



MOTIFSIM - MOTIF SIMilarity Detection Tool

Version 2.2

INPUT

Input Parameters

Number of files:	4
Number of top significant motifs:	10
Number of best matches:	5
Similarity cutoff $\geq$	0.75
Matching motif database:	UniProbe Mus Musculus
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
DREME_DM01.txt	51	1
MEME-CHIP_DM01.txt	9	2
PScanChIP_DM01.txt	27	3
RSAT_peak-motifs_DM01.txt	40	4

RESULTS

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

Dataset #: 3 **Motif ID: 69** **Motif name: NKX3-1**

Original motif Consensus sequence: ATACTTA



Reverse complement motif Consensus sequence: TAAGTAT



Best Matches for Top Significant Motif ID 69 (Highest to Lowest)

Dataset #:	4
Motif ID:	90
Motif name:	ymTACATAw
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	7
Similarity score:	0

Alignment:
HHTACATABD
-ATACTTA--

Original motif Consensus sequence: HHTACATABD

Reverse complement motif Consensus sequence: DBTATGTAHH



Dataset #: 1
 Motif ID: 10
 Motif name: Motif 10
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 7
 Similarity score: 0.00274846

Alignment:
 TATGTAD
 TAAGTAT

Original motif Consensus sequence: HTACATA



Reverse complement motif Consensus sequence: TATGTAD



Dataset #: 1
 Motif ID: 34

Motif name:	Motif 34
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	7
Similarity score:	0.00883486

Alignment:
ATATTTA
ATACTTA

Original motif Consensus sequence: ATATTTA



Reverse complement motif Consensus sequence: TAAATAT



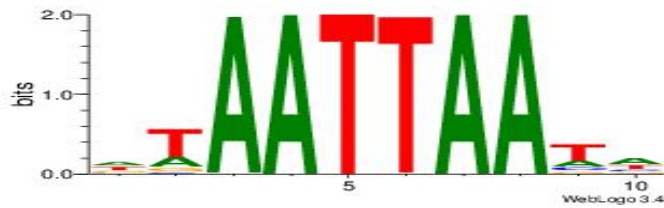
Dataset #:	4
Motif ID:	106
Motif name:	wtAATTAAtw
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	4
Number of overlap:	7
Similarity score:	0.0100679

Alignment:

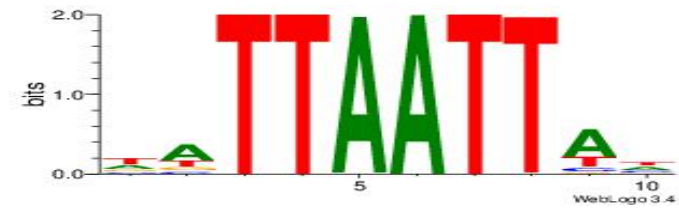
HATTAATTAD

---TAAGTAT

Original motif Consensus sequence: DTAATTAATH



Reverse complement motif Consensus sequence: HATTAATTAD



Dataset #:	4
Motif ID:	100
Motif name:	wwTAATAAww
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	3
Number of overlap:	7
Similarity score:	0.0316418

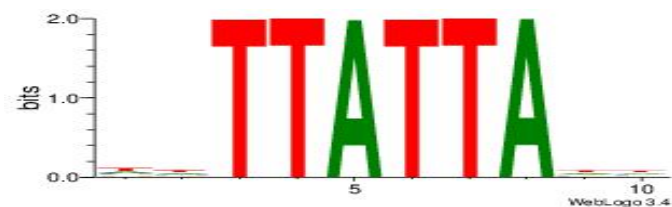
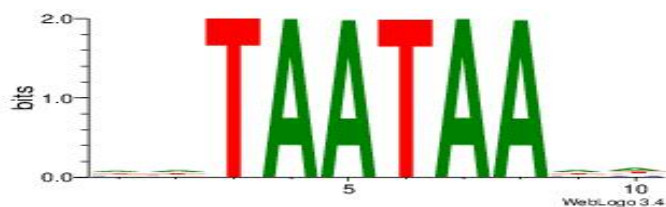
Alignment:

DDTTATTAHD

--TAAGTAT-

Original motif Consensus sequence: DHTAATAADD

Reverse complement motif Consensus sequence: DDTTATTAHD



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

Original motif Consensus sequence: TSTGTR



Reverse complement motif Consensus sequence: MACASA



Best Matches for Top Significant Motif ID 53 (Highest to Lowest)

Dataset #:	1
Motif ID:	7
Motif name:	Motif 7
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	6
Similarity score:	0.00228262

Alignment:
CACASASA
--MACASA

Original motif Consensus sequence: CACASASA



Reverse complement motif Consensus sequence: TSTSTGTG



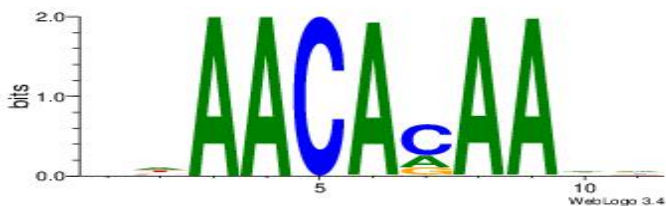
Dataset #: 4
Motif ID: 114
Motif name: awAACAcAAwa
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 4
Number of overlap: 6
Similarity score: 0.0122629

Alignment:

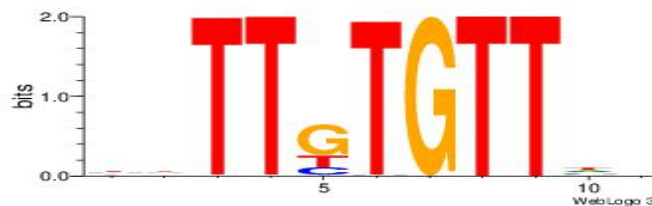
DDAACACAADV

--MACASA---

Original motif Consensus sequence: DDAACACAADV



Reverse complement motif Consensus sequence: BDTTGTGTTDD



Dataset #: 1
 Motif ID: 23
 Motif name: Motif 23
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 6
 Similarity score: 0.0137023

Alignment:
 MTSTGTA
 -TSTGTR

Original motif Consensus sequence: MTSTGTA



Reverse complement motif Consensus sequence: TACASAR



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

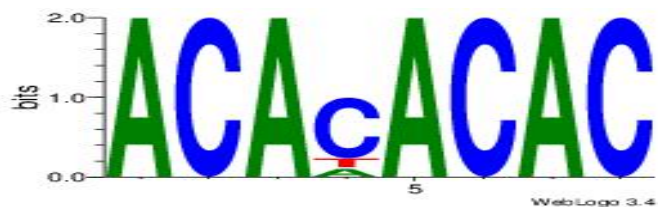
Similarity score: 0.0252334

Alignment:

GTGTGTGT

-TSTGTR-

Original motif Consensus sequence: ACACACAC



Reverse complement motif Consensus sequence: GTGTGTGT



Dataset #: 1
Motif ID: 12
Motif name: Motif 12
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 2
Number of overlap: 6
Similarity score: 0.0262273

Alignment:

MTGTGTGC

-TSTGTR-

Original motif Consensus sequence: GCACACAY

Reverse complement motif Consensus sequence: MTGTGTGC



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

Original motif Consensus sequence: TTTAAW



Reverse complement motif Consensus sequence: WWTAAA



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

Dataset #:	4
Motif ID:	91
Motif name:	wtATTTTAww
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	6
Similarity score:	0.0116421

Alignment:

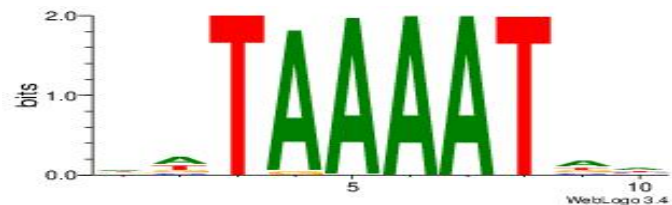
HWTAAAATHD

WWTAAA----

Original motif Consensus sequence: DHATTTTAWH



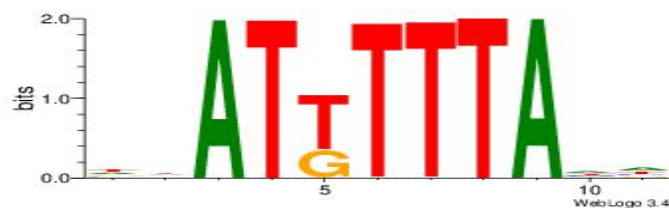
Reverse complement motif Consensus sequence: HWTAAAATHD



Dataset #: 4
 Motif ID: 108
 Motif name: wwATkTTTAww
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 6
 Number of overlap: 6
 Similarity score: 0.0118254

Alignment:
 HHTAAARATHD
 WWTAAA-----

Original motif Consensus sequence: DHATKTTTAHH



Reverse complement motif Consensus sequence: HHTAAARATHD



Dataset #: 3
 Motif ID: 70
 Motif name: Foxq1
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 6
 Similarity score: 0.0158082

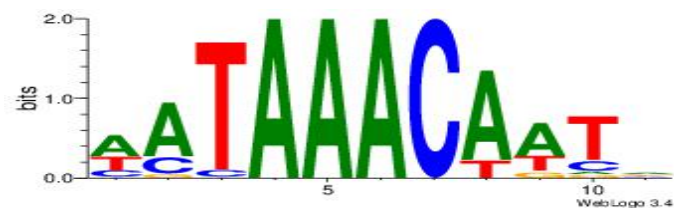
Alignment:

HATTGTTTATW
 -----TTTAWW

Original motif Consensus sequence: HATTGTTTATW



Reverse complement motif Consensus sequence: WATAACAATH



Dataset #: 2
 Motif ID: 55
 Motif name: Motif 55
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 6

Similarity score: 0.0307675

Alignment:
TTTTAAA
-WWTAAA

Original motif Consensus sequence: TTTAAAA



Reverse complement motif Consensus sequence: TTTTAAA

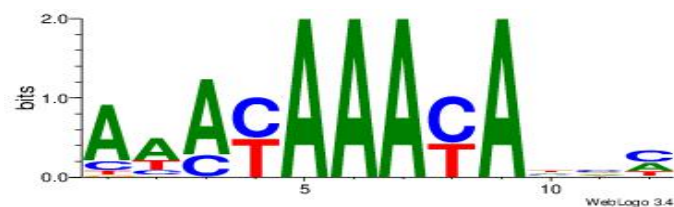
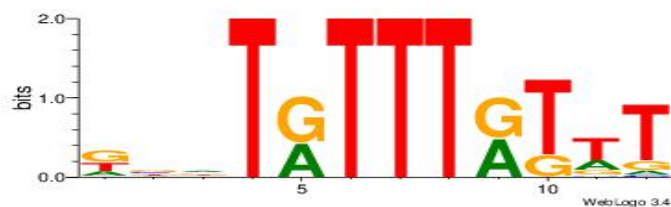


Dataset #: 3
Motif ID: 67
Motif name: FOXI1
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 6
Number of overlap: 6
Similarity score: 0.0347747

Alignment:
KBDTRTTTRTTT
-----TTTAAW-

Original motif Consensus sequence: KBDTRTTTRTTT

Reverse complement motif Consensus sequence: AAAMAAAMADBY



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

Original motif Consensus sequence: CACGB



Reverse complement motif Consensus sequence: BCGTG



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

Dataset #:	2
Motif ID:	56
Motif name:	Motif 56
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2
Number of overlap:	5
Similarity score:	0

Alignment:

CACGGA

CACGB-

Original motif Consensus sequence: CACGGA



Reverse complement motif Consensus sequence: TCCGTG



Dataset #: 4
Motif ID: 115
Motif name: ysCmAGCACwy
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 5
Similarity score: 0.0186397

Alignment:

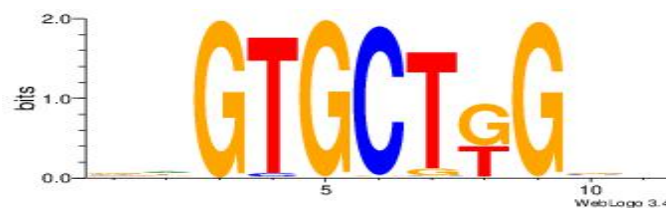
DHGTGCTRGVH

BCGTG-----

Original motif Consensus sequence: HVC MAGCACHH



Reverse complement motif Consensus sequence: DHGTGCTRGVH

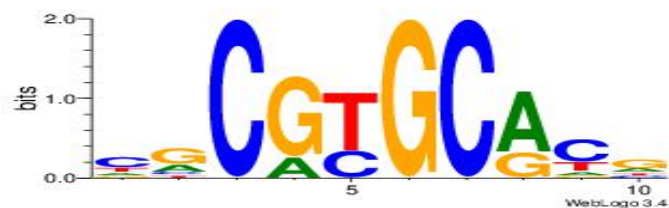


Dataset #: 4
 Motif ID: 107
 Motif name: crCGyGCRcg
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 5
 Number of overlap: 5
 Similarity score: 0.019278

Alignment:

CGCGTGCACG
 -BCGTG----

Original motif Consensus sequence: CGCGTGCACG



Reverse complement motif Consensus sequence: CGTGCACGCG

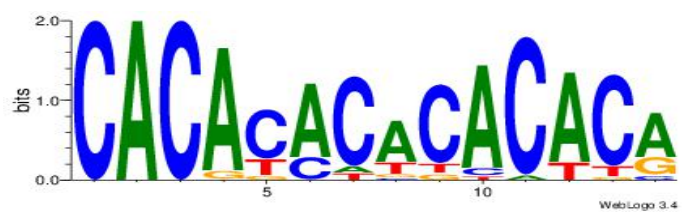


Dataset #: 2
 Motif ID: 58
 Motif name: Motif 58
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 5

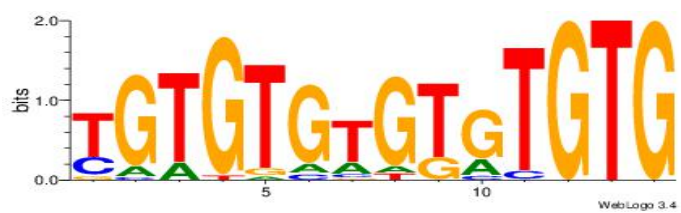
Similarity score: 0.0339655

Alignment:
CACACACACACACA
CACGB-----

Original motif Consensus sequence: CACACACACACACA



Reverse complement motif Consensus sequence: TGTGTGTGTGTGT

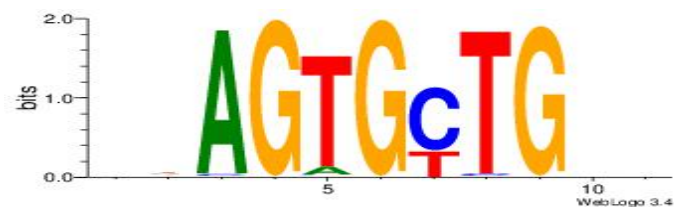
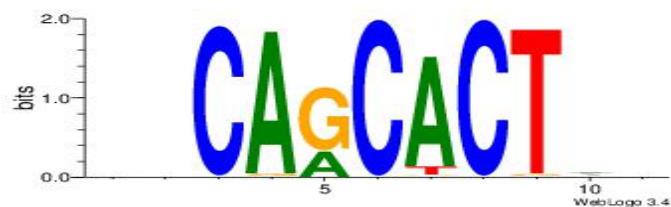


Dataset #: 4
Motif ID: 93
Motif name: cmCARCACTwr
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 6
Number of overlap: 5
Similarity score: 0.0385683

Alignment:
VHAGTGCTGHB
-BCGTG-----

Original motif Consensus sequence: BHCAGCACTHV

Reverse complement motif Consensus sequence: VHAGTGCTGHB



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

Original motif Consensus sequence: RGAAA



Reverse complement motif Consensus sequence: TTTCK



Best Matches for Top Significant Motif ID 54 (Highest to Lowest)

Dataset #:	1
Motif ID:	26
Motif name:	Motif 26
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	5
Similarity score:	0

Alignment:
 RGARGAAA
 ---RGAAA

bits

2.0

1.0

0.0

1 2 3 4 5 6 7 8 9 10

A G A G A A A

WebLogo 3.4

Alignment:
TTTCTVT
TTTCK--

Dataset #: 1
 Motif ID: 33
 Motif name: Motif 33
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 5
 Similarity score: 0.0284722

Alignment:
 CMTTTCC
 TTCK--

Original motif Consensus sequence: CMTTTCC



Reverse complement motif Consensus sequence: GGAAARG



Dataset #: 1
 Motif ID: 46
 Motif name: Motif 46
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 5

Similarity score: 0.0284722

Alignment:

GGAAASA

RGAAA--

Original motif Consensus sequence: GGAAASA



Reverse complement motif Consensus sequence: TSTTTCC



Dataset #: 1
Motif ID: 44
Motif name: Motif 44
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 3
Number of overlap: 5
Similarity score: 0.0339244

Alignment:

CATTTCT

--TTTCK

Original motif Consensus sequence: AGAAATG

Reverse complement motif Consensus sequence: CATTTCT



Dataset #: 3 Motif ID: 64 Motif name: ARID3A

Original motif Consensus sequence: ATYAAA



Reverse complement motif Consensus sequence: TTTMAT



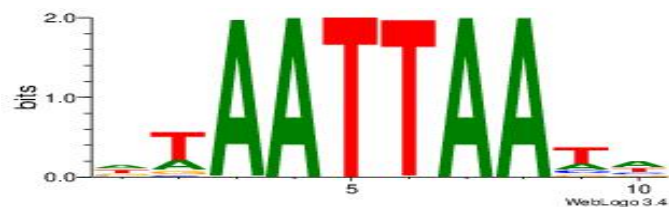
Best Matches for Top Significant Motif ID 64 (Highest to Lowest)

Dataset #:	4
Motif ID:	106
Motif name:	wtAATTAAtw
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	4
Number of overlap:	6
Similarity score:	0.0114914

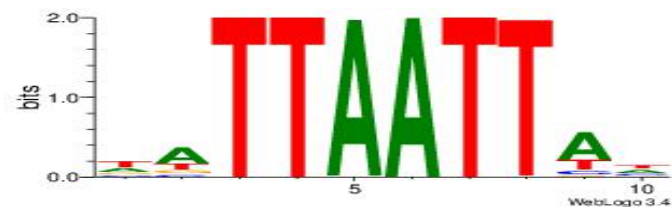
Alignment:

```
DTAATTAATH
---ATYAAA-
```

Original motif Consensus sequence: DTAATTAATH



Reverse complement motif Consensus sequence: HATTAATTAD



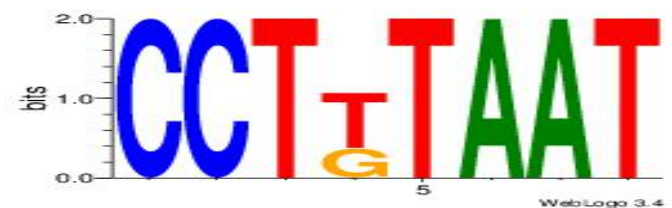
Dataset #: 1
 Motif ID: 20
 Motif name: Motif 20
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 6
 Similarity score: 0.015396

Alignment:
 ATTAMAGG
 ATYAAA--

Original motif Consensus sequence: ATTAMAGG



Reverse complement motif Consensus sequence: CCTYTAAT



Dataset #: 1
 Motif ID: 49
 Motif name: Motif 49
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 6
 Similarity score: 0.0340365

Alignment:
 KTTTATCT
 TTTMAT--

Original motif Consensus sequence: AGATAAAR



Reverse complement motif Consensus sequence: KTTTATCT



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

Similarity score: 0.0368439

Alignment:

WWTAAA

ATYAAA

Original motif Consensus sequence: TTTAWW



Reverse complement motif Consensus sequence: WWTAAA



Dataset #: 4
Motif ID: 100
Motif name: wwTAATAAww
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 5
Number of overlap: 6
Similarity score: 0.0394923

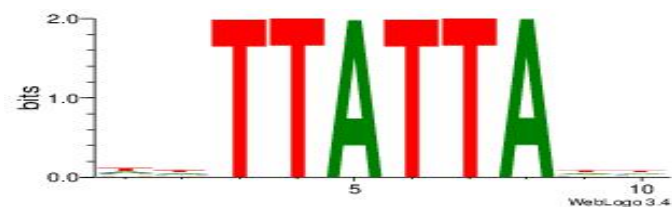
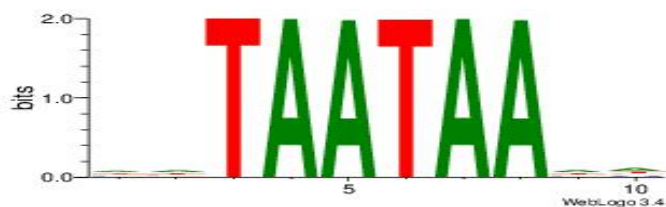
Alignment:

DHTAATAADD

TTTMAT----

Original motif Consensus sequence: DHTAATAADD

Reverse complement motif Consensus sequence: DDTTATTAHD



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

Original motif Consensus sequence: CCCASCMC



Reverse complement motif Consensus sequence: GYGSTGGG



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

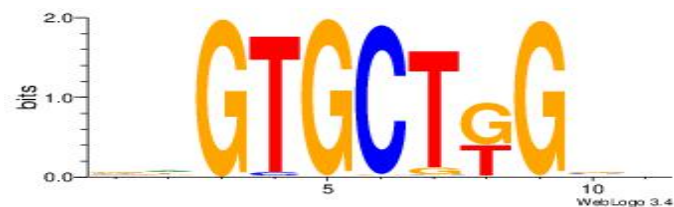
Dataset #:	4
Motif ID:	115
Motif name:	ysCmAGCACwy
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	3
Number of overlap:	8
Similarity score:	0.0212781

Alignment:
 DHGTGCTRGVH
 --GYGSTGGG--

Original motif Consensus sequence: HVCMAGCACHH



Reverse complement motif Consensus sequence: DHGTGCTRGVH

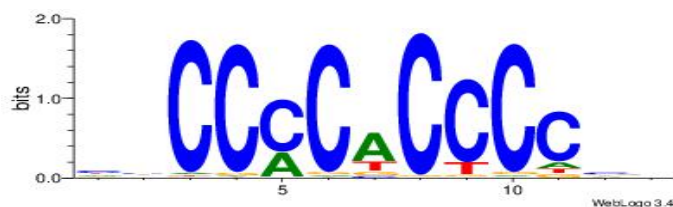


Dataset #: 4
 Motif ID: 111
 Motif name: ccCCmCaCCCCcc
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 8
 Similarity score: 0.0266863

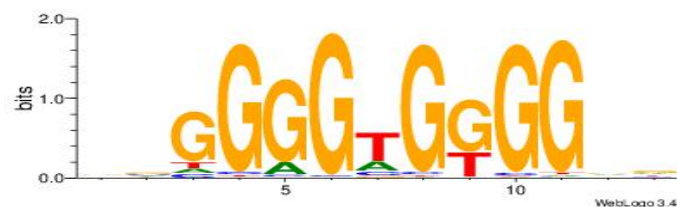
Alignment:

HBCCCCACCCCBH
 ---CCASC MC---

Original motif Consensus sequence: HBCCCCACCCCBH



Reverse complement motif Consensus sequence: DBGGGGTGGGGB

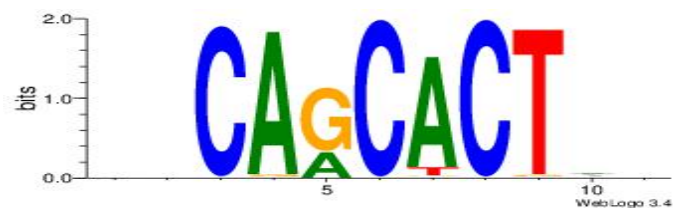


Dataset #: 4
 Motif ID: 93
 Motif name: cmCARCACTwr
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 4
 Number of overlap: 8
 Similarity score: 0.030511

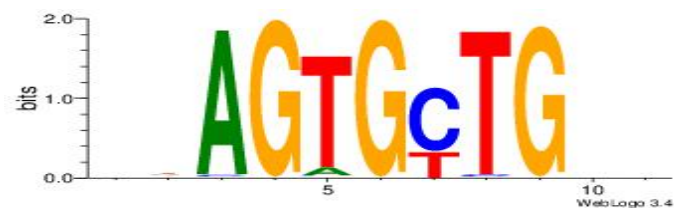
Alignment:

BHCAGCACTHV
 CCCASCMC---

Original motif Consensus sequence: BHCAGCACTHV



Reverse complement motif Consensus sequence: VHAGTGCTGHB



Dataset #: 4
 Motif ID: 119
 Motif name: cbCCAGCTCmyk
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 8

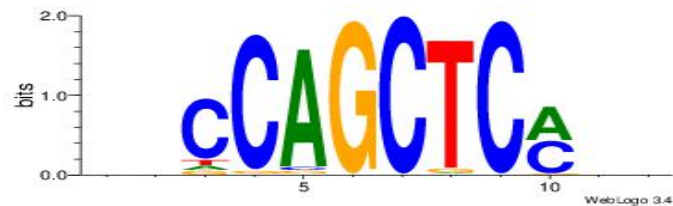
Similarity score: 0.0322039

Alignment:

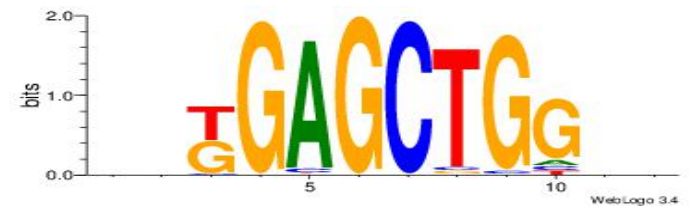
HBYGAGCTGGBB

---GYGSTGGG--

Original motif Consensus sequence: BBCCAGCTCMBD



Reverse complement motif Consensus sequence: HBYGAGCTGGBB



Dataset #: 4
Motif ID: 101
Motif name: csCACCCCg
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 8
Similarity score: 0.0415267

Alignment:

HVCACCCCB

CCCASCMC--

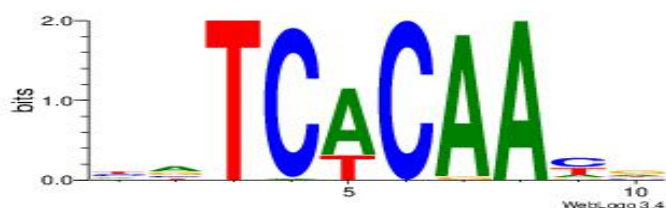
Original motif Consensus sequence: HVCACCCCB

