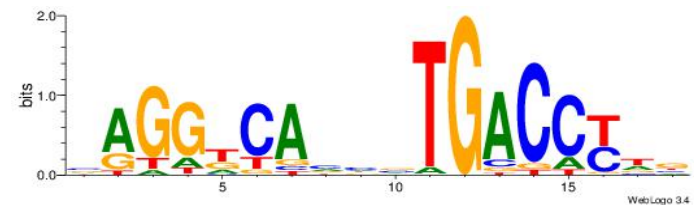
Alignment:

BAGGYCABHBTGACCKHV
--BHVCKSATTTGGMKBVV

Original motif Consensus sequence: VHRGGTCABDBTGMCCCTB



Reverse complement motif Consensus sequence: BAGGYCABHBTGACCKHV

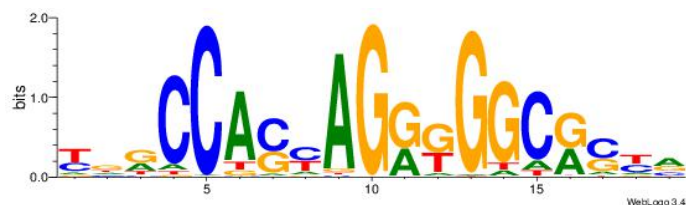


Dataset #: 3
Motif ID: 74
Motif name: CTCF
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 2
Number of overlap: 16
Similarity score: 0.0705004

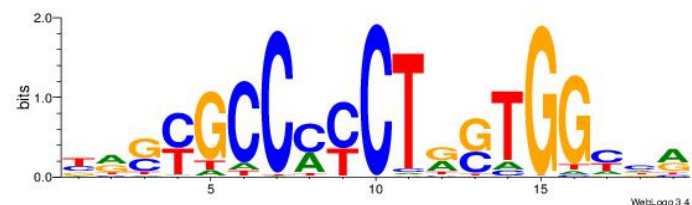
Alignment:

BMSMGCCYMCTKSTGGMHM
--BHVCKSATTTGGMKBVV--

Original motif Consensus sequence: YDRCCASYAGRKGGRSYV



Reverse complement motif Consensus sequence: BMSMGCCYMCTKSTGGMHM

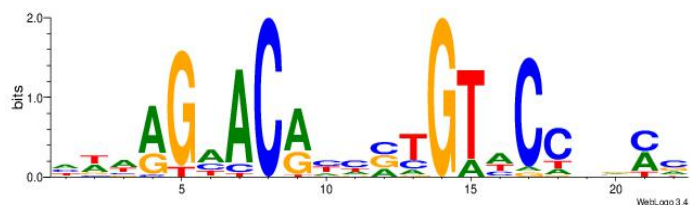


Dataset #: 3
 Motif ID: 70
 Motif name: Ar
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 16
 Similarity score: 0.0709164

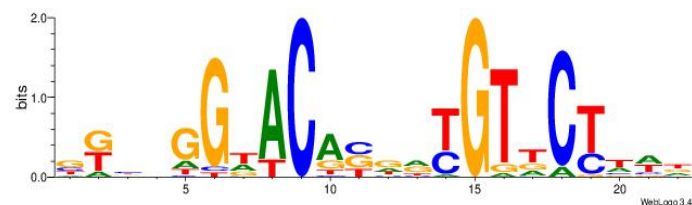
Alignment:

VRVDGGHACAVDDKGTHTDWH
 ----VBBRCCAATSRGVDB--

Original motif Consensus sequence: HWDAGHACRHHVTGTHCCHVMV

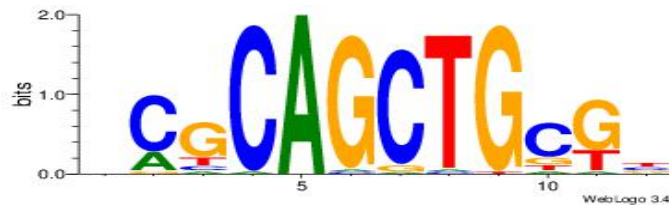


Reverse complement motif Consensus sequence: VRVDGGHACAVDDKGTHTDWH

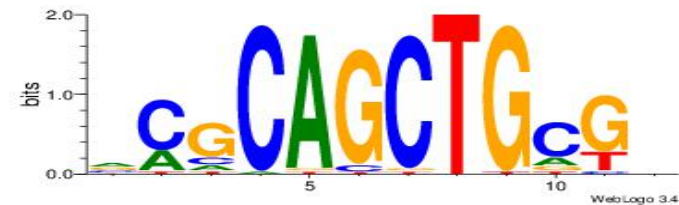


Dataset #: 3 Motif ID: 105 Motif name: NHLH1

Original motif Consensus sequence: VCGCAGCTGCGB



Reverse complement motif Consensus sequence: VCGCAGCTGCGV

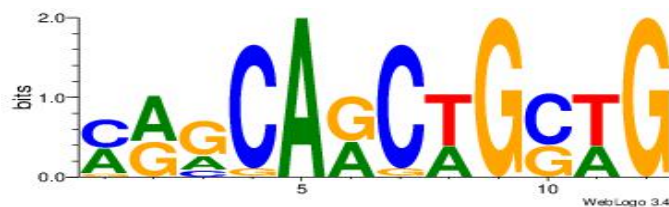


Best Matches for Motif ID 105 (Highest to Lowest)

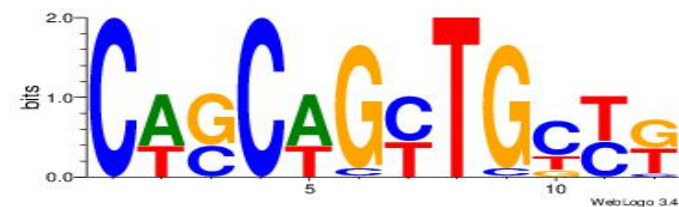
Dataset #:	3
Motif ID:	97
Motif name:	Myf
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	12
Similarity score:	0.0173692

Alignment:
 CWSCWGMTGCKR
 VCGCAGCTGCGV

Original motif Consensus sequence: MRGCARCWGSWG



Reverse complement motif Consensus sequence: CWSCWGMTGCKR

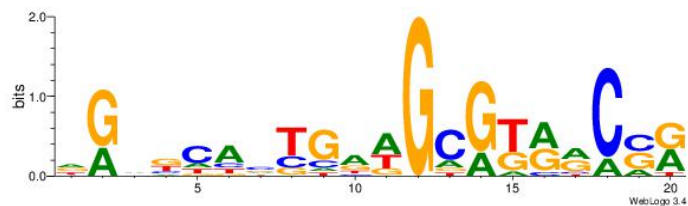


Dataset #: 3
 Motif ID: 109
 Motif name: Pax5
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 4
 Number of overlap: 12
 Similarity score: 0.0355984

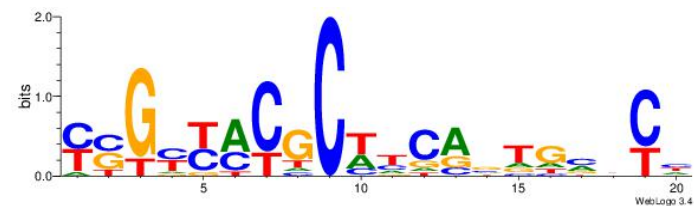
Alignment:

MSGKKRCGCWDCABTGGBCD
 -----VCGCAGCTGCGB---

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGGBCD

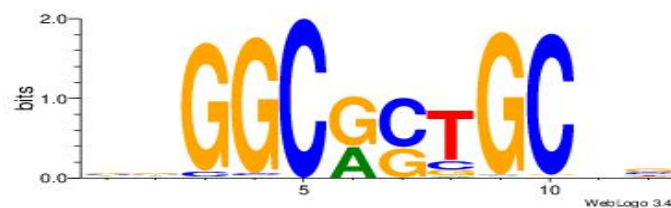


Dataset #: 4
 Motif ID: 170
 Motif name: ssGGCrSTGCRs
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward

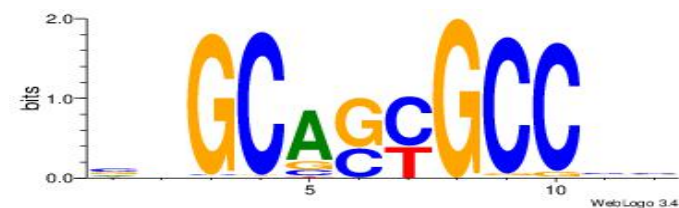
Position number: 1
Number of overlap: 12
Similarity score: 0.0376107

Alignment:
VVGGCRSTGCVB
VCGCAGCTGCGB

Original motif Consensus sequence: VVGGCRSTGCVB



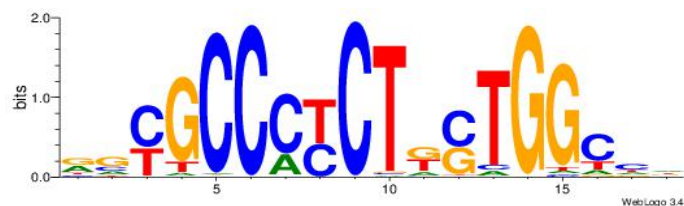
Reverse complement motif Consensus sequence: BVGCASMGCCV



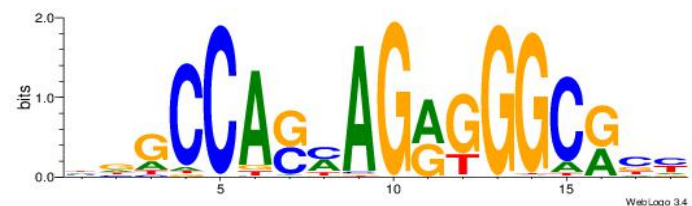
Dataset #: 4
Motif ID: 156
Motif name: rgyGCCMyCTksTGGccd
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 2
Number of overlap: 12
Similarity score: 0.0465866

Alignment:
DDGCCASYAGMGGGCKVM
-VCGCAGCTGCGV-----

Original motif Consensus sequence: RVYGCCCYCTKSTGGCHD



Reverse complement motif Consensus sequence: DDGCCASYAGMGGGCKVM

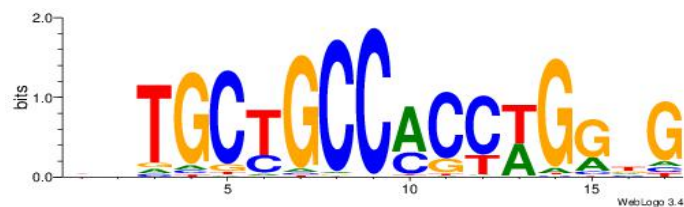


Dataset #: 4
Motif ID: 169
Motif name: yvTGCyGCCmCCwGgtG
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 2
Number of overlap: 12
Similarity score: 0.0468076

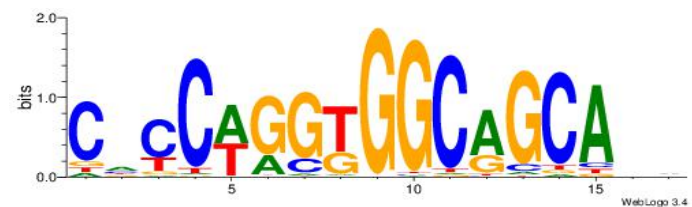
Alignment:

CDCCWGGTGGCAGCAVV
----VCGCAGCTGCGV--

Original motif Consensus sequence: BVTGCTGCCACCWGGDG



Reverse complement motif Consensus sequence: CDCCWGGTGGCAGCAVV



Dataset #: 3 Motif ID: 106 Motif name: Nkx3-2

Original motif Consensus sequence: BTRAGTGVV



Reverse complement motif Consensus sequence: BVCACTKAH



Best Matches for Motif ID 106 (Highest to Lowest)

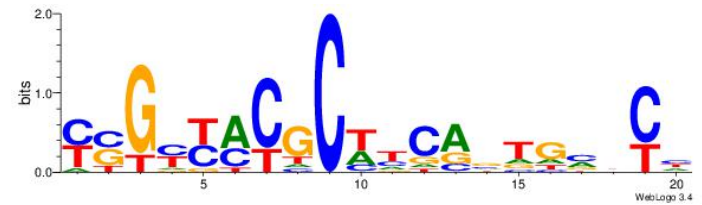
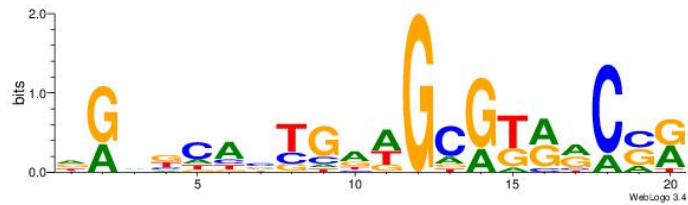
Dataset #:	3
Motif ID:	109
Motif name:	Pax5
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	8
Number of overlap:	9
Similarity score:	0.0239583

Alignment:

```
MSGKKRCGCWDCABTGBCD
----BVCACTKAH-----
```

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR

Reverse complement motif Consensus sequence:
MSGKKRCGCWDCABTGBCD

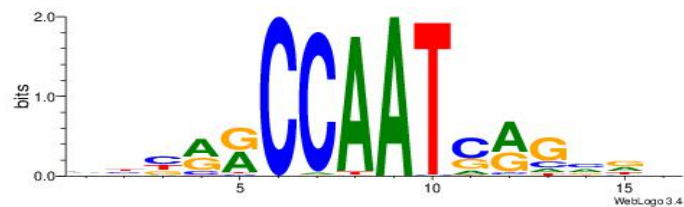


Dataset #: 3
 Motif ID: 104
 Motif name: NFYA
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 5
 Number of overlap: 9
 Similarity score: 0.0250758

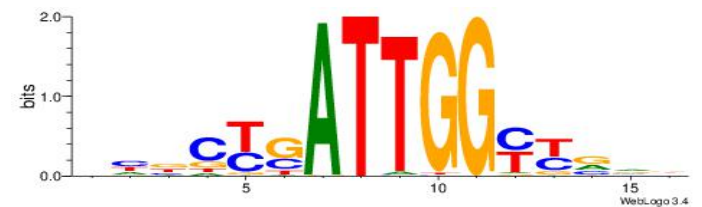
Alignment:

VBBRCCAATSRGVDB
 ---BVCACTKAH----

Original motif Consensus sequence: VBBRCCAATSRGVDB



Reverse complement motif Consensus sequence: BHVCKSATTGGMKBVV



Dataset #: 3

Motif ID: 84
 Motif name: GABPA
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 9
 Similarity score: 0.0255754

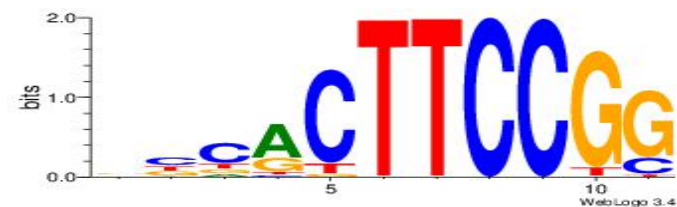
Alignment:

CCGGAAGTGVV
 --BTRAGTGVV

Original motif Consensus sequence: CCGGAAGTGVV



Reverse complement motif Consensus sequence: VVCACTTCGG



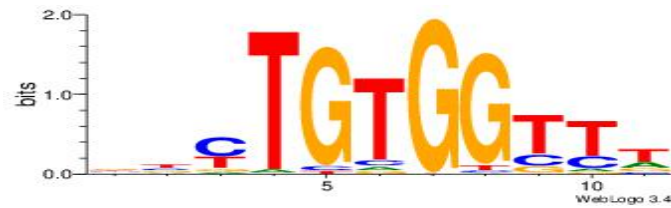
Dataset #: 3
 Motif ID: 114
 Motif name: RUNX1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 9
 Similarity score: 0.0262083

Alignment:

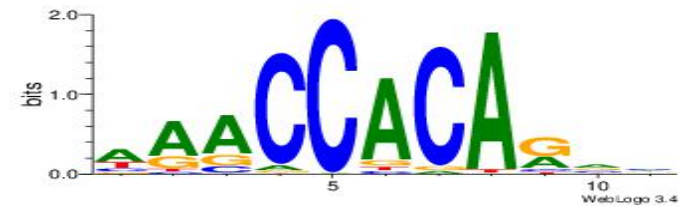
AAACCACAKVB

--BVCACTKAH

Original motif Consensus sequence: BBTGTGGTTT



Reverse complement motif Consensus sequence: AAACCACAKVB



Dataset #:	3
Motif ID:	96
Motif name:	Mycn
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	9
Similarity score:	0.0296502

Alignment:

HSCACGTGGC

-BVCACTKAH

Original motif Consensus sequence: HSCACGTGGC

Reverse complement motif Consensus sequence: GCCACGTGSD



Dataset #: 3 Motif ID: 107 Motif name: NR2F1

Original motif Consensus sequence: TGAMCTTTGMMCYT



Reverse complement motif Consensus sequence: AKGYCAAAGRTCA



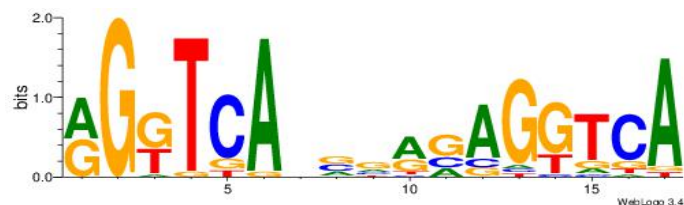
Best Matches for Motif ID 107 (Highest to Lowest)

Dataset #:	3
Motif ID:	115
Motif name:	RXRRAR_DR5
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:	0.0610709

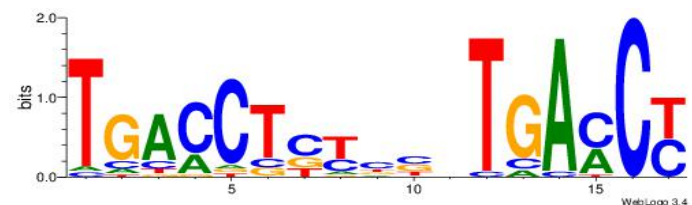
Alignment:

```
RGKTCABVVRGAGGTCA
---AKGYCAAAGRTCA
```

Original motif Consensus sequence: RGKTCABVVRGAGGTCA



Reverse complement motif Consensus sequence: TGACCTCKVVB TGAYCK

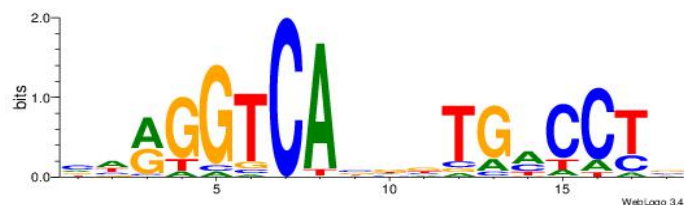


Dataset #: 3
Motif ID: 82
Motif name: ESR2
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2
Number of overlap: 14
Similarity score: 0.0695855

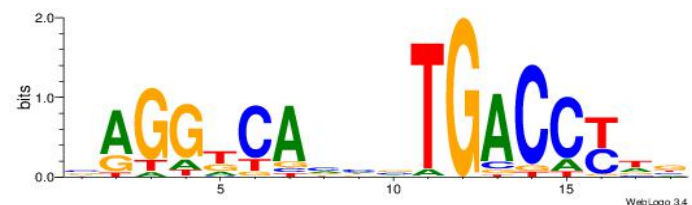
Alignment:

VHRGGTCABDBTGM CCTB
---AKGY YCAAAGRTCA-

Original motif Consensus sequence: VHRGGTCABDBTGM CCTB



Reverse complement motif Consensus sequence: BAGGYCABHBTGACCKHV

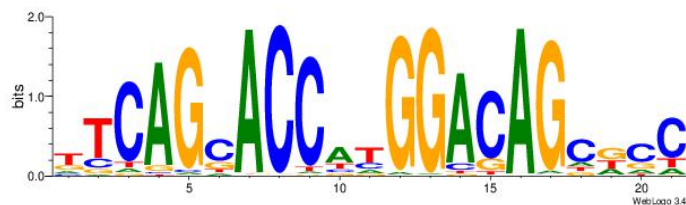


Dataset #: 3
 Motif ID: 113
 Motif name: REST
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 6
 Number of overlap: 14
 Similarity score: 0.0703341

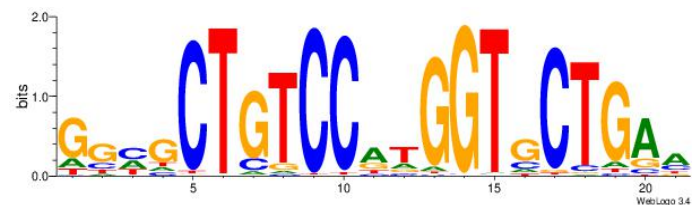
Alignment:

TTCAGCACCATGGACAGCKCC
 --AKGY YCAAAGRTCA-----

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC



Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA



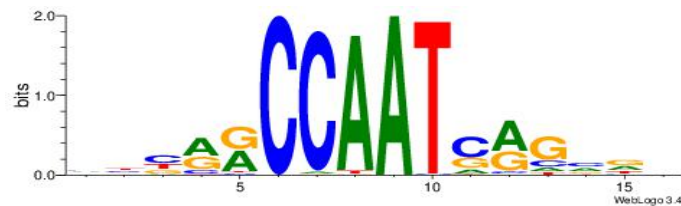
Dataset #: 3
 Motif ID: 104
 Motif name: NFYA
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3

Number of overlap: 14
Similarity score: 0.0715605

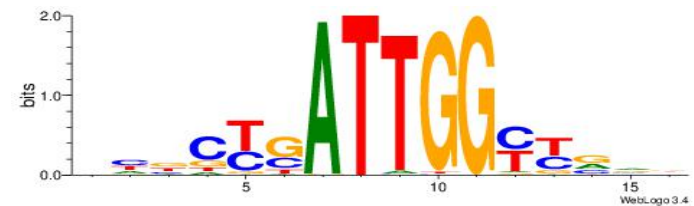
Alignment:

VBBRRCCAATSRGVDB
--TGAMCTTTGMMCYT

Original motif Consensus sequence: VBBRRCCAATSRGVDB



Reverse complement motif Consensus sequence:
BHVCKSATTGGMKBVV

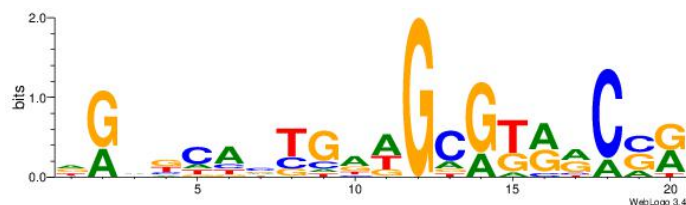


Dataset #: 3
Motif ID: 109
Motif name: Pax5
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 5
Number of overlap: 14
Similarity score: 0.0727368

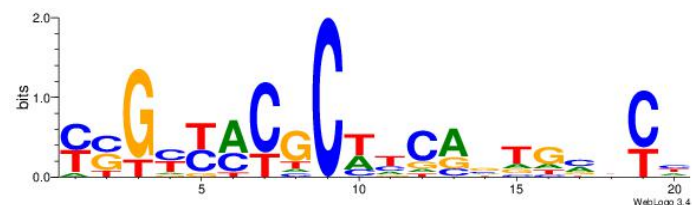
Alignment:

MSGKKRCGCWDCABTGBBCD
----TGAMCTTTGMMCYT--

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBCD



Dataset #: 3 Motif ID: 108 Motif name: NR4A2

Original motif Consensus sequence: AAGGTCAC



Reverse complement motif Consensus sequence: GTGACCTT



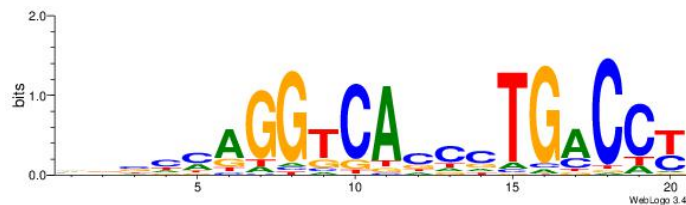
Best Matches for Motif ID 108 (Highest to Lowest)

Dataset #:	3
Motif ID:	81
Motif name:	ESR1
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	5
Number of overlap:	8
Similarity score:	0.0193781

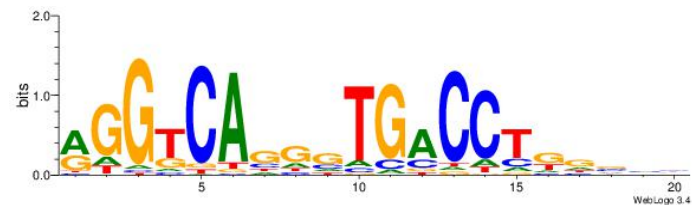
Alignment:

VDBHMAGGTCACCCTGACCY
 ----AAGGTCAC-----

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV

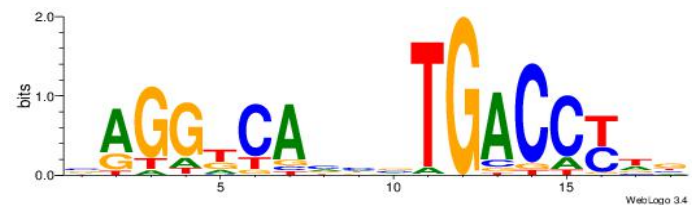
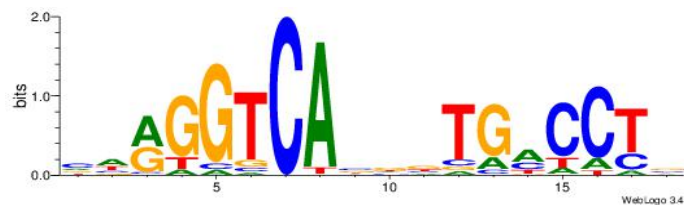


Dataset #: 3
 Motif ID: 82
 Motif name: ESR2
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 10
 Number of overlap: 8
 Similarity score: 0.0196918

Alignment:
 BAGGYCABHBTGACCKHV
 -----GTGACCTT-

Original motif Consensus sequence: VHRGGTCABDBTGMCCCTB

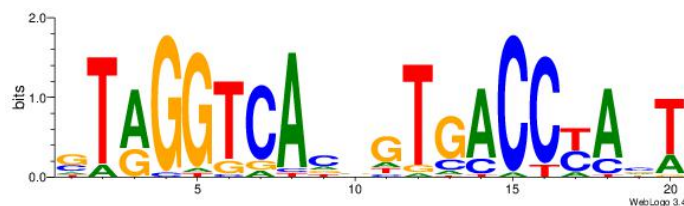
Reverse complement motif Consensus sequence: BAGGYCABHBTGACCKHV



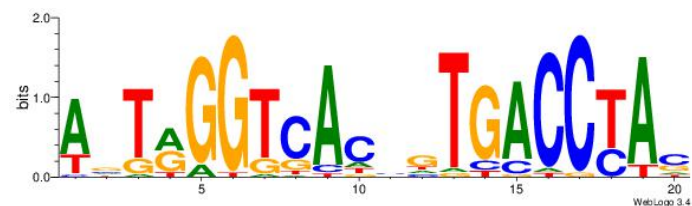
Dataset #: 3
 Motif ID: 111
 Motif name: PPARG
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 12
 Number of overlap: 8
 Similarity score: 0.0275817

Alignment:
 ABTMGGTCACBGTGACCTAS
 -----GTGACCTT-

Original motif Consensus sequence: STAGGTCACBGTGACCYABT



Reverse complement motif Consensus sequence: ABTMGGTCACBGTGACCTAS



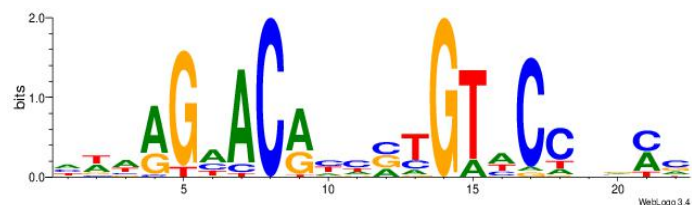
Dataset #: 3

Motif ID: 70
 Motif name: Ar
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 13
 Number of overlap: 8
 Similarity score: 0.0486154

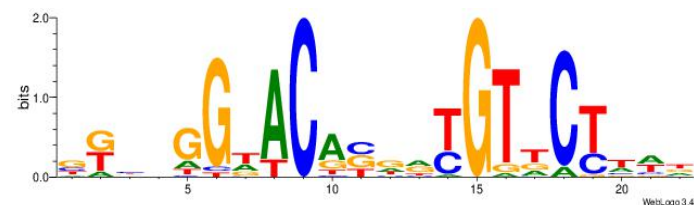
Alignment:

VRVDGGHACAVDDKGTHTDWH
 -----GTGACCTT--

Original motif Consensus sequence: HWDAGHACRHHVTGTHCCHVMV



Reverse complement motif Consensus sequence: VRVDGGHACAVDDKGTHTDWH



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: 8

Similarity score: 0.0525645

Alignment:
CTGGCCTC
GTGACCTT

Original motif Consensus sequence: CTGGCCTC

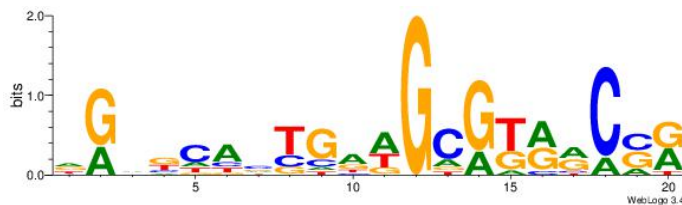


Reverse complement motif Consensus sequence: GAGGCCAG

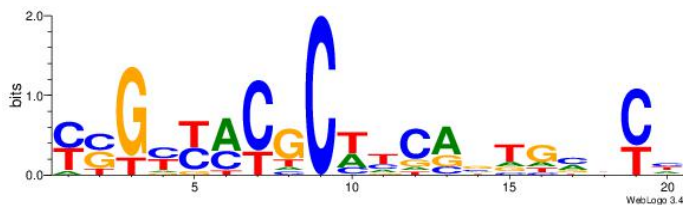


Dataset #: 3 Motif ID: 109 Motif name: Pax5

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD



Best Matches for Motif ID 109 (Highest to Lowest)

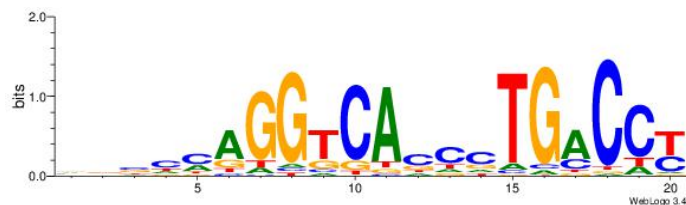
Dataset #:	3
Motif ID:	81
Motif name:	ESR1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement

Direction: Backward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.0458242

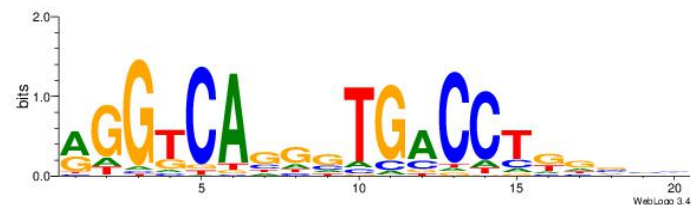
Alignment:

MGGTCAGGGTGACCTRDBHV
 MSGKKRCGCWDCABTGBBCD

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV

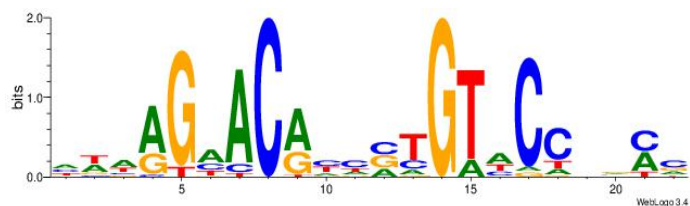


Dataset #: 3
 Motif ID: 70
 Motif name: Ar
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.052658

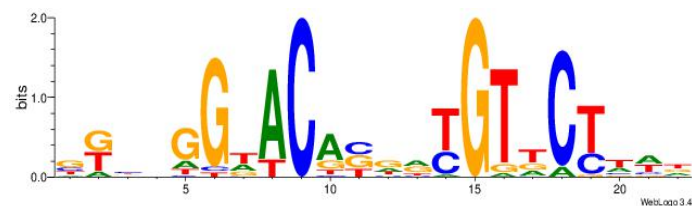
Alignment:

VRVDGGHACAVDDKGTHCTDWH
 --MSGKKRCGCWDCABTGBBCD

Original motif Consensus sequence: HWDAGHACRHHVTGTHCCHVMV



Reverse complement motif Consensus sequence: VRVDGGHACAVDDKGTHCTDWH

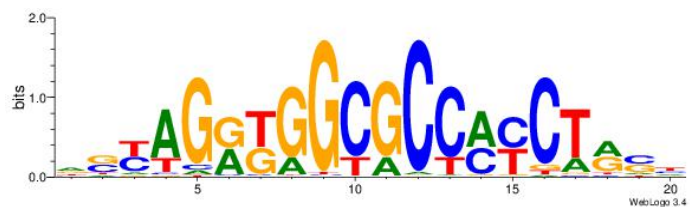


Dataset #: 4
 Motif ID: 167
 Motif name: rsyAGrkGGCGCCmyCTrsy
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.0660509

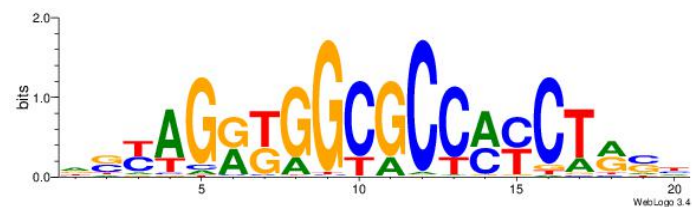
Alignment:

HSKAGKYGGCGCCRMCTMSD
 MSGKKRCGCWDCABTGBCD

Original motif Consensus sequence: DSYAGRKGGCGCCMYCTRSH



Reverse complement motif Consensus sequence: HSKAGKYGGCGCCRMCTMSD

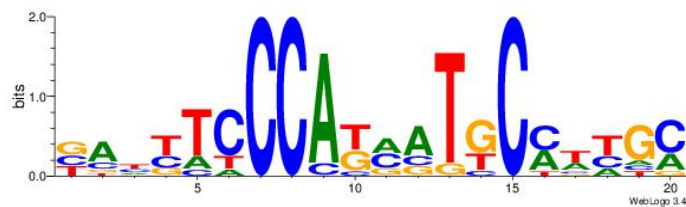


Dataset #: 3
 Motif ID: 131
 Motif name: znf143
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 19
 Similarity score: 0.552768

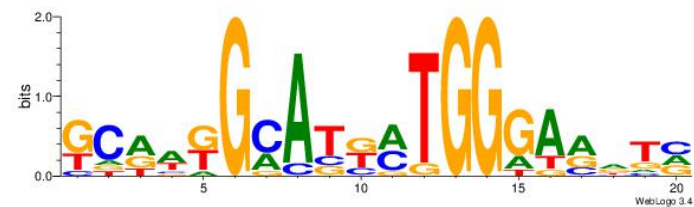
Alignment:

-BAHYTCCCAKMATGCMWYGC
 MSGKKRCGCWDCABTGBCD-

Original motif Consensus sequence: BAHYTCCCAKMATGCMWYGC



Reverse complement motif Consensus sequence: GCMWRGCATYRTGGGAMHTB



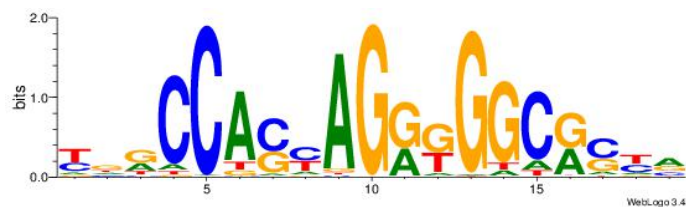
Dataset #: 3
 Motif ID: 74
 Motif name: CTCF
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1

Number of overlap: 19
 Similarity score: 0.559888

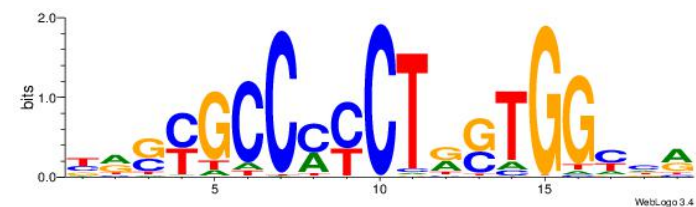
Alignment:

YDRCCASYAGRKGGCRSYV-
 DGVBCABTGDWGCGRRCR

Original motif Consensus sequence: YDRCCASYAGRKGGCRSYV

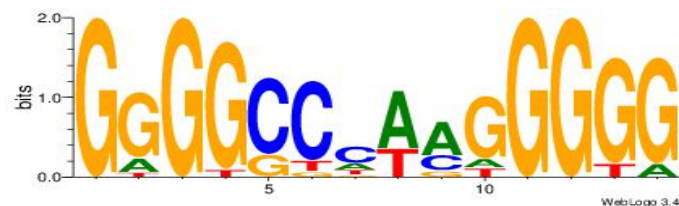


Reverse complement motif Consensus sequence: BMSMGCCYMCTKSTGGMHM

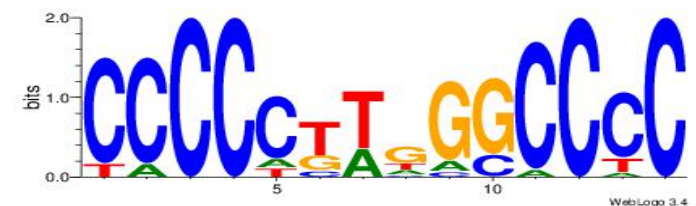


Dataset #: 3 Motif ID: 110 Motif name: PLAG1

Original motif Consensus sequence: GGGGCCAAGGGG



Reverse complement motif Consensus sequence: CCCCCTGGGCC



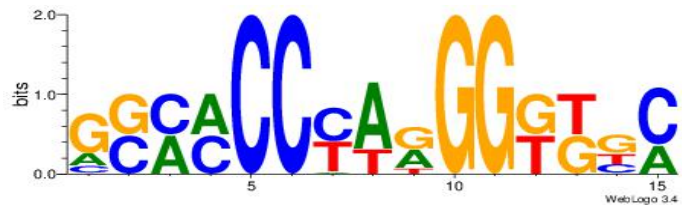
Best Matches for Motif ID 110 (Highest to Lowest)

Dataset #: 3
 Motif ID: 129
 Motif name: Zfp423
 Matching format of first motif: Original Motif

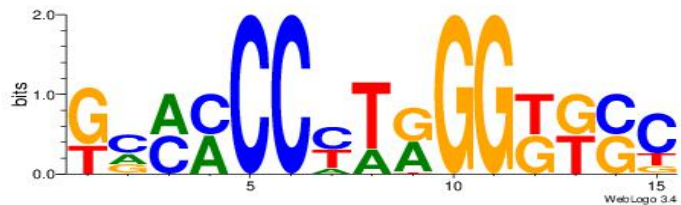
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 14
Similarity score: 0.0944264

Alignment:
GSMCCYARGGKKKC
GGGGCCCAAGGGG-

Original motif Consensus sequence: GSMCCYARGGKKKC



Reverse complement motif Consensus sequence: GYRYCCMTKGGYR



Dataset #: 4
Motif ID: 166
Motif name: CasCAGrGGGCrSy
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: 0.0955683

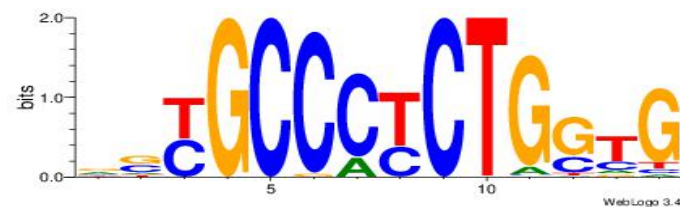
Alignment:

BSKGCCCKCTGGTG
GGGGCCCAAGGGGG

Original motif Consensus sequence: CACCAGRGGGCRSB



Reverse complement motif Consensus sequence: BSKGCCCKCTGGT



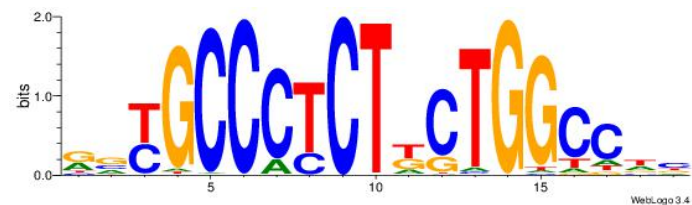
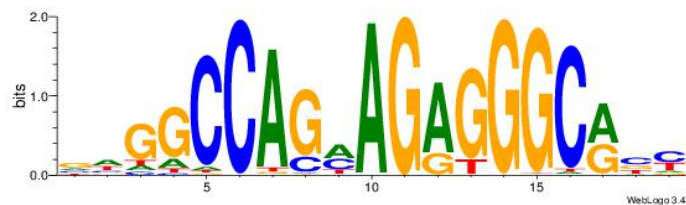
Dataset #: 4
Motif ID: 163
Motif name: gwGGCCAGmAGAGGGCrby
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 6
Number of overlap: 14
Similarity score: 0.0963962

Alignment:

VHGGCCAGMAGAGGGCRBY
GGGGCCCAAGGGGG-----

Original motif Consensus sequence: VHGGCCAGMAGAGGGCRBY

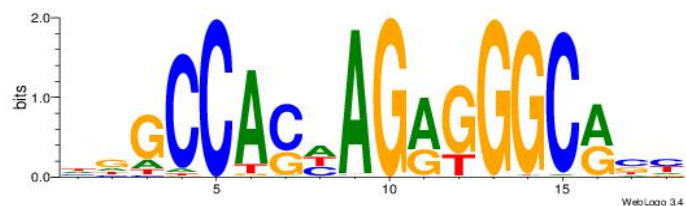
Reverse complement motif Consensus sequence:
KBKGCCCTCTYCTGGCCHV



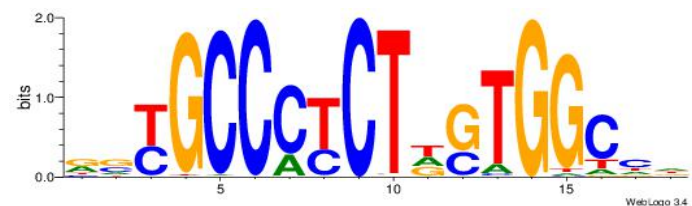
Dataset #: 4
 Motif ID: 165
 Motif name: wgGCCAshAGrGGGCrSy
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0.0984905

Alignment:
 HDGCCACHAGRGGGCRBY
 GGGGCCCAAGGGG-----

Original motif Consensus sequence: HDGCCACHAGRGGGCRBY



Reverse complement motif Consensus sequence: KBKGCCCKCTHGTGGCHH



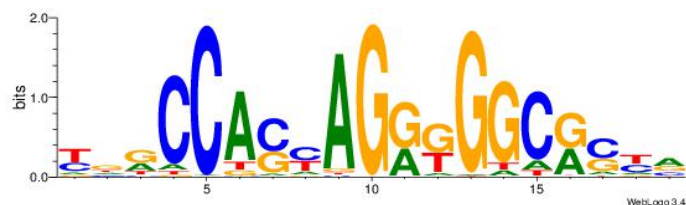
Dataset #: 3

Motif ID: 74
 Motif name: CTCF
 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: 0.0985427

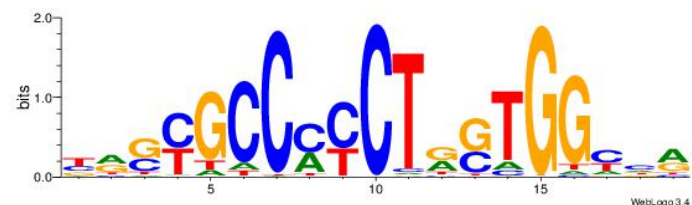
Alignment:

BMSMGCCYMCTKSTGGMHM
 -----CCCCCTTGGGCCCC

Original motif Consensus sequence: YDRCCASYAGRKGGRSYV

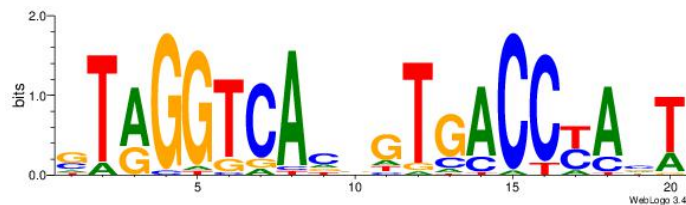


Reverse complement motif Consensus sequence: BMSMGCCYMCTKSTGGMHM

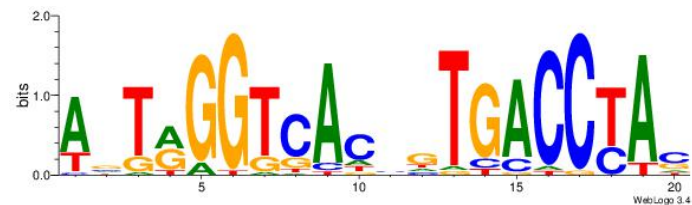


Dataset #: 3 Motif ID: 111 Motif name: PPARG

Original motif Consensus sequence: STAGGTCACBG TGACCYABT



Reverse complement motif Consensus sequence: ABTMGGTCACBG TGACCTAS



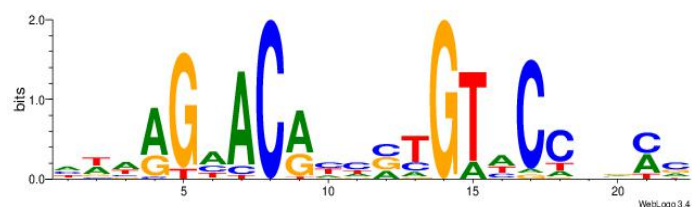
Best Matches for Motif ID 111 (Highest to Lowest)

Dataset #: 3
Motif ID: 70
Motif name: Ar
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 3
Number of overlap: 20
Similarity score: 0.0567628

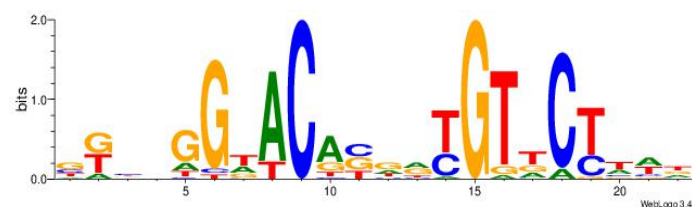
Alignment:

HWDAGHACRHHVTGTHCCHVMV
--ABTMGGTCACBGTGACCTAS

Original motif Consensus sequence: HWDAGHACRHHVTGTHCCHVMV



Reverse complement motif Consensus sequence: VRVDGGHACA VDDKGTHCTDWH

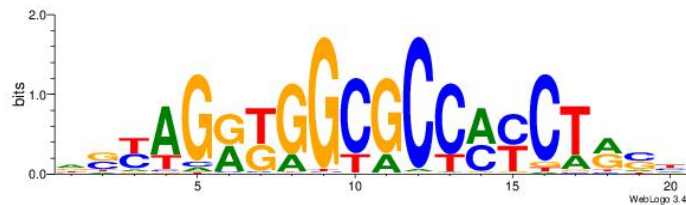


Dataset #: 4
Motif ID: 167
Motif name: rsyAGrkGGCGCCmyCTrsy
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement

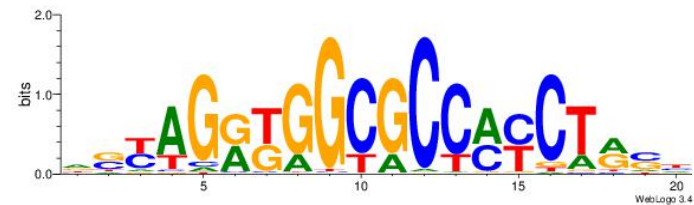
Direction: Forward
 Position number: 2
 Number of overlap: 19
 Similarity score: 0.574193

Alignment:
 HSKAGKYGGCGCCRMCTMSD-
 -STAGGTCACBG TGACCYABT

Original motif Consensus sequence: DSYAGRKGGCGCCMYCTRSH



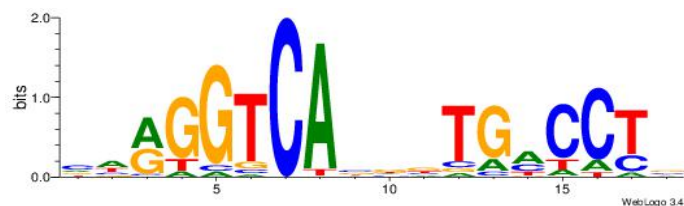
Reverse complement motif Consensus sequence: HSKAGKYGGCGCCRMCTMSD



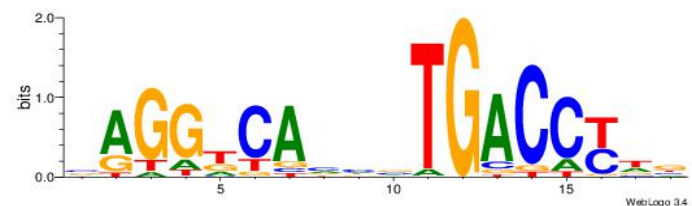
Dataset #: 3
 Motif ID: 82
 Motif name: ESR2
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 18
 Similarity score: 1.00511

Alignment:
 --BAGGYCABHBTGACCKHV
 ABTMGGTCACBG TGACCTAS

Original motif Consensus sequence: VHRGGTCABDBTGMCTB



Reverse complement motif Consensus sequence: BAGGYCABHBTGACCKHV

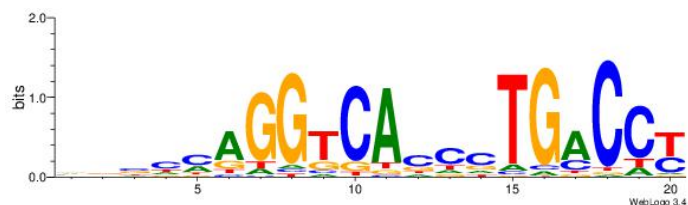


Dataset #: 3
Motif ID: 81
Motif name: ESR1
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 3
Number of overlap: 18
Similarity score: 1.01193

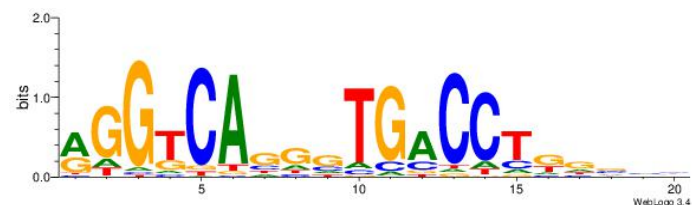
Alignment:

--VDBHMAGGTCACCCTGACCY
ABTMGGTCACBGTGACCTAS--

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV

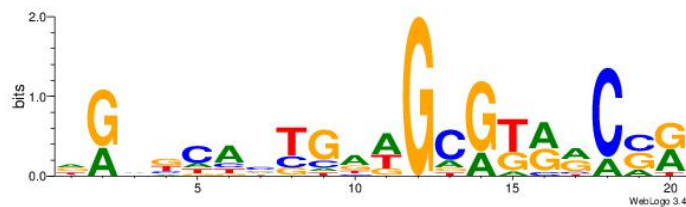


Dataset #: 3
 Motif ID: 109
 Motif name: Pax5
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3
 Number of overlap: 18
 Similarity score: 1.07268

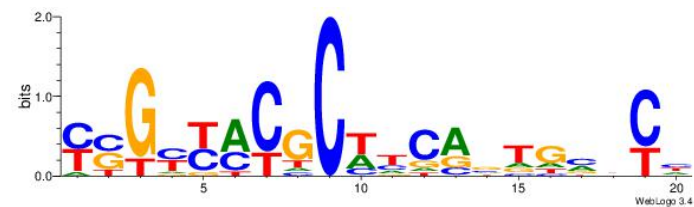
Alignment:

MSGKKRCGCWDCABTGBBCD--
 --STAGGTCACBGTGACCYABT

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR



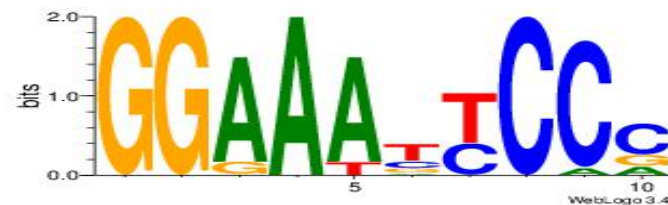
Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD



Dataset #: 3 Motif ID: 112 Motif name: RELA

Original motif Consensus sequence: GGGRATTTCC

Reverse complement motif Consensus sequence: GGAAATKCCC



Best Matches for Motif ID 112 (Highest to Lowest)

Dataset #: 3
 Motif ID: 102
 Motif name: NF-kappaB
 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: 0.00719219

Alignment:

GGMAAYKCCC

GGAAATKCCC

Original motif Consensus sequence: GGGRMTTYCC



Reverse complement motif Consensus sequence: GGMAAYKCCC



Dataset #: 3

Motif ID: 103
 Motif name: NFKB1
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 10
 Similarity score: 0.0283179

Alignment:

GGGGR TTCCCC

GGGRATTTC-

Original motif Consensus sequence: GGGGR TTCCCC



Reverse complement motif Consensus sequence: GGGGA AKCCCC



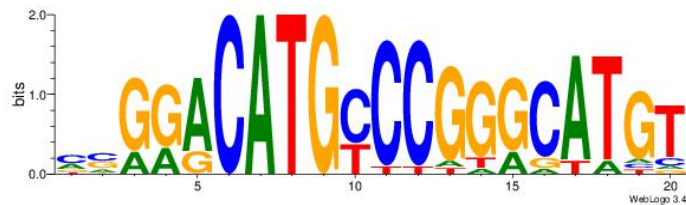
Dataset #: 3
 Motif ID: 125
 Motif name: TP53
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 9
 Number of overlap: 10
 Similarity score: 0.057648

Alignment:

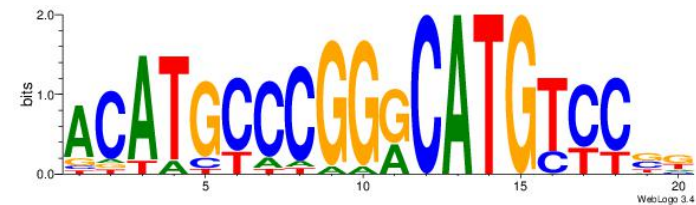
MSGGACATGYCCGGGCATGT

--GGAAATKCCC-----

Original motif Consensus sequence: MSGGACATGYCCGGGCATGT



Reverse complement motif Consensus sequence:
ACATGCCCGGKCATGTCCSR



Dataset #:	3
Motif ID:	113
Motif name:	REST
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	10
Similarity score:	0.0666417

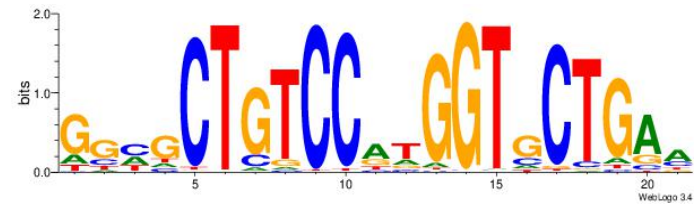
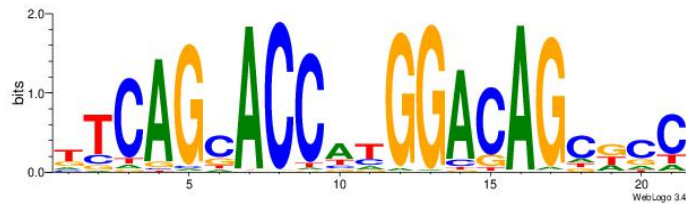
Alignment:

GGYGCTGTCCATGGTGCTGAA

GGGRATTTCC-----

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC

Reverse complement motif Consensus sequence:
GGYGCTGTCCATGGTGCTGAA



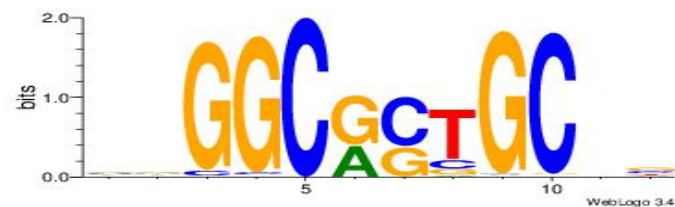
Dataset #: 4
 Motif ID: 170
 Motif name: ssGGCrSTGCrS
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 10
 Similarity score: 0.0784221

Alignment:

