



MOTIFSIM - MOTIF SIMilarity Detection Tool

Version 2.2

INPUT

Input Parameters

Number of files:	2
Number of top significant motifs:	1
Number of best matches:	1
Similarity cutoff \geq	0.75
Matching motif database:	Jaspar Core
Motif tree:	Yes
Combined similar motifs:	Yes
Output file type:	All
Output file format:	All

Input files and motif counts

File name	Count of motifs	Dataset number
U20231121_R_11-21-23_1450_InsertFile1.txt	57	1
U20231121_R_11-21-23_1450_InsertFile2.txt	57	2

RESULTS

Best Matches in Database for Each Motif (Highest to Lowest)

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

Original motif

Consensus sequence: YYRCCAATCAGAGV



Reverse complement motif

Consensus sequence: VCTCTGATTGGKKKM



Best Matches for Motif ID 1 (Highest to Lowest)

Motif ID:	MA0060.2
Motif name:	NFYA
Taxon:	Vertebrates
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	15
Similarity score:	0.0229578

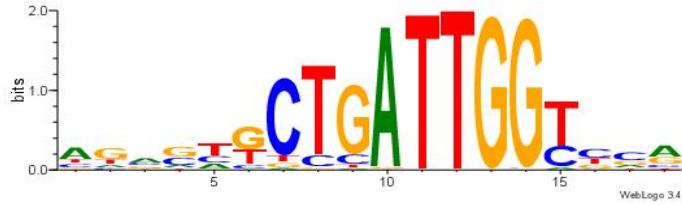
Alignment:

```
KVBACCAATCAGYMSBCT  
---VCTCTGATTGGKKKM
```

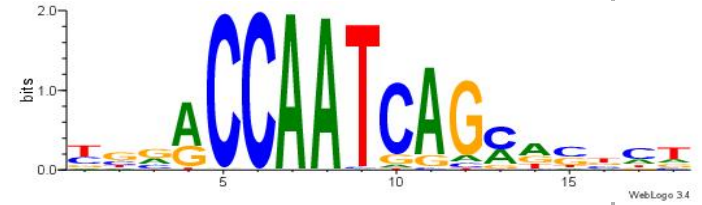
Original motif

Reverse complement motif

Consensus sequence: AGVSYKCTGATTGGTBVR



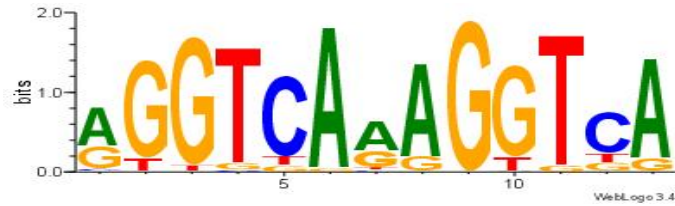
Consensus sequence: KVBACCAATCAGYMSBCT



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

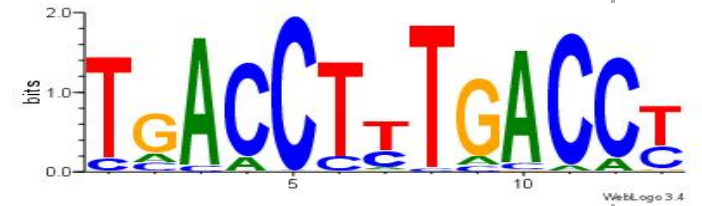
Original motif

Consensus sequence: RGGTCARAGGTCA



Reverse complement motif

Consensus sequence: TGACCTKTGACCK



Best Matches for Motif ID 2 (Highest to Lowest)

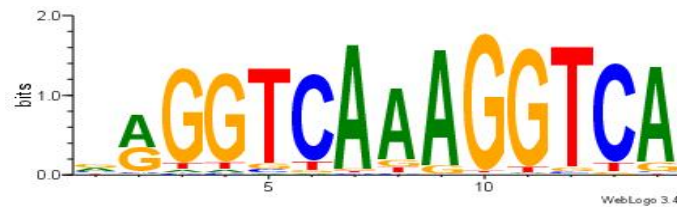
Motif ID:	MA0677.1
Motif name:	Nr2f6
Taxon:	Vertebrates
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	13
Similarity score:	0

Alignment:

VRGGTCAAAGGTCA
-RGGTCARAGGTCA

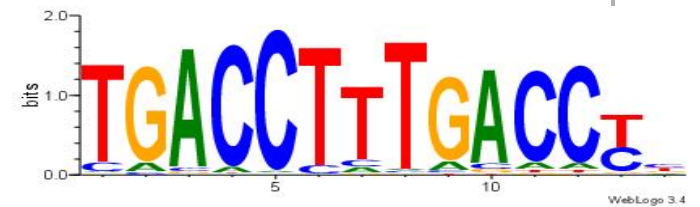
Original motif

Consensus sequence: VRGGTCAAAGGTCA



Reverse complement motif

Consensus sequence: TGACCTTTGACCKV



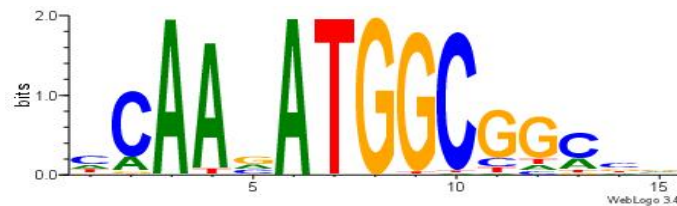
Dataset #: 1

Motif ID: 3

Motif name: Motif 3

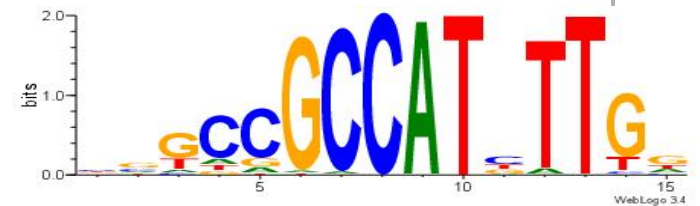
Original motif

Consensus sequence: HCAAVATGGCGGBV



Reverse complement motif

Consensus sequence: VBGCCGCCATVTTGD



Best Matches for Motif ID 3 (Highest to Lowest)

Motif ID:	MA0570.1
Motif name:	ABF1
Taxon:	Plants
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif

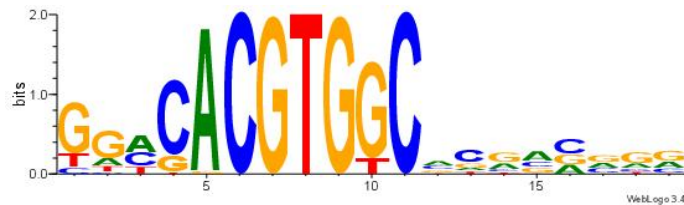
Direction: Backward
Position number: 4
Number of overlap: 15
Similarity score: 0.0784137

Alignment:

GGMCACGTGGCVCRRVVGV
-HCAAVATGGCGGCBV---

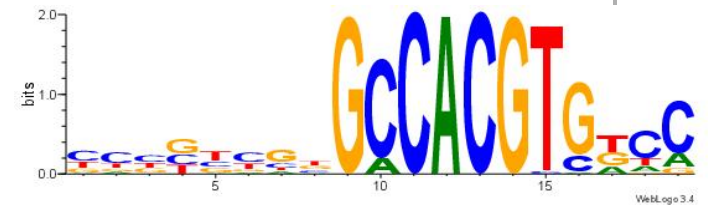
Original motif

Consensus sequence: GGMCACGTGGCVCRRVVGV



Reverse complement motif

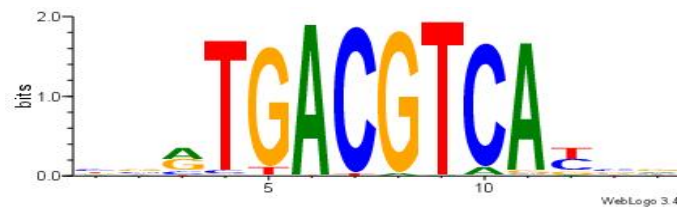
Consensus sequence: VCVVBMGBGCCACGTGYCC



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

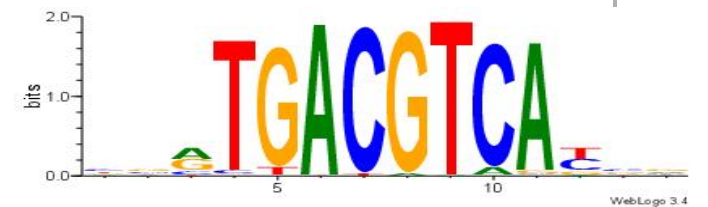
Original motif

Consensus sequence: BBRTGACGTCA



Reverse complement motif

Consensus sequence: VVMTGACGTCAKBB



Best Matches for Motif ID 4 (Highest to Lowest)

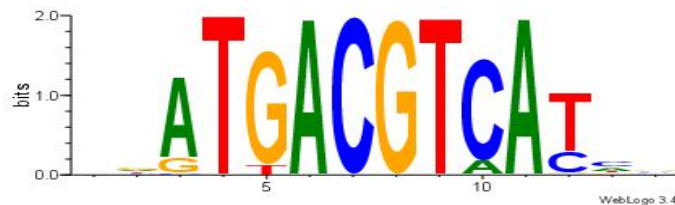
Motif ID: [MA0834.1](#)

Motif name: ATF7
 Taxon: Vertebrates
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0.0169411

Alignment:
 BDATGACGTCATHV
 BBRTGACGTCAYVV

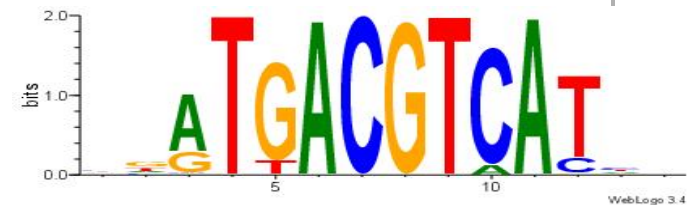
Original motif

Consensus sequence: BDATGACGTCATHV



Reverse complement motif

Consensus sequence: VDATGACGTCATHB



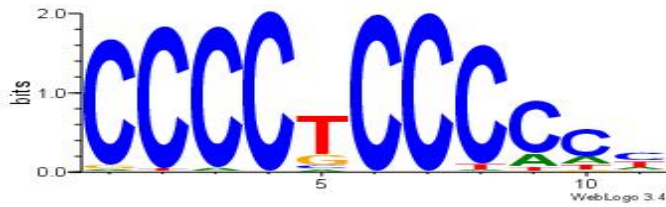
Dataset #: 1 Motif ID: 5 Motif name: Motif 5

Original motif

Consensus sequence: CCCCTCCCCCY

Reverse complement motif

Consensus sequence: KGGGGAGGGG



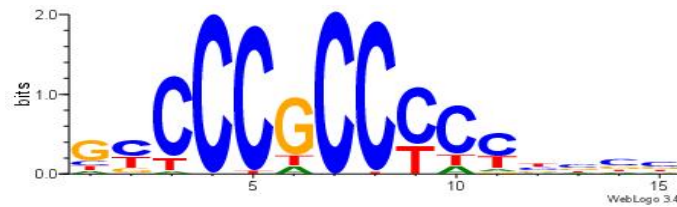
Best Matches for Motif ID 5 (Highest to Lowest)

Motif ID: [MA0516.1](#)
 Motif name: SP2
 Taxon: Vertebrates
 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: 0.0384687

Alignment:
 GYCCCGCCYCYBBBB
 -CCCCTCCCCCY---

Original motif

Consensus sequence: GYCCCGCCYCYBBBB



Reverse complement motif

Consensus sequence: BBBVKGKGGCGGGKC



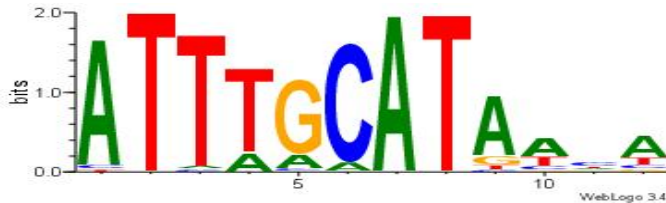
Dataset #: 1

Motif ID: 6

Motif name: Motif 6

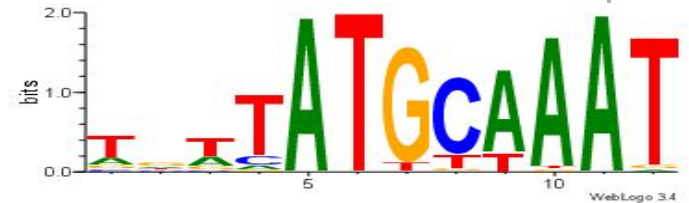
Original motif

Consensus sequence: ATTTGCATAWHA



Reverse complement motif

Consensus sequence: TDWTATGCAAAT



Best Matches for Motif ID 6 (Highest to Lowest)

Motif ID:	MA0627.1
Motif name:	Pou2f3
Taxon:	Vertebrates
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	5
Number of overlap:	12
Similarity score:	0.0149217

Alignment:

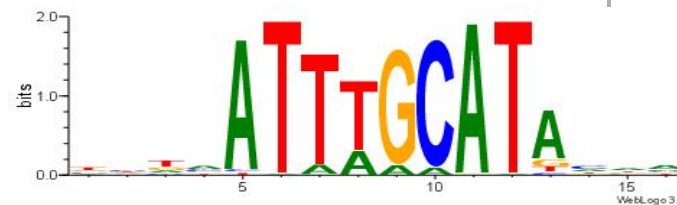
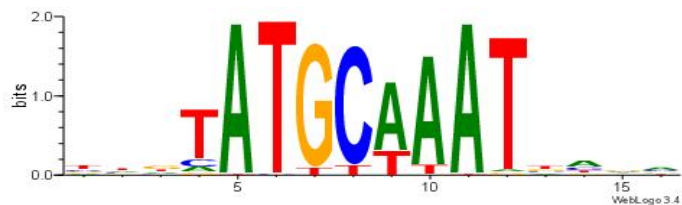
```
BHHVATTTGCATAHHV  
----ATTTGCATAWHA
```

Original motif

Consensus sequence: BHDTATGCAAATBHDV

Reverse complement motif

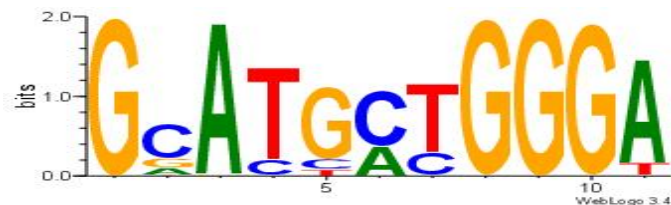
Consensus sequence: BHHVATTTGCATAHHV



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

Original motif

Consensus sequence: GCATGMTGGGA



Reverse complement motif

Consensus sequence: TCCCARCATGC



Best Matches for Motif ID 7 (Highest to Lowest)

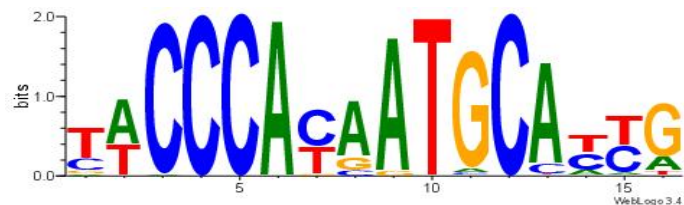
Motif ID:	MA0088.2
Motif name:	ZNF143
Taxon:	Vertebrates
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	2
Number of overlap:	11
Similarity score:	0.0572813

Alignment:

CMMTGCATTKTGGGWA
 ----GCATGMTGGGA-

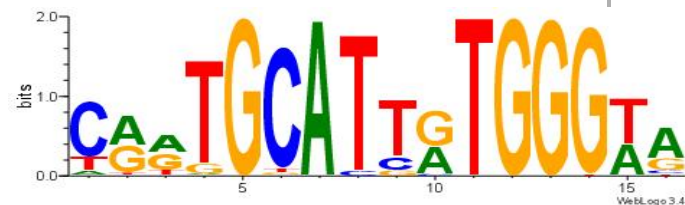
Original motif

Consensus sequence: TWCCCAAYAATGCAYYG



Reverse complement motif

Consensus sequence: CMMTGCATTKTGGGWA



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

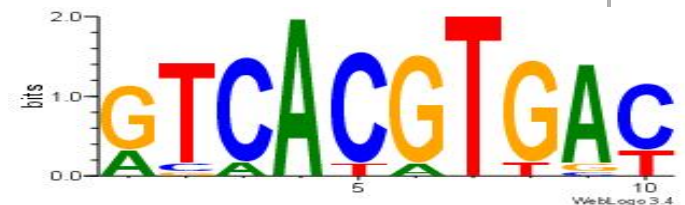
Original motif

Consensus sequence: GTCACGTGAC



Reverse complement motif

Consensus sequence: GTCACGTGAC



Best Matches for Motif ID 8 (Highest to Lowest)

Motif ID:	MA0636.1
Motif name:	BHLHE41
Taxon:	Vertebrates
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: 0.00818767

Alignment:

RTCACGTGAC

GTCACGTGAC

Original motif

Consensus sequence: RTCACGTGAC



Reverse complement motif

Consensus sequence: GTCACGTGAM



Dataset #: 1

Motif ID: 9

Motif name: Motif 9

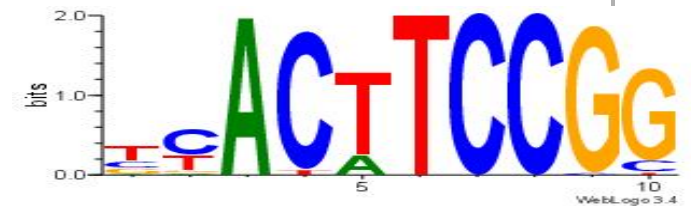
Original motif

Consensus sequence: CCGGAAGTRA



Reverse complement motif

Consensus sequence: TMACTTCCGG



Best Matches for Motif ID 9 (Highest to Lowest)

Motif ID:	MA0640.1
Motif name:	ELF3
Taxon:	Vertebrates
Matching format of first motif:	Original Motif

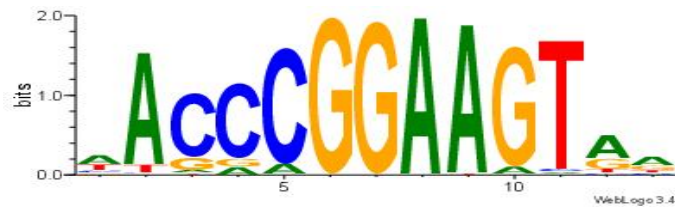
Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 10
 Similarity score: 0.0120558

Alignment:

WACCCGGAAGTAD
 ---CCGGAAGTRA

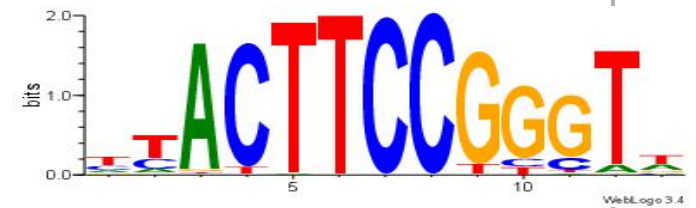
Original motif

Consensus sequence: WACCCGGAAGTAD



Reverse complement motif

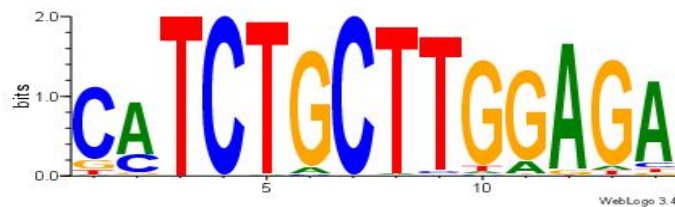
Consensus sequence: DTA C T T C C G G G T W



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

Original motif

Consensus sequence: CATCTGCTTGGAGA



Reverse complement motif

Consensus sequence: TCTCCAAGCAGATG



Best Matches for Motif ID 10 (Highest to Lowest)

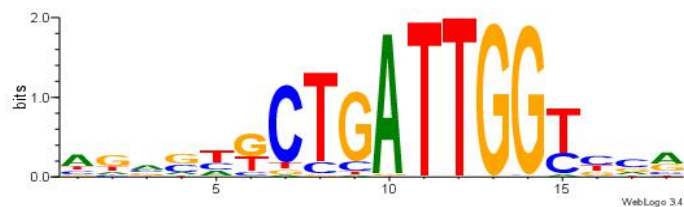
Motif ID: [MA0060.2](#)
 Motif name: NFYA
 Taxon: Vertebrates
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 14
 Similarity score: 0.0479869

Alignment:

AGVSYKCTGATTGGTBVR
 ---CATCTGCTTGGAGA-

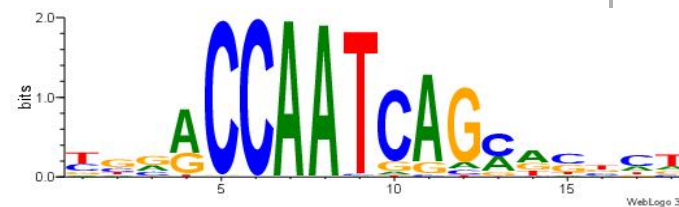
Original motif

Consensus sequence: AGVSYKCTGATTGGTBVR



Reverse complement motif

Consensus sequence: KVBACCAATCAGYMSBCT



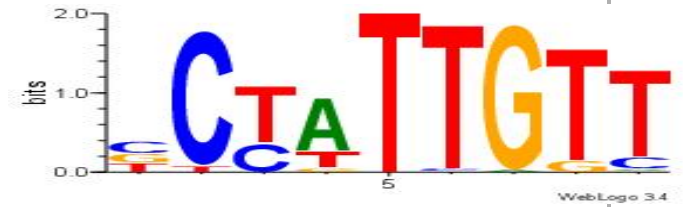
Dataset #: 1 Motif ID: 11 Motif name: Motif 11

Original motif

Consensus sequence: AACATR GV

Reverse complement motif

Consensus sequence: VCKATT GTT



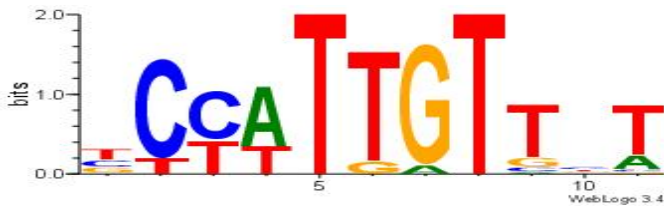
Best Matches for Motif ID 11 (Highest to Lowest)

Motif ID: [MA0445.1](#)
 Motif name: D
 Taxon: Insects
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 9
 Similarity score: 0.0214352

Alignment:
 ABAACAATKGV
 --ACAATR GV

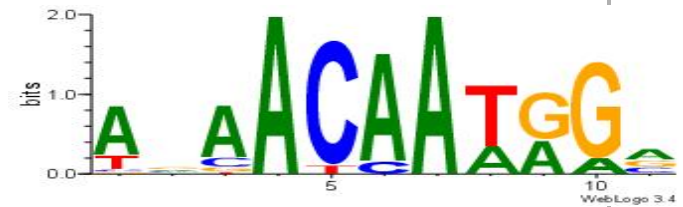
Original motif

Consensus sequence: BCYATTGTTBT



Reverse complement motif

Consensus sequence: ABAACAATKGV



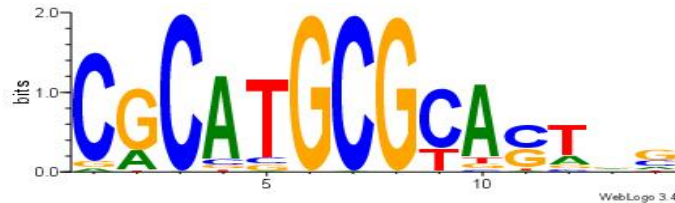
Dataset #: 1

Motif ID: 12

Motif name: Motif 12

Original motif

Consensus sequence: CGCATGCGCASTVS



Reverse complement motif

Consensus sequence: SVASTGCGCATGCG



Best Matches for Motif ID 12 (Highest to Lowest)

Motif ID: [MA0376.1](#)
Motif name: RTG3
Taxon: Fungi
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: 0.0498099

Alignment:

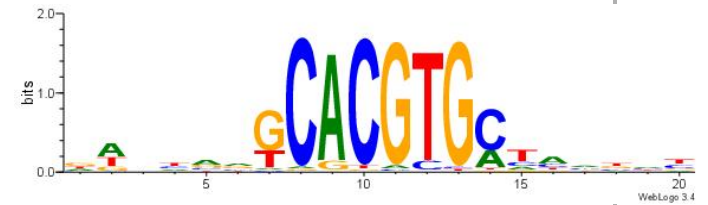
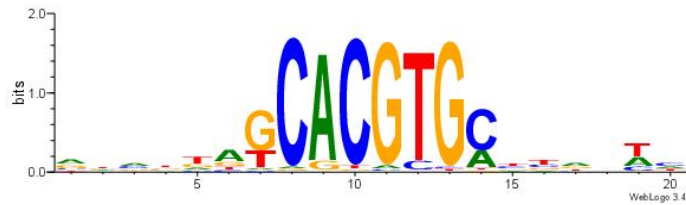
```
VDVBDAGCACGTGCBBDVWH  
-SVASTGCGCATGCG-----
```

Original motif

Consensus sequence: VDVBDAGCACGTGCBBDVWH

Reverse complement motif

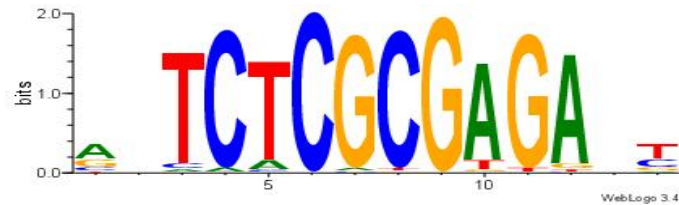
Consensus sequence: DWVDVVGACGTGCTDVBDB



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

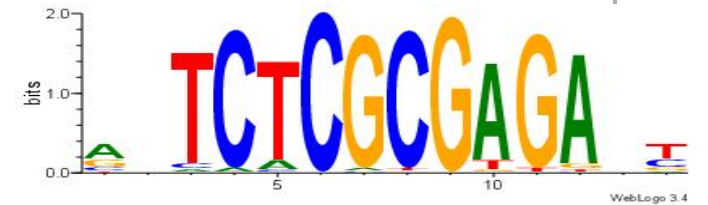
Original motif

Consensus sequence: RVTCTCGCGAGABY



Reverse complement motif

Consensus sequence: MVTCTCGCGAGABK



Best Matches for Motif ID 13 (Highest to Lowest)

Motif ID:	MA0154.3
Motif name:	EBF1
Taxon:	Vertebrates
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	14
Similarity score:	0.0477452

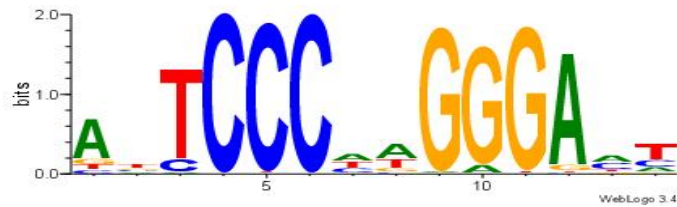
Alignment:

```

AYTCCCWHGGGAVT
MVTCTCGCGAGABK
  
```

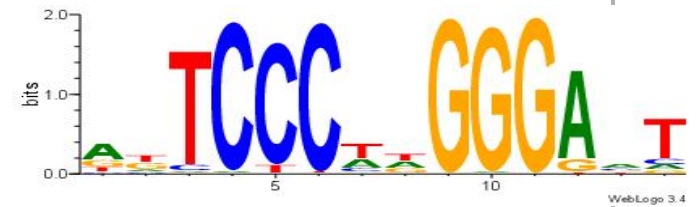

Original motif

Consensus sequence: ABTCCCHWGGGAMT



Reverse complement motif

Consensus sequence: AYTCCCWHGGGAVT



Dataset #: 1

Motif ID: 14

Motif name: Motif 14

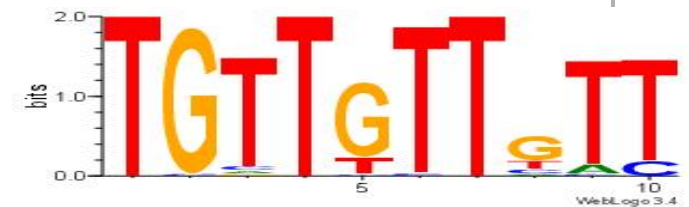
Original motif

Consensus sequence: AACAAACA



Reverse complement motif

Consensus sequence: TGTTGTTGTT



Best Matches for Motif ID 14 (Highest to Lowest)

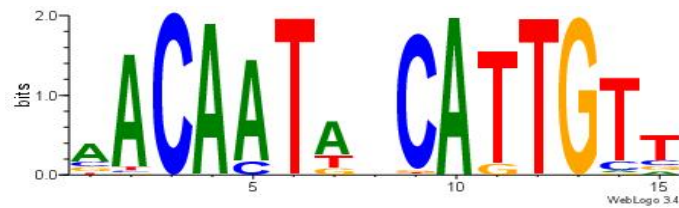
Motif ID:	MA0870.1
Motif name:	Sox1
Taxon:	Vertebrates
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	10
Similarity score:	0.0597499