Reverse complement motif Consensus sequence: BBGGGGTGVD

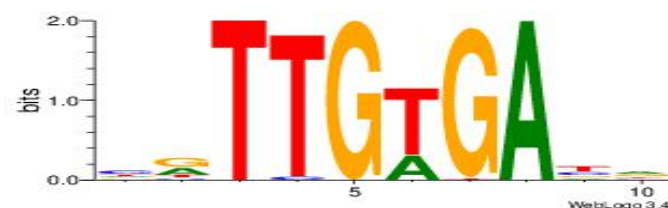


Dataset #: 4 Motif ID: 94 Motif name: yrTCWCAAyr

Original motif Consensus sequence: HVTCAAAyD



Reverse complement motif Consensus sequence: HKTTGTGABH



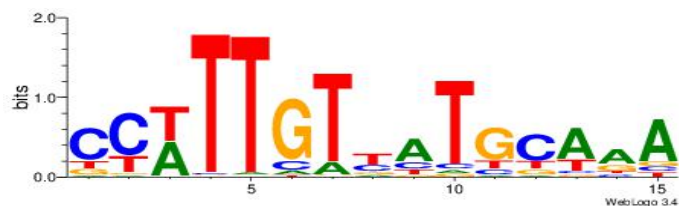
Best Matches for Top Significant Motif ID 94 (Highest to Lowest)

Dataset #:	3
Motif ID:	76
Motif name:	Sox2
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2
Number of overlap:	10
Similarity score:	0.00762497

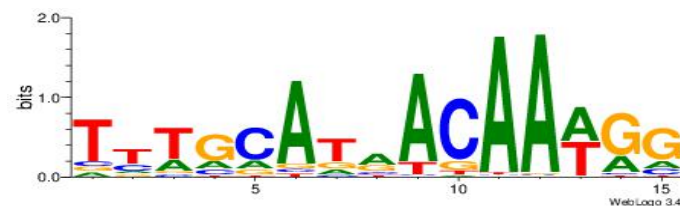
Alignment:

```
CCWTTGTYATGCAA
----HKTTGTGABH-
```

Original motif Consensus sequence: CCWTTGTYATGCAAA



Reverse complement motif Consensus sequence: TTTGCATMACAAWGG



Dataset #: 3
Motif ID: 80
Motif name: Pou5f1
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 6
Number of overlap: 10
Similarity score: 0.0127574

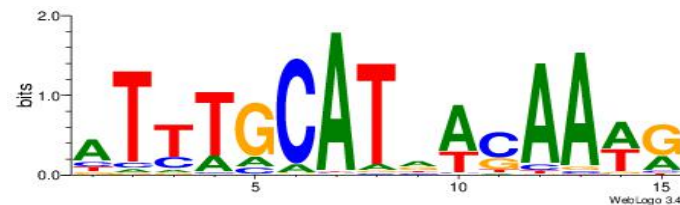
Alignment:

CWTTGTHATGCAAAT
-----HKTGTGABH

Original motif Consensus sequence: CWTTGTHATGCAAAT



Reverse complement motif Consensus sequence: ATTTGCATHACAAAT

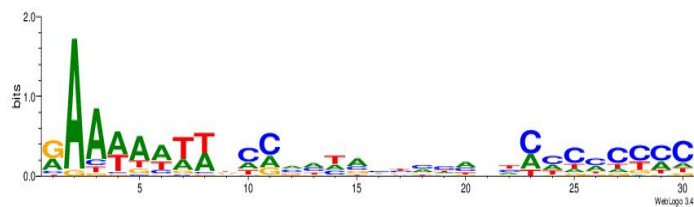


Dataset #: 3
 Motif ID: 81
 Motif name: Pax4
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 20
 Number of overlap: 10
 Similarity score: 0.0426407

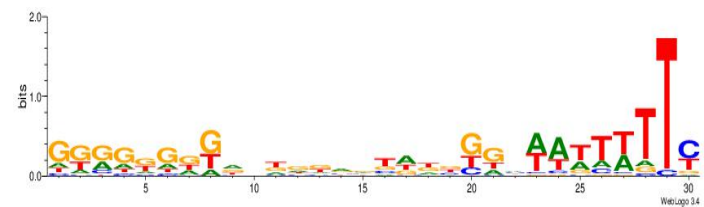
Alignment:

RAAAWATWDCMVHHVBBHHHVHMHCMCYMC
 -----HVTCACAAAYD-

Original motif Consensus sequence:
 RAAAWATWDCMVHHVBBHHHVHMHCMCYMC



Reverse complement motif Consensus sequence:
 GRKGRGDRHVHDDVBBHHBRGDWAWTWTM



Dataset #: 3
 Motif ID: 62
 Motif name: TBP
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 5

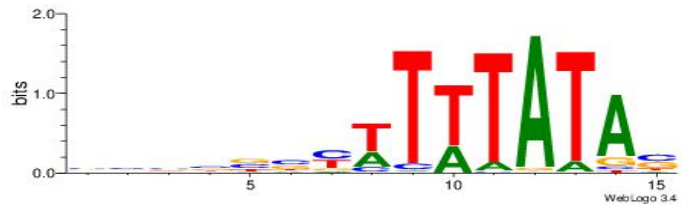
Number of overlap: 10
Similarity score: 0.0429648

Alignment:
STATAAWRVVVBV
-HVTCAAYD----

Original motif Consensus sequence: STATAAWRVVVBV



Reverse complement motif Consensus sequence: VBVVVMWTTTAT

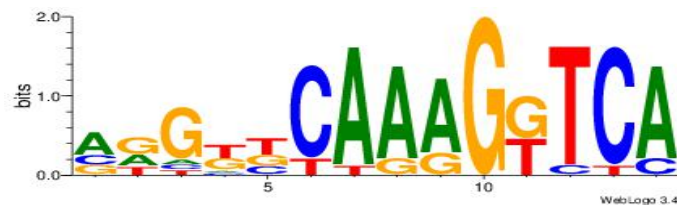


Dataset #: 3
Motif ID: 83
Motif name: NR2F1
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 10
Similarity score: 0.0463536

Alignment:
TGAMCTTTGMMCYT
HKTTGTGABH----

Original motif Consensus sequence: TGAMCTTTGMMCYT

Reverse complement motif Consensus sequence: AKGYCAAAGRTC



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

Original motif Consensus sequence: TTAAAA



Reverse complement motif Consensus sequence: TTTTAAA

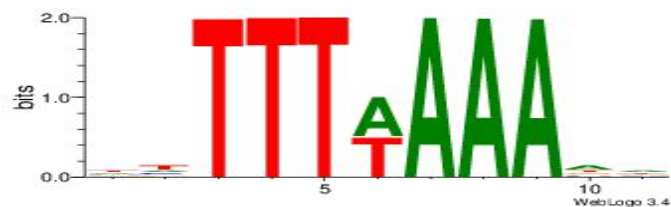


Best Matches for Top Significant Motif ID 55 (Highest to Lowest)

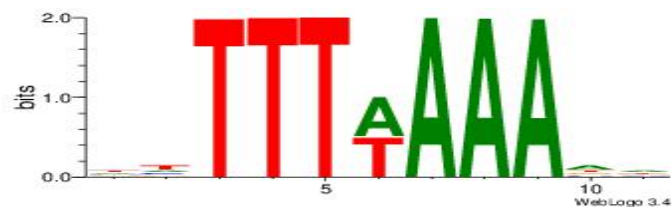
Dataset #:	4
Motif ID:	120
Motif name:	wtTTTwAAAaw
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	3
Number of overlap:	7
Similarity score:	0.00286145

Alignment:
 HHTTTWAAADD
 --TTTAAAA--

Original motif Consensus sequence: HHTTTWAAADD



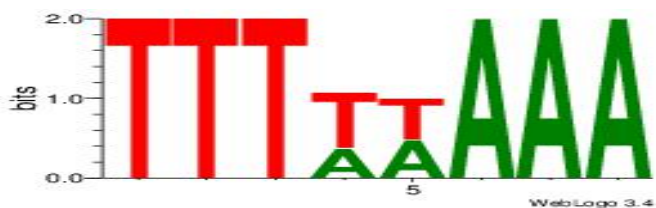
Reverse complement motif Consensus sequence: DDTTTWAAAH



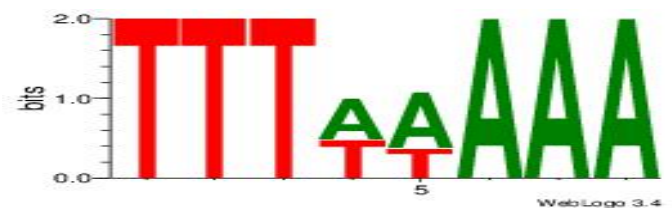
Dataset #: 1
 Motif ID: 9
 Motif name: Motif 9
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 7
 Similarity score: 0.0142562

Alignment:
 TTTWWAAA
 -TTTAAAA

Original motif Consensus sequence: TTTWWAAA



Reverse complement motif Consensus sequence: TTTWWAAA



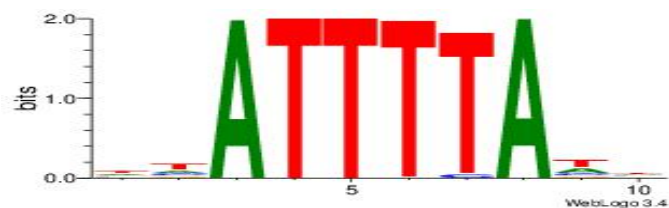
Dataset #: 4
 Motif ID: 91
 Motif name: wtATTTTAAww
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 7
 Similarity score: 0.036821

Alignment:

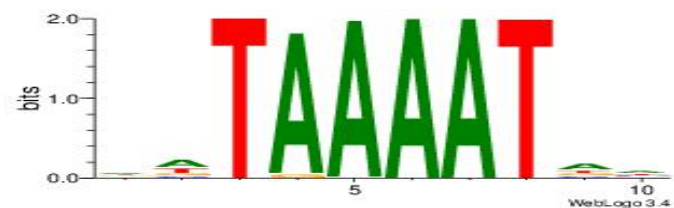
HWTAAAATHD

TTTAAAA---

Original motif Consensus sequence: DHATTTTAAWH



Reverse complement motif Consensus sequence: HWTAAAATHD

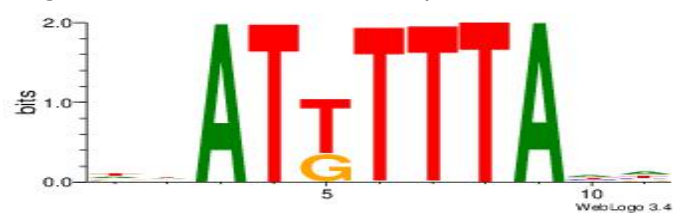


Dataset #: 4
 Motif ID: 108
 Motif name: wwATkTTTAww
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 7

Similarity score: 0.0428268

Alignment:
DHATKTTTAHH
----TTTTAAA

Original motif Consensus sequence: DHATKTTTAHH



Reverse complement motif Consensus sequence: HHTAAARATHD

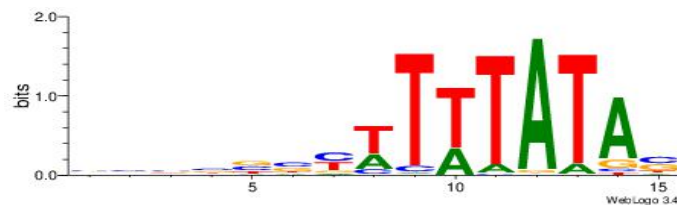
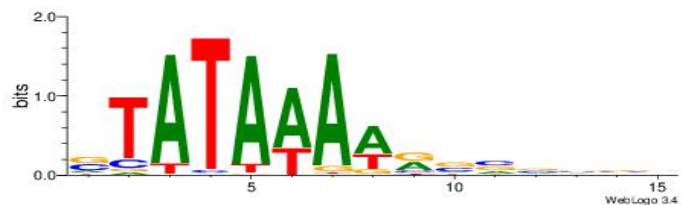


Dataset #: 3
Motif ID: 62
Motif name: TBP
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 8
Number of overlap: 7
Similarity score: 0.058454

Alignment:
VBVVVVMWTTTATAS
-----TTTTAAA-

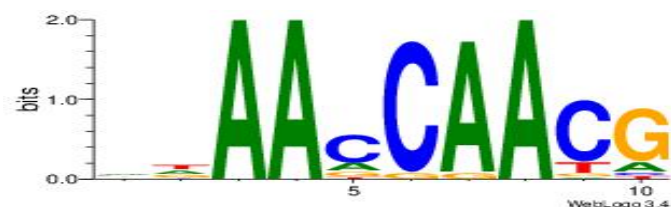
Original motif Consensus sequence: STATAAAWRVVVBV

Reverse complement motif Consensus sequence: VBVVVVMWTTTAT

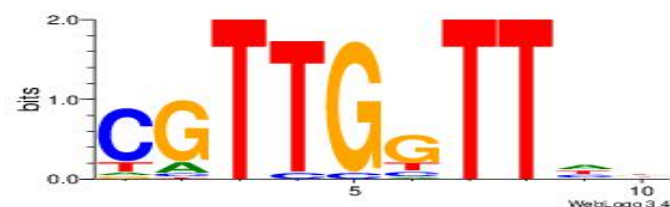


Dataset #: 4 **Motif ID: 96** **Motif name: mdAAcCAACG**

Original motif Consensus sequence: VDAACCAACG



Reverse complement motif Consensus sequence: CGTTGGTTDB



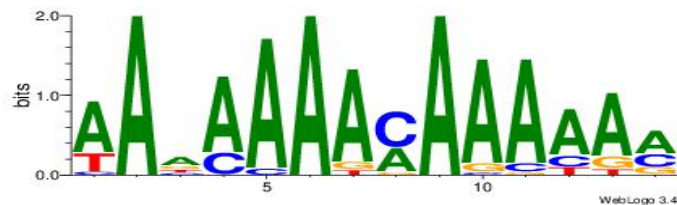
Best Matches for Top Significant Motif ID 96 (Highest to Lowest)

Dataset #:	2
Motif ID:	60
Motif name:	Motif 60
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	3
Number of overlap:	10
Similarity score:	0.0244161

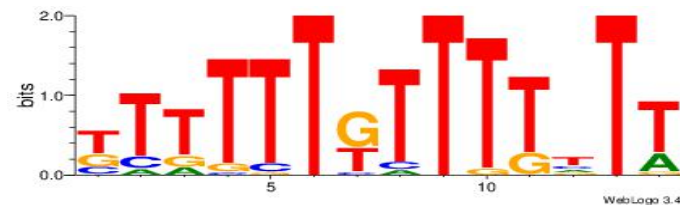
Alignment:

```
YTTTTTRTTTTDTT
--CGTTGGTTDB--
```

Original motif Consensus sequence: AADAAAAMAAAAAM



Reverse complement motif Consensus sequence: YTTTTTRTTTDTT



Dataset #: 3
 Motif ID: 70
 Motif name: Foxq1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 10
 Similarity score: 0.0266383

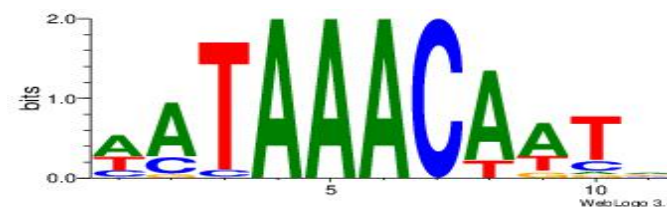
Alignment:

HATTGTTTATW
 -CGTTGGTTDB

Original motif Consensus sequence: HATTGTTTATW



Reverse complement motif Consensus sequence: WATAACAATH

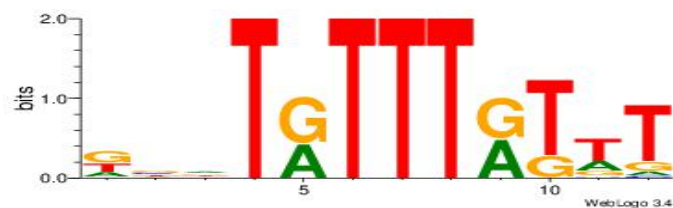


Dataset #: 3
 Motif ID: 67
 Motif name: FOXI1
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 10
 Similarity score: 0.036655

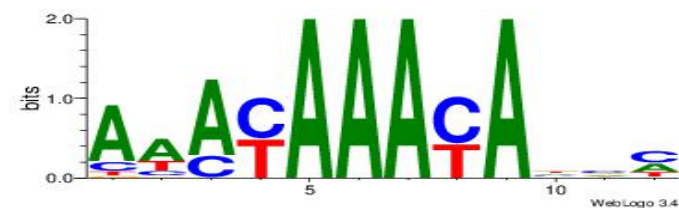
Alignment:

AAAMAAAMADBY
 VDAACCAACG--

Original motif Consensus sequence: KBDTRTTTTRTTT



Reverse complement motif Consensus sequence: AAAMAAAMADBY



Dataset #: 3
 Motif ID: 83
 Motif name: NR2F1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 10

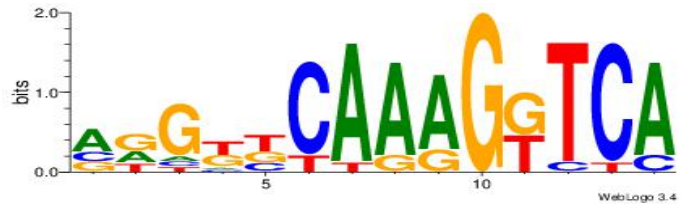
Similarity score: 0.0376121

Alignment:
TGAMCTTTGMMCYT
CGTTGGTTDB-----

Original motif Consensus sequence: TGAMCTTTGMMCYT



Reverse complement motif Consensus sequence: AKGYCAAAGRTC

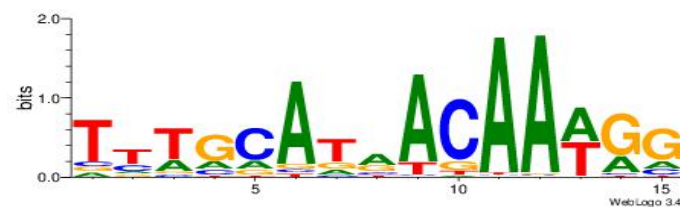
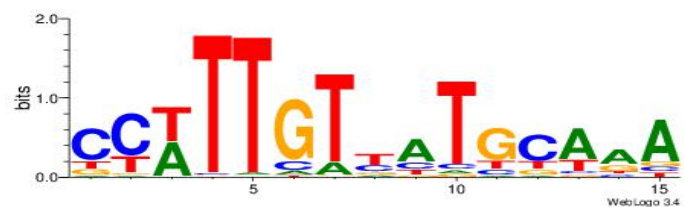


Dataset #: 3
Motif ID: 76
Motif name: Sox2
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 6
Number of overlap: 10
Similarity score: 0.0382008

Alignment:
TTTGCATMACAAWGG
VDAACCAACG-----

Original motif Consensus sequence: CCWTTGTYATGCAAA

Reverse complement motif Consensus sequence:
TTTGCATMACAAWGG



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

Dataset #: 3 Motif ID: 69 Motif name: NKX3-1

Original motif Consensus sequence: ATACTTA



Reverse complement motif Consensus sequence: TAAGTAT



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

Dataset #:	4
Motif ID:	90
Motif name:	ymTACATAyw
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	7

Similarity score: 0

Alignment:

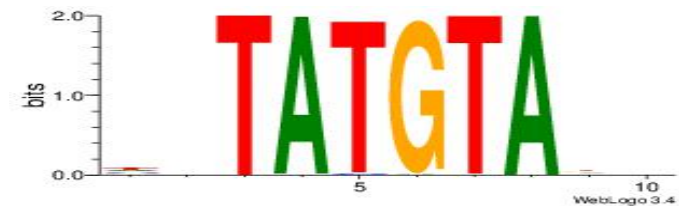
HHTACATABD

-ATACTTA--

Original motif Consensus sequence: HHTACATABD



Reverse complement motif Consensus sequence: DBTATGTAHH



Dataset #: 3
Motif ID: 66
Motif name: Lhx3
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 5
Number of overlap: 7
Similarity score: 0.000214177

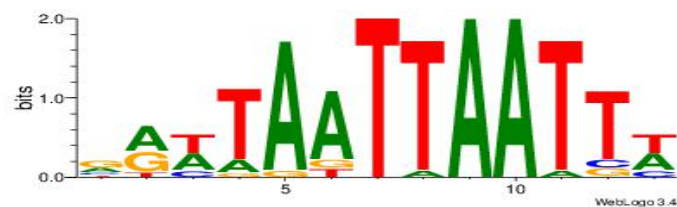
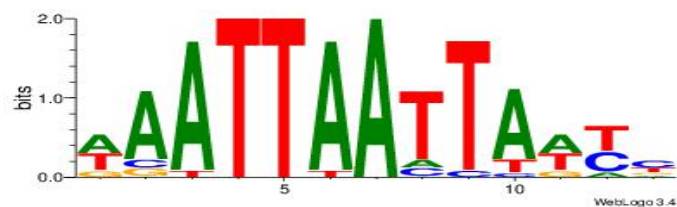
Alignment:

WAATTAATTAWYB

--TAAGTAT----

Original motif Consensus sequence: WAATTAATTAWYB

Reverse complement motif Consensus sequence: BMWTAATTAATTW



Dataset #: 1
 Motif ID: 10
 Motif name: Motif 10
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 7
 Similarity score: 0.00274846

Alignment:
 TATGTAD
 TAAGTAT

Original motif Consensus sequence: HTACATA



Reverse complement motif Consensus sequence: TATGTAD



Dataset #: 1
 Motif ID: 34

Motif name:	Motif 34
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	7
Similarity score:	0.00883486

Alignment:
ATATTTA
ATACTTA

Original motif Consensus sequence: ATATTTA



Reverse complement motif Consensus sequence: TAAATAT



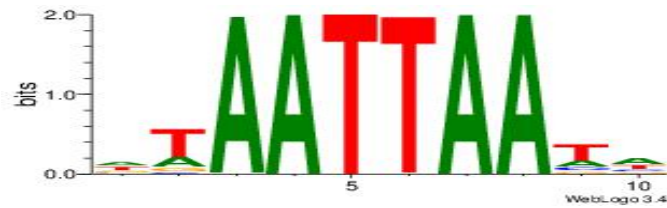
Dataset #:	4
Motif ID:	106
Motif name:	wtAATTAAtw
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	4
Number of overlap:	7
Similarity score:	0.0100679

Alignment:

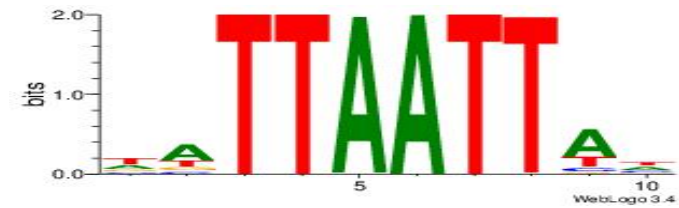
HATTAATTAD

---TAAGTAT

Original motif Consensus sequence: DTAATTAATH

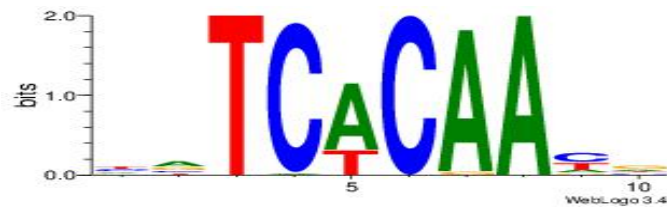


Reverse complement motif Consensus sequence: HATTAATTAD

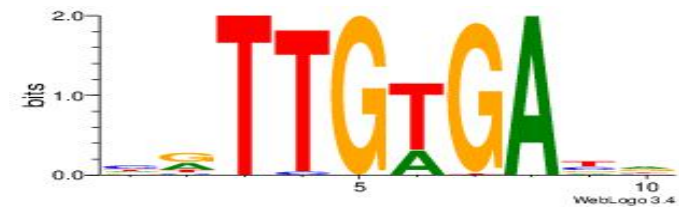


Dataset #: 4 Motif ID: 94 Motif name: yrTCWCAAyr

Original motif Consensus sequence: HVTCAAAyD



Reverse complement motif Consensus sequence: HKTTGTGABH



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

Dataset #:	4
Motif ID:	114
Motif name:	awAACAcAAwa
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1

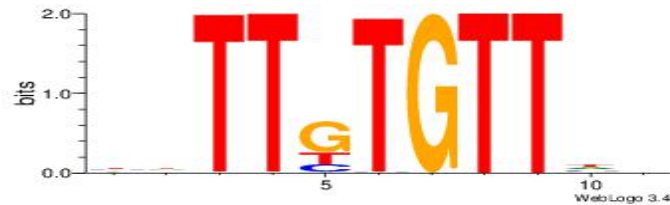
Number of overlap: 10
Similarity score: 0.00495535

Alignment:
BDTTGTGTTDD
HKTTGTGABH-

Original motif Consensus sequence: DDAACACAADV



Reverse complement motif Consensus sequence: BDTTGTGTTDD

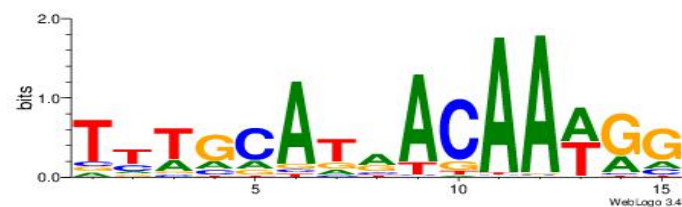
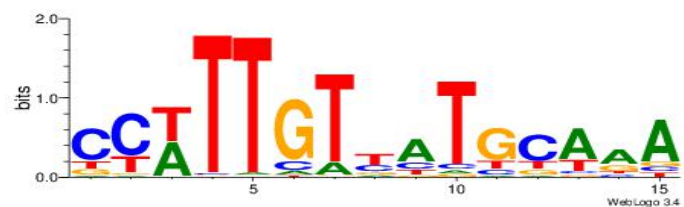


Dataset #: 3
Motif ID: 76
Motif name: Sox2
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2
Number of overlap: 10
Similarity score: 0.00762497

Alignment:
CCWTTGTYATGCAAA
----HKTTGTGABH-

Original motif Consensus sequence: CCWTTGTYATGCAAA

Reverse complement motif Consensus sequence:
TTTGCATMACAAWGG



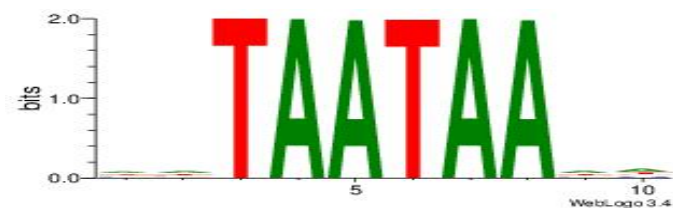
Dataset #: 4
 Motif ID: 100
 Motif name: wwTAATAAww
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 10
 Similarity score: 0.0114769

Alignment:

DDTTATTAHD

HKTTGTGABH

Original motif Consensus sequence: DHTAATAADD



Reverse complement motif Consensus sequence: DDTTATTAHD



Dataset #: 3
 Motif ID: 80

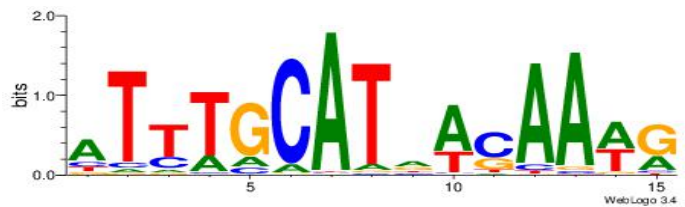
Motif name: Pou5f1
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 6
Number of overlap: 10
Similarity score: 0.0127574

