



MOTIFSIM - MOTIF SIMilarity Detection Tool

Version 2.0

INPUT

Input Parameters

Number of files:	2
Number of top significant motifs:	10
Number of best matches:	10
Similarity cutoff $\geq$	0.75
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
----------------	----------------------------	--------------------------	----------------------------

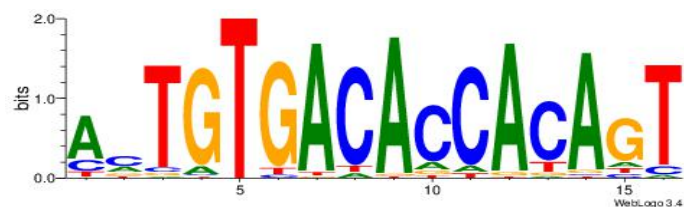


Best Matches for Top Significant Motif ID 5 (Highest to Lowest)

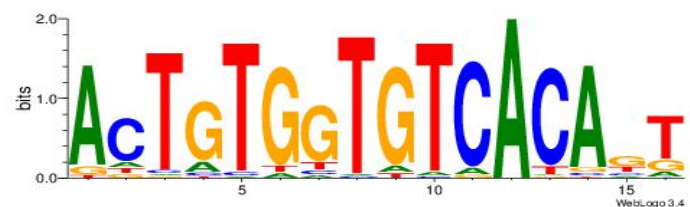
Dataset #: 2
 Motif ID: 21
 Motif name: AmTGTGACACCACAGT
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 4
 Number of overlap: 6
 Similarity score: 0.0349782

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

Original motif Consensus sequence: AMTGTGACACCACAGT



Reverse complement motif Consensus sequence: ACTGTGGTGTCACT

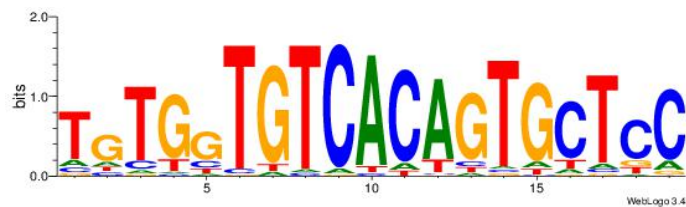


Dataset #: 2
 Motif ID: 17
 Motif name: TgTGgTGTCACAGTGCTCC
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 6
 Similarity score: 0.0362768

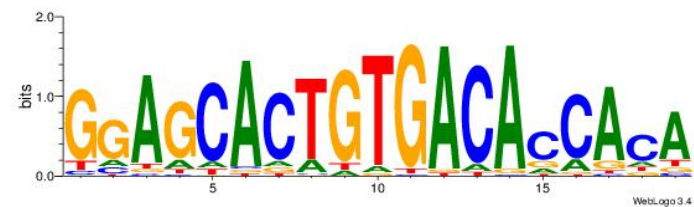
Alignment:

TGTGGTGTCACAGTGCTCC
 -HAGGTG-----

Original motif Consensus sequence: TGTGGTGTCACAGTGCTCC



Reverse complement motif Consensus sequence: GGAGCACTGTGACACCACA

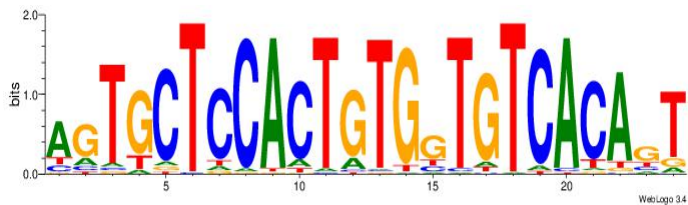


Dataset #: 2
 Motif ID: 27
 Motif name: AgTGCTCCACTGTGgTGTCACAgT
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 12

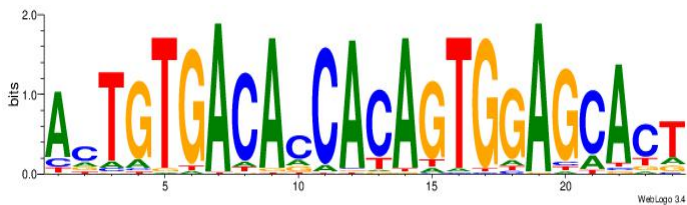
Number of overlap: 6
Similarity score: 0.0409613

Alignment:
AGTGCTCCACTGTGGTGTACAGT
-----HAGGTG-----

Original motif Consensus sequence: AGTGCTCCACTGTGGTGTACAGT



Reverse complement motif Consensus sequence: ACTGTGACACCACAGTGGAGCACT

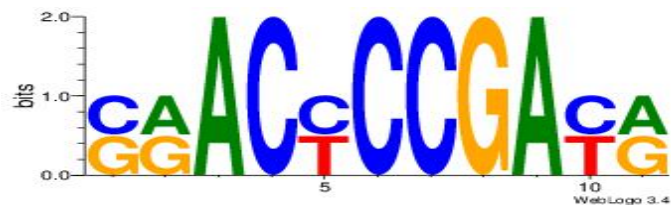


Dataset #: 2
Motif ID: 33
Motif name: srACyCCGAyr
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 3
Number of overlap: 6
Similarity score: 0.0426002

Alignment:
KKTCCGKGTKS
--HAGGTG---

Original motif Consensus sequence: SRACYCCGAYR

Reverse complement motif Consensus sequence: KKTCCGKGTKS

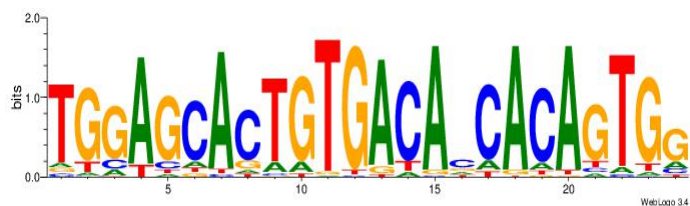


Dataset #: 2
 Motif ID: 23
 Motif name: TGGAGCACTGTGACAcCACAGTGg
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 6
 Number of overlap: 6
 Similarity score: 0.0496179

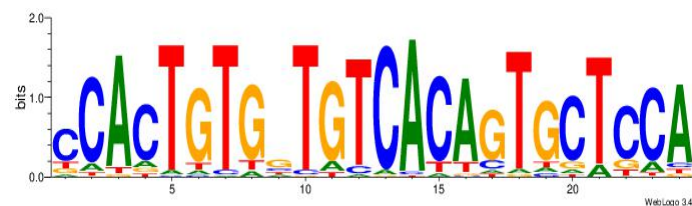
Alignment:

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

Original motif Consensus sequence: TGGAGCACTGTGACAVCACAGTGG



Reverse complement motif Consensus sequence: CCACTGTGVTGTACAGTGCTCCA

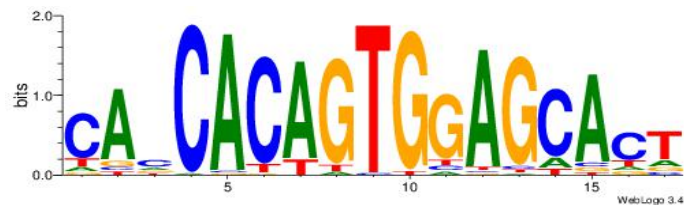


Dataset #: 2

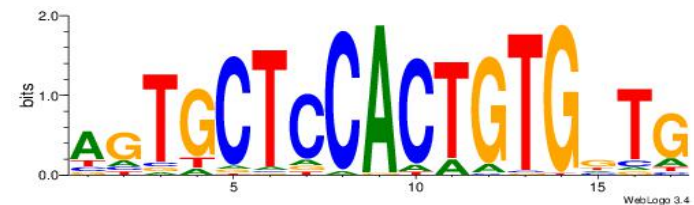
Motif ID: 26
 Motif name: CACcACAGTGGAGCAct
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 6
 Similarity score: 0.0538743

Alignment:
 CAHCACAGTGGAGCACT
 CACCTD-----

Original motif Consensus sequence: CAHCACAGTGGAGCACT



Reverse complement motif Consensus sequence: AGTGCTCCACTGTGDTG

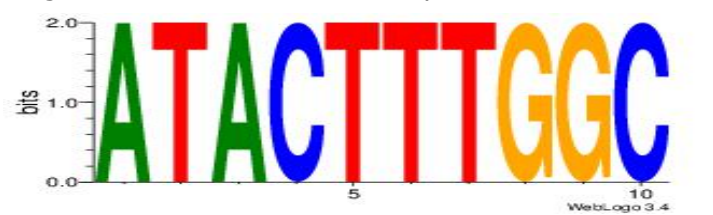


Dataset #: 2
 Motif ID: 19
 Motif name: atactttggc
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 6

Similarity score: 0.0553034

Alignment:
ATACTTTGGC
-CACCTD---

Original motif Consensus sequence: ATACTTTGGC



Reverse complement motif Consensus sequence: GCCAAAGTAT

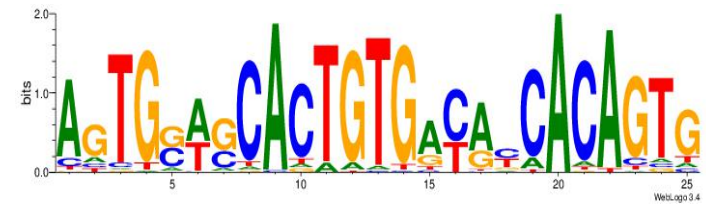
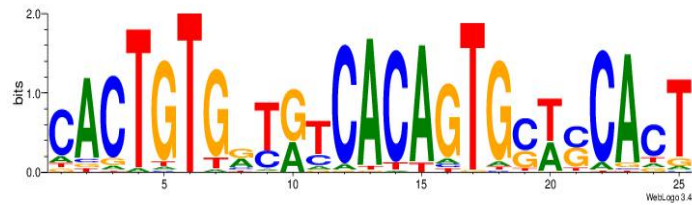


Dataset #: 2
Motif ID: 22
Motif name: CACTGTGrYrtCACAGTGswsCAcT
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 2
Number of overlap: 6
Similarity score: 0.0564649

Alignment:
AGTGSWSCACTGTGAMAMCACAGTG
-----CACCTD-

Original motif Consensus sequence:
CACTGTGRTRTCACAGTGSWSCACT

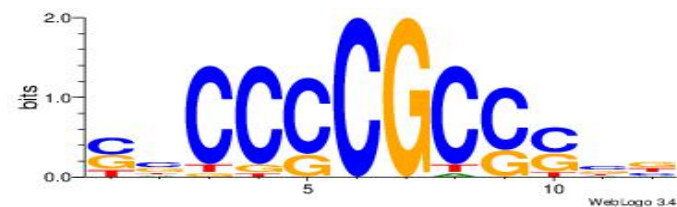
Reverse complement motif Consensus sequence:
AGTGSWSCACTGTGAMAMCACAGTG



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

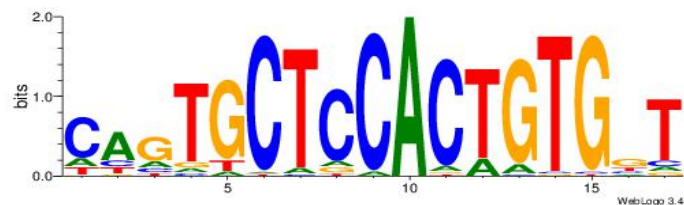


Dataset #: 2
 Motif ID: 20

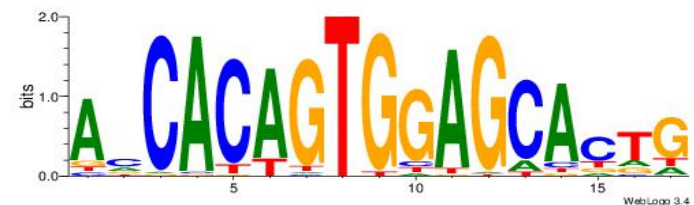
Motif name: CagTGCTCCACTGTGgT
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 8
 Number of overlap: 6
 Similarity score: 0.0594701

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

Original motif Consensus sequence: CAGTGCTCCACTGTGBT



Reverse complement motif Consensus sequence: ABCACAGTGGAGCACTG

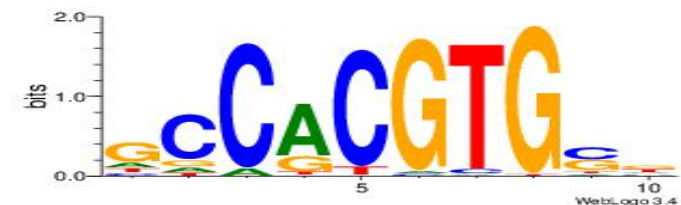


Dataset #: 1 Motif ID: 6 Motif name: Mycn

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

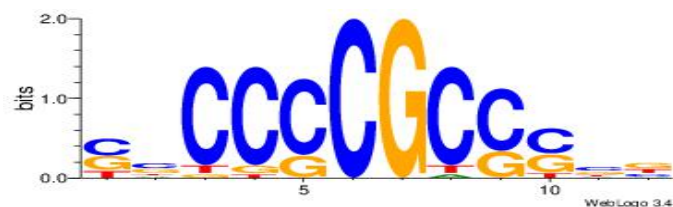


Dataset #: 2
Motif ID: 24
Motif name: ssCCCCGCSsk
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement

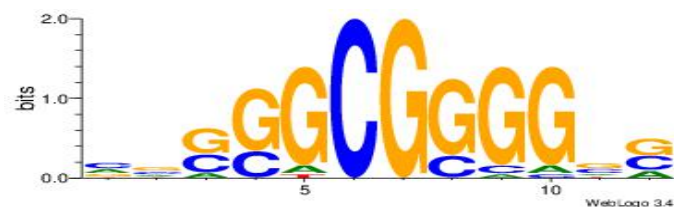
Direction: Forward
 Position number: 2
 Number of overlap: 10
 Similarity score: 0.0704988

Alignment:
 BBSGGCGGGGBS
 -HSCACGTGGC-

Original motif Consensus sequence: SBCCCCGCCSBB



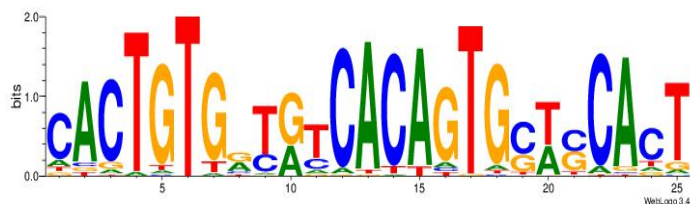
Reverse complement motif Consensus sequence: BBSGGCGGGGBS



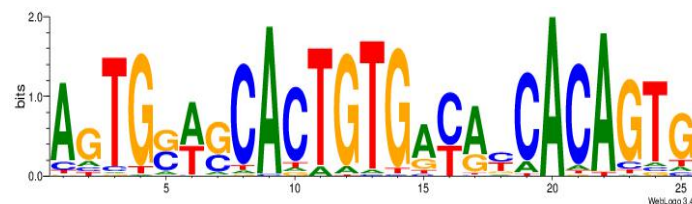
Dataset #: 2
 Motif ID: 22
 Motif name: CACTGTGrYrtCACAGTGswsCAcT
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 10
 Number of overlap: 10
 Similarity score: 0.0883224

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

Original motif Consensus sequence:
CACTGTGRTRTCACAGTGSWSCACT



Reverse complement motif Consensus sequence:
AGTGSWSCACTGTGAMAMCACAGTG

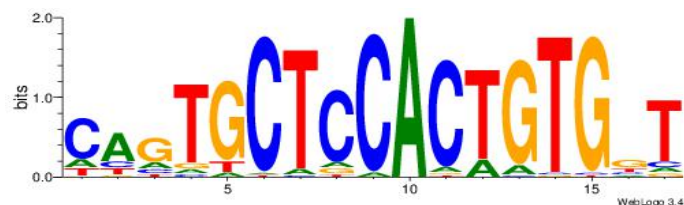


Dataset #: 2
Motif ID: 20
Motif name: CagTGCTCCACTGTGgT
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 7
Number of overlap: 10
Similarity score: 0.0943014

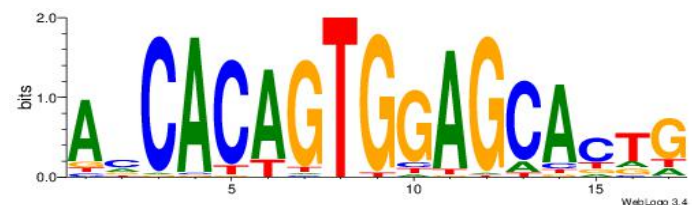
Alignment:

ABCACAGTGGAGCACTG
-GCCACGTGSD-----

Original motif Consensus sequence: CAGTGCTCCACTGTGBT



Reverse complement motif Consensus sequence:
ABCACAGTGGAGCACTG

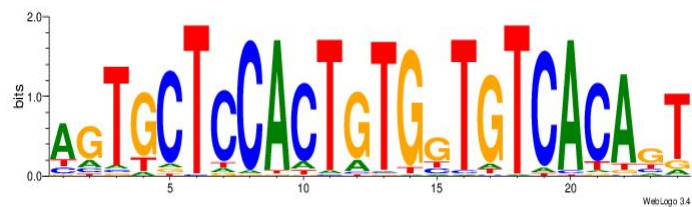


Dataset #: 2
 Motif ID: 27
 Motif name: AgTGCTCCACTGTGgTGTCACAgT
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 6
 Number of overlap: 10
 Similarity score: 0.0949359

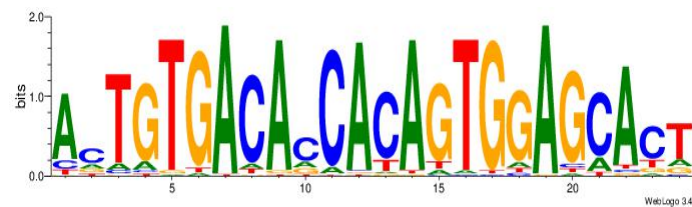
Alignment:

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

Original motif Consensus sequence: AGTGCTCCACTGTGGTGTCAcAGT



Reverse complement motif Consensus sequence: ACTGTGACACCACAGTGGAGCACT



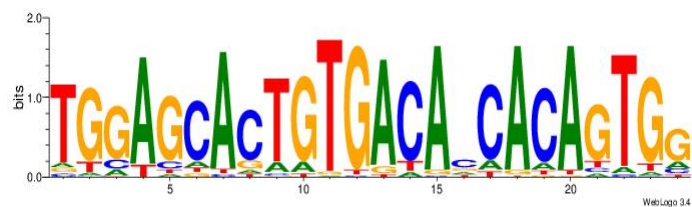
Dataset #: 2
 Motif ID: 23
 Motif name: TGGAGCACTGTGACAcCACAGTGg
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1

Number of overlap: 10
Similarity score: 0.0955115

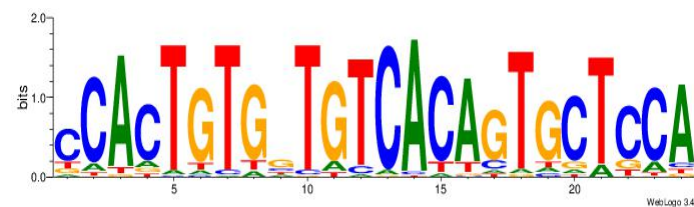
Alignment:

TGGAGCACTGTGACAVCACAGTGG
-----HSCACGTGGC

Original motif Consensus sequence: TGGAGCACTGTGACAVCACAGTGG



Reverse complement motif Consensus sequence: CCACTGTGVTGTCACAGTGCTCCA

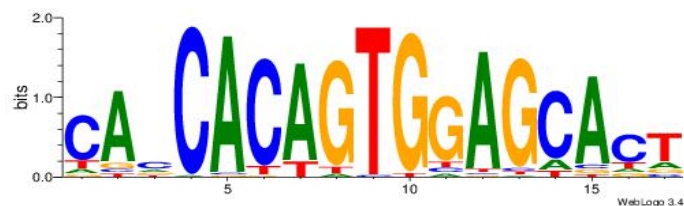


Dataset #: 2
Motif ID: 26
Motif name: CACcACAGTGGAGCAct
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 6
Number of overlap: 10
Similarity score: 0.0959628

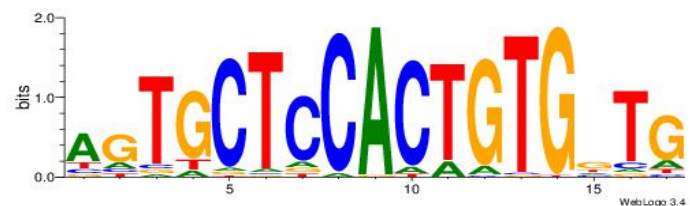
Alignment:

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

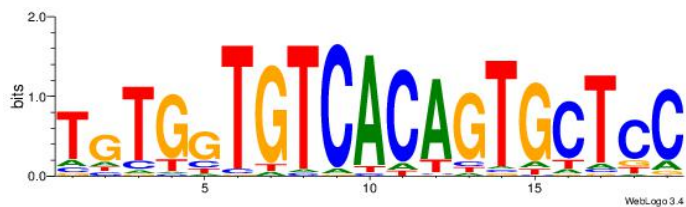


Dataset #: 2
 Motif ID: 17
 Motif name: TgTGgTGTCACAGTGCTCC
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 4
 Number of overlap: 10
 Similarity score: 0.0991692

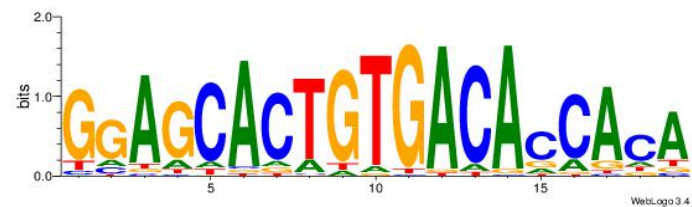
Alignment:

GGAGCACTGTGACACCACA
 ---GCCACGTGSD-----

Original motif Consensus sequence: TGTGGTGTCACAGTGCTCC



Reverse complement motif Consensus sequence: GGAGCACTGTGACACCACA

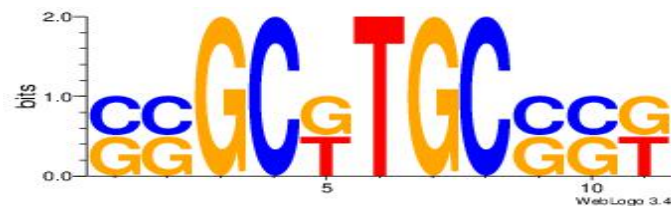


Dataset #: 2
 Motif ID: 28
 Motif name: ssGCKTGCssk
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1

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: sscCCCCGCGcs
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



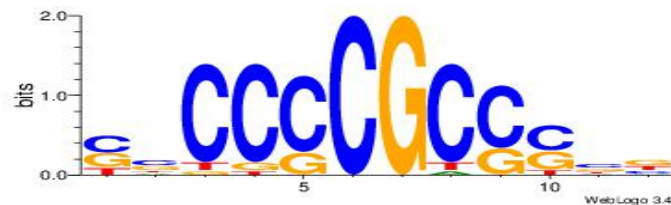
Dataset #: 2
 Motif ID: 24
 Motif name: ssCCCCGCSsk
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 10
 Similarity score: 0.0728588

Alignment:

SBCCCCGCCSBB

-DCCACGTGCV-

Original motif Consensus sequence: SBCCCCGCCSBB



Reverse complement motif Consensus sequence: BBSGGCGGGGBS

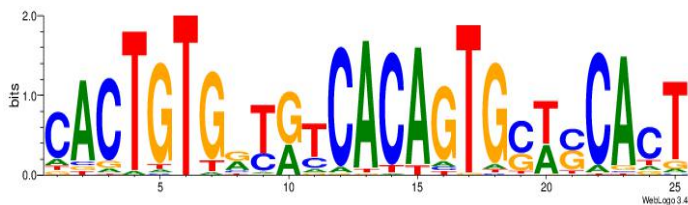


Dataset #: 2
 Motif ID: 22
 Motif name: CACTGTGrYrtCACAGTGswsCACT
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 6
 Number of overlap: 10
 Similarity score: 0.0888909

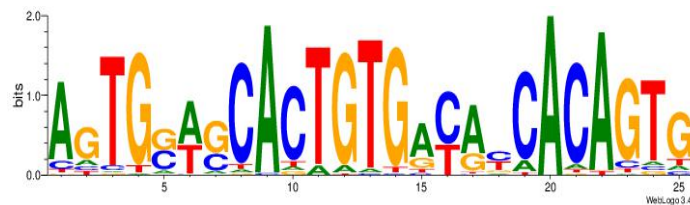
Alignment:

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

Original motif Consensus sequence:
 CACTGTGRTRTCACAGTGSWSCACT



Reverse complement motif Consensus sequence:
 AGTGSWSCACTGTGAMAMCACAGTG

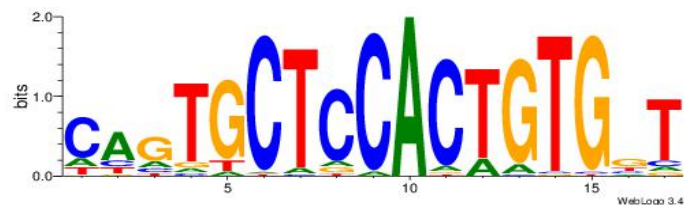


Dataset #: 2
 Motif ID: 20
 Motif name: CagTGCTCCACTGTGgT
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 7
 Number of overlap: 10
 Similarity score: 0.0955234

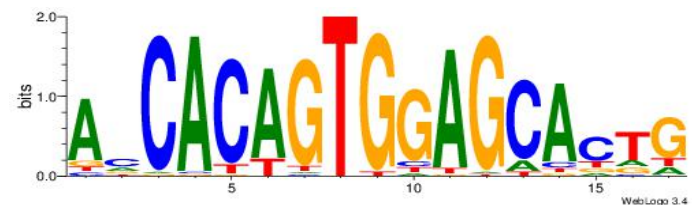
Alignment:

ABCACAGTGGAGCACTG
 -DCCACGTGCV-----

Original motif Consensus sequence: CAGTGCTCCACTGTGBT



Reverse complement motif Consensus sequence: ABCACAGTGGAGCACTG

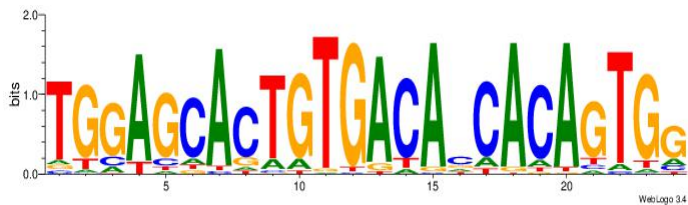


Dataset #: 2
 Motif ID: 23
 Motif name: TGGAGCACTGTGACAcCACAGTGg
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 11

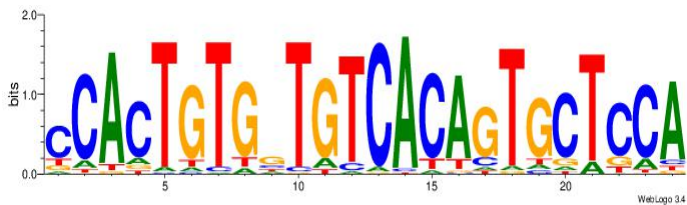
Number of overlap: 10
Similarity score: 0.0971125

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

Original motif Consensus sequence: TGGAGCACTGTGACAVCACAGTGG



Reverse complement motif Consensus sequence: CCACTGTGVTGTACAGTGCTCCA

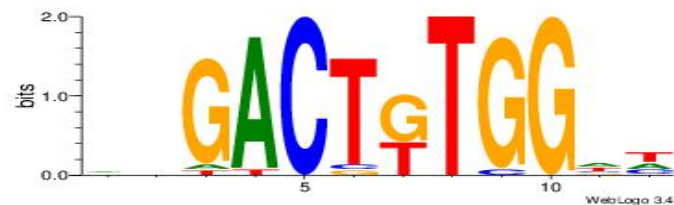
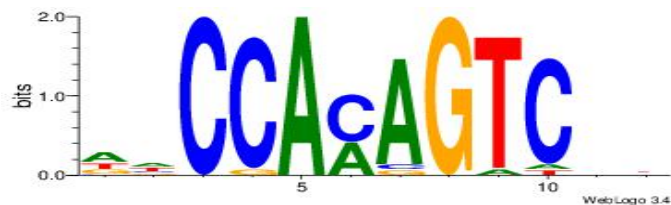


Dataset #: 2
Motif ID: 25
Motif name: wwCCAmAGTCmt
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 2
Number of overlap: 10
Similarity score: 0.0974038

Alignment:
VDGACTRTGGDD
-VGCACGTGGH-

Original motif Consensus sequence: DDCCAMAGTCHB

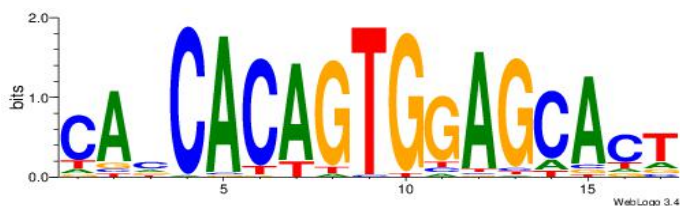
Reverse complement motif Consensus sequence: VDGACTRTGGDD



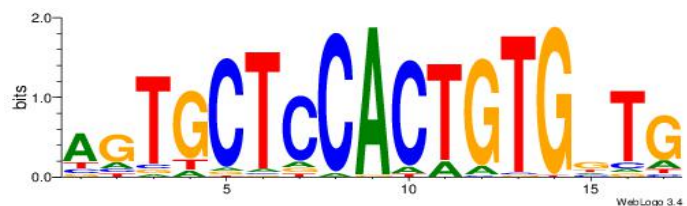
Dataset #: 2
 Motif ID: 26
 Motif name: CACcACAGTGGAGCAct
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 10
 Similarity score: 0.0979703

Alignment:
 CAHCACAGTGGAGCACT
 --DCCACGTGCV-----

Original motif Consensus sequence: CAHCACAGTGGAGCACT



Reverse complement motif Consensus sequence: AGTGCTCCACTGTGDTG



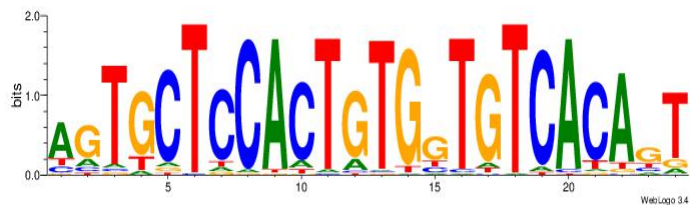
Dataset #: 2

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

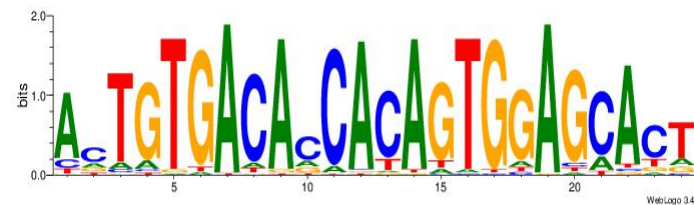
Alignment:

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

Original motif Consensus sequence: AGTGCTCCACTGTGGTGTCAAGT



Reverse complement motif Consensus sequence: ACTGTGACACCACAGTGGAGCACT

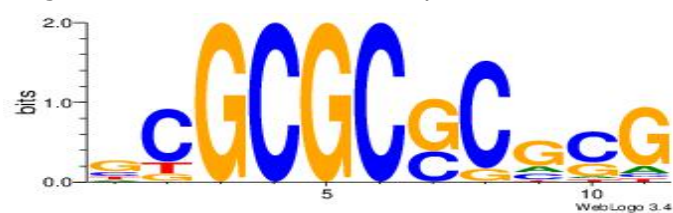


Dataset #: 2
 Motif ID: 32
 Motif name: gCGCGCsCgsG
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 10

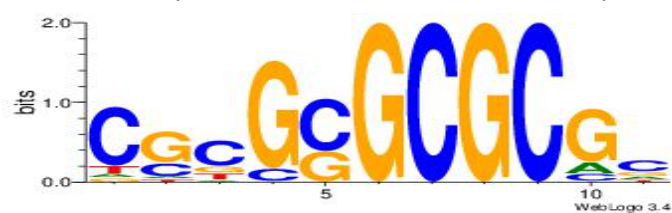
Similarity score: 0.0989125

Alignment:
CGCGSGCGCGC
VGCACGTGGH-

Original motif Consensus sequence: GCGCGCSCGCG



Reverse complement motif Consensus sequence: CGCGSGCGCGC

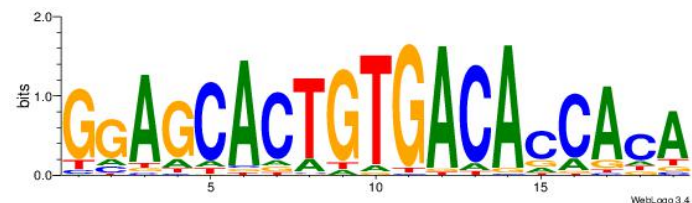
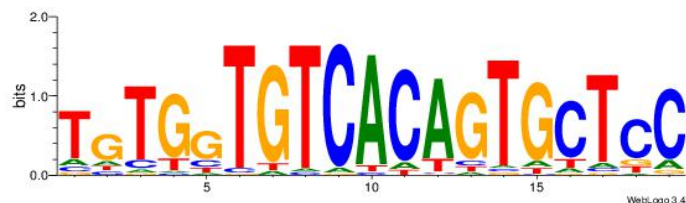


Dataset #: 2
Motif ID: 17
Motif name: TgTGgTGTCACAGTGCTCC
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 7
Number of overlap: 10
Similarity score: 0.0993196

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



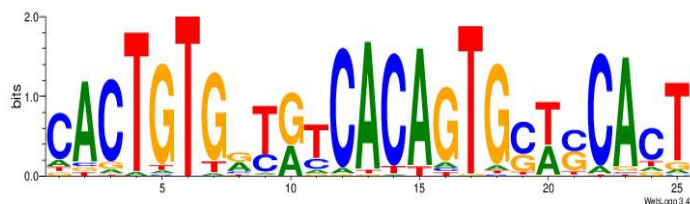
Best Matches for Top Significant Motif ID 11 (Highest to Lowest)

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

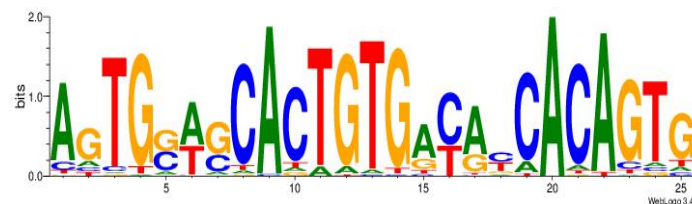
Alignment:

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

Original motif Consensus sequence:
CACTGTGRTRTCACAGTGSWSCACT



Reverse complement motif Consensus sequence:
AGTGSWSCACTGTGAMAMCACAGTG

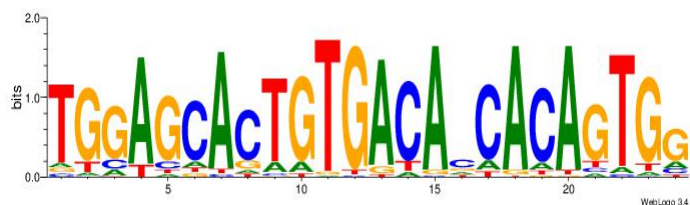


Dataset #: 2
Motif ID: 23
Motif name: TGGAGCACTGTGACAcCACAGTGg
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 8
Number of overlap: 8
Similarity score: 0.060729

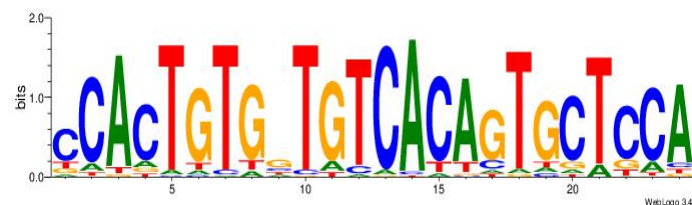
Alignment:

CCACTGTGVTGTTCACAGTGCTCCA
-----AAGGTCAC-----

Original motif Consensus sequence: TGGAGCACTGTGACAVCACAGTGG



Reverse complement motif Consensus sequence:
CCACTGTGVTGTTCACAGTGCTCCA

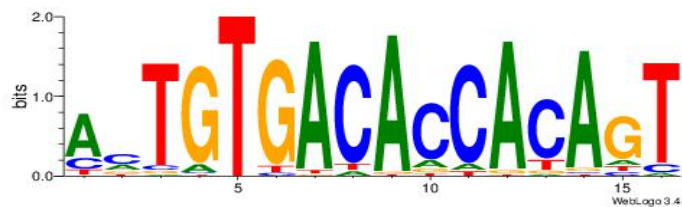


Dataset #: 2
 Motif ID: 21
 Motif name: AmTGTGACACCACAGT
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 4
 Number of overlap: 8
 Similarity score: 0.0645146

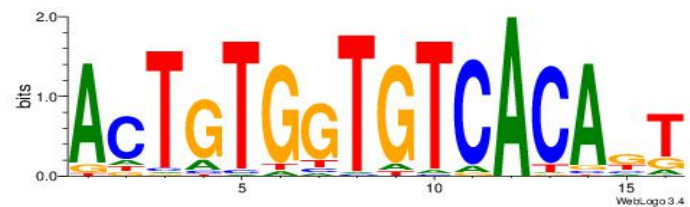
Alignment:

ACTGTGGTGTACART
 -----AAGGTCAC---

Original motif Consensus sequence: AMTGTGACACCACAGT



Reverse complement motif Consensus sequence: ACTGTGGTGTACART



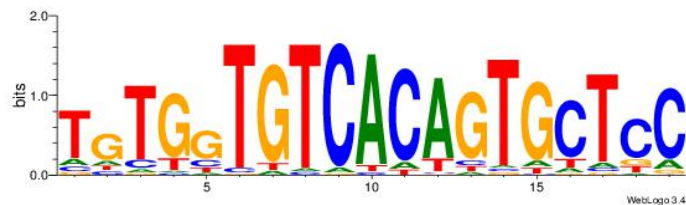
Dataset #: 2
 Motif ID: 17
 Motif name: TgTGgTGTCACAGTGCTCC
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 9

Number of overlap: 8
Similarity score: 0.0695512

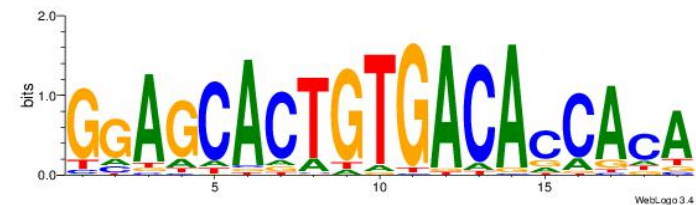
Alignment:

TGTGGTGTACAGTGCTCC
---AAGGTCAC-----

Original motif Consensus sequence: TGTGGTGTACAGTGCTCC



Reverse complement motif Consensus sequence:
GGAGCACTGTGACACCACA

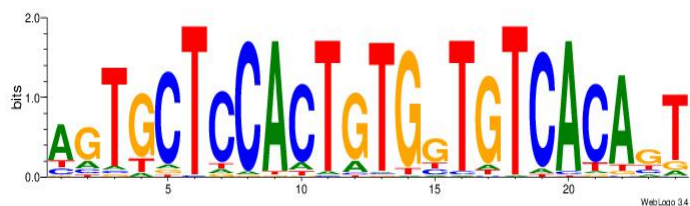


Dataset #: 2
Motif ID: 27
Motif name: AgTGCTCCACTGTGgTGTCACAgT
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 4
Number of overlap: 8
Similarity score: 0.0709831

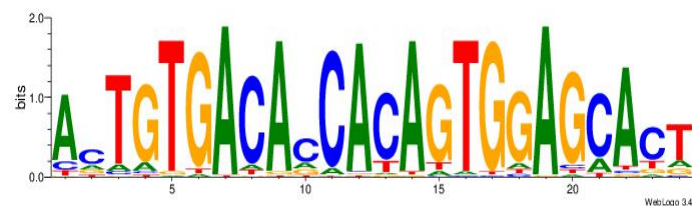
Alignment:

AGTGCTCCACTGTGGTGTACAGT
-----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

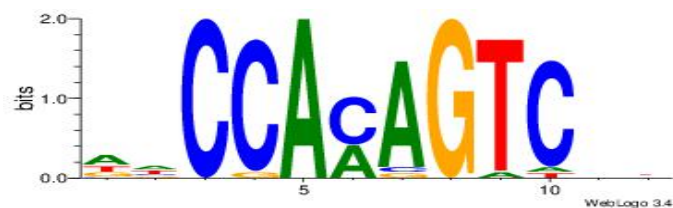


Dataset #: 2
 Motif ID: 25
 Motif name: wwCCAmAGTCmt
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 5
 Number of overlap: 8
 Similarity score: 0.0788401

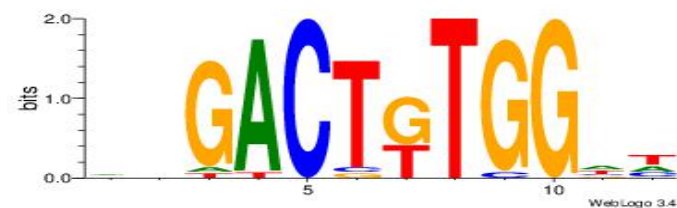
Alignment:

DDCCAMAGTCHB
 ----AAGGTCAC

Original motif Consensus sequence: DDCCAMAGTCHB



Reverse complement motif Consensus sequence: VDGACTRTGGDD

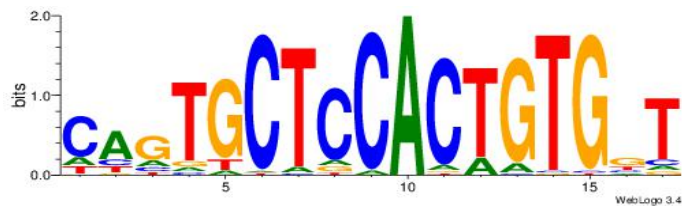


Dataset #: 2
 Motif ID: 20
 Motif name: CagTGCTCCACTGTGgT
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 10
 Number of overlap: 8

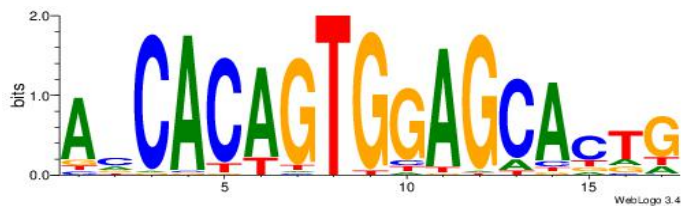
Similarity score: 0.0864039

Alignment:
ABCACAGTGGAGCACTG
-----GTGACCTT

Original motif Consensus sequence: CAGTGCTCCACTGTGBT



Reverse complement motif Consensus sequence:
ABCACAGTGGAGCACTG

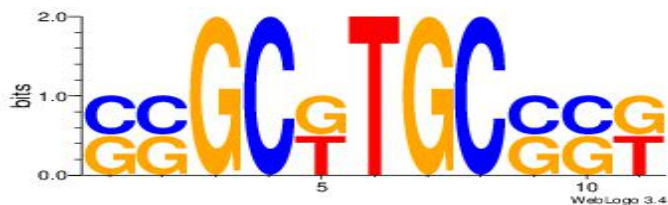


Dataset #: 2
Motif ID: 28
Motif name: ssGCKTGCssk
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 5
Number of overlap: 7
Similarity score: 0.568556

Alignment:
SSGCKTGCSSK-
----GTGACCTT

Original motif Consensus sequence: SSGCKTGCSSK

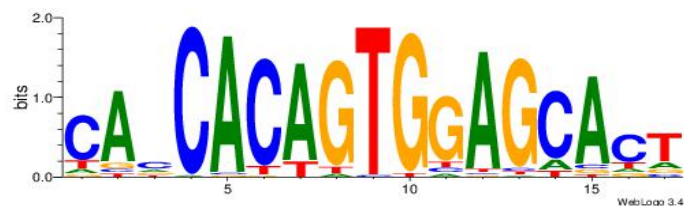
Reverse complement motif Consensus sequence: YSSGCAYGCSS



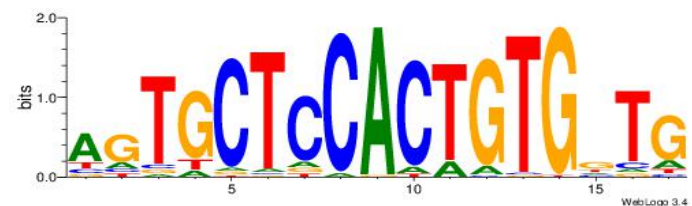
Dataset #: 2
 Motif ID: 26
 Motif name: CACcACAGTGGAGCAct
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 11
 Number of overlap: 7
 Similarity score: 0.581814

Alignment:
 CAHCACAGTGGAGCACT-
 -----GTGACCTT

Original motif Consensus sequence: CAHCACAGTGGAGCACT

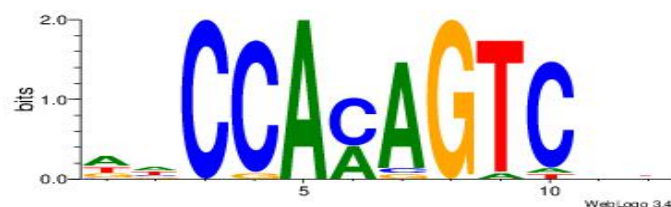


Reverse complement motif Consensus sequence: AGTGCTCCACTGTGDTG

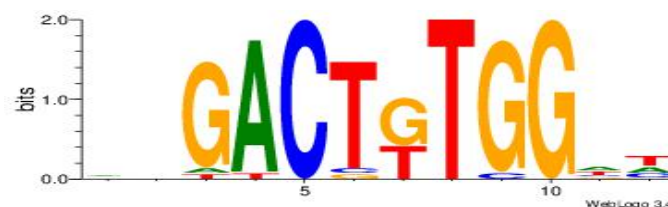


Dataset #: 2 Motif ID: 25 Motif name: wwCCAmAGTCmt

Original motif Consensus sequence: DDCCAMAGTCHB



Reverse complement motif Consensus sequence: VDGACTRTGGDD



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

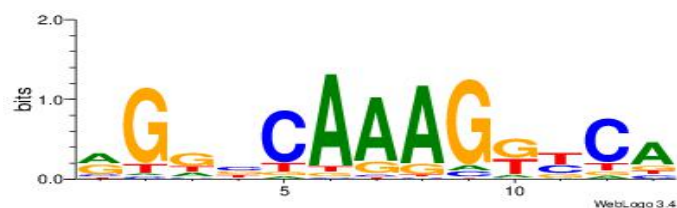
Dataset #:	1
Motif ID:	1
Motif name:	HNF4A
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	12
Similarity score:	0.032442

Alignment:

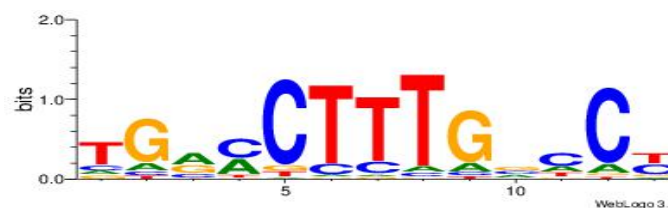
RGGBCAAAGKYCA

-DDCCAMAGTCHB

Original motif Consensus sequence: RGGBCAAAGKYCA



Reverse complement motif Consensus sequence: TGM YCTTTGBCCK

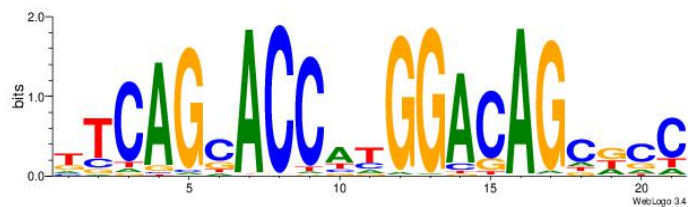


Dataset #: 1
 Motif ID: 7
 Motif name: REST
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 4
 Number of overlap: 12
 Similarity score: 0.0391228

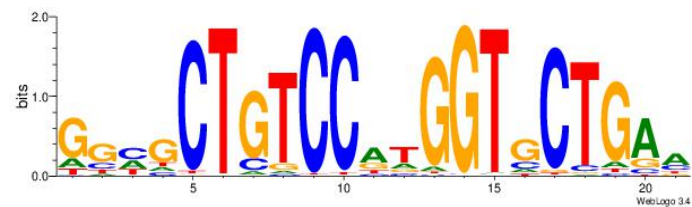
Alignment:

GYGCTGTCCATGGTGCTGAA
 ---DDCCAMAGTCHB-----

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC



Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA

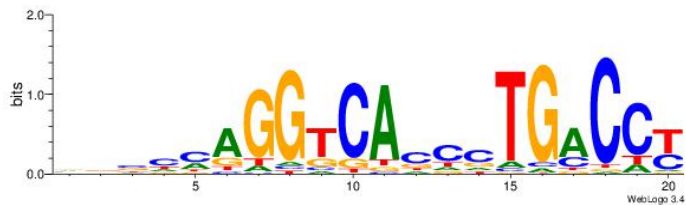


Dataset #: 1
 Motif ID: 3
 Motif name: ESR1
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1

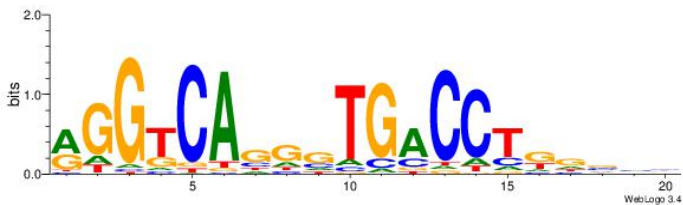
Number of overlap: 12
Similarity score: 0.0407304

Alignment:
VDBHMAGGTCACCCTGACCY
DDCCAMAGTCHB-----

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



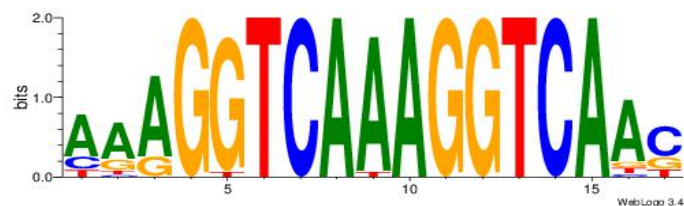
Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV



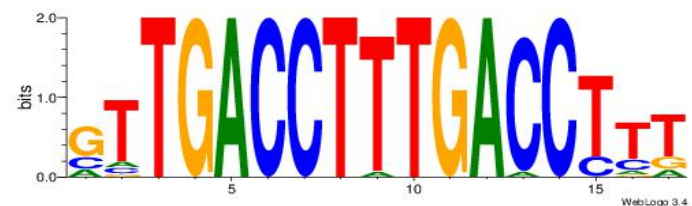
Dataset #: 1
Motif ID: 10
Motif name: NR1H2RXRA
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2
Number of overlap: 12
Similarity score: 0.0463384

Alignment:
AAAGGTCAAAGGTCAAC
----DDCCAMAGTCHB--

Original motif Consensus sequence: AAAGGTCAAAGGTCAAC



Reverse complement motif Consensus sequence: GTTGACCTTTGACCTT

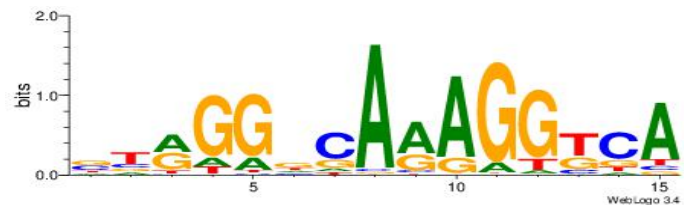


Dataset #: 1
Motif ID: 14
Motif name: PPARGRXRA
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 3
Number of overlap: 12
Similarity score: 0.0480406

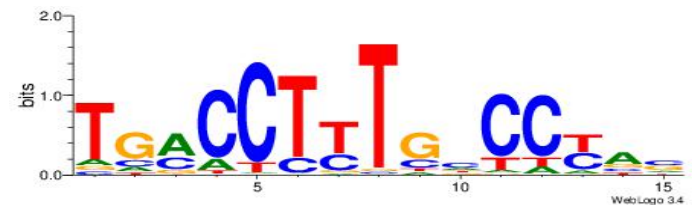
Alignment:

TGRCCTKTGHCKAB
--DDCCAMAGTCHB--

Original motif Consensus sequence: BTRGGDCARAGGKCA



Reverse complement motif Consensus sequence: TGRCCCTKTGHCKA

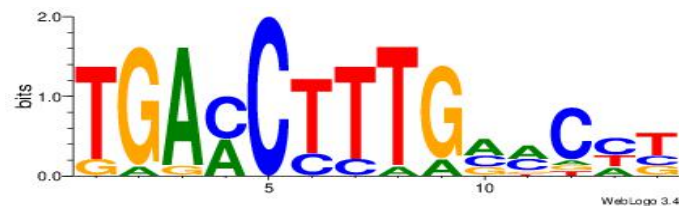


Dataset #: 1
 Motif ID: 2
 Motif name: NR2F1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 12
 Similarity score: 0.0506507

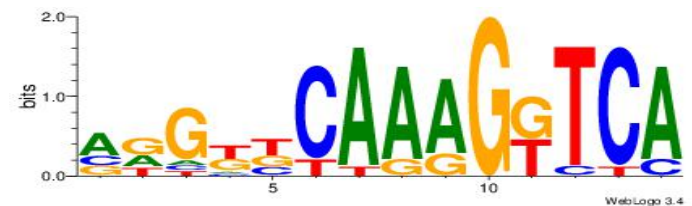
Alignment:

TGAMCTTTGMMCYT
 --VDGACTRTGGDD

Original motif Consensus sequence: TGAMCTTTGMMCYT



Reverse complement motif Consensus sequence: AKGYCAAAGRTC

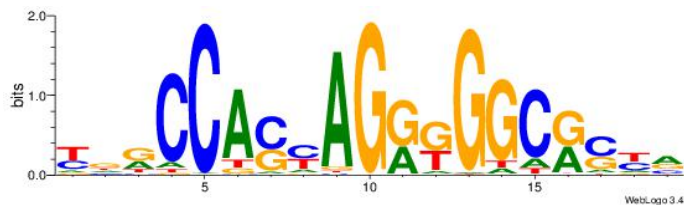


Dataset #: 1
 Motif ID: 16
 Motif name: CTCF
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 8
 Number of overlap: 12

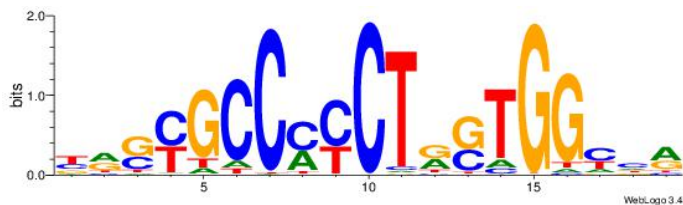
Similarity score: 0.0523578

Alignment:
BMSMGCCYMCTKSTGGMHM
DDCCAMAGTCHB-----

Original motif Consensus sequence: YDRCCASYAGRKGGCRSYV



Reverse complement motif Consensus sequence:
BMSMGCCYMCTKSTGGMHM

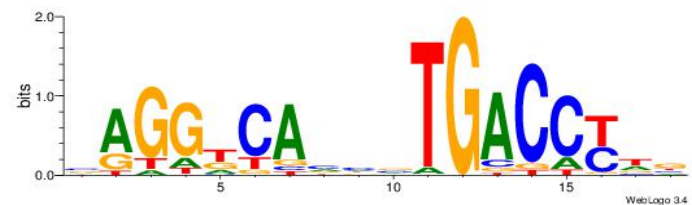
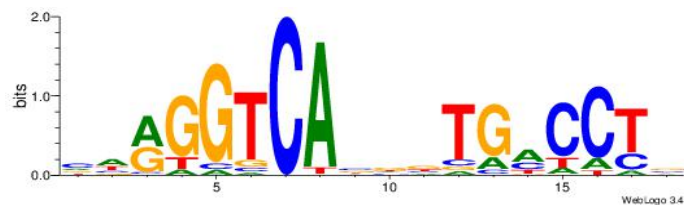


Dataset #: 1
Motif ID: 9
Motif name: ESR2
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 4
Number of overlap: 12
Similarity score: 0.0576723

Alignment:
VHRGGTCABDBTGMCTB
---DDCCAMAGTCHB---

Original motif Consensus sequence: VHRGGTCABDBTGMCTB

Reverse complement motif Consensus sequence:
BAGGYCABHBTGACCKHV

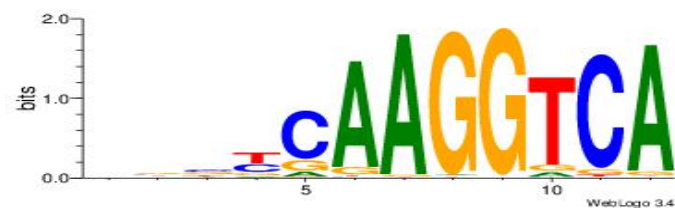


Dataset #: 1
 Motif ID: 4
 Motif name: Esrrb
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 11
 Similarity score: 0.525631

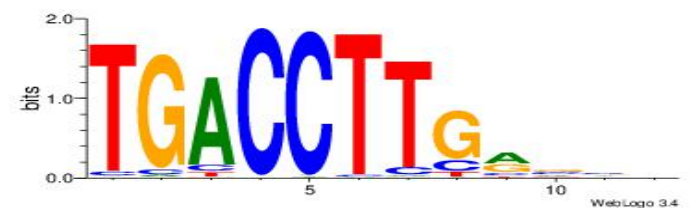
Alignment:

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
 VDGACTRGTGGDD

Original motif Consensus sequence: VGCACGTGGH

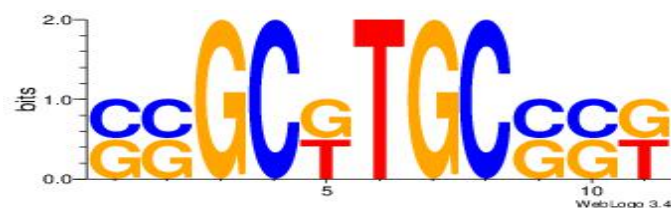


Reverse complement motif Consensus sequence: DCCACGTGCV



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

Original motif Consensus sequence: SSGCKTGCSSK



Reverse complement motif Consensus sequence: YSSGCAYGCSS



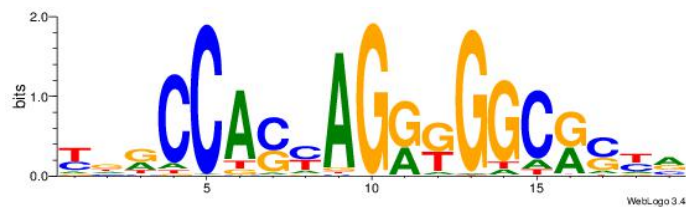
Best Matches for Top Significant Motif ID 28 (Highest to Lowest)

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

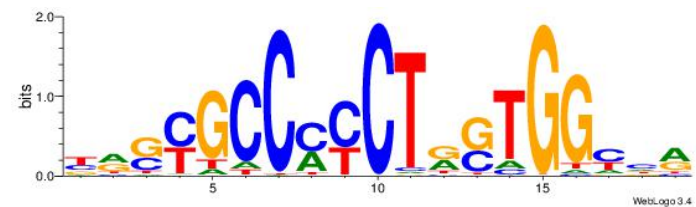
Alignment:

YDRCCASYAGRKGGRSYV
 -----SSGCKTGCSSK-

Original motif Consensus sequence: YDRCCASYAGRKGGRSYV



Reverse complement motif Consensus sequence: BMSGCCYMCTKSTGGMHM

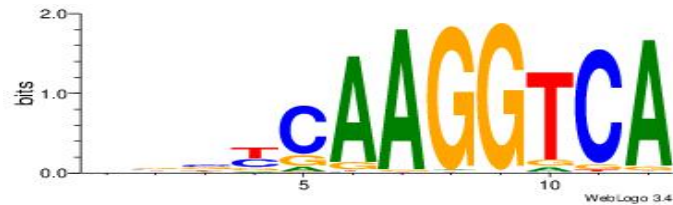


Dataset #: 1
 Motif ID: 4
 Motif name: Esrrb
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2

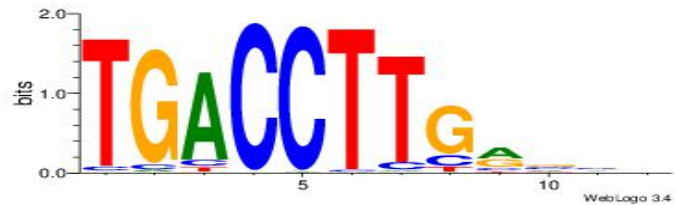
Number of overlap: 11
Similarity score: 0.0358701

Alignment:
VBBYCAAGGTCA
-YSSGCAYGCSS

Original motif Consensus sequence: VBBYCAAGGTCA



Reverse complement motif Consensus sequence: TGACCTTGMBBB

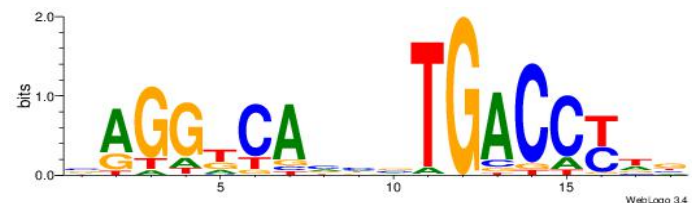
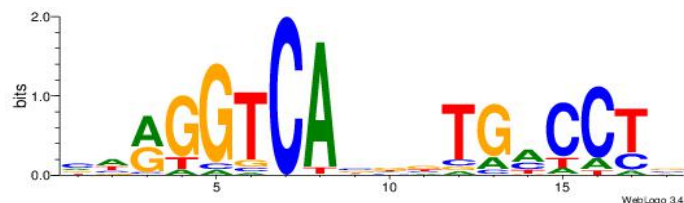


Dataset #: 1
Motif ID: 9
Motif name: ESR2
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 3
Number of overlap: 11
Similarity score: 0.0379074

Alignment:
VHRGGTCABDBTGMCTB
-----YSSGCAYGCSS--

Original motif Consensus sequence: VHRGGTCABDBTGMCTB

Reverse complement motif Consensus sequence:
BAGGYCABHBTGACCKHV

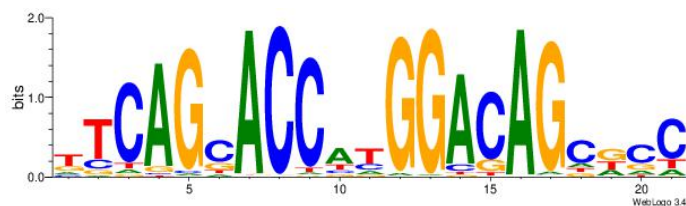


Dataset #: 1
 Motif ID: 7
 Motif name: REST
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 10
 Number of overlap: 11
 Similarity score: 0.0409322

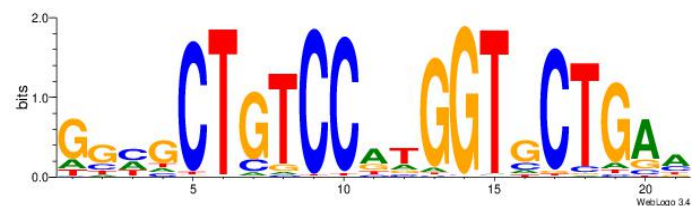
Alignment:

TTCAGCACCATGGACAGCKCC
 -YSSGCAYGCSS-----

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC



Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA



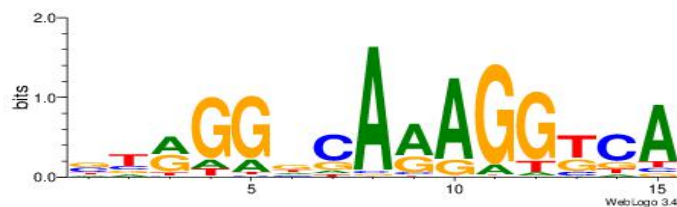
Dataset #: 1

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

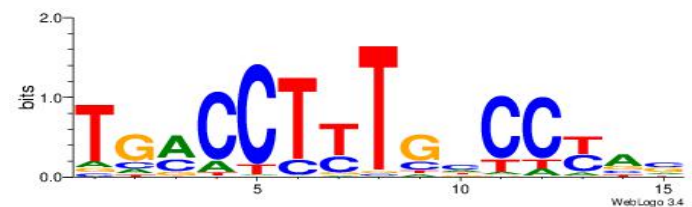
Alignment:

BTRGGDCARAGGKCA
 --YSSGCAYGCSS--

Original motif Consensus sequence: BTRGGDCARAGGKCA



Reverse complement motif Consensus sequence: TGRCCCTKTGHCCK

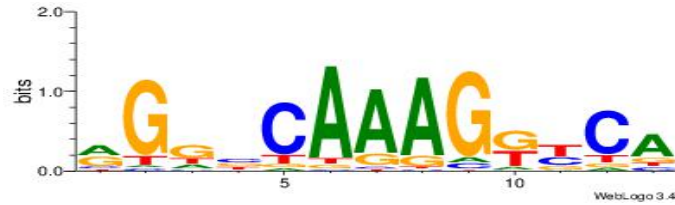


Dataset #: 1
 Motif ID: 1
 Motif name: HNF4A
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 11
 Similarity score: 0.0437981

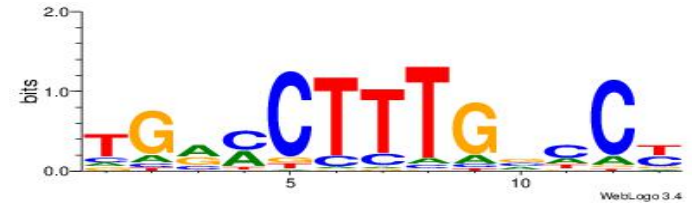
Alignment:

RGGBCAAAGKYCA
 --YSSGCAYGCSS

Original motif Consensus sequence: RGGBCAAAGKYCA



Reverse complement motif Consensus sequence: TGMYYCTTTGBCCK



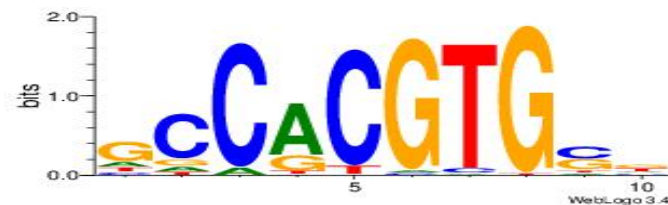
Dataset #:	1
Motif ID:	6
Motif name:	Mycn
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	10
Similarity score:	0.53887

Alignment:

GCCACGTGSD-
 SSGCKTGCSK

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

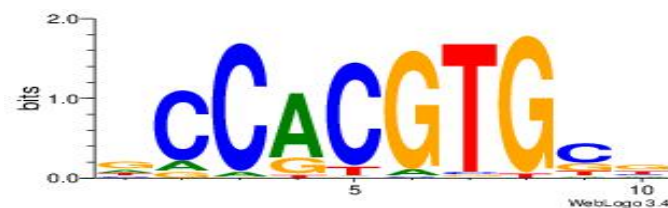
Alignment:

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

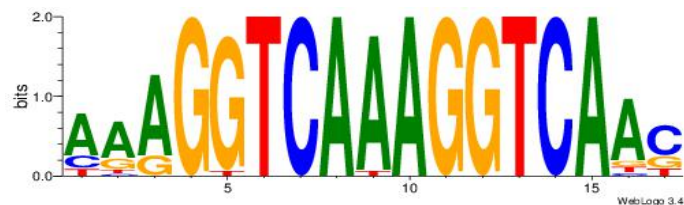
Alignment:

```

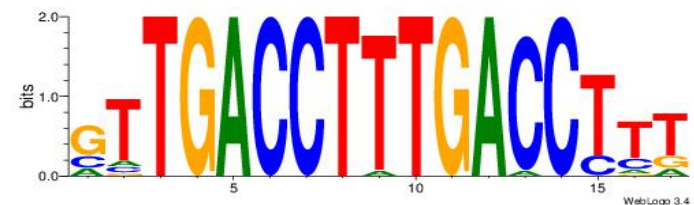
---AAAGGTCAAAGGTCAAC
YSSGCAYGCSS-----

```

Original motif Consensus sequence: AAAGGTCAAAGGTCAAC



Reverse complement motif Consensus sequence: GTTGACCTTTGACCTT

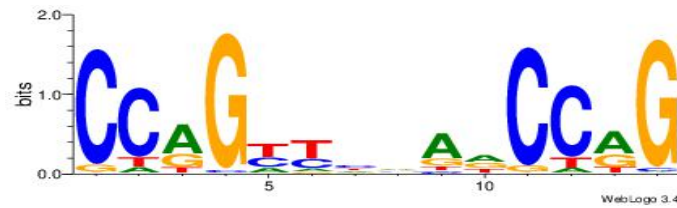


Dataset #:	1
Motif ID:	15
Motif name:	Tcfcp2l1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	7
Number of overlap:	8
Similarity score:	1.53704

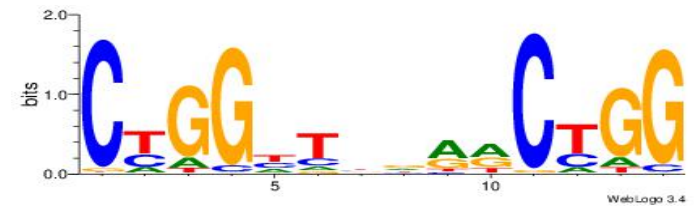
Alignment:

---CCAGYYHVADCCRG
YSSGCAYGCSS-----

Original motif Consensus sequence: CCAGYYHVADCCRG

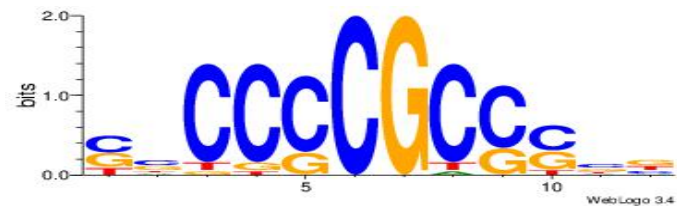


Reverse complement motif Consensus sequence: CKGGDTBDMMCTG



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)

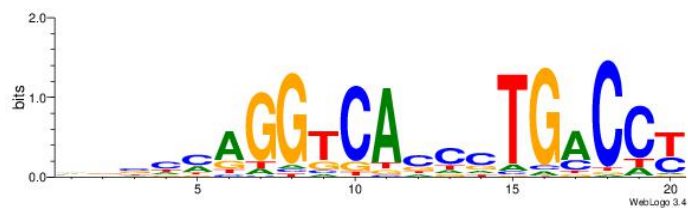
Dataset #:	1
Motif ID:	3
Motif name:	ESR1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	2

Number of overlap: 12
Similarity score: 0.063076

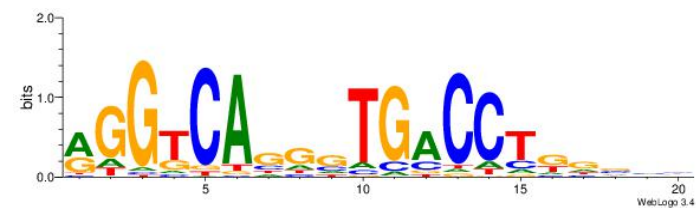
Alignment:

MGGTCAGGGTGACCTRDBHV
-----BBSGGCGGGGBS-

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV

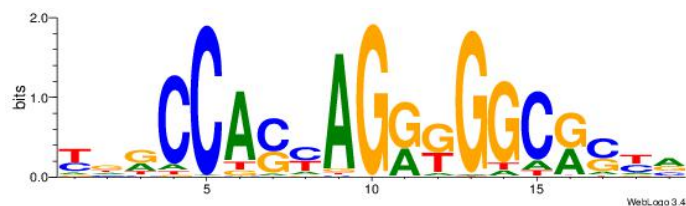


Dataset #: 1
Motif ID: 16
Motif name: CTCF
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 2
Number of overlap: 12
Similarity score: 0.0642087

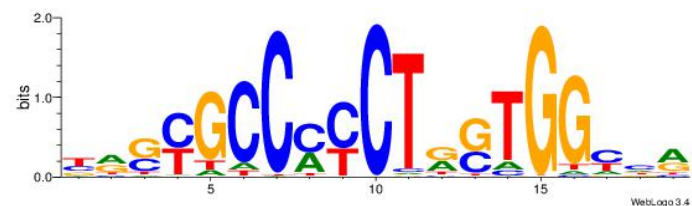
Alignment:

YDRCCASYAGRKGGRSYV
-BBSGGCGGGGBS-----

Original motif Consensus sequence: YDRCCASYAGRKGGCRSYV



Reverse complement motif Consensus sequence: BMSMGCCYMCTKSTGGMHM

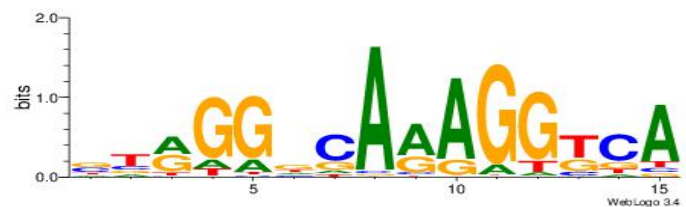


Dataset #: 1
Motif ID: 14
Motif name: PPARGRXRA
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 3
Number of overlap: 12
Similarity score: 0.0671548

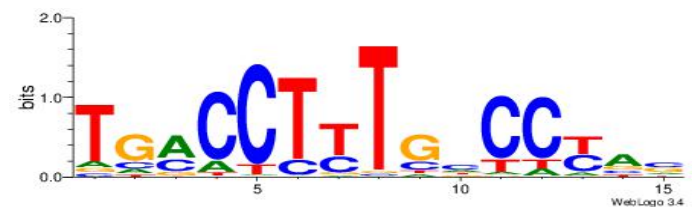
Alignment:

TGRCCTKTGHCKAB
-SBCCCCGCCSBB--

Original motif Consensus sequence: BTRGGDCARAGGKCA



Reverse complement motif Consensus sequence: TGRCCCTKTGHCKA

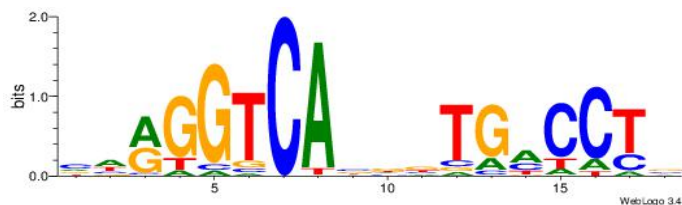


Dataset #: 1
 Motif ID: 9
 Motif name: ESR2
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 12
 Similarity score: 0.0734481

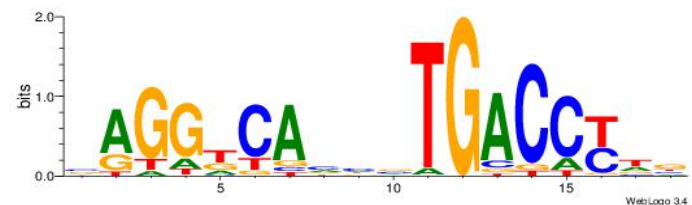
Alignment:

BAGGYCABHBTGACCKHV
 -SBCCCCGCCSBB-----

Original motif Consensus sequence: VHRGGTCABDBTGMCTB



Reverse complement motif Consensus sequence: BAGGYCABHBTGACCKHV

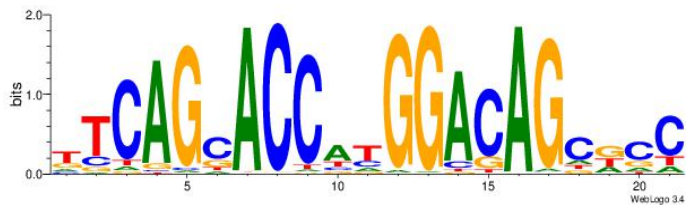


Dataset #: 1
 Motif ID: 7
 Motif name: REST
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 10

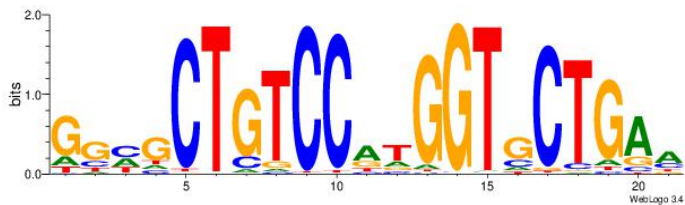
Number of overlap: 12
Similarity score: 0.0751084

Alignment:
TTCAGCACCATGGACAGCKCC
BBSGGCGGGGBS-----

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC



Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA

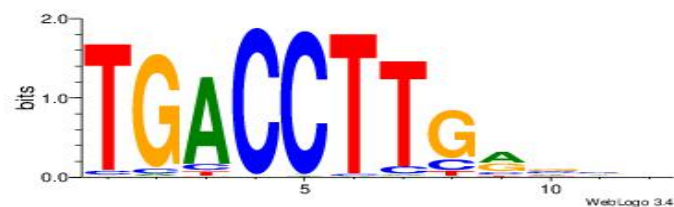
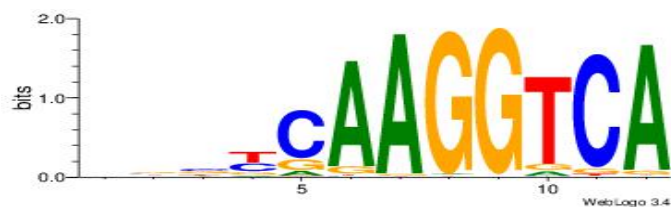


Dataset #: 1
Motif ID: 4
Motif name: Esrrb
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 2
Number of overlap: 11
Similarity score: 0.571364

Alignment:
VBBYCAAGGTCA-
-BBSGGCGGGGBS

Original motif Consensus sequence: VBBYCAAGGTCA

Reverse complement motif Consensus sequence: TGACCTTGMBBB

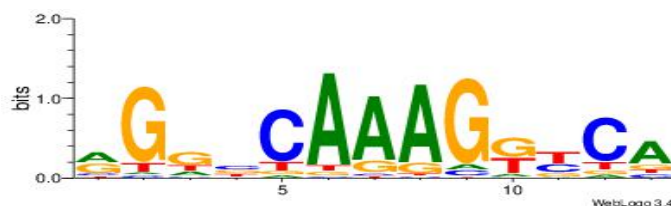


Dataset #: 1
 Motif ID: 1
 Motif name: HNF4A
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 11
 Similarity score: 0.573202

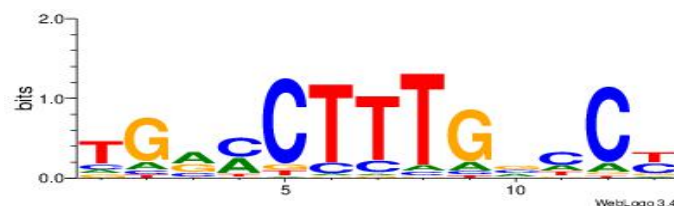
Alignment:

-TGM YCTTTGB CCK
 SBCCCCGCCSBB--

Original motif Consensus sequence: RGGBCAAAGKYCA



Reverse complement motif Consensus sequence: TGM YCTTTGB CCK



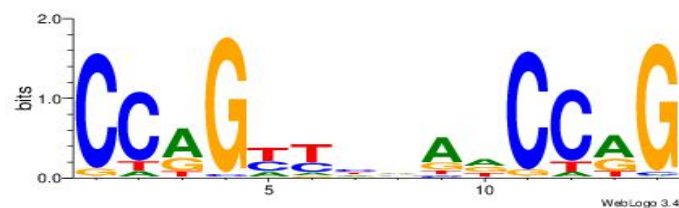
Dataset #: 1
 Motif ID: 15

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

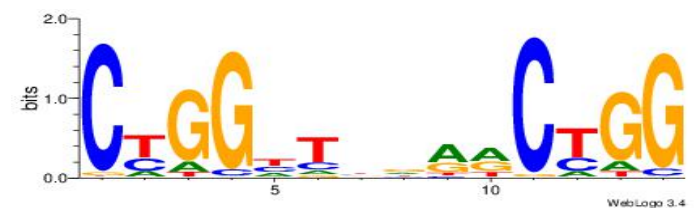
Alignment:

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

Original motif Consensus sequence: CCAGYYHVADCCRG



Reverse complement motif Consensus sequence: CKGGDTBDMCTGG

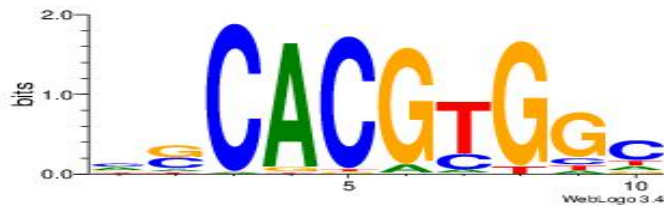


Dataset #:	1
Motif ID:	6
Motif name:	Mycn
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2
Number of overlap:	9
Similarity score:	1.57507

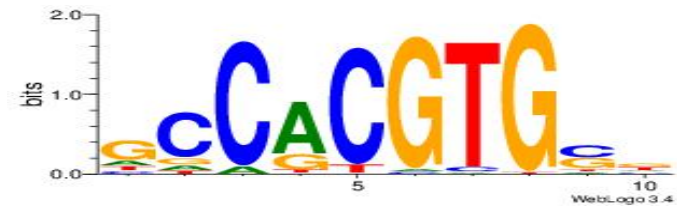
Alignment:

---HSCACGTGGC
SBCCCCGCCSBB-

Original motif Consensus sequence: HSCACGTGGC



Reverse complement motif Consensus sequence: GCCACGTGSD



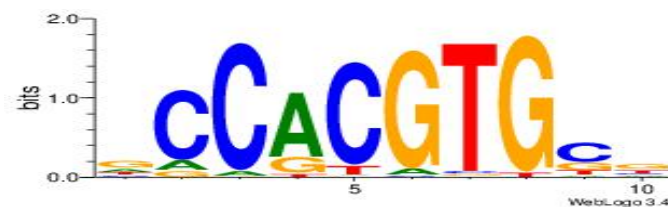
Dataset #:	1
Motif ID:	8
Motif name:	Myc
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	9
Similarity score:	1.57737

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



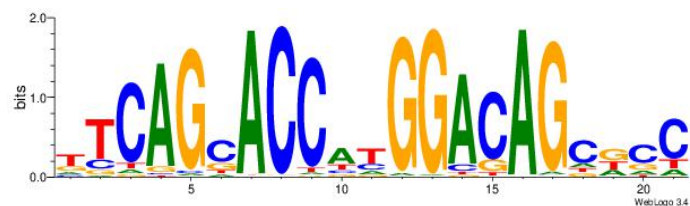
Best Matches for Top Significant Motif ID 29 (Highest to Lowest)

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

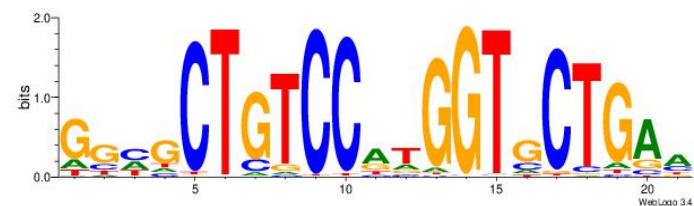
Alignment:

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


Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC



Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA

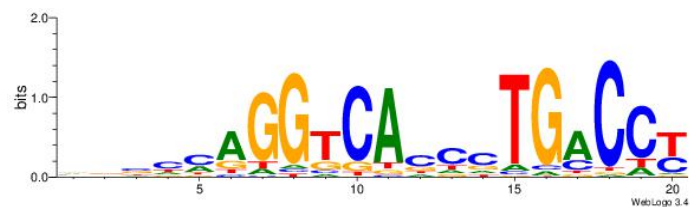


Dataset #: 1
Motif ID: 3
Motif name: ESR1
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 3
Number of overlap: 11
Similarity score: 0.0486581

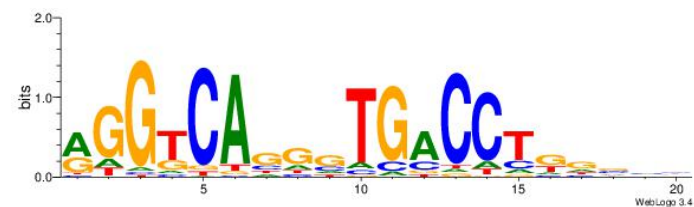
Alignment:

MGGTCAGGGTGACCTRDBHV
-----CGTGKCCGCGG--

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV

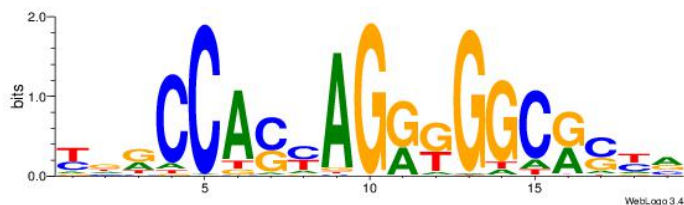


Dataset #: 1
 Motif ID: 16
 Motif name: CTCF
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 11
 Similarity score: 0.0588663

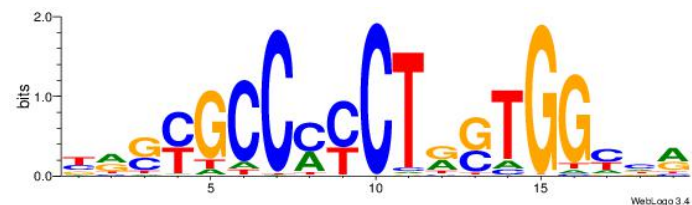
Alignment:

YDRCCASYAGRKGGRSYV
 -----CCGCGGRCACG-

Original motif Consensus sequence: YDRCCASYAGRKGGRSYV



Reverse complement motif Consensus sequence: BMSMGCCYMCTKSTGGMHM

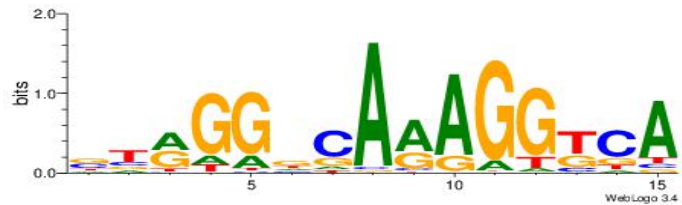


Dataset #: 1
 Motif ID: 14
 Motif name: PPARGRXRA
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2

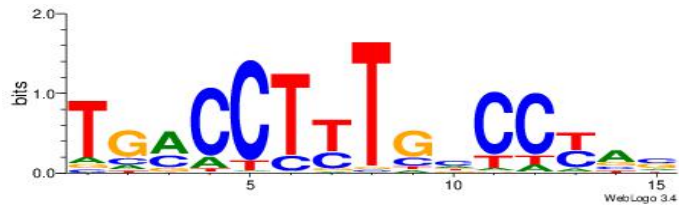
Number of overlap: 11
Similarity score: 0.0629476

Alignment:
TGRCCCTKTGHCCCKAB
---CGTGKCCGCGG-

Original motif Consensus sequence: BTRGGDCARAGGKCA



Reverse complement motif Consensus sequence: TGRCCCTKTGHCCCK

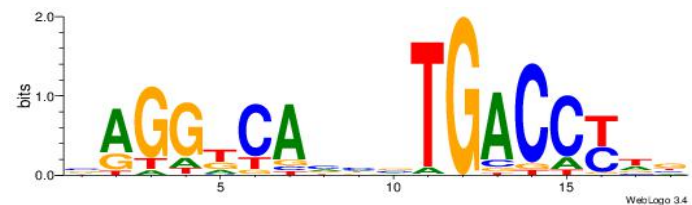
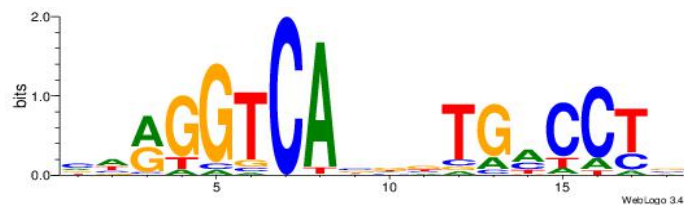


Dataset #: 1
Motif ID: 9
Motif name: ESR2
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 9
Number of overlap: 10
Similarity score: 0.551597

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

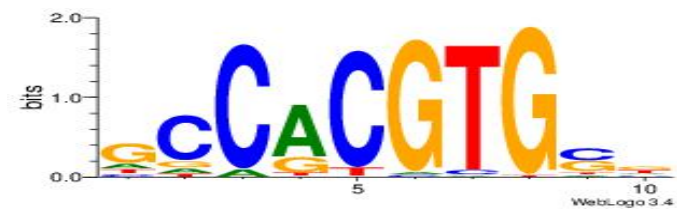
Alignment:

```
HSCACGTGGC--
-CGTGKCCGCGG
```

Original motif Consensus sequence: HSCACGTGGC



Reverse complement motif Consensus sequence: GCCACGTGSD

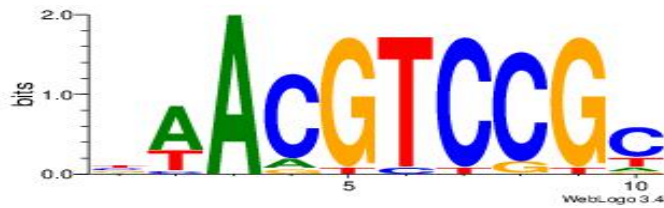


Dataset #:	1
Motif ID:	13
Motif name:	MIZF
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2
Number of overlap:	9
Similarity score:	1.04904

Alignment:

--BAACGTCCGC
CGTGKCCGCGG--

Original motif Consensus sequence: BAACGTCCGC



Reverse complement motif Consensus sequence: GCGGACGTTV



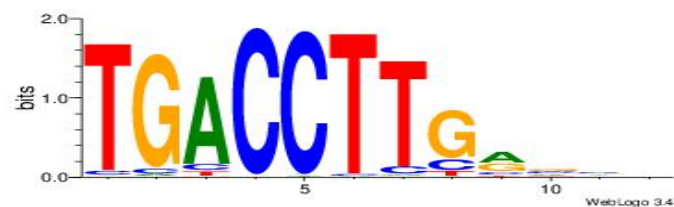
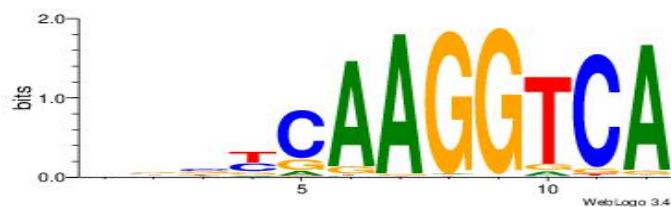
Dataset #:	1
Motif ID:	4
Motif name:	Esrb
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	4
Number of overlap:	9
Similarity score:	1.05291

Alignment:

VBBYCAAGGTCA--
---CCGCGGRCACG

Original motif Consensus sequence: VBBYCAAGGTCA

Reverse complement motif Consensus sequence: TGACCTTGMBBB

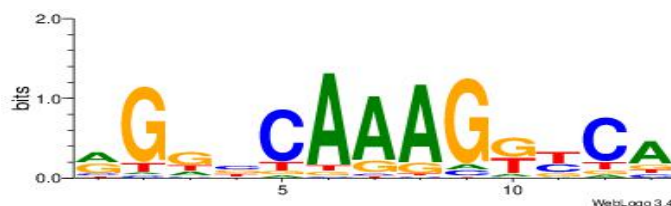


Dataset #: 1
 Motif ID: 1
 Motif name: HNF4A
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 6
 Number of overlap: 8
 Similarity score: 1.55795

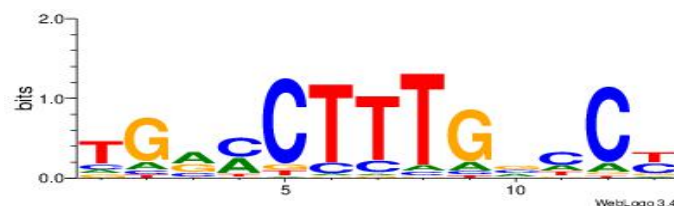
Alignment:

TGM YCTTTGBCK---
 -----CGTGKCCGCGG

Original motif Consensus sequence: RGGBCAAAGKYCA

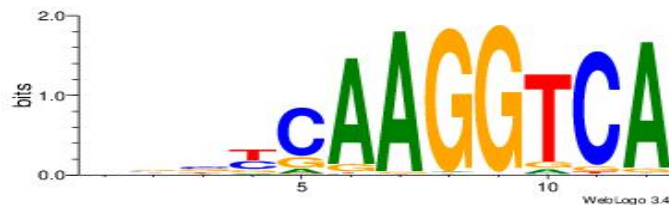


Reverse complement motif Consensus sequence: TGM YCTTTGBCK

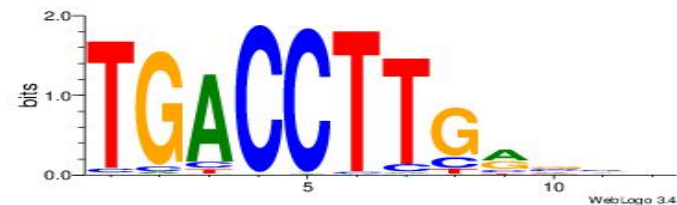


Dataset #: 1 Motif ID: 4 Motif name: Esrrb

Original motif Consensus sequence: VBBYCAAGGTCA



Reverse complement motif Consensus sequence: TGACCTTGMBBB



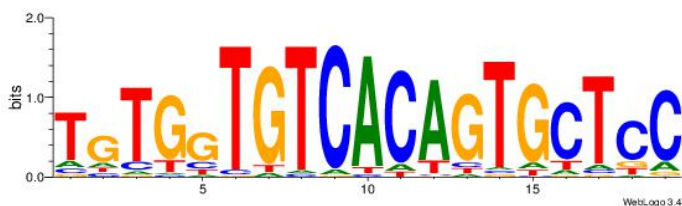
Best Matches for Top Significant Motif ID 4 (Highest to Lowest)

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

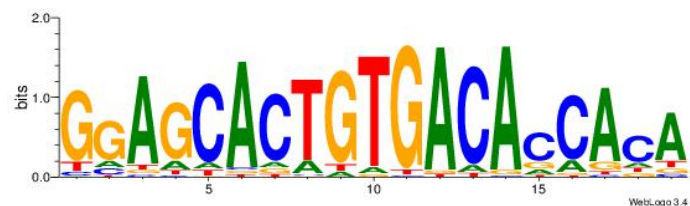
Alignment:

TGTGGTGTTCACAGTGCTCC
 -----TGACCTTGMBBB

Original motif Consensus sequence: TGTGGTGTTCACAGTGCTCC



Reverse complement motif Consensus sequence: GGAGCACTGTGACACCACA

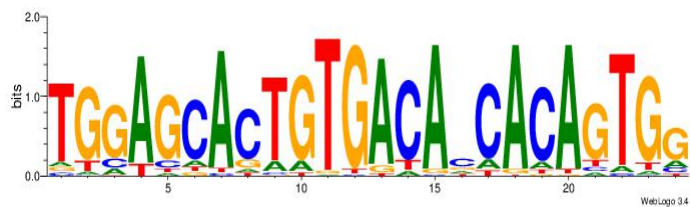


Dataset #: 2
 Motif ID: 23
 Motif name: TGGAGCACTGTGACAcCACAGTGg
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 12
 Number of overlap: 12
 Similarity score: 0.0785385

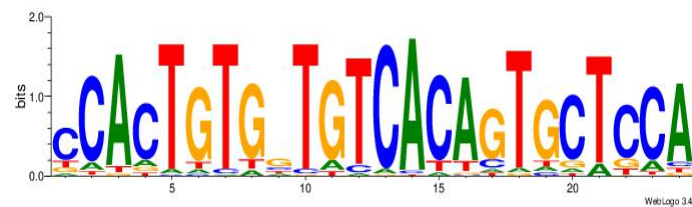
Alignment:

CCACTGTGVTGTCACAGTGCTCCA
 -----TGACCTTGMBBB-

Original motif Consensus sequence: TGGAGCACTGTGACAVCACAGTGG



Reverse complement motif Consensus sequence: CCACTGTGVTGTCACAGTGCTCCA

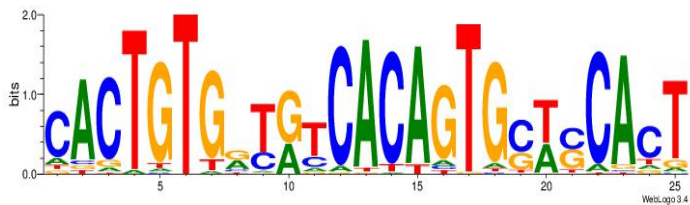


Dataset #: 2
 Motif ID: 22
 Motif name: CACTGTGrYrtCACAGTGswsCAcT
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 11

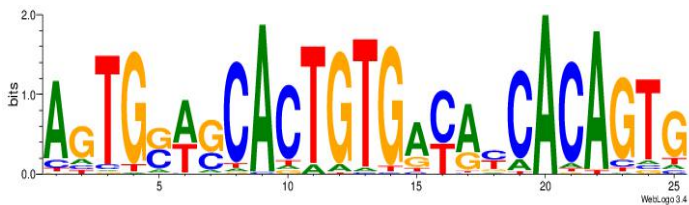
Number of overlap: 12
Similarity score: 0.0832722

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

Original motif Consensus sequence:
CACTGTGRTRTCACAGTGSWSCACT



Reverse complement motif Consensus sequence:
AGTGSWSCACTGTGAMAMCACAGTG

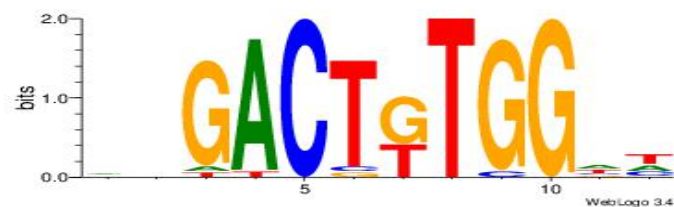
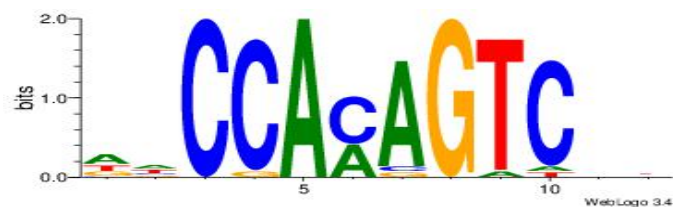


Dataset #: 2
Motif ID: 25
Motif name: wwCCAmAGTCmt
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2
Number of overlap: 11
Similarity score: 0.558919

Alignment:
-DDCCAMAGTCHB
VBBYCAAGGTCA-

Original motif Consensus sequence: DDCCAMAGTCHB

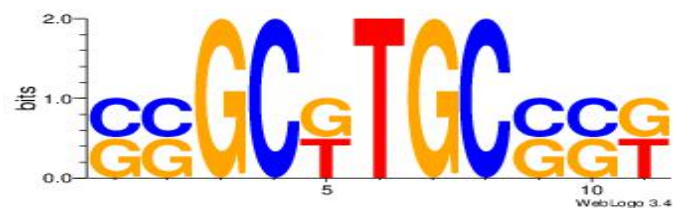
Reverse complement motif Consensus sequence: VDGACTRTGGDD



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



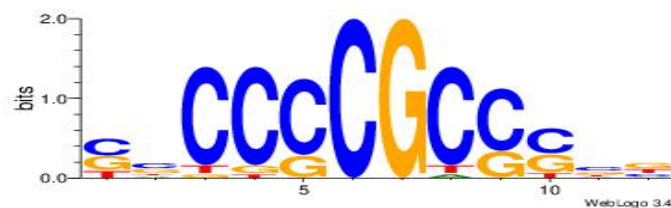
Dataset #: 2
 Motif ID: 24

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

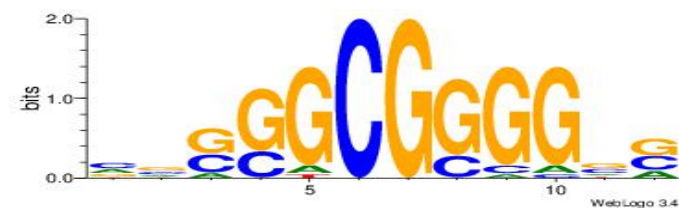
Alignment:

–SBCCCCGCCSBB
TGACCTTGMBBB–

Original motif Consensus sequence: SBCCCCGCCSBB



Reverse complement motif Consensus sequence: BBSGGCGGGBS

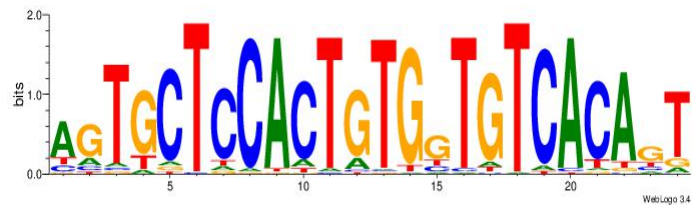


Dataset #:	2
Motif ID:	27
Motif name:	AgTGCTCCACTGTGgTGTCACAgT
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	15
Number of overlap:	10
Similarity score:	1.08683

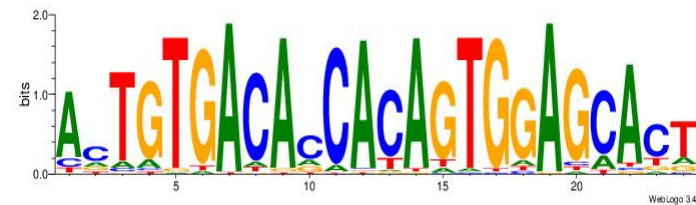
Alignment:

```
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



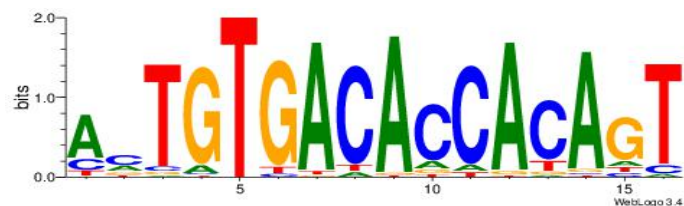
Dataset #: 2
 Motif ID: 21

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

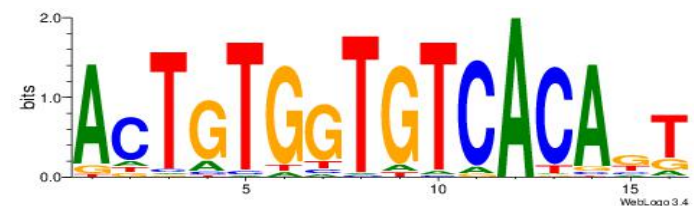
Alignment:

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

Original motif Consensus sequence: AMTGTGACACCACAGT

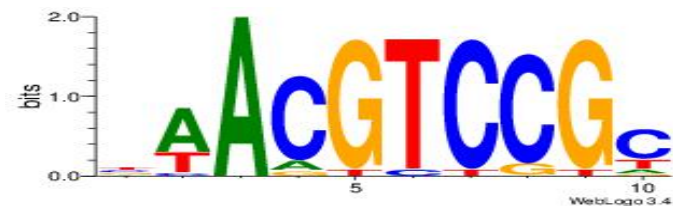


Reverse complement motif Consensus sequence: ACTGTGGTGTCACT



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: Forward
 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

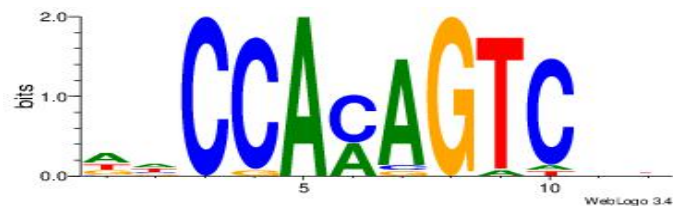


Dataset #: 2
 Motif ID: 25
 Motif name: wwCCAmAGTCmt
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 9
 Similarity score: 0.562428

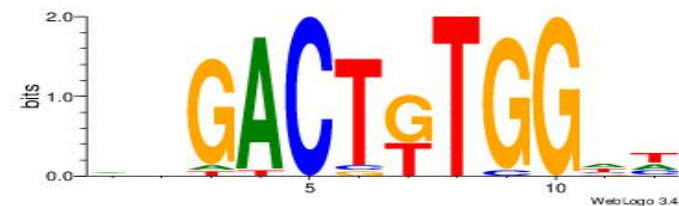
Alignment:

DDCCAMAGTCHB-
 ---BAACGTCCGC

Original motif Consensus sequence: DDCCAMAGTCHB



Reverse complement motif Consensus sequence: VDGACTRTGGDD



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



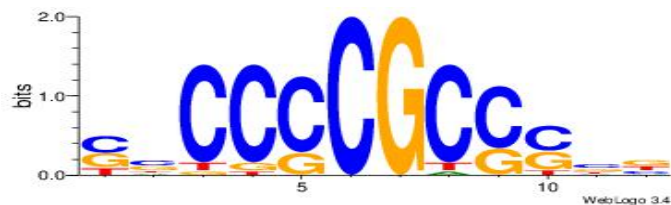
Dataset #: 2
Motif ID: 24
Motif name: ssCCCCGCSsk
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 5
Number of overlap: 8
Similarity score: 1.07197

Alignment:

BBSGGCGGGGBS--
----GCGGACGTTV

Original motif Consensus sequence: SBCCCCGCCSBB

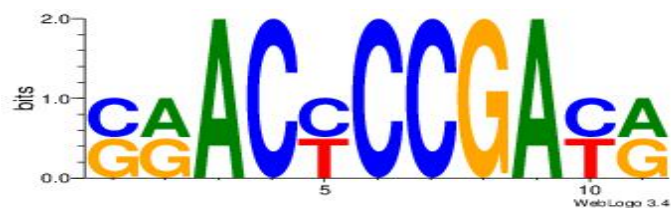
Reverse complement motif Consensus sequence: BBSGGCGGGGBS



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: KKTCCGKGTKS



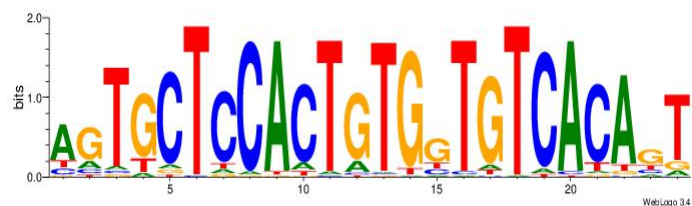
Dataset #: 2
 Motif ID: 27

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

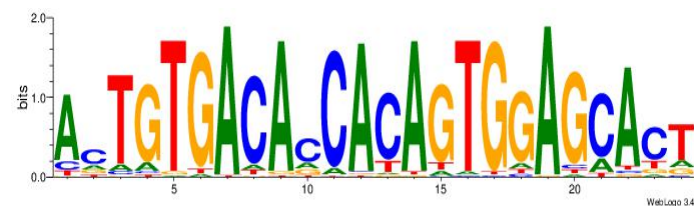
Alignment:

---AGTGCTCCACTGTGGTGTTCACAGT
 BAACGTCCGC-----

Original motif Consensus sequence: AGTGCTCCACTGTGGTGTTCACAGT



Reverse complement motif Consensus sequence: ACTGTGACACCACAGTGGAGCACT

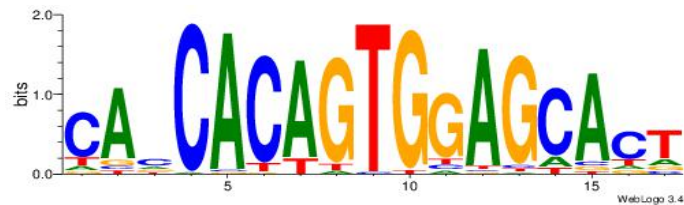


Dataset #: 2
 Motif ID: 26
 Motif name: CACcACAGTGGAGCAcT
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 11
 Number of overlap: 7
 Similarity score: 1.57176

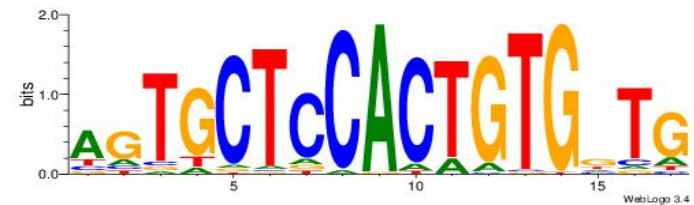
Alignment:

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

Original motif Consensus sequence: CAHCACAGTGGAGCACT



Reverse complement motif Consensus sequence: AGTGCTCCACTGTGDTG



Significant Motifs - Global and Local 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 Significant Motif ID 5 (Highest to Lowest)

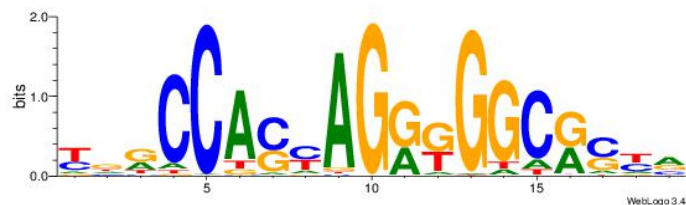
Dataset #: 1
Motif ID: 16

Motif name: CTCF
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 8
 Number of overlap: 6
 Similarity score: 0

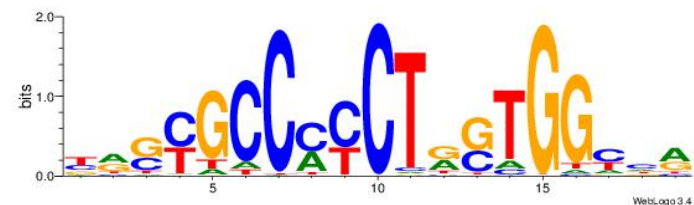
Alignment:

YDRCCASYAGRKGGRSYV
 -----HAGGTG-----

Original motif Consensus sequence: YDRCCASYAGRKGGRSYV



Reverse complement motif Consensus sequence: BMSMGCCYMCTKSTGGMHM



Dataset #: 1
 Motif ID: 12
 Motif name: RORA_1
 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: 0.00688881

Alignment:

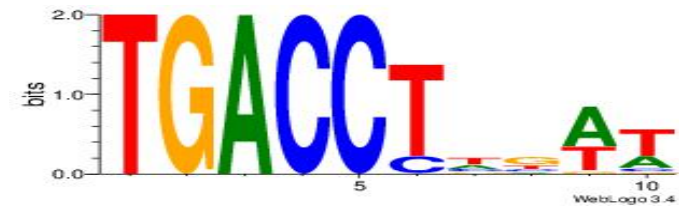
TGACCTDVWT

-CACCTD---

Original motif Consensus sequence: AWVDAGGTCA



Reverse complement motif Consensus sequence: TGACCTDVWT



Dataset #:	1
Motif ID:	7
Motif name:	REST
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	6
Number of overlap:	6
Similarity score:	0.00707323

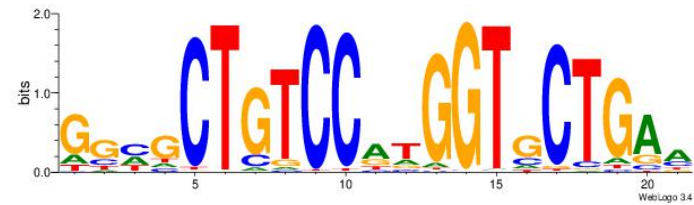
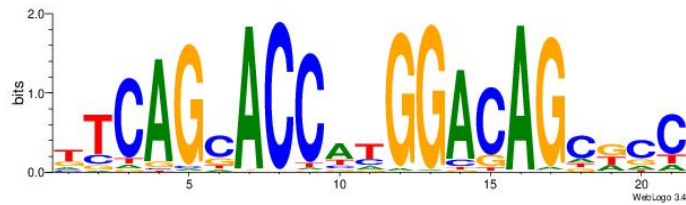
Alignment:

GGYGCTGTCCATGGTGCTGAA

-----HAGGTG-----

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC

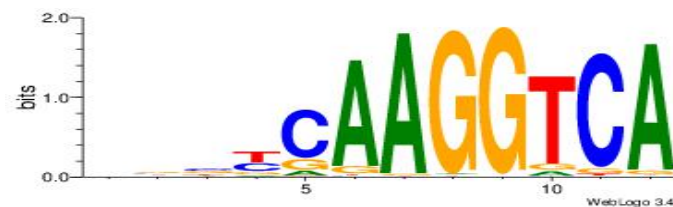
Reverse complement motif Consensus sequence:
GGYGCTGTCCATGGTGCTGAA



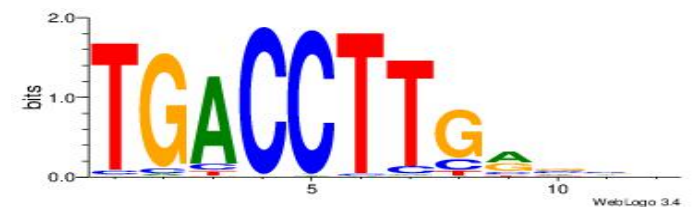
Dataset #: 1
 Motif ID: 4
 Motif name: Esrrb
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 6
 Similarity score: 0.013046

Alignment:
 VBBYCAAGGTCA
 -HAGGTG-----

Original motif Consensus sequence: VBBYCAAGGTCA



Reverse complement motif Consensus sequence: TGACCTTGMBBB



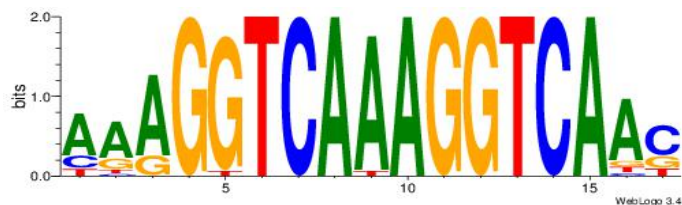
Dataset #: 1
 Motif ID: 10

Motif name:	NR1H2RXRA
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:	0.0160352

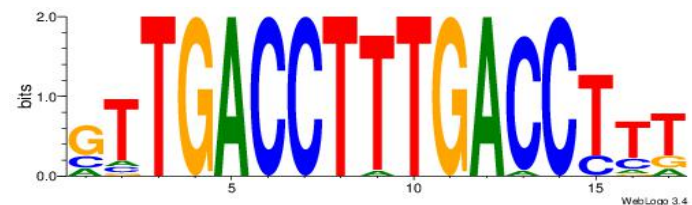
Alignment:

```
GTTGACCTTTGACCTTT
-----CACCTD-
```

Original motif Consensus sequence: AAAGGTCAAAGGTCAAC



Reverse complement motif Consensus sequence: GTTGACCTTTGACCTTT



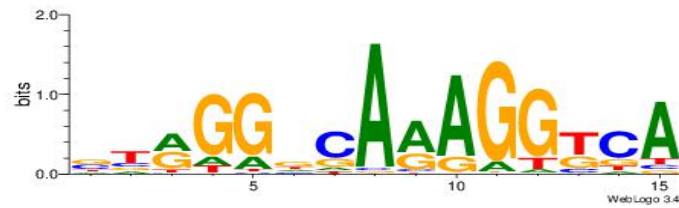
Dataset #:	1
Motif ID:	14
Motif name:	PPARGRXRA
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	9
Number of overlap:	6
Similarity score:	0.0192435

Alignment:

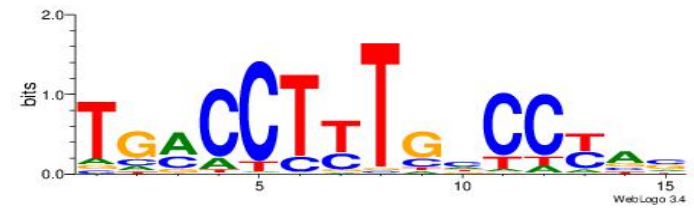
TGRCCTKTGHCKAB

-CACCTD-----

Original motif Consensus sequence: BTRGGDCARAGGKCA



Reverse complement motif Consensus sequence: TGRCCTKTGHCKK



Dataset #:	1
Motif ID:	11
Motif name:	NR4A2
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:	0.0216496

Alignment:

GTGACCTT

--CACCTD

Original motif Consensus sequence: AAGGTCAC

Reverse complement motif Consensus sequence: GTGACCTT

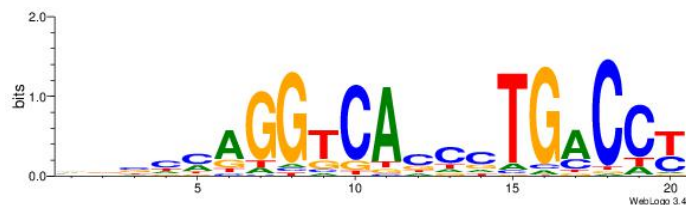


Dataset #: 1
 Motif ID: 3
 Motif name: ESR1
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 5
 Number of overlap: 6
 Similarity score: 0.022947

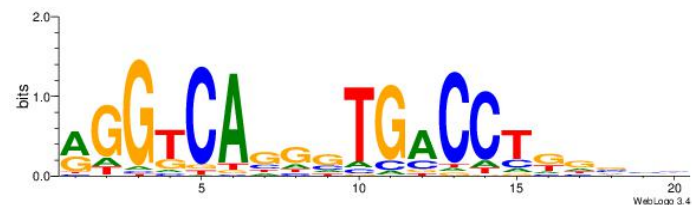
Alignment:

MGGTCAGGGTGACCTRDBHV
 ----CACCTD-----

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV



Dataset #: 1

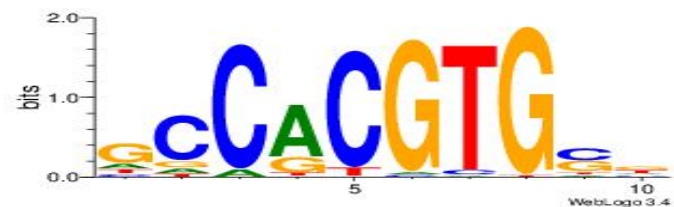
Motif ID: 6
 Motif name: Mycn
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 6
 Similarity score: 0.0246463

Alignment:
 HSCACGTGGC
 --CACCTD--

Original motif Consensus sequence: HSCACGTGGC



Reverse complement motif Consensus sequence: GCCACGTGSD



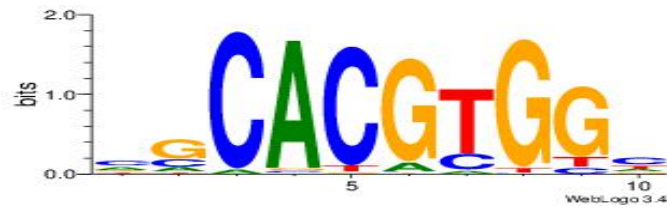
Dataset #: 1
 Motif ID: 8
 Motif name: Myc
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3
 Number of overlap: 6
 Similarity score: 0.025129

Alignment:

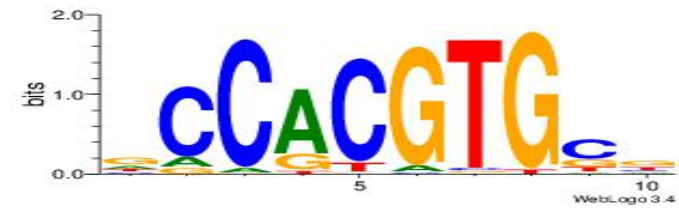
DCCACGTGCV

--HAGGTG--

Original motif Consensus sequence: VGCACGTGGH

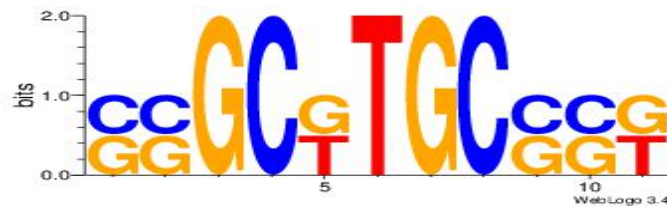


Reverse complement motif Consensus sequence: DCCACGTGCV



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

Original motif Consensus sequence: SSGCKTGCSSK



Reverse complement motif Consensus sequence: YSSGCAYGCSS



Best Matches for Significant Motif ID 28 (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:	Backward
Position number:	1

Number of overlap: 11
Similarity score: 0.00456539

Alignment:
GCGCGCSCGCG
SSGCKTGCSSK

Original motif Consensus sequence: GCGCGCSCGCG



Reverse complement motif Consensus sequence: CGCGSGCGCGC

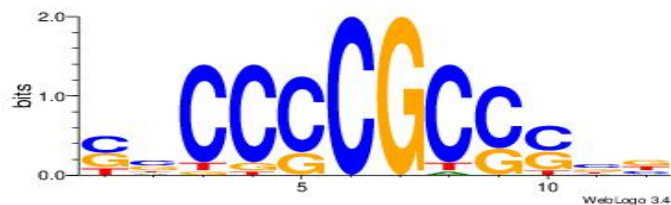


Dataset #: 2
Motif ID: 24
Motif name: ssCCCCGCSSsk
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 2
Number of overlap: 11
Similarity score: 0.0176347

Alignment:
BBSGGCGGGGBS
-YSSGCAYGCSS

Original motif Consensus sequence: SBCCCCGCCSBB

Reverse complement motif Consensus sequence: BBSGGCGGGGBS



Dataset #: 2
 Motif ID: 18
 Motif name: sscCCC G Cc c
 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: 0.0190954

Alignment:
 SBCGCGGGGSB
 YSSGCAYGCSS

Original motif Consensus sequence: BSCCCCGCGBS



Reverse complement motif Consensus sequence: SBCGCGGGGSB



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: 1
 Number of overlap: 11
 Similarity score: 0.0276515

Alignment:

CCGCGGrCACG
 SSGCKTGCSK

Original motif Consensus sequence: CCGCGGrCACG



Reverse complement motif Consensus sequence: CGTGKCCGCGG

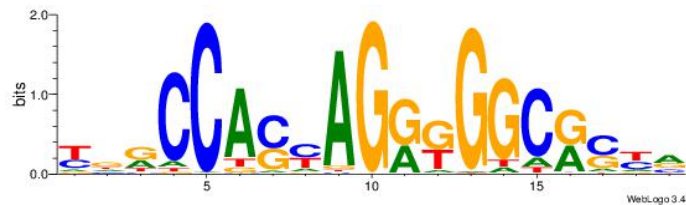


Dataset #: 1
 Motif ID: 16
 Motif name: CTCF
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 8
 Number of overlap: 11
 Similarity score: 0.0349439

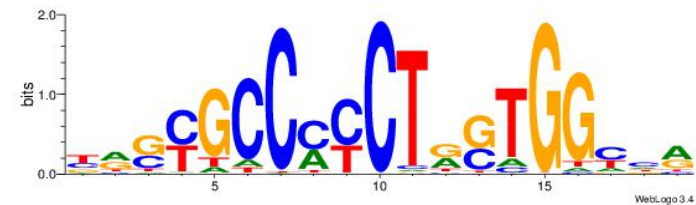
Alignment:

YDRCCASYAGRKGGRSYV
-----SSGCKTGCSSK-

Original motif Consensus sequence: YDRCCASYAGRKGGRSYV



Reverse complement motif Consensus sequence:
BMSMGCCYMCTKSTGGMHM



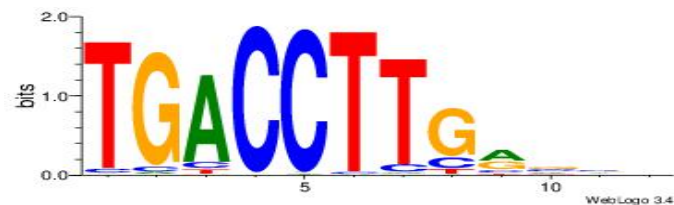
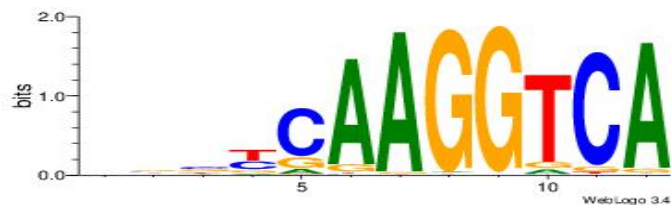
Dataset #:	1
Motif ID:	4
Motif name:	Esrrb
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	11
Similarity score:	0.0358701

Alignment:

VBBYCAAGGTCA
-YSSGCAYGCSS

Original motif Consensus sequence: VBBYCAAGGTCA

Reverse complement motif Consensus sequence: TGACCTTGMBBB

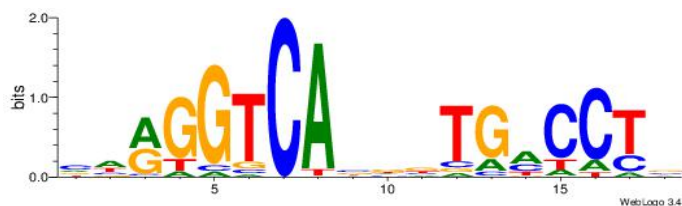


Dataset #: 1
 Motif ID: 9
 Motif name: ESR2
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 11
 Similarity score: 0.0379074

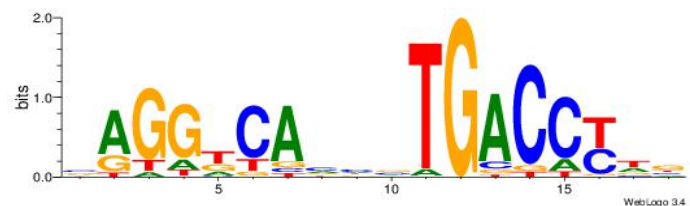
Alignment:

VHRGGTCABDBTGMCTB
 -----YSSGCAYGCSS--

Original motif Consensus sequence: VHRGGTCABDBTGMCTB



Reverse complement motif Consensus sequence: BAGGYCABHBTGACCKHV



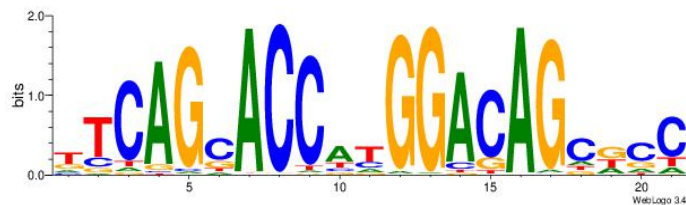
Dataset #: 1

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

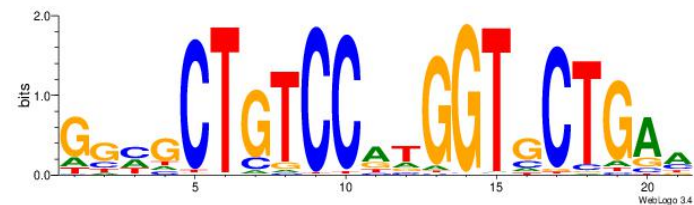
Alignment:

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

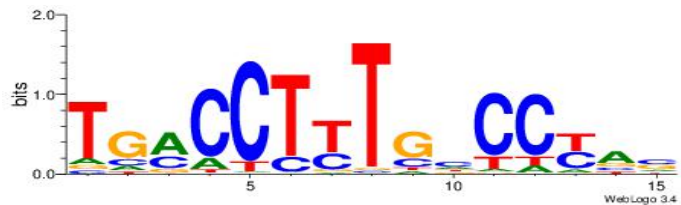
Similarity score: 0.041419

Alignment:
BTRGGDCARAGGKCA
--YSSGCAYGCSS--

Original motif Consensus sequence: BTRGGDCARAGGKCA



Reverse complement motif Consensus sequence: TGRCCCTKTGHCCCK

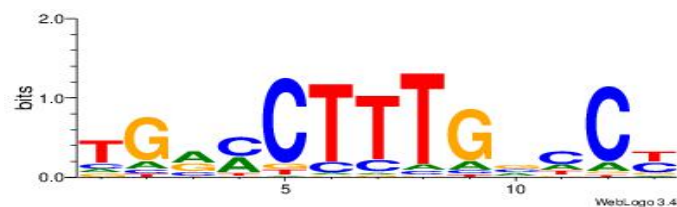
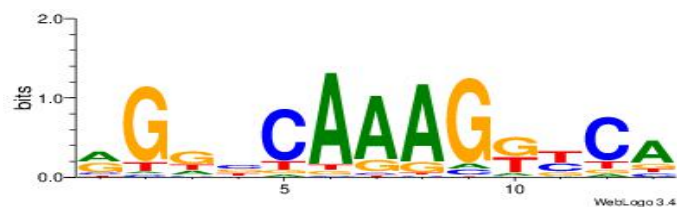


Dataset #: 1
Motif ID: 1
Motif name: HNF4A
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 11
Similarity score: 0.0437981

Alignment:
RGGBCAAAGKYCA
--YSSGCAYGCSS

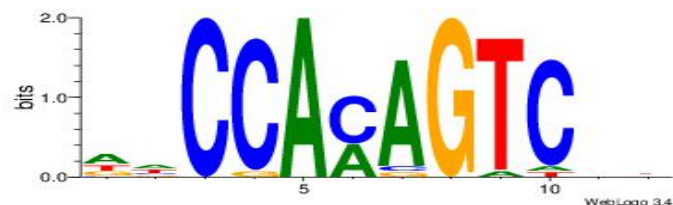
Original motif Consensus sequence: RGGBCAAAGKYCA

Reverse complement motif Consensus sequence: TGMYYTTTGBCCCK

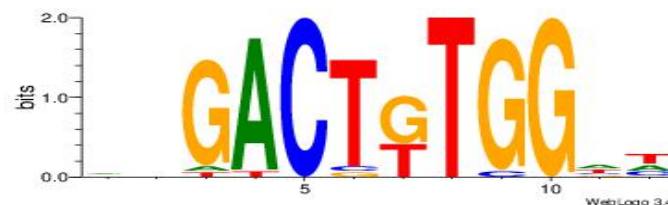


Dataset #: 2 Motif ID: 25 Motif name: wwCCAmAGTCmt

Original motif Consensus sequence: DDCCAMAGTCHB



Reverse complement motif Consensus sequence: VDGACTRTGGDD



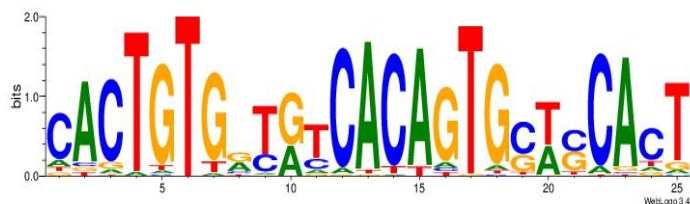
Best Matches for Significant Motif ID 25 (Highest to Lowest)

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:	9
Number of overlap:	12
Similarity score:	0.0263648

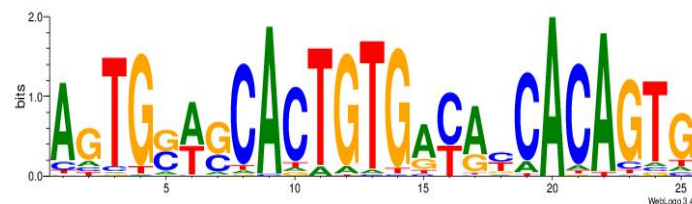
Alignment:

```
CACTGTGRTRTCACAGTGSWSCACT
-----DDCCAMAGTCHB-----
```

Original motif Consensus sequence:
CACTGTGRTRTCACAGTGSWSCACT



Reverse complement motif Consensus sequence:
AGTGSWSCACTGTGAMAMCACAGTG



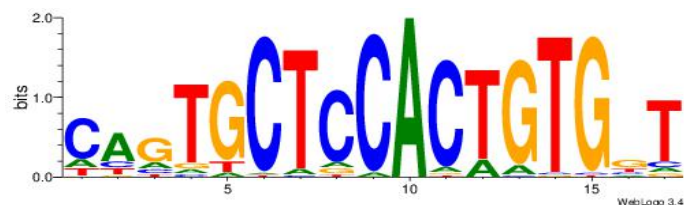
Dataset #: 2
Motif ID: 20
Motif name: CagTGCTCCACTGTGgT
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 6
Number of overlap: 12
Similarity score: 0.0282828

Alignment:

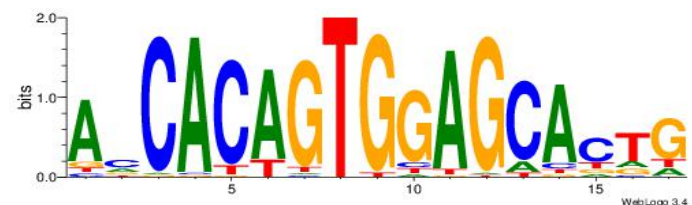
ABCACAGTGGAGCACTG

VDGACTRTGGDD-----

Original motif Consensus sequence: CAGTGCTCCACTGTGBT



Reverse complement motif Consensus sequence:
ABCACAGTGGAGCACTG

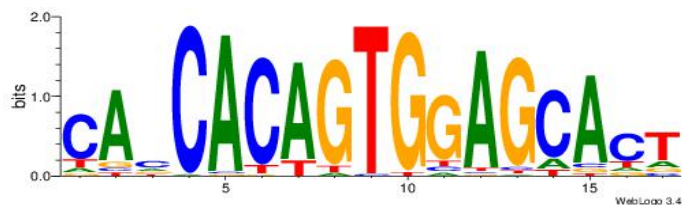


Dataset #: 2
 Motif ID: 26
 Motif name: CACACAGTGGAGCAct
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 6
 Number of overlap: 12
 Similarity score: 0.0291095

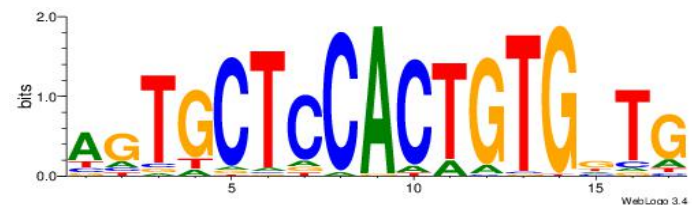
Alignment:

AGTGCTCCACTGTGDTG
 -----VDGACTRTGGDD

Original motif Consensus sequence: CAHCACAGTGGAGCACT



Reverse complement motif Consensus sequence: AGTGCTCCACTGTGDTG

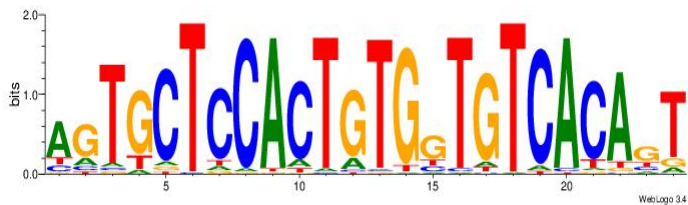


Dataset #: 2
 Motif ID: 27
 Motif name: AgTGCTCCACTGTGgTGTCACAgT
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 6

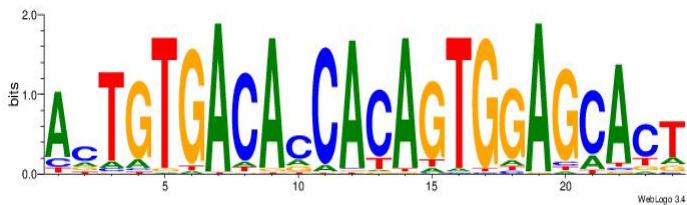
Number of overlap: 12
Similarity score: 0.0301919

Alignment:
AGTGCTCCACTGTGGTGTACAGT
-----VDGACTRTGGDD-----

Original motif Consensus sequence: AGTGCTCCACTGTGGTGTACAGT



Reverse complement motif Consensus sequence: ACTGTGACACCACAGTGGAGCACT

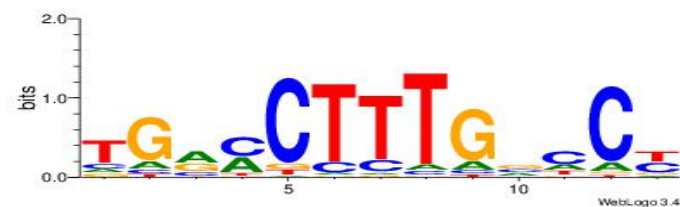
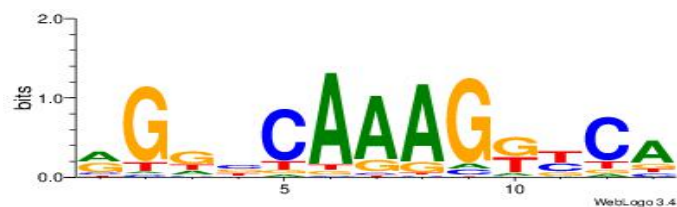


Dataset #: 1
Motif ID: 1
Motif name: HNF4A
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 2
Number of overlap: 12
Similarity score: 0.032442

Alignment:
RGGBCAAAGKYCA
-DDCCAMAGTCHB

Original motif Consensus sequence: RGGBCAAAGKYCA

Reverse complement motif Consensus sequence: TGMYYTTTGBCCK

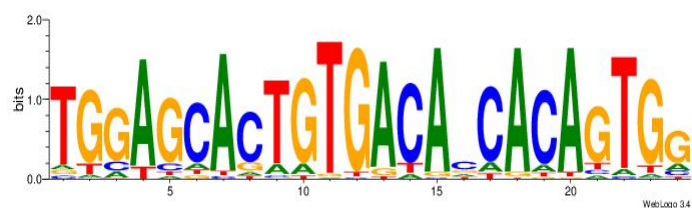


Dataset #: 2
 Motif ID: 23
 Motif name: TGGAGCACTGTGACAcCACAGTGg
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 4
 Number of overlap: 12
 Similarity score: 0.0360702

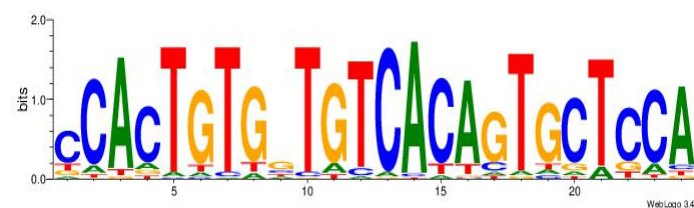
Alignment:

CCACTGTGVTGTCACAGTGCTCCA
 ---DDCCAMAGTCHB-----

Original motif Consensus sequence: TGGAGCACTGTGACAVCACAGTGG



Reverse complement motif Consensus sequence: CCACTGTGVTGTCACAGTGCTCCA



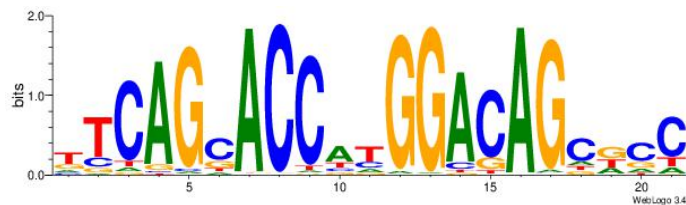
Dataset #: 1

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

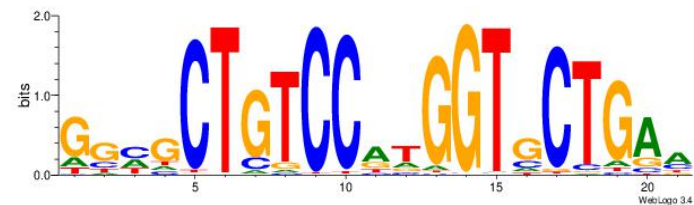
Alignment:

GYGCTGTCCATGGTGCTGAA
 ---DDCCAMAGTCHB-----

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC



Reverse complement motif Consensus sequence: GYGCTGTCCATGGTGCTGAA



Dataset #: 2
 Motif ID: 17
 Motif name: TgTGgTGTCACAGTGCTCC
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 12

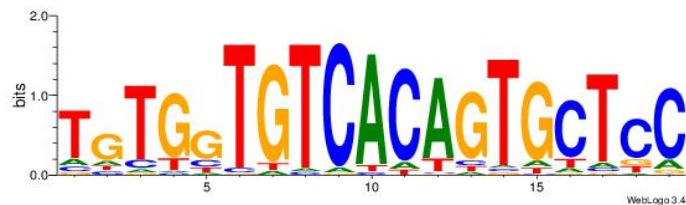
Similarity score: 0.0393782

Alignment:

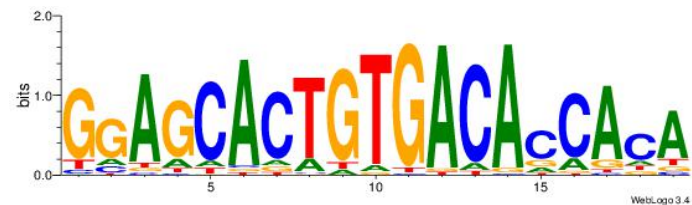
TGTGGTGTACAGTGCTCC

-----DDCCAMAGTCHB--

Original motif Consensus sequence: TGTGGTGTACAGTGCTCC



Reverse complement motif Consensus sequence:
GGAGCACTGTGACACCACA



Dataset #: 1
Motif ID: 3
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: 12
Similarity score: 0.0407304

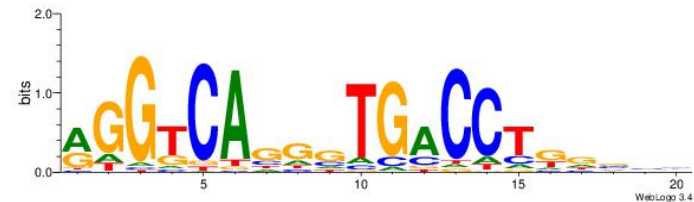
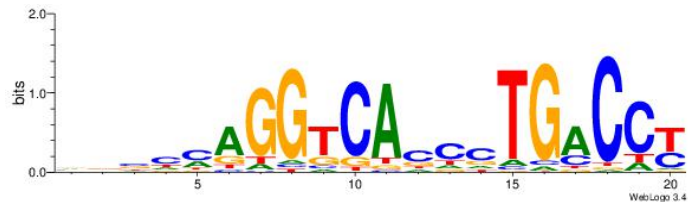
Alignment:

VDBHMAGGTCACCCTGACCY

DDCCAMAGTCHB-----

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY

Reverse complement motif Consensus sequence:
MGGTCAGGGTGACCTRDBHV

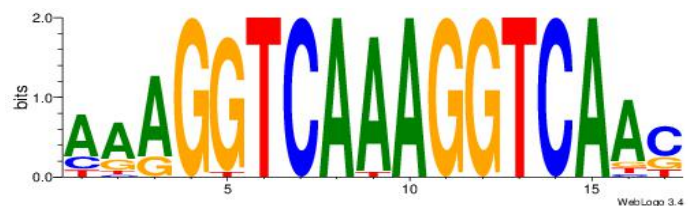


Dataset #: 1
 Motif ID: 10
 Motif name: NR1H2RXRA
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 12
 Similarity score: 0.0463384

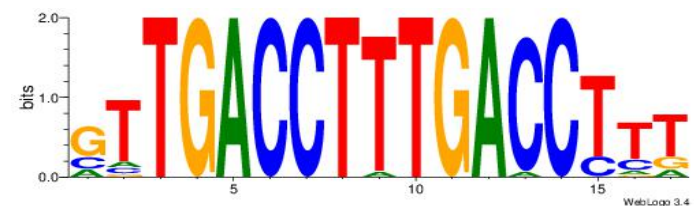
Alignment:

AAAGGTCAAAGGTCAAC
 ----DDCCAMAGTCHB-

Original motif Consensus sequence: AAAGGTCAAAGGTCAAC



Reverse complement motif Consensus sequence: GTTGACCTTTGACCTTT

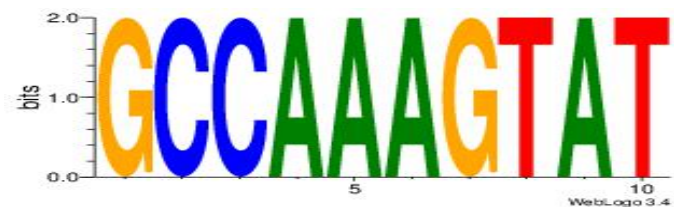


Dataset #: 2 Motif ID: 19 Motif name: atactttggc

Original motif Consensus sequence: ATACTTTGGC



Reverse complement motif Consensus sequence: GCCAAAGTAT



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

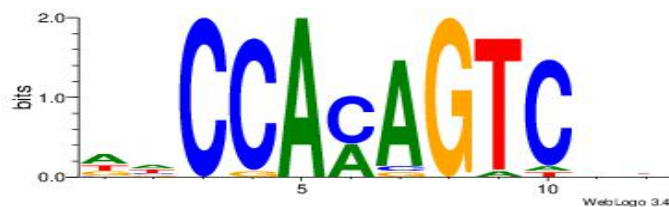
Dataset #:	2
Motif ID:	25
Motif name:	wwCCAmAGTCmt
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	10
Similarity score:	0.0215909

Alignment:

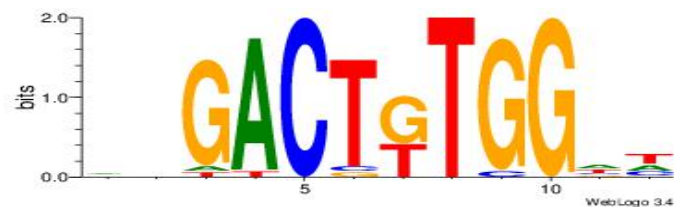
DDCCAMAGTCHB

-GCCAAAGTAT-

Original motif Consensus sequence: DDCCAMAGTCHB



Reverse complement motif Consensus sequence: VDGACTRTGGDD



Dataset #: 2
 Motif ID: 30
 Motif name: taaacgatgcc
 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: 0.0375

Alignment:

GGCATCGTTTA

GCCAAAGTAT-

Original motif Consensus sequence: TAAACGATGCC



Reverse complement motif Consensus sequence: GGCATCGTTTA



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: 5
 Number of overlap: 10

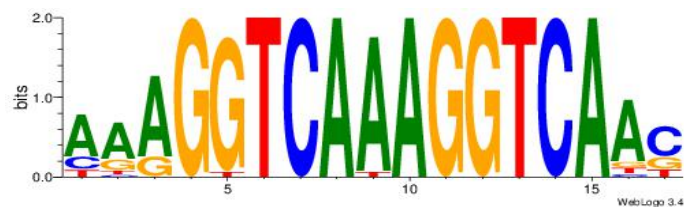
Similarity score: 0.0395

Alignment:

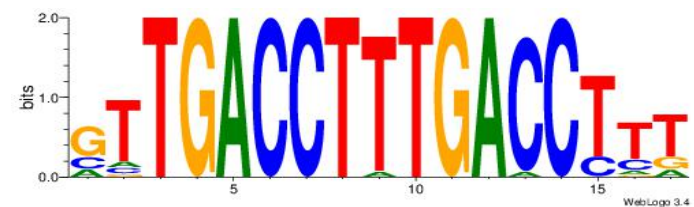
AAAGGTCAAAGGTCAAC

---GCCAAAGTAT----

Original motif Consensus sequence: AAAGGTCAAAGGTCAAC



Reverse complement motif Consensus sequence: GTTGACCTTTGACCTTT



Dataset #: 2
Motif ID: 17
Motif name: TgTGgTGTCACAGTGCTCC
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: 0.0472222

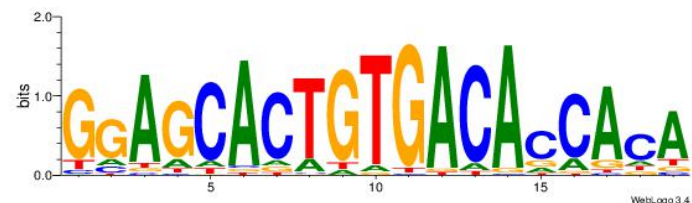
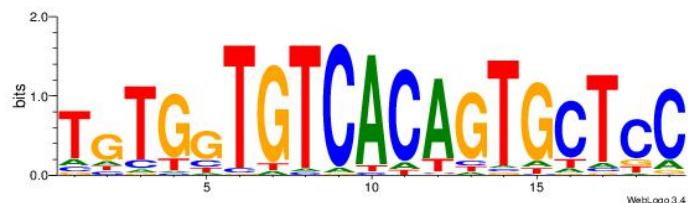
Alignment:

GGAGCACTGTGACACCACA

-----ATACTTTGGC---

Original motif Consensus sequence: TGTGGTGTACAGTGCTCC

Reverse complement motif Consensus sequence: GGAGCACTGTGACACCACA

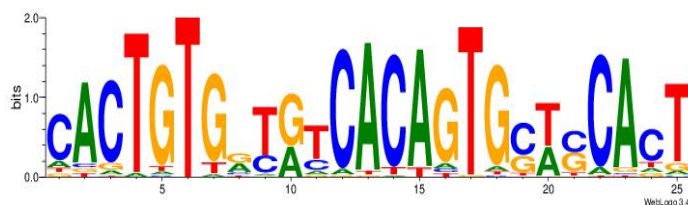


Dataset #: 2
 Motif ID: 22
 Motif name: CACTGTGrYrtCACAGTGsWsCAcT
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 10
 Number of overlap: 10
 Similarity score: 0.0474206

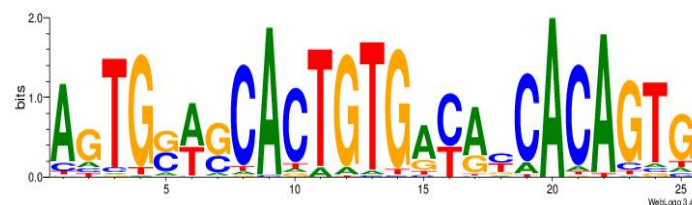
Alignment:

CACTGTGRTRTCACAGTGSWSCACT
 -----GCCAAAGTAT-----

Original motif Consensus sequence:
 CACTGTGRTRTCACAGTGSWSCACT



Reverse complement motif Consensus sequence:
 AGTGSWSCACTGTGAMAMCACAGTG



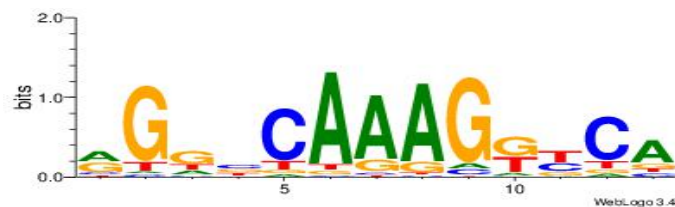
Dataset #: 1

Motif ID: 1
 Motif name: HNF4A
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3
 Number of overlap: 10
 Similarity score: 0.0483209

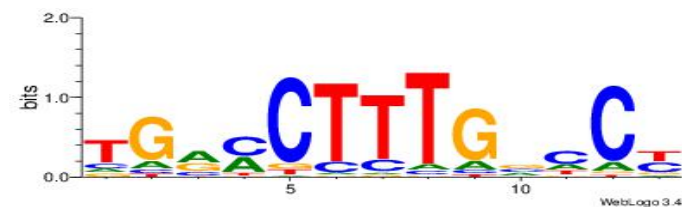
Alignment:

TGM YCTTTGB CCK
 --ATACTTTGGC--

Original motif Consensus sequence: RGGBCAAAGKYCA



Reverse complement motif Consensus sequence: TGM YCTTTGB CCK



Dataset #: 1
 Motif ID: 2
 Motif name: NR2F1
 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: 0.0490385

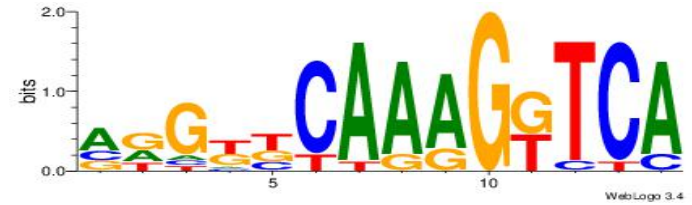
Alignment:

TGAMCTTTGMMCYT
-ATACTTTGGC---

Original motif Consensus sequence: TGAMCTTTGMMCYT



Reverse complement motif Consensus sequence: AKGYCAAAGRTC

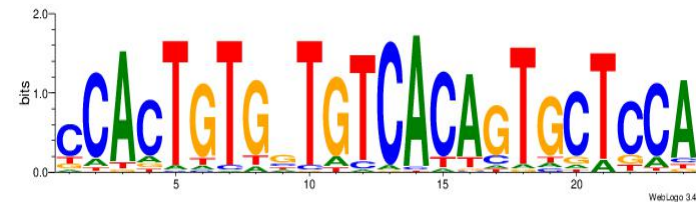
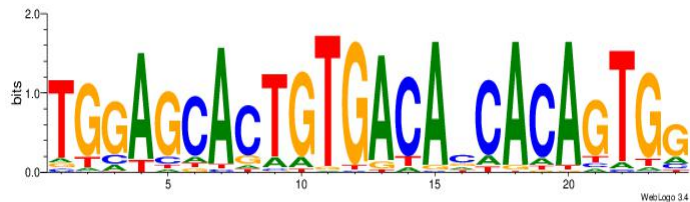


Dataset #:	2
Motif ID:	23
Motif name:	TGGAGCACTGTGACACACAGTGg
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	11
Number of overlap:	10
Similarity score:	0.0493243

Alignment:

CCACTGTGVTGTACAGTGCTCCA
-----GCCAAAGTAT-----

Original motif	Consensus sequence: TGGAGCACTGTGACAVCACAGTGG	Reverse complement motif	Consensus sequence: CCACTGTGVTGTACAGTGCTCCA
----------------	--	--------------------------	---

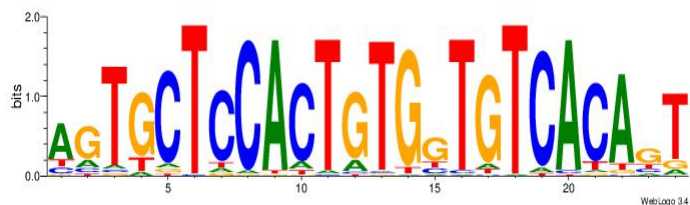


Dataset #: 2
 Motif ID: 27
 Motif name: AgTGCTCCACTGTGgTGTCACAgT
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 9
 Number of overlap: 10
 Similarity score: 0.0498239

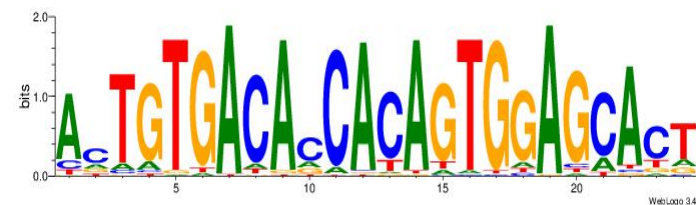
Alignment:

ACTGTGACACCACAGTGGAGCACT
 -----GCCAAAGTAT-----

Original motif Consensus sequence: AGTGCTCCACTGTGGTGTACAGT



Reverse complement motif Consensus sequence: ACTGTGACACCACAGTGGAGCACT

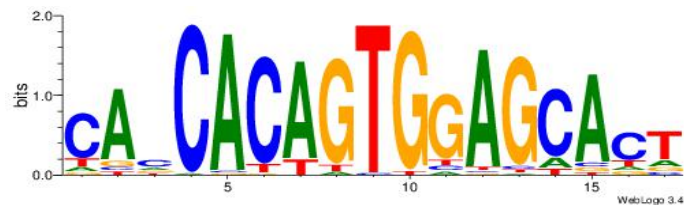


Dataset #: 2

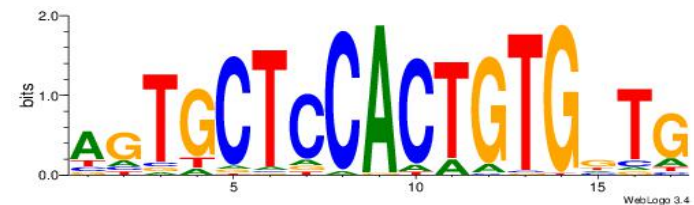
Motif ID: 26
 Motif name: CACcACAGTGGAGCAct
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 10
 Similarity score: 0.0527344

Alignment:
 AGTGCTCCACTGTGDTG
 -----ATACTTTGGC-

Original motif Consensus sequence: CAHCACAGTGGAGCACT



Reverse complement motif Consensus sequence: AGTGCTCCACTGTGDTG



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

Original motif Consensus sequence: AAGGTCAC



Reverse complement motif Consensus sequence: GTGACCTT



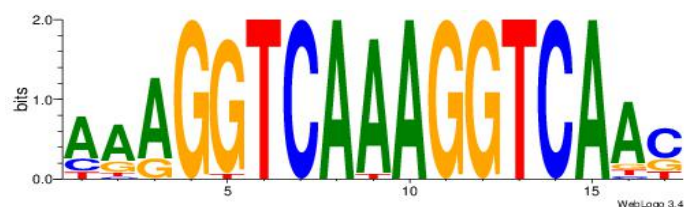
Best Matches for Significant Motif ID 11 (Highest to Lowest)

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: 9
 Number of overlap: 8
 Similarity score: 0.0167759

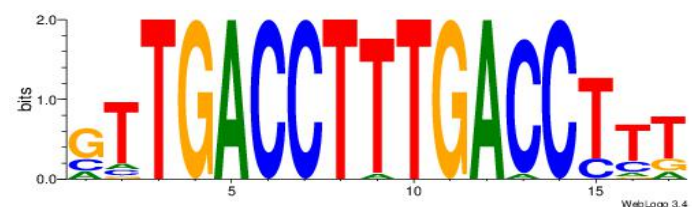
Alignment:

AAAGGTCAAAGGTCAAC
 -AAGGTCAC-----

Original motif Consensus sequence: AAAGGTCAAAGGTCAAC



Reverse complement motif Consensus sequence: GTTGACCTTTGACCTT



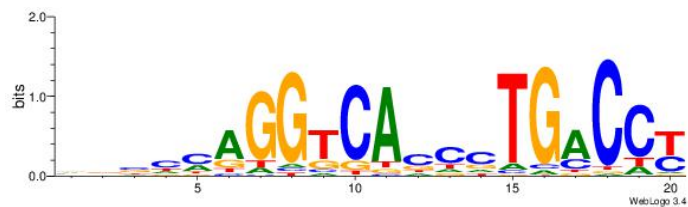
Dataset #: 1
 Motif ID: 3
 Motif name: ESR1
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif

Direction: Forward
 Position number: 5
 Number of overlap: 8
 Similarity score: 0.0195235

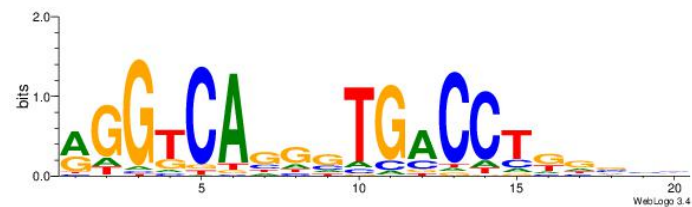
Alignment:

VDBHMAGGTCACCCTGACCY
 ----AAGGTCAC-----

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV

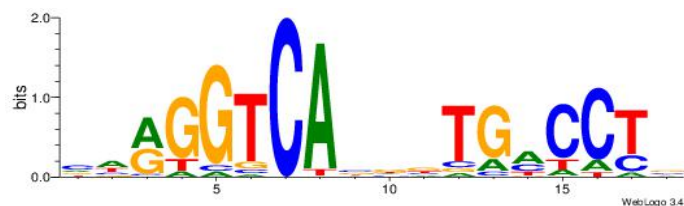


Dataset #: 1
 Motif ID: 9
 Motif name: ESR2
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 10
 Number of overlap: 8
 Similarity score: 0.0198372

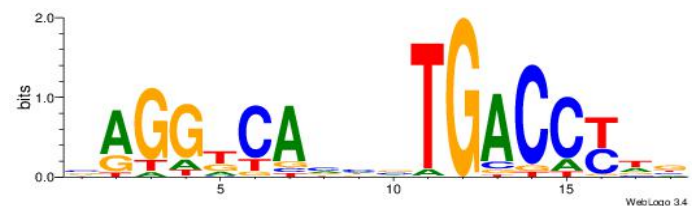
Alignment:

BAGGYCABHBTGACCKHV
 -----GTGACCTT-

Original motif Consensus sequence: VHRGGTCABDBTGMCTB



Reverse complement motif Consensus sequence: BAGGYCABHBTGACCKHV

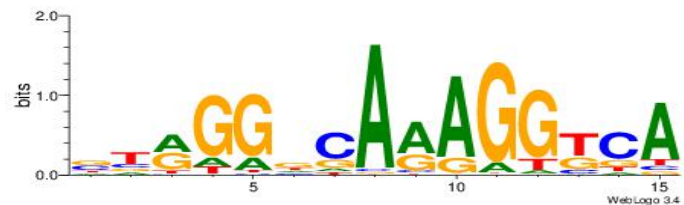


Dataset #: 1
 Motif ID: 14
 Motif name: PPARGRXRA
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 7
 Number of overlap: 8
 Similarity score: 0.0495607

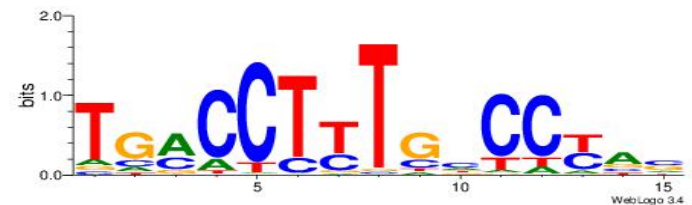
Alignment:

BTRGGDCARAGGKCA
 -AAGGTCAC-----

Original motif Consensus sequence: BTRGGDCARAGGKCA



Reverse complement motif Consensus sequence: TGRCCCTKTGHCKK

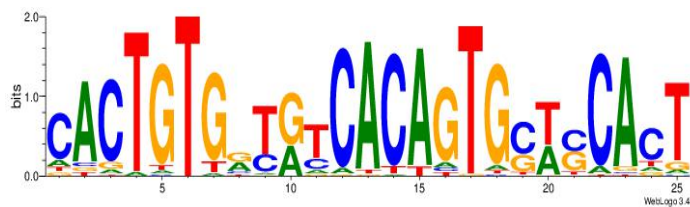


Dataset #: 2
 Motif ID: 22
 Motif name: CACTGTGrYrtCACAGTGswsCAcT
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 7
 Number of overlap: 8
 Similarity score: 0.0557243

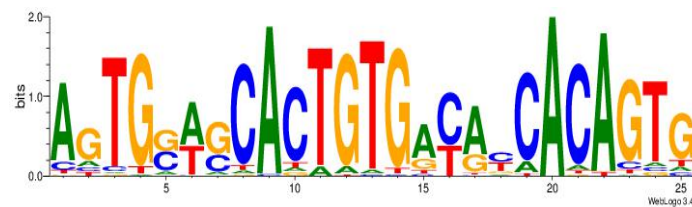
Alignment:

CACTGTGRTRTCACAGTGSWSCACT
 -----AAGGTCAC-----

Original motif Consensus sequence:
 CACTGTGRTRTCACAGTGSWSCACT



Reverse complement motif Consensus sequence:
 AGTGSWSCACTGTGAMAMCACAGTG



Dataset #: 1
 Motif ID: 2
 Motif name: NR2F1
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 7

Number of overlap: 8
Similarity score: 0.0564874

Alignment:
AKGYICAAAGRTCA
-----AAGGTCAC

Original motif Consensus sequence: TGAMCTTTGMMCYT



Reverse complement motif Consensus sequence: AKGYICAAAGRTCA

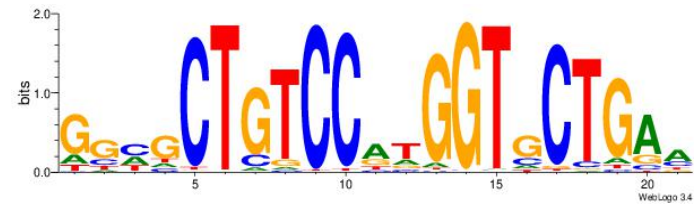
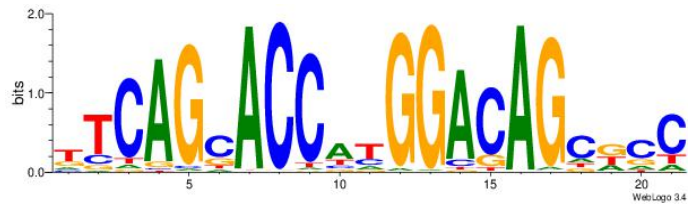


Dataset #: 1
Motif ID: 7
Motif name: REST
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 5
Number of overlap: 8
Similarity score: 0.0594649

Alignment:
GGYGCTGTCCATGGTGCTGAA
----GTGACCTT-----

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC

Reverse complement motif Consensus sequence:
GGYGCTGTCCATGGTGCTGAA

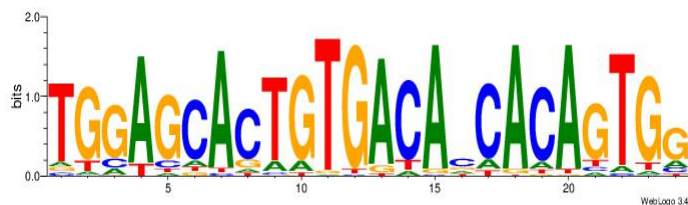


Dataset #: 2
 Motif ID: 23
 Motif name: TGGAGCACTGTGACAcCACAGTGg
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 8
 Number of overlap: 8
 Similarity score: 0.060729

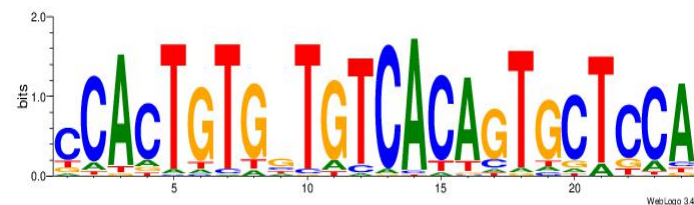
Alignment:

CCACTGTGVTGTCACAGTGCTCCA
 -----AAGGTCAC-----

Original motif Consensus sequence: TGGAGCACTGTGACAVCACAGTGG



Reverse complement motif Consensus sequence: CCACTGTGVTGTCACAGTGCTCCA

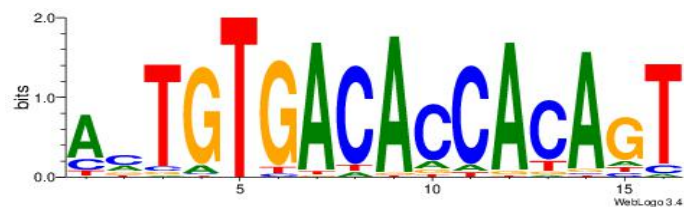


Dataset #: 2

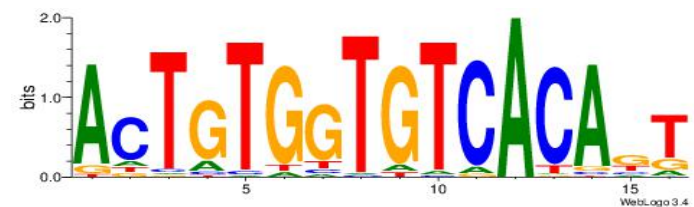
Motif ID: 21
 Motif name: AmTGTGACACCACAGT
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 6
 Number of overlap: 8
 Similarity score: 0.0645146

Alignment:
 ACTGTGGTGTACART
 -----AAGGTCAC---

Original motif Consensus sequence: AMTGTGACACCACAGT



Reverse complement motif Consensus sequence: ACTGTGGTGTACART

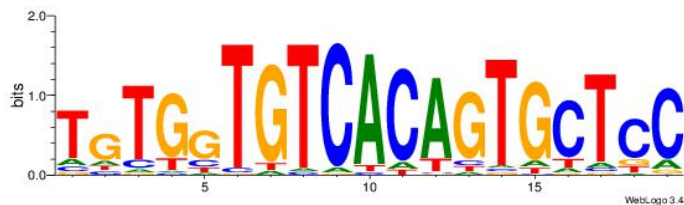


Dataset #: 2
 Motif ID: 17
 Motif name: TgTGgTGTCACAGTGCTCC
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 9
 Number of overlap: 8

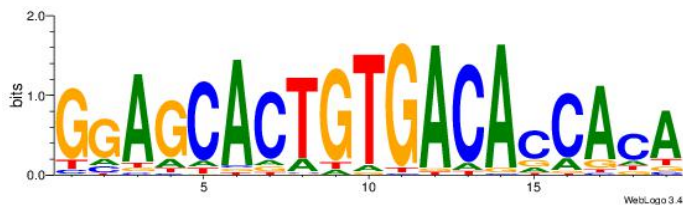
Similarity score: 0.0695512

Alignment:
TGTGGTGTACAGTGCTCC
---AAGGTCAC-----

Original motif Consensus sequence: TGTGGTGTACAGTGCTCC

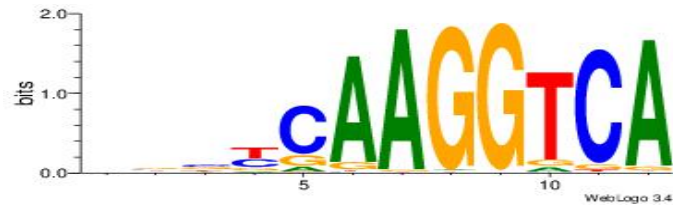


Reverse complement motif Consensus sequence: GGAGCACTGTGACACCACA

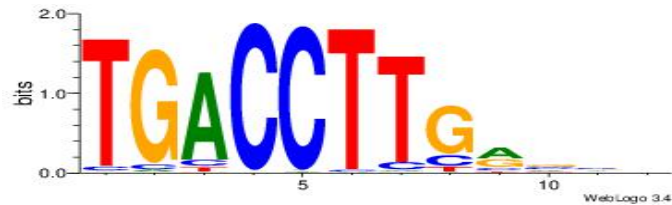


Dataset #: 1 Motif ID: 4 Motif name: Esrrb

Original motif Consensus sequence: VBBYCAAGGTCA



Reverse complement motif Consensus sequence: TGACCTGMBBB



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

Dataset #:	1
Motif ID:	2
Motif name:	NR2F1
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: 0.0442611

Alignment:
TGAMCTTTGMMCYT
--TGACCTTGMBBB

Original motif Consensus sequence: TGAMCTTTGMMCYT



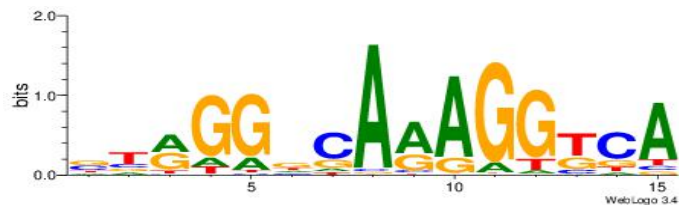
Reverse complement motif Consensus sequence: AKGYCAAAGRTC



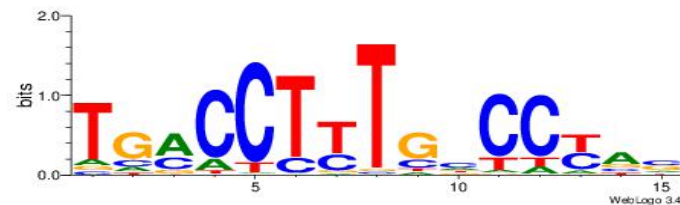
Dataset #: 1
Motif ID: 14
Motif name: PPARGRXRA
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 4
Number of overlap: 12
Similarity score: 0.04699

Alignment:
BTRGGDCARAGGKCA
---VBBYCAAGGTCA

Original motif Consensus sequence: BTRGGDCARAGGKCA



Reverse complement motif Consensus sequence: TGRCCCTKTGHCCCK

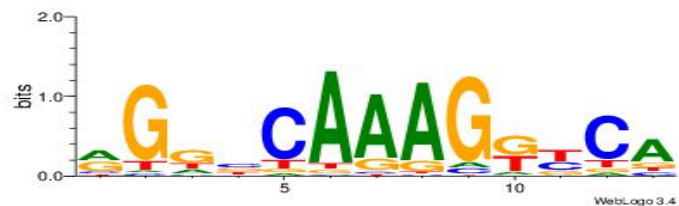


Dataset #: 1
Motif ID: 1
Motif name: HNF4A
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 12
Similarity score: 0.0470808

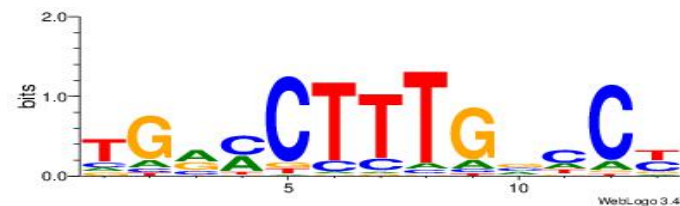
Alignment:

RGGBCAAAGKYCA
-VBBYCAAGGTCA

Original motif Consensus sequence: RGGBCAAAGKYCA



Reverse complement motif Consensus sequence: TGMYYCTTTGBCCCK

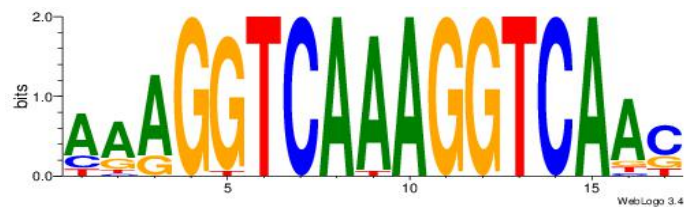


Dataset #: 1
 Motif ID: 10
 Motif name: NR1H2RXRA
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 12
 Similarity score: 0.0506977

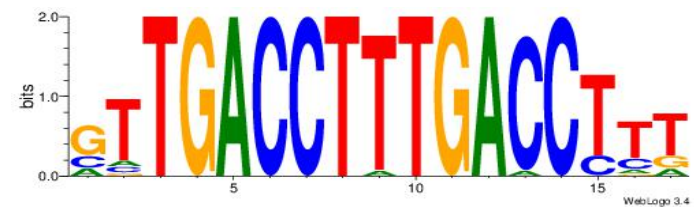
Alignment:

AAAGGTCAAAGGTCAAC
 ---VBBYCAAGGTCA--

Original motif Consensus sequence: AAAGGTCAAAGGTCAAC



Reverse complement motif Consensus sequence: GTTGACCTTTGACCTT



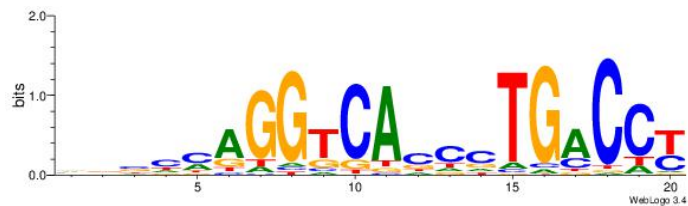
Dataset #: 1
 Motif ID: 3
 Motif name: ESR1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 9

Number of overlap: 12
Similarity score: 0.0628484

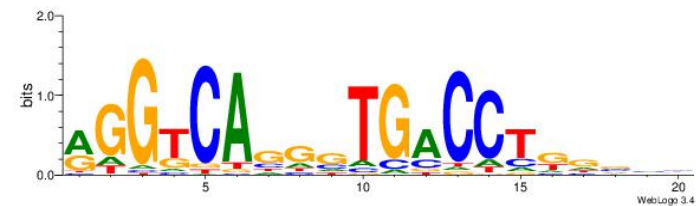
Alignment:

VDBHMAGGTCACCCTGACCY
TGACCTTGMBBB-----

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV

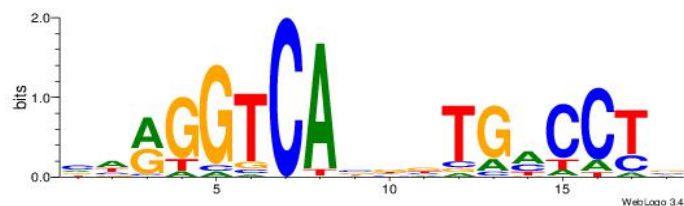


Dataset #: 1
Motif ID: 9
Motif name: ESR2
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 6
Number of overlap: 12
Similarity score: 0.0694613

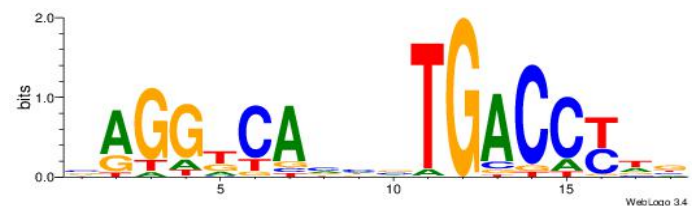
Alignment:

VHRGGTCABDBTGMCCCTB
-----TGACCTTGMBBB-

Original motif Consensus sequence: VHRGGTCABDBTGMCTB



Reverse complement motif Consensus sequence: BAGGYCABHBTGACCKHV

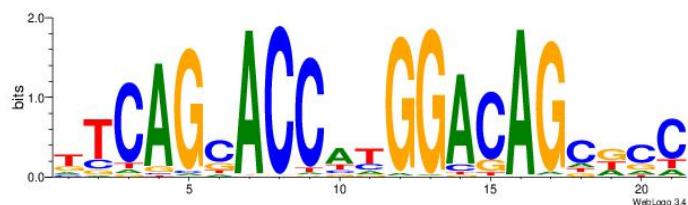


Dataset #: 1
 Motif ID: 7
 Motif name: REST
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 5
 Number of overlap: 12
 Similarity score: 0.0713236

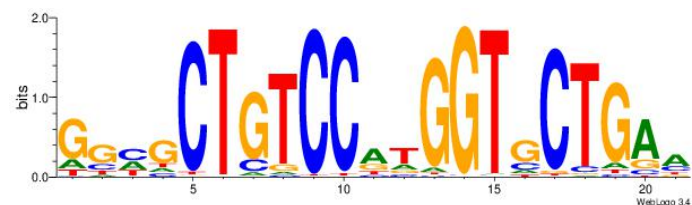
Alignment:

TTCAGCACCATGGACAGCKCC
 ----VBBYCAAGGTCA-----

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC



Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGTCTGAA

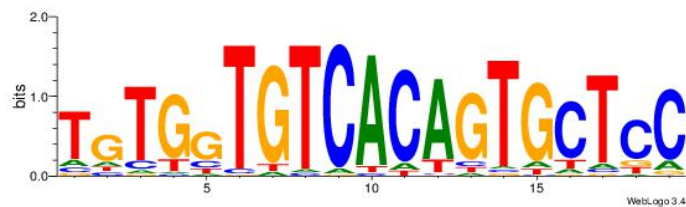


Dataset #: 2
 Motif ID: 17
 Motif name: TgTGgTGTCACAGTGCTCC
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 12
 Similarity score: 0.0772556

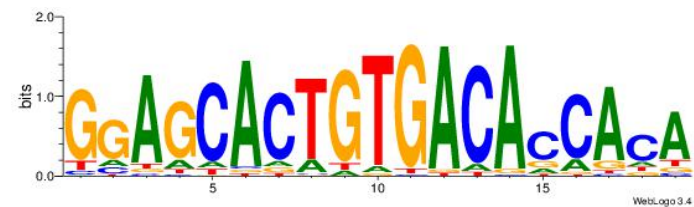
Alignment:

TGTGGTGTCACAGTGCTCC
 -----TGACCTTGMBBB

Original motif Consensus sequence: TGTGGTGTCACAGTGCTCC



Reverse complement motif Consensus sequence: GGAGCACTGTGACACCACA



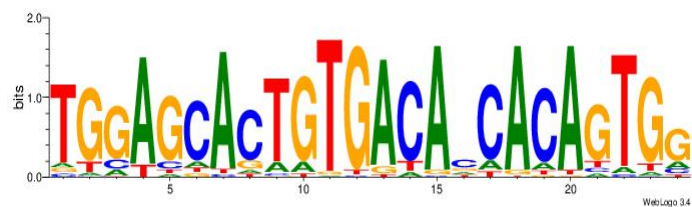
Dataset #: 2
 Motif ID: 23
 Motif name: TGGAGCACTGTGACAcCACAGTGg
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 12

Number of overlap: 12
Similarity score: 0.0785385

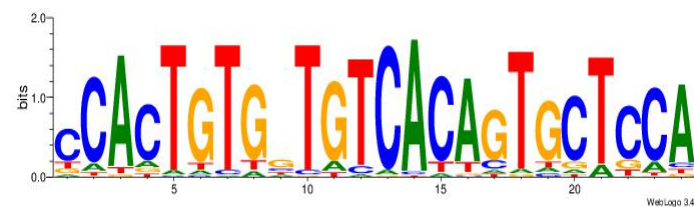
Alignment:

CCACTGTGVTGTCACAGTGCTCCA
-----TGACCTTGMBBB-

Original motif Consensus sequence: TGGAGCACTGTGACAVCACAGTGG



Reverse complement motif Consensus sequence: CCACTGTGVTGTCACAGTGCTCCA

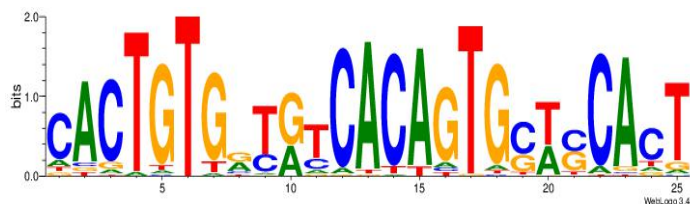


Dataset #: 2
Motif ID: 22
Motif name: CACTGTGGrYrtCACAGTGswsCAcT
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 4
Number of overlap: 12
Similarity score: 0.0832722

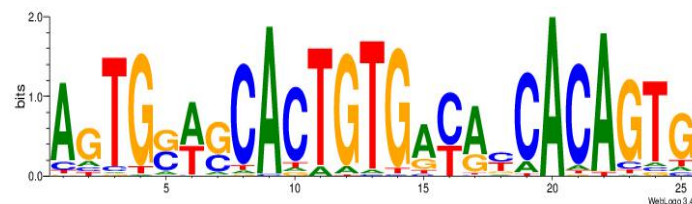
Alignment:

AGTGSWSCACTGTGAMAMCACAGTG
---VBBYCAAGGTCA-----

Original motif Consensus sequence:
CACTGTGRTRTCACAGTGSWSCACT

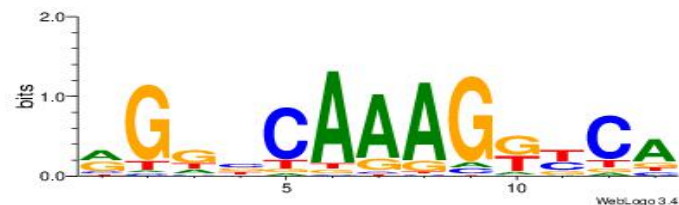


Reverse complement motif Consensus sequence:
AGTGSWSCACTGTGAMAMCACAGTG

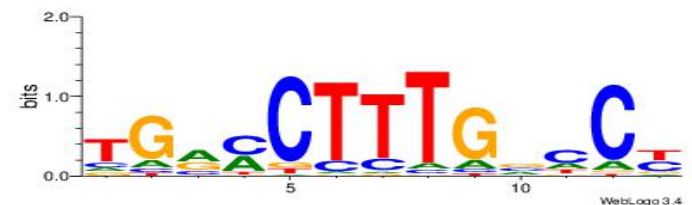


Dataset #: 1 Motif ID: 1 Motif name: HNF4A

Original motif Consensus sequence: RGGBCAAAGKYCA



Reverse complement motif Consensus sequence: TGMYCTTTGBCK



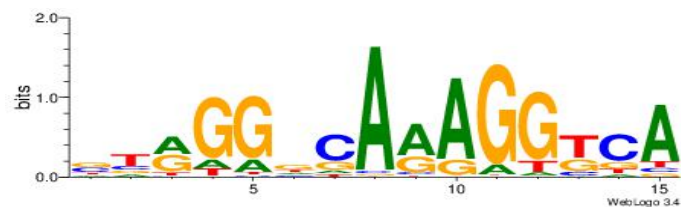
Best Matches for Significant Motif ID 1 (Highest to Lowest)

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

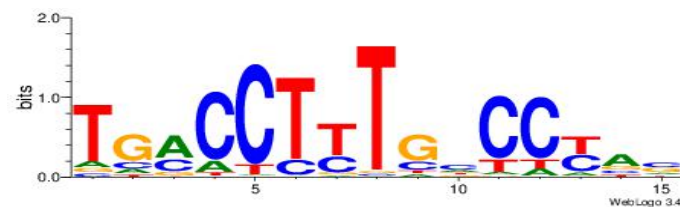
Alignment:

BTRGGDCARAGGKCA
--RGGBCAAAGKYCA

Original motif Consensus sequence: BTRGGDCARAGGKCA



Reverse complement motif Consensus sequence: TGRCCCTKGHCCK

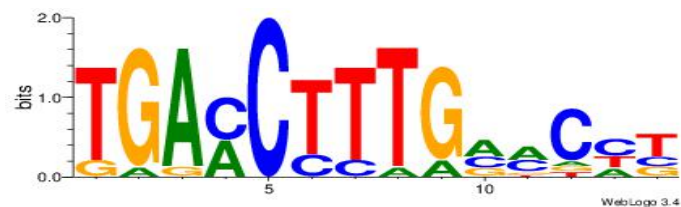


Dataset #: 1
Motif ID: 2
Motif name: NR2F1
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 2
Number of overlap: 13
Similarity score: 0.0227413

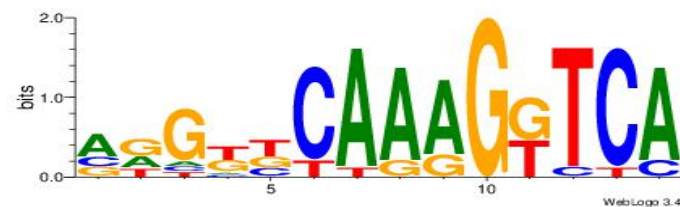
Alignment:

AKGYCAAAGRTCA
-RGGBCAAAGKYCA

Original motif Consensus sequence: TGAMCTTTGMMCYT



Reverse complement motif Consensus sequence: AKGYCAAAGRTCA



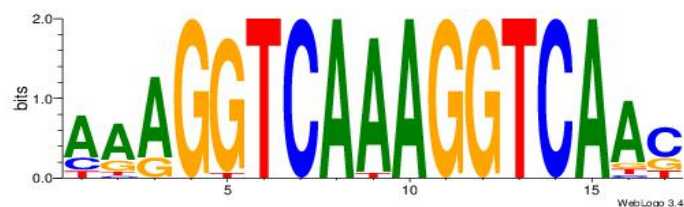
Dataset #: 1
 Motif ID: 10
 Motif name: NR1H2RXRA
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 13
 Similarity score: 0.0423023

Alignment:

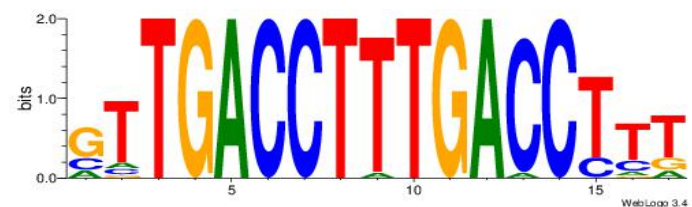
AAAGGTCAAAGGTCAAC

--RGGBCAAAGKYCA--

Original motif Consensus sequence: AAAGGTCAAAGGTCAAC



Reverse complement motif Consensus sequence: GTTGACCTTTGACCTT



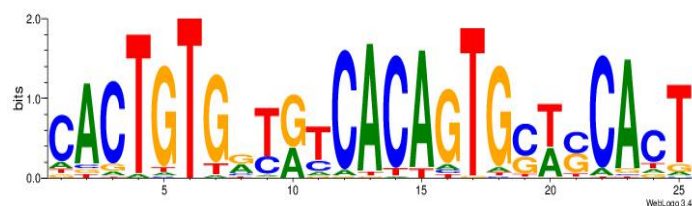
Dataset #: 2
 Motif ID: 22
 Motif name: CACTGTGrYrtCACAGTGswsCAcT
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward

Position number: 6
 Number of overlap: 13
 Similarity score: 0.0557654

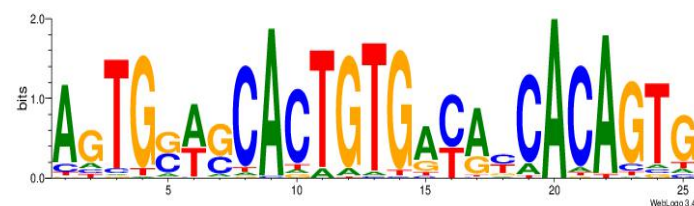
Alignment:

CACTGTGRTRTCACAGTGSWSCACT
 -----RGGBCAAAGKYCA-----

Original motif Consensus sequence:
 CACTGTGRTRTCACAGTGSWSCACT



Reverse complement motif Consensus sequence:
 AGTGSWSCACTGTGAMAMCACAGTG

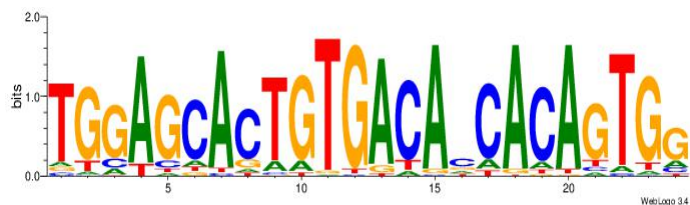


Dataset #: 2
 Motif ID: 23
 Motif name: TGGAGCACTGTGACACACAGTGg
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 4
 Number of overlap: 13
 Similarity score: 0.0656443

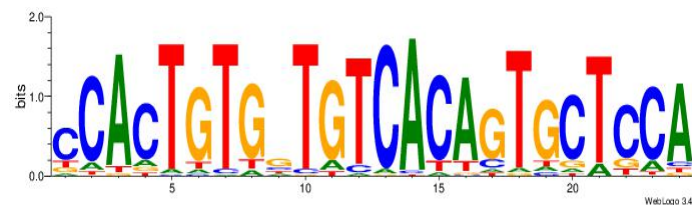
Alignment:

CCACTGTGVTGTCACAGTGCTCCA
 -----RGGBCAAAGKYCA----

Original motif Consensus sequence: TGGAGCACTGTGACAVCACAGTGG



Reverse complement motif Consensus sequence: CCACTGTGVTGTACAGTGCTCCA

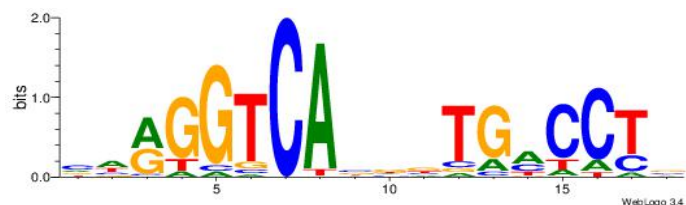


Dataset #: 1
Motif ID: 9
Motif name: ESR2
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 3
Number of overlap: 13
Similarity score: 0.0671615

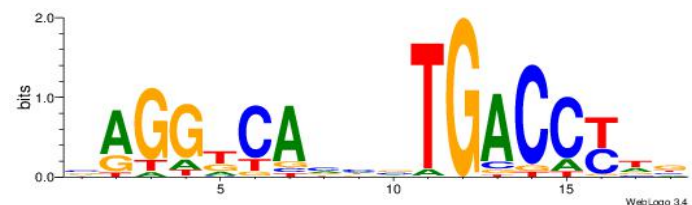
Alignment:

VHRGGTCABDBTGMCTB
--RGGBCAAAGKYCA---

Original motif Consensus sequence: VHRGGTCABDBTGMCTB



Reverse complement motif Consensus sequence: BAGGYCABHBTGACCKHV

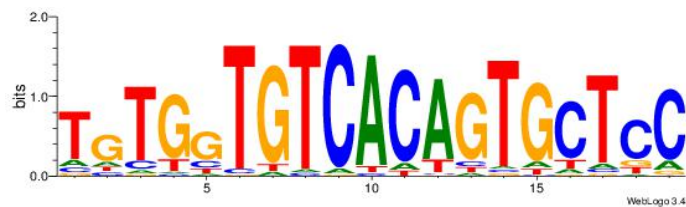


Dataset #: 2
 Motif ID: 17
 Motif name: TgTGgTGTCACAGTGCTCC
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 13
 Similarity score: 0.0681338

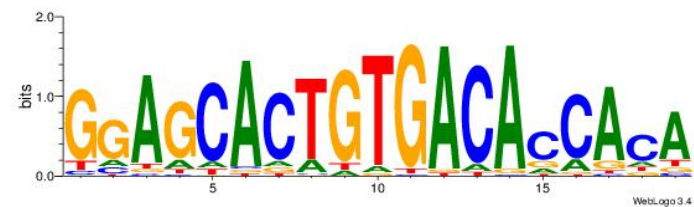
Alignment:

TGTGGTGTCACAGTGCTCC
 ----RGGBCAAAGKYCA--

Original motif Consensus sequence: TGTGGTGTCACAGTGCTCC



Reverse complement motif Consensus sequence: GGAGCACTGTGACACCACA



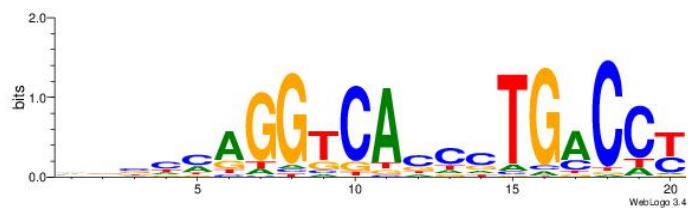
Dataset #: 1
 Motif ID: 3
 Motif name: ESR1
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1

Number of overlap: 13
Similarity score: 0.0711137

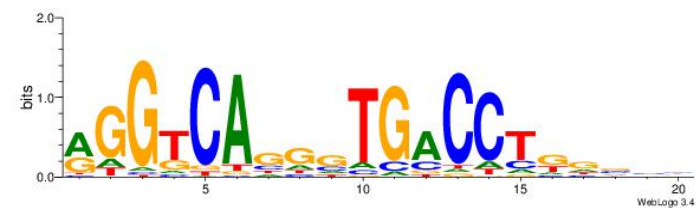
Alignment:

MGGTCAGGGTGACCTRDBHV
RGGBCAAAGKYCA-----

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV

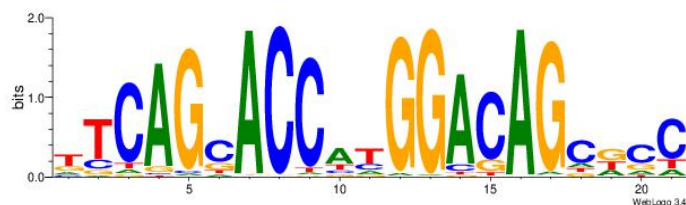


Dataset #: 1
Motif ID: 7
Motif name: REST
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 6
Number of overlap: 13
Similarity score: 0.0741922

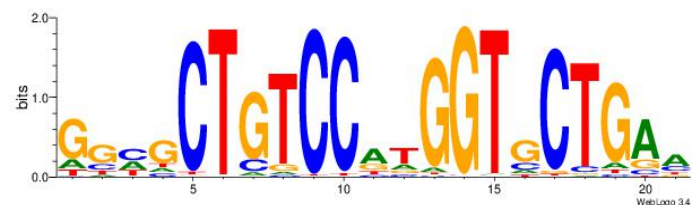
Alignment:

GGYGCTGTCCATGGTGCTGAA
-----TGM YCTTTGBCK---

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC



Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA

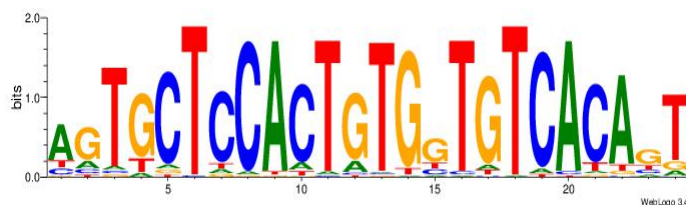


Dataset #: 2
Motif ID: 27
Motif name: AgTGCTCCACTGTGgTGTCACAgT
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 6
Number of overlap: 13
Similarity score: 0.0799096

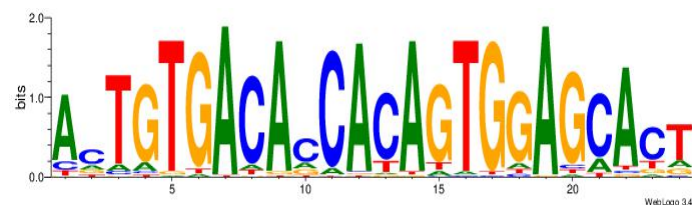
Alignment:

ACTGTGACACCACAGTGGAGCACT
-----RGGBCAAAGKYCA-----

Original motif Consensus sequence: AGTGCTCCACTGTGGTGTCACAGT



Reverse complement motif Consensus sequence: ACTGTGACACCACAGTGGAGCACT

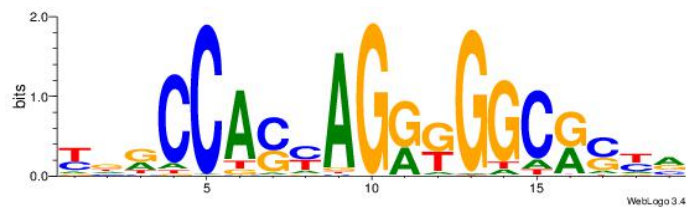


Dataset #: 1
 Motif ID: 16
 Motif name: CTCF
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 13
 Similarity score: 0.0850642

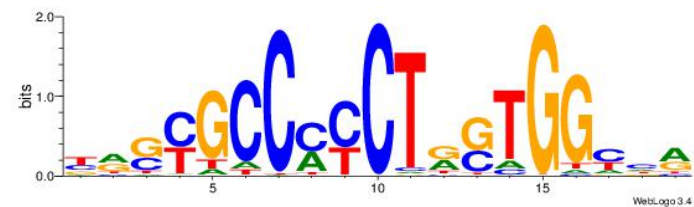
Alignment:

YDRCCASYAGRKGGRSYV
 ---RGGBCAAAGKYCA---

Original motif Consensus sequence: YDRCCASYAGRKGGRSYV



Reverse complement motif Consensus sequence: BMSMGCCYMCTKSTGGMHM



Dataset #: 1 Motif ID: 12 Motif name: RORA_1

Original motif Consensus sequence: AWVDAGGTCA

Reverse complement motif Consensus sequence: TGACCTDVWT



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

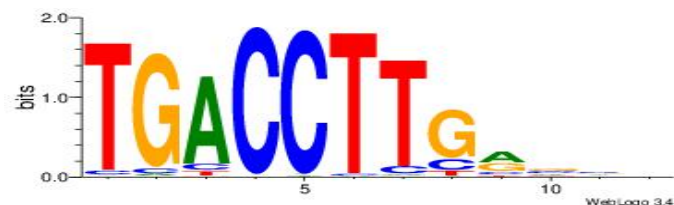
Dataset #: 1
 Motif ID: 4
 Motif name: Esrrb
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 10
 Similarity score: 0.029401

Alignment:
 VBBYCAAGGTCA
 --AWVDAGGTCA

Original motif Consensus sequence: VBBYCAAGGTCA



Reverse complement motif Consensus sequence: TGACCTTGMBBB



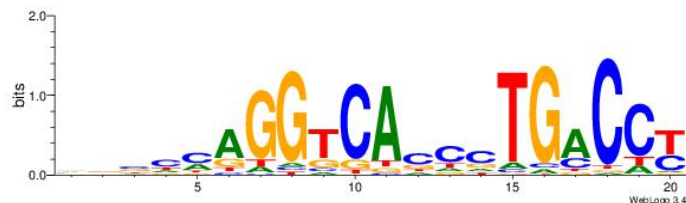
Dataset #: 1

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: 10
 Similarity score: 0.0417851

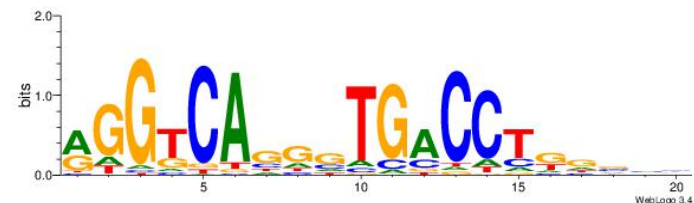
Alignment:

MGGTCAGGGTGACCTRDBHV
 -----TGACCTDVWT-

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV

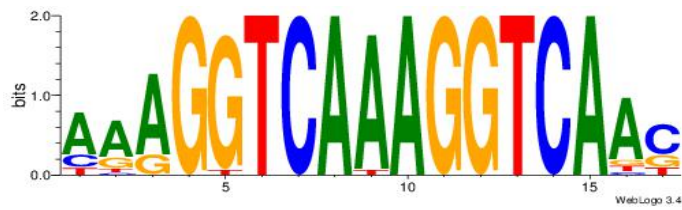


Dataset #: 1
 Motif ID: 10
 Motif name: NR1H2RXRA
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 6
 Number of overlap: 10

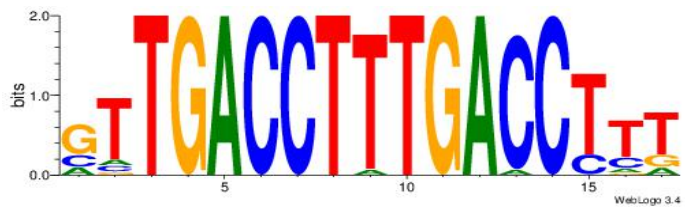
Similarity score: 0.05425

Alignment:
AAAGGTCAAAGGTCAAC
-----AWVDAGGTCA--

Original motif Consensus sequence: AAAGGTCAAAGGTCAAC



Reverse complement motif Consensus sequence: GTTGACCTTTGACCTTT

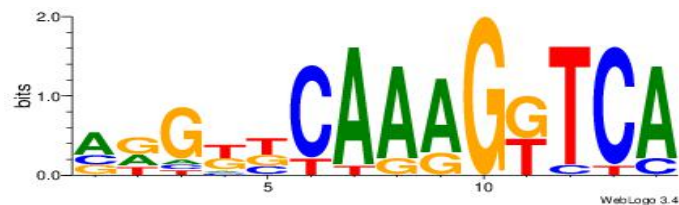


Dataset #: 1
Motif ID: 2
Motif name: NR2F1
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 5
Number of overlap: 10
Similarity score: 0.0654808

Alignment:
TGAMCTTTGMMCYT
-----TGACCTDVWT

Original motif Consensus sequence: TGAMCTTTGMMCYT

Reverse complement motif Consensus sequence: AKGYCAAAGRTC

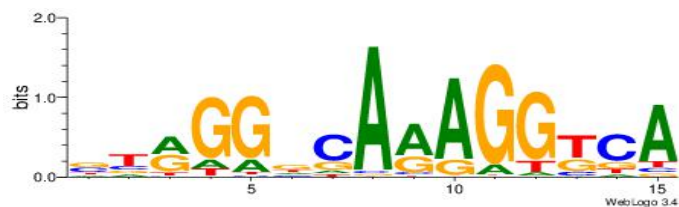


Dataset #: 1
 Motif ID: 14
 Motif name: PPARGRXRA
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 10
 Similarity score: 0.06668

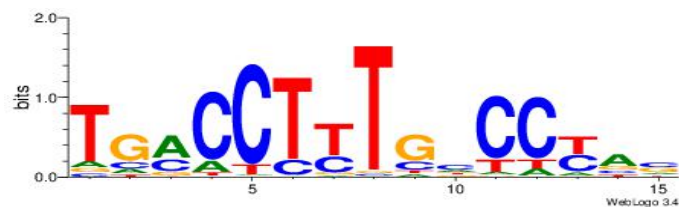
Alignment:

BTRGGDCARAGGKCA
 -----AWVDAGGTCA

Original motif Consensus sequence: BTRGGDCARAGGKCA



Reverse complement motif Consensus sequence: TGRCCCTKTGHCCCK



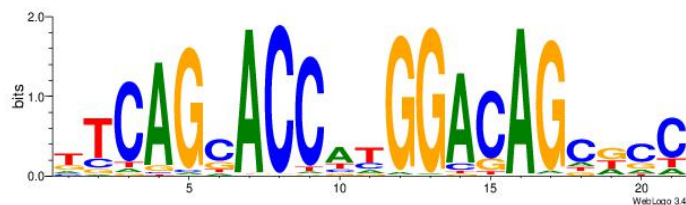
Dataset #: 1
 Motif ID: 7

Motif name:	REST
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:	0.0755608

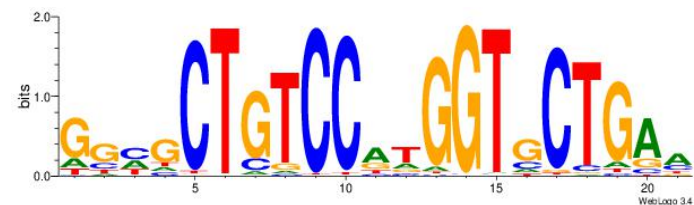
Alignment:

```
TTCAGCACCATGGACAGCKCC
-----AWVDAGGTCA-----
```

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC



Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA



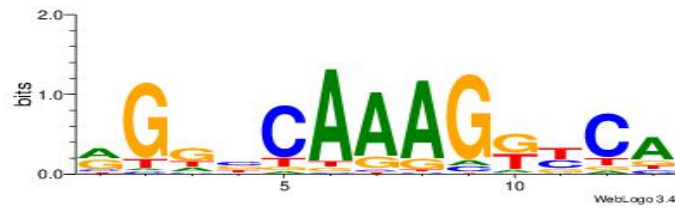
Dataset #:	1
Motif ID:	1
Motif name:	HNF4A
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	4
Number of overlap:	10
Similarity score:	0.0803396

Alignment:

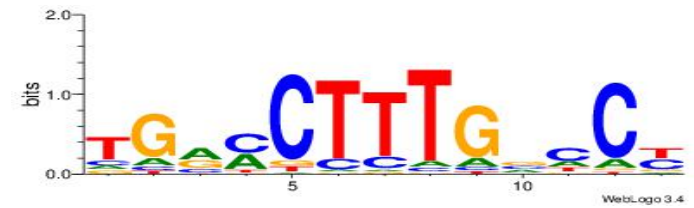
RGGBCAAAGKYCA

---AWVDAGGTCA

Original motif Consensus sequence: RGGBCAAAGKYCA



Reverse complement motif Consensus sequence: TGMYYCTTTGBCCK



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: 10

Number of overlap: 10

Similarity score: 0.0889306

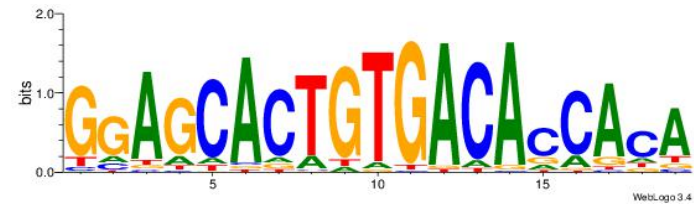
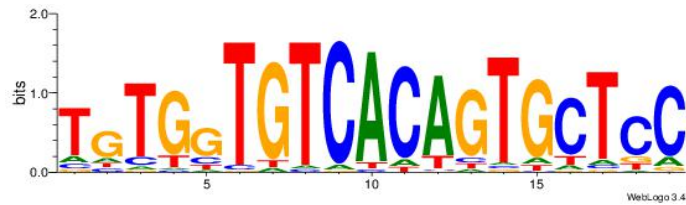
Alignment:

GGAGCACTGTGACACCACA

-----TGACCTDVWT

Original motif Consensus sequence: TGTGGTGTCACAGTGCTCC

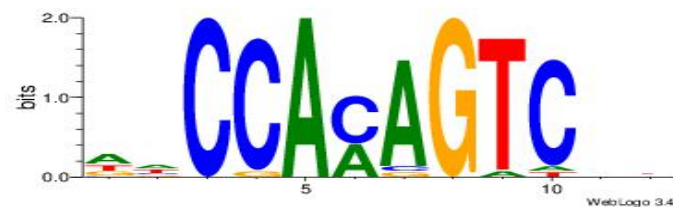
Reverse complement motif Consensus sequence:
GGAGCACTGTGACACCACA



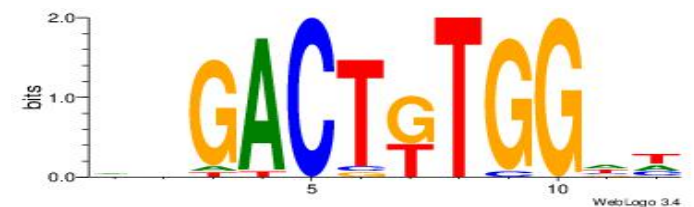
Dataset #: 2
 Motif ID: 25
 Motif name: wwCCAmAGTCmt
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 10
 Similarity score: 0.09225

Alignment:
 DDCCAMAGTCHB
 -AWVDAGGTCA-

Original motif Consensus sequence: DDCCAMAGTCHB



Reverse complement motif Consensus sequence: VDGACTRTGGDD



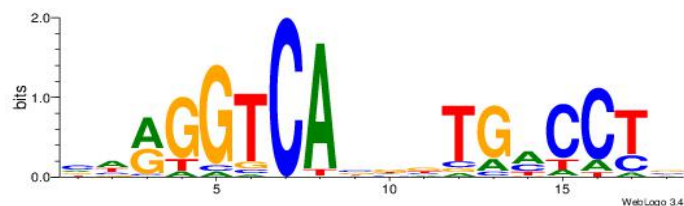
Dataset #: 1
 Motif ID: 9

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: 10
 Similarity score: 0.0988214

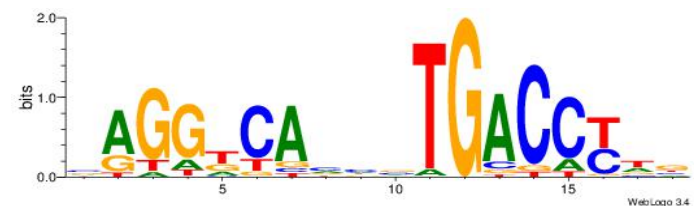
Alignment:

BAGGYCABHBTGACCKHV
 -----AWVDAGGTCA----

Original motif Consensus sequence: VHRGGTCABDBTGMCCCTB



Reverse complement motif Consensus sequence: BAGGYCABHBTGACCKHV



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

Original motif Consensus sequence: HSCACGTGGC



Reverse complement motif Consensus sequence: GCCACGTGSD



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

Dataset #: 1
Motif ID: 8
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:

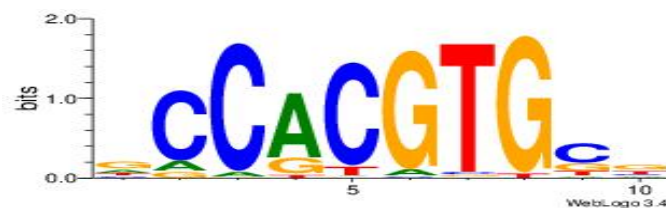
DCCACGTGCV

GCCACGTGSD

Original motif Consensus sequence: VGCACGTGGH



Reverse complement motif Consensus sequence: DCCACGTGCV



Dataset #: 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



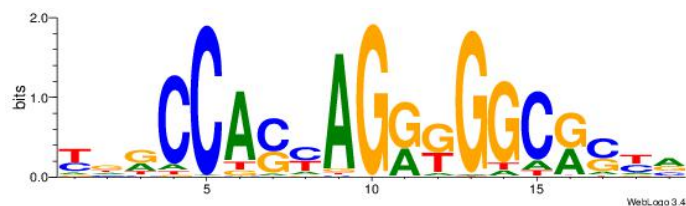
Reverse complement motif Consensus sequence: SBCGCGGGGSB



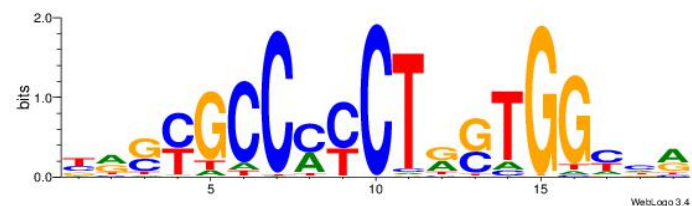
Dataset #: 1
Motif ID: 16
Motif name: CTCF
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 6
Number of overlap: 10
Similarity score: 0.0679017

Alignment:
YDRCCASYAGRKGGCRSYV
-----HSCACGTGGC-----

Original motif Consensus sequence: YDRCCASYAGRKGGCRSYV



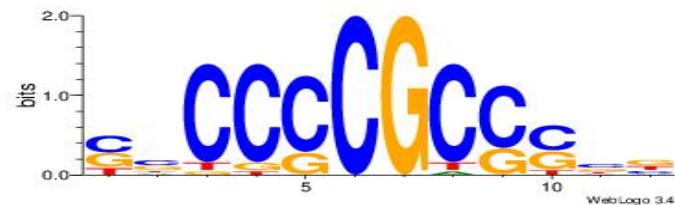
Reverse complement motif Consensus sequence: BMSGCCYMCTKSTGGMHM



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

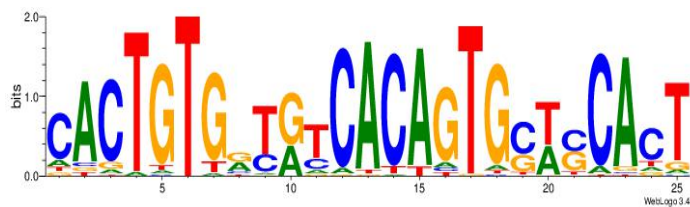


Dataset #: 2
 Motif ID: 22
 Motif name: CACTGTGrYrtCACAGTGswsCAcT
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 10
 Number of overlap: 10
 Similarity score: 0.0883224

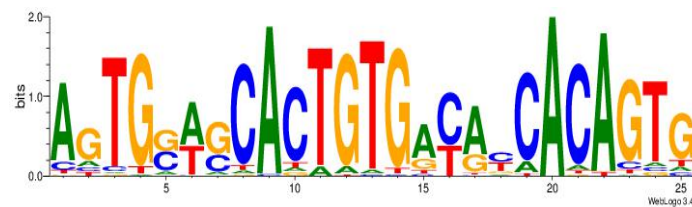
Alignment:

AGTGSWSCACTGTGAMAMCACAGTG
 -----GCCACGTGSD-----

Original motif Consensus sequence:
 CACTGTGRTRTCACAGTGSWSCACT



Reverse complement motif Consensus sequence:
 AGTGSWSCACTGTGAMAMCACAGTG



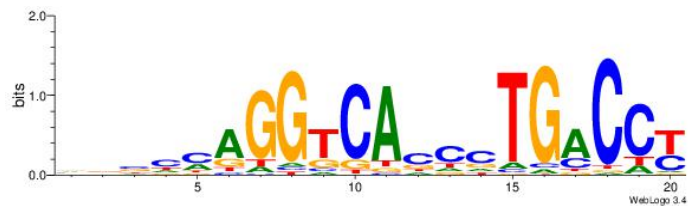
Dataset #: 1
 Motif ID: 3
 Motif name: ESR1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3

Number of overlap: 10
Similarity score: 0.089863

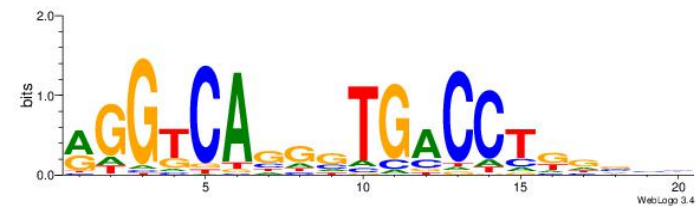
Alignment:

MGGTCAGGGTGACCTRDBHV
-----GCCACGTGSD--

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV

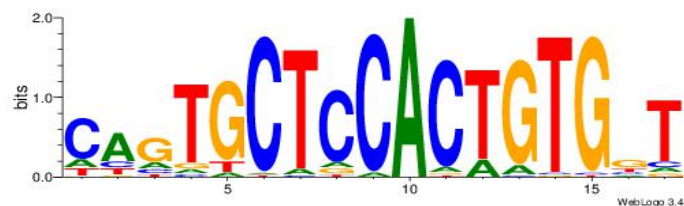


Dataset #: 2
Motif ID: 20
Motif name: CagTGCTCCACTGTGgT
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 7
Number of overlap: 10
Similarity score: 0.0943014

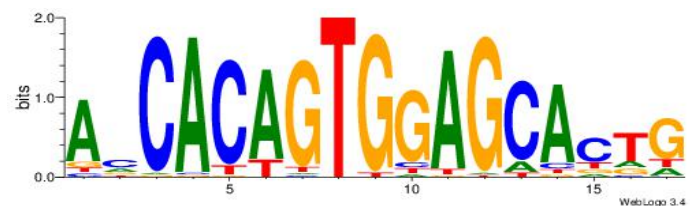
Alignment:

ABCACAGTGGAGCACTG
-GCCACGTGSD-----

Original motif Consensus sequence: CAGTGCTCCACTGTGBT



Reverse complement motif Consensus sequence: ABCACAGTGGAGCACTG

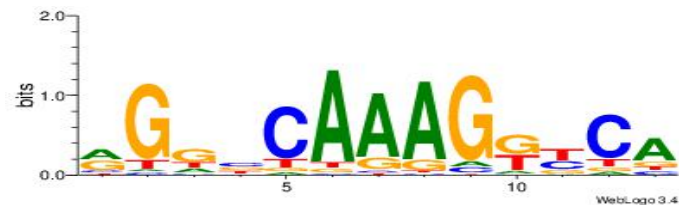


Dataset #: 1
Motif ID: 1
Motif name: HNF4A
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 2
Number of overlap: 10
Similarity score: 0.0947124

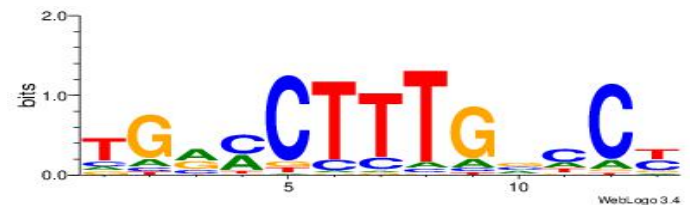
Alignment:

TGMYCTTTGBCK
-GCCACGTGSD--

Original motif Consensus sequence: RGGBCAAAGKYCA



Reverse complement motif Consensus sequence: TGMYCTTTGBCK

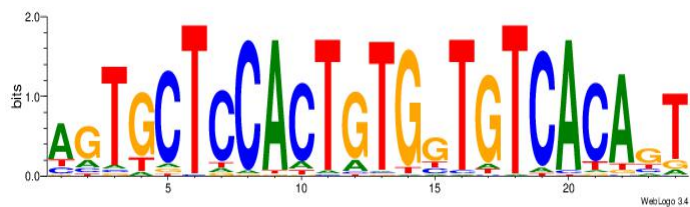


Dataset #: 2
 Motif ID: 27
 Motif name: AgTGCTCCACTGTGgTGTCACAgT
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 6
 Number of overlap: 10
 Similarity score: 0.0949359

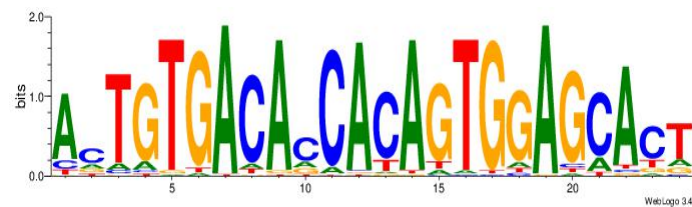
Alignment:

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

Original motif Consensus sequence: AGTGCTCCACTGTGGTGTTCACAGT



Reverse complement motif Consensus sequence: ACTGTGACACCACAGTGGAGCACT

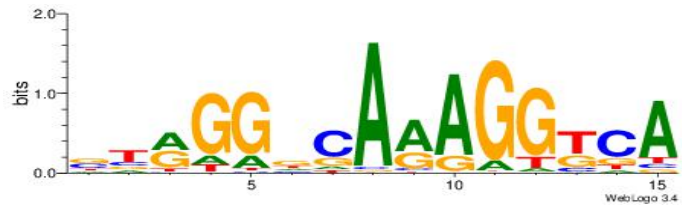


Dataset #: 1
 Motif ID: 14
 Motif name: PPARGRXRA
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 5

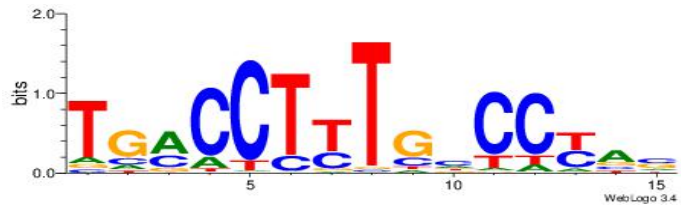
Number of overlap: 10
Similarity score: 0.0954444

Alignment:
TGRCCCTKTGHCCCKAB
-GCCACGTGSD-----

Original motif Consensus sequence: BTRGGDCARAGGKCA

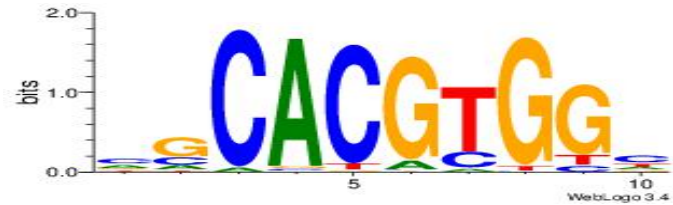


Reverse complement motif Consensus sequence: TGRCCCTKTGHCCCK

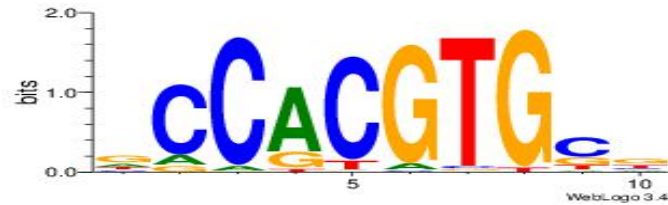


Dataset #: 1 Motif ID: 8 Motif name: Myc

Original motif Consensus sequence: VGCACGTGGH



Reverse complement motif Consensus sequence: DCCACGTGCV



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

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: 1
 Number of overlap: 10
 Similarity score: 0

Alignment:

HSCACGTGGC

VGCACGTGGH

Original motif Consensus sequence: HSCACGTGGC



Reverse complement motif Consensus sequence: GCCACGTGSD



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

Alignment:

BSCCCCGCGBS

-DCCACGTGCV

Original motif Consensus sequence: BSCCCCGCGBS



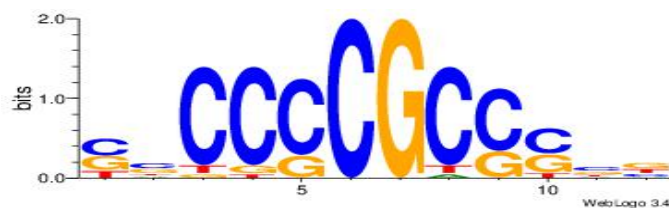
Reverse complement motif Consensus sequence: SBCGCGGGGSB



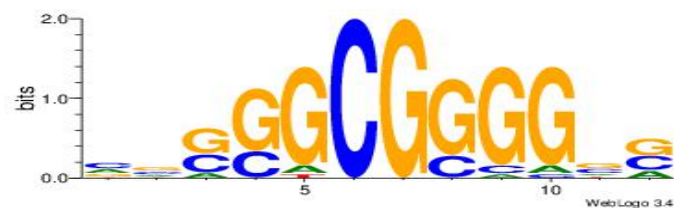
Dataset #: 2
Motif ID: 24
Motif name: ssCCCCGCSSsk
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2
Number of overlap: 10
Similarity score: 0.0728588

Alignment:
SBCCCCGCCSBB
-DCCACGTGCV-

Original motif Consensus sequence: SBCCCCGCCSBB



Reverse complement motif Consensus sequence: BBSGGCGGGGBS

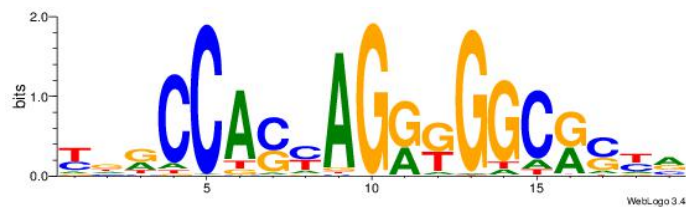


Dataset #: 1
 Motif ID: 16
 Motif name: CTCF
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 8
 Number of overlap: 10
 Similarity score: 0.0754257

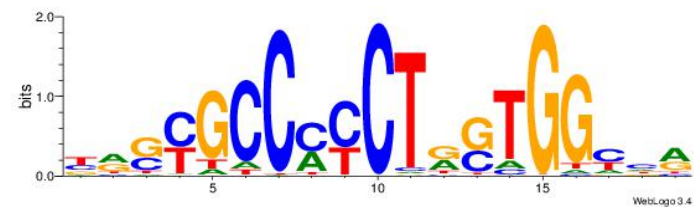
Alignment:

YDRCCASYAGRKGGRSYV
 --DCCACGTGCV-----

Original motif Consensus sequence: YDRCCASYAGRKGGRSYV



Reverse complement motif Consensus sequence: BMSMGCCYMCTKSTGGMHM

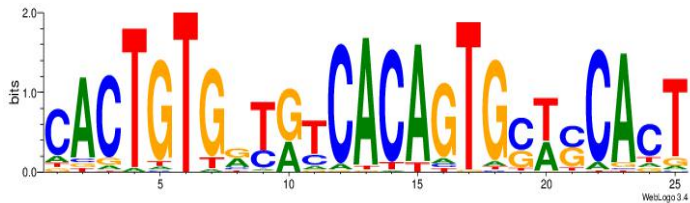


Dataset #: 2
 Motif ID: 22
 Motif name: CACTGTGrYrtCACAGTGswsCAcT
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 6

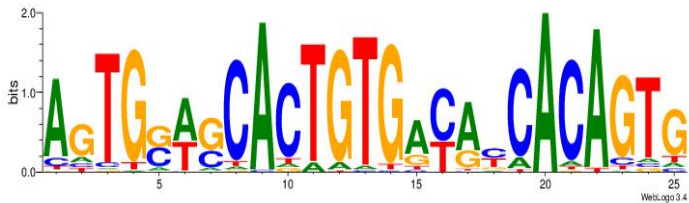
Number of overlap: 10
Similarity score: 0.0888909

Alignment:
CACTGTGRTRTCACAGTGSWSCACT
-----DCCACGTGCV-----

Original motif Consensus sequence:
CACTGTGRTRTCACAGTGSWSCACT



Reverse complement motif Consensus sequence:
AGTGSWSCACTGTGAMAMCACAGTG

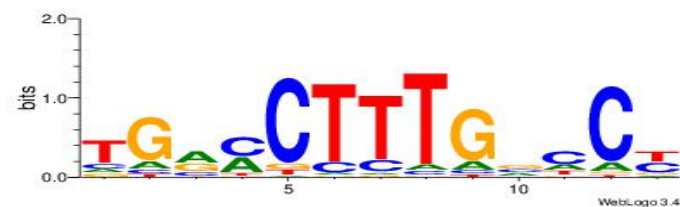
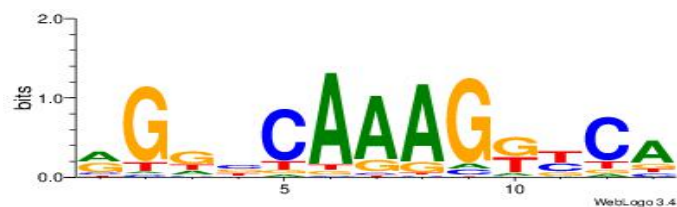


Dataset #: 1
Motif ID: 1
Motif name: HNF4A
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 10
Similarity score: 0.0934488

Alignment:
TGMCTTTGBCK
---VGCACGTGGH

Original motif Consensus sequence: RGGBCAAAGKYCA

Reverse complement motif Consensus sequence: TGMCTTTGBCK

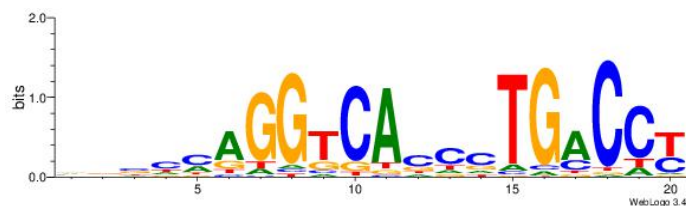


Dataset #: 1
 Motif ID: 3
 Motif name: ESR1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 9
 Number of overlap: 10
 Similarity score: 0.0940438

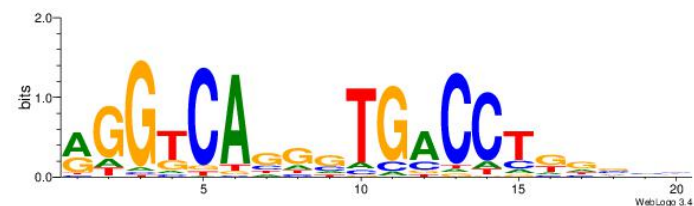
Alignment:

MGGTCAGGGTGACCTRDBHV
 -----DCCACGTGCV--

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV

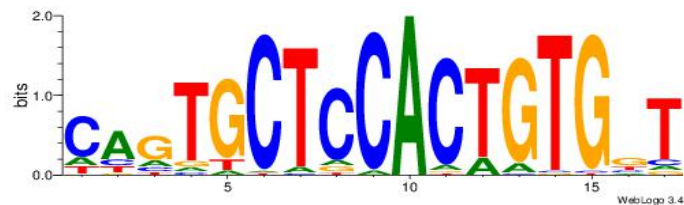


Dataset #: 2

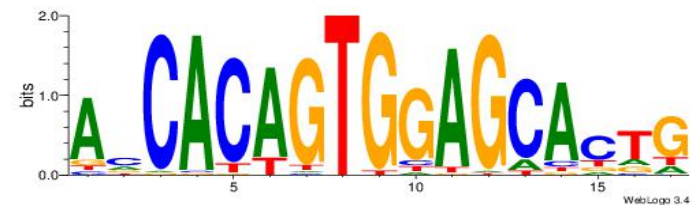
Motif ID: 20
 Motif name: CagTGCTCCACTGTGgT
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 7
 Number of overlap: 10
 Similarity score: 0.0955234

Alignment:
 ABCACAGTGGAGCACTG
 -DCCACGTGCV-----

Original motif Consensus sequence: CAGTGCTCCACTGTGBT



Reverse complement motif Consensus sequence: ABCACAGTGGAGCACTG



Dataset #: 1
 Motif ID: 9
 Motif name: ESR2
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 5
 Number of overlap: 10

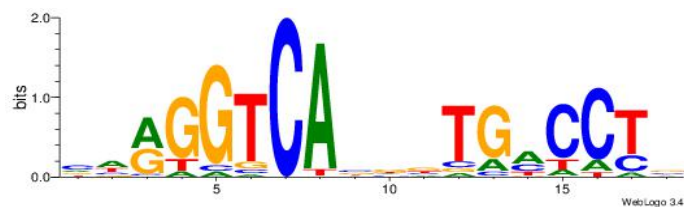
Similarity score: 0.0968598

Alignment:

VHRGGTCABDBTGMCTB

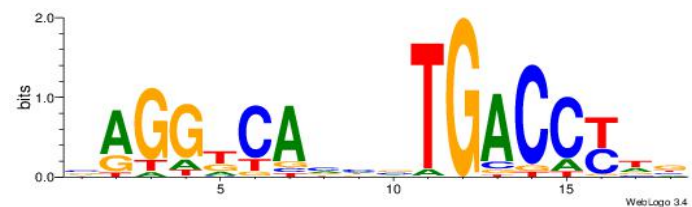
-----VGCACGTGGH-----

Original motif Consensus sequence: VHRGGTCABDBTGMCTB



Reverse complement motif
BAGGYCABHBTGACCKHV

Consensus sequence:



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

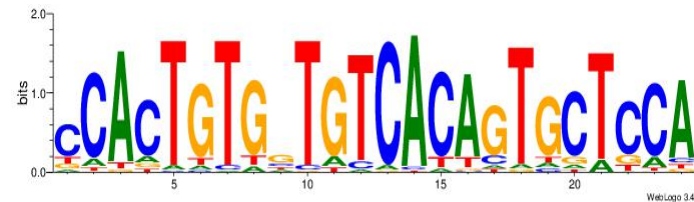
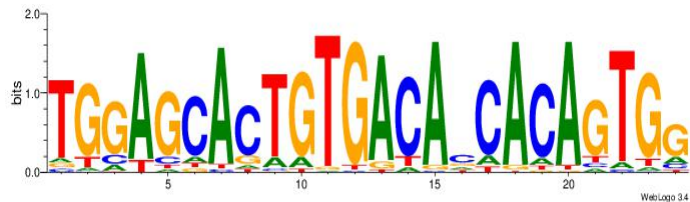
Alignment:

TGGAGCACTGTGACAVCACAGTGG

-----DCCACGTGCV-----

Original motif Consensus sequence: TGGAGCACTGTGACAVCACAGTGG

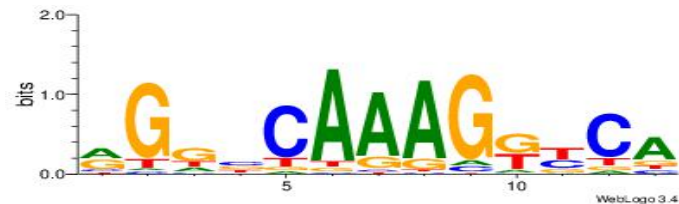
Reverse complement motif Consensus sequence:
CCTACTGTGVTGTACAGTGCTCCA



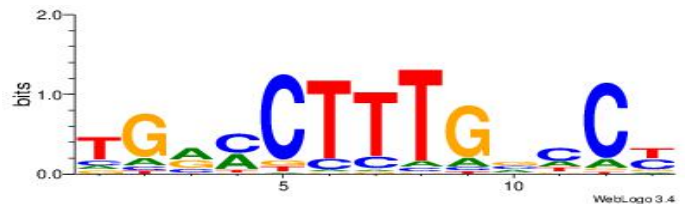
Best Matches for Each Motif (Highest to Lowest)

Dataset #: 1 Motif ID: 1 Motif name: HNF4A

Original motif Consensus sequence: RGGBCAAAGKYCA



Reverse complement motif Consensus sequence: TGMYCTTTGBCCK



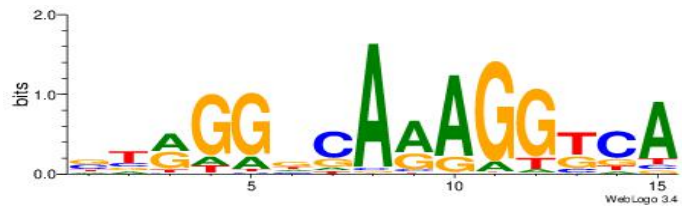
Best Matches for Motif ID 1 (Highest to Lowest)

Dataset #:	1
Motif ID:	14
Motif name:	PPARGRXRA
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	3
Number of overlap:	13

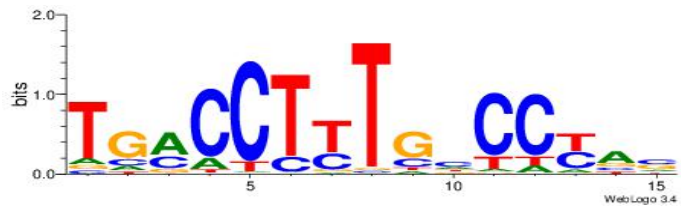
Similarity score: 0

Alignment:
BTRGGDCARAGGKCA
--RGGBCAAAGKYCA

Original motif Consensus sequence: BTRGGDCARAGGKCA



Reverse complement motif Consensus sequence: TGRCCCTKTGHCCCK

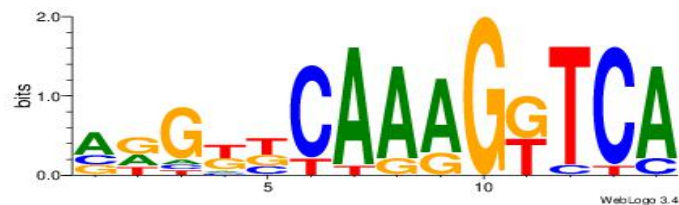


Dataset #: 1
Motif ID: 2
Motif name: NR2F1
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 2
Number of overlap: 13
Similarity score: 0.0227413

Alignment:
AKGY YCAAAGRTCA
-RGGBCAAAGKYCA

Original motif Consensus sequence: TGAMCTTTGMMCYT

Reverse complement motif Consensus sequence: AKGY YCAAAGRTC

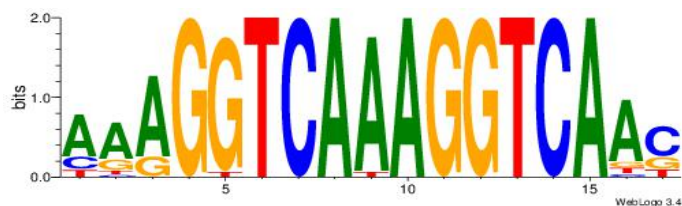


Dataset #: 1
 Motif ID: 10
 Motif name: NR1H2RXRA
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 13
 Similarity score: 0.0423023

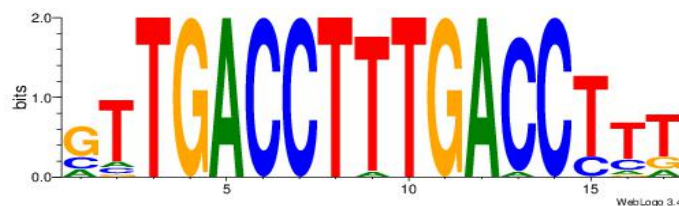
Alignment:

AAAGGTCAAAGGTCAAC
 --RGGBCAAAGKYCA--

Original motif Consensus sequence: AAAGGTCAAAGGTCAAC



Reverse complement motif Consensus sequence: GTTGACCTTTGACCTTT



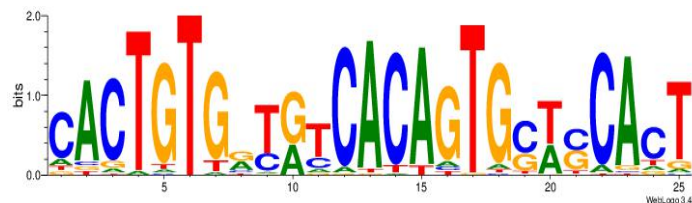
Dataset #: 2

Motif ID: 22
 Motif name: CACTGTGrYrtCACAGTGsWsCAcT
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 6
 Number of overlap: 13
 Similarity score: 0.0557654

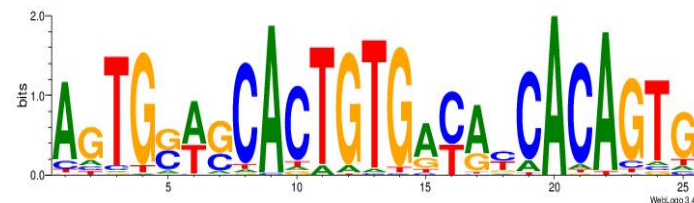
Alignment:

CACTGTGRTRTCACAGTGSWSCACT
 -----RGGBCAAAGKYCA-----

Original motif Consensus sequence:
 CACTGTGRTRTCACAGTGSWSCACT



Reverse complement motif Consensus sequence:
 AGTGSWSCACTGTGAMAMCACAGTG

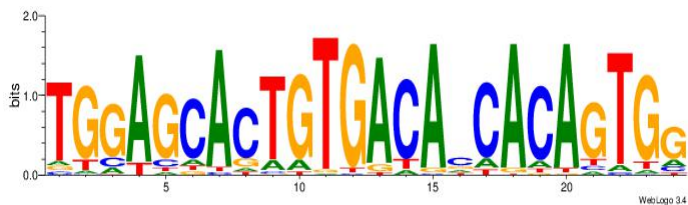


Dataset #: 2
 Motif ID: 23
 Motif name: TGGAGCACTGTGACAcCACAGTGg
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 4
 Number of overlap: 13

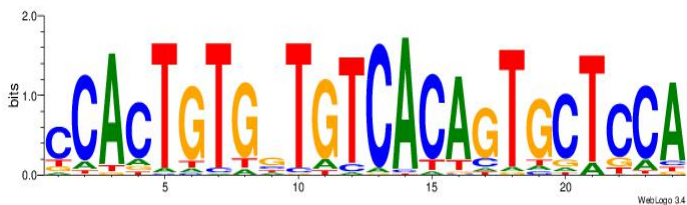
Similarity score: 0.0656443

Alignment:
CCACTGTGVTGTCACAGTGCTCCA
-----RGGBCAAAGKYCA---

Original motif Consensus sequence: TGGAGCACTGTGACAVCACAGTGG



Reverse complement motif Consensus sequence: CCACTGTGVTGTCACAGTGCTCCA

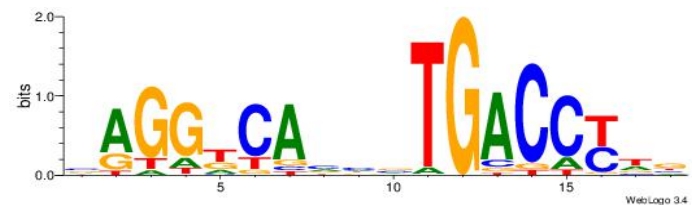
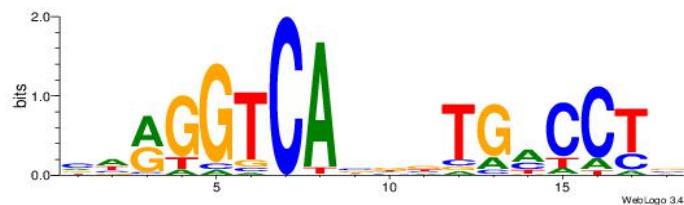


Dataset #: 1
Motif ID: 9
Motif name: ESR2
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 3
Number of overlap: 13
Similarity score: 0.0671615

Alignment:
VHRGGTCABDBTGMCTB
--RGGBCAAAGKYCA---

Original motif Consensus sequence: VHRGGTCABDBTGMCTB

Reverse complement motif Consensus sequence: BAGGYCABHBTGACCKHV

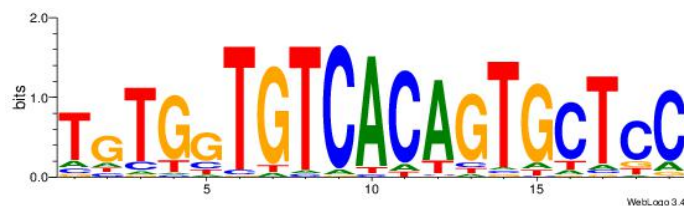


Dataset #: 2
 Motif ID: 17
 Motif name: TgTGgTGTCACAGTGCTCC
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 13
 Similarity score: 0.0681338

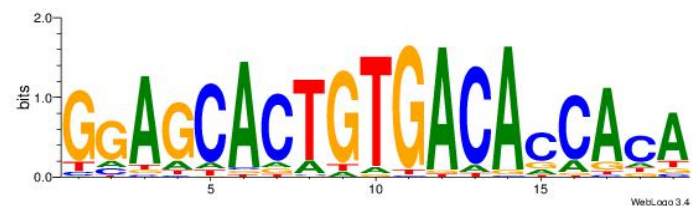
Alignment:

TGTGGTGTCACAGTGCTCC
 ----RGGBCAAAGKYCA--

Original motif Consensus sequence: TGTGGTGTCACAGTGCTCC



Reverse complement motif Consensus sequence:
 GGAGCACTGTGACACCACA



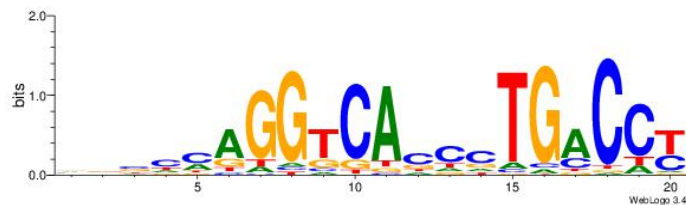
Dataset #: 1

Motif ID: 3
 Motif name: ESR1
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 13
 Similarity score: 0.0711137

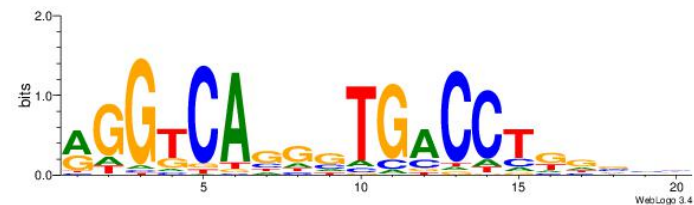
Alignment:

MGGTCAGGGTGACCTRDBHV
 RGGBCAAAGKYCA-----

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV

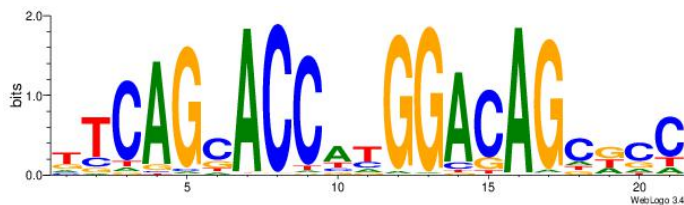


Dataset #: 1
 Motif ID: 7
 Motif name: REST
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 6
 Number of overlap: 13

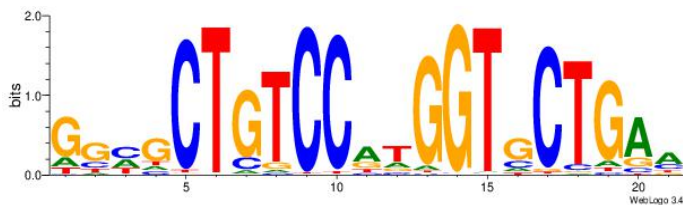
Similarity score: 0.0741922

Alignment:
GGYGCTGTCCATGGTGCTGAA
-----TGM YCTTTGBCK---

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC



Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA

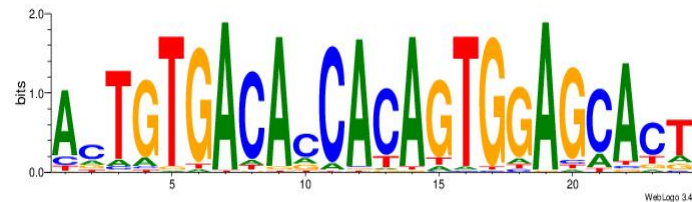
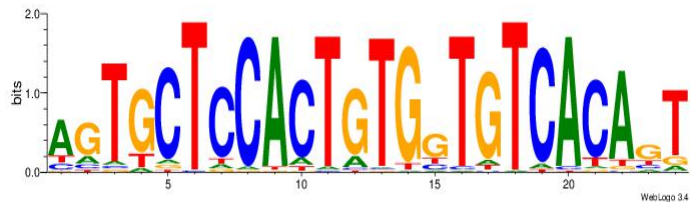


Dataset #: 2
Motif ID: 27
Motif name: AgTGCTCCACTGTGgTGTCACAgT
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 6
Number of overlap: 13
Similarity score: 0.0799096

Alignment:
ACTGTGACACCACAGTGGAGCACT
-----RGGBCAAAGKYCA-----

Original motif Consensus sequence: AGTGCTCCACTGTGGTGTACAGT

Reverse complement motif Consensus sequence: ACTGTGACACCACAGTGGAGCACT

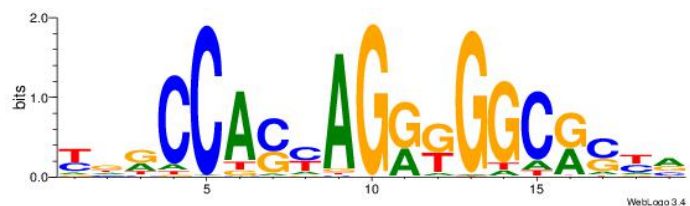


Dataset #: 1
 Motif ID: 16
 Motif name: CTCF
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 13
 Similarity score: 0.0850642

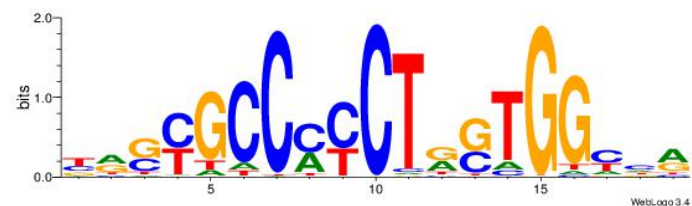
Alignment:

YDRCCASYAGRKGGRSYV
 ---RGGBCAAAGKYCA---

Original motif Consensus sequence: YDRCCASYAGRKGGRSYV



Reverse complement motif Consensus sequence: BMSMGCCYMCTKSTGGMHM

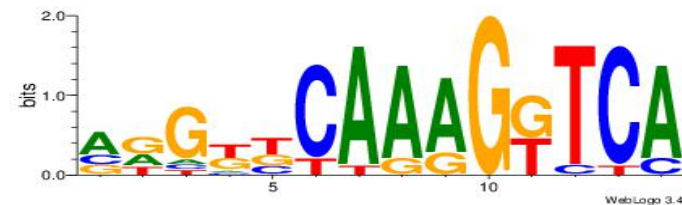


Dataset #: 1 Motif ID: 2 Motif name: NR2F1

Original motif Consensus sequence: TGAMCTTTGMMCYT



Reverse complement motif Consensus sequence: AKGYCAAAGRTC



Best Matches for Motif ID 2 (Highest to Lowest)

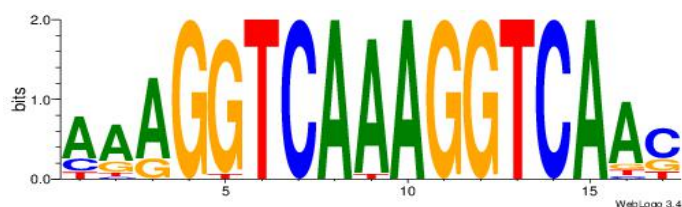
Dataset #:	1
Motif ID:	10
Motif name:	NR1H2RXRA
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	2
Number of overlap:	14
Similarity score:	0.0174588

Alignment:

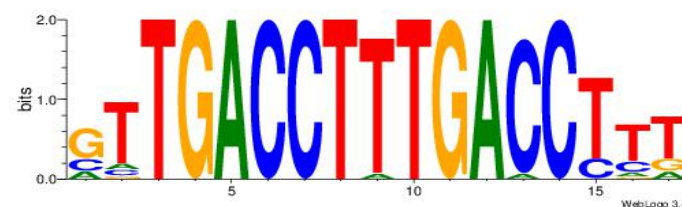
GTTGACCTTTGACCTTT

--TGAMCTTTGMMCYT--

Original motif Consensus sequence: AAAGGTCAAAGGTCAAC



Reverse complement motif Consensus sequence: GTTGACCTTTGACCTTT



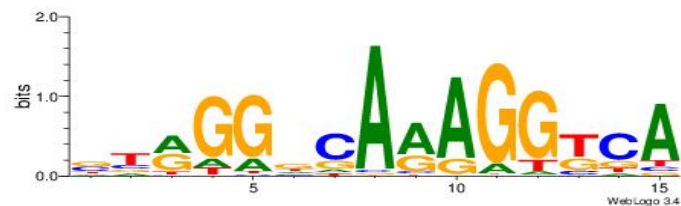
Dataset #: 1
 Motif ID: 14
 Motif name: PPARGRXRA
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 14
 Similarity score: 0.0278283

Alignment:

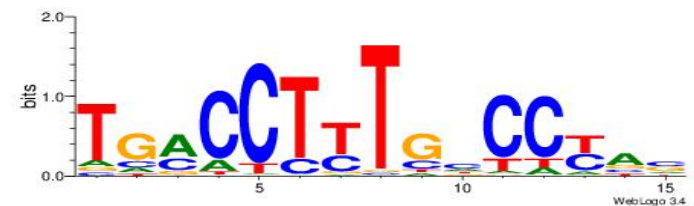
TGRCCTKTGHCKAB

TGAMCTTTGMMCYT-

Original motif Consensus sequence: BTRGGDCARAGGKCA



Reverse complement motif Consensus sequence: TGRCCCTKTGHCKA

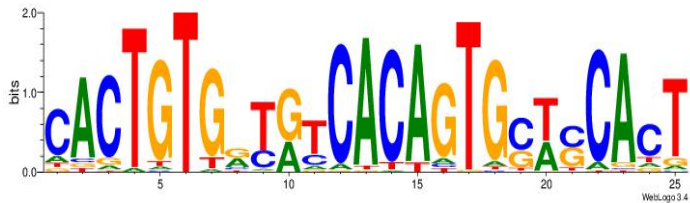


Dataset #: 2
 Motif ID: 22
 Motif name: CACTGTGrYrtCACAGTGswsCAcT
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 7
 Number of overlap: 14

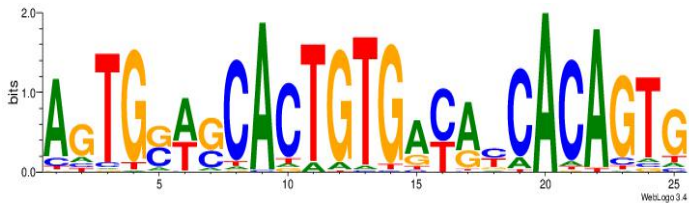
Similarity score: 0.0597647

Alignment:
AGTGSWSCACTGTGAMAMCACAGTG
-----TGAMCTTTGMMCYT-----

Original motif Consensus sequence:
CACTGTGRTRTCACAGTGSWSCACT



Reverse complement motif Consensus sequence:
AGTGSWSCACTGTGAMAMCACAGTG

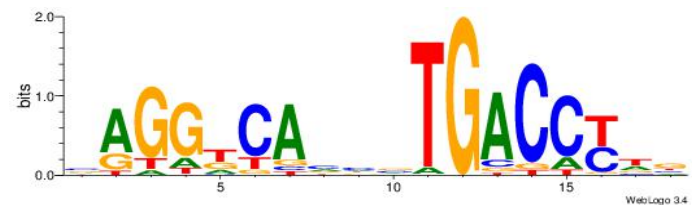
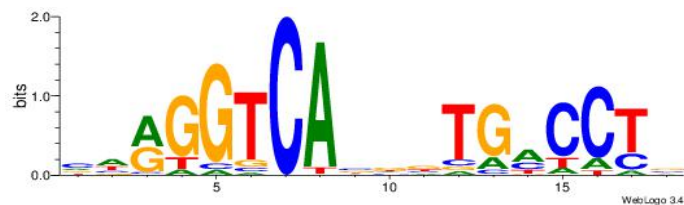


Dataset #: 1
Motif ID: 9
Motif name: ESR2
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 2
Number of overlap: 14
Similarity score: 0.0710475

Alignment:
BAGGYCABHBTGACCKHV
---TGAMCTTTGMMCYT---

Original motif Consensus sequence: VHRGGTCABDBTGMCTB

Reverse complement motif Consensus sequence:
BAGGYCABHBTGACCKHV

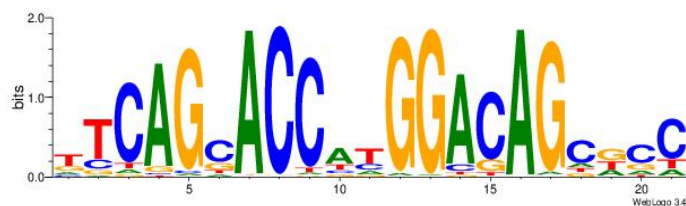


Dataset #: 1
 Motif ID: 7
 Motif name: REST
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 6
 Number of overlap: 14
 Similarity score: 0.071796

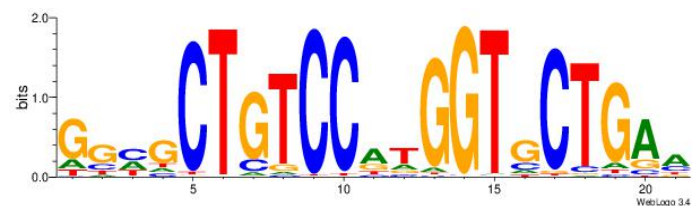
Alignment:

TTCAGCACCATGGACAGCKCC
 --AKGYCYAAAGRTCA-----

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC



Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA

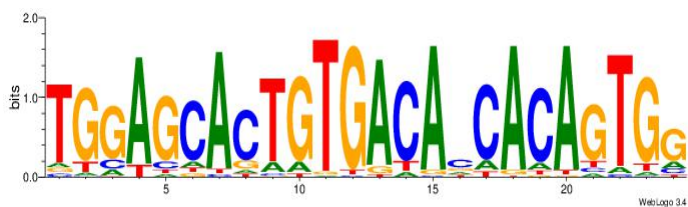


Dataset #: 2

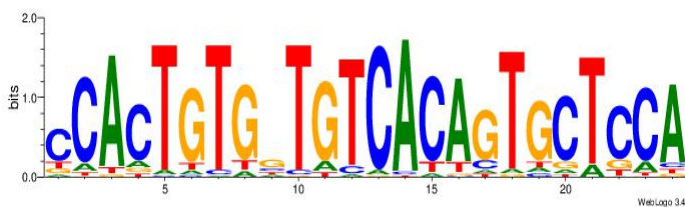
Motif ID: 23
Motif name: TGGAGCACTGTGACAcCACAGTGg
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 8
Number of overlap: 14
Similarity score: 0.0737285

Alignment:
TGGAGCACTGTGACAVCACAGTGG
---TGAMCTTTGMMCYT-----

Original motif Consensus sequence: TGGAGCACTGTGACAVCACAGTGG



Reverse complement motif Consensus sequence: CCACTGTGVTGTACAGTGCTCCA

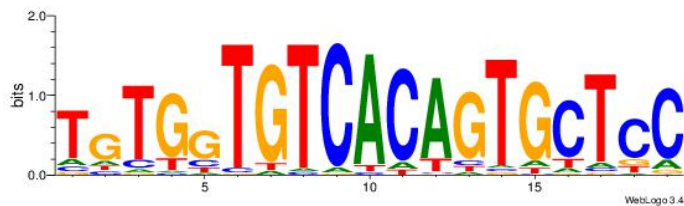


Dataset #: 2
Motif ID: 17
Motif name: TgTGgTGTCACAGTGCTCC
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 4
Number of overlap: 14

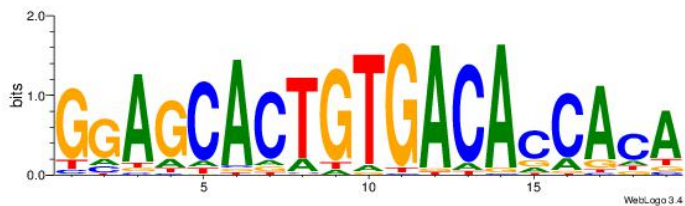
Similarity score: 0.0739698

Alignment:
GGAGCACTGTGACACCACA
--TGAMCTTTGMMCYT---

Original motif Consensus sequence: TGTGGTGTACAGTGCTCC



Reverse complement motif Consensus sequence:
GGAGCACTGTGACACCACA

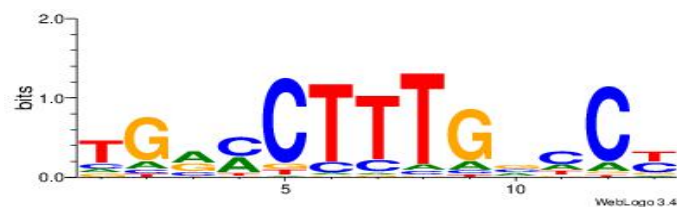
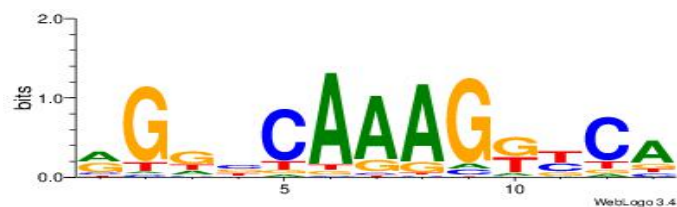


Dataset #: 1
Motif ID: 1
Motif name: HNF4A
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 13
Similarity score: 0.514048

Alignment:
-TGMCTTTGBCCK
TGAMCTTTGMMCYT

Original motif Consensus sequence: RGGBCAAAGKYCA

Reverse complement motif Consensus sequence: TGMCTTTGBCCK

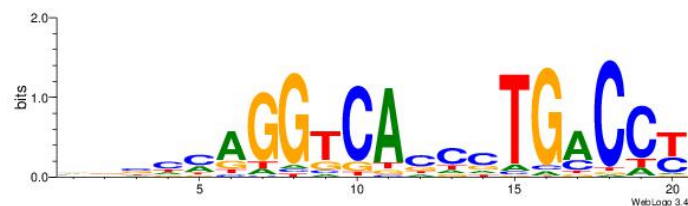


Dataset #: 1
 Motif ID: 3
 Motif name: ESR1
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 8
 Number of overlap: 13
 Similarity score: 0.569869

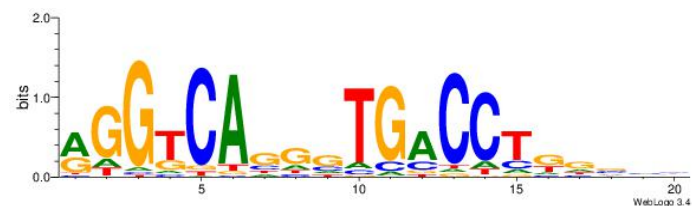
Alignment:

VDBHMAGGTCACCCTGACCY-
 -----TGAMCTTTGMMCYT

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV



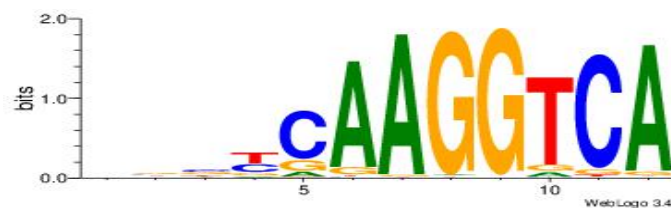
Dataset #: 1

Motif ID: 4
 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: 12
 Similarity score: 1.0303

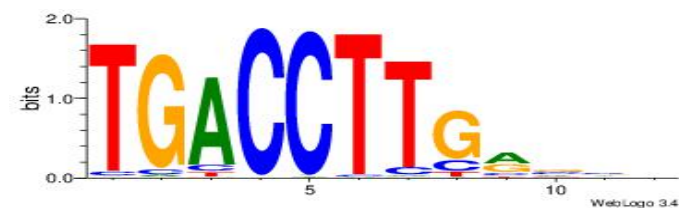
Alignment:

--VBBYCAAGGTCA
 AKGYCAAAGRTCA

Original motif Consensus sequence: VBBYCAAGGTCA

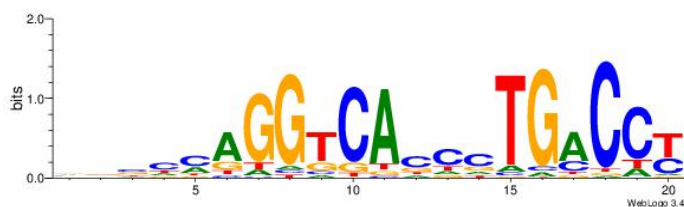


Reverse complement motif Consensus sequence: TGACCTTGMBBB

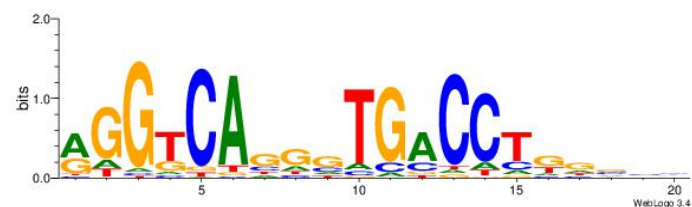


Dataset #: 1 Motif ID: 3 Motif name: ESR1

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV



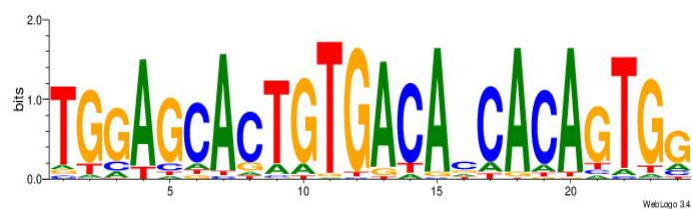
Best Matches for Motif ID 3 (Highest to Lowest)

Dataset #: 2
Motif ID: 23
Motif name: TGGAGCACTGTGACAcCACAGTGg
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 2
Number of overlap: 20
Similarity score: 0.0722586

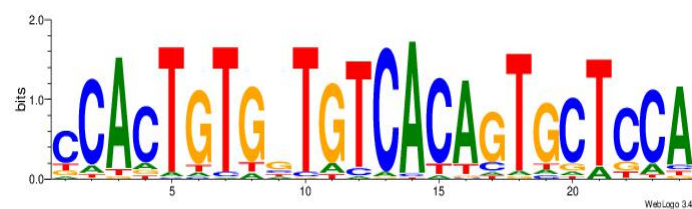
Alignment:

```
CCACTGTGVTGTCACAGTGCTCCA  
---VDBHMAGGTCACCCTGACCY-
```

Original motif Consensus sequence: TGGAGCACTGTGACAVCACAGTGG



Reverse complement motif Consensus sequence: CCACTGTGVTGTCACAGTGCTCCA



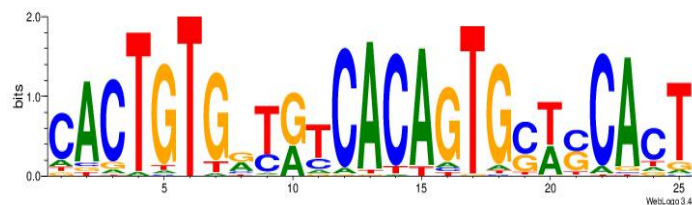
Dataset #: 2
Motif ID: 22
Motif name: CACTGTGrYrtCACAGTGswsCAcT
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif

Direction: Forward
 Position number: 3
 Number of overlap: 20
 Similarity score: 0.0818971

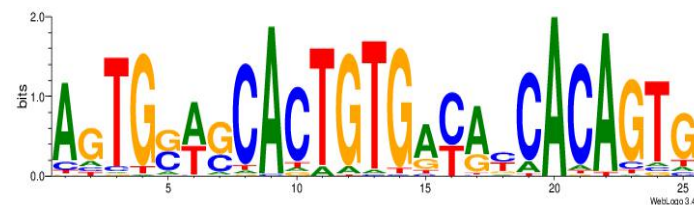
Alignment:

CACTGTGRTRTCACAGTGSWSCACT
 --VDBHMAGGTCACCCTGACCY---

Original motif Consensus sequence:
 CACTGTGRTRTCACAGTGSWSCACT



Reverse complement motif Consensus sequence:
 AGTGSWSCACTGTGAMAMCACAGTG

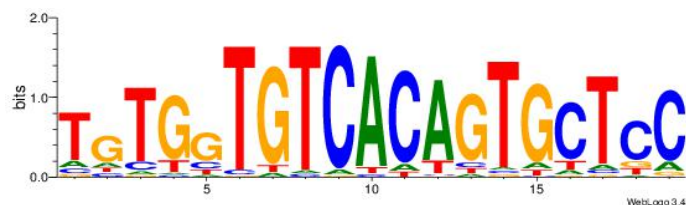


Dataset #: 2
 Motif ID: 17
 Motif name: TgTGgTGTCACAGTGCTCC
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 19
 Similarity score: 0.566376

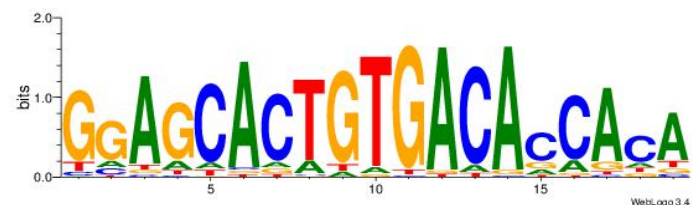
Alignment:

-TGTGGTGTTCACAGTGCTCC
 VDBHMAGGTCACCCTGACCY

Original motif Consensus sequence: TGTGGTGTACAGTGCTCC



Reverse complement motif Consensus sequence: GGAGCACTGTGACACCACA

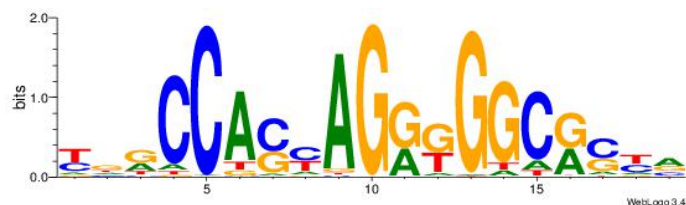


Dataset #: 1
Motif ID: 16
Motif name: CTCF
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 19
Similarity score: 0.579928

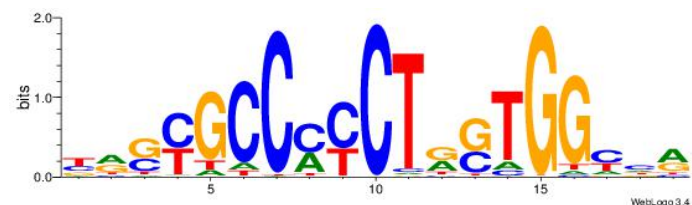
Alignment:

-BMSMGCCYMCTKSTGGMHM
VDBHMAAGGTCACCCTGACCY

Original motif Consensus sequence: YDRCCASYAGRKGGRSYV



Reverse complement motif Consensus sequence: BMSMGCCYMCTKSTGGMHM

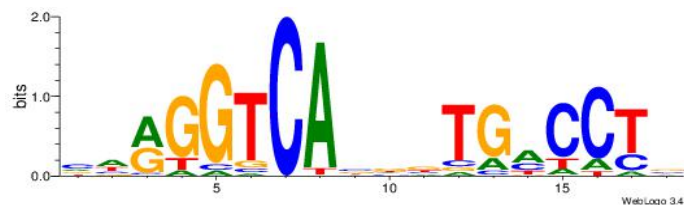


Dataset #: 1
 Motif ID: 9
 Motif name: ESR2
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 17
 Similarity score: 1.50287

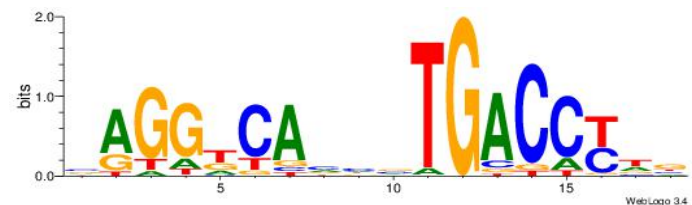
Alignment:

---VHRGGTCABDBTGMCTB
 VDBHMAGGTCACCCTGACCY-

Original motif Consensus sequence: VHRGGTCABDBTGMCTB



Reverse complement motif Consensus sequence: BAGGYCABHBTGACCKHV



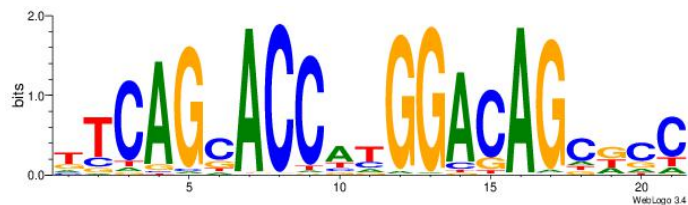
Dataset #: 1
 Motif ID: 7
 Motif name: REST
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 6

Number of overlap: 16
Similarity score: 2.07409

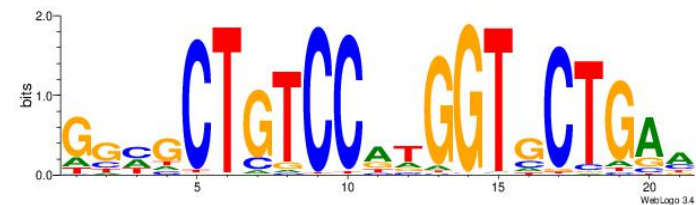
Alignment:

TTCAGCACCATGGACAGCKCC-----
-----VDBHMAGGTCACCCTGACCY

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC



Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA

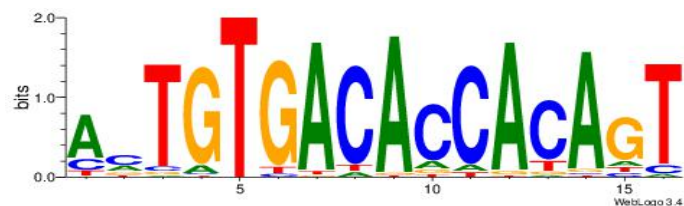


Dataset #: 2
Motif ID: 21
Motif name: AmTGTGACACCACAGT
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 2
Number of overlap: 15
Similarity score: 2.57517

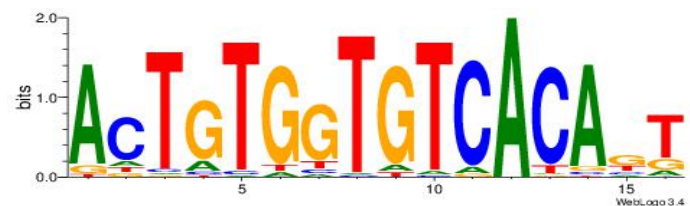
Alignment:

ACTGTGGTGTACART-----
-VDBHMAGGTCACCCTGACCY

Original motif Consensus sequence: AMTGTGACACCACAGT



Reverse complement motif Consensus sequence: ACTGTGGTGTGCACART

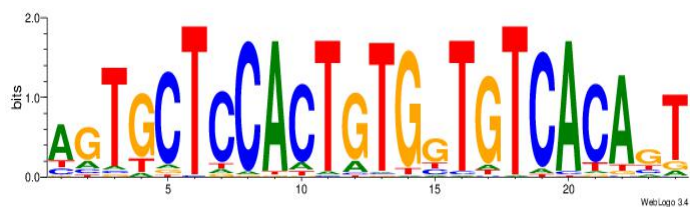


Dataset #: 2
Motif ID: 27
Motif name: AgTGCTCCACTGTGgTGTCACAgT
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 10
Number of overlap: 15
Similarity score: 2.57594

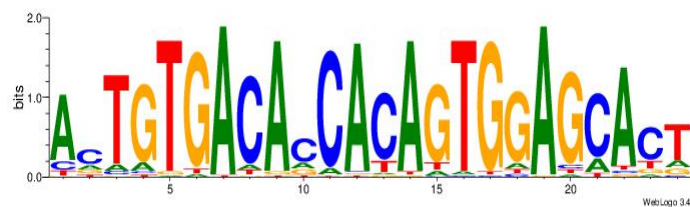
Alignment:

-----ACTGTGACACCACAGTGGAGCACT
MGGTCAGGGTGACCTRDBHV-----

Original motif Consensus sequence: AGTGCTCCACTGTGGTGTGCACAGT



Reverse complement motif Consensus sequence: ACTGTGACACCACAGTGGAGCACT

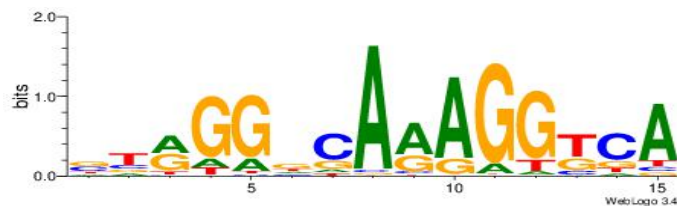


Dataset #: 1
 Motif ID: 14
 Motif name: PPARGRXRA
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 14
 Similarity score: 3.07055

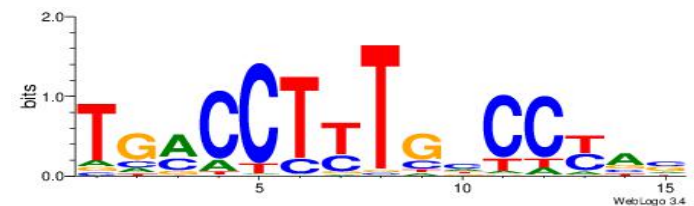
Alignment:

-----BTRGGDCARAGGKCA
 MGGTCAGGGTGACCTRDBHV-

Original motif Consensus sequence: BTRGGDCARAGGKCA



Reverse complement motif Consensus sequence: TGRCCCTKGHCCK

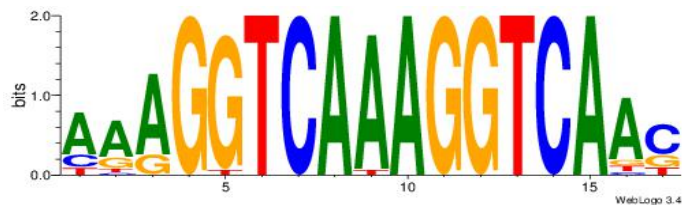


Dataset #: 1
 Motif ID: 10
 Motif name: NR1H2RXRA
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 5
 Number of overlap: 13

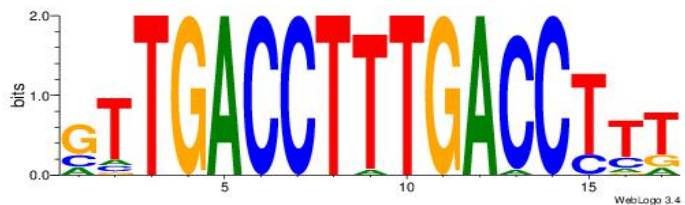
Similarity score: 3.5678

Alignment:
AAAGGTCAAAGGTCAAC-----
----VDBHMAGGTCACCCTGACCY

Original motif Consensus sequence: AAAGGTCAAAGGTCAAC

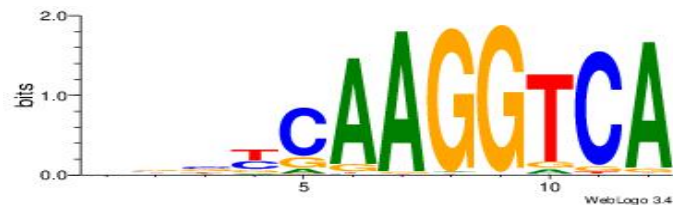


Reverse complement motif Consensus sequence: GTTGACCTTTGACCTT

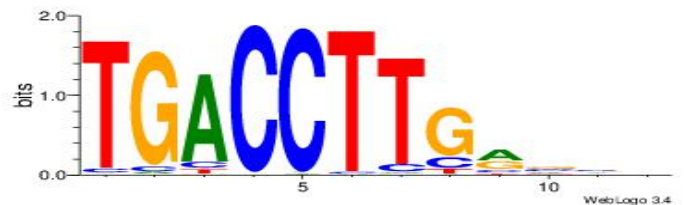


Dataset #: 1 Motif ID: 4 Motif name: Esrrb

Original motif Consensus sequence: VBBYCAAGGTCA



Reverse complement motif Consensus sequence: TGACCTTGMBBB



Best Matches for Motif ID 4 (Highest to Lowest)

Dataset #:	1
Motif ID:	2
Motif name:	NR2F1
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: 0.0442611

Alignment:

TGAMCTTTGMMCYT
 --TGACCTTGMBBB

Original motif Consensus sequence: TGAMCTTTGMMCYT



Reverse complement motif Consensus sequence: AKGYCAAAGRTC

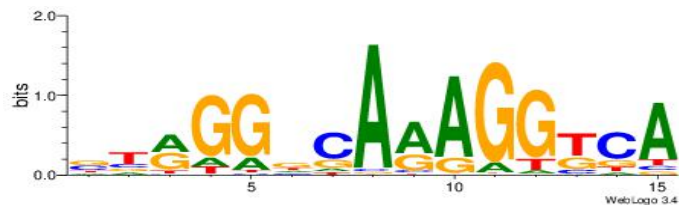


Dataset #: 1
 Motif ID: 14
 Motif name: PPARGRXRA
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 12
 Similarity score: 0.04699

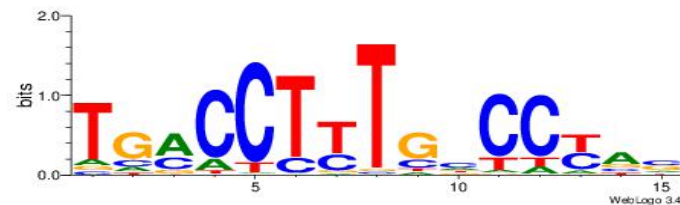
Alignment:

BTRGGDCARAGGKCA
 ---VBBYCAAGGTCA

Original motif Consensus sequence: BTRGGDCARAGGKCA



Reverse complement motif Consensus sequence: TGRCCCTKTGHCCCK

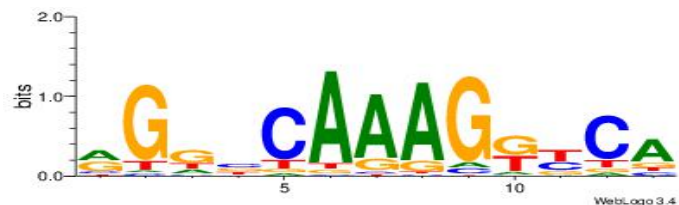


Dataset #: 1
Motif ID: 1
Motif name: HNF4A
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 12
Similarity score: 0.0470808

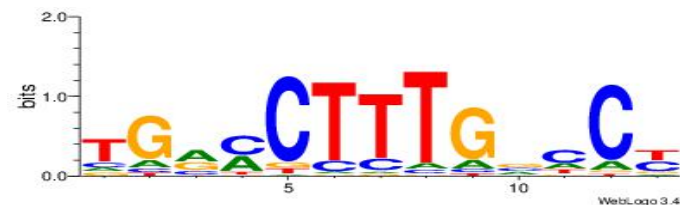
Alignment:

RGGBCAAAGKYCA
-VBBYCAAGGTCA

Original motif Consensus sequence: RGGBCAAAGKYCA



Reverse complement motif Consensus sequence: TGMYYCTTTGBCCCK

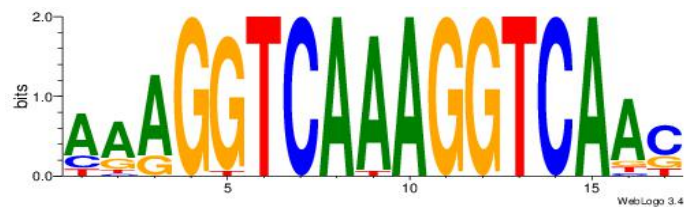


Dataset #: 1
 Motif ID: 10
 Motif name: NR1H2RXRA
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 12
 Similarity score: 0.0506977

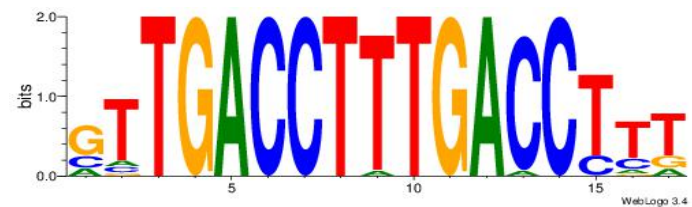
Alignment:

AAAGGTCAAAGGTCAAC
 ---VBBYCAAGGTCA--

Original motif Consensus sequence: AAAGGTCAAAGGTCAAC



Reverse complement motif Consensus sequence: GTTGACCTTTGACCTT



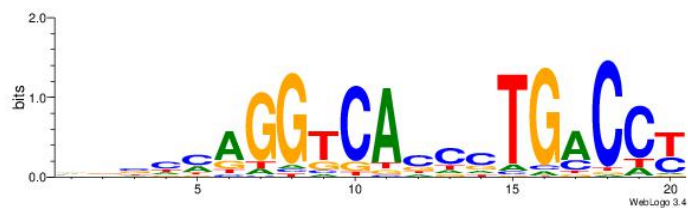
Dataset #: 1
 Motif ID: 3
 Motif name: ESR1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 9

Number of overlap: 12
Similarity score: 0.0628484

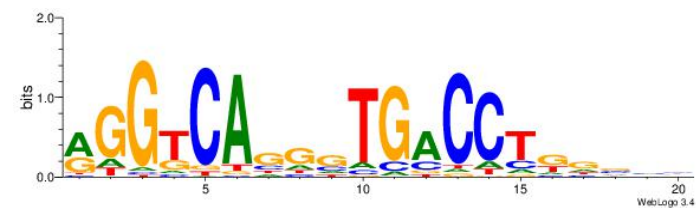
Alignment:

VDBHMAGGTCACCCTGACCY
TGACCTTGMBBB-----

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV

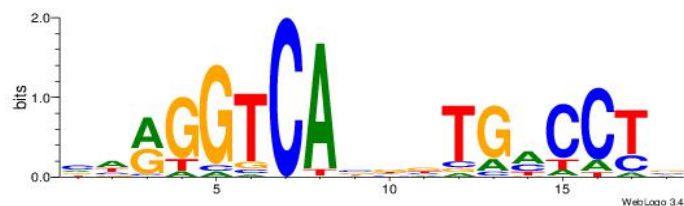


Dataset #: 1
Motif ID: 9
Motif name: ESR2
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 6
Number of overlap: 12
Similarity score: 0.0694613

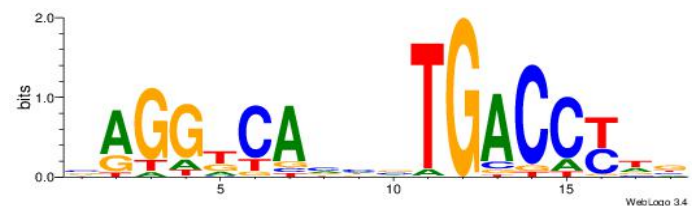
Alignment:

VHRGGTCABDBTGMCCCTB
-----TGACCTTGMBBB-

Original motif Consensus sequence: VHRGGTCABDBTGMCTB



Reverse complement motif Consensus sequence: BAGGYCABHBTGACCKHV

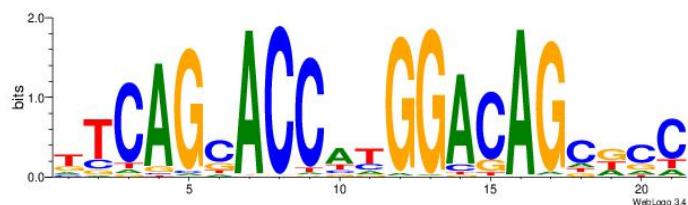


Dataset #: 1
 Motif ID: 7
 Motif name: REST
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 5
 Number of overlap: 12
 Similarity score: 0.0713236

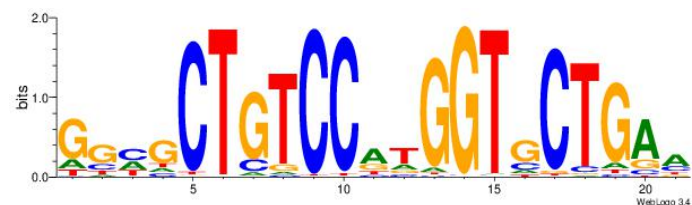
Alignment:

TTCAGCACCATGGACAGCKCC
 ----VBBYCAAGGTCA-----

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC



Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGTCTGAA

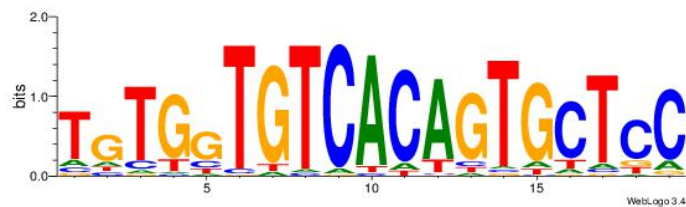


Dataset #: 2
 Motif ID: 17
 Motif name: TgTGgTGTCACAGTGCTCC
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 12
 Similarity score: 0.0772556

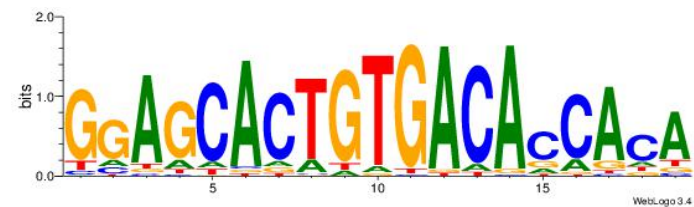
Alignment:

TGTGGTGTCACAGTGCTCC
 -----TGACCTTGMBBB

Original motif Consensus sequence: TGTGGTGTCACAGTGCTCC



Reverse complement motif Consensus sequence: GGAGCACTGTGACACCACA

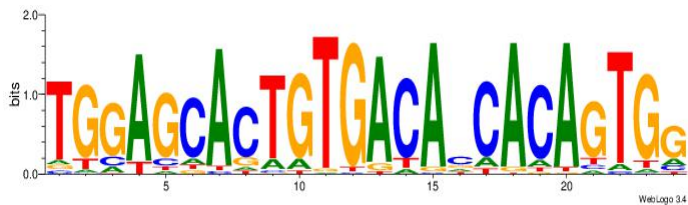


Dataset #: 2
 Motif ID: 23
 Motif name: TGGAGCACTGTGACAcCACAGTGg
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 12

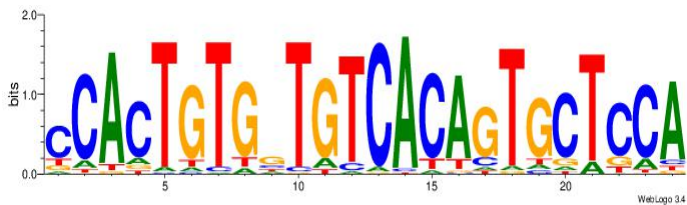
Number of overlap: 12
Similarity score: 0.0785385

Alignment:
CCACTGTGVTGTCACAGTGCTCCA
-----TGACCTTGMBBB-

Original motif Consensus sequence: TGGAGCACTGTGACAVCACAGTGG



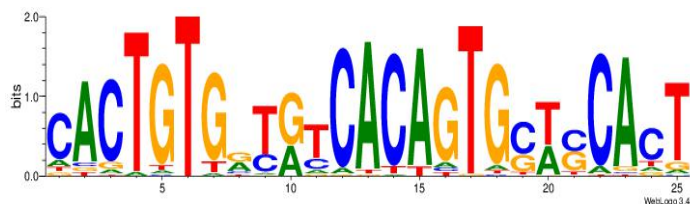
Reverse complement motif Consensus sequence: CCACTGTGVTGTCACAGTGCTCCA



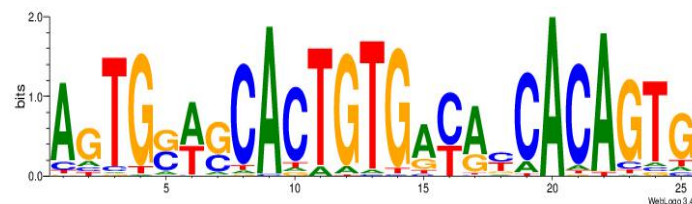
Dataset #: 2
Motif ID: 22
Motif name: CACTGTGGrYrtCACAGTGswsCAcT
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 4
Number of overlap: 12
Similarity score: 0.0832722

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

Original motif Consensus sequence:
CACTGTGRTRTCACAGTGSWSCACT



Reverse complement motif Consensus sequence:
AGTGSWSCACTGTGAMAMCACAGTG



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

Original motif Consensus sequence: CACCTD



Reverse complement motif Consensus sequence: HAGGTG



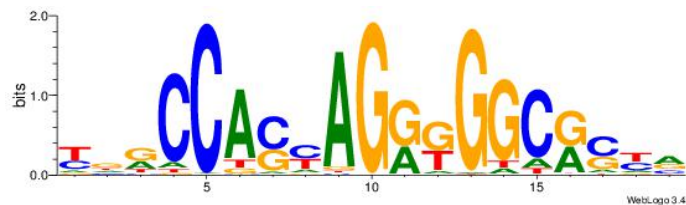
Best Matches for Motif ID 5 (Highest to Lowest)

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:	8
Number of overlap:	6
Similarity score:	0

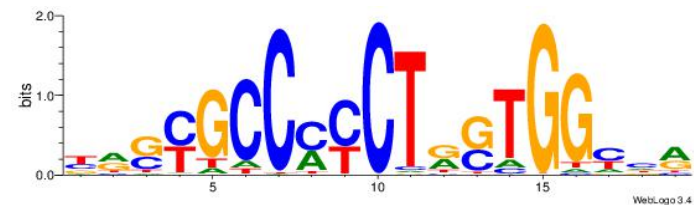
Alignment:

YDRCCASYAGRKGGRSYV
 -----HAGGTG-----

Original motif Consensus sequence: YDRCCASYAGRKGGRSYV



Reverse complement motif Consensus sequence: BMSMGCCYMCTKSTGGMHM



Dataset #:	1
Motif ID:	12
Motif name:	RORA_1
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:	0.00688881

Alignment:
 TGACCTDVWT
 -CACCTD----

Original motif Consensus sequence: AWVDAGGTCA

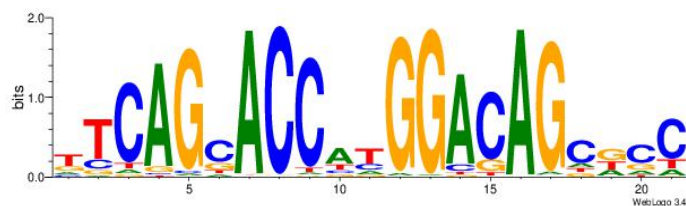
Reverse complement motif Consensus sequence: TGACCTDVWT



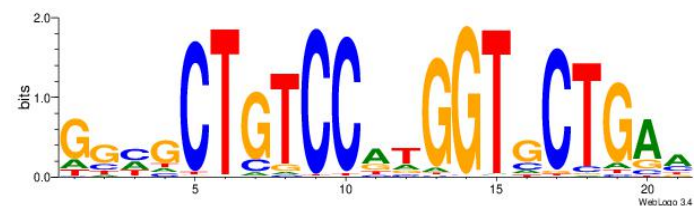
Dataset #: 1
 Motif ID: 7
 Motif name: REST
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 6
 Number of overlap: 6
 Similarity score: 0.00707323

Alignment:
 GYGCTGTCCATGGTGCTGAA
 -----HAGGTG-----

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC



Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA

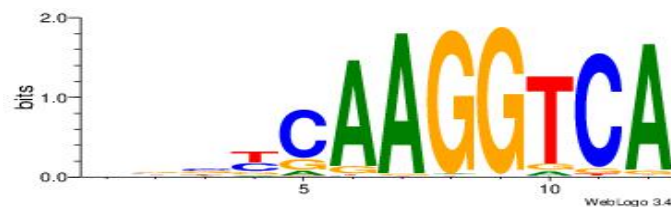


Dataset #: 1

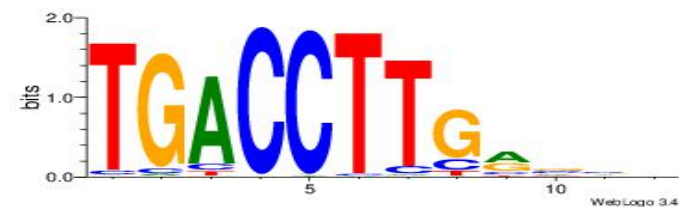
Motif ID: 4
 Motif name: Esrrb
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 6
 Similarity score: 0.013046

Alignment:
 VBBYCAAGGTCA
 -HAGGTG-----

Original motif Consensus sequence: VBBYCAAGGTCA



Reverse complement motif Consensus sequence: TGACCTTGMBBB



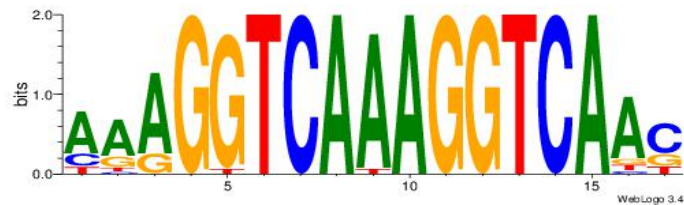
Dataset #: 1
 Motif ID: 10
 Motif name: NR1H2RXRA
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 6
 Similarity score: 0.0160352

Alignment:

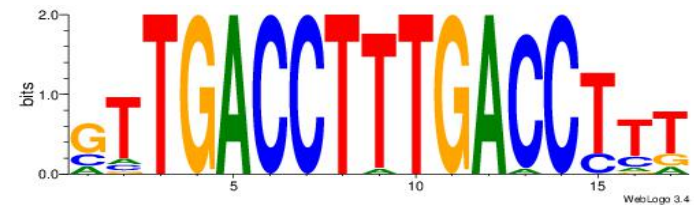
GTGACCTTTGACCTTT

-----CACCTD-

Original motif Consensus sequence: AAAGGTCAAAGGTCAAC



Reverse complement motif Consensus sequence:
GTTGACCTTTGACCTTT



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:	9
Number of overlap:	6
Similarity score:	0.0192435

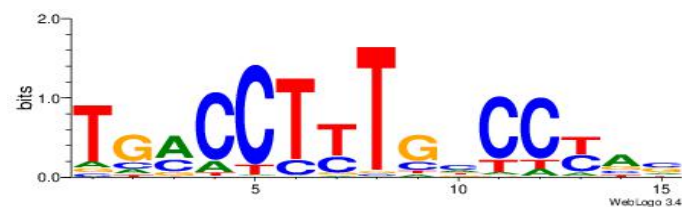
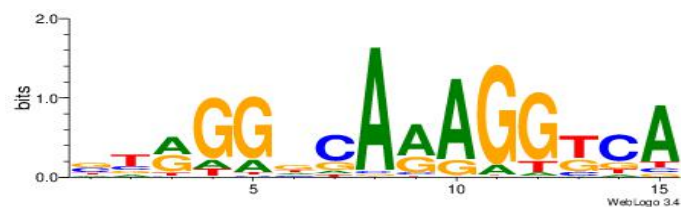
Alignment:

TGRCCTKTGHCKAB

-CACCTD-----

Original motif Consensus sequence: BTRGGDCARAGGKCA

Reverse complement motif Consensus sequence: TGRCCTKTGHCKAB



Dataset #: 1
 Motif ID: 11
 Motif name: NR4A2
 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: 0.0216496

Alignment:
 GTGACCTT
 --CACCTD

Original motif Consensus sequence: AAGGTCAC



Reverse complement motif Consensus sequence: GTGACCTT



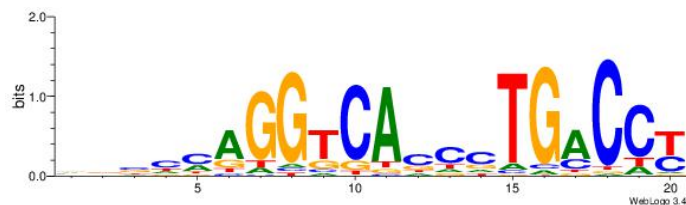
Dataset #: 1
 Motif ID: 3

Motif name: ESR1
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 5
 Number of overlap: 6
 Similarity score: 0.022947

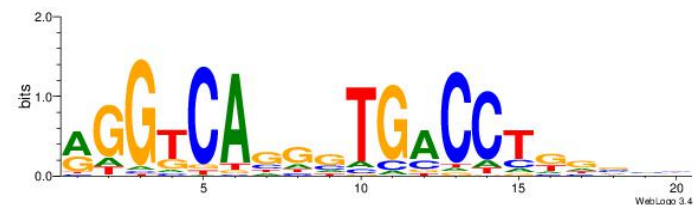
Alignment:

MGGTCAGGGTGACCTRDBHV
 ----CACCTD-----

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV



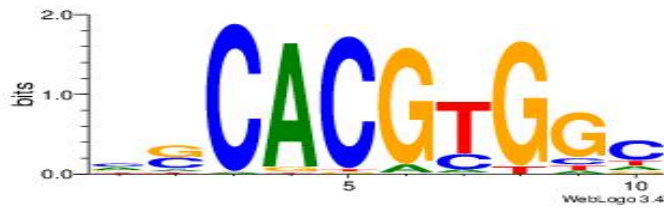
Dataset #: 1
 Motif ID: 6
 Motif name: Mycn
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 6
 Similarity score: 0.0246463

Alignment:

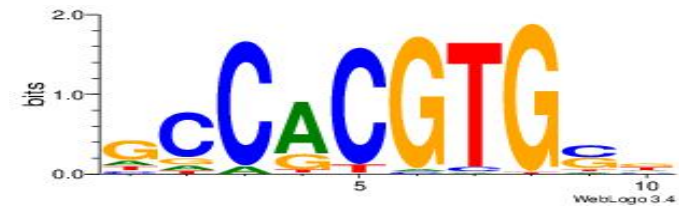
HSCACGTGGC

--CACCTD--

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:	Reverse Complement
Direction:	Forward
Position number:	3
Number of overlap:	6
Similarity score:	0.025129

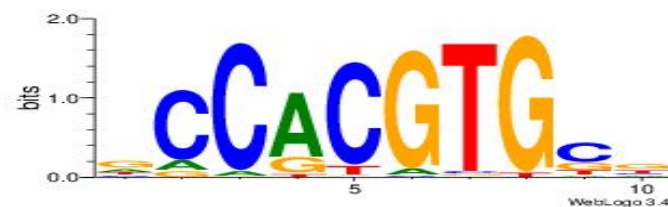
Alignment:

DCCACGTGCV

--HAGGTG--

Original motif Consensus sequence: VGCACGTGGH

Reverse complement motif Consensus sequence: DCCACGTGCV



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

Original motif Consensus sequence: HSCACGTGGC



Reverse complement motif Consensus sequence: GCCACGTGSD



Best Matches for Motif ID 6 (Highest to Lowest)

Dataset #:	1
Motif ID:	8
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 #: 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:

BSCCCCGCGBS

-GCCACGTGSD

Original motif Consensus sequence: BSCCCCGCGBS



Reverse complement motif Consensus sequence: SBCGCGGGGSB

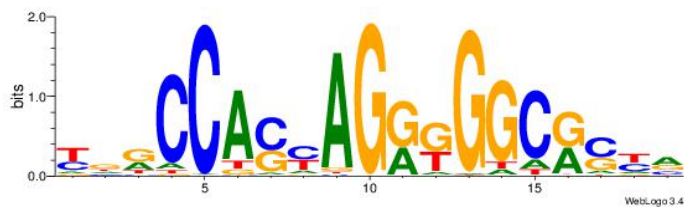


Dataset #: 1
 Motif ID: 16
 Motif name: CTCF
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 6
 Number of overlap: 10
 Similarity score: 0.0679017

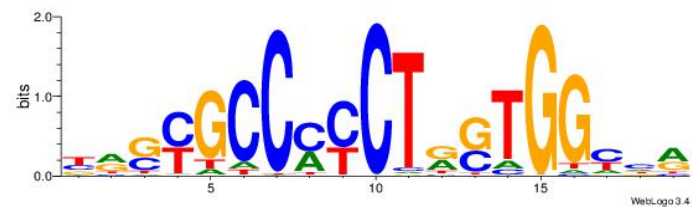
Alignment:

YDRCCASYAGRKGGRSYV
 -----HSCACGTGGC-----

Original motif Consensus sequence: YDRCCASYAGRKGGRSYV



Reverse complement motif Consensus sequence: BMSGCCYMCTKSTGGMHM



Dataset #: 2
 Motif ID: 24
 Motif name: ssCCCCGCSSsk
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2

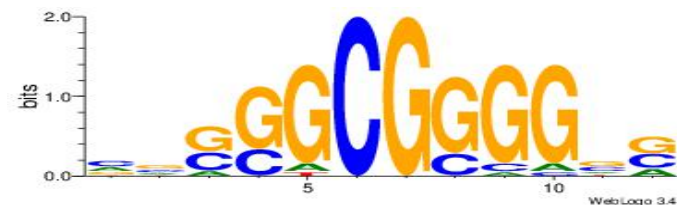
Number of overlap: 10
Similarity score: 0.0704988

Alignment:
BBSGGCGGGGBS
-HSCACGTGGC-

Original motif Consensus sequence: SBCCCCGCCSBB



Reverse complement motif Consensus sequence: BBSGGCGGGGBS

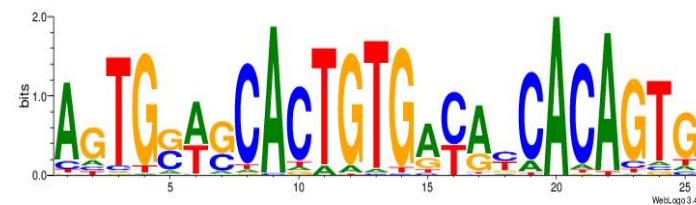
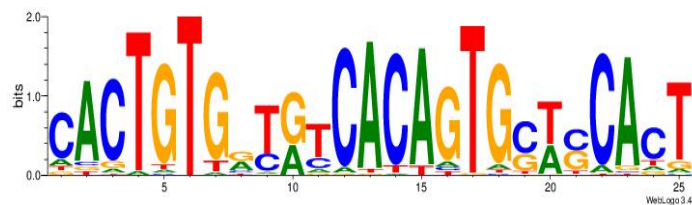


Dataset #: 2
Motif ID: 22
Motif name: CACTGTGrYrtCACAGTGswsCAcT
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 10
Number of overlap: 10
Similarity score: 0.0883224

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

Original motif Consensus sequence:
CACTGTGRTRTCACAGTGSWSCACT

Reverse complement motif Consensus sequence:
AGTGSWSCACTGTGAMAMCACAGTG

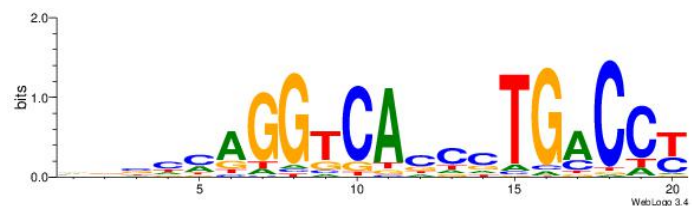


Dataset #: 1
 Motif ID: 3
 Motif name: ESR1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 10
 Similarity score: 0.089863

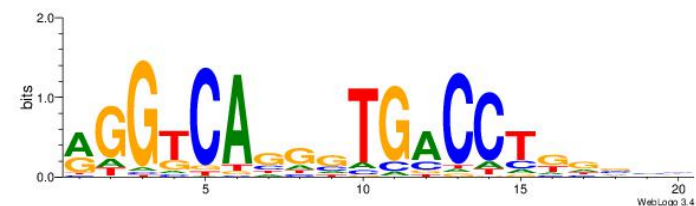
Alignment:

MGGTCAGGGTGACCTRDBHV
 -----GCCACGTGSD--

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV



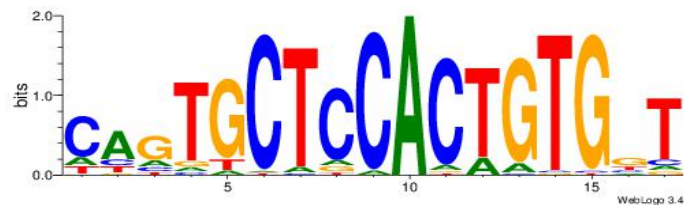
Dataset #: 2

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

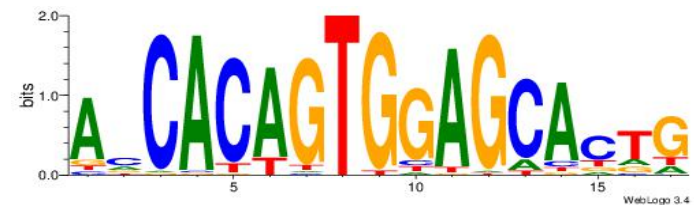
Alignment:

ABCACAGTGGAGCACTG
 -GCCACGTGSD-----

Original motif Consensus sequence: CAGTGCTCCACTGTGBT



Reverse complement motif Consensus sequence: ABCACAGTGGAGCACTG



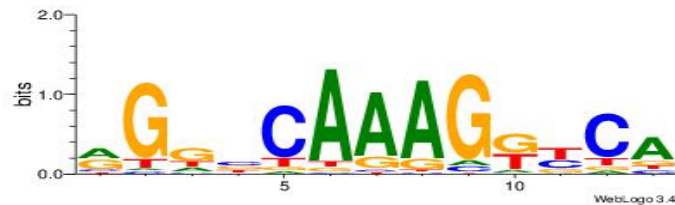
Dataset #: 1
 Motif ID: 1
 Motif name: HNF4A
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 10

Similarity score: 0.0947124

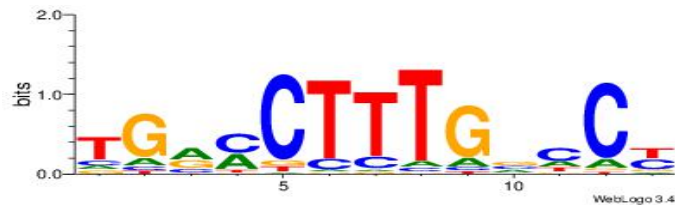
Alignment:

TGMYCTTTGBCK
-GCCACGTGSD--

Original motif Consensus sequence: RGGBCAAAGKYCA



Reverse complement motif Consensus sequence: TGMYCTTTGBCK

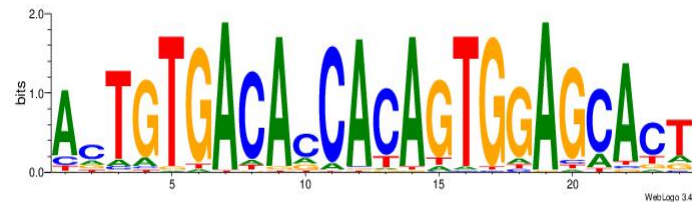
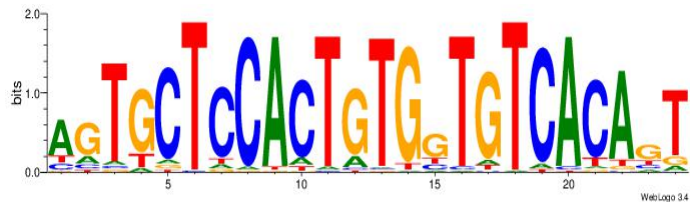


Dataset #: 2
Motif ID: 27
Motif name: AgTGCTCCACTGTGgTGTCACAgT
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 6
Number of overlap: 10
Similarity score: 0.0949359

Alignment:

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

Original motif Consensus sequence: AGTGCTCCACTGTGGTGTACAGT Reverse complement motif Consensus sequence: ACTGTGACACCACAGTGGAGCACT

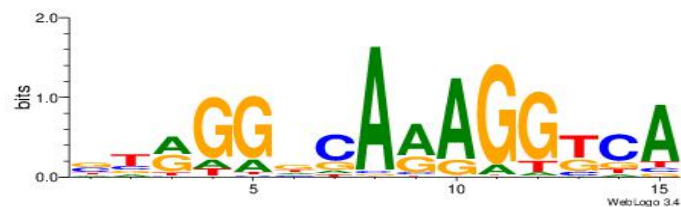


Dataset #: 1
 Motif ID: 14
 Motif name: PPARGRXRA
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 5
 Number of overlap: 10
 Similarity score: 0.0954444

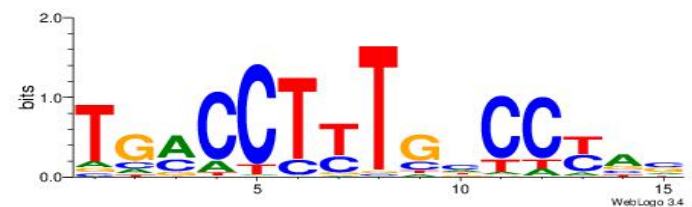
Alignment:

TGRCCCTKTGHCCCKAB
 -GCCACGTGSD-----

Original motif Consensus sequence: BTRGGDCARAGGKCA

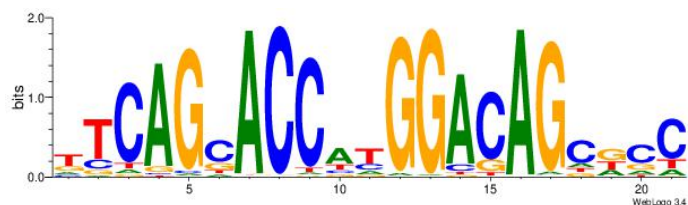


Reverse complement motif Consensus sequence: TGRCCCTKTGHCCCKAB

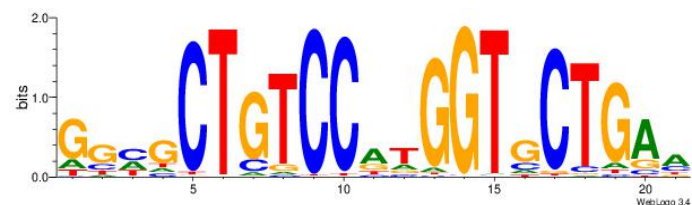


Dataset #: 1 Motif ID: 7 Motif name: REST

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC



Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA



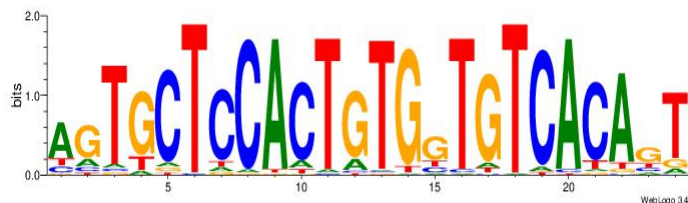
Best Matches for Motif ID 7 (Highest to Lowest)

Dataset #: 2
 Motif ID: 27
 Motif name: AgTGCTCCACTGTGgTGTCACAgT
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 6
 Number of overlap: 19
 Similarity score: 0.0605225

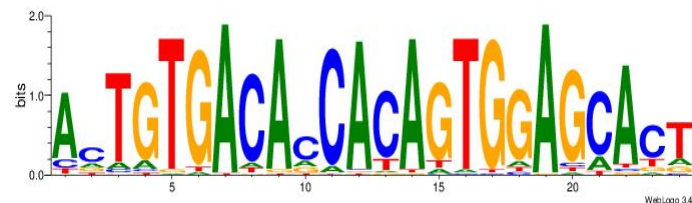
Alignment:

```
--AGTGCTCCACTGTGGTGTCACAGT
GGYGCTGTCCATGGTGCTGAA-----
```

Original motif Consensus sequence: AGTGCTCCACTGTGGTGTCACAGT



Reverse complement motif Consensus sequence: ACTGTGACACCACAGTGGAGCACT

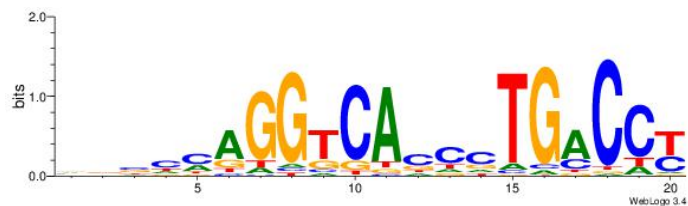


Dataset #: 1
 Motif ID: 3
 Motif name: ESR1
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 5
 Number of overlap: 16
 Similarity score: 1.56264

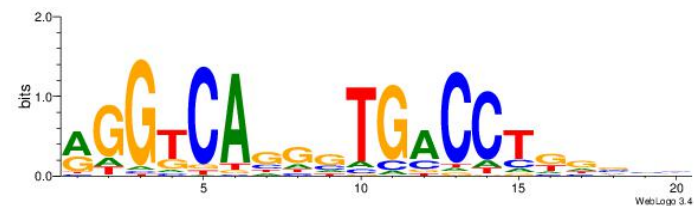
Alignment:

-----VDBHMAGGTCACCCTGACCY
 TTCAGCACCATGGACAGCKCC-----

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV



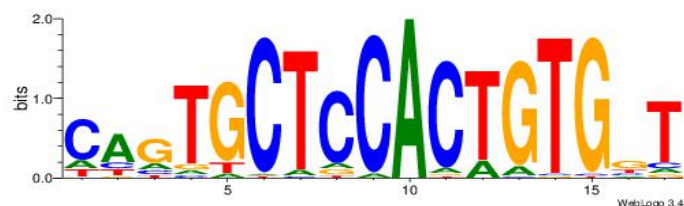
Dataset #: 2
 Motif ID: 20
 Motif name: CagTGCTCCACTGTGgT
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward

Position number: 4
Number of overlap: 14
Similarity score: 2.57032

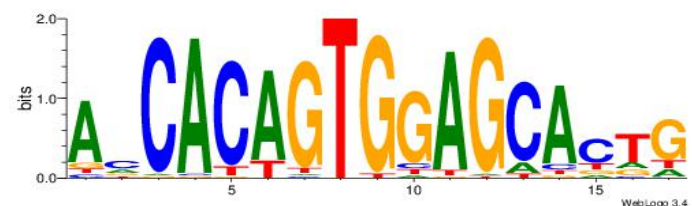
Alignment:

-----ABCACAGTGGAGCACTG
GGYGCTGTCCATGGTGCTGAA---

Original motif Consensus sequence: CAGTGCTCCACTGTGBT



Reverse complement motif Consensus sequence:
ABCACAGTGGAGCACTG

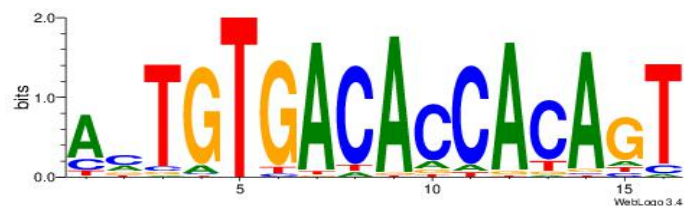


Dataset #: 2
Motif ID: 21
Motif name: AmTGTGACACCACAGT
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 3
Number of overlap: 14
Similarity score: 2.57054

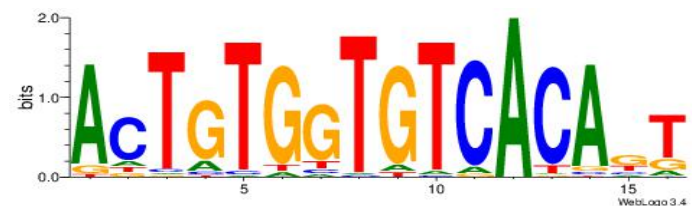
Alignment:

ACTGTGGTGTCACART-----
--GGYGCTGTCCATGGTGCTGAA

Original motif Consensus sequence: AMTGTGACACCACAGT



Reverse complement motif Consensus sequence: ACTGTGGTGTCACT

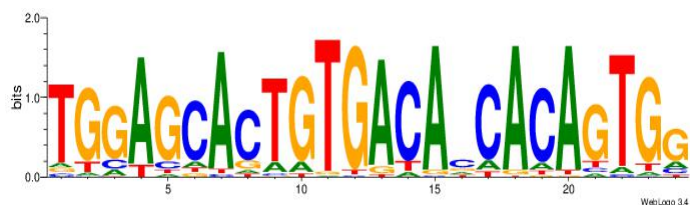


Dataset #: 2
 Motif ID: 23
 Motif name: TGGAGCACTGTGACAcCACAGTGg
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 12
 Number of overlap: 13
 Similarity score: 3.04841

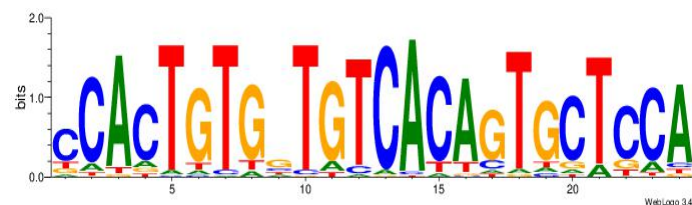
Alignment:

TGGAGCACTGTGACAVCACAGTGG-----
 -----TTCAGCACCATGGACAGCKCC

Original motif Consensus sequence: TGGAGCACTGTGACAVCACAGTGG



Reverse complement motif Consensus sequence: CCACTGTGVTGTCACTGCTCCA

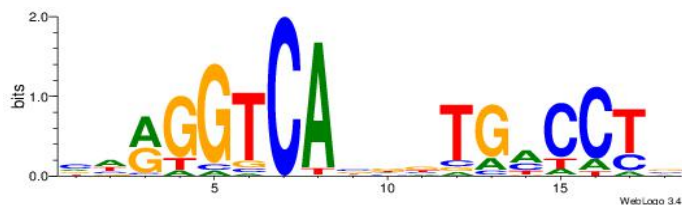


Dataset #: 1
 Motif ID: 9
 Motif name: ESR2
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 6
 Number of overlap: 13
 Similarity score: 3.05156

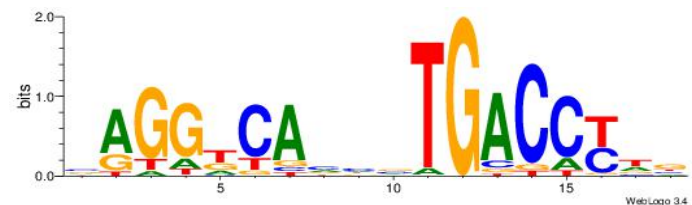
Alignment:

BAGGYCABHBTGACCKHV-----
 -----GGYGCTGTCCATGGTGCTGAA

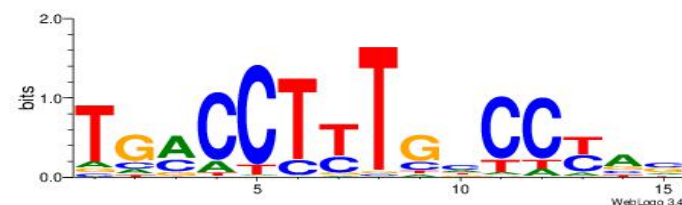
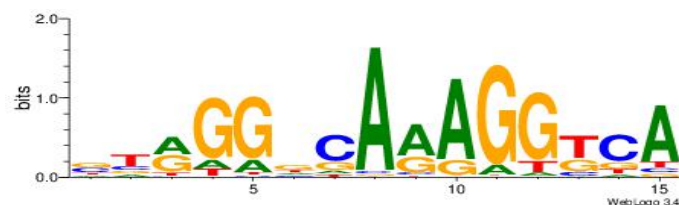
Original motif Consensus sequence: VHRGGTCABDBTGMCTB



Reverse complement motif Consensus sequence: BAGGYCABHBTGACCKHV



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: 1

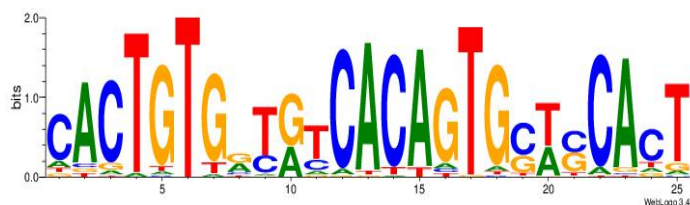


Dataset #: 2
 Motif ID: 22
 Motif name: CACTGTGrYrtCACAGTGswsCACT
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 14
 Number of overlap: 12
 Similarity score: 3.55903

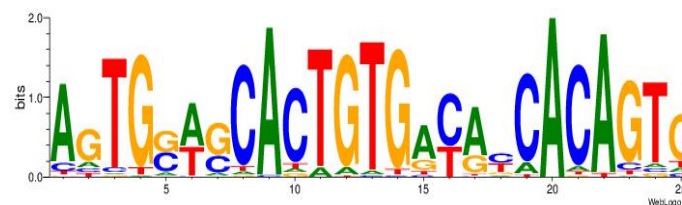
Alignment:

AGTGSWSCACTGTGAMAMCACAGTG-----
 -----TTCAGCACCATGGACAGCKCC

Original motif Consensus sequence:
 CACTGTGRTRTCACAGTGSWSCACT



Reverse complement motif Consensus sequence:
 AGTGSWSCACTGTGAMAMCACAGTG



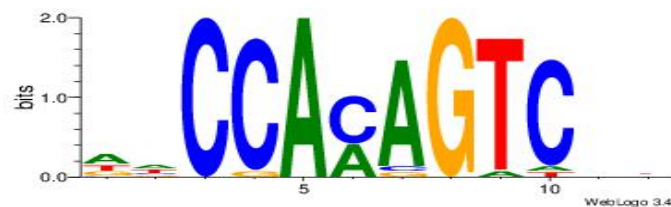
Dataset #: 2

Motif ID: 25
 Motif name: wwCCAmAGTCmt
 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: 3.56306

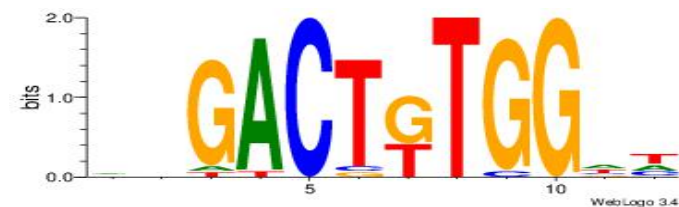
Alignment:

VDGACTRTGGDD-----
 GYGCTGTCCATGGTGCTGAA

Original motif Consensus sequence: DDCCAMAGTCHB



Reverse complement motif Consensus sequence: VDGACTRTGGDD



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

Original motif Consensus sequence: VGCACGTGGH



Reverse complement motif Consensus sequence: DCCACGTGCV



Best Matches for Motif ID 8 (Highest to Lowest)

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: 1
 Number of overlap: 10
 Similarity score: 0

Alignment:

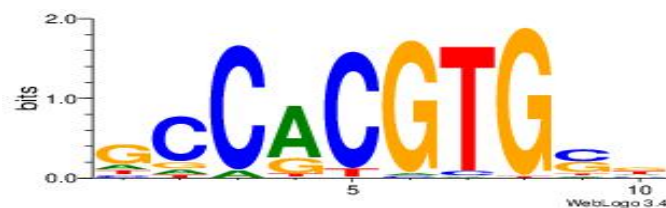
HSCACGTGGC

VGCACGTGGH

Original motif Consensus sequence: HSCACGTGGC



Reverse complement motif Consensus sequence: GCCACGTGSD



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

Alignment:
BSCCCCGCGBS
-DCCACGTGCV

Original motif Consensus sequence: BSCCCCGCGBS



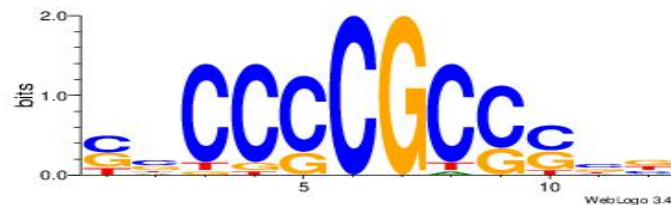
Reverse complement motif Consensus sequence: SBCGCGGGGSB



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:
SBCCCGCCSBB
-DCCACGTGCV-

Original motif Consensus sequence: SBCCCCGCCSBB



Reverse complement motif Consensus sequence: BBSGGCGGGGBS

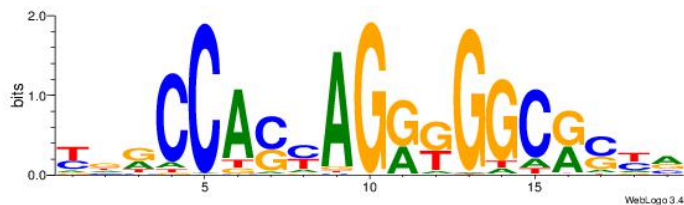


Dataset #: 1
 Motif ID: 16
 Motif name: CTCF
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 8
 Number of overlap: 10
 Similarity score: 0.0754257

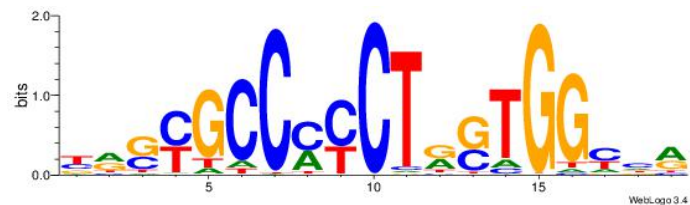
Alignment:

YDRCCASYAGRKGGRSYV
 --DCCACGTGCV-----

Original motif Consensus sequence: YDRCCASYAGRKGGRSYV



Reverse complement motif Consensus sequence: BMSMGCCYMCTKSTGGMHM

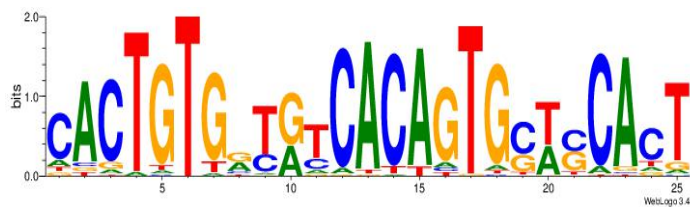


Dataset #: 2
 Motif ID: 22
 Motif name: CACTGTGrYrtCACAGTGswsCAcT
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 6
 Number of overlap: 10
 Similarity score: 0.0888909

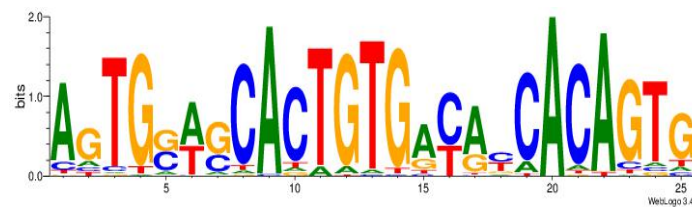
Alignment:

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

Original motif Consensus sequence:
 CACTGTGRTRTCACAGTGSWSCACT



Reverse complement motif Consensus sequence:
 AGTGSWSCACTGTGAMAMCACAGTG

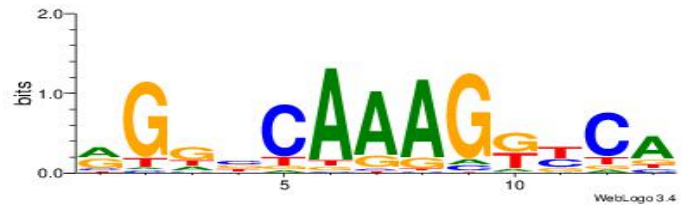


Dataset #: 1
 Motif ID: 1
 Motif name: HNF4A
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1

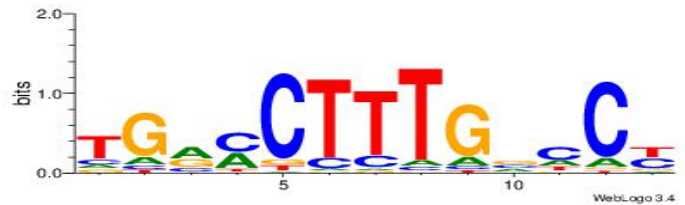
Number of overlap: 10
Similarity score: 0.0934488

Alignment:
TGM YCTTTGB CCK
---VGCACGTGGH

Original motif Consensus sequence: RGGBCAAAGKYCA



Reverse complement motif Consensus sequence: TGM YCTTTGB CCK

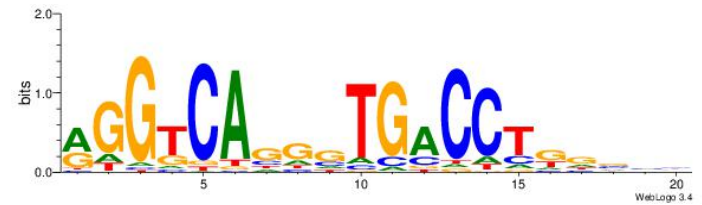
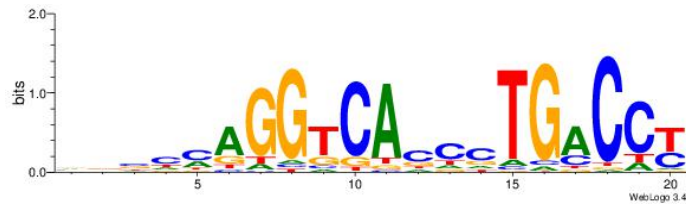


Dataset #: 1
Motif ID: 3
Motif name: ESR1
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 9
Number of overlap: 10
Similarity score: 0.0940438

Alignment:
MGGTCAGGGTGACCTRDBHV
-----DCCACGTGCV--

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY

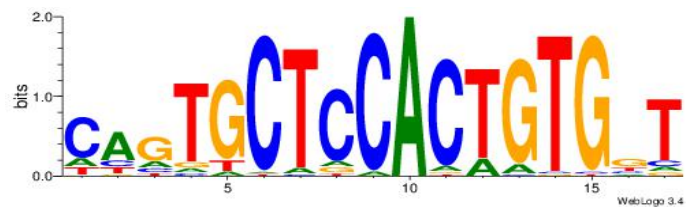
Reverse complement motif Consensus sequence:
MGGTCAGGGTGACCTRDBHV



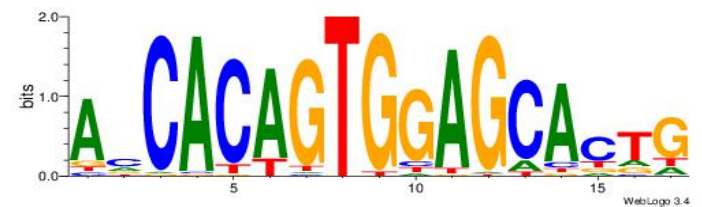
Dataset #: 2
 Motif ID: 20
 Motif name: CagTGCTCCACTGTGgT
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 7
 Number of overlap: 10
 Similarity score: 0.0955234

Alignment:
 ABCACAGTGGAGCACTG
 -DCCACGTGCV-----

Original motif Consensus sequence: CAGTGCTCCACTGTGBT



Reverse complement motif Consensus sequence: ABCACAGTGGAGCACTG



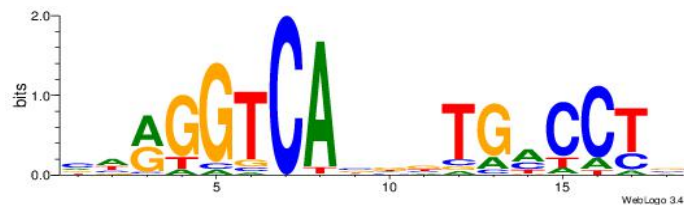
Dataset #: 1

Motif ID: 9
 Motif name: ESR2
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 5
 Number of overlap: 10
 Similarity score: 0.0968598

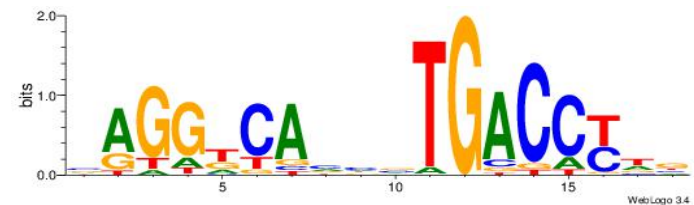
Alignment:

VHRGGTCABDBTGMCCCTB
 ----VGCACGTGGH----

Original motif Consensus sequence: VHRGGTCABDBTGMCCCTB



Reverse complement motif Consensus sequence: BAGGYCABHBTGACCKHV

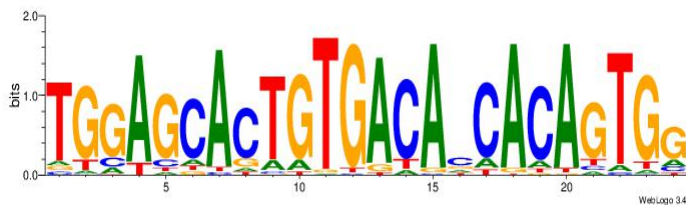


Dataset #: 2
 Motif ID: 23
 Motif name: TGGAGCACTGTGACAcCACAGTGg
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 11
 Number of overlap: 10

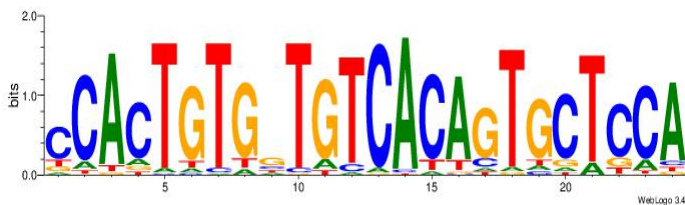
Similarity score: 0.0971125

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

Original motif Consensus sequence: TGGAGCACTGTGACAVCACAGTGG

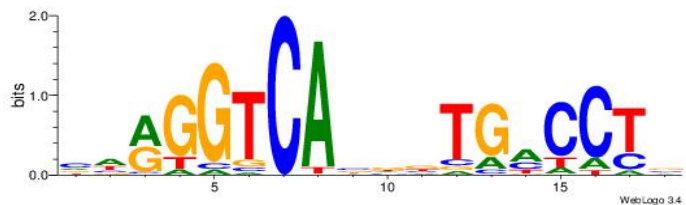


Reverse complement motif Consensus sequence: CCACTGTGVTGTCACAGTGCTCCA

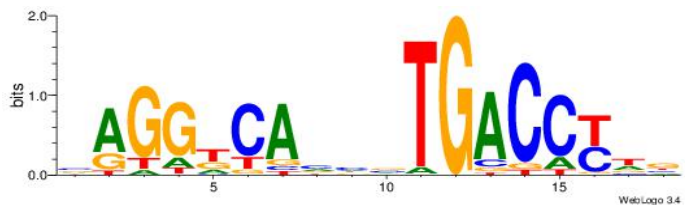


Dataset #: 1 Motif ID: 9 Motif name: ESR2

Original motif Consensus sequence: VHRGGTCABDBTGMCTB



Reverse complement motif Consensus sequence: BAGGYCABHBTGACCKHV



Best Matches for Motif ID 9 (Highest to Lowest)

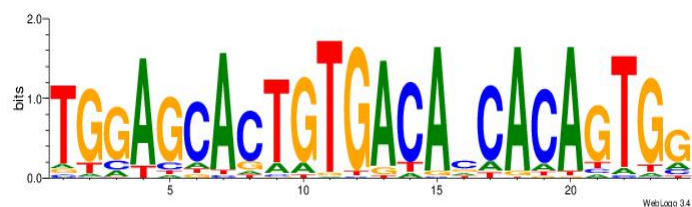
Dataset #: 2
Motif ID: 23
Motif name: TGGAGCACTGTGACAcCACAGTGg
Matching format of first motif: Original Motif

Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	7
Number of overlap:	18
Similarity score:	0.0717757

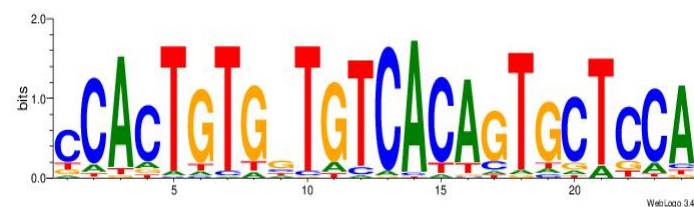
Alignment:

```
CCACTGTGVTGTCACAGTGCTCCA
-----VHRGGTCABDBTGMCTB
```

Original motif Consensus sequence: TGGAGCACTGTGACAVCACAGTGG



Reverse complement motif Consensus sequence: CCACTGTGVTGTCACAGTGCTCCA

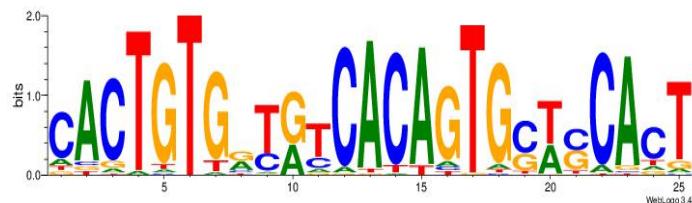


Dataset #:	2
Motif ID:	22
Motif name:	CACTGTGrYrtCACAGTGswsCAcT
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	7
Number of overlap:	18
Similarity score:	0.0815903

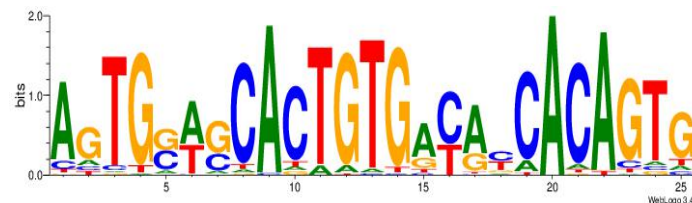
Alignment:

AGTGSWSCACTGTGAMAMCACAGTG
 -VHRGGTCABDBTGMCTB-----

Original motif Consensus sequence:
 CACTGTGRTRTCACAGTGSWSCACT



Reverse complement motif Consensus sequence:
 AGTGSWSCACTGTGAMAMCACAGTG

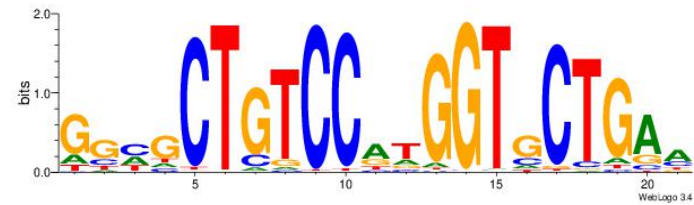
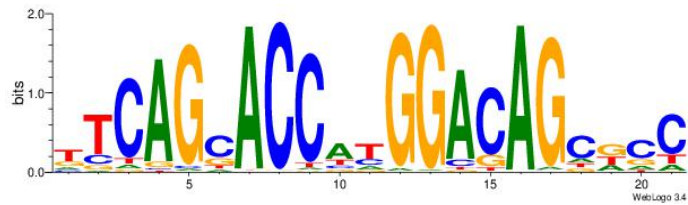


Dataset #:	1
Motif ID:	7
Motif name:	REST
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	3
Number of overlap:	18
Similarity score:	0.0916961

Alignment:
 GYGCTGTCCATGGTGCTGAA
 -VHRGGTCABDBTGMCTB--

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC

Reverse complement motif Consensus sequence:
 GYGCTGTCCATGGTGCTGAA

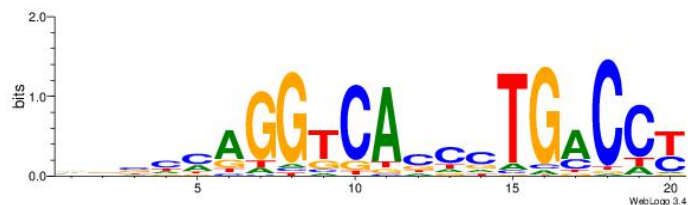


Dataset #: 1
 Motif ID: 3
 Motif name: ESR1
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 17
 Similarity score: 0.511812

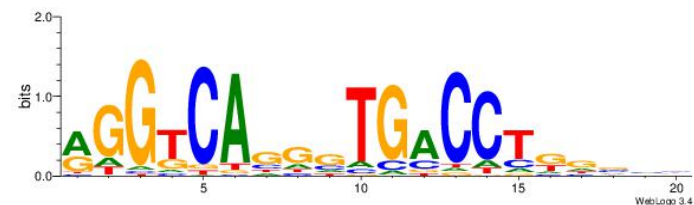
Alignment:

VDBHMAGGTCACCCTGACCY-
 ---VHRGGTCABDBTGMCTB

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV



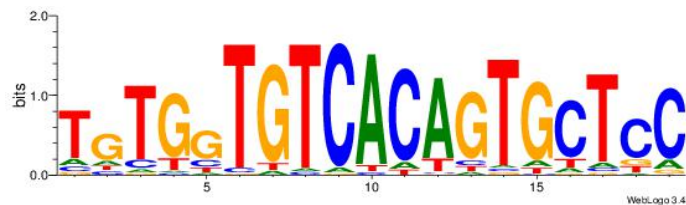
Dataset #: 2

Motif ID: 17
 Motif name: TgTGgTGTCACAGTGCTCC
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 17
 Similarity score: 0.569595

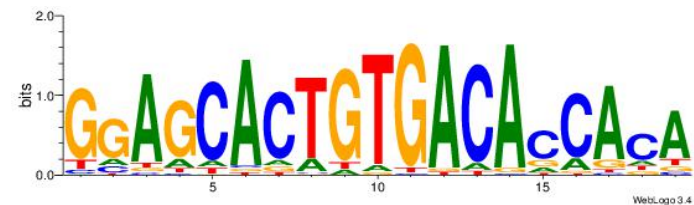
Alignment:

TGTGGTGTCACAGTGCTCC-
 --VHRGGTCABDBTGMCTB

Original motif Consensus sequence: TGTGGTGTCACAGTGCTCC



Reverse complement motif Consensus sequence: GGAGCACTGTGACACCACA

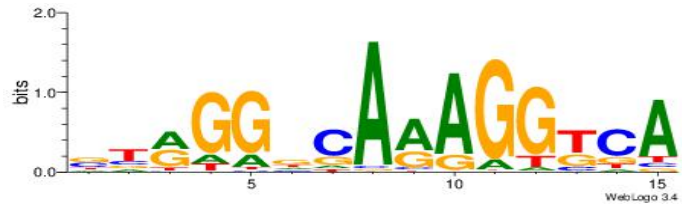


Dataset #: 1
 Motif ID: 14
 Motif name: PPARGRXRA
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 15

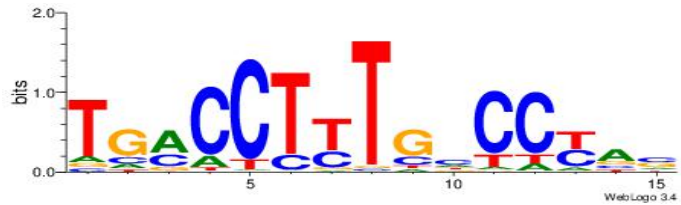
Similarity score: 1.56699

Alignment:
BTRGGDCARAGGKCA---
VHRGGTCABDBTGMCTB

Original motif Consensus sequence: BTRGGDCARAGGKCA



Reverse complement motif Consensus sequence: TGRCCCTKTGHCCCK

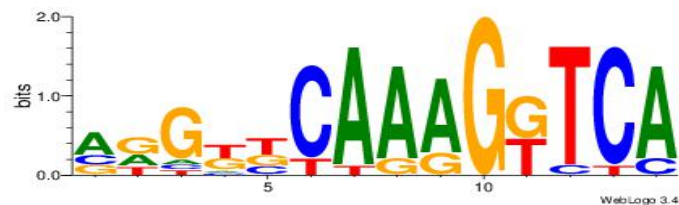


Dataset #: 1
Motif ID: 2
Motif name: NR2F1
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 14
Similarity score: 2.08921

Alignment:
----TGAMCTTTGMMCYT
VHRGGTCABDBTGMCTB

Original motif Consensus sequence: TGAMCTTTGMMCYT

Reverse complement motif Consensus sequence: AKGYCAAAGRTC

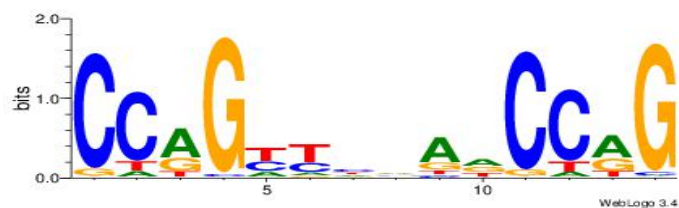


Dataset #: 1
 Motif ID: 15
 Motif name: Tcfcp2l1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 14
 Similarity score: 2.09109

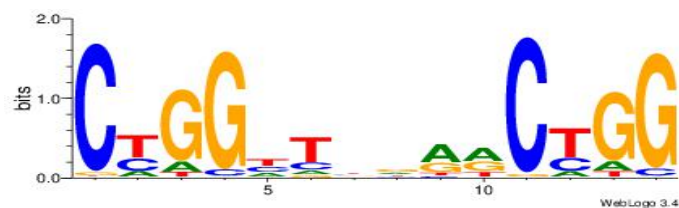
Alignment:

----CCAGYYHVADCCRG
 BAGGYCABHBTGACCKHV

Original motif Consensus sequence: CCAGYYHVADCCRG



Reverse complement motif Consensus sequence: CKGGDTBDMMCTC



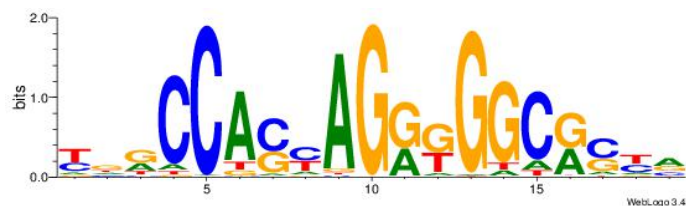
Dataset #: 1
 Motif ID: 16

Motif name: CTCF
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 7
 Number of overlap: 13
 Similarity score: 2.58379

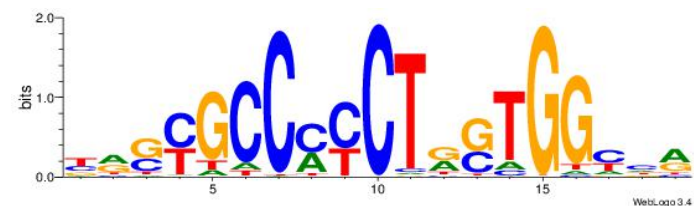
Alignment:

YDRCCASYAGRKGGRSYV-----
 -----VHRGGTCABDBTGMCCTB

Original motif Consensus sequence: YDRCCASYAGRKGGRSYV



Reverse complement motif Consensus sequence: BMSMGCCYMCTKSTGGMHM

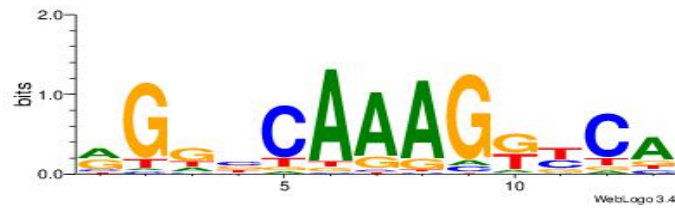


Dataset #: 1
 Motif ID: 1
 Motif name: HNF4A
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 13
 Similarity score: 2.59263

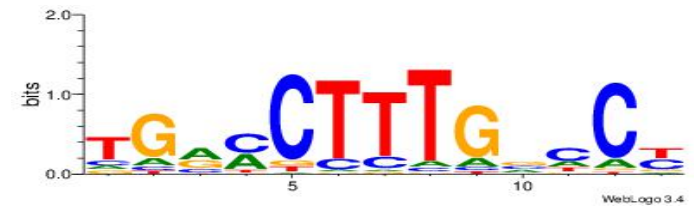
Alignment:

-----RGGBCAAAGKYCA
BAGGYCABHBTGACCKHV

Original motif Consensus sequence: RGGBCAAAGKYCA

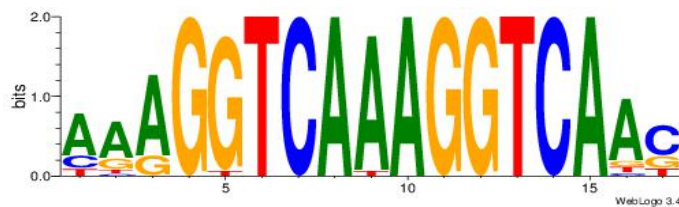


Reverse complement motif Consensus sequence: TGM YCTTTGBCCK

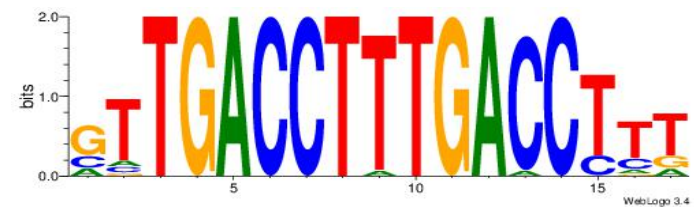


Dataset #: 1 Motif ID: 10 Motif name: NR1H2RXRA

Original motif Consensus sequence: AAAGGTCAAAGGTCAAC



Reverse complement motif Consensus sequence:
GTTGACCTTTGACCTTT



Best Matches for Motif ID 10 (Highest to Lowest)

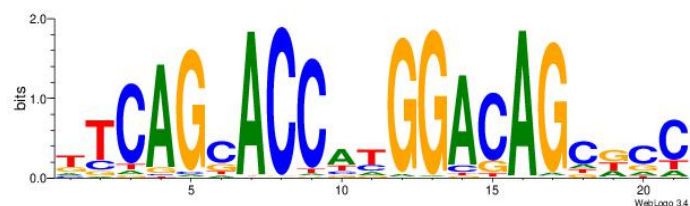
Dataset #:	1
Motif ID:	7
Motif name:	REST
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward

Position number: 4
 Number of overlap: 17
 Similarity score: 0.0911991

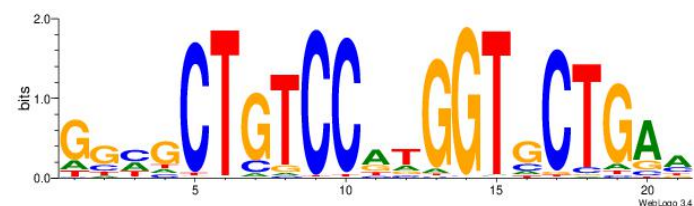
Alignment:

GGYGCTGTCCATGGTGCTGAA
 ---GTTGACCTTTGACCTTT-

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC



Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA

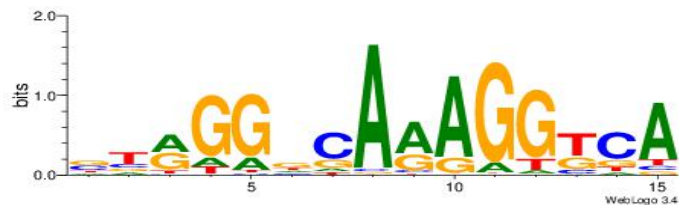


Dataset #: 1
 Motif ID: 14
 Motif name: PPARGRXRA
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 15
 Similarity score: 1.05945

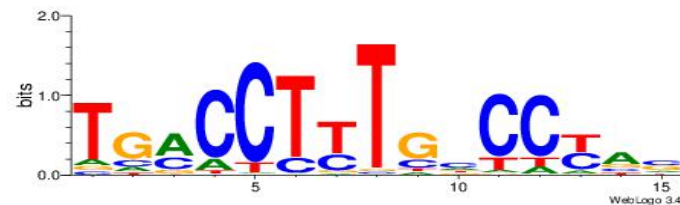
Alignment:

BTRGGDCARAGGKCA--
 AAAGGTCAAAGGTCAAC

Original motif Consensus sequence: BTRGGDCARAGGKCA



Reverse complement motif Consensus sequence: TGRCCCTKTGHCCCK



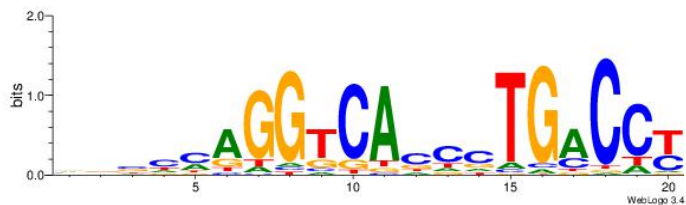
Dataset #: 1
 Motif ID: 3
 Motif name: ESR1
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 8
 Number of overlap: 13
 Similarity score: 2.08514

Alignment:

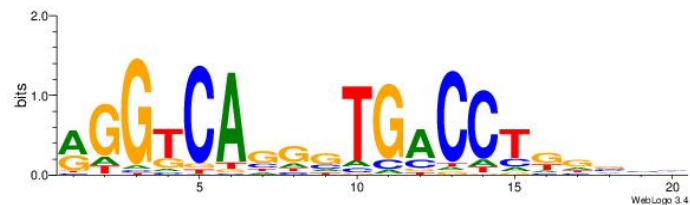
```

----VDBHMAGGTCACCCTGACCY
AAAGGTCAAAGGTCAAC-----
  
```

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRD BHV

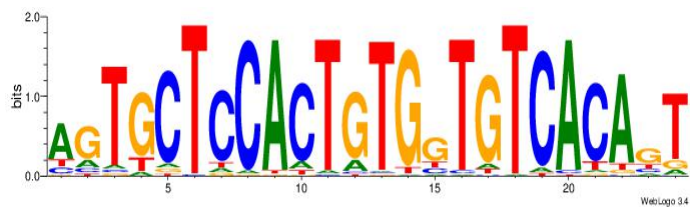


Dataset #: 2
 Motif ID: 27
 Motif name: AgTGCTCCACTGTGgTGTCACAgT
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 13
 Number of overlap: 12
 Similarity score: 2.59961

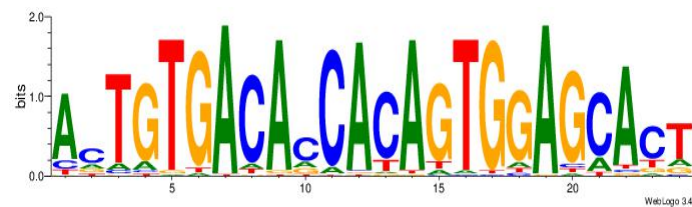
Alignment:

AGTGCTCCACTGTGGTGTACAGT-----
 -----AAAGGTCAAAGGTCAAC

Original motif Consensus sequence: AGTGCTCCACTGTGGTGTACAGT



Reverse complement motif Consensus sequence: ACTGTGACACCACAGTGGAGCACT



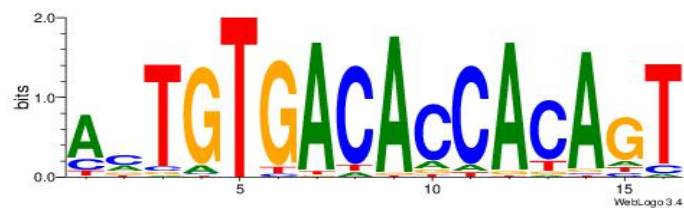
Dataset #: 2
 Motif ID: 21
 Motif name: AmTGTGACACCACAGT
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 5

Number of overlap: 12
Similarity score: 2.59967

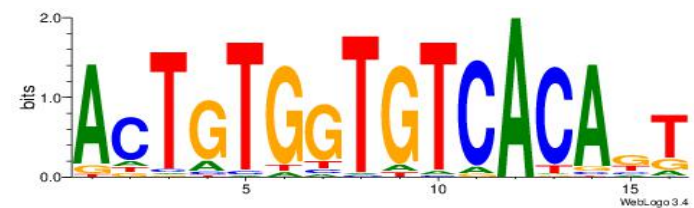
Alignment:

ACTGTGGTGTACART-----
-----AAAGGTCAAAGGTCAAC

Original motif Consensus sequence: AMTGTGACACCACAGT



Reverse complement motif Consensus sequence:
ACTGTGGTGTACART

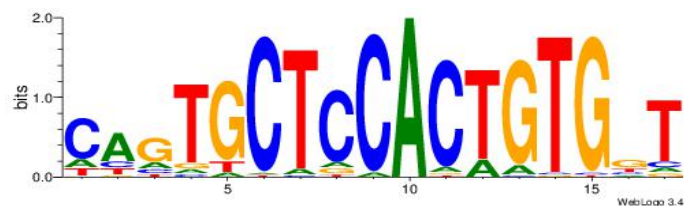


Dataset #: 2
Motif ID: 20
Motif name: CagTGCTCCACTGTGgT
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 7
Number of overlap: 11
Similarity score: 3.09731

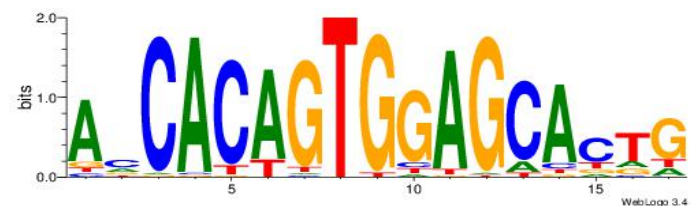
Alignment:

-----CAGTGCTCCACTGTGBT
AAAGGTCAAAGGTCAAC-----

Original motif Consensus sequence: CAGTGCTCCACTGTGBT



Reverse complement motif Consensus sequence: ABCACAGTGGAGCACTG

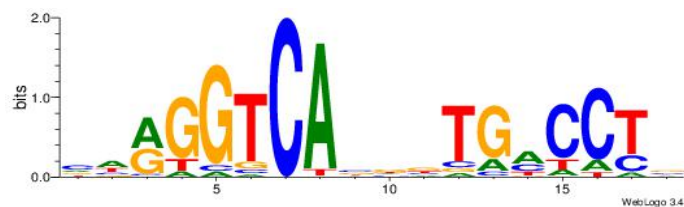


Dataset #: 1
Motif ID: 9
Motif name: ESR2
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 9
Number of overlap: 10
Similarity score: 3.56221

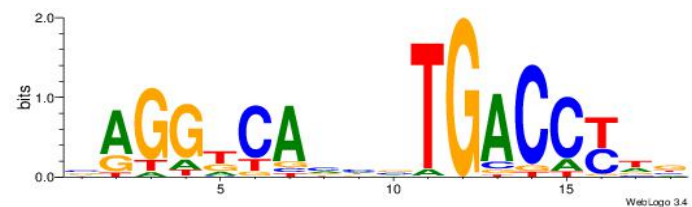
Alignment:

BAGGYCABHBTGACCKHV-----
-----GTTGACCTTTGACCTTT

Original motif Consensus sequence: VHRGGTCABDBTGMCTB



Reverse complement motif Consensus sequence: BAGGYCABHBTGACCKHV



Dataset #: 1
 Motif ID: 13
 Motif name: MIZF
 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: 3.5855

Alignment:

-----BAACGTCCGC
 AAAGGTCAAAGGTCAAC

Original motif Consensus sequence: BAACGTCCGC



Reverse complement motif Consensus sequence: GCGGACGTTT



Dataset #: 1
 Motif ID: 2
 Motif name: NR2F1
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 6
 Number of overlap: 9

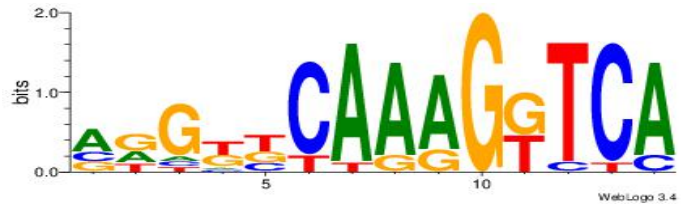
Similarity score: 4.07454

Alignment:
AKGY YCAAAGRTCA-----
-----AAAGGTCAAAGGTCAAC

Original motif Consensus sequence: TGAMCTTTGMMCYT



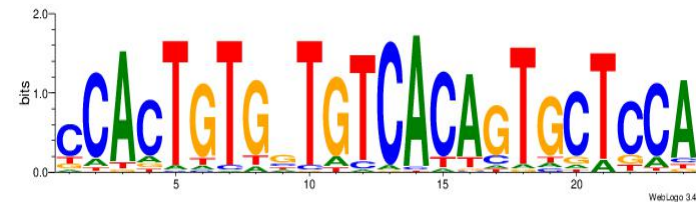
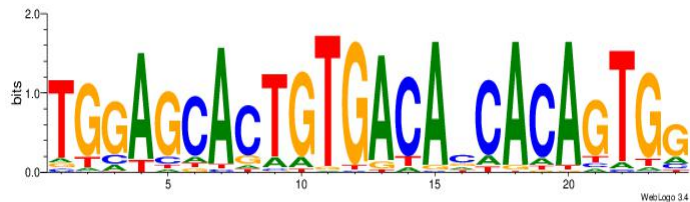
Reverse complement motif Consensus sequence: AKGY YCAAAGRTCA



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: 16
Number of overlap: 9
Similarity score: 4.09479

Alignment:
-----TGGAGCACTGTGACAVCACAGTGG
GTTGACCTTTGACCTTT-----

Original motif Consensus sequence: TGGAGCACTGTGACAVCACAGTGG Reverse complement motif Consensus sequence: CCACTGTGVTGTACAGTGCTCCA



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

Original motif Consensus sequence: AAGGTCAC



Reverse complement motif Consensus sequence: GTGACCTT



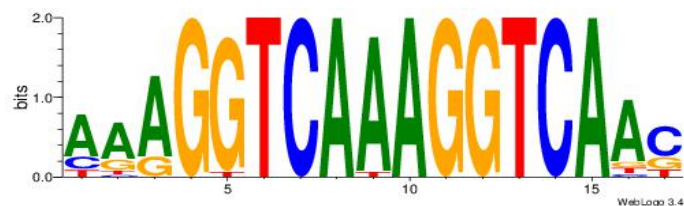
Best Matches for Motif ID 11 (Highest to Lowest)

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:	9
Number of overlap:	8
Similarity score:	0.0167759

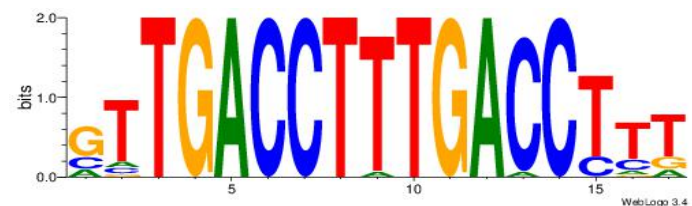
Alignment:

```
AAAGGTCAAAGGTCAAC
-AAGGTCAC-----
```

Original motif Consensus sequence: AAAGGTCAAAGGTCAAC



Reverse complement motif Consensus sequence: GTTGACCTTTGACCTT

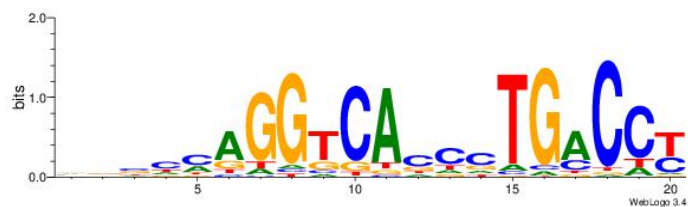


Dataset #: 1
Motif ID: 3
Motif name: ESR1
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 5
Number of overlap: 8
Similarity score: 0.0195235

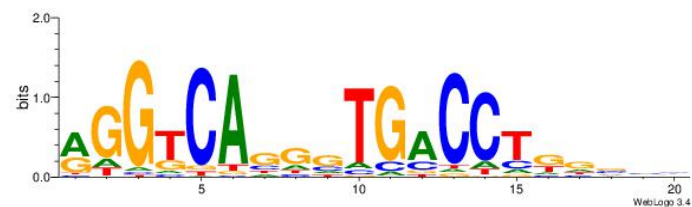
Alignment:

VDBHMAGGTCACCCTGACCY
-----AAGGTCAC-----

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV

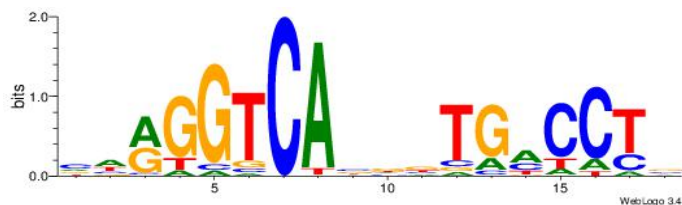


Dataset #: 1
 Motif ID: 9
 Motif name: ESR2
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 10
 Number of overlap: 8
 Similarity score: 0.0198372

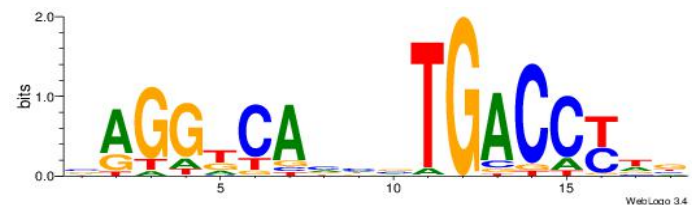
Alignment:

BAGGYCABHBTGACCKHV
 -----GTGACCTT-

Original motif Consensus sequence: VHRGGTCABDBTGMCTB



Reverse complement motif Consensus sequence: BAGGYCABHBTGACCKHV

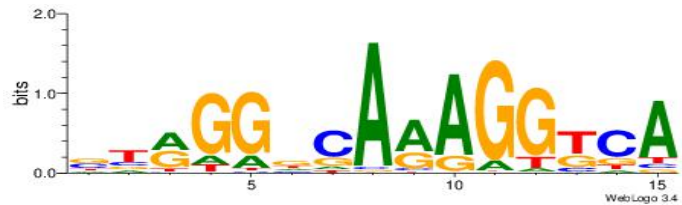


Dataset #: 1
 Motif ID: 14
 Motif name: PPARGRXRA
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 7

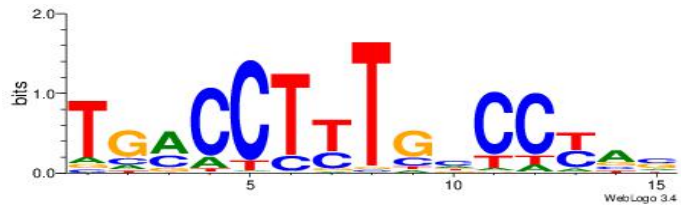
Number of overlap: 8
Similarity score: 0.0495607

Alignment:
BTRGGDCARAGGKCA
-AAGGTCAC-----

Original motif Consensus sequence: BTRGGDCARAGGKCA



Reverse complement motif Consensus sequence: TGRCCCTKTGHCCCK

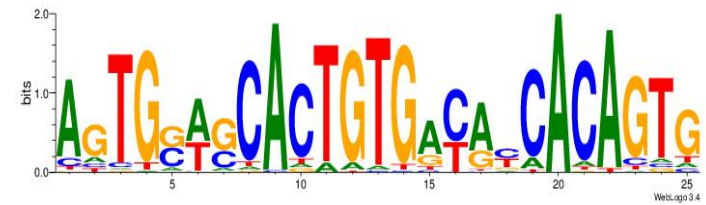
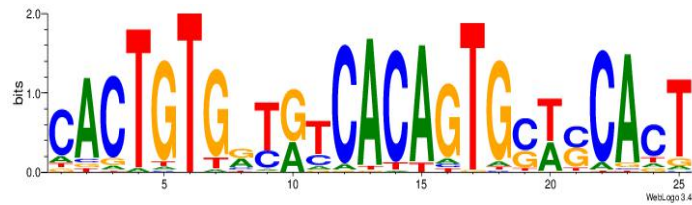


Dataset #: 2
Motif ID: 22
Motif name: CACTGTGrYrtCACAGTGswsCAcT
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 7
Number of overlap: 8
Similarity score: 0.0557243

Alignment:
CACTGTGRTRTCACAGTGSWSCACT
-----AAGGTCAC-----

Original motif Consensus sequence:
CACTGTGRTRTCACAGTGSWSCACT

Reverse complement motif Consensus sequence:
AGTGSWSCACTGTGAMAMCACAGTG



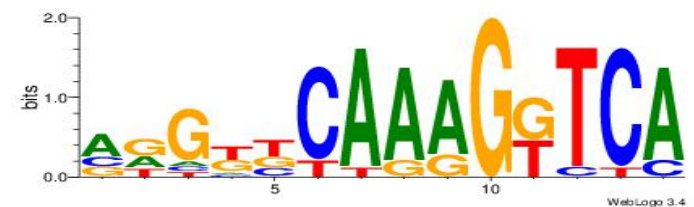
Dataset #: 1
 Motif ID: 2
 Motif name: NR2F1
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 7
 Number of overlap: 8
 Similarity score: 0.0564874

Alignment:
 AKGYCAAAGRTCA
 -----AAGGTCAC

Original motif Consensus sequence: TGAMCTTTGMMCYT



Reverse complement motif Consensus sequence: AKGYCAAAGRTCA



Dataset #: 1
 Motif ID: 7

Motif name:	REST
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:	0.0594649

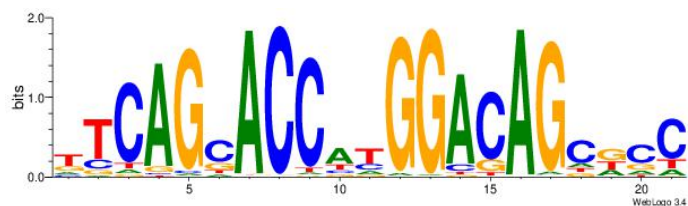
Alignment:

```

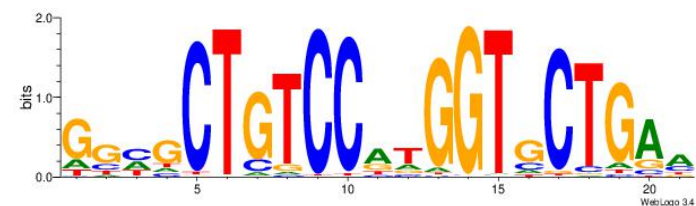
GGYGCTGTCCATGGTGCTGAA
----GTGACCTT-----

```

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC



Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA

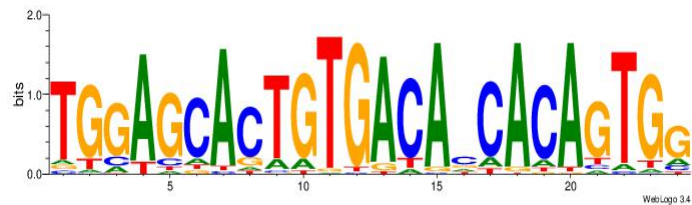


Dataset #:	2
Motif ID:	23
Motif name:	TGGAGCACTGTGACACACAGTGg
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	8
Number of overlap:	8
Similarity score:	0.060729

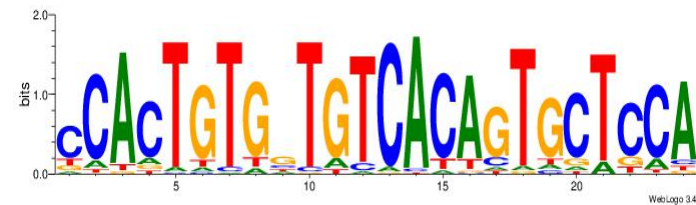
Alignment:

CCACTGTGVTGTCACAGTGCTCCA
-----AAGGTCAC-----

Original motif Consensus sequence: TGGAGCACTGTGACAVCACAGTGG



Reverse complement motif Consensus sequence: CCACTGTGVTGTCACAGTGCTCCA



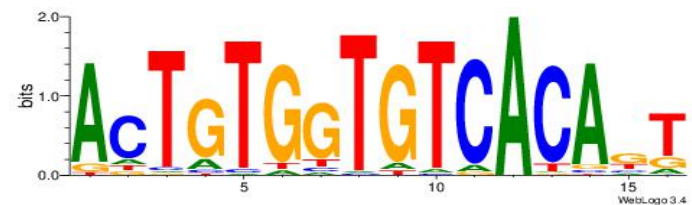
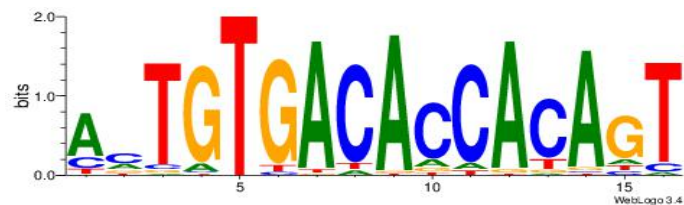
Dataset #:	2
Motif ID:	21
Motif name:	AmTGTGACACCACAGT
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	6
Number of overlap:	8
Similarity score:	0.0645146

Alignment:

ACTGTGGTGTACART
-----AAGGTCAC---

Original motif Consensus sequence: AMTGTGACACCACAGT

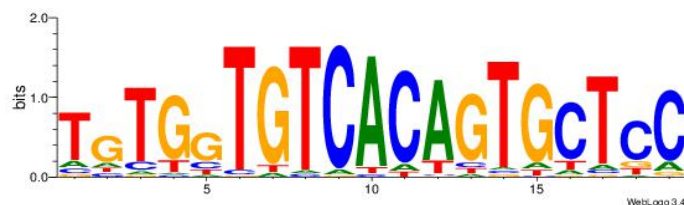
Reverse complement motif Consensus sequence: ACTGTGGTGTACART



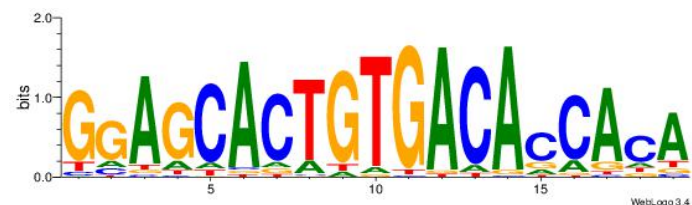
Dataset #: 2
 Motif ID: 17
 Motif name: TgTGgTGTCACAGTGCTCC
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 9
 Number of overlap: 8
 Similarity score: 0.0695512

Alignment:
 TGTGGTGTACAGTGCTCC
 ---AAGGTCAC-----

Original motif Consensus sequence: TGTGGTGTACAGTGCTCC



Reverse complement motif Consensus sequence: GGAGCACTGTGACACCACA



Dataset #: 1 Motif ID: 12 Motif name: RORA_1

Original motif Consensus sequence: AWVDAGGTCA



Reverse complement motif Consensus sequence: TGACCTDVWT



Best Matches for Motif ID 12 (Highest to Lowest)

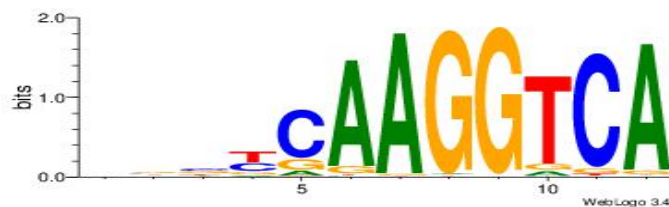
Dataset #:	1
Motif ID:	4
Motif name:	Esrb
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	10
Similarity score:	0.029401

Alignment:

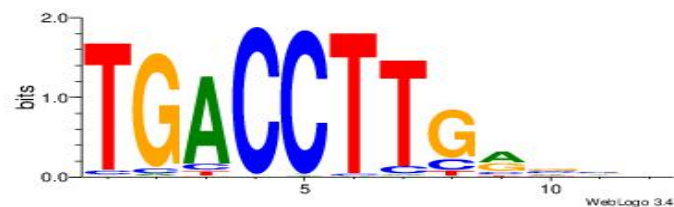
VBBYCAAGGTCA

--AWVDAGGTCA

Original motif Consensus sequence: VBBYCAAGGTCA



Reverse complement motif Consensus sequence: TGACCTGMBBB

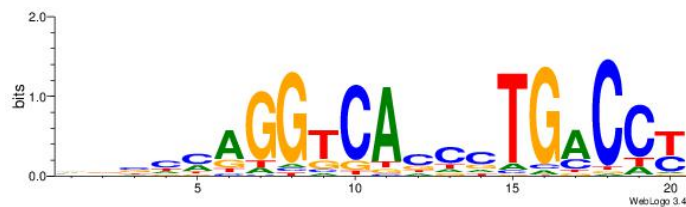


Dataset #: 1
 Motif ID: 3
 Motif name: ESR1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 10
 Similarity score: 0.0417851

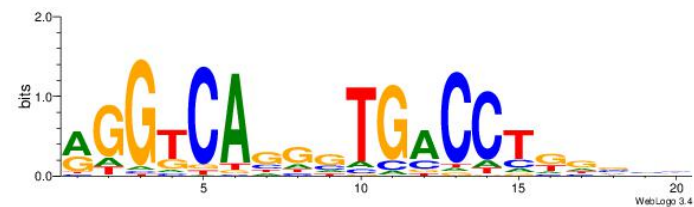
Alignment:

MGGTCAGGGTGACCTRDBHV
 -----TGACCTDVWT-

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV

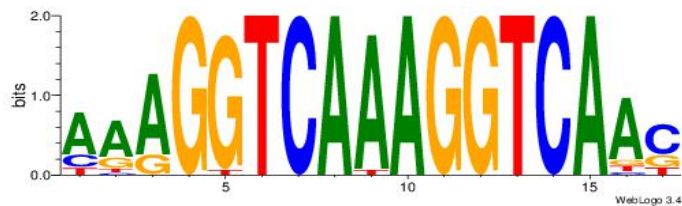


Dataset #: 1
 Motif ID: 10
 Motif name: NR1H2RXRA
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 6

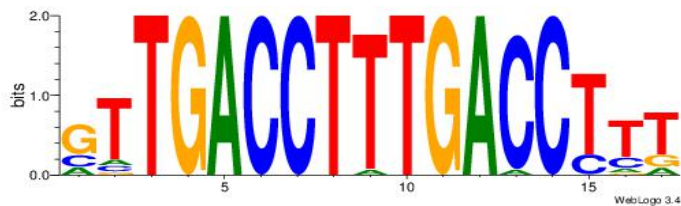
Number of overlap: 10
Similarity score: 0.05425

Alignment:
AAAGGTCAAAGGTCAAC
-----AWVDAGGTCA--

Original motif Consensus sequence: AAAGGTCAAAGGTCAAC



Reverse complement motif Consensus sequence: GTTGACCTTTGACCTTT

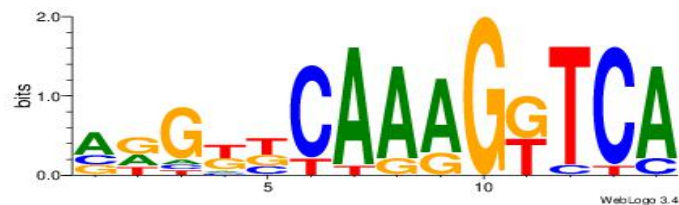


Dataset #: 1
Motif ID: 2
Motif name: NR2F1
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 5
Number of overlap: 10
Similarity score: 0.0654808

Alignment:
TGAMCTTTGMMCYT
-----TGACCTDVWT

Original motif Consensus sequence: TGAMCTTTGMMCYT

Reverse complement motif Consensus sequence: AKGYCAAAGRTC

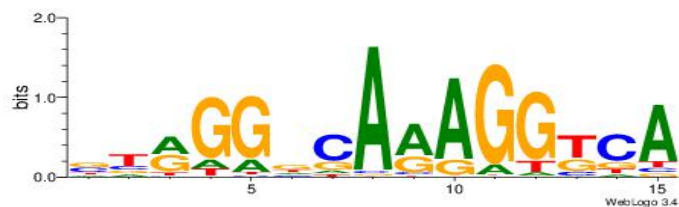


Dataset #: 1
 Motif ID: 14
 Motif name: PPARGRXRA
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 10
 Similarity score: 0.06668

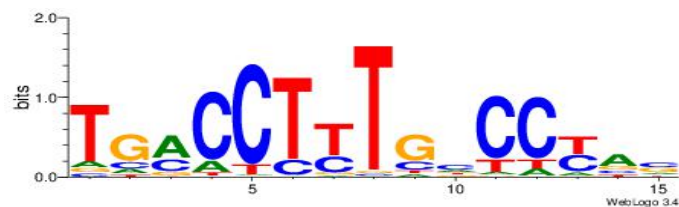
Alignment:

BTRGGDCARAGGKCA
 -----AWVDAGGTCA

Original motif Consensus sequence: BTRGGDCARAGGKCA



Reverse complement motif Consensus sequence: TGRCCCTKTGHCCCK



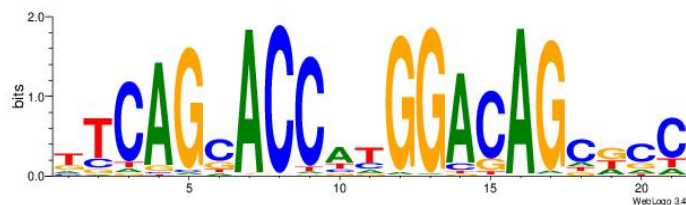
Dataset #: 1
 Motif ID: 7

Motif name:	REST
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:	0.0755608

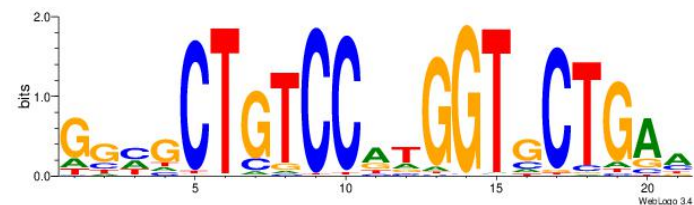
Alignment:

```
TTCAGCACCATGGACAGCKCC
-----AWVDAGGTCA-----
```

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC



Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA



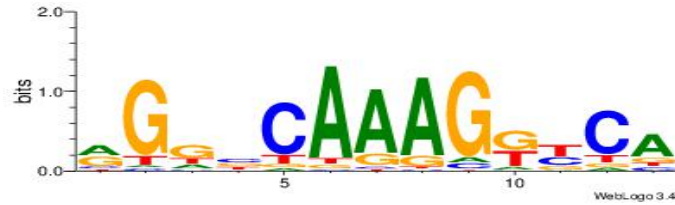
Dataset #:	1
Motif ID:	1
Motif name:	HNF4A
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	4
Number of overlap:	10
Similarity score:	0.0803396

Alignment:

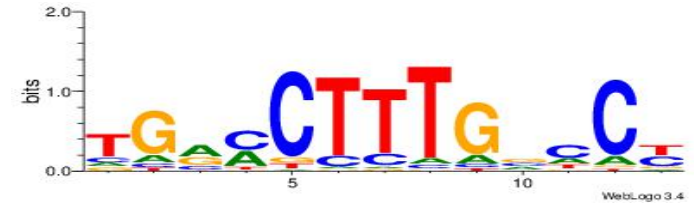
RGGBCAAAGKYCA

---AWVDAGGTCA

Original motif Consensus sequence: RGGBCAAAGKYCA



Reverse complement motif Consensus sequence: TGM YCTTTGBCC



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: 10

Number of overlap: 10

Similarity score: 0.0889306

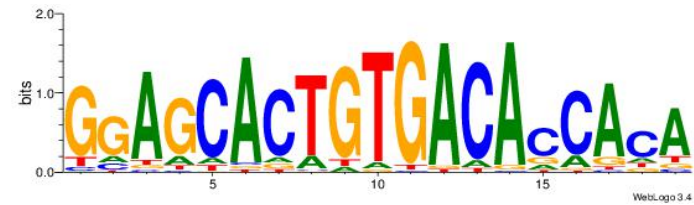
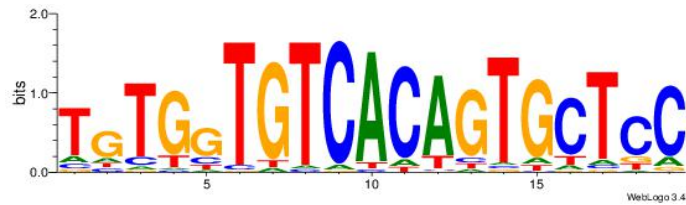
Alignment:

GGAGCACTGTGACACCACA

-----TGACCTDVWT

Original motif Consensus sequence: TGTGGTGTCACAGTGCTCC

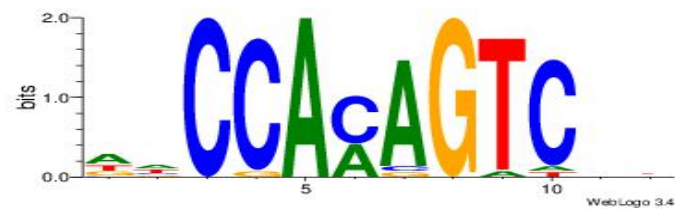
Reverse complement motif Consensus sequence:
GGAGCACTGTGACACCACA



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: 10
 Similarity score: 0.09225

Alignment:
 DDCCAMAGTCHB
 -AWVDAGGTCA-

Original motif Consensus sequence: DDCCAMAGTCHB



Reverse complement motif Consensus sequence: VDGACTRTGGDD



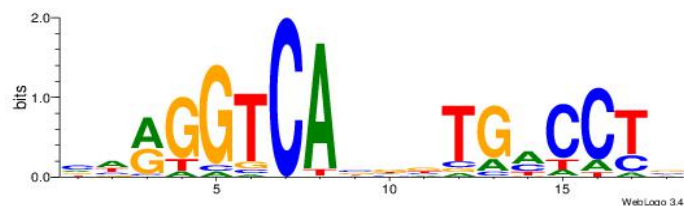
Dataset #: 1
 Motif ID: 9

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: 10
 Similarity score: 0.0988214

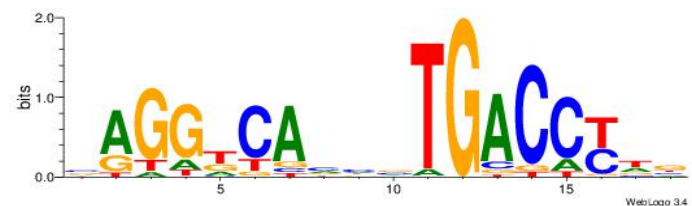
Alignment:

BAGGYCABHBTGACCKHV
 -----AWVDAGGTCA----

Original motif Consensus sequence: VHRGGTCABDBTGMCCCTB



Reverse complement motif Consensus sequence: BAGGYCABHBTGACCKHV



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

Original motif Consensus sequence: BAACGTCCGC



Reverse complement motif Consensus sequence: GCGGACGTTT



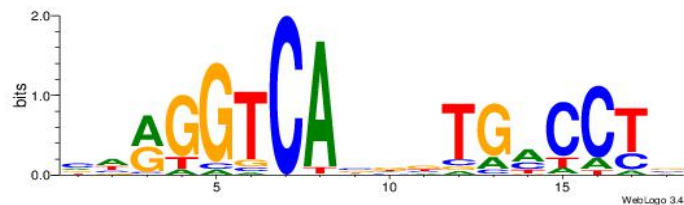
Best Matches for Motif ID 13 (Highest to Lowest)

Dataset #: 1
Motif ID: 9
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: 0.0605777

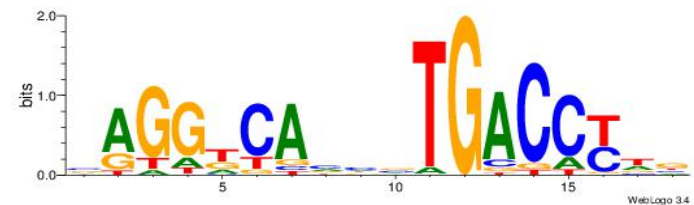
Alignment:

```
BAGGYCABHBTGACCKHV  
-----GCGGACGTTV
```

Original motif Consensus sequence: VHRGGTCABDBTGMCTB



Reverse complement motif Consensus sequence: BAGGYCABHBTGACCKHV

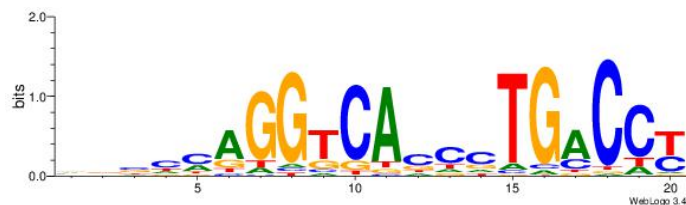


Dataset #: 1
Motif ID: 3
Motif name: ESR1
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif

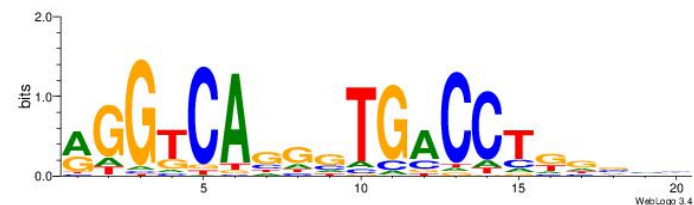
Direction: Backward
 Position number: 8
 Number of overlap: 10
 Similarity score: 0.0614567

Alignment:
 VDBHMAGGTCACCCTGACCY
 ---BAACGTCCGC-----

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



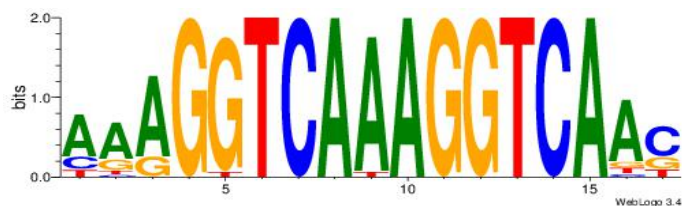
Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV



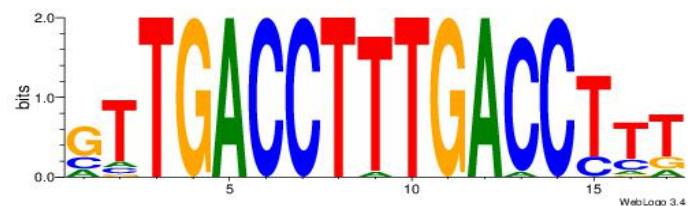
Dataset #: 1
 Motif ID: 10
 Motif name: NR1H2RXRA
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 10
 Similarity score: 0.0646071

Alignment:
 AAAGGTCAAAGGTCAAC
 -----BAACGTCCGC

Original motif Consensus sequence: AAAGGTCAAAGGTCAAC



Reverse complement motif Consensus sequence: GTTGACCTTTGACCTTT



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

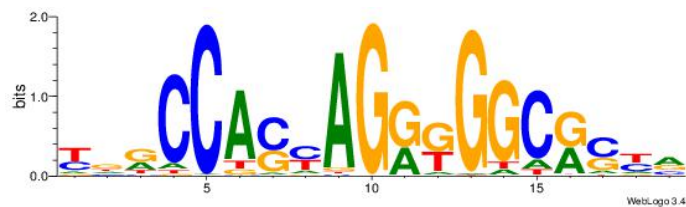


Dataset #: 1
 Motif ID: 16
 Motif name: CTCF
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 10
 Number of overlap: 10
 Similarity score: 0.0697767

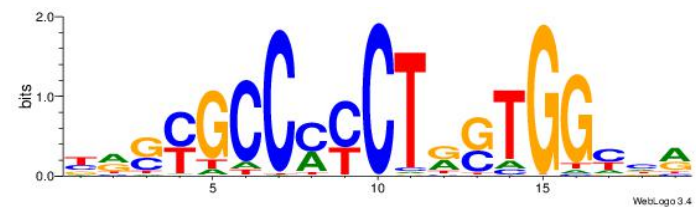
Alignment:

BSMGCCYMCTKSTGGMHM
 BAACGTCCGC-----

Original motif Consensus sequence: YDRCCASYAGRKGGCRSYV



Reverse complement motif Consensus sequence: BSMGCCYMCTKSTGGMHM

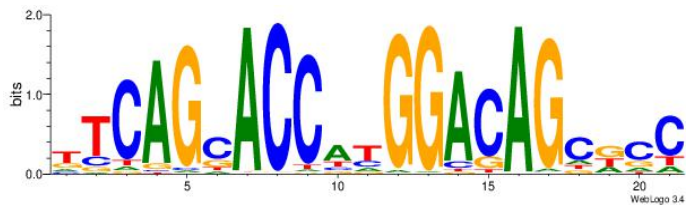


Dataset #: 1
 Motif ID: 7
 Motif name: REST
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3

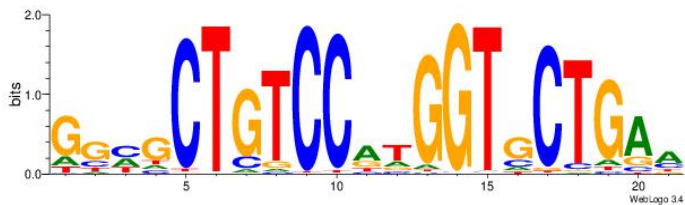
Number of overlap: 10
Similarity score: 0.0708149

Alignment:
GGYGCTGTCCATGGTGCTGAA
-----BAACGTCCGC--

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC



Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA



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



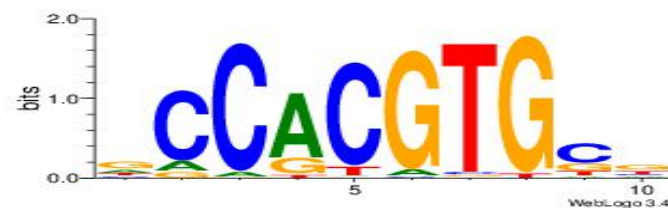
Dataset #: 1
 Motif ID: 8
 Motif name: Myc
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 9
 Similarity score: 0.555645

Alignment:
 VGCACGTGGH-
 -GCGGACGTTV

Original motif Consensus sequence: VGCACGTGGH



Reverse complement motif Consensus sequence: DCCACGTGCV



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 #:	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:	0.561179

Alignment:

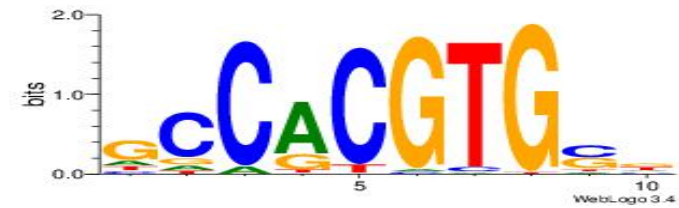
HSCACGTGGC-

-GCGGACGTTV

Original motif Consensus sequence: HSCACGTGGC



Reverse complement motif Consensus sequence: GCCACGTGSD

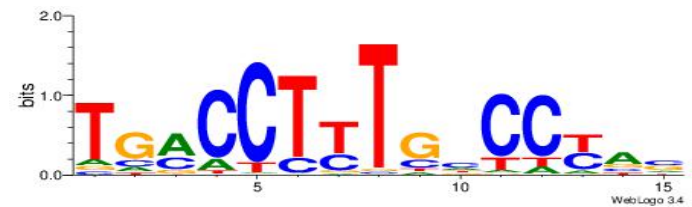


Dataset #: 1 Motif ID: 14 Motif name: PPARGRXRA

Original motif Consensus sequence: BTRGGDCARAGGKCA



Reverse complement motif Consensus sequence: TGRCCCTKTGHCKK



Best Matches for Motif ID 14 (Highest to Lowest)

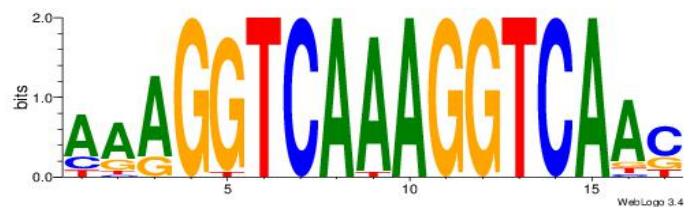
Dataset #:	1
Motif ID:	10
Motif name:	NR1H2RXRA
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	3

Number of overlap: 15
Similarity score: 0.0442974

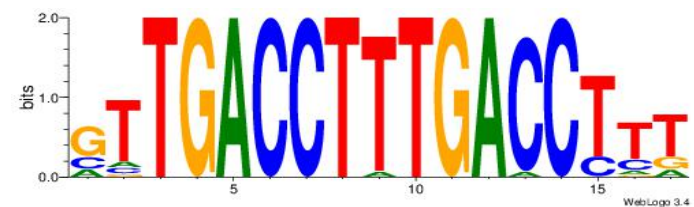
Alignment:

AAAGGTCAAAGGTCAAC
BTRGGDCARAGGKCA--

Original motif Consensus sequence: AAAGGTCAAAGGTCAAC



Reverse complement motif Consensus sequence:
GTTGACCTTTGACCTTT

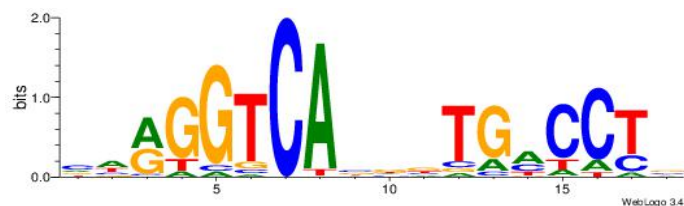


Dataset #: 1
Motif ID: 9
Motif name: ESR2
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 4
Number of overlap: 15
Similarity score: 0.0602408

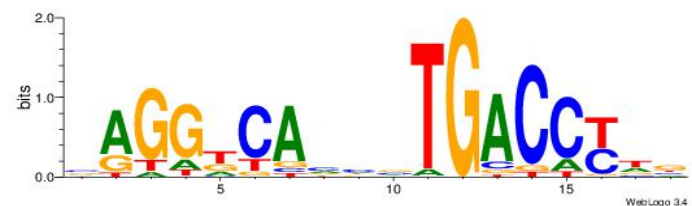
Alignment:

VHRGGTCABDBTGMCTB
BTRGGDCARAGGKCA---

Original motif Consensus sequence: VHRGGTCABDBTGMCTB



Reverse complement motif Consensus sequence: BAGGYCABHBTGACCKHV

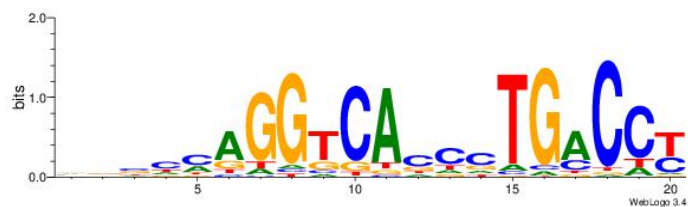


Dataset #: 1
 Motif ID: 3
 Motif name: ESR1
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 15
 Similarity score: 0.0723092

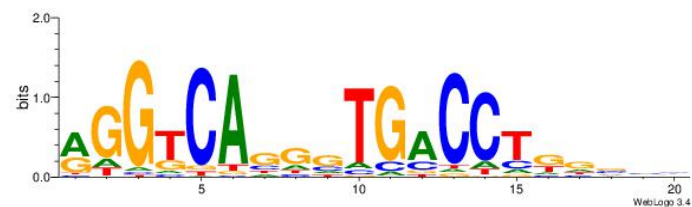
Alignment:

VDBHMAGGTCACCCTGACCY
 ---BTRGGDCARAGGKCA--

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV

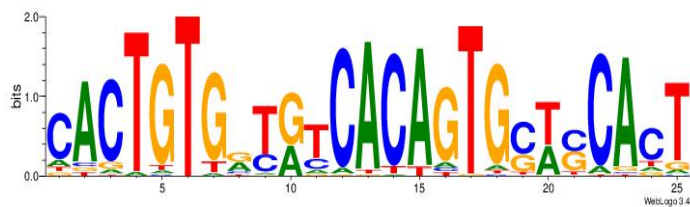


Dataset #: 2
 Motif ID: 22
 Motif name: CACTGTGrYrtCACAGTGswsCAcT
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 6
 Number of overlap: 15
 Similarity score: 0.0741352

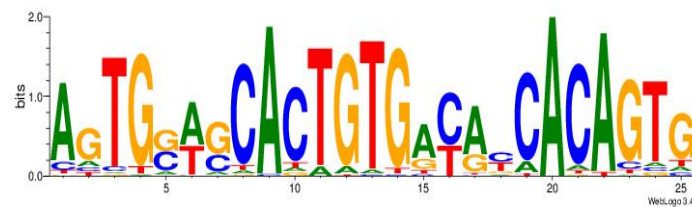
Alignment:

CACTGTGRTRTCACAGTGSWSCACT
 -----BTRGGDCARAGGKCA-----

Original motif Consensus sequence:
 CACTGTGRTRTCACAGTGSWSCACT



Reverse complement motif Consensus sequence:
 AGTGSWSCACTGTGAMAMCACAGTG



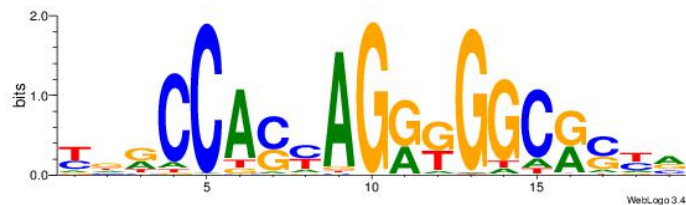
Dataset #: 1
 Motif ID: 16
 Motif name: CTCF
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2

Number of overlap: 15
Similarity score: 0.0786357

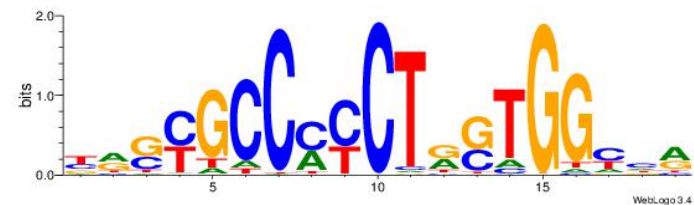
Alignment:

YDRCCASYAGRKGGRSYV
-BTRGGDCARAGGKCA---

Original motif Consensus sequence: YDRCCASYAGRKGGRSYV



Reverse complement motif Consensus sequence: BMSMGCCYMCTKSTGGMHM

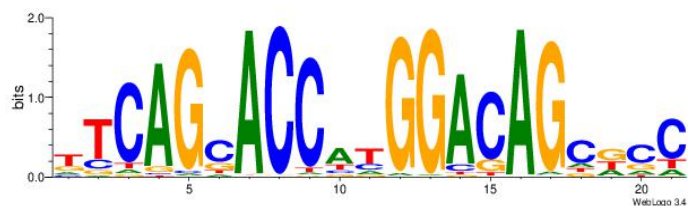


Dataset #: 1
Motif ID: 7
Motif name: REST
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 2
Number of overlap: 15
Similarity score: 0.0796159

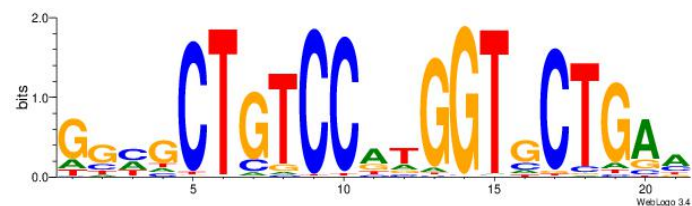
Alignment:

TTCAGCACCATGGACAGCKCC
-BTRGGDCARAGGKCA-----

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC



Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA

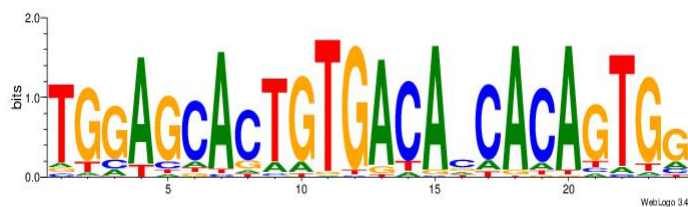


Dataset #: 2
Motif ID: 23
Motif name: TGGAGCACTGTGACAcCACAGTGg
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 7
Number of overlap: 15
Similarity score: 0.0813414

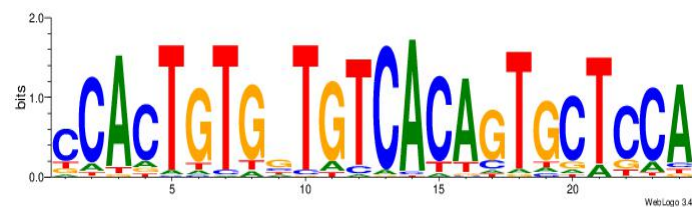
Alignment:

CCACTGTGVTGTACAGTGCTCCA
-----BTRGGDCARAGGKCA---

Original motif Consensus sequence: TGGAGCACTGTGACAVCACAGTGG



Reverse complement motif Consensus sequence: CCACTGTGVTGTACAGTGCTCCA

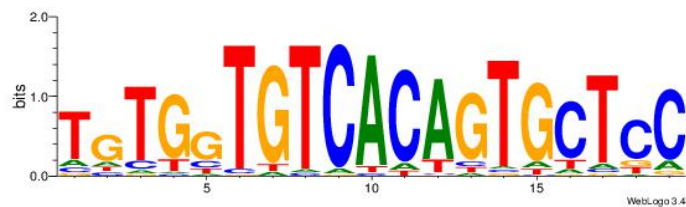


Dataset #: 2
 Motif ID: 17
 Motif name: TgTGgTGTCACAGTGCTCC
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 15
 Similarity score: 0.0818655

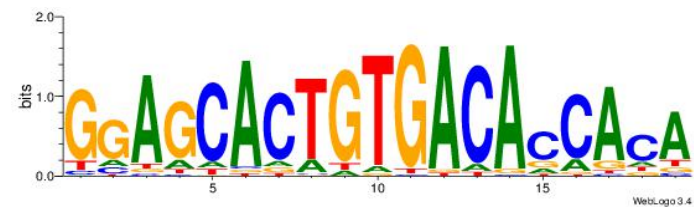
Alignment:

TGTGGTGTCACAGTGCTCC
 --BTRGGDCARAGGKCA--

Original motif Consensus sequence: TGTGGTGTCACAGTGCTCC



Reverse complement motif Consensus sequence: GGAGCACTGTGACACCACA



Dataset #: 1
 Motif ID: 2
 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: 14
Similarity score: 0.536521

Alignment:
AKGY YCAAAGRTCA-
BTRGGDCARAGGKCA

Original motif Consensus sequence: TGAMCTTTGMMCYT



Reverse complement motif Consensus sequence: AKGY YCAAAGRTCA

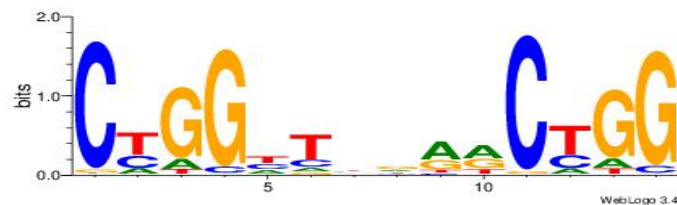
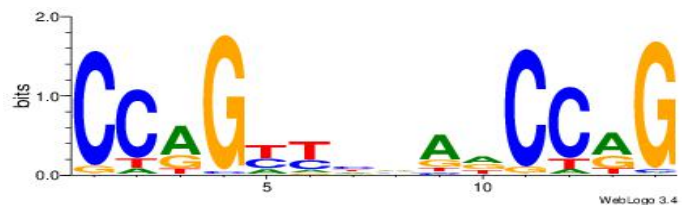


Dataset #: 1
Motif ID: 15
Motif name: Tcfcp2l1
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 14
Similarity score: 0.584465

Alignment:
-CKGGDTBDMMCTGG
TGRCC TKTGHCKAB

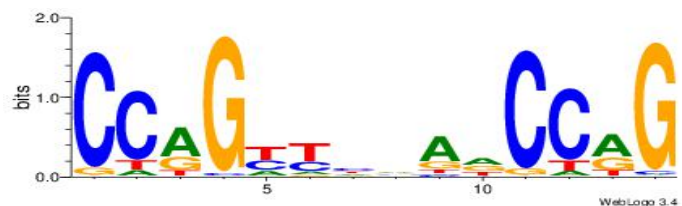
Original motif Consensus sequence: CCAGYYHVADCCRG

Reverse complement motif Consensus sequence: CKGGDTBDMMCTGG

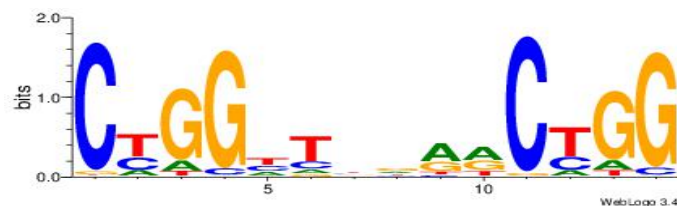


Dataset #: 1 Motif ID: 15 Motif name: Tcfcp2l1

Original motif Consensus sequence: CCAGYYHVADCCRG



Reverse complement motif Consensus sequence: CKGGDTBDMMCTG



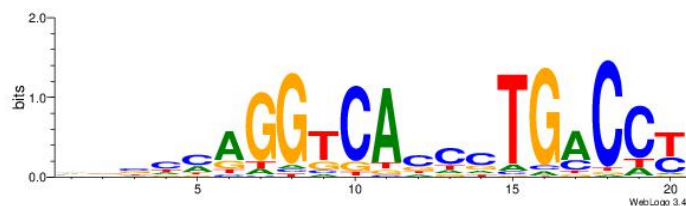
Best Matches for Motif ID 15 (Highest to Lowest)

Dataset #:	1
Motif ID:	3
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:	0.0453398

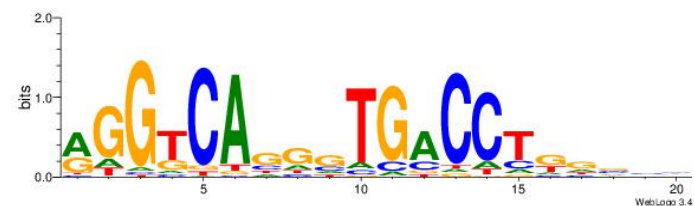
Alignment:

```
MGGTCAGGGTGACCTRDBHV
---CCAGYYHVADCCRG---
```

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV

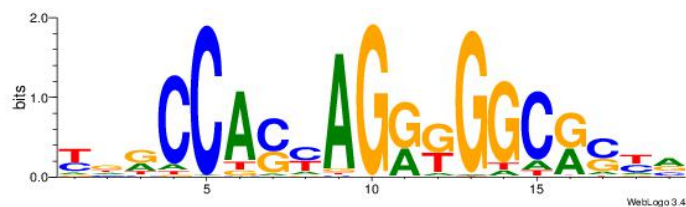


Dataset #: 1
 Motif ID: 16
 Motif name: CTCF
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 14
 Similarity score: 0.0491111

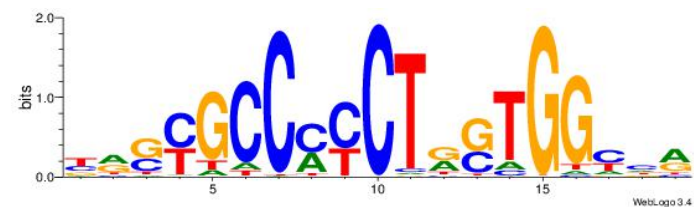
Alignment:

YDRCCASYAGRKGGRSYV
 ---CCAGYYHVADCCRG--

Original motif Consensus sequence: YDRCCASYAGRKGGRSYV



Reverse complement motif Consensus sequence: BMSMGCCYMCTKSTGGMHM

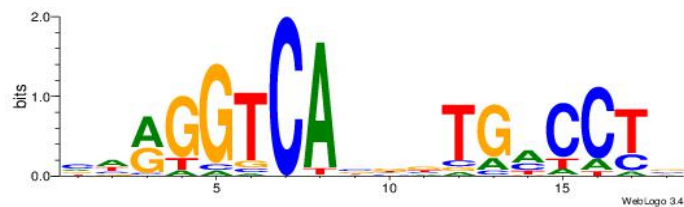


Dataset #: 1
 Motif ID: 9
 Motif name: ESR2
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0.0568174

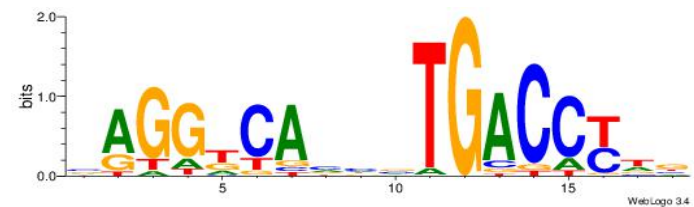
Alignment:

VHRGGTCABDBTGMCTB
 ----CKGGDTBDMCTGG

Original motif Consensus sequence: VHRGGTCABDBTGMCTB



Reverse complement motif Consensus sequence: BAGGYCABHBTGACCKHV

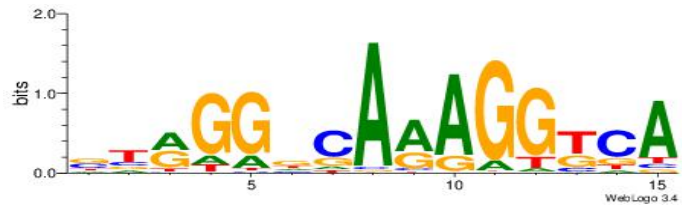


Dataset #: 1
 Motif ID: 14
 Motif name: PPARGRXRA
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1

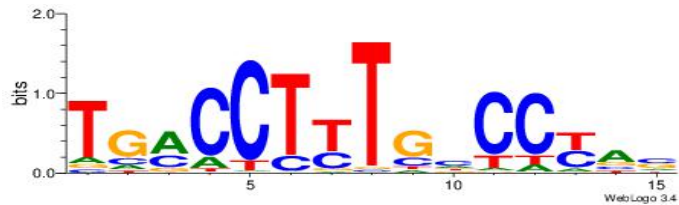
Number of overlap: 14
Similarity score: 0.0569399

Alignment:
TGRCCCTKTGHCCCKAB
-CKGGDTBDMMCTGG

Original motif Consensus sequence: BTRGGDCARAGGKCA



Reverse complement motif Consensus sequence: TGRCCCTKTGHCCCK

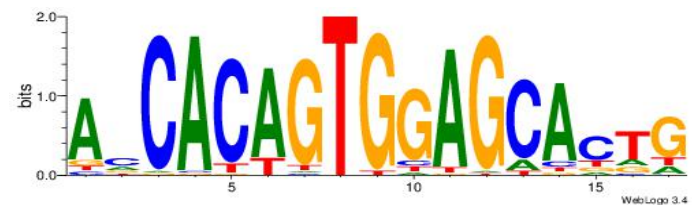
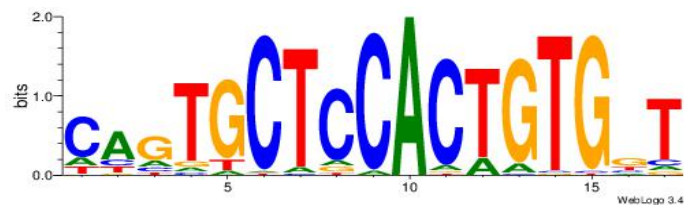


Dataset #: 2
Motif ID: 20
Motif name: CagTGCTCCACTGTGgT
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 5
Number of overlap: 13
Similarity score: 0.551995

Alignment:
ABCACAGTGGAGCACTG-
----CKGGDTBDMMCTGG

Original motif Consensus sequence: CAGTGCTCCACTGTGBT

Reverse complement motif Consensus sequence:
ABCACAGTGGAGCACTG

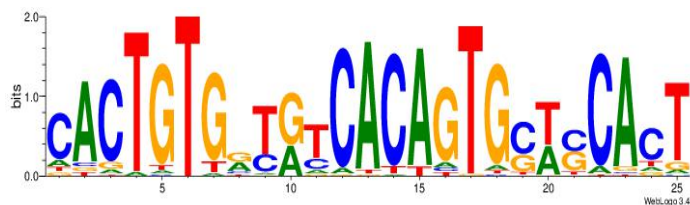


Dataset #: 2
 Motif ID: 22
 Motif name: CACTGTGrYrtCACAGTGsWsCAcT
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 14
 Number of overlap: 12
 Similarity score: 1.05046

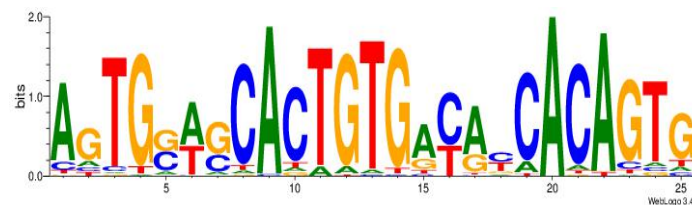
Alignment:

CACTGTGRTRTCACAGTGSWSCACT--
 -----CKGGDTBDMMCTGG

Original motif Consensus sequence:
 CACTGTGRTRTCACAGTGSWSCACT



Reverse complement motif Consensus sequence:
 AGTGSWSCACTGTGAMAMCACAGTG



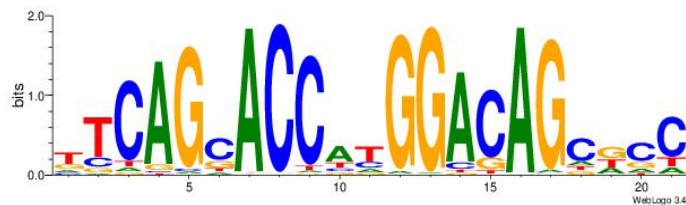
Dataset #: 1

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: 1.05111

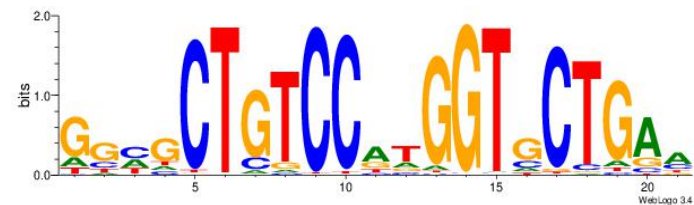
Alignment:

--TTCAGCACCATGGACAGCKCC
 CKGGDTBDMCTGG-----

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC



Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA

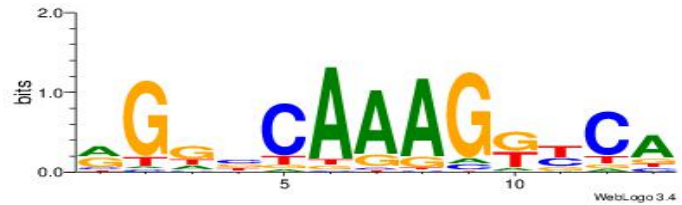


Dataset #: 1
 Motif ID: 1
 Motif name: HNF4A
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 12

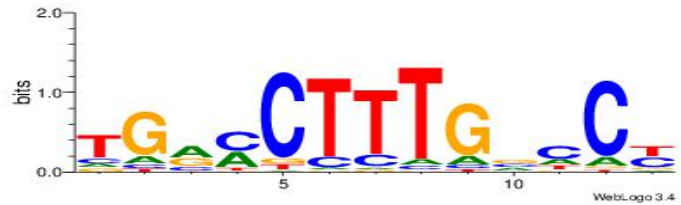
Similarity score: 1.05387

Alignment:
TGM YCTTTGB CCK--
-CKGGDTB DMMCTGG

Original motif Consensus sequence: RGGBCAAAGKYCA



Reverse complement motif Consensus sequence: TGM YCTTTGB CCK

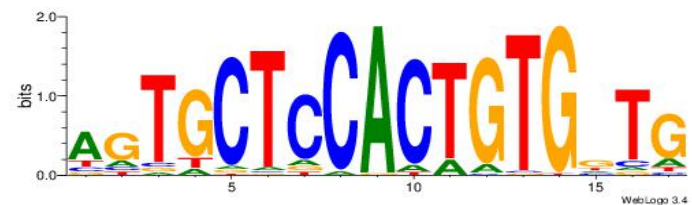
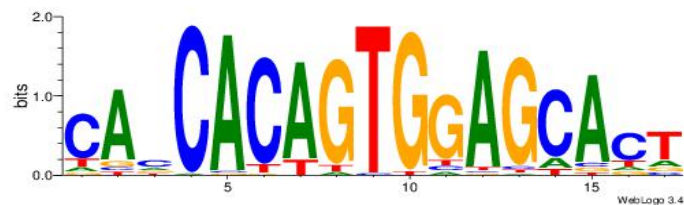


Dataset #: 2
Motif ID: 26
Motif name: CACACAGTGGAGCACT
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 6
Number of overlap: 12
Similarity score: 1.05541

Alignment:
CAHCACAGTGGAGCACT--
-----CKGGDTB DMMCTGG

Original motif Consensus sequence: CAHCACAGTGGAGCACT

Reverse complement motif Consensus sequence:
AGTGCTCCACTGTGDTG

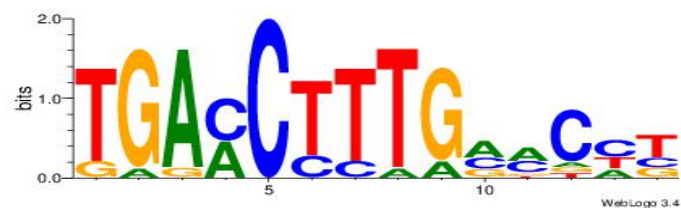


Dataset #: 1
 Motif ID: 2
 Motif name: NR2F1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 4
 Number of overlap: 11
 Similarity score: 1.55702

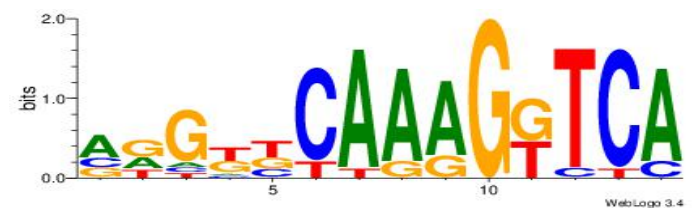
Alignment:

---AKGYCAAAGRTCA
 CKGGDTBDMCTGG---

Original motif Consensus sequence: TGAMCTTTGMMCYT

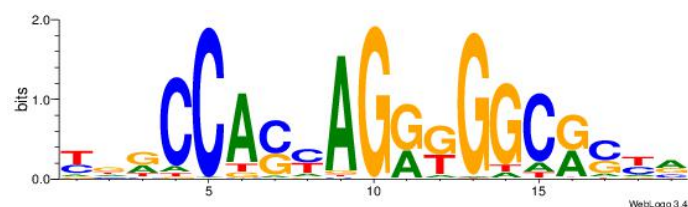


Reverse complement motif Consensus sequence: AKGYCAAAGRTC

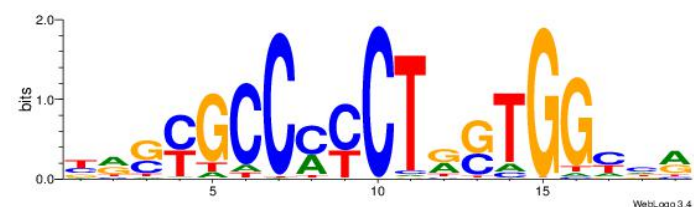


Dataset #: 1 Motif ID: 16 Motif name: CTCF

Original motif Consensus sequence: YDRCCASYAGRKGGRSYV



Reverse complement motif Consensus sequence: BMSMGCCYMCTKSTGGMHM



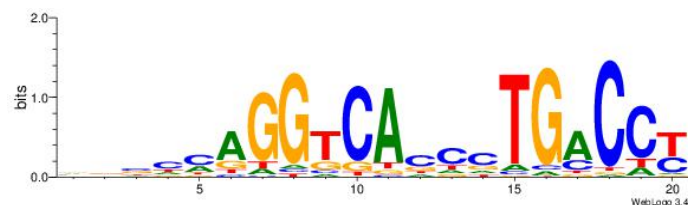
Best Matches for Motif ID 16 (Highest to Lowest)

Dataset #:	1
Motif ID:	3
Motif name:	ESR1
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:	0.0655511

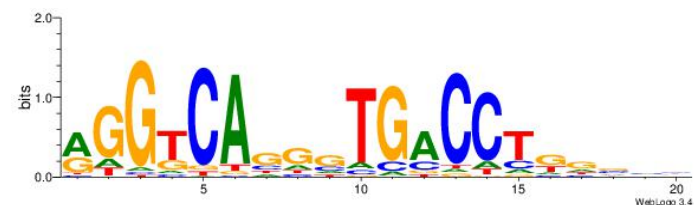
Alignment:

MGGTCAGGGTGACCTRDBHV
 -YDRCCASYAGRKGGRSYV

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV

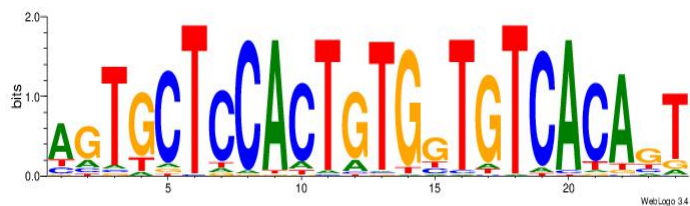


Dataset #: 2
 Motif ID: 27
 Motif name: AgTGCTCCACTGTGgTGTCACAgT
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 7
 Number of overlap: 18
 Similarity score: 0.563463

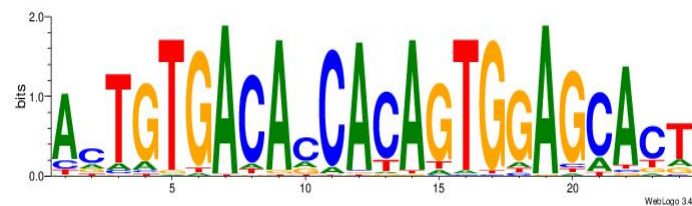
Alignment:

ACTGTGACACCACAGTGGAGCACT-
 -----YDRCCASYAGRKGGRSYV

Original motif Consensus sequence: AGTGCTCCACTGTGGTGTTCACAGT



Reverse complement motif Consensus sequence: ACTGTGACACCACAGTGGAGCACT



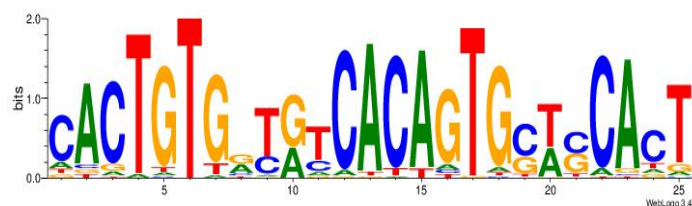
Dataset #: 2
 Motif ID: 22
 Motif name: CACTGTGrYrtCACAGTGswsCAcT
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward

Position number: 8
 Number of overlap: 18
 Similarity score: 0.566264

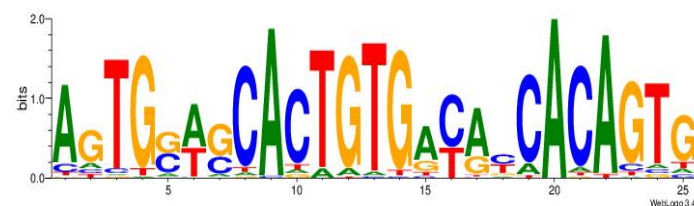
Alignment:

–AGTGSWSCACTGTGAMAMCACAGTG
 BSMGCCYMCTKSTGGMHM-----

Original motif Consensus sequence:
 CACTGTGRTRTCACAGTGSWSCACT



Reverse complement motif Consensus sequence:
 AGTGSWSCACTGTGAMAMCACAGTG

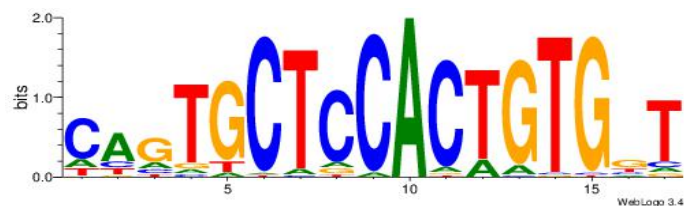


Dataset #: 2
 Motif ID: 20
 Motif name: CagTGCTCCACTGTGgT
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 17
 Similarity score: 1.05236

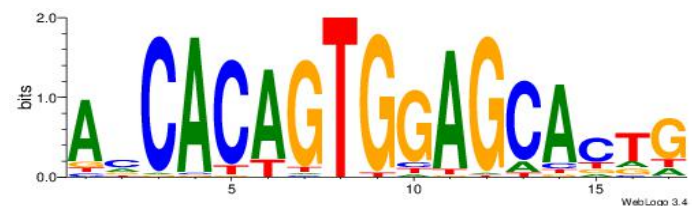
Alignment:

--ABCACAGTGGAGCACTG
 YDRCCASYAGRKGGRSYV

Original motif Consensus sequence: CAGTGCTCCACTGTGBT



Reverse complement motif Consensus sequence: ABCACAGTGGAGCACTG

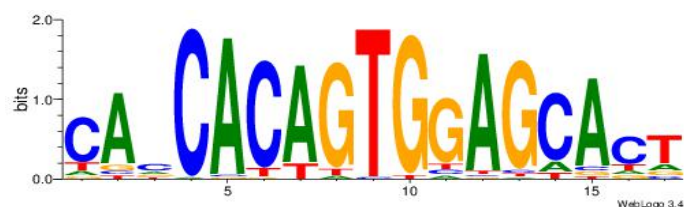


Dataset #: 2
Motif ID: 26
Motif name: CACACAGTGGAGCACT
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 3
Number of overlap: 15
Similarity score: 2.06184

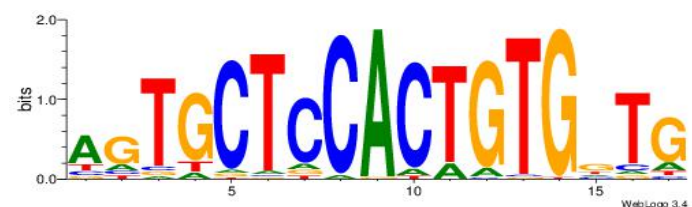
Alignment:

----CAHCACAGTGGAGCACT
YDRCCASYAGRKGGRSYV--

Original motif Consensus sequence: CAHCACAGTGGAGCACT



Reverse complement motif Consensus sequence: AGTGCTCCACTGTGDTG

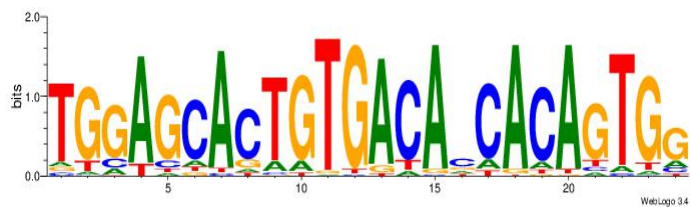


Dataset #: 2
 Motif ID: 23
 Motif name: TGGAGCACTGTGACAcCACAGTGg
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 10
 Number of overlap: 15
 Similarity score: 2.06698

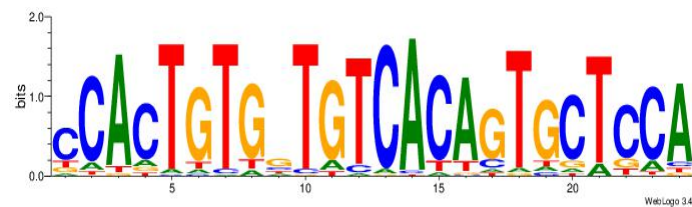
Alignment:

TGGAGCACTGTGACAVCACAGTGG----
 -----YDRCCASYAGRKGGRSYV

Original motif Consensus sequence: TGGAGCACTGTGACAVCACAGTGG



Reverse complement motif Consensus sequence: CCACTGTGVTGTACAGTGCTCCA

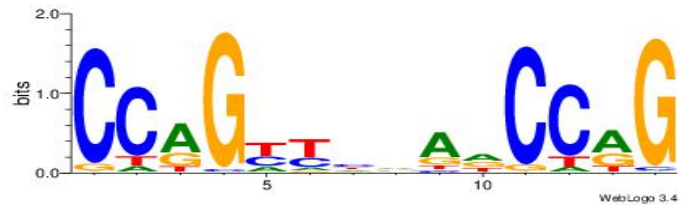


Dataset #: 1
 Motif ID: 15
 Motif name: Tcfcp2l1
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2

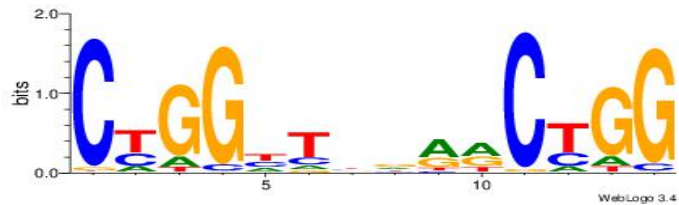
Number of overlap: 13
Similarity score: 3.05613

Alignment:
-----CCAGYYHVADCCRG
YDRCCASYAGRKGCCRSYV-

Original motif Consensus sequence: CCAGYYHVADCCRG



Reverse complement motif Consensus sequence: CKGGDTBDMMCTG

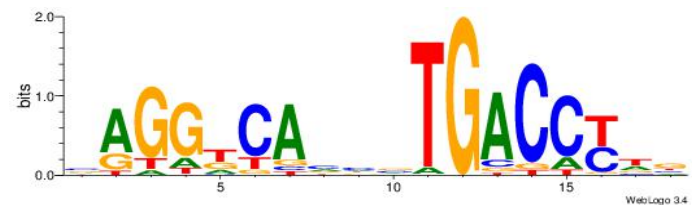
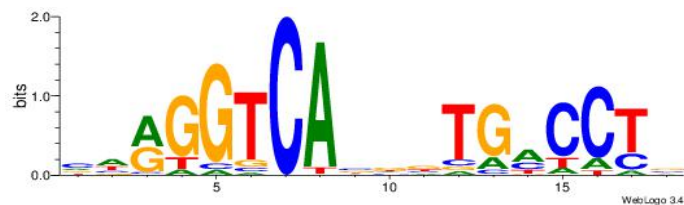


Dataset #: 1
Motif ID: 9
Motif name: ESR2
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 6
Number of overlap: 13
Similarity score: 3.06048

Alignment:
-----VHRGGTCABDBTGMCTB
YDRCCASYAGRKGCCRSYV-----

Original motif Consensus sequence: VHRGGTCABDBTGMCTB

Reverse complement motif Consensus sequence:
BAGGYCABHBTGACCKHV

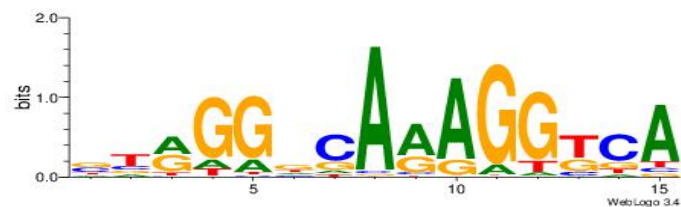


Dataset #: 1
 Motif ID: 14
 Motif name: PPARGRXRA
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 13
 Similarity score: 3.06565

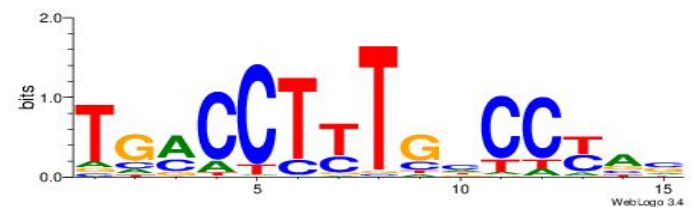
Alignment:

-----BTRGGDCARAGGKCA
 YDRCCASYAGRKGGCRSYV--

Original motif Consensus sequence: BTRGGDCARAGGKCA



Reverse complement motif Consensus sequence: TGRCCCTKTGHCCCK



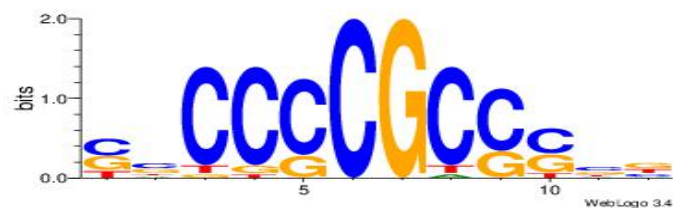
Dataset #: 2
 Motif ID: 24

Motif name: ssCCCCGCSssk
 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: 3.56185

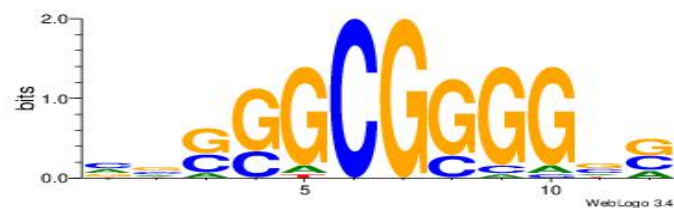
Alignment:

SBCCCCGCCSBB-----
 BSMGCCCYMCTKSTGGMHM

Original motif Consensus sequence: SBCCCCGCCSBB

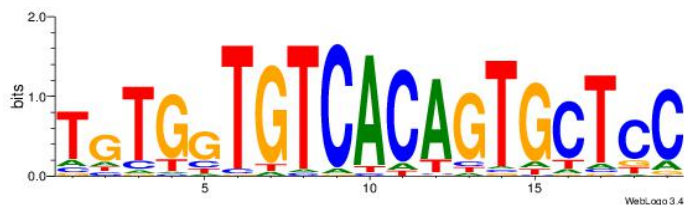


Reverse complement motif Consensus sequence: BBSGGCGGGBS

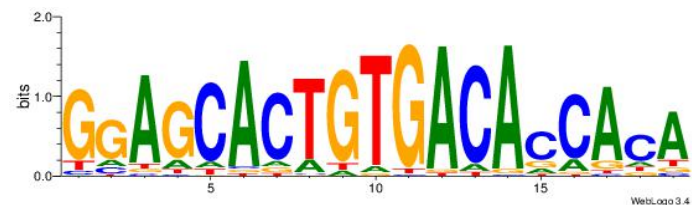


Dataset #: 2 Motif ID: 17 Motif name: TgTGgTGTCACAGTGCTCC

Original motif Consensus sequence: TGTGGTGTCACAGTGCTCC



Reverse complement motif Consensus sequence:
GGAGCACTGTGACACCACA



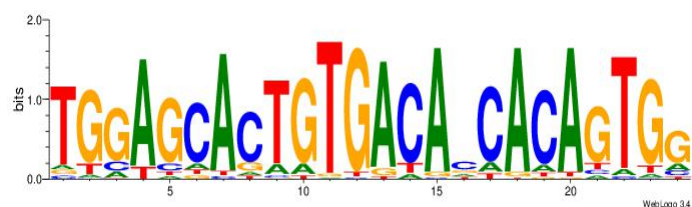
Best Matches for Motif ID 17 (Highest to Lowest)

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: 5
 Number of overlap: 19
 Similarity score: 0

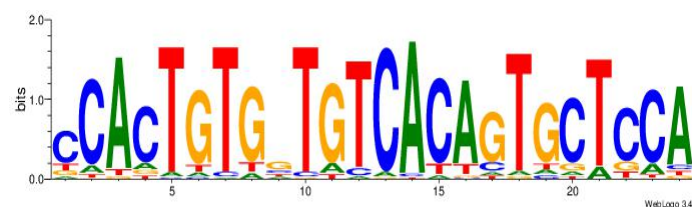
Alignment:

TGGAGCACTGTGACAVCACAGTGG
 -GGAGCACTGTGACACCACA-----

Original motif Consensus sequence: TGGAGCACTGTGACAVCACAGTGG



Reverse complement motif Consensus sequence: CCACTGTGVTGTACAGTGCTCCA



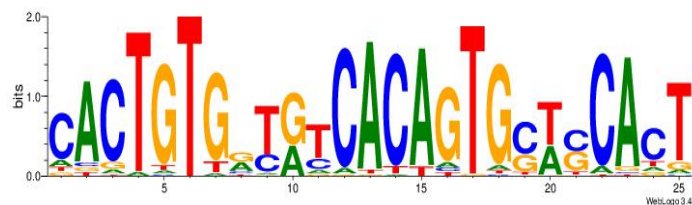
Dataset #: 2
 Motif ID: 22
 Motif name: CACTGTGrYrtCACAGTGsWsCAcT
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif

Direction: Backward
 Position number: 4
 Number of overlap: 19
 Similarity score: 0.0217259

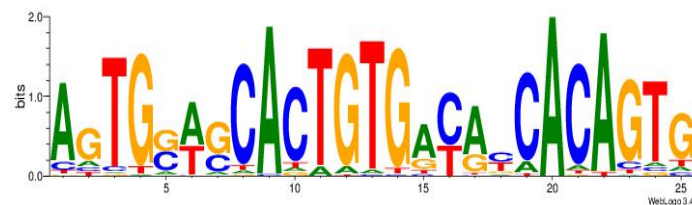
Alignment:

CACTGTGRTRTCACAGTGSWSCACT
 ---TGTGGTGTTCACAGTGCTCC---

Original motif Consensus sequence:
 CACTGTGRTRTCACAGTGSWSCACT



Reverse complement motif Consensus sequence:
 AGTGSWSCACTGTGAMAMCACAGTG

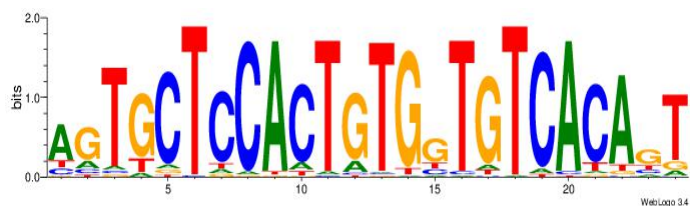


Dataset #: 2
 Motif ID: 27
 Motif name: AgTGCTCCACTGTGgTGTCACAgT
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3
 Number of overlap: 19
 Similarity score: 0.074816

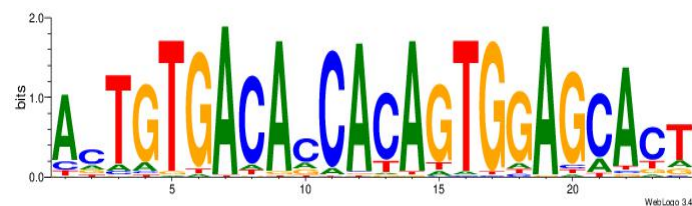
Alignment:

ACTGTGACACCACAGTGGAGCACT
 --TGTGGTGTTCACAGTGCTCC---

Original motif Consensus sequence: AGTGCTCCACTGTGGTGTACAGT



Reverse complement motif Consensus sequence: ACTGTGACACCACAGTGGAGCACT

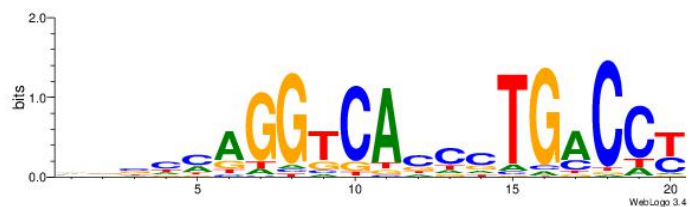


Dataset #: 1
Motif ID: 3
Motif name: ESR1
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 2
Number of overlap: 19
Similarity score: 0.0857262

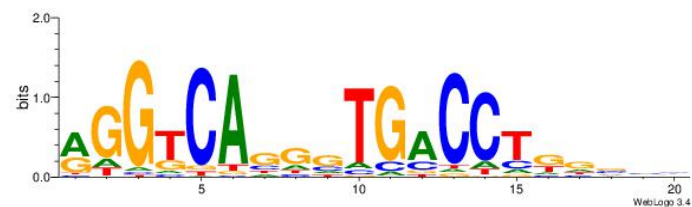
Alignment:

VDBHMAGGTCACCCTGACCY
-TGTGGTGTACAGTGCTCC

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV

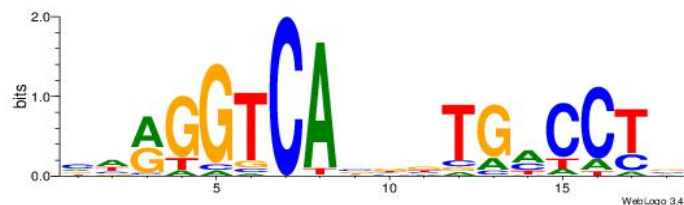


Dataset #: 1
 Motif ID: 9
 Motif name: ESR2
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 17
 Similarity score: 1.08001

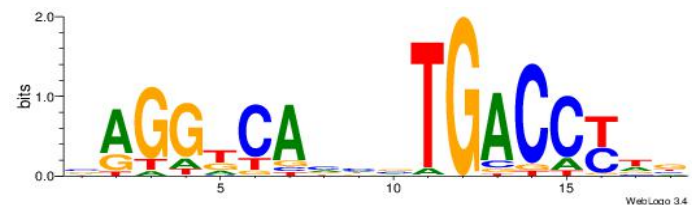
Alignment:

--VHRGGTCABDBTGMCTB
 TGTGGTGTACAGTGCTCC-

Original motif Consensus sequence: VHRGGTCABDBTGMCTB



Reverse complement motif Consensus sequence: BAGGYCABHBTGACCKHV



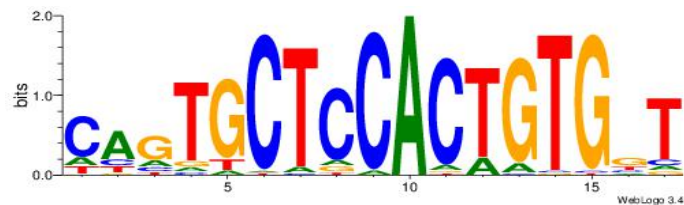
Dataset #: 2
 Motif ID: 20
 Motif name: CagTGCTCCACTGTGgT
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1

Number of overlap: 17
Similarity score: 1.08847

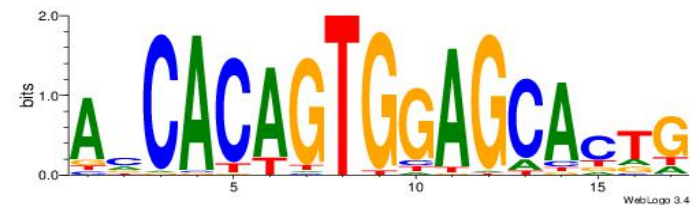
Alignment:

CAGTGCTCCACTGTGBT--
TGTGGTGTACAGTGCTCC

Original motif Consensus sequence: CAGTGCTCCACTGTGBT



Reverse complement motif Consensus sequence: ABCACAGTGGAGCACTG

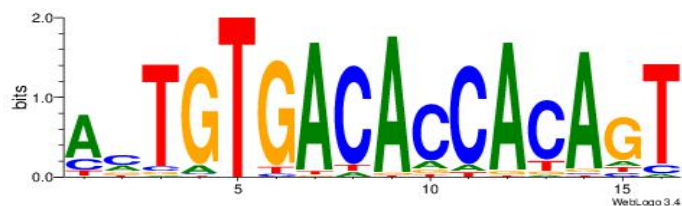


Dataset #: 2
Motif ID: 21
Motif name: AmTGTGACACCACAGT
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 16
Similarity score: 1.59452

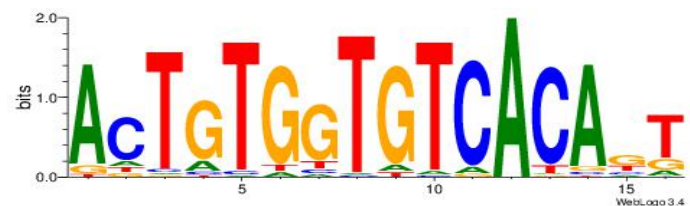
Alignment:

ACTGTGGTGTACART---
GGAGCACTGTGACACCACA

Original motif Consensus sequence: AMTGTGACACCACAGT



Reverse complement motif Consensus sequence: ACTGTGGTGTCCACART

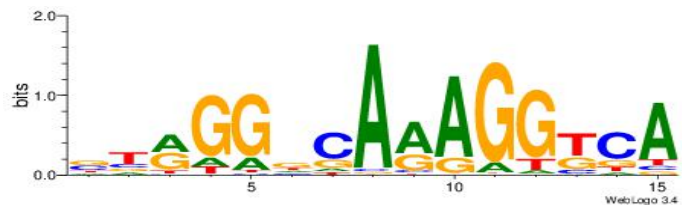


Dataset #: 1
Motif ID: 14
Motif name: PPARGRXRA
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 15
Similarity score: 2.10007

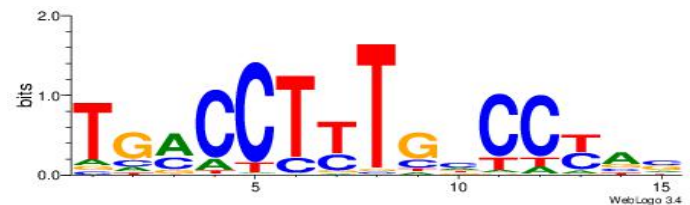
Alignment:

BTRGGDCARAGGKCA-----
GGAGCACTGTGACACCACA

Original motif Consensus sequence: BTRGGDCARAGGKCA



Reverse complement motif Consensus sequence: TGRCCCTKTGHCCCK

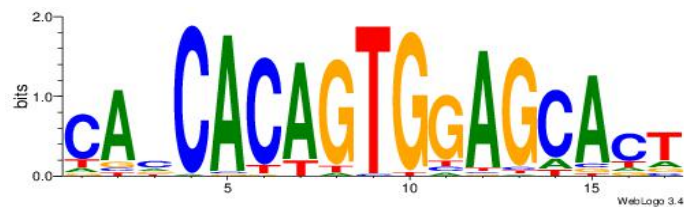


Dataset #: 2
 Motif ID: 26
 Motif name: CACACAGTGGAGCACT
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 4
 Number of overlap: 14
 Similarity score: 2.57554

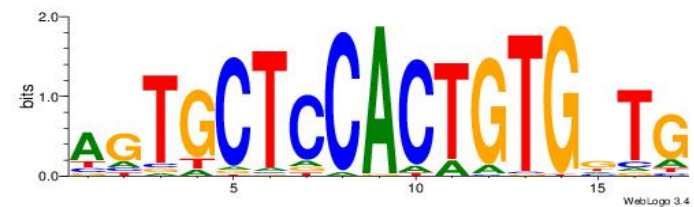
Alignment:

-----CAHCACAGTGGAGCACT
 TGTGGTGTCACTGTCTCC---

Original motif Consensus sequence: CAHCACAGTGGAGCACT



Reverse complement motif Consensus sequence: AGTGCTCCACTGTGDTG



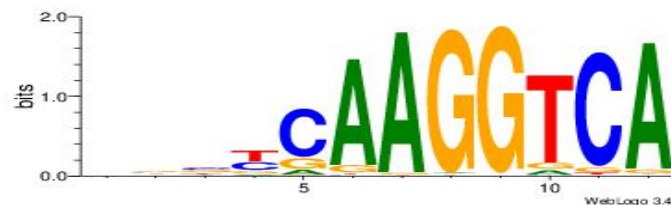
Dataset #: 1
 Motif ID: 4
 Motif name: Esrrb
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1

Number of overlap: 12
Similarity score: 3.58914

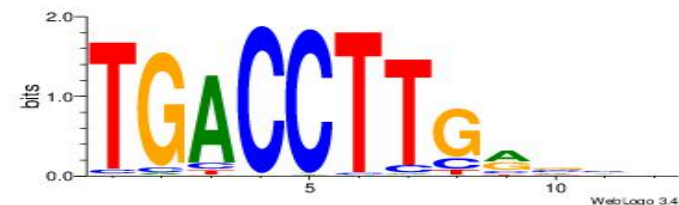
Alignment:

-----VBBYCAAGGTCA
GGAGCACTGTGACACCACA

Original motif Consensus sequence: VBBYCAAGGTCA

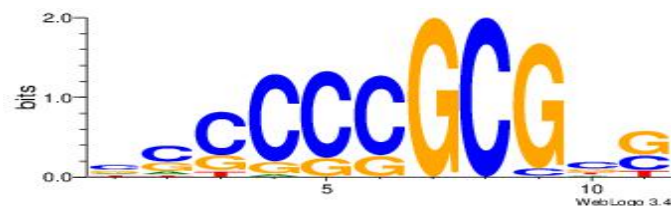


Reverse complement motif Consensus sequence: TGACCTTGMBBB



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

Original motif Consensus sequence: BSCCCCGCGBS



Reverse complement motif Consensus sequence: SBCGCGGGGSB



Best Matches for Motif ID 18 (Highest to Lowest)

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

Alignment:
 BBSGGCGGGGBS
 -SBCGCGGGGSB

Original motif Consensus sequence: SBCCCCGCCSBB



Reverse complement motif Consensus sequence: BBSGGCGGGGBS



Dataset #: 2
 Motif ID: 32
 Motif name: gCGCGCsCgsG
 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: 0.0417227

Alignment:
 CGCGSGCGCGC
 SBCGCGGGGSB

Original motif Consensus sequence: GCGCGCSCGCG



Reverse complement motif Consensus sequence: CGCGSGCGCGC

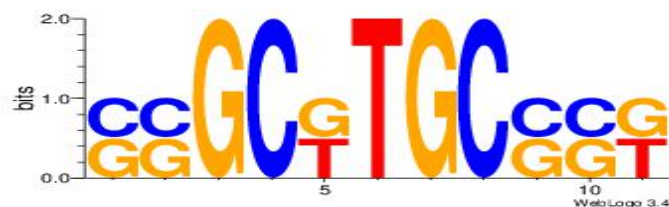


Dataset #: 2
 Motif ID: 28
 Motif name: ssGCKTGCssk
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.0523123

Alignment:

SSGCKTGCSSK
 BSCCCGCGBS

Original motif Consensus sequence: SSGCKTGCSSK



Reverse complement motif Consensus sequence: YSSGCAYGCSS

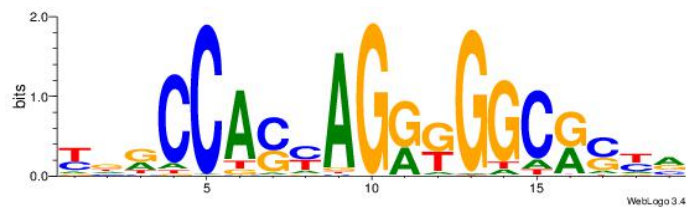


Dataset #: 1
 Motif ID: 16
 Motif name: CTCF
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 7
 Number of overlap: 11
 Similarity score: 0.0564004

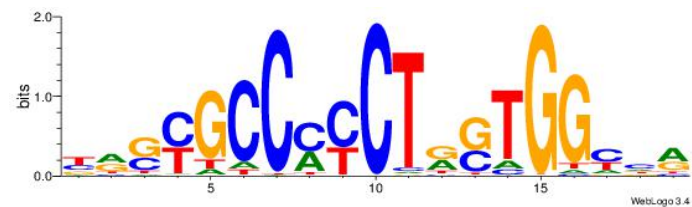
Alignment:

YDRCCASYAGRKGGCRSYV
 --SBCGCGGGGSB-----

Original motif Consensus sequence: YDRCCASYAGRKGGCRSYV



Reverse complement motif Consensus sequence: BMSMGCCYMCTKSTGGMHM

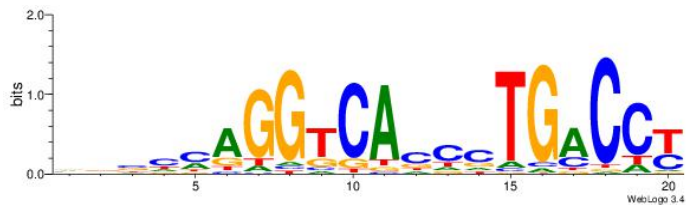


Dataset #: 1
 Motif ID: 3
 Motif name: ESR1
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1

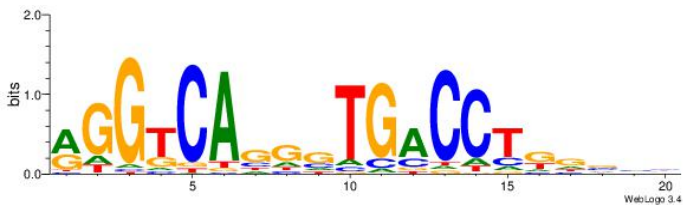
Number of overlap: 11
Similarity score: 0.0734979

Alignment:
MGGTCAGGGTGACCTRDBHV
BSCCCCGCGBS-----

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV



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: 1
Number of overlap: 11
Similarity score: 0.0757081

Alignment:
CCGCGGRCACG
BSCCCCGCGBS

Original motif Consensus sequence: CCGCGGRCACG

Reverse complement motif Consensus sequence: CGTGKCCGCGG

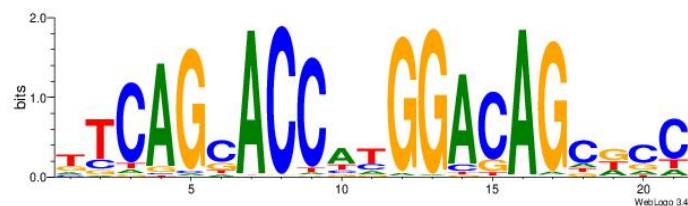


Dataset #: 1
 Motif ID: 7
 Motif name: REST
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 11
 Number of overlap: 11
 Similarity score: 0.0758097

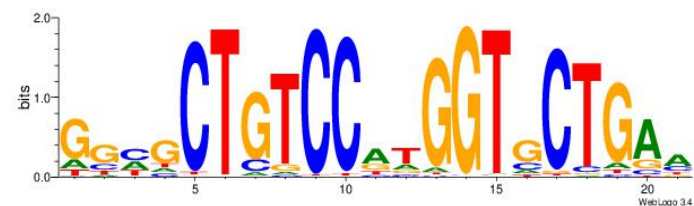
Alignment:

GYGCTGTCCATGGTGCTGAA
 SBCGCGGGGSB-----

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC



Reverse complement motif Consensus sequence: GYGCTGTCCATGGTGCTGAA



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: 0.535606

Alignment:

-VGCACGTGGH
 SBCGCGGGGSB

Original motif Consensus sequence: VGCACGTGGH



Reverse complement motif Consensus sequence: DCCACGTGCV

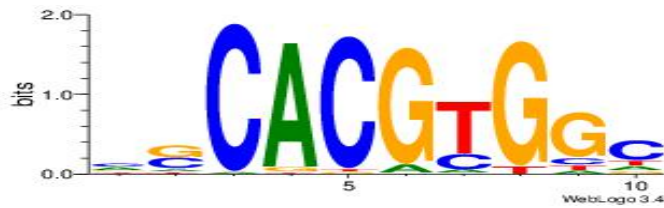


Dataset #: 1
 Motif ID: 6
 Motif name: Mycn
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 10
 Similarity score: 0.536235

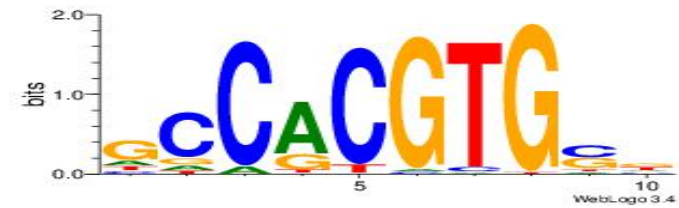
Alignment:

-HSCACGTGGC
SBCGCGGGGSB

Original motif Consensus sequence: HSCACGTGGC



Reverse complement motif Consensus sequence: GCCACGTGSD



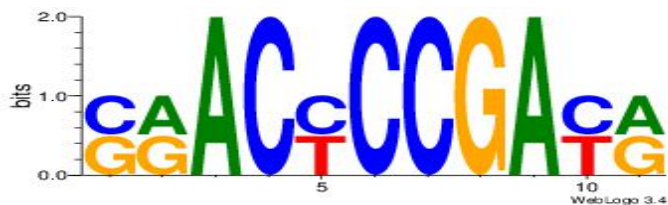
Dataset #:	2
Motif ID:	33
Motif name:	srACyCCGAyr
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	2
Number of overlap:	10
Similarity score:	0.571697

Alignment:

KKTCGGKGTKS-
-SBCGCGGGGSB

Original motif Consensus sequence: SRACYCCGAYR

Reverse complement motif Consensus sequence: KKTCGGKGTKS



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

Original motif Consensus sequence: ATACTTTGGC



Reverse complement motif Consensus sequence: GCCAAAGTAT

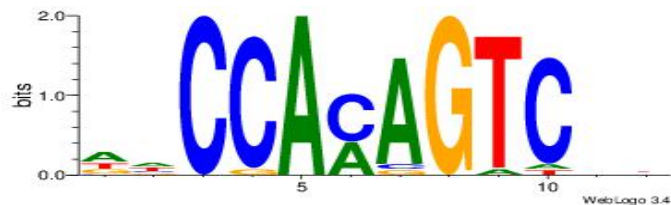


Best Matches for Motif ID 19 (Highest to Lowest)

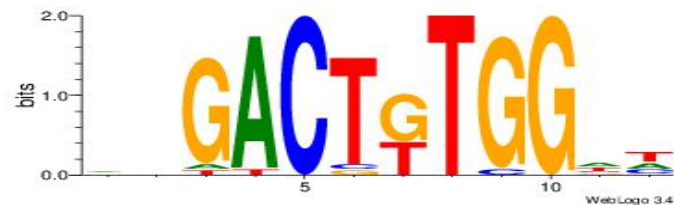
Dataset #:	2
Motif ID:	25
Motif name:	wwCCAmAGTCmt
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	10
Similarity score:	0.0215909

Alignment:
 DDCCAMAGTCHB
 -GCCAAAGTAT-

Original motif Consensus sequence: DDCCAMAGTCHB



Reverse complement motif Consensus sequence: VDGACTRTGGDD



Dataset #: 2
Motif ID: 30
Motif name: taaacgatgcc
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: 0.0375

Alignment:

GGCATCGTTTA

GCCAAAGTAT-

Original motif Consensus sequence: TAAACGATGCC



Reverse complement motif Consensus sequence: GGCATCGTTTA

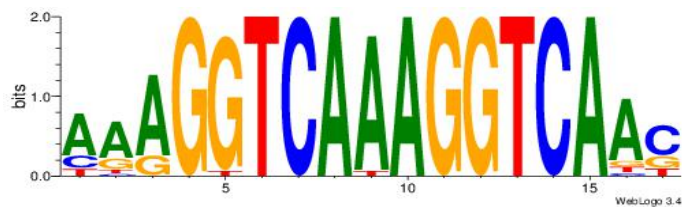


Dataset #: 1
 Motif ID: 10
 Motif name: NR1H2RXRA
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 5
 Number of overlap: 10
 Similarity score: 0.0395

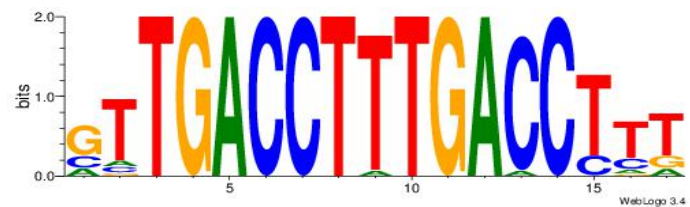
Alignment:

AAAGGTCAAAGGTCAAC
 ---GCCAAAGTAT----

Original motif Consensus sequence: AAAGGTCAAAGGTCAAC



Reverse complement motif Consensus sequence: GTTGACCTTTGACCTT



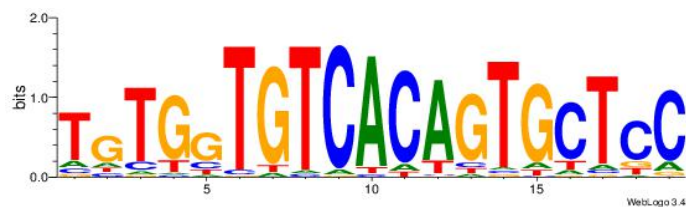
Dataset #: 2
 Motif ID: 17
 Motif name: TgTGgTGTCACAGTGCTCC
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 4

Number of overlap: 10
Similarity score: 0.0472222

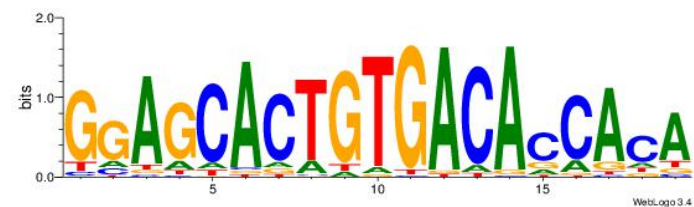
Alignment:

GGAGCACTGTGACACCACA
-----ATACTTTGGC---

Original motif Consensus sequence: TGTGGTGTACAGTGCTCC



Reverse complement motif Consensus sequence: GGAGCACTGTGACACCACA

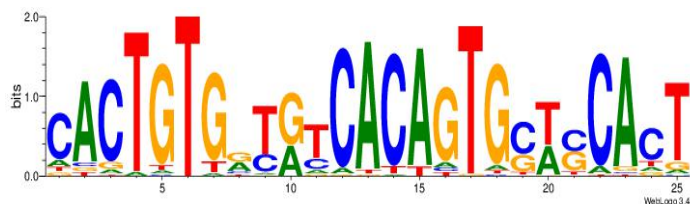


Dataset #: 2
Motif ID: 22
Motif name: CACTGTGrYrtCACAGTGsWsCAcT
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 10
Number of overlap: 10
Similarity score: 0.0474206

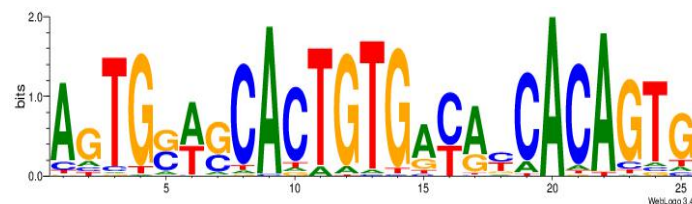
Alignment:

CACTGTGRTRTCACAGTGSWSCACT
-----GCCAAAGTAT-----

Original motif Consensus sequence:
CACTGTGRTRTCACAGTGSWSCACT



Reverse complement motif Consensus sequence:
AGTGSWSCACTGTGAMAMCACAGTG

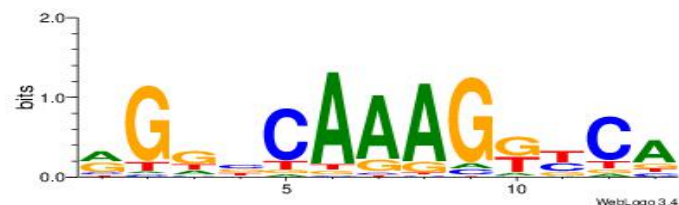


Dataset #: 1
Motif ID: 1
Motif name: HNF4A
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 3
Number of overlap: 10
Similarity score: 0.0483209

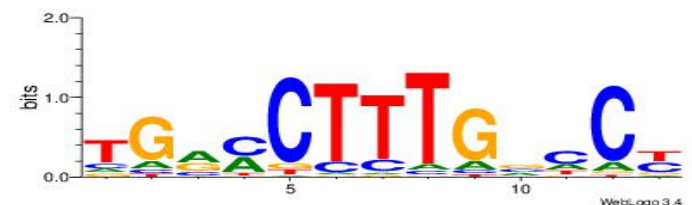
Alignment:

TGMYCTTTGBCCK
--ATACTTTGGC--

Original motif Consensus sequence: RGGBCAAAGKYCA



Reverse complement motif Consensus sequence: TGMYCTTTGBCCK

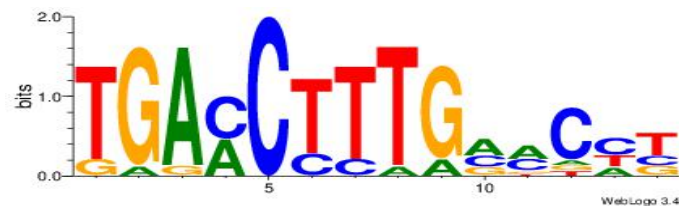


Dataset #: 1
 Motif ID: 2
 Motif name: NR2F1
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 10
 Similarity score: 0.0490385

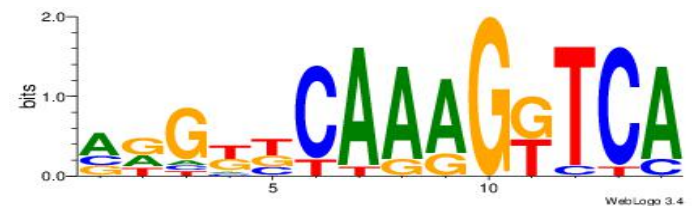
Alignment:

TGAMCTTTGMMCYT
 -ATACTTTGGC---

Original motif Consensus sequence: TGAMCTTTGMMCYT



Reverse complement motif Consensus sequence: AKGYCAAAGRTC



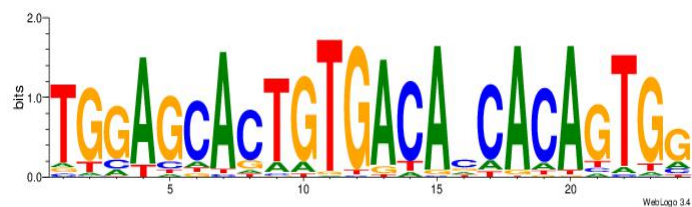
Dataset #: 2
 Motif ID: 23
 Motif name: TGGAGCACTGTGACAcCACAGTGg
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 11
 Number of overlap: 10

Similarity score: 0.0493243

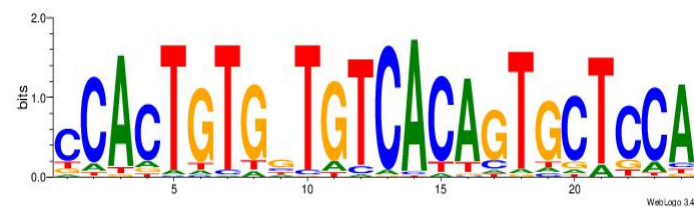
Alignment:

CCACTGTGVTGTCACAGTGCTCCA
-----GCCAAAGTAT-----

Original motif Consensus sequence: TGGAGCACTGTGACAVCACAGTGG



Reverse complement motif Consensus sequence: CCACTGTGVTGTCACAGTGCTCCA



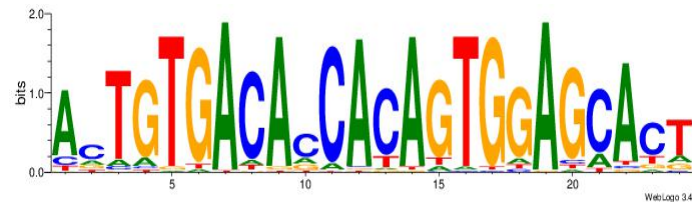
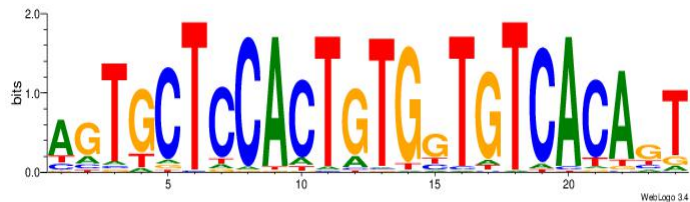
Dataset #: 2
Motif ID: 27
Motif name: AgTGCTCCACTGTGgTGTCACAgT
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 9
Number of overlap: 10
Similarity score: 0.0498239

Alignment:

ACTGTGACACCACAGTGGAGCACT
-----GCCAAAGTAT-----

Original motif Consensus sequence: AGTGCTCCACTGTGGTGTACAGT

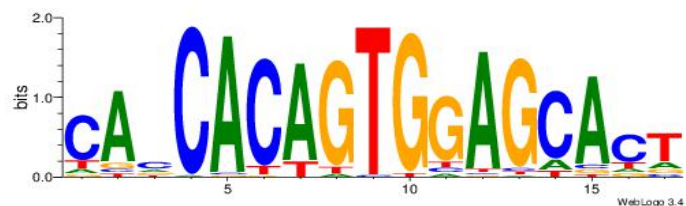
Reverse complement motif Consensus sequence: ACTGTGACACCACAGTGGAGCACT



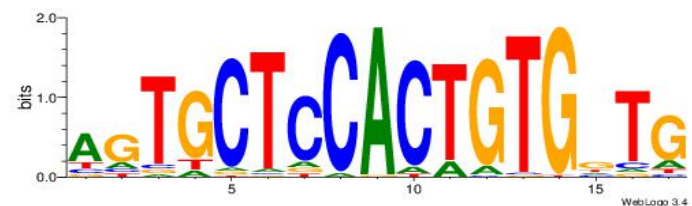
Dataset #: 2
 Motif ID: 26
 Motif name: CACcACAGTGGAGCAcT
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 10
 Similarity score: 0.0527344

Alignment:
 AGTGCTCCACTGTGDTG
 -----ATACTTTGGC-

Original motif Consensus sequence: CAHCACAGTGGAGCACT

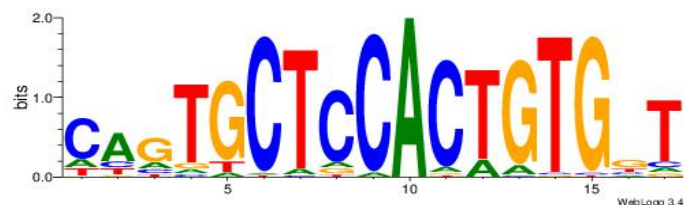


Reverse complement motif Consensus sequence: AGTGCTCCACTGTGDTG

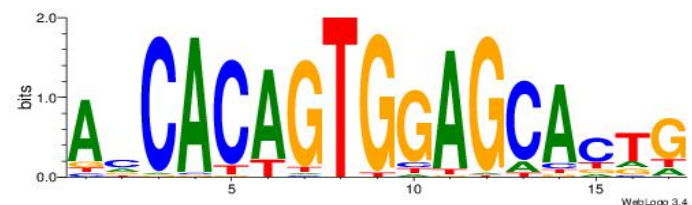


Dataset #: 2 Motif ID: 20 Motif name: CagTGCTCCACTGTGgT

Original motif Consensus sequence: CAGTGCTCCACTGTGBT



Reverse complement motif Consensus sequence: ABCACAGTGGAGCACTG



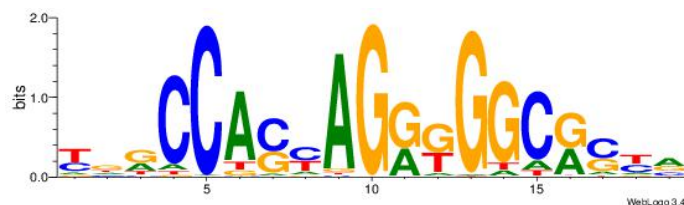
Best Matches for Motif ID 20 (Highest to Lowest)

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:	1
Number of overlap:	17
Similarity score:	0.0957051

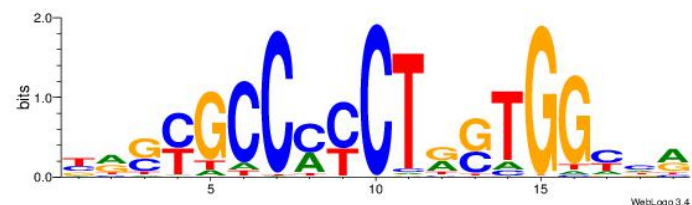
Alignment:

```
BMSMGCCYMCTKSTGGMHM
--CAGTGCTCCACTGTGBT
```

Original motif Consensus sequence: YDRCCASYAGRKGGRSYV



Reverse complement motif Consensus sequence: BMSMGCCYMCTKSTGGMHM

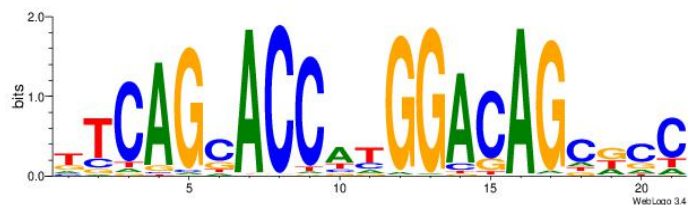


Dataset #: 1
 Motif ID: 7
 Motif name: REST
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 17
 Similarity score: 0.0975871

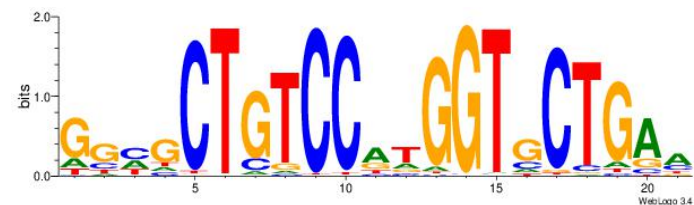
Alignment:

TTCAGCACCATGGACAGCKCC
 -ABCACAGTGGAGCACTG---

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC



Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA



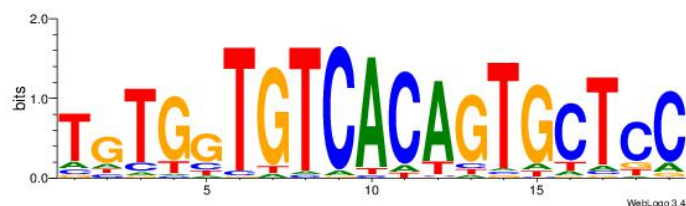
Dataset #: 2
 Motif ID: 17
 Motif name: TgTGgTGTCACAGTGCTCC
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward

Position number: 3
 Number of overlap: 17
 Similarity score: 0.0980868

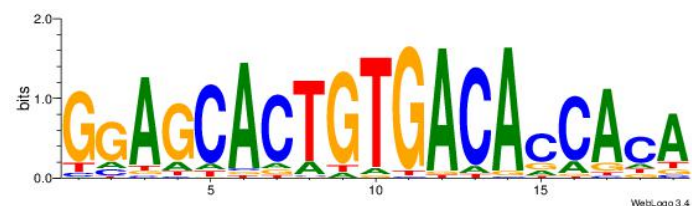
Alignment:

TGTGGTGTACAGTGCTCC
 CAGTGCTCCACTGTGCT--

Original motif Consensus sequence: TGTGGTGTACAGTGCTCC



Reverse complement motif Consensus sequence: GGAGCACTGTGACACCACA

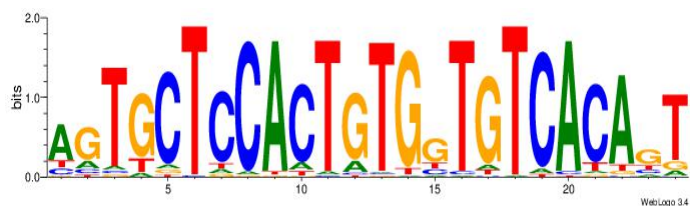


Dataset #: 2
 Motif ID: 27
 Motif name: AgTGCTCCACTGTGgTGTCACAgT
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 17
 Similarity score: 0.099784

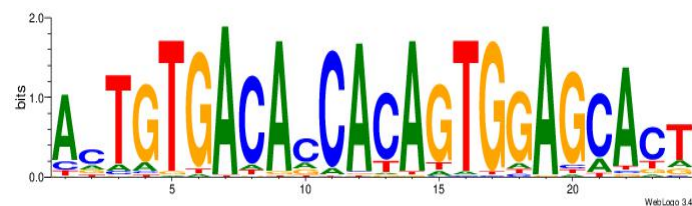
Alignment:

AGTGCTCCACTGTGGTGTACAGT
 -----ABCACAGTGGAGCACTG--

Original motif Consensus sequence: AGTGCTCCACTGTGGTGTACAGT



Reverse complement motif Consensus sequence: ACTGTGACACCACAGTGGAGCACT

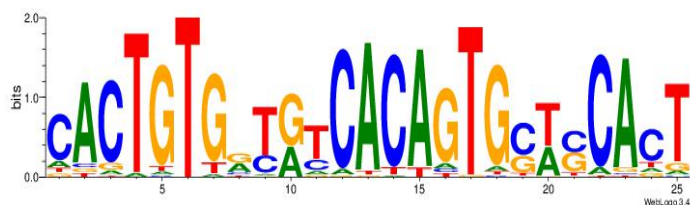


Dataset #: 2
 Motif ID: 22
 Motif name: CACTGTGrYrtCACAGTGswsCAcT
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 6
 Number of overlap: 17
 Similarity score: 0.104226

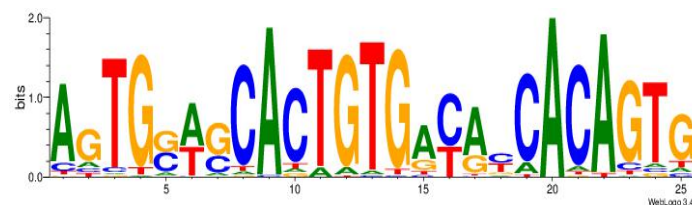
Alignment:

AGTGSWSCACTGTGAMAMCACAGTG
 -----ABCACAGTGGAGCACTG----

Original motif Consensus sequence: CACTGTGRTRTCACAGTGSWSCACT



Reverse complement motif Consensus sequence: AGTGSWSCACTGTGAMAMCACAGTG

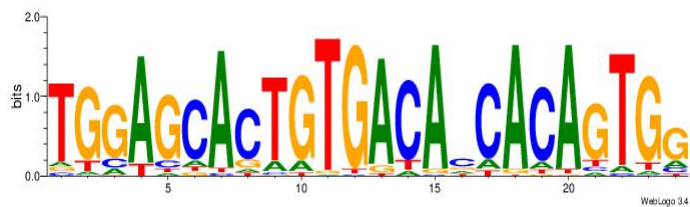


Dataset #: 2
 Motif ID: 23
 Motif name: TGGAGCACTGTGACAcCACAGTGg
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 5
 Number of overlap: 17
 Similarity score: 0.107548

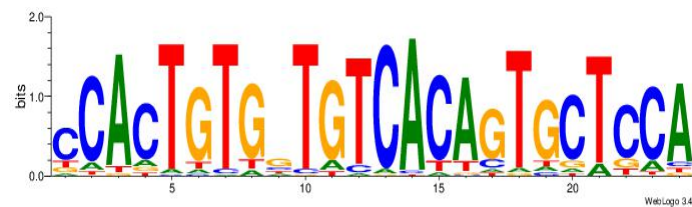
Alignment:

TGGAGCACTGTGACAVCACAGTGG
 ---ABCACAGTGGAGCACTG----

Original motif Consensus sequence: TGGAGCACTGTGACAVCACAGTGG



Reverse complement motif Consensus sequence: CCACTGTGVTGTACAGTGCTCCA



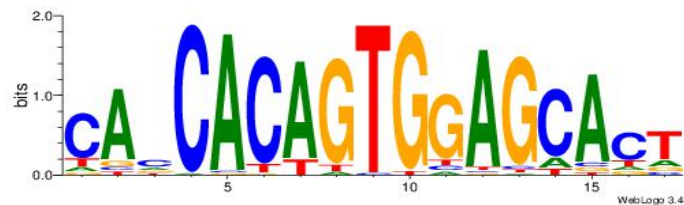
Dataset #: 2
 Motif ID: 26
 Motif name: CACcACAGTGGAGCAct
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2

Number of overlap: 16
Similarity score: 0.5

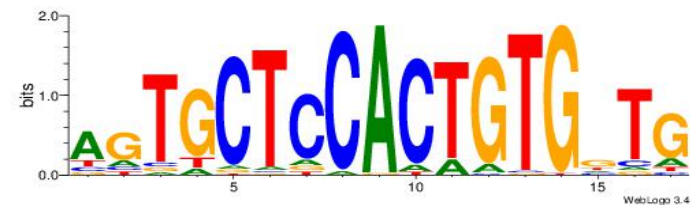
Alignment:

CAHCACAGTGGAGCACT-
-ABCACAGTGGAGCACTG

Original motif Consensus sequence: CAHCACAGTGGAGCACT



Reverse complement motif Consensus sequence:
AGTGCTCCACTGTGDTG

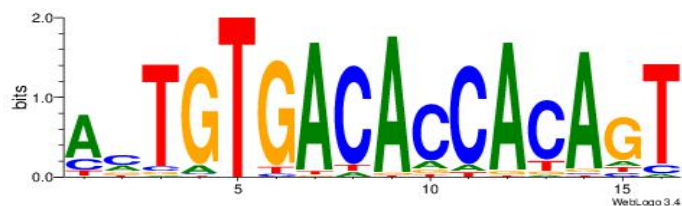


Dataset #: 2
Motif ID: 21
Motif name: AmTGTGACACCACAGT
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 16
Similarity score: 0.607943

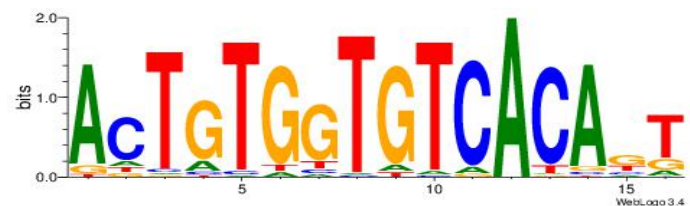
Alignment:

-AMTGTGACACCACAGT
CAGTGCTCCACTGTGBT

Original motif Consensus sequence: AMTGTGACACCACAGT



Reverse complement motif Consensus sequence: ACTGTGGTGTACART

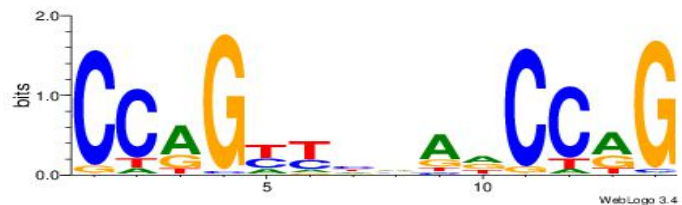


Dataset #: 1
Motif ID: 15
Motif name: Tcfcp2l1
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 2
Number of overlap: 13
Similarity score: 2.1063

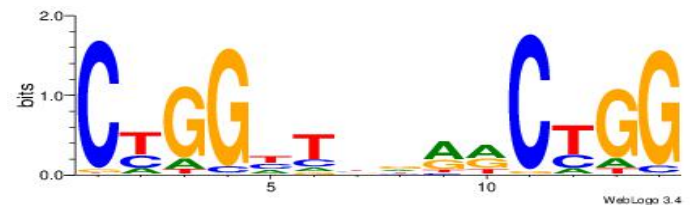
Alignment:

----CKGGDTBDMMCTGG
ABCACAGTGGAGCACTG--

Original motif Consensus sequence: CCAGYYHVADCCRG



Reverse complement motif Consensus sequence: CKGGDTBDMMCTGG

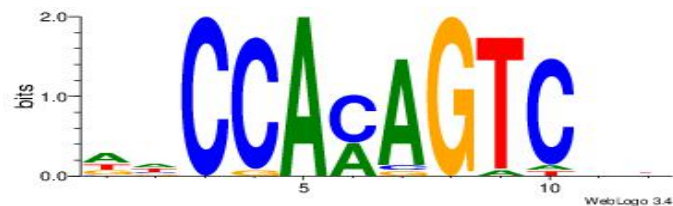


Dataset #: 2
 Motif ID: 25
 Motif name: wwCCAmAGTCmt
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 12
 Similarity score: 2.58308

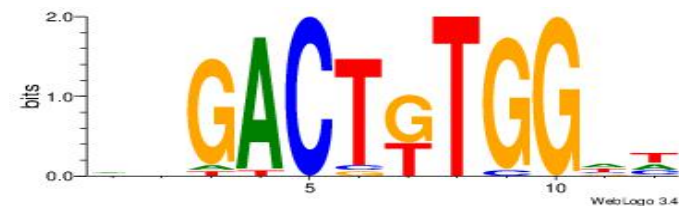
Alignment:

VDGACTRTGGDD-----
 ABCACAGTGGAGCACTG

Original motif Consensus sequence: DDCCAMAGTCHB



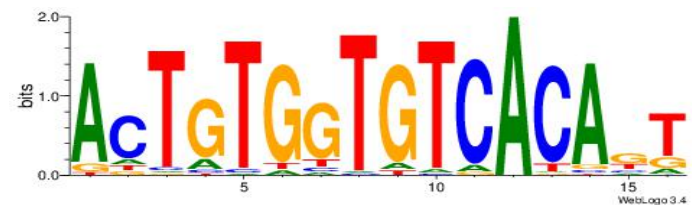
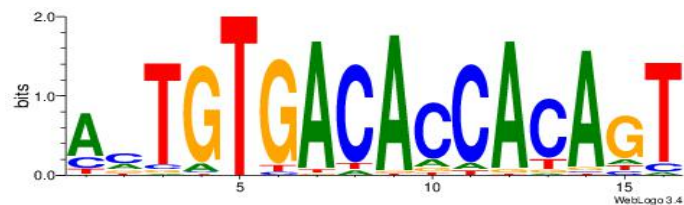
Reverse complement motif Consensus sequence: VDGACTRTGGDD



Dataset #: 2 Motif ID: 21 Motif name: AmTGTGACACCACAGT

Original motif Consensus sequence: AMTGTGACACCACAGT

Reverse complement motif Consensus sequence:
ACTGTGGTGTACART



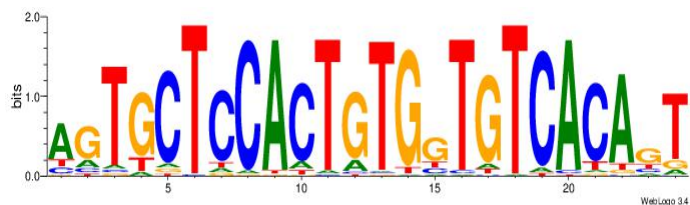
Best Matches for Motif ID 21 (Highest to Lowest)

Dataset #: 2
 Motif ID: 27
 Motif name: AgTGCTCCACTGTGgTGTCACAgT
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 16
 Similarity score: 0

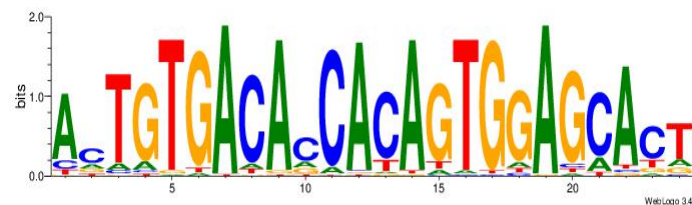
Alignment:

ACTGTGACACCACAGTGGAGCACT
 AMTGTGACACCACAGT-----

Original motif Consensus sequence: AGTGCTCCACTGTGGTGTCAcAGT



Reverse complement motif Consensus sequence: ACTGTGACACCACAGTGGAGCACT

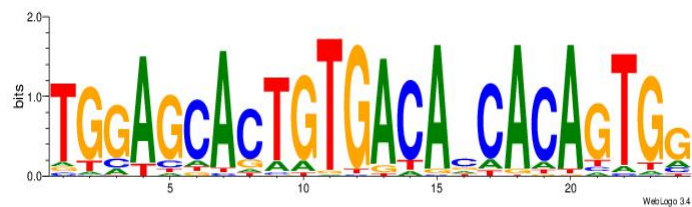


Dataset #: 2
 Motif ID: 23
 Motif name: TGGAGCACTGTGACAcCACAGTGg
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3
 Number of overlap: 16
 Similarity score: 0.00171837

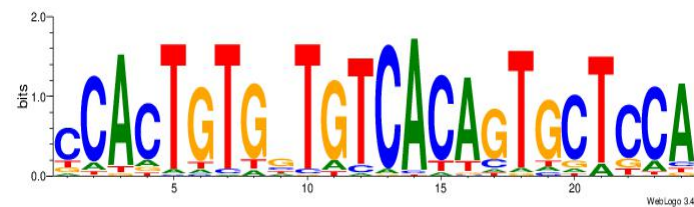
Alignment:

CCACTGTGVTGTCACAGTGCTCCA
 --ACTGTGGTGTACART-----

Original motif Consensus sequence: TGGAGCACTGTGACAVCACAGTGG



Reverse complement motif Consensus sequence: CCACTGTGVTGTCACAGTGCTCCA



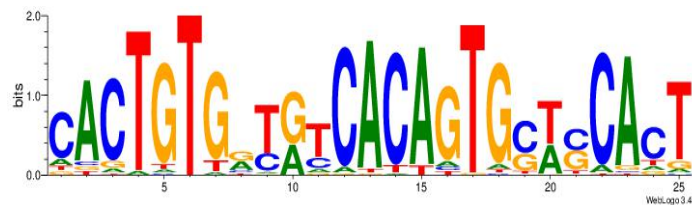
Dataset #: 2
 Motif ID: 22
 Motif name: CACTGTGrYrtCACAGTGswsCAcT
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2

Number of overlap: 16
Similarity score: 0.0197279

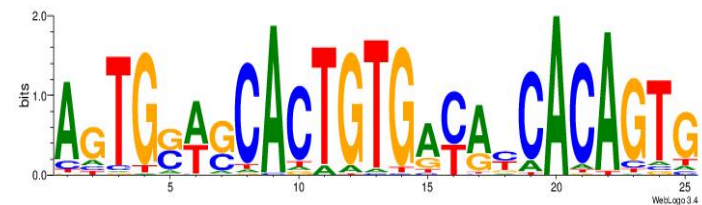
Alignment:

CACTGTGRTRTCACAGTGSWSCACT
-ACTGTGGTGTACART-----

Original motif Consensus sequence:
CACTGTGRTRTCACAGTGSWSCACT



Reverse complement motif Consensus sequence:
AGTGSWSCACTGTGAMAMCACAGTG

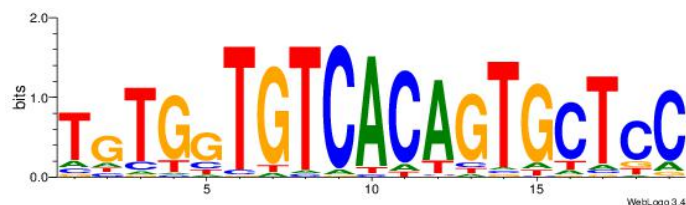


Dataset #: 2
Motif ID: 17
Motif name: TgTGgTGTCACAGTGCTCC
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 4
Number of overlap: 16
Similarity score: 0.0950937

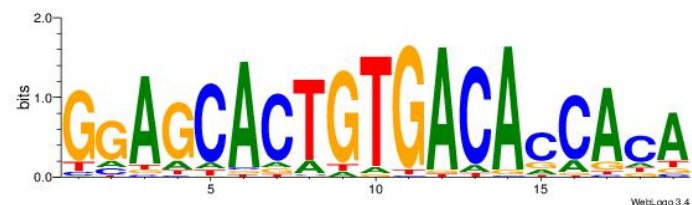
Alignment:

GGAGCACTGTGACACCACA
ACTGTGGTGTACART---

Original motif Consensus sequence: TGTGGTGTACAGTGCTCC



Reverse complement motif Consensus sequence: GGAGCACTGTGACACCACA

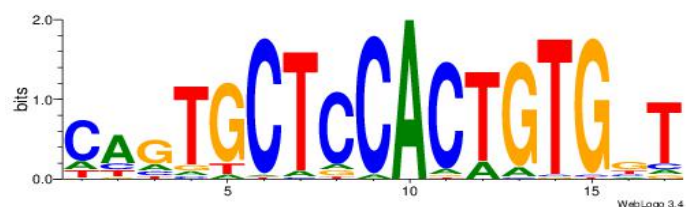


Dataset #: 2
Motif ID: 20
Motif name: CagTGCTCCACTGTGgT
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 16
Similarity score: 0.0988969

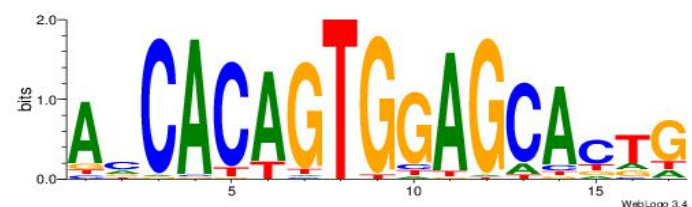
Alignment:

CAGTGCTCCACTGTGBT
-AMTGTGACACCACAGT

Original motif Consensus sequence: CAGTGCTCCACTGTGBT



Reverse complement motif Consensus sequence: ABCACAGTGGAGCACTG

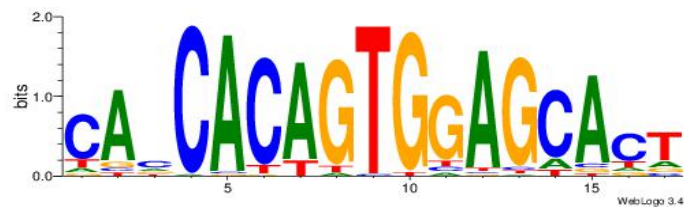


Dataset #: 2
 Motif ID: 26
 Motif name: CACACAGTGGAGCACT
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 16
 Similarity score: 0.101875

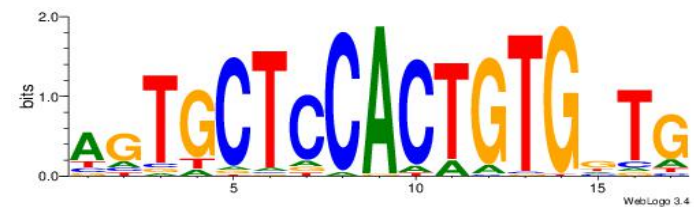
Alignment:

AGTGCTCCACTGTGDTG
 AMTGTGACACCACAGT-

Original motif Consensus sequence: CAHCACAGTGGAGCACT



Reverse complement motif Consensus sequence: AGTGCTCCACTGTGDTG



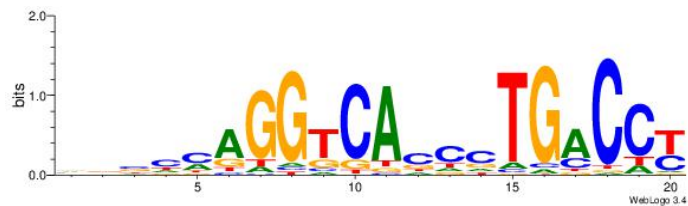
Dataset #: 1
 Motif ID: 3
 Motif name: ESR1
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 6

Number of overlap: 15
Similarity score: 0.595092

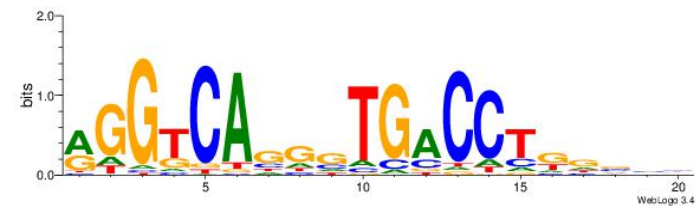
Alignment:

-MGGTCAGGGTGACCTRDBHV
AMTGTGACACCACAGT-----

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif Consensus sequence:
MGGTCAGGGTGACCTRDBHV

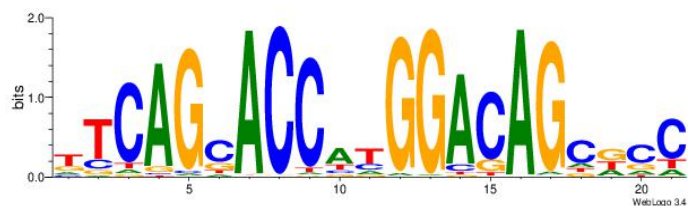


Dataset #: 1
Motif ID: 7
Motif name: REST
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 8
Number of overlap: 14
Similarity score: 1.1019

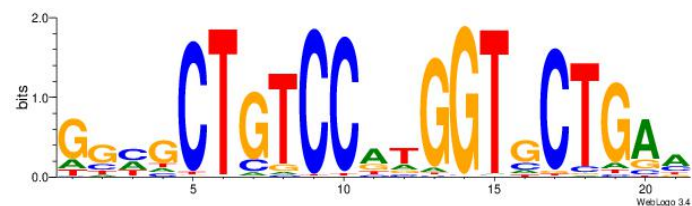
Alignment:

--GGYGCTGTCCATGGTGCTGAA
ACTGTGGTGTACART-----

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC



Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA

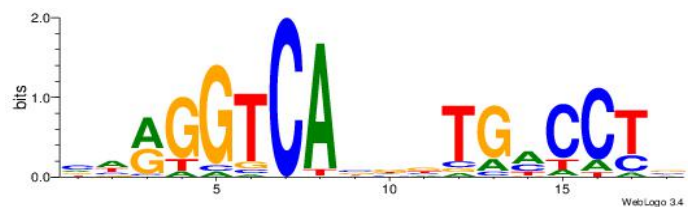


Dataset #: 1
Motif ID: 9
Motif name: ESR2
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 7
Number of overlap: 12
Similarity score: 2.07799

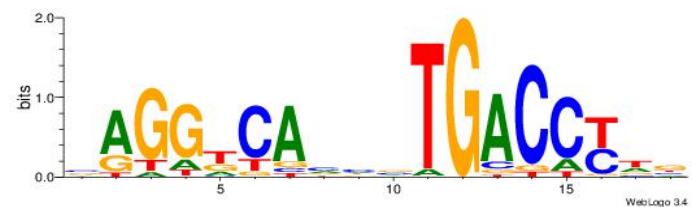
Alignment:

----BAGGYCABHBTGACCKHV
AMTGTGACACCACAGT-----

Original motif Consensus sequence: VHRGGTCABDBTGMCTB



Reverse complement motif Consensus sequence: BAGGYCABHBTGACCKHV

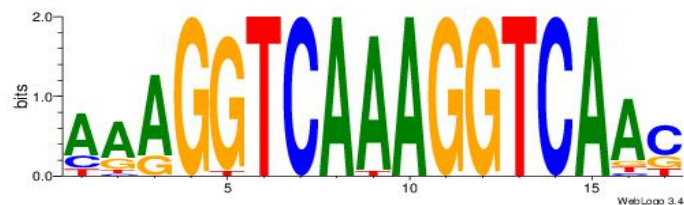


Dataset #: 1
 Motif ID: 10
 Motif name: NR1H2RXRA
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 6
 Number of overlap: 12
 Similarity score: 2.10225

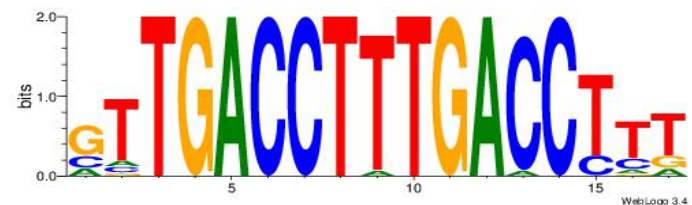
Alignment:

----GTTGACCTTTGACCTTT
 AMTGTGACACCACAGT-----

Original motif Consensus sequence: AAAGGTCAAAGGTCAAC



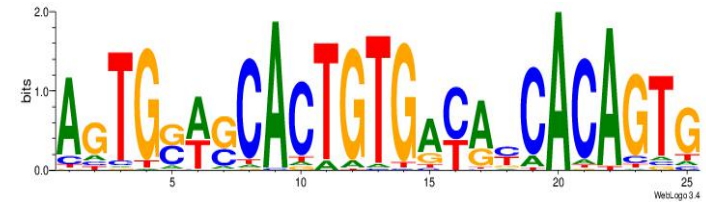
Reverse complement motif Consensus sequence: GTTGACCTTTGACCTTT



Dataset #: 2 Motif ID: 22 Motif name: CACTGTGrYrtCACAGTGswsCAcT

Original motif Consensus sequence:
CACTGTGRTRTCACAGTGSWSCACT

Reverse complement motif Consensus sequence:
AGTGSWSCACTGTGAMAMCACAGTG

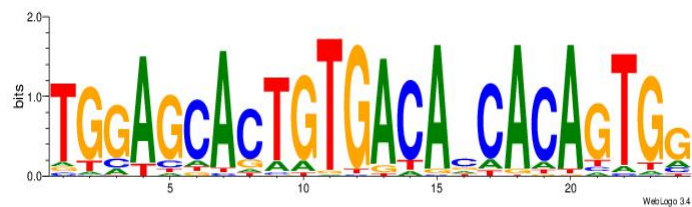


Dataset #: 2
 Motif ID: 23
 Motif name: TGGAGCACTGTGACAcCACAGTGg
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 23
 Similarity score: 0.500966

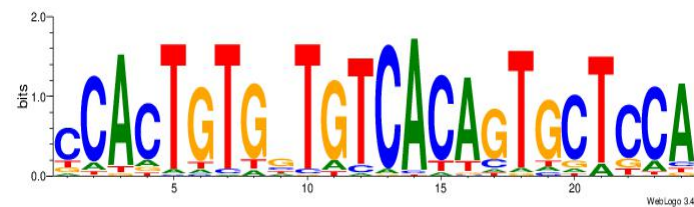
Alignment:

--TGGAGCACTGTGACAVCACAGTGG
 AGTGSWSCACTGTGAMAMCACAGTG-

Original motif Consensus sequence: TGGAGCACTGTGACAVCACAGTGG



Reverse complement motif Consensus sequence: CCACTGTGVTGTACAGTGCTCCA



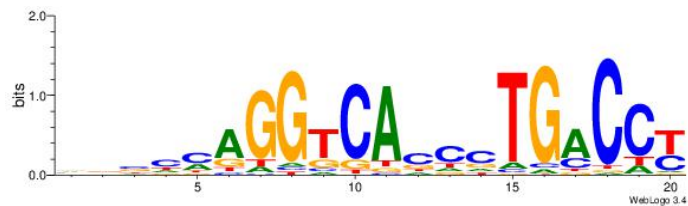
Dataset #: 1
 Motif ID: 3
 Motif name: ESR1
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3

Number of overlap: 18
Similarity score: 3.08246

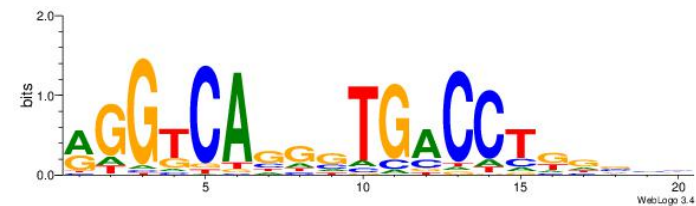
Alignment:

MGGTCAGGGTGACCTRDBHV-----
--CACTGTGRTRTCACAGTGSWSACT

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV

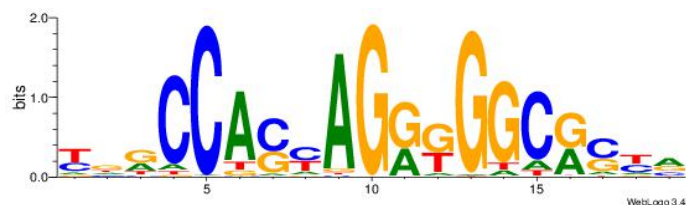


Dataset #: 1
Motif ID: 16
Motif name: CTCF
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 2
Number of overlap: 18
Similarity score: 3.08842

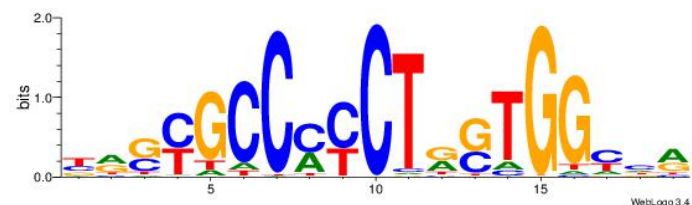
Alignment:

BMSMGCCYMCTKSTGGMHM-----
-AGTGSWSACTGTGAMAMCACAGTG

Original motif Consensus sequence: YDRCCASYAGRKGGRSYV



Reverse complement motif Consensus sequence: BMSMGCCYMCTKSTGGMHM

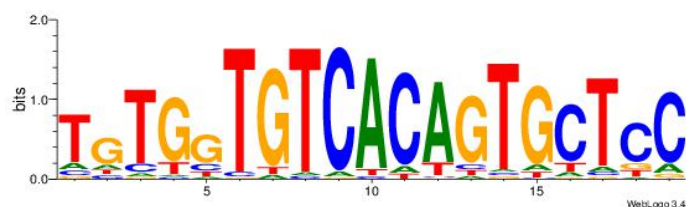


Dataset #: 2
 Motif ID: 17
 Motif name: TgTgGTGCACAGTGCTCC
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 18
 Similarity score: 3.08984

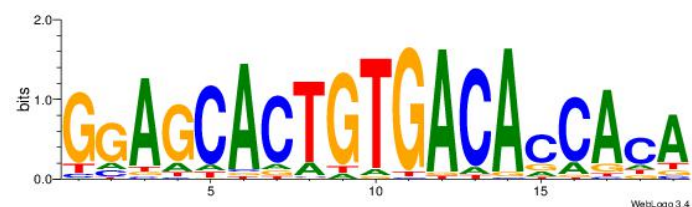
Alignment:

GGAGCACTGTGACACCACA-----
 -CACTGTGRTRTCACAGTGSWSCACT

Original motif Consensus sequence: TGTGGTGTGCACAGTGCTCC



Reverse complement motif Consensus sequence: GGAGCACTGTGACACCACA

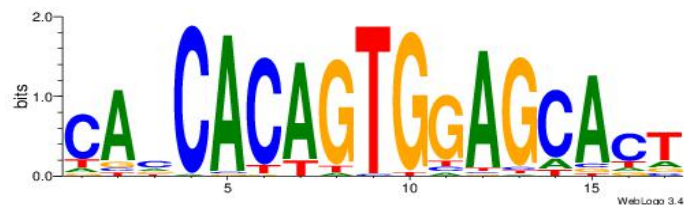


Dataset #: 2
 Motif ID: 26
 Motif name: CACACAGTGGAGCAct
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 17
 Similarity score: 3.52449

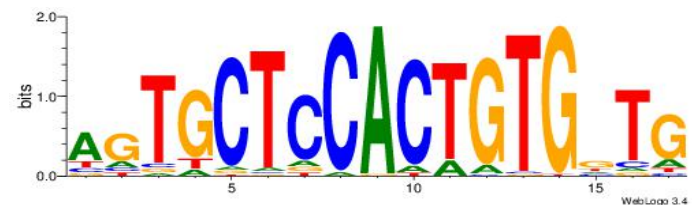
Alignment:

-----CAHCACAGTGGAGCACT
 CACTGTGRTRTCACAGTGSWSCACT

Original motif Consensus sequence: CAHCACAGTGGAGCACT



Reverse complement motif Consensus sequence: AGTGCTCCACTGTGDTG



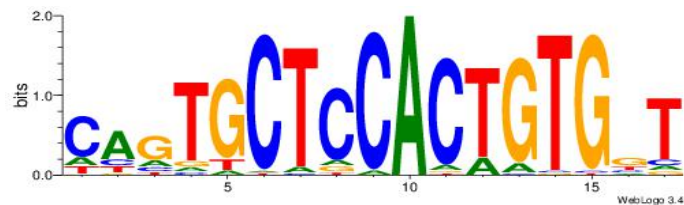
Dataset #: 2
 Motif ID: 20
 Motif name: CagTGCTCCACTGTGgT
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2

Number of overlap: 16
Similarity score: 4.02265

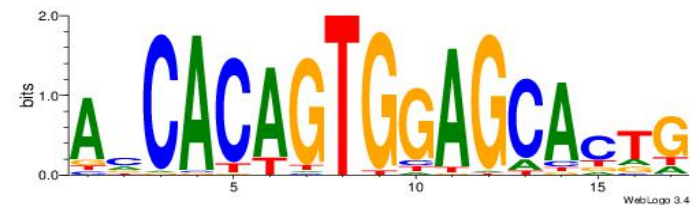
Alignment:

-----CAGTGCTCCACTGTGBT
AGTGSWSCACTGTGAMAMCACAGTG-

Original motif Consensus sequence: CAGTGCTCCACTGTGBT



Reverse complement motif Consensus sequence:
ABCACAGTGGAGCACTG

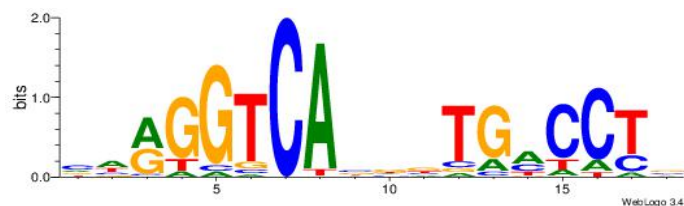


Dataset #: 1
Motif ID: 9
Motif name: ESR2
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 6
Number of overlap: 13
Similarity score: 5.58301

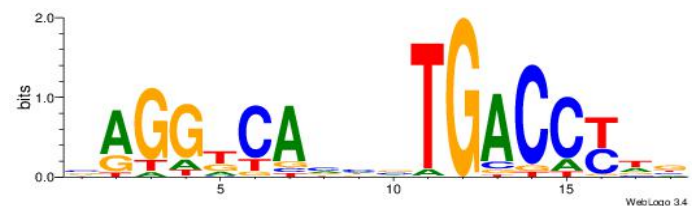
Alignment:

VHRGGTCABDBTGMCTB-----
-----AGTGSWSCACTGTGAMAMCACAGTG

Original motif Consensus sequence: VHRGGTCABDBTGMCTB



Reverse complement motif Consensus sequence: BAGGYCABHBTGACCKHV

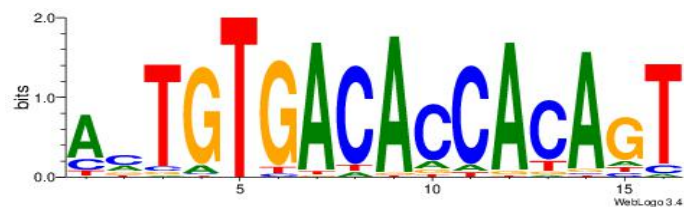


Dataset #: 2
 Motif ID: 21
 Motif name: AmTGTGACACCACAGT
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 4
 Number of overlap: 13
 Similarity score: 5.58597

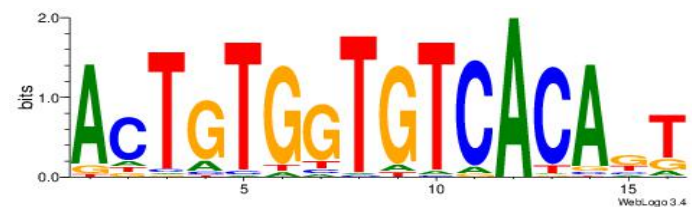
Alignment:

ACTGTGGTGTACART-----
 ---CACTGTGRTRTCACAGTGSWSCACT

Original motif Consensus sequence: AMTGTGACACCACAGT



Reverse complement motif Consensus sequence: ACTGTGGTGTACART

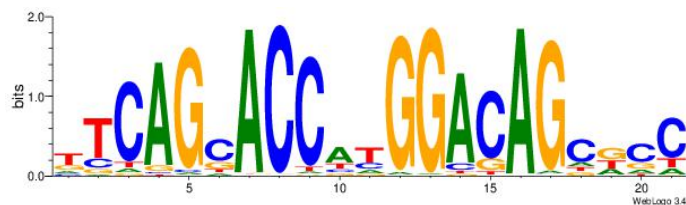


Dataset #: 1
 Motif ID: 7
 Motif name: REST
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 10
 Number of overlap: 12
 Similarity score: 6.07826

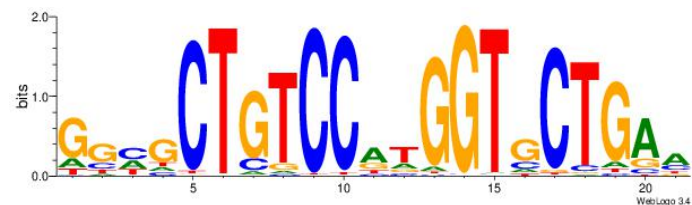
Alignment:

-----GGYGCTGTCCATGGTGCTGAA
 CACTGTGRTRTCACAGTGSWSCACT-----

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC

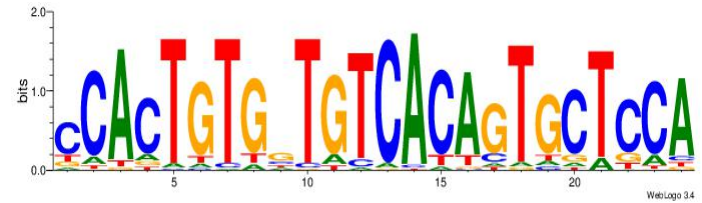
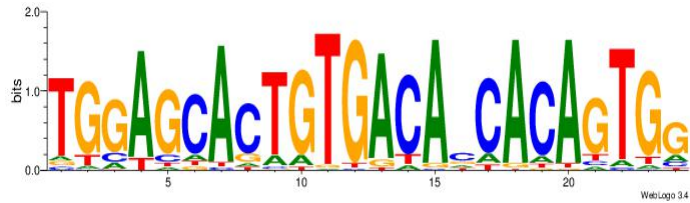


Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA



Dataset #: 2 Motif ID: 23 Motif name: TGGAGCACTGTGACAcCACAGTGg

Original motif Consensus sequence: TGGAGCACTGTGACAVCACAGTGg Reverse complement motif Consensus sequence: CCACTGTGVTGTACAGTGCTCCA



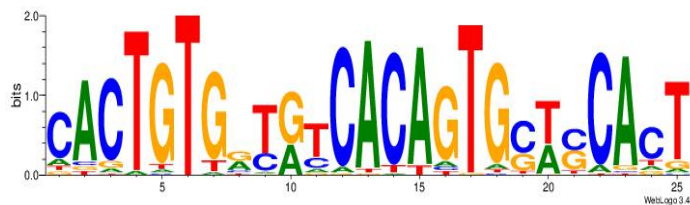
Best Matches for Motif ID 23 (Highest to Lowest)

Dataset #: 2
 Motif ID: 22
 Motif name: CACTGTGrYrtCACAGTGsWsCAcT
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 23
 Similarity score: 0.0136536

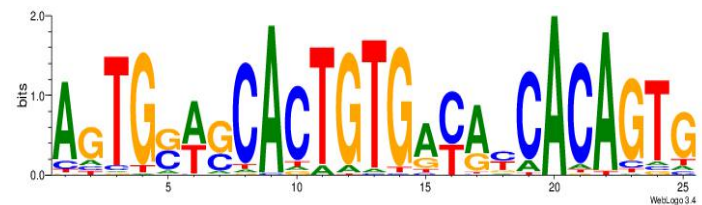
Alignment:

CACTGTGRTRTCACAGTGSWSCACT-
 --CCACTGTGVTGTCACAGTGCTCCA

Original motif Consensus sequence:
 CACTGTGRTRTCACAGTGSWSCACT



Reverse complement motif Consensus sequence:
 AGTGSWSCACTGTGAMAMCACAGTG

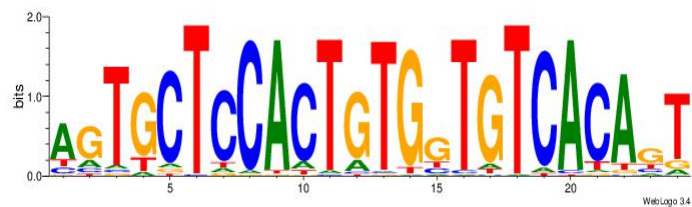


Dataset #: 2
 Motif ID: 27
 Motif name: AgTGCTCCACTGTGgTGTCACAgT
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 22
 Similarity score: 0.560082

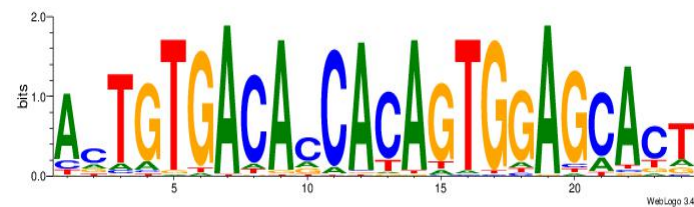
Alignment:

--ACTGTGACACCACAGTGGAGCACT
 CCACTGTGVTGTCACAGTGCTCCA--

Original motif Consensus sequence: AGTGCTCCACTGTGGTGTTCACAGT



Reverse complement motif Consensus sequence: ACTGTGACACCACAGTGGAGCACT



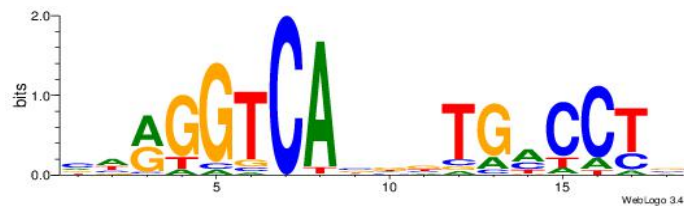
Dataset #: 1
 Motif ID: 9
 Motif name: ESR2
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1

Number of overlap: 18
Similarity score: 2.5833

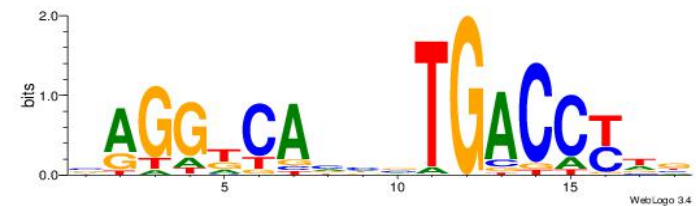
Alignment:

-----BAGGYCABHBTGACCKHV
TGGAGCACTGTGACAVCACAGTGG

Original motif Consensus sequence: VHRGGTCABDBTGMCTB



Reverse complement motif Consensus sequence: BAGGYCABHBTGACCKHV

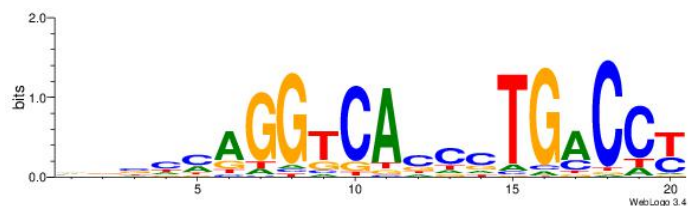


Dataset #: 1
Motif ID: 3
Motif name: ESR1
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 4
Number of overlap: 17
Similarity score: 3.10239

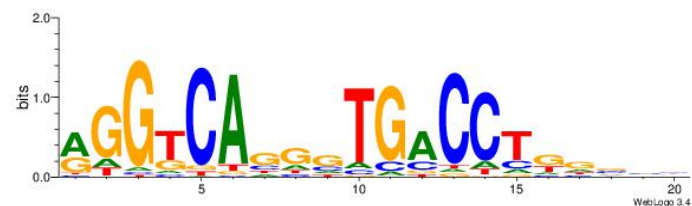
Alignment:

MGGTCAGGGTGACCTRDBHV-----
---CCACTGTGVTGTCACAGTGCTCCA

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV

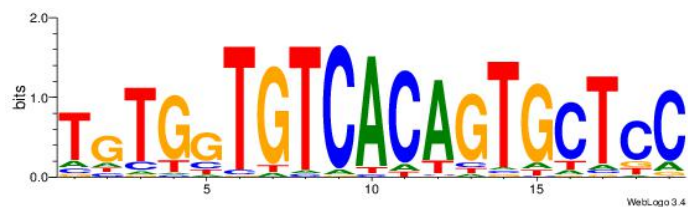


Dataset #: 2
Motif ID: 17
Motif name: TgTgTGTGTCACAGTGCTCC
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 4
Number of overlap: 16
Similarity score: 3.56015

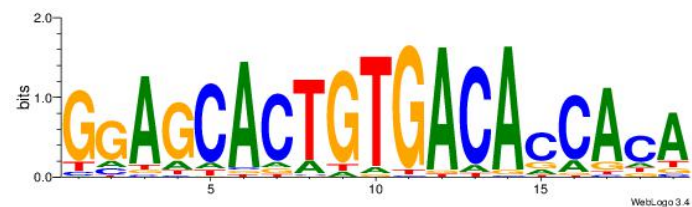
Alignment:

GGAGCACTGTGACACCACA-----
---CCACTGTGVTGTCACAGTGCTCCA

Original motif Consensus sequence: TGTGGTGTGTCACAGTGCTCC



Reverse complement motif Consensus sequence: GGAGCACTGTGACACCACA

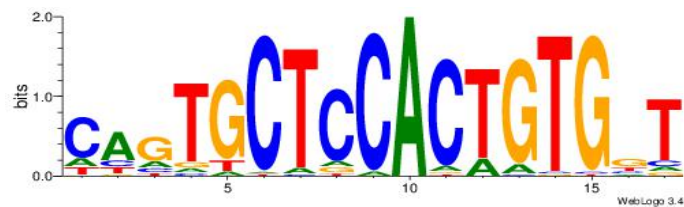


Dataset #: 2
 Motif ID: 20
 Motif name: CagTGCTCCACTGTGgT
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 16
 Similarity score: 3.58845

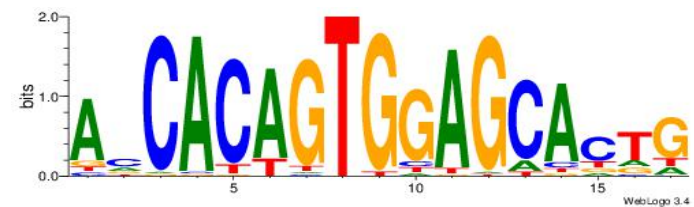
Alignment:

ABCACAGTGGAGCACTG-----
 -CCACTGTGVTGTCACAGTGCTCCA

Original motif Consensus sequence: CAGTGCTCCACTGTGBT



Reverse complement motif Consensus sequence: ABCACAGTGGAGCACTG



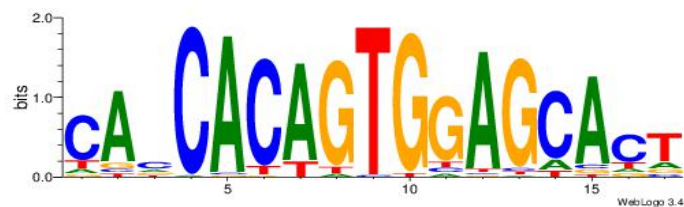
Dataset #: 2
 Motif ID: 26
 Motif name: CACcACAGTGGAGCAct
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3

Number of overlap: 15
Similarity score: 4.07113

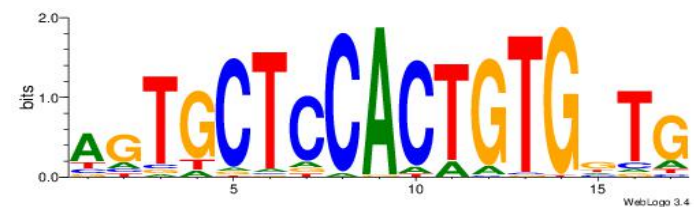
Alignment:

AGTGCTCCACTGTGDTG-----
--TGGAGCACTGTGACAVCACAGTGG

Original motif Consensus sequence: CAHCACAGTGGAGCACT



Reverse complement motif Consensus sequence:
AGTGCTCCACTGTGDTG

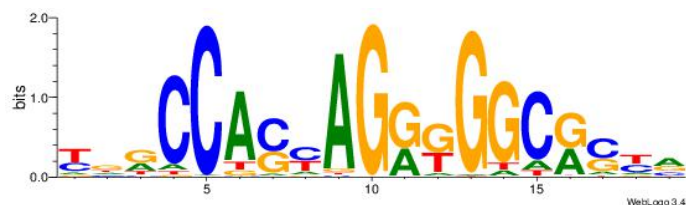


Dataset #: 1
Motif ID: 16
Motif name: CTCF
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 5
Number of overlap: 15
Similarity score: 4.10183

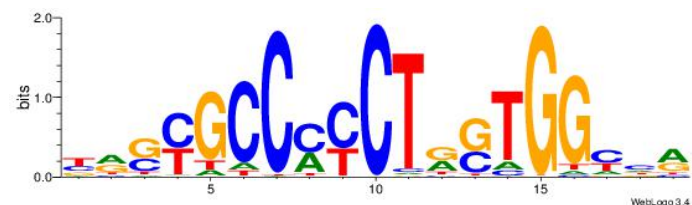
Alignment:

-----YDRCCASYAGRKGGRSYV
TGGAGCACTGTGACAVCACAGTGG----

Original motif Consensus sequence: YDRCCASYAGRKGGCRSYV



Reverse complement motif Consensus sequence: BMSMGCCYMCTKSTGGMHM

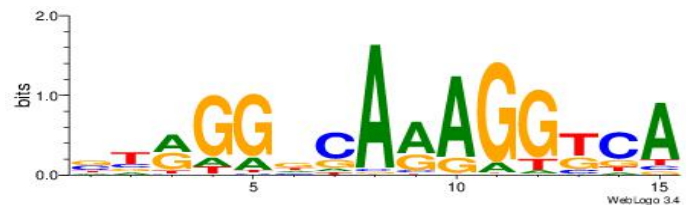


Dataset #: 1
 Motif ID: 14
 Motif name: PPARGRXRA
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 14
 Similarity score: 4.60325

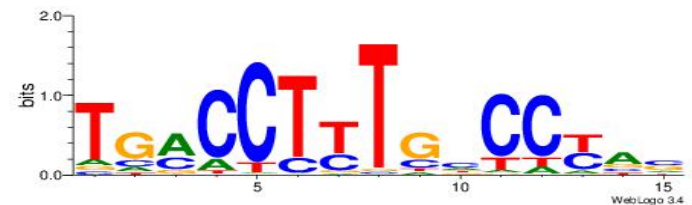
Alignment:

BTRGGDCARAGGKCA-----
 -TGGAGCACTGTGACAVCACAGTGG

Original motif Consensus sequence: BTRGGDCARAGGKCA



Reverse complement motif Consensus sequence: TGRCCCTKTGHCKK

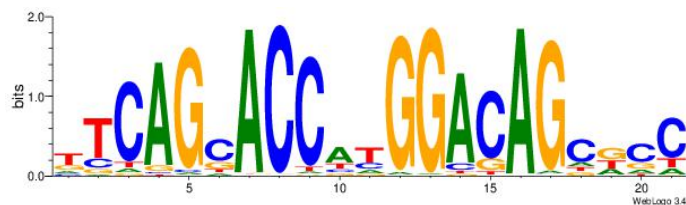


Dataset #: 1
 Motif ID: 7
 Motif name: REST
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 9
 Number of overlap: 13
 Similarity score: 5.08033

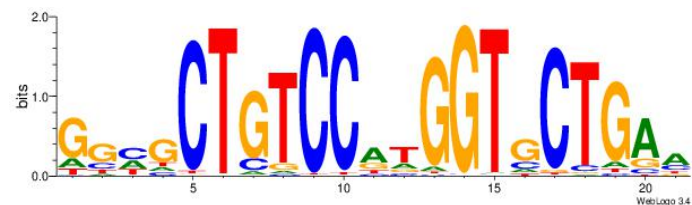
Alignment:

-----TTCAGCACCATGGACAGCKCC
 TGGAGCACTGTGACAVCACAGTGG-----

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC



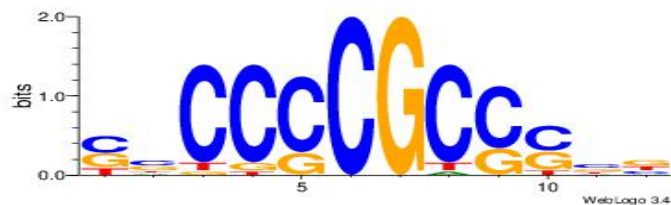
Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA



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

Original motif Consensus sequence: SBCCCCGCCSBB

Reverse complement motif Consensus sequence: BBSGGCGGGGBS



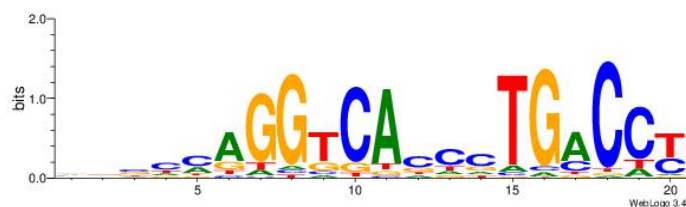
Best Matches for Motif ID 24 (Highest to Lowest)

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

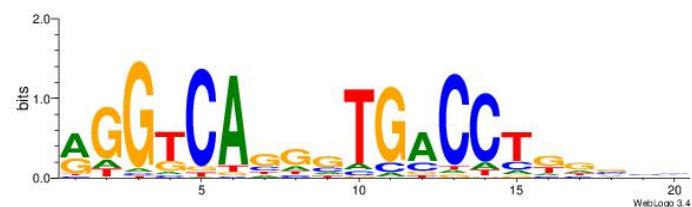
Alignment:

MGGTCAGGGTGACCTRDBHV
 -----BBSGGCGGGGBS-

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV

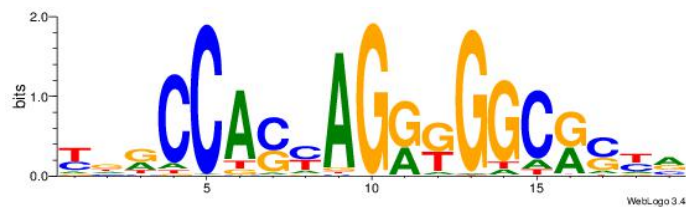


Dataset #: 1
 Motif ID: 16
 Motif name: CTCF
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 12
 Similarity score: 0.0642087

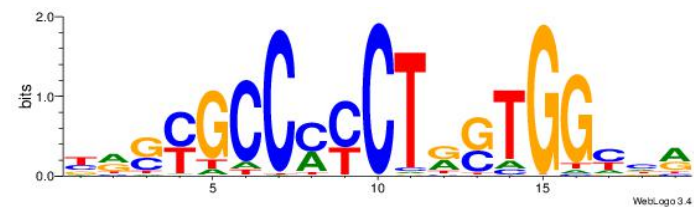
Alignment:

YDRCCASYAGRKGGRSYV
 -BBSGGCGGGGBS-----

Original motif Consensus sequence: YDRCCASYAGRKGGRSYV



Reverse complement motif Consensus sequence: BMSMGCCYMCTKSTGGMHM

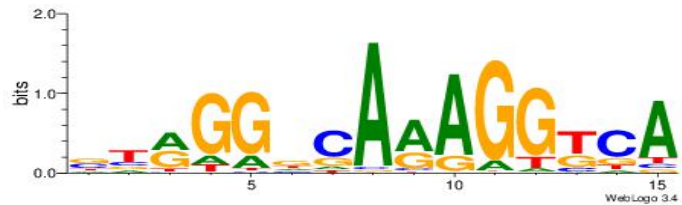


Dataset #: 1
 Motif ID: 14
 Motif name: PPARGRXRA
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3

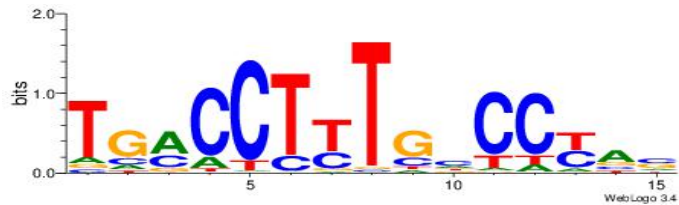
Number of overlap: 12
Similarity score: 0.0671548

Alignment:
TGRCCCTKTGHCCCKAB
-SBCCCCGCCSBB--

Original motif Consensus sequence: BTRGGDCARAGGKCA



Reverse complement motif Consensus sequence: TGRCCCTKTGHCCCK

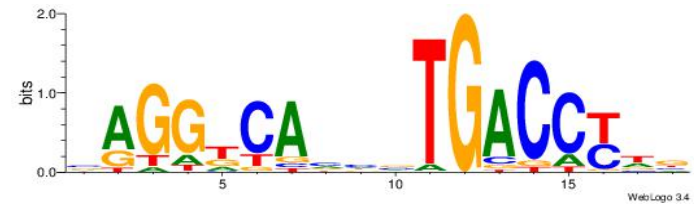
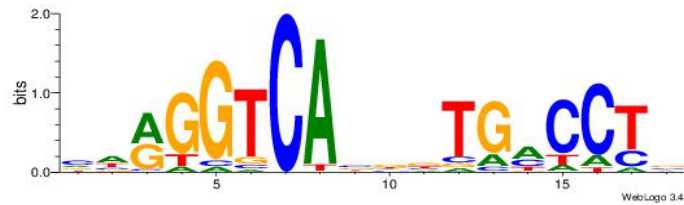


Dataset #: 1
Motif ID: 9
Motif name: ESR2
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 2
Number of overlap: 12
Similarity score: 0.0734481

Alignment:
BAGGYCABHBTGACCKHV
-SBCCCCGCCSBB-----

Original motif Consensus sequence: VHRGGTCABDBTGMCTB

Reverse complement motif Consensus sequence:
BAGGYCABHBTGACCKHV

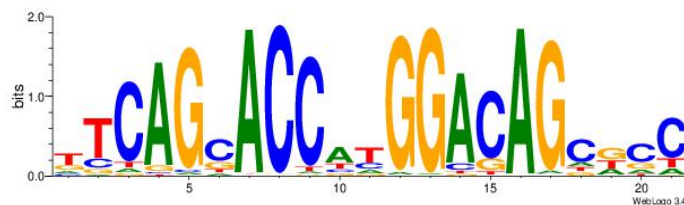


Dataset #: 1
 Motif ID: 7
 Motif name: REST
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 10
 Number of overlap: 12
 Similarity score: 0.0751084

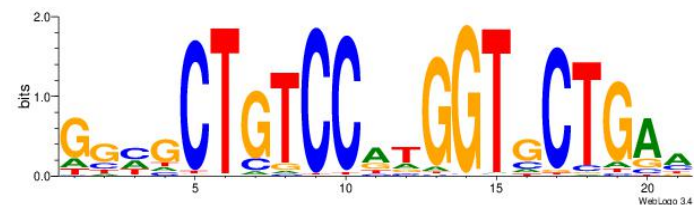
Alignment:

TTCAGCACCATGGACAGCKCC
 BBSGGCGGGGBS-----

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC



Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA



Dataset #: 2

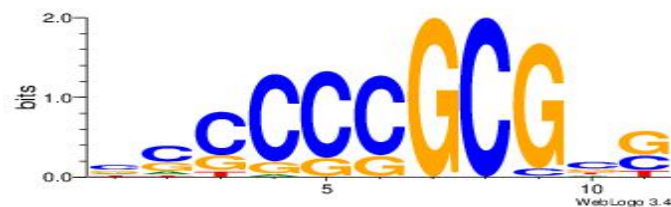
Motif ID: 18
 Motif name: sscCCCCGCGcs
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.5

Alignment:

–SBCGCGGGGSB

BBSGGCGGGGS

Original motif Consensus sequence: BSCCCCGCGBS



Reverse complement motif Consensus sequence: SBCGCGGGGSB



Dataset #: 2
 Motif ID: 32
 Motif name: gCGCGCsCgsG
 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: 0.548902

Alignment:

-CGCGSGCGCGC
BBSGGCGGGGBS

Original motif Consensus sequence: GCGCGCSCGCG



Reverse complement motif Consensus sequence: CGCGSGCGCGC



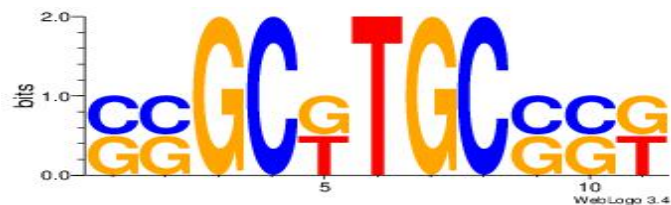
Dataset #:	2
Motif ID:	28
Motif name:	ssGCKTGCssk
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	11
Similarity score:	0.550852

Alignment:

-YSSGCAYGCSS
BBSGGCGGGGBS

Original motif Consensus sequence: SSGCKTGCSSK

Reverse complement motif Consensus sequence: YSSGCAYGCSS



Dataset #: 2
 Motif ID: 29
 Motif name: cCGCGGrCACG
 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: 0.56634

Alignment:
 CGTGKCCGCGG-
 BBSGGCGGGGBS

Original motif Consensus sequence: CCGCGGrCACG



Reverse complement motif Consensus sequence: CGTGKCCGCGG



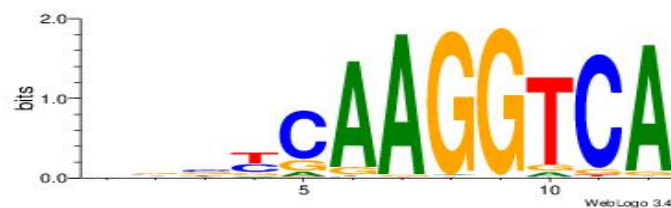
Dataset #: 1
 Motif ID: 4

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

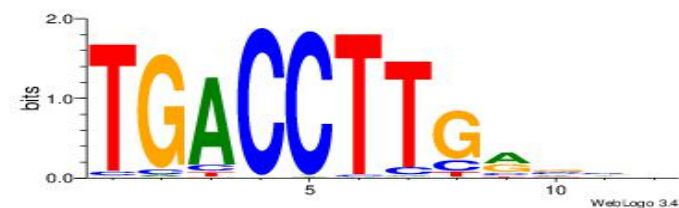
Alignment:

VBBYCAAGGTCA-
 -BBSGGCGGGGBS

Original motif Consensus sequence: VBBYCAAGGTCA

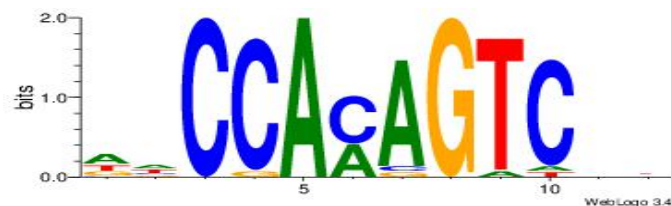


Reverse complement motif Consensus sequence: TGACCTTGMBBB

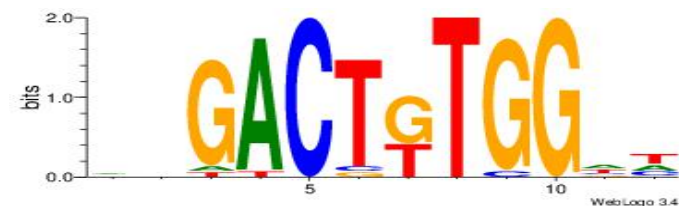


Dataset #: 2 Motif ID: 25 Motif name: wwCCAmAGTCmt

Original motif Consensus sequence: DDCCAMAGTCHB



Reverse complement motif Consensus sequence: VDGACTRTGGDD



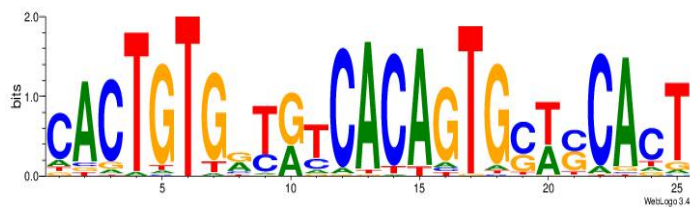
Best Matches for Motif ID 25 (Highest to Lowest)

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: 9
 Number of overlap: 12
 Similarity score: 0.0263648

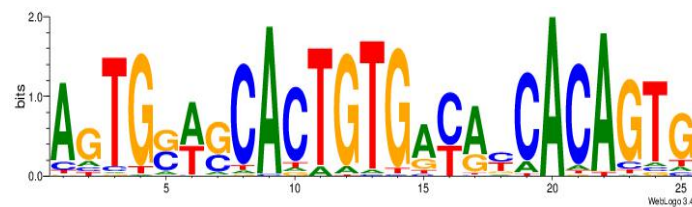
Alignment:

CACTGTGRTRTCACAGTGSWSCACT
 -----DDCCAMAGTCHB-----

Original motif Consensus sequence:
 CACTGTGRTRTCACAGTGSWSCACT



Reverse complement motif Consensus sequence:
 AGTGSWSCACTGTGAMAMCACAGTG



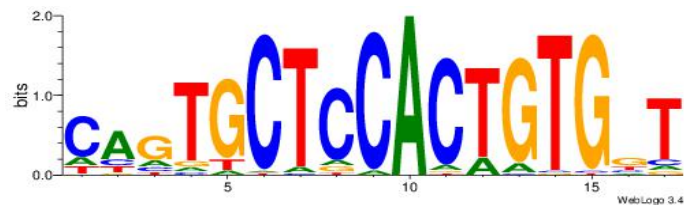
Dataset #: 2
 Motif ID: 20
 Motif name: CagTGCTCCACTGTGgT
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 6

Number of overlap: 12
Similarity score: 0.0282828

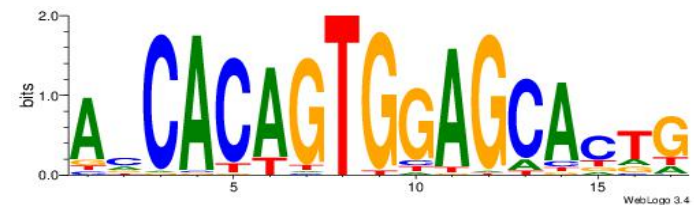
Alignment:

ABCACAGTGGAGCACTG
VDGACTRTGGDD-----

Original motif Consensus sequence: CAGTGCTCCACTGTGBT



Reverse complement motif Consensus sequence:
ABCACAGTGGAGCACTG

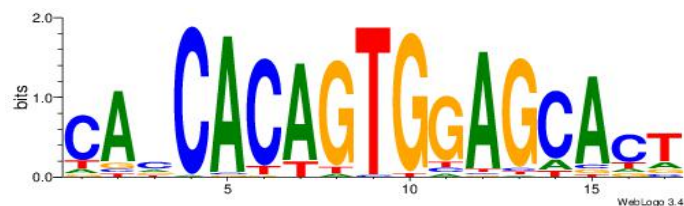


Dataset #: 2
Motif ID: 26
Motif name: CACACAGTGGAGCAct
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 6
Number of overlap: 12
Similarity score: 0.0291095

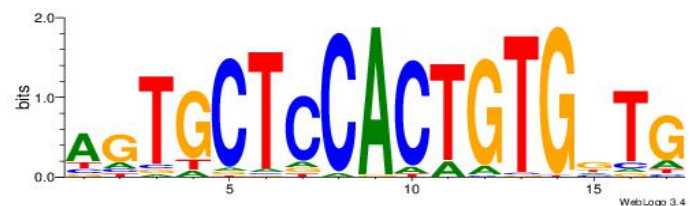
Alignment:

AGTGCTCCACTGTGDTG
-----VDGACTRTGGDD

Original motif Consensus sequence: CAHCACAGTGGAGCACT



Reverse complement motif Consensus sequence: AGTGCTCCACTGTGDTG

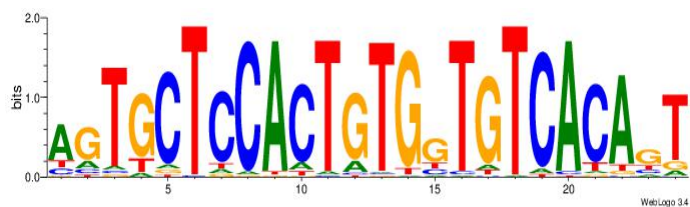


Dataset #: 2
Motif ID: 27
Motif name: AgTGCTCCACTGTGgTGTCACAgT
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 6
Number of overlap: 12
Similarity score: 0.0301919

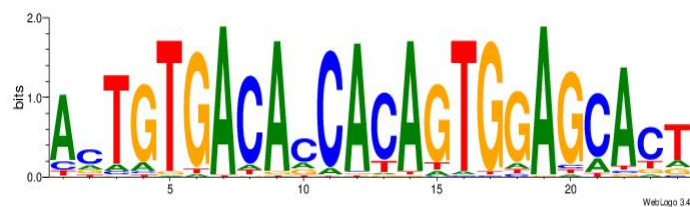
Alignment:

AGTGCTCCACTGTGGTGTTCACAGT
-----VDGACTRTGGDD-----

Original motif Consensus sequence: AGTGCTCCACTGTGGTGTTCACAGT



Reverse complement motif Consensus sequence: ACTGTGACACCACAGTGGAGCACT

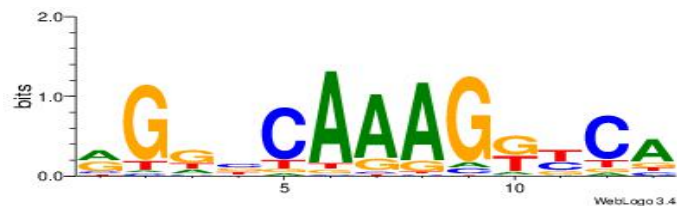


Dataset #: 1
 Motif ID: 1
 Motif name: HNF4A
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 12
 Similarity score: 0.032442

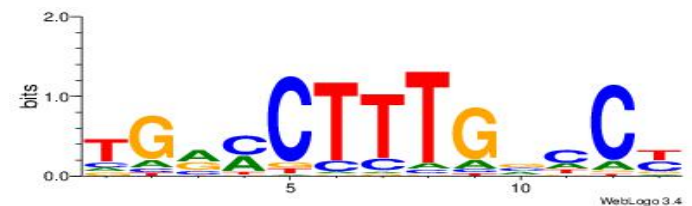
Alignment:

RGGBCAAAGKYCA
 -DDCCAMAGTCHB

Original motif Consensus sequence: RGGBCAAAGKYCA



Reverse complement motif Consensus sequence: TGMYYCTTTGBCCK

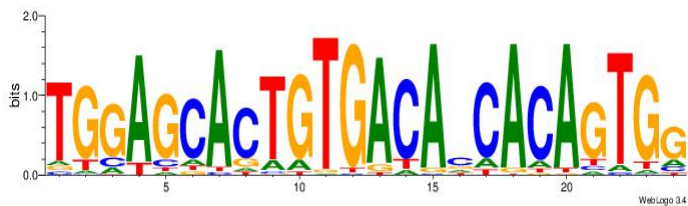


Dataset #: 2
 Motif ID: 23
 Motif name: TGGAGCACTGTGACAcCACAGTGg
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 4
 Number of overlap: 12

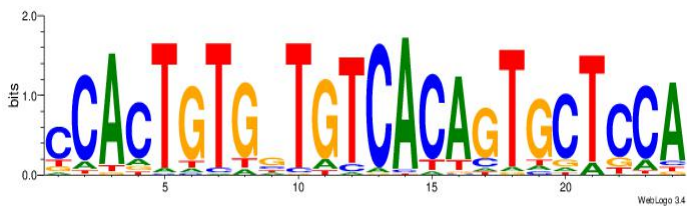
Similarity score: 0.0360702

Alignment:
C C A C T G T G V T G T C A C A G T G C T C C A
---D D C C A M A G T C H B-----

Original motif Consensus sequence: TGGAGCACTGTGACAVCACAGTGG



Reverse complement motif Consensus sequence: CCACTGTGVTGTGCACAGTGCTCCA

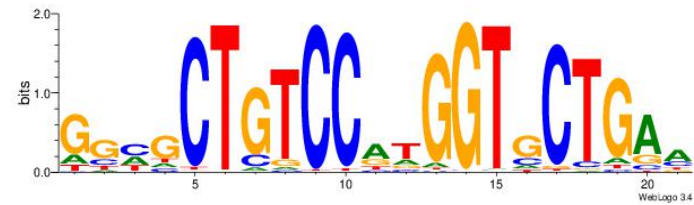
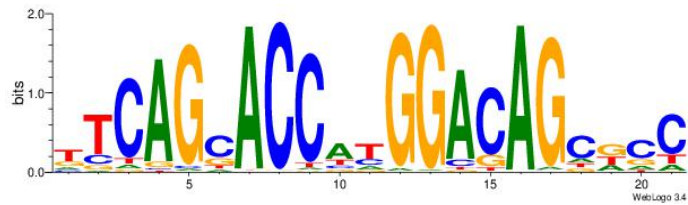


Dataset #: 1
Motif ID: 7
Motif name: REST
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 4
Number of overlap: 12
Similarity score: 0.0391228

Alignment:
G G Y G C T G T C C A T G G T G C T G A A
---D D C C A M A G T C H B-----

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC

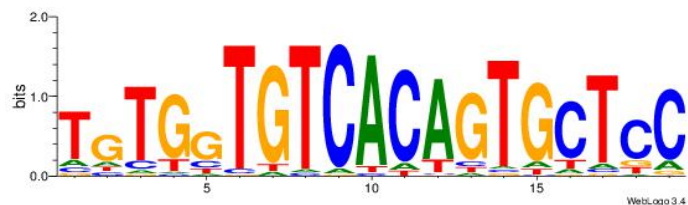
Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA



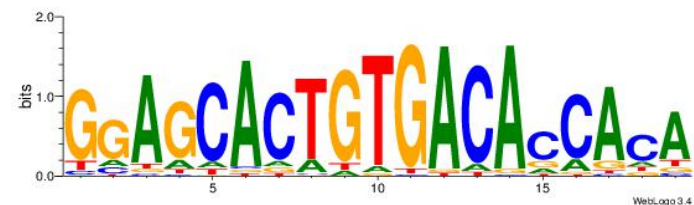
Dataset #: 2
 Motif ID: 17
 Motif name: TgTGgTGTCACAGTGCTCC
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 12
 Similarity score: 0.0393782

Alignment:
 TGTGGTGTCACAGTGCTCC
 -----DDCCAMAGTCHB--

Original motif Consensus sequence: TGTGGTGTCACAGTGCTCC



Reverse complement motif Consensus sequence: GGAGCACTGTGACACCACA



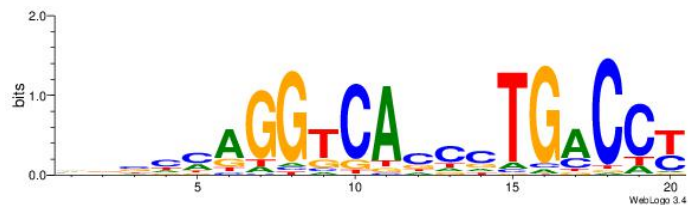
Dataset #: 1

Motif ID: 3
 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: 12
 Similarity score: 0.0407304

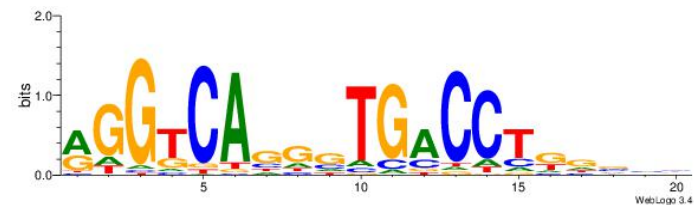
Alignment:

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

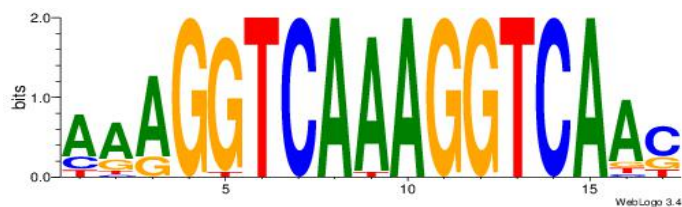
Similarity score: 0.0463384

Alignment:

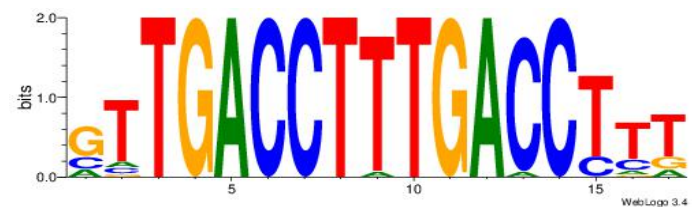
AAAGGTCAAAGGTCAAC

----DDCCAMAGTCHB--

Original motif Consensus sequence: AAAGGTCAAAGGTCAAC

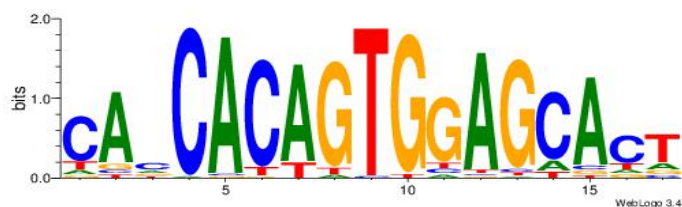


Reverse complement motif Consensus sequence: GTTGACCTTTGACCTT

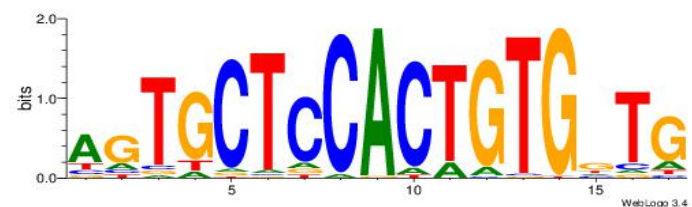


Dataset #: 2 Motif ID: 26 Motif name: CACACAGTGGAGCACT

Original motif Consensus sequence: CAHCACAGTGGAGCACT



Reverse complement motif Consensus sequence: AGTGCTCCACTGTGDTG



Best Matches for Motif ID 26 (Highest to Lowest)

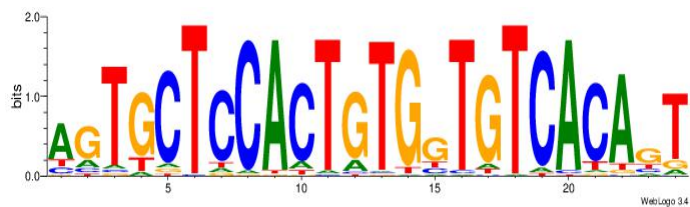
Dataset #:	2
Motif ID:	27
Motif name:	AgTGCTCCACTGTGgTGTCACAgT
Matching format of first motif:	Reverse Complement

Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	17
Similarity score:	0.00742502

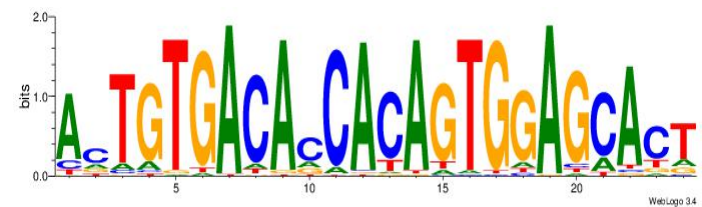
Alignment:

```
AGTGCTCCACTGTGGTGTACAGT
AGTGCTCCACTGTGDTG-----
```

Original motif Consensus sequence: AGTGCTCCACTGTGGTGTACAGT



Reverse complement motif Consensus sequence: ACTGTGACACCACAGTGGAGCACT

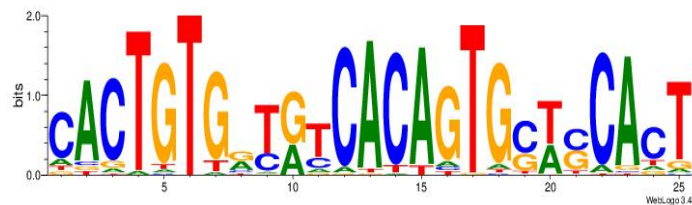


Dataset #:	2
Motif ID:	22
Motif name:	CACTGTGrYrtCACAGTGswsCAcT
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	9
Number of overlap:	17
Similarity score:	0.0456803

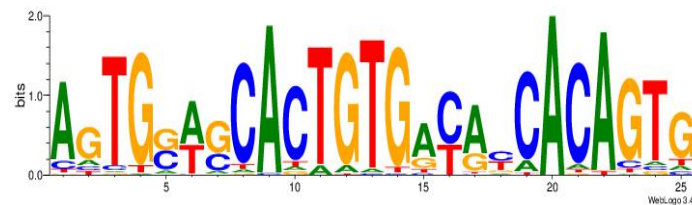
Alignment:

CACTGTGRTRTCACAGTGSWSCACT
 -----CAHCACAGTGGAGCACT

Original motif Consensus sequence:
 CACTGTGRTRTCACAGTGSWSCACT



Reverse complement motif Consensus sequence:
 AGTGSWSCACTGTGAMAMCACAGTG

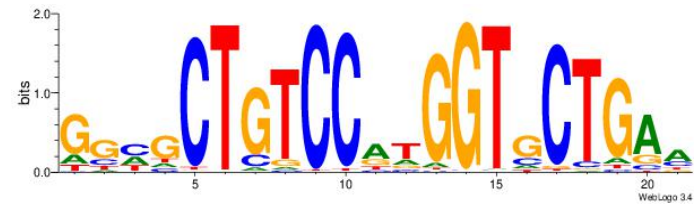
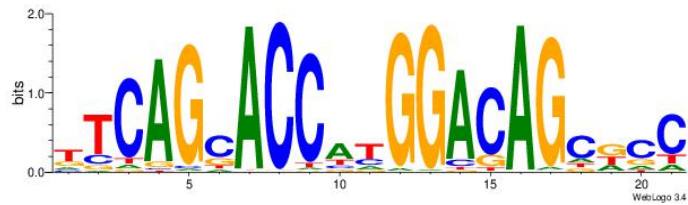


Dataset #:	1
Motif ID:	7
Motif name:	REST
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	3
Number of overlap:	17
Similarity score:	0.0894884

Alignment:
 TTCAGCACCATGGACAGCKCC
 --CAHCACAGTGGAGCACT--

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC

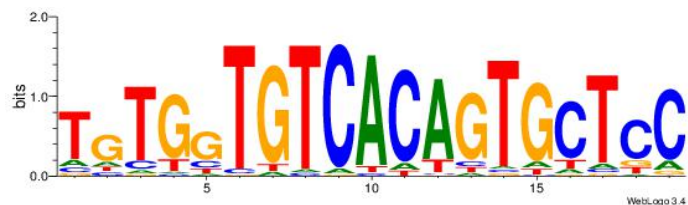
Reverse complement motif Consensus sequence:
 GYGCTGTCCATGGTGCTGAA



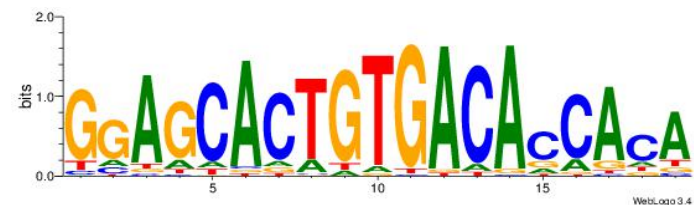
Dataset #: 2
 Motif ID: 17
 Motif name: TgTGgTGTCACAGTGCTCC
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 17
 Similarity score: 0.0962536

Alignment:
 GGAGCACTGTGACACCACA
 -CAHCACAGTGGAGCACT-

Original motif Consensus sequence: TGTGGTGTGTCACAGTGCTCC



Reverse complement motif Consensus sequence: GGAGCACTGTGACACCACA

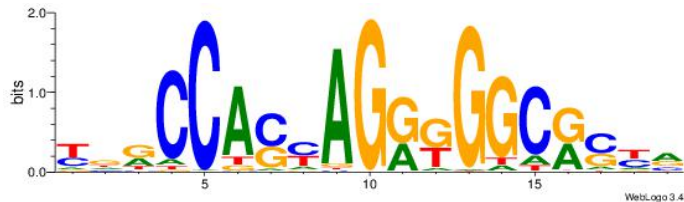


Dataset #: 1

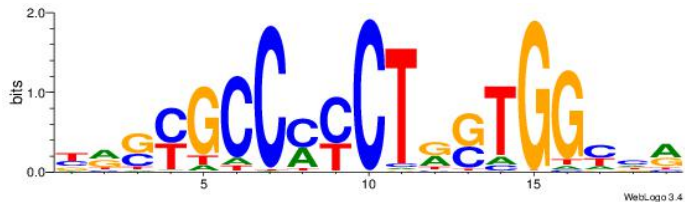
Motif ID: 16
Motif name: CTCF
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 2
Number of overlap: 17
Similarity score: 0.0978126

Alignment:
YDRCCASYAGRKGGRSYV
-CAHCACAGTGGAGCACT-

Original motif Consensus sequence: YDRCCASYAGRKGGRSYV



Reverse complement motif Consensus sequence: BMSMGCCYMCTKSTGGMHM

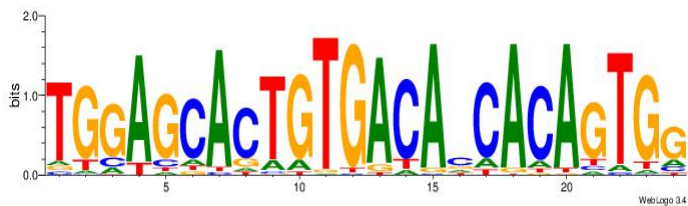


Dataset #: 2
Motif ID: 23
Motif name: TGGAGCACTGTGACAcCACAGTGg
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 3
Number of overlap: 17

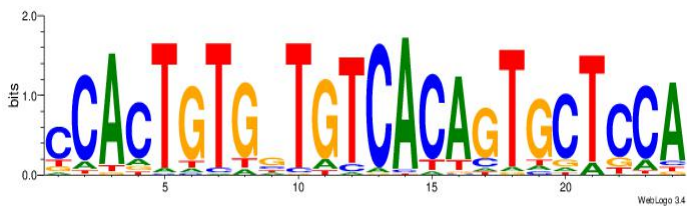
Similarity score: 0.106708

Alignment:
CCACTGTGVTGTCACAGTGCTCCA
-----AGTGCTCCACTGTGDTG--

Original motif Consensus sequence: TGGAGCACTGTGACAVCACAGTGG



Reverse complement motif Consensus sequence: CCACTGTGVTGTCACAGTGCTCCA

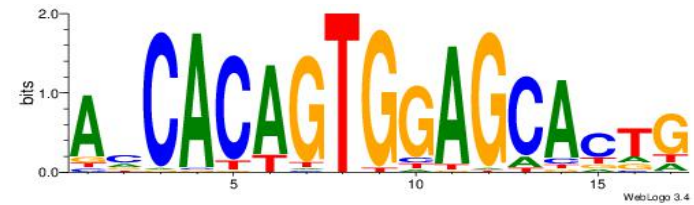
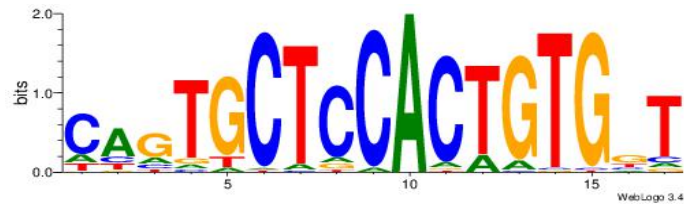


Dataset #: 2
Motif ID: 20
Motif name: CagTGCTCCACTGTGgT
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 2
Number of overlap: 16
Similarity score: 0.5

Alignment:
ABCACAGTGGAGCACTG-
-CAHCACAGTGGAGCACT

Original motif Consensus sequence: CAGTGCTCCACTGTGBT

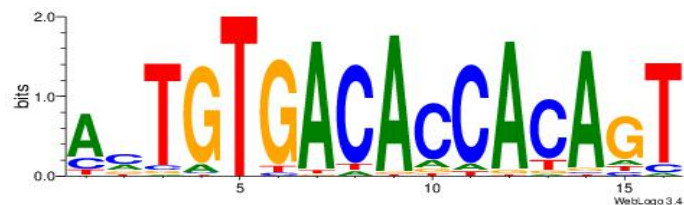
Reverse complement motif Consensus sequence: ABCACAGTGGAGCACTG



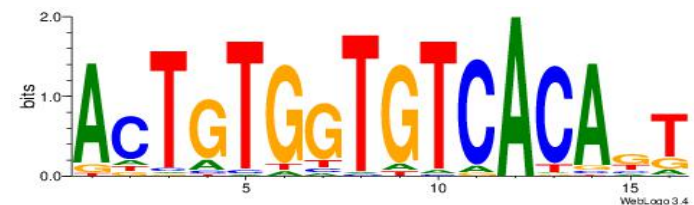
Dataset #: 2
 Motif ID: 21
 Motif name: AmTGTGACACCACAGT
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 16
 Similarity score: 0.610921

Alignment:
 ACTGTGGTGTACART-
 CAHCACAGTGGAGCACT

Original motif Consensus sequence: AMTGTGACACCACAGT



Reverse complement motif Consensus sequence: ACTGTGGTGTACART



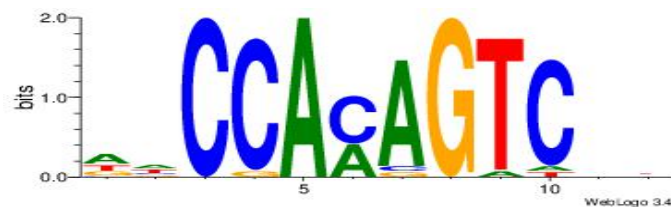
Dataset #: 2

Motif ID: 25
 Motif name: wwCCAmAGTCmt
 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: 2.5839

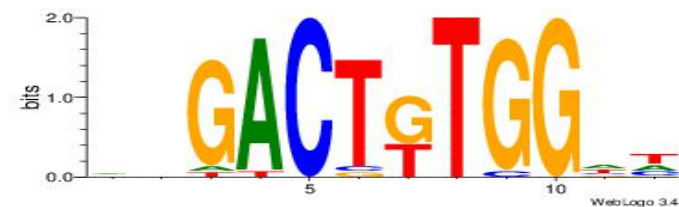
Alignment:

-----VDGACTRTGGDD
 AGTGCTCCACTGTGDTG

Original motif Consensus sequence: DDCCAMAGTCHB



Reverse complement motif Consensus sequence: VDGACTRTGGDD

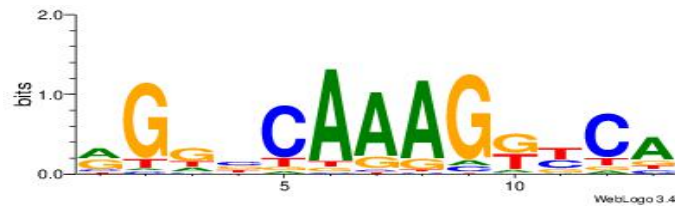


Dataset #: 1
 Motif ID: 1
 Motif name: HNF4A
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 12
 Similarity score: 2.60332

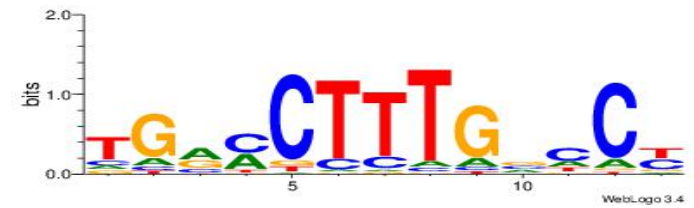
Alignment:

```
-----TGM YCTTTGBCKK
AGTGCTCCACTGTGDTG-
```

Original motif Consensus sequence: RGGBCAAAGKYCA

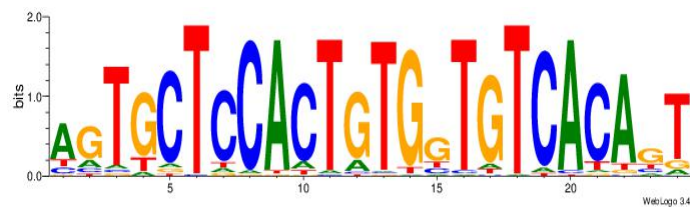


Reverse complement motif Consensus sequence: TGM YCTTTGBCKK

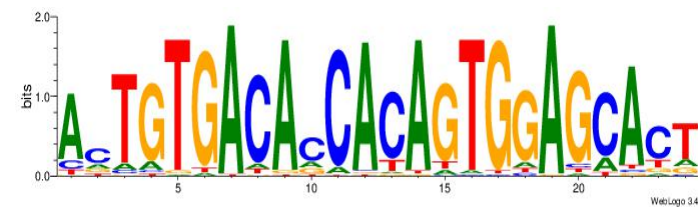


Dataset #: 2 Motif ID: 27 Motif name: AgTGCTCCACTGTGgTGTCACAgT

Original motif Consensus sequence: AGTGCTCCACTGTGGTGTACAGT



Reverse complement motif Consensus sequence: ACTGTGACACCACAGTGGAGCACT



Best Matches for Motif ID 27 (Highest to Lowest)

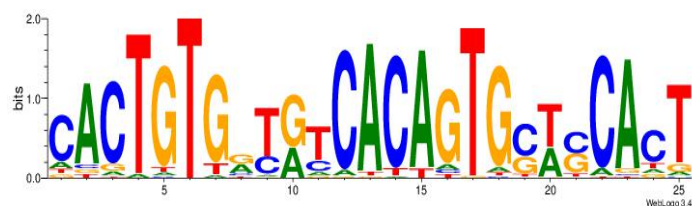
Dataset #:	2
Motif ID:	22
Motif name:	CACTGTGrYrtCACAGTGsWsCACT
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward

Position number: 2
 Number of overlap: 24
 Similarity score: 0.0409586

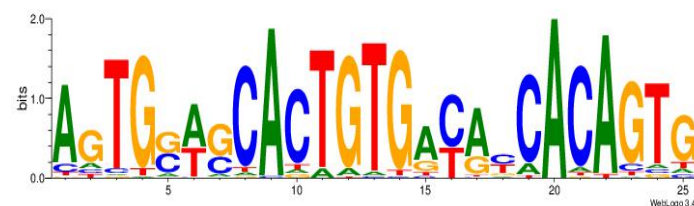
Alignment:

AGTGSWSCACTGTGAMAMCACAGTG
 -AGTGCTCCACTGTGGTGTACAGT

Original motif Consensus sequence:
 CACTGTGRTRTCACAGTGSWSCACT



Reverse complement motif Consensus sequence:
 AGTGSWSCACTGTGAMAMCACAGTG

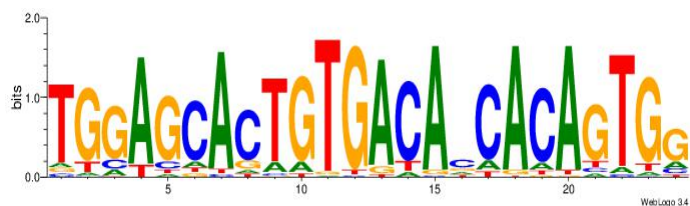


Dataset #: 2
 Motif ID: 23
 Motif name: TGGAGCACTGTGACAcCACAGTGg
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3
 Number of overlap: 22
 Similarity score: 1.06364

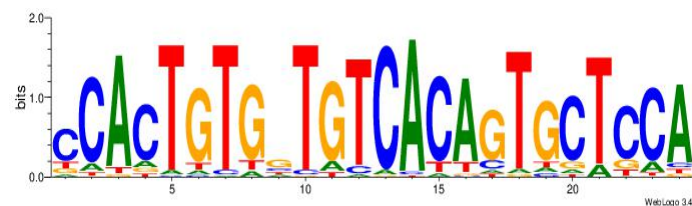
Alignment:

CCACTGTGVTGTCACAGTGCTCCA--
 --ACTGTGACACCACAGTGGAGCACT

Original motif Consensus sequence: TGGAGCACTGTGACAVCACAGTGG



Reverse complement motif Consensus sequence: CCACTGTGVTGTACAGTGCTCCA

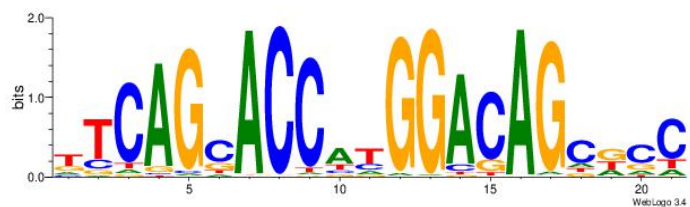


Dataset #: 1
 Motif ID: 7
 Motif name: REST
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 19
 Similarity score: 2.59599

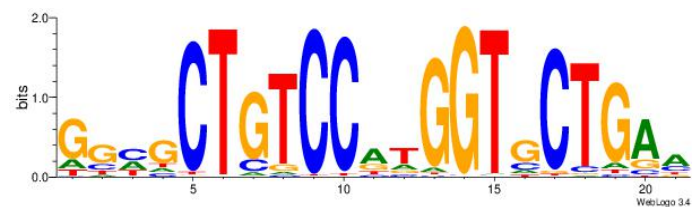
Alignment:

TTCAGCACCATGGACAGCKCC-----
 --ACTGTGACACCACAGTGGAGCACT

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC



Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGTCTGAA

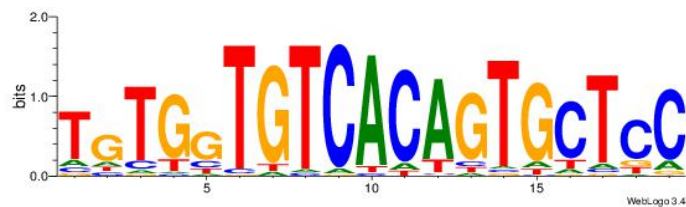


Dataset #: 2
 Motif ID: 17
 Motif name: TgTGgTGTCACAGTGCTCC
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 18
 Similarity score: 3.10123

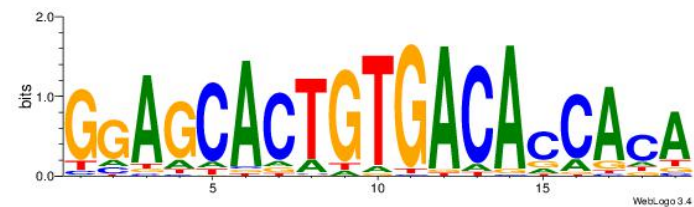
Alignment:

-----GGAGCACTGTGACACCACA
 ACTGTGACACCACAGTGGAGCACT-

Original motif Consensus sequence: TGTGGTGTCACAGTGCTCC



Reverse complement motif Consensus sequence: GGAGCACTGTGACACCACA



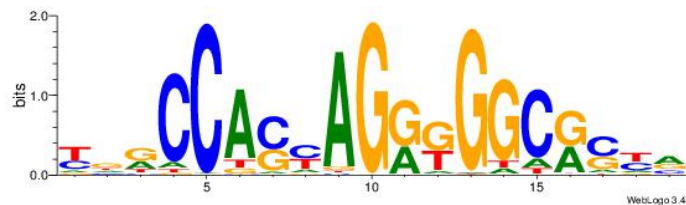
Dataset #: 1
 Motif ID: 16
 Motif name: CTCF
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2

Number of overlap: 18
Similarity score: 3.10186

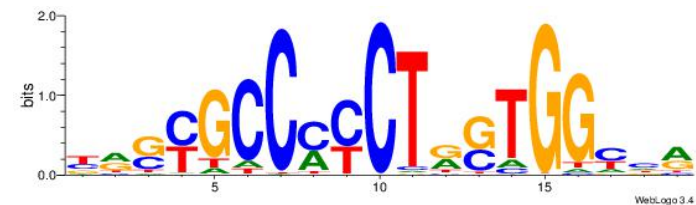
Alignment:

-----BMSMGCCYMCTKSTGGMHM
AGTGCTCCACTGTGGTGTCACAGT-

Original motif Consensus sequence: YDRCCASYAGRKGGRSYV



Reverse complement motif Consensus sequence: BMSMGCCYMCTKSTGGMHM

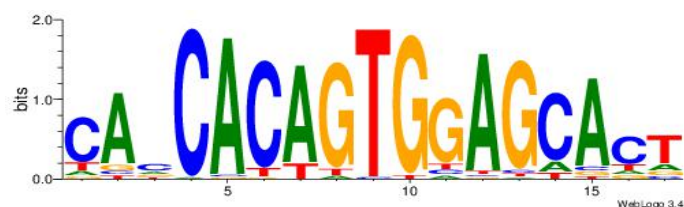


Dataset #: 2
Motif ID: 26
Motif name: CACACAGTGGAGCAct
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 17
Similarity score: 3.50248

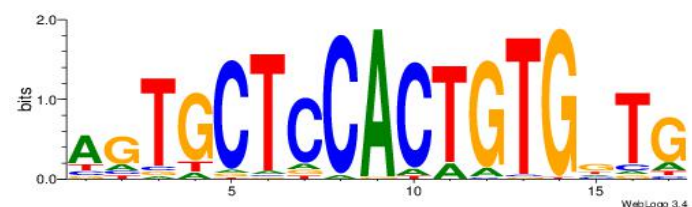
Alignment:

-----AGTGCTCCACTGTGDTG
AGTGCTCCACTGTGGTGTCACAGT

Original motif Consensus sequence: CAHCACAGTGGAGCACT



Reverse complement motif Consensus sequence: AGTGCTCCACTGTGDTG

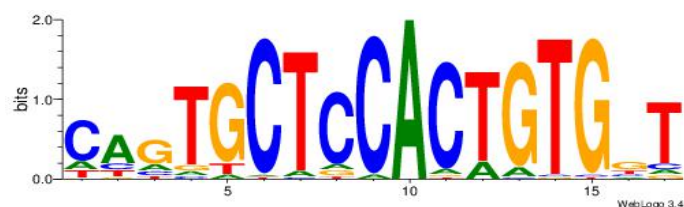


Dataset #: 2
Motif ID: 20
Motif name: CagTGCTCCACTGTGgT
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 2
Number of overlap: 16
Similarity score: 4

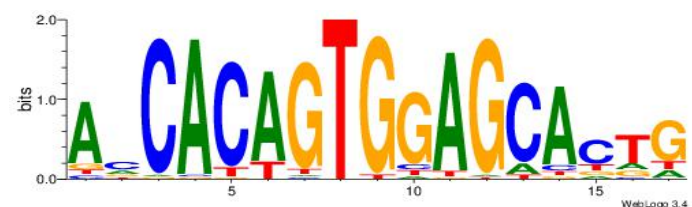
Alignment:

CAGTGCTCCACTGTGBT-----
-AGTGCTCCACTGTGGTGTACAGT

Original motif Consensus sequence: CAGTGCTCCACTGTGBT



Reverse complement motif Consensus sequence: ABCACAGTGGAGCACTG

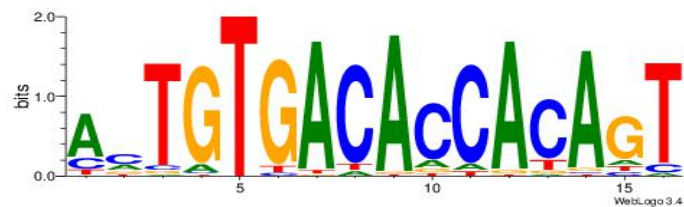


Dataset #: 2
 Motif ID: 21
 Motif name: AmTGTGACACCACAGT
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 16
 Similarity score: 4.0041

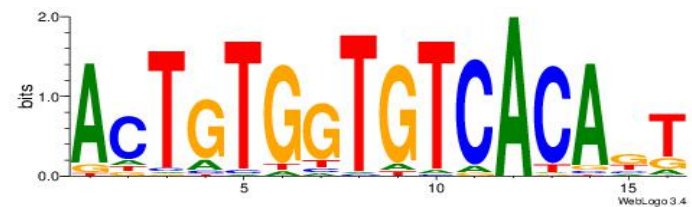
Alignment:

-----AMTGTGACACCACAGT
 ACTGTGACACCACAGTGGAGCACT

Original motif Consensus sequence: AMTGTGACACCACAGT



Reverse complement motif Consensus sequence: ACTGTGGTGTCACT



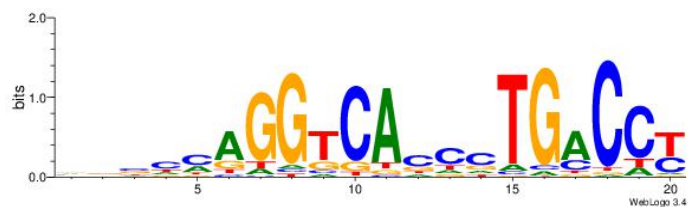
Dataset #: 1
 Motif ID: 3
 Motif name: ESR1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 6

Number of overlap: 15
Similarity score: 4.59996

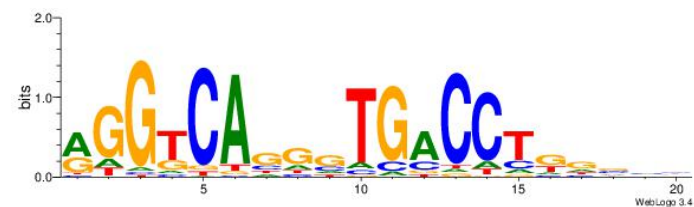
Alignment:

MGGTCAGGGTGACCTRDBHV-----
-----ACTGTGACACCACAGTGGAGCACT

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif Consensus sequence:
MGGTCAGGGTGACCTRDBHV

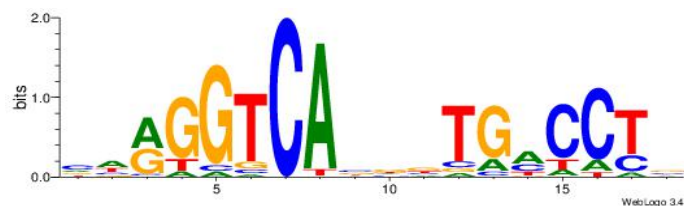


Dataset #: 1
Motif ID: 9
Motif name: ESR2
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 7
Number of overlap: 12
Similarity score: 6.08041

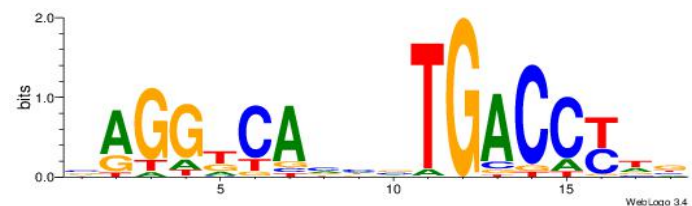
Alignment:

-----VHRGGTCABDBTGMCCCTB
AGTGCTCCACTGTGGTGTCACAGT-----

Original motif Consensus sequence: VHRGGTCABDBTGMCTB

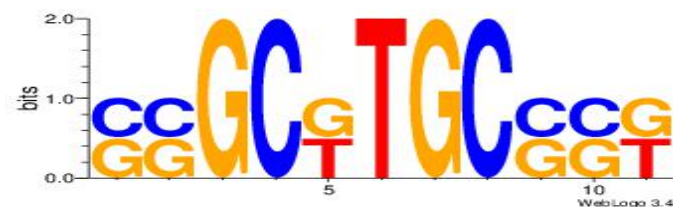


Reverse complement motif Consensus sequence: BAGGYCABHBTGACCKHV



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

Original motif Consensus sequence: SSGCKTGCSSK



Reverse complement motif Consensus sequence: YSSGCAYGCSS



Best Matches for Motif ID 28 (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:	Backward
Position number:	1
Number of overlap:	11
Similarity score:	0.00456539

Alignment:

GCGCGCSCGCG
SSGCKTGCSSK

Original motif Consensus sequence: GCGCGCSCGCG



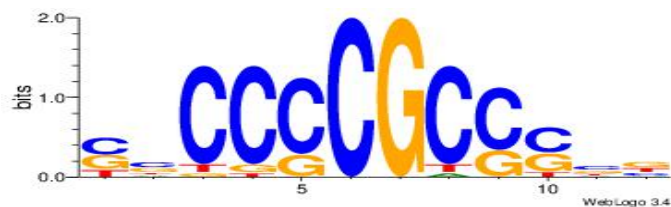
Reverse complement motif Consensus sequence: CGCGSGCGCGC



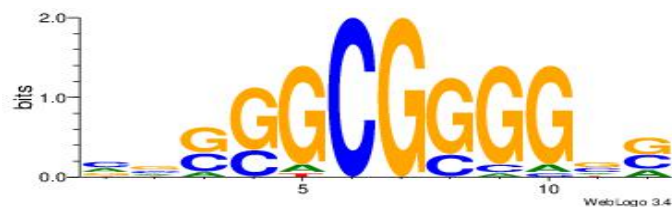
Dataset #: 2
Motif ID: 24
Motif name: ssCCCCGCSsk
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 2
Number of overlap: 11
Similarity score: 0.0176347

Alignment:
BBSGGCGGGGBS
-YSSGCAYGCSS

Original motif Consensus sequence: SBCCCCGCCSBB



Reverse complement motif Consensus sequence: BBSGGCGGGGBS



Dataset #: 2
 Motif ID: 18
 Motif name: sscCCCGCGcs
 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: 0.0190954

Alignment:

SBCGCGGGGSB

YSSGCAYGCSS

Original motif Consensus sequence: BSCCCCGCGBS



Reverse complement motif Consensus sequence: SBCGCGGGGSB



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: 1

Number of overlap: 11
Similarity score: 0.0276515

Alignment:
CCGCGGRCACG
SSGCKTGCSSK

Original motif Consensus sequence: CCGCGGRCACG



Reverse complement motif Consensus sequence: CGTGKCCGCGG

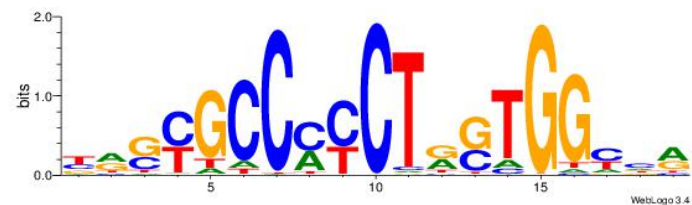
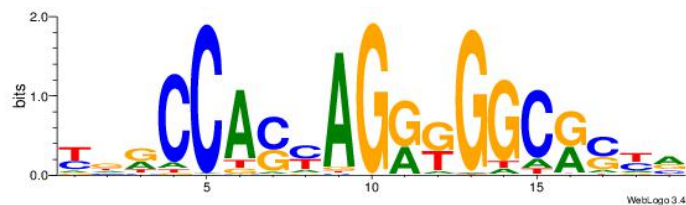


Dataset #: 1
Motif ID: 16
Motif name: CTCF
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 8
Number of overlap: 11
Similarity score: 0.0349439

Alignment:
YDRCCASYAGRKGGRSYV
-----SSGCKTGCSSK-

Original motif Consensus sequence: YDRCCASYAGRKGGRSYV

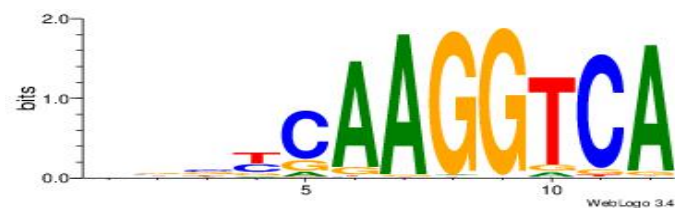
Reverse complement motif Consensus sequence:
BMSMGCCYMCTKSTGGMHM



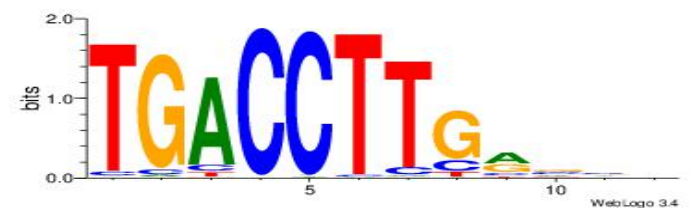
Dataset #: 1
 Motif ID: 4
 Motif name: Esrrb
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.0358701

Alignment:
 VBBYCAAGGTCA
 -YSSGCAYGCSS

Original motif Consensus sequence: VBBYCAAGGTCA



Reverse complement motif Consensus sequence: TGACCTTGMBBB



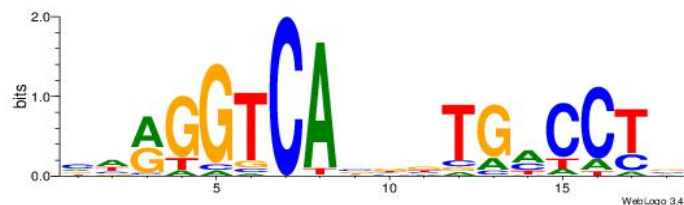
Dataset #: 1
 Motif ID: 9

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

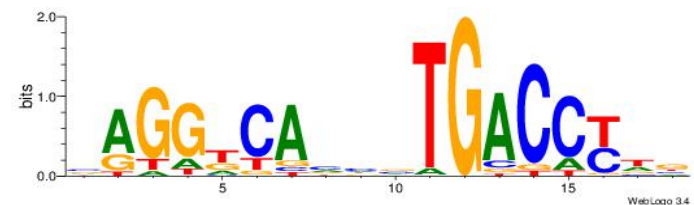
Alignment:

```
VHRGGTCABDBTGMCTB
-----YSSGCAYGCSS--
```

Original motif Consensus sequence: VHRGGTCABDBTGMCTB



Reverse complement motif Consensus sequence: BAGGYCABHBTGACCKHV

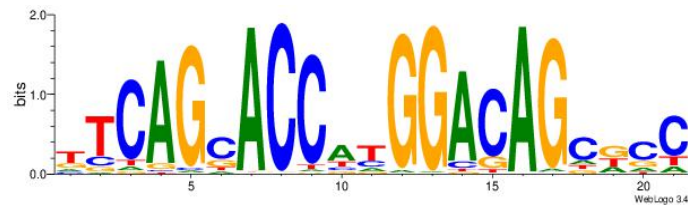


Dataset #:	1
Motif ID:	7
Motif name:	REST
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	10
Number of overlap:	11
Similarity score:	0.0409322

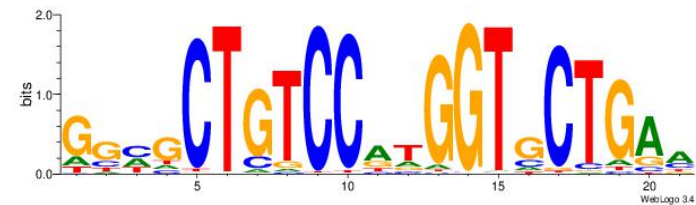
Alignment:

TTCAGCACCATGGACAGCKCC
-YSSGCAYGCSS-----

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC



Reverse complement motif Consensus sequence:
GGYGCTGTCCATGGTGCTGAA



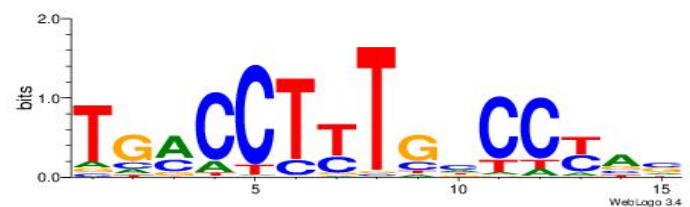
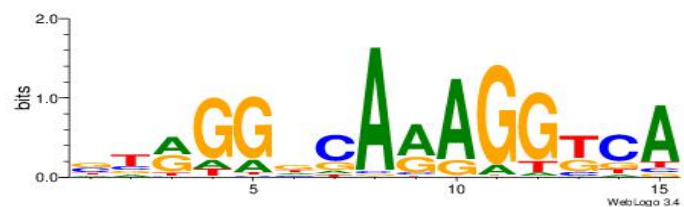
Dataset #:	1
Motif ID:	14
Motif name:	PPARGRXRA
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	3
Number of overlap:	11
Similarity score:	0.041419

Alignment:

BTRGGDCARAGGKCA
--YSSGCAYGCSS--

Original motif Consensus sequence: BTRGGDCARAGGKCA

Reverse complement motif Consensus sequence: TGRCCCTKTGHCKK

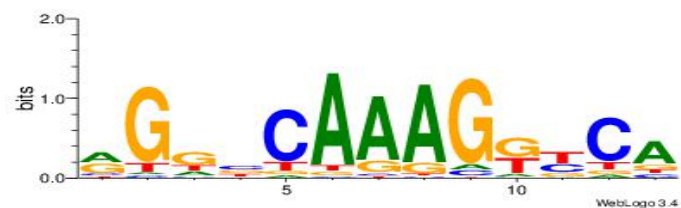


Dataset #: 1
 Motif ID: 1
 Motif name: HNF4A
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.0437981

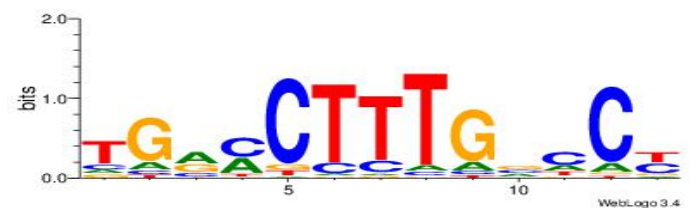
Alignment:

RGGBCAAAGKYCA
 --YSSGCAYGCSS

Original motif Consensus sequence: RGGBCAAAGKYCA



Reverse complement motif Consensus sequence: TGMYCTTTGBCCCK



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

Original motif Consensus sequence: CCGCGGRCACG



Reverse complement motif Consensus sequence: CGTGKCCGCGG



Best Matches for Motif ID 29 (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:	Backward
Position number:	1
Number of overlap:	11
Similarity score:	0.010473

Alignment:

GCGCGCSCGCG

CCGCGGRCACG

Original motif Consensus sequence: GCGCGCSCGCG



Reverse complement motif Consensus sequence: CGCGSGCGCGC

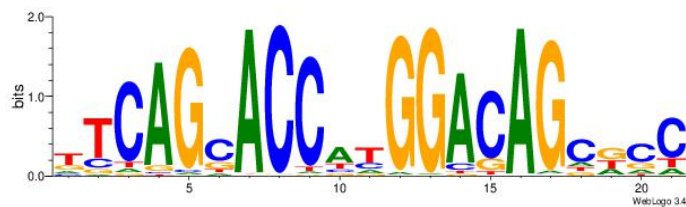


Dataset #: 1
 Motif ID: 7
 Motif name: REST
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 4
 Number of overlap: 11
 Similarity score: 0.0484441

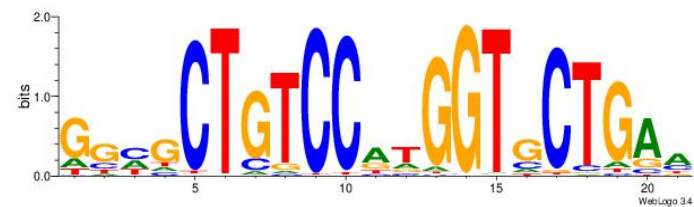
Alignment:

TTCAGCACCATGGACAGCKCC
 -----CCGCGGRCACG---

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC



Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA

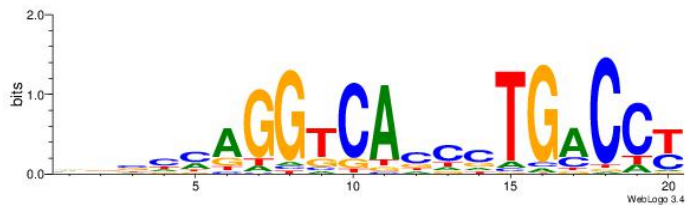


Dataset #: 1
 Motif ID: 3
 Motif name: ESR1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3

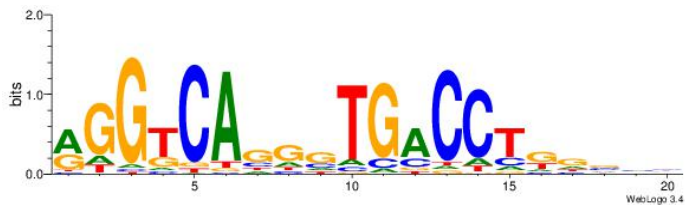
Number of overlap: 11
Similarity score: 0.0486581

Alignment:
MGGTCAGGGTGACCTRDBHV
-----CGTGKCCGCGG--

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV

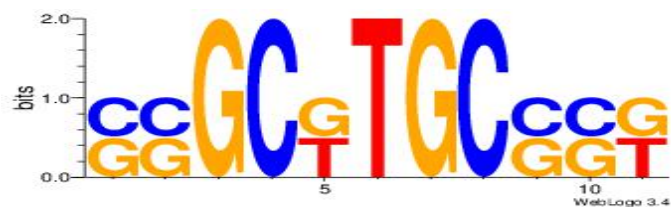


Dataset #: 2
Motif ID: 28
Motif name: ssGCKTGCssk
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 11
Similarity score: 0.0503056

Alignment:
SSGCKTGCSK
CCGCGGRCACG

Original motif Consensus sequence: SSGCKTGCSK

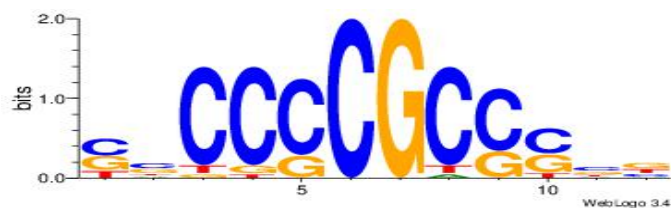
Reverse complement motif Consensus sequence: YSSGCAYGCSS



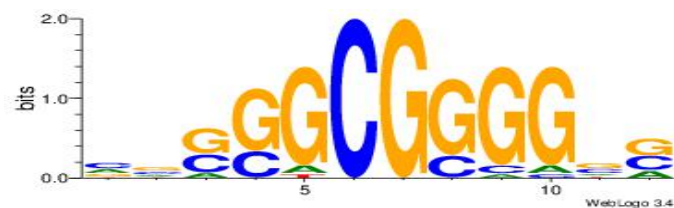
Dataset #: 2
 Motif ID: 24
 Motif name: ssCCCCGCSsk
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 11
 Similarity score: 0.055777

Alignment:
 BBSGGCGGGGBS
 CGTGKCCGCGG-

Original motif Consensus sequence: SBCCCCGCCSBB



Reverse complement motif Consensus sequence: BBSGGCGGGGBS



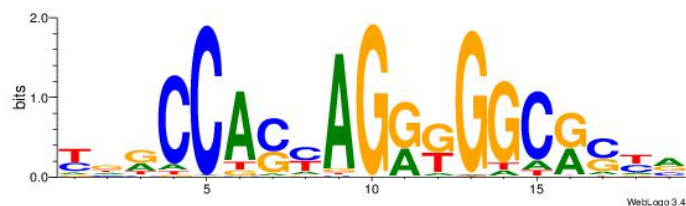
Dataset #: 1
 Motif ID: 16

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: 11
 Similarity score: 0.0588663

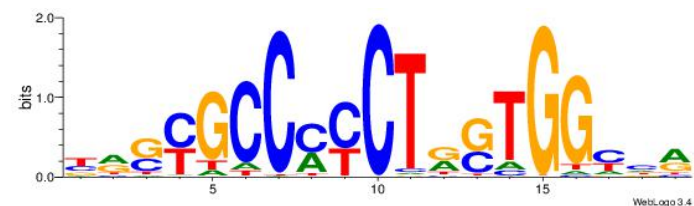
Alignment:

YDRCCASYAGRKGGRSYV
 -----CCGCGGRCACG-

Original motif Consensus sequence: YDRCCASYAGRKGGRSYV



Reverse complement motif Consensus sequence: BMSMGCCYMCTKSTGGMHM



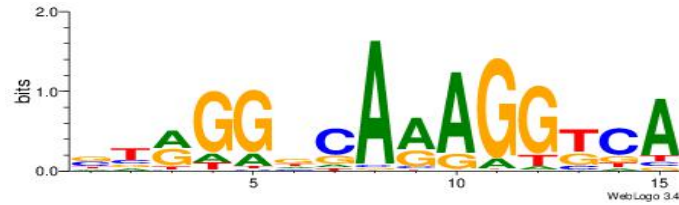
Dataset #: 1
 Motif ID: 14
 Motif name: PPARGRXRA
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 4
 Number of overlap: 11
 Similarity score: 0.0629476

Alignment:

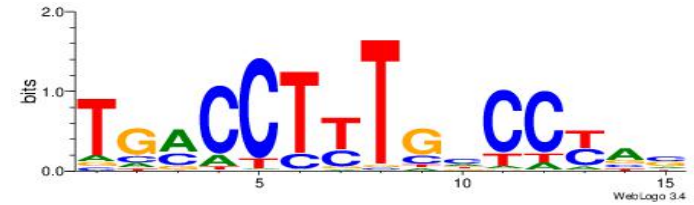
TGRCCTKTGHCKAB

---CGTGKCCGCGG--

Original motif Consensus sequence: BTRGGDCARAGGKCA



Reverse complement motif Consensus sequence: TGRCCTKTGHCKAB



Dataset #:	2
Motif ID:	18
Motif name:	sscCCCGCGcs
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:	0.0651451

Alignment:

BSCCCCGCGBS

CCGCGGRCACG

Original motif Consensus sequence: BSCCCCGCGBS

Reverse complement motif Consensus sequence: SBCGCGGGGSB

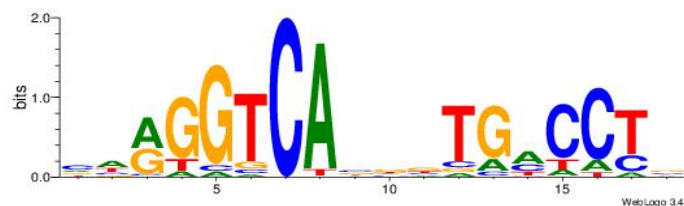


Dataset #: 1
 Motif ID: 9
 Motif name: ESR2
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 9
 Number of overlap: 10
 Similarity score: 0.551597

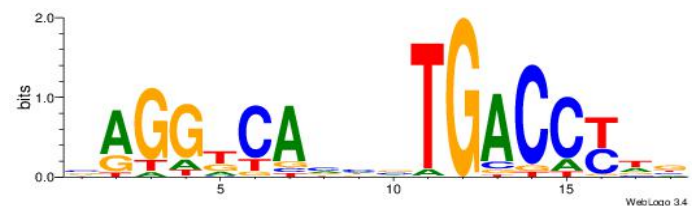
Alignment:

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

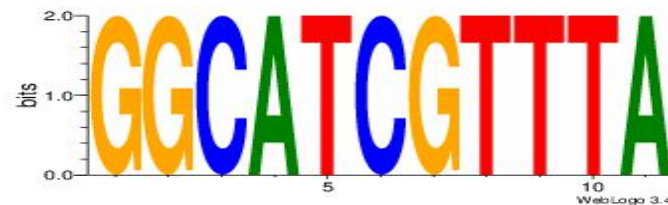


Dataset #: 2 Motif ID: 30 Motif name: taaacgatgcc

Original motif Consensus sequence: TAAACGATGCC



Reverse complement motif Consensus sequence: GGCATCGTTTA



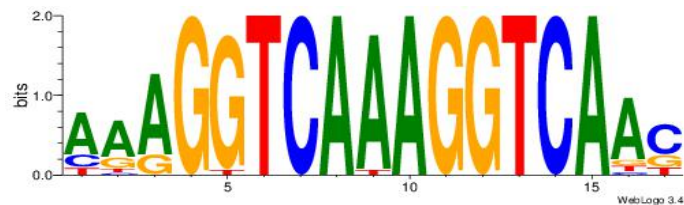
Best Matches for Motif ID 30 (Highest to Lowest)

Dataset #: 1
Motif ID: 10
Motif name: NR1H2RXRA
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: 0.0511364

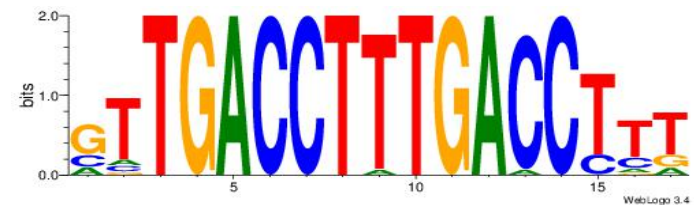
Alignment:

```
GTGACCTTTGACCTTT  
----TAAACGATGCC--
```

Original motif Consensus sequence: AAAGGTCAAAGGTCAAC



Reverse complement motif Consensus sequence:
GTTGACCTTTGACCTTT



Dataset #: 1
Motif ID: 2
Motif name: NR2F1
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: 0.0563811

Alignment:
 TGAMCTTTGMMCYT
 TAAACGATGCC---

Original motif Consensus sequence: TGAMCTTTGMMCYT



Reverse complement motif Consensus sequence: AKGYCAAAGRTC



Dataset #: 2
 Motif ID: 19
 Motif name: atactttggc
 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: 0.5375

Alignment:
 GCCAAAGTAT-
 GGCATCGTTTA

Original motif Consensus sequence: ATACTTTGGC



Reverse complement motif Consensus sequence: GCCAAAGTAT



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: 2
Number of overlap: 10
Similarity score: 0.5625

Alignment:

-CGTCCGTATAG

GGCATCGTTTA-

Original motif Consensus sequence: CTATACGGACG



Reverse complement motif Consensus sequence: CGTCCGTATAG

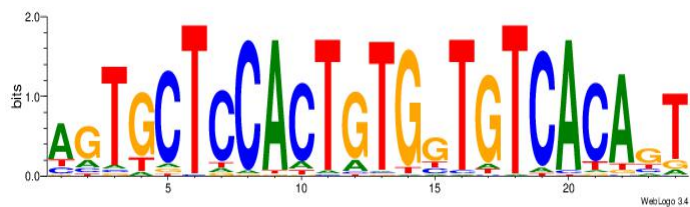


Dataset #: 2
 Motif ID: 27
 Motif name: AgTGCTCCACTGTGgTGTCACAgT
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 17
 Number of overlap: 8
 Similarity score: 1.55502

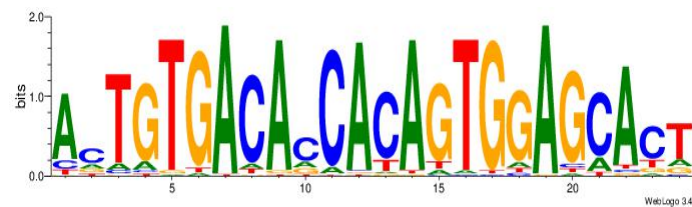
Alignment:

ACTGTGACACCACAGTGGAGCACT---
 -----TAAACGATGCC

Original motif Consensus sequence: AGTGCTCCACTGTGGTGTTCACAGT



Reverse complement motif Consensus sequence: ACTGTGACACCACAGTGGAGCACT



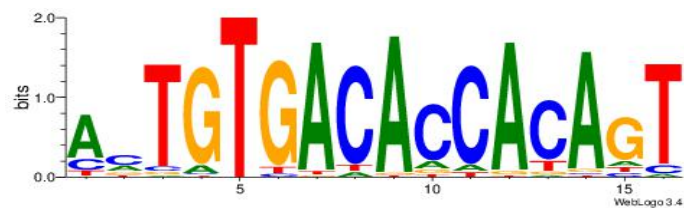
Dataset #: 2
 Motif ID: 21
 Motif name: AmTGTGACACCACAGT
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 9

Number of overlap: 8
Similarity score: 1.55908

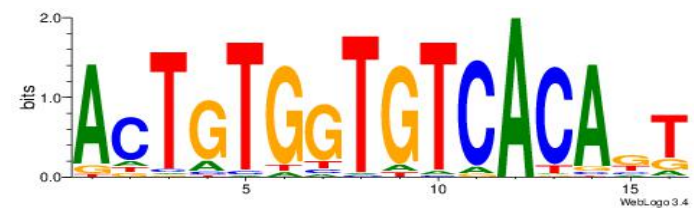
Alignment:

---AMTGTGACACCACAGT
TAAACGATGCC-----

Original motif Consensus sequence: AMTGTGACACCACAGT



Reverse complement motif Consensus sequence:
ACTGTGGTGTCACT



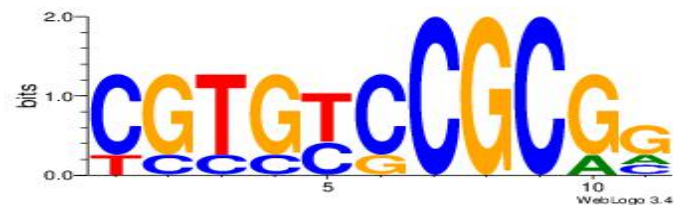
Dataset #: 2
Motif ID: 29
Motif name: cCGCGGrCACG
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 4
Number of overlap: 8
Similarity score: 1.5625

Alignment:

CGTGKCCGCGG---
---GGCATCGTTTA

Original motif Consensus sequence: CCGCGGrCACG

Reverse complement motif Consensus sequence: CGTGKCCGCGG

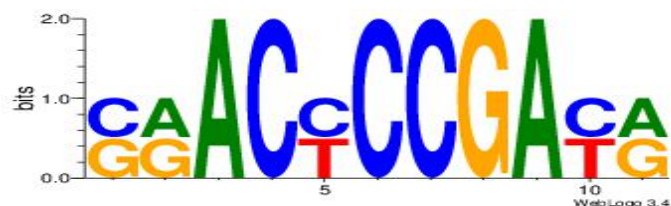


Dataset #: 2
 Motif ID: 33
 Motif name: srACyCCGAYr
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 5
 Number of overlap: 7
 Similarity score: 2.04464

Alignment:

----SRACYCCGAYR
 TAAACGATGCC----

Original motif Consensus sequence: SRACYCCGAYR



Reverse complement motif Consensus sequence: KTCGGKGT



Dataset #: 1
 Motif ID: 16

Motif name:	CTCF
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	13
Number of overlap:	7
Similarity score:	2.05416

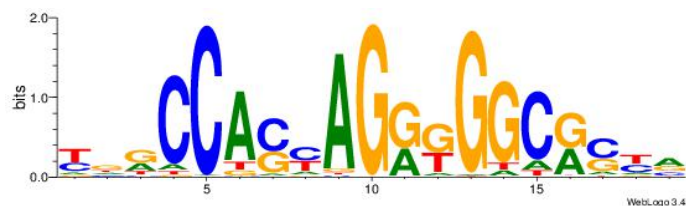
Alignment:

```

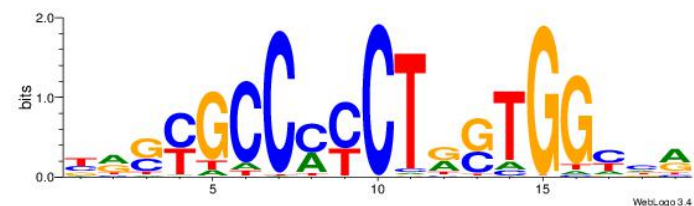
BMSMGCCYMCTKSTGGMHM-----
-----TAAACGATGCC

```

Original motif Consensus sequence: YDRCCASYAGRKGGRSYV



Reverse complement motif Consensus sequence: BMSMGCCYMCTKSTGGMHM

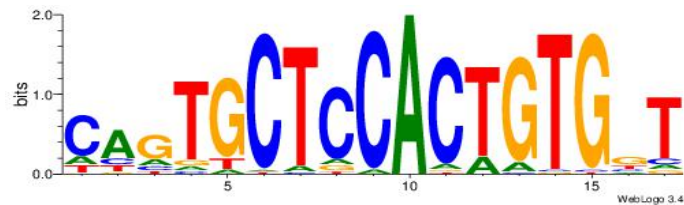


Dataset #:	2
Motif ID:	20
Motif name:	CagTGCTCCACTGTGgT
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	11
Number of overlap:	7
Similarity score:	2.05952

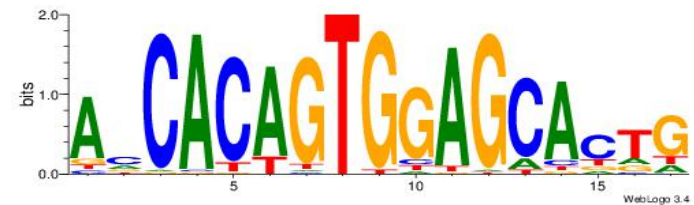
Alignment:

```
----CAGTGCTCCACTGTGBT  
TAAACGATGCC-----
```

Original motif Consensus sequence: CAGTGCTCCACTGTGBT



Reverse complement motif Consensus sequence: ABCACAGTGGAGCACTG



Dataset #: 2 Motif ID: 31 Motif name: ctatacggacg

Original motif Consensus sequence: CTATACGGACG



Reverse complement motif Consensus sequence: CGTCCGTATAG



Best Matches for Motif ID 31 (Highest to Lowest)

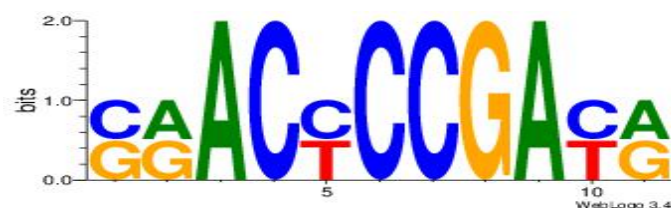
Dataset #:	2
Motif ID:	33
Motif name:	srACyCCGAYr
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward

Position number: 1
Number of overlap: 11
Similarity score: 0.0803571

Alignment:

SRACYCCGAYR
CTATACGGACG

Original motif Consensus sequence: SRACYCCGAYR



Reverse complement motif Consensus sequence: KKTCGGKGTKS



Dataset #: 2
Motif ID: 30
Motif name: taaacgatgcc
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: 0.580357

Alignment:

-TAAACGATGCC
CTATACGGACG-

Original motif Consensus sequence: TAAACGATGCC

Reverse complement motif Consensus sequence: GGCATCGTTTA

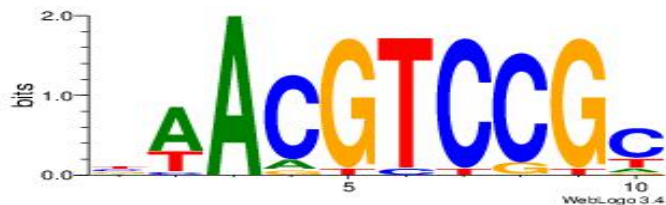


Dataset #: 1
 Motif ID: 13
 Motif name: MIZF
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 9
 Similarity score: 1.0623

Alignment:

GCGGACGTTV--
 -CGTCCGTATAG

Original motif Consensus sequence: BAACGTCCGC



Reverse complement motif Consensus sequence: GCGGACGTTV



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: 2
 Number of overlap: 9
 Similarity score: 1.06647

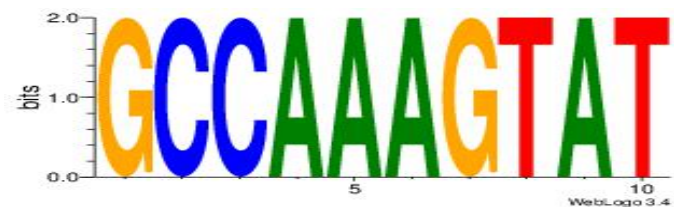
Alignment:

--ATACTTTGGC
 CTATACGGACG-

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: 1.07758

Alignment:

--CCGCGGRCACG
CTATACGGACG--

Original motif Consensus sequence: CCGCGGRCACG



Reverse complement motif Consensus sequence: CGTGKCCGCGG



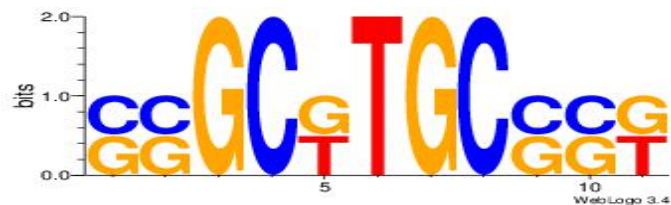
Dataset #:	2
Motif ID:	28
Motif name:	ssGCKTGCssk
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	4
Number of overlap:	8
Similarity score:	1.56473

Alignment:

---SSGCKTGCSSK
CGTCCGTATAG---

Original motif Consensus sequence: SSGCKTGCSSK

Reverse complement motif Consensus sequence: YSSGCAYGCSS



Dataset #: 2
 Motif ID: 32
 Motif name: gCGCGCsCgsG
 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: 1.57871

Alignment:
 GCGCGCSCGCG---
 ---CGTCCGTATAG

Original motif Consensus sequence: GCGCGCSCGCG



Reverse complement motif Consensus sequence: CGCGSGCGCGC



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:	6
Number of overlap:	7
Similarity score:	2.06779

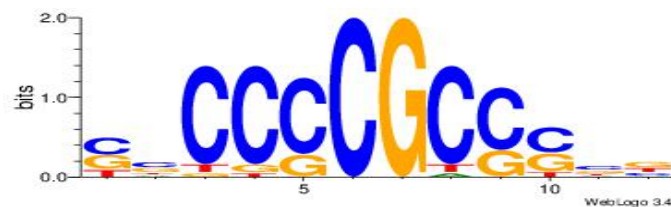
Alignment:

```

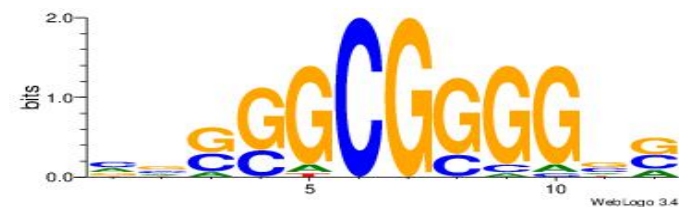
BBSGGCGGGGBS-----
-----CTATACGGACG

```

Original motif Consensus sequence: SBCCCCGCCSBB



Reverse complement motif Consensus sequence: BBSGGCGGGGBS

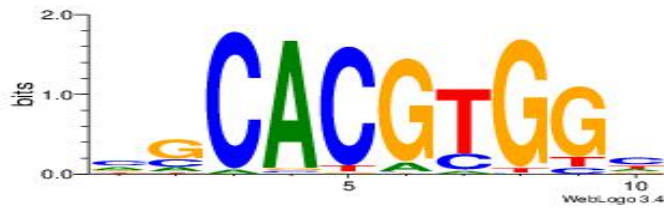


Dataset #:	1
Motif ID:	8
Motif name:	Myc
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	5
Number of overlap:	6
Similarity score:	2.54768

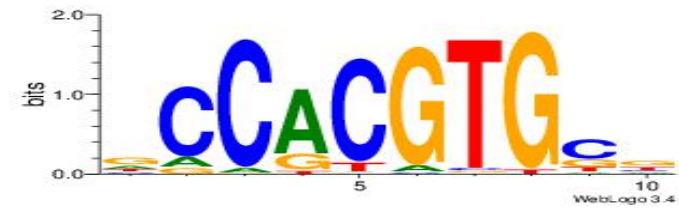
Alignment:

DCCACGTGCV-----
-----CGTCCGTATAG

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:	Reverse Complement
Direction:	Forward
Position number:	5
Number of overlap:	6
Similarity score:	2.55363

Alignment:

GCCACGTGSD-----
-----CGTCCGTATAG

Original motif Consensus sequence: HSCACGTGGC

Reverse complement motif Consensus sequence: GCCACGTGSD



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

Original motif Consensus sequence: GCGCGCSCGCG



Reverse complement motif Consensus sequence: CGCGSGCGCGC



Best Matches for Motif ID 32 (Highest to Lowest)

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:	1
Number of overlap:	11
Similarity score:	0.0131931

Alignment:
CCGCGGRCACG
GCGCGCSCGCG

Original motif Consensus sequence: CCGCGGRCACG



Reverse complement motif Consensus sequence: CGTGKCCGCGG

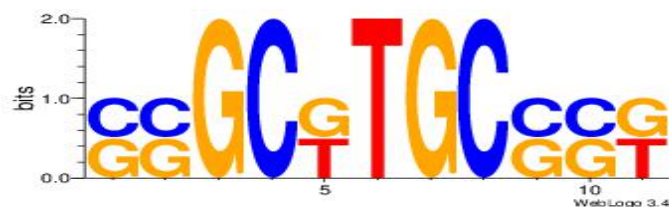


Dataset #: 2
Motif ID: 28
Motif name: ssGCKTGCssk
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 11
Similarity score: 0.0299395

Alignment:

SSGCKTGCSSK
GCGCGCSCGCG

Original motif Consensus sequence: SSGCKTGCSSK



Reverse complement motif Consensus sequence: YSSGCAYGCSS



Dataset #: 2
 Motif ID: 18
 Motif name: sscCCCGCGcs
 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: 0.0338798

Alignment:

BSCCCGCGBS
 GCGCGCSCGCG

Original motif Consensus sequence: BSCCCGCGBS



Reverse complement motif Consensus sequence: SBCGCGGGGSB

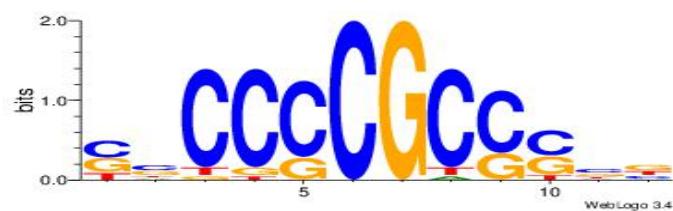


Dataset #: 2
 Motif ID: 24
 Motif name: ssCCCCGCSsk
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 11

Similarity score: 0.0410595

Alignment:
BBSGGCGGGGBS
-CGCGSGCGCGC

Original motif Consensus sequence: SBCCCCGCCSBB



Reverse complement motif Consensus sequence: BBSGGCGGGGBS

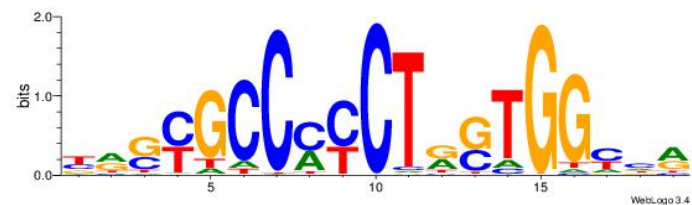
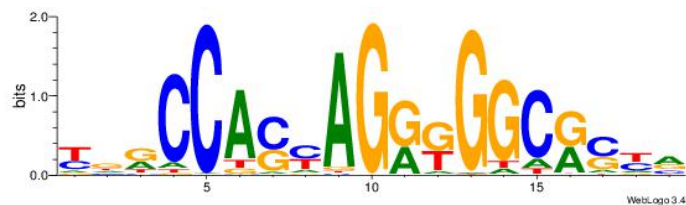


Dataset #: 1
Motif ID: 16
Motif name: CTCF
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 7
Number of overlap: 11
Similarity score: 0.0537298

Alignment:
BMSMGCCYMCTKSTGGMHM
-----GCGCGCSCGCG--

Original motif Consensus sequence: YDRCCASYAGRKGGCRSYV

Reverse complement motif Consensus sequence:
BMSMGCCYMCTKSTGGMHM

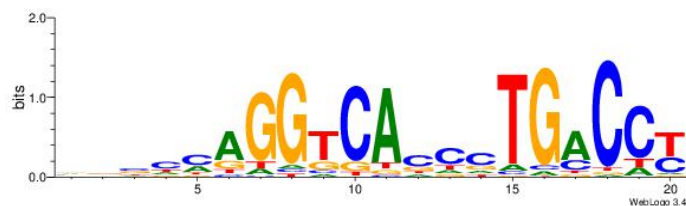


Dataset #: 1
 Motif ID: 3
 Motif name: ESR1
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 7
 Number of overlap: 11
 Similarity score: 0.0651602

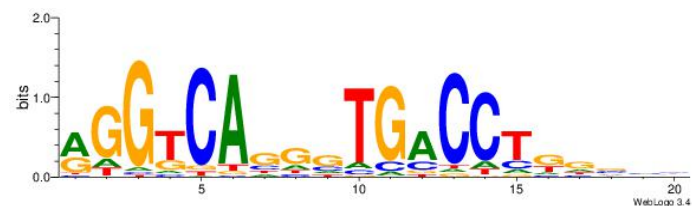
Alignment:

MGGTCAGGGTGACCTRDBHV
 ---GCGCGSCGCG-----

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV



Dataset #: 1

Motif ID: 13
 Motif name: MIZF
 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: 0.55601

Alignment:

BAACGTCCGC-
 GCGCGCSCGCG

Original motif Consensus sequence: BAACGTCCGC



Reverse complement motif Consensus sequence: GCGGACGTTT

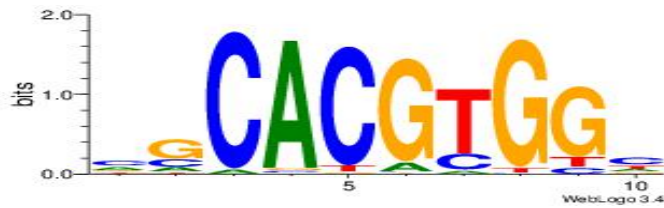


Dataset #: 1
 Motif ID: 8
 Motif name: Myc
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 10
 Similarity score: 0.561823

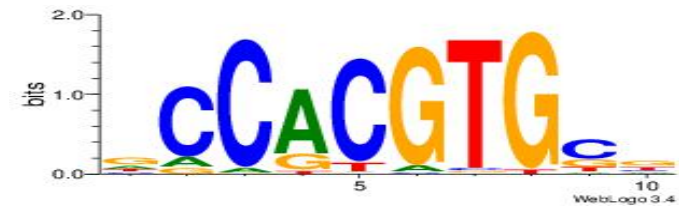
Alignment:

DCCACGTGCV-
GCGCGCSCGCG

Original motif Consensus sequence: VGCACGTGGH



Reverse complement motif Consensus sequence: DCCACGTGCV



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:	1
Number of overlap:	10
Similarity score:	0.561904

Alignment:

-HSCACGTGGC
GCGCGCSCGCG

Original motif Consensus sequence: HSCACGTGGC

Reverse complement motif Consensus sequence: GCCACGTGSD



Dataset #: 2
 Motif ID: 31
 Motif name: ctatacggacg
 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: 1.56956

Alignment:

---CTATACGGACG

CGCGSGCGCGC---

Original motif Consensus sequence: CTATACGGACG

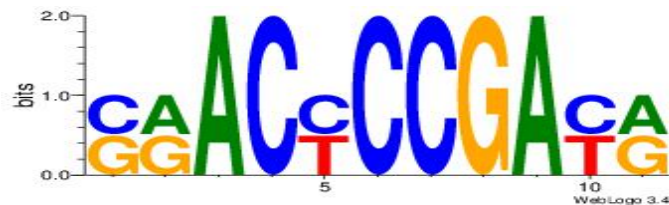


Reverse complement motif Consensus sequence: CGTCCGTATAG



Dataset #: 2 Motif ID: 33 Motif name: srACyCCGAyr

Original motif Consensus sequence: SRACYCCGAYR



Reverse complement motif Consensus sequence: KKTCCGGKGTKS



Best Matches for Motif ID 33 (Highest to Lowest)

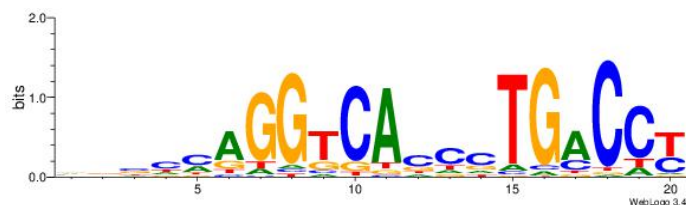
Dataset #:	1
Motif ID:	3
Motif name:	ESR1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	2
Number of overlap:	11
Similarity score:	0.0287254

Alignment:

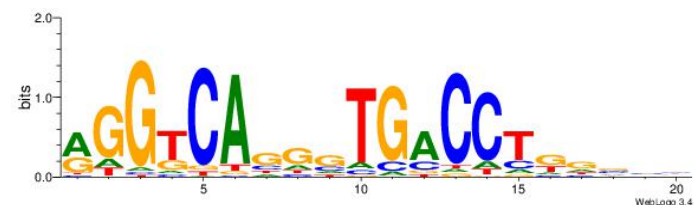
```

MGGTCAGGGTGACCTRDBHV
-KKTCGGKGTKS-----
  
```

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV

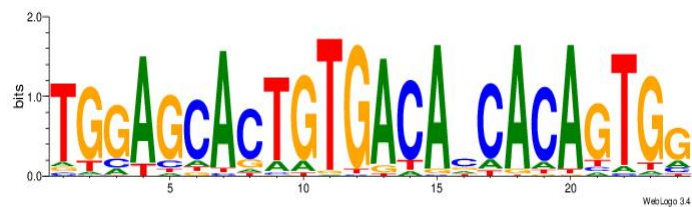


Dataset #: 2
 Motif ID: 23
 Motif name: TGGAGCACTGTGACAcCACAGTGg
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 5
 Number of overlap: 11
 Similarity score: 0.0316919

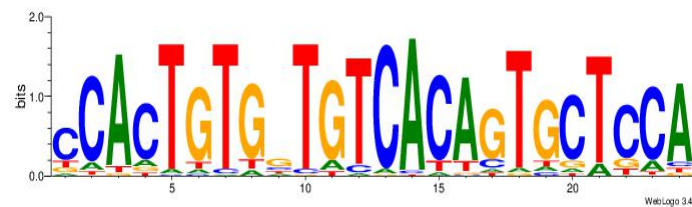
Alignment:

CCACTGTGVTGTCACAGTGCTCCA
 -----KKTGGGKGTKS-----

Original motif Consensus sequence: TGGAGCACTGTGACAVCACAGTGG



Reverse complement motif Consensus sequence: CCACTGTGVTGTCACAGTGCTCCA



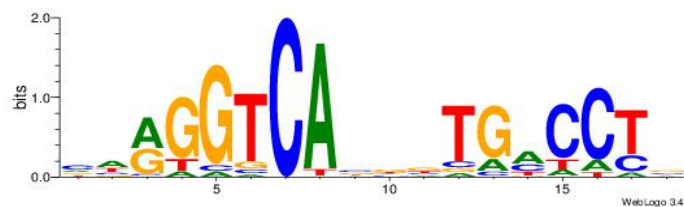
Dataset #: 1
 Motif ID: 9
 Motif name: ESR2
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 5

Number of overlap: 11
Similarity score: 0.032424

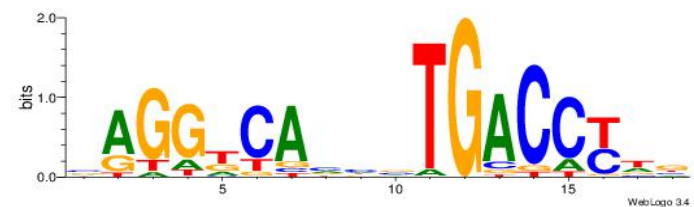
Alignment:

BAGGYCABHBTGACCKHV
---SRACYCCGAYR----

Original motif Consensus sequence: VHRGGTCABDBTGMCTB



Reverse complement motif Consensus sequence: BAGGYCABHBTGACCKHV

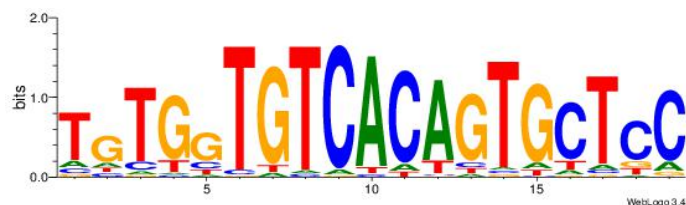


Dataset #: 2
Motif ID: 17
Motif name: TgTGgTGTCACAGTGCTCC
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 6
Number of overlap: 11
Similarity score: 0.0326389

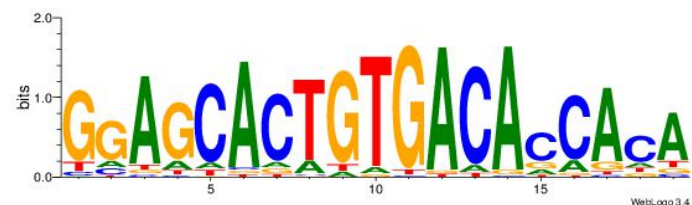
Alignment:

GGAGCACTGTGACACCACA
-----SRACYCCGAYR---

Original motif Consensus sequence: TGTGGTGTACAGTGCTCC



Reverse complement motif Consensus sequence: GGAGCACTGTGACACCACA

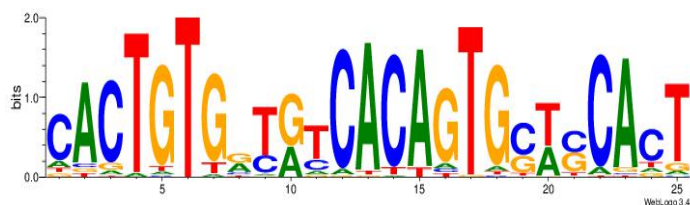


Dataset #: 2
 Motif ID: 22
 Motif name: CACTGTGrYrtCACAGTGswsCAcT
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 7
 Number of overlap: 11
 Similarity score: 0.0342172

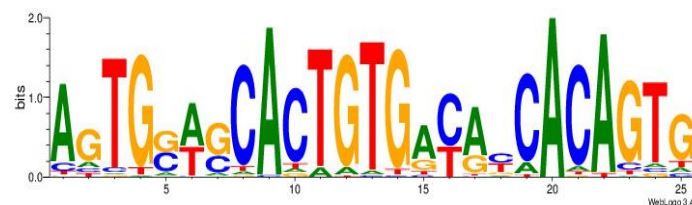
Alignment:

AGTGSWSCACTGTGAMAMCACAGTG
 -----SRACYCCGAYR-----

Original motif Consensus sequence: CACTGTGRTRTCACAGTGSWSCACT



Reverse complement motif Consensus sequence: AGTGSWSCACTGTGAMAMCACAGTG

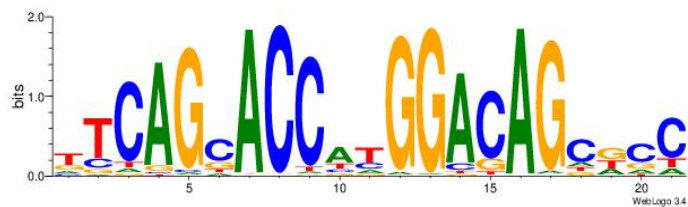


Dataset #: 1
 Motif ID: 7
 Motif name: REST
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 5
 Number of overlap: 11
 Similarity score: 0.0347246

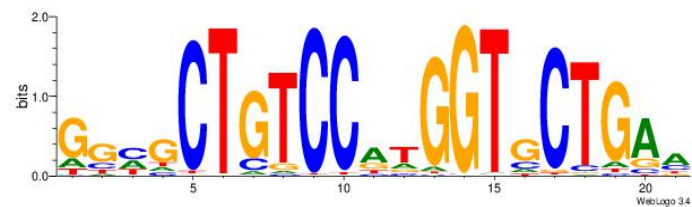
Alignment:

GYGCTGTCCATGGTGCTGAA
 -----KKTCCGGKGTGS-----

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC



Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA



Dataset #: 2
 Motif ID: 31
 Motif name: ctatacggacg
 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: 0.0430556

Alignment:
CTATACGGACG
SRACYCCGAYR

Original motif Consensus sequence: CTATACGGACG



Reverse complement motif Consensus sequence: CGTCCGTATAG

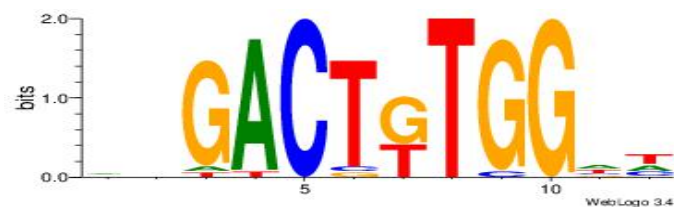
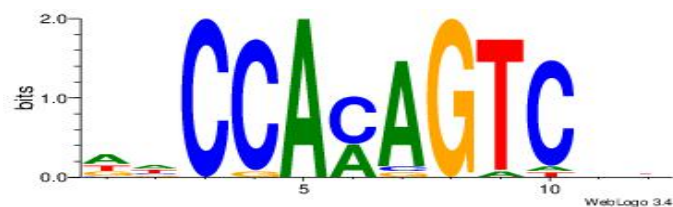


Dataset #: 2
Motif ID: 25
Motif name: wwCCAmAGTCmt
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 2
Number of overlap: 11
Similarity score: 0.0430556

Alignment:
DDCCAMAGTCHB
-KKTCCGKGTKS

Original motif Consensus sequence: DDCCAMAGTCHB

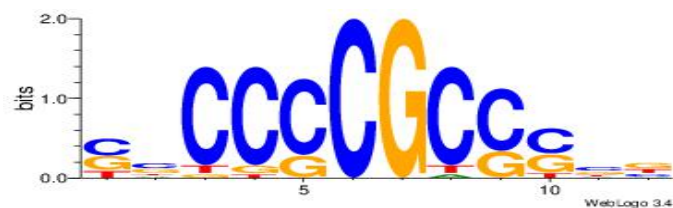
Reverse complement motif Consensus sequence: VDGACTRTGGDD



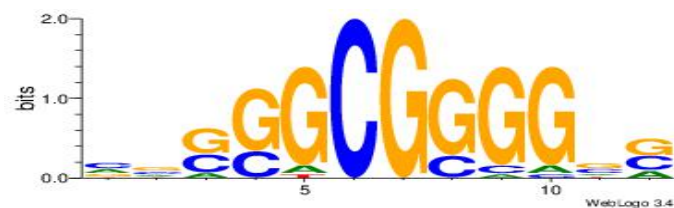
Dataset #: 2
 Motif ID: 24
 Motif name: ssCCCCGCSsk
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3
 Number of overlap: 10
 Similarity score: 0.513889

Alignment:
 BBSGGCGGGGBS-
 --KKTCGGKGTKS

Original motif Consensus sequence: SBCCCCGCCSBB



Reverse complement motif Consensus sequence: BBSGGCGGGGBS



Dataset #: 2
 Motif ID: 18

Motif name:	sscCCCGCGcs
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:	0.535703

Alignment:

-SBCGCGGGGSB
 KKTCGGKGTKS-

Original motif Consensus sequence: BSCCCCGCGBS



Reverse complement motif Consensus sequence: SBCGCGGGGSB



Results created by MOTIFSIM on 09-23-2015 12:19:03
 Runtime: 43.9155 seconds.

MOTIFSIM is written by Ngoc Tam L. Tran
 Motif logo generated by [weblogo](http://weblogo.threeplusone.com)