Alignment:

```
ACAATGBTATTGTT
-----TGTTGTTGTT
```

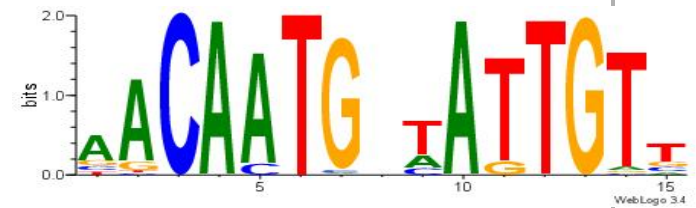
Original motif

Consensus sequence: ACAATAVCATTGTT



Reverse complement motif

Consensus sequence: ACAATGBTATTGTT



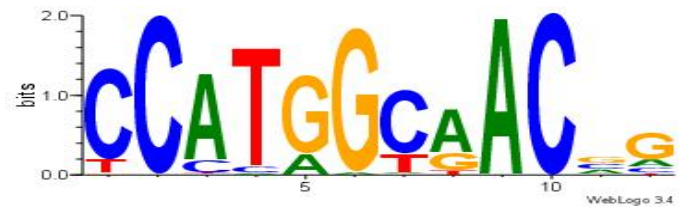
Dataset #: 1

Motif ID: 15

Motif name: Motif 15

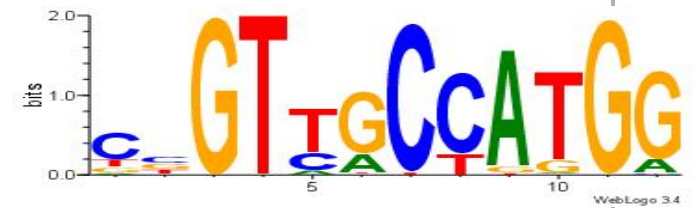
Original motif

Consensus sequence: CCATGGCAACVG



Reverse complement motif

Consensus sequence: CVGTTGCCATGG



Best Matches for Motif ID 15 (Highest to Lowest)

Motif ID:	MA0138.2
Motif name:	REST
Taxon:	Vertebrates
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement

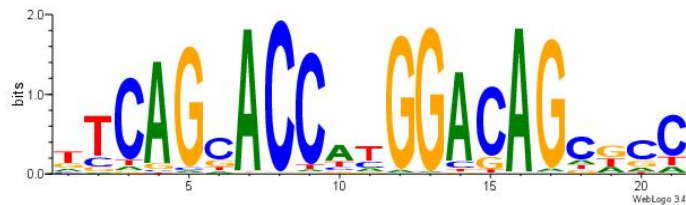
Direction: Backward
 Position number: 8
 Number of overlap: 12
 Similarity score: 0.0637808

Alignment:

GGYGCTGTCCATGGTGCTGAA
 --CVGTTGCCATGG-----

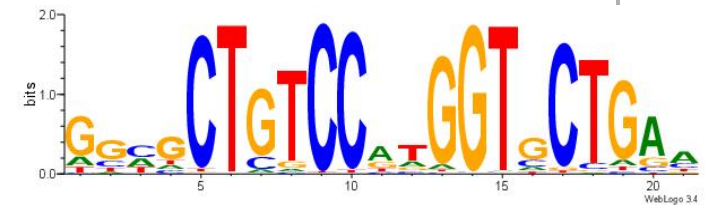
Original motif

Consensus sequence: TTCAGCACCATGGACAGCKCC



Reverse complement motif

Consensus sequence: GGYGCTGTCCATGGTGCTGAA



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

Original motif

Consensus sequence: TCCCGCCVW



Reverse complement motif

Consensus sequence: WBGCGGGA



Best Matches for Motif ID 16 (Highest to Lowest)

Motif ID: [MA0758.1](#)

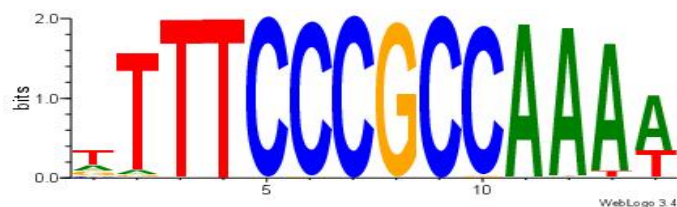
Motif name: E2F7
 Taxon: Vertebrates
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 4
 Number of overlap: 9
 Similarity score: 0.0204536

Alignment:

TTTTGGCGGGAAAA
 --WBGGCGGGA---

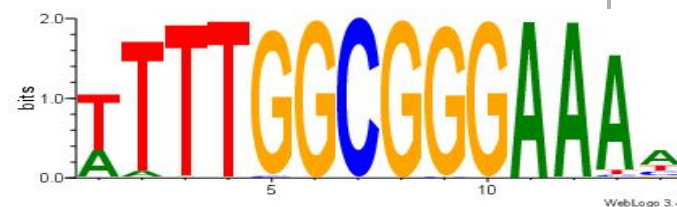
Original motif

Consensus sequence: TTTTCCCGCCAAA



Reverse complement motif

Consensus sequence: TTTTGGCGGGAAAA



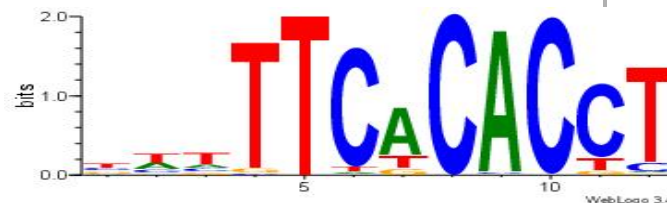
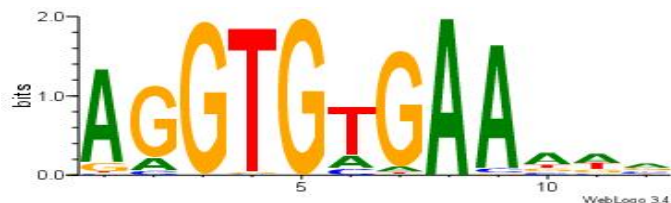
Dataset #: 1 Motif ID: 17 Motif name: Motif 17

Original motif

Consensus sequence: AGGTGTGAAWV

Reverse complement motif

Consensus sequence: BWTTTCACACCT



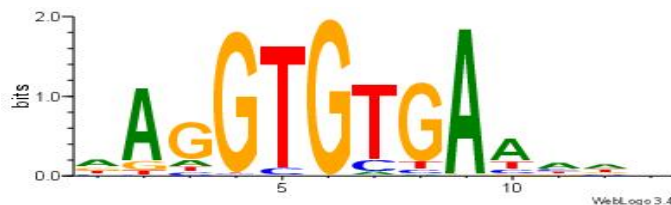
Best Matches for Motif ID 17 (Highest to Lowest)

Motif ID: [MA0800.1](#)
 Motif name: EOMES
 Taxon: Vertebrates
 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: 0.0126084

Alignment:
 HDHTTCACACCTD
 BWTTTCACACCT-

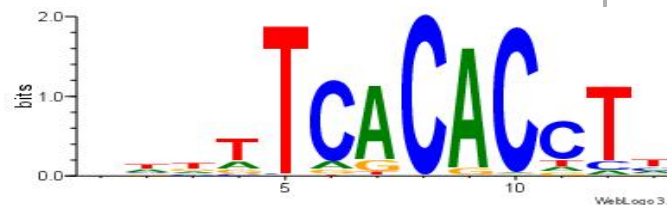
Original motif

Consensus sequence: DAGGTGTGAAHDH



Reverse complement motif

Consensus sequence: HDHTTCACACCTD



Dataset #: 1

Motif ID: 18

Motif name: Motif 18

Original motif

Consensus sequence: GMTAATTA



Reverse complement motif

Consensus sequence: TAATTAYC



Best Matches for Motif ID 18 (Highest to Lowest)

Motif ID: [MA0904.1](#)
Motif name: Hoxb5
Taxon: Vertebrates
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 7
Number of overlap: 8
Similarity score: 0.0176518

Alignment:

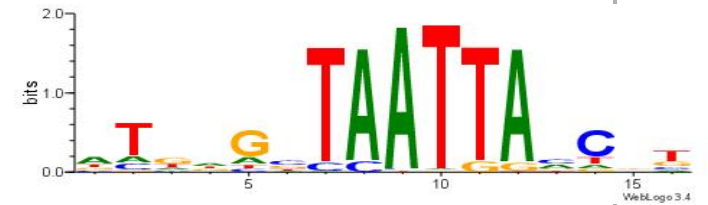
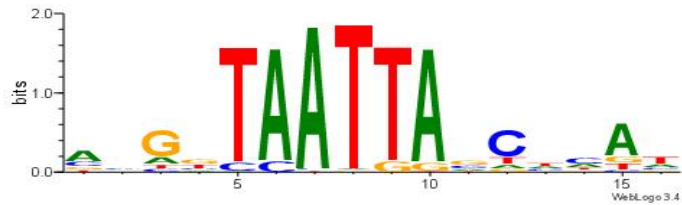
```
HTDHGVTAAATTABCDT  
-----TAATTAYC--
```

Original motif

Consensus sequence: AHGBTAATTAVCHHAH

Reverse complement motif

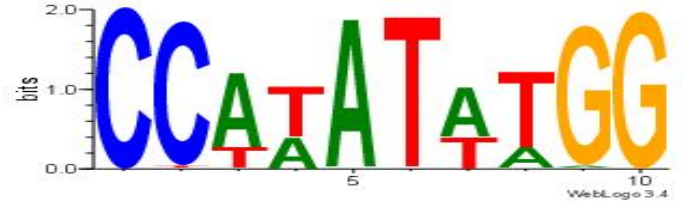
Consensus sequence: HTDHGVTAAATTABCDT



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

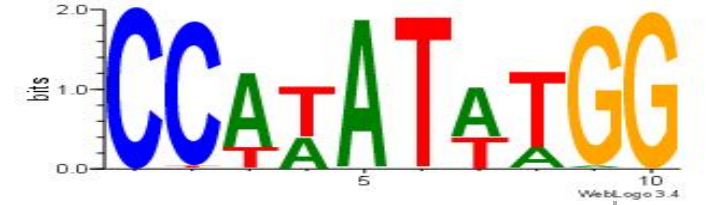
Original motif

Consensus sequence: CCAWATWTGG



Reverse complement motif

Consensus sequence: CCAWATWTGG



Best Matches for Motif ID 19 (Highest to Lowest)

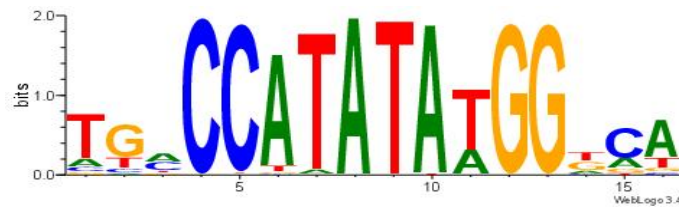
Motif ID:	MA0083.3
Motif name:	SRF
Taxon:	Vertebrates
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	4
Number of overlap:	10
Similarity score:	0

Alignment:

TGMCCATATATGGKCA
---CCAWATWTGG---

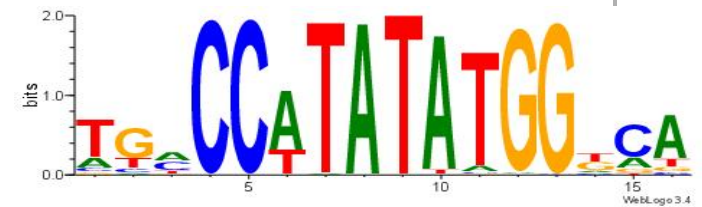
Original motif

Consensus sequence: TGMCCATATATGGKCA



Reverse complement motif

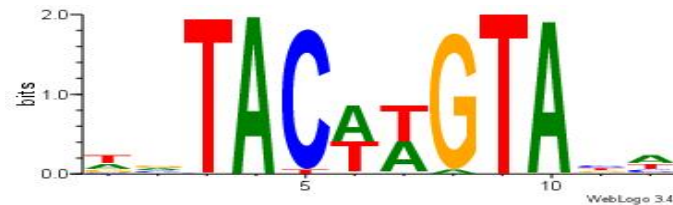
Consensus sequence: TGRCCATATATGGYCA



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

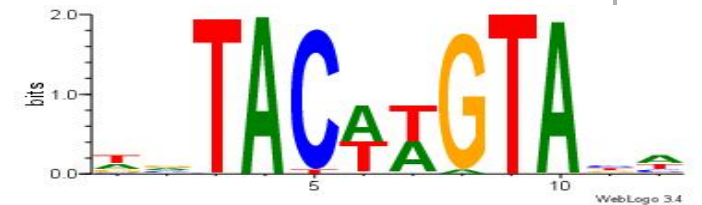
Original motif

Consensus sequence: DVTACWWGTABH



Reverse complement motif

Consensus sequence: HBTACWWGTAVD



Best Matches for Motif ID 20 (Highest to Lowest)

Motif ID:	MA0941.1
Motif name:	ABF2
Taxon:	Plants
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	12

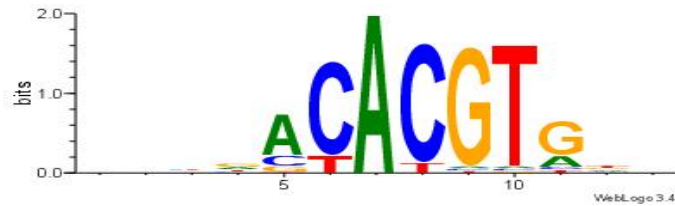
Similarity score: 0.0341371

Alignment:

DDCACGTGTHHBB
HBTACWWGTAVD-

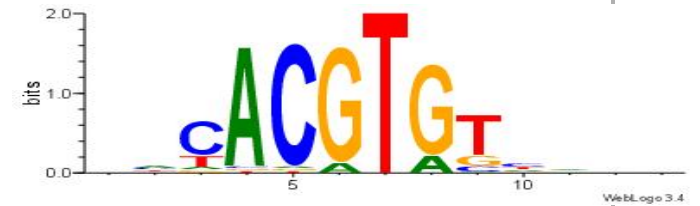
Original motif

Consensus sequence: BDBDACACGTGDB



Reverse complement motif

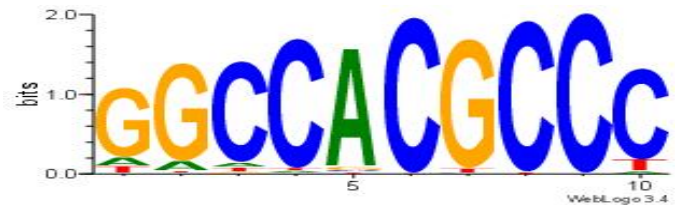
Consensus sequence: DDCACGTGTHHBB



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

Original motif

Consensus sequence: GGCCACGCC



Reverse complement motif

Consensus sequence: GGGCGTGGCC



Best Matches for Motif ID 21 (Highest to Lowest)

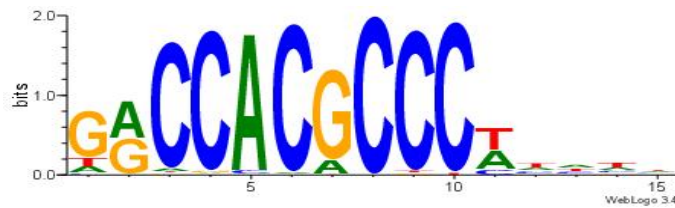
Motif ID: [MA0742.1](#)
Motif name: Klf12
Taxon: Vertebrates
Matching format of first motif: Original Motif

Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 10
 Similarity score: 0

Alignment:
 GRCCACGCCCWHHHH
 GGCCACGCCC-----

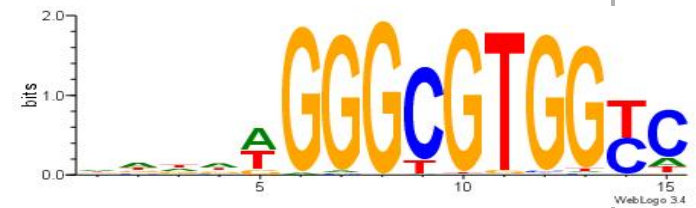
Original motif

Consensus sequence: GRCCACGCCCWHHHH



Reverse complement motif

Consensus sequence: HHHHWGGGCGTGGKC



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

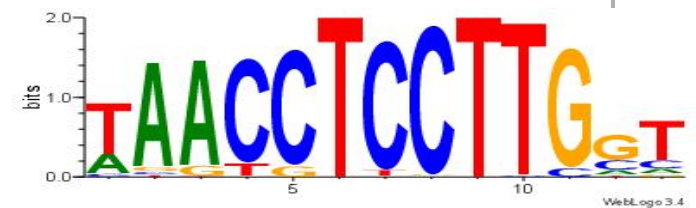
Original motif

Consensus sequence: ACCAAGGAGGTTA



Reverse complement motif

Consensus sequence: TAACCTCCTTGGT



Best Matches for Motif ID 22 (Highest to Lowest)

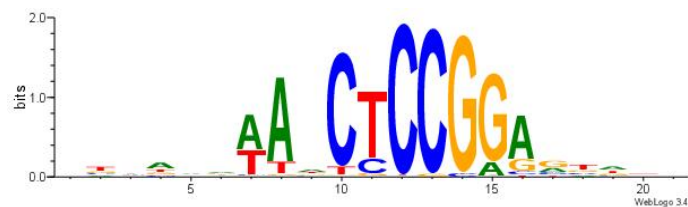
Motif ID: [MA0308.1](#)
 Motif name: GSM1
 Taxon: Fungi
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 4
 Number of overlap: 13
 Similarity score: 0.0653916

Alignment:

HDDVVTCCGGAGDTWDDDHVH
 ---ACCAAGGAGGTTA-----

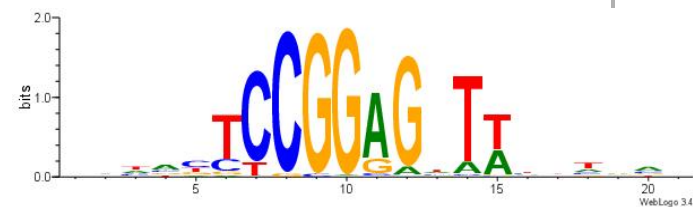
Original motif

Consensus sequence: HBHDDDWADCTCCGGAVBDDH



Reverse complement motif

Consensus sequence: HDDVVTCCGGAGDTWDDDHVH



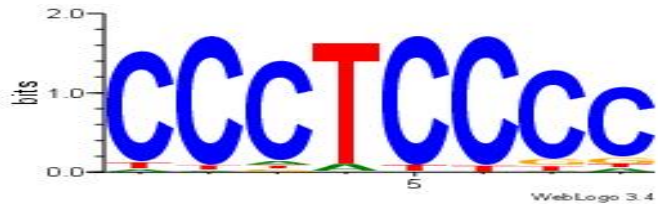
Dataset #: 1 Motif ID: 23 Motif name: Motif 23

Original motif

Consensus sequence: CCCTCCCC

Reverse complement motif

Consensus sequence: GGGGAGGG



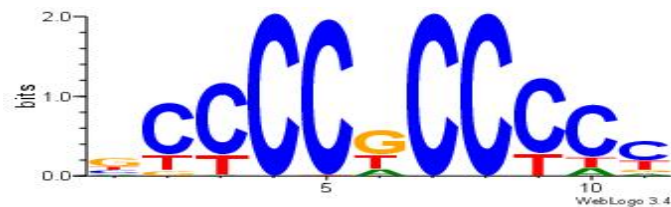
Best Matches for Motif ID 23 (Highest to Lowest)

Motif ID: [MA0079.3](#)
 Motif name: SP1
 Taxon: Vertebrates
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 8
 Similarity score: 0.0246016

Alignment:
 BCCCCKCCCCC
 --CCCTCCCC-

Original motif

Consensus sequence: BCCCCKCCCCC



Reverse complement motif

Consensus sequence: GGGGYGGGGB



Dataset #: 1

Motif ID: 24

Motif name: Motif 24

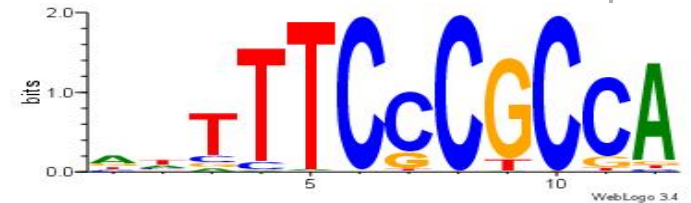
Original motif

Consensus sequence: TGGCGGAAADH



Reverse complement motif

Consensus sequence: HDTTCCCGCCA



Best Matches for Motif ID 24 (Highest to Lowest)

Motif ID:	MA0541.1
Motif name:	efl-1
Taxon:	Nematodes
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:	0.0282826

Alignment:

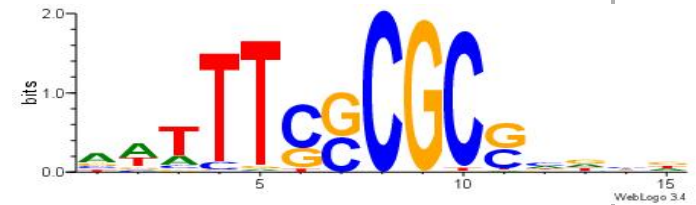
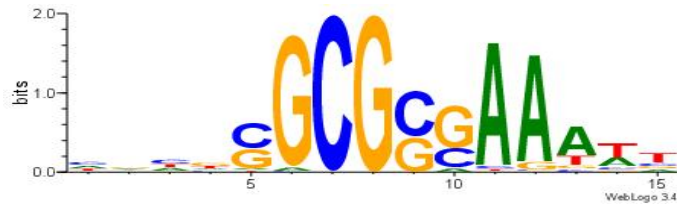
```
HDHDSGCGSGAAAWT  
---TGGCGGAAADH
```

Original motif

Consensus sequence: HDHDSGCGSGAAAWT

Reverse complement motif

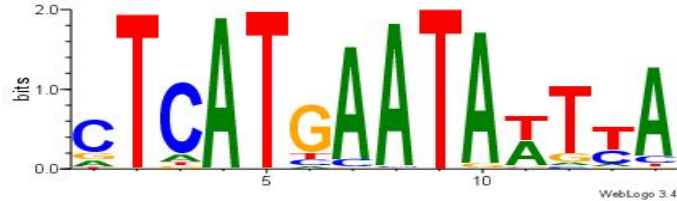
Consensus sequence: AWTTCSCGCSHDHD



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

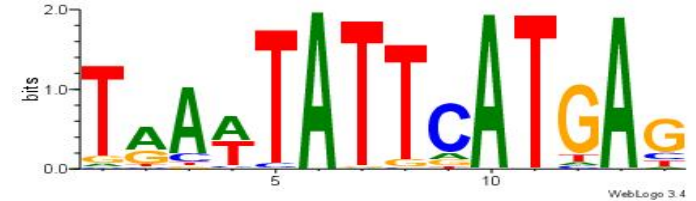
Original motif

Consensus sequence: CTCATGAATAWTYA



Reverse complement motif

Consensus sequence: TMAWTATTCATGAG



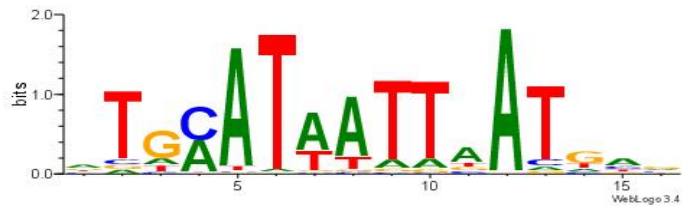
Best Matches for Motif ID 25 (Highest to Lowest)

Motif ID:	MA0791.1
Motif name:	POU4F3
Taxon:	Vertebrates
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:	0.0563832

Alignment:
 VHCATTAATWATRCAD
 --TMAWTATTCATGAG

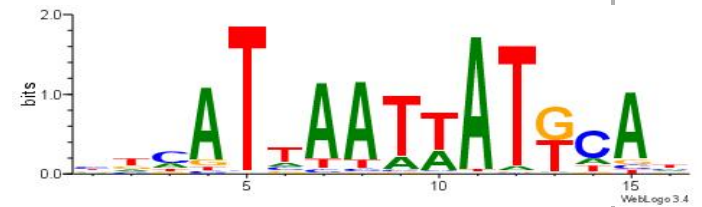
Original motif

Consensus sequence: DTGMATWATTAATGHV



Reverse complement motif

Consensus sequence: VHCATTAATWATRCAD



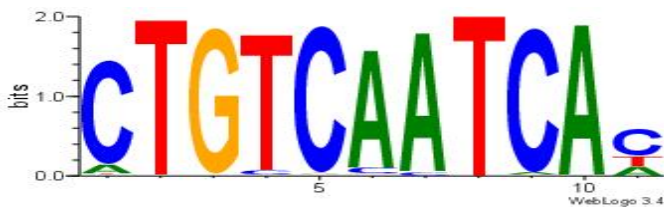
Dataset #: 1

Motif ID: 26

Motif name: Motif 26

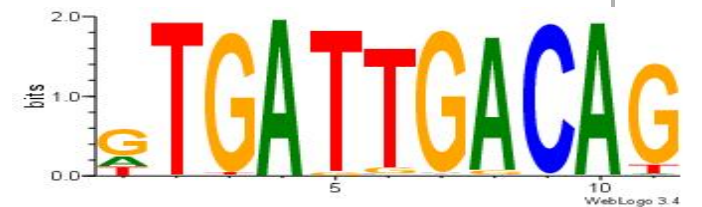
Original motif

Consensus sequence: CTGTCAATCAC



Reverse complement motif

Consensus sequence: GTGATTGACAG



Best Matches for Motif ID 26 (Highest to Lowest)

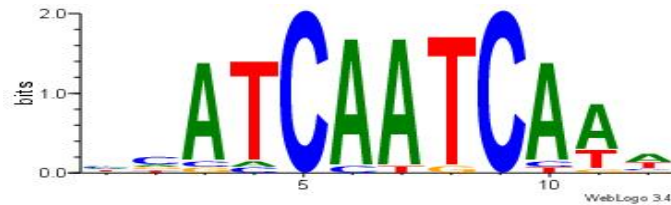
Motif ID:	MA0070.1
Motif name:	PBX1
Taxon:	Vertebrates
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	11
Similarity score:	0.0642241

Alignment:

WTTGATTGATBD
-GTGATTGACAG

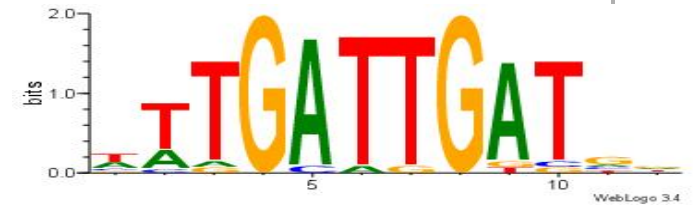
Original motif

Consensus sequence: HBATCAATCAAW



Reverse complement motif

Consensus sequence: WTTGATTGATBD



Dataset #: 1

Motif ID: 27

Motif name: Motif 27

Original motif

Consensus sequence: CAGGTAAG



Reverse complement motif

Consensus sequence: CTTACCTG



Best Matches for Motif ID 27 (Highest to Lowest)

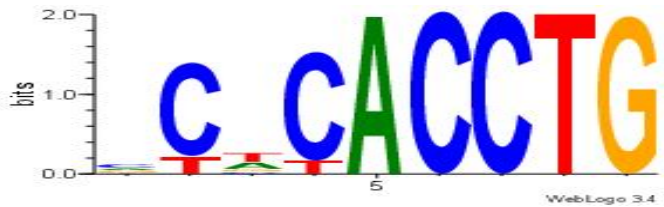
Motif ID:	MA0103.2
Motif name:	ZEB1
Taxon:	Vertebrates
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement

Direction: Forward
Position number: 1
Number of overlap: 8
Similarity score: 0.00667179

Alignment:
CAGGTG^WGV
CAGGTAAG-

Original motif

Consensus sequence: VCWCACCTG



Reverse complement motif

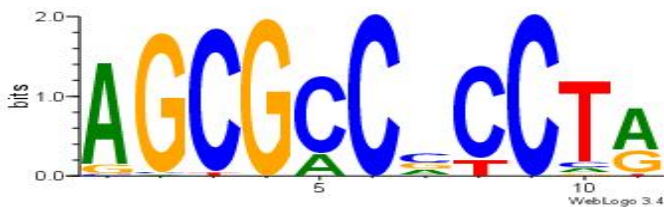
Consensus sequence: CAGGTG^WGV



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

Original motif

Consensus sequence: AGCGCCVCCTR



Reverse complement motif

Consensus sequence: KAGGVGGCGCT



Best Matches for Motif ID 28 (Highest to Lowest)

Motif ID: [MA0531.1](#)

Motif name: CTCF
 Taxon: Insects
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 5
 Number of overlap: 11
 Similarity score: 0.0422441

Alignment:

BCVMYAGRTGGCGCY
 ----KAGGVGGCGCT

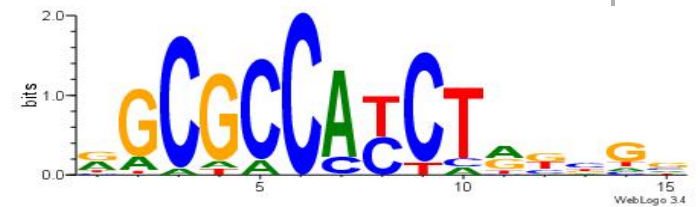
Original motif

Consensus sequence: BCVMYAGRTGGCGCY



Reverse complement motif

Consensus sequence: KGCGCCAKCTMRVGB



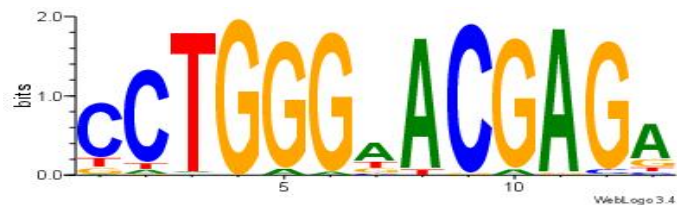
Dataset #: 1 Motif ID: 29 Motif name: Motif 29

Original motif

Consensus sequence: CCTGGGAACGAGA

Reverse complement motif

Consensus sequence: TCTCGTCCCAGG



Best Matches for Motif ID 29 (Highest to Lowest)