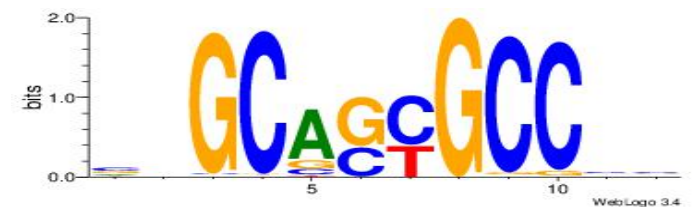
VVGGCRSTGCVB

--GGAAATKCCC

Original motif Consensus sequence: VVGGCRSTGCVB

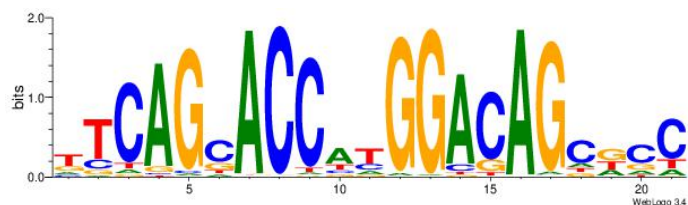


Reverse complement motif Consensus sequence: BVGCASMGCCVV

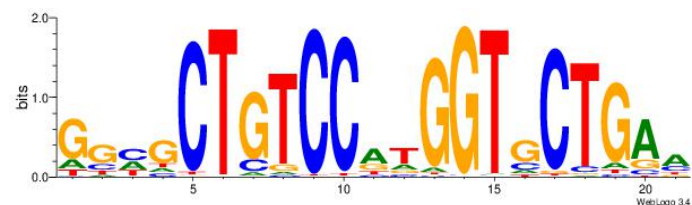


Dataset #: 3 Motif ID: 113 Motif name: REST

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC



Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA



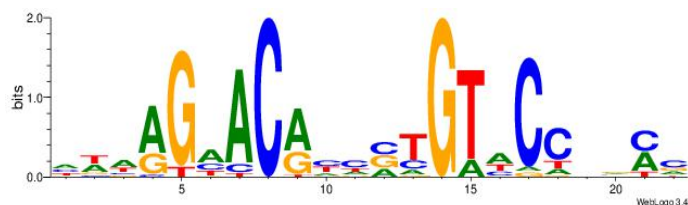
Best Matches for Motif ID 113 (Highest to Lowest)

Dataset #:	3
Motif ID:	70
Motif name:	Ar
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	21
Similarity score:	0.0685835

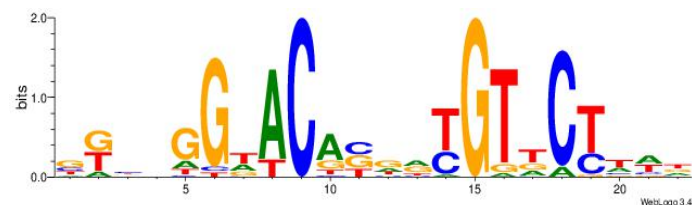
Alignment:

VRVDGGHACAVDDKGTHCTDWH
 -GGYGCTGTCCATGGTGCTGAA

Original motif Consensus sequence: HWDAGHACRHHVTGTHCCHVMV



Reverse complement motif Consensus sequence: VRVDGGHACAVDDKGTHCTDWH

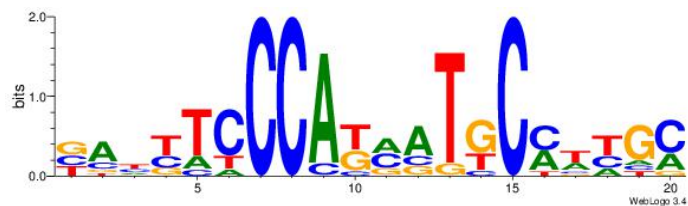


Dataset #: 3
 Motif ID: 131
 Motif name: znf143
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 19
 Similarity score: 1.0683

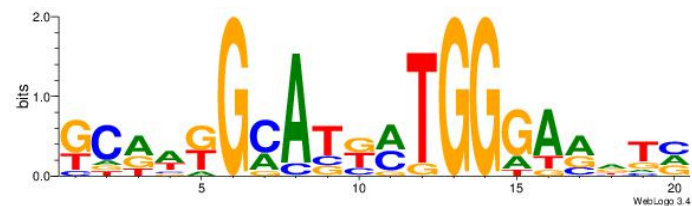
Alignment:

GCMWRGCATYRTGGGAMHTB--
 -TTCAGCACCATGGACAGCKCC

Original motif Consensus sequence: BAHYTCCCAKMATGCMWYGC



Reverse complement motif Consensus sequence: GCMWRGCATYRTGGGAMHTB



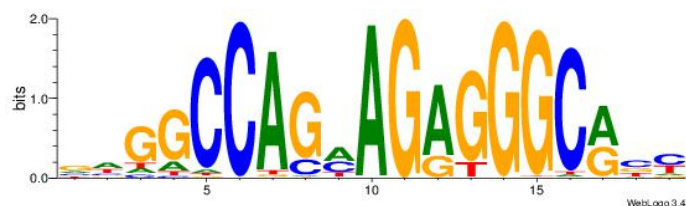
Dataset #: 4
 Motif ID: 163
 Motif name: gwGGCCAGmAGAGGGCrby
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward

Position number: 1
Number of overlap: 19
Similarity score: 1.07477

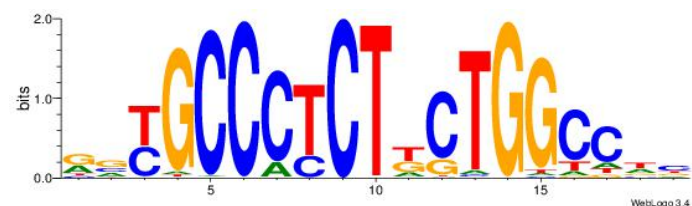
Alignment:

--VHGGCCAGMAGAGGGCRBY
TTCAGCACCATGGACAGCKCC

Original motif Consensus sequence: VHGGCCAGMAGAGGGCRBY



Reverse complement motif Consensus sequence: KBKGCCCTCTYCTGGCCHV

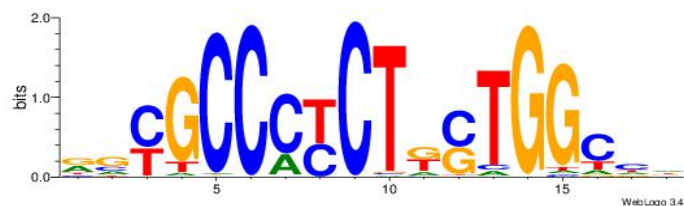


Dataset #: 4
Motif ID: 156
Motif name: rgyGCCMyCTksTGGccd
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 18
Similarity score: 1.57039

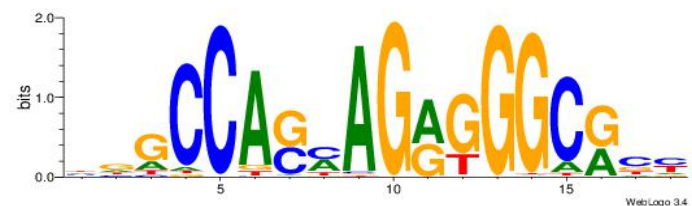
Alignment:

---DDGCCASYAGMGGGCKVM
TTCAGCACCATGGACAGCKCC

Original motif Consensus sequence: RYVGCCCYCTKSTGGCHD



Reverse complement motif Consensus sequence: DDGCCASYAGMGGGCKVM

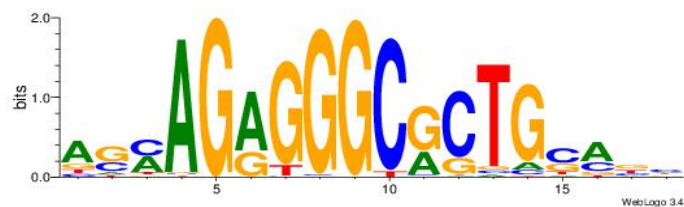


Dataset #: 4
Motif ID: 149
Motif name: asmAGRGGGCrCTGsmkc
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 18
Similarity score: 1.57097

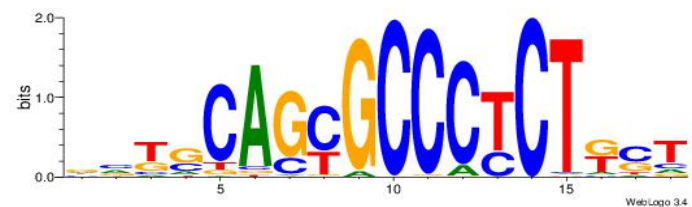
Alignment:

DBTSCAGMGCCCTCTRST---
GGYGCTGTCCATGGTGCTGAA

Original motif Consensus sequence: ASMAGAGGGCRCTGSABH

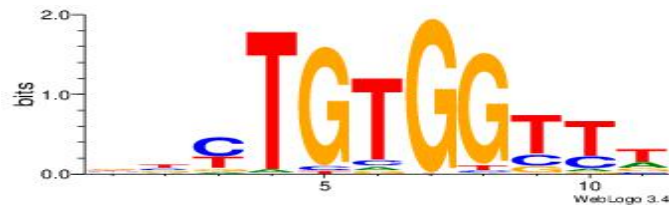


Reverse complement motif Consensus sequence: DBTSCAGMGCCCTCTRST

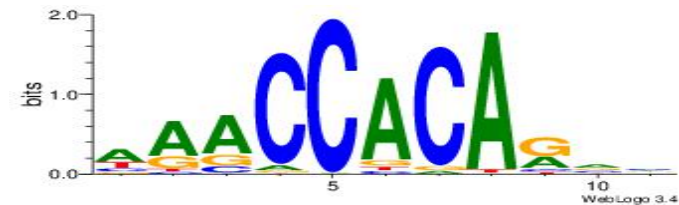


Dataset #: 3 Motif ID: 114 Motif name: RUNX1

Original motif Consensus sequence: BBYTGTGGTTT



Reverse complement motif Consensus sequence: AAACCACAKVB



Best Matches for Motif ID 114 (Highest to Lowest)

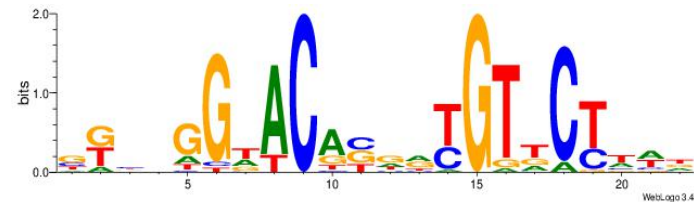
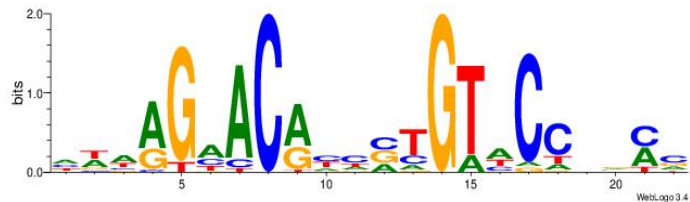
Dataset #:	3
Motif ID:	70
Motif name:	Ar
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	11
Number of overlap:	11
Similarity score:	0.0360379

Alignment:

```
VRVDGGHACAVDDKGTHTDWH
-BBYTGTGGTTT-----
```

Original motif Consensus sequence: HWDAGHACRHHVTGTHCCHVMV

Reverse complement motif Consensus sequence:
VRVDGGHACAVDDKGTHTDWH

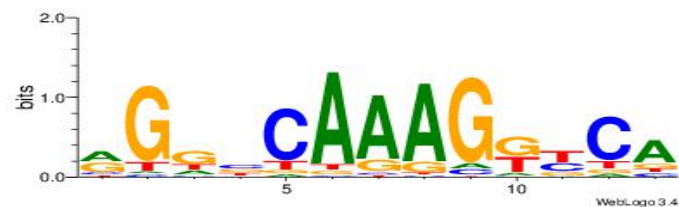


Dataset #: 3
 Motif ID: 87
 Motif name: HNF4A
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.0433682

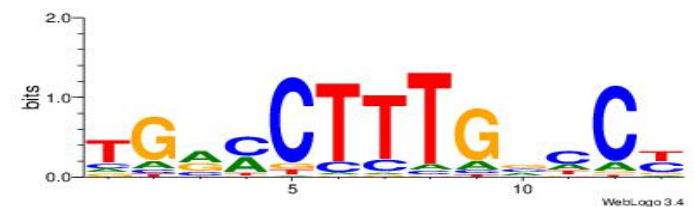
Alignment:

RGGBCAAAGKYCA
 --AAACCACAKVB

Original motif Consensus sequence: RGGBCAAAGKYCA



Reverse complement motif Consensus sequence: TGM YCTTTGBCCK



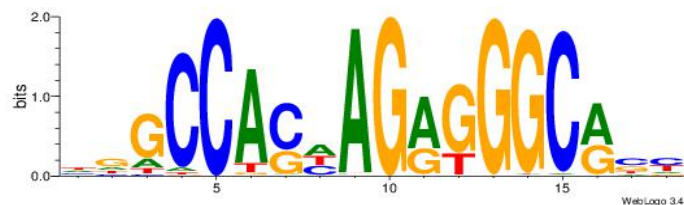
Dataset #: 4
 Motif ID: 165

Motif name: wgGCCAshAGrGGGCrSy
 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: 0.0447401

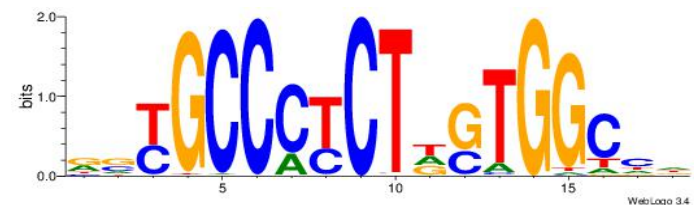
Alignment:

KBKGCCCKCTHGTGGCHH
 -----BBYTGTGGTTT

Original motif Consensus sequence: HDGCCACHAGRGGGCRBY



Reverse complement motif Consensus sequence: KBKGCCCKCTHGTGGCHH



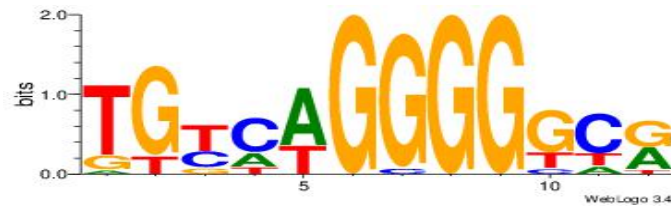
Dataset #: 3
 Motif ID: 88
 Motif name: INSM1
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.0456894

Alignment:

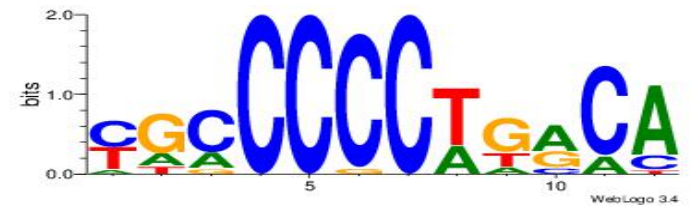
TGYCAGGGGGCR

-BBYTGTGGTTT

Original motif Consensus sequence: TGYCAGGGGGCR



Reverse complement motif Consensus sequence: MGCCCCCTGMCA



Dataset #:	4
Motif ID:	156
Motif name:	rgyGCCMyCTksTGGccd
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	8
Number of overlap:	11
Similarity score:	0.0459745

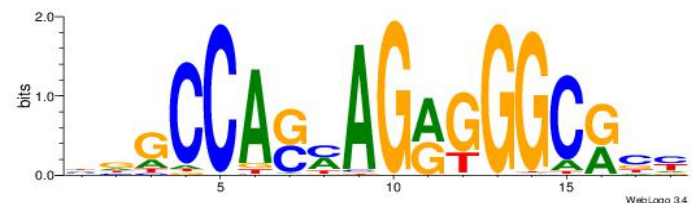
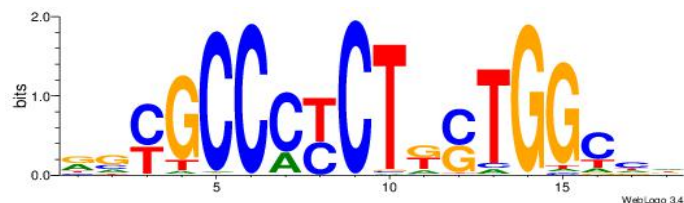
Alignment:

RVYGCCCYCTKSTGGCHD

-----BBYTGTGGTTT

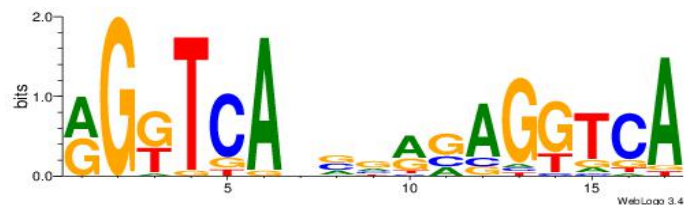
Original motif Consensus sequence: RVYGCCCYCTKSTGGCHD

Reverse complement motif Consensus sequence:
DDGCCASYAGMGGGCKVM

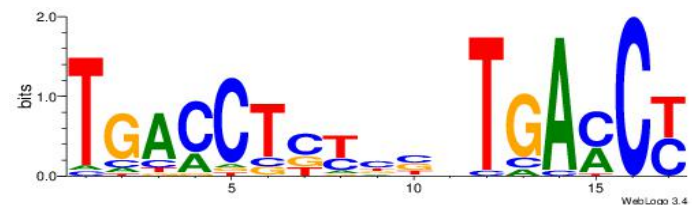


Dataset #: 3 Motif ID: 115 Motif name: RXRRAR_DR5

Original motif Consensus sequence: RGKTCABVVRGAGGTCA



Reverse complement motif Consensus sequence: TGACCTCKVVBGTGAYCK



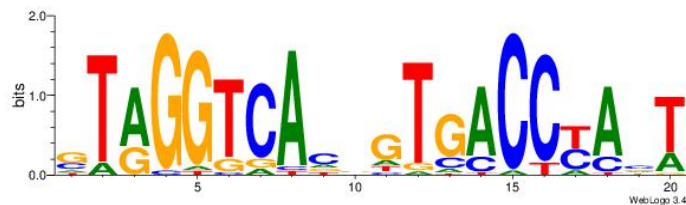
Best Matches for Motif ID 115 (Highest to Lowest)

Dataset #:	3
Motif ID:	111
Motif name:	PPARG
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:	0.0471437

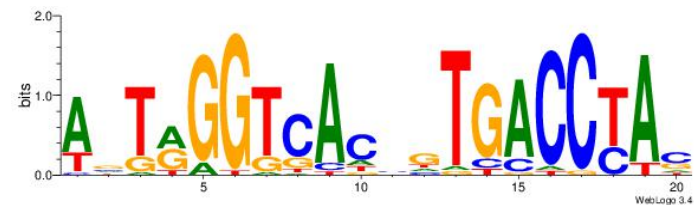
Alignment:

STAGGTCACBGTGACCYABT
 --RGKTCABVVRGAGGTCA-

Original motif Consensus sequence: STAGGTCACBGTGACCYABT



Reverse complement motif Consensus sequence: ABTMGGTCACBGTGACCTAS

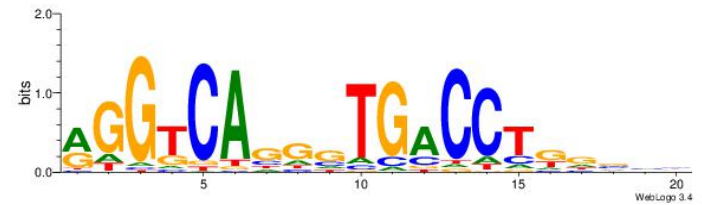
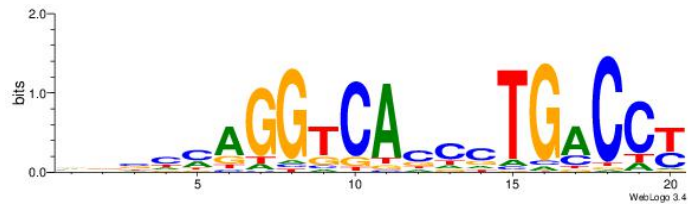


Dataset #:	3
Motif ID:	81
Motif name:	ESR1
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	17
Similarity score:	0.0543729

Alignment:
 MGGTCAGGGTGACCTRDBHV
 ---RGKTCABVVRGAGGTCA

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY

Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV

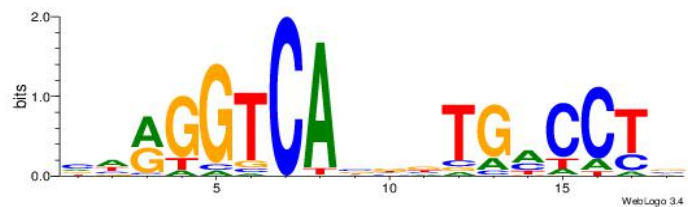


Dataset #: 3
 Motif ID: 82
 Motif name: ESR2
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 17
 Similarity score: 0.058015

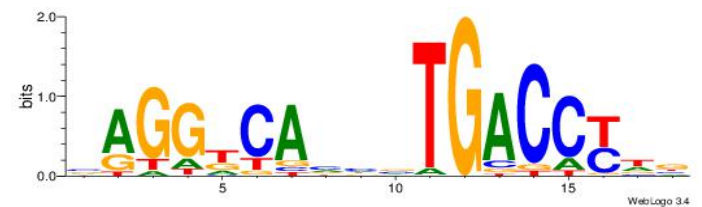
Alignment:

VHRGGTCABDBTGMCTB
 -TGACCTCKVVB TGAYCK

Original motif Consensus sequence: VHRGGTCABDBTGMCTB



Reverse complement motif Consensus sequence: BAGGYCABHBTGACCKHV



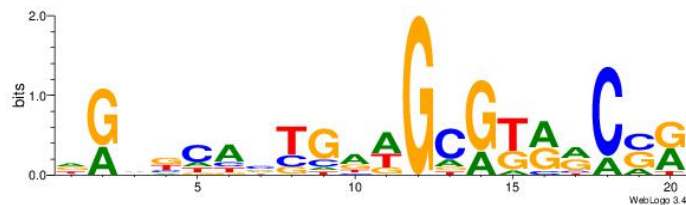
Dataset #: 3

Motif ID: 109
 Motif name: Pax5
 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: 0.0584167

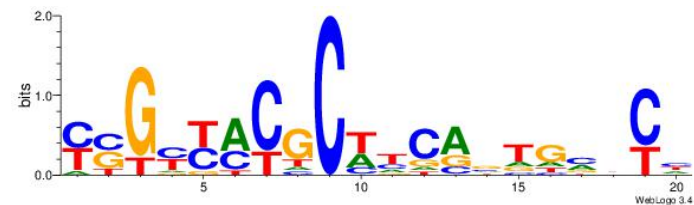
Alignment:

MSGKKRCGCWDCABTGBBCD
 ---TGACCTCKVVB TGAYCK

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD

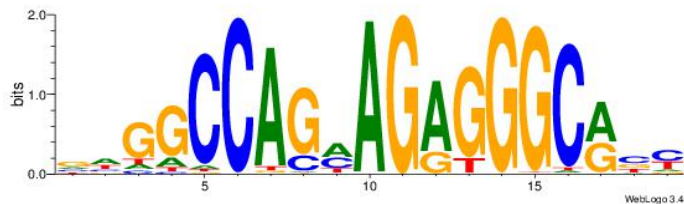


Dataset #: 4
 Motif ID: 163
 Motif name: gwGGCCAGmAGAGGGCrby
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3
 Number of overlap: 17

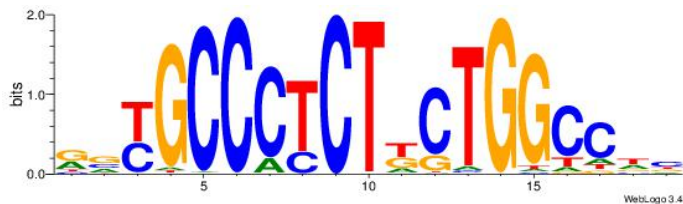
Similarity score: 0.0732845

Alignment:
KBKGCCCTCTYCTGGCCHV
--TGACCTCKVVB TGAYCK

Original motif Consensus sequence: VHGGCCAGMAGAGGGCRBY

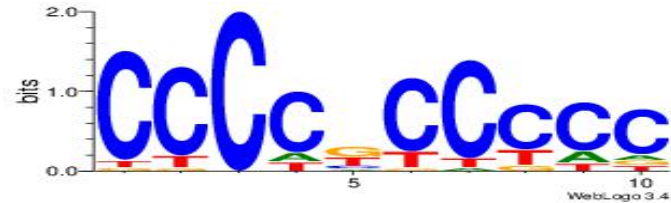


Reverse complement motif Consensus sequence: KBKGCCCTCTYCTGGCCHV

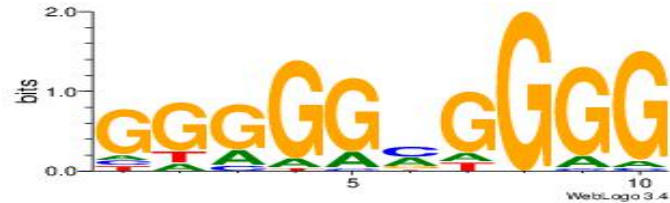


Dataset #: 3 Motif ID: 116 Motif name: SP1

Original motif Consensus sequence: CCCCKCCCC



Reverse complement motif Consensus sequence: GGGGGYGGGG



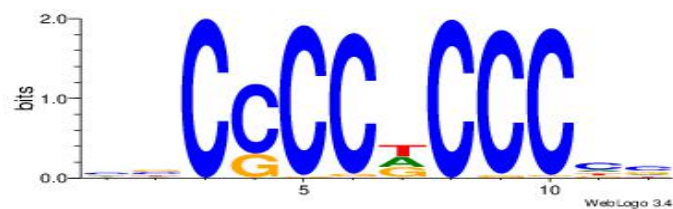
Best Matches for Motif ID 116 (Highest to Lowest)

Dataset #:	4
Motif ID:	155
Motif name:	csCSCCdCCCcs
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif

Direction: Forward
 Position number: 3
 Number of overlap: 10
 Similarity score: 0.0226218

Alignment:
 VBCCCCDCCCHV
 --CCCKCCCCC

Original motif Consensus sequence: VBCCCCDCCCHV



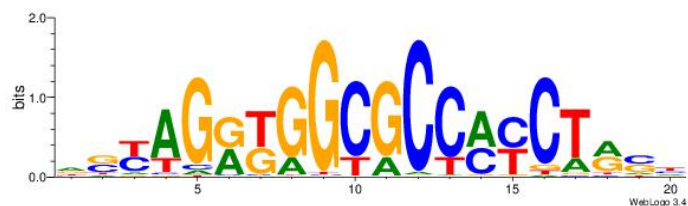
Reverse complement motif Consensus sequence: VDGGGDGGGGBV



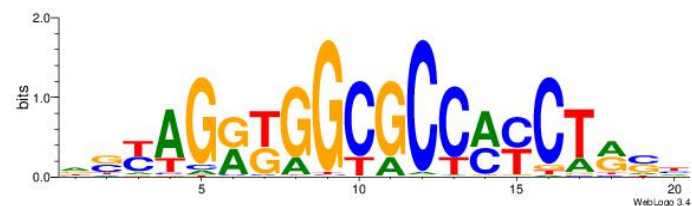
Dataset #: 4
 Motif ID: 167
 Motif name: rsyAGrkGGCGCCmyCTrsy
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 10
 Number of overlap: 10
 Similarity score: 0.0535317

Alignment:
 HSKAGKYGGCGCCRMCTMSD
 -GGGGGYGGG-----

Original motif Consensus sequence: DSYAGRKGCGCCMYCTRSH



Reverse complement motif Consensus sequence: HSKAGKYGGCGCCRMCTMSD

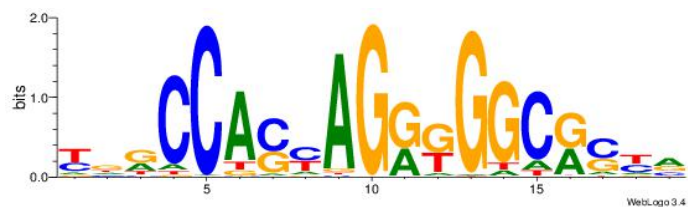


Dataset #: 3
 Motif ID: 74
 Motif name: CTCF
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 10
 Number of overlap: 10
 Similarity score: 0.0604118

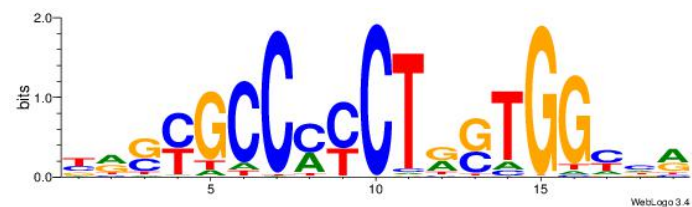
Alignment:

YDRCCASYAGRKGGRSYV
 GGGGGYGGGG-----

Original motif Consensus sequence: YDRCCASYAGRKGGRSYV



Reverse complement motif Consensus sequence: BMSMGCCYMCTKSTGGMHM

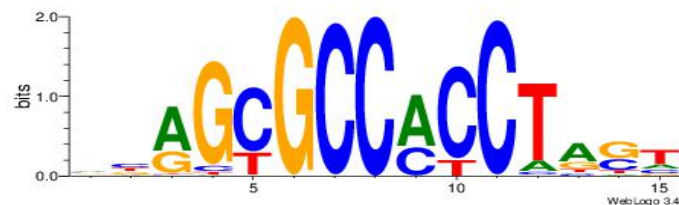


Dataset #: 4
 Motif ID: 146
 Motif name: myrGYGCCmCCTast
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 5
 Number of overlap: 10
 Similarity score: 0.0650794

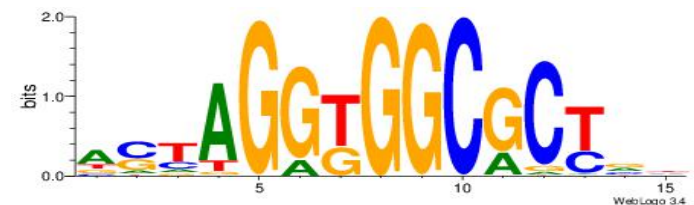
Alignment:

ASTAGGYGGCGCTBB
 -GGGGGYGGGG-----

Original motif Consensus sequence: VBAGCGCCMCCTAST



Reverse complement motif Consensus sequence: ASTAGGYGGCGCTBB

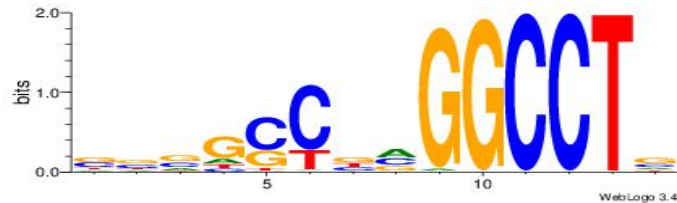


Dataset #: 3
 Motif ID: 130
 Motif name: Zfx
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 5
 Number of overlap: 10

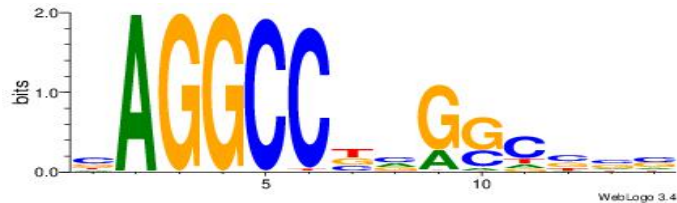
Similarity score: 0.0664832

Alignment:
VAGGCCBBGGCVBB
----CCCCCKCCCCC

Original motif Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif Consensus sequence: VAGGCCBBGGCVBB

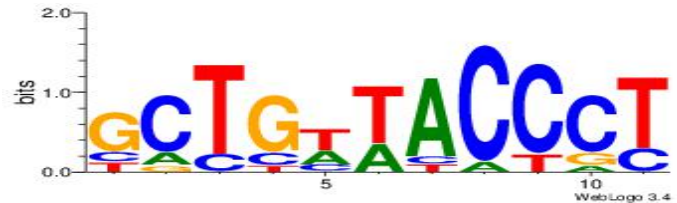


Dataset #: 3 Motif ID: 117 Motif name: Spz1

Original motif Consensus sequence: AGGGTAWCAGC



Reverse complement motif Consensus sequence: GCTGWTACCCT



Best Matches for Motif ID 117 (Highest to Lowest)

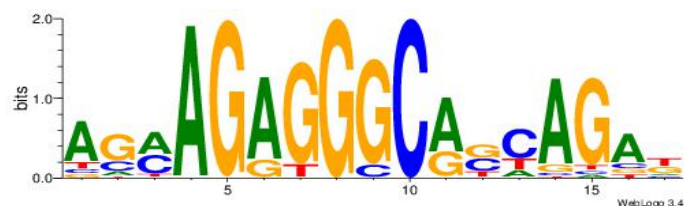
Dataset #:	4
Motif ID:	143
Motif name:	AgmAGAGGGCrscAGak
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward

Position number: 6
 Number of overlap: 11
 Similarity score: 0.0235542

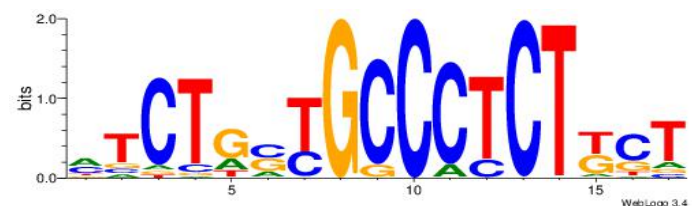
Alignment:

RTCTGSTGCCCTCTYCT
 -GCTGWTACCCT-----

Original motif Consensus sequence: AGMAGAGGGCASCAGAK



Reverse complement motif Consensus sequence: RTCTGSTGCCCTCTYCT

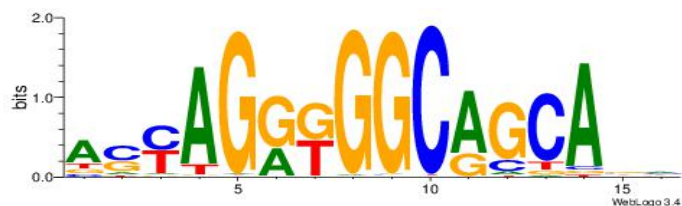


Dataset #: 4
 Motif ID: 164
 Motif name: asyAGrkGGCRGCAGa
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 6
 Number of overlap: 11
 Similarity score: 0.0381204

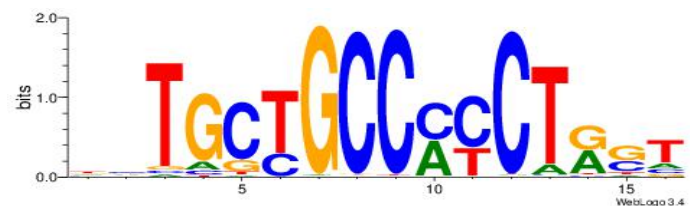
Alignment:

ASYAGRKGGCAGCABH
 -----AGGGTAWCAGC

Original motif Consensus sequence: ASYAGRKGGCAGCABH



Reverse complement motif Consensus sequence: HBTGCTGCCYMCTKST

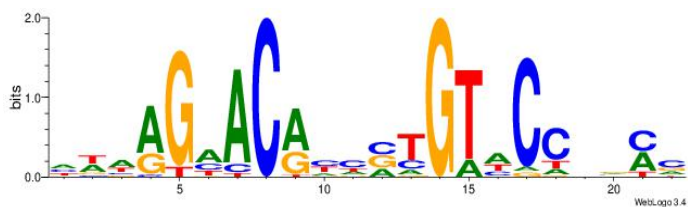


Dataset #: 3
 Motif ID: 70
 Motif name: Ar
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 11
 Similarity score: 0.0401654

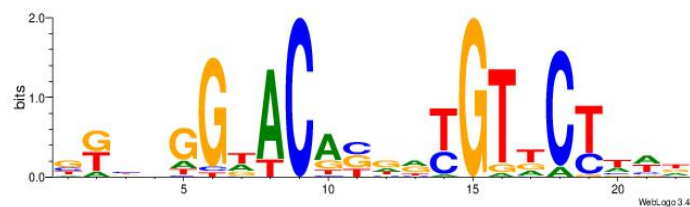
Alignment:

VRVDGGHACAVDDKGTHTCDWH
 -GCTGWTACCCT-----

Original motif Consensus sequence: HWDAGHACRHHVTGTHCCHVMV



Reverse complement motif Consensus sequence: VRVDGGHACAVDDKGTHTCDWH

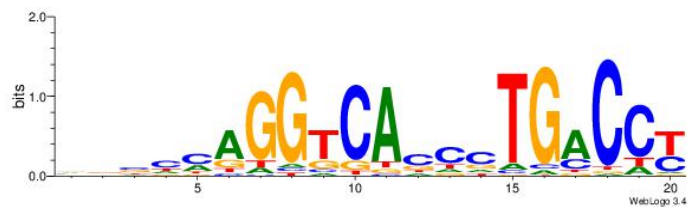


Dataset #: 3
 Motif ID: 81
 Motif name: ESR1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 5
 Number of overlap: 11
 Similarity score: 0.0458949

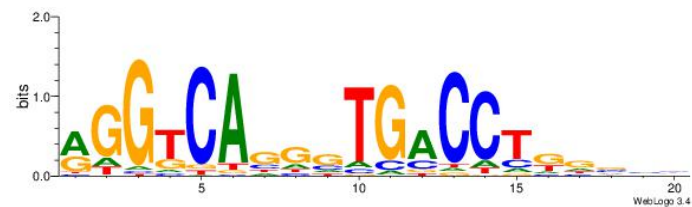
Alignment:

VDBHMAGGTCACCCTGACCY
 -----GCTGWTACCCT-----

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV

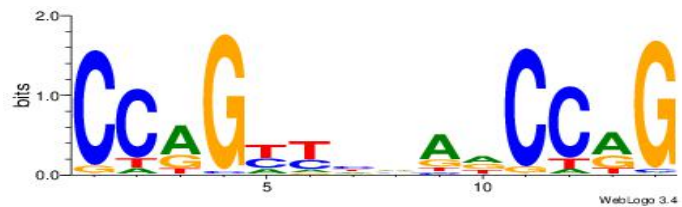


Dataset #: 3
 Motif ID: 122
 Motif name: Tcfcp2l1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4

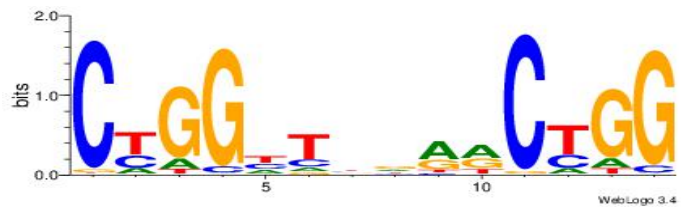
Number of overlap: 11
Similarity score: 0.0503934

Alignment:
CCAGYYHVADCCRG
---GCTGWTACCCT

Original motif Consensus sequence: CCAGYYHVADCCRG

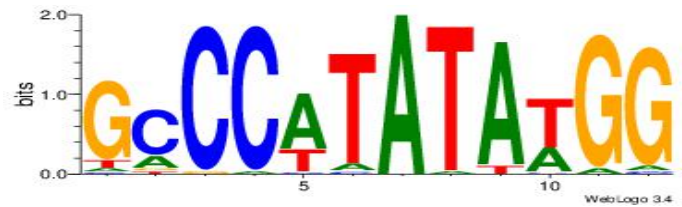


Reverse complement motif Consensus sequence: CKGGDTBDMMCTG

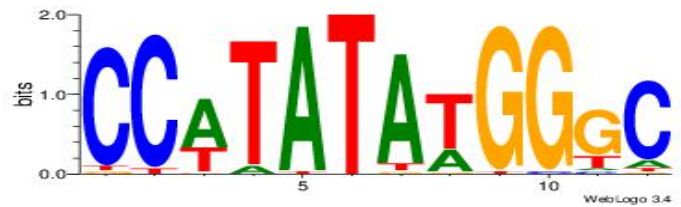


Dataset #: 3 Motif ID: 118 Motif name: SRF

Original motif Consensus sequence: GCCCATATATGG



Reverse complement motif Consensus sequence: CCATATATGGGC



Best Matches for Motif ID 118 (Highest to Lowest)

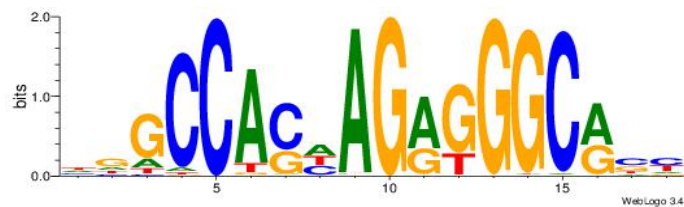
Dataset #: 4
Motif ID: 165
Motif name: wgGCCAshAGrGGGCrSy
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement

Direction: Backward
 Position number: 3
 Number of overlap: 12
 Similarity score: 0.0548555

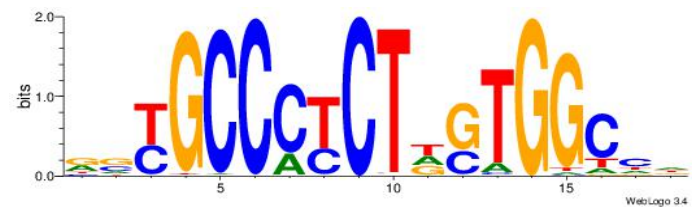
Alignment:

KBKGCCCKCTHGTGGCHH
 ----CCATATATGGGC--

Original motif Consensus sequence: HDGCCACHAGRGGGCRBY



Reverse complement motif Consensus sequence: KBKGCCCKCTHGTGGCHH

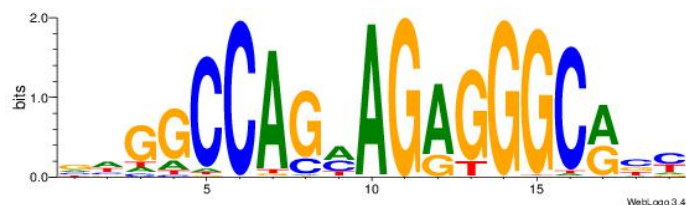


Dataset #: 4
 Motif ID: 163
 Motif name: gwGGCCAGmAGAGGGCrby
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 5
 Number of overlap: 12
 Similarity score: 0.0556649

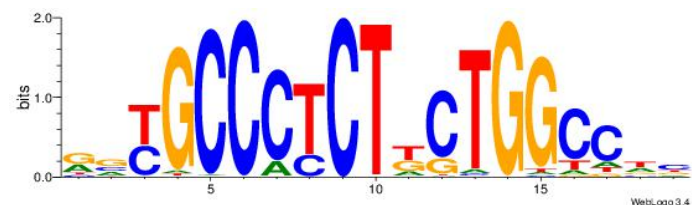
Alignment:

KBKGCCCTCTYCTGGCCHV
 ---GCCCATATATGG----

Original motif Consensus sequence: VHGGCCAGMAGAGGGCRBY



Reverse complement motif Consensus sequence: KBKGCCCTCTYCTGGCCHV

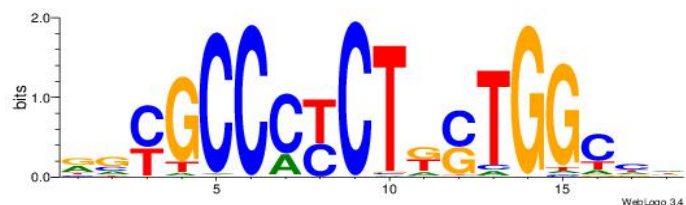


Dataset #: 4
Motif ID: 156
Motif name: rgyGCCMyCTksTGGccd
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 3
Number of overlap: 12
Similarity score: 0.0558448

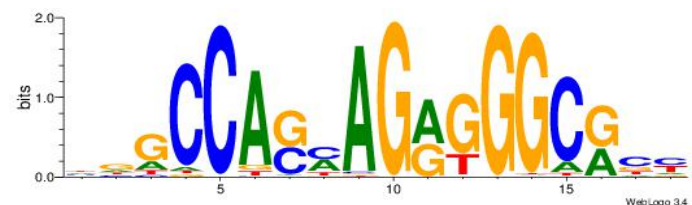
Alignment:

DDGCCASYAGMGGGCKVM
--GCCCATATATGG----

Original motif Consensus sequence: RVYGCCCYCTKSTGGCHD



Reverse complement motif Consensus sequence: DDGCCASYAGMGGGCKVM

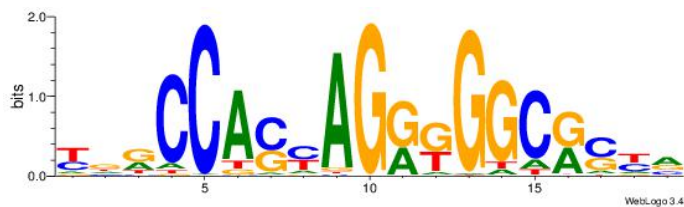


Dataset #: 3
 Motif ID: 74
 Motif name: CTCF
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 4
 Number of overlap: 12
 Similarity score: 0.0566321

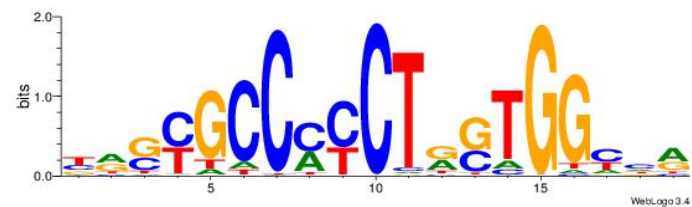
Alignment:

YDRCCASYAGRKGGCRSYV
 ----CCATATATGGGC---

Original motif Consensus sequence: YDRCCASYAGRKGGCRSYV



Reverse complement motif Consensus sequence: BMSMGCCYMCTKSTGGMHM

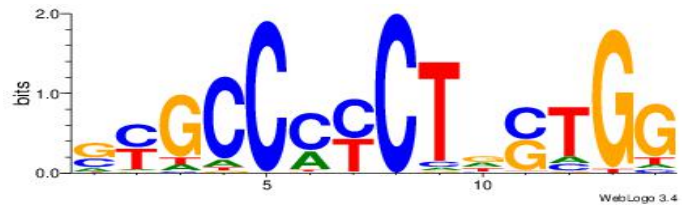


Dataset #: 2
 Motif ID: 67
 Motif name: Motif 67
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3

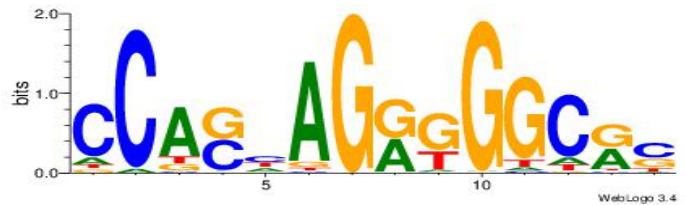
Number of overlap: 12
Similarity score: 0.0566949

Alignment:
CCASHAGKGGGCKS
CCATATATGGGC--

Original motif Consensus sequence: SYGCCCYCTDSTGG

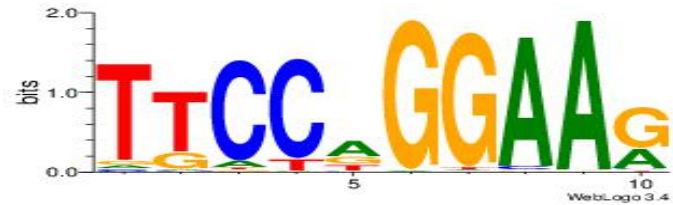


Reverse complement motif Consensus sequence: CCASHAGKGGGCKS

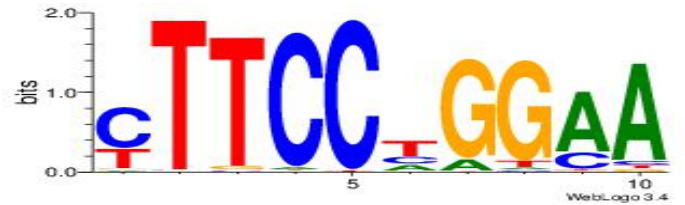


Dataset #: 3 Motif ID: 119 Motif name: Stat3

Original motif Consensus sequence: TTCCAGGAAG



Reverse complement motif Consensus sequence: CTTCTGGAA



Best Matches for Motif ID 119 (Highest to Lowest)

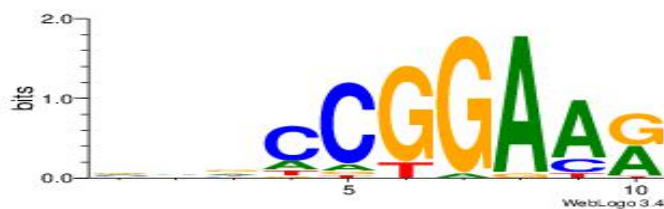
Dataset #: 3
Motif ID: 79
Motif name: ELK1
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement

Direction: Backward
 Position number: 1
 Number of overlap: 10
 Similarity score: 0.0612721

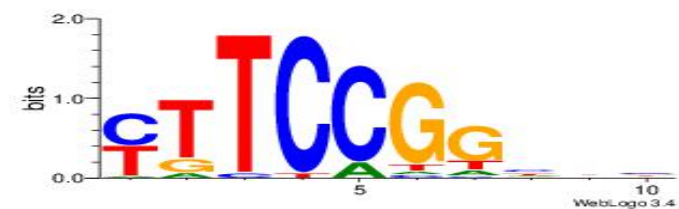
Alignment:

MTTCCGGHBV
 CTCCTGGAA

Original motif Consensus sequence: VDDCCGGAAR



Reverse complement motif Consensus sequence: MTTCCGGHBV

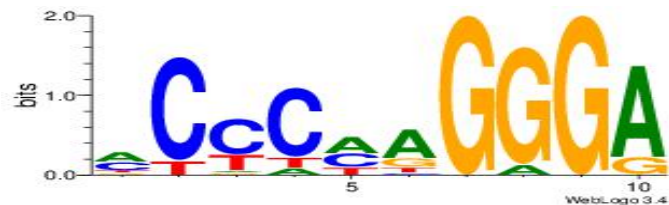


Dataset #: 3
 Motif ID: 77
 Motif name: EBF1
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 10
 Similarity score: 0.0803002

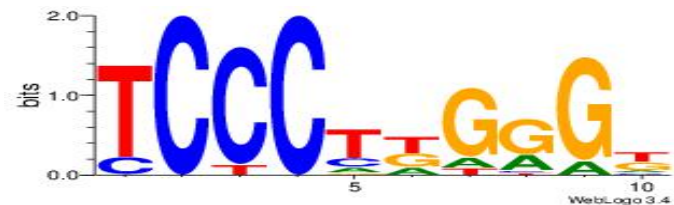
Alignment:

TCCCTYGGGY
 TTCCAGGAAG

Original motif Consensus sequence: MCCCMAAGGA



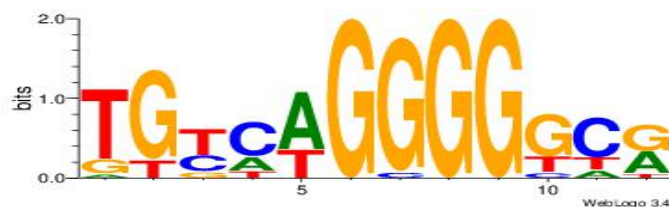
Reverse complement motif Consensus sequence: TCCCTYGGGY



Dataset #: 3
 Motif ID: 88
 Motif name: INSM1
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 10
 Similarity score: 0.0834676

Alignment:
 TGYCAGGGGGCR
 TTCCAGGAAG--

Original motif Consensus sequence: TGYCAGGGGGCR



Reverse complement motif Consensus sequence: MGCCCCCTGMCA

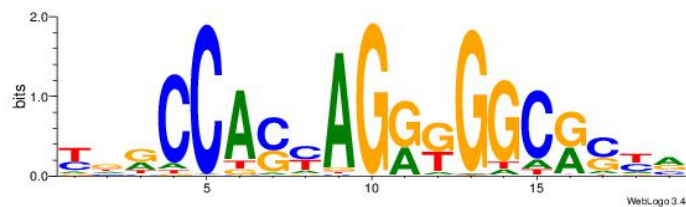


Dataset #: 3
 Motif ID: 74
 Motif name: CTCF
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 10
 Similarity score: 0.0852106

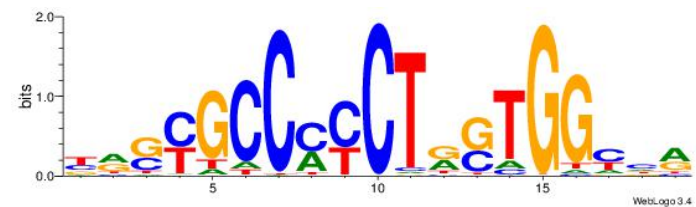
Alignment:

YDRCCASYAGRKGGRSYV
 -TTCCAGGAAG-----

Original motif Consensus sequence: YDRCCASYAGRKGGRSYV



Reverse complement motif Consensus sequence: BMSGCCYMCTKSTGGMHM



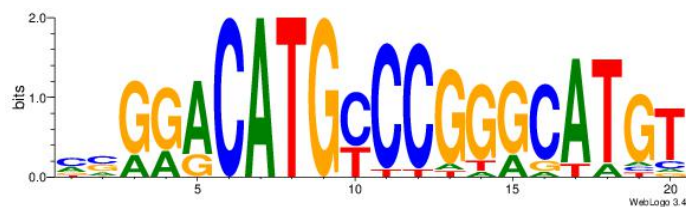
Dataset #: 3
 Motif ID: 125
 Motif name: TP53
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 8

Number of overlap: 10
Similarity score: 0.087969

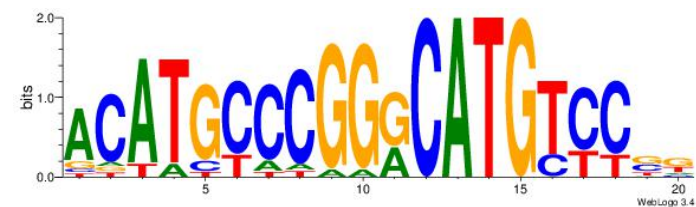
Alignment:

MSGGACATGYCCGGGCATGT
-----CTTCCTGGAA----

Original motif Consensus sequence: MSGGACATGYCCGGGCATGT



Reverse complement motif Consensus sequence: ACATGCCCCGKCATGTCCSR



Dataset #: 3 Motif ID: 120 Motif name: T

Original motif Consensus sequence: CTAGGTGTGAA



Reverse complement motif Consensus sequence: TTCACACCTAG



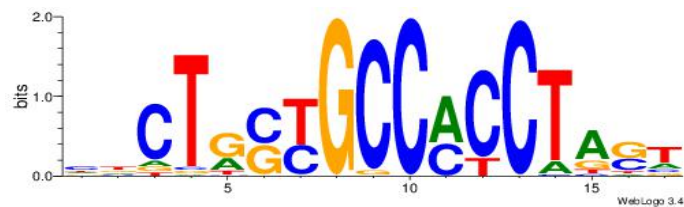
Best Matches for Motif ID 120 (Highest to Lowest)

Dataset #: 4
Motif ID: 144
Motif name: ctCTrsyGCCmCCTast
Matching format of first motif: Reverse Complement

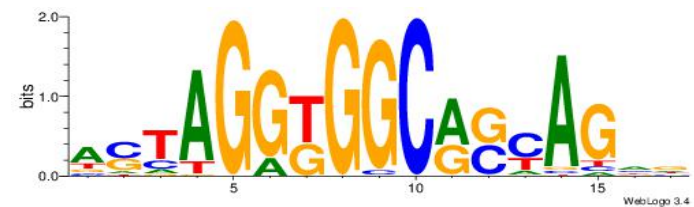
Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 6
 Number of overlap: 11
 Similarity score: 0.0559721

Alignment:
 HDCTGSYGCCMCCTAST
 -----TTCACACCTAG--

Original motif Consensus sequence: HDCTGSYGCCMCCTAST



Reverse complement motif Consensus sequence:
 ASTAGGYGGCMSCAGDD

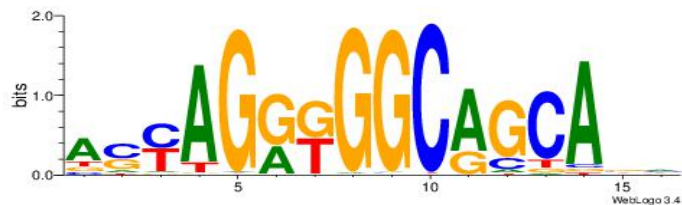


Dataset #: 4
 Motif ID: 164
 Motif name: asyAGrkGGCRGCaga
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 11
 Similarity score: 0.0641201