Alignment:
CWTGTHATGCAAAT
-----HKTGTGABH

Original motif Consensus sequence: CWTGTHATGCAAAT



Reverse complement motif Consensus sequence: ATTTGCATHACAAAT



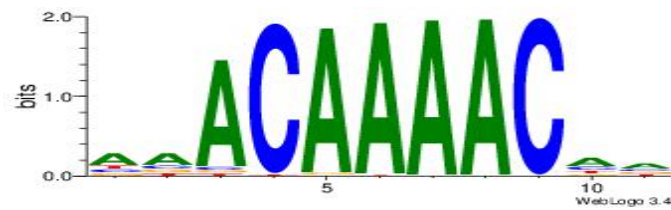
Dataset #: 4
Motif ID: 89
Motif name: aaACAAAACaa
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 10
Similarity score: 0.0208363

Alignment:

AAACAAAACHV

HVTCACAAYD-

Original motif Consensus sequence: AAACAAAACHV



Reverse complement motif Consensus sequence: BHGTTTTGTTT



Dataset #: 3 Motif ID: 77 Motif name: Sox5

Original motif Consensus sequence: HAACAAT



Reverse complement motif Consensus sequence: ATTGTTT



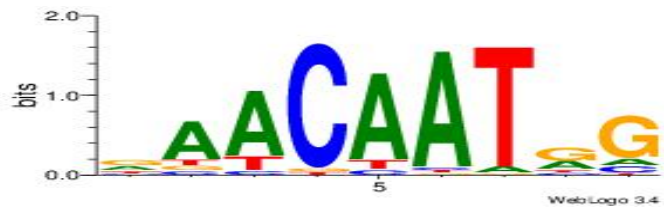
Best Matches for Significant Motif ID 77 (Highest to Lowest)

Dataset #:	3
Motif ID:	87
Motif name:	SOX9
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	3

Number of overlap: 7
Similarity score: 0

Alignment:
CMATTGTTH
--ATTGTTH

Original motif Consensus sequence: DAACAATRG



Reverse complement motif Consensus sequence: CMATTGTTH

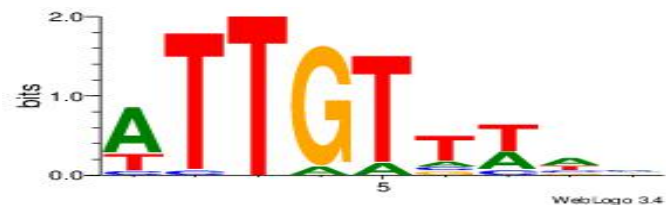
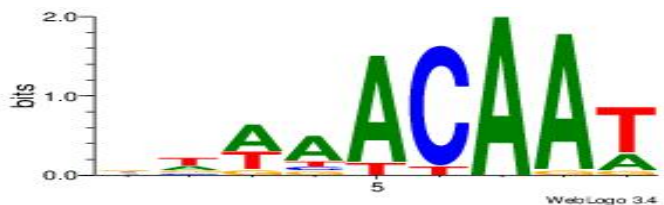


Dataset #: 3
Motif ID: 73
Motif name: SRY
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 7
Similarity score: 0.0011033

Alignment:
ATTGTTWDB
ATTGTTH--

Original motif Consensus sequence: BDWAACAAT

Reverse complement motif Consensus sequence: ATTGTTWDB

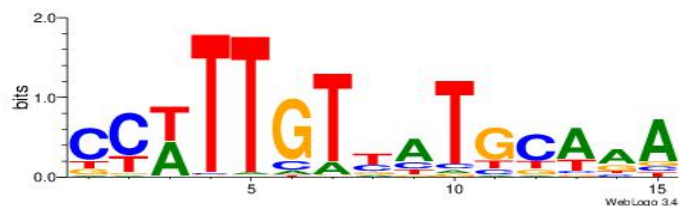


Dataset #: 3
 Motif ID: 76
 Motif name: Sox2
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 7
 Number of overlap: 7
 Similarity score: 0.022869

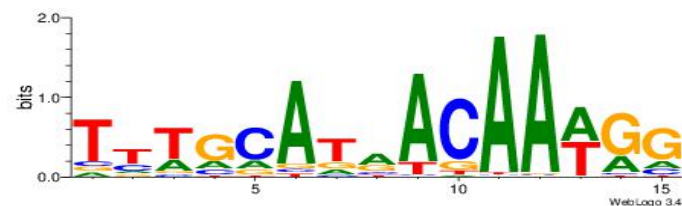
Alignment:

CCWTTGTYATGCAAA
 -----ATTGTTH--

Original motif Consensus sequence: CCWTTGTYATGCAAA



Reverse complement motif Consensus sequence: TTTGCATMACAAWGG



Dataset #: 3

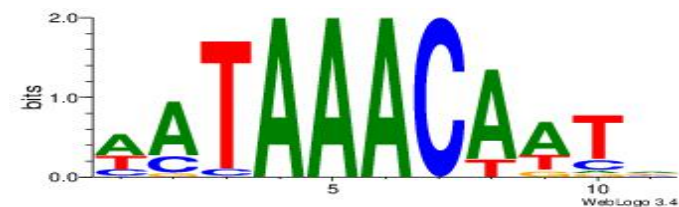
Motif ID:	70
Motif name:	Foxq1
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	4
Number of overlap:	7
Similarity score:	0.0242658

Alignment:
WATAACAATH
-HACAAT---

Original motif Consensus sequence: HATTGTTTATW



Reverse complement motif Consensus sequence: WATAACAATH



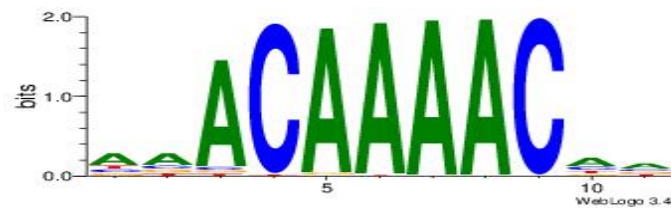
Dataset #:	4
Motif ID:	89
Motif name:	aaACAAAACaa
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	7
Similarity score:	0.0278776

Alignment:

AAACAAAACHV

HAACAAT----

Original motif Consensus sequence: AAACAAAACHV



Reverse complement motif Consensus sequence: BHGTTTTGTTT



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

Original motif Consensus sequence: TSTGTR



Reverse complement motif Consensus sequence: MACASA



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

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

Number of overlap: 6
 Similarity score: 0.00228262

Alignment:
 TSTSTGTG
 TSTGTR--

Original motif Consensus sequence: CACASASA



Reverse complement motif Consensus sequence: TSTSTGTG

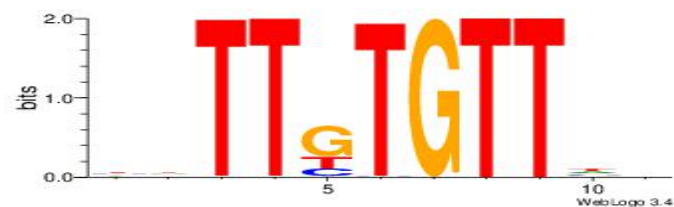


Dataset #: 4
 Motif ID: 114
 Motif name: awAACAcAAwa
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 4
 Number of overlap: 6
 Similarity score: 0.0122629

Alignment:
 DDAACACAADV
 --MACASA---

Original motif Consensus sequence: DDAACACAADV

Reverse complement motif Consensus sequence: BDTTGTGTTDD



Dataset #: 1
 Motif ID: 23
 Motif name: Motif 23
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 6
 Similarity score: 0.0137023

Alignment:
 MTSTGTA
 -TSTGTR

Original motif Consensus sequence: MTSTGTA



Reverse complement motif Consensus sequence: TACASAR

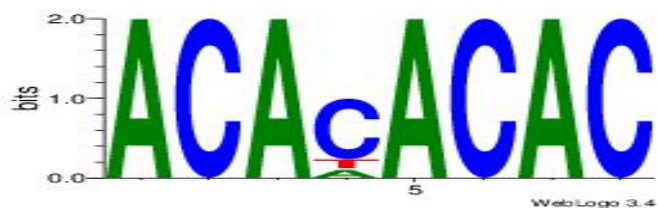


Dataset #: 1
 Motif ID: 2

Motif name:	Motif 2
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	2
Number of overlap:	6
Similarity score:	0.0252334

Alignment:
GTGTGTGT
-TSTGTR-

Original motif Consensus sequence: ACACACAC



Reverse complement motif Consensus sequence: GTGTGTGT



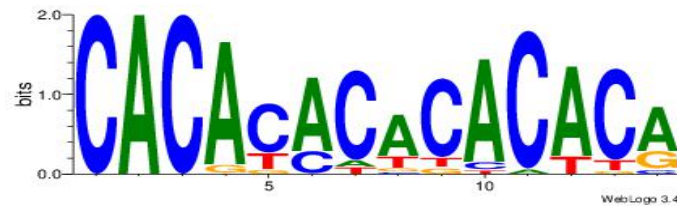
Dataset #:	2
Motif ID:	58
Motif name:	Motif 58
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	6
Similarity score:	0.025412

Alignment:

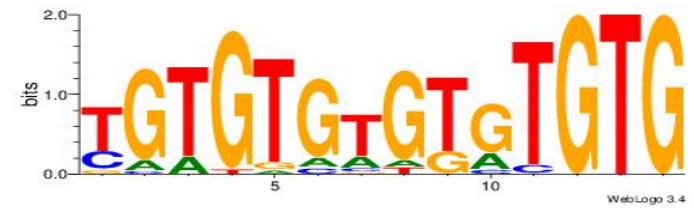
CACACACACACACA

MACASA-----

Original motif Consensus sequence: CACACACACACACA

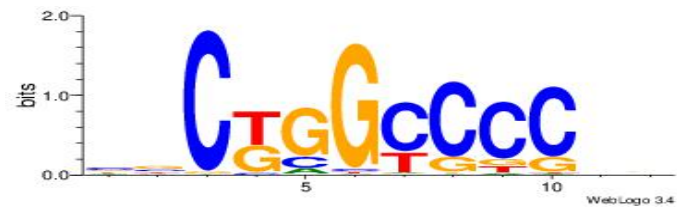


Reverse complement motif Consensus sequence: TGTGTGTGTGTGT



Dataset #: 4 Motif ID: 102 Motif name: ssCkGGYCCCsg

Original motif Consensus sequence: BBCKGGCCCCV



Reverse complement motif Consensus sequence: VVGGGGCCRBBB



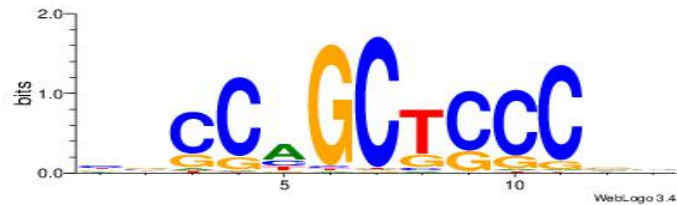
Best Matches for Significant Motif ID 102 (Highest to Lowest)

Dataset #:	4
Motif ID:	103
Motif name:	csCCaGCTCCCgs
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	2

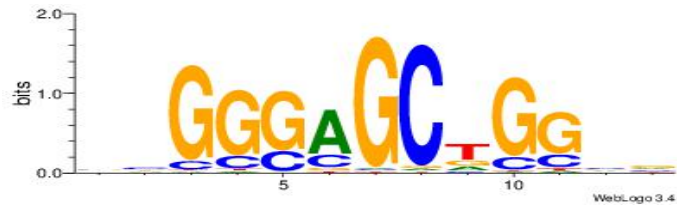
Number of overlap: 12
Similarity score: 0.00699729

Alignment:
BVGGGAGCTGGBB
-VVGGGGCCRBB

Original motif Consensus sequence: BBCCAGCTCCCVB



Reverse complement motif Consensus sequence: BVGGGAGCTGGBB

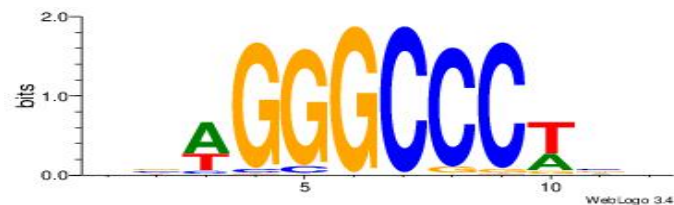
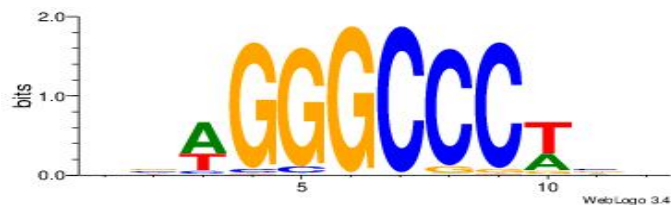


Dataset #: 4
Motif ID: 124
Motif name: cswGGGCCCwsg
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 12
Similarity score: 0.00901563

Alignment:
VVWGGGCCCWBB
BBCKGGCCCVV

Original motif Consensus sequence: VVWGGGCCCWBB

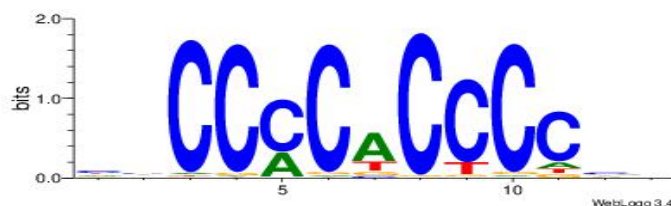
Reverse complement motif Consensus sequence: BBWGGGCCCWVV



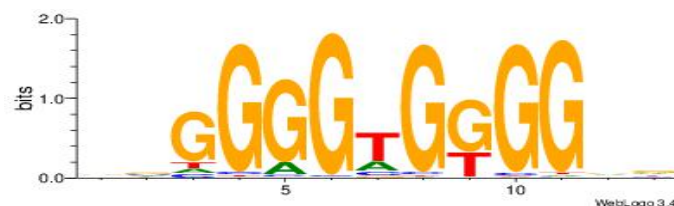
Dataset #: 4
 Motif ID: 111
 Motif name: ccCCmCaCCCCcc
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 12
 Similarity score: 0.015463

Alignment:
 DBGGGGTGGGGBD
 VVGGGGCCRGBB-

Original motif Consensus sequence: HBCCCCACCCCBH



Reverse complement motif Consensus sequence: DBGGGGTGGGGB



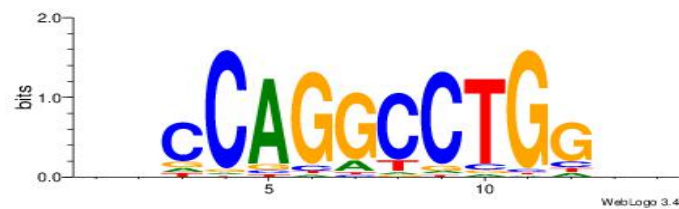
Dataset #: 4
 Motif ID: 122

Motif name:	hsCCAGGCCTGGsr
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:	0.0222107

Alignment:

HVCCAGGCCTGGBD
 -BBCKGGCCCCVV-

Original motif Consensus sequence: HVCCAGGCCTGGBD



Reverse complement motif Consensus sequence: HBCCAGGCCTGGV



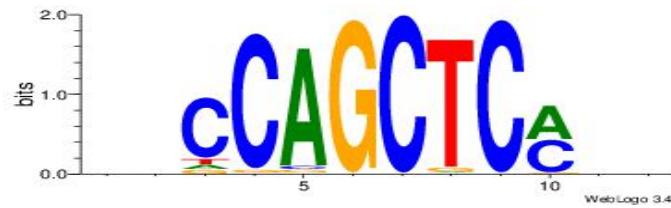
Dataset #:	4
Motif ID:	119
Motif name:	cbCCAGCTCmyk
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	12
Similarity score:	0.0277516

Alignment:

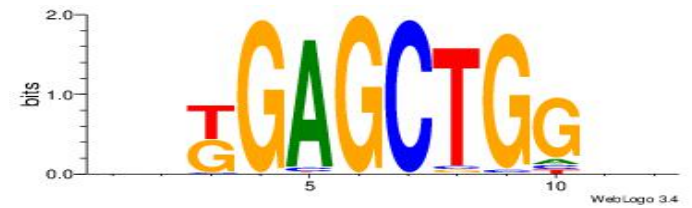
BBCCAGCTCMBD

BBCKGGCCCCVV

Original motif Consensus sequence: BBCCAGCTCMBD



Reverse complement motif Consensus sequence: HBYGAGCTGGBB



Dataset #: 4 Motif ID: 95 Motif name: rmATGCTAww

Original motif Consensus sequence: DHATGCTADH



Reverse complement motif Consensus sequence: HDTAGCATHD



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

Dataset #:	4
Motif ID:	91
Motif name:	wtATTTTAww
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1

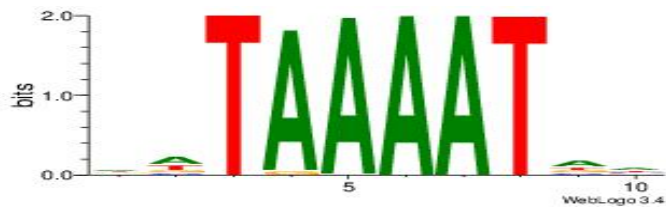
Number of overlap: 10
Similarity score: 0.00863735

Alignment:
DHATTTTAWH
DHATGCTADH

Original motif Consensus sequence: DHATTTTAWH



Reverse complement motif Consensus sequence: HWTAAAATHD

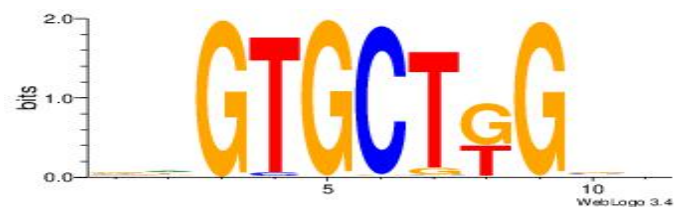


Dataset #: 4
Motif ID: 115
Motif name: ysCmAGCACwy
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 10
Similarity score: 0.0142021

Alignment:
DHGTGCTRGVH
DHATGCTADH-

Original motif Consensus sequence: HVCMAGCACHH

Reverse complement motif Consensus sequence: DHGTGCTRGVH



Dataset #: 3
 Motif ID: 80
 Motif name: Pou5f1
 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: 0.0215325

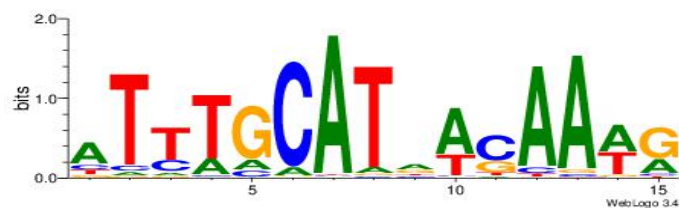
Alignment:

CWTGTHATGCAAAT
 -----DHATGCTADH

Original motif Consensus sequence: CWTGTHATGCAAAT



Reverse complement motif Consensus sequence: ATTTGCATHACAAAT

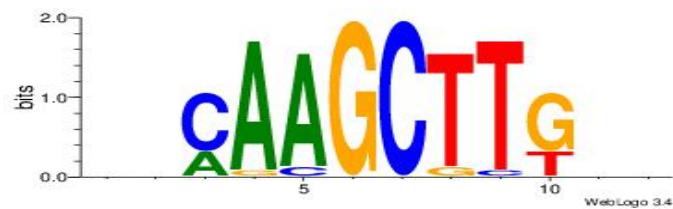


Dataset #: 4
 Motif ID: 123

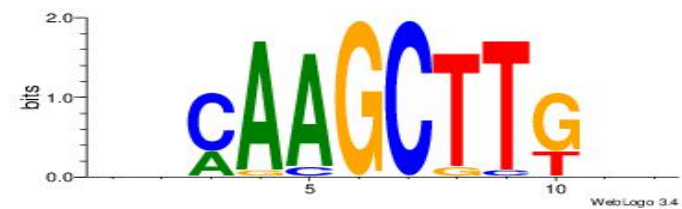
Motif name: asMAAGCTTKst
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 10
 Similarity score: 0.0234838

Alignment:
 HBCAAGCTTGVD
 -DHATGCTADH-

Original motif Consensus sequence: HBCAAGCTTGVD



Reverse complement motif Consensus sequence: DVCAAGCTTGBH



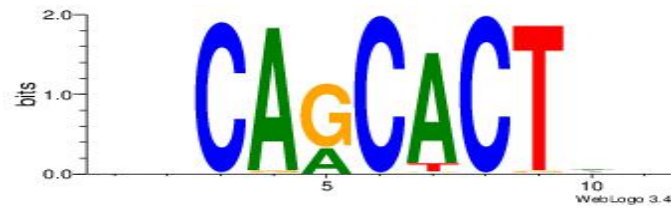
Dataset #: 4
 Motif ID: 93
 Motif name: cmCARCACTwr
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 10
 Similarity score: 0.0266703

Alignment:

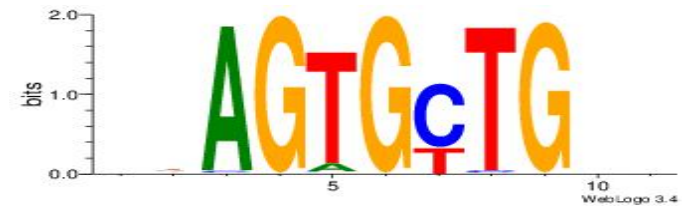
VHAGTGCTGHB

DHATGCTADH-

Original motif Consensus sequence: BHCAGCACTHV



Reverse complement motif Consensus sequence: VHAGTGCTGHB



Dataset #: 4 Motif ID: 105 Motif name: ccGCAGCCss

Original motif Consensus sequence: VCGCAGCCBB



Reverse complement motif Consensus sequence: BBGGCTGCGV



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

Dataset #:	4
Motif ID:	126
Motif name:	yvTGCAGsCAcg
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	2

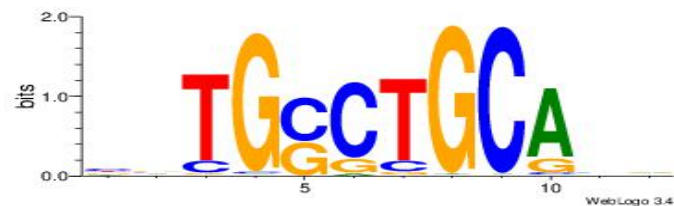
Number of overlap: 10
Similarity score: 0

Alignment:
VBTGSCTGCAVB
-BBGGCTGCGV-

Original motif Consensus sequence: BVTGCAGSCABV



Reverse complement motif Consensus sequence: VBTGSCTGCAVB

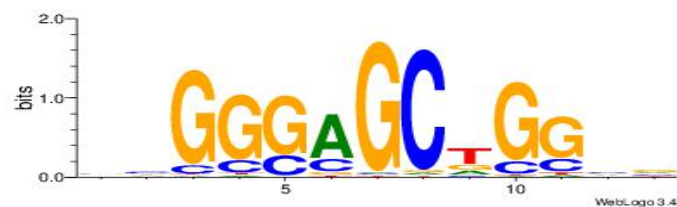
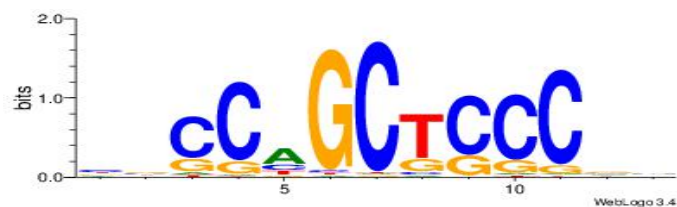


Dataset #: 4
Motif ID: 103
Motif name: csCCaGCTCCCgs
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 10
Similarity score: 0.0101194

Alignment:
BVGGGAGCTGGBB
BBGGCTGCGV---

Original motif Consensus sequence: BBCCAGCTCCCVB

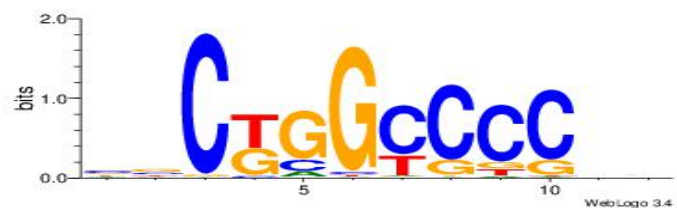
Reverse complement motif Consensus sequence: BVGGGAGCTGGBB



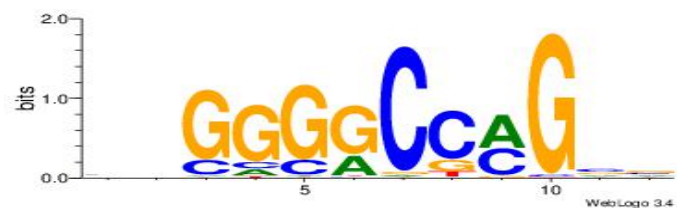
Dataset #: 4
 Motif ID: 102
 Motif name: ssCkGGYCCCsg
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 10
 Similarity score: 0.0260007

Alignment:
 BBCKGGCCCCVV
 BBGGCTGCGV--

Original motif Consensus sequence: BBCKGGCCCCVV



Reverse complement motif Consensus sequence: VVGGGGCCCRBB

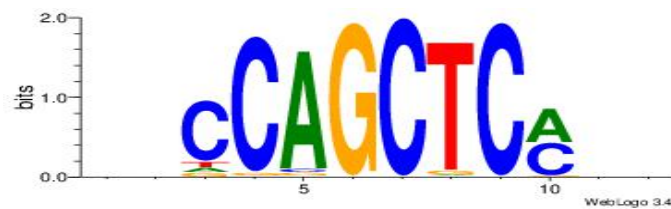


Dataset #: 4
 Motif ID: 119

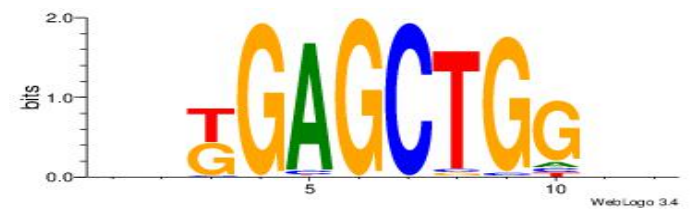
Motif name: cbCCAGCTCmyk
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3
 Number of overlap: 10
 Similarity score: 0.0296738

Alignment:
 HBYGAGCTGGBB
 --BBGGCTGCGV

Original motif Consensus sequence: BBCCAGCTCMBD



Reverse complement motif Consensus sequence: HBYGAGCTGGBB



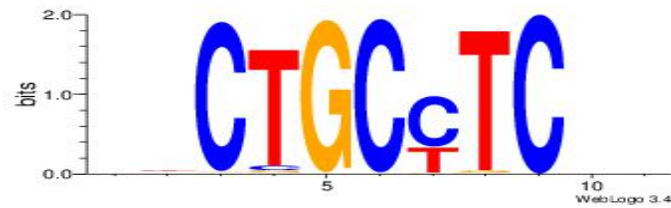
Dataset #: 4
 Motif ID: 116
 Motif name: dyCTGCyTCyc
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 10
 Similarity score: 0.0303133

