



MOTIFSIM - MOTIF SIMilarity Detection Tool

Version 2.1

INPUT

Input Parameters

Number of files:	2
Number of top significant motifs:	10
Number of best matches:	10
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
PScanChIP_DM05.txt	16	1
RSAT_peak-motifs_DM05.txt	17	2

RESULTS

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

Dataset #: 1 Motif ID: 5 Motif name: ZEB1

Original motif Consensus sequence: CACCTD



Reverse complement motif Consensus sequence: HAGGTG

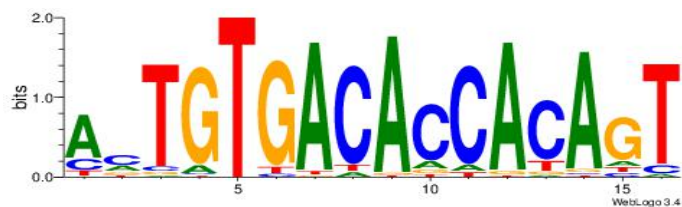


Best Matches for Top Significant Motif ID 5 (Highest to Lowest)

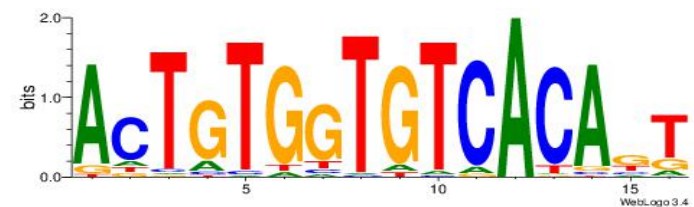
Dataset #: 2
 Motif ID: 21
 Motif name: AmTGTGACACCACAGT
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 4
 Number of overlap: 6
 Similarity score: 0.0349782

Alignment:
 AMTGTGACACCACAGT
 -----CACCTD----

Original motif Consensus sequence: AMTGTGACACCACAGT



Reverse complement motif Consensus sequence: ACTGTGGTGTACART

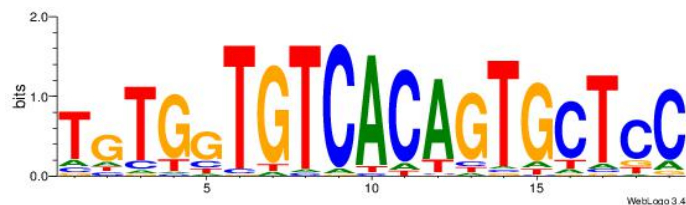


Dataset #: 2
 Motif ID: 17
 Motif name: TgTGgTGTCACAGTGCTCC
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 6
 Similarity score: 0.0362768

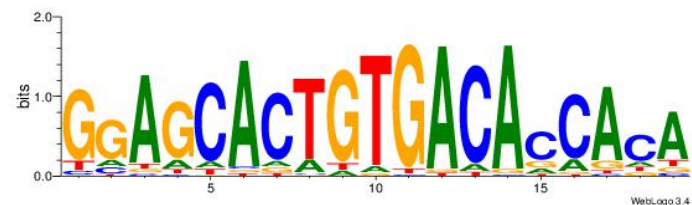
Alignment:

TGTGGTGTACAGTGCTCC
 -HAGGTG-----

Original motif Consensus sequence: TGTGGTGTACAGTGCTCC



Reverse complement motif Consensus sequence: GGAGCACTGTGACACCACA



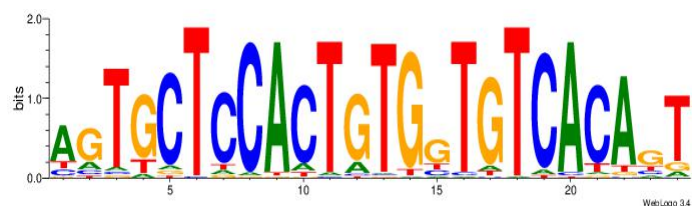
Dataset #: 2
 Motif ID: 27
 Motif name: AgTGCTCCACTGTGgTGTCACAgT
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward

Position number: 12
 Number of overlap: 6
 Similarity score: 0.0409613

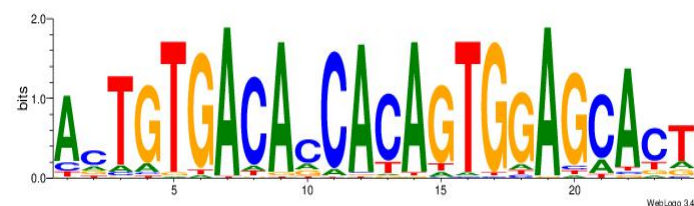
Alignment:

AGTGCTCCACTGTGGTGTACAGT
 -----HAGGTG-----

Original motif Consensus sequence: AGTGCTCCACTGTGGTGTACAGT



Reverse complement motif Consensus sequence: ACTGTGACACCACAGTGGAGCACT

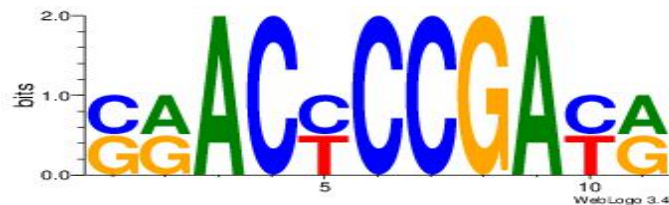


Dataset #: 2
 Motif ID: 33
 Motif name: srACyCCGAyr
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3
 Number of overlap: 6
 Similarity score: 0.0426002

Alignment:

KKTCGGKGTKS
 --HAGGTG---

Original motif Consensus sequence: SRACYCCGAYR



Reverse complement motif Consensus sequence: KKTCCGGKGTKS

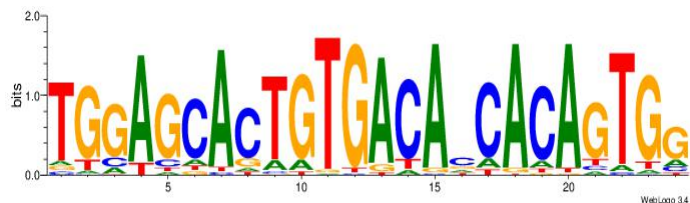


Dataset #: 2
 Motif ID: 23
 Motif name: TGGAGCACTGTGACACACAGTGg
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 6
 Number of overlap: 6
 Similarity score: 0.0496179

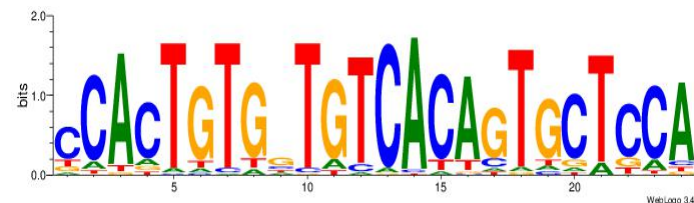
Alignment:

TGGAGCACTGTGACAVCACAGTGG
 -----CACCTD-----

Original motif Consensus sequence: TGGAGCACTGTGACAVCACAGTGG



Reverse complement motif Consensus sequence: CCACTGTGVTGTACAGTGCTCCA

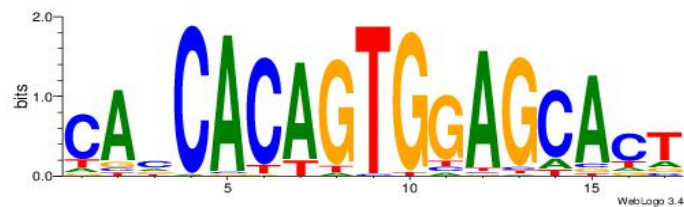


Dataset #: 2
 Motif ID: 26
 Motif name: CACACAGTGGAGCAct
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 6
 Similarity score: 0.0538743

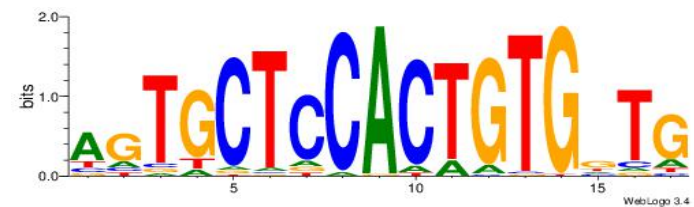
Alignment:

AGTGCTCCACTGTGDTG
 -----HAGGTG

Original motif Consensus sequence: CAHCACAGTGGAGCACT



Reverse complement motif Consensus sequence: AGTGCTCCACTGTGDTG



Dataset #: 2
 Motif ID: 19
 Motif name: atactttggc
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2

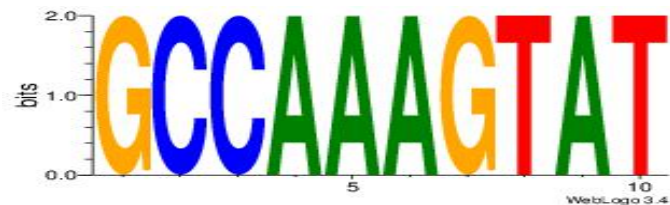
Number of overlap: 6
Similarity score: 0.0553034

Alignment:
ATACTTTGGC
-CACCTD---

Original motif Consensus sequence: ATACTTTGGC



Reverse complement motif Consensus sequence: GCCAAAGTAT

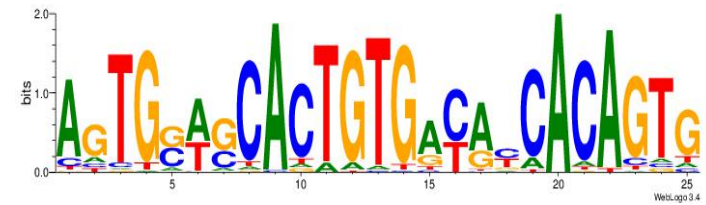
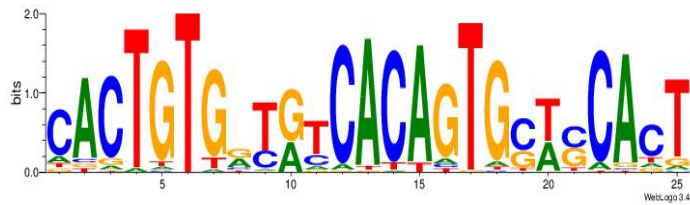


Dataset #: 2
Motif ID: 22
Motif name: CACTGTGrYrtCACAGTGsWsCAcT
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 19
Number of overlap: 6
Similarity score: 0.0564649

Alignment:
AGTGSWSCACTGTGAMAMCACAGTG
-----CACCTD-

Original motif Consensus sequence:
CACTGTGRTRTCACAGTGSWSCACT

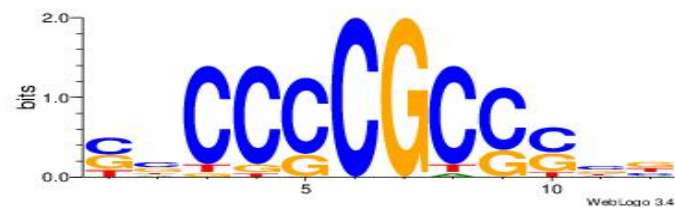
Reverse complement motif Consensus sequence:
AGTGSWSCACTGTGAMAMCACAGTG



Dataset #: 2
 Motif ID: 24
 Motif name: ssCCCCGCSsk
 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: 0.0571854

Alignment:
 SBCCCCGCCSBB
 -----CACCTD-

Original motif Consensus sequence: SBCCCCGCCSBB



Reverse complement motif Consensus sequence: BBSGGCGGGBS

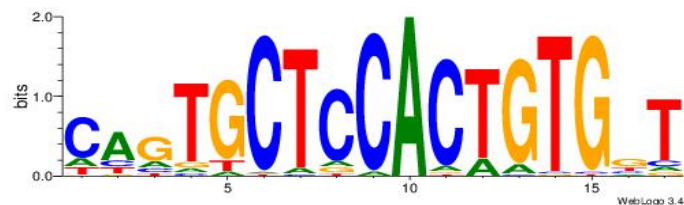


Dataset #: 2
 Motif ID: 20

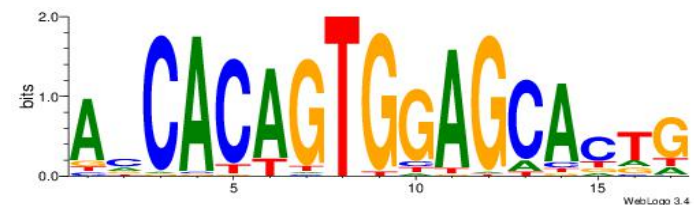
Motif name: CagTGCTCCACTGTGgT
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 8
 Number of overlap: 6
 Similarity score: 0.0594701

Alignment:
 ABCACAGTGGAGCACTG
 ----HAGGTG-----

Original motif Consensus sequence: CAGTGCTCCACTGTGBT



Reverse complement motif Consensus sequence: ABCACAGTGGAGCACTG

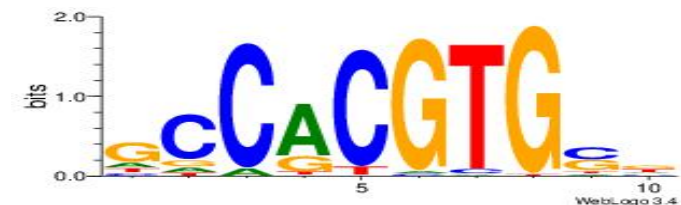


Dataset #: 1 Motif ID: 6 Motif name: Mycn

Original motif Consensus sequence: HSCACGTGGC



Reverse complement motif Consensus sequence: GCCACGTGSD



Best Matches for Top Significant Motif ID 6 (Highest to Lowest)

Dataset #: 2
Motif ID: 18
Motif name: sscCCCGCGcs
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: 0.0654819

Alignment:

BSCCCGCGBS
-GCCACGTGSD

Original motif Consensus sequence: BSCCCGCGBS



Reverse complement motif Consensus sequence: SBCGCGGGGSB



Dataset #: 2
Motif ID: 24
Motif name: ssCCCCGCSsk
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: 0.0704988

Alignment:
 BBSGGCGGGGBS
 -HSCACGTGGC-

Original motif Consensus sequence: SBCCCCGCCSBB



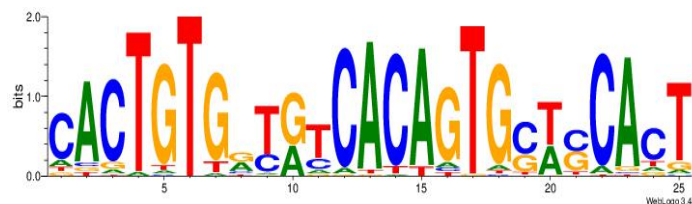
Reverse complement motif Consensus sequence: BBSGGCGGGGBS



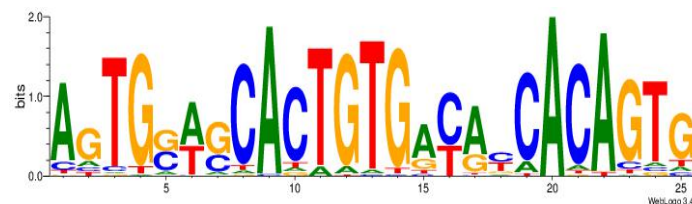
Dataset #: 2
 Motif ID: 22
 Motif name: CACTGTGrYrtCACAGTGswsCAcT
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 10
 Number of overlap: 10
 Similarity score: 0.0883224