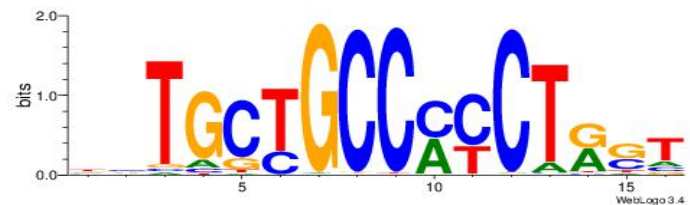
Alignment:

ASYAGRKGGCAGCABH
-CTAGGTGTGAA-----

Original motif Consensus sequence: ASYAGRKGGCAGCABH



Reverse complement motif Consensus sequence:
HBTGCTGCCYMCTKST



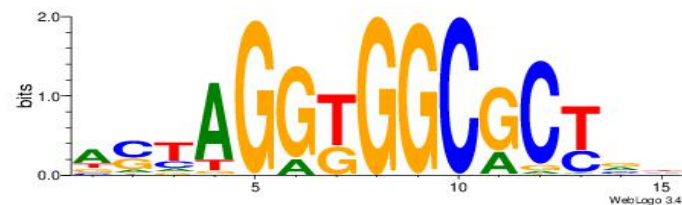
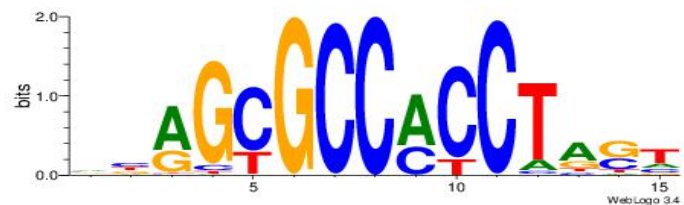
Dataset #:	4
Motif ID:	146
Motif name:	myrYGCCmCCTast
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	4
Number of overlap:	11
Similarity score:	0.0654989

Alignment:

VBAGCGCCMCCTAST
---TTCACACCTAG-

Original motif Consensus sequence: VBAGCGCCMCCTAST

Reverse complement motif Consensus sequence: ASTAGGYGGCGCT

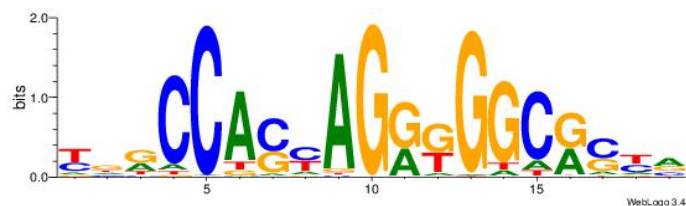


Dataset #: 3
 Motif ID: 74
 Motif name: CTCF
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 11
 Similarity score: 0.0692022

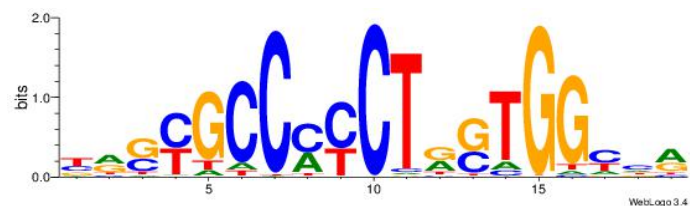
Alignment:

YDRCCASYAGRKGGRSYV
 -----CTAGGTGTGAA--

Original motif Consensus sequence: YDRCCASYAGRKGGRSYV



Reverse complement motif Consensus sequence: BMSMGCCYMCTKSTGGMHM



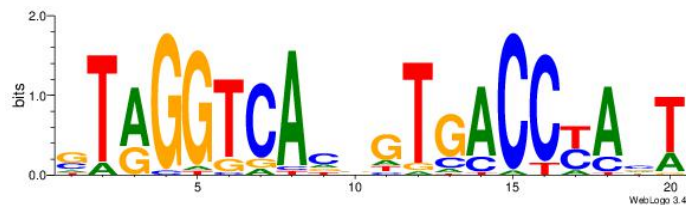
Dataset #: 3

Motif ID: 111
 Motif name: PPARG
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 10
 Number of overlap: 11
 Similarity score: 0.070764

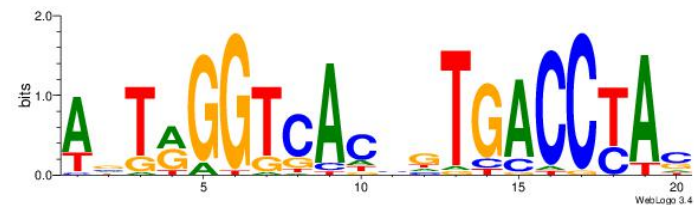
Alignment:

ABTMGGTCACBG TGACCTAS
 -----TTCACACCTAG

Original motif Consensus sequence: STAGGTCACBG TGACCYABT

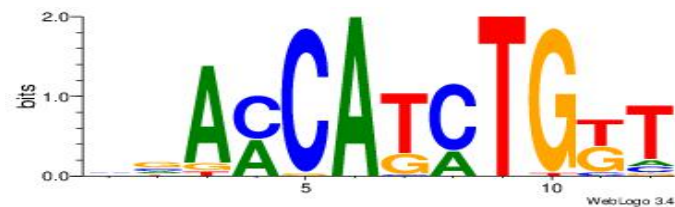


Reverse complement motif Consensus sequence: ABTMGGTCACBG TGACCTAS



Dataset #: 3 Motif ID: 121 Motif name: TAL1TCF3

Original motif Consensus sequence: HVAMCATCTGKT



Reverse complement motif Consensus sequence: ARCAGATGRTVD



Best Matches for Motif ID 121 (Highest to Lowest)

Dataset #: 4
Motif ID: 147
Motif name: asCAGrkGGCrSy
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: 0.0388867

Alignment:

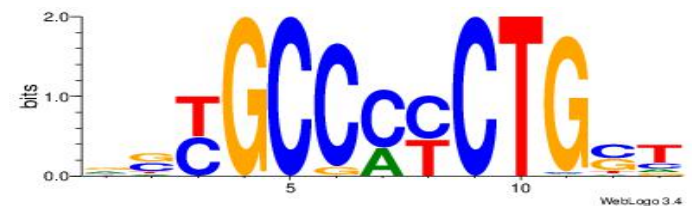
ASCAGRGGGCRSB

ARCAGATGRTVD-

Original motif Consensus sequence: ASCAGRGGGCRSB



Reverse complement motif Consensus sequence: BSKGCCCMCTGST

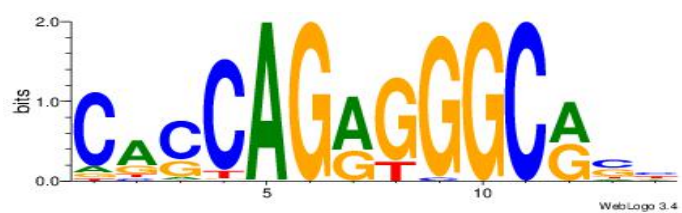


Dataset #: 4
Motif ID: 166
Motif name: CasCAGrGGGCrSy
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement

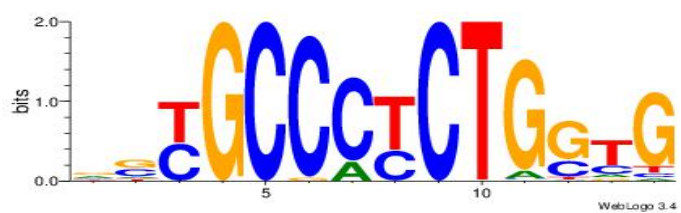
Direction: Forward
Position number: 2
Number of overlap: 12
Similarity score: 0.0389554

Alignment:
BSKGCCCKCTGGTG
-HVAMCATCTGKT-

Original motif Consensus sequence: CACCAGRGGGCRSB



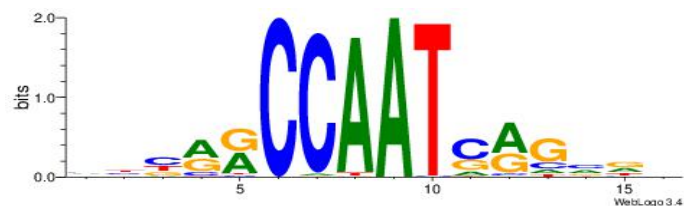
Reverse complement motif Consensus sequence: BSKGCCCKCTGGT



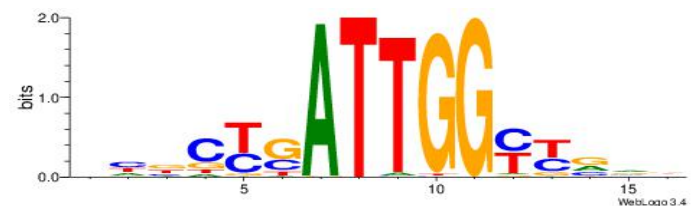
Dataset #: 3
Motif ID: 104
Motif name: NFYA
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 4
Number of overlap: 12
Similarity score: 0.0418463

Alignment:
BHVCKSATTTGGMKBVV
---HVAMCATCTGKT-

Original motif Consensus sequence: VBBRCCAATSRGVDB



Reverse complement motif Consensus sequence: BHVCKSATTGGMKBVV



Dataset #: 4
Motif ID: 151
Motif name: agrCCAGmAGrg
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: 0.0439721

Alignment:

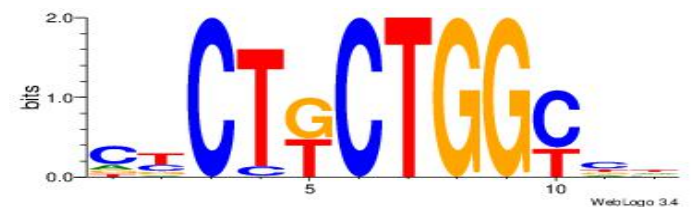
HV GCCAGMAGRG

HVAMCATCTGKT

Original motif Consensus sequence: HVGCCAGMAGRG



Reverse complement motif Consensus sequence: CKCTRCTGGCVH

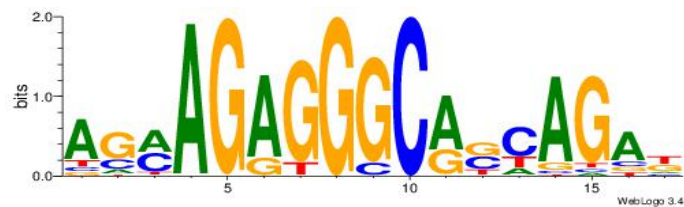


Dataset #: 4
 Motif ID: 143
 Motif name: AgmAGAGGGCrscAGak
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 6
 Number of overlap: 12
 Similarity score: 0.0474478

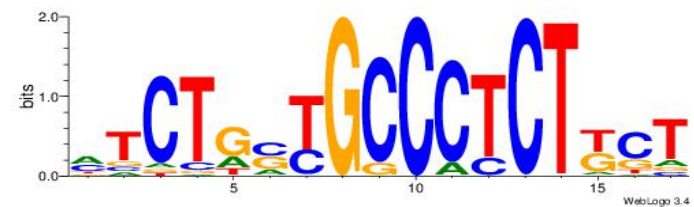
Alignment:

AGMAGAGGGCASCAGAK
 ARCAGATGRTVD-----

Original motif Consensus sequence: AGMAGAGGGCASCAGAK



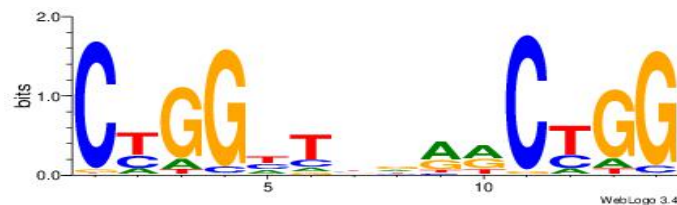
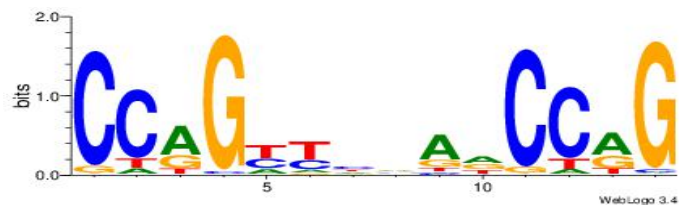
Reverse complement motif Consensus sequence: RTCTGSTGCCCTCTYCT



Dataset #: 3 Motif ID: 122 Motif name: Tcfcp2l1

Original motif Consensus sequence: CCAGYYHVADCCRG

Reverse complement motif Consensus sequence: CKGGDTBDMMCTG



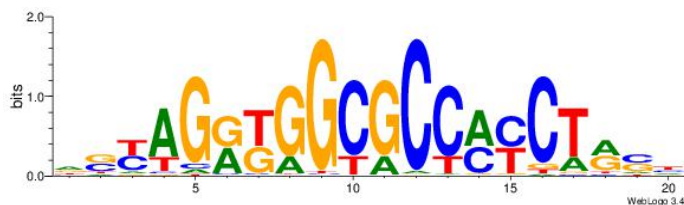
Best Matches for Motif ID 122 (Highest to Lowest)

Dataset #: 4
 Motif ID: 167
 Motif name: rsyAGrkGGCGCCmyCTrsy
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 6
 Number of overlap: 14
 Similarity score: 0.0620246

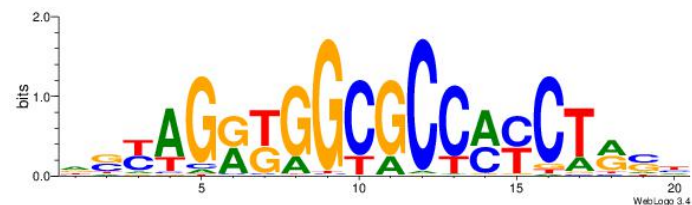
Alignment:

DSYAGRKGCGCCMYCTRSH
 -----CKGGDTBDMCTGG-

Original motif Consensus sequence: DSYAGRKGCGCCMYCTRSH



Reverse complement motif Consensus sequence: HSKAGKYGGCGCCRMCTMSD

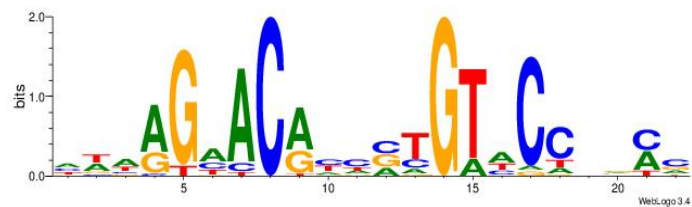


Dataset #: 3
 Motif ID: 70
 Motif name: Ar
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 7
 Number of overlap: 14
 Similarity score: 0.0642855

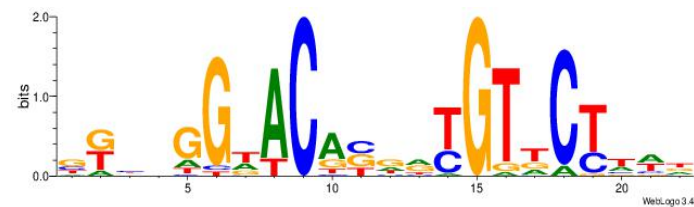
Alignment:

HWDAGHACRHHVTGTHCCHVMV
 -----CCAGYYHVADCCRG--

Original motif Consensus sequence: HWDAGHACRHHVTGTHCCHVMV



Reverse complement motif Consensus sequence: VRVDGGHACA VDDKGTCTDWH



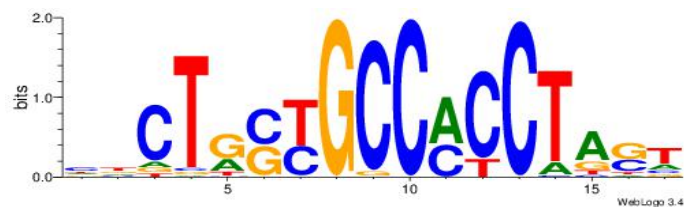
Dataset #: 4
 Motif ID: 144
 Motif name: ctCTrsyGCCmCCTast
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2

Number of overlap: 14
Similarity score: 0.0675705

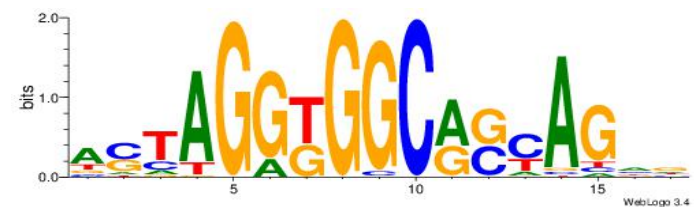
Alignment:

HDCTGSYGCCMCCTAST
--CKGGDTBDMMCTGG--

Original motif Consensus sequence: HDCTGSYGCCMCCTAST



Reverse complement motif Consensus sequence:
ASTAGGYGGCMSCAGDD

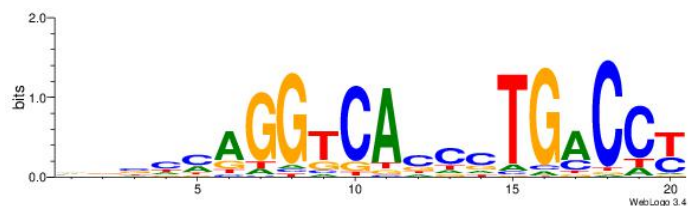


Dataset #: 3
Motif ID: 81
Motif name: ESR1
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 4
Number of overlap: 14
Similarity score: 0.0676841

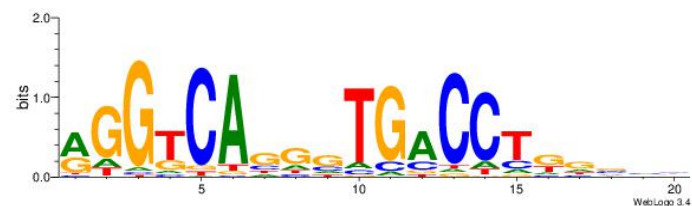
Alignment:

MGGTCAGGGTGACCTRDBHV
---CCAGYYHVADCCRG---

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDDBHV

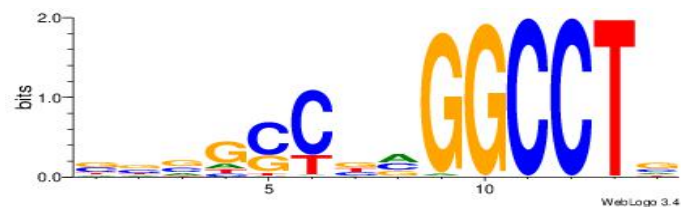


Dataset #: 3
Motif ID: 130
Motif name: Zfx
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 14
Similarity score: 0.0677766

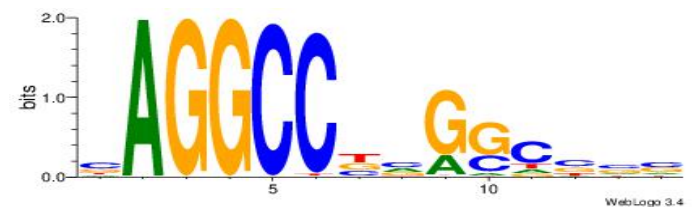
Alignment:

BBVGCCBVGGCCTV
CCAGYYHVADCCRG

Original motif Consensus sequence: BBVGCCBVGGCCTV

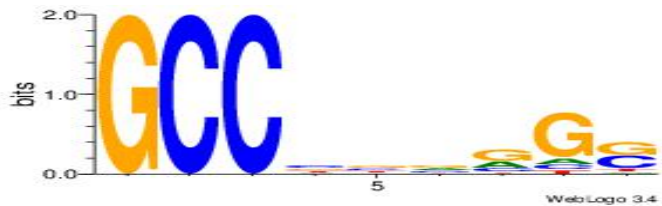


Reverse complement motif Consensus sequence: VAGGCCBBGGCV

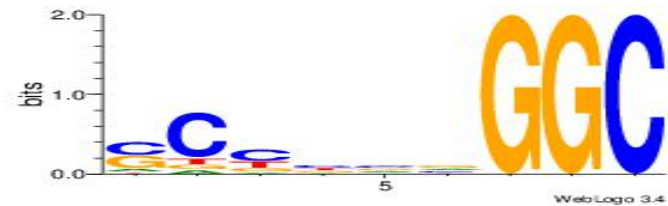


Dataset #: 3 Motif ID: 123 Motif name: TFAP2A

Original motif Consensus sequence: GCCBBVRGS



Reverse complement motif Consensus sequence: SCMVBGGC



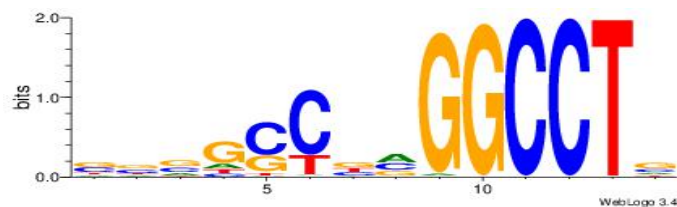
Best Matches for Motif ID 123 (Highest to Lowest)

Dataset #:	3
Motif ID:	130
Motif name:	Zfx
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:	0.0365038

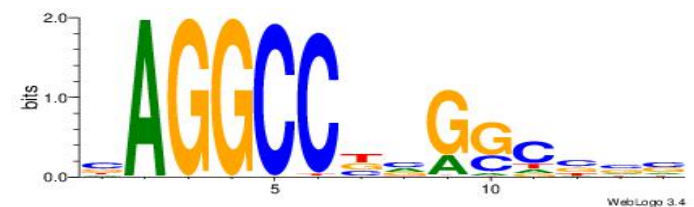
Alignment:

VAGGCCBBGGCVBB
 ---GCCBBVRGS---

Original motif Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif Consensus sequence: VAGGCCBBGGCVBB



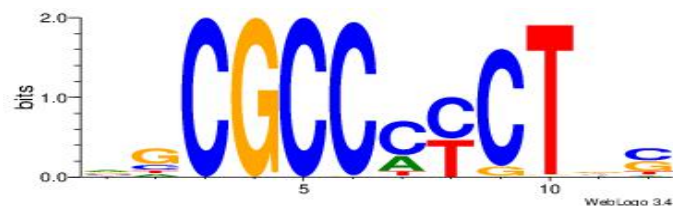
Dataset #: 4
 Motif ID: 137
 Motif name: rgCGCCmyCTgs
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 4
 Number of overlap: 9
 Similarity score: 0.0578475

Alignment:

SHAGKGGGCGCB

SCMVBBGGC---

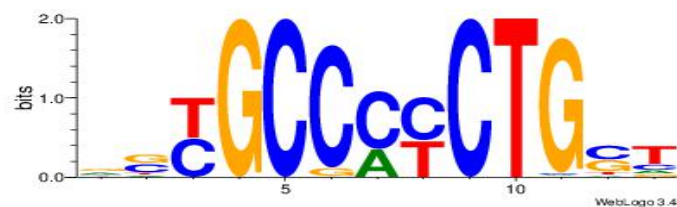
Original motif Consensus sequence: VGCGCCCYCTDS



Reverse complement motif Consensus sequence: SHAGKGGGCGCB



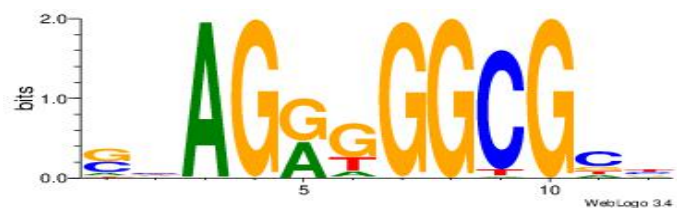
Dataset #: 3
 Motif ID: 124
 Motif name: TLX1NFIC
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3



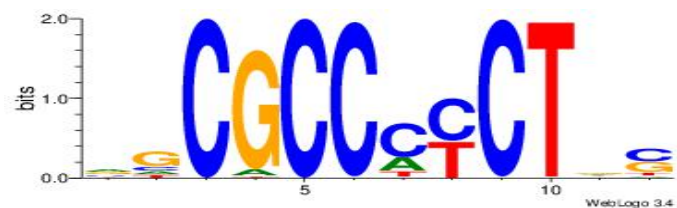
Dataset #: 4
 Motif ID: 153
 Motif name: scAGrkGGCGcy
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 4
 Number of overlap: 9
 Similarity score: 0.0640748

Alignment:
 SHAGRGGGCGCB
 SCMVBGGC---

Original motif Consensus sequence: SHAGRGGGCGCB

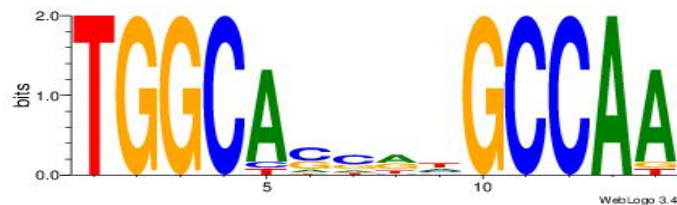


Reverse complement motif Consensus sequence: VCGCCCMCTDS

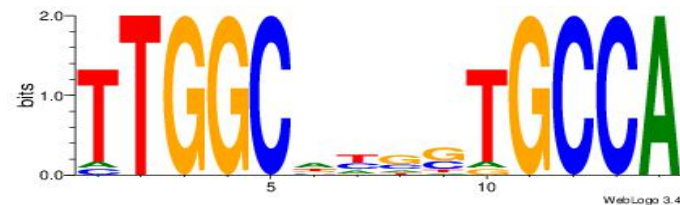


Dataset #: 3 Motif ID: 124 Motif name: TLX1NFIC

Original motif Consensus sequence: TGGCASBDHGCCAA



Reverse complement motif Consensus sequence: TTGGCHDBSTGCC



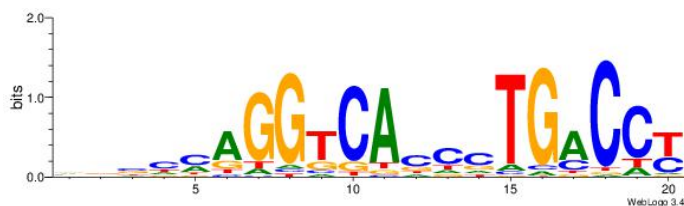
Best Matches for Motif ID 124 (Highest to Lowest)

Dataset #:	3
Motif ID:	81
Motif name:	ESR1
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:	0.0758334

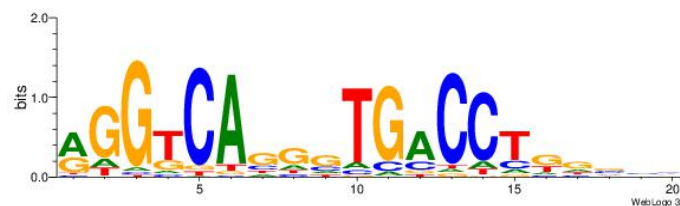
Alignment:

```
VDBHMAGGTCACCCTGACCY
-----TGGCASBDHGCCAA
```

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRD BHV

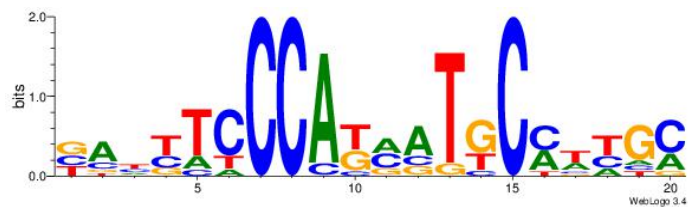


Dataset #: 3
 Motif ID: 131
 Motif name: znf143
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 4
 Number of overlap: 14
 Similarity score: 0.0763138

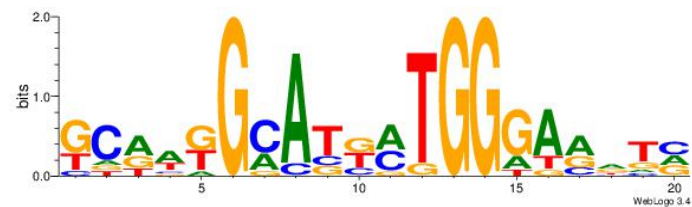
Alignment:

GCMWRGCATYRTGGGAMHTB
 ---TGGCASBDHGCCAA---

Original motif Consensus sequence: BAHYTCCCAKMATGCMWYGC



Reverse complement motif Consensus sequence: GCMWRGCATYRTGGGAMHTB



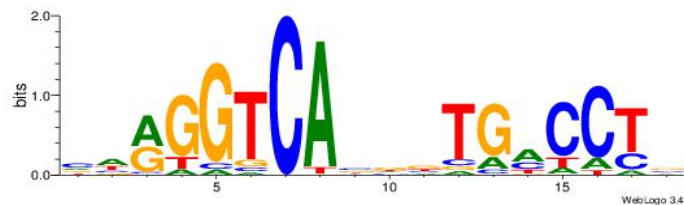
Dataset #: 3
 Motif ID: 82
 Motif name: ESR2
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2

Number of overlap: 14
Similarity score: 0.0777688

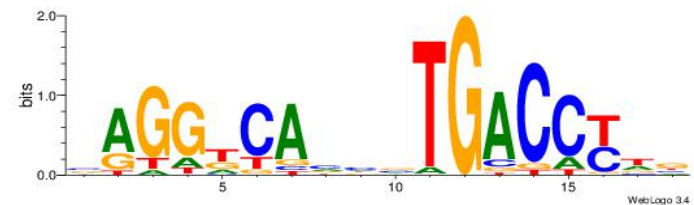
Alignment:

VHRGGTCABDBTGMCTB
---TGGCASBDHGCCAA--

Original motif Consensus sequence: VHRGGTCABDBTGMCTB



Reverse complement motif Consensus sequence: BAGGYCABHBTGACCKHV

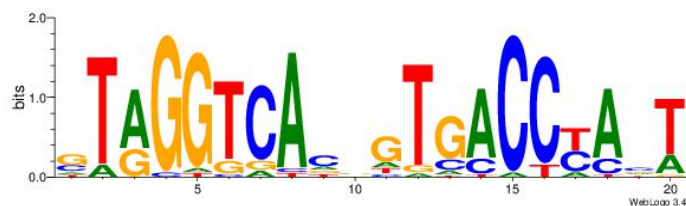


Dataset #: 3
Motif ID: 111
Motif name: PPARG
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 4
Number of overlap: 14
Similarity score: 0.0838712

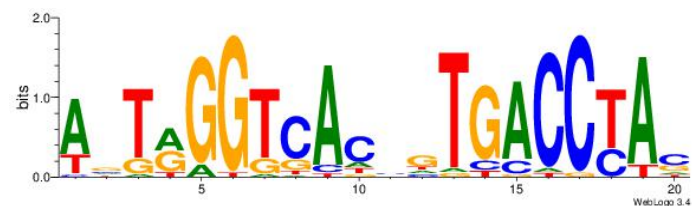
Alignment:

STAGGTCACBGTGACCYABT
---TGGCASBDHGCCAA---

Original motif Consensus sequence: STAGGTCACBG TGACCYABT



Reverse complement motif Consensus sequence: ABTMGGTCACBG TGACCTAS

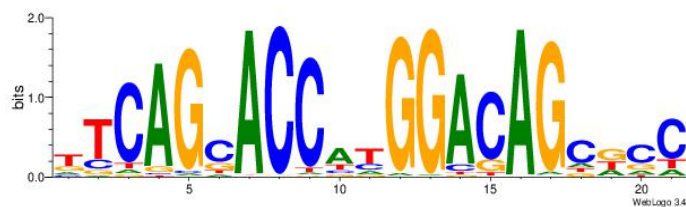


Dataset #: 3
Motif ID: 113
Motif name: REST
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 6
Number of overlap: 14
Similarity score: 0.0916353

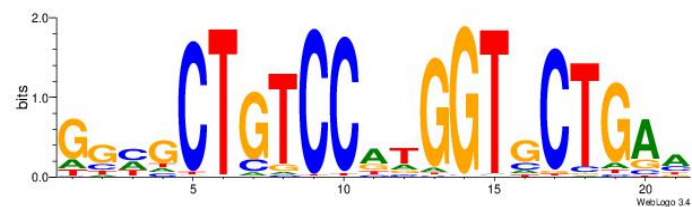
Alignment:

TTCAGCACCATGGACAGCKCC
--TGGCASBDHGCCAA-----

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC

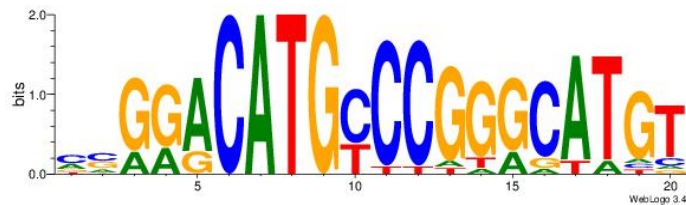


Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA

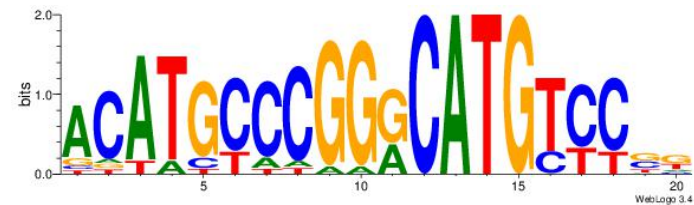


Dataset #: 3 Motif ID: 125 Motif name: TP53

Original motif Consensus sequence: MSGGACATGYCCGGGCATGT



Reverse complement motif Consensus sequence: ACATGCCCGGKCATGTCCSR



Best Matches for Motif ID 125 (Highest to Lowest)

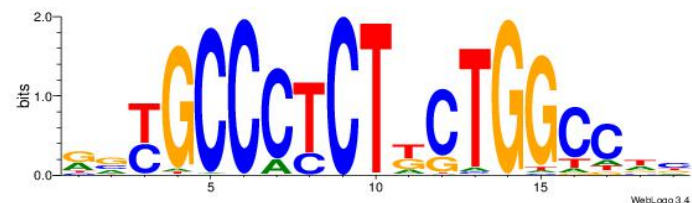
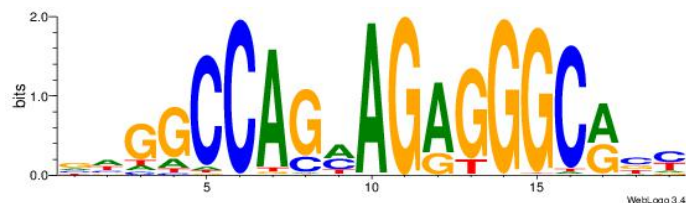
Dataset #:	4
Motif ID:	163
Motif name:	gwGGCCAGmAGAGGGCrby
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	19
Similarity score:	0.0641029

Alignment:

-KBKGCCCTCTYCTGGCCHV
ACATGCCCGGKCATGTCCSR

Original motif Consensus sequence: VHGGCCAGMAGAGGGCRBY

Reverse complement motif Consensus sequence:
KBKGCCCTCTYCTGGCCHV

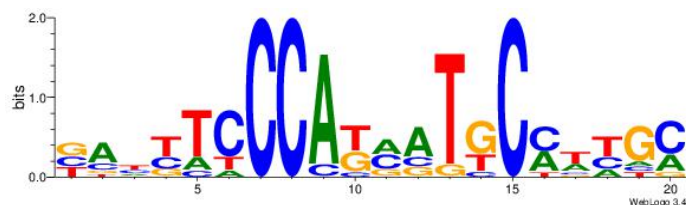


Dataset #: 3
 Motif ID: 131
 Motif name: znf143
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 19
 Similarity score: 0.0730057

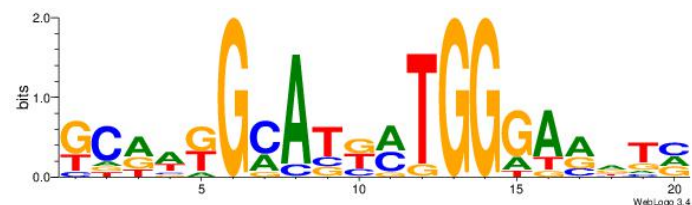
Alignment:

–BAHYTCCCAKMATGCMWYGC
 ACATGCCCGGKCATGTCCSR–

Original motif Consensus sequence: BAHYTCCCAKMATGCMWYGC



Reverse complement motif Consensus sequence: GCMWRGCATYRTGGGAMHTB



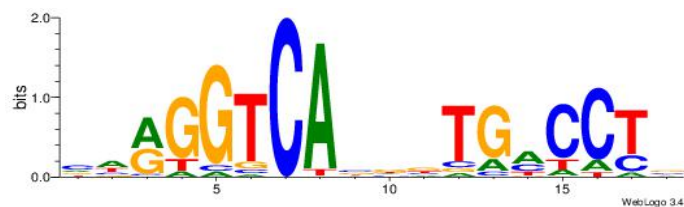
Dataset #: 3

Motif ID: 82
 Motif name: ESR2
 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: 2.07342

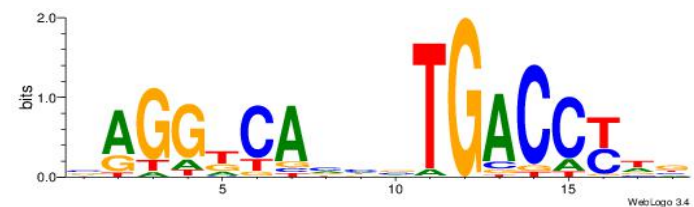
Alignment:

-----BAGGYCABHBTGACCKHV
 MSGGACATGYCCGGGCATGT---

Original motif Consensus sequence: VHRGGTCABDBTGMCTB



Reverse complement motif Consensus sequence: BAGGYCABHBTGACCKHV

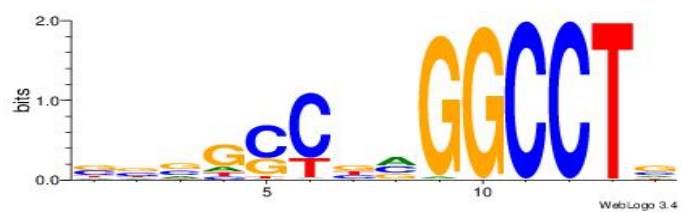


Dataset #: 3
 Motif ID: 130
 Motif name: Zfx
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 14

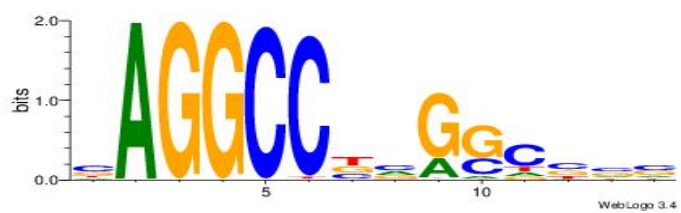
Similarity score: 2.55908

Alignment:
-----VAGGCCBBGGCVBB
ACATGCCCGGKCATGTCCSR

Original motif Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif Consensus sequence: VAGGCCBBGGCVBB

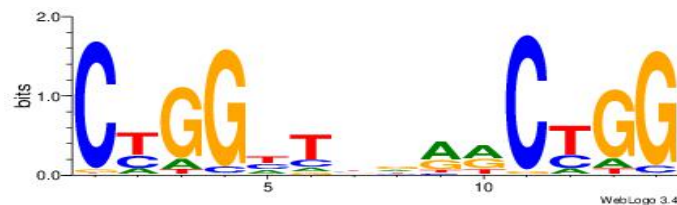
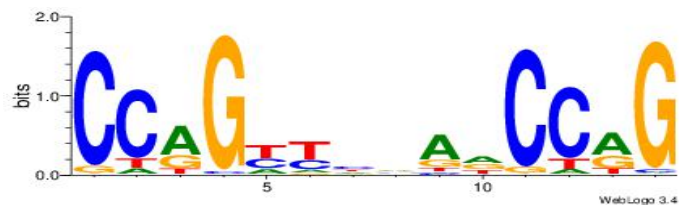


Dataset #: 3
Motif ID: 122
Motif name: Tcfcp2l1
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 14
Similarity score: 2.56997

Alignment:
-----CKGGDTBDMMCTGG
MSGGACATGYCCGGGCATGT

Original motif Consensus sequence: CCAGYYHVADCCRG

Reverse complement motif Consensus sequence: CKGGDTBDMMCTGG



Dataset #: 3 Motif ID: 126 Motif name: USF1

Original motif Consensus sequence: CACGTGR



Reverse complement motif Consensus sequence: MCACGTG



Best Matches for Motif ID 126 (Highest to Lowest)

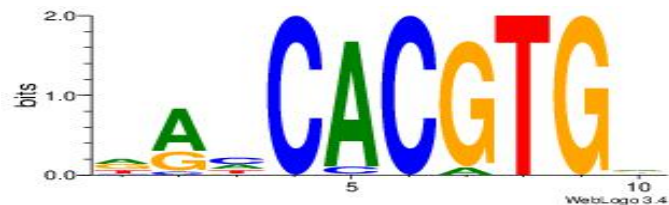
Dataset #:	3
Motif ID:	91
Motif name:	MAX
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	3
Number of overlap:	7
Similarity score:	0

Alignment:

BCACGTGDTD

--CACGTGR--

Original motif Consensus sequence: DAHCACGTGD



Reverse complement motif Consensus sequence: BCACGTGDTD



Dataset #: 3
Motif ID: 95
Motif name: MYCMAX
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2
Number of overlap: 7
Similarity score: 0.0108143

Alignment:

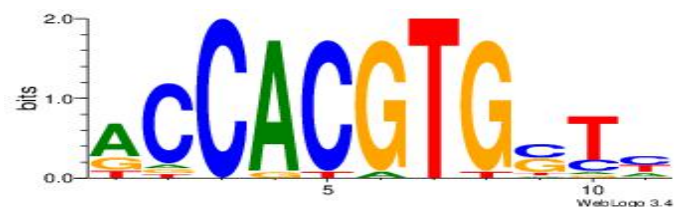
RASCACGTGGT

---CACGTGR--

Original motif Consensus sequence: RASCACGTGGT



Reverse complement motif Consensus sequence: ACCACGTGSTM



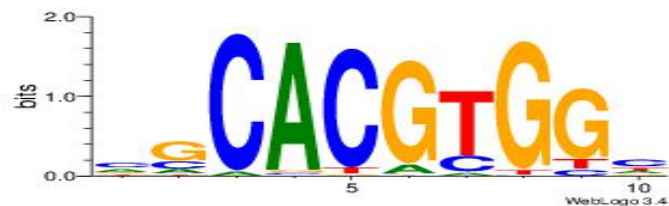
Dataset #: 3
 Motif ID: 94
 Motif name: Myc
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 7
 Similarity score: 0.0198377

Alignment:

VGCACGTGGH

--CACGTGR--

Original motif Consensus sequence: VGCACGTGGH



Reverse complement motif Consensus sequence: DCCACGTGCV

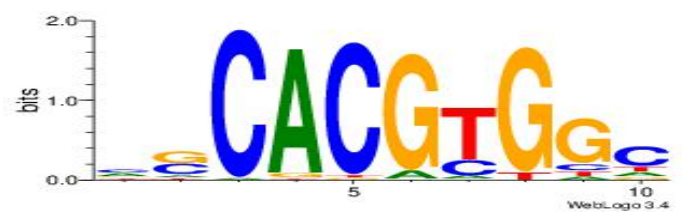


Dataset #: 3
 Motif ID: 96
 Motif name: Mycn
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 7

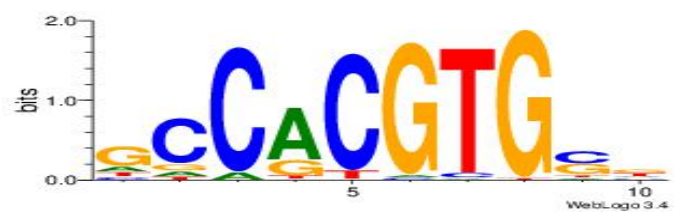
Similarity score: 0.0207062

Alignment:
HSCACGTGGC
--CACGTGR--

Original motif Consensus sequence: HSCACGTGGC



Reverse complement motif Consensus sequence: GCCACGTGSD



Dataset #: 3
Motif ID: 86
Motif name: HIF1AARNT
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 7
Similarity score: 0.0436113

Alignment:
VBACGTGV
-MCACGTG

Original motif Consensus sequence: VBACGTGV

Reverse complement motif Consensus sequence: VCACGTBV



Dataset #: 3 Motif ID: 127 Motif name: YY1

Original motif Consensus sequence: RCCATB



Reverse complement motif Consensus sequence: BATGGM



Best Matches for Motif ID 127 (Highest to Lowest)

Dataset #:	2
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:	2
Number of overlap:	6
Similarity score:	0.00122549

Alignment:

KCCATCT

-RCCATB

Original motif Consensus sequence: AGATGGY



Reverse complement motif Consensus sequence: KCCATCT



Dataset #:	1
Motif ID:	12
Motif name:	Motif 12
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	3
Number of overlap:	6
Similarity score:	0.00857843

Alignment:
GAGCCATC
RCCATB--

Original motif Consensus sequence: GATGGCTC



Reverse complement motif Consensus sequence: GAGCCATC

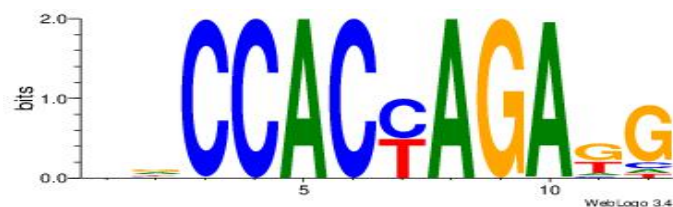


Dataset #: 4
 Motif ID: 145
 Motif name: grCCACyAGAkG
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 6
 Similarity score: 0.022036

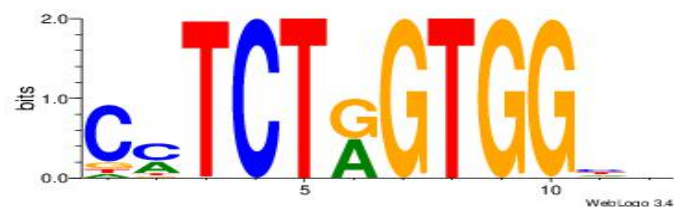
Alignment:

CYTCTKGTGGHH
 -----BATGGM-

Original motif Consensus sequence: DDCCACYAGAKG



Reverse complement motif Consensus sequence: CYTCTKGTGGHH

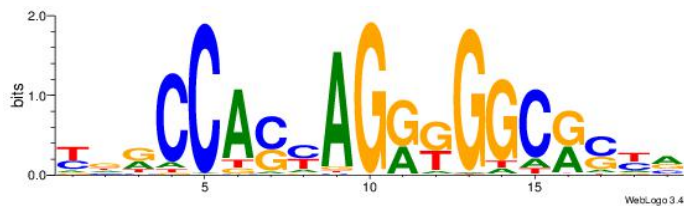


Dataset #: 3
 Motif ID: 74
 Motif name: CTCF
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 6

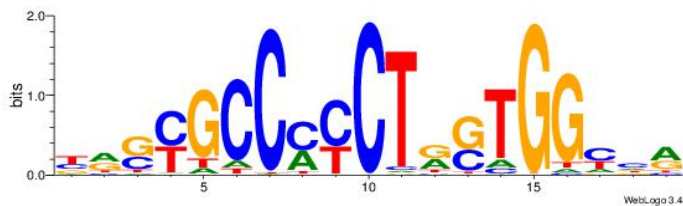
Similarity score: 0.0220417

Alignment:
BMSGCCYMCTKSTGGMHM
-----BATGGM--

Original motif Consensus sequence: YDRCCASYAGRKGGRSYV



Reverse complement motif Consensus sequence:
BMSGCCYMCTKSTGGMHM

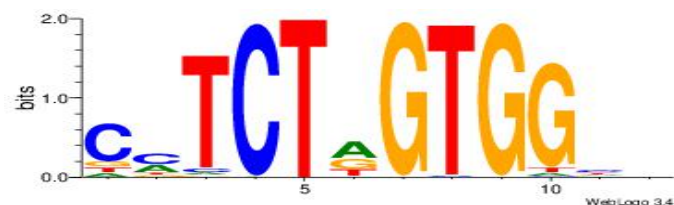
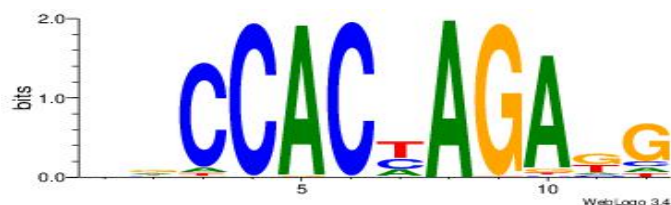


Dataset #: 4
Motif ID: 138
Motif name: grCCACyAGAkG
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 2
Number of overlap: 6
Similarity score: 0.0223679

Alignment:
DDCCACYAGAKG
-RCCATB-----

Original motif Consensus sequence: DDCCACYAGAKG

Reverse complement motif Consensus sequence: CYTCTMGTGGHH



Dataset #: 3 Motif ID: 128 Motif name: ZEB1

Original motif Consensus sequence: CACCTD



Reverse complement motif Consensus sequence: HAGGTG



Best Matches for Motif ID 128 (Highest to Lowest)

Dataset #:	3
Motif ID:	120
Motif name:	T
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	2
Number of overlap:	6
Similarity score:	0.0192581

Alignment:

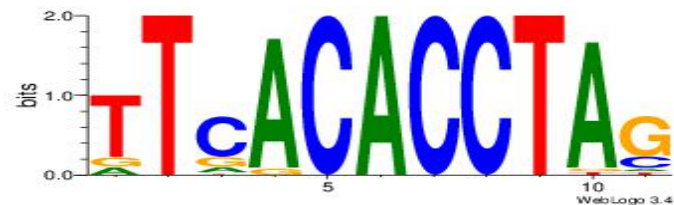
TTCACACCTAG

-CACCTD----

Original motif Consensus sequence: CTAGGTGTGAA



Reverse complement motif Consensus sequence: TTCACACCTAG

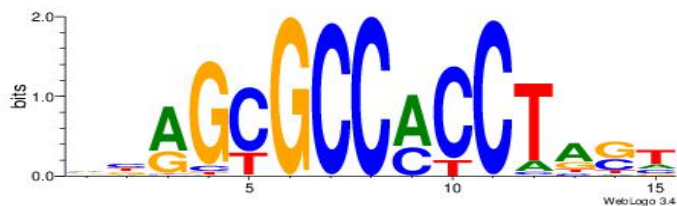


Dataset #: 4
 Motif ID: 146
 Motif name: myrGYGCCmCCTast
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 6
 Similarity score: 0.0325288

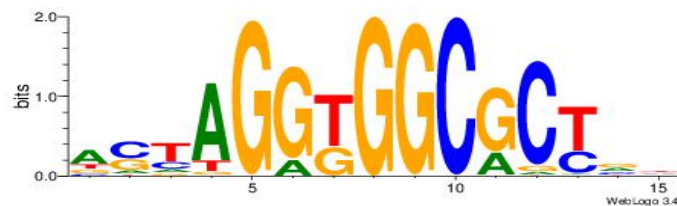
Alignment:

VBAGCGCCMCCTAST
 -----CACCTD--

Original motif Consensus sequence: VBAGCGCCMCCTAST



Reverse complement motif Consensus sequence: ASTAGGYGGCGCT

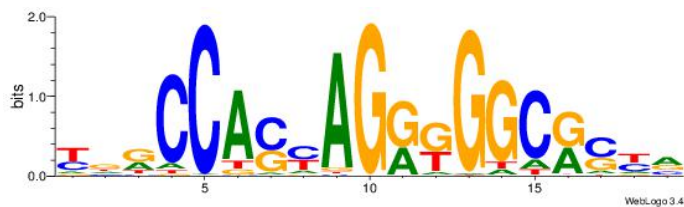


Dataset #: 3
 Motif ID: 74
 Motif name: CTCF
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 8
 Number of overlap: 6
 Similarity score: 0.0341274

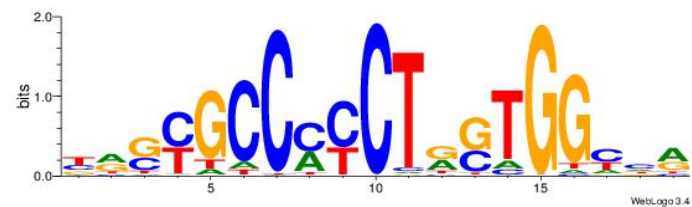
Alignment:

BSMGCCYMCTKSTGGMHM
 -----CACCTD-----

Original motif Consensus sequence: YDRCCASYAGRKGGRSYV



Reverse complement motif Consensus sequence: BSMGCCYMCTKSTGGMHM

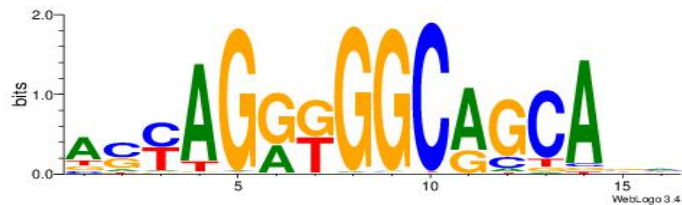


Dataset #: 4
 Motif ID: 164
 Motif name: asyAGrkGGCRGCaga
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3

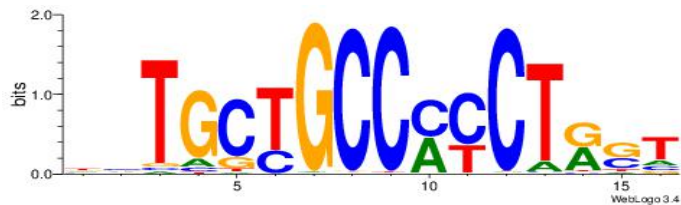
Number of overlap: 6
Similarity score: 0.0351031

Alignment:
ASYAGRKGGCAGCABH
--HAGGTG-----

Original motif Consensus sequence: ASYAGRKGGCAGCABH



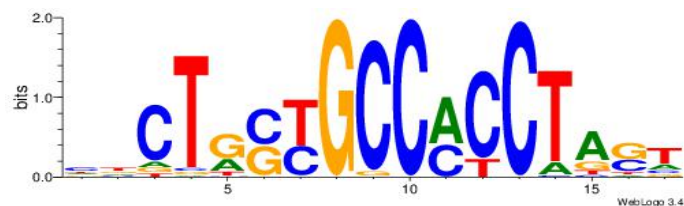
Reverse complement motif Consensus sequence:
HBTGCTGCCYMCTKST



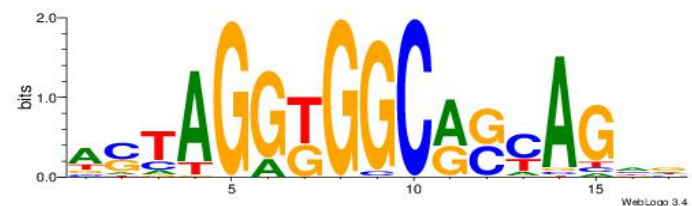
Dataset #: 4
Motif ID: 144
Motif name: ctCTrsyGCCmCCTast
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 3
Number of overlap: 6
Similarity score: 0.0356696

Alignment:
HDCTGSYGCCMCCTAST
-----CACCTD--

Original motif Consensus sequence: HDCTGSYGCCMCCTAST

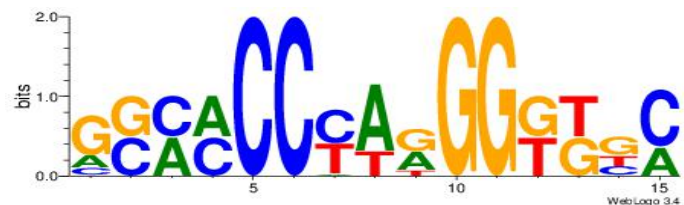


Reverse complement motif Consensus sequence: ASTAGGYGGCMSCAGDD

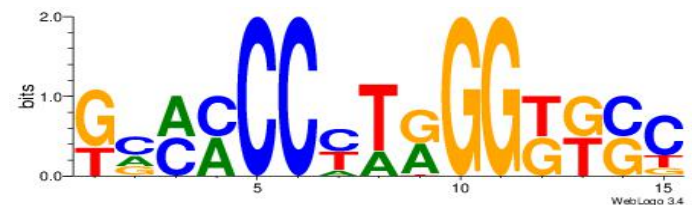


Dataset #: 3 Motif ID: 129 Motif name: Zfp423

Original motif Consensus sequence: GSMMCCYARGGKKKC



Reverse complement motif Consensus sequence: GYRYCCMTKGGYR



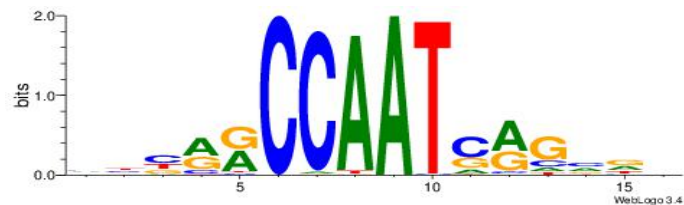
Best Matches for Motif ID 129 (Highest to Lowest)

Dataset #:	3
Motif ID:	104
Motif name:	NFYA
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:	0.0358106