Alignment:

DHCTGCTCHB

-BBGGCTGCGV

Original motif Consensus sequence: DHCTGCTCHB



Reverse complement motif Consensus sequence: BHGAKGCAGHH



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

Original motif Consensus sequence: CACGB



Reverse complement motif Consensus sequence: BCGTG



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

Dataset #:	2
Motif ID:	56
Motif name:	Motif 56
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	2

Number of overlap: 5
Similarity score: 0

Alignment:

TCCGTG
-BCGTG

Original motif Consensus sequence: CACGGA



Reverse complement motif Consensus sequence: TCCGTG



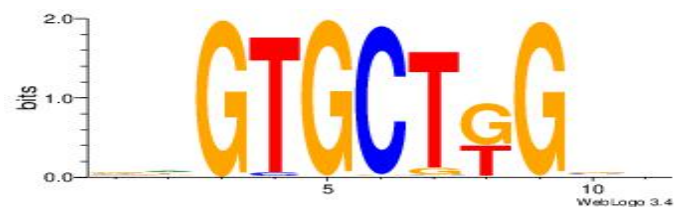
Dataset #: 4
Motif ID: 115
Motif name: ysCmAGCACwy
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 5
Similarity score: 0.0186397

Alignment:

DHGTGCTRGVH
BCGTG-----

Original motif Consensus sequence: HVCmAGCACHH

Reverse complement motif Consensus sequence: DHGTGCTRGVH



Dataset #: 4
 Motif ID: 107
 Motif name: crCGyGCRcg
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 5
 Similarity score: 0.019278

Alignment:

CGCGTGCACG

-BCGTG----

Original motif Consensus sequence: CGCGTGCACG



Reverse complement motif Consensus sequence: CGTGCACGCG



Dataset #: 1
 Motif ID: 12

Motif name:	Motif 12
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	4
Number of overlap:	5
Similarity score:	0.0246242

Alignment:
GCACACAY
---CACGB

Original motif Consensus sequence: GCACACAY



Reverse complement motif Consensus sequence: MTGTGTGC



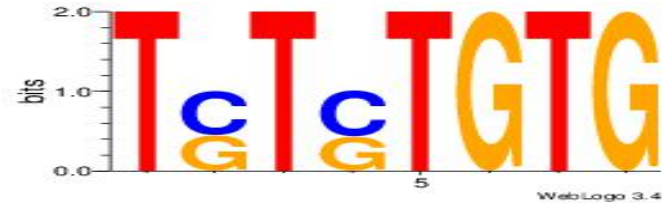
Dataset #:	1
Motif ID:	7
Motif name:	Motif 7
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	5
Similarity score:	0.0336642

Alignment:
CACASASA
CACGB---

Original motif Consensus sequence: CACASASA



Reverse complement motif Consensus sequence: TSTSTGTG



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

Original motif Consensus sequence: TTTAWW



Reverse complement motif Consensus sequence: WWTAAA



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

Dataset #:	4
Motif ID:	91
Motif name:	wtATTTTAww
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1

Number of overlap: 6
Similarity score: 0.0116421

Alignment:
HWTAAAATHD
WWTAAA-----

Original motif Consensus sequence: DHATTTTAWH



Reverse complement motif Consensus sequence: HWTAAAATHD

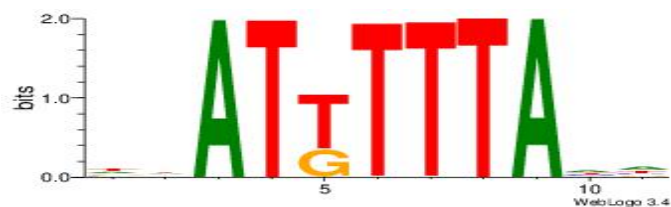


Dataset #: 4
Motif ID: 108
Motif name: wwATkTTTAww
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 6
Similarity score: 0.0118254

Alignment:
DHATKTTTAHH
-----TTTAWW

Original motif Consensus sequence: DHATKTTTAHH

Reverse complement motif Consensus sequence: HHTAAARATHD



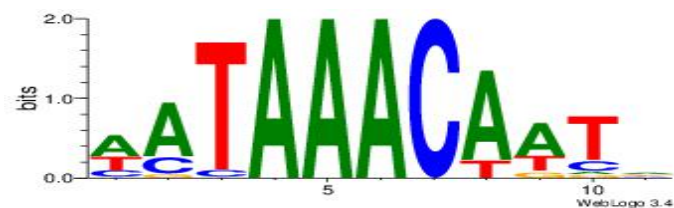
Dataset #: 3
 Motif ID: 70
 Motif name: Foxq1
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 6
 Similarity score: 0.0158082

Alignment:
 HATTGTTTATW
 -----TTTAWW

Original motif Consensus sequence: HATTGTTTATW



Reverse complement motif Consensus sequence: WATAACAATH



Dataset #: 1
 Motif ID: 3

Motif name:	Motif 3
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	6
Similarity score:	0.0300892

Alignment:
 AWATAMA
 WWTAAA-

Original motif Consensus sequence: AWATAMA



Reverse complement motif Consensus sequence: TYTATWT



Dataset #:	2
Motif ID:	55
Motif name:	Motif 55
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2
Number of overlap:	6
Similarity score:	0.0307675

Alignment:

TTTAAAA

TTTAWW-

Original motif Consensus sequence: TTTAAAA

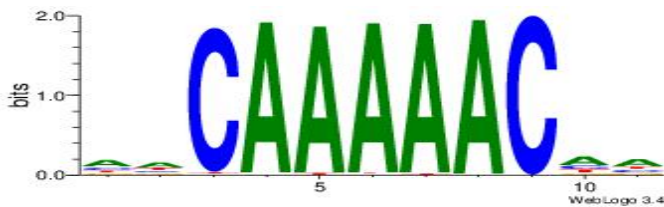


Reverse complement motif Consensus sequence: TTTTAAA

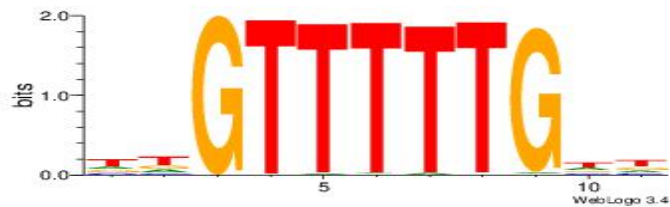


Dataset #: 4 Motif ID: 109 Motif name: aaCAAAAACaa

Original motif Consensus sequence: HHCAAAAACHH



Reverse complement motif Consensus sequence: HHGTTTTTGHH



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

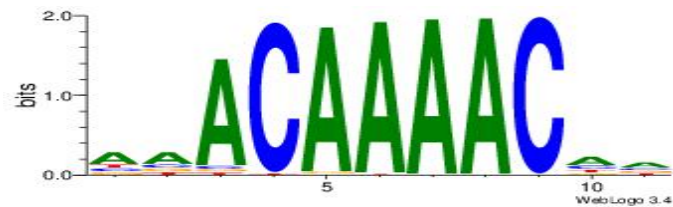
Dataset #:	4
Motif ID:	89
Motif name:	aaACAAAACaa
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1

Number of overlap: 11
Similarity score: 0.00652588

Alignment:

BHGTTTTGTTT
HHGTTTTTGHH

Original motif Consensus sequence: AACAAAAACHV



Reverse complement motif Consensus sequence: BHGTTTTGTTT



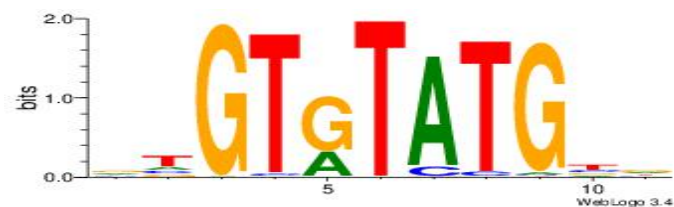
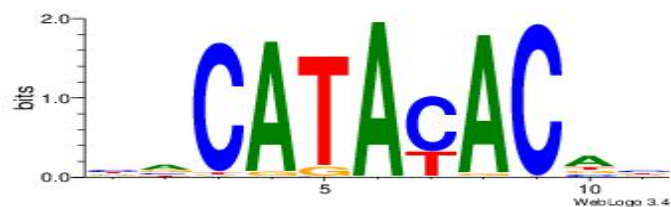
Dataset #: 4
Motif ID: 117
Motif name: yaCATAYACay
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 11
Similarity score: 0.0113253

Alignment:

DTGTGTATGBD
HHGTTTTTGHH

Original motif Consensus sequence: HVCATACACAH

Reverse complement motif Consensus sequence: DTGTGTATGBD



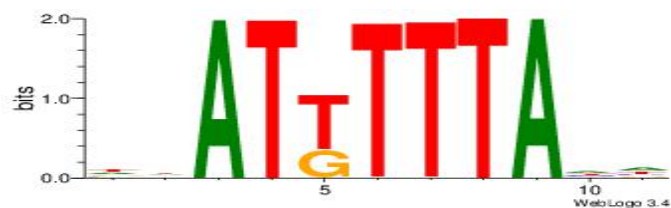
Dataset #: 4
 Motif ID: 108
 Motif name: wwATkTTTAww
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.0251184

Alignment:

DHATKTTTAHH

HHGTTTTTGGH

Original motif Consensus sequence: DHATKTTTAHH



Reverse complement motif Consensus sequence: HHTAAARATHD

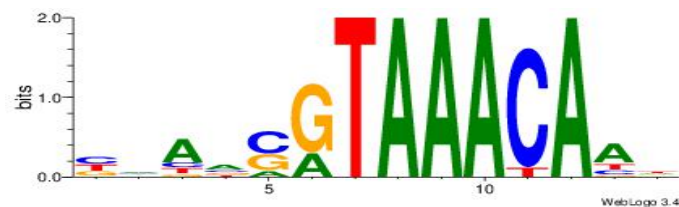


Dataset #: 3
 Motif ID: 75

Motif name: FOXF2
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 11
 Similarity score: 0.0278186

Alignment:
 BHADSGTAAACAAD
 --HHCAAAAACHH--

Original motif Consensus sequence: BHADSGTAAACAAD



Reverse complement motif Consensus sequence: DTTGTTACSBTB



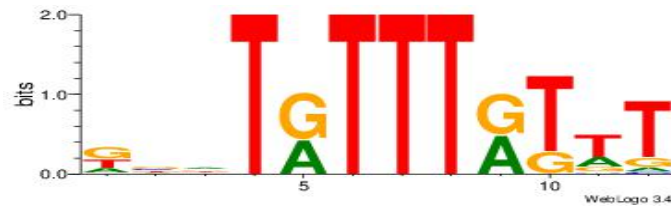
Dataset #: 3
 Motif ID: 67
 Motif name: FOXI1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 11
 Similarity score: 0.0320335

Alignment:

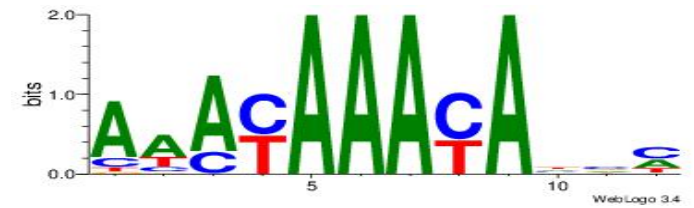
KBDTRTTTTRTTT

-HHGTTTTTGH

Original motif Consensus sequence: KBDTRTTTTRTTT



Reverse complement motif Consensus sequence: AAAMAAAMADBY



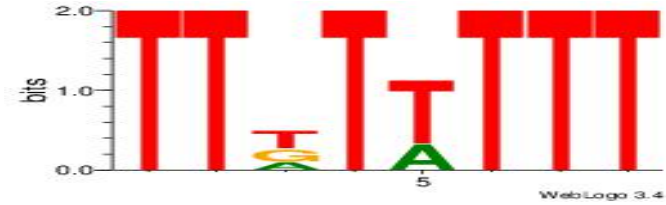
Best Matches for Each Motif (Highest to Lowest)

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

Original motif Consensus sequence: AAAAAMAA



Reverse complement motif Consensus sequence: TTYTTTTT



Best Matches for Motif ID 1 (Highest to Lowest)

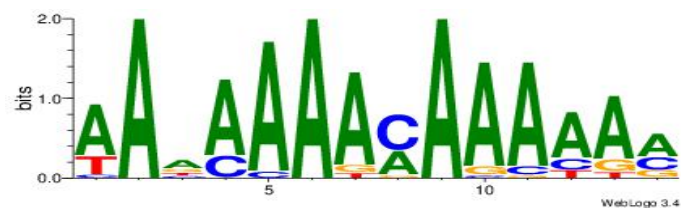
Dataset #: 2
Motif ID: 60

Motif name:	Motif 60
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	3
Number of overlap:	8
Similarity score:	0.0315879

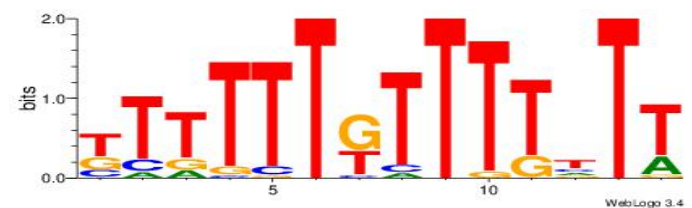
Alignment:

AADAAAAMAAAAAM
 --AAAAAMAA-----

Original motif Consensus sequence: AADAAAAMAAAAAM



Reverse complement motif Consensus sequence: YTTTTTRTTTTDTT



Dataset #:	1
Motif ID:	5
Motif name:	Motif 5
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:	0.0375279

Alignment:
AAASAAAA
AAAAAMAA

Original motif Consensus sequence: AAASAAAA



Reverse complement motif Consensus sequence: TTTTSTTT



Dataset #:	4
Motif ID:	109
Motif name:	aaCAAAAACaa
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	4
Number of overlap:	8
Similarity score:	0.0446212

Alignment:
HHCAAAAACHH
---AAAAAMAA

Original motif Consensus sequence: HHCAAAAACHH

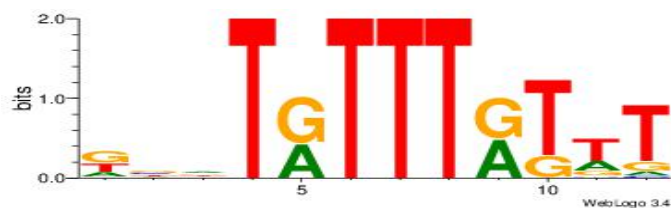
Reverse complement motif Consensus sequence: HHGTTTTTGHH



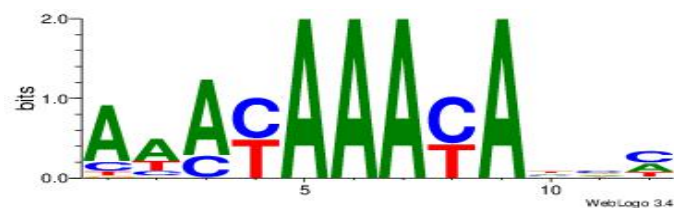
Dataset #: 3
 Motif ID: 67
 Motif name: FOXI1
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 8
 Similarity score: 0.0453228

Alignment:
 AAAMAAAMADBY
 --AAAAAMAA--

Original motif Consensus sequence: KBDTRTTTTRTTT



Reverse complement motif Consensus sequence: AAAMAAAMADBY



Dataset #: 4
 Motif ID: 114

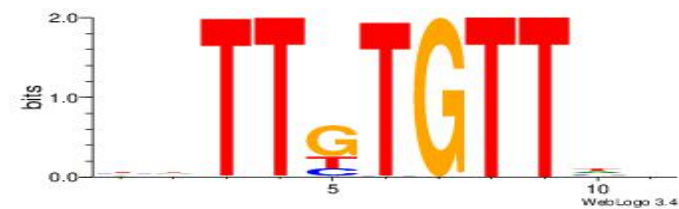
Motif name: awAACAcAAwa
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 8
 Similarity score: 0.0467797

Alignment:
 DDAACACAADV
 -AAAAAMAA--

Original motif Consensus sequence: DDAACACAADV



Reverse complement motif Consensus sequence: BDTTGTGTTDD



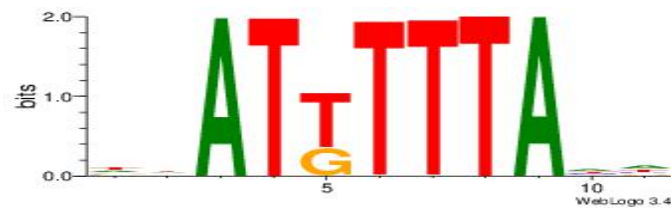
Dataset #: 4
 Motif ID: 108
 Motif name: wwATkTTTAww
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 4
 Number of overlap: 8
 Similarity score: 0.0570668

Alignment:

DHATKTTTAHH

TTYTTTTT---

Original motif Consensus sequence: DHATKTTTAHH

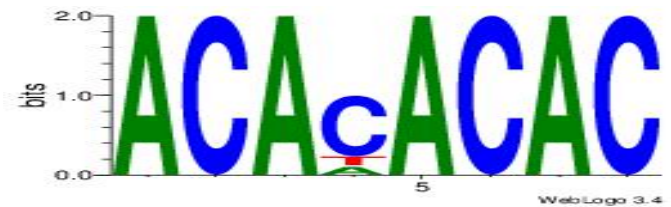


Reverse complement motif Consensus sequence: HHTAAARATHD



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

Original motif Consensus sequence: ACACACAC



Reverse complement motif Consensus sequence: GTGTGTGT



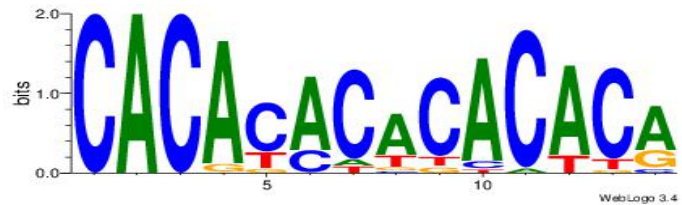
Best Matches for Motif ID 2 (Highest to Lowest)

Dataset #:	2
Motif ID:	58
Motif name:	Motif 58
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	6

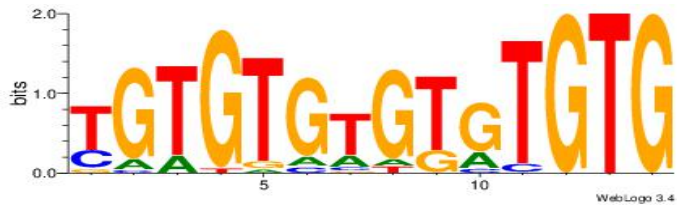
Number of overlap: 8
Similarity score: 0.0337866

Alignment:
TGTGTGTGTGTG
-----GTGTGTGT-

Original motif Consensus sequence: CACACACACACACA



Reverse complement motif Consensus sequence: TGTGTGTGTGTG

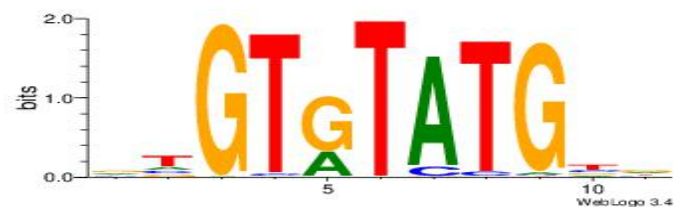
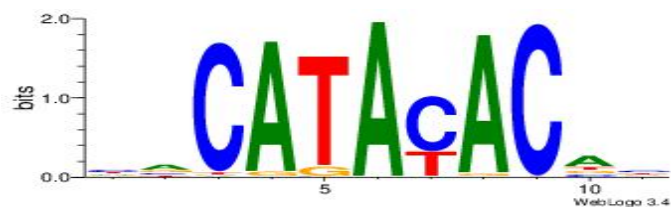


Dataset #: 4
Motif ID: 117
Motif name: yaCATAYACay
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 3
Number of overlap: 8
Similarity score: 0.0556866

Alignment:
DTGTGTATGBD
--GTGTGTGT-

Original motif Consensus sequence: HVCATACACAH

Reverse complement motif Consensus sequence: DTGTGTATGBD



Dataset #: 1
 Motif ID: 12
 Motif name: Motif 12
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 8
 Similarity score: 0.0626247

Alignment:
 GCACACAY
 ACACACAC

Original motif Consensus sequence: GCACACAY



Reverse complement motif Consensus sequence: MTGTGTGC



Dataset #: 1
 Motif ID: 21

Motif name:	Motif 21
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	8
Similarity score:	0.0696577

Alignment:
AAACAAAC
ACACACAC

Original motif Consensus sequence: AAACAAAC



Reverse complement motif Consensus sequence: GTTTGTTT



Dataset #:	1
Motif ID:	37
Motif name:	Motif 37
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	8
Similarity score:	0.07313

Alignment:
GYATGTGY
GTGTGTGT

Original motif Consensus sequence: GYATGTGY



Reverse complement motif Consensus sequence: KCACATKC



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

Original motif Consensus sequence: AWATAMA



Reverse complement motif Consensus sequence: TYTATWT



Best Matches for Motif ID 3 (Highest to Lowest)

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

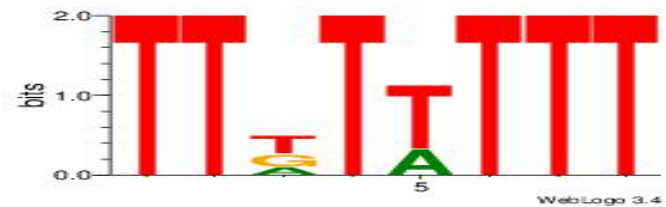
Number of overlap: 7
Similarity score: 0.00716822

Alignment:
AAAAAMAA
AWATAMA-

Original motif Consensus sequence: AAAAAMAA



Reverse complement motif Consensus sequence: TTYTTTTT



Dataset #: 1
Motif ID: 49
Motif name: Motif 49
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 7
Similarity score: 0.021456

Alignment:
KTTTATCT
-TYTATWT

Original motif Consensus sequence: AGATAAAR

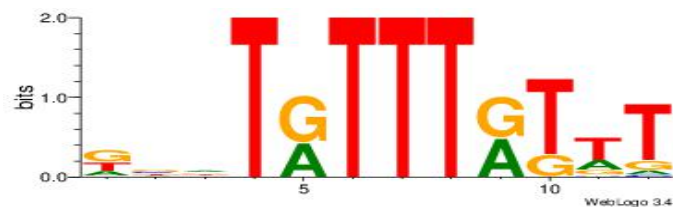
Reverse complement motif Consensus sequence: KTTTATCT



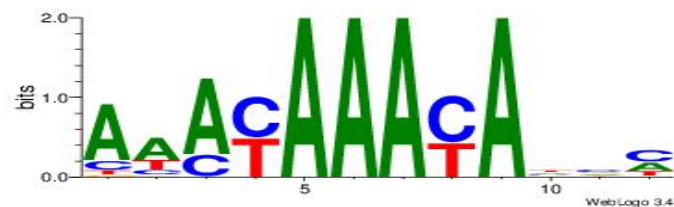
Dataset #: 3
 Motif ID: 67
 Motif name: FOXI1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 6
 Number of overlap: 7
 Similarity score: 0.0260643

Alignment:
 KBDTRTTTTRTTT
 -----TYTATWT

Original motif Consensus sequence: KBDTRTTTTRTTT



Reverse complement motif Consensus sequence: AAAMAAAMADBY



Dataset #: 2
 Motif ID: 60

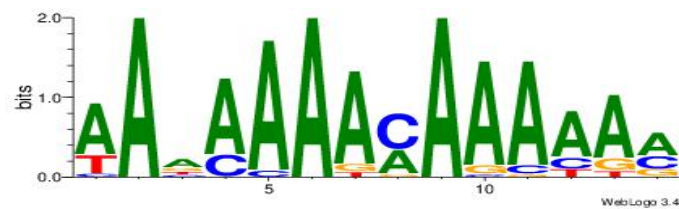
Motif name:	Motif 60
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	5
Number of overlap:	7
Similarity score:	0.031739

Alignment:

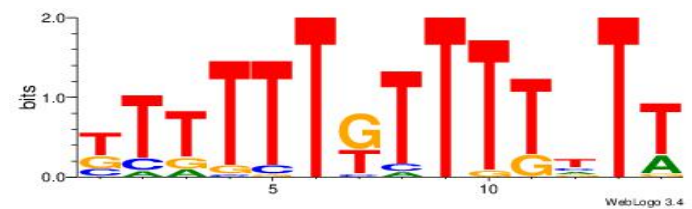
```

YTTTTTRTTTDTT
---TYTATWT----
```

Original motif Consensus sequence: AADAAAAMAAAAAM



Reverse complement motif Consensus sequence: YTTTTTRTTTDTT



Dataset #:	4
Motif ID:	90
Motif name:	ymTACATAyw
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	4
Number of overlap:	7
Similarity score:	0.034879

Alignment:

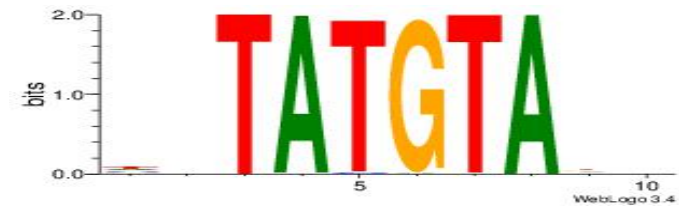
DBTATGTAHH

TYTATWT---

Original motif Consensus sequence: HHTACATABD



Reverse complement motif Consensus sequence: DBTATGTAHH



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

Original motif Consensus sequence: GAGRMAGR



Reverse complement motif Consensus sequence: KCTRMCTC



Best Matches for Motif ID 4 (Highest to Lowest)

Dataset #:	4
Motif ID:	116
Motif name:	dyCTGCyTCyc
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	2

Number of overlap: 8
Similarity score: 0.0229288

Alignment:
BHGA KGCAGHH
--GAGRMAGR--

Original motif Consensus sequence: DHCTGCYTCHB



Reverse complement motif Consensus sequence: BHGA KGCAGHH



Dataset #: 4
Motif ID: 113
Motif name: htCTGyKTCbt
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 3
Number of overlap: 8
Similarity score: 0.0339962

Alignment:
HVGAAMCAGVH
--GAGRMAGR--

Original motif Consensus sequence: HBCTGYTTCBH

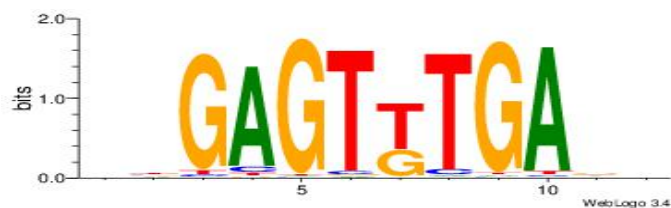
Reverse complement motif Consensus sequence: HVGAAMCAGVH