Alignment:
 AGTGSWSCACTGTGAMAMCACAGTG
 -----GCCACGTGSD-----

Original motif Consensus sequence:
CACTGTGRTRTCACAGTGSWSCACT



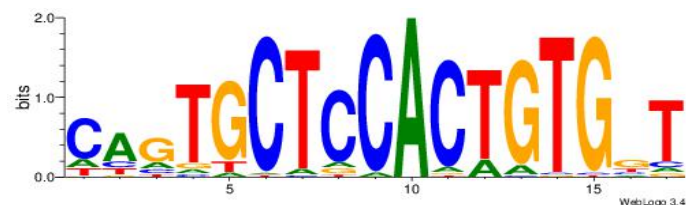
Reverse complement motif Consensus sequence:
AGTGSWSCACTGTGAMAMCACAGTG



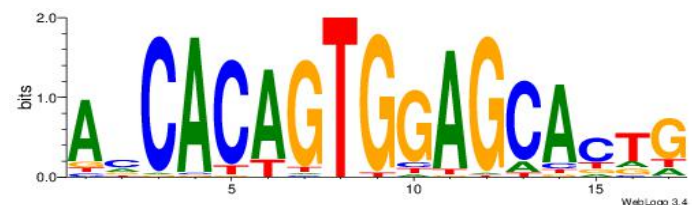
Dataset #: 2
Motif ID: 20
Motif name: CagTGCTCCACTGTGgT
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 7
Number of overlap: 10
Similarity score: 0.0943014

Alignment:
ABCACAGTGGAGCACTG
-GCCACGTGSD-----

Original motif Consensus sequence: CAGTGCTCCACTGTGBT



Reverse complement motif Consensus sequence:
ABCACAGTGGAGCACTG

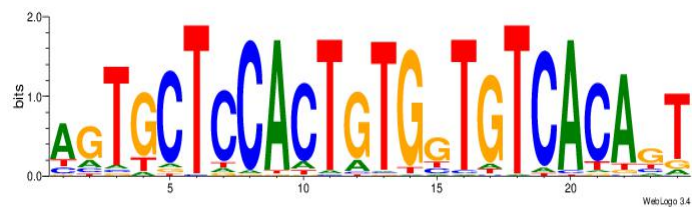


Dataset #: 2
 Motif ID: 27
 Motif name: AgTGCTCCACTGTGgTGTCACAgT
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 6
 Number of overlap: 10
 Similarity score: 0.0949359

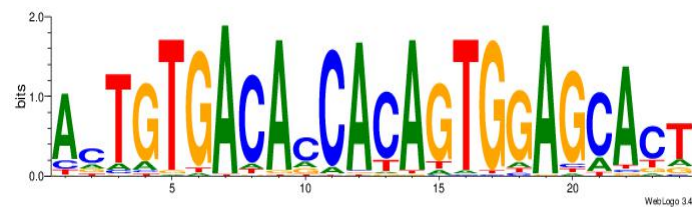
Alignment:

ACTGTGACACCACAGTGGAGCACT
 -----GCCACGTGSD-----

Original motif Consensus sequence: AGTGCTCCACTGTGGTGTCAcAGT



Reverse complement motif Consensus sequence: ACTGTGACACCACAGTGGAGCACT



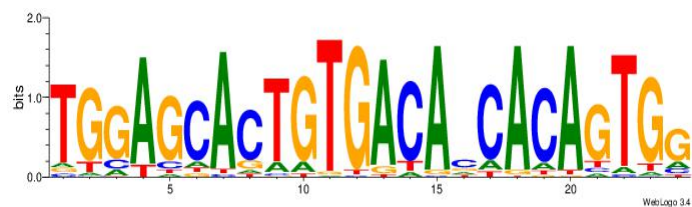
Dataset #: 2
 Motif ID: 23
 Motif name: TGGAGCACTGTGACAcCACAGTGg
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1

Number of overlap: 10
Similarity score: 0.0955115

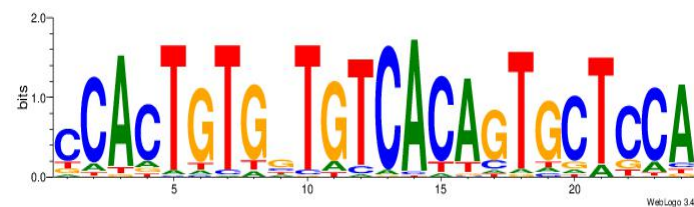
Alignment:

TGGAGCACTGTGACAVCACAGTGG
-----HSCACGTGGC

Original motif Consensus sequence: TGGAGCACTGTGACAVCACAGTGG



Reverse complement motif Consensus sequence: CCACTGTGVTGTCACAGTGCTCCA

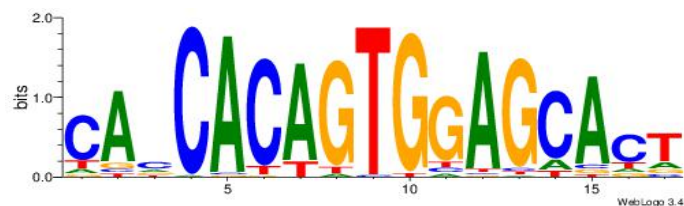


Dataset #: 2
Motif ID: 26
Motif name: CACcACAGTGGAGCAct
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 3
Number of overlap: 10
Similarity score: 0.0959628

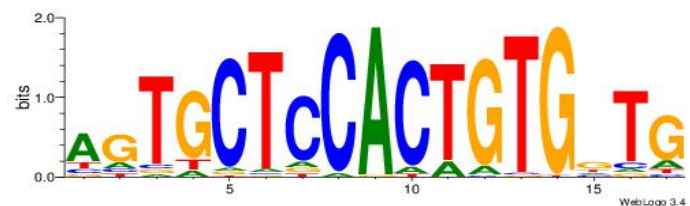
Alignment:

CAHCACAGTGGAGCACT
--GCCACGTGSD-----

Original motif Consensus sequence: CAHCACAGTGGAGCACT



Reverse complement motif Consensus sequence: AGTGCTCCACTGTGDTG



Dataset #: 2
Motif ID: 32
Motif name: gCGCGCsCgsG
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: 0.0989932

Alignment:
GCGCGCSCGCG
-HSCACGTGGC

Original motif Consensus sequence: GCGCGCSCGCG



Reverse complement motif Consensus sequence: CGCGSGCGCGC

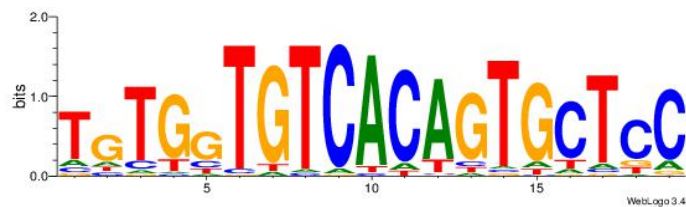


Dataset #: 2
 Motif ID: 17
 Motif name: TgTGgTGTCACAGTGCTCC
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 4
 Number of overlap: 10
 Similarity score: 0.0991692

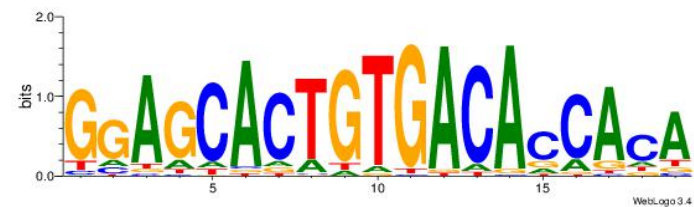
Alignment:

GGAGCACTGTGACACCACA
 ---GCCACGTGSD-----

Original motif Consensus sequence: TGTGGTGTCACAGTGCTCC



Reverse complement motif Consensus sequence: GGAGCACTGTGACACCACA

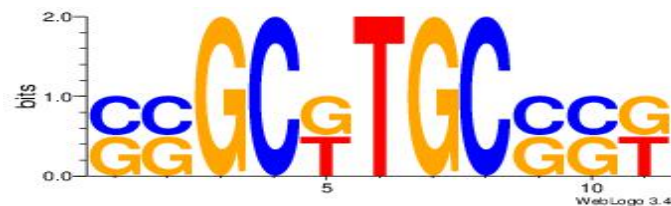


Dataset #: 2
 Motif ID: 28
 Motif name: ssGCKTGCssk
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1

Number of overlap: 10
Similarity score: 0.101333

Alignment:
YSSGCAYGCSS
HSCACGTGGC-

Original motif Consensus sequence: SSGCKTGCSSK



Reverse complement motif Consensus sequence: YSSGCAYGCSS



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

Original motif Consensus sequence: VGCACGTGGH



Reverse complement motif Consensus sequence: DCCACGTGCV



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

Dataset #: 2
Motif ID: 18
Motif name: sscCCCGCGcs
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: 0.064853

Alignment:

BSCCCCGCGBS

-DCCACGTGCV

Original motif Consensus sequence: BSCCCCGCGBS



Reverse complement motif Consensus sequence: SBCGCGGGGSB



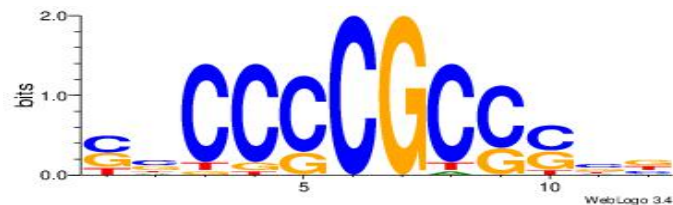
Dataset #: 2
 Motif ID: 24
 Motif name: ssCCCCGCSsk
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 10
 Similarity score: 0.0728588

Alignment:

SBCCCCGCCSBB

-DCCACGTGCV-

Original motif Consensus sequence: SBCCCCGCCSBB



Reverse complement motif Consensus sequence: BBSGGCGGGGBS

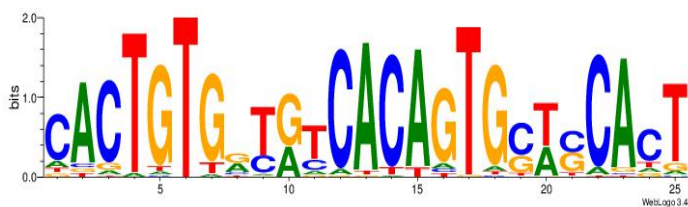


Dataset #: 2
 Motif ID: 22
 Motif name: CACTGTGrYrtCACAGTGswsCACT
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 6
 Number of overlap: 10
 Similarity score: 0.0888909

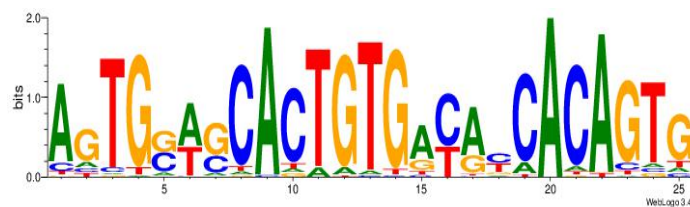
Alignment:

CACTGTGRTRTCACAGTGSWSCACT
 -----DCCACGTGCV-----

Original motif Consensus sequence:
 CACTGTGRTRTCACAGTGSWSCACT



Reverse complement motif Consensus sequence:
 AGTGSWSCACTGTGAMAMCACAGTG

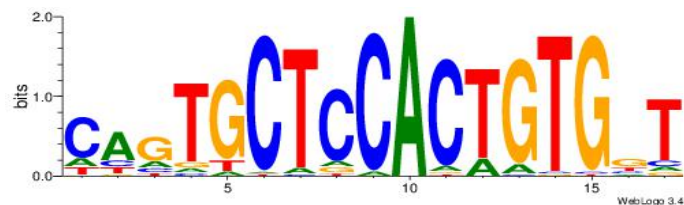


Dataset #: 2
 Motif ID: 20
 Motif name: CagTGCTCCACTGTGgT
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 7
 Number of overlap: 10
 Similarity score: 0.0955234

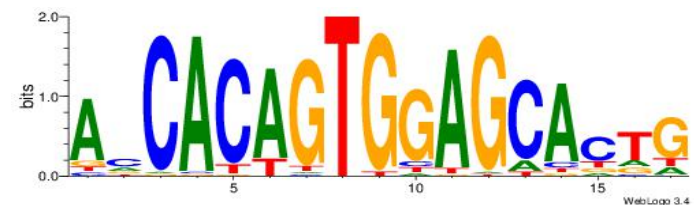
Alignment:

ABCACAGTGGAGCACTG
 -DCCACGTGCV-----

Original motif Consensus sequence: CAGTGCTCCACTGTGBT



Reverse complement motif Consensus sequence: ABCACAGTGGAGCACTG

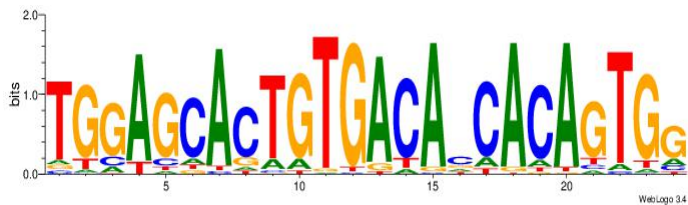


Dataset #: 2
 Motif ID: 23
 Motif name: TGGAGCACTGTGACAcCACAGTGg
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 11

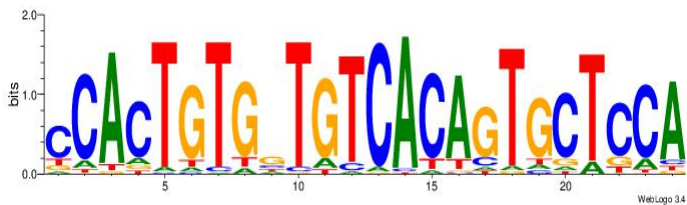
Number of overlap: 10
Similarity score: 0.0971125

Alignment:
TGGAGCACTGTGACAVCACAGTGG
----DCCACGTGCV-----

Original motif Consensus sequence: TGGAGCACTGTGACAVCACAGTGG



Reverse complement motif Consensus sequence: CCACTGTGVTGTACAGTGCTCCA

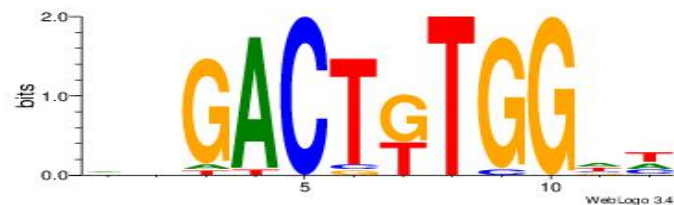
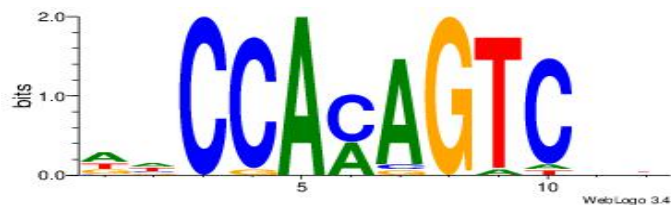