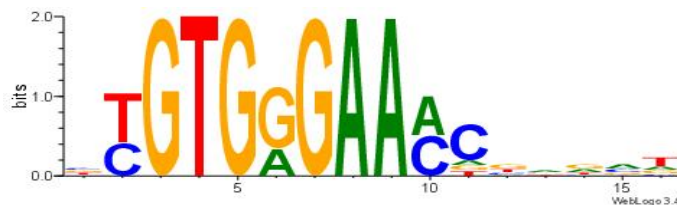
Motif ID: [MA0085.1](#)
 Motif name: Su(H)
 Taxon: Insects
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 13
 Similarity score: 0.0866213

Alignment:

BYGTGGGAAMCBDDVD
 -CCTGGGAACGAGA--

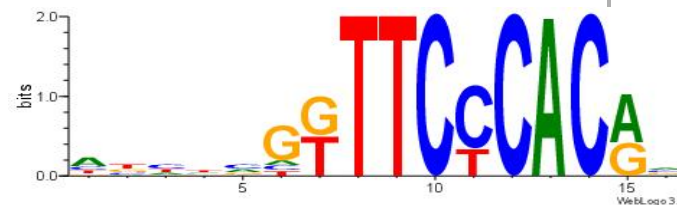
Original motif

Consensus sequence: BYGTGGGAAMCBDDVD



Reverse complement motif

Consensus sequence: DBHBBGYTTCCACMB



Dataset #: 1

Motif ID: 30

Motif name: Motif 30

Original motif

Consensus sequence: RTGACGTASD



Reverse complement motif

Consensus sequence: DSTACGTCAK



Best Matches for Motif ID 30 (Highest to Lowest)

Motif ID:	MA0097.1
Motif name:	bZIP911
Taxon:	Plants
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:	0.0406054

Alignment:

GRCCACGTCAKC

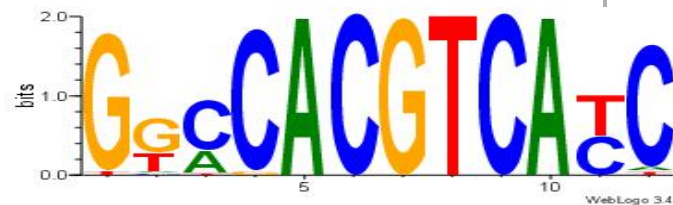
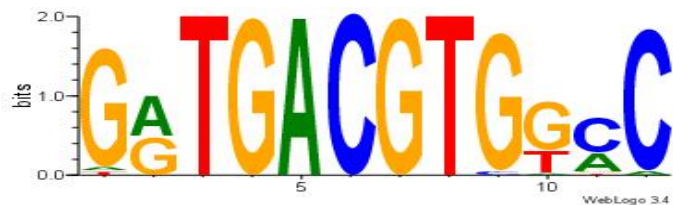
-DSTACGTCAK-

Original motif

Consensus sequence: GRTGACGTGGMC

Reverse complement motif

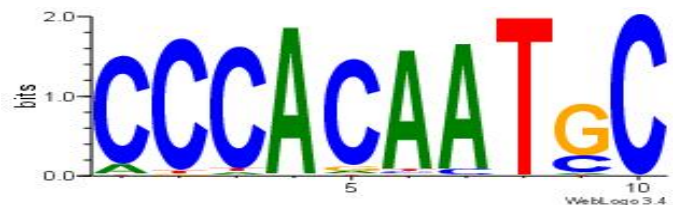
Consensus sequence: GRCCACGTCAKC



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

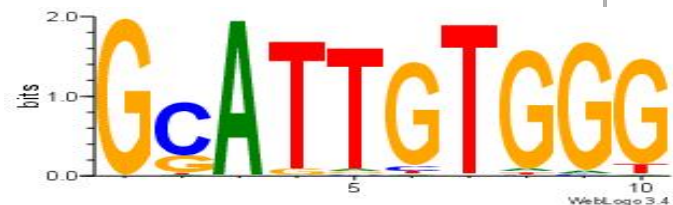
Original motif

Consensus sequence: CCCACAATGC



Reverse complement motif

Consensus sequence: GCATTGTGGG



Best Matches for Motif ID 31 (Highest to Lowest)

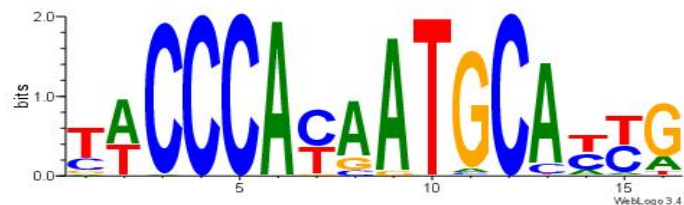
Motif ID:	MA0088.2
Motif name:	ZNF143
Taxon:	Vertebrates
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	5
Number of overlap:	10
Similarity score:	0.0155351

Alignment:

TWCCAYAATGCAYYG
--CCCACAATGC----

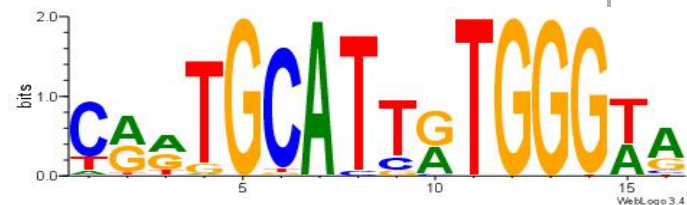
Original motif

Consensus sequence: TWCCAYAATGCAYYG



Reverse complement motif

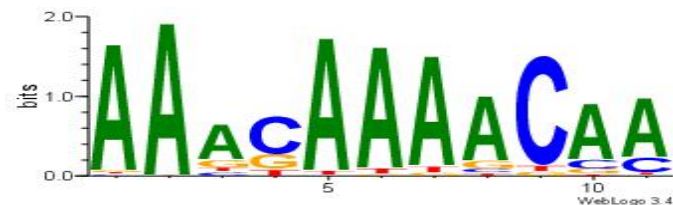
Consensus sequence: CMMTGCATTKTGGGWA



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

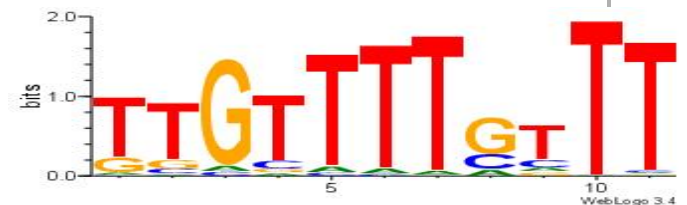
Original motif

Consensus sequence: AAACAAAACAA



Reverse complement motif

Consensus sequence: TTGTTTGT



Best Matches for Motif ID 32 (Highest to Lowest)

Motif ID:	MA0296.1
Motif name:	FKH1
Taxon:	Fungi
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	9

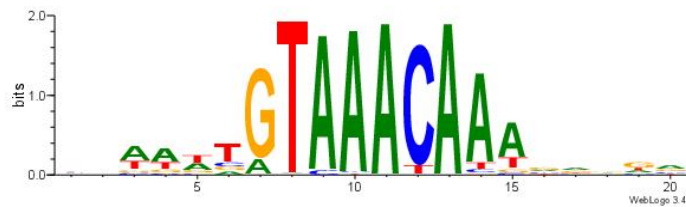
Number of overlap: 11
Similarity score: 0.0515149

Alignment:

BHHDVTTTGTTTACAWWWHV
-TTGTTTTGTTT-----

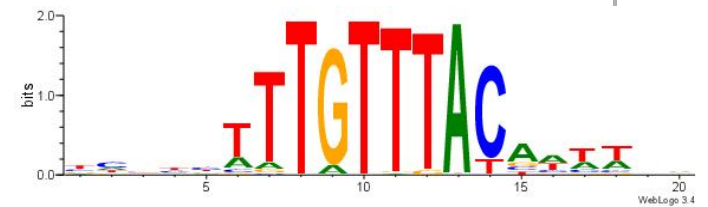
Original motif

Consensus sequence: BDWWWTGTAAACAAVDDD



Reverse complement motif

Consensus sequence: BHHDVTTTGTTTACAWWWHV



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

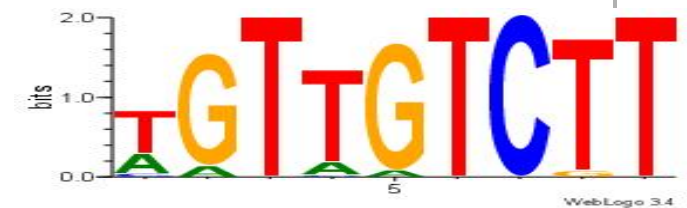
Original motif

Consensus sequence: AAGACAACA



Reverse complement motif

Consensus sequence: TGTTGTCTT



Best Matches for Motif ID 33 (Highest to Lowest)

Motif ID: [MA0029.1](#)
Motif name: Mecom
Taxon: Vertebrates

Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 9
 Similarity score: 0.0220224

Alignment:
 AAGAYAAGATAABA
 -----AAGACAACA

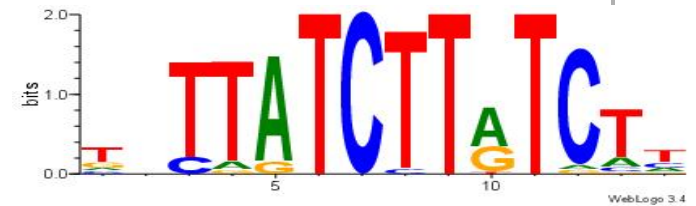
Original motif

Consensus sequence: AAGAYAAGATAABA



Reverse complement motif

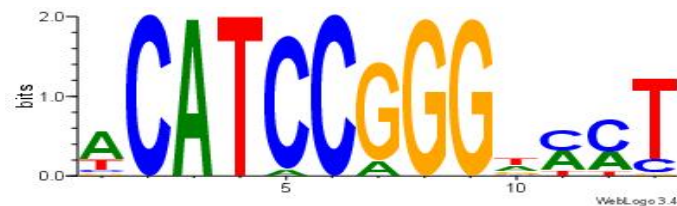
Consensus sequence: TBTTATCTTMTCTT



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

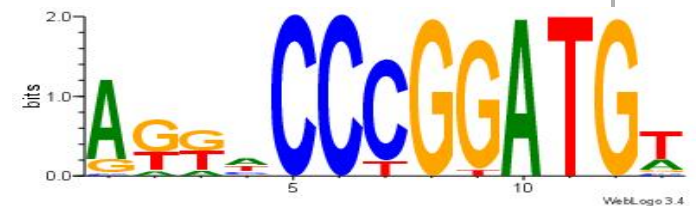
Original motif

Consensus sequence: ACATCCGGDMMT



Reverse complement motif

Consensus sequence: ARRDCCCGGATGT



Best Matches for Motif ID 34 (Highest to Lowest)

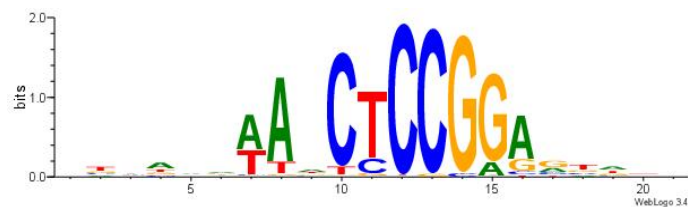
Motif ID: [MA0308.1](#)
 Motif name: GSM1
 Taxon: Fungi
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 8
 Number of overlap: 13
 Similarity score: 0.0730858

Alignment:

HDDVVTCCGGAGDTWDDDHVH
 -ARRDCCCGGATGT-----

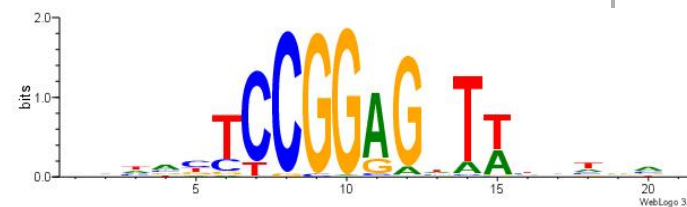
Original motif

Consensus sequence: HBHDDDWADCTCCGGAVBDDH



Reverse complement motif

Consensus sequence: HDDVVTCCGGAGDTWDDDHVH



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

Original motif

Consensus sequence: AAAAYAAACAA

Reverse complement motif

Consensus sequence: TTGTTTKTTTT



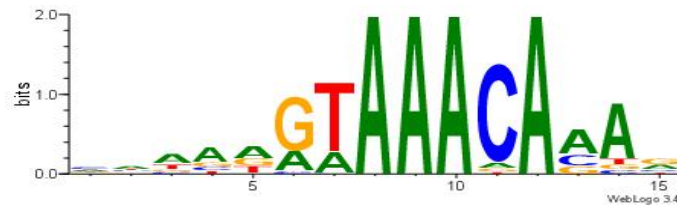
Best Matches for Motif ID 35 (Highest to Lowest)

Motif ID: [MA0481.1](#)
 Motif name: FOXP1
 Taxon: Vertebrates
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 11
 Similarity score: 0.0452708

Alignment:
 HHDADGTAAACAAAV
 --AAAAYAAACAA--

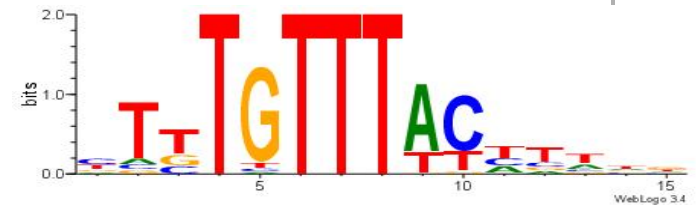
Original motif

Consensus sequence: HHDADGTAAACAAAV



Reverse complement motif

Consensus sequence: VTTTGTTTACDTHD



Dataset #: 1

Motif ID: 36

Motif name: Motif 36

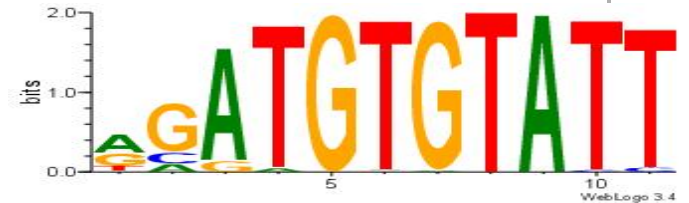
Original motif

Consensus sequence: AATACACATCY



Reverse complement motif

Consensus sequence: MGATGTGTATT



Best Matches for Motif ID 36 (Highest to Lowest)

Motif ID: [MA0040.1](#)
Motif name: Foxq1
Taxon: Vertebrates
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: 0.0480007

Alignment:

HATTGTTTATW

AATACACATCY

Original motif

Consensus sequence: HATTGTTTATW

Reverse complement motif

Consensus sequence: WATAACAATH



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

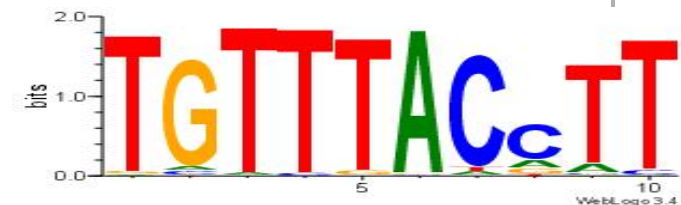
Original motif

Consensus sequence: AAGGTTAACA



Reverse complement motif

Consensus sequence: TGTTACCT



Best Matches for Motif ID 37 (Highest to Lowest)

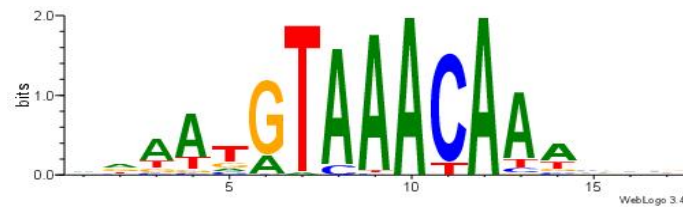
Motif ID:	MA0852.1
Motif name:	Foxk1
Taxon:	Vertebrates
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	3
Number of overlap:	10
Similarity score:	0.0286025

Alignment:

DDAATGTAAACAAAVVB
--AAGGTAAACA-----

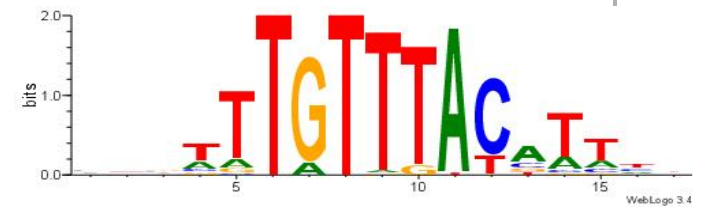
Original motif

Consensus sequence: DDAATGTAAACAAAVVB



Reverse complement motif

Consensus sequence: BBVTTTGTTTACATTD



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

Original motif

Consensus sequence: CGCCGCCA



Reverse complement motif

Consensus sequence: TGGCGCG



Best Matches for Motif ID 38 (Highest to Lowest)

Motif ID:	MA1034.1
Motif name:	Os05g0497200
Taxon:	Plants
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	8

Similarity score: 0.00831137

Alignment:

CGSCGCCR

CGCCGCCA

Original motif

Consensus sequence: CGSCGCCR



Reverse complement motif

Consensus sequence: KGGCGSCG



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

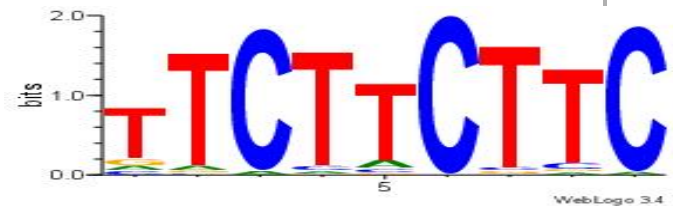
Original motif

Consensus sequence: GAAGAAGAA



Reverse complement motif

Consensus sequence: TTCTTCTTC



Best Matches for Motif ID 39 (Highest to Lowest)

Motif ID:	MA0377.1
Motif name:	SFL1
Taxon:	Fungi
Matching format of first motif:	Reverse Complement

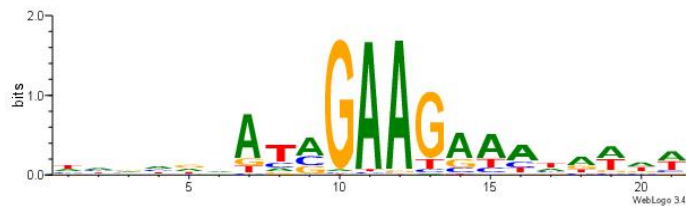
Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 4
 Number of overlap: 9
 Similarity score: 0.034731

Alignment:

WDWDHTTTCTTCYATHHHVHH
 ---TTCTTCTTC-----

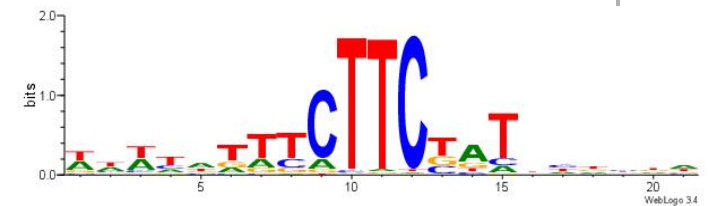
Original motif

Consensus sequence: HHVHDHATMGAAGAAHDWDW



Reverse complement motif

Consensus sequence: WDWDHTTTCTTCYATHHHVHH



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

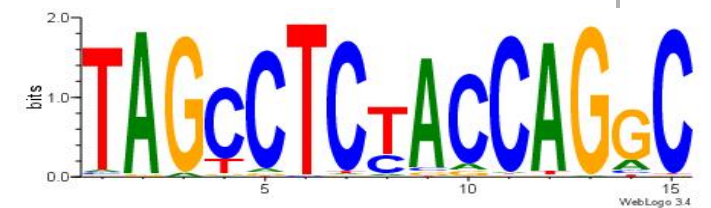
Original motif

Consensus sequence: GCCTGGTAGAGGCTA



Reverse complement motif

Consensus sequence: TAGCCTCTACCAGGC



Best Matches for Motif ID 40 (Highest to Lowest)

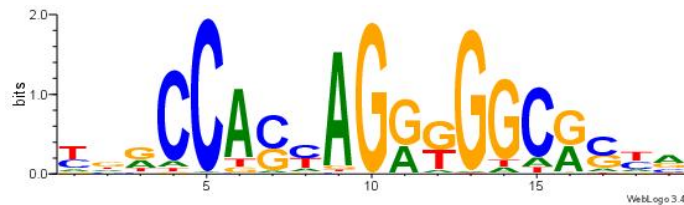
Motif ID: [MA0139.1](#)
 Motif name: CTCF
 Taxon: Vertebrates
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 15
 Similarity score: 0.0871174

Alignment:

YDRCCASYAGRKGGCRSYV
 ----GCCTGGTAGAGGCTA

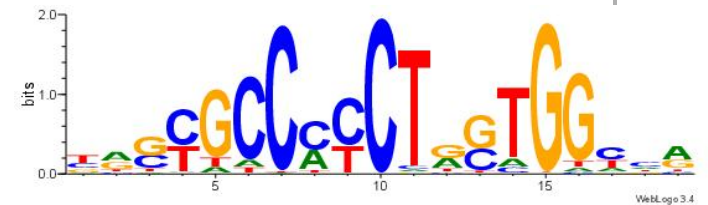
Original motif

Consensus sequence: YDRCCASYAGRKGGCRSYV



Reverse complement motif

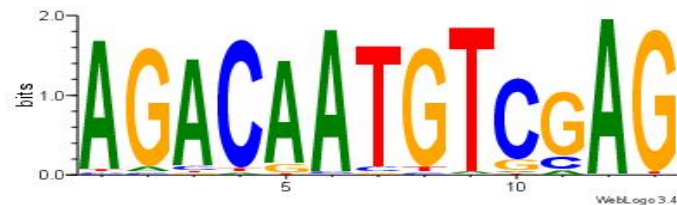
Consensus sequence: BMSMGCCYMCTKSTGGMHH



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

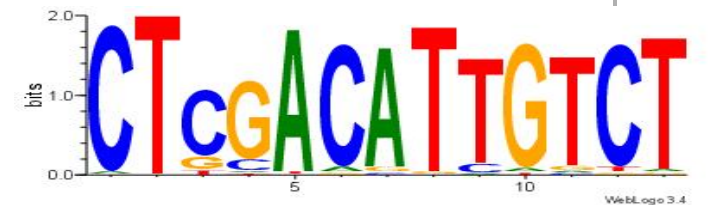
Original motif

Consensus sequence: AGACAATGTCGAG



Reverse complement motif

Consensus sequence: CTCGACATTGTCT



Best Matches for Motif ID 41 (Highest to Lowest)

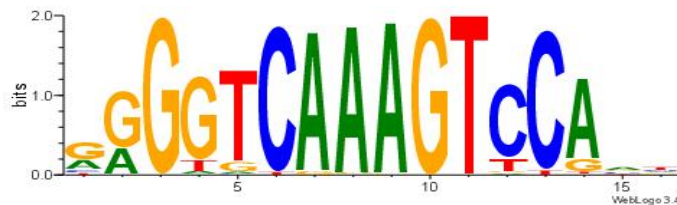
Motif ID: [MA0114.3](#)
Motif name: Hnf4a
Taxon: Vertebrates
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 2
Number of overlap: 13
Similarity score: 0.0795723

Alignment:

```
HBTGGACTTTGACCCM  
-CTCGACATTGTCT--
```

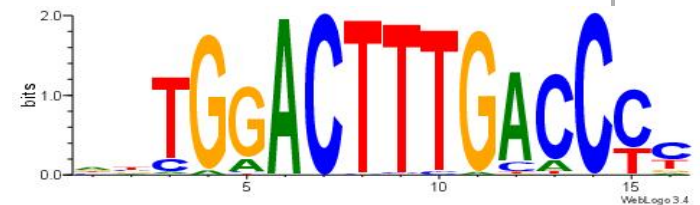
Original motif

Consensus sequence: RGGGTCAAAGTCCA



Reverse complement motif

Consensus sequence: HBTGGACTTTGACCCM



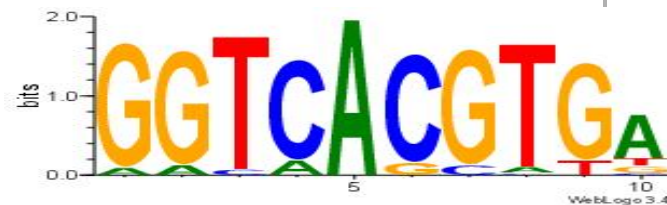
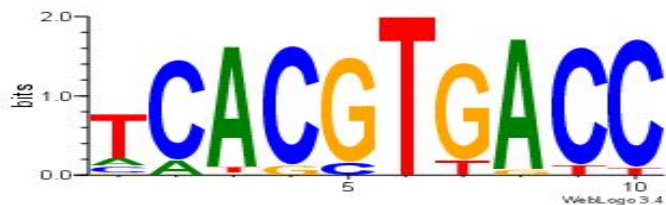
Dataset #: 1 **Motif ID: 42** **Motif name: Motif 42**

Original motif

Consensus sequence: TCACGTGACC

Reverse complement motif

Consensus sequence: GGTCACGTGA

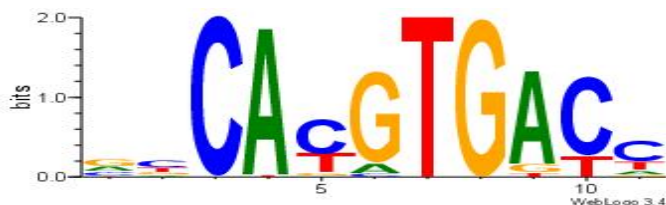


Best Matches for Motif ID 42 (Highest to Lowest)

Motif ID: [MA0093.2](#)
 Motif name: USF1
 Taxon: Vertebrates
 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: 0.0323214

Alignment:
 VBCAYGTGACC
 -TCACGTGACC

Original motif
 Consensus sequence: VBCAYGTGACC



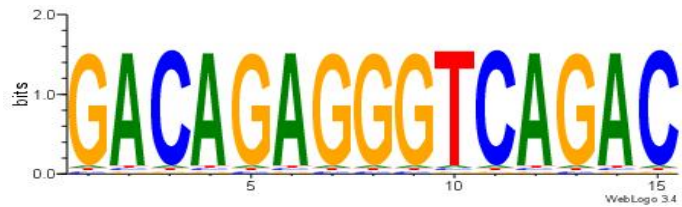
Reverse complement motif
 Consensus sequence: GGTcACGTG



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

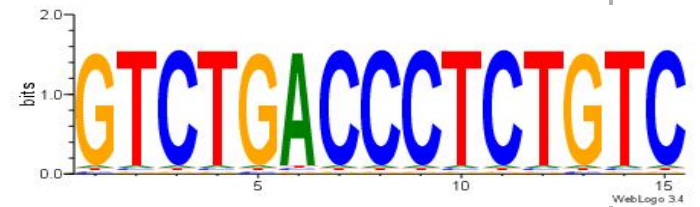
Original motif

Consensus sequence: GACAGAGGGTCAGAC



Reverse complement motif

Consensus sequence: GTCTGACCCTCTGTC



Best Matches for Motif ID 43 (Highest to Lowest)

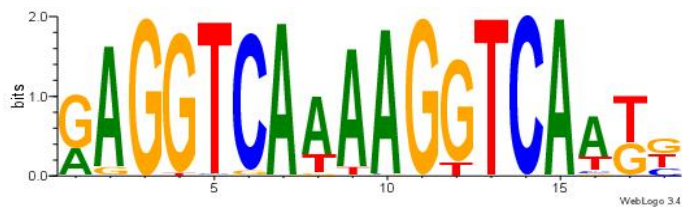
Motif ID: [MA0729.1](#)
Motif name: RARA
Taxon: Vertebrates
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 15
Similarity score: 0.0856351

Alignment:

GAGGTCAAAGGTCAAKK
---GACAGAGGGTCAGAC

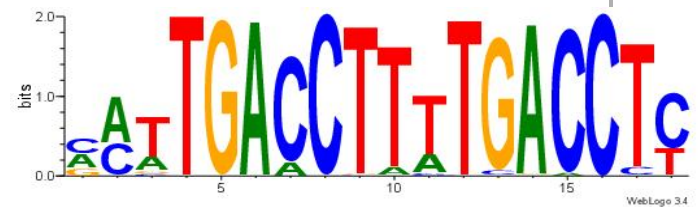
Original motif

Consensus sequence: GAGGTCAAAGGTCAAKK



Reverse complement motif

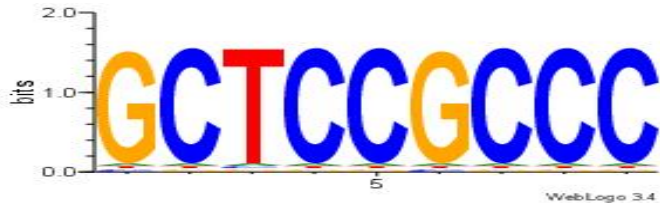
Consensus sequence: YRTTGACCTTTTGACCTC



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

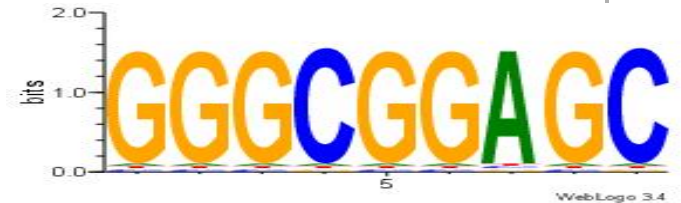
Original motif

Consensus sequence: GCTCCGCC



Reverse complement motif

Consensus sequence: GGGCGGAGC



Best Matches for Motif ID 44 (Highest to Lowest)

Motif ID:	MA0685.1
Motif name:	SP4
Taxon:	Vertebrates
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	6
Number of overlap:	9
Similarity score:	0.0231825

Alignment:

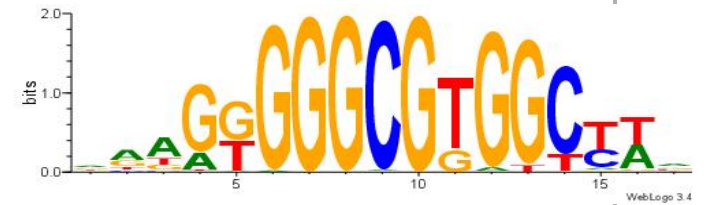
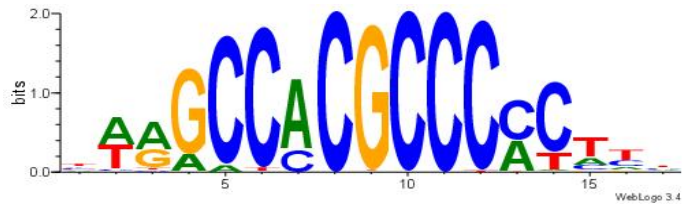
```
BWRGCCACGCCCMCTYH  
---GCTCCGCC-----
```

Original motif

Consensus sequence: BWRGCCACGCCCMCTYH

Reverse complement motif

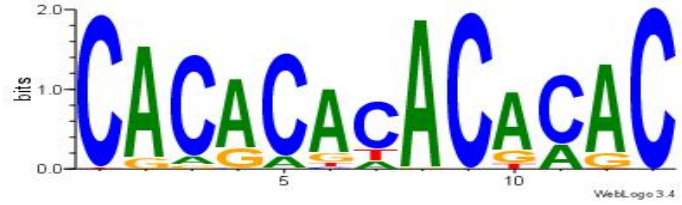
Consensus sequence: HMAGRGGGCGTGGCKWV



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

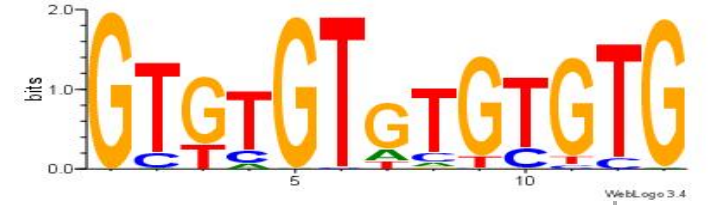
Original motif

Consensus sequence: CACACACACAC



Reverse complement motif

Consensus sequence: GTGTGTGTGTG



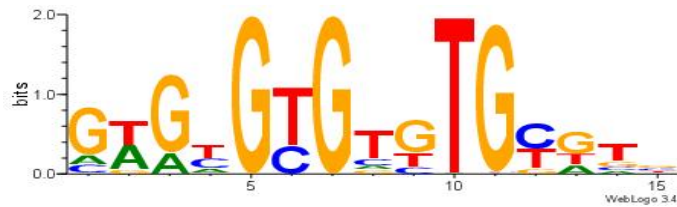
Best Matches for Motif ID 45 (Highest to Lowest)

Motif ID:	MA0538.1
Motif name:	daf-12
Taxon:	Nematodes
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	13
Similarity score:	0.0427041

Alignment:
 BACKCACACACMCWC
 GTGTGTGTGTGTG--

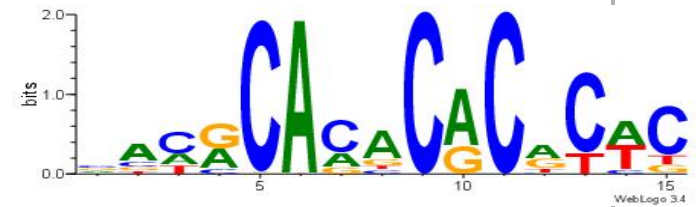
Original motif

Consensus sequence: GWGYGTGTGTGYGTB



Reverse complement motif

Consensus sequence: BACKCACACACMCWC



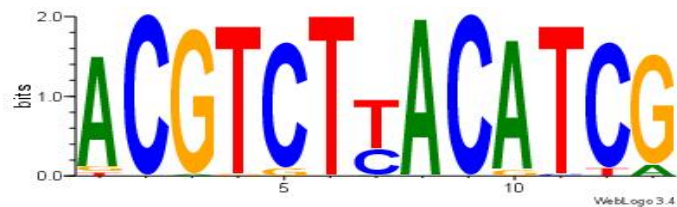
Dataset #: 1

Motif ID: 46

Motif name: Motif 46

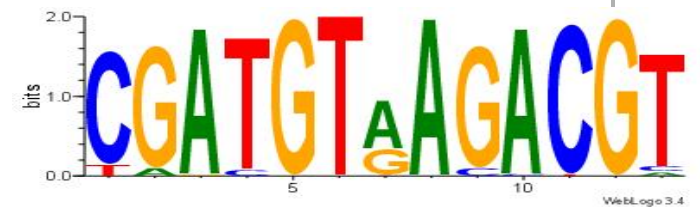
Original motif

Consensus sequence: ACGTCTYACATCG



Reverse complement motif

Consensus sequence: CGATGTMAGACGT



Best Matches for Motif ID 46 (Highest to Lowest)

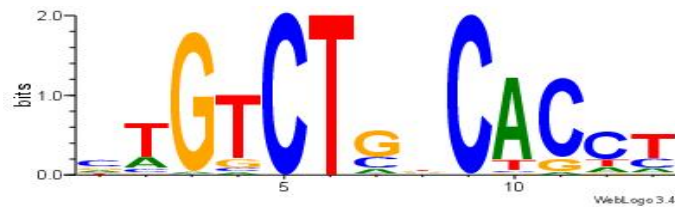
Motif ID:	MA0513.1
Motif name:	SMAD2::SMAD3::SMAD4
Taxon:	Vertebrates
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	13
Similarity score:	0.0949021

Alignment:

AGGTGDCAGACAV
CGATGTMAGACGT

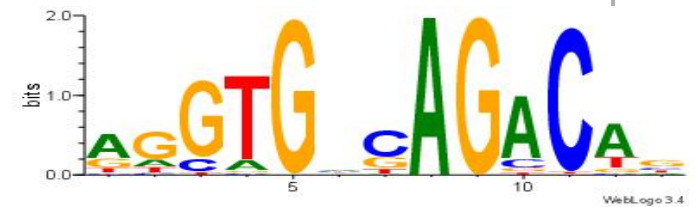
Original motif

Consensus sequence: VTGTCTGDCACCT



Reverse complement motif

Consensus sequence: AGGTGDCAGACAV



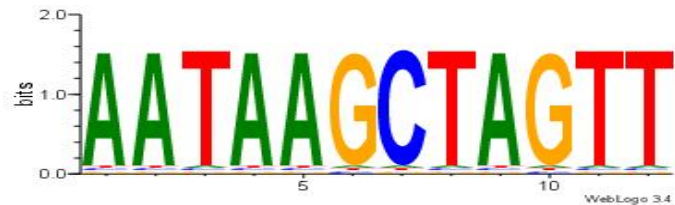
Dataset #: 1

Motif ID: 47

Motif name: Motif 47

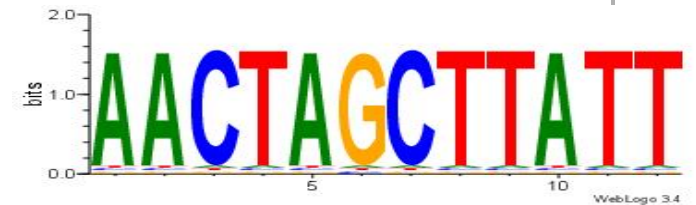
Original motif

Consensus sequence: AATAAGCTAGTT



Reverse complement motif

Consensus sequence: AACTAGCTTATT



Best Matches for Motif ID 47 (Highest to Lowest)

Motif ID:	MA0788.1
Motif name:	POU3F3
Taxon:	Vertebrates
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif

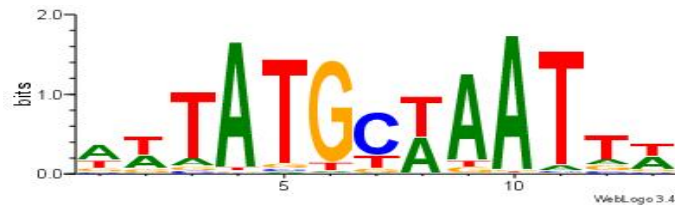
Direction: Backward
Position number: 2
Number of overlap: 12
Similarity score: 0.0583819

Alignment:

WWTATGCWAATTW
AATAAGCTAGTT-

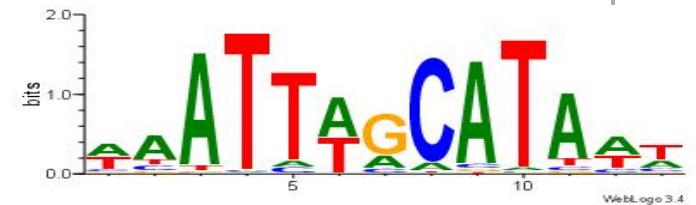
Original motif

Consensus sequence: WWTATGCWAATTW



Reverse complement motif

Consensus sequence: WAATTWGCATAWW



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

Original motif

Consensus sequence: CAGACRAC



Reverse complement motif

Consensus sequence: GTKGTCTG



Best Matches for Motif ID 48 (Highest to Lowest)

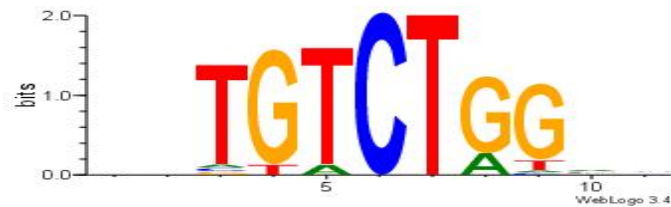
Motif ID: [MA0925.1](#)

Motif name: sma-4
 Taxon: Nematodes
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 8
 Similarity score: 0.0307066

Alignment:
 DVTGTCTGGVB
 ---CAGACRAC

Original motif

Consensus sequence: DVTGTCTGGVB



Reverse complement motif

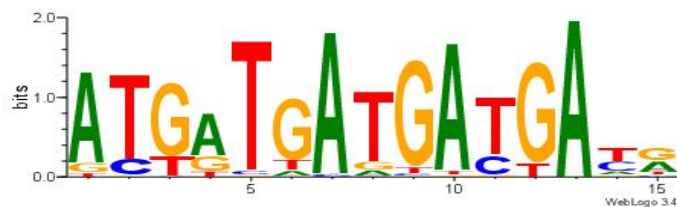
Consensus sequence: BBCCAGACAVB



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

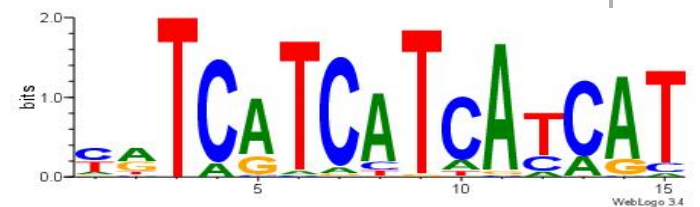
Original motif

Consensus sequence: ATGATGATGATGAYR



Reverse complement motif

Consensus sequence: MMTCATCATCATCAT



Best Matches for Motif ID 49 (Highest to Lowest)

Motif ID: [MA0547.1](#)
Motif name: skn-1
Taxon: Nematodes
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: 0.0545893

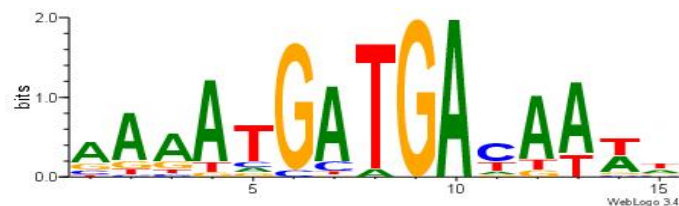
Alignment:

AAAATGATGACAAWD

ATGATGATGATGAYR

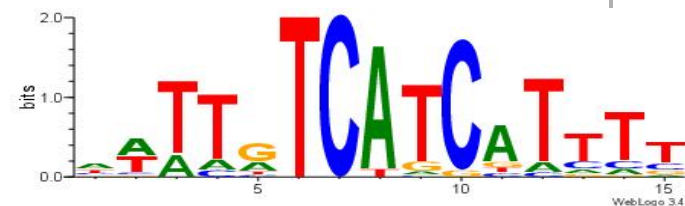
Original motif

Consensus sequence: AAAATGATGACAAWD



Reverse complement motif

Consensus sequence: DWTTGTCATCATTTT



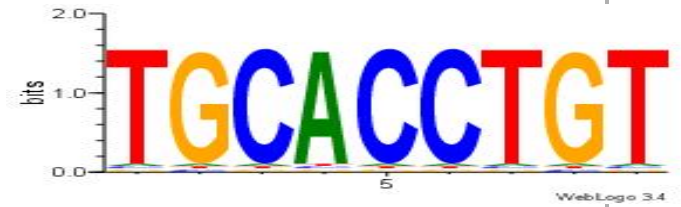
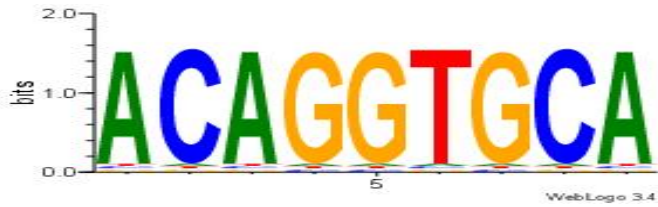
Dataset #: 1 **Motif ID: 50** **Motif name: Motif 50**

Original motif

Consensus sequence: ACAGGTGCA

Reverse complement motif

Consensus sequence: TGCACCTGT



Best Matches for Motif ID 50 (Highest to Lowest)

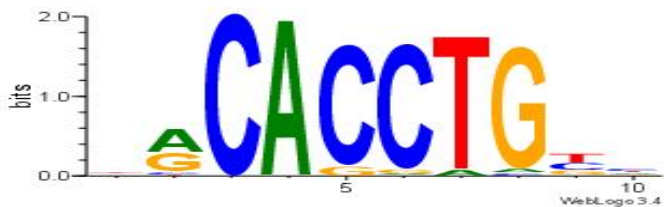
Motif ID: [MA0824.1](#)
 Motif name: ID4
 Taxon: Vertebrates
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 9
 Similarity score: 0.0401018

Alignment:

DRCACCTGBH
 TGCACCTGT-

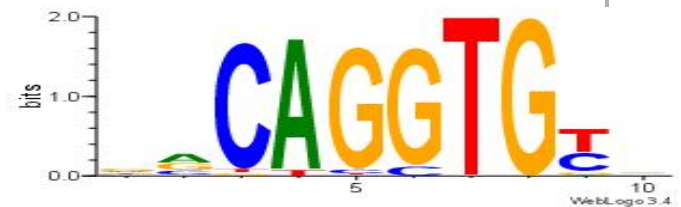
Original motif

Consensus sequence: DRCACCTGBH



Reverse complement motif

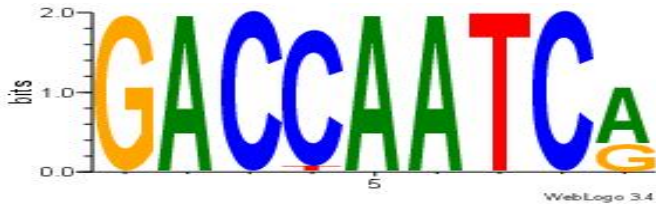
Consensus sequence: DVCAGGTGKD



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

Original motif

Consensus sequence: GACCAATCA



Reverse complement motif

Consensus sequence: TGATTGGTC



Best Matches for Motif ID 51 (Highest to Lowest)

Motif ID: [MA0060.2](#)
Motif name: NFYA
Taxon: Vertebrates
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 3
Number of overlap: 9
Similarity score: 0.0180131

Alignment:

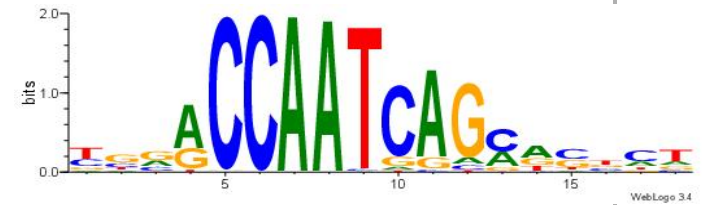
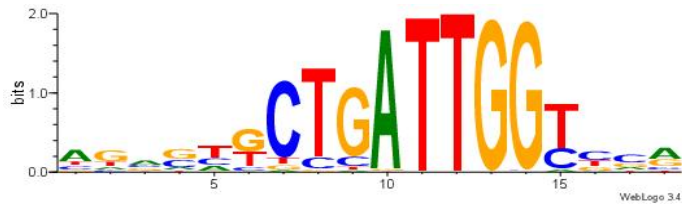
```
AGVSYKCTGATTGGTBVR  
-----TGATTGGTC--
```

Original motif

Consensus sequence: AGVSYKCTGATTGGTBVR

Reverse complement motif

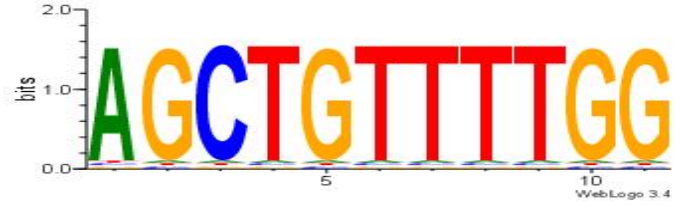
Consensus sequence: KVBACCAATCAGYMSBCT



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

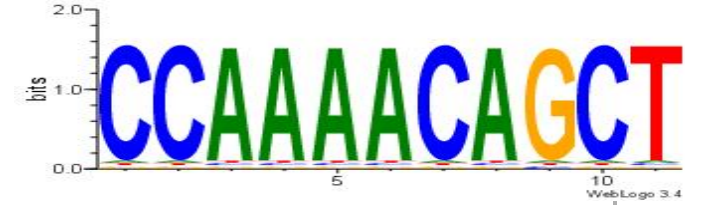
Original motif

Consensus sequence: AGCTGTTTGG



Reverse complement motif

Consensus sequence: CCAAACAGCT



Best Matches for Motif ID 52 (Highest to Lowest)

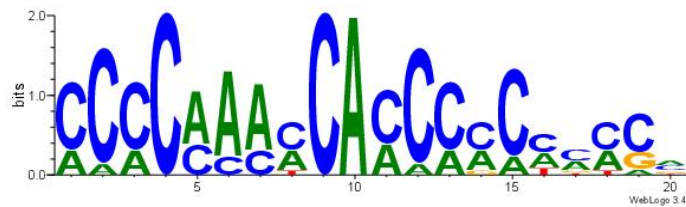
Motif ID:	MA0073.1
Motif name:	RREB1
Taxon:	Vertebrates
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	3
Number of overlap:	11
Similarity score:	0.0758389

Alignment:

CCCCMAAMCAMCCMCMMMC
 --CCAAAACAGCT-----

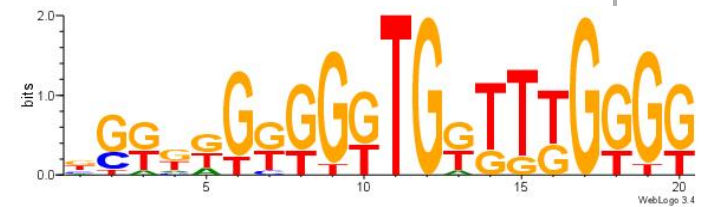
Original motif

Consensus sequence: CCCCMAAMCAMCCMCMMMC



Reverse complement motif

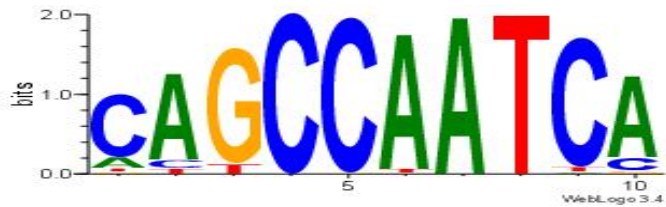
Consensus sequence: BGRRRGRGGRTGRTTYGGGG



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

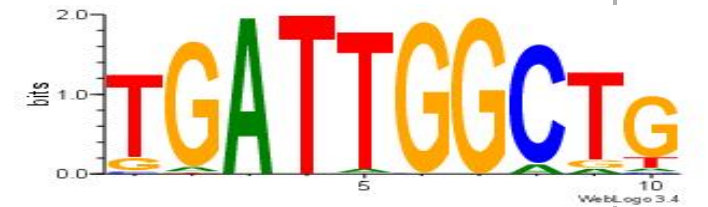
Original motif

Consensus sequence: CAGCCAATCA



Reverse complement motif

Consensus sequence: TGATTGGCTG



Best Matches for Motif ID 53 (Highest to Lowest)

Motif ID:	MA0314.1
Motif name:	HAP3
Taxon:	Fungi
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	3

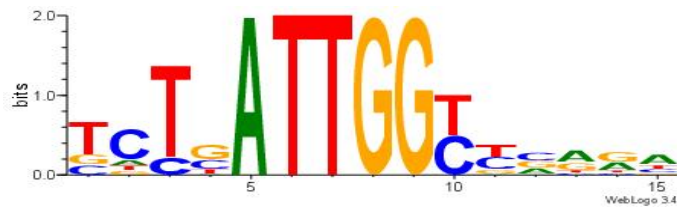
Number of overlap: 10
Similarity score: 0.0179107

Alignment:

TCTSATTGGYYVRRRA
--TGATTGGCTG---

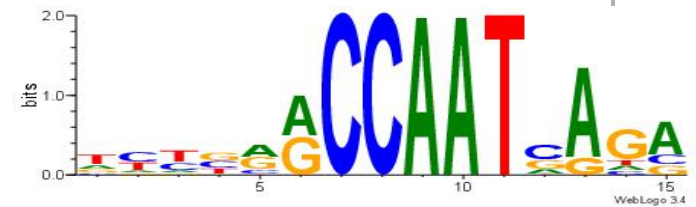
Original motif

Consensus sequence: TCTSATTGGYYVRRRA



Reverse complement motif

Consensus sequence: TMKVMMCCAATSAGA



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

Original motif

Consensus sequence: ATGCAAAT



Reverse complement motif

Consensus sequence: ATTTGCAT



Best Matches for Motif ID 54 (Highest to Lowest)

Motif ID: [MA0507.1](#)
Motif name: POU2F2
Taxon: Vertebrates

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:	0.00743635

Alignment:
 AKATGCAAATDDH
 --ATGCAAAT---

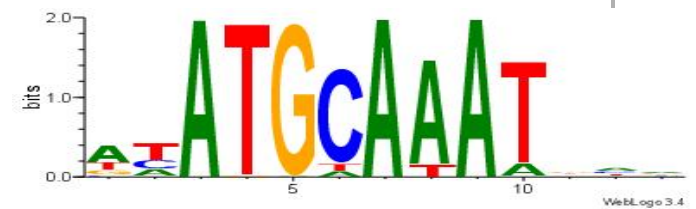
Original motif

Consensus sequence: HDHATTTGCATRT



Reverse complement motif

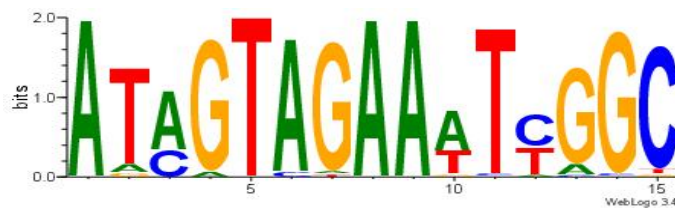
Consensus sequence: AKATGCAAATDDH



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

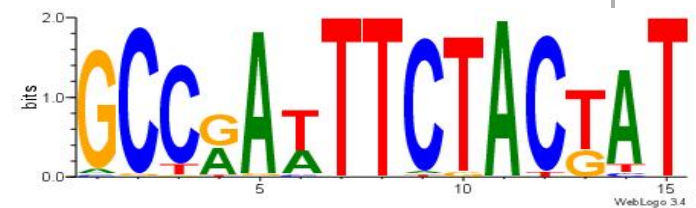
Original motif

Consensus sequence: ATAGTAGAAATCGGC



Reverse complement motif

Consensus sequence: GCCKAWTTCTACTAT



Best Matches for Motif ID 55 (Highest to Lowest)

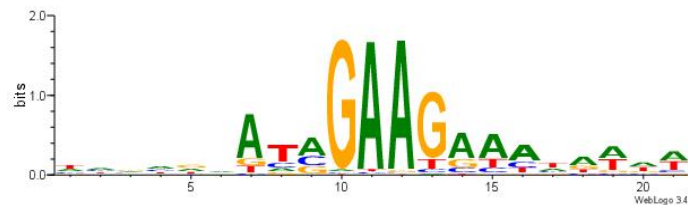
Motif ID: [MA0377.1](#)
Motif name: SFL1
Taxon: Fungi
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 7
Number of overlap: 15
Similarity score: 0.0860145

Alignment:

```
WDWDHTTTCTTCYATHHHVHH  
GCKKAWTTCTACTAT-----
```

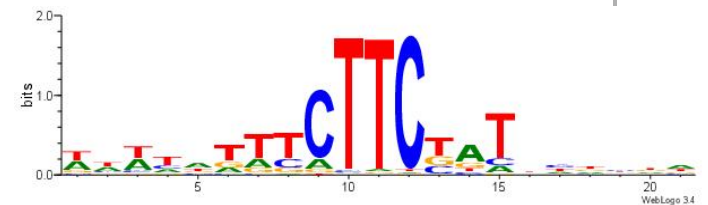
Original motif

Consensus sequence: HHVHDHATMGAAGAAHDWDW



Reverse complement motif

Consensus sequence: WDWDHTTTCTTCYATHHHVHH



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

Original motif

Consensus sequence: HRCTGCAGYD

Reverse complement motif

Consensus sequence: DMCTGCAGKH



Best Matches for Motif ID 56 (Highest to Lowest)

Motif ID: [MA0355.1](#)
 Motif name: PHD1
 Taxon: Fungi
 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: 0.00587276

Alignment:

BVBTGCARSB
 HRCTGCAGYD

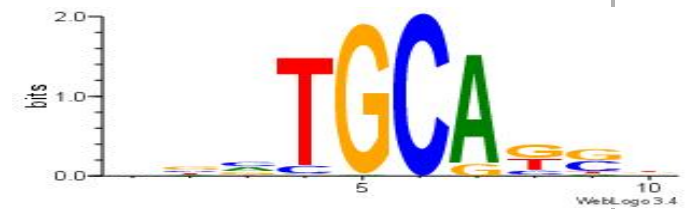
Original motif

Consensus sequence: VSMTGCABVV



Reverse complement motif

Consensus sequence: BVBTGCARSB



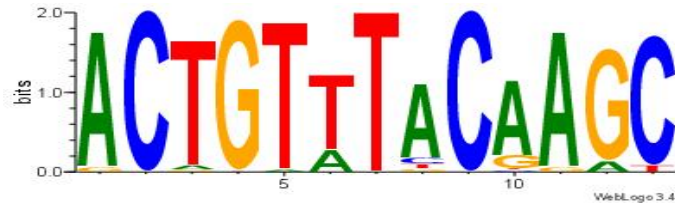
Dataset #: 1

Motif ID: 57

Motif name: Motif 57

Original motif

Consensus sequence: ACTGTTACAAGC



Reverse complement motif

Consensus sequence: GCTTGTAACAGT



Best Matches for Motif ID 57 (Highest to Lowest)

Motif ID:	MA0296.1
Motif name:	FKH1
Taxon:	Fungi
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	3
Number of overlap:	13
Similarity score:	0.0709953

Alignment:

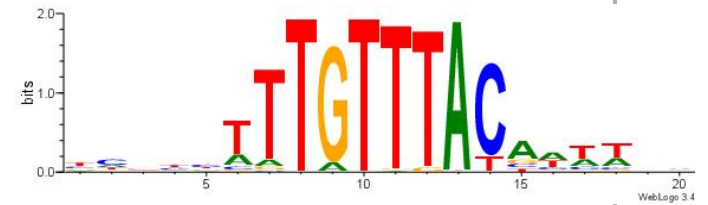
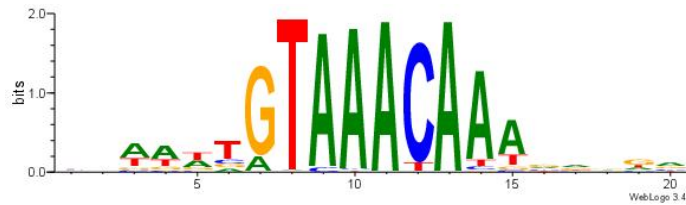
```
BHHDVTTTGTTTACAWWWHV  
-----ACTGTTTACAAGC--
```

Original motif

Consensus sequence: BDWWWTGTAAACAAVDDDDV

Reverse complement motif

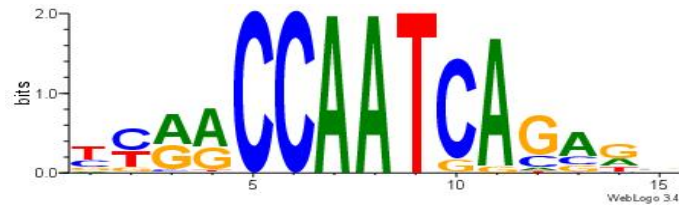
Consensus sequence: BHHDVTTTGTTTACAWWWHV



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

Original motif

Consensus sequence: YRRC~~CAAT~~CAGAGV



Reverse complement motif

Consensus sequence: VCTCTGATTGGKKKM



Best Matches for Motif ID 58 (Highest to Lowest)