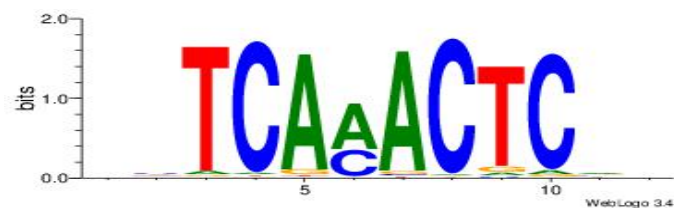
Dataset #: 4
 Motif ID: 112
 Motif name: ctGAGTktGAgg
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 8
 Similarity score: 0.0422491

Alignment:
 HHTCARACTCVV
 --KCTRMCTC--

Original motif Consensus sequence: VBGAGTKTGADD



Reverse complement motif Consensus sequence: HHTCARACTCVV

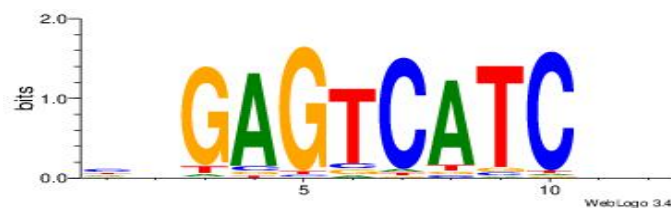


Dataset #: 4
 Motif ID: 121

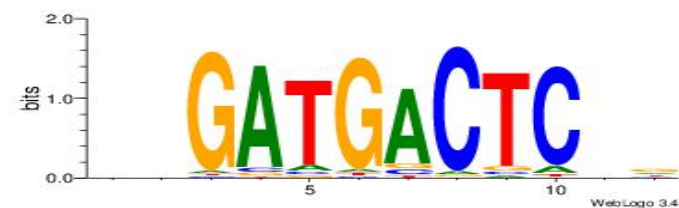
Motif name:	ctGAGTCATCkb
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	3
Number of overlap:	8
Similarity score:	0.0508307

Alignment:
 BHGATGACTCDD
 --KCTRMCTC--

Original motif Consensus sequence: HDGAGTCATCDB



Reverse complement motif Consensus sequence: BHGATGACTCDD



Dataset #:	1
Motif ID:	18
Motif name:	Motif 18
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	8
Similarity score:	0.0519824

Alignment:

GRRAGAGA

GAGRMAGR

Original motif Consensus sequence: GRRAGAGA



Reverse complement motif Consensus sequence: TCTCTMKC

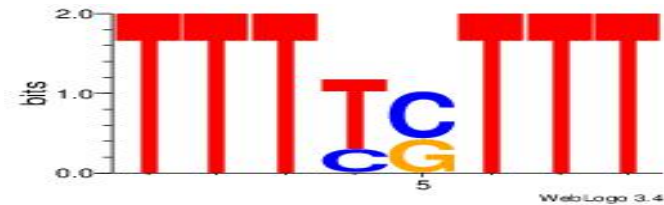


Dataset #: 1 Motif ID: 5 Motif name: Motif 5

Original motif Consensus sequence: AAASAAA



Reverse complement motif Consensus sequence: TTTTSTTT



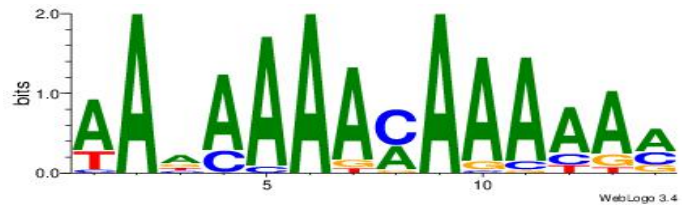
Best Matches for Motif ID 5 (Highest to Lowest)

Dataset #:	2
Motif ID:	60
Motif name:	Motif 60
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	5

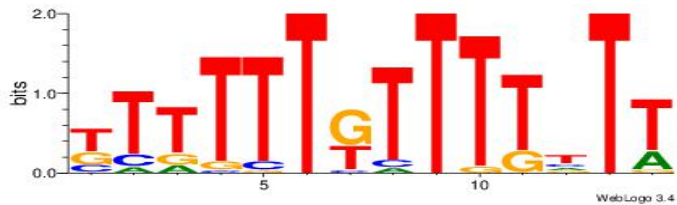
Number of overlap: 8
Similarity score: 0.0229557

Alignment:
AADAAAAMAAAAAM
-----AAASAAAA--

Original motif Consensus sequence: AADAAAAMAAAAAM



Reverse complement motif Consensus sequence: YTTTTTRTTTTDTT

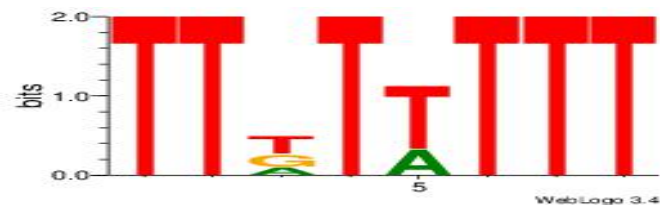


Dataset #: 1
Motif ID: 1
Motif name: Motif 1
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 8
Similarity score: 0.0330694

Alignment:
TTYTTTTT
TTTTSTTT

Original motif Consensus sequence: AAAAAMAA

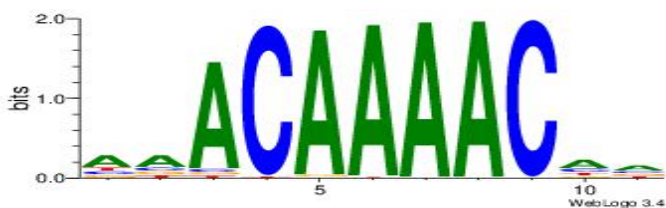
Reverse complement motif Consensus sequence: TTYTTTTT



Dataset #: 4
 Motif ID: 89
 Motif name: aaACAAACaa
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 4
 Number of overlap: 8
 Similarity score: 0.0345209

Alignment:
 BHGTTTTGTTT
 ---TTTTSTTT

Original motif Consensus sequence: AAACAAACHV



Reverse complement motif Consensus sequence: BHGTTTTGTTT



Dataset #: 1
 Motif ID: 21

Motif name:	Motif 21
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	8
Similarity score:	0.0346745

Alignment:
AAACAAAC
AAASAAAA

Original motif Consensus sequence: AAACAAAC



Reverse complement motif Consensus sequence: GTTTGTTT



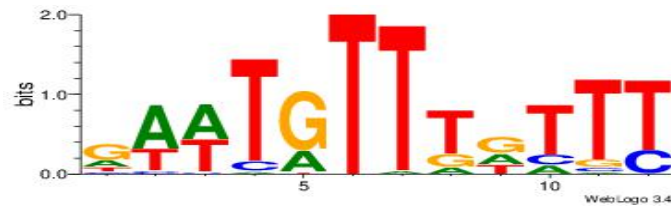
Dataset #:	3
Motif ID:	65
Motif name:	Foxd3
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	8
Similarity score:	0.0440489

Alignment:

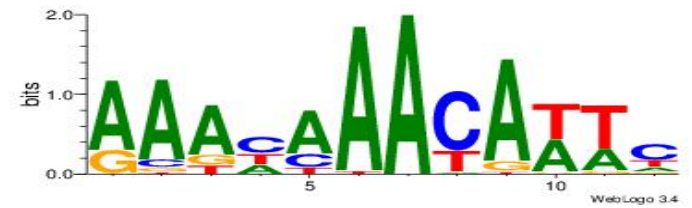
AAAHAAACAWTC

AAASAAAA-----

Original motif Consensus sequence: GAWTGTTTDTTT



Reverse complement motif Consensus sequence: AAAHAAACAWTC



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

Original motif Consensus sequence: CCCASCMC



Reverse complement motif Consensus sequence: GYGSTGGG



Best Matches for Motif ID 6 (Highest to Lowest)

Dataset #:	1
Motif ID:	22
Motif name:	Motif 22
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: 0.00727797

Alignment:
MCCACCAC
CCCASCMC

Original motif Consensus sequence: GTGGTGGY



Reverse complement motif Consensus sequence: MCCACCAC

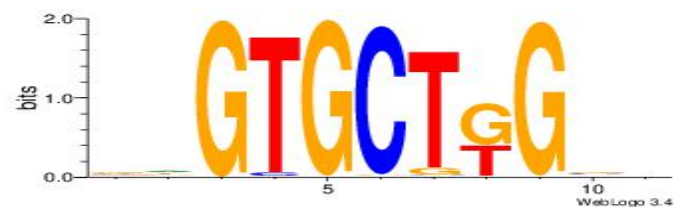


Dataset #: 4
Motif ID: 115
Motif name: ysCmAGCACwy
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 3
Number of overlap: 8
Similarity score: 0.0212781

Alignment:
DHGTGCTRGVH
--GYGSTGGG--

Original motif Consensus sequence: HVCMAGCACHH

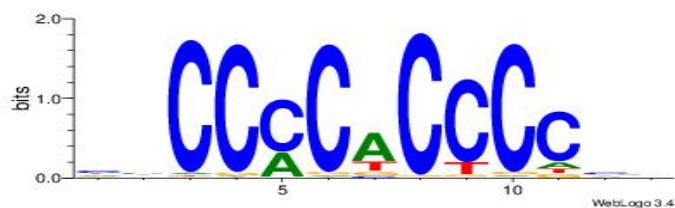
Reverse complement motif Consensus sequence: DHGTGCTRGVH



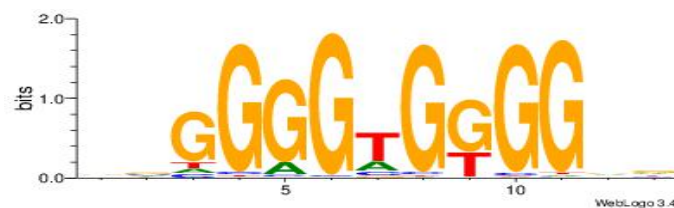
Dataset #: 4
 Motif ID: 111
 Motif name: ccCCmCaCCCCcc
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 8
 Similarity score: 0.0266863

Alignment:
 HBCCCCACCCCBH
 ---CCCASCMC--

Original motif Consensus sequence: HBCCCCACCCCBH



Reverse complement motif Consensus sequence: DBGGGTGGGB



Dataset #: 1
 Motif ID: 42

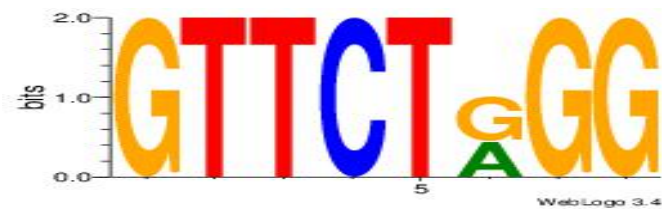
Motif name:	Motif 42
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	8
Similarity score:	0.030487

Alignment:
GTTCTKGG
GYGSTGGG

Original motif Consensus sequence: CCYAGAAC



Reverse complement motif Consensus sequence: GTTCTKGG



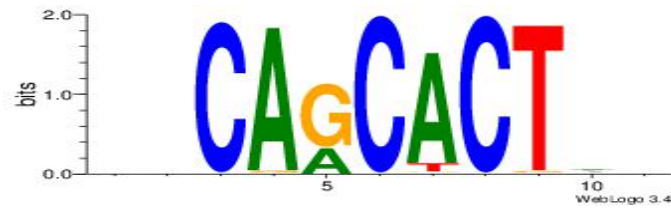
Dataset #:	4
Motif ID:	93
Motif name:	cmCARCACTwr
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	4
Number of overlap:	8
Similarity score:	0.030511

Alignment:

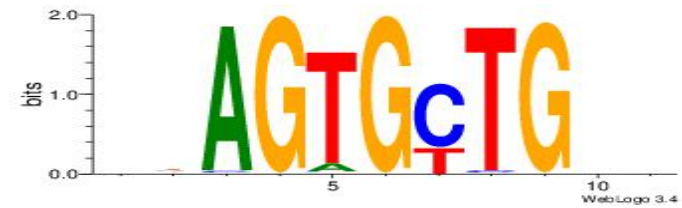
BHCAGCACTHV

CCCASCMC---

Original motif Consensus sequence: BHCAGCACTHV



Reverse complement motif Consensus sequence: VHAGTGCTGHB

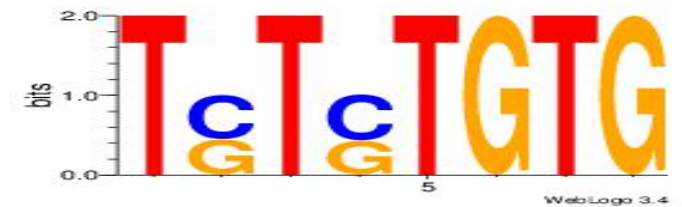


Dataset #: 1 Motif ID: 7 Motif name: Motif 7

Original motif Consensus sequence: CACASASA



Reverse complement motif Consensus sequence: TSTSTGTG



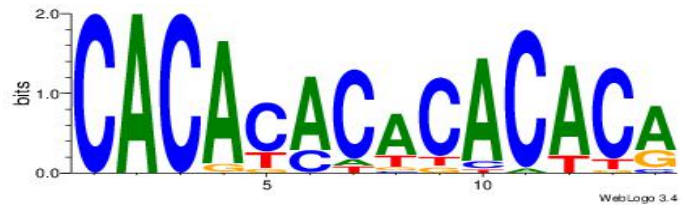
Best Matches for Motif ID 7 (Highest to Lowest)

Dataset #:	2
Motif ID:	58
Motif name:	Motif 58
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	7

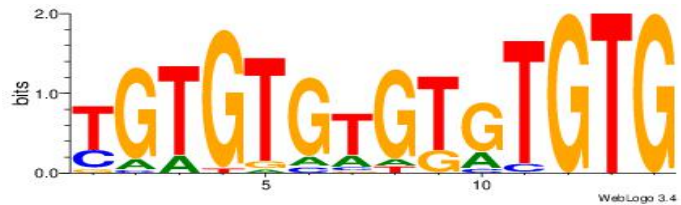
Number of overlap: 8
Similarity score: 0.0271648

Alignment:
TGTGTGTGTGTG
-----TSTSTGTG

Original motif Consensus sequence: CACACACACACA



Reverse complement motif Consensus sequence: TGTGTGTGTGTG

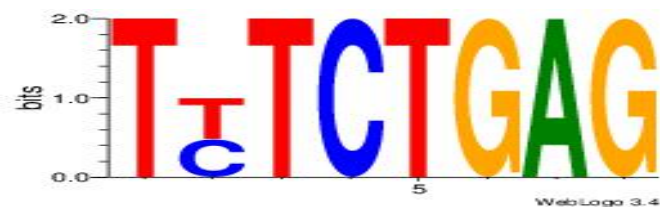


Dataset #: 1
Motif ID: 41
Motif name: Motif 41
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 8
Similarity score: 0.0361772

Alignment:
CTCAGARA
CACASASA

Original motif Consensus sequence: CTCAGARA

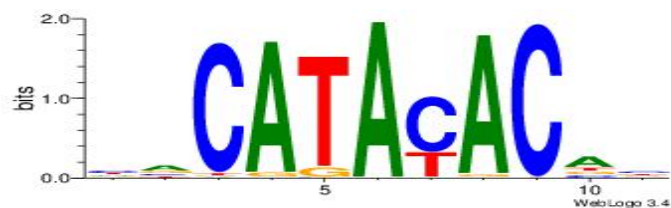
Reverse complement motif Consensus sequence: TKTCTGAG



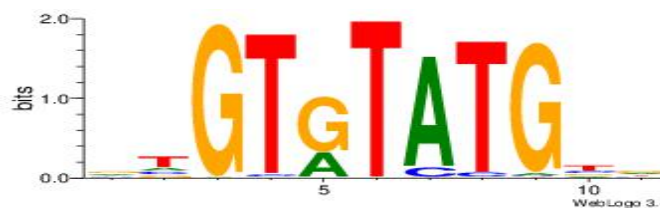
Dataset #: 4
 Motif ID: 117
 Motif name: yaCATAYACay
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 8
 Similarity score: 0.0572872

Alignment:
 DTGTGTATGBD
 -TSTSTGTG--

Original motif Consensus sequence: HVCATACACAH



Reverse complement motif Consensus sequence: DTGTGTATGBD

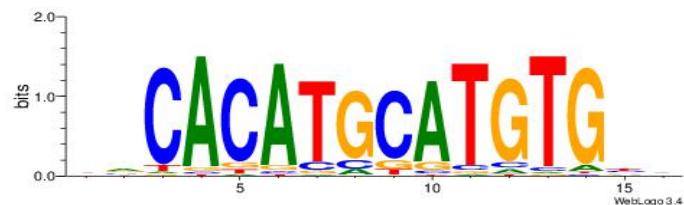


Dataset #: 4
 Motif ID: 118

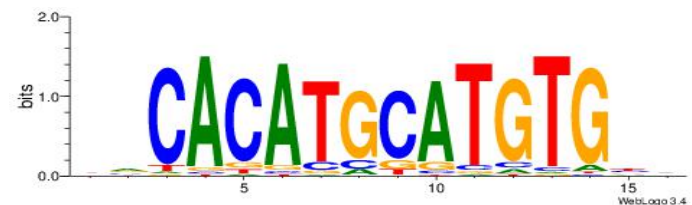
Motif name: yrCACATGCATGTGyr
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 7
 Number of overlap: 8
 Similarity score: 0.0627214

Alignment:
 HVCACATGCATGTGBD
 --CACASASA-----

Original motif Consensus sequence: HVCACATGCATGTGBD



Reverse complement motif Consensus sequence: DVCACATGCATGTGBH



Dataset #: 4
 Motif ID: 114
 Motif name: awAACAcAAwa
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 8
 Similarity score: 0.0715956

Alignment:

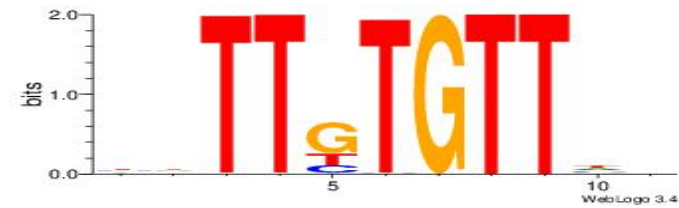
DDAACACAADV

--CACASASA--

Original motif Consensus sequence: DDAACACAADV



Reverse complement motif Consensus sequence: BDTTGTGTTDD



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

Original motif Consensus sequence: CTGGCYTY



Reverse complement motif Consensus sequence: KAGCCAG



Best Matches for Motif ID 8 (Highest to Lowest)

Dataset #:	4
Motif ID:	97
Motif name:	sgArGCCACg
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2

Number of overlap: 8
Similarity score: 0.0352649

Alignment:
SGARGCCACG
-KAKGCCAG-

Original motif Consensus sequence: SGARGCCACG



Reverse complement motif Consensus sequence: CGTGGCKTCS



Dataset #: 4
Motif ID: 92
Motif name: cgAKGyCACg
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2
Number of overlap: 8
Similarity score: 0.0406315

Alignment:
CGAGGYCACV
-KAKGCCAG-

Original motif Consensus sequence: CGAGGYCACV

Reverse complement motif Consensus sequence: VGTGMCCTCG



Dataset #: 1
 Motif ID: 27
 Motif name: Motif 27
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 8
 Similarity score: 0.0419581

Alignment:
 CTGCCTKY
 CTGGCYTY

Original motif Consensus sequence: CTGCCTKY



Reverse complement motif Consensus sequence: KRAGGCAG



Dataset #: 1
 Motif ID: 31

Motif name:	Motif 31
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	8
Similarity score:	0.0519508

Alignment:
CTGWSCTC
CTGGCYTY

Original motif Consensus sequence: CTGWSCTC



Reverse complement motif Consensus sequence: GAGSWCAG



Dataset #:	1
Motif ID:	11
Motif name:	Motif 11
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	8
Similarity score:	0.0648749

Alignment:
CTGDGTTC
CTGGCYTY

Original motif Consensus sequence: CTGDGTTC

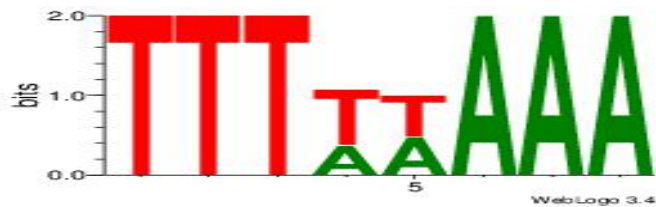


Reverse complement motif Consensus sequence: GAACDCAG



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

Original motif Consensus sequence: TTTWWAAA



Reverse complement motif Consensus sequence: TTTWWAAA



Best Matches for Motif ID 9 (Highest to Lowest)

Dataset #:	4
Motif ID:	120
Motif name:	wtTTTwAAAaw
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2

Number of overlap: 8
Similarity score: 0

Alignment:
HHTTTWAAADD
-TTTWAAA--

Original motif Consensus sequence: HHTTTWAAADD



Reverse complement motif Consensus sequence: DDTTTWAAHH

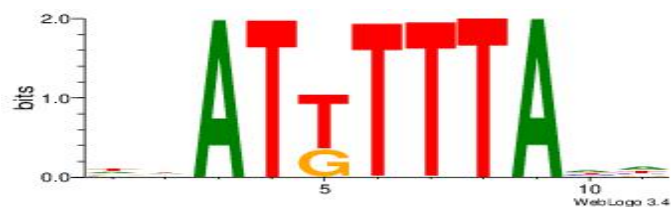


Dataset #: 4
Motif ID: 108
Motif name: wwATkTTTAww
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 8
Similarity score: 0.0472911

Alignment:
DHATKTTTAHH
---TTTWAAA

Original motif Consensus sequence: DHATKTTTAHH

Reverse complement motif Consensus sequence: HHTAAARATHD

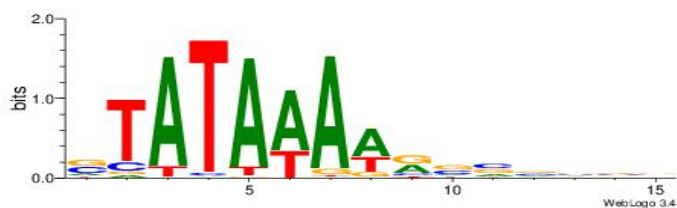


Dataset #: 3
 Motif ID: 62
 Motif name: TBP
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 8
 Similarity score: 0.0552987

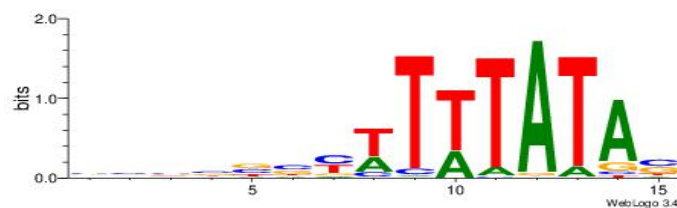
Alignment:

STATAAAWRVVVBV
 -TTTWAAA-----

Original motif Consensus sequence: STATAAAWRVVVBV



Reverse complement motif Consensus sequence: VBVVVVMWTTTAT



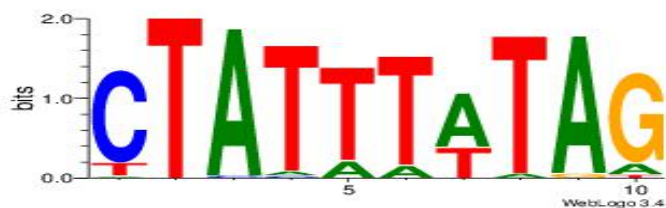
Dataset #: 3
 Motif ID: 61

Motif name: MEF2A
 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: 0.0641646

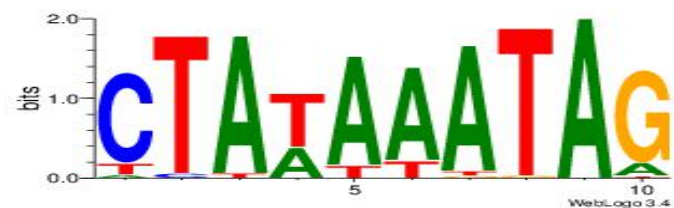
Alignment:

CTATTTWTAG
 -TTTWWAAA-

Original motif Consensus sequence: CTATTTWTAG



Reverse complement motif Consensus sequence: CTAWAAATAG



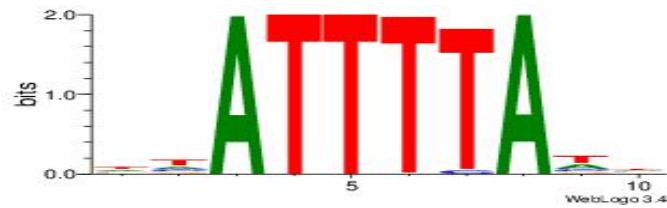
Dataset #: 4
 Motif ID: 91
 Motif name: wtATTTTAww
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 8
 Similarity score: 0.0724871

Alignment:

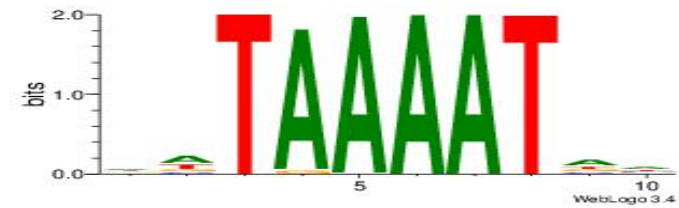
HWTAAAATHD

TTTWAAA--

Original motif Consensus sequence: DHATTTTAWH



Reverse complement motif Consensus sequence: HWTAAAATHD



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

Original motif Consensus sequence: HTACATA



Reverse complement motif Consensus sequence: TATGTAD



Best Matches for Motif ID 10 (Highest to Lowest)

Dataset #:	4
Motif ID:	90
Motif name:	ymTACATyW
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	3

Number of overlap: 7
Similarity score: 0

Alignment:
HHTACATABD
-HTACATA--

Original motif Consensus sequence: HHTACATABD



Reverse complement motif Consensus sequence: DBTATGTAHH



Dataset #: 3
Motif ID: 69
Motif name: NKX3-1
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 7
Similarity score: 0.0460238

Alignment:
TAAGTAT
TATGTAD

Original motif Consensus sequence: AACTTA

Reverse complement motif Consensus sequence: TAAGTAT



Dataset #: 4
 Motif ID: 114
 Motif name: awAACAcAAwa
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 4
 Number of overlap: 7
 Similarity score: 0.0619118

Alignment:

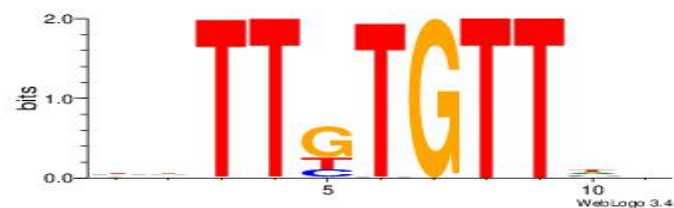
BDTTGTGTTDD

---TATGTAD-

Original motif Consensus sequence: DDAACACAADV



Reverse complement motif Consensus sequence: BDTTGTGTTDD

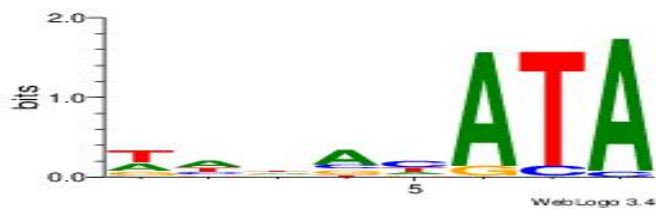


Dataset #: 3
 Motif ID: 63

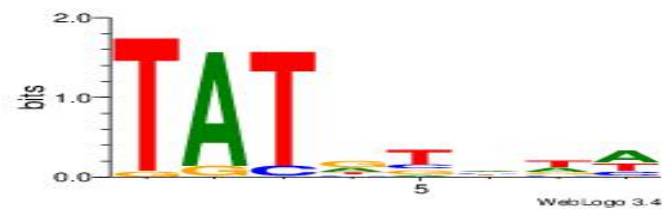
Motif name: FOXL1
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 7
 Similarity score: 0.0663597

Alignment:
 WHDAHATA
 -HTACATA

Original motif Consensus sequence: WHDAHATA



Reverse complement motif Consensus sequence: TATDTHW



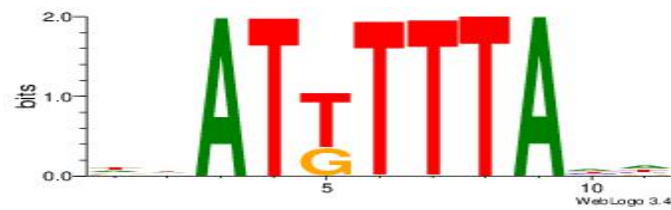
Dataset #: 4
 Motif ID: 108
 Motif name: wwATkTTTAww
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 4
 Number of overlap: 7
 Similarity score: 0.0688346

Alignment:

HHTAAARATHD

-HTACATA---

Original motif Consensus sequence: DHATKTTTAHH



Reverse complement motif Consensus sequence: HHTAAARATHD

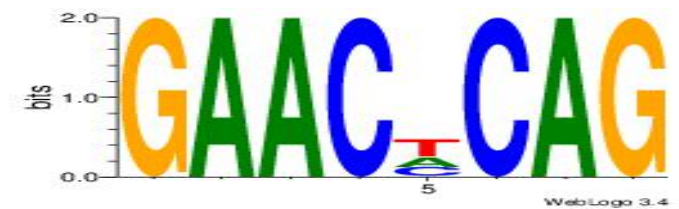


Dataset #: 1 Motif ID: 11 Motif name: Motif 11

Original motif Consensus sequence: CTGDGTTC



Reverse complement motif Consensus sequence: GAACDCAG



Best Matches for Motif ID 11 (Highest to Lowest)

Dataset #:	1
Motif ID:	31
Motif name:	Motif 31
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1

Number of overlap: 8
Similarity score: 0.0558383

Alignment:
CTGWSCTC
CTGDGTTC

Original motif Consensus sequence: CTGWSCTC



Reverse complement motif Consensus sequence: GAGSWCAG



Dataset #: 1
Motif ID: 12
Motif name: Motif 12
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 8
Similarity score: 0.0780567

Alignment:
MTGTGTGC
CTGDGTTC

Original motif Consensus sequence: GCACACAY

Reverse complement motif Consensus sequence: MTGTGTGC



Dataset #: 1
 Motif ID: 27
 Motif name: Motif 27
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 8
 Similarity score: 0.0849877

Alignment:
 KRAGGCAG
 GAACDCAG

Original motif Consensus sequence: CTGCCTKY



Reverse complement motif Consensus sequence: KRAGGCAG



Dataset #: 1
 Motif ID: 8

Motif name:	Motif 8
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:	0.0874939

Alignment:
CTGGCYTY
CTGDGTTC

Original motif Consensus sequence: CTGGCYTY



Reverse complement motif Consensus sequence: KAKGCCAG



Dataset #:	4
Motif ID:	114
Motif name:	awAACAcAAwa
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	8
Similarity score:	0.0916924

Alignment:

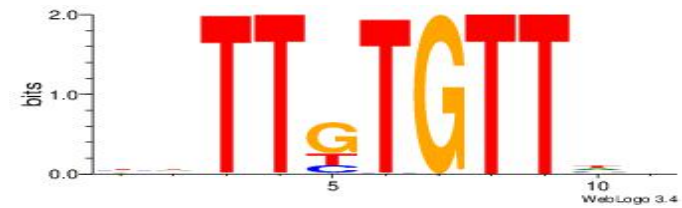
DDAACACAADV

-GAACDCAG--

Original motif Consensus sequence: DDAACACAADV



Reverse complement motif Consensus sequence: BDTTGTGTTDD



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

Original motif Consensus sequence: GCACACAY



Reverse complement motif Consensus sequence: MTGTGTGC



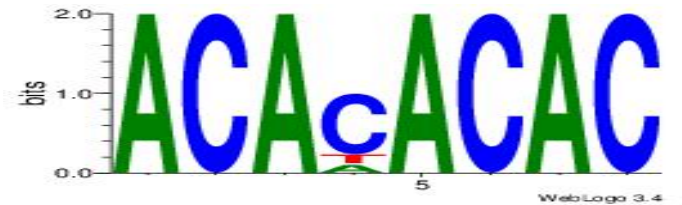
Best Matches for Motif ID 12 (Highest to Lowest)

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

Number of overlap: 8
Similarity score: 0.0388776

Alignment:
ACACACAC
GCACACAY

Original motif Consensus sequence: ACACACAC



Reverse complement motif Consensus sequence: GTGTGTGT

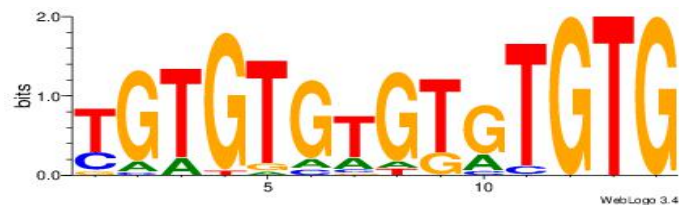
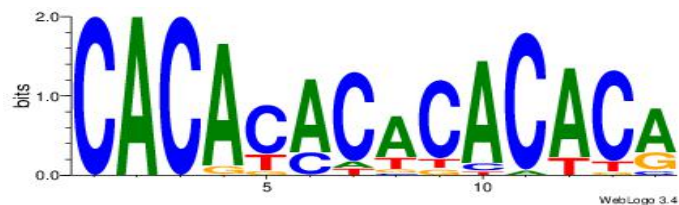


Dataset #: 2
Motif ID: 58
Motif name: Motif 58
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 6
Number of overlap: 8
Similarity score: 0.0509001

Alignment:
CACACACACACA
-GCACACAY-----

Original motif Consensus sequence: CACACACACACA

Reverse complement motif Consensus sequence: TGTGTGTGTGT



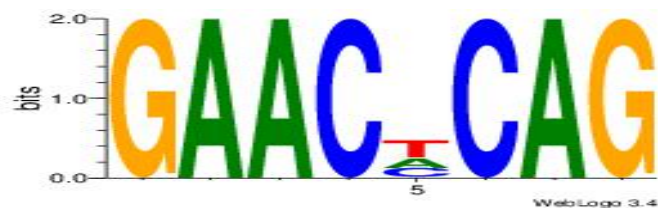
Dataset #: 1
 Motif ID: 11
 Motif name: Motif 11
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 8
 Similarity score: 0.0543096

Alignment:
 GAACDCAG
 GCACACAY

Original motif Consensus sequence: CTGDGTTC



Reverse complement motif Consensus sequence: GAACDCAG



Dataset #: 4
 Motif ID: 126

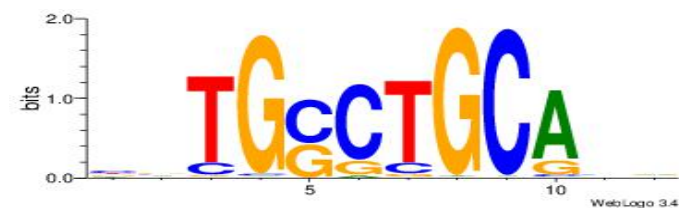
Motif name: yvTGCAGsCAcg
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 8
 Similarity score: 0.0573852

Alignment:
 BVTGCAGSCABV
 ---GCACACAY-

Original motif Consensus sequence: BVTGCAGSCABV



Reverse complement motif Consensus sequence: VBTGSCTGCAVB



Dataset #: 1
 Motif ID: 37
 Motif name: Motif 37
 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: 0.0626478

Alignment:
KCACATKC
GCACACAY

Original motif Consensus sequence: GYATGTGY



Reverse complement motif Consensus sequence: KCACATKC



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

Original motif Consensus sequence: GGAAGSAR



Reverse complement motif Consensus sequence: MTSCTTCC



Best Matches for Motif ID 13 (Highest to Lowest)

Dataset #:	1
Motif ID:	17
Motif name:	Motif 17
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1

Number of overlap: 8
Similarity score: 0.0653924

Alignment:
GGGAGGRR
GGAAGSAR

Original motif Consensus sequence: GGGAGGRR



Reverse complement motif Consensus sequence: MMCCTCCC

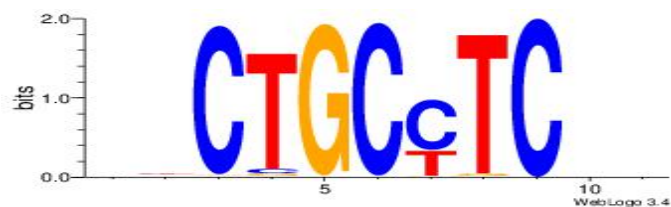


Dataset #: 4
Motif ID: 116
Motif name: dyCTGCyTCyc
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 3
Number of overlap: 8
Similarity score: 0.0796555

Alignment:
DHCTGCTCHB
--MTSCTTCC--

Original motif Consensus sequence: DHCTGCTCHB

Reverse complement motif Consensus sequence: BHGAKGCAGHH



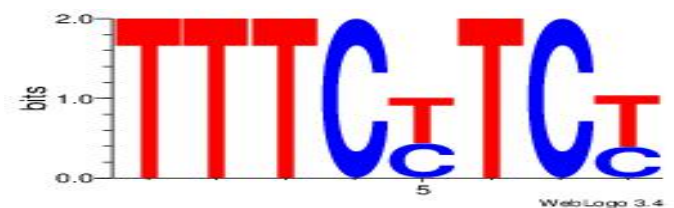
Dataset #: 1
 Motif ID: 26
 Motif name: Motif 26
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 8
 Similarity score: 0.0803708

Alignment:
 RGARGAAA
 GGAAGSAR

Original motif Consensus sequence: RGARGAAA



Reverse complement motif Consensus sequence: TTTCTCK



Dataset #: 4
 Motif ID: 113

Motif name:	htCTGyKTCbt
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	3
Number of overlap:	8
Similarity score:	0.0857132

Alignment:

HBCTGYTTCBH
 --MTSCTTCC--

Original motif Consensus sequence: HBCTGYTTCBH



Reverse complement motif Consensus sequence: HVGAAMCAGVH



Dataset #:	1
Motif ID:	27
Motif name:	Motif 27
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	8
Similarity score:	0.0948401

Alignment:
KRAGGCAG
GGAAGSAR

Original motif Consensus sequence: CTGCCTKY



Reverse complement motif Consensus sequence: KRAGGCAG



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

Original motif Consensus sequence: KAAAATR



Reverse complement motif Consensus sequence: MATTTTY



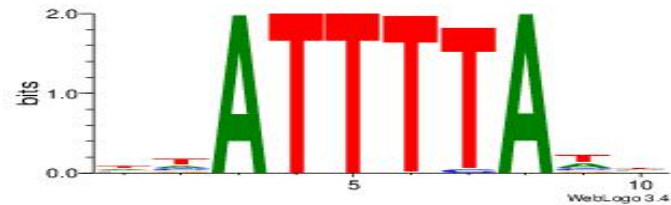
Best Matches for Motif ID 14 (Highest to Lowest)

Dataset #:	4
Motif ID:	91
Motif name:	wtATTTTAww
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	2

Number of overlap: 7
Similarity score: 0.0107308

Alignment:
HWTAAAATHD
--KAAAATR--

Original motif Consensus sequence: DHATTTTAWH



Reverse complement motif Consensus sequence: HWTAAAATHD

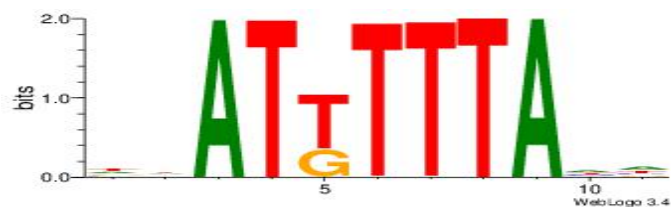


Dataset #: 4
Motif ID: 108
Motif name: wwATkTTTAww
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 2
Number of overlap: 7
Similarity score: 0.0228401

Alignment:
DHATKTTTAHH
-MATTTY---

Original motif Consensus sequence: DHATKTTTAHH

Reverse complement motif Consensus sequence: HHTAAARATHD



Dataset #: 1
 Motif ID: 44
 Motif name: Motif 44
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 7
 Similarity score: 0.0324742

Alignment:
 CATTTCT
 MATTTTY

Original motif Consensus sequence: AGAAATG



Reverse complement motif Consensus sequence: CATTTCT



Dataset #: 3
 Motif ID: 87

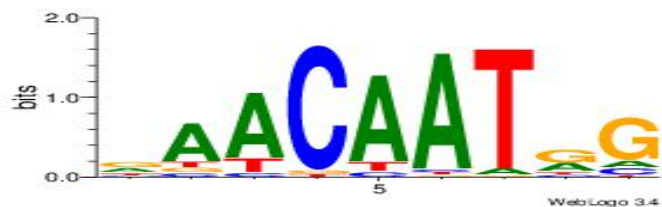
Motif name:	SOX9
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	2
Number of overlap:	7
Similarity score:	0.0488777

Alignment:

CMATTGTH

-MATTTY-

Original motif Consensus sequence: DAACAATRG



Reverse complement motif Consensus sequence: CMATTGTH



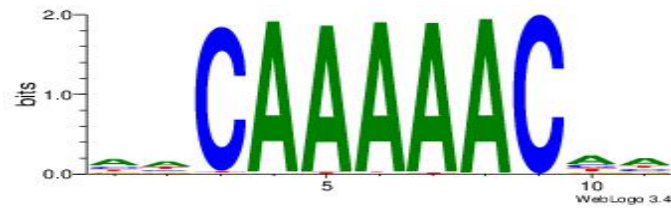
Dataset #:	4
Motif ID:	109
Motif name:	aaCAAAAACaa
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	2
Number of overlap:	7
Similarity score:	0.0510773

Alignment:

HHGTTTTTGHH

-MATTTTY---

Original motif Consensus sequence: HHCAAAAACHH



Reverse complement motif Consensus sequence: HHGTTTTTGHH



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

Original motif Consensus sequence: AGCCCWGG



Reverse complement motif Consensus sequence: CCWGGGCT



Best Matches for Motif ID 15 (Highest to Lowest)

Dataset #:	1
Motif ID:	51
Motif name:	Motif 51
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1

Number of overlap: 8
Similarity score: 0.0387232

Alignment:
AGAGCWGG
AGCCCWGG

Original motif Consensus sequence: AGAGCWGG



Reverse complement motif Consensus sequence: CCWGCTCT

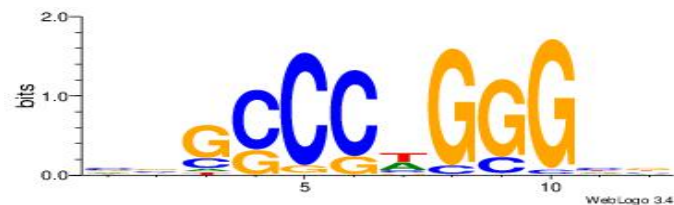
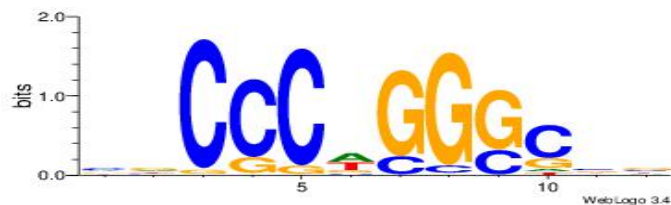


Dataset #: 4
Motif ID: 104
Motif name: cgCCCwGGScsg
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 8
Similarity score: 0.0422017

Alignment:
VDCCCWGGGCBB
AGCCCWGG----

Original motif Consensus sequence: VDCCCWGGGCBB

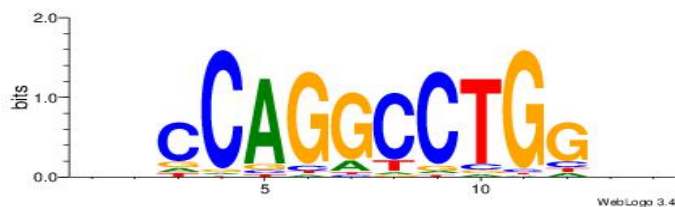
Reverse complement motif Consensus sequence: BBGCCCWGGGHV



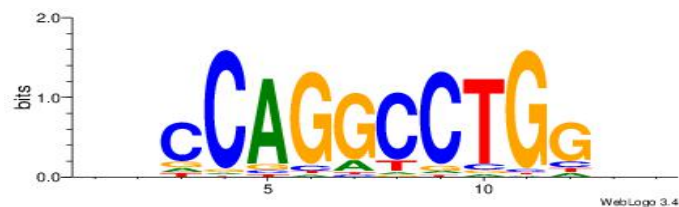
Dataset #: 4
 Motif ID: 122
 Motif name: hsCCAGGCCTGGsr
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 5
 Number of overlap: 8
 Similarity score: 0.0482193

Alignment:
 HVCCAGGCCTGGBD
 --CCWGGGCT----

Original motif Consensus sequence: HVCCAGGCCTGGBD



Reverse complement motif Consensus sequence: HBCCAGGCCTGGV



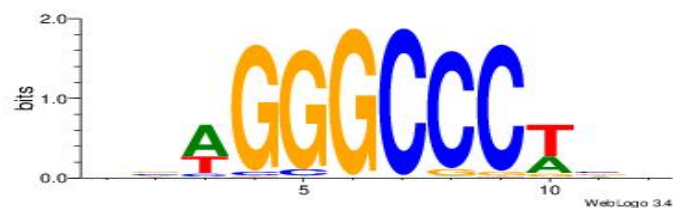
Dataset #: 4
 Motif ID: 124

Motif name: cswGGGCCCwsg
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 5
 Number of overlap: 8
 Similarity score: 0.0580747

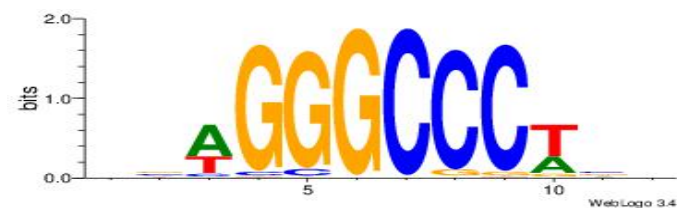
Alignment:

BBWGGGCCCWVV
 ----AGCCCWGG

Original motif Consensus sequence: VVWGGGCCCWBB



Reverse complement motif Consensus sequence: BBWGGGCCCWVV



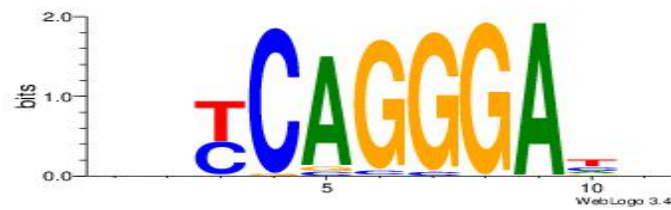
Dataset #: 4
 Motif ID: 127
 Motif name: rryCAGGGAyw
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 8
 Similarity score: 0.0593634

Alignment:

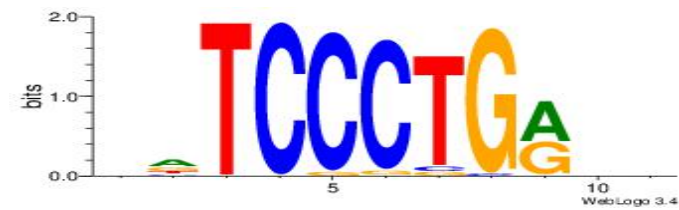
DDYCAGGGAHD

--CCWGGGCT--

Original motif Consensus sequence: DDYCAGGGAHD



Reverse complement motif Consensus sequence: DHTCCCTGMDD



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

Original motif Consensus sequence: GAGCCATC



Reverse complement motif Consensus sequence: GATGGCTC



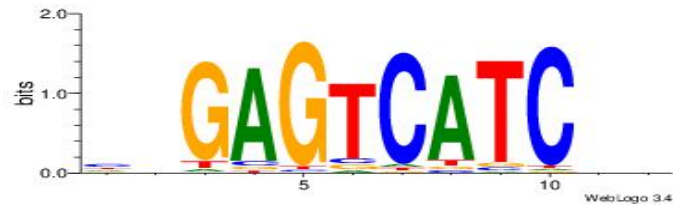
Best Matches for Motif ID 16 (Highest to Lowest)

Dataset #:	4
Motif ID:	121
Motif name:	ctGAGTCATCkb
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	3

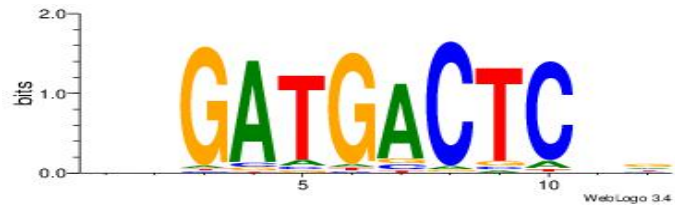
Number of overlap: 8
Similarity score: 0.0217603

Alignment:
HDGAGTCATCDB
--GAGCCATC--

Original motif Consensus sequence: HDGAGTCATCDB



Reverse complement motif Consensus sequence: BHGATGACTCDD



Dataset #: 1
Motif ID: 4
Motif name: Motif 4
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 8
Similarity score: 0.0643454

Alignment:
KCTRMCTC
GATGGCTC

Original motif Consensus sequence: GAGRMAGR

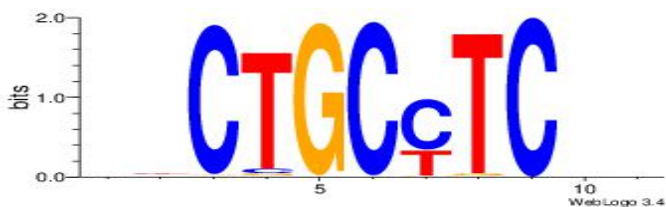
Reverse complement motif Consensus sequence: KCTRMCTC



Dataset #: 4
 Motif ID: 116
 Motif name: dyCTGCyTCyc
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 8
 Similarity score: 0.0716659

Alignment:
 BHGAKGCAGHH
 --GAGCCATC--

Original motif Consensus sequence: DHCTGCTCHB



Reverse complement motif Consensus sequence: BHGAKGCAGHH



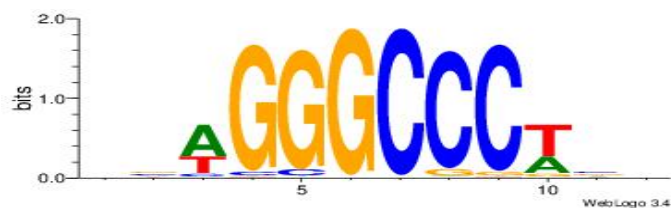
Dataset #: 4
 Motif ID: 124

Motif name: cswGGGCCCwsg
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 4
 Number of overlap: 8
 Similarity score: 0.0726629

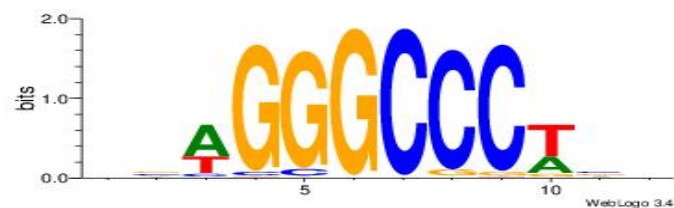
Alignment:

BBWGGGCCCWVV
 ---GAGCCATC-

Original motif Consensus sequence: VVWGGGCCCWBB



Reverse complement motif Consensus sequence: BBWGGGCCCWVV



Dataset #: 4
 Motif ID: 97
 Motif name: sgArGCCACg
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 8
 Similarity score: 0.0739514

Alignment:

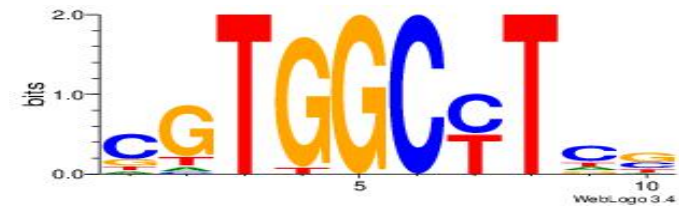
CGTGGCKTCS

GATGGCTC--

Original motif Consensus sequence: SGARGCCACG



Reverse complement motif Consensus sequence: CGTGGCKTCS



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

Original motif Consensus sequence: GGGAGGRR



Reverse complement motif Consensus sequence: MMCCTCCC



Best Matches for Motif ID 17 (Highest to Lowest)

Dataset #:	1
Motif ID:	13
Motif name:	Motif 13
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1

Number of overlap: 8
Similarity score: 0.0153924

Alignment:
GGAAGSAR
GGGAGGRR

Original motif Consensus sequence: GGAAGSAR



Reverse complement motif Consensus sequence: MTSCTTCC

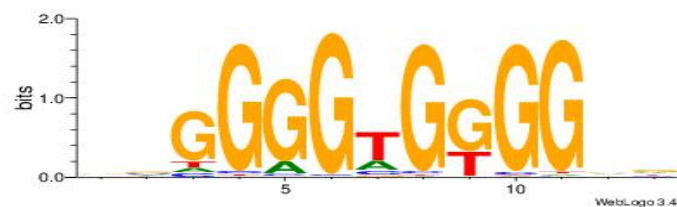
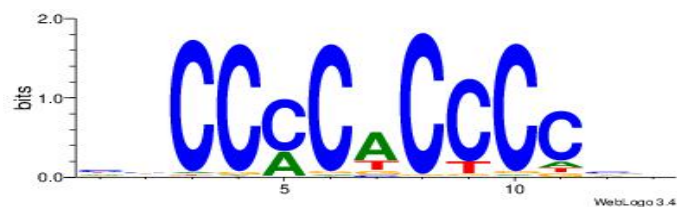


Dataset #: 4
Motif ID: 111
Motif name: ccCCmCaCCCCcc
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 4
Number of overlap: 8
Similarity score: 0.0180858