Dataset #: 2
Motif ID: 25
Motif name: wwCCAmAGTCmt
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 2
Number of overlap: 10
Similarity score: 0.0974038

Alignment:
VDGACTRTGGDD
-VGCACGTGGH-

Original motif Consensus sequence: DDCCAMAGTCHB

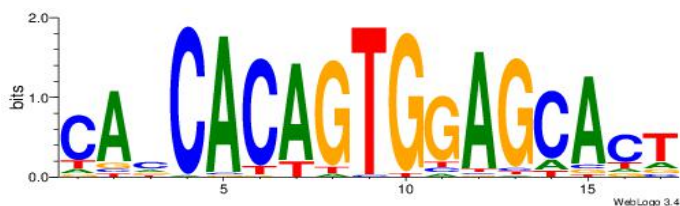
Reverse complement motif Consensus sequence: VDGACTRTGGDD



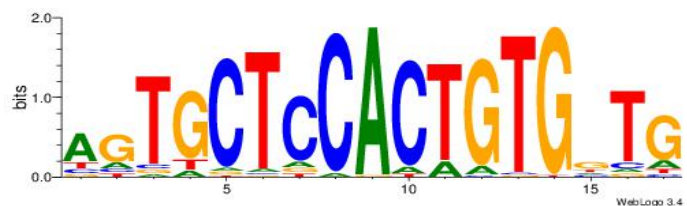
Dataset #: 2
 Motif ID: 26
 Motif name: CACcACAGTGGAGCAct
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 10
 Similarity score: 0.0979703

Alignment:
 CAHCACAGTGGAGCACT
 --DCCACGTGCV-----

Original motif Consensus sequence: CAHCACAGTGGAGCACT



Reverse complement motif Consensus sequence: AGTGCTCCACTGTGDTG



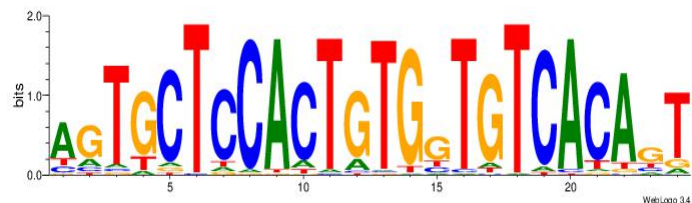
Dataset #: 2

Motif ID: 27
 Motif name: AgTGCTCCACTGTGgTGTCACAgT
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 6
 Number of overlap: 10
 Similarity score: 0.0980018

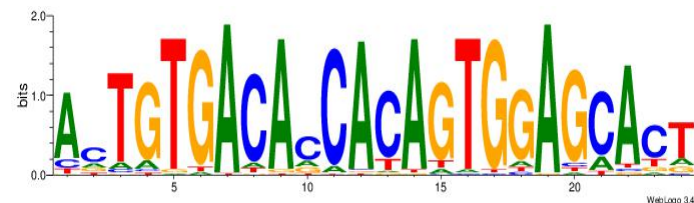
Alignment:

ACTGTGACACCACAGTGGAGCACT
 -----DCCACGTGCV-----

Original motif Consensus sequence: AGTGCTCCACTGTGGTGTCAAGT



Reverse complement motif Consensus sequence: ACTGTGACACCACAGTGGAGCACT

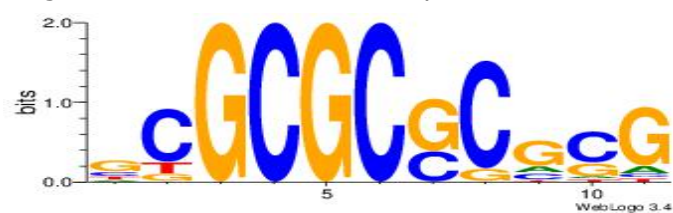


Dataset #: 2
 Motif ID: 32
 Motif name: gCGCGCsCgsG
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 10

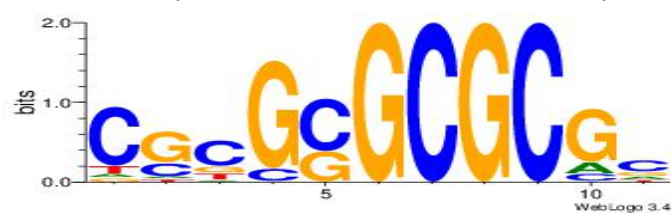
Similarity score: 0.0989125

Alignment:
CGCGSGCGCGC
VGCACGTGGH-

Original motif Consensus sequence: GCGCGCSCGCG



Reverse complement motif Consensus sequence: CGCGSGCGCGC

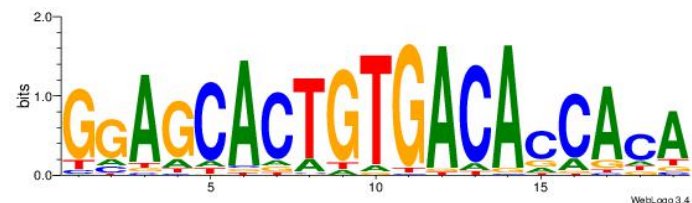
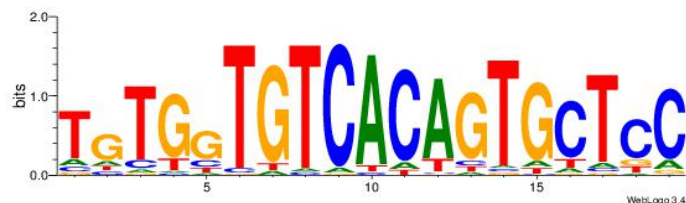


Dataset #: 2
Motif ID: 17
Motif name: TgTGgTGTCACAGTGCTCC
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 7
Number of overlap: 10
Similarity score: 0.0993196

Alignment:
GGAGCACTGTGACACCACA
---DCCACGTGCV-----

Original motif Consensus sequence: TGTGGTGTACAGTGCTCC

Reverse complement motif Consensus sequence:
GGAGCACTGTGACACCACA



Dataset #: 1 Motif ID: 11 Motif name: NR4A2

Original motif Consensus sequence: AAGGTCAC



Reverse complement motif Consensus sequence: GTGACCTT



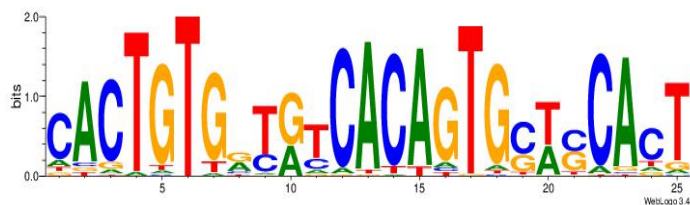
Best Matches for Top Significant Motif ID 11 (Highest to Lowest)

Dataset #:	2
Motif ID:	22
Motif name:	CACTGTGrYrtCACAGTGswsCAcT
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	7
Number of overlap:	8
Similarity score:	0.0557243

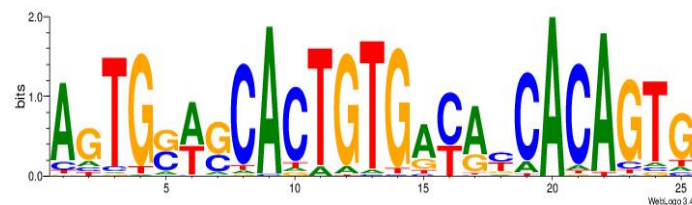
Alignment:

```
CACTGTGRTRTCACAGTGSWSCACT
-----AAGGTCAC-----
```

Original motif Consensus sequence:
CACTGTGRTRTCACAGTGSWSCACT



Reverse complement motif Consensus sequence:
AGTGSWSCACTGTGAMAMCACAGTG

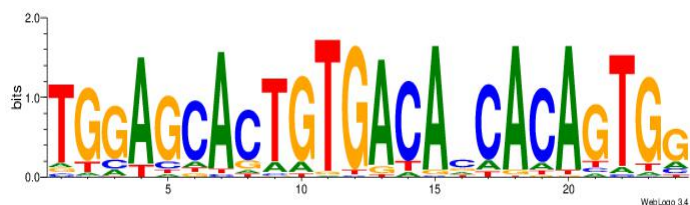


Dataset #: 2
Motif ID: 23
Motif name: TGGAGCACTGTGACAcCACAGTGg
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 8
Number of overlap: 8
Similarity score: 0.060729

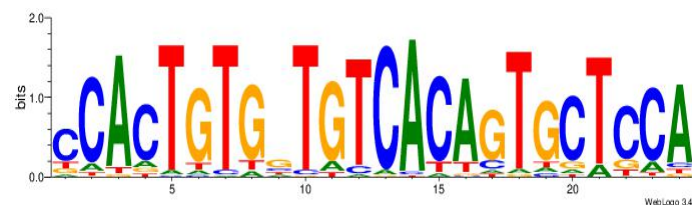
Alignment:

CCACTGTGVTGTACAGTGCTCCA
-----AAGGTCAC-----

Original motif Consensus sequence: TGGAGCACTGTGACAVCACAGTGG



Reverse complement motif Consensus sequence:
CCACTGTGVTGTACAGTGCTCCA

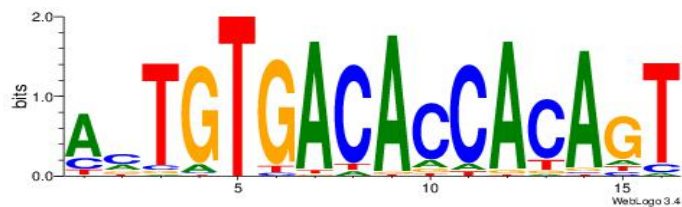


Dataset #: 2
 Motif ID: 21
 Motif name: AmTGTGACACCACAGT
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 4
 Number of overlap: 8
 Similarity score: 0.0645146

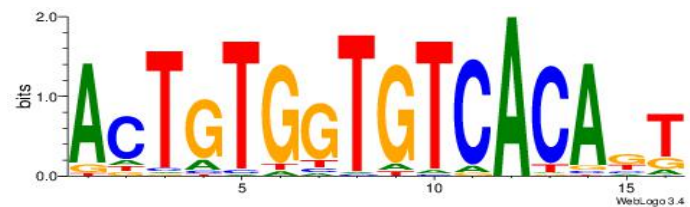
Alignment:

ACTGTGGTGTACART
 -----AAGGTCAC---

Original motif Consensus sequence: AMTGTGACACCACAGT



Reverse complement motif Consensus sequence: ACTGTGGTGTACART

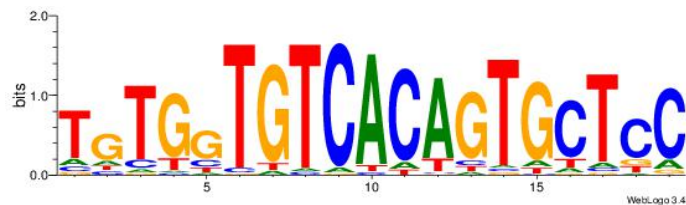


Dataset #: 2
 Motif ID: 17
 Motif name: TgTGgTGTCACAGTGCTCC
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4

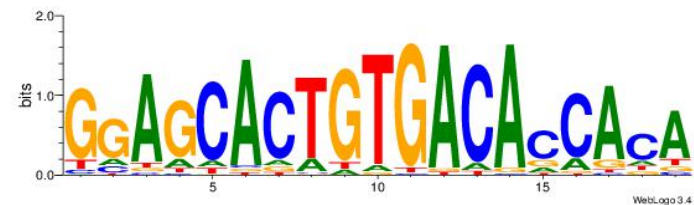
Number of overlap: 8
 Similarity score: 0.0695512

Alignment:
 TGTGGTGTTCACAGTGCTCC
 ---AAGGTCAC-----

Original motif Consensus sequence: TGTGGTGTTCACAGTGCTCC



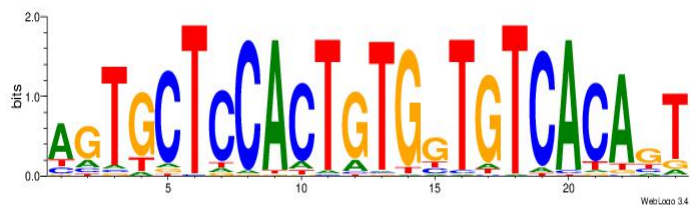
Reverse complement motif Consensus sequence: GGAGCACTGTGACACCACA



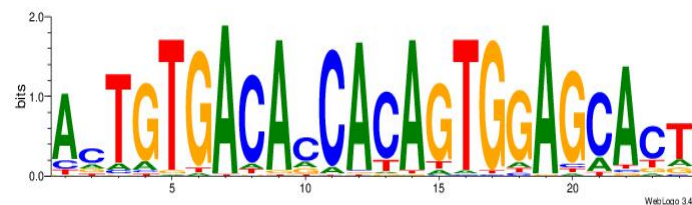
Dataset #: 2
 Motif ID: 27
 Motif name: AgTGCTCCACTGTGgTGTCACAgT
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 4
 Number of overlap: 8
 Similarity score: 0.0709831

Alignment:
 AGTGCTCCACTGTGGTGTTCACAGT
 -----AAGGTCAC---

Original motif Consensus sequence: AGTGCTCCACTGTGGTGTACAGT



Reverse complement motif Consensus sequence: ACTGTGACACCACAGTGGAGCACT



Dataset #: 2
Motif ID: 29
Motif name: cCGCGGrCACG
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: 0.0772292

Alignment:
CCGCGGRCACG
--AAGGTCAC--

Original motif Consensus sequence: CCGCGGRCACG



Reverse complement motif Consensus sequence: CGTGKCCGCGG

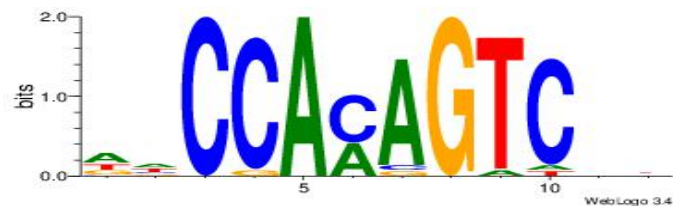


Dataset #: 2
 Motif ID: 25
 Motif name: wwCCAmAGTCmt
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 5
 Number of overlap: 8
 Similarity score: 0.0788401

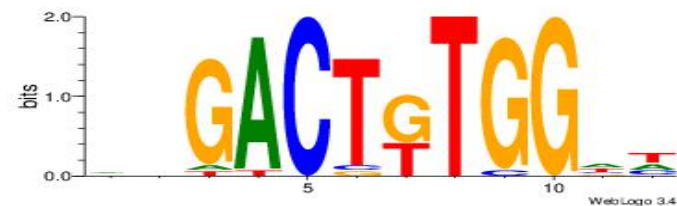
Alignment:

DDCCAMAGTCHB
 ----AAGGTCAC

Original motif Consensus sequence: DDCCAMAGTCHB



Reverse complement motif Consensus sequence: VDGACTRTGGDD

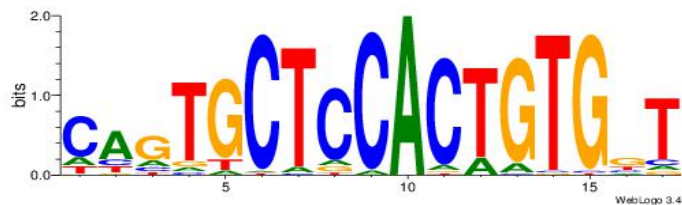


Dataset #: 2
 Motif ID: 20
 Motif name: CagTGCTCCACTGTGgT
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 10
 Number of overlap: 8

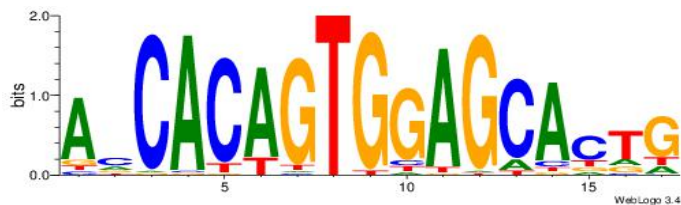
Similarity score: 0.0864039

Alignment:
ABCACAGTGGAGCACTG
-----GTGACCTT

Original motif Consensus sequence: CAGTGCTCCACTGTGBT



Reverse complement motif Consensus sequence:
ABCACAGTGGAGCACTG

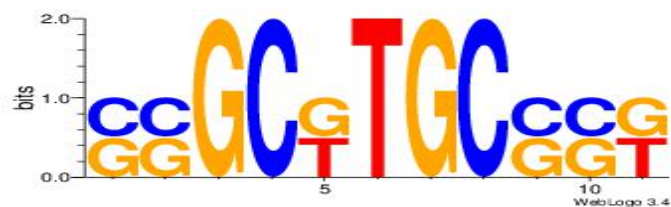


Dataset #: 2
Motif ID: 28
Motif name: ssGCKTGCssk
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 5
Number of overlap: 7
Similarity score: 0.568556

Alignment:
SSGCKTGCSSK-
----GTGACCTT

Original motif Consensus sequence: SSGCKTGCSSK

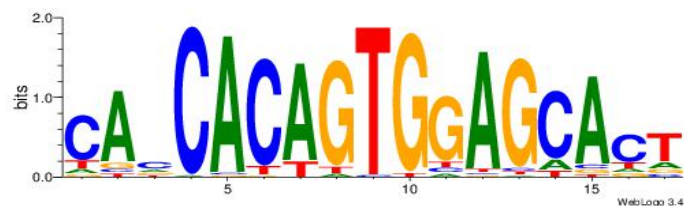
Reverse complement motif Consensus sequence: YSSGCAYGCSS



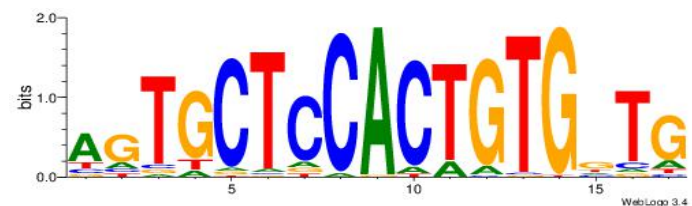
Dataset #: 2
 Motif ID: 26
 Motif name: CACcACAGTGGAGCAct
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 11
 Number of overlap: 7
 Similarity score: 0.581814

Alignment:
 CAHCACAGTGGAGCACT-
 -----GTGACCTT

Original motif Consensus sequence: CAHCACAGTGGAGCACT

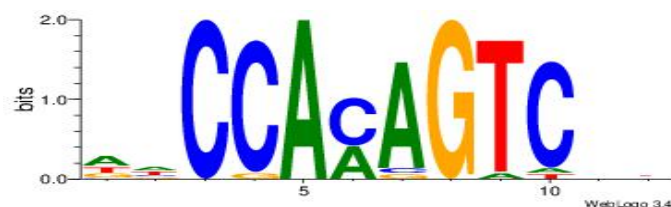


Reverse complement motif Consensus sequence: AGTGCTCCACTGTGDTG

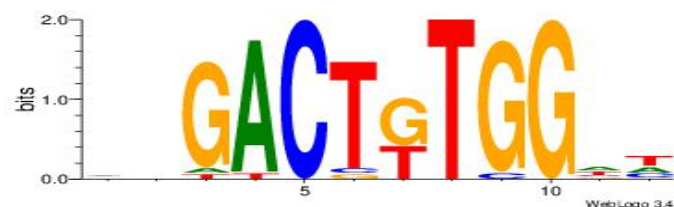


Dataset #: 2 Motif ID: 25 Motif name: wwCCAmAGTCmt

Original motif Consensus sequence: DDCCAMAGTCHB



Reverse complement motif Consensus sequence: VDGACTRTGGDD



Best Matches for Top Significant Motif ID 25 (Highest to Lowest)

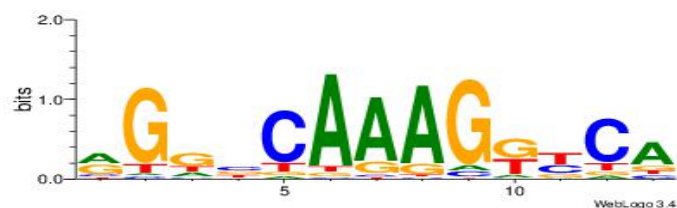
Dataset #:	1
Motif ID:	1
Motif name:	HNF4A
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	12
Similarity score:	0.032442

Alignment:

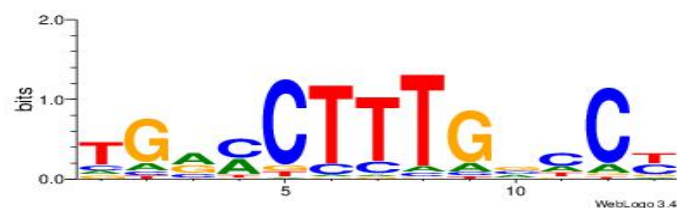
RGGBCAAAGKYCA

–DDCCAMAGTCHB

Original motif Consensus sequence: RGGBCAAAGKYCA



Reverse complement motif Consensus sequence: TGMYCTTTGBCCK

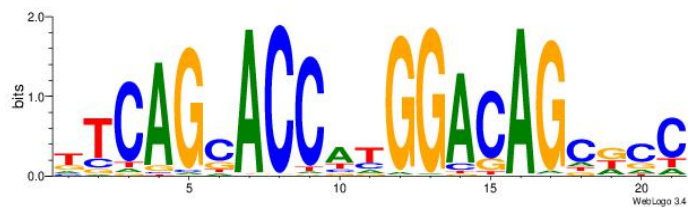


Dataset #: 1
 Motif ID: 7
 Motif name: REST
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 4
 Number of overlap: 12
 Similarity score: 0.0391228

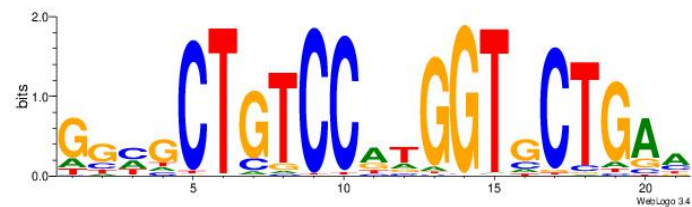
Alignment:

GYGCTGTCCATGGTGCTGAA
 ---DDCCAMAGTCHB-----

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC



Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA



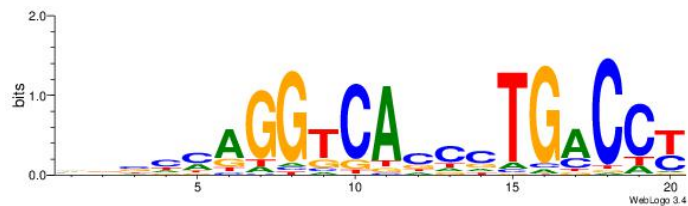
Dataset #: 1
 Motif ID: 3
 Motif name: ESR1
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 9

Number of overlap: 12
Similarity score: 0.0407304

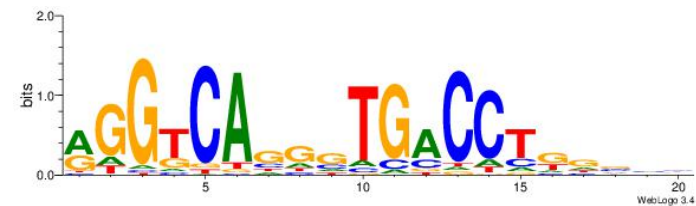
Alignment:

VDBHMAGGTCACCCTGACCY
DDCCAMAGTCHB-----

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV

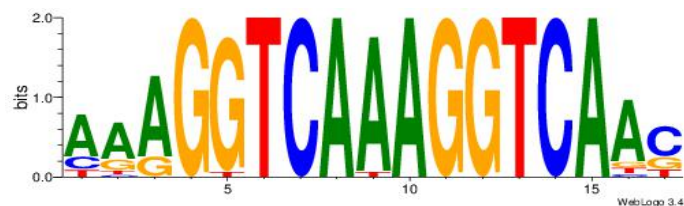


Dataset #: 1
Motif ID: 10
Motif name: NR1H2RXRA
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2
Number of overlap: 12
Similarity score: 0.0463384

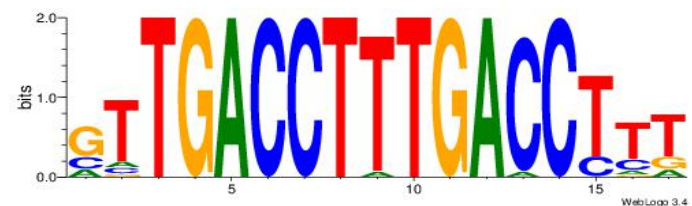
Alignment:

AAAGGTCAAAGGTCAAC
----DDCCAMAGTCHB--

Original motif Consensus sequence: AAAGGTCAAAGGTCAAC



Reverse complement motif Consensus sequence: GTTGACCTTTGACCTT

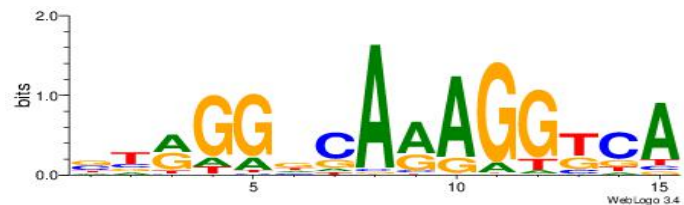


Dataset #: 1
Motif ID: 14
Motif name: PPARGRXRA
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 3
Number of overlap: 12
Similarity score: 0.0480406

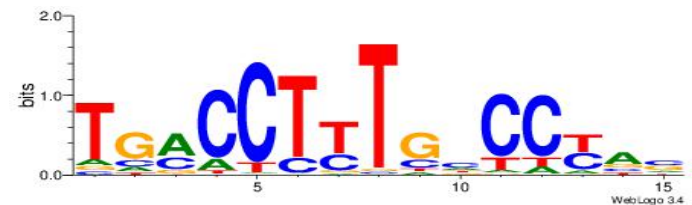
Alignment:

TGRCCTKTGHCKAB
--DDCCAMAGTCHB--

Original motif Consensus sequence: BTRGGDCARAGGKCA



Reverse complement motif Consensus sequence: TGRCCCTKTGHCKA

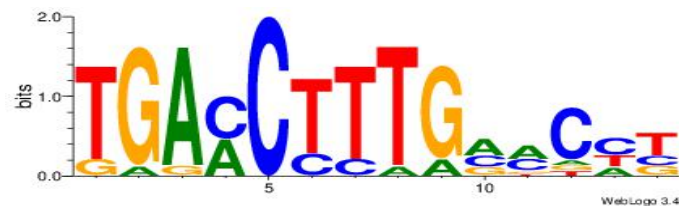


Dataset #: 1
 Motif ID: 2
 Motif name: NR2F1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 12
 Similarity score: 0.0506507

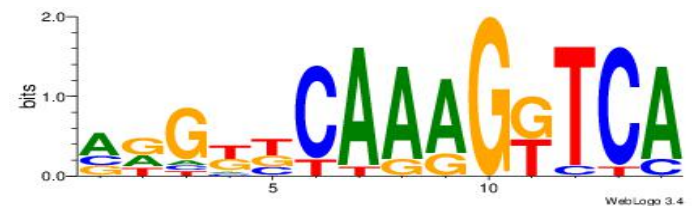
Alignment:

TGAMCTTTGMMCYT
 --VDGACTRTGGDD

Original motif Consensus sequence: TGAMCTTTGMMCYT



Reverse complement motif Consensus sequence: AKGYCAAAGRTC

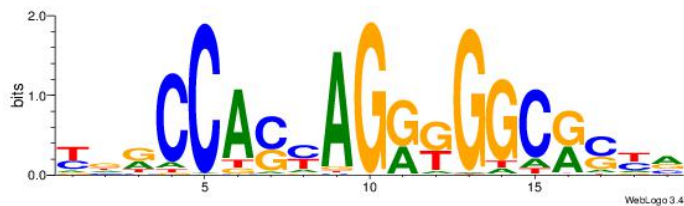


Dataset #: 1
 Motif ID: 16
 Motif name: CTCF
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 8
 Number of overlap: 12

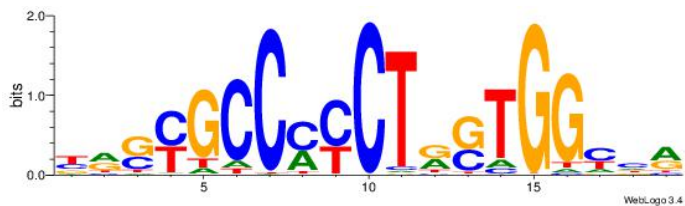
Similarity score: 0.0523578

Alignment:
BMSMGCCYMCTKSTGGMHM
DDCCAMAGTCHB-----

Original motif Consensus sequence: YDRCCASYAGRKGGCRSYV



Reverse complement motif Consensus sequence:
BMSMGCCYMCTKSTGGMHM

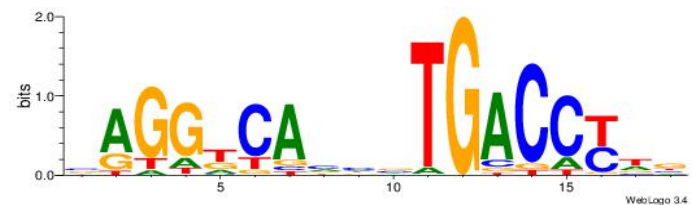
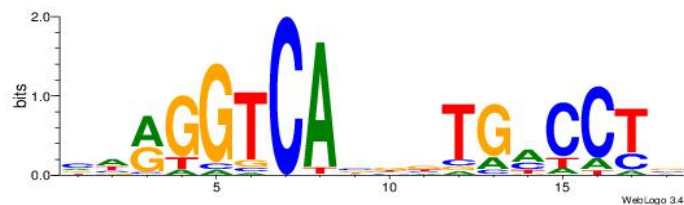


Dataset #: 1
Motif ID: 9
Motif name: ESR2
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 4
Number of overlap: 12
Similarity score: 0.0576723