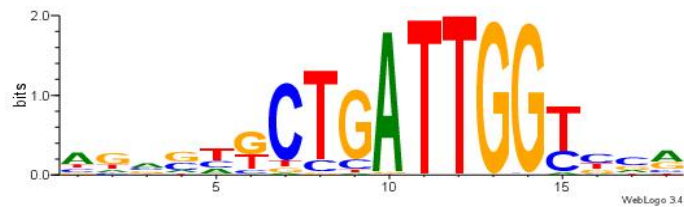
Motif ID:	MA0060.2
Motif name:	NFYA
Taxon:	Vertebrates
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	4
Number of overlap:	15
Similarity score:	0.0229578

Alignment:

AGVSYKCTGATTGGTBVR
---VCTCTGATTGGKKKM

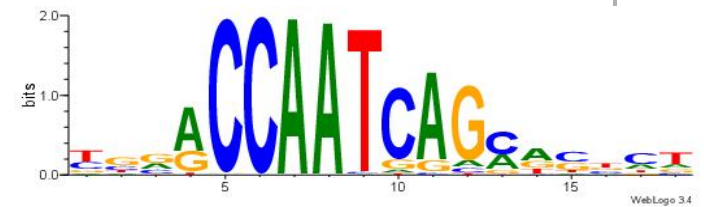
Original motif

Consensus sequence: AGVSYKCTGATTGGTBVR



Reverse complement motif

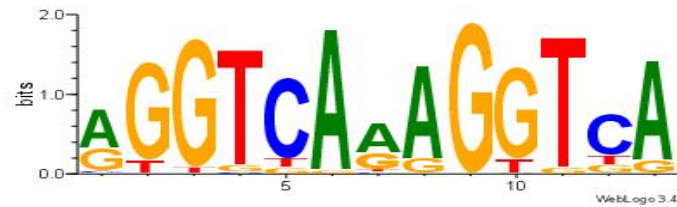
Consensus sequence: KVBACCAATCAGYMSBCT



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

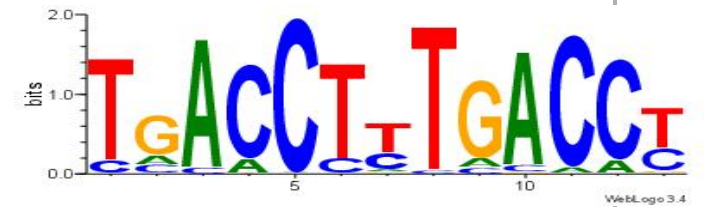
Original motif

Consensus sequence: RGGTCARAGGTCA



Reverse complement motif

Consensus sequence: TGACCTKTGACCK



Best Matches for Motif ID 59 (Highest to Lowest)

Motif ID:	MA0677.1
Motif name:	Nr2f6
Taxon:	Vertebrates
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1

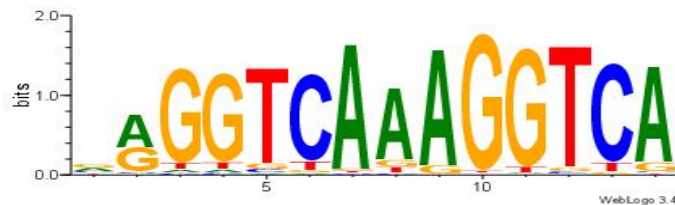
Number of overlap: 13
Similarity score: 0

Alignment:

TGACCTTTGACCKV
TGACCTKTGACCK-

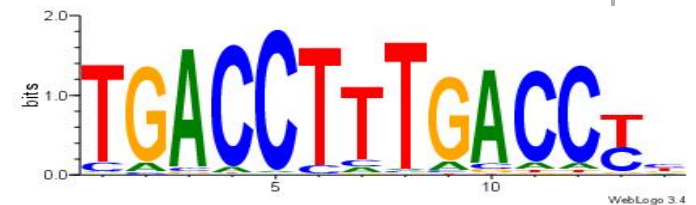
Original motif

Consensus sequence: VRGGTCAAAGGTCA



Reverse complement motif

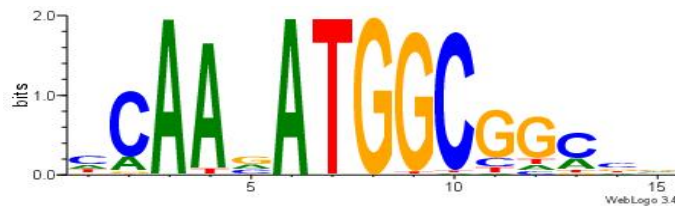
Consensus sequence: TGACCTTTGACCKV



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

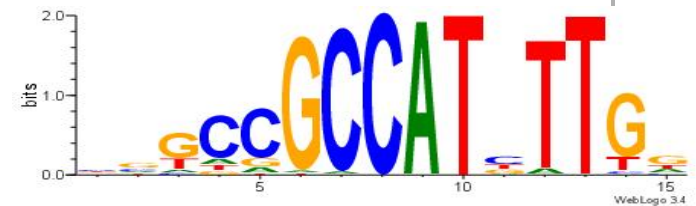
Original motif

Consensus sequence: HCAAVATGGCGGCBV



Reverse complement motif

Consensus sequence: VBGCCGCCATVTTGD



Best Matches for Motif ID 60 (Highest to Lowest)

Motif ID: [MA0570.1](#)
Motif name: ABF1
Taxon: Plants

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:	0.0784137

Alignment:

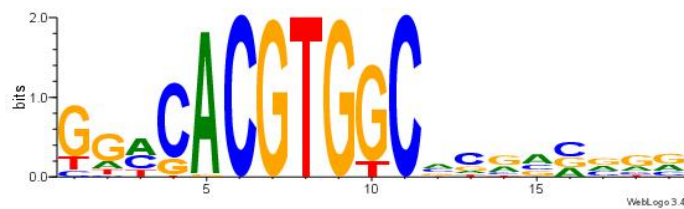
```

GGMCACGTGGCVCRRVVVGV
-HCAAVATGGCGGCBV---

```

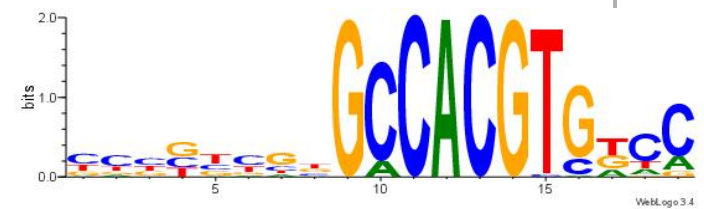
Original motif

Consensus sequence: GGMCACGTGGCVCRRVVVGV



Reverse complement motif

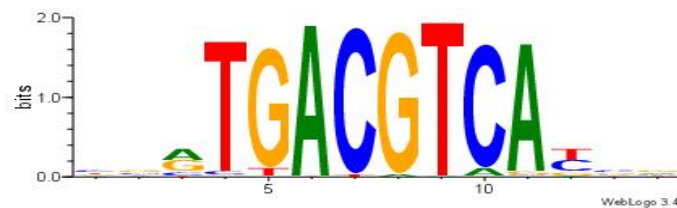
Consensus sequence: VCVVBMGBGCCACGTGYCC



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

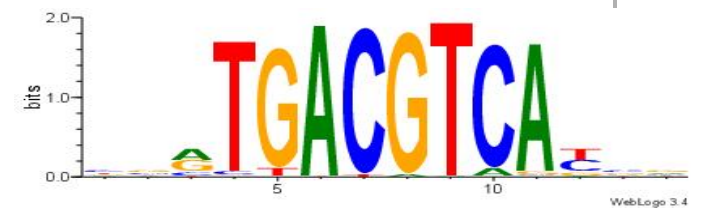
Original motif

Consensus sequence: BBRTGACGTCAYVV



Reverse complement motif

Consensus sequence: VVMTGACGTCAYVV



Best Matches for Motif ID 61 (Highest to Lowest)

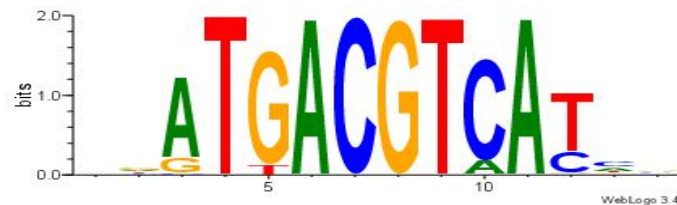
Motif ID: [MA0834.1](#)
Motif name: ATF7
Taxon: Vertebrates
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 14
Similarity score: 0.0169411

Alignment:

BDATGACGTCATHV
BBRTGACGTCAYVV

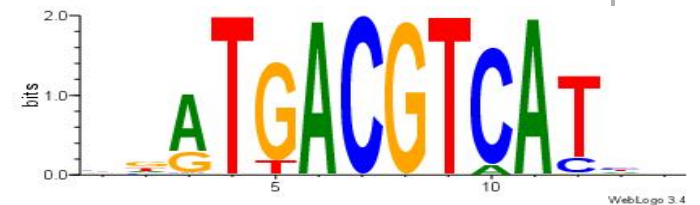
Original motif

Consensus sequence: BDATGACGTCATHV



Reverse complement motif

Consensus sequence: VDATGACGTCATHB



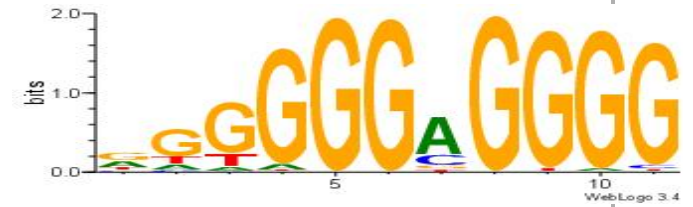
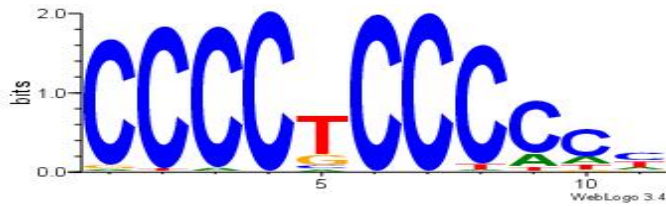
Dataset #: 2 Motif ID: 62 Motif name: Motif 62

Original motif

Consensus sequence: CCCCTCCCCCY

Reverse complement motif

Consensus sequence: KGGGGGAGGGG



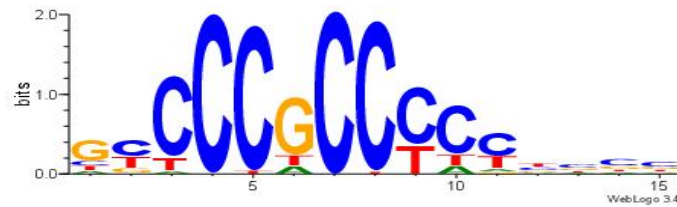
Best Matches for Motif ID 62 (Highest to Lowest)

Motif ID: [MA0516.1](#)
 Motif name: SP2
 Taxon: Vertebrates
 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: 0.0384687

Alignment:
 GYCCCGCCYCYBBBB
 -CCCCTCCCCCY---

Original motif

Consensus sequence: GYCCCGCCYCYBBBB



Reverse complement motif

Consensus sequence: BBBVKGKGGCGGGKC



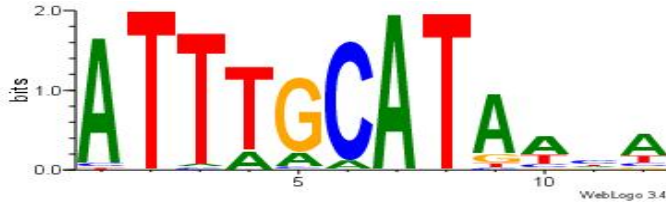
Dataset #: 2

Motif ID: 63

Motif name: Motif 63

Original motif

Consensus sequence: ATTTGCATAWHA



Reverse complement motif

Consensus sequence: TDWTATGCAAAT



Best Matches for Motif ID 63 (Highest to Lowest)

Motif ID:	MA0627.1
Motif name:	Pou2f3
Taxon:	Vertebrates
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	5
Number of overlap:	12
Similarity score:	0.0149217

Alignment:

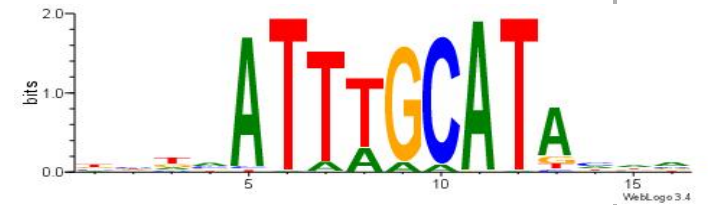
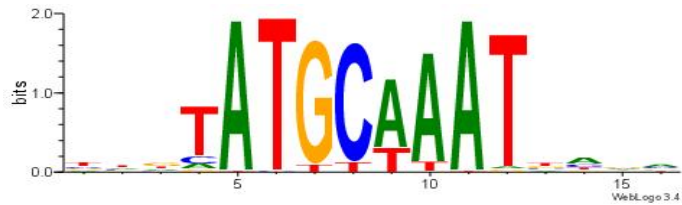
```
BHHVATTTGCATAHHV  
----ATTTGCATAWHA
```

Original motif

Consensus sequence: BHDTATGCAAATBHDV

Reverse complement motif

Consensus sequence: BHHVATTTGCATAHHV



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

Original motif

Consensus sequence: GCATGMTGGGA



Reverse complement motif

Consensus sequence: TCCCARCATGC



Best Matches for Motif ID 64 (Highest to Lowest)

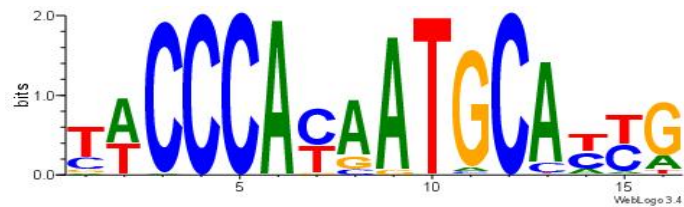
Motif ID:	MA0088.2
Motif name:	ZNF143
Taxon:	Vertebrates
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	2
Number of overlap:	11
Similarity score:	0.0572813

Alignment:

CMMTGCATTKTGGGWA
 ----GCATGMTGGGA-

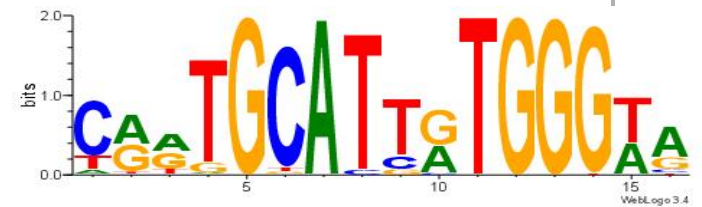
Original motif

Consensus sequence: TWCCCAAYAATGCAYYG



Reverse complement motif

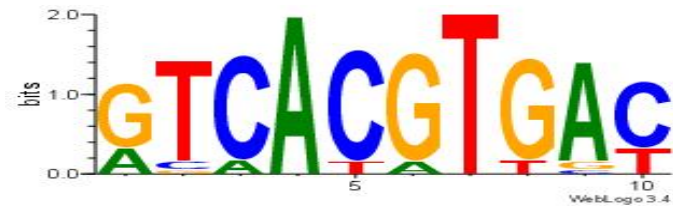
Consensus sequence: CMMTGCATTKTGGGWA



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

Original motif

Consensus sequence: GTCACGTGAC



Reverse complement motif

Consensus sequence: GTCACGTGAC



Best Matches for Motif ID 65 (Highest to Lowest)

Motif ID:	MA0636.1
Motif name:	BHLHE41
Taxon:	Vertebrates
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: 0.00818767

Alignment:

RTCACGTGAC

GTCACGTGAC

Original motif

Consensus sequence: RTCACGTGAC



Reverse complement motif

Consensus sequence: GTCACGTGAM



Dataset #: 2

Motif ID: 66

Motif name: Motif 66

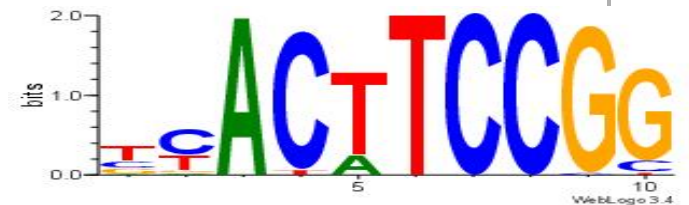
Original motif

Consensus sequence: CCGGAAGTRA



Reverse complement motif

Consensus sequence: TMACTTCCGG



Best Matches for Motif ID 66 (Highest to Lowest)

Motif ID:	MA0640.1
Motif name:	ELF3
Taxon:	Vertebrates
Matching format of first motif:	Original Motif

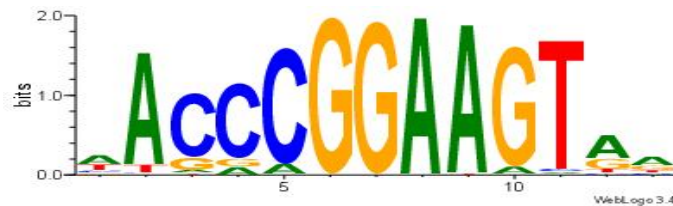
Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 10
 Similarity score: 0.0120558

Alignment:

WACCCGGAAGTAD
 ---CCGGAAGTRA

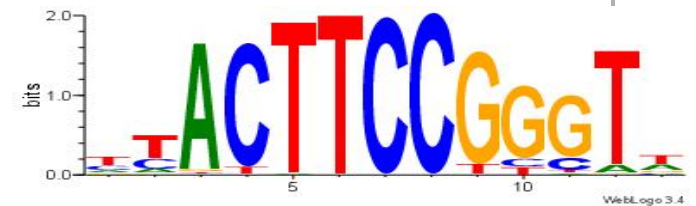
Original motif

Consensus sequence: WACCCGGAAGTAD



Reverse complement motif

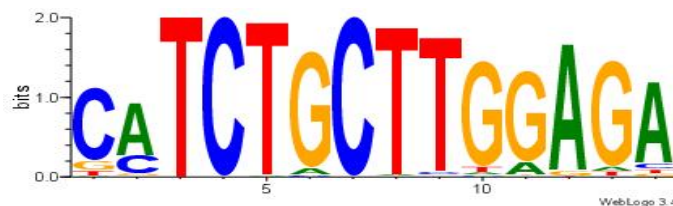
Consensus sequence: DTA CTTCCGGGTW



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

Original motif

Consensus sequence: CATCTGCTTGGAGA



Reverse complement motif

Consensus sequence: TCTCCAAGCAGATG



Best Matches for Motif ID 67 (Highest to Lowest)

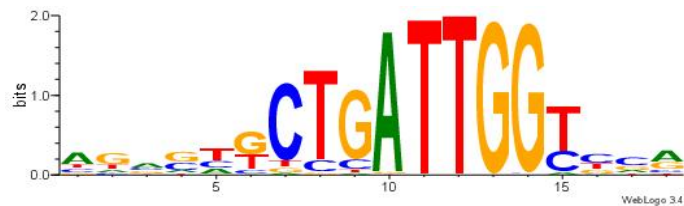
Motif ID: [MA0060.2](#)
 Motif name: NFYA
 Taxon: Vertebrates
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 14
 Similarity score: 0.0479869

Alignment:

AGVSYKCTGATTGGTBVR
 ---CATCTGCTTGGAGA-

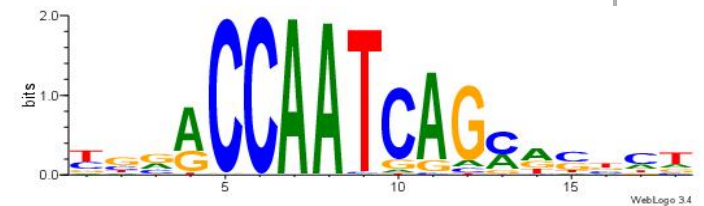
Original motif

Consensus sequence: AGVSYKCTGATTGGTBVR



Reverse complement motif

Consensus sequence: KVBACCAATCAGYMSBCT



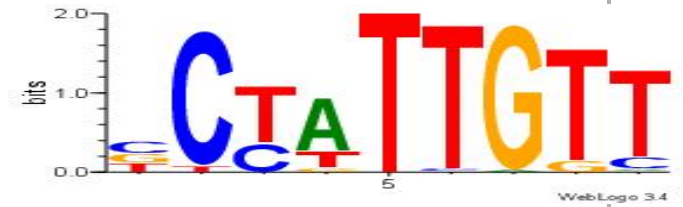
Dataset #: 2 Motif ID: 68 Motif name: Motif 68

Original motif

Consensus sequence: AACATR GV

Reverse complement motif

Consensus sequence: VCKATT GTT



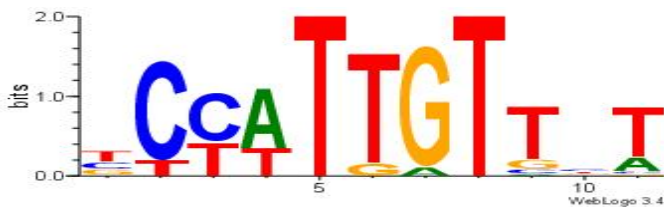
Best Matches for Motif ID 68 (Highest to Lowest)

Motif ID: [MA0445.1](#)
 Motif name: D
 Taxon: Insects
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3
 Number of overlap: 9
 Similarity score: 0.0214352

Alignment:
 ABAACAATKGV
 --ACAATR GV

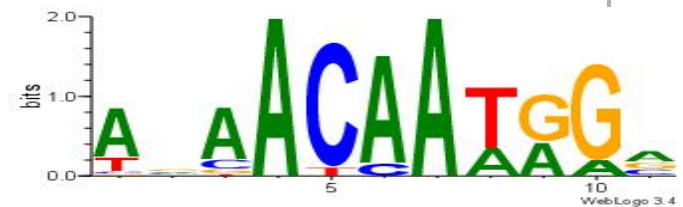
Original motif

Consensus sequence: BCYATTGTTBT



Reverse complement motif

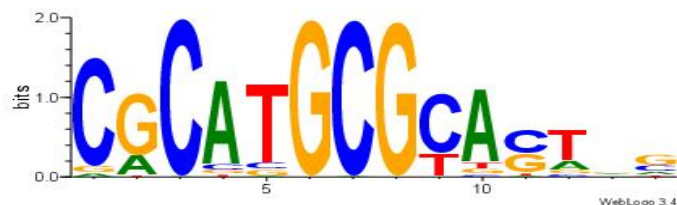
Consensus sequence: ABAACAATKGV



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

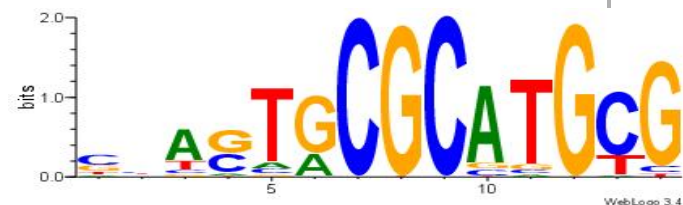
Original motif

Consensus sequence: CGCATGCGCASTVS



Reverse complement motif

Consensus sequence: SVASTGCGCATGCG



Best Matches for Motif ID 69 (Highest to Lowest)

Motif ID:	MA0376.1
Motif name:	RTG3
Taxon:	Fungi
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:	0.0498099

Alignment:

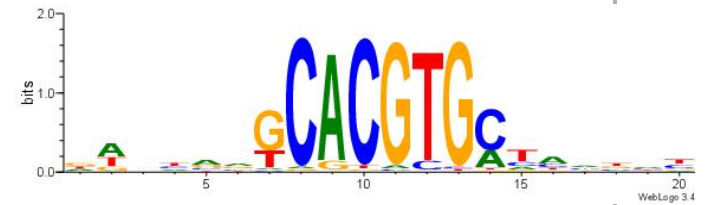
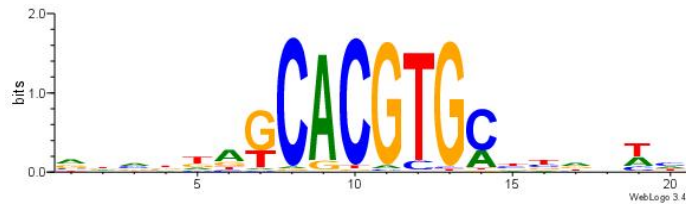
```
VDVBDAGCACGTGCBBDVWH  
-SVASTGCGCATGCG-----
```

Original motif

Consensus sequence: VDVBDAGCACGTGCBBDVWH

Reverse complement motif

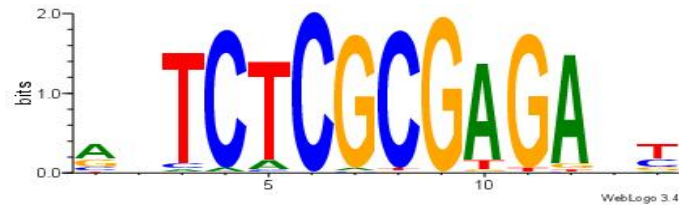
Consensus sequence: DWVDVVGACGTGCTDVVBD



Dataset #: 2 Motif ID: 70 Motif name: Motif 70

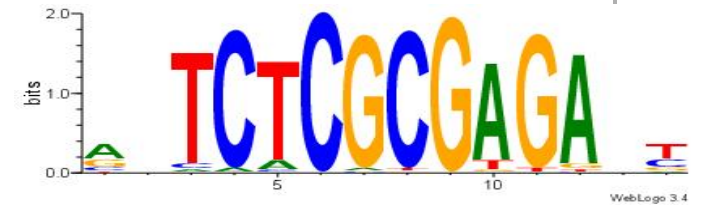
Original motif

Consensus sequence: RVTCTCGCGAGABY



Reverse complement motif

Consensus sequence: MVTCTCGCGAGABK



Best Matches for Motif ID 70 (Highest to Lowest)

Motif ID:	MA0154.3
Motif name:	EBF1
Taxon:	Vertebrates
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	14
Similarity score:	0.0477452

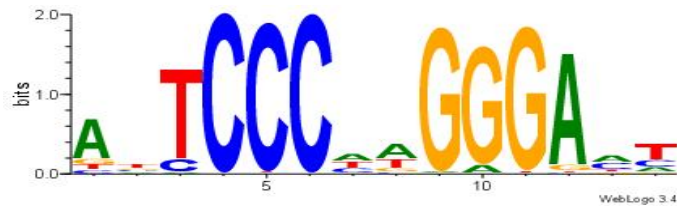
Alignment:

```

AYTCCCWHGGGAVT
MVTCTCGCGAGABK
  
```

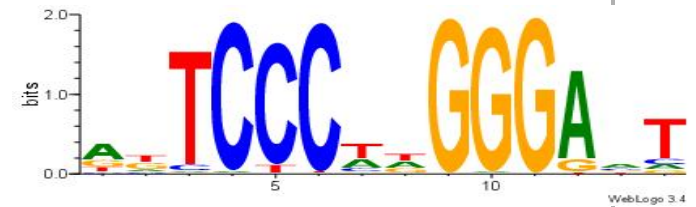
Original motif

Consensus sequence: ABTCCCHWGGGAMT



Reverse complement motif

Consensus sequence: AYTCCCWHGGGAVT



Dataset #: 2

Motif ID: 71

Motif name: Motif 71

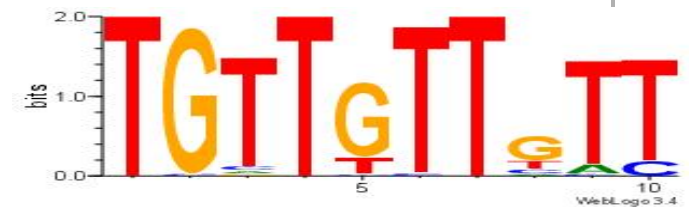
Original motif

Consensus sequence: AACAAACA



Reverse complement motif

Consensus sequence: TGTTGTTGTT



Best Matches for Motif ID 71 (Highest to Lowest)

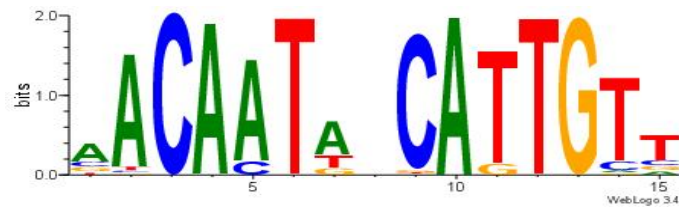
Motif ID:	MA0870.1
Motif name:	Sox1
Taxon:	Vertebrates
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	10
Similarity score:	0.0597499

Alignment:

ACAATGBTATTGTT
 -----TGTGTGTTGTT

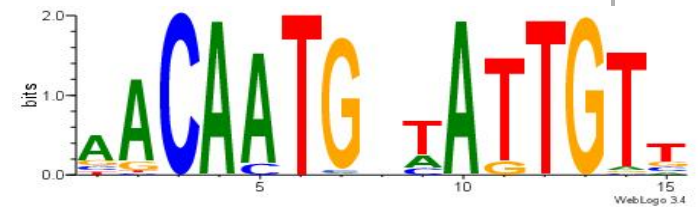
Original motif

Consensus sequence: ACAATAVCATTGTT



Reverse complement motif

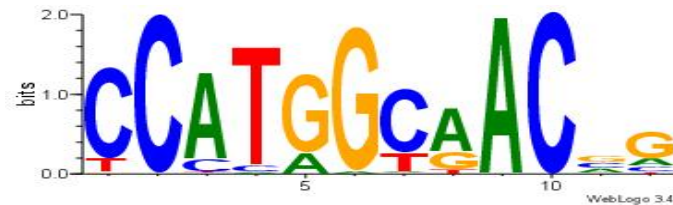
Consensus sequence: ACAATGBTATTGTT



Dataset #: 2 Motif ID: 72 Motif name: Motif 72

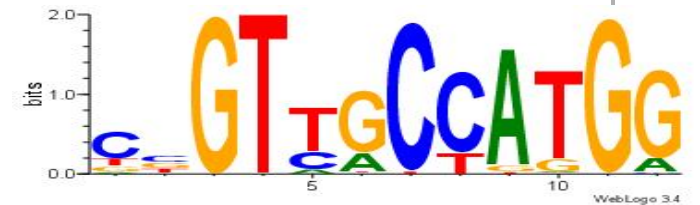
Original motif

Consensus sequence: CCATGGCAACVG



Reverse complement motif

Consensus sequence: CVGTTGCCATGG



Best Matches for Motif ID 72 (Highest to Lowest)