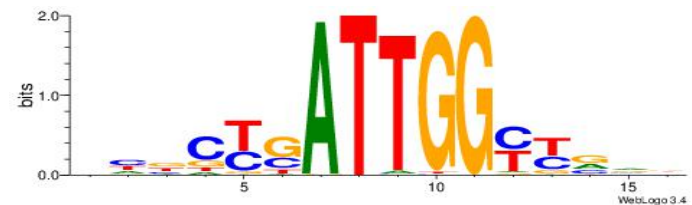
Alignment:

BHVCKSATGGMKBVV
GYRYCCMTKGGYRSC-

Original motif Consensus sequence: VBBRCCAATSRGVDB



Reverse complement motif Consensus sequence:
BHVCKSATGGMKBVV



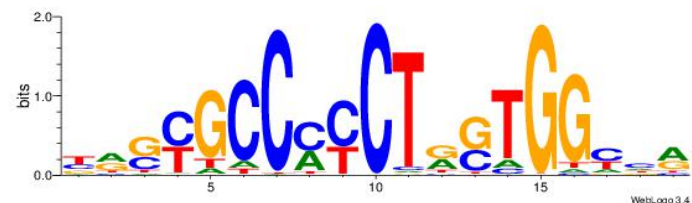
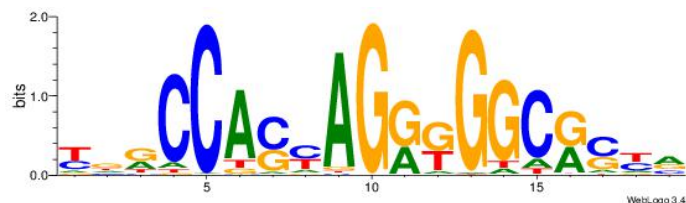
Dataset #:	3
Motif ID:	74
Motif name:	CTCF
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	3
Number of overlap:	15
Similarity score:	0.0359705

Alignment:

BMSMGCCYMCTKSTGGMHM
--GYRYCCMTKGGYRSC--

Original motif Consensus sequence: YDRCCASYAGRKGGRSYV

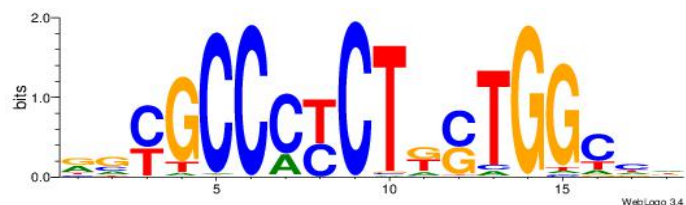
Reverse complement motif Consensus sequence:
BMSMGCCYMCTKSTGGMHM



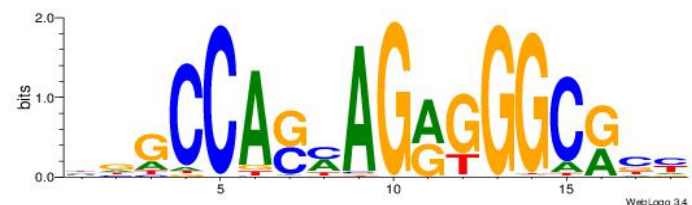
Dataset #: 4
 Motif ID: 156
 Motif name: rgyGCCMyCTksTGGccd
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 15
 Similarity score: 0.0382225

Alignment:
 RVYGCCCYCTKSTGGCHD
 -GYRYCCMTKGGYRSC--

Original motif Consensus sequence: RVYGCCCYCTKSTGGCHD



Reverse complement motif Consensus sequence: DDGCCASYAGMGGGCKVM



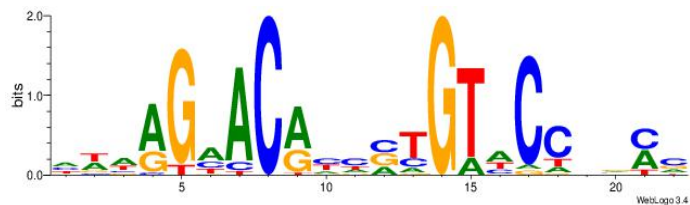
Dataset #: 3

Motif ID: 70
 Motif name: Ar
 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: 0.0429662

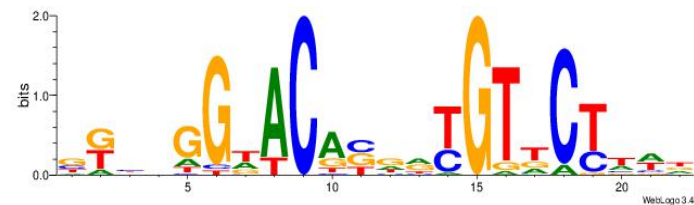
Alignment:

HWDAGHACRHHVTGTHCCHVMV
 ---GSMCCYARGGKKKC---

Original motif Consensus sequence: HWDAGHACRHHVTGTHCCHVMV



Reverse complement motif Consensus sequence: VRVDGGHACAVDDKGTHCTDWH

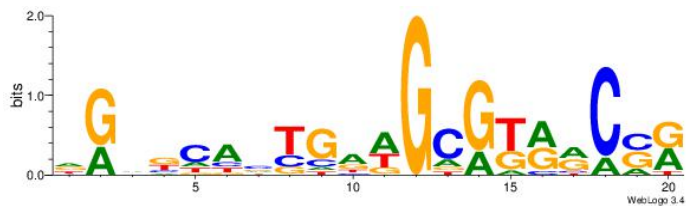


Dataset #: 3
 Motif ID: 109
 Motif name: Pax5
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 15

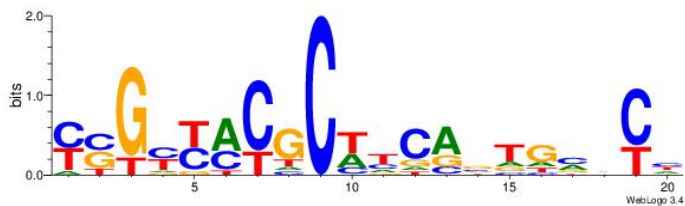
Similarity score: 0.0430294

Alignment:
DGVBCABTGDWGCGRRCR
--GSMCCYARGGKKKC---

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR

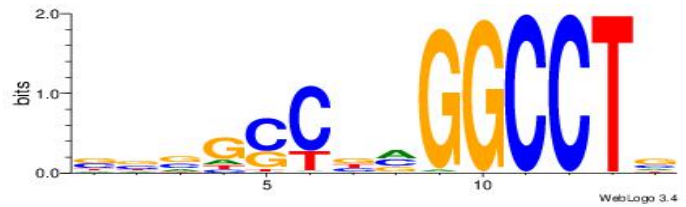


Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBCD

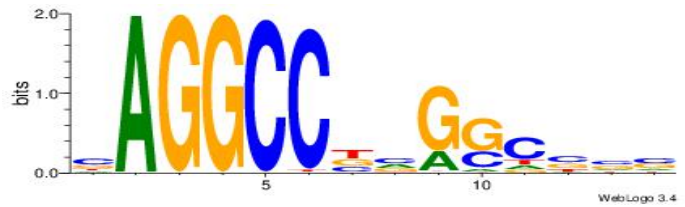


Dataset #: 3 Motif ID: 130 Motif name: Zfx

Original motif Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif Consensus sequence: VAGGCCBBGGCV



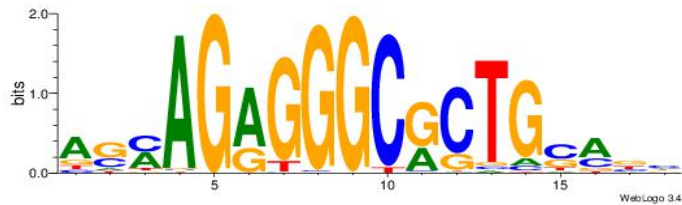
Best Matches for Motif ID 130 (Highest to Lowest)

Dataset #:	4
Motif ID:	149
Motif name:	asmAGRGGGCrCTGsmkc
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement

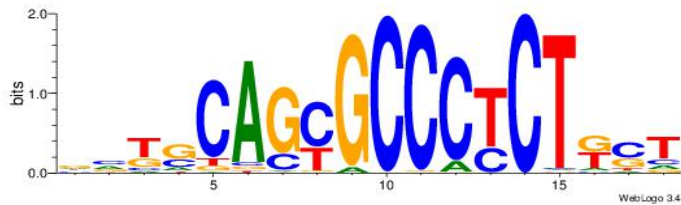
Direction: Forward
Position number: 1
Number of overlap: 14
Similarity score: 0.0651255

Alignment:
DBTSCAGMGCCCTCTRST
BBVGCCBVGGCCTV----

Original motif Consensus sequence: ASMAGAGGGCRCTGSABH



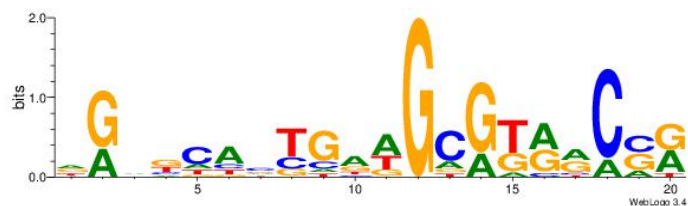
Reverse complement motif Consensus sequence: DBTSCAGMGCCCTCTRST



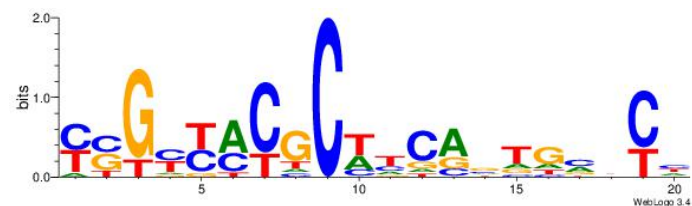
Dataset #: 3
Motif ID: 109
Motif name: Pax5
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 5
Number of overlap: 14
Similarity score: 0.0724025

Alignment:
DGVBCABTGDWGCGRRCR
--BBVGCCBVGGCCTV----

Original motif Consensus sequence: DGVBCABTGDWGCGRRCRCSR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBBCD

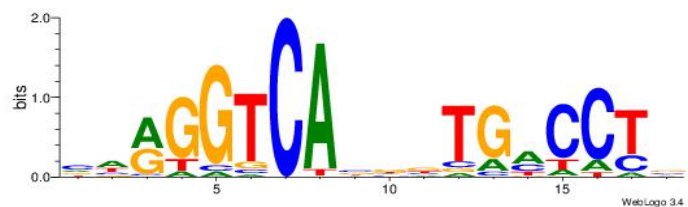


Dataset #: 3
Motif ID: 82
Motif name: ESR2
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2
Number of overlap: 14
Similarity score: 0.0748557

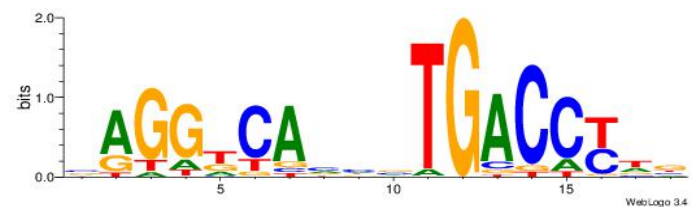
Alignment:

VHRGGTCABDBTGMCCCTB
---VAGGCCBBGGCVBB-

Original motif Consensus sequence: VHRGGTCABDBTGMCCCTB



Reverse complement motif Consensus sequence: BAGGYCABHBTGACCKHV

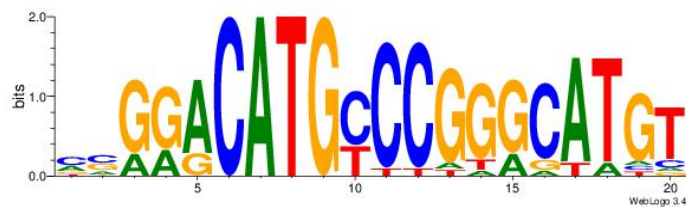


Dataset #: 3
 Motif ID: 125
 Motif name: TP53
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 6
 Number of overlap: 14
 Similarity score: 0.0763693

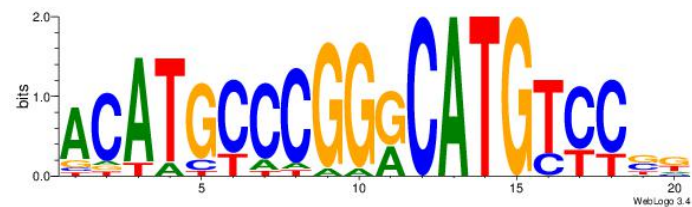
Alignment:

ACATGCCCGGKCATGTCCSR
 -----BBVGCCBVGGCCTV-

Original motif Consensus sequence: MSGGACATGYCCGGGCATGT



Reverse complement motif Consensus sequence: ACATGCCCGGKCATGTCCSR



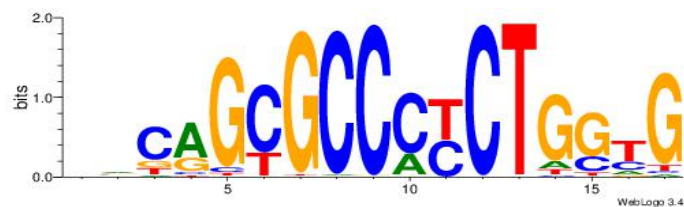
Dataset #: 4
 Motif ID: 168
 Motif name: yrcrGYGCCMyCTGGtG
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1

Number of overlap: 14
Similarity score: 0.0830122

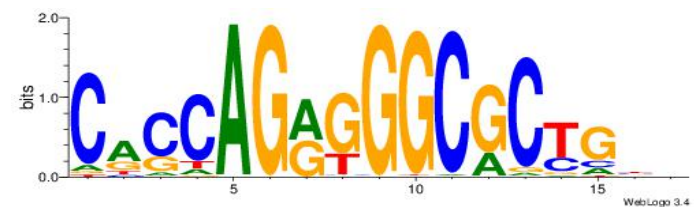
Alignment:

HVCAGCGCCCYCTGGTG
BBVGCCBVGGCCTV---

Original motif Consensus sequence: HVCAGCGCCCYCTGGTG

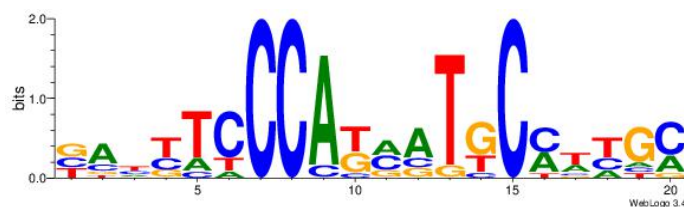


Reverse complement motif Consensus sequence: CACCAGMGGGCGCTGBD

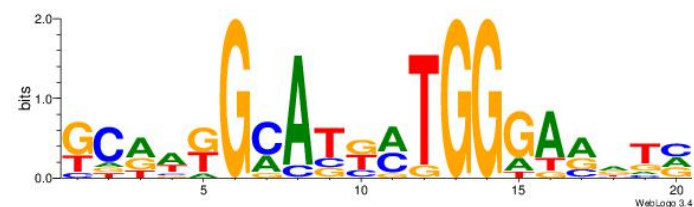


Dataset #: 3 Motif ID: 131 Motif name: znf143

Original motif Consensus sequence: BAHYTCCCAKMATGCMWYGC



Reverse complement motif Consensus sequence: GCMWRGCATYRTGGGAMHTB



Best Matches for Motif ID 131 (Highest to Lowest)

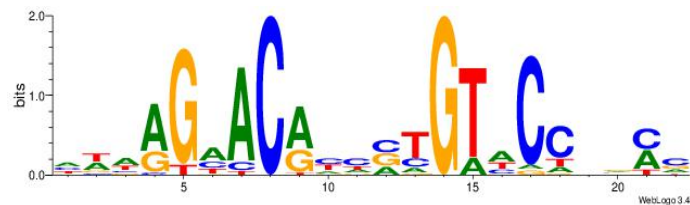
Dataset #: 3
Motif ID: 70
Motif name: Ar

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:	0.0555912

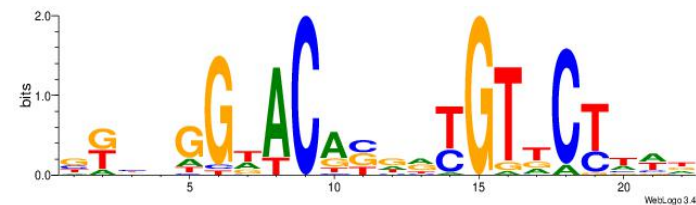
Alignment:

```
VRVDGGHACAVDDKGTHCTDWH
GCMWRGCATYRTGGGAMHTB--
```

Original motif Consensus sequence: HWDAGHACRHHVTGTHCCHVMV



Reverse complement motif Consensus sequence: VRVDGGHACAVDDKGTHCTDWH

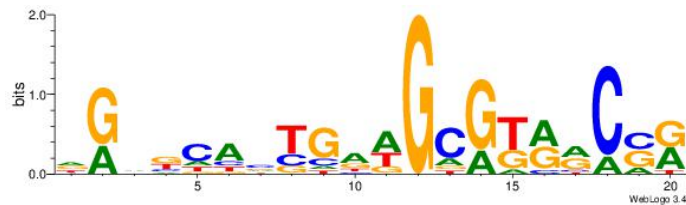


Dataset #:	3
Motif ID:	109
Motif name:	Pax5
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	19
Similarity score:	0.554242

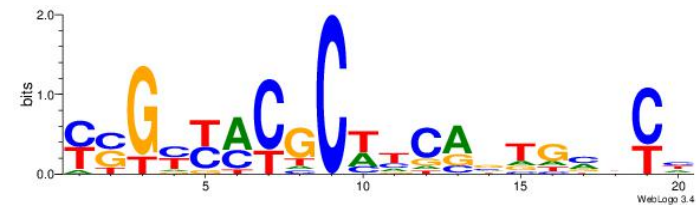
Alignment:

DGVBCABTGDWGCGRRCR-
-GCMWRGCATYRTGGGAMHTB

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR



Reverse complement motif Consensus sequence:
MSGKKRCGCWDCABTGBCD



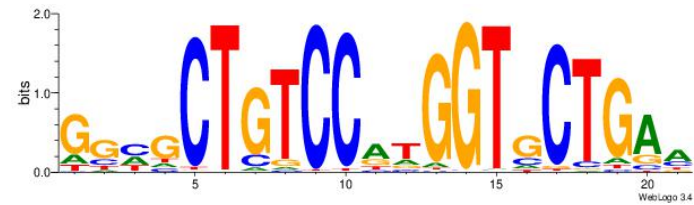
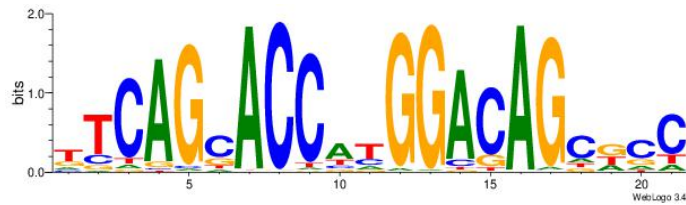
Dataset #:	3
Motif ID:	113
Motif name:	REST
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	3
Number of overlap:	19
Similarity score:	0.558571

Alignment:

-GGYGCTGTCCATGGTGCTGAA
BAHYTCCCAKMATGCMWYGC--

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC

Reverse complement motif Consensus sequence:
GGYGCTGTCCATGGTGCTGAA

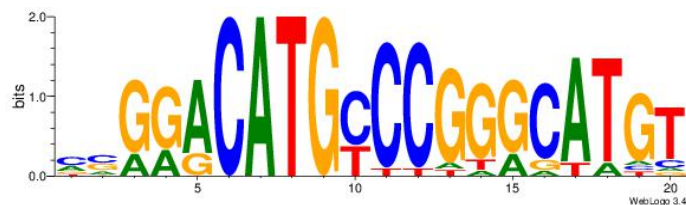


Dataset #: 3
 Motif ID: 125
 Motif name: TP53
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 19
 Similarity score: 0.566085

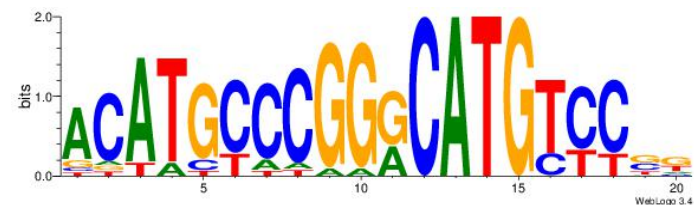
Alignment:

MSGGACATGYCCGGGCATGT-
 -GCMWRGCATYRTGGGAMHTB

Original motif Consensus sequence: MSGGACATGYCCGGGCATGT



Reverse complement motif Consensus sequence: ACATGCCCGGKCATGTCCSR



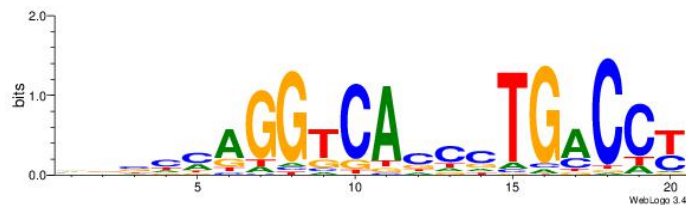
Dataset #: 3

Motif ID: 81
 Motif name: ESR1
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 18
 Similarity score: 1.05907

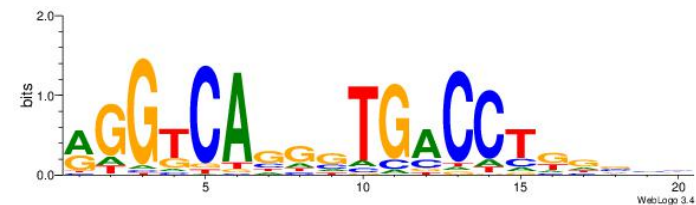
Alignment:

VDBHMAGGTCACCCTGACCY--
 --BAHYTCCCAKMATGCMWYGC

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV



Dataset #: 3 Motif ID: 132 Motif name: ZNF354C

Original motif Consensus sequence: MTCCAC



Reverse complement motif Consensus sequence: GTGGAY



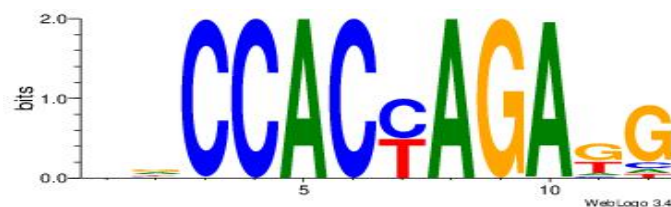
Best Matches for Motif ID 132 (Highest to Lowest)

Dataset #: 4
Motif ID: 145
Motif name: grCCACyAGAkG
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 7
Number of overlap: 6
Similarity score: 0.0253111

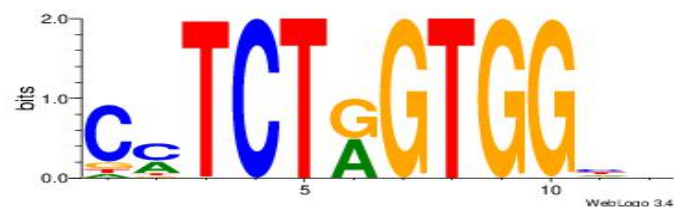
Alignment:

CYTCTKGTGGHH
-----GTGGAY

Original motif Consensus sequence: DDCCACYAGAKG



Reverse complement motif Consensus sequence: CYTCTKGTGGHH



Dataset #: 4
Motif ID: 158
Motif name: grCCACwAGrk
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement

Direction: Forward
Position number: 6
Number of overlap: 6
Similarity score: 0.0266594

Alignment:
YMCTWGTGGHH
-----GTGGAY

Original motif Consensus sequence: DDCCACWAGRK



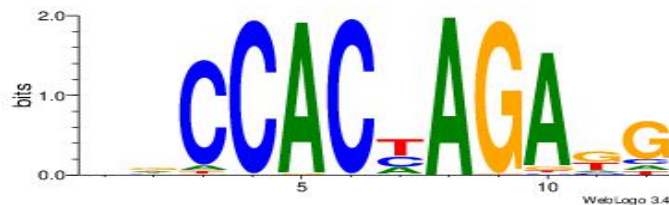
Reverse complement motif Consensus sequence: YMCTWGTGGHH



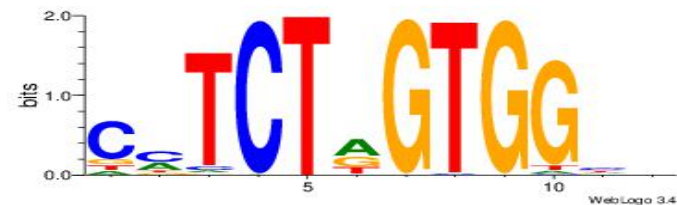
Dataset #: 4
Motif ID: 138
Motif name: grCCACyAGAkG
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 7
Number of overlap: 6
Similarity score: 0.0292621

Alignment:
CYTCTMGTGGHH
-----GTGGAY

Original motif Consensus sequence: DDCCACYAGAKG



Reverse complement motif Consensus sequence: CYTCTMGTGGHH

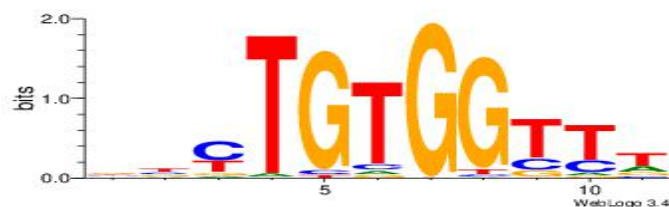


Dataset #: 3
Motif ID: 114
Motif name: RUNX1
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 5
Number of overlap: 6
Similarity score: 0.0470937

Alignment:

BBYTGTGGTTT
-GTGGAY----

Original motif Consensus sequence: BBYTGTGGTTT



Reverse complement motif Consensus sequence: AAACCACAKVB



Dataset #: 1
 Motif ID: 9
 Motif name: Motif 9
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 6
 Similarity score: 0.0507812

Alignment:
 SWGCCACC
 -MTCCAC-

Original motif Consensus sequence: GGTGGCWS



Reverse complement motif Consensus sequence: SWGCCACC



Dataset #: 4 Motif ID: 133 Motif name: shAGrGGGCAGy

Original motif Consensus sequence: SHAGRGGGCABH



Reverse complement motif Consensus sequence: DBTGCCCKCTDS



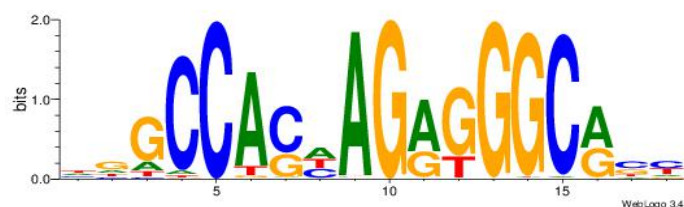
Best Matches for Motif ID 133 (Highest to Lowest)

Dataset #: 4
Motif ID: 165
Motif name: wgGCCAshAGrGGGCrSy
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 7
Number of overlap: 12
Similarity score: 0.00159897

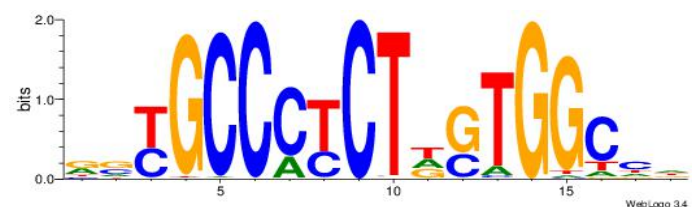
Alignment:

```
HDGCCACHAGRGGGCRBY  
-----SHAGRGGGCABH
```

Original motif Consensus sequence: HDGCCACHAGRGGGCRBY



Reverse complement motif Consensus sequence: KBKGCCCKCTHGTGGCHH

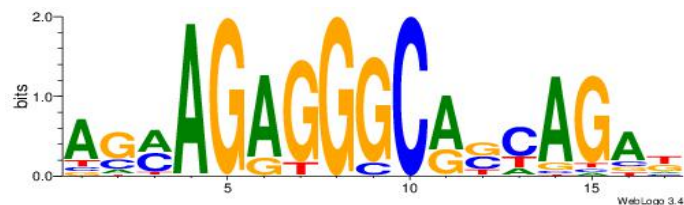


Dataset #: 4
Motif ID: 143
Motif name: AgmAGAGGGCrscAGak
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif

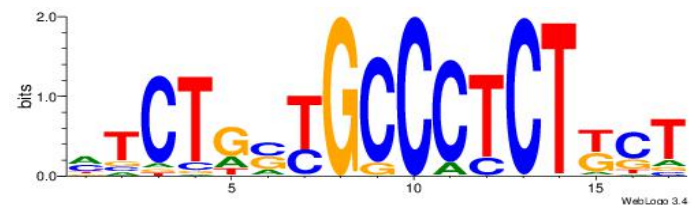
Direction: Backward
 Position number: 5
 Number of overlap: 12
 Similarity score: 0.00815796

Alignment:
 AGMAGAGGGCASCAGAK
 -SHAGRGGGCABH----

Original motif Consensus sequence: AGMAGAGGGCASCAGAK



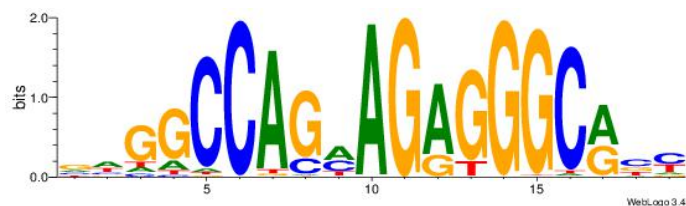
Reverse complement motif Consensus sequence: RTCTGSTGCCCTCTYCT



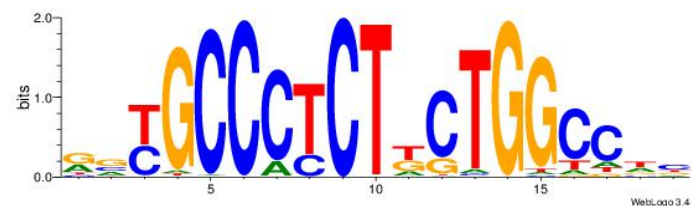
Dataset #: 4
 Motif ID: 163
 Motif name: gwGGCCAGmAGAGGGCrby
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 8
 Number of overlap: 12
 Similarity score: 0.0109424

Alignment:
 VHGGCCAGMAGAGGGCRBY
 -----SHAGRGGGCABH

Original motif Consensus sequence: VHGGCCAGMAGAGGGCRBY



Reverse complement motif Consensus sequence: KBKGCCCTCTYCTGGCCHV



Dataset #: 4
Motif ID: 166
Motif name: CasCAGrGGGCrSy
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: 0.0124424

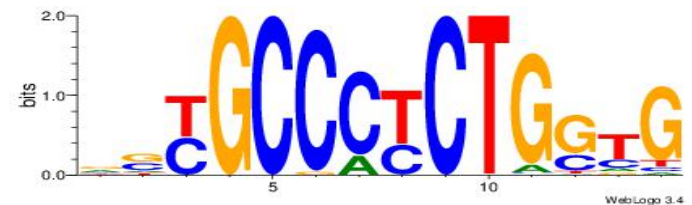
Alignment:

BSKGCCCKCTGGTG
DBTGCCCKCTDS--

Original motif Consensus sequence: CACCAGRGGGCRSB



Reverse complement motif Consensus sequence: BSKGCCCKCTGGT



Dataset #: 4
 Motif ID: 147
 Motif name: asCAGrkGGCrSy
 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: 0.0128393

Alignment:

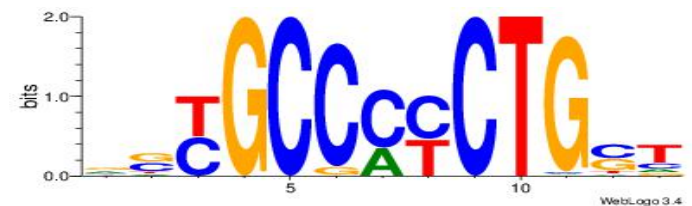
ASCAGRGGGCRSB

–SHAGRGGGCABH

Original motif Consensus sequence: ASCAGRGGGCRSB



Reverse complement motif Consensus sequence: BSKGCCCCMCTGST



Dataset #: 4 Motif ID: 134 Motif name: ssCGwGCGss

Original motif Consensus sequence: BSCGWGCGBV



Reverse complement motif Consensus sequence: VBCGCWCGSB



Best Matches for Motif ID 134 (Highest to Lowest)

Dataset #: 4
Motif ID: 135
Motif name: ssCGGCCGss
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: 0.0113669

Alignment:

BSCGGCCGSV

VBCGCWCGSB

Original motif Consensus sequence: BSCGGCCGSV



Reverse complement motif Consensus sequence: VSCGGCCGSB

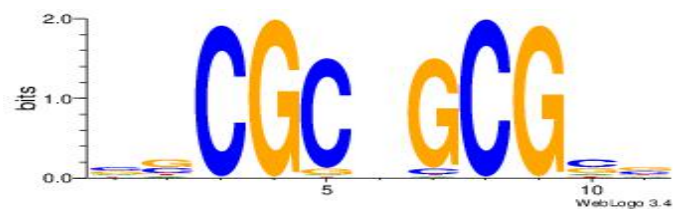


Dataset #: 4
Motif ID: 161
Motif name: ssCGCwGCGss
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif

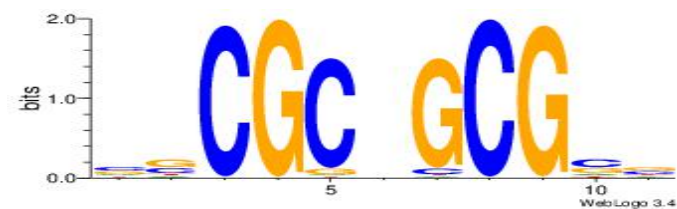
Direction: Backward
 Position number: 2
 Number of overlap: 10
 Similarity score: 0.0473417

Alignment:
 VSCGCDGCGSB
 VBCGCWCGSB-

Original motif Consensus sequence: VSCGCDGCGSB



Reverse complement motif Consensus sequence: BSCGCDGCGSV



Dataset #: 4
 Motif ID: 152
 Motif name: yrCATGCAyr
 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: 0.0541916

Alignment:
 BRCATGCABD
 BSCGWGCGBV

Original motif Consensus sequence: BRCATGCABD



Reverse complement motif Consensus sequence: HVTGCATGKV



Dataset #: 4
Motif ID: 158
Motif name: grCCACwAGrk
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 2
Number of overlap: 10
Similarity score: 0.0546634

Alignment:

DDCCACWAGRK
-VBCGCWCGSB

Original motif Consensus sequence: DDCCACWAGRK



Reverse complement motif Consensus sequence: YMCTWGTGGHH

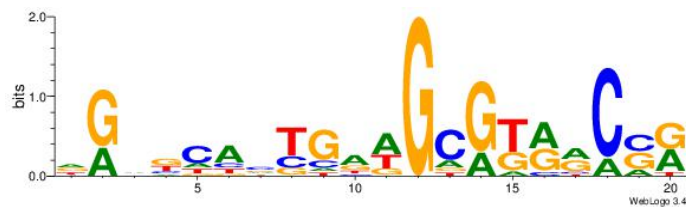


Dataset #: 3
 Motif ID: 109
 Motif name: Pax5
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 7
 Number of overlap: 10
 Similarity score: 0.0551638

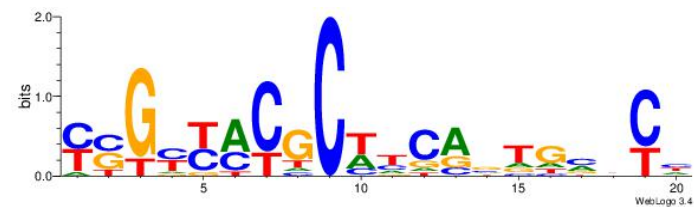
Alignment:

DGVBCABTGDWGCGRRCR
 -----BSCGWGCBV-----

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD



Dataset #: 4 Motif ID: 135 Motif name: ssCGGCCGss

Original motif Consensus sequence: BSCGGCCGSV

Reverse complement motif Consensus sequence: VSCGGCCGSB



Best Matches for Motif ID 135 (Highest to Lowest)

Dataset #: 4
 Motif ID: 134
 Motif name: ssCGwGCGss
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 10
 Similarity score: 0

Alignment:

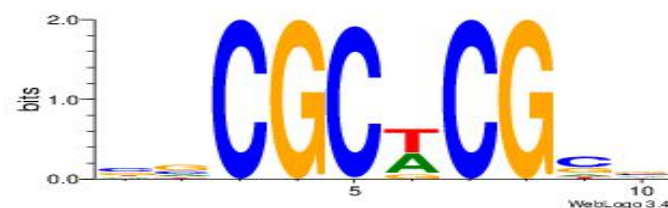
BSCGWGCGBV

VSCGGCCGSB

Original motif Consensus sequence: BSCGWGCGBV



Reverse complement motif Consensus sequence: VBCGOWCGSB



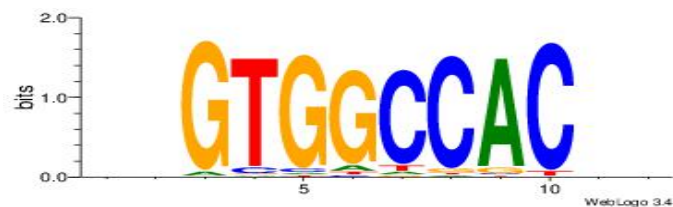
Dataset #: 4

Motif ID: 171
 Motif name: ysGTGGCCACsr
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 10
 Similarity score: 0.0413265

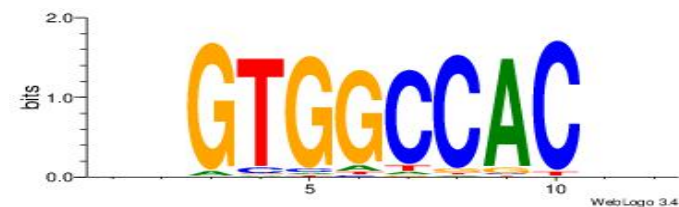
Alignment:

BVGTGGCCACBV
 -VSCGGCCGSB-

Original motif Consensus sequence: BVGTGGCCACBV



Reverse complement motif Consensus sequence: VBGTGGCCACVB

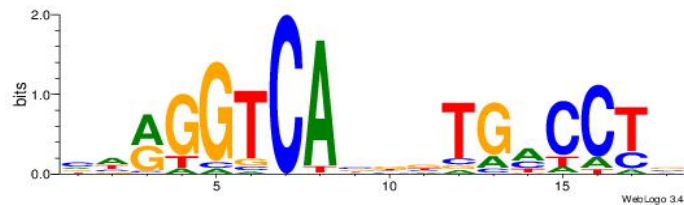


Dataset #: 3
 Motif ID: 82
 Motif name: ESR2
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 10
 Similarity score: 0.0424008

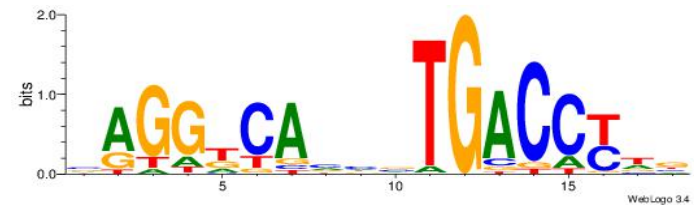
Alignment:

BAGGYCABHBTGACCKHV
-----VSCGGCCGSB

Original motif Consensus sequence: VHRGGTCABDBTGMCTB



Reverse complement motif Consensus sequence:
BAGGYCABHBTGACCKHV



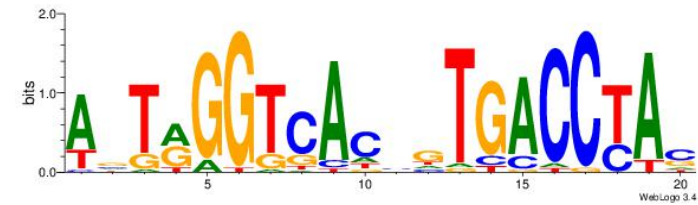
Dataset #:	3
Motif ID:	111
Motif name:	PPARG
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	2
Number of overlap:	10
Similarity score:	0.046338

Alignment:

ABTMGGTCACBGTGACCTAS
-VSCGGCCGSB-----

Original motif Consensus sequence: STAGGTCACBGTGACCYABT

Reverse complement motif Consensus sequence:
ABTMGGTCACBGTGACCTAS



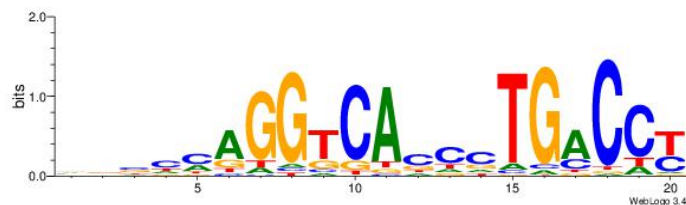
Dataset #:	3
Motif ID:	81
Motif name:	ESR1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	8
Number of overlap:	10
Similarity score:	0.0468951

Alignment:

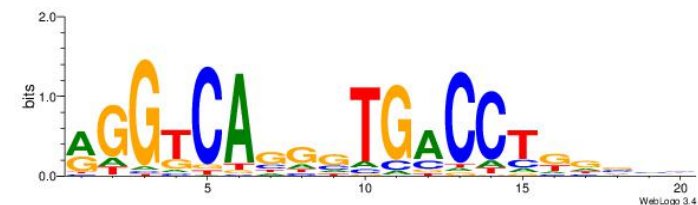
MGGTCAGGGTGACCTRDBHV

-----VSCGGCCGSB----

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif Consensus sequence:
MGGTCAGGGTGACCTRDBHV

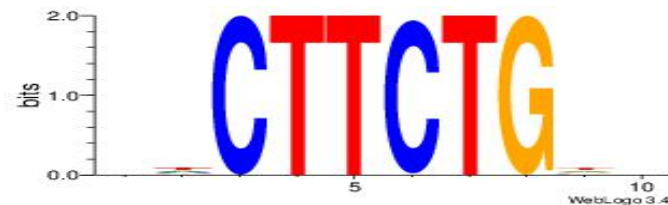


Dataset #: 4 Motif ID: 136 Motif name: dwCAGAAGwh

Original motif Consensus sequence: DHCAGAAAGDH



Reverse complement motif Consensus sequence: HDCTTCTGHD



Best Matches for Motif ID 136 (Highest to Lowest)

Dataset #: 4
 Motif ID: 151
 Motif name: agrCCAGmAGrg
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 10
 Similarity score: 0.00562474

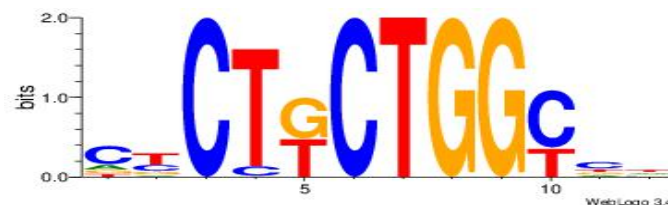
Alignment:

HVGCCAGMAGRG
 --DHCAGAAAGDH

Original motif Consensus sequence: HVGCCAGMAGRG



Reverse complement motif Consensus sequence: CKCTRCTGGCVH



Dataset #: 4
 Motif ID: 141
 Motif name: raCAAAACam
 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: 0.0107169

Alignment:

DACAAAACAH

DHCAGAAGDH

Original motif Consensus sequence: DACAAAACAH



Reverse complement motif Consensus sequence: HTGTTTTGTD



Dataset #: 4
 Motif ID: 158
 Motif name: grCCACwAGrk
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 10

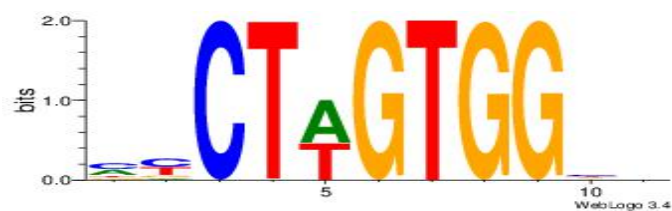
Similarity score: 0.0167426

Alignment:
DDCCACWAGRK
-DHCAGAAGDH

Original motif Consensus sequence: DDCCACWAGRK



Reverse complement motif Consensus sequence: YMCTWGTGGHH

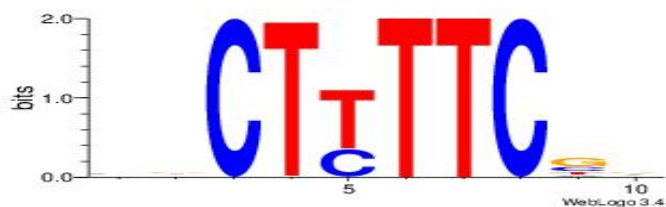


Dataset #: 4
Motif ID: 139
Motif name: mkCTyTTCsg
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 10
Similarity score: 0.0207259

Alignment:
HBCTTTTCBD
HDCTTCTGHD

Original motif Consensus sequence: HBCTTTTCBD

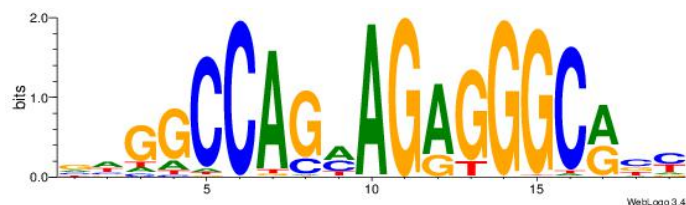
Reverse complement motif Consensus sequence: HBGAAAAGBD



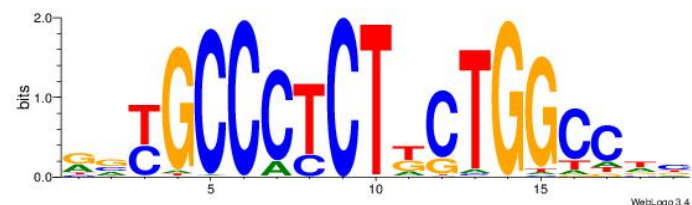
Dataset #: 4
 Motif ID: 163
 Motif name: gwGGCCAGmAGAGGGCrby
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 10
 Similarity score: 0.0212719

Alignment:
 VHGGCCAGMAGAGGGCRBY
 ---DHCAGAAGDH-----

Original motif Consensus sequence: VHGGCCAGMAGAGGGCRBY

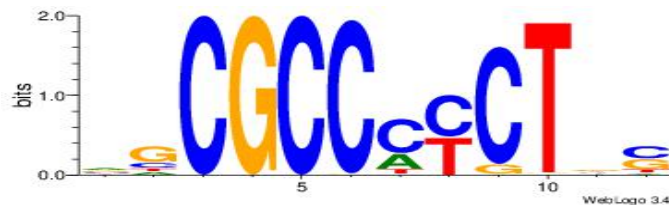


Reverse complement motif Consensus sequence: KBKGCCCTCTYCTGGCCHV

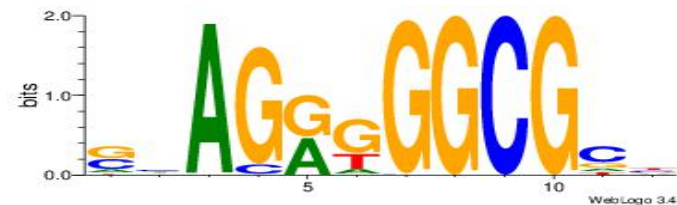


Dataset #: 4 Motif ID: 137 Motif name: rgCGCCmyCTgs

Original motif Consensus sequence: VGCGCCCYCTDS



Reverse complement motif Consensus sequence: SHAGKGGGCGCB



Best Matches for Motif ID 137 (Highest to Lowest)

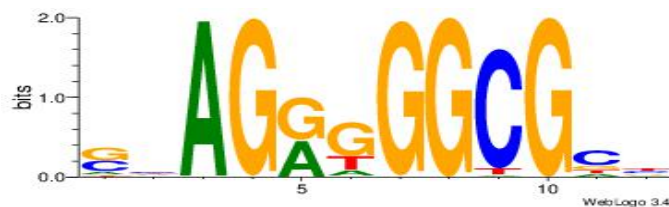
Dataset #:	4
Motif ID:	153
Motif name:	scAGrkGGCGcy
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	12
Similarity score:	0

Alignment:

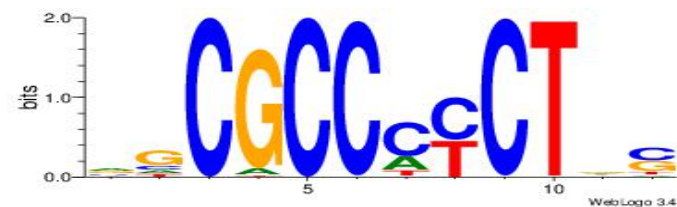
VGCGCCCMCTDS

VGCGCCCYCTDS

Original motif Consensus sequence: SHAGRGGGCGCB



Reverse complement motif Consensus sequence: VGCGCCCMCTDS

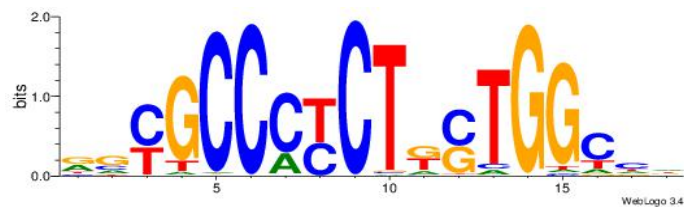


Dataset #: 4
 Motif ID: 156
 Motif name: rgyGCCMyCTksTGGccd
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 7
 Number of overlap: 12
 Similarity score: 0.00894839

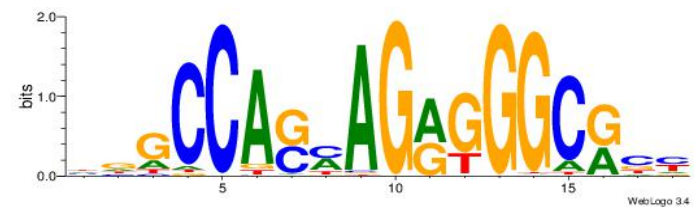
Alignment:

RVYGCCCYCTKSTGGCHD
 VGCGCCCYCTDS-----

Original motif Consensus sequence: RVYGCCCYCTKSTGGCHD



Reverse complement motif Consensus sequence: DDGCCASYAGMGGGCKVM

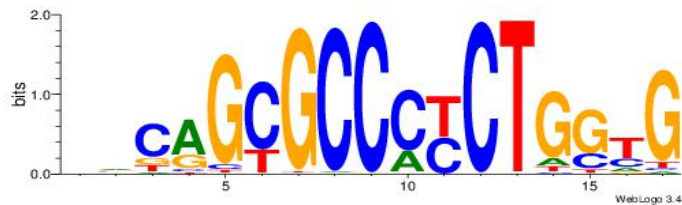


Dataset #: 4
 Motif ID: 168
 Motif name: yrcrGYGCCMyCTGGtG
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3

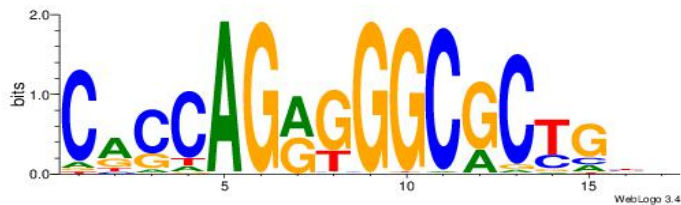
Number of overlap: 12
Similarity score: 0.0183868

Alignment:
HVCAGCGCCCYCTGGTG
---VCGGCCCYCTDS--

Original motif Consensus sequence: HVCAGCGCCCYCTGGTG



Reverse complement motif Consensus sequence: CACCAGMGGGCGCTGBD

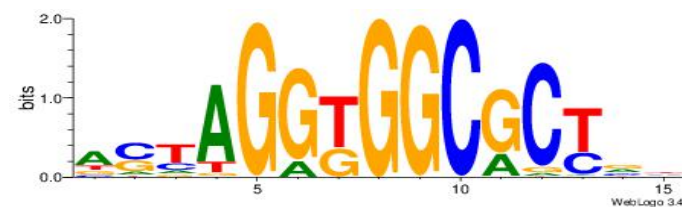
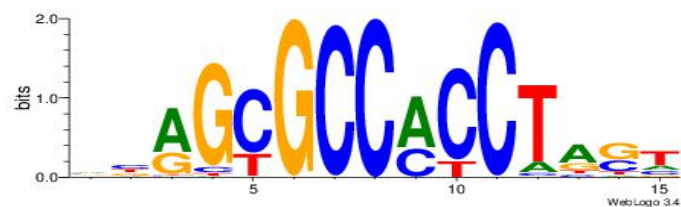


Dataset #: 4
Motif ID: 146
Motif name: myrGYGCCmCCTast
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 3
Number of overlap: 12
Similarity score: 0.0261893

Alignment:
VBAGCGCCMCCTAST
--VCGGCCCYCTDS-

Original motif Consensus sequence: VBAGCGCCMCCTAST

Reverse complement motif Consensus sequence: ASTAGGYGGCGCT



Dataset #: 4
 Motif ID: 147
 Motif name: asCAGrkGGCrSy
 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: 0.0284224

Alignment:

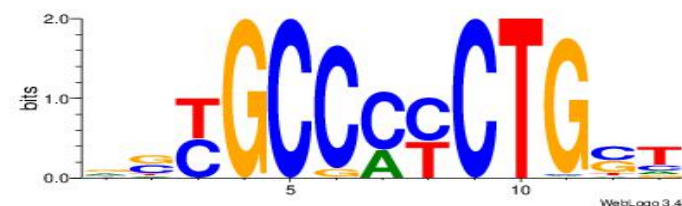
ASCAGRGGGCRSB

–SHAGKGGGCGCB

Original motif Consensus sequence: ASCAGRGGGCRSB

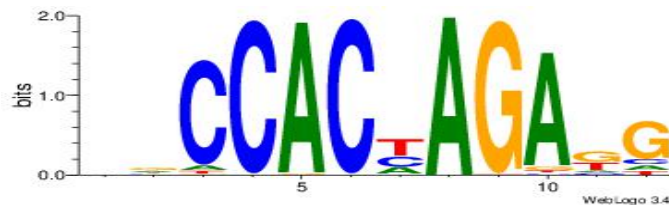


Reverse complement motif Consensus sequence: BSKGCCCMCTGST

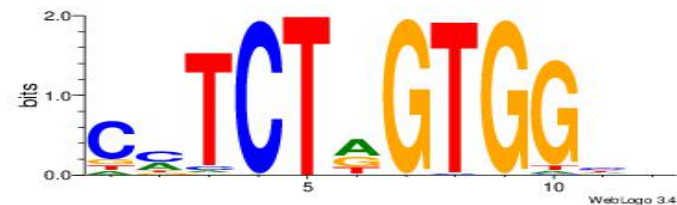


Dataset #: 4 Motif ID: 138 Motif name: grCCACyAGAkG

Original motif Consensus sequence: DDCCACYAGAKG



Reverse complement motif Consensus sequence: CYTCTMGTGGHH



Best Matches for Motif ID 138 (Highest to Lowest)

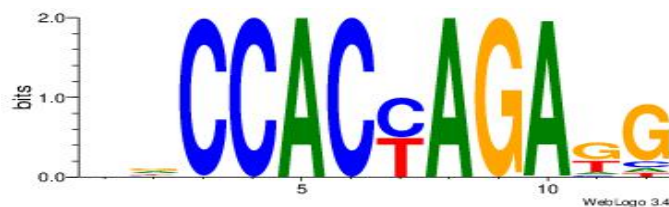
Dataset #:	4
Motif ID:	145
Motif name:	grCCACyAGAkG
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	12
Similarity score:	0

Alignment:

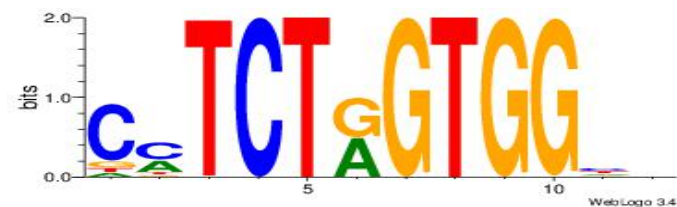
DDCCACYAGAKG

DDCCACYAGAKG

Original motif Consensus sequence: DDCCACYAGAKG



Reverse complement motif Consensus sequence: CYTCTKGTGGHH

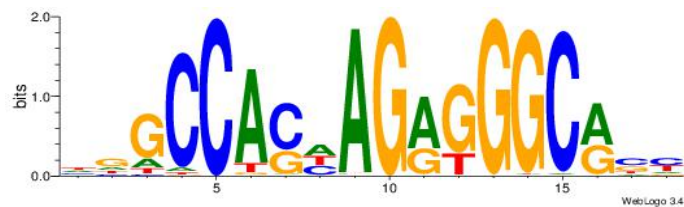


Dataset #: 4
 Motif ID: 165
 Motif name: wgGCCAshAGrGGGCrSy
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 12
 Similarity score: 0.0317718