Alignment:
VHRGGTCABDBTGMCCCTB
---DDCCAMAGTCHB---

Original motif Consensus sequence: VHRGGTCABDBTGMCCCTB

Reverse complement motif Consensus sequence:
BAGGYCABHBTGACCKHV

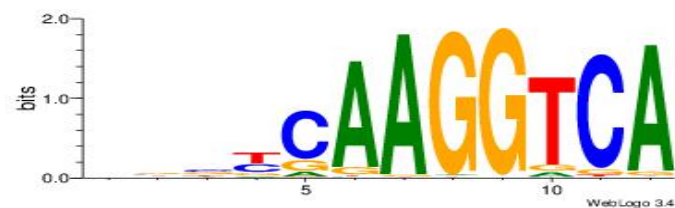


Dataset #: 1
 Motif ID: 4
 Motif name: Esrrb
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 11
 Similarity score: 0.525631

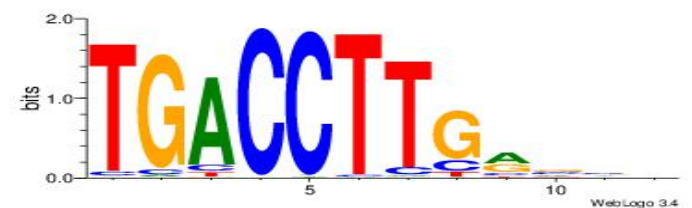
Alignment:

VBBYCAAGGTCA-
 -DDCCAMAGTCHB

Original motif Consensus sequence: VBBYCAAGGTCA



Reverse complement motif Consensus sequence: TGACCTTGMBBB



Dataset #: 1
 Motif ID: 8

Motif name:	Myc
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:	1.0578

Alignment:

--VGCACGTGGH

VDGACTRTGGDD

Original motif Consensus sequence: VGCACGTGGH

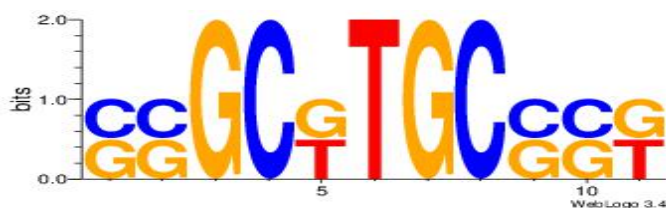


Reverse complement motif Consensus sequence: DCCACGTGCV



Dataset #: 2 Motif ID: 28 Motif name: ssGCKTGCssk

Original motif Consensus sequence: SSGCKTGCSSK



Reverse complement motif Consensus sequence: YSSGCAYGCSS



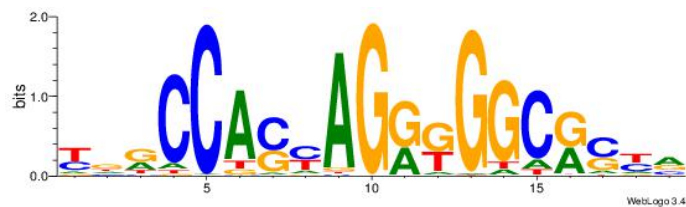
Best Matches for Top Significant Motif ID 28 (Highest to Lowest)

Dataset #: 1
 Motif ID: 16
 Motif name: CTCF
 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: 0.0349439

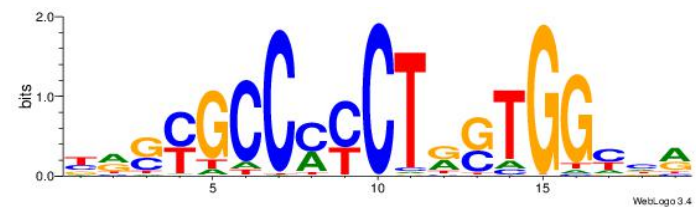
Alignment:

YDRCCASYAGRKGGRSYV
 -----SSGCKTGCSSK-

Original motif Consensus sequence: YDRCCASYAGRKGGRSYV



Reverse complement motif Consensus sequence: BMSMGCCYMCTKSTGGMHM

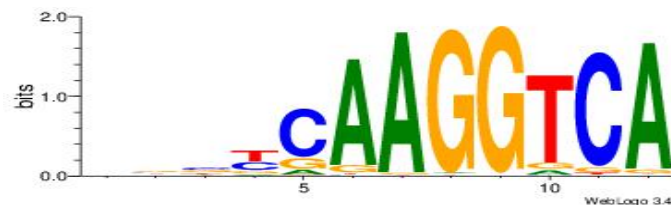


Dataset #: 1
 Motif ID: 4
 Motif name: Esrrb
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2

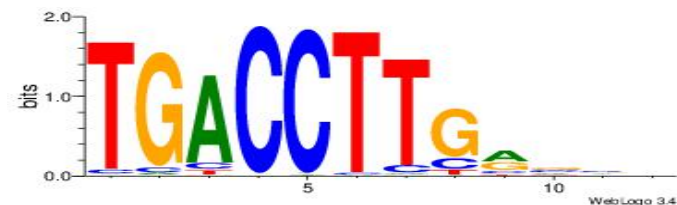
Number of overlap: 11
Similarity score: 0.0358701

Alignment:
VBBYCAAGGTCA
-YSSGCAYGCSS

Original motif Consensus sequence: VBBYCAAGGTCA



Reverse complement motif Consensus sequence: TGACCTTGMBBB

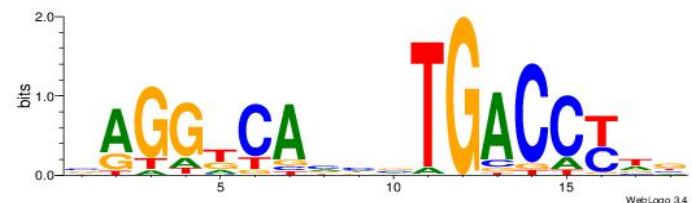
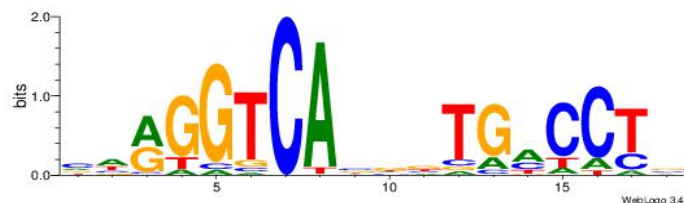


Dataset #: 1
Motif ID: 9
Motif name: ESR2
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 3
Number of overlap: 11
Similarity score: 0.0379074

Alignment:
VHRGGTCABDBTGMCTB
-----YSSGCAYGCSS--

Original motif Consensus sequence: VHRGGTCABDBTGMCTB

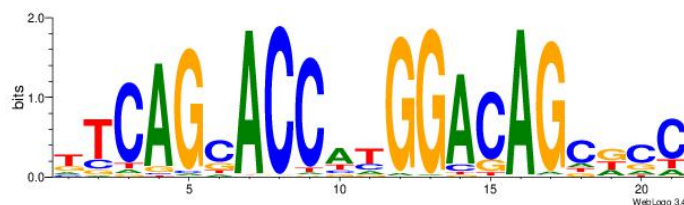
Reverse complement motif Consensus sequence:
BAGGYCABHBTGACCKHV



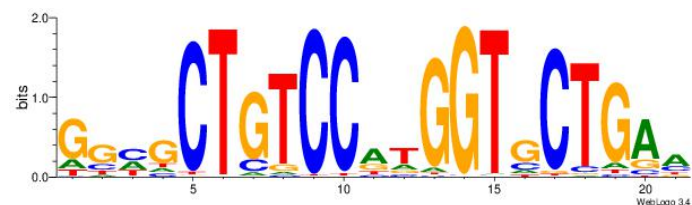
Dataset #: 1
 Motif ID: 7
 Motif name: REST
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 10
 Number of overlap: 11
 Similarity score: 0.0409322

Alignment:
 TTCAGCACCATGGACAGCKCC
 -YSSGCAYGCSS-----

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC



Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA

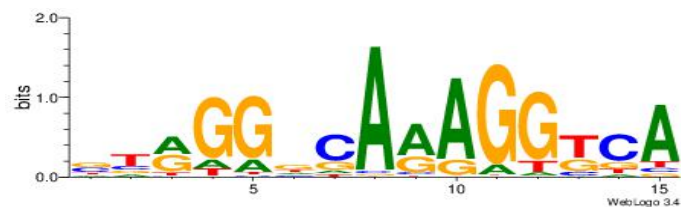


Dataset #: 1

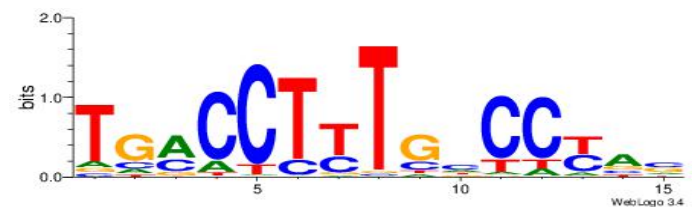
Motif ID: 14
 Motif name: PPARGRXRA
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 11
 Similarity score: 0.041419

Alignment:
 BTRGGDCARAGGKCA
 --YSSGCAYGCSS--

Original motif Consensus sequence: BTRGGDCARAGGKCA



Reverse complement motif Consensus sequence: TGRCCTKTGHCCK



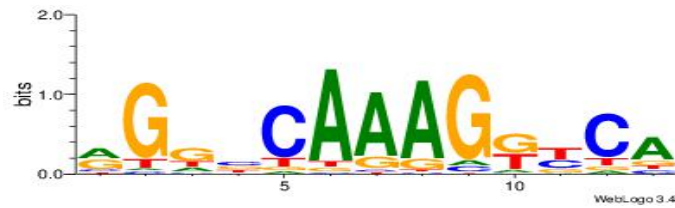
Dataset #: 1
 Motif ID: 1
 Motif name: HNF4A
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 11
 Similarity score: 0.0437981

Alignment:

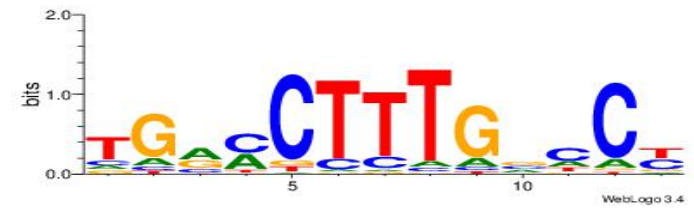
RGGBCAAAGKYCA

--YSSGCAYGCSS

Original motif Consensus sequence: RGGBCAAAGKYCA



Reverse complement motif Consensus sequence: TGM YCTTTGBCCK



Dataset #:	1
Motif ID:	6
Motif name:	Mycn
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:	0.53887

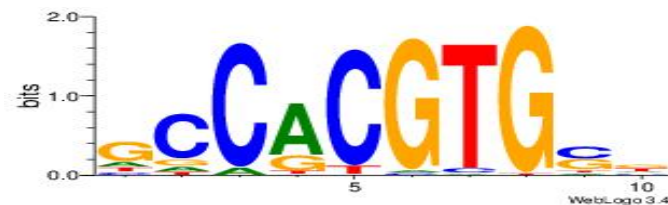
Alignment:

GCCACGTGSD-

SSGCKTGCSSK

Original motif Consensus sequence: HSCACGTGGC

Reverse complement motif Consensus sequence: GCCACGTGSD



Dataset #: 1
 Motif ID: 8
 Motif name: Myc
 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: 0.542915

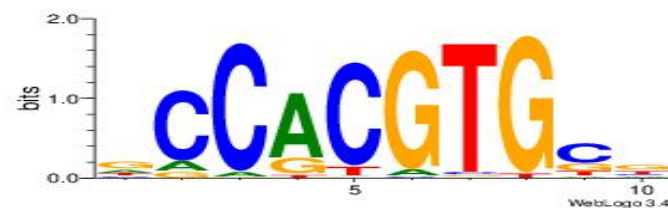
Alignment:

DCCACGTGCV-
 SSGCKTGCSK

Original motif Consensus sequence: VGCACGTGGH



Reverse complement motif Consensus sequence: DCCACGTGCV



Dataset #: 1
 Motif ID: 10

Motif name:	NR1H2RXRA
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	10
Number of overlap:	8
Similarity score:	1.53583

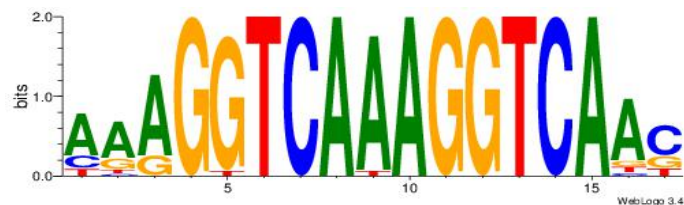
Alignment:

```

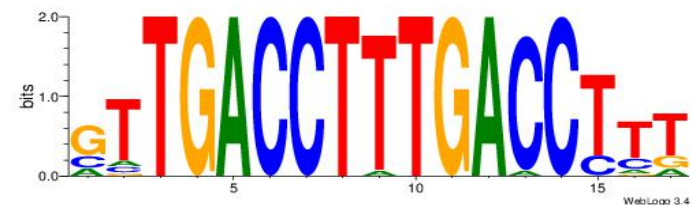
---AAAGGTCAAAGGTCAAC
YSSGCAYGCSS-----

```

Original motif Consensus sequence: AAAGGTCAAAGGTCAAC



Reverse complement motif Consensus sequence: GTTGACCTTTGACCTT

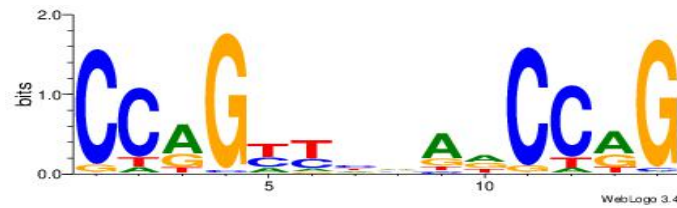


Dataset #:	1
Motif ID:	15
Motif name:	Tcfcp2l1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	7
Number of overlap:	8
Similarity score:	1.53704

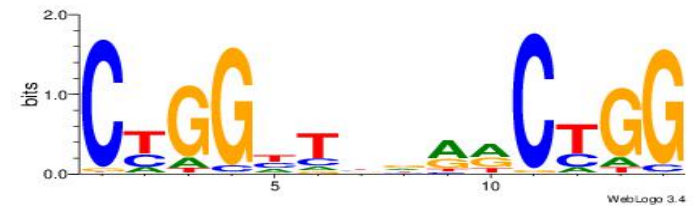
Alignment:

---CCAGYYHVADCCRG
YSSGCAYGCSS-----

Original motif Consensus sequence: CCAGYYHVADCCRG

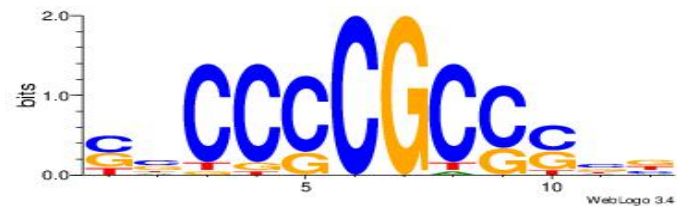


Reverse complement motif Consensus sequence: CKGGDTBDMMCTG



Dataset #: 2 Motif ID: 24 Motif name: ssCCCCGCSsk

Original motif Consensus sequence: SBCCCCGCCSBB



Reverse complement motif Consensus sequence: BBSGGCGGGGBS



Best Matches for Top Significant Motif ID 24 (Highest to Lowest)