Motif ID:	MA0138.2
Motif name:	REST
Taxon:	Vertebrates
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	8

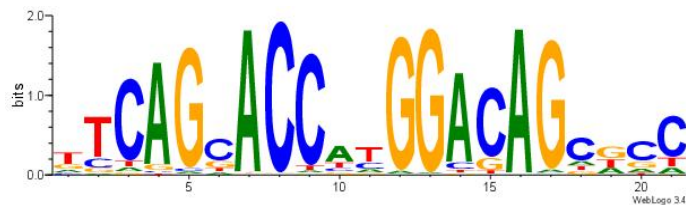
Number of overlap: 12
Similarity score: 0.0637808

Alignment:

GGYGCTGTCCATGGTGCTGAA
--CVGTTGCCATGG-----

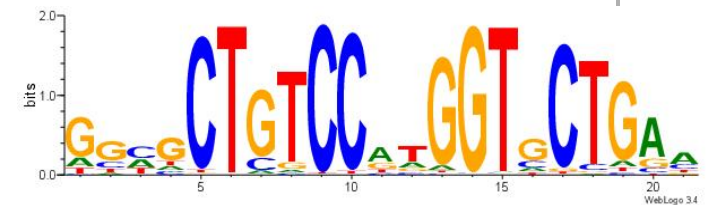
Original motif

Consensus sequence: TTCAGCACCATGGACAGCKCC



Reverse complement motif

Consensus sequence: GGYGCTGTCCATGGTGCTGAA



Dataset #: 2 Motif ID: 73 Motif name: Motif 73

Original motif

Consensus sequence: TCCCGCCVW



Reverse complement motif

Consensus sequence: WBGCGGGA



Best Matches for Motif ID 73 (Highest to Lowest)

Motif ID: [MA0758.1](#)
Motif name: E2F7
Taxon: Vertebrates

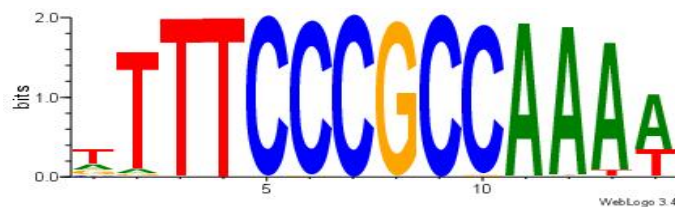
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	4
Number of overlap:	9
Similarity score:	0.0204536

Alignment:

```
TTTTGGCGGGAAAA
--WBGCGGGA---
```

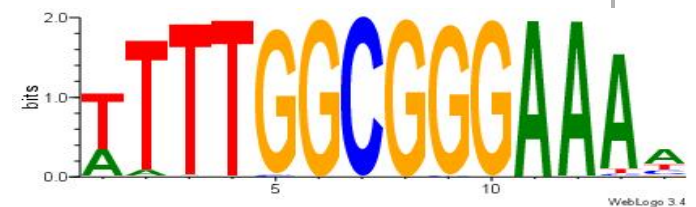
Original motif

Consensus sequence: TTTTCCCGCCAAAA



Reverse complement motif

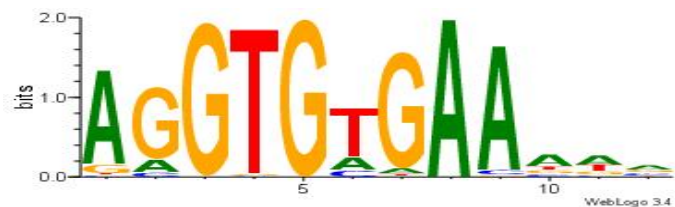
Consensus sequence: TTTTGGCGGGAAAA



Dataset #: 2 Motif ID: 74 Motif name: Motif 74

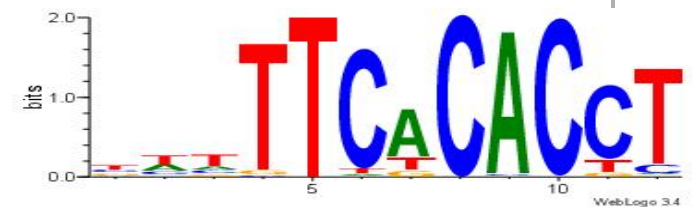
Original motif

Consensus sequence: AGGTGTGAAWV



Reverse complement motif

Consensus sequence: BWTTTCACACCT



Best Matches for Motif ID 74 (Highest to Lowest)

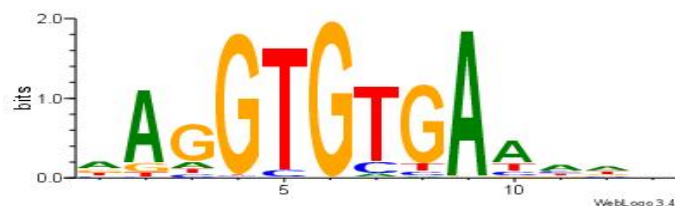
Motif ID: [MA0800.1](#)
Motif name: EOMES
Taxon: Vertebrates
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 2
Number of overlap: 12
Similarity score: 0.0126084

Alignment:

HDHTTCACACCTD
BWTTCACACCT-

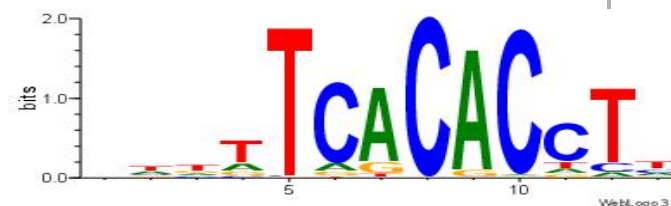
Original motif

Consensus sequence: DAGGTGTGAAHDH



Reverse complement motif

Consensus sequence: HDHTTCACACCTD



Dataset #: 2 Motif ID: 75 Motif name: Motif 75

Original motif

Consensus sequence: GMTAATTA

Reverse complement motif

Consensus sequence: TAATTAYC



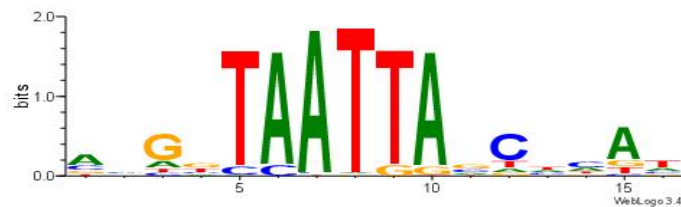
Best Matches for Motif ID 75 (Highest to Lowest)

Motif ID: [MA0904.1](#)
 Motif name: Hoxb5
 Taxon: Vertebrates
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 7
 Number of overlap: 8
 Similarity score: 0.0176518

Alignment:
 HTDHGVTAAATTABCDT
 -----TAATTAYC--

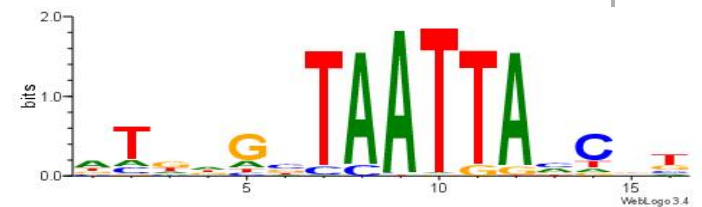
Original motif

Consensus sequence: AHGBTAATTAVCHHAH



Reverse complement motif

Consensus sequence: HTDHGVTAAATTABCDT



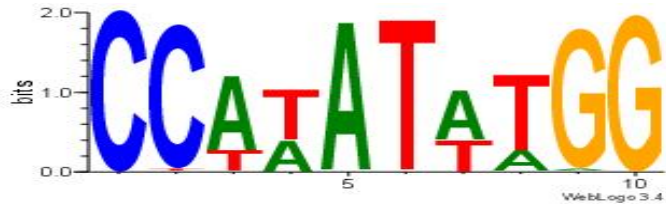
Dataset #: 2

Motif ID: 76

Motif name: Motif 76

Original motif

Consensus sequence: CCAWATWTGG



Reverse complement motif

Consensus sequence: CCAWATWTGG



Best Matches for Motif ID 76 (Highest to Lowest)

Motif ID: [MA0083.3](#)
Motif name: SRF
Taxon: Vertebrates
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

Alignment:

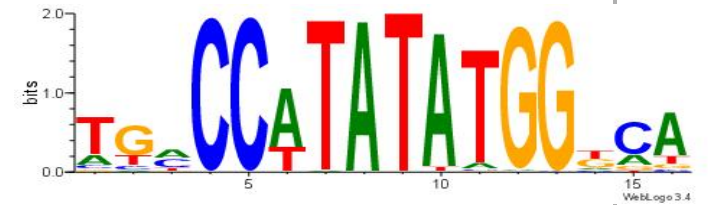
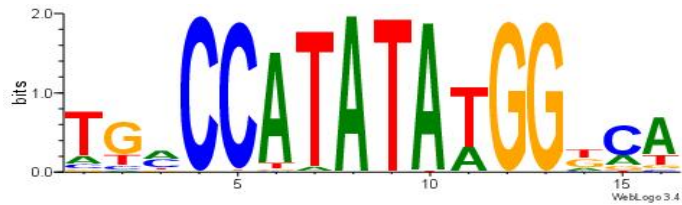
```
TGMCCATATATGGKCA  
---CCAWATWTGG---
```

Original motif

Consensus sequence: TGMCCATATATGGKCA

Reverse complement motif

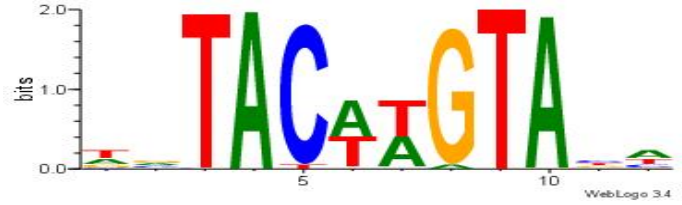
Consensus sequence: TGRCCATATATGGYCA



Dataset #: 2 Motif ID: 77 Motif name: Motif 77

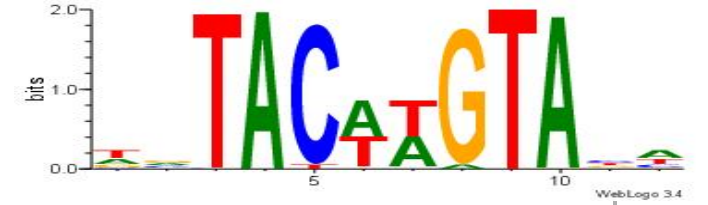
Original motif

Consensus sequence: DVTACWWGTABH



Reverse complement motif

Consensus sequence: HBTACWWGTAVD



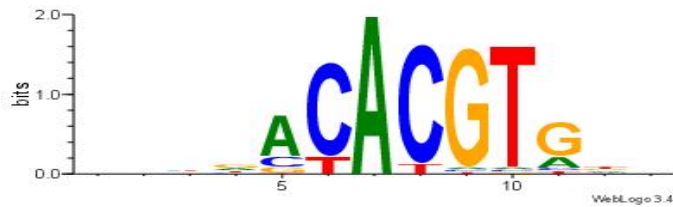
Best Matches for Motif ID 77 (Highest to Lowest)

Motif ID:	MA0941.1
Motif name:	ABF2
Taxon:	Plants
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	12
Similarity score:	0.0341371

Alignment:
 DDCACGTGTHHBB
 HBTACWWGTAVD-

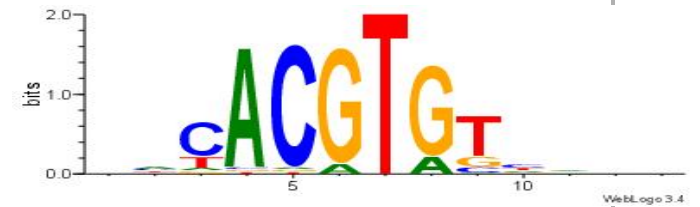
Original motif

Consensus sequence: BDBDACACGTGDB



Reverse complement motif

Consensus sequence: DDCACGTGTHHBB



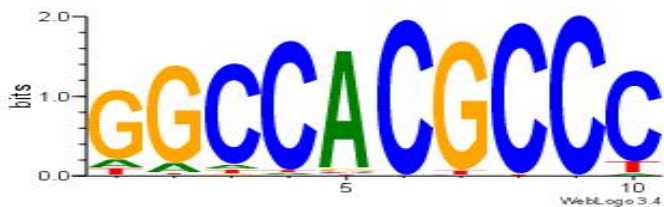
Dataset #: 2

Motif ID: 78

Motif name: Motif 78

Original motif

Consensus sequence: GGCCACGCC



Reverse complement motif

Consensus sequence: GGGCGTGGCC



Best Matches for Motif ID 78 (Highest to Lowest)

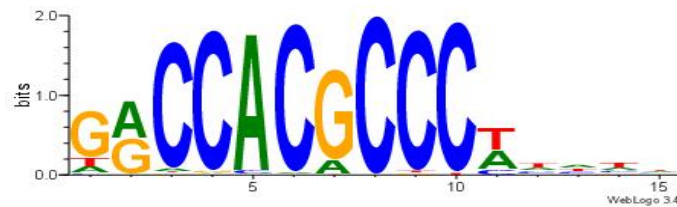
Motif ID:	MA0742.1
Motif name:	Klf12
Taxon:	Vertebrates
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	10
Similarity score:	0

Alignment:

GRCCACGCCCWHHHH
GGCCACGCC-----

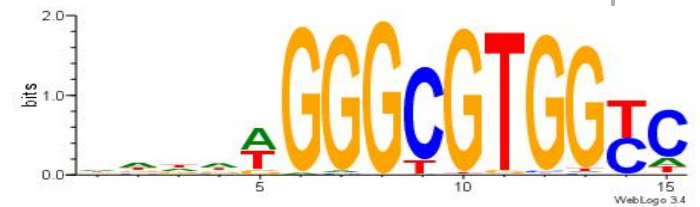
Original motif

Consensus sequence: GRCCACGCCCWHHHH



Reverse complement motif

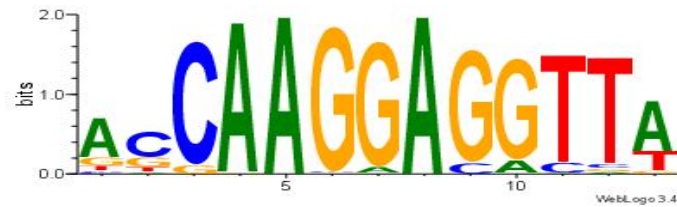
Consensus sequence: HHHHWGGGCGTGGKC



Dataset #: 2 Motif ID: 79 Motif name: Motif 79

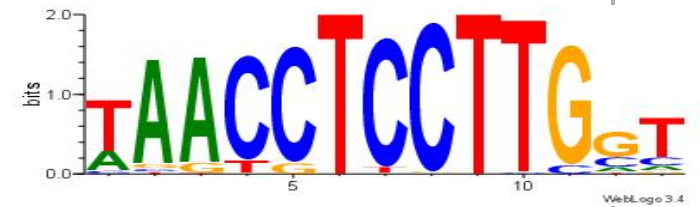
Original motif

Consensus sequence: ACCAAGGAGGTTA



Reverse complement motif

Consensus sequence: TAACCTCCTTGGT



Best Matches for Motif ID 79 (Highest to Lowest)

Motif ID:	MA0308.1
Motif name:	GSM1
Taxon:	Fungi
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	4

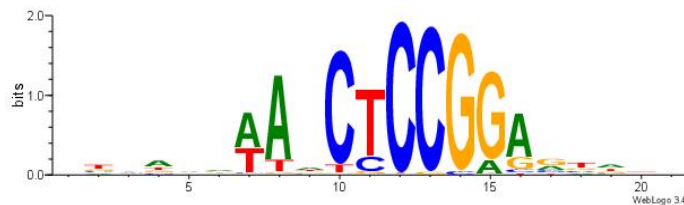
Number of overlap: 13
Similarity score: 0.0653916

Alignment:

HDDVVTCCGGAGDTWDDDHVH
---ACCAAGGAGGTTA-----

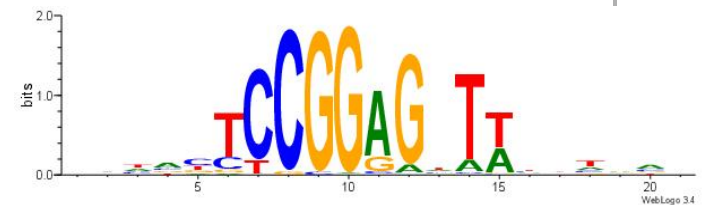
Original motif

Consensus sequence: HBHDDDWADCTCCGGAVBDDH



Reverse complement motif

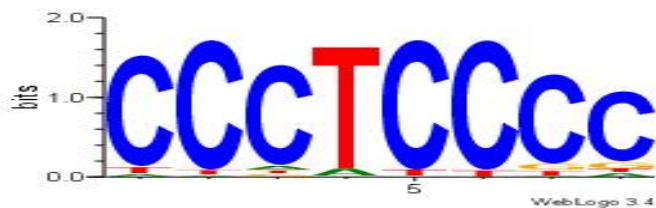
Consensus sequence: HDDVVTCCGGAGDTWDDDHVH



Dataset #: 2 Motif ID: 80 Motif name: Motif 80

Original motif

Consensus sequence: CCCTCCCC



Reverse complement motif

Consensus sequence: GGGGAGGG



Best Matches for Motif ID 80 (Highest to Lowest)

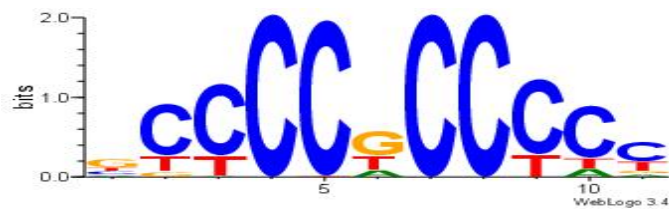
Motif ID: [MA0079.3](#)
Motif name: SP1
Taxon: Vertebrates

Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2
Number of overlap:	8
Similarity score:	0.0246016

Alignment:
 BCCCCKCCCC
 --CCCTCCCC-

Original motif

Consensus sequence: BCCCCKCCCC



Reverse complement motif

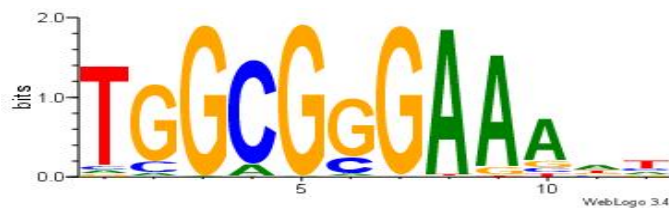
Consensus sequence: GGGGYGGGG



Dataset #: 2 Motif ID: 81 Motif name: Motif 81

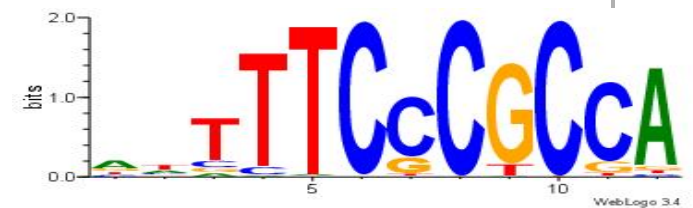
Original motif

Consensus sequence: TGGCGGAAADH



Reverse complement motif

Consensus sequence: HDTTCCCGCCA



Best Matches for Motif ID 81 (Highest to Lowest)

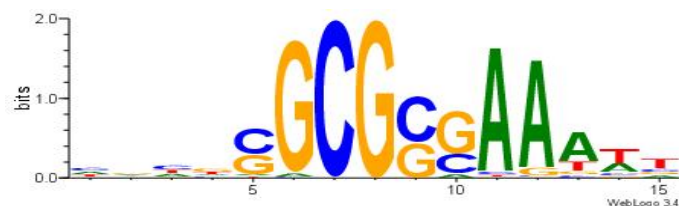
Motif ID: [MA0541.1](#)
Motif name: efl-1
Taxon: Nematodes
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 4
Number of overlap: 12
Similarity score: 0.0282826

Alignment:

```
HDHDSGCGSGAAAWT  
---TGGCGGGAAADH
```

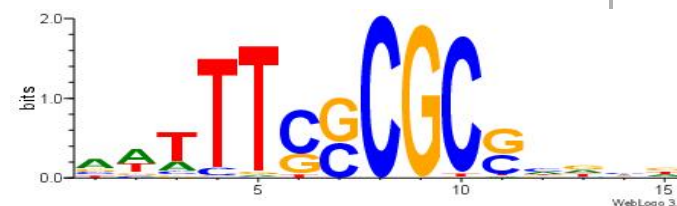
Original motif

Consensus sequence: HDHDSGCGSGAAAWT



Reverse complement motif

Consensus sequence: AWTTCSCGCSHDHD



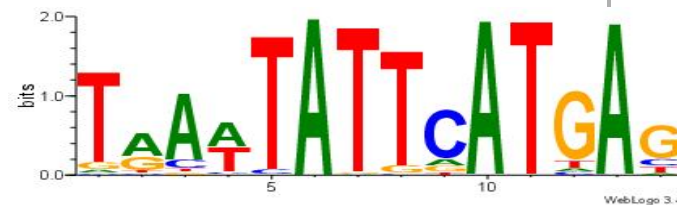
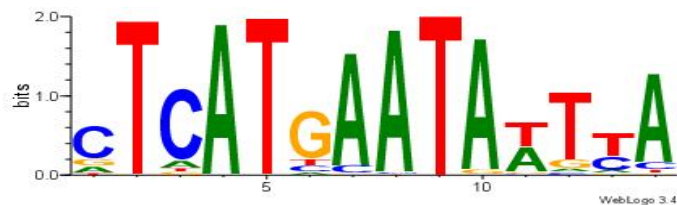
Dataset #: 2 Motif ID: 82 Motif name: Motif 82

Original motif

Consensus sequence: CTCATGAATAWTYA

Reverse complement motif

Consensus sequence: TMAWTATTCATGAG

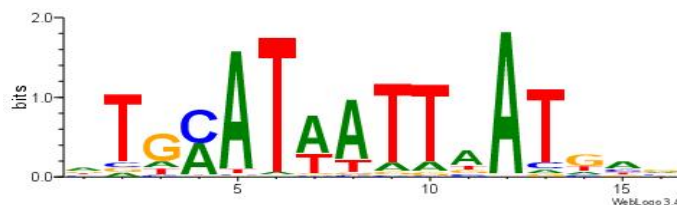


Best Matches for Motif ID 82 (Highest to Lowest)

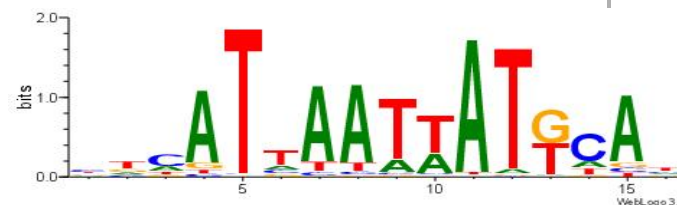
Motif ID: [MA0791.1](#)
 Motif name: POU4F3
 Taxon: Vertebrates
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0.0563832

Alignment:
 VHCATTAATWATRCAD
 --TMAWTATTCATGAG

Original motif
 Consensus sequence: DTGMATWATTAATGHV



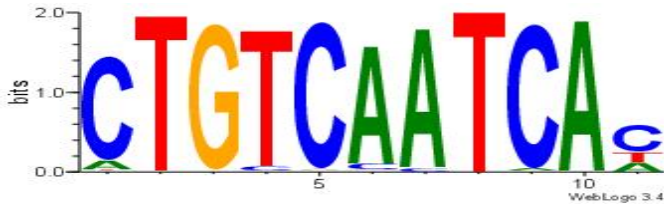
Reverse complement motif
 Consensus sequence: VHCATTAATWATRCAD



Dataset #: 2 Motif ID: 83 Motif name: Motif 83

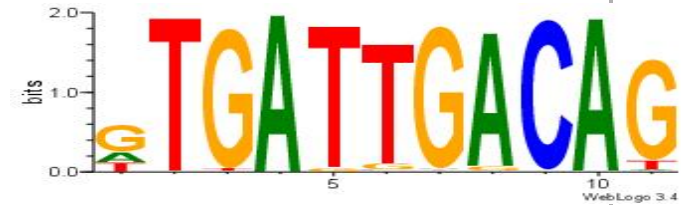
Original motif

Consensus sequence: CTGTC AATCA C



Reverse complement motif

Consensus sequence: GTGATTGACAG



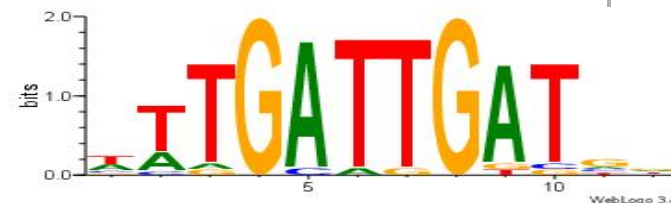
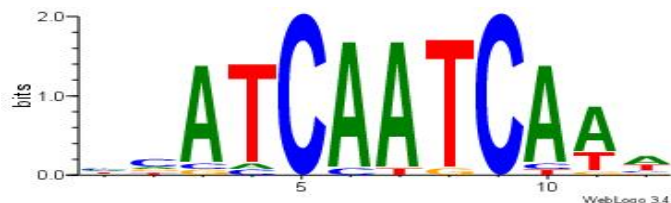
Best Matches for Motif ID 83 (Highest to Lowest)

Motif ID: [MA0070.1](#)
Motif name: PBX1
Taxon: Vertebrates
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: 0.0642241

Alignment:
WTTGATTGATBD
-GTGATTGACAG

Original motif
Consensus sequence: HBATCAATCAAW

Reverse complement motif
Consensus sequence: WTTGATTGATBD



Dataset #: 2 Motif ID: 84 Motif name: Motif 84

Original motif

Consensus sequence: CAGGTAAG



Reverse complement motif

Consensus sequence: CTTACCTG



Best Matches for Motif ID 84 (Highest to Lowest)

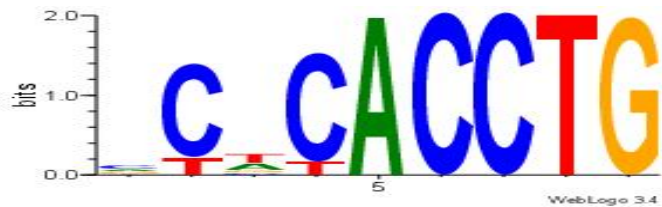
Motif ID:	MA0103.2
Motif name:	ZEB1
Taxon:	Vertebrates
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	8
Similarity score:	0.00667179

Alignment:

CAGGTGwGV
CAGGTAAG-

Original motif

Consensus sequence: VCWCACCTG



Reverse complement motif

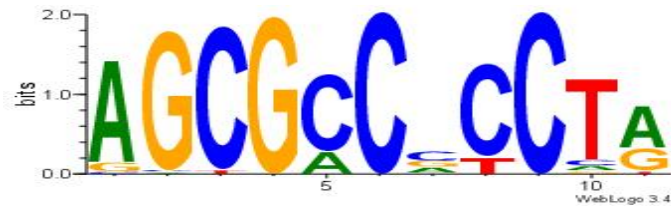
Consensus sequence: CAGGTGwGV



Dataset #: 2 Motif ID: 85 Motif name: Motif 85

Original motif

Consensus sequence: AGCGCCVCCTR



Reverse complement motif

Consensus sequence: KAGGVGGCGCT



Best Matches for Motif ID 85 (Highest to Lowest)

Motif ID:	MA0531.1
Motif name:	CTCF
Taxon:	Insects
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: 0.0422441

Alignment:

KGCGCCAKCTMRVGB
----KAGGVGGCGCT

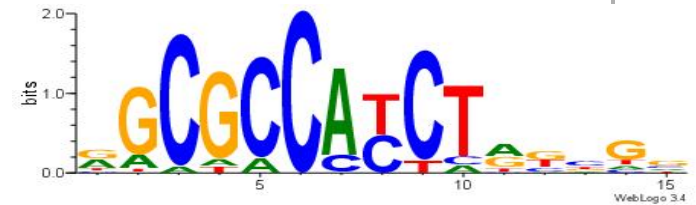
Original motif

Consensus sequence: BCVMYAGRTGGCGCY



Reverse complement motif

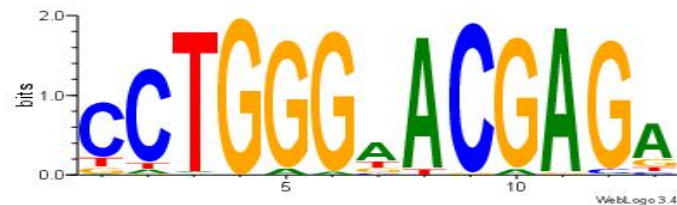
Consensus sequence: KGCGCCAKCTMRVGB



Dataset #: 2 Motif ID: 86 Motif name: Motif 86

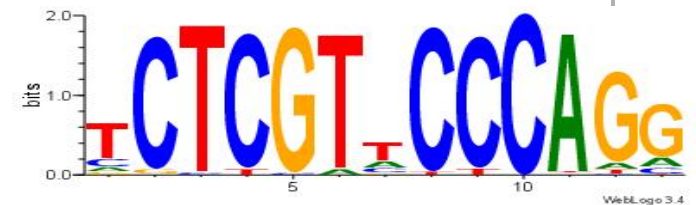
Original motif

Consensus sequence: CCTGGGAACGAGA



Reverse complement motif

Consensus sequence: TCTCGTCCAGG



Best Matches for Motif ID 86 (Highest to Lowest)