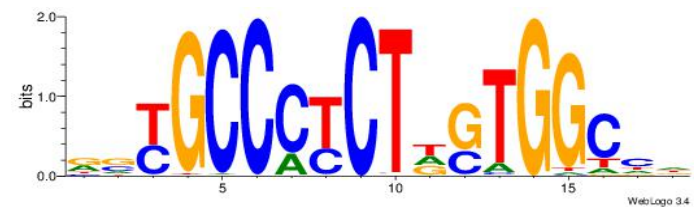
Alignment:

HDGCCACHAGRGGGCRBY
 -DDCCACYAGAKG-----

Original motif Consensus sequence: HDGCCACHAGRGGGCRBY



Reverse complement motif Consensus sequence: KBKGCCCKCTHGTGGCHH



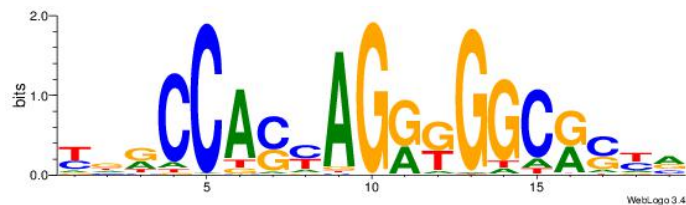
Dataset #: 3
 Motif ID: 74
 Motif name: CTCF
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 7

Number of overlap: 12
Similarity score: 0.0332329

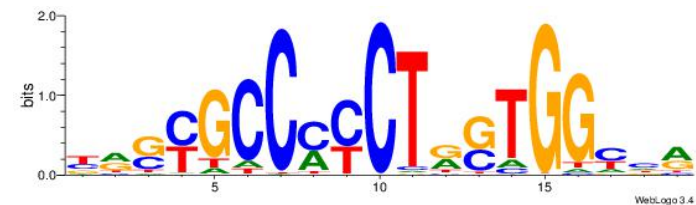
Alignment:

YDRCCASYAGRKGGRSYV
-DDCCACYAGAKG-----

Original motif Consensus sequence: YDRCCASYAGRKGGRSYV



Reverse complement motif Consensus sequence: BMSMGCCYMCTKSTGGMHM

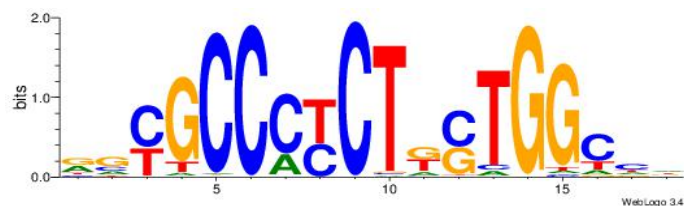


Dataset #: 4
Motif ID: 156
Motif name: rgyGCCMyCTksTGGccd
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 6
Number of overlap: 12
Similarity score: 0.0390921

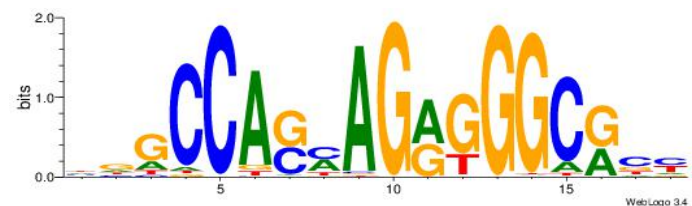
Alignment:

DDGCCASYAGMGGGCKVM
-DDCCACYAGAKG-----

Original motif Consensus sequence: RYVCCCCYCTKSTGGCHD



Reverse complement motif Consensus sequence: DDGCCASYAGMGGGCKVM

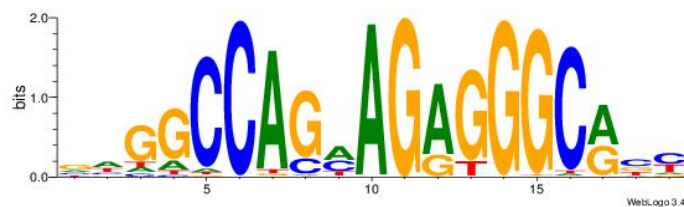


Dataset #: 4
Motif ID: 163
Motif name: gwGGCCAGmAGAGGGCrby
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 3
Number of overlap: 12
Similarity score: 0.0478776

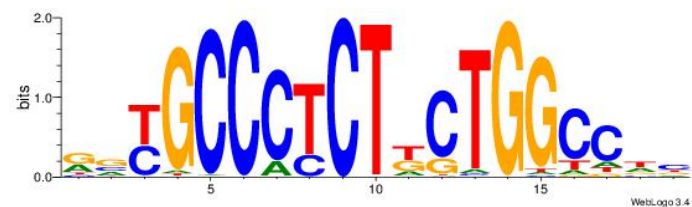
Alignment:

VHGGCCAGMAGAGGGCRBY
--DDCCACYAGAKG-----

Original motif Consensus sequence: VHGGCCAGMAGAGGGCRBY

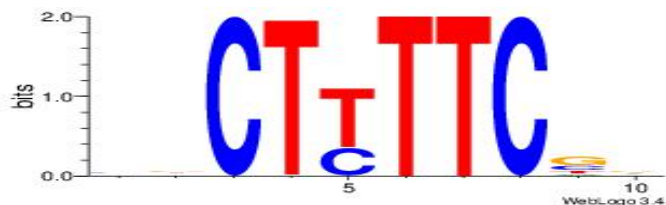


Reverse complement motif Consensus sequence: KBKGCCCTCTYCTGGCCHV



Dataset #: 4 Motif ID: 139 Motif name: mkCTyTTCsg

Original motif Consensus sequence: HBCTTTTCBD



Reverse complement motif Consensus sequence: HBGAAAAGBD



Best Matches for Motif ID 139 (Highest to Lowest)

Dataset #:	4
Motif ID:	140
Motif name:	vkCKCTkCGk
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:	0.000582108

Alignment:

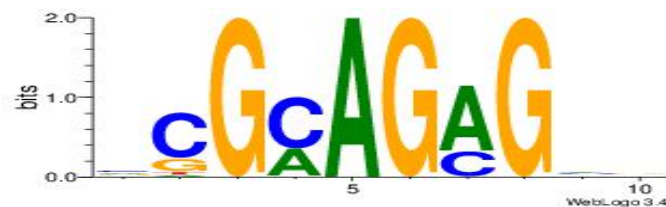
VDCTCTKCGB

HBCTTTTCBD

Original motif Consensus sequence: VDCTCTKCGB



Reverse complement motif Consensus sequence: BCGYAGAGDV

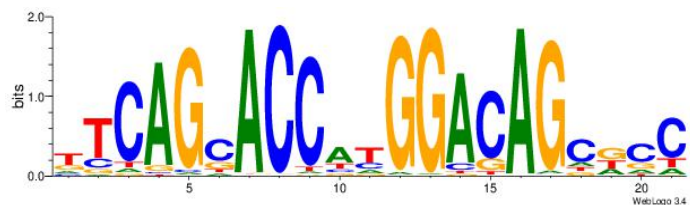


Dataset #: 3
 Motif ID: 113
 Motif name: REST
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 10
 Number of overlap: 10
 Similarity score: 0.0260893

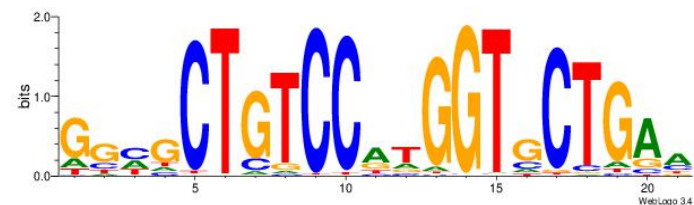
Alignment:

GYGCTGTCCATGGTGCTGAA
 -----HBCTTTTCBD--

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC



Reverse complement motif Consensus sequence: GYGCTGTCCATGGTGCTGAA



Dataset #: 4
 Motif ID: 136
 Motif name: dwCAGAAGwh
 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: 0.0271307

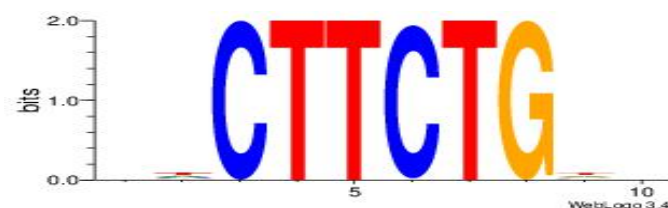
Alignment:

DHCAGAAGDH
HBGAAAAGBD

Original motif Consensus sequence: DHCAGAAGDH



Reverse complement motif Consensus sequence: HDCTTCTGHD



Dataset #: 4
Motif ID: 142
Motif name: ctCTTAACyw
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: 0.0279851

Alignment:

HHCTTAACHD
HBCTTTTCBD

Original motif Consensus sequence: HHCTTAACHD

Reverse complement motif Consensus sequence: DDGTTAAGHD



Dataset #: 4
 Motif ID: 141
 Motif name: raCAAAACam
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 10
 Similarity score: 0.0368067

Alignment:

HTGTTTTGTD

HBCTTTTCBD

Original motif Consensus sequence: DACAAAACAH

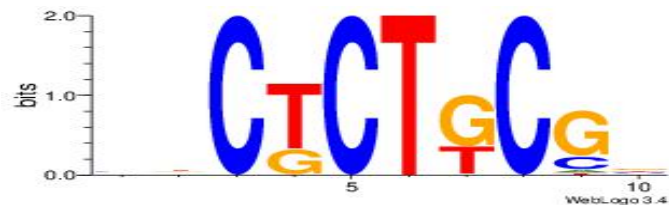


Reverse complement motif Consensus sequence: HTGTTTTGTD



Dataset #: 4 Motif ID: 140 Motif name: vkCKCTkCGk

Original motif Consensus sequence: VDCTCTKCGB



Reverse complement motif Consensus sequence: BCGYAGAGDV



Best Matches for Motif ID 140 (Highest to Lowest)

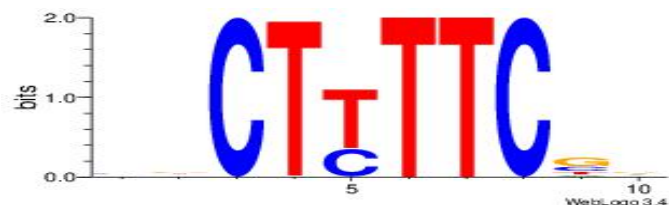
Dataset #:	4
Motif ID:	139
Motif name:	mkCTyTTCsg
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	10
Similarity score:	0.00351595

Alignment:

HBCTTTTCBD

VDCTCTKCGB

Original motif Consensus sequence: HBCTTTTCBD



Reverse complement motif Consensus sequence: HBGAAAAGBD



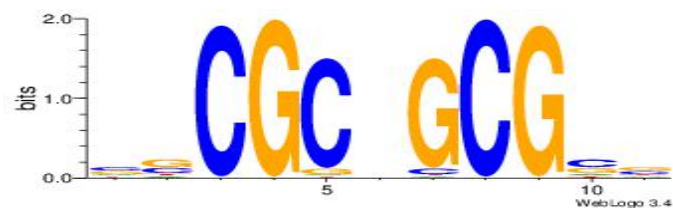
Dataset #: 4
 Motif ID: 161
 Motif name: ssCGCwGCGss
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 10
 Similarity score: 0.0202536

Alignment:

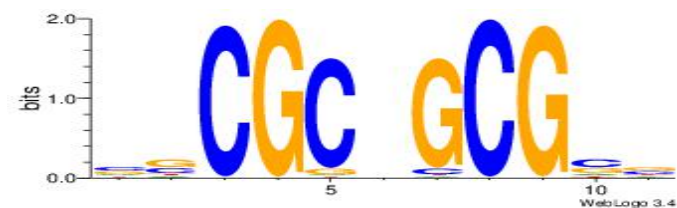
VSCGCDGCGSB

VDCTCTKCGB-

Original motif Consensus sequence: VSCGCDGCGSB



Reverse complement motif Consensus sequence: BSCGCDGCGSV



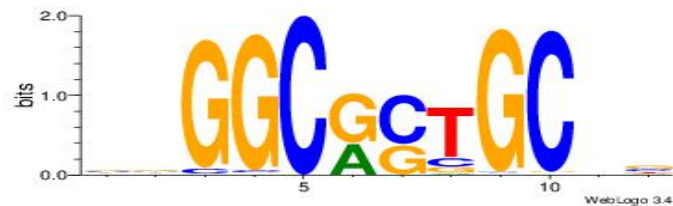
Dataset #: 4
 Motif ID: 170
 Motif name: ssGGCrSTGCrS
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 10

Similarity score: 0.0403601

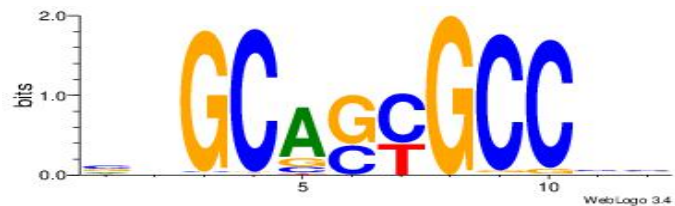
Alignment:

VVGGCRSTGCVB
--VDCTCTKCGB

Original motif Consensus sequence: VVGGCRSTGCVB



Reverse complement motif Consensus sequence: BVGCASMGCCVV



Dataset #: 4
Motif ID: 154
Motif name: csCsCCTCCcc
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2
Number of overlap: 10
Similarity score: 0.0407996

Alignment:

VBCCCCTCCHB
VDCTCTKCGB-

Original motif Consensus sequence: VBCCCCTCCHB

Reverse complement motif Consensus sequence: BDGGAGGGGBV

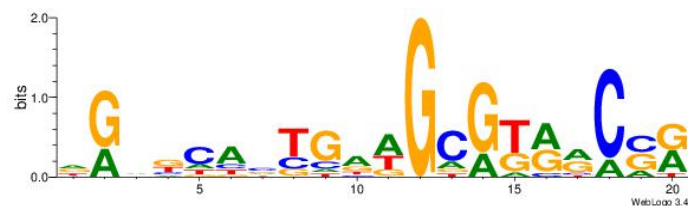


Dataset #: 3
 Motif ID: 109
 Motif name: Pax5
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 7
 Number of overlap: 10
 Similarity score: 0.0447624

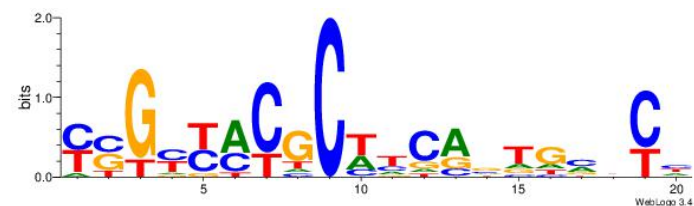
Alignment:

DGVBCABTGDWGCGRRCR
 ----BCGYAGAGDV-----

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD



Dataset #: 4 Motif ID: 141 Motif name: raCAAAACam

Original motif Consensus sequence: DACAAAACAH



Reverse complement motif Consensus sequence: HTGTTTGTGTD



Best Matches for Motif ID 141 (Highest to Lowest)

Dataset #: 4
Motif ID: 136
Motif name: dwCAGAAGwh
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: 0.0286451

Alignment:

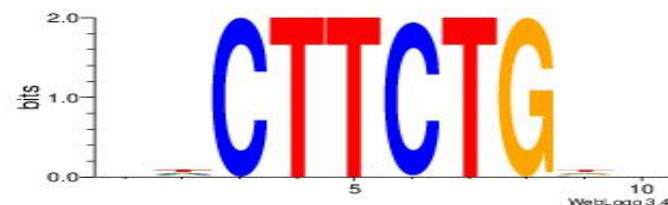
DHCAGAAGDH

DACAAAACAH

Original motif Consensus sequence: DHCAGAAGDH



Reverse complement motif Consensus sequence: HDCTTCTGHD



Dataset #: 4
 Motif ID: 142
 Motif name: ctCTTAACyw
 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: 0.0383253

Alignment:

DDGTTAAGHD

HTGTTTTGTD

Original motif Consensus sequence: HHCTTAACHD



Reverse complement motif Consensus sequence: DDGTTAAGHD

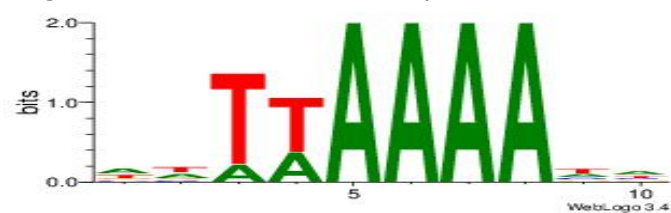


Dataset #: 4
 Motif ID: 148
 Motif name: wwTwAAAAww
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 10

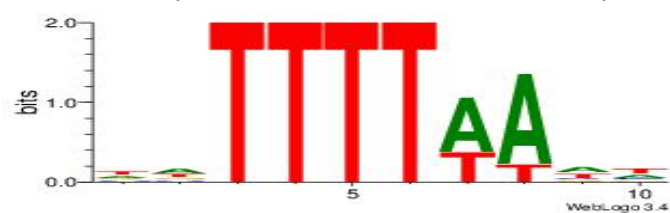
Similarity score: 0.0458158

Alignment:
DDTWAAAAHH
DACAACAACAH

Original motif Consensus sequence: DDTWAAAAHH



Reverse complement motif Consensus sequence: HHTTTTWADD

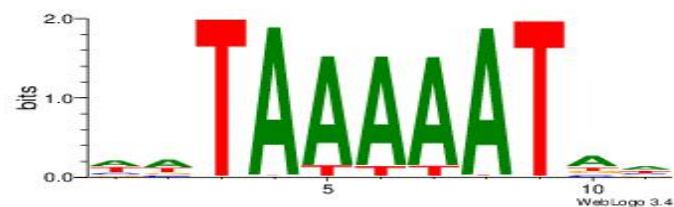
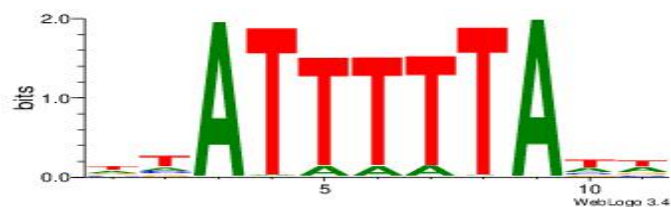


Dataset #: 4
Motif ID: 157
Motif name: wtATTTTAAww
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 2
Number of overlap: 10
Similarity score: 0.0464408

Alignment:
WWTAAAAATAD
-DACAACAACAH

Original motif Consensus sequence: DTATTTTAAWW

Reverse complement motif Consensus sequence: WWTAAAAATAD



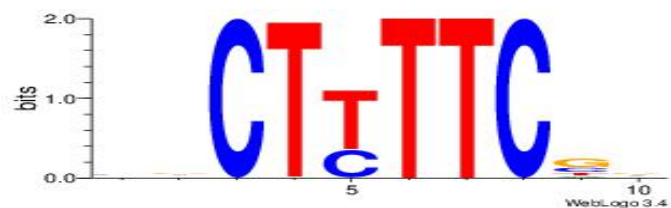
Dataset #: 4
 Motif ID: 139
 Motif name: mkCTyTTCsg
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 10
 Similarity score: 0.0483302

Alignment:

HBGAAAAGBD

DACAAAACAH

Original motif Consensus sequence: HBCTTTTCBD



Reverse complement motif Consensus sequence: HBGAAAAGBD



Dataset #: 4 **Motif ID: 142** **Motif name: ctCTTAACyw**

Original motif Consensus sequence: HHCTTAACHD



Reverse complement motif Consensus sequence: DDGTTAAGHD



Best Matches for Motif ID 142 (Highest to Lowest)

Dataset #:	4
Motif ID:	141
Motif name:	raCAAAACam
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:	0.0459536

Alignment:

HTGTTTTGTD

DDGTTAAGHD

Original motif Consensus sequence: DACAAAACAH



Reverse complement motif Consensus sequence: HTGTTTTGTD



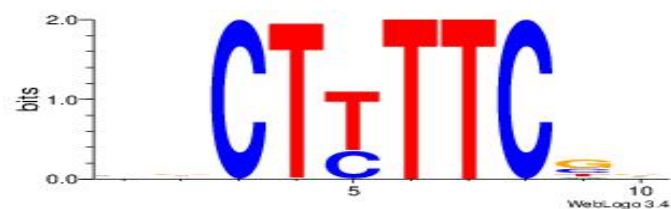
Dataset #: 4
 Motif ID: 139
 Motif name: mkCTyTTCsg
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 10
 Similarity score: 0.0471369

Alignment:

HBCTTTTCBD

HHCTTAACHD

Original motif Consensus sequence: HBCTTTTCBD



Reverse complement motif Consensus sequence: HBGAAAAGBD



Dataset #: 4
 Motif ID: 136
 Motif name: dwCAGAAGwh
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 10

Similarity score: 0.0550541

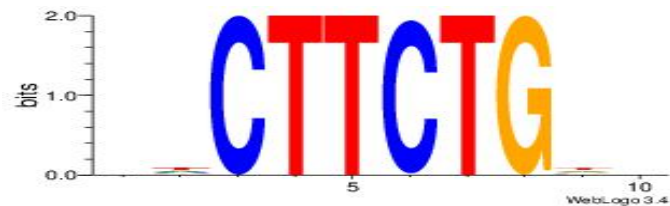
Alignment:

DHCAGAAGDH
DDGTTAAGHD

Original motif Consensus sequence: DHCAGAAGDH



Reverse complement motif Consensus sequence: HDCTTCTGHD



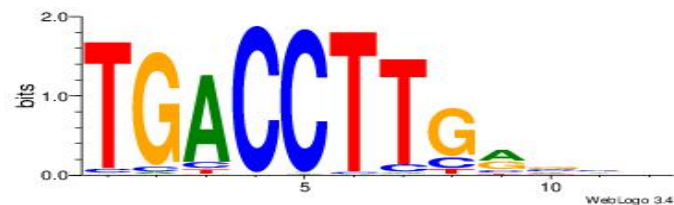
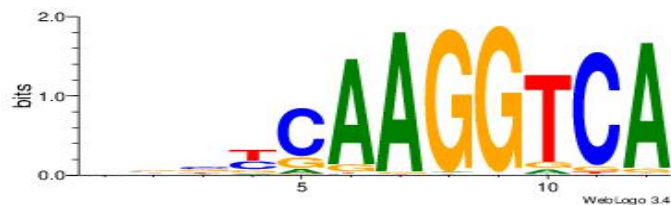
Dataset #: 3
Motif ID: 83
Motif name: Esrrb
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 10
Similarity score: 0.0663739

Alignment:

VBBYCAAGGTCA
--DDGTTAAGHD

Original motif Consensus sequence: VBBYCAAGGTCA

Reverse complement motif Consensus sequence: TGACCTTGMBBB

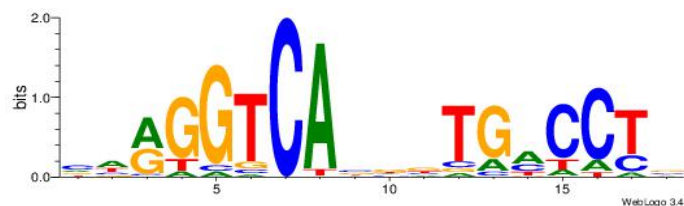


Dataset #: 3
 Motif ID: 82
 Motif name: ESR2
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 10
 Similarity score: 0.0691225

Alignment:

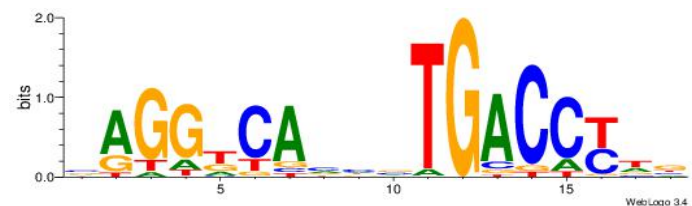
BAGGYCABHBTGACCKHV
 -HHCTTAACHD-----

Original motif Consensus sequence: VHRGGTCABDBTGMCTB



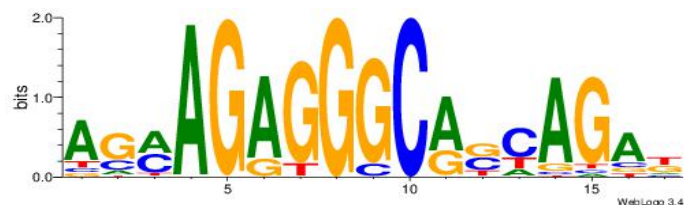
Reverse complement motif
BAGGYCABHBTGACCKHV

Consensus sequence:

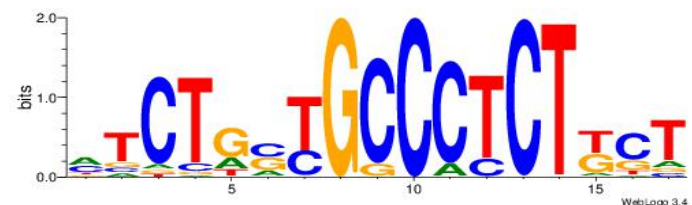


Dataset #: 4 Motif ID: 143 Motif name: AgmAGAGGGCrscAGak

Original motif Consensus sequence: AGMAGAGGGCASCAGAK



Reverse complement motif Consensus sequence: RTCTGSTGCCCTCTYCT



Best Matches for Motif ID 143 (Highest to Lowest)

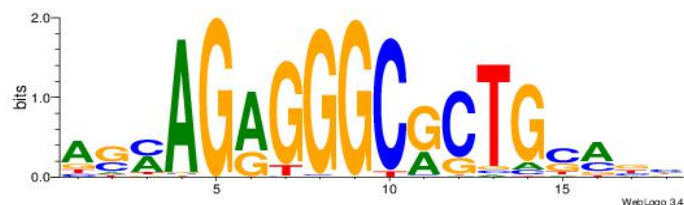
Dataset #:	4
Motif ID:	149
Motif name:	asmAGRGGGCrCTGsmkc
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2
Number of overlap:	17
Similarity score:	0.0311468

Alignment:

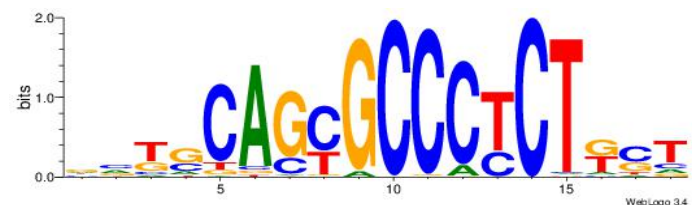
ASMAGAGGGCRCTGSABH

AGMAGAGGGCASCAGAK-

Original motif Consensus sequence: ASMAGAGGGCRCTGSABH



Reverse complement motif Consensus sequence: DBTSCAGMGCCCTCTRST

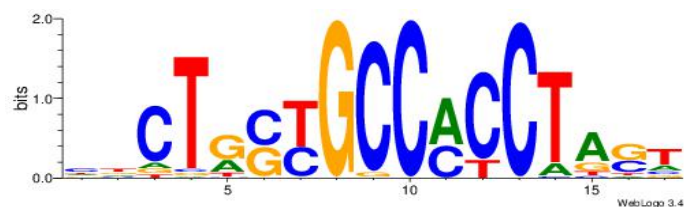


Dataset #: 4
 Motif ID: 144
 Motif name: ctCTrsyGCCmCCTast
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 17
 Similarity score: 0.0415124

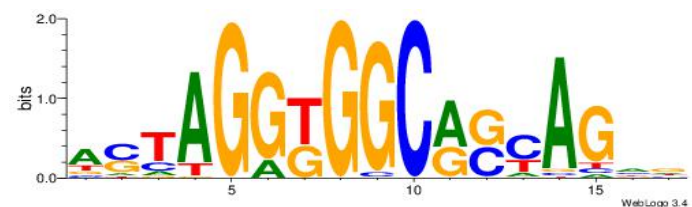
Alignment:

HDCTGSYGCCMCCTAST
 RTCTGSTGCCCTCTYCT

Original motif Consensus sequence: HDCTGSYGCCMCCTAST



Reverse complement motif Consensus sequence: ASTAGGYGGCMSCAGDD



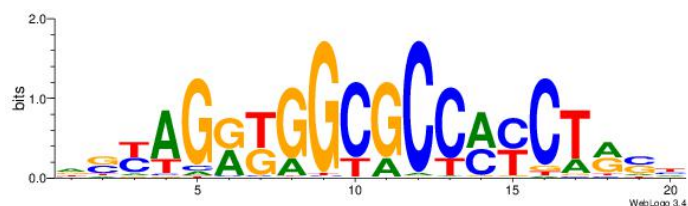
Dataset #: 4
 Motif ID: 167
 Motif name: rsyAGrkGGCGCCmyCTrsy
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward

Position number: 1
Number of overlap: 17
Similarity score: 0.0702327

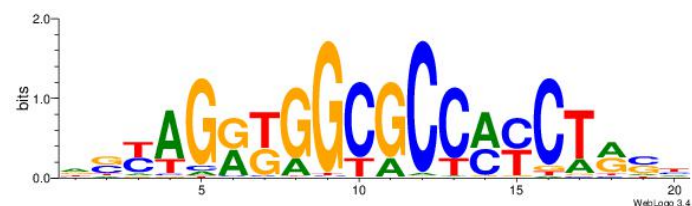
Alignment:

DSYAGRKGGCGCCMYCTRSH
AGMAGAGGGCASCAGAK---

Original motif Consensus sequence: DSYAGRKGGCGCCMYCTRSH



Reverse complement motif Consensus sequence: HSKAGKYGGCGCCRMCTMSD

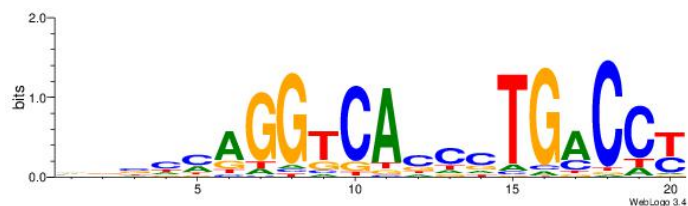


Dataset #: 3
Motif ID: 81
Motif name: ESR1
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 4
Number of overlap: 17
Similarity score: 0.0915393

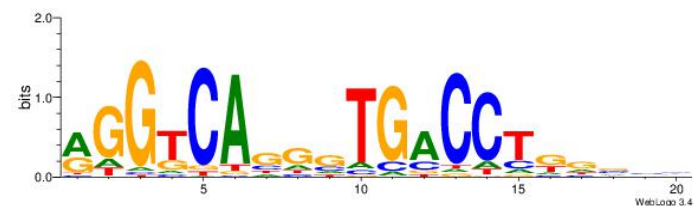
Alignment:

VDBHMAGGTCACCCTGACCY
AGMAGAGGGCASCAGAK---

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



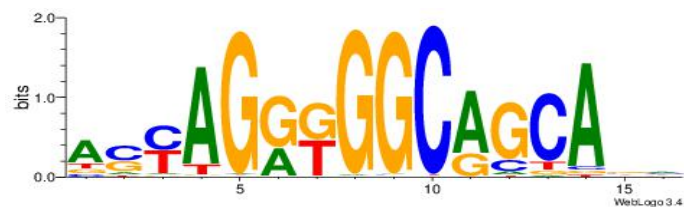
Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV



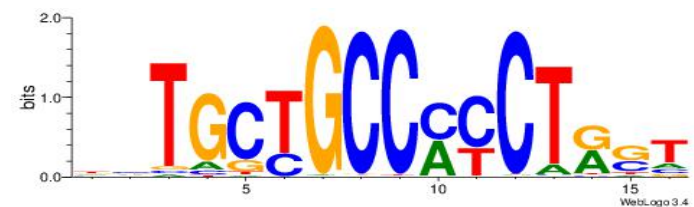
Dataset #: 4
Motif ID: 164
Motif name: asyAGrkGGCRGCa
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 16
Similarity score: 0.531077

Alignment:
ASYAGRKGGCAGCABH-
AGMAGAGGGCASCAGAK

Original motif Consensus sequence: ASYAGRKGGCAGCABH

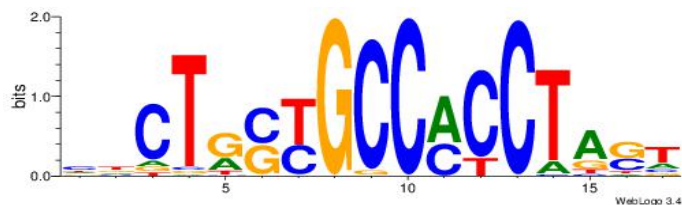


Reverse complement motif Consensus sequence: HBTGCTGCCYMCTKST

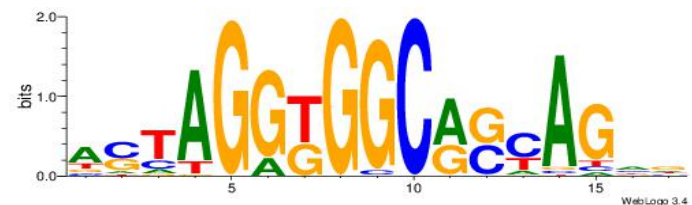


Dataset #: 4 Motif ID: 144 Motif name: ctCTrsyGCCmCCTast

Original motif Consensus sequence: HDCTGSYGCCMCCTAST



Reverse complement motif Consensus sequence: ASTAGGYGGCMSCAGDD



Best Matches for Motif ID 144 (Highest to Lowest)

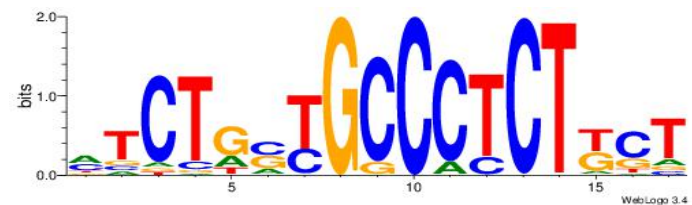
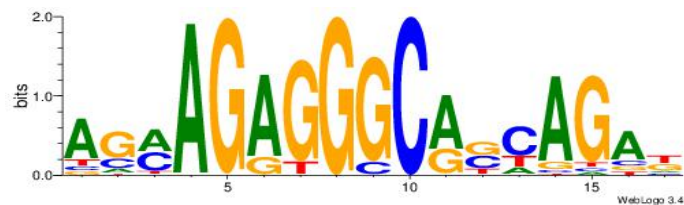
Dataset #:	4
Motif ID:	143
Motif name:	AgmAGAGGGCrscAGak
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	17
Similarity score:	0.0216483

Alignment:

AGMAGAGGGCASCAGAK
ASTAGGYGGCMSCAGDD

Original motif Consensus sequence: AGMAGAGGGCASCAGAK

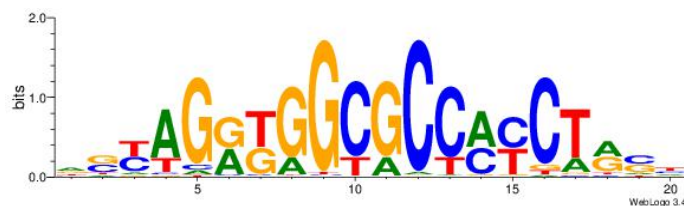
Reverse complement motif Consensus sequence:
RTCTGSTGCCCTCTYCT



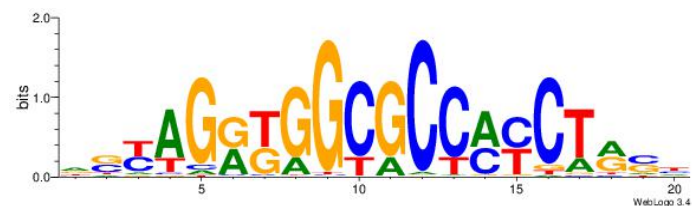
Dataset #: 4
 Motif ID: 167
 Motif name: rsyAGrkGGCGCCmyCTrsy
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 17
 Similarity score: 0.0316423

Alignment:
 DSYAGRKGGCGCCMYCTRSH
 ---HDCTGSYGCCMCCTAST

Original motif Consensus sequence: DSYAGRKGGCGCCMYCTRSH



Reverse complement motif Consensus sequence: HSKAGKYGGCGCCRMCTMSD



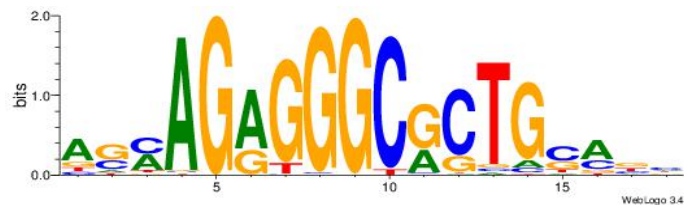
Dataset #: 4

Motif ID: 149
 Motif name: asmAGRGGGCrCTGsmkc
 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: 0.040379

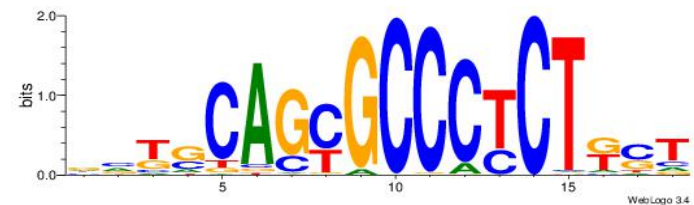
Alignment:

DBTSCAGMGCCCTCTRST
 -HDCTGSYGCCMCCTAST

Original motif Consensus sequence: ASMAGAGGGCRCTGSABH



Reverse complement motif Consensus sequence: DBTSCAGMGCCCTCTRST

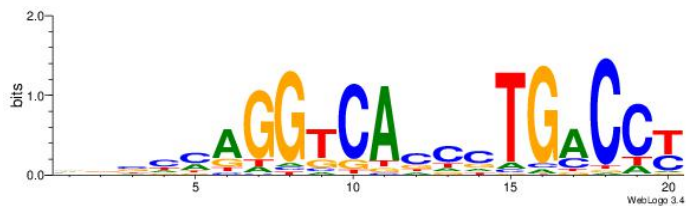


Dataset #: 3
 Motif ID: 81
 Motif name: ESR1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 4
 Number of overlap: 17

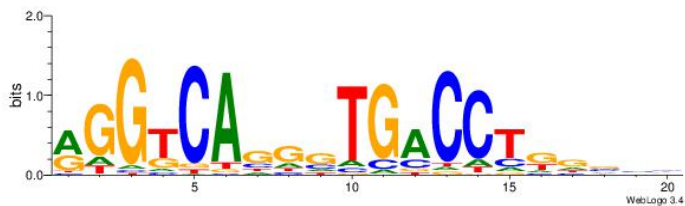
Similarity score: 0.0748345

Alignment:
MGGTCAGGGTGACCTRDBHV
---ASTAGGYGGCMSCAGDD

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV

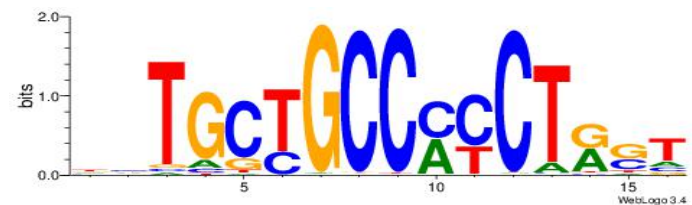
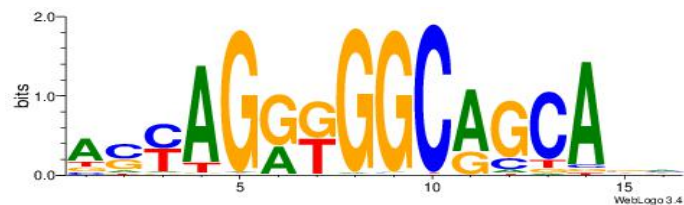


Dataset #: 4
Motif ID: 164
Motif name: asyAGrkGGCRGCa
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 16
Similarity score: 0.503247

Alignment:
ASYAGRKGGCAGCABH-
ASTAGGYGGCMSCAGDD

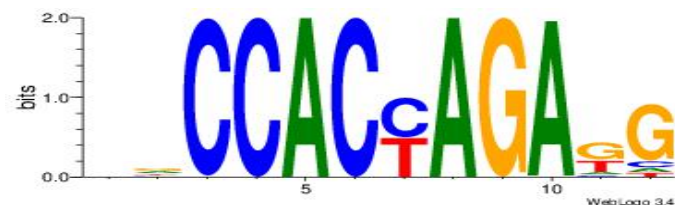
Original motif Consensus sequence: ASYAGRKGGCAGCABH

Reverse complement motif Consensus sequence: HBTGCTGCCYMCTKST

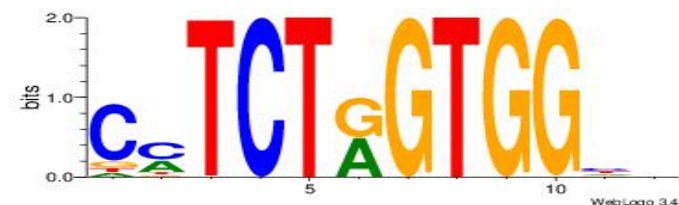


Dataset #: 4 Motif ID: 145 Motif name: grCCACyAGAkG

Original motif Consensus sequence: DDCCACYAGAKG



Reverse complement motif Consensus sequence: CYTCTKGTGGHH

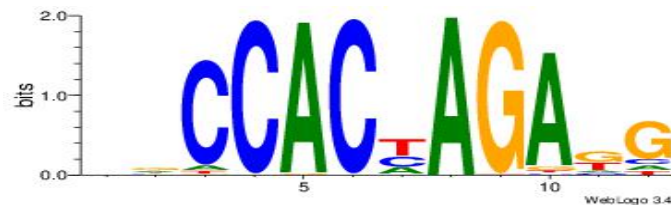


Best Matches for Motif ID 145 (Highest to Lowest)

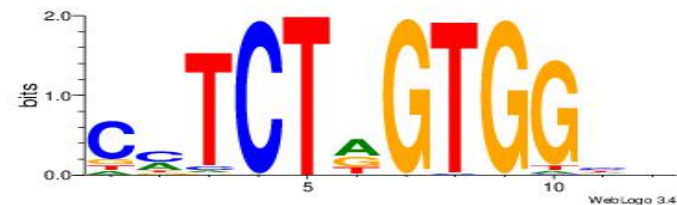
Dataset #:	4
Motif ID:	138
Motif name:	grCCACyAGAkG
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	12
Similarity score:	0

Alignment:
DDCCACYAGAKG
DDCCACYAGAKG

Original motif Consensus sequence: DDCCACYAGAKG



Reverse complement motif Consensus sequence: CYTCTMGTGGHH

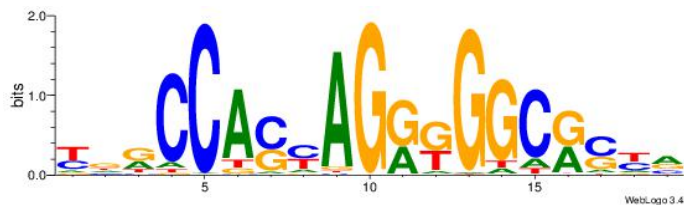


Dataset #: 3
 Motif ID: 74
 Motif name: CTCF
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 12
 Similarity score: 0.0323771

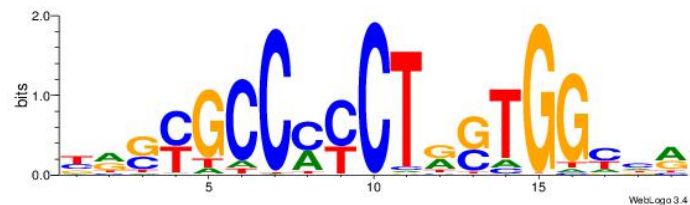
Alignment:

YDRCCASYAGRKGGRSYV
 -DDCCACYAGAKG-----

Original motif Consensus sequence: YDRCCASYAGRKGGRSYV



Reverse complement motif Consensus sequence: BMSMGCCYMCTKSTGGMHM

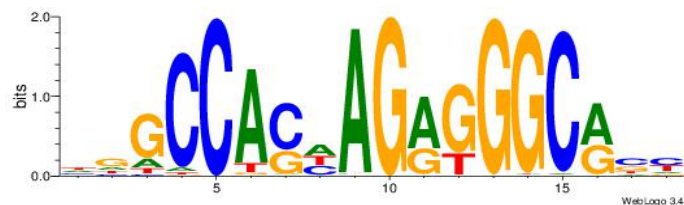


Dataset #: 4
 Motif ID: 165
 Motif name: wgGCCAshAGrGGGCrSy
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 6
 Number of overlap: 12
 Similarity score: 0.0347955

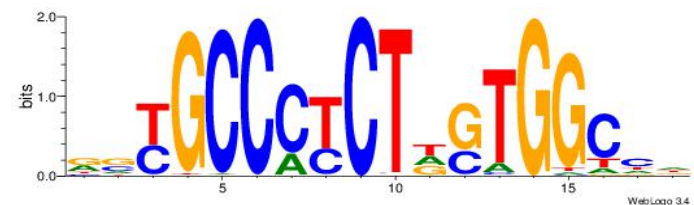
Alignment:

HDGCCACHAGRGGGCRBY
 -DDCCACYAGAKG-----

Original motif Consensus sequence: HDGCCACHAGRGGGCRBY



Reverse complement motif Consensus sequence: KBKGCCCKCTHGTGGCHH



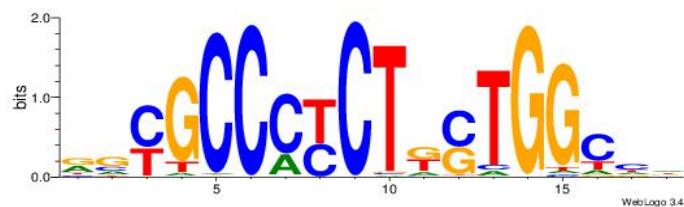
Dataset #: 4
 Motif ID: 156
 Motif name: rgyGCCMyCTksTGGccd
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 6

Number of overlap: 12
Similarity score: 0.0388427

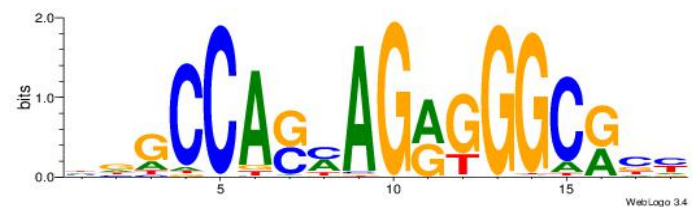
Alignment:

DDGCCASYAGMGGGCKVM
-DDCCACYAGAKG-----

Original motif Consensus sequence: RYVGCCCYCTKSTGGCHD



Reverse complement motif Consensus sequence: DDGCCASYAGMGGGCKVM

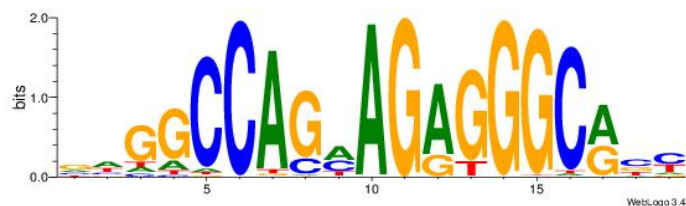


Dataset #: 4
Motif ID: 163
Motif name: gwGGCCAGmAGAGGGCrby
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 3
Number of overlap: 12
Similarity score: 0.0502736

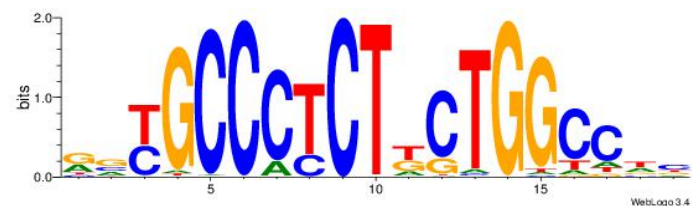
Alignment:

VHGGCCAGMAGAGGGCRBY
--DDCCACYAGAKG-----

Original motif Consensus sequence: VHGGCCAGMAGAGGGCRBY

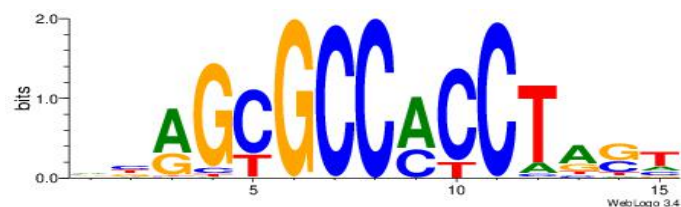


Reverse complement motif Consensus sequence: KBKGCCCTCTYCTGGCCHV

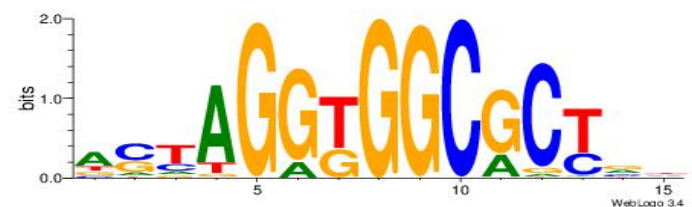


Dataset #: 4 Motif ID: 146 Motif name: myrGYGCCmCCTast

Original motif Consensus sequence: VBAGCGCCMCCTAST



Reverse complement motif Consensus sequence: ASTAGGYGGCGCT



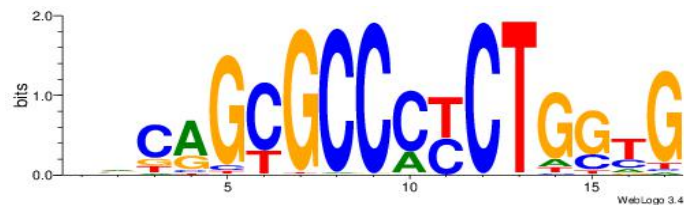
Best Matches for Motif ID 146 (Highest to Lowest)

Dataset #:	4
Motif ID:	168
Motif name:	yrerGYGCCMyCTGGtG
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:	0.00670638

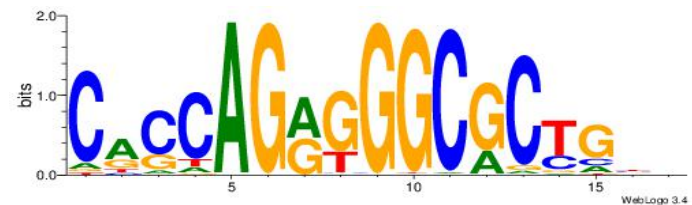
Alignment:

HVCAGCGCCCYCTGGTG
-VBAGCGCCMCCTAST-

Original motif Consensus sequence: HVCAGCGCCCYCTGGTG



Reverse complement motif Consensus sequence:
CACCAGMGGGCGCTGBD

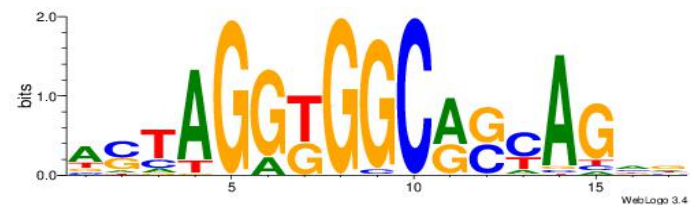
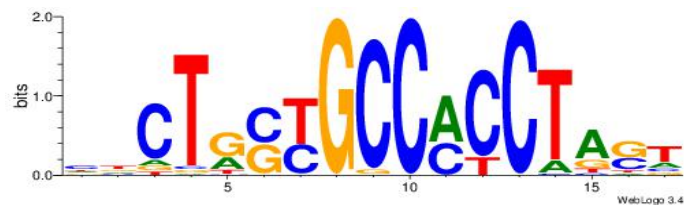


Dataset #: 4
Motif ID: 144
Motif name: ctCTrsyGCCmCCTast
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 3
Number of overlap: 15
Similarity score: 0.0118351

Alignment:
HDCTGSYGCCMCCTAST
--VBAGCGCCMCCTAST

Original motif Consensus sequence: HDCTGSYGCCMCCTAST

Reverse complement motif Consensus sequence:
ASTAGGYGGCMSCAGDD

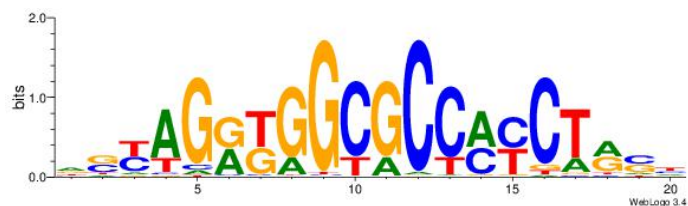


Dataset #: 4
 Motif ID: 167
 Motif name: rsyAGrkGGCGCCmyCTrsy
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 6
 Number of overlap: 15
 Similarity score: 0.0178333

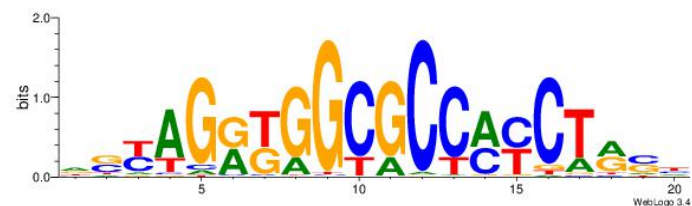
Alignment:

DSYAGRKGCGCCMYCTRSH
 -----VBAGCGCCMCCTAST

Original motif Consensus sequence: DSYAGRKGCGCCMYCTRSH



Reverse complement motif Consensus sequence: HSKAGKYGGCGCCRMCTMSD



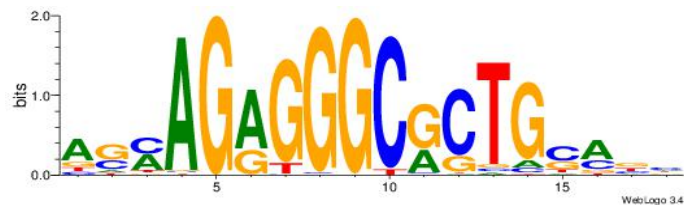
Dataset #: 4

Motif ID: 149
 Motif name: asmAGRGGGCrCTGsmkc
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 15
 Similarity score: 0.0324399

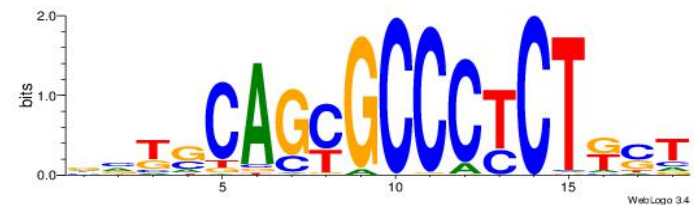
Alignment:

DBTSCAGMGCCCTCTRST
 ---VBAGCGCCMCCTAST

Original motif Consensus sequence: ASMAGAGGGCRCTGSABH



Reverse complement motif Consensus sequence: DBTSCAGMGCCCTCTRST

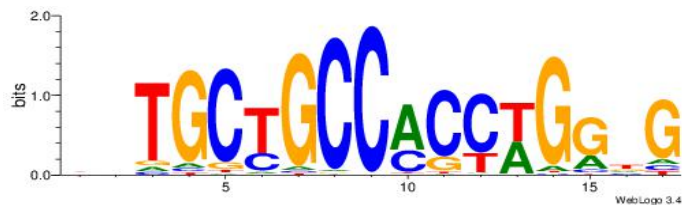


Dataset #: 4
 Motif ID: 169
 Motif name: yVTGCyGCCmCCwGgtG
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 15

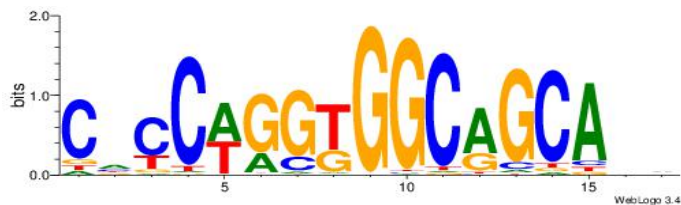
Similarity score: 0.0457506

Alignment:
BVTGCTGCCACCWGGDG
-VBAGCGCCMCCTAST-

Original motif Consensus sequence: BVTGCTGCCACCWGGDG



Reverse complement motif Consensus sequence: CDCCWGGTGGCAGCAVV



Dataset #: 4 Motif ID: 147 Motif name: asCAGrkGGCrSy

Original motif Consensus sequence: ASCAGRGGGCRSB



Reverse complement motif Consensus sequence: BSKGCCCMCTGST



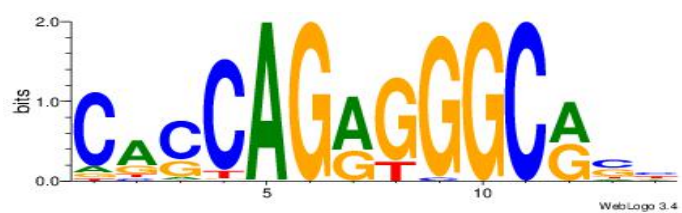
Best Matches for Motif ID 147 (Highest to Lowest)