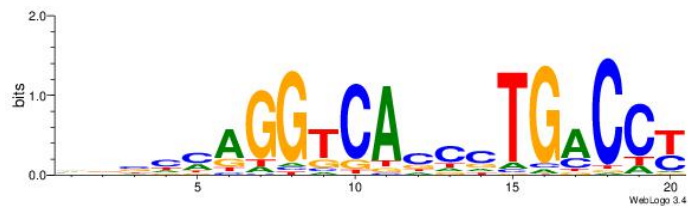
Dataset #:	1
Motif ID:	3
Motif name:	ESR1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	2

Number of overlap: 12
Similarity score: 0.063076

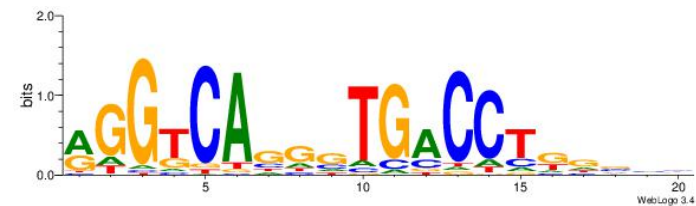
Alignment:

MGGTCAGGGTGACCTRDBHV
-----BBSGGCGGGGBS--

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV

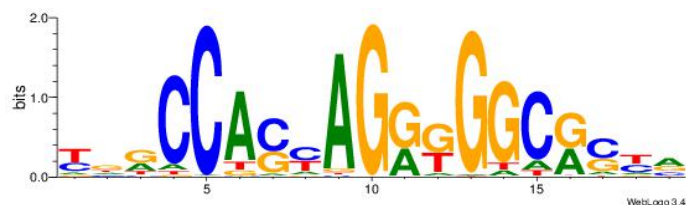


Dataset #: 1
Motif ID: 16
Motif name: CTCF
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 2
Number of overlap: 12
Similarity score: 0.0642087

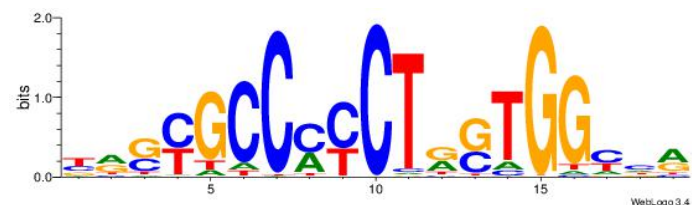
Alignment:

YDRCCASYAGRKGGRSYV
-BBSGGCGGGGBS-----

Original motif Consensus sequence: YDRCCASYAGRKGGRSYV



Reverse complement motif Consensus sequence: BMSMGCCYMCTKSTGGMHM

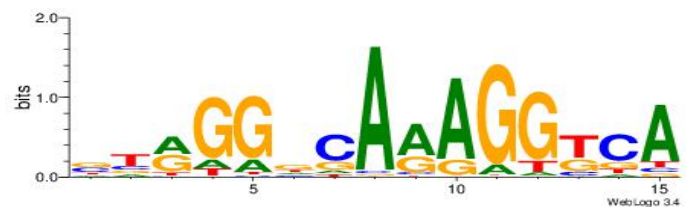


Dataset #: 1
 Motif ID: 14
 Motif name: PPARGRXRA
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 12
 Similarity score: 0.0671548

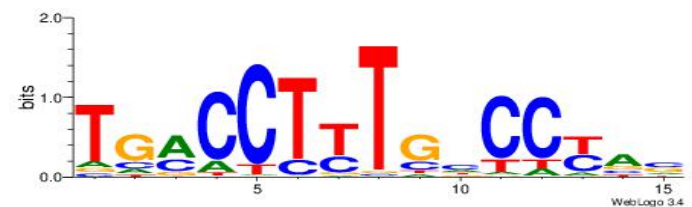
Alignment:

TGRCCTKTGHCKAB
 -SBCCCCGCCSBB--

Original motif Consensus sequence: BTRGGDCARAGGKCA



Reverse complement motif Consensus sequence: TGRCCCTKTGHCKK

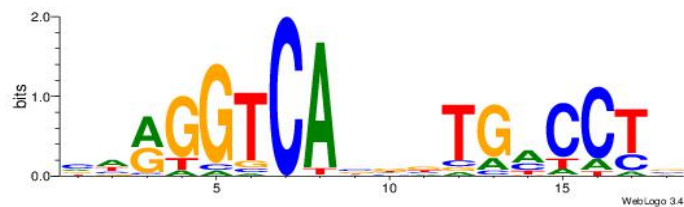


Dataset #: 1
 Motif ID: 9
 Motif name: ESR2
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 12
 Similarity score: 0.0734481

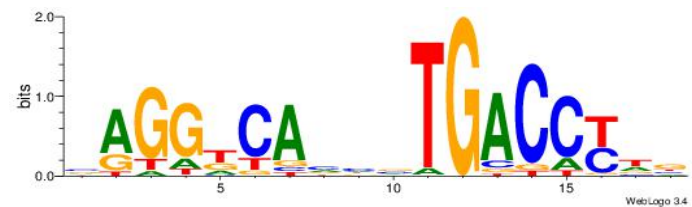
Alignment:

BAGGYCABHBTGACCKHV
 -SBCCCCGCCSBB-----

Original motif Consensus sequence: VHRGGTCABDBTGMCTB



Reverse complement motif Consensus sequence: BAGGYCABHBTGACCKHV

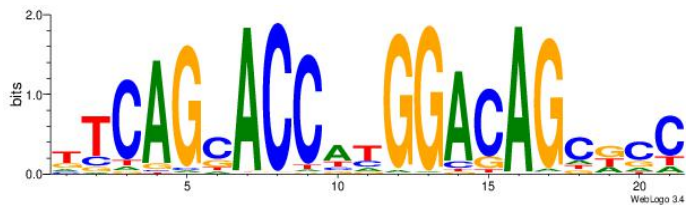


Dataset #: 1
 Motif ID: 7
 Motif name: REST
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 10

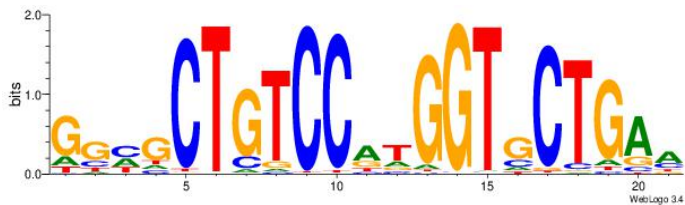
Number of overlap: 12
Similarity score: 0.0751084

Alignment:
TTCAGCACCATGGACAGCKCC
BBSGGCGGGGBS-----

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC



Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA

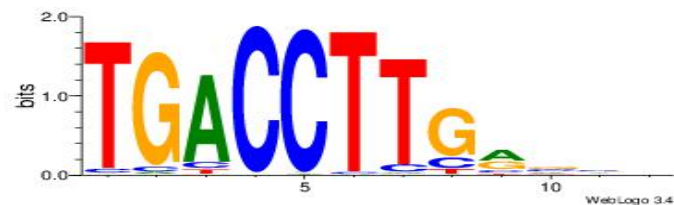
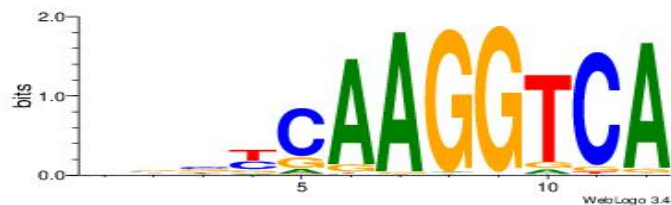


Dataset #: 1
Motif ID: 4
Motif name: Esrrb
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 2
Number of overlap: 11
Similarity score: 0.571364

Alignment:
VBBYCAAGGTCA-
-BBSGGCGGGGBS

Original motif Consensus sequence: VBBYCAAGGTCA

Reverse complement motif Consensus sequence: TGACCTTGMBBB

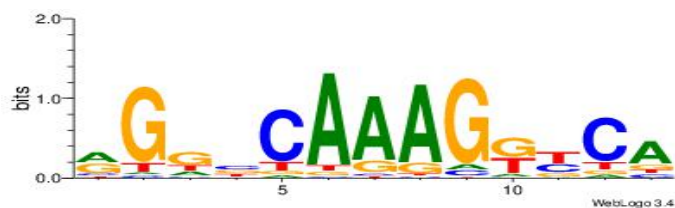


Dataset #: 1
 Motif ID: 1
 Motif name: HNF4A
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 11
 Similarity score: 0.573202

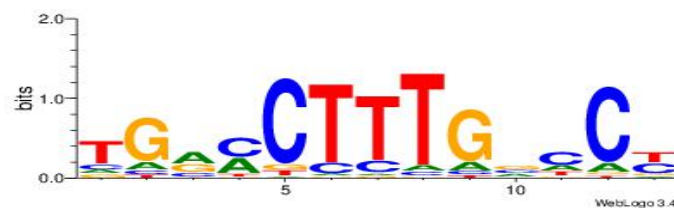
Alignment:

-TGM YCTTTGBCK
 SBCCCCGCCSBB--

Original motif Consensus sequence: RGGBCAAAGKYCA



Reverse complement motif Consensus sequence: TGM YCTTTGBCK



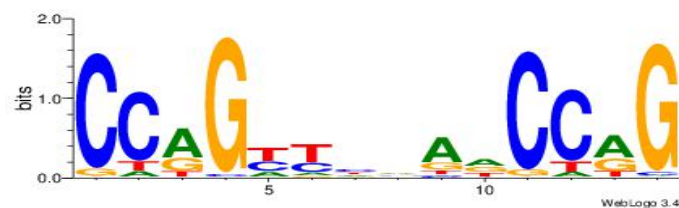
Dataset #: 1
 Motif ID: 15

Motif name:	Tcfcp2l1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	6
Number of overlap:	9
Similarity score:	1.54913

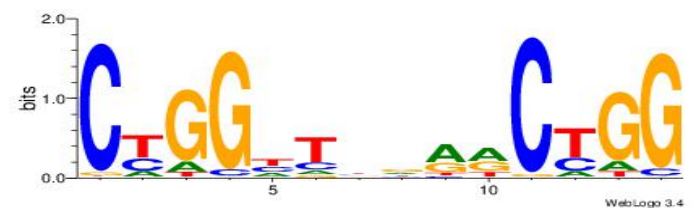
Alignment:

```
CKGGDTBDMCTGG---
-----BBSGGCGGGGBS
```

Original motif Consensus sequence: CCAGYYHVADCCRG



Reverse complement motif Consensus sequence: CKGGDTBDMCTGG

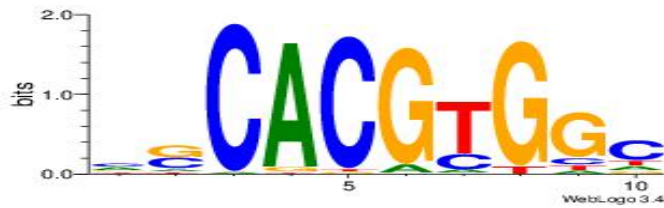


Dataset #:	1
Motif ID:	6
Motif name:	Mycn
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2
Number of overlap:	9
Similarity score:	1.57507

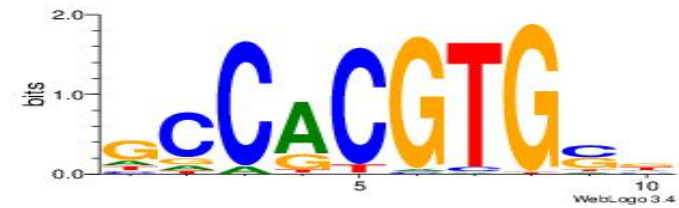
Alignment:

---HSCACGTGGC
SBCCCCGCCSBB-

Original motif Consensus sequence: HSCACGTGGC



Reverse complement motif Consensus sequence: GCCACGTGSD



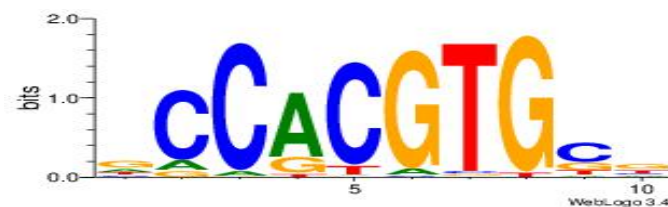
Dataset #:	1
Motif ID:	8
Motif name:	Myc
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	9
Similarity score:	1.57737

Alignment:

VGCACGTGGH---
-BBSGGCGGGGBS

Original motif Consensus sequence: VGCACGTGGH

Reverse complement motif Consensus sequence: DCCACGTGCV



Dataset #: 2 Motif ID: 29 Motif name: cCGCGGrCACG

Original motif Consensus sequence: CCGCGGRCACG



Reverse complement motif Consensus sequence: CGTGKCCGCGG



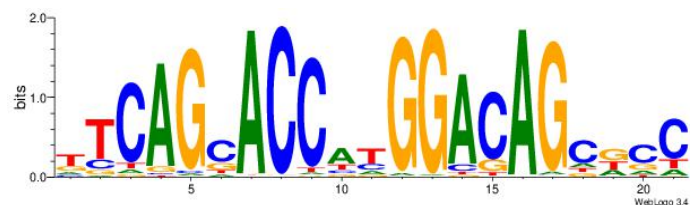
Best Matches for Top Significant Motif ID 29 (Highest to Lowest)

Dataset #:	1
Motif ID:	7
Motif name:	REST
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	4
Number of overlap:	11
Similarity score:	0.0484441

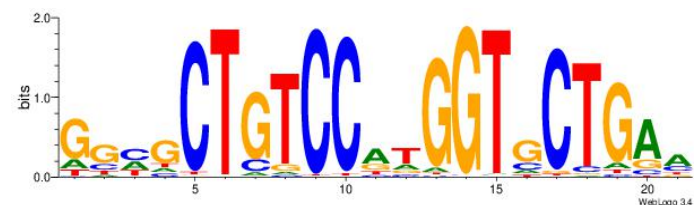
Alignment:

```
TTCAGCACCATGGACAGCKCC
-----CCGCGGRCACG----
```


Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC



Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA

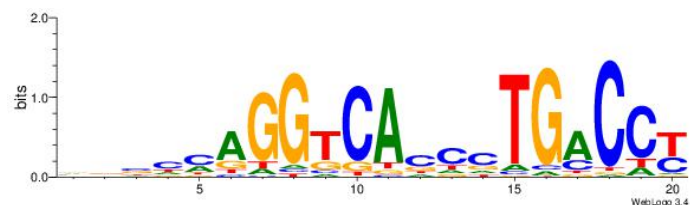


Dataset #: 1
 Motif ID: 3
 Motif name: ESR1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 11
 Similarity score: 0.0486581