Motif ID: [MA0085.1](#)
Motif name: Su(H)
Taxon: Insects
Matching format of first motif: Original Motif

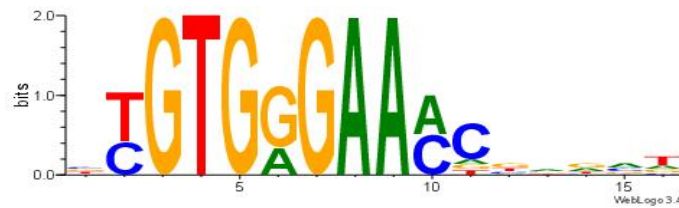
Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 13
 Similarity score: 0.0866213

Alignment:

BYGTGGGAAMCBDDVD
 -CCTGGGAACGAGA--

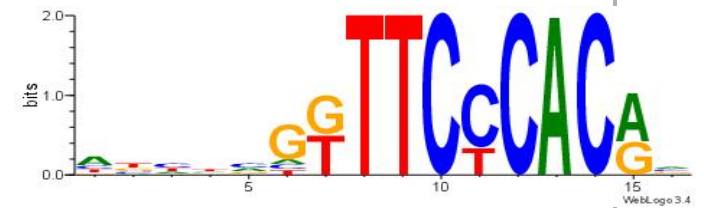
Original motif

Consensus sequence: BYGTGGGAAMCBDDVD



Reverse complement motif

Consensus sequence: DBHBBGYTTCACMB



Dataset #: 2 Motif ID: 87 Motif name: Motif 87

Original motif

Consensus sequence: RTGACGTASD



Reverse complement motif

Consensus sequence: DSTACGTCAK



Best Matches for Motif ID 87 (Highest to Lowest)

Motif ID: [MA0097.1](#)
 Motif name: bZIP911
 Taxon: Plants
 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: 0.0406054

Alignment:
 GRCCACGTCACK
 -DSTACGTCAK-

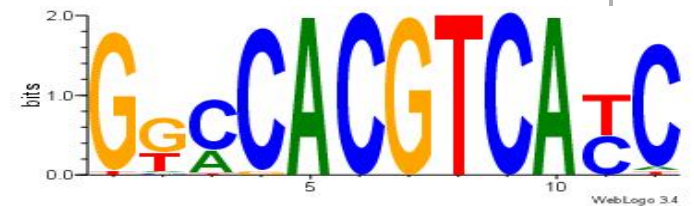
Original motif

Consensus sequence: GRTGACGTGGMC



Reverse complement motif

Consensus sequence: GRCCACGTCACK



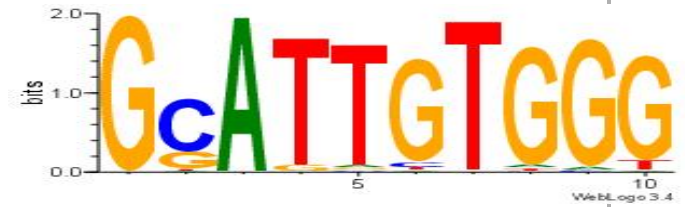
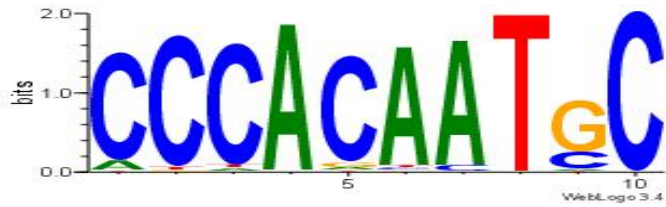
Dataset #: 2 Motif ID: 88 Motif name: Motif 88

Original motif

Consensus sequence: CCCACAATGC

Reverse complement motif

Consensus sequence: GCATTGTGGG



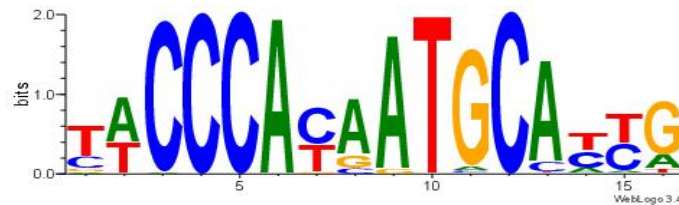
Best Matches for Motif ID 88 (Highest to Lowest)

Motif ID: [MA0088.2](#)
 Motif name: ZNF143
 Taxon: Vertebrates
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 5
 Number of overlap: 10
 Similarity score: 0.0155351

Alignment:
 CMMTGCATTKTGGGWA
 ----GCATTGTGGG--

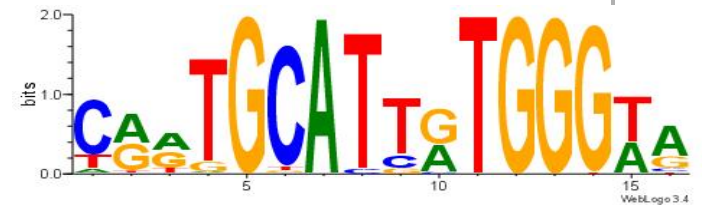
Original motif

Consensus sequence: TWCCCA YAATGCAYYG



Reverse complement motif

Consensus sequence: CMMTGCATTKTGGGWA



Dataset #: 2 **Motif ID: 89** **Motif name: Motif 89**

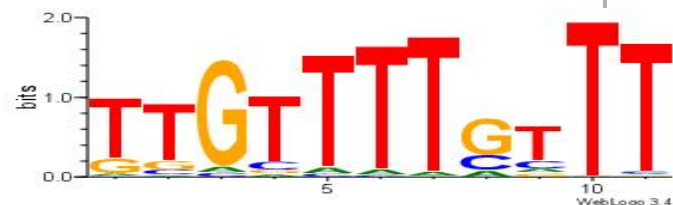
Original motif

Consensus sequence: AAACAAAACAA



Reverse complement motif

Consensus sequence: TTGTTTGT



Best Matches for Motif ID 89 (Highest to Lowest)

Motif ID:	MA0296.1
Motif name:	FKH1
Taxon:	Fungi
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	9
Number of overlap:	11
Similarity score:	0.0515149

Alignment:

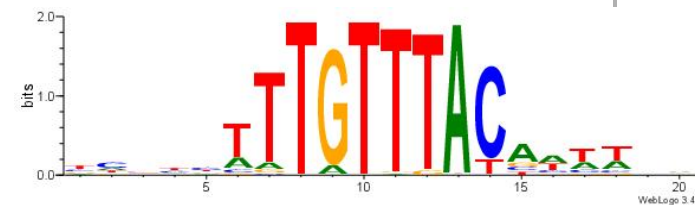
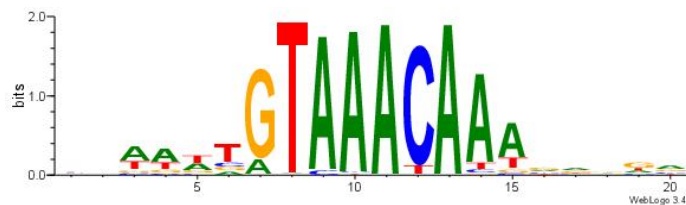
```
BHHDVTTTGTTTACAWWHV  
-TTGTTTGTTT-----
```

Original motif

Consensus sequence: BDWWWTGTAAACAAVDDDDV

Reverse complement motif

Consensus sequence: BHHDVTTTGTTTACAWWHV



Dataset #: 2 Motif ID: 90 Motif name: Motif 90

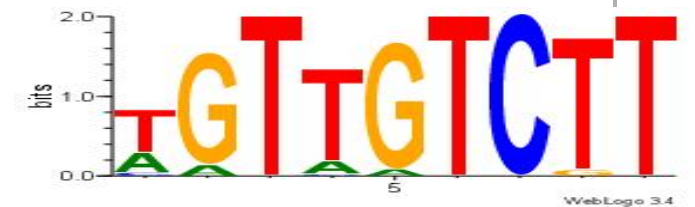
Original motif

Consensus sequence: AAGACAACA



Reverse complement motif

Consensus sequence: TGTTGTCTT



Best Matches for Motif ID 90 (Highest to Lowest)

Motif ID:	MA0029.1
Motif name:	Mecom
Taxon:	Vertebrates
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	9
Similarity score:	0.0220224

Alignment:

AAGAYAAGATAABA
-----AAGACAACA

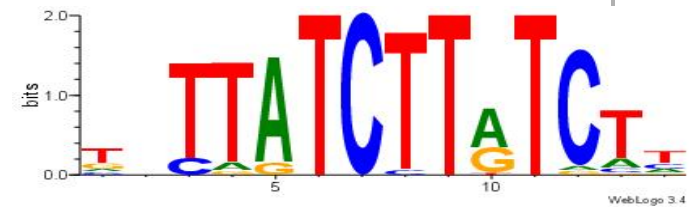
Original motif

Consensus sequence: AAGAYAAGATAABA



Reverse complement motif

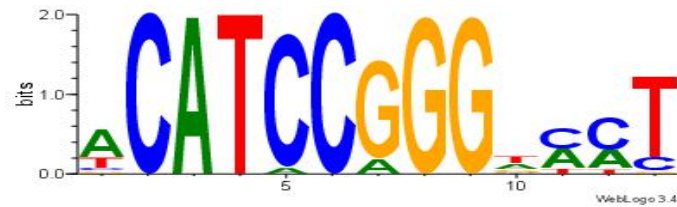
Consensus sequence: TBTTATCTTMTCTT



Dataset #: 2 Motif ID: 91 Motif name: Motif 91

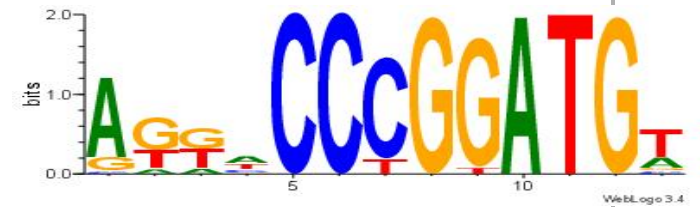
Original motif

Consensus sequence: ACATCCGGDMMT



Reverse complement motif

Consensus sequence: ARRDCCCGGATGT



Best Matches for Motif ID 91 (Highest to Lowest)

Motif ID:	MA0308.1
Motif name:	GSM1
Taxon:	Fungi
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	8

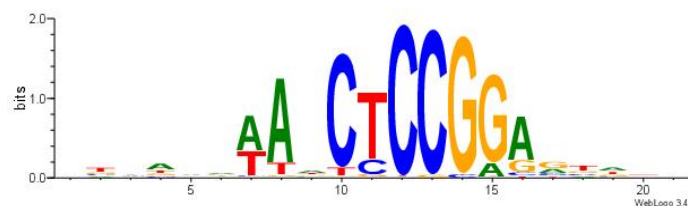
Number of overlap: 13
Similarity score: 0.0730858

Alignment:

HDDVVTCCGGAGDTWDDDHVH
-ARRDCCCGGATGT-----

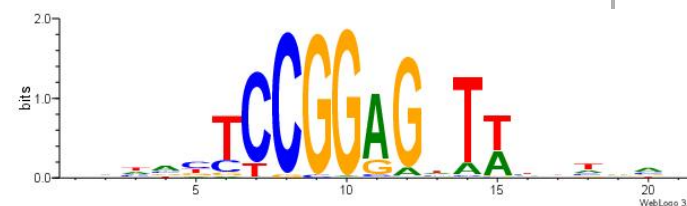
Original motif

Consensus sequence: HBHDDDWADCTCCGGAVBDDH



Reverse complement motif

Consensus sequence: HDDVVTCCGGAGDTWDDDHVH



Dataset #: 2 Motif ID: 92 Motif name: Motif 92

Original motif

Consensus sequence: AAAAYAAACAA



Reverse complement motif

Consensus sequence: TTGTTTKTTTT



Best Matches for Motif ID 92 (Highest to Lowest)

Motif ID: [MA0481.1](#)
Motif name: FOXP1
Taxon: Vertebrates

Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	3
Number of overlap:	11
Similarity score:	0.0452708

Alignment:

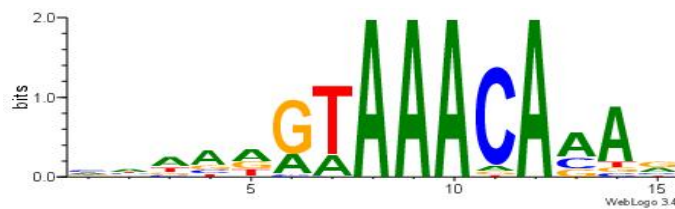
```

HHDADGTAAACAAAV
--AAAAYAAACAA--

```

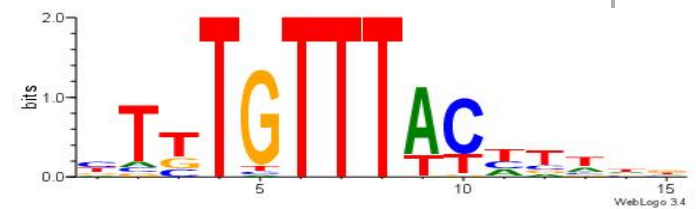
Original motif

Consensus sequence: HHDADGTAAACAAAV



Reverse complement motif

Consensus sequence: VTTTGTTTACDTHD



Dataset #: 2 Motif ID: 93 Motif name: Motif 93

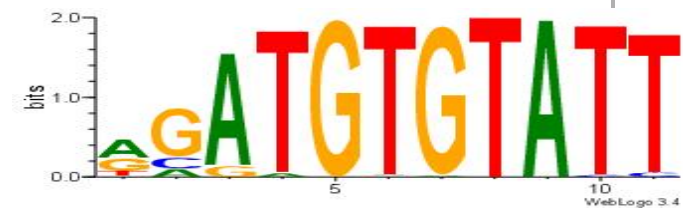
Original motif

Consensus sequence: AATACACATCY



Reverse complement motif

Consensus sequence: MGATGTGTATT



Best Matches for Motif ID 93 (Highest to Lowest)

Motif ID: [MA0040.1](#)
Motif name: Foxq1
Taxon: Vertebrates
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: 0.0480007

Alignment:

WATAACAATH
AATACACATCY

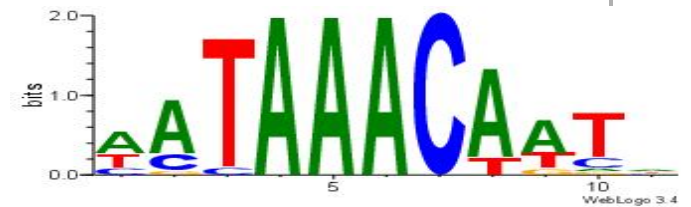
Original motif

Consensus sequence: HATTGTTTATW



Reverse complement motif

Consensus sequence: WATAACAATH



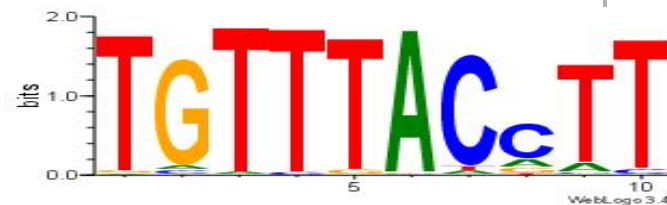
Dataset #: 2 Motif ID: 94 Motif name: Motif 94

Original motif

Consensus sequence: AAGGTAAACA

Reverse complement motif

Consensus sequence: TGTTTACCTT



Best Matches for Motif ID 94 (Highest to Lowest)

Motif ID: [MA0852.1](#)
 Motif name: Foxk1
 Taxon: Vertebrates
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 10
 Similarity score: 0.0286025

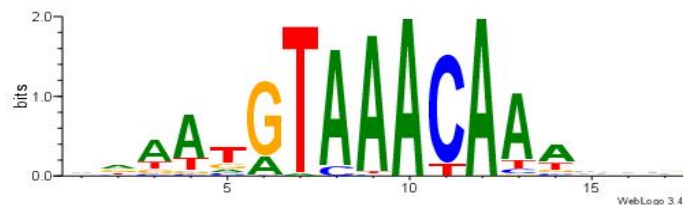
Alignment:

```

DDAATGTAAACAAAVVB
--AAGGTAAACA-----
  
```

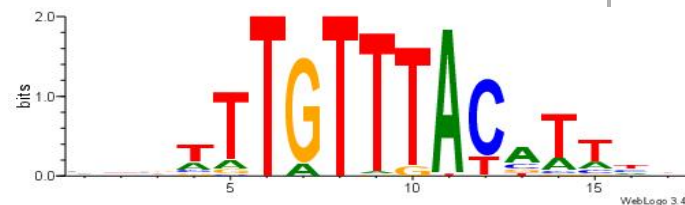
Original motif

Consensus sequence: DDAATGTAAACAAAVVB



Reverse complement motif

Consensus sequence: BBVTTTGTTTACATTDD



Dataset #: 2

Motif ID: 95

Motif name: Motif 95

Original motif

Consensus sequence: CGCCGCCA



Reverse complement motif

Consensus sequence: TGGCGGCG



Best Matches for Motif ID 95 (Highest to Lowest)

Motif ID: [MA1034.1](#)
Motif name: Os05g0497200
Taxon: Plants
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 8
Similarity score: 0.00831137

Alignment:
CGSCGCCR
CGCCGCCA

Original motif
Consensus sequence: CGSCGCCR

Reverse complement motif
Consensus sequence: KGGCGSCG



Dataset #: 2 Motif ID: 96 Motif name: Motif 96

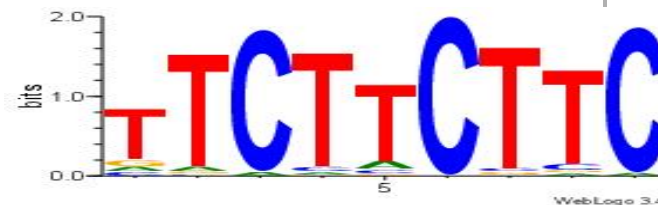
Original motif

Consensus sequence: GAAGAAGAA



Reverse complement motif

Consensus sequence: TTCTTCTTC



Best Matches for Motif ID 96 (Highest to Lowest)

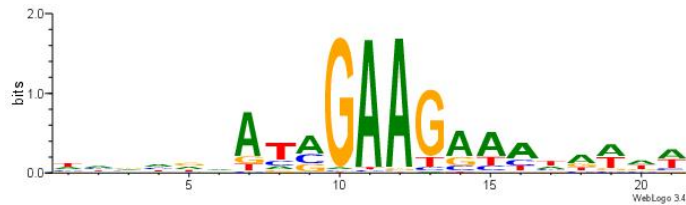
Motif ID:	MA0377.1
Motif name:	SFL1
Taxon:	Fungi
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	4
Number of overlap:	9
Similarity score:	0.034731

Alignment:

WDWDHTTTCTTCYATHHHVHH
 ---TTCTTCTTC-----

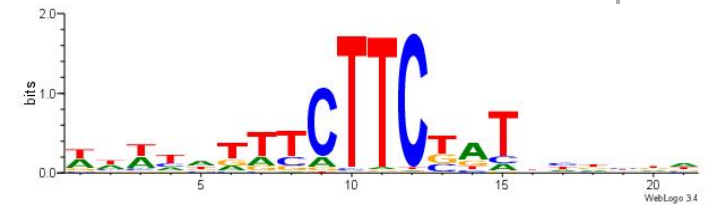
Original motif

Consensus sequence: HHVHDHATMGAAGAAHWDWD



Reverse complement motif

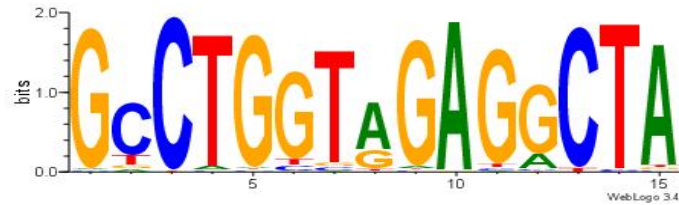
Consensus sequence: WDWDHTTTCTTCYATHHHVHH



Dataset #: 2 Motif ID: 97 Motif name: Motif 97

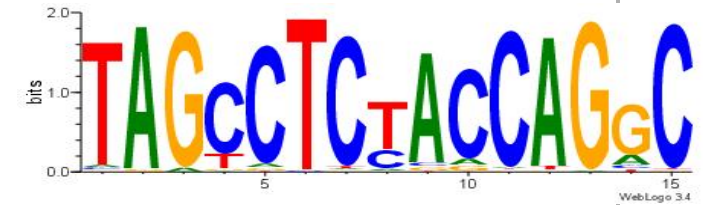
Original motif

Consensus sequence: GCCTGGTAGAGGCTA



Reverse complement motif

Consensus sequence: TAGCCTCTACCAGGC



Best Matches for Motif ID 97 (Highest to Lowest)

Motif ID:	MA0139.1
Motif name:	CTCF
Taxon:	Vertebrates
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	15

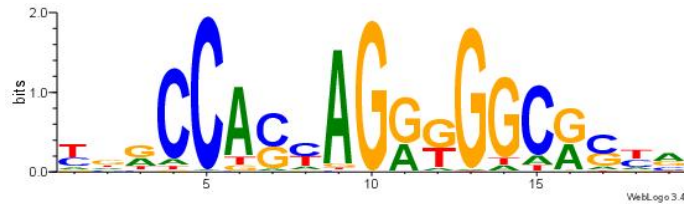
Similarity score: 0.0871174

Alignment:

YDRCCASYAGRKGGCRSYV
----GCCTGGTAGAGGCTA

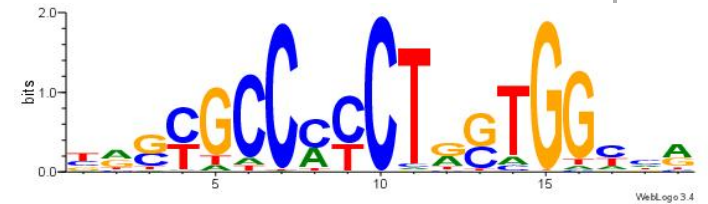
Original motif

Consensus sequence: YDRCCASYAGRKGGCRSYV



Reverse complement motif

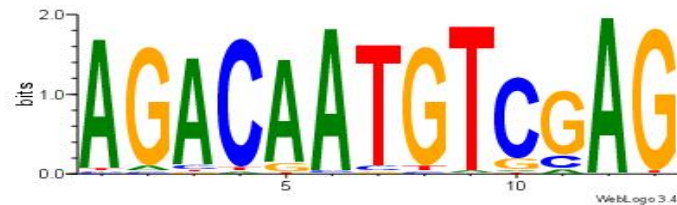
Consensus sequence: BMSGCCYMCTKSTGGMHH



Dataset #: 2 Motif ID: 98 Motif name: Motif 98

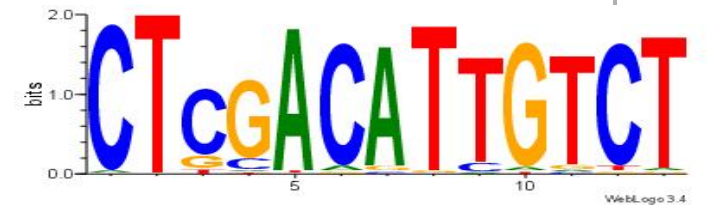
Original motif

Consensus sequence: AGACAATGTCGAG



Reverse complement motif

Consensus sequence: CTCGACATTGTCT



Best Matches for Motif ID 98 (Highest to Lowest)

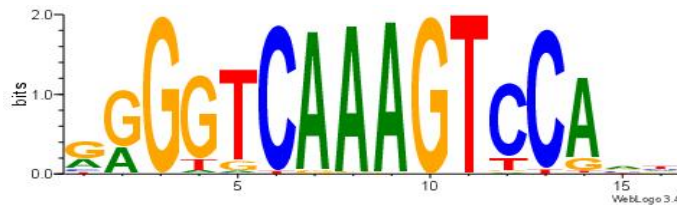
Motif ID: [MA0114.3](#)
Motif name: Hnf4a
Taxon: Vertebrates
Matching format of first motif: Reverse Complement

Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 13
 Similarity score: 0.0795723

Alignment:
 HBTGGACTTTGACCCM
 -CTCGACATTGTCT--

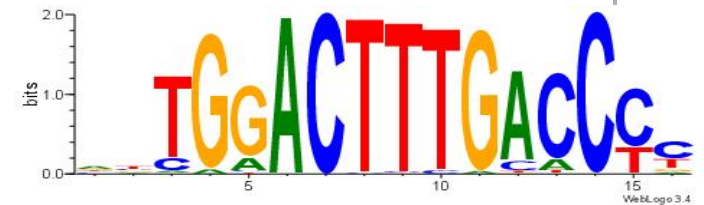
Original motif

Consensus sequence: RGGGTCAAAGTCCA



Reverse complement motif

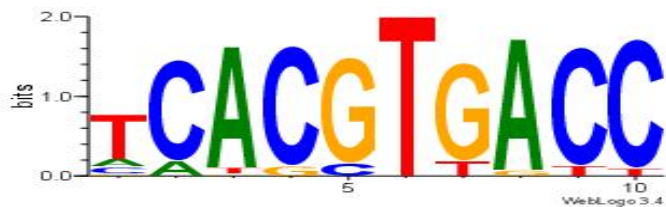
Consensus sequence: HBTGGACTTTGACCCM



Dataset #: 2 Motif ID: 99 Motif name: Motif 99

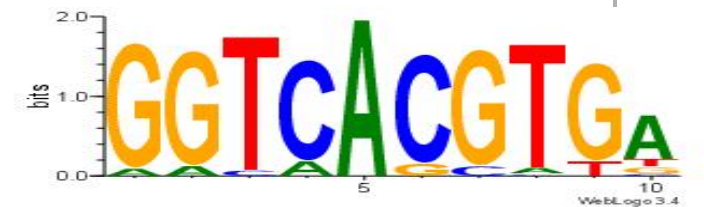
Original motif

Consensus sequence: TCACGTGACC



Reverse complement motif

Consensus sequence: GGTCACGTGA



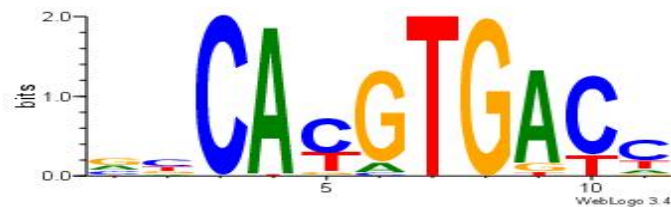
Best Matches for Motif ID 99 (Highest to Lowest)

Motif ID: [MA0093.2](#)
 Motif name: USF1
 Taxon: Vertebrates
 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: 0.0323214

Alignment:
 VBCAYGTGACC
 -TCACGTGACC

Original motif

Consensus sequence: VBCAYGTGACC



Reverse complement motif

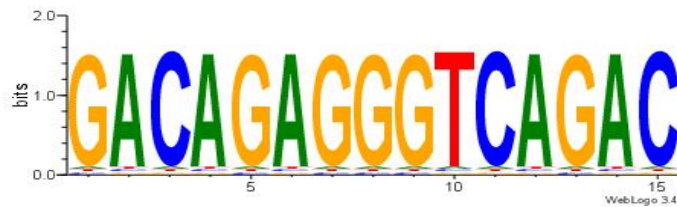
Consensus sequence: GGTCACKTGBV



Dataset #: 2 Motif ID: 100 Motif name: Motif 100

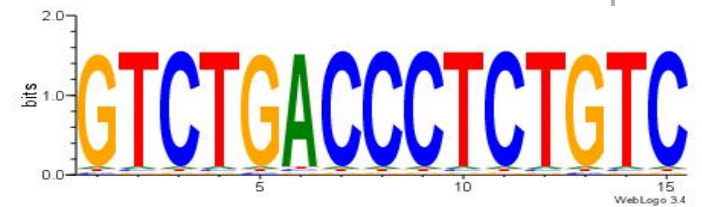
Original motif

Consensus sequence: GACAGAGGGTCAGAC



Reverse complement motif

Consensus sequence: GTCTGACCCTCTGTC



Best Matches for Motif ID 100 (Highest to Lowest)

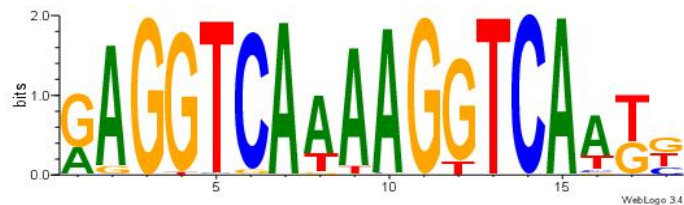
Motif ID: [MA0729.1](#)
Motif name: RARA
Taxon: Vertebrates
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 15
Similarity score: 0.0856351

Alignment:

```
GAGGTCAAAGGTCAAKK  
---GACAGAGGGTCAGAC
```

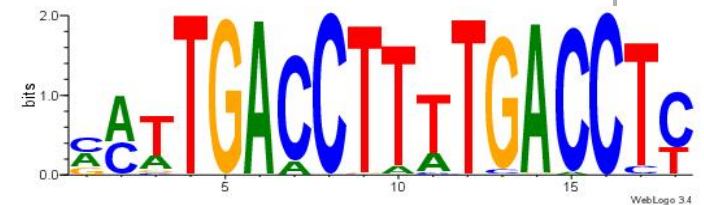
Original motif

Consensus sequence: GAGGTCAAAGGTCAAKK



Reverse complement motif

Consensus sequence: YRTTGACCTTTTGACCTC



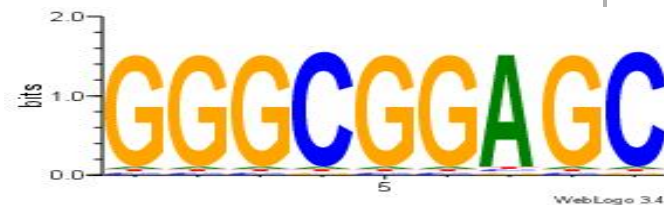
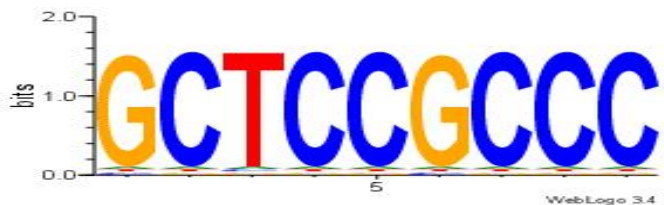
Dataset #: 2 Motif ID: 101 Motif name: Motif 101