Dataset #:	4
Motif ID:	166
Motif name:	CasCAGrGGGCrSy
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: 0.00871755

Alignment:
CACCAGRGGGCRSB
-ASCAGRGGGCRSB

Original motif Consensus sequence: CACCAGRGGGCRSB



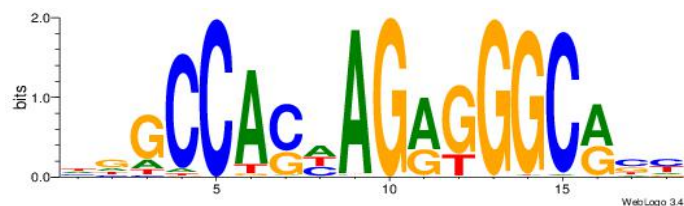
Reverse complement motif Consensus sequence: BSKGCCCKCTGGT



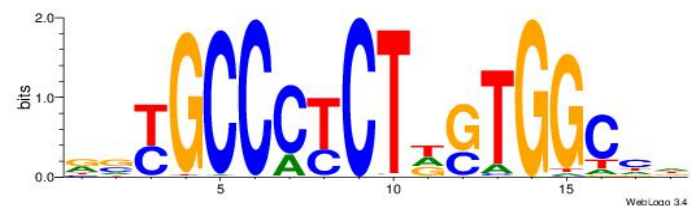
Dataset #: 4
Motif ID: 165
Motif name: wgGCCAshAGrGGGCrSy
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 13
Similarity score: 0.0301924

Alignment:
HDGCCACHAGRGGGCRBY
-----ASCAGRGGGCRSB

Original motif Consensus sequence: HDGCCACHAGRGGGCRBY



Reverse complement motif Consensus sequence: KBKGCCCKCTHGTGGCHH

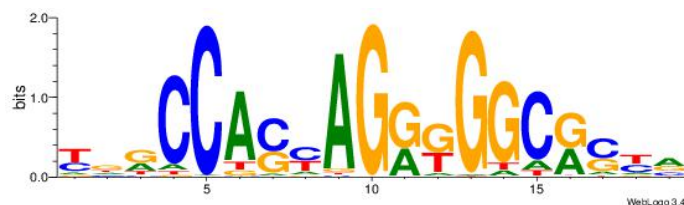


Dataset #: 3
Motif ID: 74
Motif name: CTCF
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 6
Number of overlap: 13
Similarity score: 0.0305318

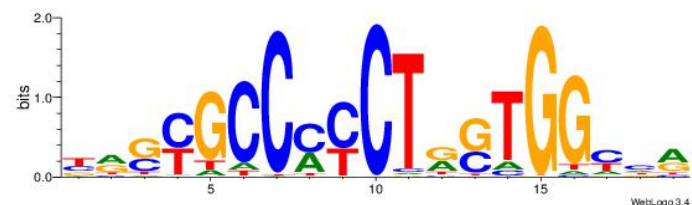
Alignment:

YDRCCASYAGRKGGRSYV
-----ASCAGRGGGCRSB-

Original motif Consensus sequence: YDRCCASYAGRKGGRSYV



Reverse complement motif Consensus sequence: BMSMGCCYMCTKSTGGMHM

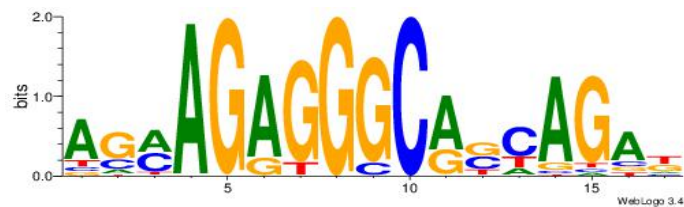


Dataset #: 4
 Motif ID: 143
 Motif name: AgmAGAGGGCrscAGak
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 5
 Number of overlap: 13
 Similarity score: 0.0348963

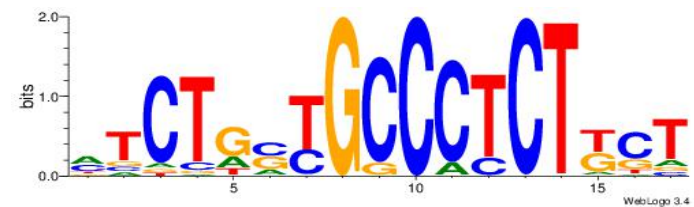
Alignment:

AGMAGAGGGCASCAGAK
 ASCAGRGGGCRSB-----

Original motif Consensus sequence: AGMAGAGGGCASCAGAK



Reverse complement motif Consensus sequence: RTCTGSTGCCCTCTYCT

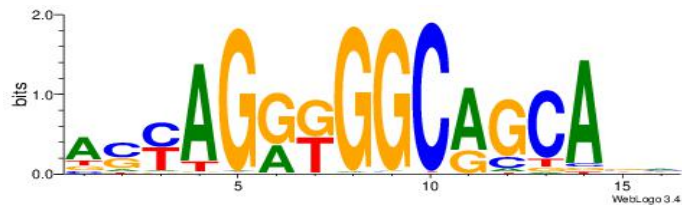


Dataset #: 4
 Motif ID: 164
 Motif name: asyAGrkGGCRGCaga
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1

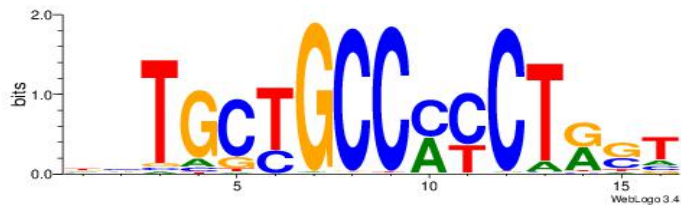
Number of overlap: 13
Similarity score: 0.0366623

Alignment:
HBTGCTGCCYMCTKST
---BSKGCCCMCTGST

Original motif Consensus sequence: ASYAGRKGGCAGCABH



Reverse complement motif Consensus sequence: HBTGCTGCCYMCTKST

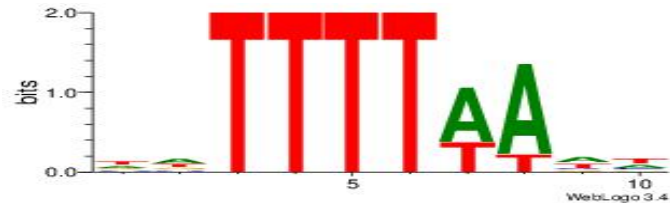


Dataset #: 4 Motif ID: 148 Motif name: wwTwAAAAww

Original motif Consensus sequence: DDTWAAAAHH



Reverse complement motif Consensus sequence: HHTTTTWADD



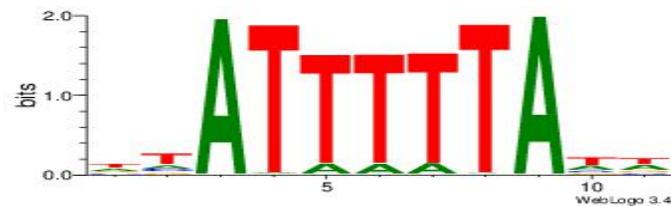
Best Matches for Motif ID 148 (Highest to Lowest)

Dataset #: 4
Motif ID: 157
Motif name: wtATTTTTAww
Matching format of first motif: Original Motif

Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 10
 Similarity score: 0.0143677

Alignment:
 WWTAAAAATAD
 DDTWAAAAHH-

Original motif Consensus sequence: DTATTTTAAWW



Reverse complement motif Consensus sequence: WWTAAAAATAD



Dataset #: 4
 Motif ID: 150
 Motif name: waATwAAAATAww
 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: 0.0146704

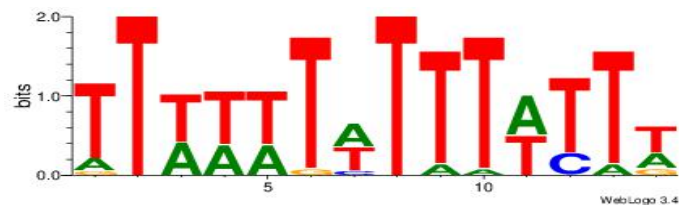
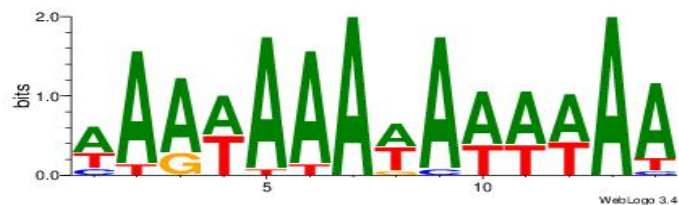
Alignment:

--HHTTTTWADD--

Alignment:

```
TTWWWTWTTTWTTW
---HHTTTTWADD---
```

Reverse complement motif Consensus sequence:
TTWWWTWTTTWTWW



Dataset #: 4
 Motif ID: 141
 Motif name: raCAAAACam
 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: 0.0504274

Alignment:

DACAAAACAH

DDTWAAAHH

Original motif Consensus sequence: DACAAAACAH



Reverse complement motif Consensus sequence: HTGTTTGTG



Dataset #: 4
 Motif ID: 142

Motif name: ctCTTAACyw
 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: 0.0669752

Alignment:

HHCTTAACHD
 DDTWAAAAHH

Original motif Consensus sequence: HHCTTAACHD

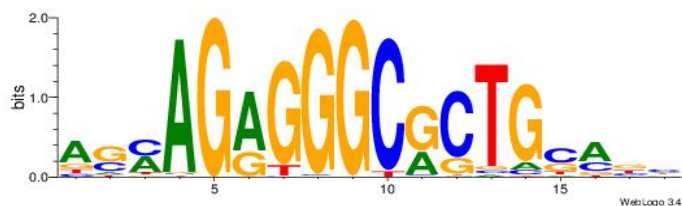


Reverse complement motif Consensus sequence: DDGTTAAGHD

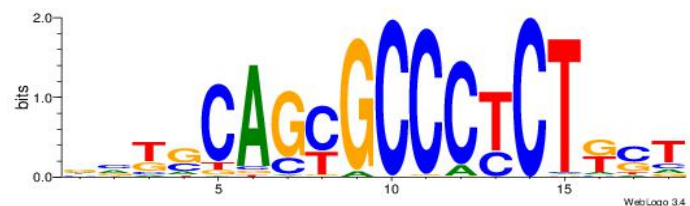


Dataset #: 4 Motif ID: 149 Motif name: asmAGRGGGCrCTGsmkc

Original motif Consensus sequence: ASMAGAGGGCRCTGSABH



Reverse complement motif Consensus sequence: DBTSCAGMGCCCTCTRST



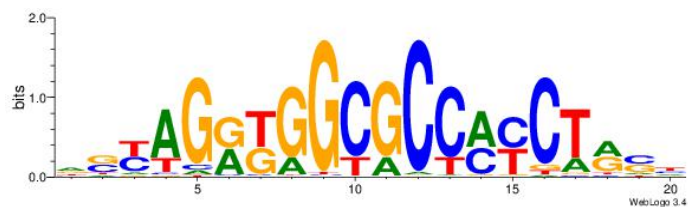
Best Matches for Motif ID 149 (Highest to Lowest)

Dataset #: 4
Motif ID: 167
Motif name: rsyAGrkGGCGCCmyCTrsy
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: 0.0599593

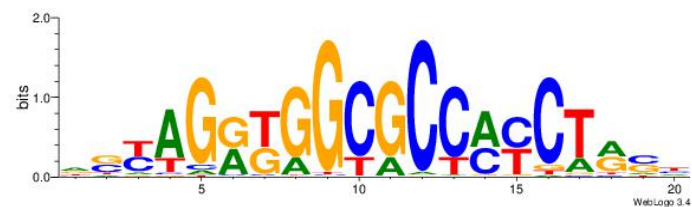
Alignment:

DSYAGRKGCGCCMYCTRSH
ASMAGAGGGCRCTGSABH--

Original motif Consensus sequence: DSYAGRKGCGCCMYCTRSH



Reverse complement motif Consensus sequence: HSKAGKYGGCGCCRMCTMSD



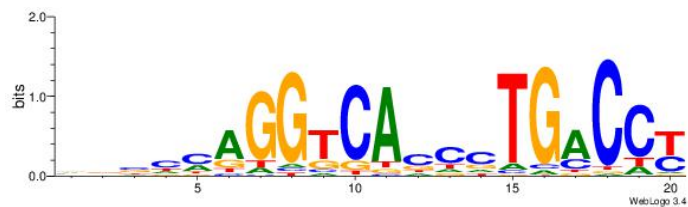
Dataset #: 3
Motif ID: 81
Motif name: ESR1
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif

Direction: Forward
 Position number: 3
 Number of overlap: 18
 Similarity score: 0.0884279

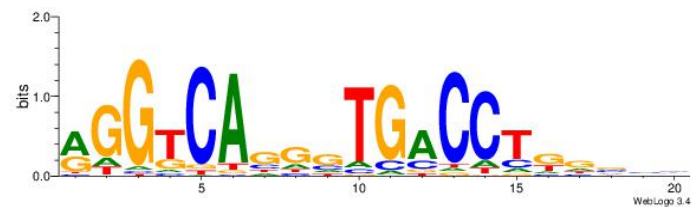
Alignment:

VDBHMAGGTCACCCTGACCY
 --DBTSCAGMGCCCTCTRST

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV

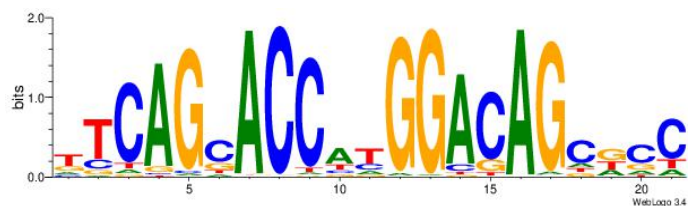


Dataset #: 3
 Motif ID: 113
 Motif name: REST
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 18
 Similarity score: 0.0932033

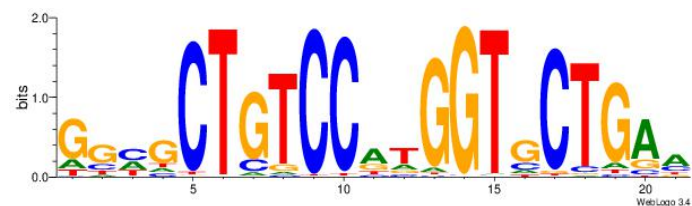
Alignment:

GGYGCTGTCCATGGTGCTGAA
 DBTSCAGMGCCCTCTRST---

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC



Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA

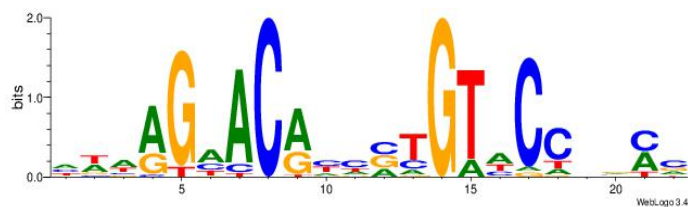


Dataset #: 3
Motif ID: 70
Motif name: Ar
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 18
Similarity score: 0.0976041

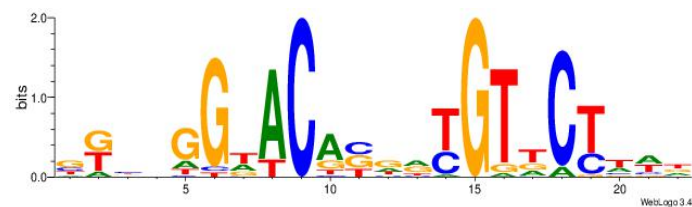
Alignment:

HWDAGHACRHHVTGTHCCHVMV
ASMAGAGGGCRCTGSABH----

Original motif Consensus sequence: HWDAGHACRHHVTGTHCCHVMV



Reverse complement motif Consensus sequence: VRVDGGHACAVDDKGTHCTDWH

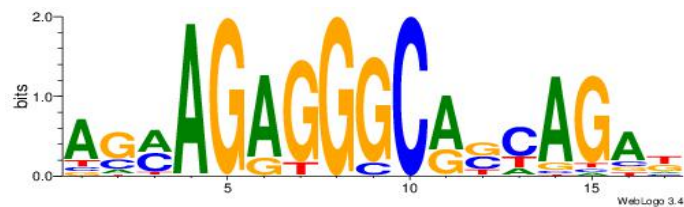


Dataset #: 4
 Motif ID: 143
 Motif name: AgmAGAGGGCrscAGak
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 17
 Similarity score: 0.529694

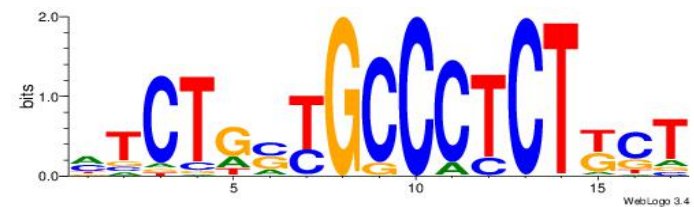
Alignment:

AGMAGAGGGCASCAGAK-
 ASMAGAGGGCRCTGSABH

Original motif Consensus sequence: AGMAGAGGGCASCAGAK



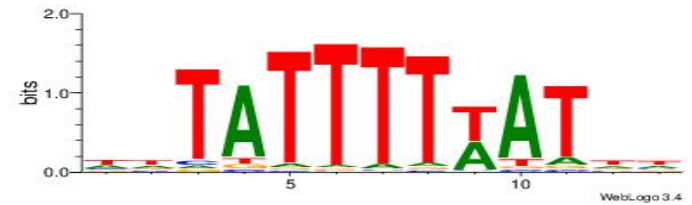
Reverse complement motif Consensus sequence: RTCTGSTGCCCTCTYCT



Dataset #: 4 Motif ID: 150 Motif name: waATwAAAATAww

Original motif Consensus sequence: DHATWAAAATAHD

Reverse complement motif Consensus sequence: DHTATTTTWATHD



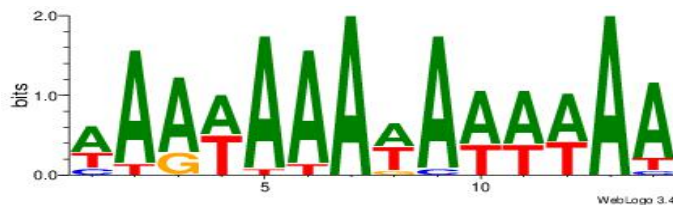
Best Matches for Motif ID 150 (Highest to Lowest)

Dataset #: 2
 Motif ID: 68
 Motif name: Motif 68
 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: 0.0403377

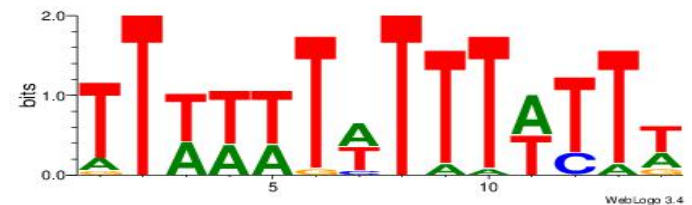
Alignment:

TTWWWTWTTTWTTW
 -DHTATTTTWATHD

Original motif Consensus sequence: WAAWAAWAWWWAA



Reverse complement motif Consensus sequence: TTWWWTWTTTWTTW

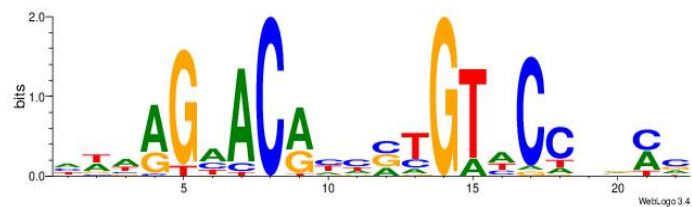


Dataset #: 3
 Motif ID: 70
 Motif name: Ar
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 13
 Similarity score: 0.0805462

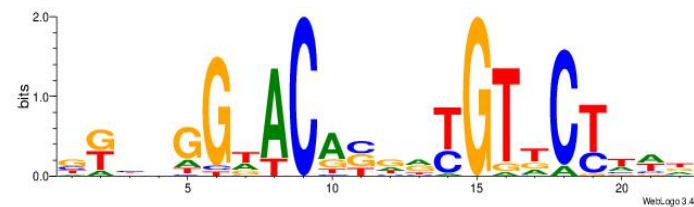
Alignment:

HWDAGHACRHHVTGTHCCHVMV
 DHATWAAAATAHD-----

Original motif Consensus sequence: HWDAGHACRHHVTGTHCCHVMV



Reverse complement motif Consensus sequence: VRVDGGHACA VDDKGTHCTDWH

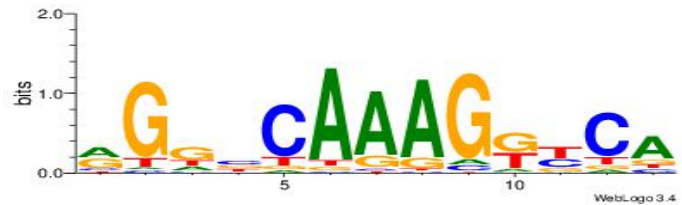


Dataset #: 3
 Motif ID: 87
 Motif name: HNF4A
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1

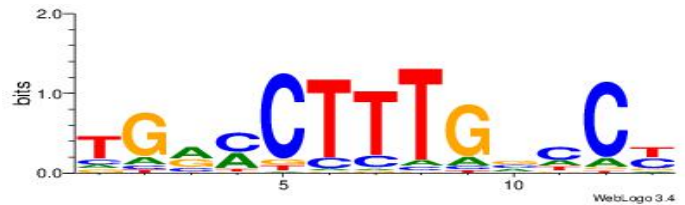
Number of overlap: 13
Similarity score: 0.081608

Alignment:
RGGBCAAAGKYCA
DHATWAAAATAHD

Original motif Consensus sequence: RGGBCAAAGKYCA



Reverse complement motif Consensus sequence: TGMYCTTTGBCK

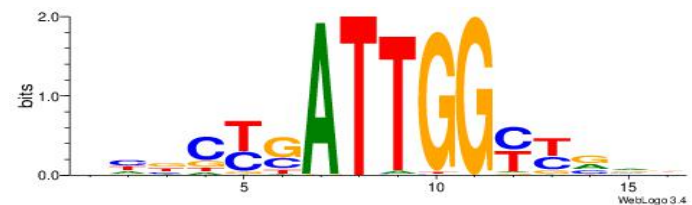
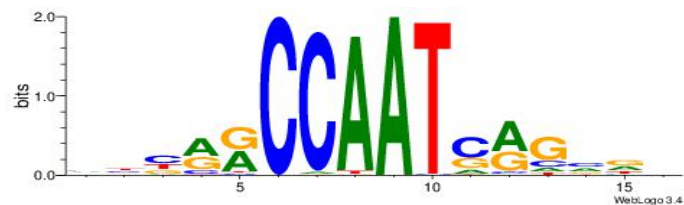


Dataset #: 3
Motif ID: 104
Motif name: NFYA
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 2
Number of overlap: 13
Similarity score: 0.0831397

Alignment:
BHVCKSATTTGGMKBVV
--DHTATTTTWATHD--

Original motif Consensus sequence: VBBRCCAATSRGVDB

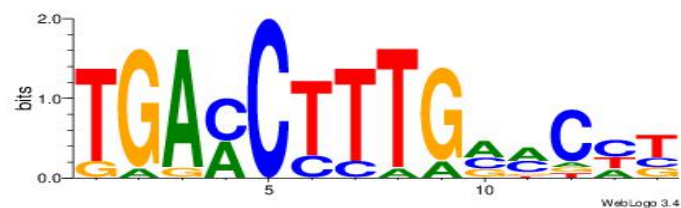
Reverse complement motif Consensus sequence:
BHVCKSATTTGGMKBVV



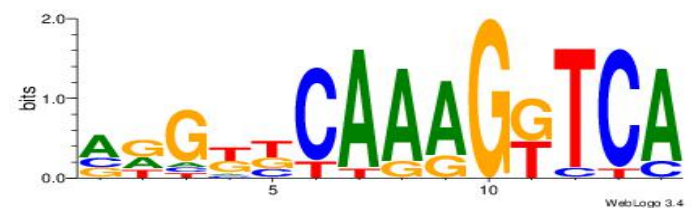
Dataset #: 3
 Motif ID: 107
 Motif name: NR2F1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 13
 Similarity score: 0.0856949

Alignment:
 TGAMCTTTGMMCYT
 DHTATTTTWATHD-

Original motif Consensus sequence: TGAMCTTTGMMCYT



Reverse complement motif Consensus sequence: AKGYCAAAGRTC

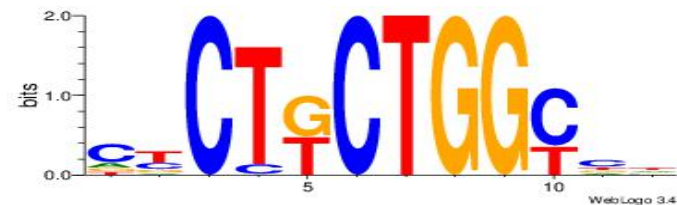


Dataset #: 4 Motif ID: 151 Motif name: agrCCAGmAGrg

Original motif Consensus sequence: HVGCCAGMAGRG



Reverse complement motif Consensus sequence: CKCTRCTGGCVH



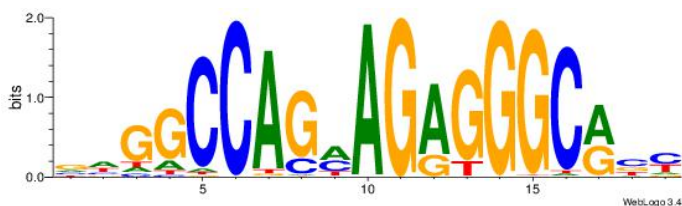
Best Matches for Motif ID 151 (Highest to Lowest)

Dataset #:	4
Motif ID:	163
Motif name:	gwGGCCAGmAGAGGGCrby
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:	0.00116274

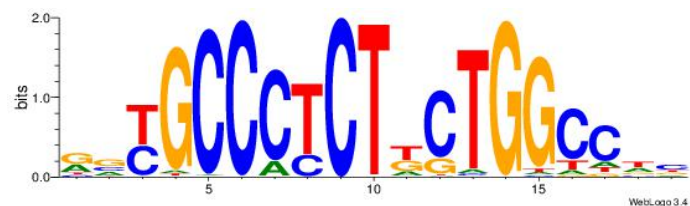
Alignment:

```
VHGGCCAGMAGAGGGCRBY
-HVGGCCAGMAGRG-----
```

Original motif Consensus sequence: VHGGCCAGMAGAGGGCRBY



Reverse complement motif Consensus sequence: KBKGCCCTCTYCTGGCCHV

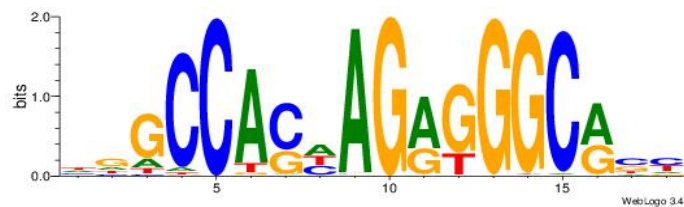


Dataset #: 4
 Motif ID: 165
 Motif name: wgGCCAshAGrGGGCrSy
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 12
 Similarity score: 0.0104581

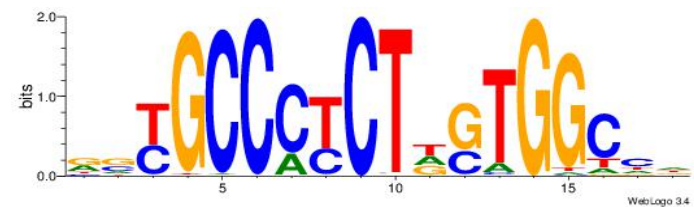
Alignment:

HDGCCACHAGRGGGCRBY
 HVGCCAGMAGRG-----

Original motif Consensus sequence: HDGCCACHAGRGGGCRBY



Reverse complement motif Consensus sequence: KBKGCCCKCTHGTGGCHH



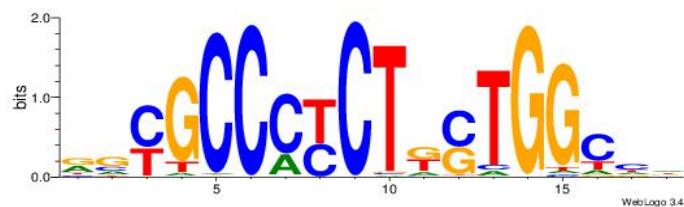
Dataset #: 4
 Motif ID: 156
 Motif name: rgyGCCMyCTksTGGccd
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1

Number of overlap: 12
Similarity score: 0.0140707

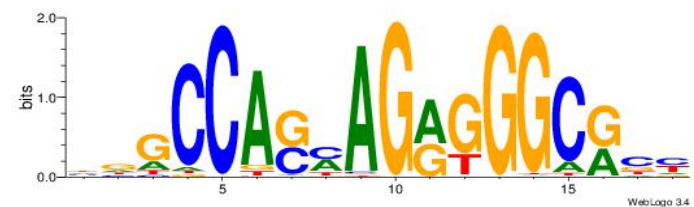
Alignment:

RVYGCCCYCTKSTGGCHD
-----CKCTRCTGGCVH

Original motif Consensus sequence: RVYGCCCYCTKSTGGCHD



Reverse complement motif Consensus sequence: DDGCCASYAGMGGGCKVM

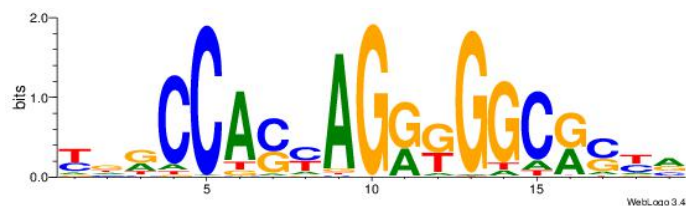


Dataset #: 3
Motif ID: 74
Motif name: CTCF
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 12
Similarity score: 0.0214576

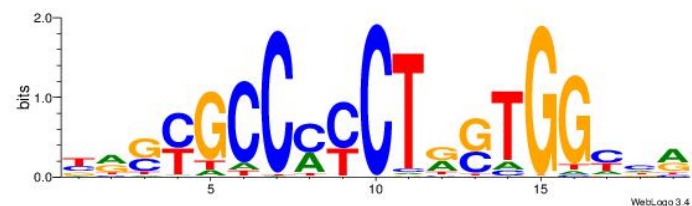
Alignment:

YDRCCASYAGRKGGCRSYV
HVGCCAGMAGR-----

Original motif Consensus sequence: YDRCCASYAGRKGGRSYV



Reverse complement motif Consensus sequence: BSMGCCYMCTKSTGGMHM

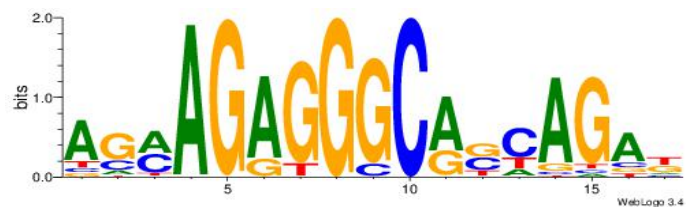


Dataset #: 4
Motif ID: 143
Motif name: AgmAGAGGGCrscAGak
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 6
Number of overlap: 12
Similarity score: 0.0481806

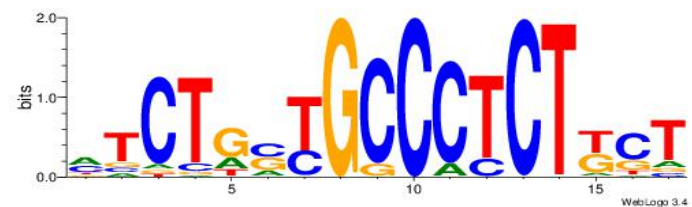
Alignment:

AGMAGAGGGCASCAGAK
-----HVGCCAGMAGRG

Original motif Consensus sequence: AGMAGAGGGCASCAGAK



Reverse complement motif Consensus sequence: RTCTGSTGCCCTCTYCT



Dataset #: 4 Motif ID: 152 Motif name: yrCATGCAYr

Original motif Consensus sequence: BRCATGCABD



Reverse complement motif Consensus sequence: HVTGCATGKV



Best Matches for Motif ID 152 (Highest to Lowest)

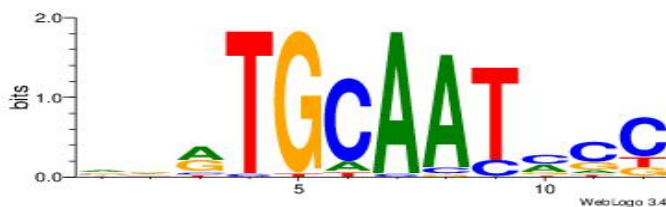
Dataset #:	3
Motif ID:	75
Motif name:	Ddit3Cebpa
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	10
Similarity score:	0.0420406

Alignment:

VDRITGCAATMCC

-HVTGCATGKV-

Original motif Consensus sequence: VDRITGCAATMCC



Reverse complement motif Consensus sequence: GGRATTGCAKHB

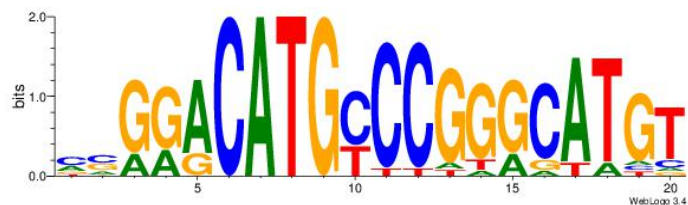


Dataset #: 3
 Motif ID: 125
 Motif name: TP53
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 4
 Number of overlap: 10
 Similarity score: 0.0472223

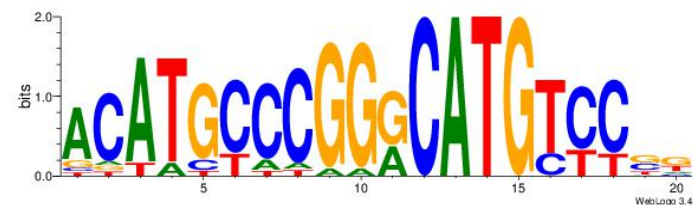
Alignment:

ACATGCCCGGKCATGTCCSR
 -----HVTGCATGKV---

Original motif Consensus sequence: MSGGACATGYCCGGGCATGT



Reverse complement motif Consensus sequence:
ACATGCCCGGKCATGTCCSR



Dataset #: 4
 Motif ID: 134
 Motif name: ssCGwGCGss
 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: 0.055087

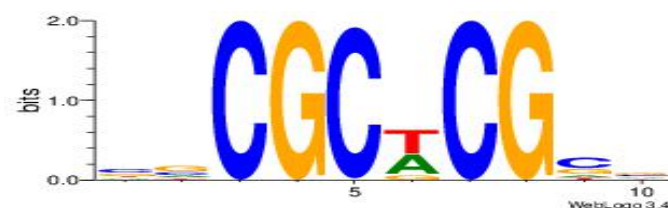
Alignment:

BSCGWGCGBV
BRCATGCABD

Original motif Consensus sequence: BSCGWGCGBV



Reverse complement motif Consensus sequence: VBCGWCGBS

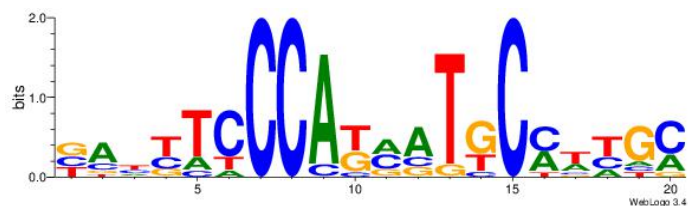


Dataset #: 3
Motif ID: 131
Motif name: znf143
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 11
Number of overlap: 10
Similarity score: 0.0551971

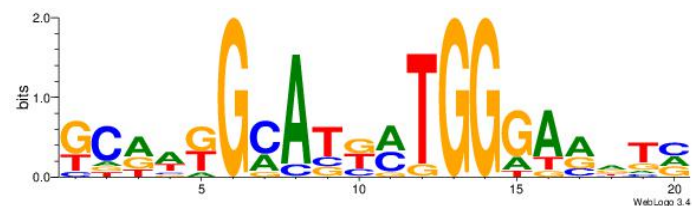
Alignment:

GCMWRGCATYRTGGGAMHTB
-----BRCATGCABD

Original motif Consensus sequence: BAHYTCCCAKMATGCMWYGC



Reverse complement motif Consensus sequence: GCMWRGCATYRTGGGAMHTB



Dataset #: 4
Motif ID: 159
Motif name: kkAAGAGCAsy
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: 0.0606344

Alignment:

HVTGCTCTTBH

HVTGCATGKV-

Original motif Consensus sequence: DBAAGAGCAVH

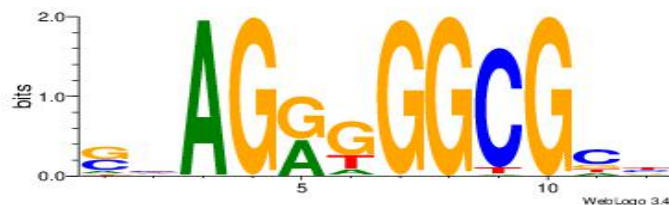


Reverse complement motif Consensus sequence: HVTGCTCTTBH

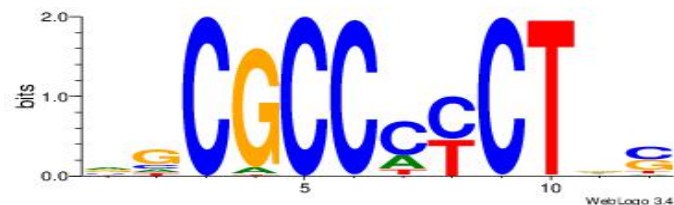


Dataset #: 4 **Motif ID: 153** **Motif name: scAGrkGGCGcy**

Original motif Consensus sequence: SHAGRGGGCGCB



Reverse complement motif Consensus sequence: VCGGCCCMCTDS



Best Matches for Motif ID 153 (Highest to Lowest)

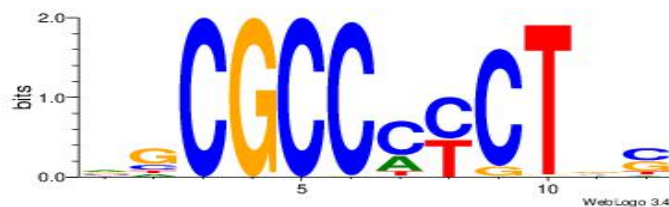
Dataset #:	4
Motif ID:	137
Motif name:	rgCGCCmyCTgs
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	12
Similarity score:	0

Alignment:

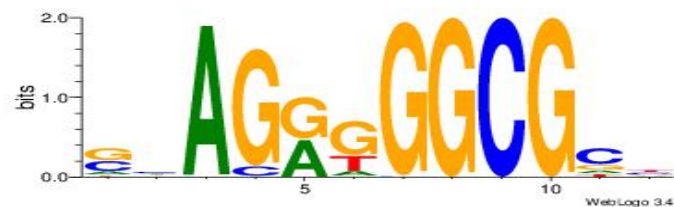
SHAGKGGGCGCB

SHAGRGGGCGCB

Original motif Consensus sequence: VCGGCCCYCTDS



Reverse complement motif Consensus sequence: SHAGKGGGCGCB



Dataset #: 4
Motif ID: 147
Motif name: asCAGrkGGCrsy
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: 0.0112071

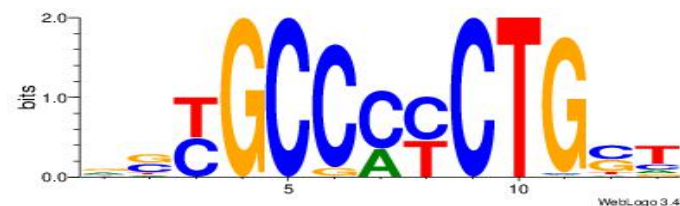
Alignment:

ASCAGRGGGCRSB
-SHAGRGGGCGCB

Original motif Consensus sequence: ASCAGRGGGCRSB



Reverse complement motif Consensus sequence: BSKGCCCMCTGST



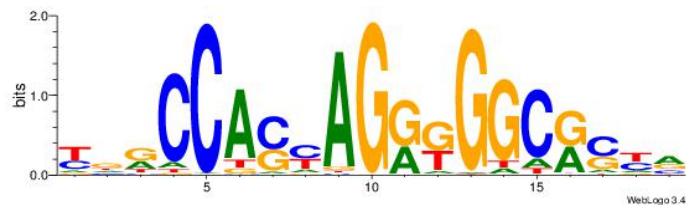
Dataset #: 3
Motif ID: 74
Motif name: CTCF
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 7

Number of overlap: 12
Similarity score: 0.0133899

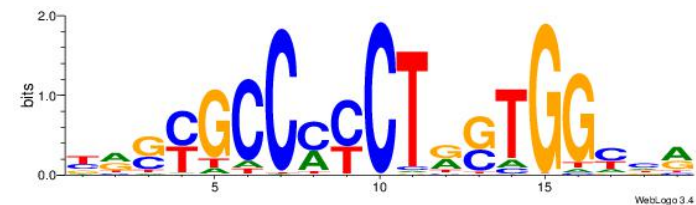
Alignment:

YDRCCASYAGRKGGRSYV
-----SHAGRGGGCGCB-

Original motif Consensus sequence: YDRCCASYAGRKGGRSYV



Reverse complement motif Consensus sequence:
BMSMGCCYMCTKSTGGMHM

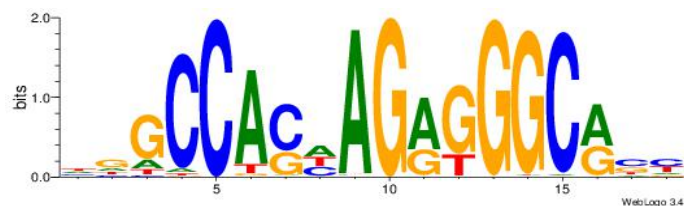


Dataset #: 4
Motif ID: 165
Motif name: wgGCCAshAGrGGGCrSy
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 12
Similarity score: 0.0146442

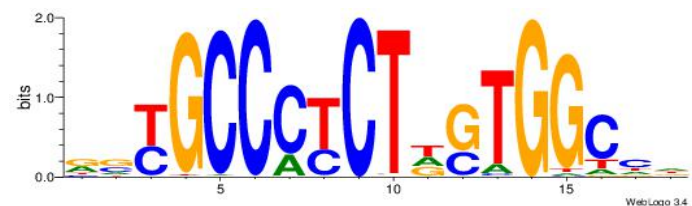
Alignment:

HDGCCACHAGRGGGCRBY
-----SHAGRGGGCGCB

Original motif Consensus sequence: HDGCCACHAGRGGGCRBY



Reverse complement motif Consensus sequence: KBKGCCCKCTHGTGGCHH



Dataset #: 4
Motif ID: 166
Motif name: CasCAGrGGGCrSy
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: 0.0200811

Alignment:

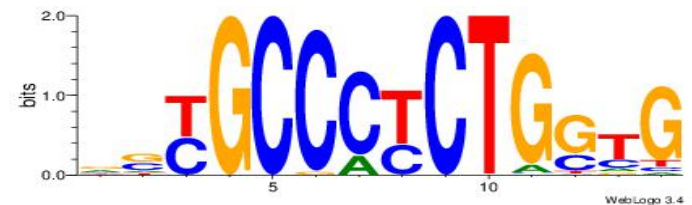
CACCAGRGGGCRSB

--SHAGRGGGCGCB

Original motif Consensus sequence: CACCAGRGGGCRSB



Reverse complement motif Consensus sequence: BSKGCCCKCTGGT



Dataset #: 4 Motif ID: 154 Motif name: csCsCCTCCcc

Original motif Consensus sequence: VBCCCCTCCHB



Reverse complement motif Consensus sequence: BDGGAGGGGBV

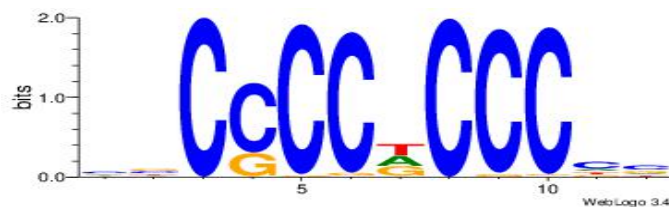


Best Matches for Motif ID 154 (Highest to Lowest)

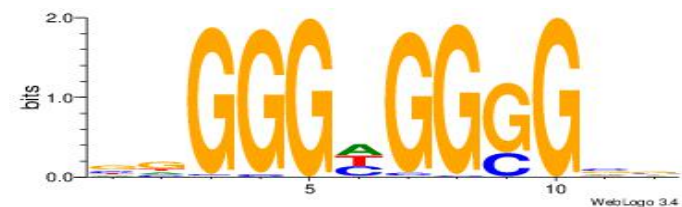
Dataset #: 4
 Motif ID: 155
 Motif name: csCSCCdCCCcs
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0

Alignment:
 VBCCCCDCCCHV
 VBCCCCTCCHB-

Original motif Consensus sequence: VBCCCCDCCCHV



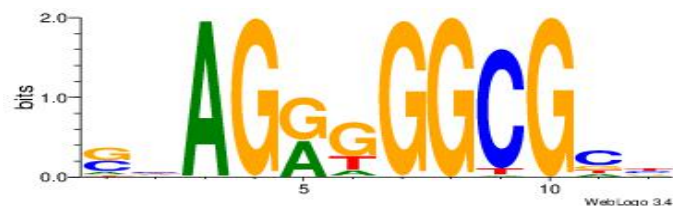
Reverse complement motif Consensus sequence: VDGGGDGGGGBV



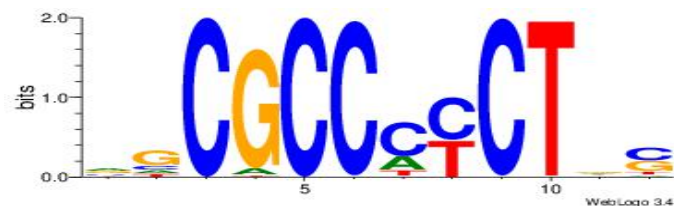
Dataset #: 4
 Motif ID: 153
 Motif name: scAGrkGGCGcy
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.0415573

Alignment:
 SHAGRGGGCGCB
 BDGGAGGGGBV-

Original motif Consensus sequence: SHAGRGGGCGCB



Reverse complement motif Consensus sequence: VGCGCCCMCTDS



Dataset #: 4
 Motif ID: 137
 Motif name: rgCGCCmyCTgs
 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: 0.0446252

Alignment:
SHAGKGGGCGCB
-BDGGAGGGGBV

Original motif Consensus sequence: VGCGCCCYCTDS



Reverse complement motif Consensus sequence: SHAGKGGGCGCB



Dataset #: 4
Motif ID: 162
Motif name: ccAsCCCCAcc
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: 0.049712

Alignment:
DBTGGGGSTVD
BDGGAGGGGBV

Original motif Consensus sequence: HVASCCCCABH

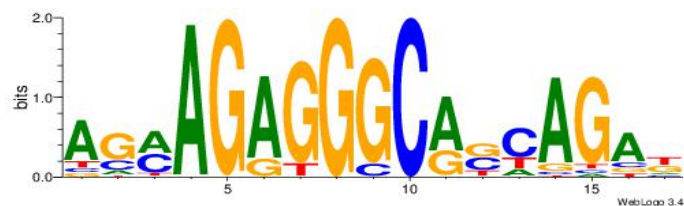
Reverse complement motif Consensus sequence: DBTGGGGSTVD



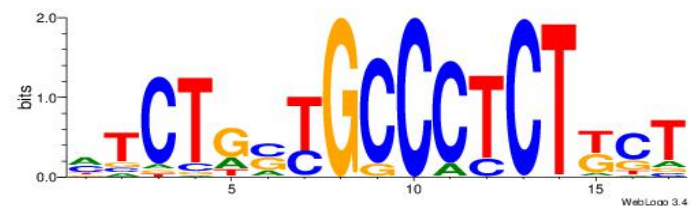
Dataset #: 4
 Motif ID: 143
 Motif name: AgmAGAGGGCrscAGak
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 11
 Similarity score: 0.0533559

Alignment:
 AGMAGAGGGCASCAGAK
 -----BDGGAGGGGBV-

Original motif Consensus sequence: AGMAGAGGGCASCAGAK

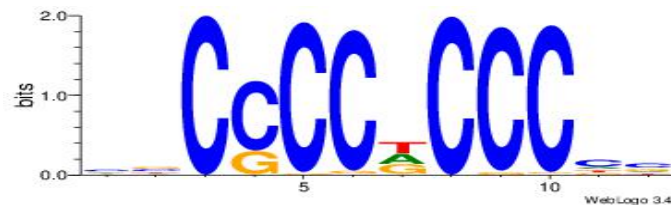


Reverse complement motif Consensus sequence:
 RTCTGSTGCCCTCTYCT

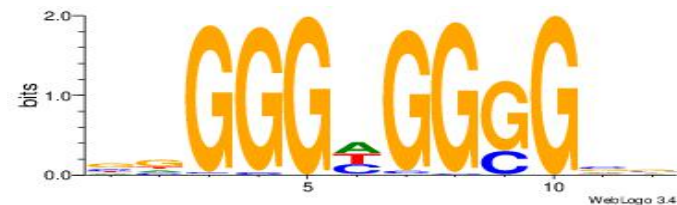


Dataset #: 4 Motif ID: 155 Motif name: csCSCCdCCCcs

Original motif Consensus sequence: VBCCCCDCCCHV



Reverse complement motif Consensus sequence: VDGGGDGGGGBV



Best Matches for Motif ID 155 (Highest to Lowest)

Dataset #:	4
Motif ID:	137
Motif name:	rgCGCCmyCTgs
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:	0.0604731

Alignment:

SHAGKGGGCGCB

VDGGGDGGGGBV

Original motif Consensus sequence: VGC GCCCYCTDS



Reverse complement motif Consensus sequence: SHAGKGGGCGCB



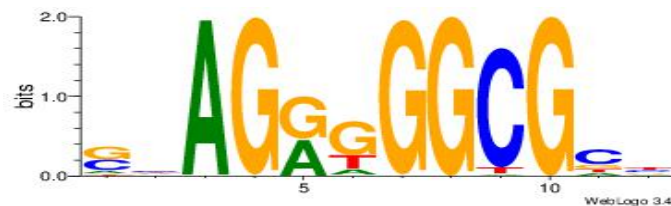
Dataset #: 4
 Motif ID: 153
 Motif name: scAGrkGGCGcy
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 12
 Similarity score: 0.0624586

Alignment:

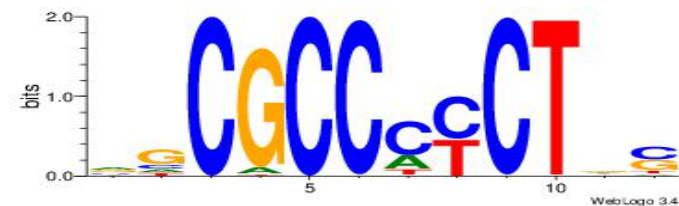
VGCGCCCMCTDS

VBCCCCDCCCHV

Original motif Consensus sequence: SHAGRGGGCGCB



Reverse complement motif Consensus sequence: VGCGCCCMCTDS

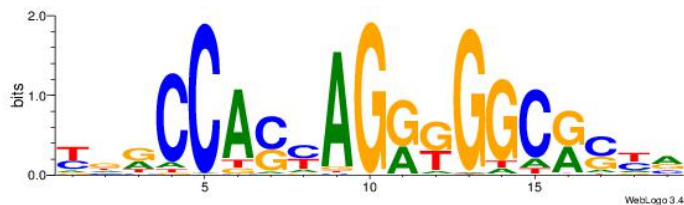


Dataset #: 3
 Motif ID: 74
 Motif name: CTCF
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 7
 Number of overlap: 12

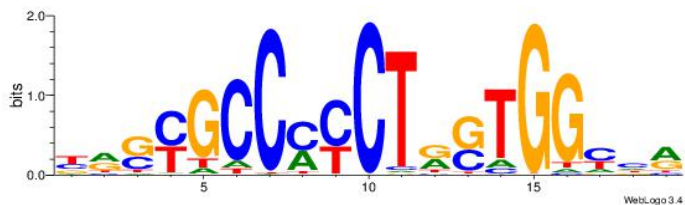
Similarity score: 0.0800509

Alignment:
BMSMGCCYMCTKSTGGMHM
-----VBCCCCDCCCHV-

Original motif Consensus sequence: YDRCCASYAGRKGGRSYV



Reverse complement motif Consensus sequence:
BMSMGCCYMCTKSTGGMHM

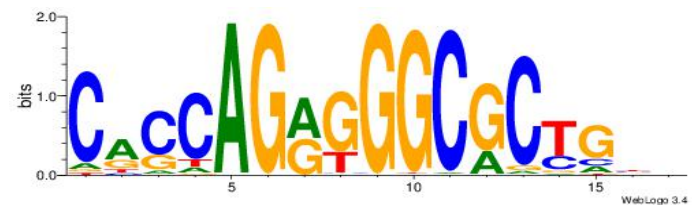
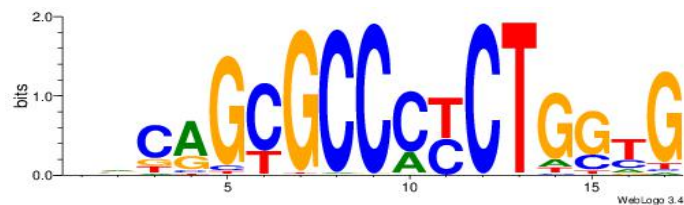


Dataset #: 4
Motif ID: 168
Motif name: yrcrYGCCMyCTGGtG
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 12
Similarity score: 0.0810683

Alignment:
HVCAGCGCCCYCTGGTG
VBCCCCDCCCHV-----

Original motif Consensus sequence: HVCAGCGCCCYCTGGTG

Reverse complement motif Consensus sequence:
CACCAGMGGGCGCTGBD



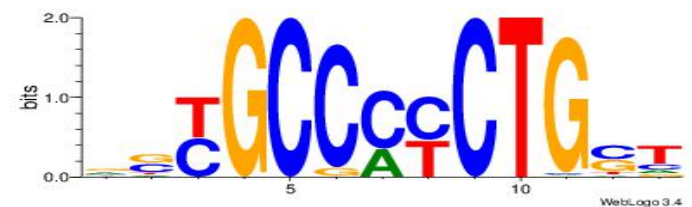
Dataset #: 4
 Motif ID: 147
 Motif name: asCAGrkGGCrSy
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 12
 Similarity score: 0.0823049

Alignment:
 BSKGCCCMCTGST
 -VBCCCCDCCCHV

Original motif Consensus sequence: ASCAGRGGGCRSB

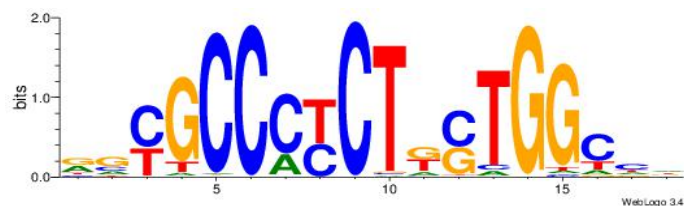


Reverse complement motif Consensus sequence: BSKGCCCMCTGST

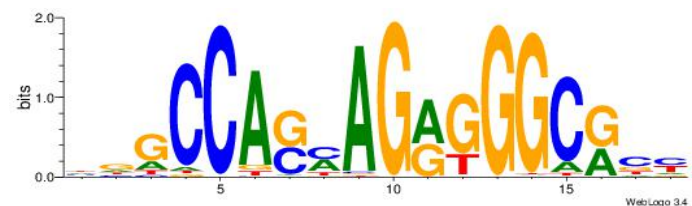


Dataset #: 4 Motif ID: 156 Motif name: rgyGCCMyCTksTGGccd

Original motif Consensus sequence: RYVGCCCYCTKSTGGCHD



Reverse complement motif Consensus sequence: DDGCCASYAGMGGGCKVM



Best Matches for Motif ID 156 (Highest to Lowest)

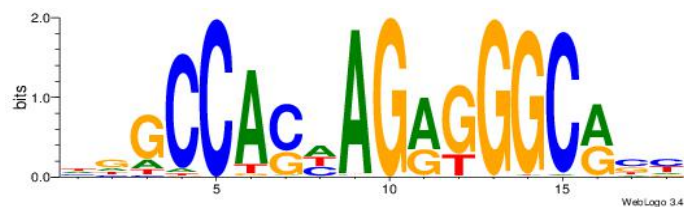
Dataset #:	4
Motif ID:	165
Motif name:	wgGCCAshAGrGGGCrSy
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	18
Similarity score:	0.0156448

Alignment:

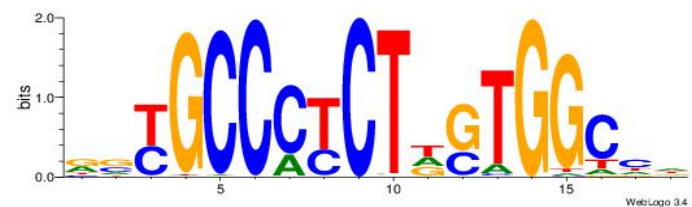
```

HDGCCACHAGRGGGCRBY
DDGCCASYAGMGGGCKVM
  
```

Original motif Consensus sequence: HDGCCACHAGRGGGCRBY



Reverse complement motif Consensus sequence: KBKGCCCKCTHGTGGCHH

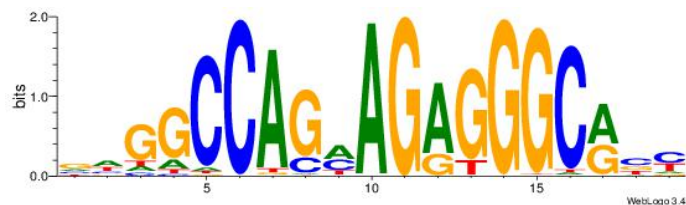


Dataset #: 4
 Motif ID: 163
 Motif name: gwGGCCAGmAGAGGGCrby
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 18
 Similarity score: 0.0201276

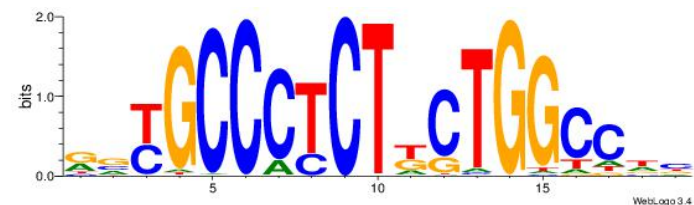
Alignment:

VHGGCCAGMAGAGGGCRBY
 -DDGCCASYAGMGGGCKVM

Original motif Consensus sequence: VHGGCCAGMAGAGGGCRBY



Reverse complement motif Consensus sequence: KBKGCCCTCTYCTGGCCHV



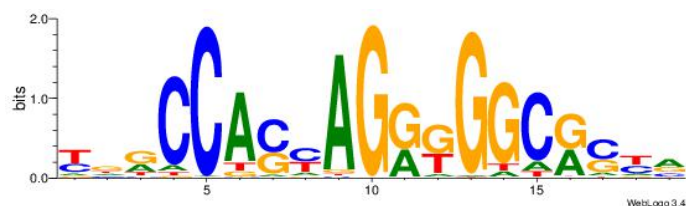
Dataset #: 3
 Motif ID: 74
 Motif name: CTCF
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward

Position number: 1
Number of overlap: 18
Similarity score: 0.0207204

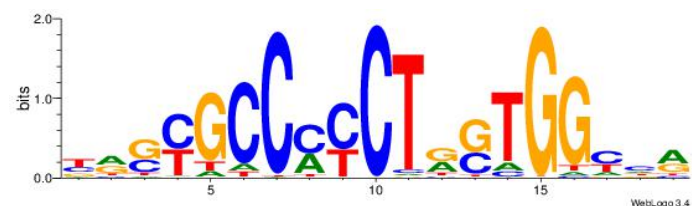
Alignment:

YDRCCASYAGRKGGRSYV
-DDGCCASYAGMGGGCKVM

Original motif Consensus sequence: YDRCCASYAGRKGGRSYV



Reverse complement motif Consensus sequence: BMSMGCCYMCTKSTGGMHM

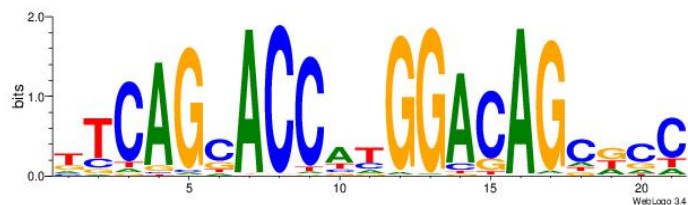


Dataset #: 3
Motif ID: 113
Motif name: REST
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 18
Similarity score: 0.0950319

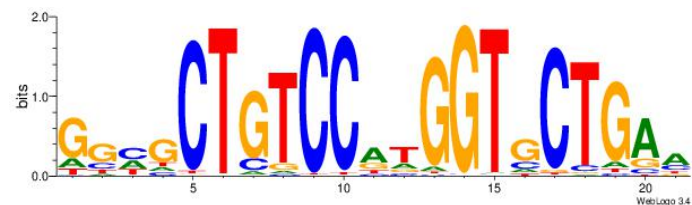
Alignment:

GGYGCTGTCCATGGTGCTGAA
---RVYGCCCYCTKSTGGCHD

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC



Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA

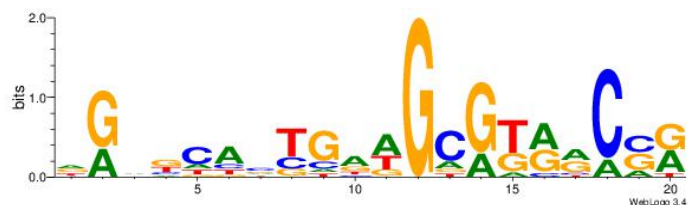


Dataset #: 3
Motif ID: 109
Motif name: Pax5
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 18
Similarity score: 0.09559

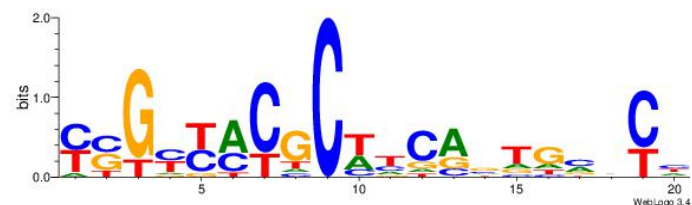
Alignment:

MSGKKRCGCWDCABTGBBCD
--RVYGCCCYCTKSTGGCHD

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR

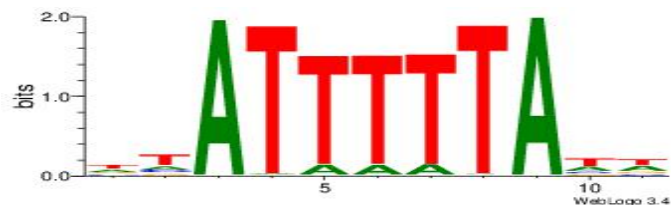


Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD



Dataset #: 4 Motif ID: 157 Motif name: wtATTTTTAww

Original motif Consensus sequence: DTATTTTTAww



Reverse complement motif Consensus sequence: WWTAAAAATAD



Best Matches for Motif ID 157 (Highest to Lowest)

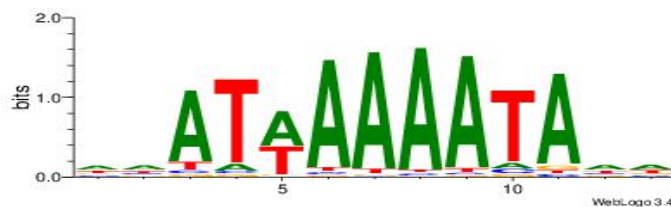
Dataset #: 4
Motif ID: 150
Motif name: waATwAAAATAww
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 2
Number of overlap: 11
Similarity score: 0

Alignment:

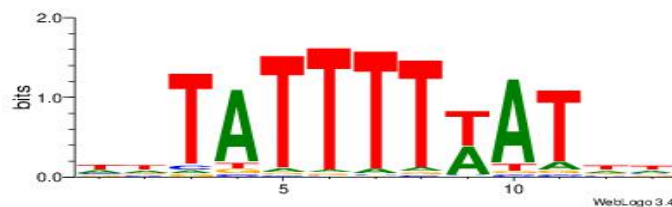
DHTATTTTWATHD

-DTATTTTTAww-

Original motif Consensus sequence: DHATWAAAATAHD



Reverse complement motif Consensus sequence: DHTATTTTWATHD

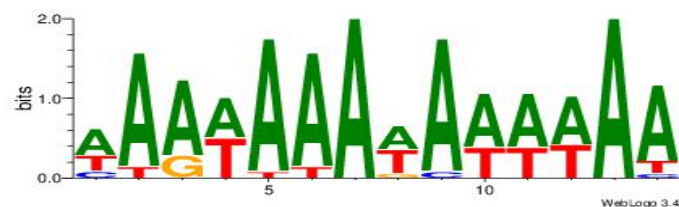


Dataset #: 2
 Motif ID: 68
 Motif name: Motif 68
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 11
 Similarity score: 0.0323073

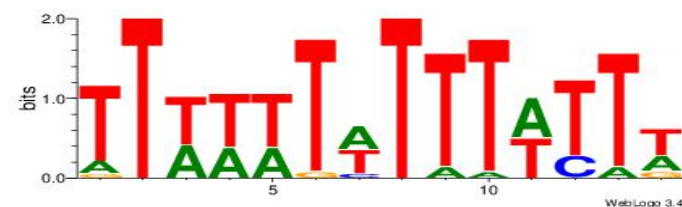
Alignment:

TTWWWTWTTTWTTW
 -DTATTTTAAWW--

Original motif Consensus sequence: WAAWAAAWAWWWAA



Reverse complement motif Consensus sequence: TTWWWTWTTTWTTW

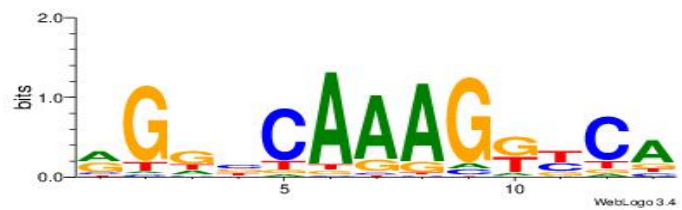


Dataset #: 3
 Motif ID: 87
 Motif name: HNF4A
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward

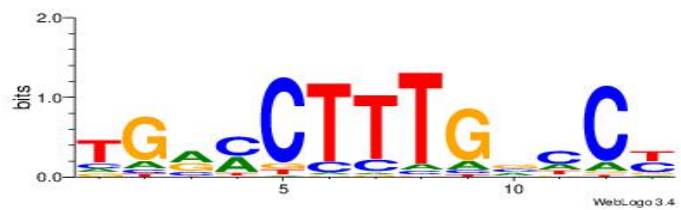
Position number: 1
Number of overlap: 11
Similarity score: 0.0727314

Alignment:
RGGBCAAAGKYCA
WWTAAAAATAD--

Original motif Consensus sequence: RGGBCAAAGKYCA



Reverse complement motif Consensus sequence: TGMYCTTTGBCCK

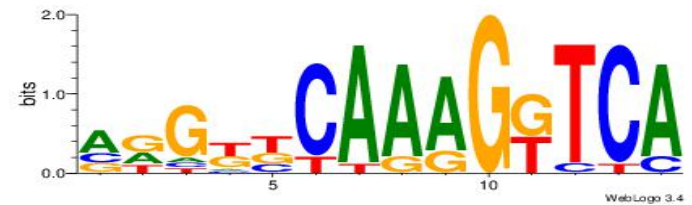


Dataset #: 3
Motif ID: 107
Motif name: NR2F1
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 4
Number of overlap: 11
Similarity score: 0.0739182

Alignment:
AKGYCAAAGRTCA
---WWTAAAAATAD

Original motif Consensus sequence: TGAMCTTTGMMCYT

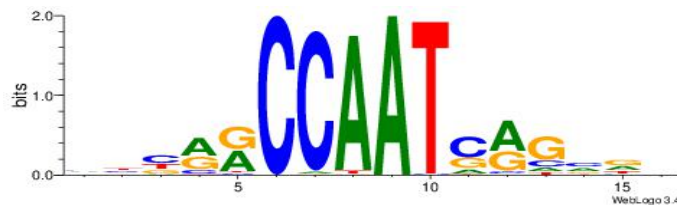
Reverse complement motif Consensus sequence: AKGYCAAAGRTCA



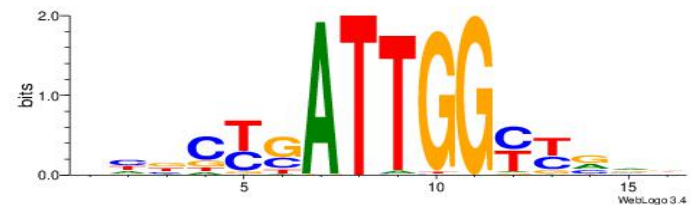
Dataset #: 3
 Motif ID: 104
 Motif name: NFYA
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 5
 Number of overlap: 11
 Similarity score: 0.0755742

Alignment:
 BHVCKSATTTGGMKBVV
 -DTATTTTAAW----

Original motif Consensus sequence: VBBRCCAATSRGVDB



Reverse complement motif Consensus sequence: BHVCKSATTTGGMKBVV



Dataset #: 4 Motif ID: 158 Motif name: grCCACwAGrk

Original motif Consensus sequence: DDCCACWAGRK



Reverse complement motif Consensus sequence: YMCTWGTGGHH



Best Matches for Motif ID 158 (Highest to Lowest)

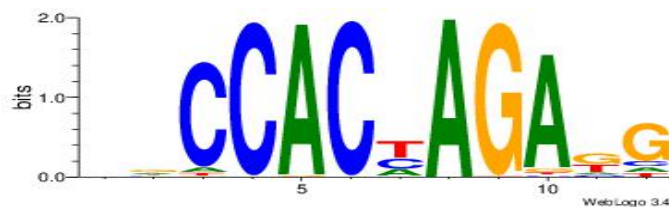
Dataset #:	4
Motif ID:	138
Motif name:	grCCACyAGAkG
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	11
Similarity score:	0.0013909

Alignment:

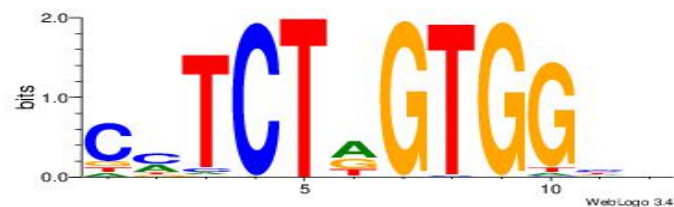
DDCCACYAGAKG

DDCCACWAGRK-

Original motif Consensus sequence: DDCCACYAGAKG



Reverse complement motif Consensus sequence: CYTCTMGTGGHH



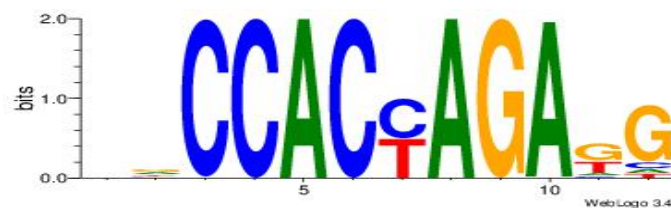
Dataset #: 4
 Motif ID: 145
 Motif name: grCCACyAGAkG
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 11
 Similarity score: 0.00619044

Alignment:

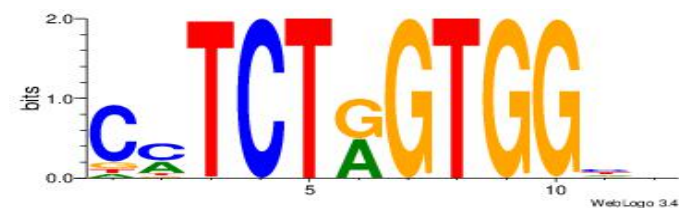
DDCCACYAGAKG

DDCCACWAGRK-

Original motif Consensus sequence: DDCCACYAGAKG



Reverse complement motif Consensus sequence: CYTCTKGTGGHH

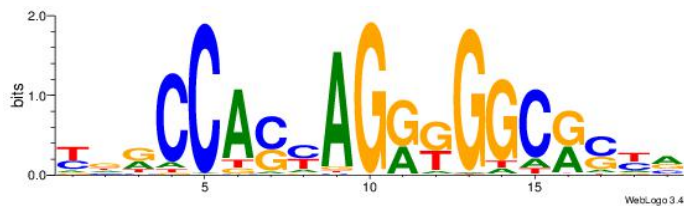


Dataset #: 3
 Motif ID: 74
 Motif name: CTCF
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 8
 Number of overlap: 11

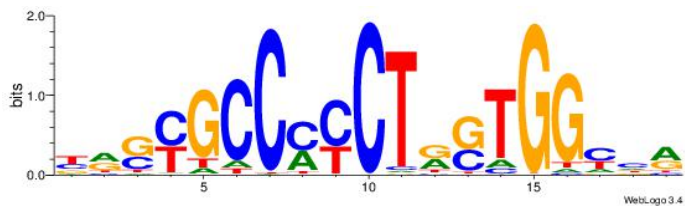
Similarity score: 0.0223616

Alignment:
BMSMGCCYMCTKSTGGMHM
-----YMCTWGTGGHH-

Original motif Consensus sequence: YDRCCASYAGRKGGCRSYV



Reverse complement motif Consensus sequence:
BMSMGCCYMCTKSTGGMHM

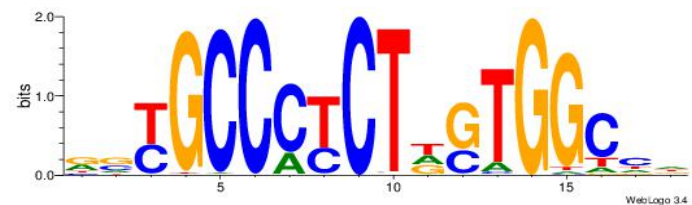
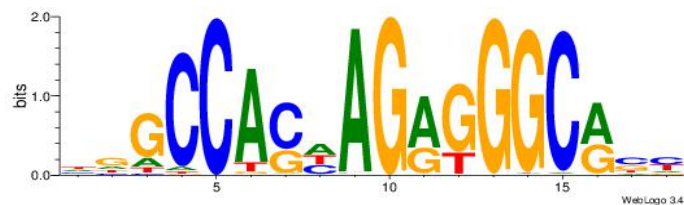


Dataset #: 4
Motif ID: 165
Motif name: wgGCCAshAGrGGGCrSy
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 7
Number of overlap: 11
Similarity score: 0.0228739

Alignment:
HDGCCACHAGRGGGCRBY
-DDCCACWAGRK-----

Original motif Consensus sequence: HDGCCACHAGRGGGCRBY

Reverse complement motif Consensus sequence:
KBKGCCCKCTHGTGGCHH



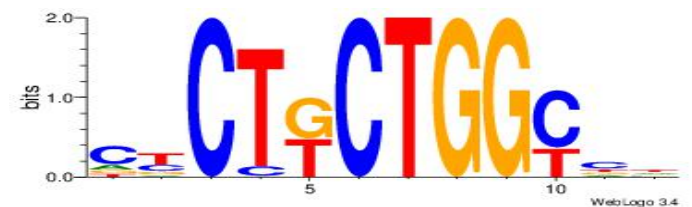
Dataset #: 4
 Motif ID: 151
 Motif name: agrCCAGmAGrg
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.0330864

Alignment:
 HVGCCAGMAGRG
 -DDCCACWAGRK

Original motif Consensus sequence: HVGCCAGMAGRG



Reverse complement motif Consensus sequence: CKCTRCTGGCVH

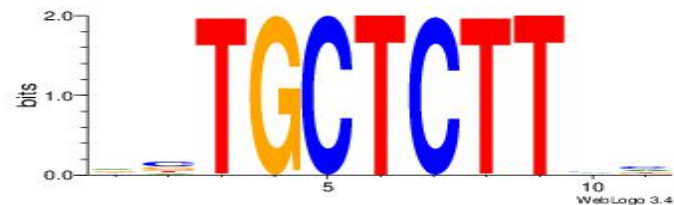


Dataset #: 4 Motif ID: 159 Motif name: kkAAGAGCAsy

Original motif Consensus sequence: DBAAGAGCAVH



Reverse complement motif Consensus sequence: HVTGCTCTTBH



Best Matches for Motif ID 159 (Highest to Lowest)

Dataset #:	4
Motif ID:	160
Motif name:	brCAGGGCCrs
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:	0.0212428

Alignment:

BBGGCCCTGBB

HVTGCTCTTBH

Original motif Consensus sequence: BVCAGGGCCVB



Reverse complement motif Consensus sequence: BBGGCCCTGBB



Dataset #: 4
 Motif ID: 133
 Motif name: shAGrGGGCAgy
 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: 0.0322726

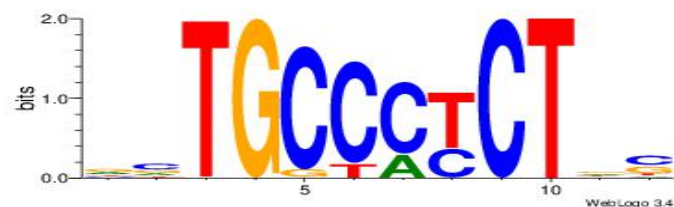
Alignment:

SHAGRGGGCABH
 -DBAAGAGCAVH

Original motif Consensus sequence: SHAGRGGGCABH



Reverse complement motif Consensus sequence: DBTGCCCKCTDS

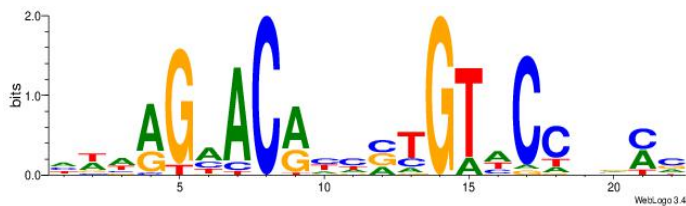


Dataset #: 3
 Motif ID: 70
 Motif name: Ar
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 11

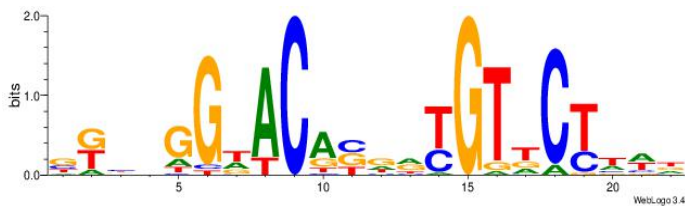
Similarity score: 0.0353029

Alignment:
VRVDGGHACAVDDKGTHCTDWH
-----HVTGCTCTTBH

Original motif Consensus sequence: HWDAGHACRHHVTGTHCCHVMV



Reverse complement motif Consensus sequence: VRVDGGHACAVDDKGTHCTDWH

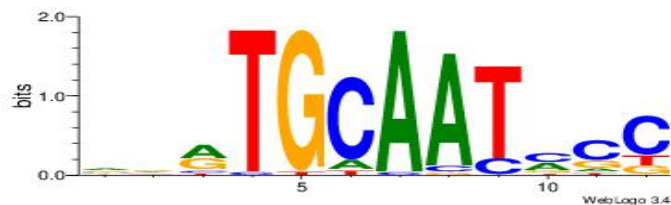


Dataset #: 3
Motif ID: 75
Motif name: Ddit3Cebpa
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 11
Similarity score: 0.0380063

Alignment:
VDRTGCAATMCC
HVTGCTCTTBH-

Original motif Consensus sequence: VDRTGCAATMCC

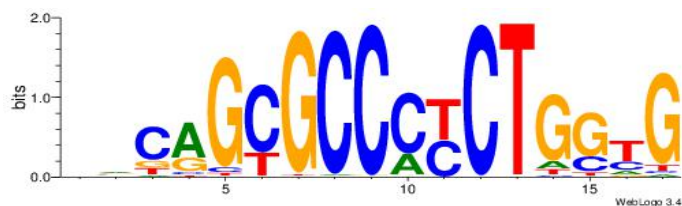
Reverse complement motif Consensus sequence: GGRATTGCAKHB



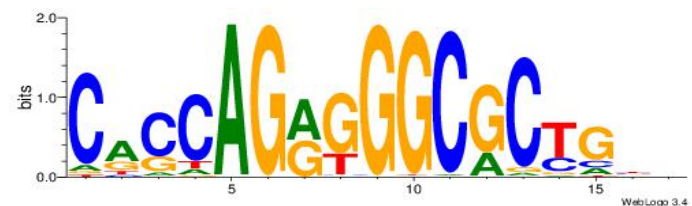
Dataset #: 4
 Motif ID: 168
 Motif name: yrcrYGCCMyCTGGtG
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.0432631

Alignment:
 CACCAGMGGGCGCTGBD
 -----HVTGCTCTTBH

Original motif Consensus sequence: HVCAGCGCCCYCTGGTG



Reverse complement motif Consensus sequence: CACCAGMGGGCGCTGBD



Dataset #: 4 Motif ID: 160 Motif name: brCAGGGCCrs

Original motif Consensus sequence: BVCAGGGCCVB



Reverse complement motif Consensus sequence: BBGGCCCTGGBB



Best Matches for Motif ID 160 (Highest to Lowest)

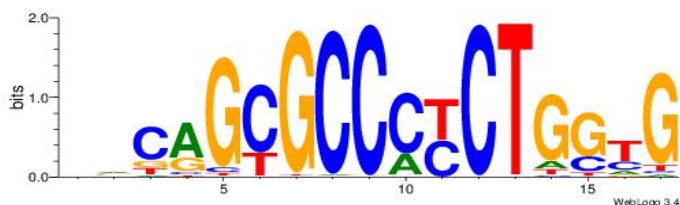
Dataset #:	4
Motif ID:	168
Motif name:	yrerGYGCCMyCTGGtG
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	11
Similarity score:	0.0430085

Alignment:

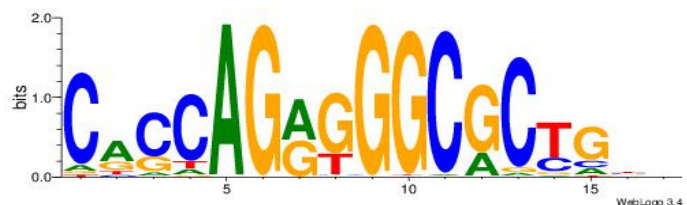
HVCAGCGCCCYCTGGTG

BVCAGGGCCVB-----

Original motif Consensus sequence: HVCAGCGCCCYCTGGTG



Reverse complement motif Consensus sequence: CACCAGMGGGCGCTGBD

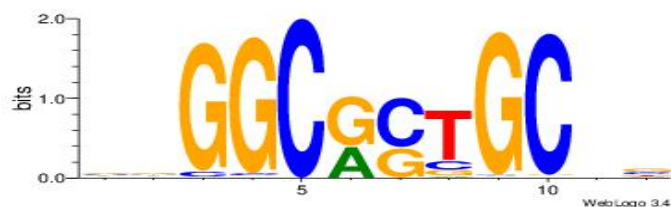


Dataset #: 4
 Motif ID: 170
 Motif name: ssGGCrSTGCrS
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 11
 Similarity score: 0.0438378

Alignment:

BVGCASMGCCVV
 -BVCAGGGCCVB

Original motif Consensus sequence: VVGGCRSTGCVB



Reverse complement motif Consensus sequence: BVGCASMGCCVV



Dataset #: 4
 Motif ID: 159
 Motif name: kkAAGAGCAsy
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 11

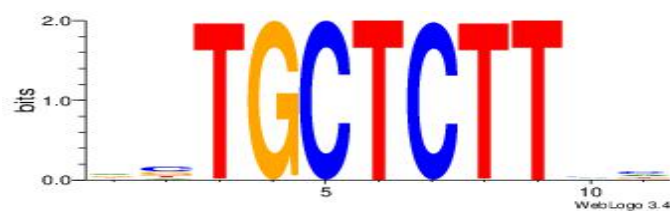
Similarity score: 0.0567379

Alignment:
HVTGCTCTTBH
BBGGCCCTGBB

Original motif Consensus sequence: DBAAGAGCAVH



Reverse complement motif Consensus sequence: HVTGCTCTTBH

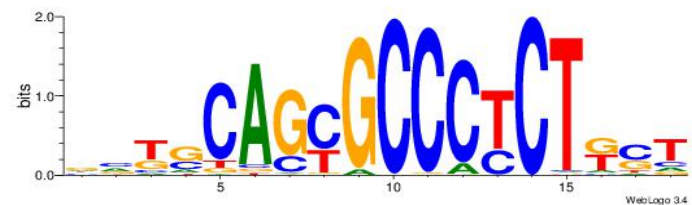
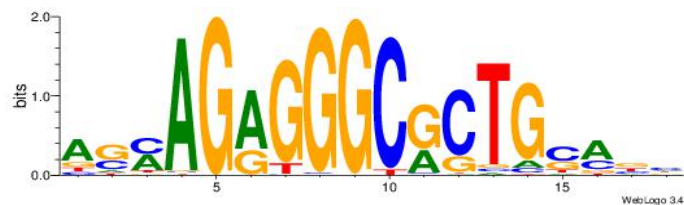


Dataset #: 4
Motif ID: 149
Motif name: asmAGRGGGCrCTGsmkc
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 3
Number of overlap: 11
Similarity score: 0.0583002

Alignment:
ASMAGAGGGCRCTGSABH
--BBGGCCCTGBB-----

Original motif Consensus sequence: ASMAGAGGGCRCTGSABH

Reverse complement motif Consensus sequence:
DBTSCAGMGCCCTCTRST

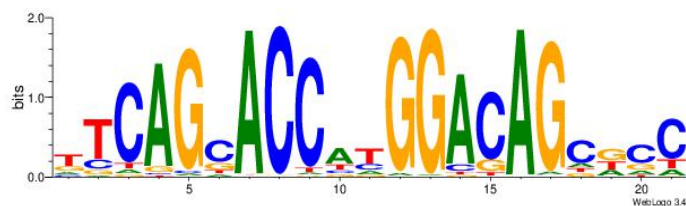


Dataset #: 3
 Motif ID: 113
 Motif name: REST
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 11
 Number of overlap: 11
 Similarity score: 0.0603368

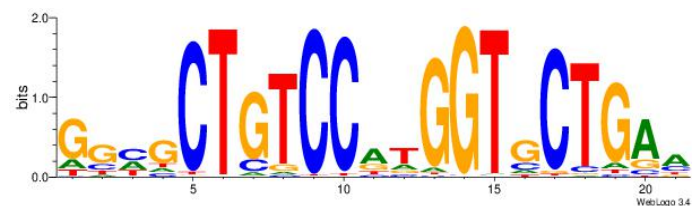
Alignment:

TTCAGCACCATGGACAGCKCC
 BVCAGGGCCVB-----

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC

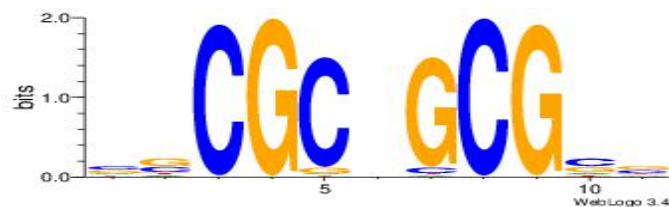


Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA

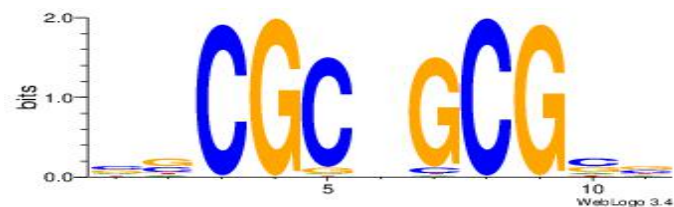


Dataset #: 4 Motif ID: 161 Motif name: ssCGCwGCGss

Original motif Consensus sequence: VSCGCDGCGSB



Reverse complement motif Consensus sequence: BSCGCDGCGSV

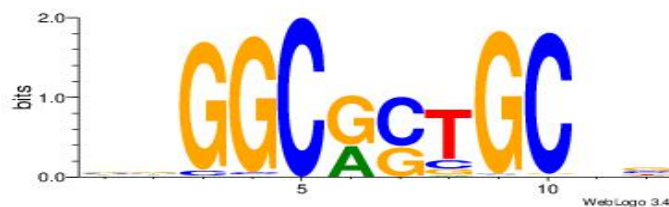


Best Matches for Motif ID 161 (Highest to Lowest)

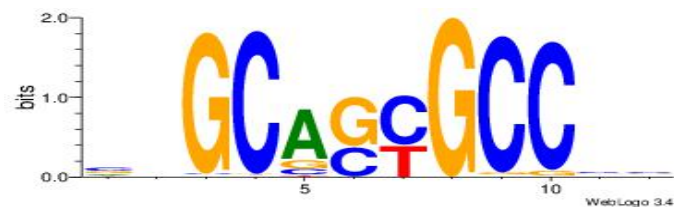
Dataset #: 4
 Motif ID: 170
 Motif name: ssGGCrSTGCrS
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 11
 Similarity score: 0.0546471

Alignment:
 VVGGCRSTGCVB
 BSCGCDGCGSV-

Original motif Consensus sequence: VVGGCRSTGCVB



Reverse complement motif Consensus sequence: BVGCASMGCCVV

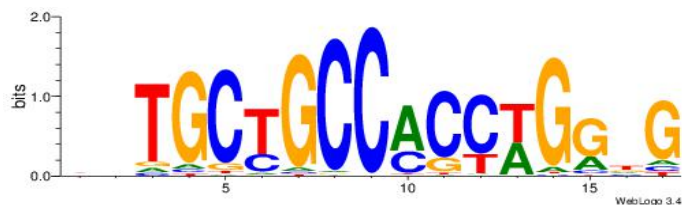


Dataset #: 4
 Motif ID: 169
 Motif name: yvTGCyGCCmCCwGgtG
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.0565318

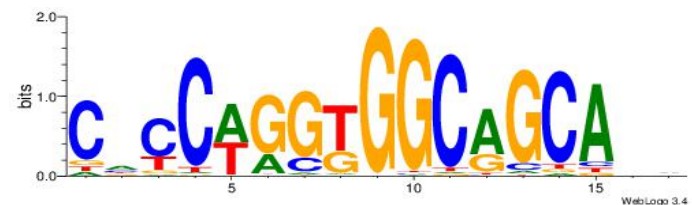
Alignment:

CDCCWGGTGGCAGCAVV
 -----BSCGCDGCGSV

Original motif Consensus sequence: BVTGCTGCCACCWGGDG



Reverse complement motif Consensus sequence: CDCCWGGTGGCAGCAVV

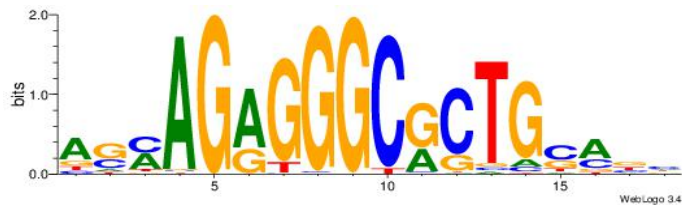


Dataset #: 4
 Motif ID: 149
 Motif name: asmAGRGGGCrCTGsmkc
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1

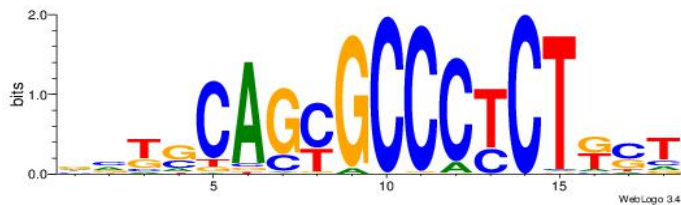
Number of overlap: 11
Similarity score: 0.0580603

Alignment:
DBTSCAGMGCCCTCTRST
BSCGCDGCGSV-----

Original motif Consensus sequence: ASMAGAGGGCRCTGSABH



Reverse complement motif Consensus sequence: DBTSCAGMGCCCTCTRST



Dataset #: 4
Motif ID: 154
Motif name: csCsCCTCCcc
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: 0.0592711

Alignment:
VBCCCCTCCHB
BSCGCDGCGSV

Original motif Consensus sequence: VBCCCCTCCHB

Reverse complement motif Consensus sequence: BDGGAGGGGBV



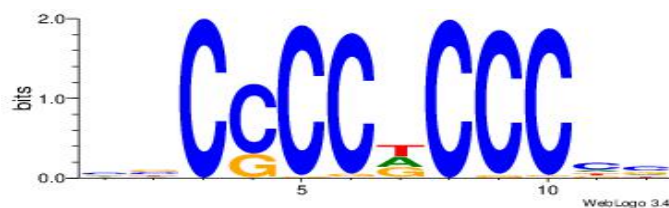
Dataset #: 4
 Motif ID: 155
 Motif name: csCSCCdCCCcs
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 11
 Similarity score: 0.0599572

Alignment:

VDGGGDGGGGBV

VSCGCDGCGSB-

Original motif Consensus sequence: VBCCCCDCCCHV



Reverse complement motif Consensus sequence: VDGGGDGGGGBV



Dataset #: 4 Motif ID: 162 Motif name: ccAsCCCCAcc

Original motif Consensus sequence: HVASCCCCABH



Reverse complement motif Consensus sequence: DBTGGGGSTVD



Best Matches for Motif ID 162 (Highest to Lowest)

Dataset #:	4
Motif ID:	154
Motif name:	csCsCCTCCcc
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:	0.0318935

Alignment:

BDGGAGGGGBV

DBTGGGGSTVD

Original motif Consensus sequence: VBCCCCTCCHB



Reverse complement motif Consensus sequence: BDGGAGGGGBV

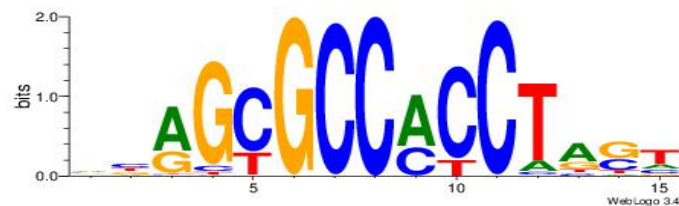


Dataset #: 4
 Motif ID: 146
 Motif name: myrGYGCCmCCTast
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 5
 Number of overlap: 11
 Similarity score: 0.0360618

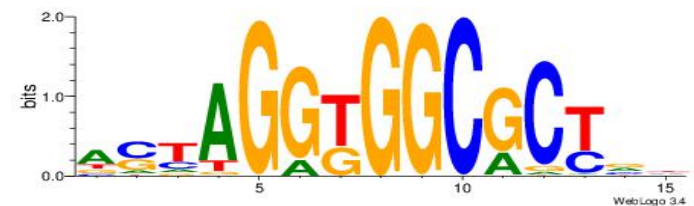
Alignment:

VBAGCGCCMCCTAST
 HVASCCCCABH----

Original motif Consensus sequence: VBAGCGCCMCCTAST



Reverse complement motif Consensus sequence: ASTAGGYGGCGCT

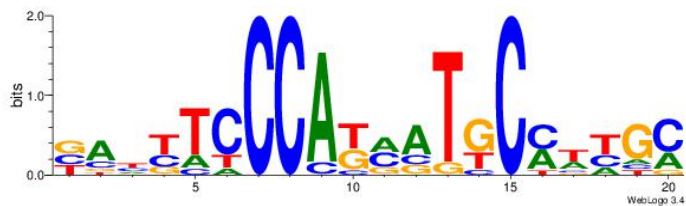


Dataset #: 3
 Motif ID: 131
 Motif name: znf143
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 10
 Number of overlap: 11

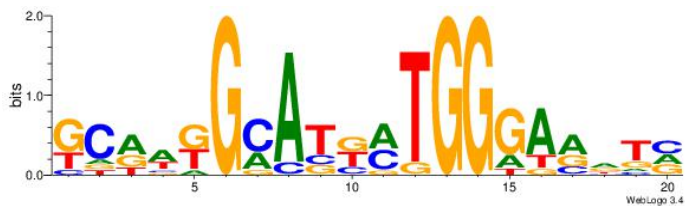
Similarity score: 0.0409371

Alignment:
BAHYTCCCAKMATGCMWYGC
HVASCCCCABH-----

Original motif Consensus sequence: BAHYTCCCAKMATGCMWYGC



Reverse complement motif Consensus sequence: GCMWRGCATYRTGGGAMHTB

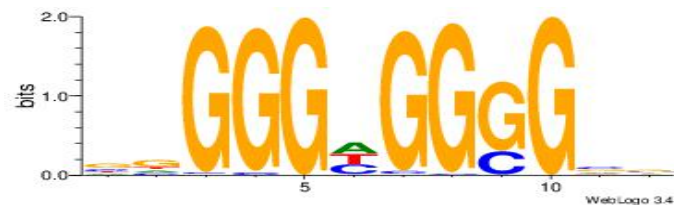
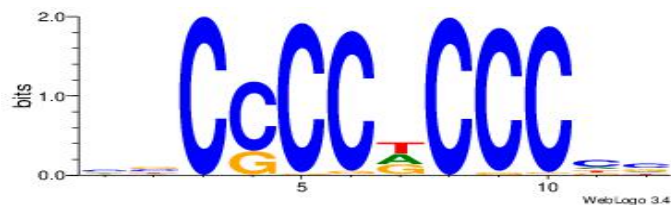


Dataset #: 4
Motif ID: 155
Motif name: csCSCCdCCCcs
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 2
Number of overlap: 11
Similarity score: 0.0412348

Alignment:
VDGGGDGGGGBV
-DBTGGGGSTVD

Original motif Consensus sequence: VBCCCCDCCCHV

Reverse complement motif Consensus sequence: VDGGGDGGGGBV

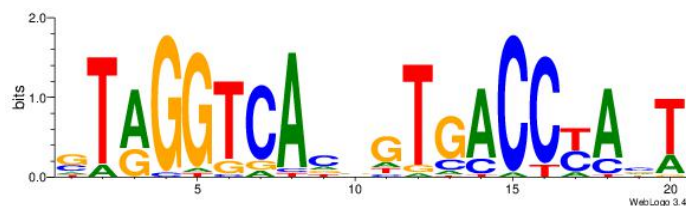


Dataset #: 3
 Motif ID: 111
 Motif name: PPARG
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.0446625

Alignment:

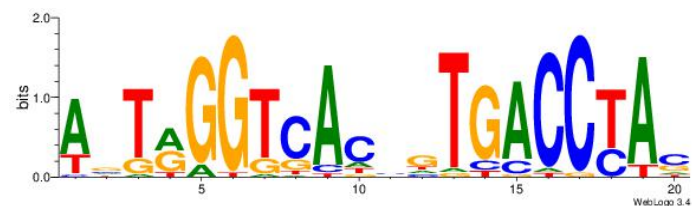
STAGGTCACBG TGACCYABT
 -----HVASCCCCABH

Original motif Consensus sequence: STAGGTCACBG TGACCYABT



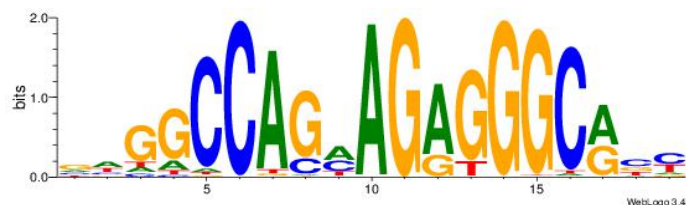
Reverse complement motif
ABTMGGTCACBG TGACCTAS

Consensus sequence:

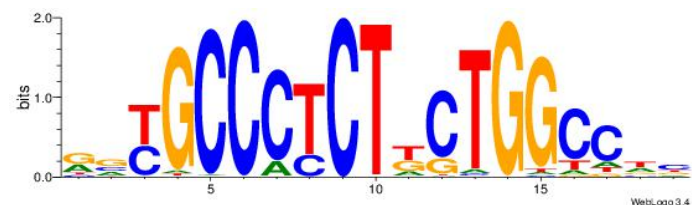


Dataset #: 4 **Motif ID: 163** **Motif name: gwGGCCAGmAGAGGGCrby**

Original motif Consensus sequence: VHGGCCAGMAGAGGGCRBY



Reverse complement motif Consensus sequence: KBKGCCCTCTYCTGGCCHV



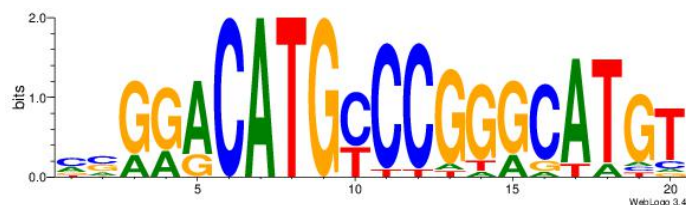
Best Matches for Motif ID 163 (Highest to Lowest)

Dataset #: 3
 Motif ID: 125
 Motif name: TP53
 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: 0.0964434

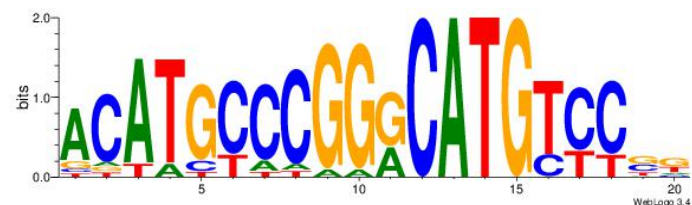
Alignment:

ACATGCCCGGKCATGTCCSR
 -KBKGCCCTCTYCTGGCCHV

Original motif Consensus sequence: MSGGACATGYCCGGGCATGT



Reverse complement motif Consensus sequence: ACATGCCCGGKCATGTCCSR

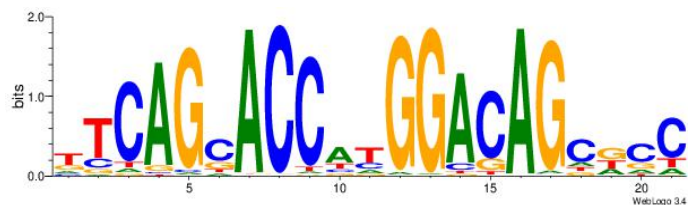


Dataset #: 3
 Motif ID: 113
 Motif name: REST
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 19
 Similarity score: 0.104301

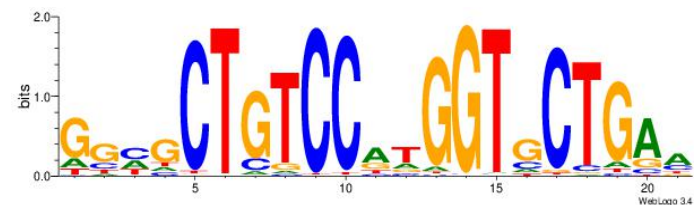
Alignment:

TTCAGCACCATGGACAGCKCC
 --VHGGCCAGMAGAGGGCRBY

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC



Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA



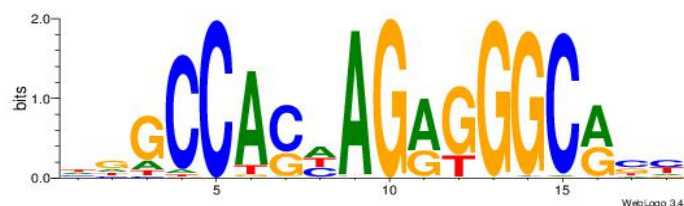
Dataset #: 4
 Motif ID: 165
 Motif name: wgGCCAshAGrGGGCrSy
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward

Position number: 1
Number of overlap: 18
Similarity score: 0.502859

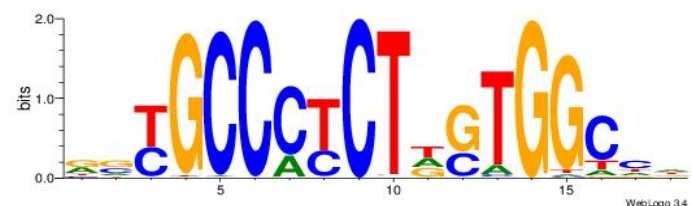
Alignment:

KBKGCCCKCTHGTGGCHH-
KBKGCCCTCTYCTGGCCHV

Original motif Consensus sequence: HDGCCACHAGRGGGCRBY



Reverse complement motif Consensus sequence: KBKGCCCKCTHGTGGCHH

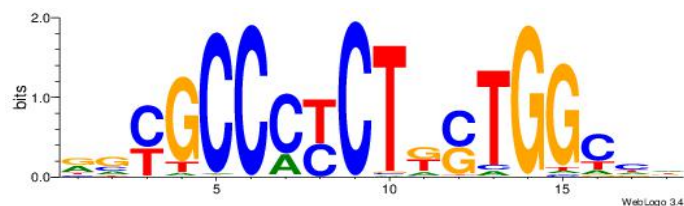


Dataset #: 4
Motif ID: 156
Motif name: rgyGCCMyCTksTGGccd
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 18
Similarity score: 0.525011

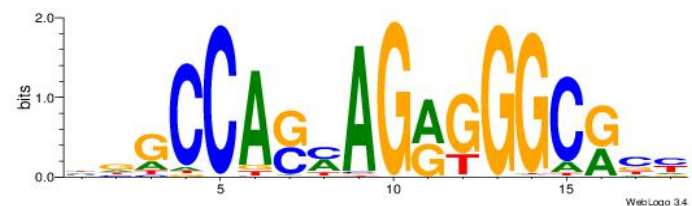
Alignment:

-RVYGCCCYCTKSTGGCHD
KBKGCCCTCTYCTGGCCHV

Original motif Consensus sequence: RYVGCCCYCTKSTGGCHD



Reverse complement motif Consensus sequence: DDGCCASYAGMGGGCKVM

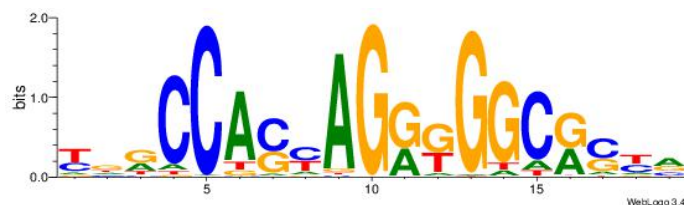


Dataset #: 3
Motif ID: 74
Motif name: CTCF
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2
Number of overlap: 18
Similarity score: 0.529309

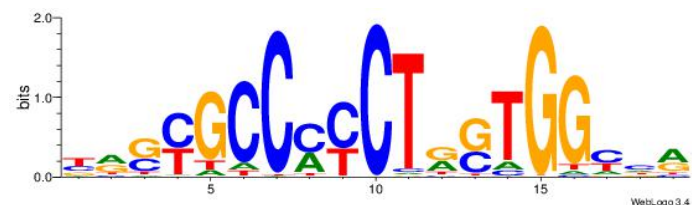
Alignment:

–YDRCCASYAGRKGGRSYV
VHGGCCAGMAGAGGGCRBY–

Original motif Consensus sequence: YDRCCASYAGRKGGRSYV

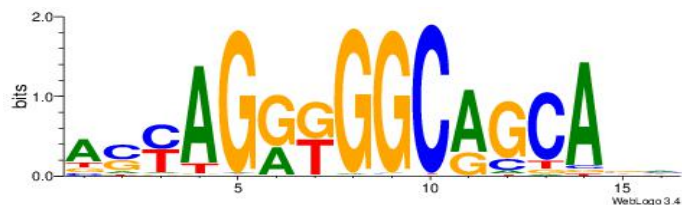


Reverse complement motif Consensus sequence: BMSMGCCYMCTKSTGGMHM

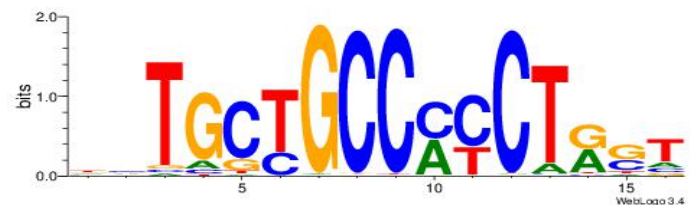


Dataset #: 4 Motif ID: 164 Motif name: asyAGrkGGCRGCaGa

Original motif Consensus sequence: ASYAGRKGGCAGCABH



Reverse complement motif Consensus sequence: HBTGCTGCCYMCTKST



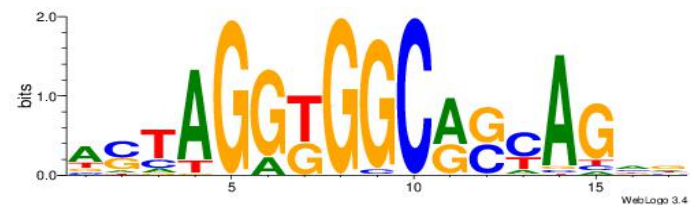
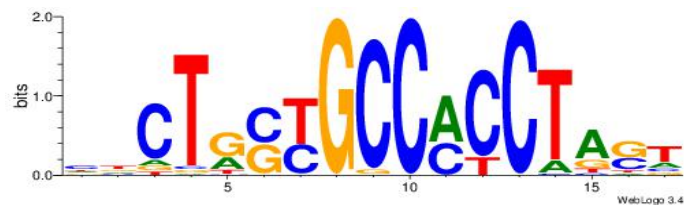
Best Matches for Motif ID 164 (Highest to Lowest)

Dataset #:	4
Motif ID:	144
Motif name:	ctCTrsyGCCmCCTast
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:	0.0253571

Alignment:
 HDCTGSYGCCMCCTAST
 HBTGCTGCCYMCTKST-

Original motif Consensus sequence: HDCTGSYGCCMCCTAST

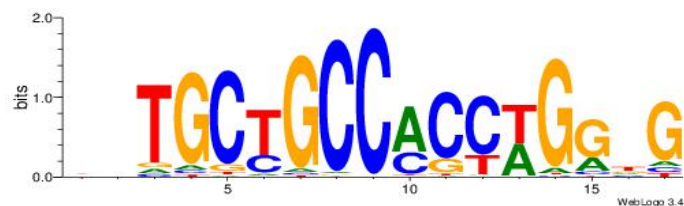
Reverse complement motif Consensus sequence: ASTAGGYGGCMSCAGDD



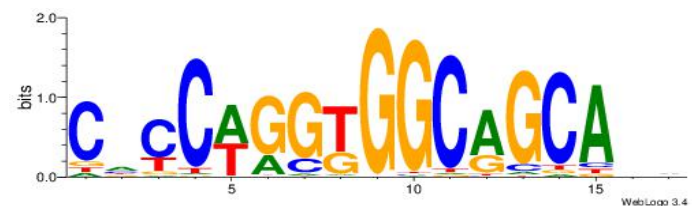
Dataset #: 4
 Motif ID: 169
 Motif name: yVTGCyGCCmCCwGgtG
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 16
 Similarity score: 0.0299559

Alignment:
 CDCCWGGTGGCAGCAVV
 -ASYAGRKGGCAGCABH

Original motif Consensus sequence: BVTGCTGCCACCWGGDG



Reverse complement motif Consensus sequence: CDCCWGGTGGCAGCAVV



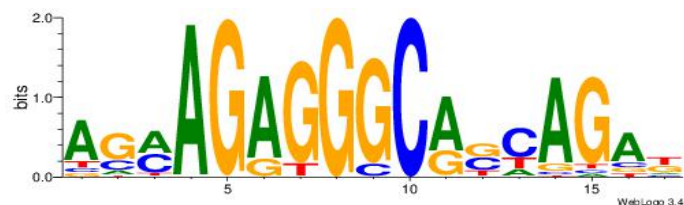
Dataset #: 4

Motif ID: 143
 Motif name: AgmAGAGGGCrscAGak
 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: 0.0333221

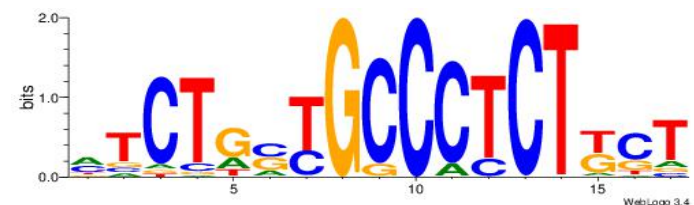
Alignment:

AGMAGAGGGCASCAGAK
 ASYAGRKGGCAGCABH-

Original motif Consensus sequence: AGMAGAGGGCASCAGAK



Reverse complement motif Consensus sequence: RTCTGSTGCCCTCTYCT

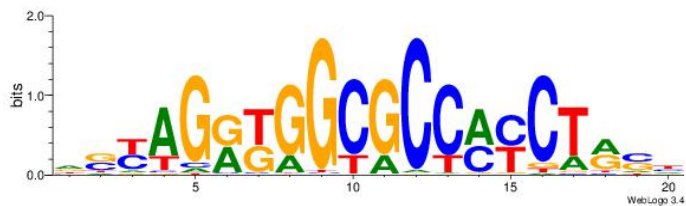


Dataset #: 4
 Motif ID: 167
 Motif name: rsyAGrkGGCGCCmyCTrsy
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 5
 Number of overlap: 16