Alignment:
HBCCCCACCCCBH
--MMCTCCC---

Original motif Consensus sequence: HBCCCCACCCCBH

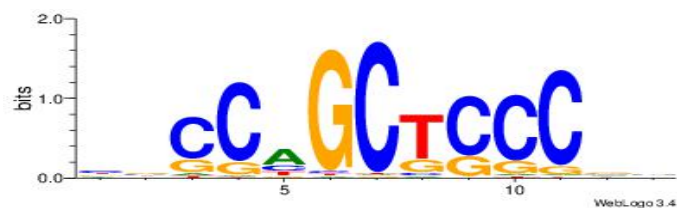
Reverse complement motif Consensus sequence: DBGGGGTGGGGB



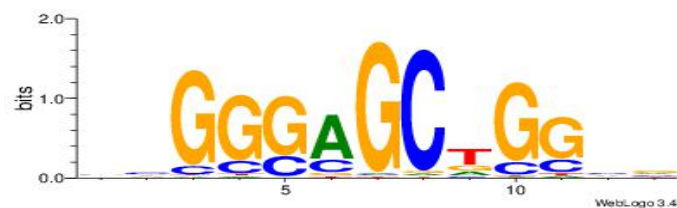
Dataset #: 4
 Motif ID: 103
 Motif name: csCCaGCTCCCgs
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 8
 Similarity score: 0.0339203

Alignment:
 BBCCAGCTCCCVB
 ---MMCTCCC--

Original motif Consensus sequence: BBCCAGCTCCCVB



Reverse complement motif Consensus sequence: BVGGGAGCTGGBB



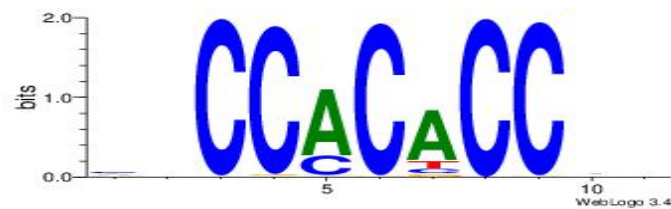
Dataset #: 4
 Motif ID: 110

Motif name:	cmCCACACCcm
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	8
Similarity score:	0.0373897

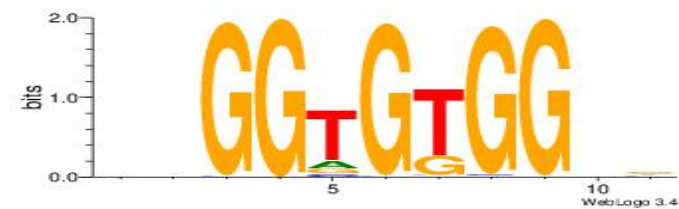
Alignment:

HVCCACACCBV
 MMCCTCCC---

Original motif Consensus sequence: HVCCACACCBV



Reverse complement motif Consensus sequence: VBGGTGTGGBD



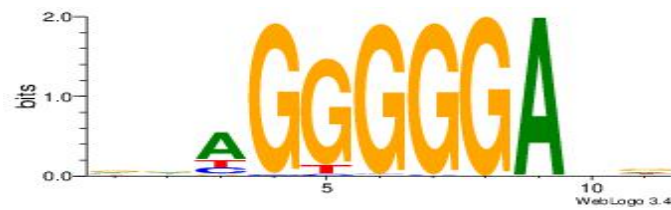
Dataset #:	4
Motif ID:	99
Motif name:	graGGGGGArr
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	4
Number of overlap:	8
Similarity score:	0.0403428

Alignment:

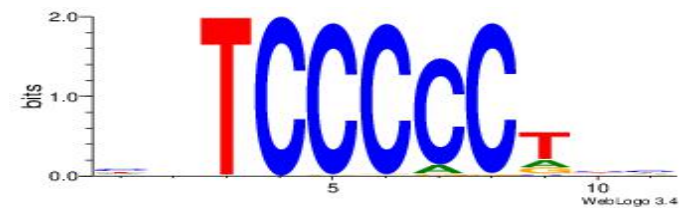
DVAGGGGGADD

---GGGAGGRR

Original motif Consensus sequence: DVAGGGGGADD



Reverse complement motif Consensus sequence: HDTCCCCCTVH



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

Original motif Consensus sequence: GRRAGAGA



Reverse complement motif Consensus sequence: TCTCTMKC



Best Matches for Motif ID 18 (Highest to Lowest)

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

Number of overlap: 8
Similarity score: 0.0524813

Alignment:
GAGRMAGR
GRRAGAGA

Original motif Consensus sequence: GAGRMAGR



Reverse complement motif Consensus sequence: KCTRMCTC



Dataset #: 4
Motif ID: 113
Motif name: htCTGyKTCbt
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 3
Number of overlap: 8
Similarity score: 0.0543958

Alignment:
HVGAAMCAGVH
--GRRAGAGA--

Original motif Consensus sequence: HBCTGYTTCBH

Reverse complement motif Consensus sequence: HVGAAMCAGVH



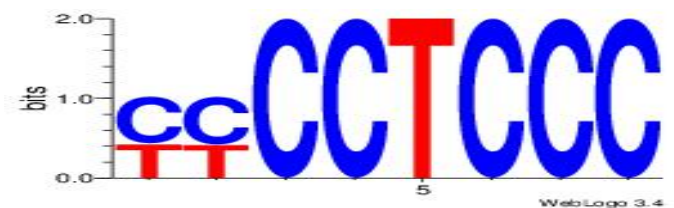
Dataset #: 1
 Motif ID: 17
 Motif name: Motif 17
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 8
 Similarity score: 0.0594801

Alignment:
 GGGAGGRR
 GRRAGAGA

Original motif Consensus sequence: GGGAGGRR



Reverse complement motif Consensus sequence: MMCCTCCC



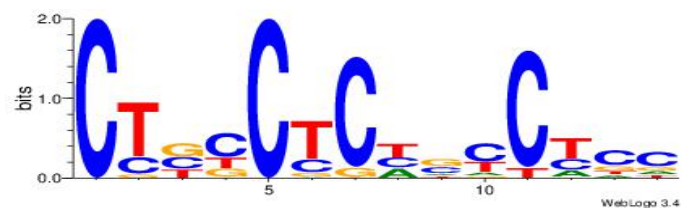
Dataset #: 2
 Motif ID: 59

Motif name:	Motif 59
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	4
Number of overlap:	8
Similarity score:	0.0602419

Alignment:

CTBCCTCHSYCYCC
 ---TCTCTMKC---

Original motif Consensus sequence: CTBCCTCHSYCYCC



Reverse complement motif Consensus sequence: GGMGKSHGAGGB



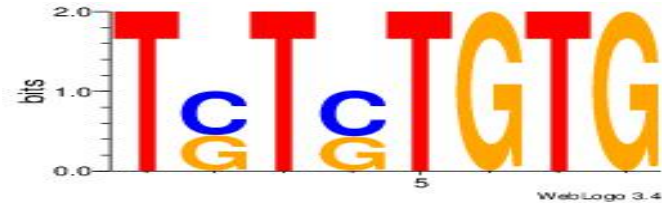
Dataset #:	1
Motif ID:	7
Motif name:	Motif 7
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	8
Similarity score:	0.0675926

Alignment:
CACASASA
GRRAGAGA

Original motif Consensus sequence: CACASASA



Reverse complement motif Consensus sequence: TSTSTGTG



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

Original motif Consensus sequence: CCTGGARC



Reverse complement motif Consensus sequence: GKTCCAGG



Best Matches for Motif ID 19 (Highest to Lowest)

Dataset #:	1
Motif ID:	42
Motif name:	Motif 42
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1

Number of overlap: 8
Similarity score: 0.0610815

Alignment:
CCYAGAAC
CCTGGARC

Original motif Consensus sequence: CCYAGAAC



Reverse complement motif Consensus sequence: GTTCTKGG

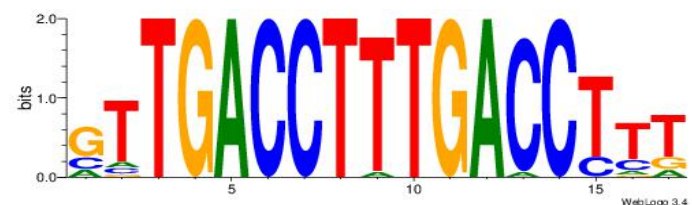
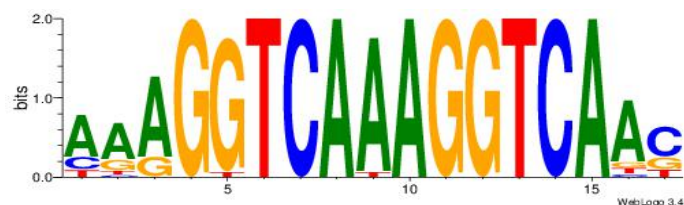


Dataset #: 3
Motif ID: 84
Motif name: NR1H2RXRA
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 4
Number of overlap: 8
Similarity score: 0.0814394

Alignment:
AAAGGTCAAAGGTCAAC
---GKTCCAGG-----

Original motif Consensus sequence: AAAGGTCAAAGGTCAAC

Reverse complement motif Consensus sequence:
GTTGACCTTTGACCTTT



Dataset #: 1
 Motif ID: 20
 Motif name: Motif 20
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 8
 Similarity score: 0.0952394

Alignment:
 ATTAMAGG
 GKTCCAGG

Original motif Consensus sequence: ATTAMAGG



Reverse complement motif Consensus sequence: CCTYTAAT

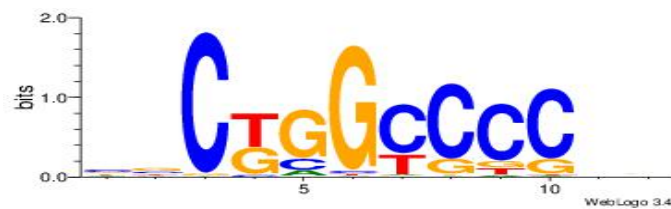


Dataset #: 4
 Motif ID: 102

Motif name: ssCkGGYCCCsg
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 8
 Similarity score: 0.0966701

Alignment:
 VVGGGGCCRBBB
 ---GKTCCAGG-

Original motif Consensus sequence: BBCKGGCCCCV



Reverse complement motif Consensus sequence: VVGGGGCCRBBB



Dataset #: 1
 Motif ID: 15
 Motif name: Motif 15
 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: 0.0972534

Alignment:
CCWGGGCT
CCTGGARC

Original motif Consensus sequence: AGCCCWGG



Reverse complement motif Consensus sequence: CCWGGGCT



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

Original motif Consensus sequence: ATTAMAGG



Reverse complement motif Consensus sequence: CCTYTAAT



Best Matches for Motif ID 20 (Highest to Lowest)

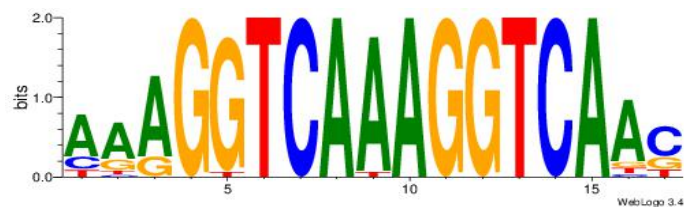
Dataset #:	3
Motif ID:	84
Motif name:	NR1H2RXRA
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	6

Number of overlap: 8
Similarity score: 0.0699525

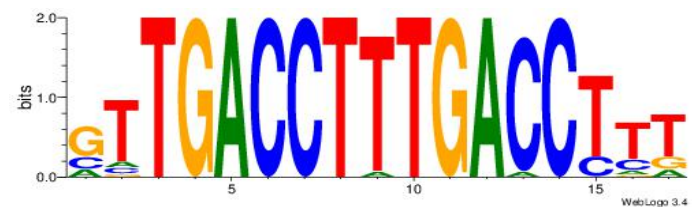
Alignment:

GTTGACCTTTGACCTTT
-----CCTYTAAT-----

Original motif Consensus sequence: AAAGGTCAAAGGTCAAC



Reverse complement motif Consensus sequence:
GTTGACCTTTGACCTTT



Dataset #: 1
Motif ID: 19
Motif name: Motif 19
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 8
Similarity score: 0.0931208

Alignment:

CCTGGARC
CCTYTAAT

Original motif Consensus sequence: CCTGGARC

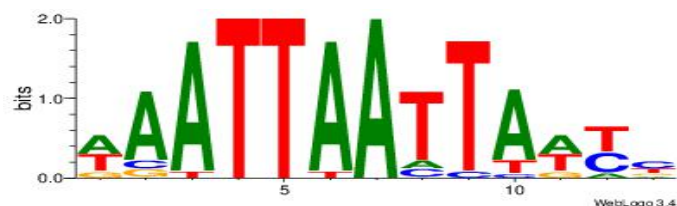
Reverse complement motif Consensus sequence: GKTCCAGG



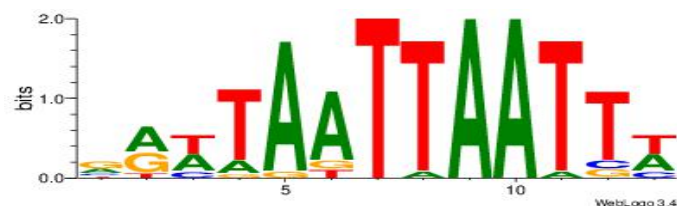
Dataset #: 3
 Motif ID: 66
 Motif name: Lhx3
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 8
 Similarity score: 0.0993275

Alignment:
 BMWTAATTAATTW
 ---CCTYTAAT--

Original motif Consensus sequence: WAATTAATTAWYB



Reverse complement motif Consensus sequence: BMWTAATTAATTW



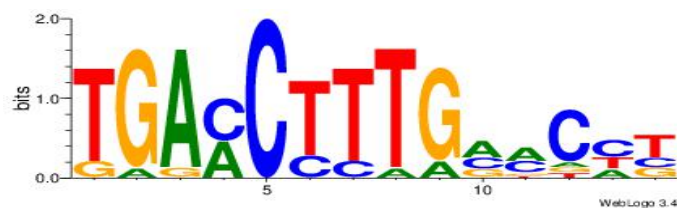
Dataset #: 3
 Motif ID: 83

Motif name:	NR2F1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	4
Number of overlap:	8
Similarity score:	0.100049

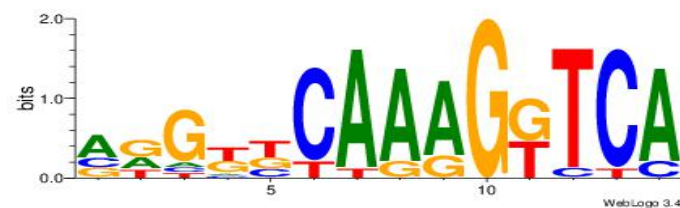
Alignment:

```
TGAMCTTTGMMCYT
---CCTYTAAT---
```

Original motif Consensus sequence: TGAMCTTTGMMCYT



Reverse complement motif Consensus sequence: AKGYCAAAGRTCA



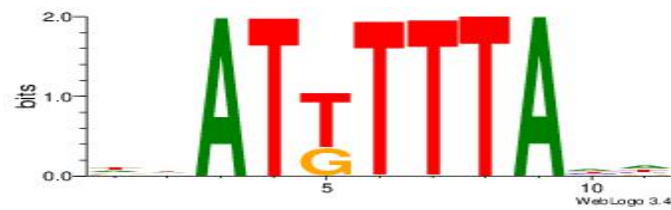
Dataset #:	4
Motif ID:	108
Motif name:	wwATkTTTAww
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	4
Number of overlap:	8
Similarity score:	0.101957

Alignment:

HHTAAARATHD

ATTAMAGG---

Original motif Consensus sequence: DHATKTTTAHH



Reverse complement motif Consensus sequence: HHTAAARATHD



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

Original motif Consensus sequence: AAACAAAC



Reverse complement motif Consensus sequence: GTTTGTTT



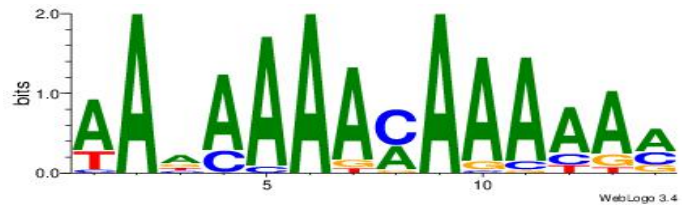
Best Matches for Motif ID 21 (Highest to Lowest)

Dataset #:	2
Motif ID:	60
Motif name:	Motif 60
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	5

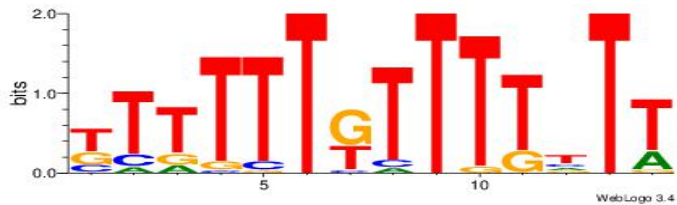
Number of overlap: 8
Similarity score: 0.0392428

Alignment:
AADAAAAMAAAAAM
-----AAACAAAC--

Original motif Consensus sequence: AADAAAAMAAAAAM



Reverse complement motif Consensus sequence: YTTTTTRTTTTDTT

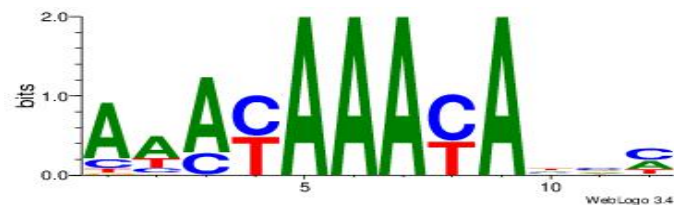
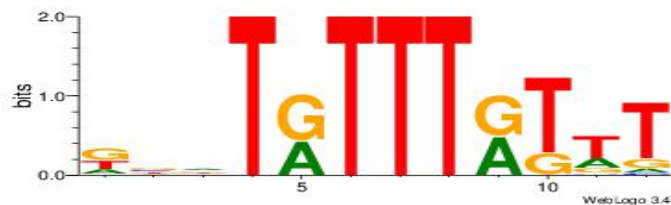


Dataset #: 3
Motif ID: 67
Motif name: FOXI1
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 8
Similarity score: 0.0439051

Alignment:
AAAMAAAMADBY
AAACAAAC----

Original motif Consensus sequence: KBDTRTTTTRTTT

Reverse complement motif Consensus sequence: AAAMAAAMADBY



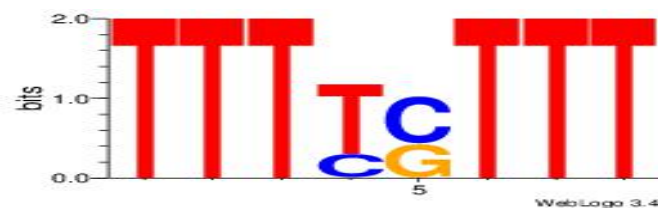
Dataset #: 1
 Motif ID: 5
 Motif name: Motif 5
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 8
 Similarity score: 0.0458289

Alignment:
 AAASAAAA
 AAACAAAC

Original motif Consensus sequence: AAASAAAA



Reverse complement motif Consensus sequence: TTTTSTTT



Dataset #: 3
 Motif ID: 65

Motif name:	Foxd3
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:	0.0463073

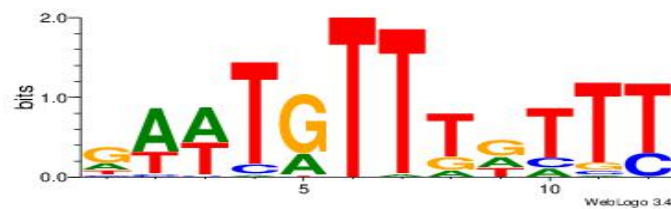
Alignment:

```

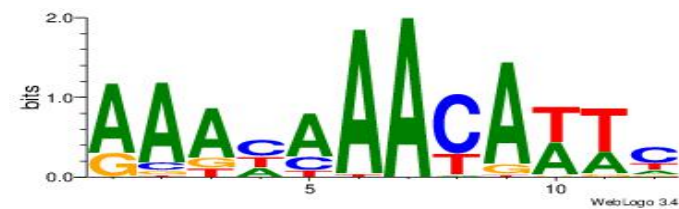
AAAHAAACAWTC
AAACAAAC-----

```

Original motif Consensus sequence: GAWTGTTTDTTT



Reverse complement motif Consensus sequence: AAAHAAACAWTC



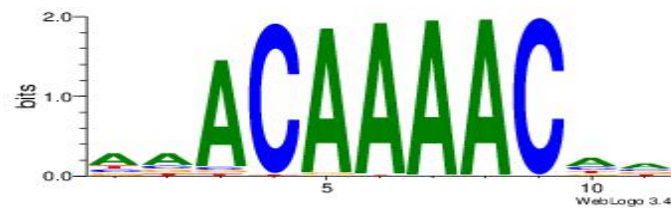
Dataset #:	4
Motif ID:	89
Motif name:	aaACAAAACaa
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	4
Number of overlap:	8
Similarity score:	0.0522284

Alignment:

BHGTTTTGT

---GTTTGT

Original motif Consensus sequence: AAACAAACHV



Reverse complement motif Consensus sequence: BHGTTTTGT



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

Original motif Consensus sequence: GTGGTGGY



Reverse complement motif Consensus sequence: MCCACCAC



Best Matches for Motif ID 22 (Highest to Lowest)

Dataset #:	1
Motif ID:	6
Motif name:	Motif 6
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: 0.0503283

Alignment:
GYGSTGGG
GTGGTGGY

Original motif Consensus sequence: CCCASCMC



Reverse complement motif Consensus sequence: GYGSTGGG

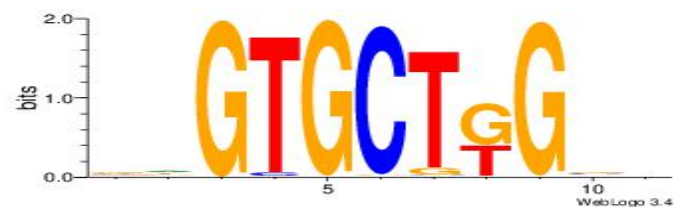


Dataset #: 4
Motif ID: 115
Motif name: ysCmAGCACwy
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 3
Number of overlap: 8
Similarity score: 0.0623778

Alignment:
HVCMAGCACHH
-MCCACCAC--

Original motif Consensus sequence: HVCMAGCACHH

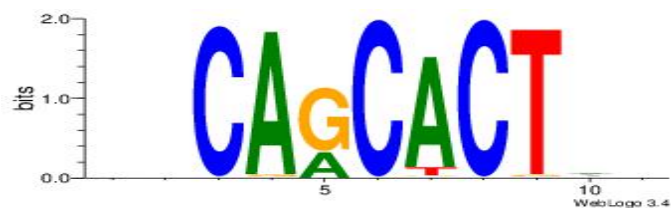
Reverse complement motif Consensus sequence: DHGTGCTRGVH



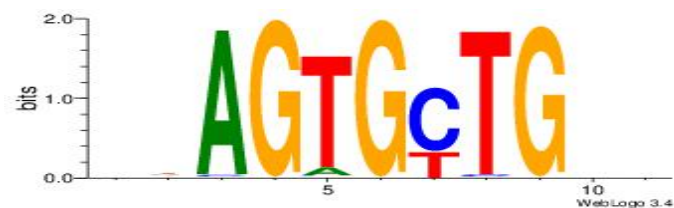
Dataset #: 4
 Motif ID: 93
 Motif name: cmCARCACTwr
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 4
 Number of overlap: 8
 Similarity score: 0.0725856

Alignment:
 BHCAGCACTHV
 MCCACCAC---

Original motif Consensus sequence: BHCAGCACTHV



Reverse complement motif Consensus sequence: VHAGTGCTGHB



Dataset #: 4
 Motif ID: 101

Motif name:	csCACCCCgg
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	8
Similarity score:	0.0756613

Alignment:

HVCACCCBB
MCCACCAC--

Original motif Consensus sequence: HVCACCCBB



Reverse complement motif Consensus sequence: BBGGGGTGVD



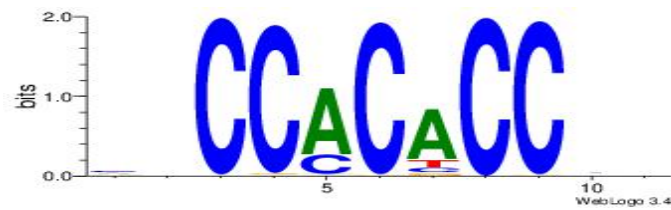
Dataset #:	4
Motif ID:	110
Motif name:	cmCCACACCcm
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	3
Number of overlap:	8
Similarity score:	0.0823897

Alignment:

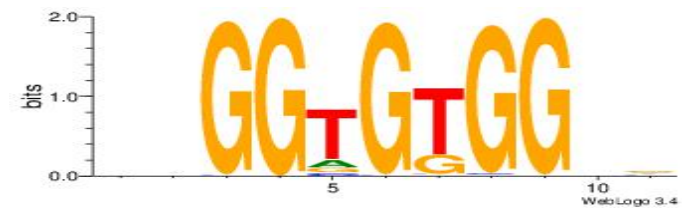
HVCCACACCBV

-MCCACCAC--

Original motif Consensus sequence: HVCCACACCBV



Reverse complement motif Consensus sequence: VBGGTGTGGBD



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

Original motif Consensus sequence: MTSTGTA



Reverse complement motif Consensus sequence: TACASAR



Best Matches for Motif ID 23 (Highest to Lowest)

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

Number of overlap: 7
Similarity score: 0.0172404

Alignment:
TSTSTGTG
MTSTGTA-

Original motif Consensus sequence: CACASASA



Reverse complement motif Consensus sequence: TSTSTGTG



Dataset #: 4
Motif ID: 90
Motif name: ymTACATAw
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2
Number of overlap: 7
Similarity score: 0.0191193

Alignment:
HHTACATABD
--TACASAR-

Original motif Consensus sequence: HHTACATABD

Reverse complement motif Consensus sequence: DBTATGTAHH



Dataset #: 1
 Motif ID: 12
 Motif name: Motif 12
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 7
 Similarity score: 0.03188

Alignment:
 GCACACAY
 TACASAR-

Original motif Consensus sequence: GCACACAY



Reverse complement motif Consensus sequence: MTGTGTGC



Dataset #: 4
 Motif ID: 114

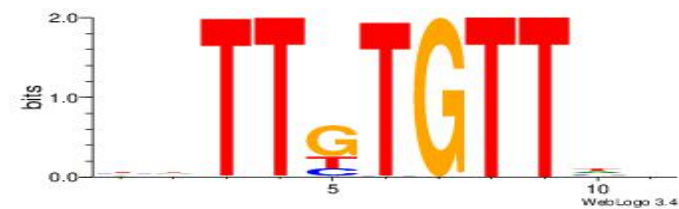
Motif name: awAACAcAAwa
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 7
 Similarity score: 0.0346685

Alignment:
 DDAACACAADV
 --TACASAR--

Original motif Consensus sequence: DDAACACAADV



Reverse complement motif Consensus sequence: BDTTGTGTTDD



Dataset #: 3
 Motif ID: 75
 Motif name: FOXF2
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 7
 Similarity score: 0.0372723