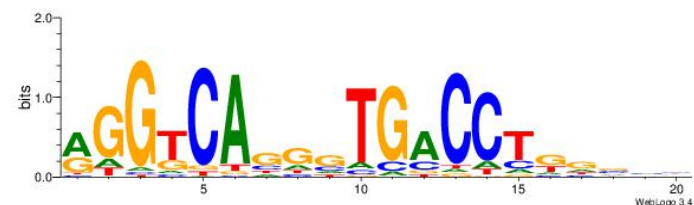
Alignment:

MGGTCAGGGTGACCTRDBHV
 -----CGTGKCCGCGG--

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV

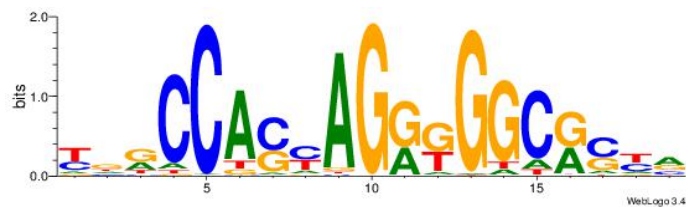


Dataset #: 1
 Motif ID: 16
 Motif name: CTCF
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 8
 Number of overlap: 11
 Similarity score: 0.0588663

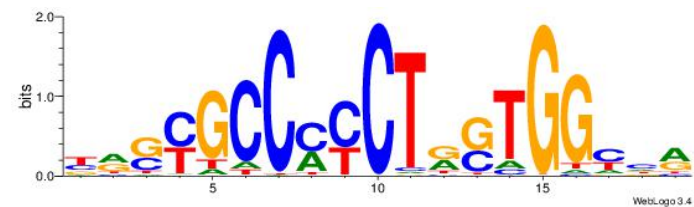
Alignment:

YDRCCASYAGRKGGRSYV
 -----CCGCGGRCACG-

Original motif Consensus sequence: YDRCCASYAGRKGGRSYV



Reverse complement motif Consensus sequence: BMSMGCCYMCTKSTGGMHM

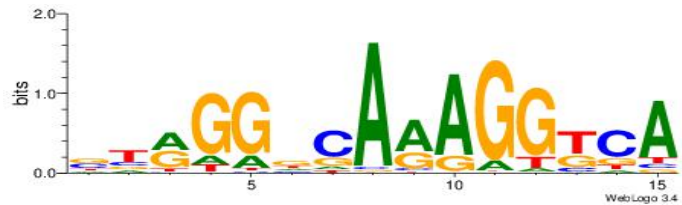


Dataset #: 1
 Motif ID: 14
 Motif name: PPARGRXRA
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2

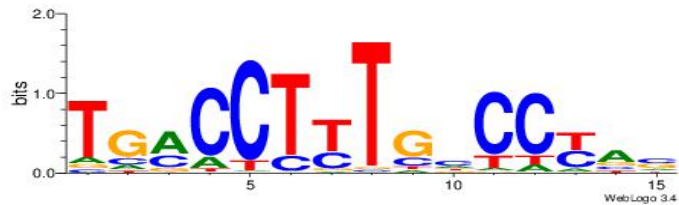
Number of overlap: 11
Similarity score: 0.0629476

Alignment:
TGRCCTKTGHCKAB
---CGTGKCCGCGG-

Original motif Consensus sequence: BTRGGDCARAGGKCA



Reverse complement motif Consensus sequence: TGRCCTKTGHCKAB

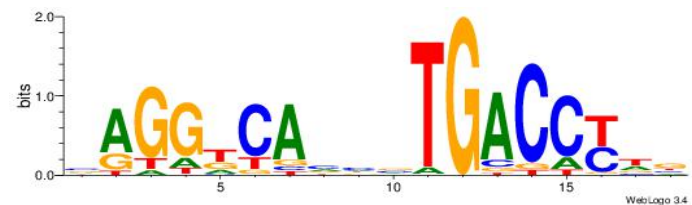
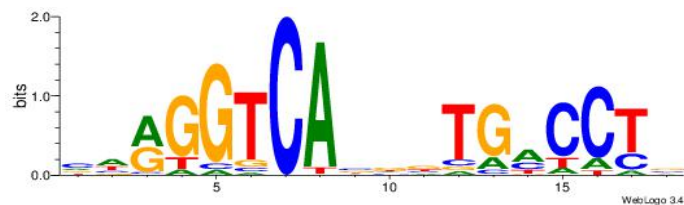


Dataset #: 1
Motif ID: 9
Motif name: ESR2
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 9
Number of overlap: 10
Similarity score: 0.551597

Alignment:
BAGGYCABHBTGACCKHV-
-----CGTGKCCGCGG

Original motif Consensus sequence: VHRGGTCABDBTGMCTB

Reverse complement motif Consensus sequence:
BAGGYCABHBTGACCKHV



Dataset #: 1
 Motif ID: 8
 Motif name: Myc
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 9
 Similarity score: 1.0488

Alignment:

VGCACGTGGH--
 -CGTGKCCGCGG

Original motif Consensus sequence: VGCACGTGGH



Reverse complement motif Consensus sequence: DCCACGTGCV



Dataset #: 1
 Motif ID: 6

Motif name:	Mycn
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	9
Similarity score:	1.04892

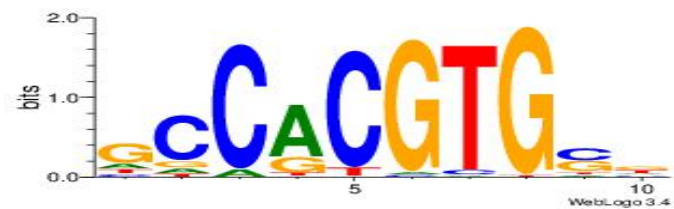
Alignment:

```
HSCACGTGGC--
-CGTGKCCGCGG
```

Original motif Consensus sequence: HSCACGTGGC



Reverse complement motif Consensus sequence: GCCACGTGSD

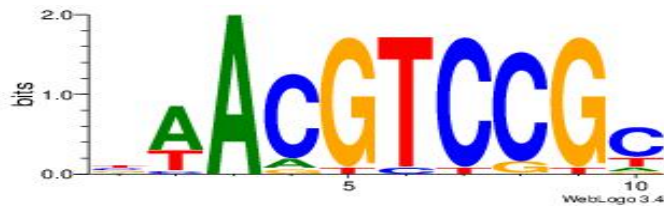


Dataset #:	1
Motif ID:	13
Motif name:	MIZF
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2
Number of overlap:	9
Similarity score:	1.04904

Alignment:

--BAACGTCCGC
CGTGKCCGCGG--

Original motif Consensus sequence: BAACGTCCGC



Reverse complement motif Consensus sequence: GCGGACGTTV



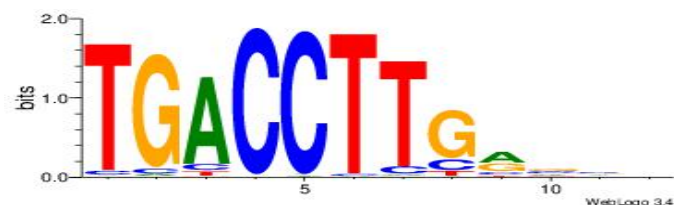
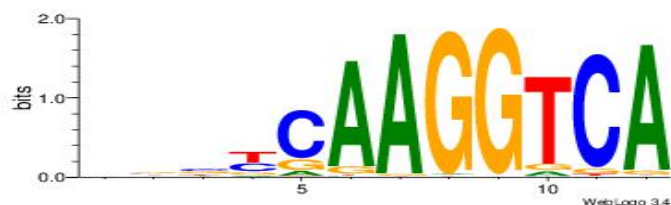
Dataset #:	1
Motif ID:	4
Motif name:	Esrb
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	4
Number of overlap:	9
Similarity score:	1.05291

Alignment:

VBBYCAAGGTCA--
---CCGCGGRCACG

Original motif Consensus sequence: VBBYCAAGGTCA

Reverse complement motif Consensus sequence: TGACCTTGMBBB

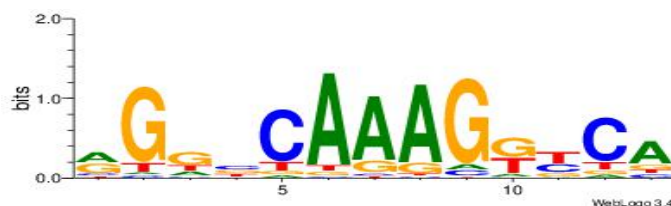


Dataset #: 1
 Motif ID: 1
 Motif name: HNF4A
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 6
 Number of overlap: 8
 Similarity score: 1.55795

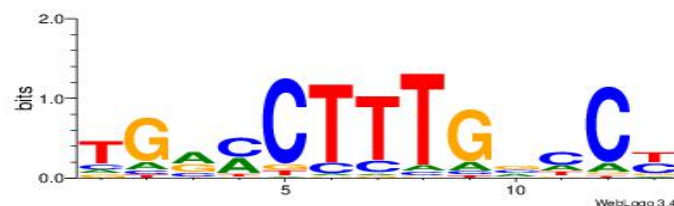
Alignment:

TGM YCTTTGBCK---
 -----CGTGKCCGCGG

Original motif Consensus sequence: RGGBCAAAGKYCA

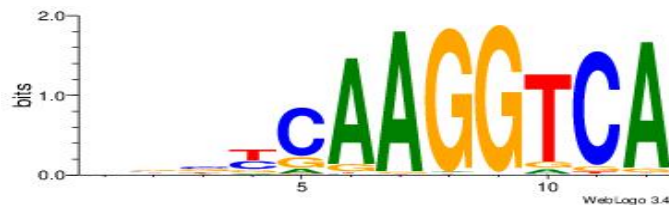


Reverse complement motif Consensus sequence: TGM YCTTTGBCK

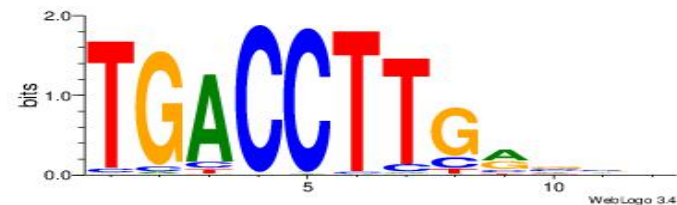


Dataset #: 1 Motif ID: 4 Motif name: Esrrb

Original motif Consensus sequence: VBBYCAAGGTCA



Reverse complement motif Consensus sequence: TGACCTTGMBBB



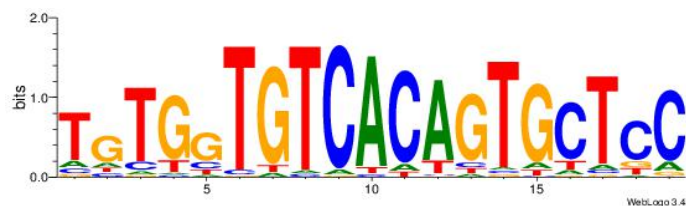
Best Matches for Top Significant Motif ID 4 (Highest to Lowest)

Dataset #: 2
 Motif ID: 17
 Motif name: TgTGgTGTCACAGTGCTCC
 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: 0.0772556

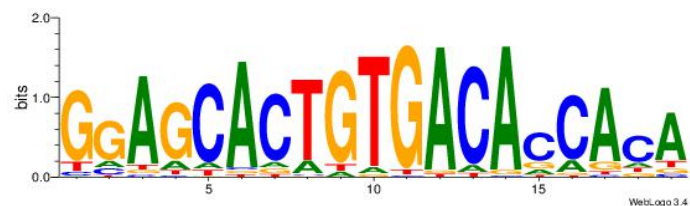
Alignment:

TGTGGTGTTCACAGTGCTCC
 -----TGACCTTGMBBB

Original motif Consensus sequence: TGTGGTGTTCACAGTGCTCC



Reverse complement motif Consensus sequence: GGAGCACTGTGACACCACA

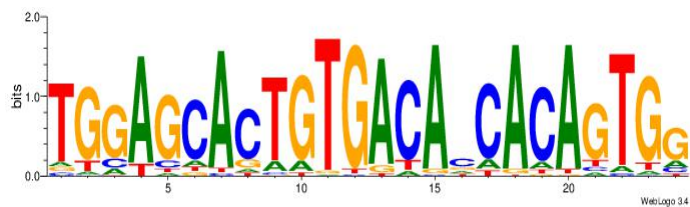


Dataset #: 2
 Motif ID: 23
 Motif name: TGGAGCACTGTGACAcCACAGTGg
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 12
 Number of overlap: 12
 Similarity score: 0.0785385

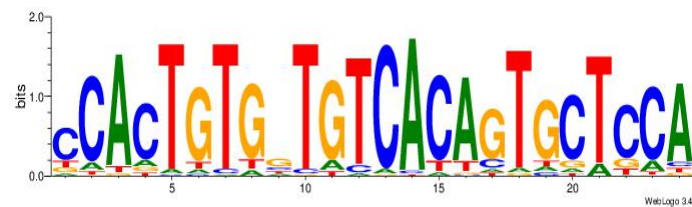
Alignment:

CCACTGTGVTGTCACAGTGCTCCA
 -----TGACCTTGMBBB-

Original motif Consensus sequence: TGGAGCACTGTGACAVCACAGTGG



Reverse complement motif Consensus sequence: CCACTGTGVTGTCACAGTGCTCCA

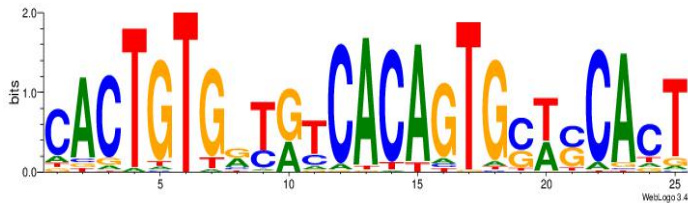


Dataset #: 2
 Motif ID: 22
 Motif name: CACTGTGrYrtCACAGTGswsCAcT
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 11

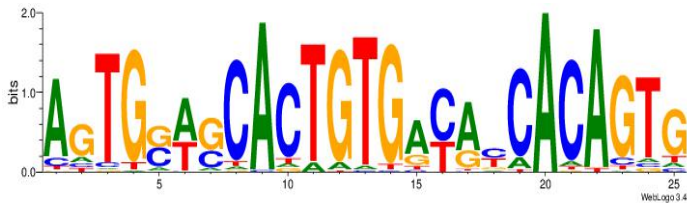
Number of overlap: 12
Similarity score: 0.0832722

Alignment:
AGTGSWSCACTGTGAMAMCACAGTG
---VBBYCAAGGTCA-----

Original motif Consensus sequence:
CACTGTGRTRTCACAGTGSWSCACT



Reverse complement motif Consensus sequence:
AGTGSWSCACTGTGAMAMCACAGTG

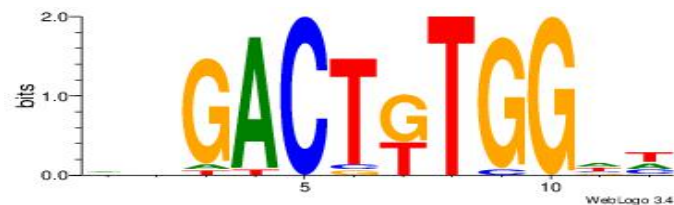
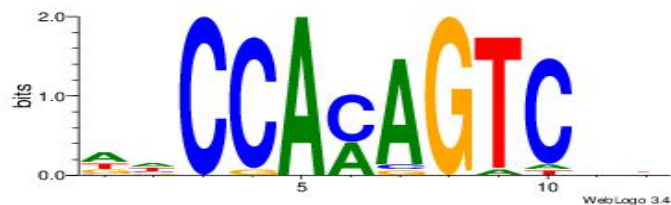