Original motif

Consensus sequence: GCTCCGCC

Reverse complement motif

Consensus sequence: GGGCGGAGC



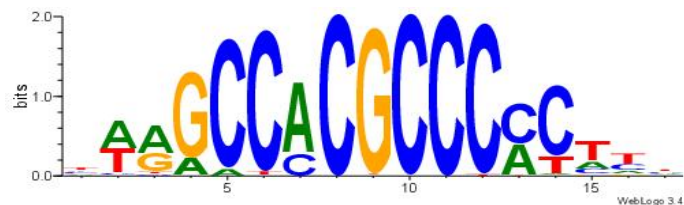
Best Matches for Motif ID 101 (Highest to Lowest)

Motif ID: [MA0685.1](#)
 Motif name: SP4
 Taxon: Vertebrates
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 6
 Number of overlap: 9
 Similarity score: 0.0231825

Alignment:
 BWRGCCACGCCCMCTYH
 ---GCTCCGCC-----

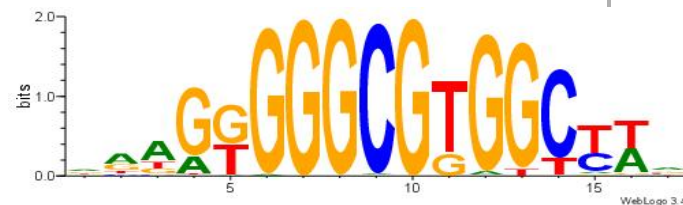
Original motif

Consensus sequence: BWRGCCACGCCCMCTYH



Reverse complement motif

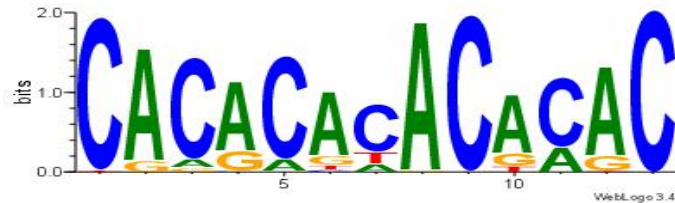
Consensus sequence: HMAGRGGGCGTGGCKWV



Dataset #: 2 **Motif ID: 102** **Motif name: Motif 102**

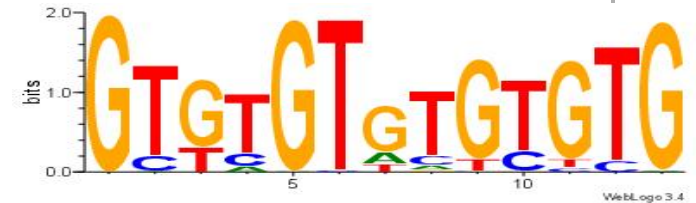
Original motif

Consensus sequence: CACACACACAC



Reverse complement motif

Consensus sequence: GTGTGTGTGTG



Best Matches for Motif ID 102 (Highest to Lowest)

Motif ID:	MA0538.1
Motif name:	daf-12
Taxon:	Nematodes
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	13
Similarity score:	0.0427041

Alignment:

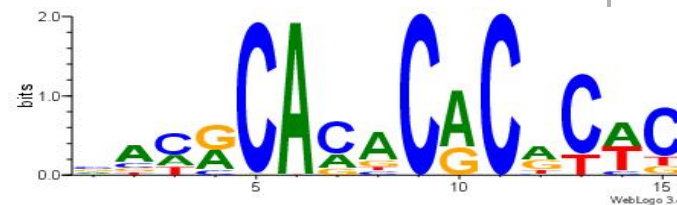
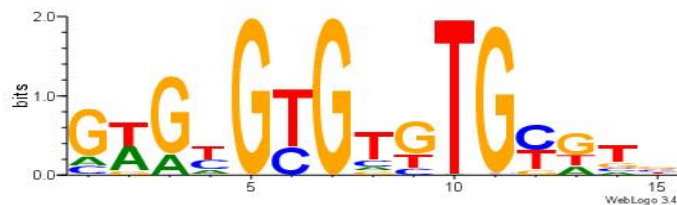
```
BACKCACACACMCWC  
GTGTGTGTGTGTG--
```

Original motif

Consensus sequence: GWGYGTGTGTGYGTB

Reverse complement motif

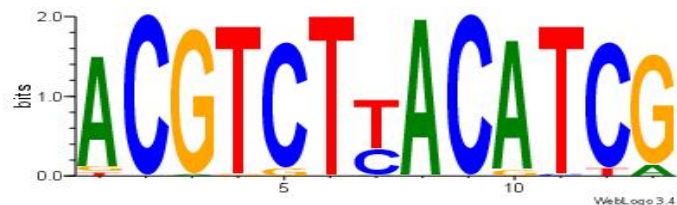
Consensus sequence: BACKCACACACMCWC



Dataset #: 2 Motif ID: 103 Motif name: Motif 103

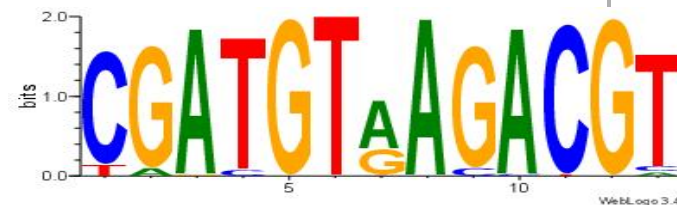
Original motif

Consensus sequence: ACGTCTYACATCG



Reverse complement motif

Consensus sequence: CGATGTMAGACGT



Best Matches for Motif ID 103 (Highest to Lowest)

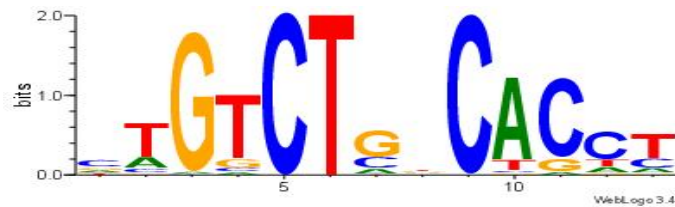
Motif ID:	MA0513.1
Motif name:	SMAD2::SMAD3::SMAD4
Taxon:	Vertebrates
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	13
Similarity score:	0.0949021

Alignment:

AGGTGDCAGACAV
CGATGTMAGACGT

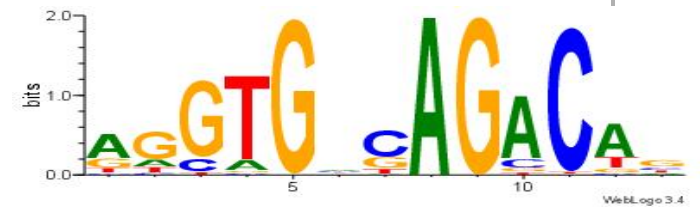
Original motif

Consensus sequence: VTGTCTGDCACCT



Reverse complement motif

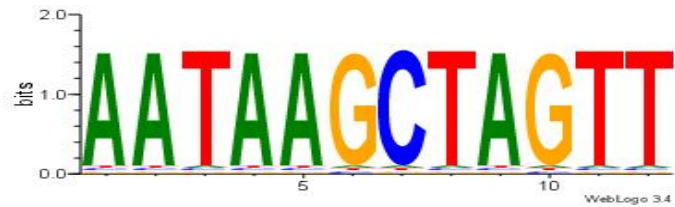
Consensus sequence: AGGTGDCAGACAV



Dataset #: 2 Motif ID: 104 Motif name: Motif 104

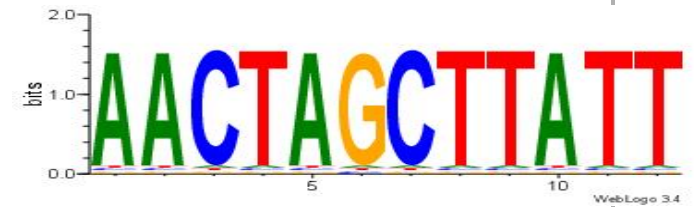
Original motif

Consensus sequence: AATAAGCTAGTT



Reverse complement motif

Consensus sequence: AACTAGCTTATT



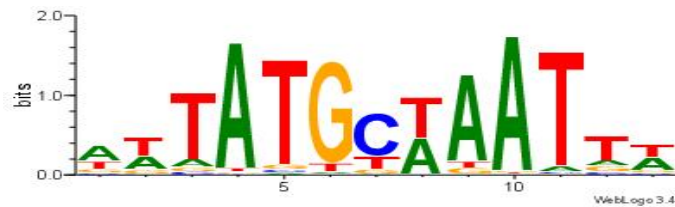
Best Matches for Motif ID 104 (Highest to Lowest)

Motif ID:	MA0788.1
Motif name:	POU3F3
Taxon:	Vertebrates
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2

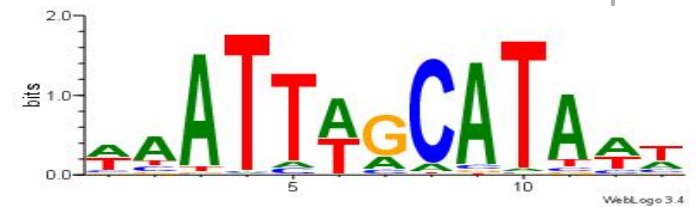
Number of overlap: 12
Similarity score: 0.0583819

Alignment:
WWTATGCWAATTW
AATAAGCTAGTT-

Original motif
Consensus sequence: WWTATGCWAATTW



Reverse complement motif
Consensus sequence: WAATTWGCATAWW



Dataset #: 2 Motif ID: 105 Motif name: Motif 105

Original motif
Consensus sequence: CAGACRAC



Reverse complement motif
Consensus sequence: GTKGTCTG



Best Matches for Motif ID 105 (Highest to Lowest)

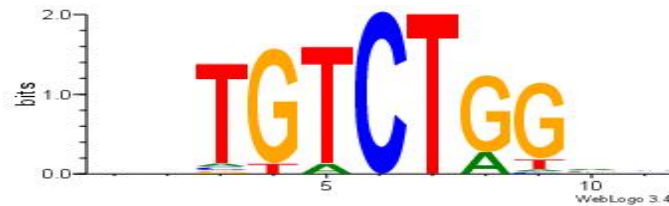
Motif ID: [MA0925.1](#)
Motif name: sma-4
Taxon: Nematodes

Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	8
Similarity score:	0.0307066

Alignment:
DVTGTCTGGVB
---CAGACRAC

Original motif

Consensus sequence: DVTGTCTGGVB



Reverse complement motif

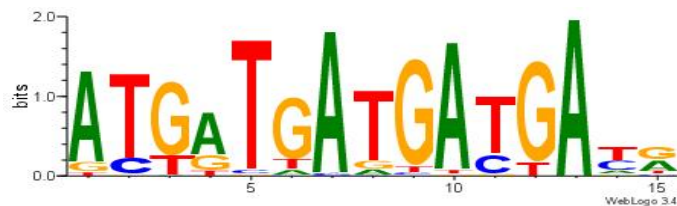
Consensus sequence: BBCCAGACA VB



Dataset #: 2 Motif ID: 106 Motif name: Motif 106

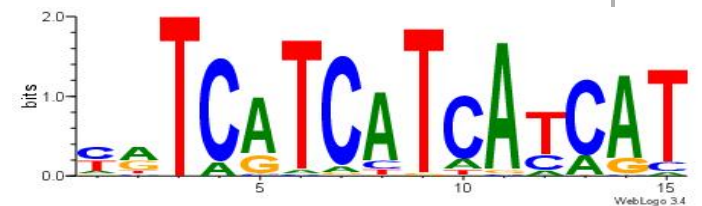
Original motif

Consensus sequence: ATGATGATGATGAYR



Reverse complement motif

Consensus sequence: MMTCATCATCATCAT



Best Matches for Motif ID 106 (Highest to Lowest)

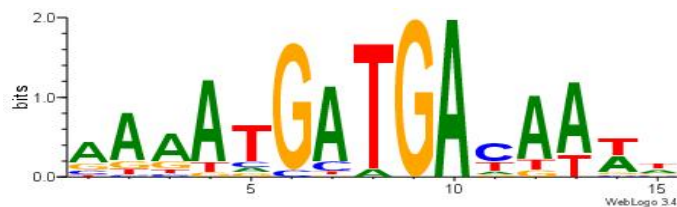
Motif ID: [MA0547.1](#)
 Motif name: skn-1
 Taxon: Nematodes
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 15
 Similarity score: 0.0545893

Alignment:

AAAATGATGACAAWD
 ATGATGATGATGAYR

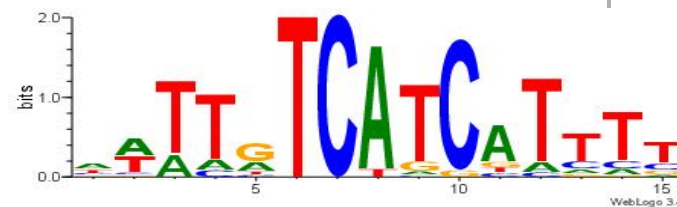
Original motif

Consensus sequence: AAAATGATGACAAWD



Reverse complement motif

Consensus sequence: DWTTGTCATCATTTT



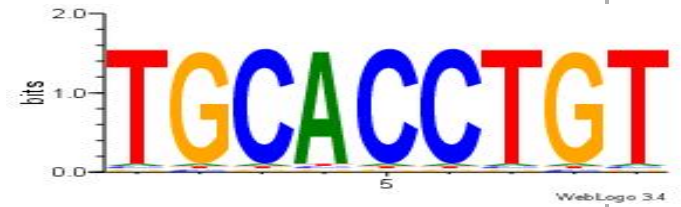
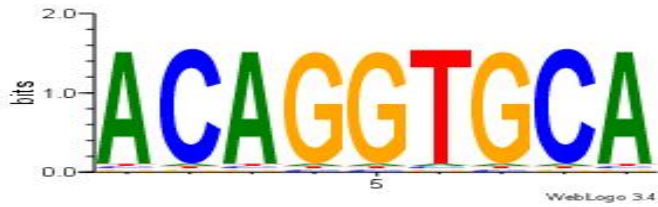
Dataset #: 2 Motif ID: 107 Motif name: Motif 107

Original motif

Consensus sequence: ACAGGTGCA

Reverse complement motif

Consensus sequence: TGCACCTGT



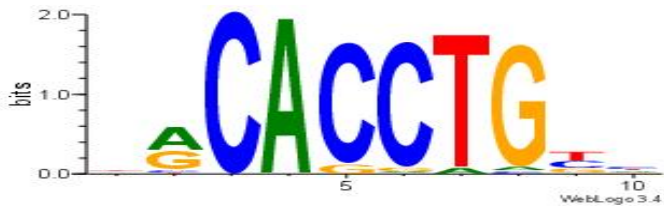
Best Matches for Motif ID 107 (Highest to Lowest)

Motif ID: [MA0824.1](#)
 Motif name: ID4
 Taxon: Vertebrates
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 9
 Similarity score: 0.0401018

Alignment:
 DRCACCTGBH
 TGCACCTGT-

Original motif

Consensus sequence: DRCACCTGBH



Reverse complement motif

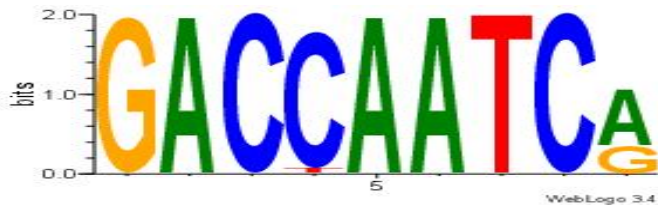
Consensus sequence: DVCAGGTGKD



Dataset #: 2 Motif ID: 108 Motif name: Motif 108

Original motif

Consensus sequence: GACCAATCA



Reverse complement motif

Consensus sequence: TGATTGGTC



Best Matches for Motif ID 108 (Highest to Lowest)

Motif ID: [MA0060.2](#)
Motif name: NFYA
Taxon: Vertebrates
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 3
Number of overlap: 9
Similarity score: 0.0180131

Alignment:

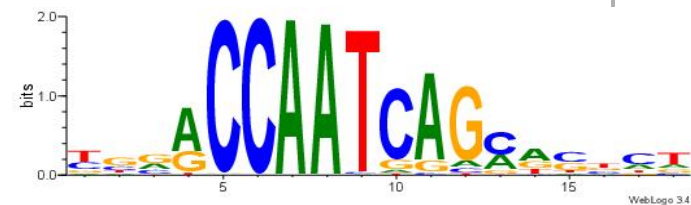
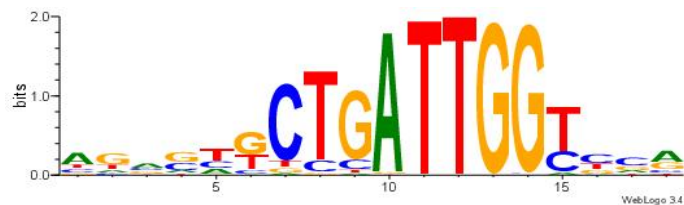
```
AGVSYKCTGATTGGTBVR  
-----TGATTGGTC--
```

Original motif

Consensus sequence: AGVSYKCTGATTGGTBVR

Reverse complement motif

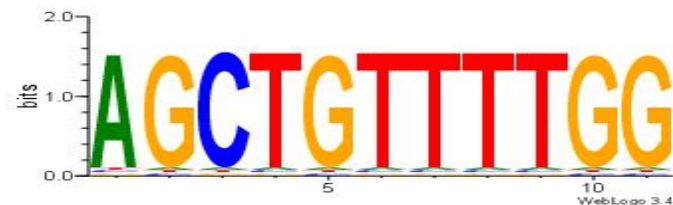
Consensus sequence: KVBACCAATCAGYMSBCT



Dataset #: 2 Motif ID: 109 Motif name: Motif 109

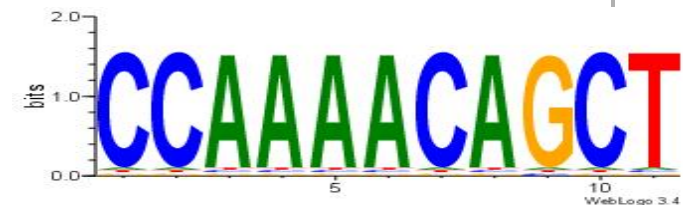
Original motif

Consensus sequence: AGCTGTTTGG



Reverse complement motif

Consensus sequence: CCAAACAGCT



Best Matches for Motif ID 109 (Highest to Lowest)

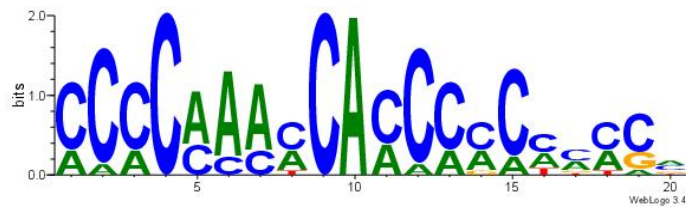
Motif ID:	MA0073.1
Motif name:	RREB1
Taxon:	Vertebrates
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	3
Number of overlap:	11
Similarity score:	0.0758389

Alignment:

CCCCMAAMCAMCCMCMMMC
 --CCAAAACAGCT-----

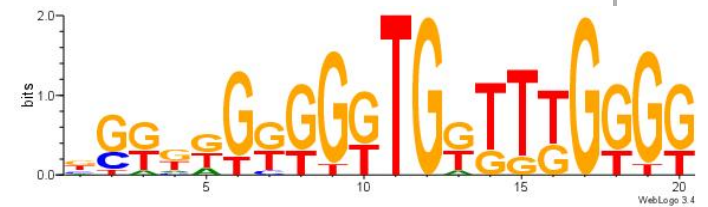
Original motif

Consensus sequence: CCCCMAAMCAMCCMCMMMC



Reverse complement motif

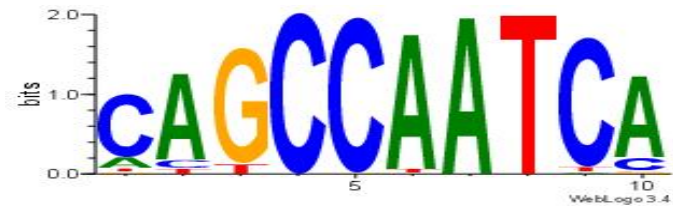
Consensus sequence: BGRRRGRGGRTGRTTYGGGG



Dataset #: 2 Motif ID: 110 Motif name: Motif 110

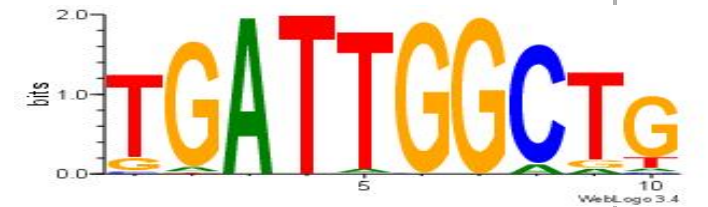
Original motif

Consensus sequence: CAGCCAATCA



Reverse complement motif

Consensus sequence: TGATTGGCTG



Best Matches for Motif ID 110 (Highest to Lowest)

Motif ID:	MA0314.1
Motif name:	HAP3
Taxon:	Fungi
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	3

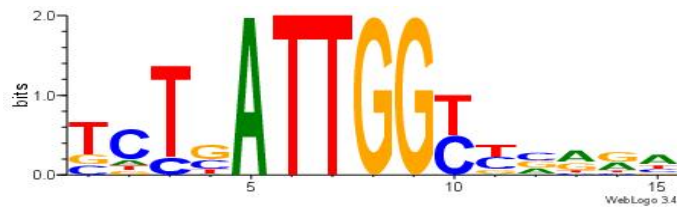
Number of overlap: 10
Similarity score: 0.0179107

Alignment:

TCTSATTGGYYVRRR
--TGATTGGCTG---

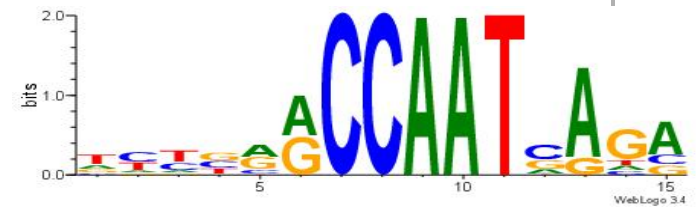
Original motif

Consensus sequence: TCTSATTGGYYVRRR



Reverse complement motif

Consensus sequence: TMKVMMCCAATSAGA



Dataset #: 2 Motif ID: 111 Motif name: Motif 111

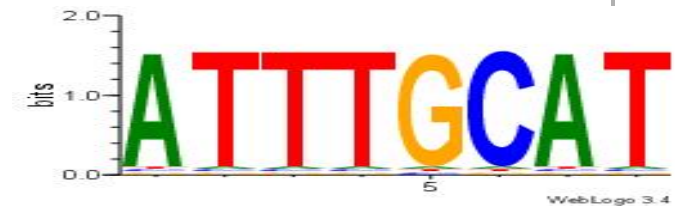
Original motif

Consensus sequence: ATGCAAAT



Reverse complement motif

Consensus sequence: ATTTGCAT



Best Matches for Motif ID 111 (Highest to Lowest)

Motif ID: [MA0507.1](#)
Motif name: POU2F2
Taxon: Vertebrates

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:	0.00743635

Alignment:
 AKATGCAAATDDH
 --ATGCAAAT---

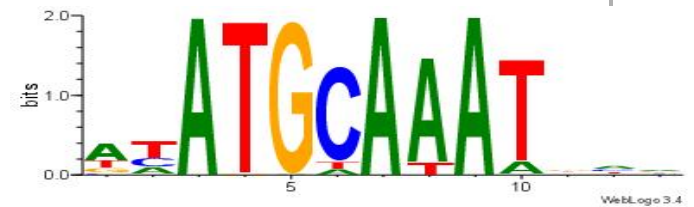
Original motif

Consensus sequence: HDHATTTGCATRT



Reverse complement motif

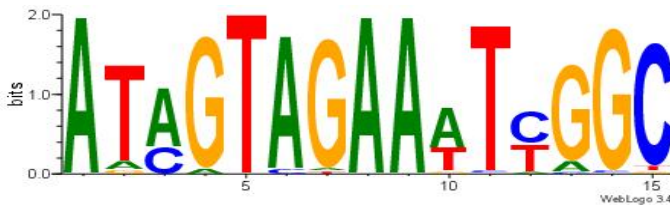
Consensus sequence: AKATGCAAATDDH



Dataset #: 2 Motif ID: 112 Motif name: Motif 112

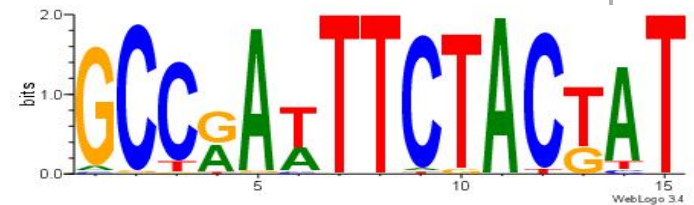
Original motif

Consensus sequence: ATAGTAGAAWTYGGC



Reverse complement motif

Consensus sequence: GCCKAWTTCTACTAT



Best Matches for Motif ID 112 (Highest to Lowest)

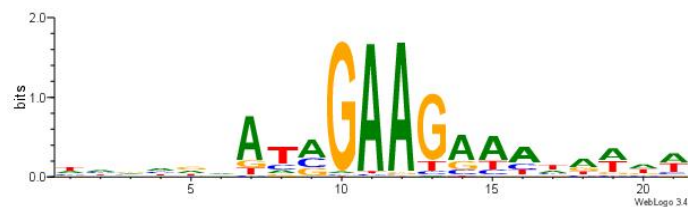
Motif ID: [MA0377.1](#)
Motif name: SFL1
Taxon: Fungi
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 7
Number of overlap: 15
Similarity score: 0.0860145

Alignment:

```
WDWDHTTTCTTCYATHHHVHH  
GCKKAWTTCTACTAT-----
```

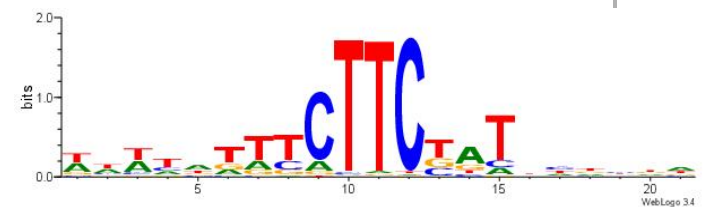
Original motif

Consensus sequence: HHVHDHATMGAAGAAHDWDW



Reverse complement motif

Consensus sequence: WDWDHTTTCTTCYATHHHVHH



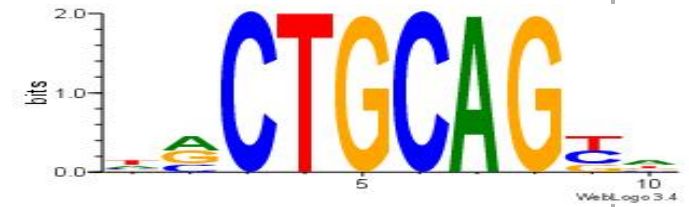
Dataset #: 2 Motif ID: 113 Motif name: Motif 113

Original motif

Consensus sequence: HRCTGCAGYD

Reverse complement motif

Consensus sequence: DMCTGCAGKH



Best Matches for Motif ID 113 (Highest to Lowest)

Motif ID: [MA0355.1](#)
 Motif name: PHD1
 Taxon: Fungi
 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: 0.00587276

Alignment:

BVBTGCARSB
 HRCTGCAGYD

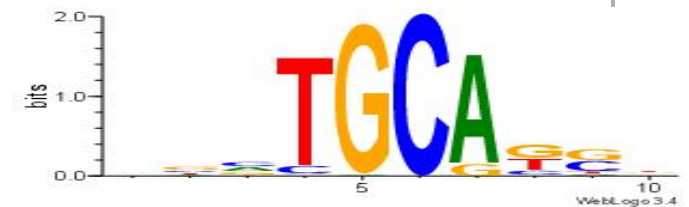
Original motif

Consensus sequence: VSMTGCABVV



Reverse complement motif

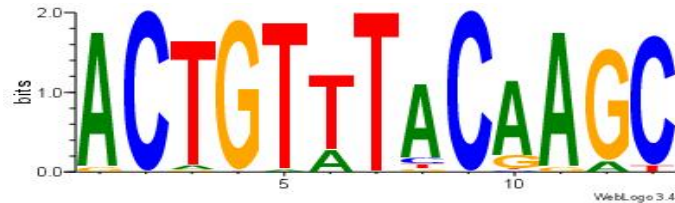
Consensus sequence: BVBTGCARSB



Dataset #: 2 Motif ID: 114 Motif name: Motif 114

Original motif

Consensus sequence: ACTGTTACAAGC



Reverse complement motif

Consensus sequence: GCTTGTAACAGT



Best Matches for Motif ID 114 (Highest to Lowest)

Motif ID:	MA0296.1
Motif name:	FKH1
Taxon:	Fungi
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	3
Number of overlap:	13
Similarity score:	0.0709953

Alignment:

```
BHHDVTTTGTTCACAWWHV  
-----ACTGTTTACAAGC--
```

Original motif

Consensus sequence: BDWWWTGTAAACAAVDDDDV

Reverse complement motif

Consensus sequence: BHHDVTTTGTTCACAWWHV



Results created by MOTIFSIM on 11-21-2023 16:21:43
Runtime: 3497.06 seconds

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