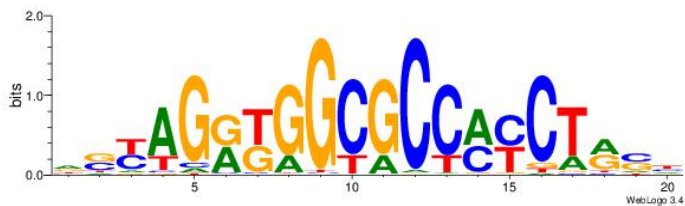
Similarity score: 0.0458621

Alignment:
DSYAGRKGCGCCMYCTRSH
ASYAGRKGCGCAGCABH----

Original motif Consensus sequence: DSYAGRKGCGCCMYCTRSH



Reverse complement motif Consensus sequence:
HSKAGKYGGCGCCRMCTMSD

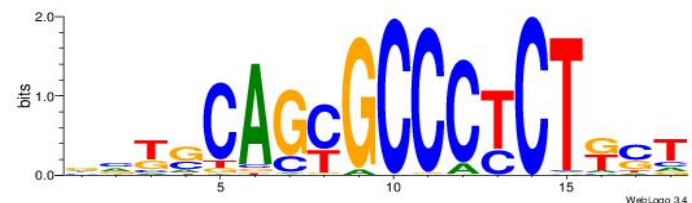
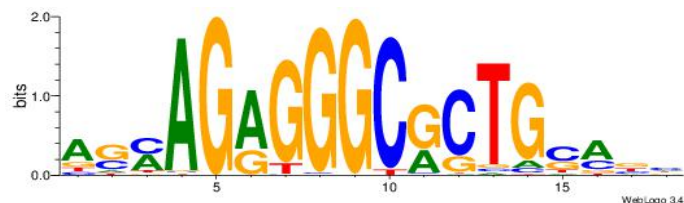


Dataset #: 4
Motif ID: 149
Motif name: asmAGRGGGCrCTGsmkc
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 16
Similarity score: 0.0529808

Alignment:
ASMAGAGGGCRCTGSABH
ASYAGRKGCGCAGCABH--

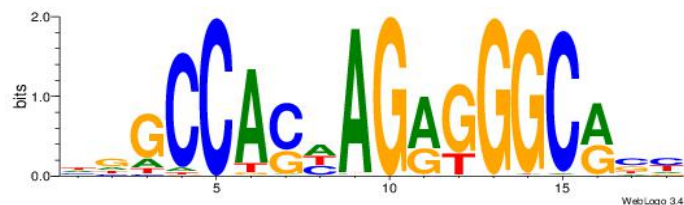
Original motif Consensus sequence: ASMAGAGGGCRCTGSABH

Reverse complement motif Consensus sequence:
DBTSCAGMGCCCTCTRST

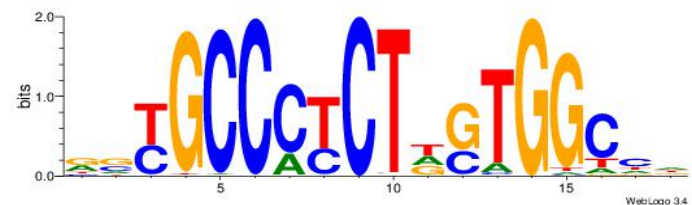


Dataset #: 4 Motif ID: 165 Motif name: wgGCCAshAGrGGGCrSy

Original motif Consensus sequence: HDGCCACHAGRGGGCRBY



Reverse complement motif Consensus sequence: KBKGCCCKCTHGTGGCHH



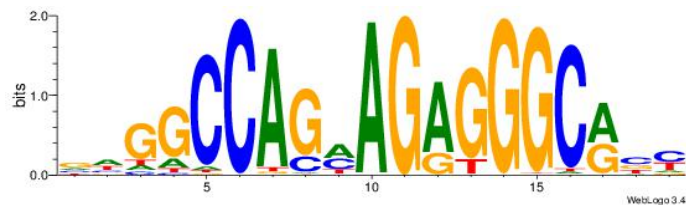
Best Matches for Motif ID 165 (Highest to Lowest)

Dataset #:	4
Motif ID:	163
Motif name:	gwGGCCAGmAGAGGGCrby
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	18
Similarity score:	0.00922625

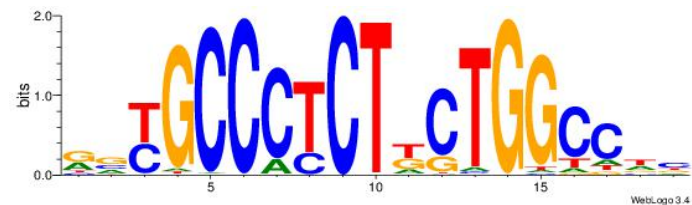
Alignment:

VHGGCCAGMAGAGGGCRBY
-HDGCCACHAGRGGGCRBY

Original motif Consensus sequence: VHGGCCAGMAGAGGGCRBY



Reverse complement motif Consensus sequence: KBKGGCCTCTYCTGGCCHV

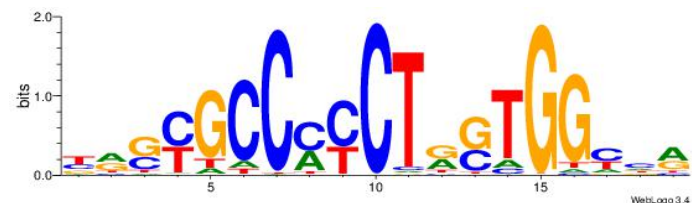
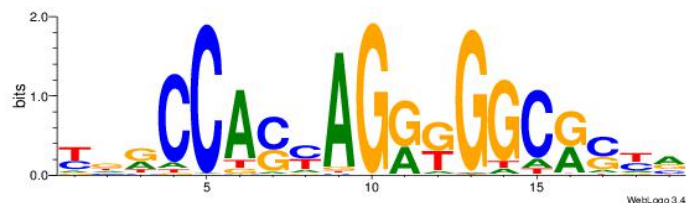


Dataset #:	3
Motif ID:	74
Motif name:	CTCF
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2
Number of overlap:	18
Similarity score:	0.0205802

Alignment:
YDRCCASYAGRKGGCRSYV
HDGCCACHAGRGGGCRBY-

Original motif Consensus sequence: YDRCCASYAGRKGGCRSYV

Reverse complement motif Consensus sequence: BMSMGCCYMCTKSTGGMHM



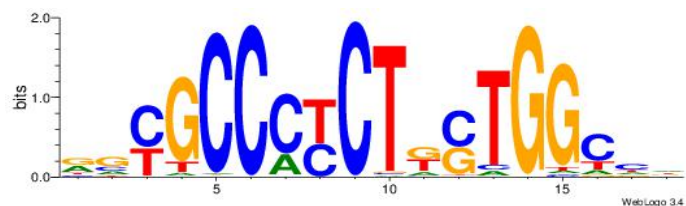
Dataset #: 4
 Motif ID: 156
 Motif name: rgyGCCMyCTksTGGccd
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 18
 Similarity score: 0.0268949

Alignment:

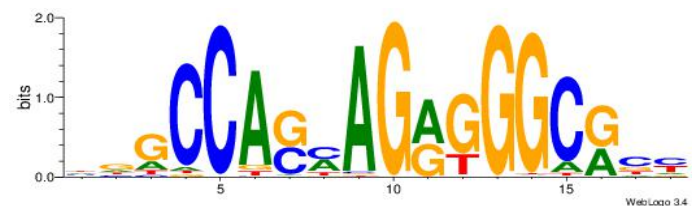
RVYGCCCYCTKSTGGCHD

KBKGCCCKCTHGTGGCHH

Original motif Consensus sequence: RVYGCCCYCTKSTGGCHD



Reverse complement motif Consensus sequence: DDGCCASYAGMGGGCKVM



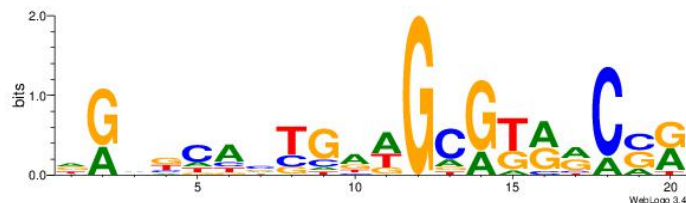
Dataset #: 3

Motif ID: 109
 Motif name: Pax5
 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: 0.103512

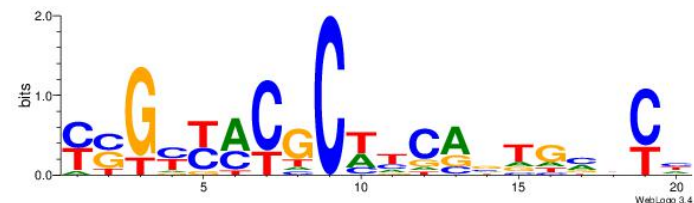
Alignment:

MSGKKRCGCWDCABTGBBCD
 --KBKGCCCKCTHGTGGCHH

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD

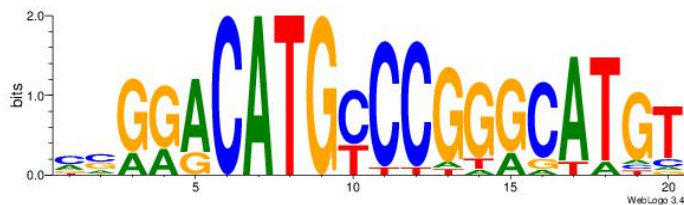


Dataset #: 3
 Motif ID: 125
 Motif name: TP53
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 18

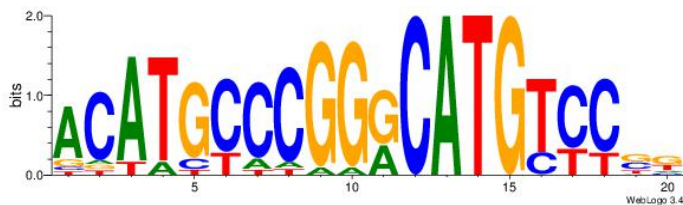
Similarity score: 0.105007

Alignment:
ACATGCCCGGKCATGTCCSR
-KBKGCCCKCTHGTGGCHH-

Original motif Consensus sequence: MSGGACATGYCCGGGCATGT



Reverse complement motif Consensus sequence: ACATGCCCGGKCATGTCCSR



Dataset #: 4 Motif ID: 166 Motif name: CasCAGrGGGCrSy

Original motif Consensus sequence: CACCAGRGGGCRSB



Reverse complement motif Consensus sequence: BSKGCCCKCTGGT



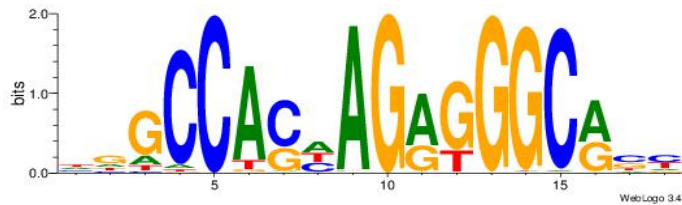
Best Matches for Motif ID 166 (Highest to Lowest)

Dataset #:	4
Motif ID:	165
Motif name:	wgGCCAshAGrGGGCrSy
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif

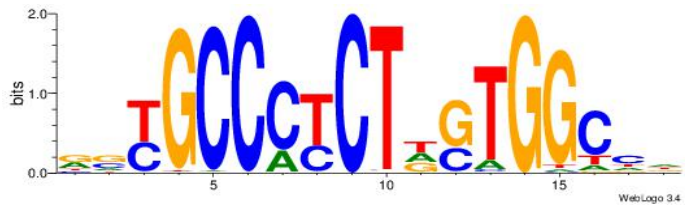
Direction: Forward
Position number: 5
Number of overlap: 14
Similarity score: 0.015353

Alignment:
HDGCCACHAGRGGGCRBY
----CACCAGRGGGCRSB

Original motif Consensus sequence: HDGCCACHAGRGGGCRBY



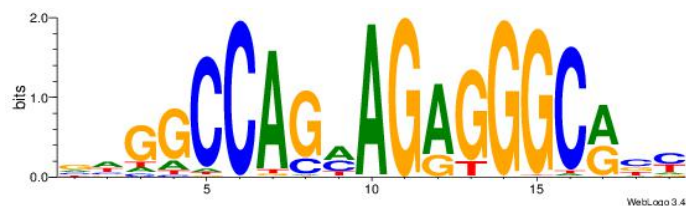
Reverse complement motif Consensus sequence: KBKGCCCKCTHGTGGCHH



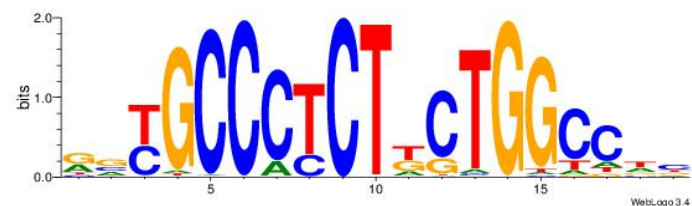
Dataset #: 4
Motif ID: 163
Motif name: gwGGCCAGmAGAGGGCrby
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 14
Similarity score: 0.0273616

Alignment:
VHGGCCAGMAGAGGGCRBY
-----CACCAGRGGGCRSB

Original motif Consensus sequence: VHGGCCAGMAGAGGGCRBY



Reverse complement motif Consensus sequence: KBKGCCCTCTYCTGGCCHV

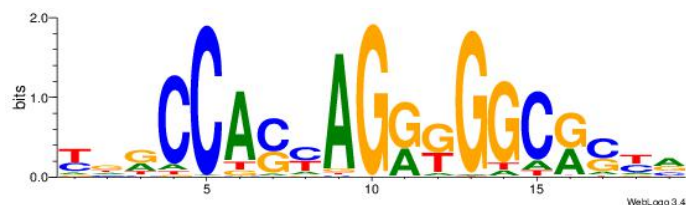


Dataset #: 3
Motif ID: 74
Motif name: CTCF
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 5
Number of overlap: 14
Similarity score: 0.0281629

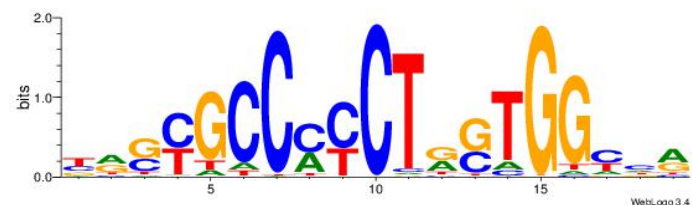
Alignment:

YDRCCASYAGRKGGRSYV
----CACCAGRGGGCRSB-

Original motif Consensus sequence: YDRCCASYAGRKGGRSYV



Reverse complement motif Consensus sequence: BMSMGCCYMCTKSTGGMHM

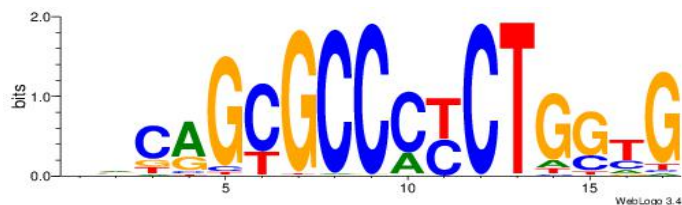


Dataset #: 4
 Motif ID: 168
 Motif name: yrcrGYGCCMyCTGGtG
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0.03743

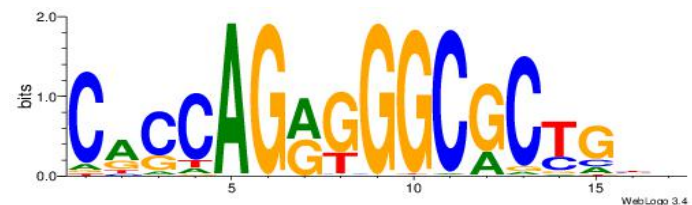
Alignment:

CACCAGMGGGCGCTGBD
 CACCAGRGGGCRSB---

Original motif Consensus sequence: HVCAGCGCCCYCTGGTG



Reverse complement motif Consensus sequence: CACCAGMGGGCGCTGBD

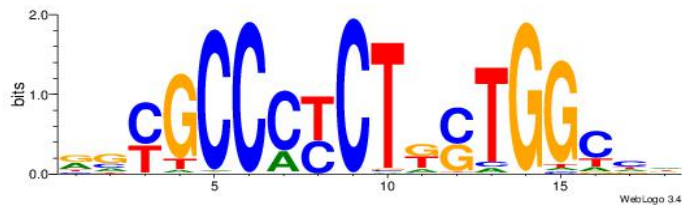


Dataset #: 4
 Motif ID: 156
 Motif name: rgyGCCMyCTksTGGccd
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 5

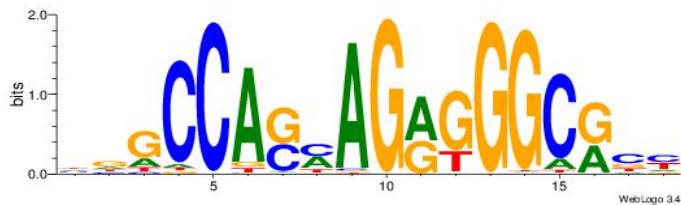
Number of overlap: 14
Similarity score: 0.043415

Alignment:
RVYGCCCYCTKSTGGCHD
----BSKGCCCKCTGGTG

Original motif Consensus sequence: RVYGCCCYCTKSTGGCHD

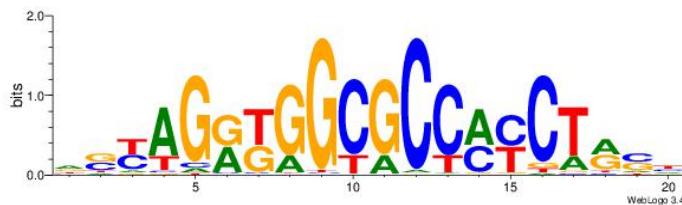


Reverse complement motif Consensus sequence: DDGCCASYAGMGGGCKVM

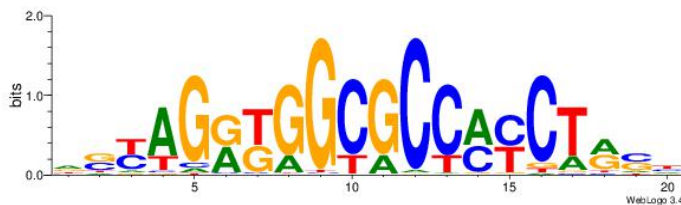


Dataset #: 4 Motif ID: 167 Motif name: rsyAGrkGGCGCCmyCTrsy

Original motif Consensus sequence: DSYAGRKGGCGCCMYCTRSH



Reverse complement motif Consensus sequence: HSKAGKYGGCGCCRMCTMSD



Best Matches for Motif ID 167 (Highest to Lowest)

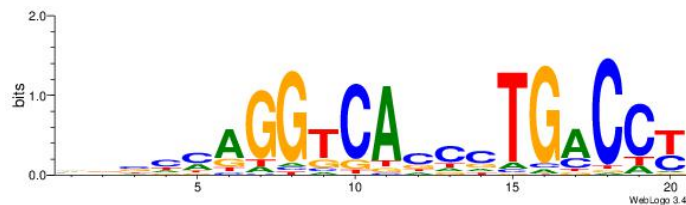
Dataset #: 3
Motif ID: 81
Motif name: ESR1

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:	0.0672057

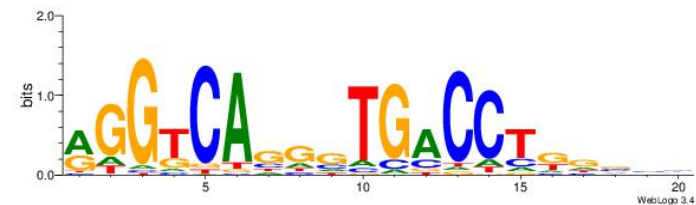
Alignment:

```
VDBHMAGGTCACCCTGACCY
DSYAGRKGCGCCMYCTRSH
```

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV

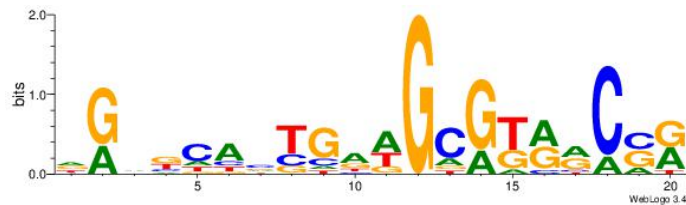


Dataset #:	3
Motif ID:	109
Motif name:	Pax5
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	20
Similarity score:	0.0747165

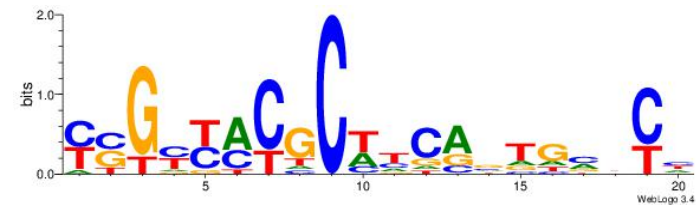
Alignment:

MSGKKRCGCWDCABTGBB
CD
HSKAGKYGGCGCCRMCTMSD

Original motif Consensus sequence: DGVBCABTGDWGCGRRC



Reverse complement motif Consensus sequence:
MSGKKRCGCWDCABTGBB
CD



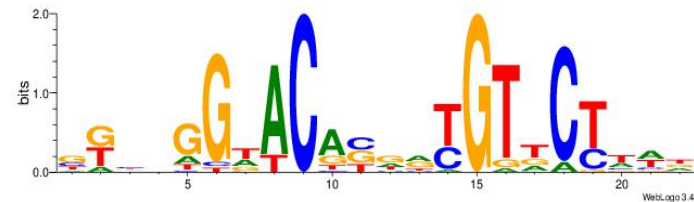
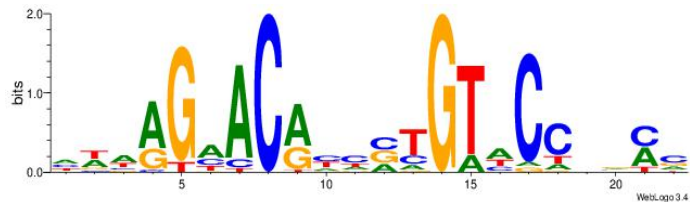
Dataset #:	3
Motif ID:	70
Motif name:	Ar
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	4
Number of overlap:	19
Similarity score:	0.57268

Alignment:

HWDAGHACRHHVTGTHCCHVMV-
---DSYAGRKGCGCCMYCTRSH

Original motif Consensus sequence: HWDAGHACRHHVTGTHCCHVMV

Reverse complement motif Consensus sequence:
VRVDGGHACAVDDKGTHCTDWH

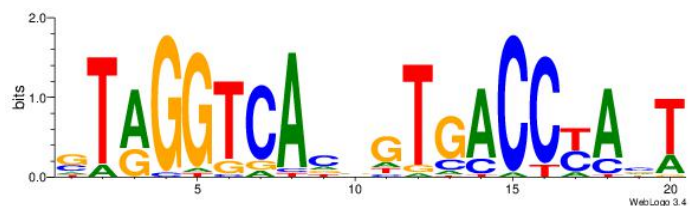


Dataset #: 3
 Motif ID: 111
 Motif name: PPARG
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 19
 Similarity score: 0.57362

Alignment:

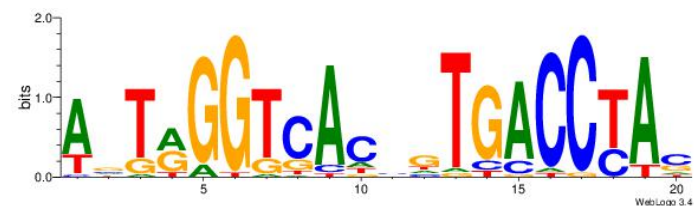
-ABTMGGTCACBGTGACCTAS
 DSYAGRKGGCGCCMYCTRSH-

Original motif Consensus sequence: STAGGTCACBGTGACCYABT



Reverse complement motif
ABTMGGTCACBGTGACCTAS

Consensus sequence:



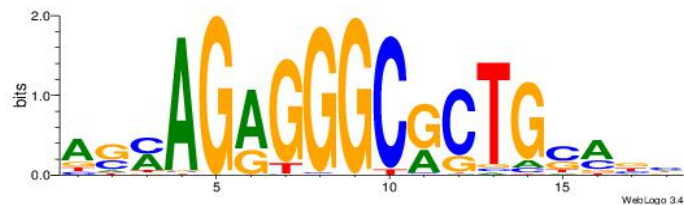
Dataset #: 4

Motif ID: 149
 Motif name: asmAGRGGGCrCTGsmkc
 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: 1.03519

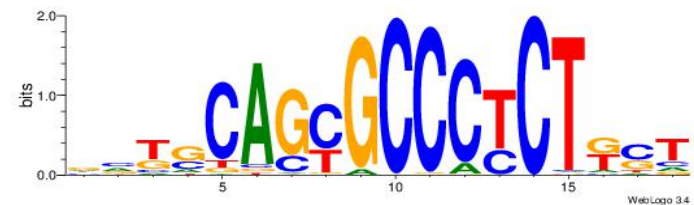
Alignment:

ASMAGAGGGCRCTGSABH--
 DSYAGRKGCGCCMYCTRSH

Original motif Consensus sequence: ASMAGAGGGCRCTGSABH

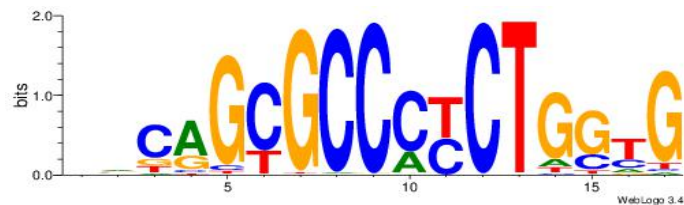


Reverse complement motif Consensus sequence: DBTSCAGMGCCCTCTRST

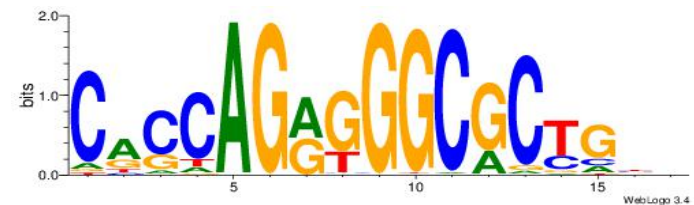


Dataset #: 4 Motif ID: 168 Motif name: yrcrGYGCCMyCTGGtG

Original motif Consensus sequence: HVCAGCGCCCYCTGGTG



Reverse complement motif Consensus sequence: CACCAGMGGGCGCTGBD



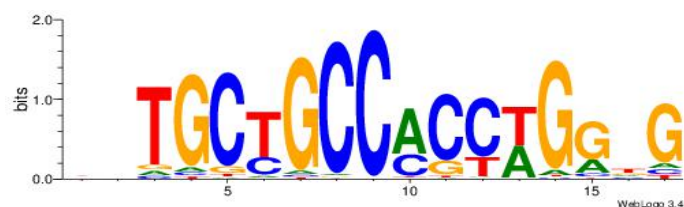
Best Matches for Motif ID 168 (Highest to Lowest)

Dataset #: 4
Motif ID: 169
Motif name: yvTGCyGCCmCCwGgtG
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: 0.0386724

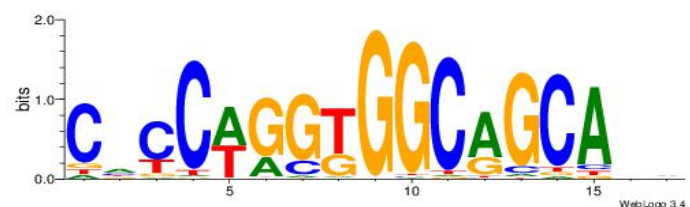
Alignment:

BVTGCTGCCACCWGGDG
HVCAGCGCCCYCTGGTG

Original motif Consensus sequence: BVTGCTGCCACCWGGDG



Reverse complement motif Consensus sequence: CDCCWGGTGGCAGCAVV



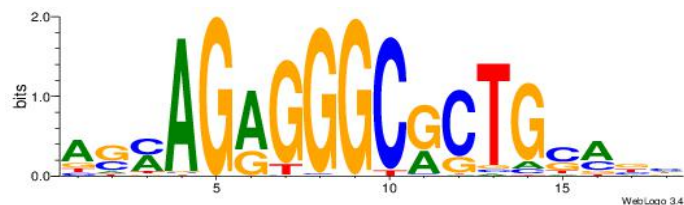
Dataset #: 4
Motif ID: 149
Motif name: asmAGRGGGCrCTGsmkc
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement

Direction: Forward
 Position number: 2
 Number of overlap: 17
 Similarity score: 0.0542719

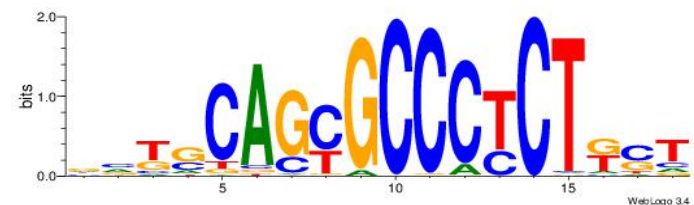
Alignment:

DBTSCAGMGCCCTCTRST
 -CACCAGMGGGCGCTGBD

Original motif Consensus sequence: ASMAGAGGGCRCTGSABH



Reverse complement motif Consensus sequence: DBTSCAGMGCCCTCTRST

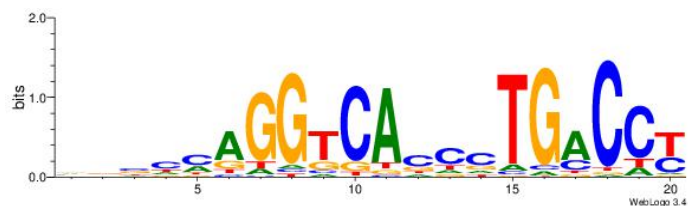


Dataset #: 3
 Motif ID: 81
 Motif name: ESR1
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 17
 Similarity score: 0.0695994

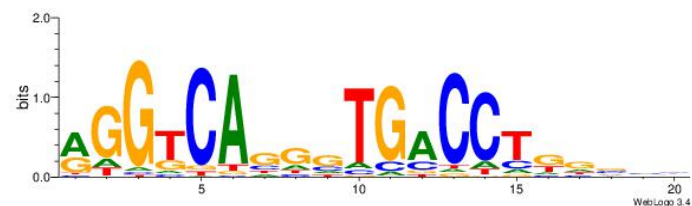
Alignment:

VDBHMAGGTCACCCTGACCY
 --HVCAGCGCCCYCTGGTG-

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV

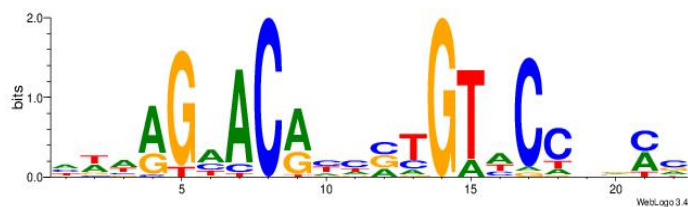


Dataset #: 3
Motif ID: 70
Motif name: Ar
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 17
Similarity score: 0.074879

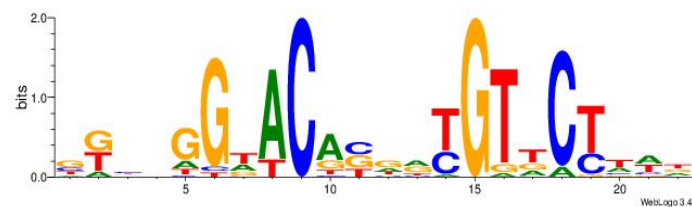
Alignment:

HWDAGHACRHHVTGTHCCHVMV
HVCAGCGCCCYCTGGTG-----

Original motif Consensus sequence: HWDAGHACRHHVTGTHCCHVMV



Reverse complement motif Consensus sequence: VRVDGGHACAVDDKGTHCTDWH

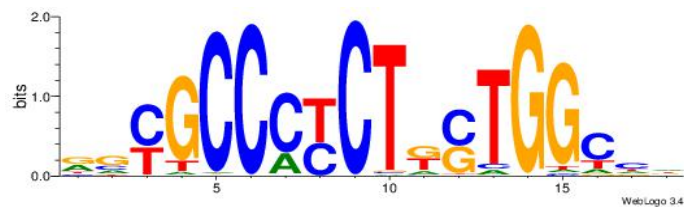


Dataset #: 4
 Motif ID: 156
 Motif name: rgyGCCMyCTksTGGccd
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 17
 Similarity score: 0.076934

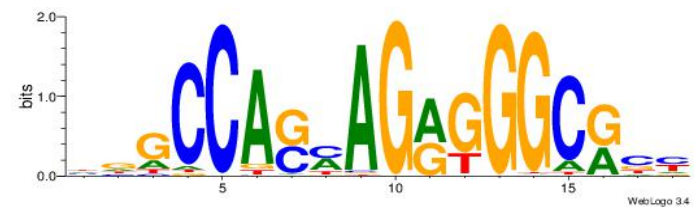
Alignment:

RVYGCCCYCTKSTGGCHD
 HVCAGCGCCCYCTGGTG-

Original motif Consensus sequence: RVYGCCCYCTKSTGGCHD



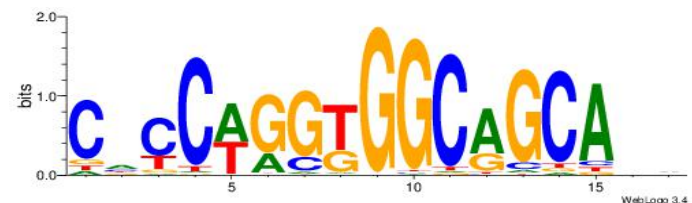
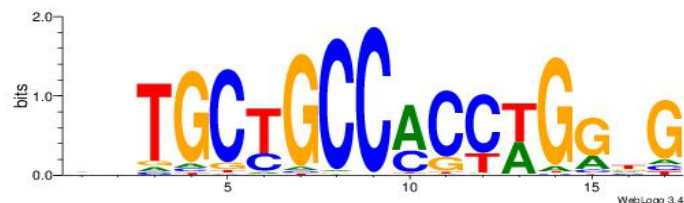
Reverse complement motif Consensus sequence: DDGCCASYAGMGGGCKVM



Dataset #: 4 Motif ID: 169 Motif name: yvTGCyGCCmCCwGgtG

Original motif Consensus sequence: BVTGCTGCCACCWGGDG

Reverse complement motif Consensus sequence: CDCCWGGTGGCAGCAVV



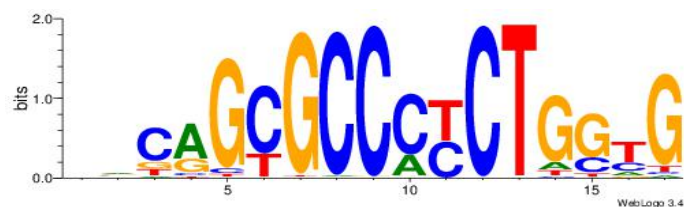
Best Matches for Motif ID 169 (Highest to Lowest)

Dataset #: 4
 Motif ID: 168
 Motif name: yrcrGYGCCMyCTGGtG
 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: 0.0263455

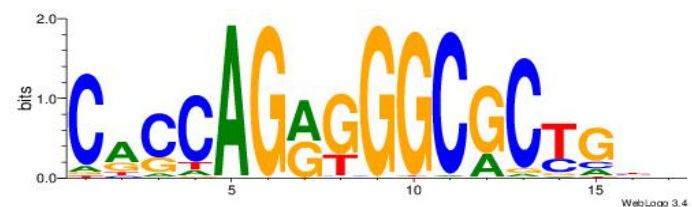
Alignment:

HVCAGCGCCCYCTGGTG
 BVTGCTGCCACCWGGDG

Original motif Consensus sequence: HVCAGCGCCCYCTGGTG



Reverse complement motif Consensus sequence: CACCAGMGGGCGCTGBD

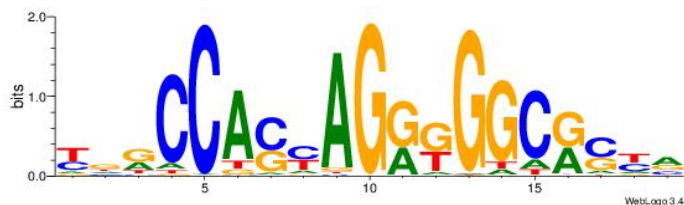


Dataset #: 3
 Motif ID: 74
 Motif name: CTCF
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 17
 Similarity score: 0.0578732

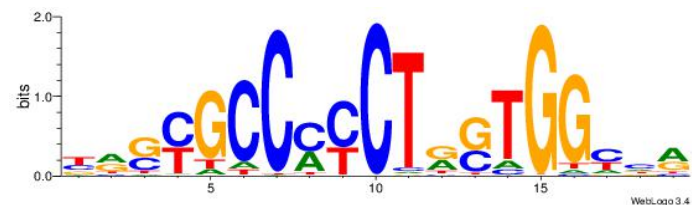
Alignment:

BSMGCCYMCTKSTGGMHM
 -BVTGCTGCCACCGGDG-

Original motif Consensus sequence: YDRCCASYAGRKGGRSYV



Reverse complement motif Consensus sequence: BSMGCCYMCTKSTGGMHM

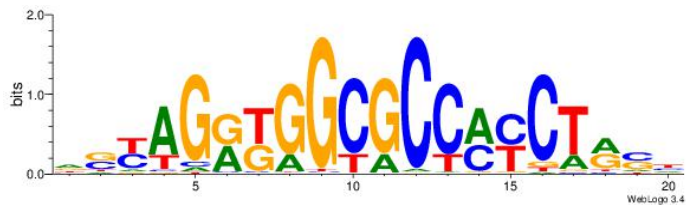


Dataset #: 4
 Motif ID: 167
 Motif name: rsyAGrkGGCGCCmyCTrsy
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3

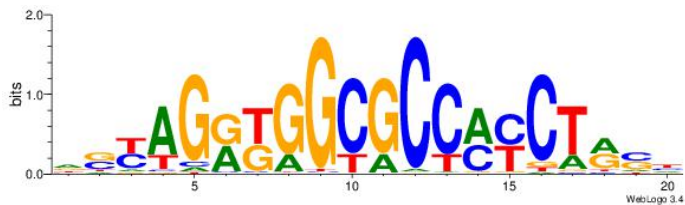
Number of overlap: 17
Similarity score: 0.0596753

Alignment:
HSKAGKYGGCGCCRMCTMSD
--BVTGCTGCCACCWGGDG--

Original motif Consensus sequence: DSYAGRKGGCGCCMYCTRSH



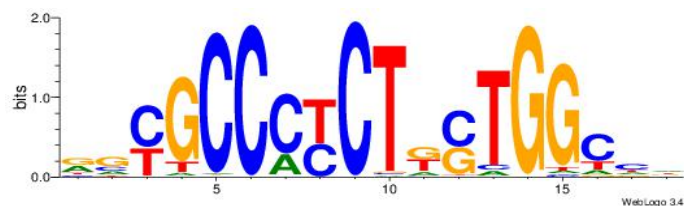
Reverse complement motif Consensus sequence: HSKAGKYGGCGCCRMCTMSD



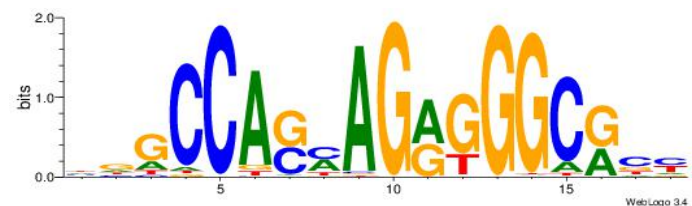
Dataset #: 4
Motif ID: 156
Motif name: rgyGCCMyCTksTGGccd
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 17
Similarity score: 0.0597938

Alignment:
RVYGCCCYCTKSTGGCHD
BVTGCTGCCACCWGGDG--

Original motif Consensus sequence: RYVCCCCYCTKSTGGCHD



Reverse complement motif Consensus sequence: DDGCCASYAGMGGGCKVM

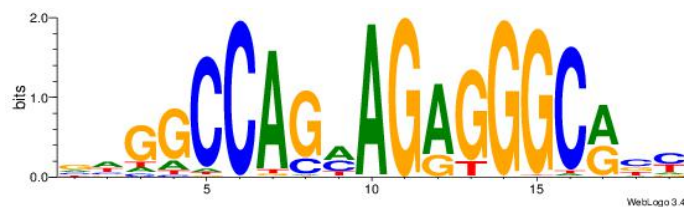


Dataset #: 4
 Motif ID: 163
 Motif name: gwGGCCAGmAGAGGGCrby
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 17
 Similarity score: 0.0605716

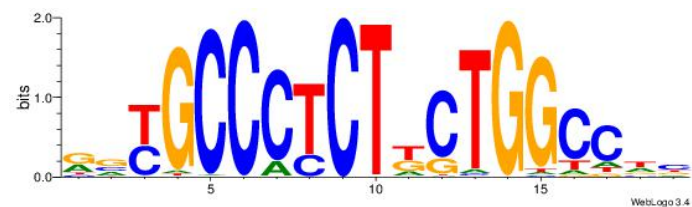
Alignment:

VHGGCCAGMAGAGGGCRBY
 CDCCWGGTGGCAGCAVV--

Original motif Consensus sequence: VHGGCCAGMAGAGGGCRBY

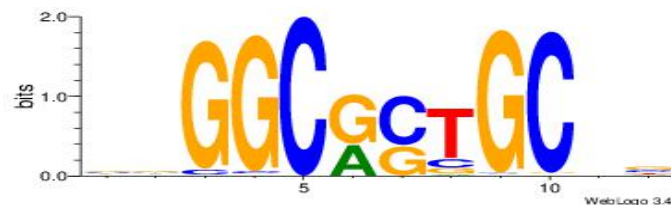


Reverse complement motif Consensus sequence: KBKGCCCTCTYCTGGCCHV

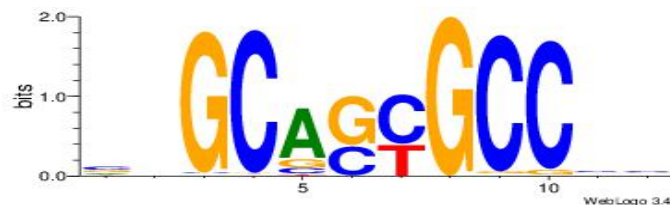


Dataset #: 4 Motif ID: 170 Motif name: ssGGCrSTGCrS

Original motif Consensus sequence: VVGGCRSTGCVB



Reverse complement motif Consensus sequence: BVGCASMGCCVV



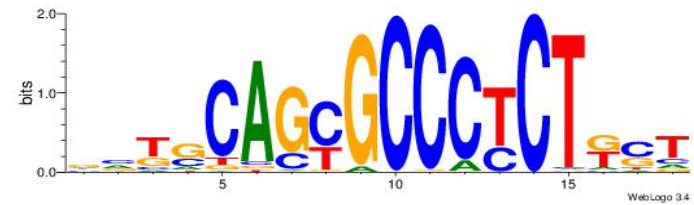
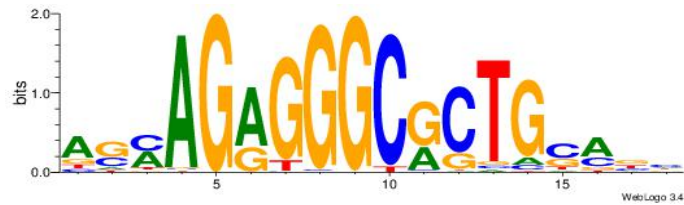
Best Matches for Motif ID 170 (Highest to Lowest)

Dataset #:	4
Motif ID:	149
Motif name:	asmAGRGGGCrCTGsmkc
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:	0.038906

Alignment:
ASMAGAGGGCRCTGSABH
-----VVGGCRSTGCVB-

Original motif Consensus sequence: ASMAGAGGGCRCTGSABH

Reverse complement motif Consensus sequence:
DBTSCAGMGCCCTCTRST



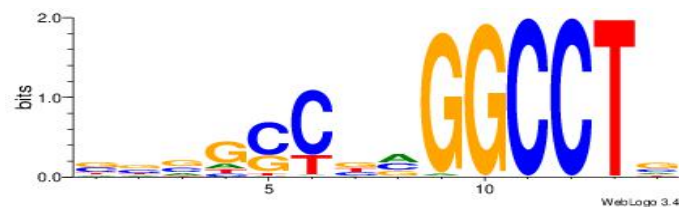
Dataset #: 3
 Motif ID: 130
 Motif name: Zfx
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 12
 Similarity score: 0.0768177

Alignment:

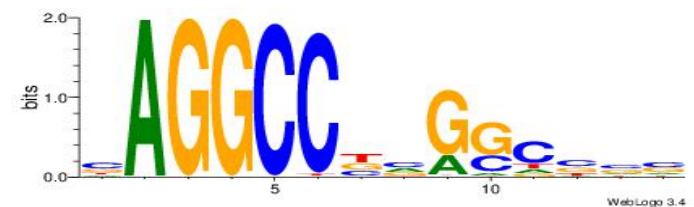
BBVGCCBVGGCCTV

BVGCASMGCCVV--

Original motif Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif Consensus sequence: VAGGCCBBGGCCTV



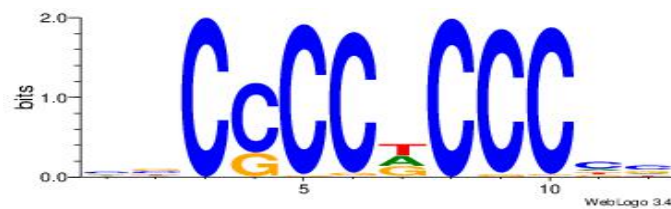
Dataset #: 4
 Motif ID: 155

Motif name:	csCSCCdCCCcs
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:	0.0798188

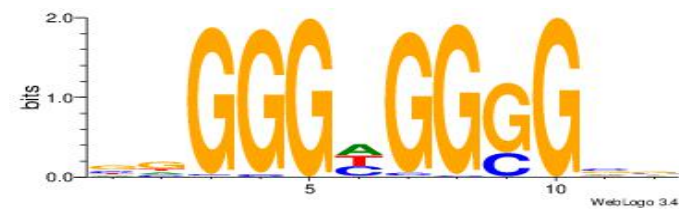
Alignment:

VBCCCCDCCCHV
BVGCCASMGCCVV

Original motif Consensus sequence: VBCCCCDCCCHV



Reverse complement motif Consensus sequence: VDGGGDGGGGBV



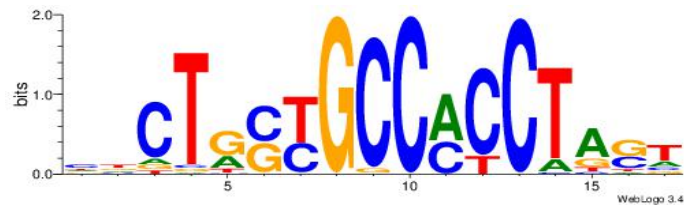
Dataset #:	4
Motif ID:	144
Motif name:	ctCTrsyGCCmCCTast
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	12
Similarity score:	0.0800293

Alignment:

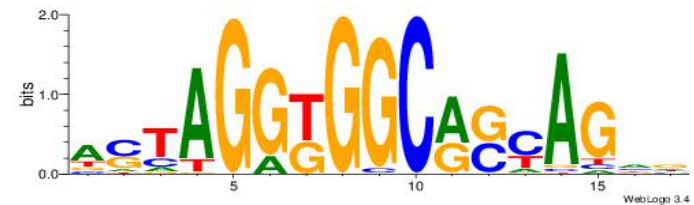
ASTAGGYGGCMSCAGDD

VVGGCRSTGCVB-----

Original motif Consensus sequence: HDCTGSYGCCMCCTAST



Reverse complement motif Consensus sequence:
ASTAGGYGGCMSCAGDD



Dataset #:	4
Motif ID:	146
Motif name:	myrGYGCCmCCTast
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:	0.0817044

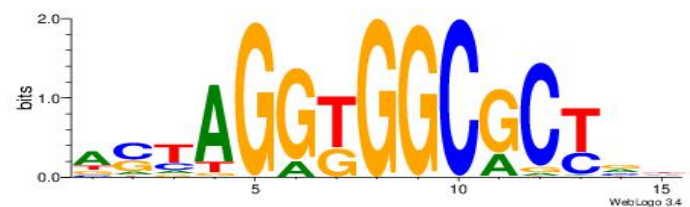
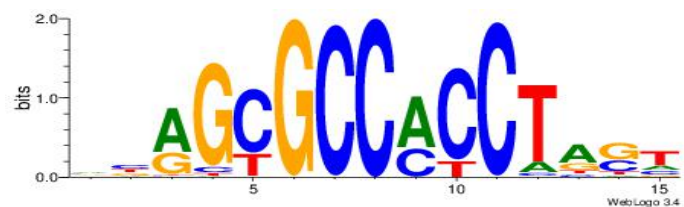
Alignment:

VBAGCGCCMCCTAST

--BVGCA SMGCCVV--

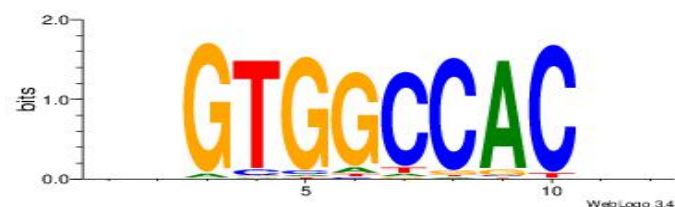
Original motif Consensus sequence: VBAGCGCCMCCTAST

Reverse complement motif Consensus sequence: ASTAGGYGGCGCT

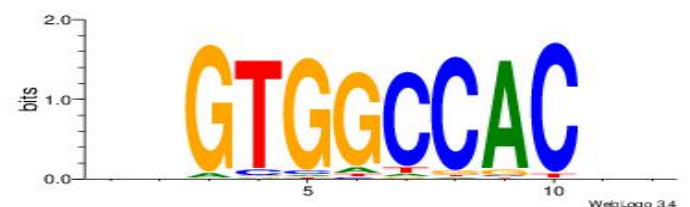


Dataset #: 4 Motif ID: 171 Motif name: ysGTGGCCACsr

Original motif Consensus sequence: BVGTGGCCACBV



Reverse complement motif Consensus sequence: VBGTGGCCACVB



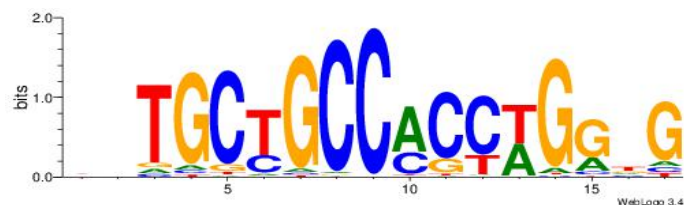
Best Matches for Motif ID 171 (Highest to Lowest)

Dataset #:	4
Motif ID:	169
Motif name:	yvTGCyGCCmCCwGgtG
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:	0.0325062

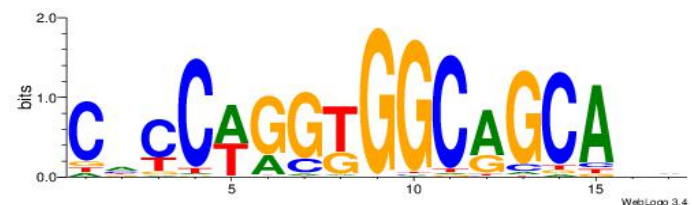
Alignment:

```
BVTGCTGCCACCWGGDG
----VBGTGGCCACVB--
```

Original motif Consensus sequence: BVTGCTGCCACCWGGDG



Reverse complement motif Consensus sequence: CDCCWGGTGGCAGCAVV

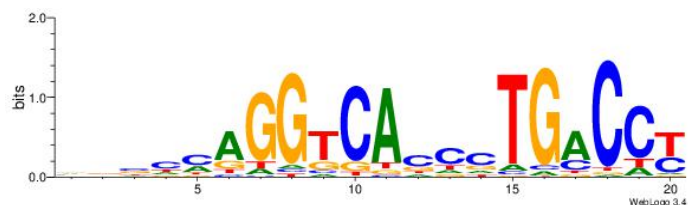


Dataset #: 3
Motif ID: 81
Motif name: ESR1
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 3
Number of overlap: 12
Similarity score: 0.0344223

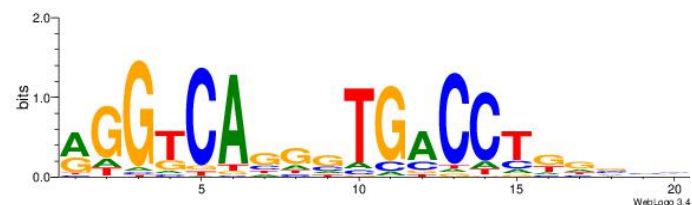
Alignment:

MGGTCAGGGTGACCTRDBHV
-----VBGTGGCCACVB--

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV

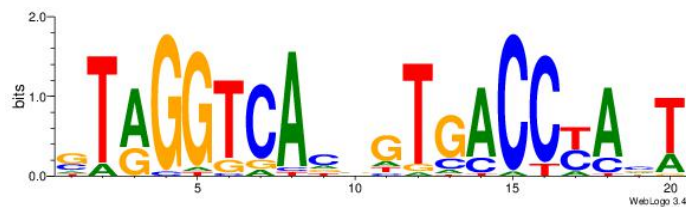


Dataset #: 3
 Motif ID: 111
 Motif name: PPARG
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 12
 Similarity score: 0.0381861

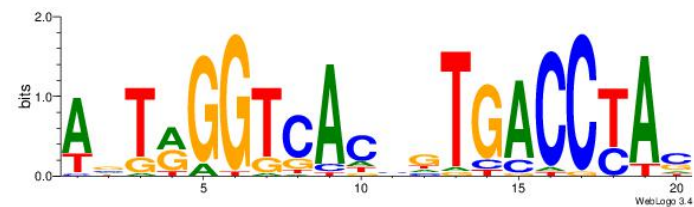
Alignment:

ABTMGGTCACBGTGACCTAS
 -----BVGTGGCCACBV

Original motif Consensus sequence: STAGGTCACBGTGACCYABT



Reverse complement motif Consensus sequence: ABTMGGTCACBGTGACCTAS

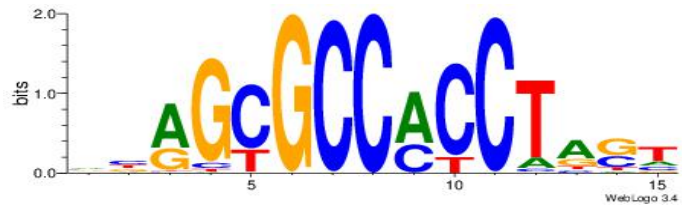


Dataset #: 4
 Motif ID: 146
 Motif name: myrGYGCCmCCTast
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1

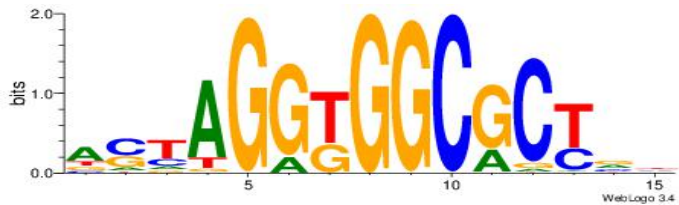
Number of overlap: 12
Similarity score: 0.0484805

Alignment:
ASTAGGYGGCGCTBB
BVTGGCCACBV---

Original motif Consensus sequence: V BAGCGCCMCCTAST



Reverse complement motif Consensus sequence: ASTAGGYGGCGCT

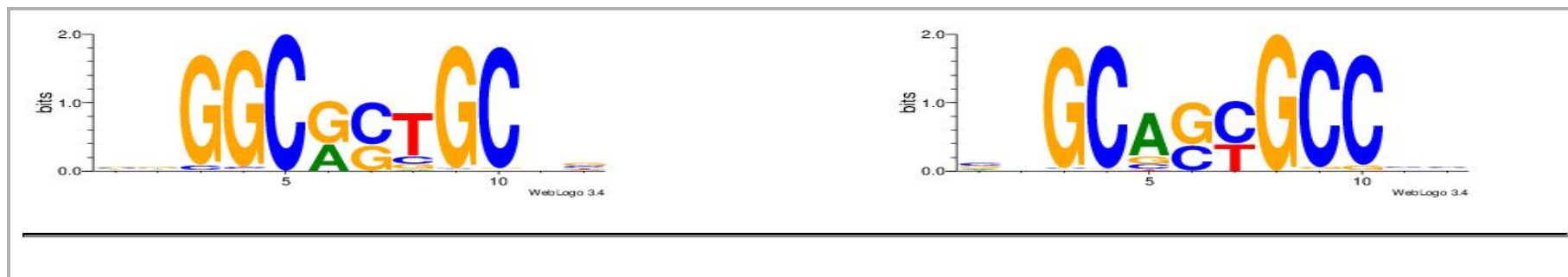


Dataset #: 4
Motif ID: 170
Motif name: ssGGCrSTGCrs
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 12
Similarity score: 0.0498451

Alignment:
BVGCA SMGCCVV
BVTGGCCACBV

Original motif Consensus sequence: V VGGCRSTGCVB

Reverse complement motif Consensus sequence: BVGCASMGCCVV



Results created by MOTIFSIM on 11-19-2016 22:45:25
Runtime: 1028.98 seconds

MOTIFSIM is written by Ngoc Tam L. Tran
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