Dataset #: 2
Motif ID: 25
Motif name: wwCCAmAGTCmt
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2
Number of overlap: 11
Similarity score: 0.558919

Alignment:
-DDCCAMAGTCHB
VBBYCAAGGTCA-

Original motif Consensus sequence: DDCCAMAGTCHB

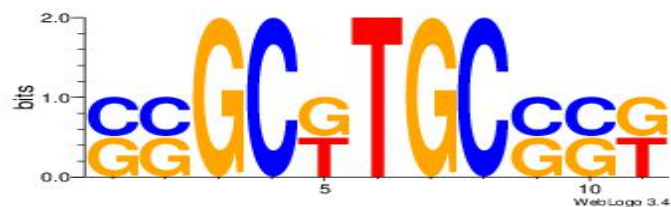
Reverse complement motif Consensus sequence: VDGACTRTGGDD



Dataset #: 2
 Motif ID: 28
 Motif name: ssGCKTGCssk
 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: 0.581406

Alignment:
 -SSGCKTGCSSK
 TGACCTTGMBBB

Original motif Consensus sequence: SSGCKTGCSSK



Reverse complement motif Consensus sequence: YSSGCAYGCSS



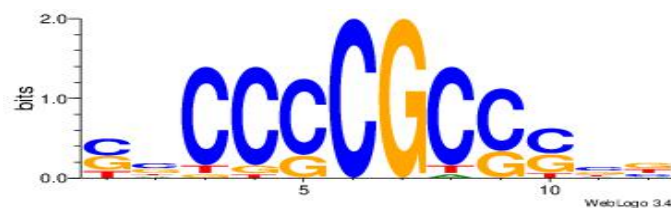
Dataset #: 2
 Motif ID: 24

Motif name: ssCCCCGCSsk
 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: 0.583683

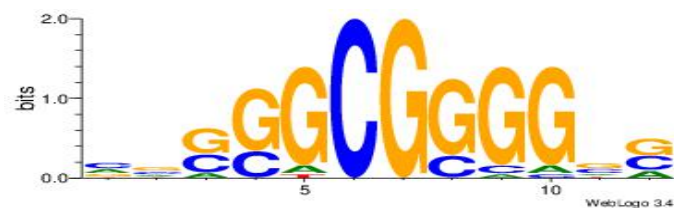
Alignment:

-SBCCCCGCCSBB
 TGACCTTGMBBB-

Original motif Consensus sequence: SBCCCCGCCSBB



Reverse complement motif Consensus sequence: BBSGGCGGGBS

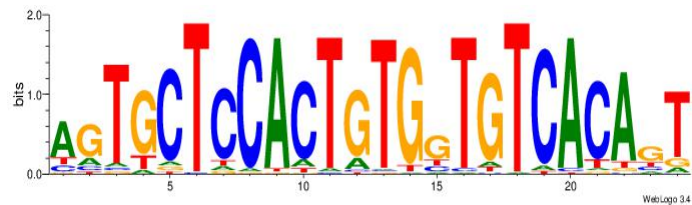


Dataset #: 2
 Motif ID: 27
 Motif name: AgTGCTCCACTGTGgTGTCACAgT
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 15
 Number of overlap: 10
 Similarity score: 1.08683

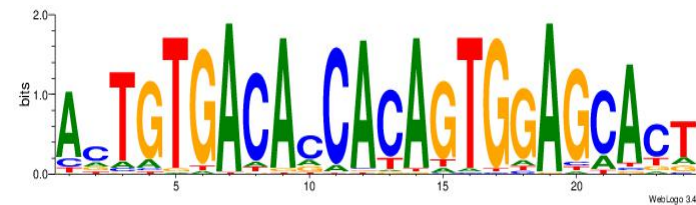
Alignment:

```
AGTGCTCCACTGTGGTGTACAGT--  
-----VBBYCAAGGTCA
```

Original motif Consensus sequence: AGTGCTCCACTGTGGTGTACAGT



Reverse complement motif Consensus sequence: ACTGTGACACCACAGTGGAGCACT



Dataset #:	2
Motif ID:	19
Motif name:	atactttggc
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:	1.08726

Alignment:

```
--GCCAAAGTAT  
VBBYCAAGGTCA
```

Original motif Consensus sequence: ATACTTTGGC

Reverse complement motif Consensus sequence: GCCAAAGTAT



Dataset #: 2
 Motif ID: 29
 Motif name: cCGCGGrCACG
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 9
 Similarity score: 1.57579

Alignment:

---CCGCGGRCACG
 VBBYCAAGGTCA--

Original motif Consensus sequence: CCGCGGRCACG



Reverse complement motif Consensus sequence: CGTGKCCGCGG



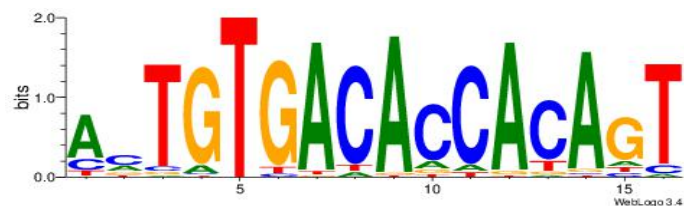
Dataset #: 2
 Motif ID: 21

Motif name: AmTGTGACACCACAGT
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 10
 Number of overlap: 7
 Similarity score: 2.57595

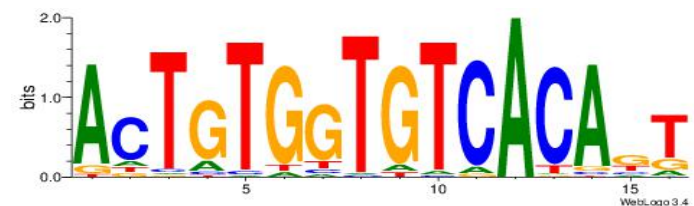
Alignment:

-----AMTGTGACACCACAGT
 VBBYCAAGGTCA-----

Original motif Consensus sequence: AMTGTGACACCACAGT

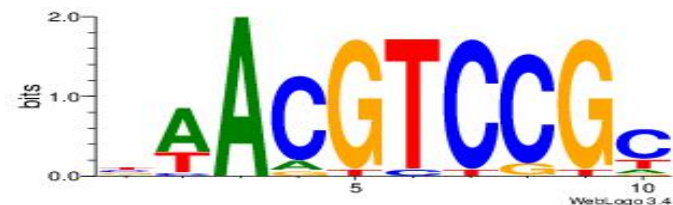


Reverse complement motif Consensus sequence: ACTGTGGTGTCACT



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

Original motif Consensus sequence: BAACGTCCGC



Reverse complement motif Consensus sequence: GCGGACGTTT



Best Matches for Top Significant Motif ID 13 (Highest to Lowest)

Dataset #: 2
 Motif ID: 32
 Motif name: gCGCGCsCgsG
 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: 0.0651598

Alignment:

GCGCGCSCGCG

BAACGTCCGC-

Original motif Consensus sequence: GCGCGCSCGCG



Reverse complement motif Consensus sequence: CGCGSGCGCGC



Dataset #: 2
 Motif ID: 19
 Motif name: atactttggc
 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: 0.0803571

Alignment:

ATACTTTGGC

BAACGTCCGC

Original motif Consensus sequence: ATACTTTGGC



Reverse complement motif Consensus sequence: GCCAAAGTAT



Dataset #: 2
 Motif ID: 29
 Motif name: cCGCGGrCACG
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 9
 Similarity score: 0.560913

Alignment:

CCGCGGrCACG-

--GCGGACGTTV

Original motif Consensus sequence: CCGCGGRCACG



Reverse complement motif Consensus sequence: CGTGKCCGCGG



Dataset #: 2
Motif ID: 31
Motif name: ctatacggacg
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 3
Number of overlap: 9
Similarity score: 0.562302

Alignment:

-CGTCCGTATAG

GCGGACGTTV--

Original motif Consensus sequence: CTATACGGACG



Reverse complement motif Consensus sequence: CGTCCGTATAG

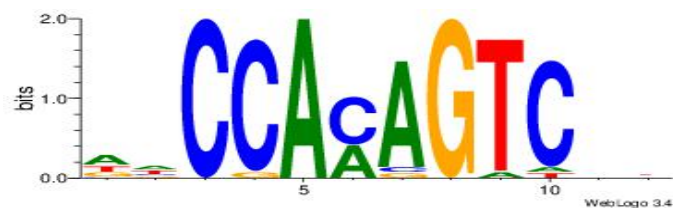


Dataset #: 2
 Motif ID: 25
 Motif name: wwCCAmAGTCmt
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 9
 Similarity score: 0.562428

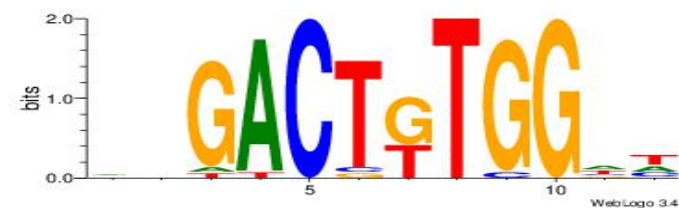
Alignment:

DDCCAMAGTCHB-
 ---BAACGTCCGC

Original motif Consensus sequence: DDCCAMAGTCHB



Reverse complement motif Consensus sequence: VDGACTRTGGDD



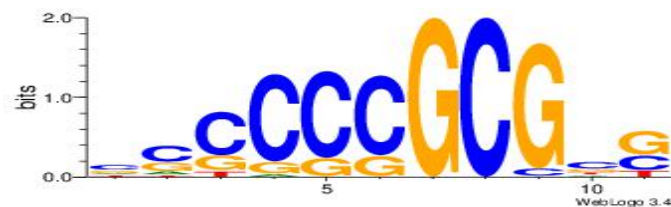
Dataset #: 2
 Motif ID: 18
 Motif name: sscCCCCGCGcs
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 4
 Number of overlap: 8

Similarity score: 1.06446

Alignment:

SBCGCGGGGSB--
---GCGGACGTTV

Original motif Consensus sequence: BSCCCCGCGBS



Reverse complement motif Consensus sequence: SBCGCGGGGSB



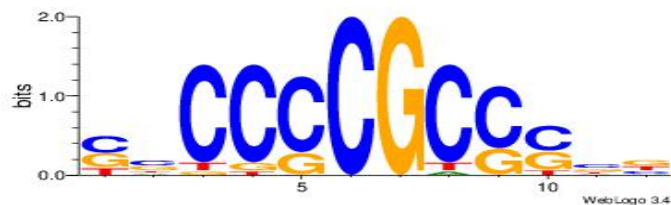
Dataset #: 2
Motif ID: 24
Motif name: ssCCCCGCSsk
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 5
Number of overlap: 8
Similarity score: 1.07197

Alignment:

BBSGGCGGGGBS--
----GCGGACGTTV

Original motif Consensus sequence: SBCCCCGCCSBB

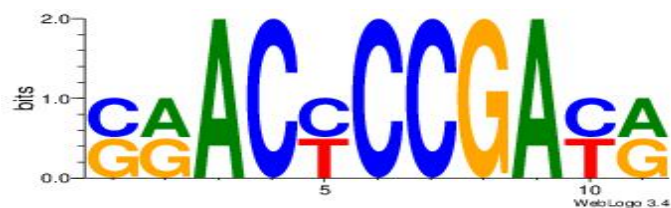
Reverse complement motif Consensus sequence: BBSGGCGGGGBS



Dataset #: 2
 Motif ID: 33
 Motif name: srACyCCGAYr
 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: 1.55

Alignment:
 SRACYCCGAYR---
 ----GCGGACGTTV

Original motif Consensus sequence: SRACYCCGAYR



Reverse complement motif Consensus sequence: KKTCGGKGTKS



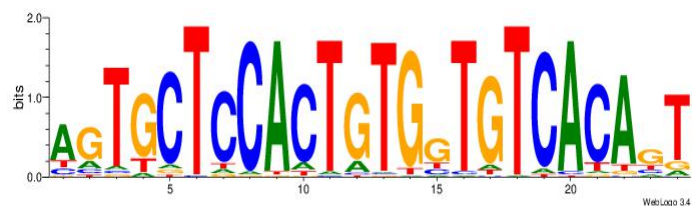
Dataset #: 2
 Motif ID: 27

Motif name: AgTGCTCCACTGTGgTGTCACAgT
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 18
 Number of overlap: 7
 Similarity score: 1.5706

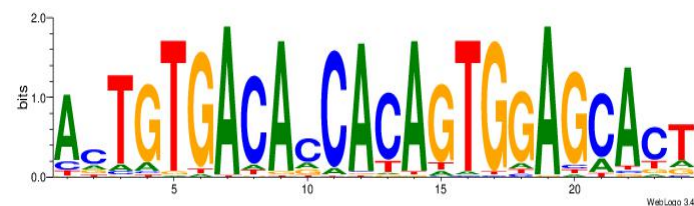
Alignment:

---AGTGCTCCACTGTGGTGTTCACAGT
 BAACGTCCGC-----

Original motif Consensus sequence: AGTGCTCCACTGTGGTGTTCACAGT



Reverse complement motif Consensus sequence: ACTGTGACACCACAGTGGAGCACT

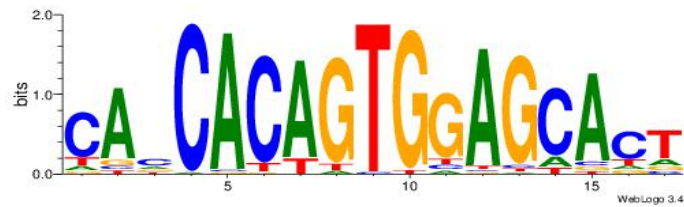


Dataset #: 2
 Motif ID: 26
 Motif name: CACcACAGTGGAGCAct
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 11
 Number of overlap: 7
 Similarity score: 1.57176

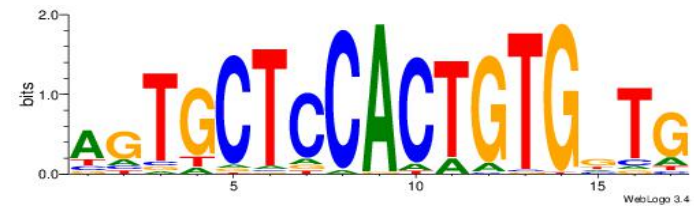
Alignment:

```
CAHCACAGTGGAGCACT---  
-----GCGGACGTTV
```

Original motif Consensus sequence: CAHCACAGTGGAGCACT



Reverse complement motif Consensus sequence:
AGTGCTCCACTGTGDTG



Results created by MOTIFSIM on 11-20-2016 21:11:03

Runtime: 725.149 seconds

MOTIFSIM is written by Ngoc Tam L. Tran

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