Alignment:

BHADSGTAAACAAD

-----TACASAR-

Original motif Consensus sequence: BHADSGTAAACAAD



Reverse complement motif Consensus sequence: DTTGTTTACSBTB



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

Original motif Consensus sequence: CACGB



Reverse complement motif Consensus sequence: BCGTG



Best Matches for Motif ID 24 (Highest to Lowest)

Dataset #:	2
Motif ID:	56
Motif name:	Motif 56
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	2

Number of overlap: 5
Similarity score: 0

Alignment:

TCCGTG
-BCGTG

Original motif Consensus sequence: CACGGA



Reverse complement motif Consensus sequence: TCCGTG



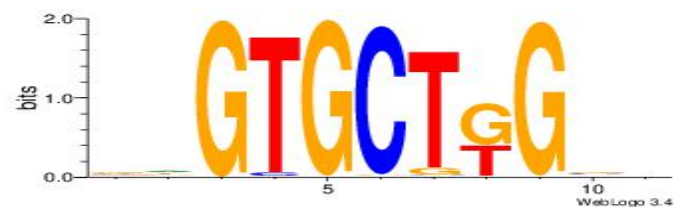
Dataset #: 4
Motif ID: 115
Motif name: ysCmAGCACwy
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 5
Similarity score: 0.0186397

Alignment:

DHGTGCTRGVH
BCGTG-----

Original motif Consensus sequence: HVCMAGCACHH

Reverse complement motif Consensus sequence: DHGTGCTRGVH



Dataset #: 4
 Motif ID: 107
 Motif name: crCGyGCRcg
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 5
 Similarity score: 0.019278

Alignment:

CGCGTGCACG

-BCGTG----

Original motif Consensus sequence: CGCGTGCACG



Reverse complement motif Consensus sequence: CGTGCACGCG



Dataset #: 1
 Motif ID: 12

Motif name:	Motif 12
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	4
Number of overlap:	5
Similarity score:	0.0246242

Alignment:
GCACACAY
---CACGB

Original motif Consensus sequence: GCACACAY



Reverse complement motif Consensus sequence: MTGTGTGC



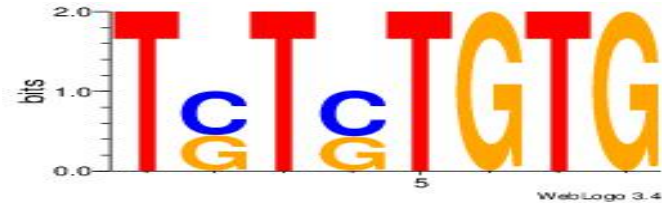
Dataset #:	1
Motif ID:	7
Motif name:	Motif 7
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	5
Similarity score:	0.0336642

Alignment:
CACASASA
CACGB---

Original motif Consensus sequence: CACASASA



Reverse complement motif Consensus sequence: TSTSTGTG



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

Original motif Consensus sequence: TTTAWW



Reverse complement motif Consensus sequence: WWTAAA



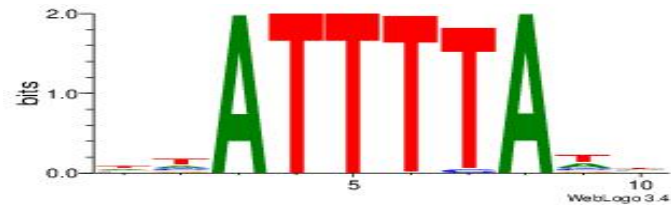
Best Matches for Motif ID 25 (Highest to Lowest)

Dataset #:	4
Motif ID:	91
Motif name:	wtATTTTAww
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1

Number of overlap: 6
Similarity score: 0.0116421

Alignment:
HWTAAAATHD
WWTAAA-----

Original motif Consensus sequence: DHATTTTAWH



Reverse complement motif Consensus sequence: HWTAAAATHD

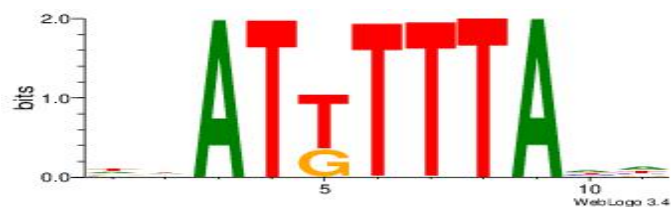


Dataset #: 4
Motif ID: 108
Motif name: wwATkTTTAww
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 6
Similarity score: 0.0118254

Alignment:
DHATKTTTAHH
-----TTTAWW

Original motif Consensus sequence: DHATKTTTAHH

Reverse complement motif Consensus sequence: HHTAAARATHD



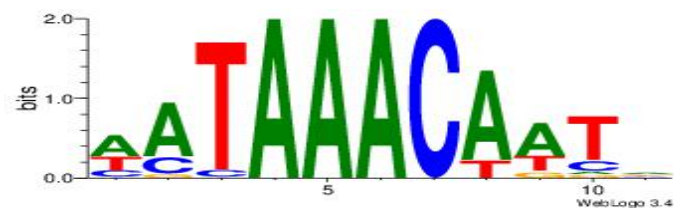
Dataset #: 3
 Motif ID: 70
 Motif name: Foxq1
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 6
 Similarity score: 0.0158082

Alignment:
 HATTGTTTATW
 -----TTTAWW

Original motif Consensus sequence: HATTGTTTATW



Reverse complement motif Consensus sequence: WATAACAATH



Dataset #: 1
 Motif ID: 3

Motif name:	Motif 3
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	6
Similarity score:	0.0300892

Alignment:
 AWATAMA
 WWTAAA-

Original motif Consensus sequence: AWATAMA



Reverse complement motif Consensus sequence: TYTATWT



Dataset #:	2
Motif ID:	55
Motif name:	Motif 55
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2
Number of overlap:	6
Similarity score:	0.0307675

Alignment:

TTTAAAA

TTTAWW-

Original motif Consensus sequence: TTTAAAA



Reverse complement motif Consensus sequence: TTTTAAA

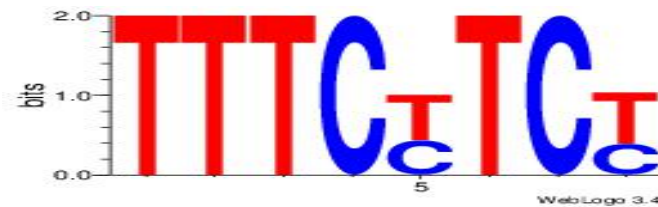


Dataset #: 1 Motif ID: 26 Motif name: Motif 26

Original motif Consensus sequence: RGARGAAA



Reverse complement motif Consensus sequence: TTTCKTCK



Best Matches for Motif ID 26 (Highest to Lowest)

Dataset #:	3
Motif ID:	71
Motif name:	Evi1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	4

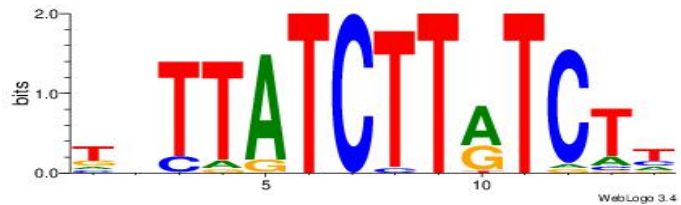
Number of overlap: 8
Similarity score: 0.0776207

Alignment:
TBTTATCTTMTCTT
---TTTCKTCK---

Original motif Consensus sequence: AAGAYAAGATAABA



Reverse complement motif Consensus sequence: TBTTATCTTMTCTT

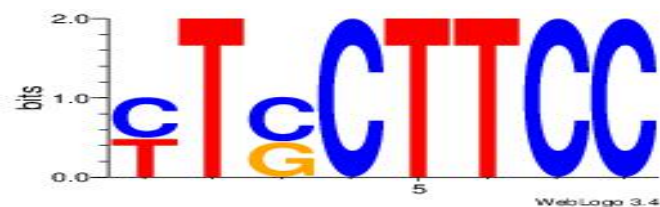


Dataset #: 1
Motif ID: 13
Motif name: Motif 13
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 8
Similarity score: 0.0795772

Alignment:
GGAAGSAR
RGARGAAA

Original motif Consensus sequence: GGAAGSAR

Reverse complement motif Consensus sequence: MTSCTTCC



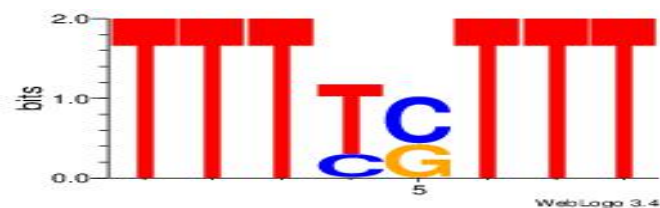
Dataset #: 1
 Motif ID: 5
 Motif name: Motif 5
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 8
 Similarity score: 0.0833075

Alignment:
 AAASAAAA
 RGARGAAA

Original motif Consensus sequence: AAASAAAA



Reverse complement motif Consensus sequence: TTTTSTTT



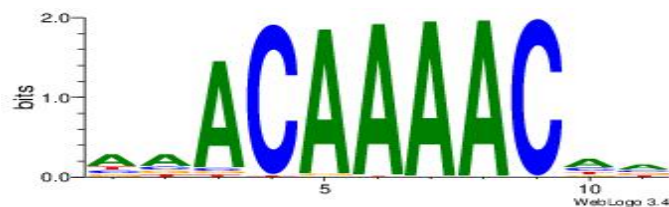
Dataset #: 4
 Motif ID: 89

Motif name:	aaACAAAACaa
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	4
Number of overlap:	8
Similarity score:	0.087026

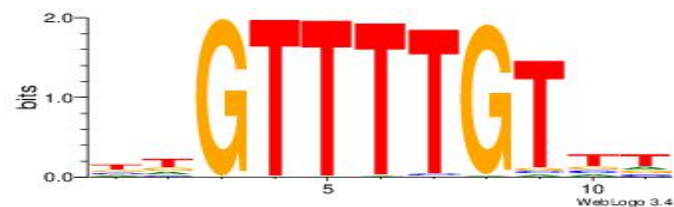
Alignment:

```
BHGTTTTGTTT
---TTTCKTCK
```

Original motif Consensus sequence: AAACAAAACHV



Reverse complement motif Consensus sequence: BHGTTTTGTTT



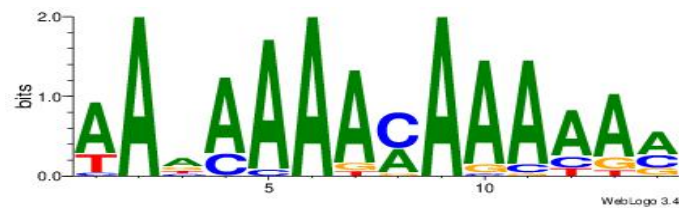
Dataset #:	2
Motif ID:	60
Motif name:	Motif 60
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	4
Number of overlap:	8
Similarity score:	0.0876612

Alignment:

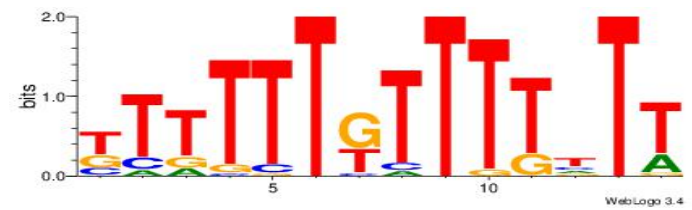
YTTTTTRTTTTDTT

---TTTCKTCK---

Original motif Consensus sequence: AADAAAAMAAAAAM



Reverse complement motif Consensus sequence: YTTTTTRTTTTDTT



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

Original motif Consensus sequence: CTGCCTKY



Reverse complement motif Consensus sequence: KRAGGCAG



Best Matches for Motif ID 27 (Highest to Lowest)

Dataset #:	1
Motif ID:	39
Motif name:	Motif 39
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: 0.0247901

Alignment:
CTGYCTGT
CTGCCTKY

Original motif Consensus sequence: ACAGMCAG



Reverse complement motif Consensus sequence: CTGYCTGT

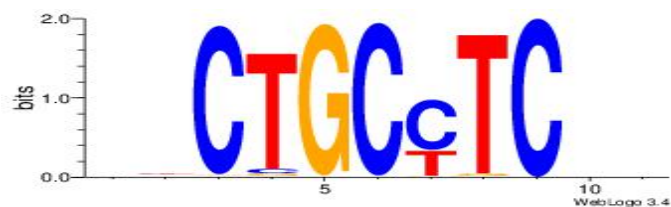


Dataset #: 4
Motif ID: 116
Motif name: dyCTGCyTCyc
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 3
Number of overlap: 8
Similarity score: 0.0249073

Alignment:
BHGAKGCAGHH
-KRAGGCAG--

Original motif Consensus sequence: DHCTGCTCHB

Reverse complement motif Consensus sequence: BHGAKGCAGHH



Dataset #: 1
 Motif ID: 8
 Motif name: Motif 8
 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: 0.0407877

Alignment:
 CTGGCYTY
 CTGCCTKY

Original motif Consensus sequence: CTGGCYTY



Reverse complement motif Consensus sequence: KAKGCCAG



Dataset #: 4
 Motif ID: 126

Motif name:	yvTGCAGsCAcg
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	2
Number of overlap:	8
Similarity score:	0.0601303

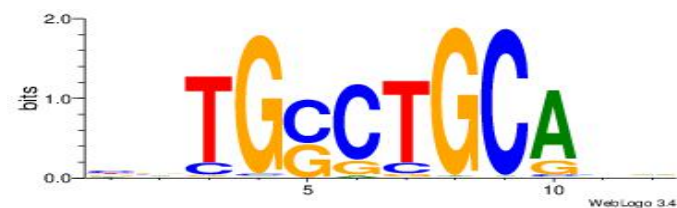
Alignment:

VBTGsCTGCAVB
 -CTGCCTKY---

Original motif Consensus sequence: BVTGCAGSCABV



Reverse complement motif Consensus sequence: VBTGSCTGCAVB



Dataset #:	1
Motif ID:	11
Motif name:	Motif 11
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	8
Similarity score:	0.0611983

Alignment:
GAACDCAG
KRAGGCAG

Original motif Consensus sequence: CTGDGTTTC



Reverse complement motif Consensus sequence: GAACDCAG



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

Original motif Consensus sequence: AVAGAAA



Reverse complement motif Consensus sequence: TTTCTVT



Best Matches for Motif ID 28 (Highest to Lowest)

Dataset #:	1
Motif ID:	5
Motif name:	Motif 5
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2

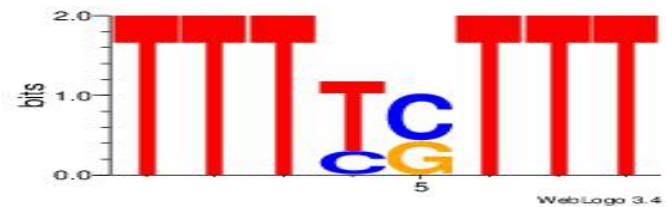
Number of overlap: 7
Similarity score: 0.034392

Alignment:
AAASAAAA
AVAGAAA-

Original motif Consensus sequence: AAASAAAA



Reverse complement motif Consensus sequence: TTTTSTTT



Dataset #: 1
Motif ID: 49
Motif name: Motif 49
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 7
Similarity score: 0.0458576

Alignment:
AGATAAAR
AVAGAAA-

Original motif Consensus sequence: AGATAAAR

Reverse complement motif Consensus sequence: KTTTATCT



Dataset #: 1
 Motif ID: 21
 Motif name: Motif 21
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 7
 Similarity score: 0.0461542

Alignment:
 AAACAAAC
 AVAGAAA-

Original motif Consensus sequence: AAACAAAC



Reverse complement motif Consensus sequence: GTTTGTTT



Dataset #: 1
 Motif ID: 18

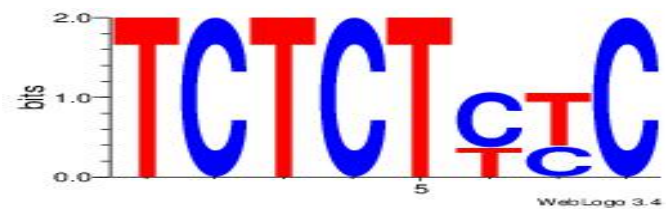
Motif name:	Motif 18
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	2
Number of overlap:	7
Similarity score:	0.047492

Alignment:
TCTCTMKC
TTTCTVT-

Original motif Consensus sequence: GRRAGAGA



Reverse complement motif Consensus sequence: TCTCTMKC



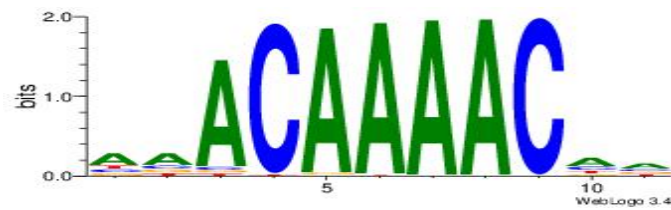
Dataset #:	4
Motif ID:	89
Motif name:	aaACAAAACaa
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	5
Number of overlap:	7
Similarity score:	0.055017

Alignment:

AAACAAAACHV

AVAGAAA-----

Original motif Consensus sequence: AAACAAAACHV



Reverse complement motif Consensus sequence: BHGTTTTGTTT



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

Original motif Consensus sequence: CCMGCCCC



Reverse complement motif Consensus sequence: GGGCYGG



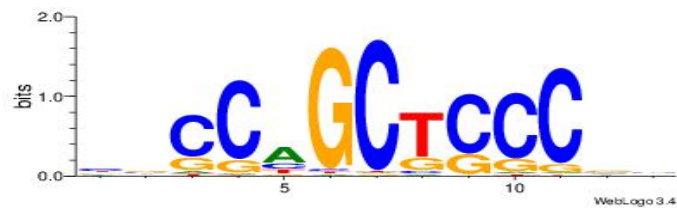
Best Matches for Motif ID 29 (Highest to Lowest)

Dataset #:	4
Motif ID:	103
Motif name:	csCCaGCTCCCgs
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	4

Number of overlap: 8
Similarity score: 0.0420068

Alignment:
BVGGGAGCTGGBB
---GGGGCYGG--

Original motif Consensus sequence: BBCCAGCTCCCVB



Reverse complement motif Consensus sequence: BVGGGAGCTGGBB

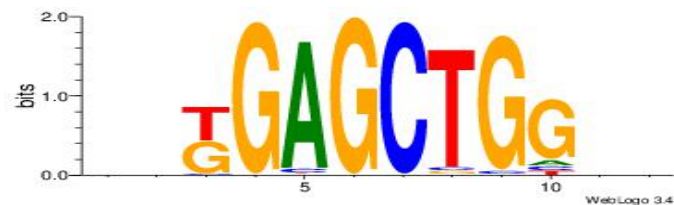
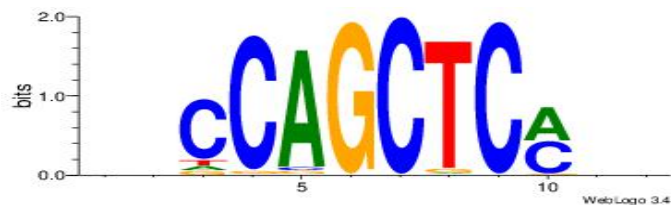


Dataset #: 4
Motif ID: 119
Motif name: cbCCAGCTCmyk
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 3
Number of overlap: 8
Similarity score: 0.0430311

Alignment:
BBCCAGCTCMBD
--CCMGCCCC--

Original motif Consensus sequence: BBCCAGCTCMBD

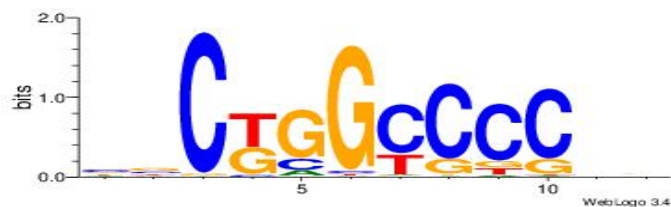
Reverse complement motif Consensus sequence: HBYGAGCTGGBB



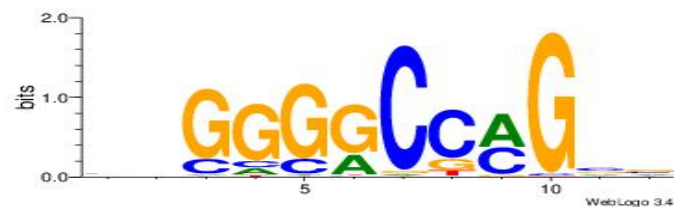
Dataset #: 4
 Motif ID: 102
 Motif name: ssCkGGYCCCsg
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 8
 Similarity score: 0.0462922

Alignment:
 VVGGGGCCRBBB
 --GGGGCYGG--

Original motif Consensus sequence: BBCKGGCCCCVV



Reverse complement motif Consensus sequence: VVGGGGCCRBBB



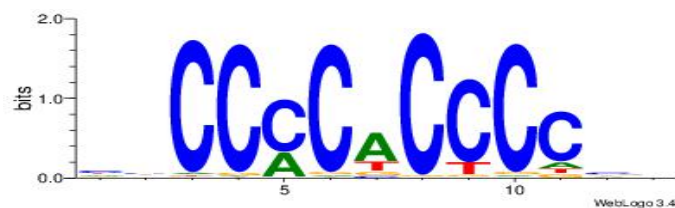
Dataset #: 4
 Motif ID: 111

Motif name: ccCCmCaCCCCcc
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 8
 Similarity score: 0.051245

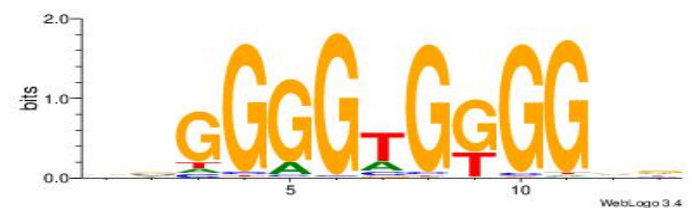
Alignment:

HBCCCCACCCCBH
 ---CCMGCCCC--

Original motif Consensus sequence: HBCCCCACCCCBH



Reverse complement motif Consensus sequence: DBGGGGTGGGGB



Dataset #: 4
 Motif ID: 115
 Motif name: ysCmAGCACwy
 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: 0.0556862

Alignment:

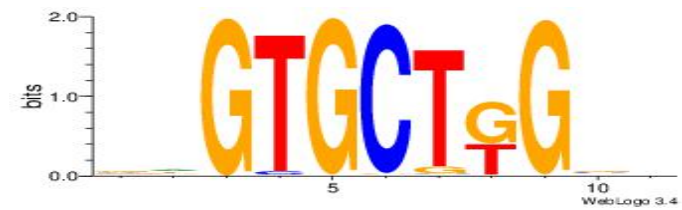
HVCMAGCACHH

--CCMGCCCC--

Original motif Consensus sequence: HVCMAGCACHH



Reverse complement motif Consensus sequence: DHGTGCTRGVH

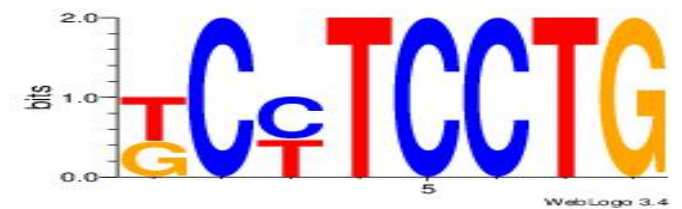


Dataset #: 1 Motif ID: 30 Motif name: Motif 30

Original motif Consensus sequence: CAGGARGM



Reverse complement motif Consensus sequence: YCMTCTTG



Best Matches for Motif ID 30 (Highest to Lowest)

Dataset #:	1
Motif ID:	47
Motif name:	Motif 47
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1

Number of overlap: 8
Similarity score: 0.0890875

Alignment:
KGCTGCTG
YCMTCCTG

Original motif Consensus sequence: KGCTGCTG



Reverse complement motif Consensus sequence: CAGCAGCR



Dataset #: 1
Motif ID: 4
Motif name: Motif 4
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: 0.0957719

Alignment:
GAGRMAGR
CAGGARGM

Original motif Consensus sequence: GAGRMAGR

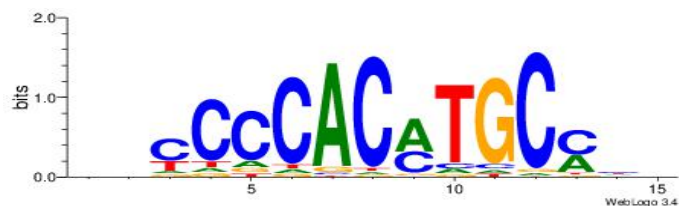
Reverse complement motif Consensus sequence: KCTRMCTC



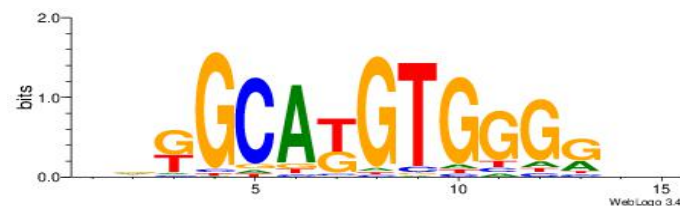
Dataset #: 4
 Motif ID: 98
 Motif name: myyCCCACmTGCmyr
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 8
 Similarity score: 0.0969866

Alignment:
 HBCCCCACMTGCMHV
 ---YCMTCCTG----

Original motif Consensus sequence: HBCCCCACMTGCMHV



Reverse complement motif Consensus sequence: VDRGCAYGTGGGGVD



Dataset #: 4

Motif ID: 127
 Motif name: rryCAGGGAyw
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 8
 Similarity score: 0.0975352

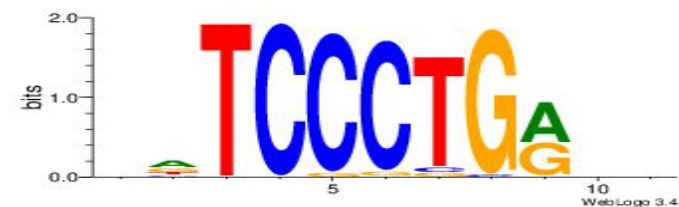
Alignment:

DDYCAGGGAHD
 ---CAGGARGM

Original motif Consensus sequence: DDYCAGGGAHD



Reverse complement motif Consensus sequence: DHTCCCTGMDD



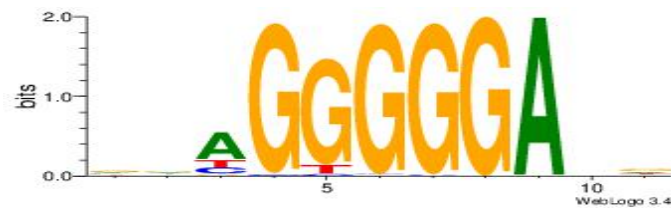
Dataset #: 4
 Motif ID: 99
 Motif name: graGGGGGArr
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 8
 Similarity score: 0.0989909

Alignment:

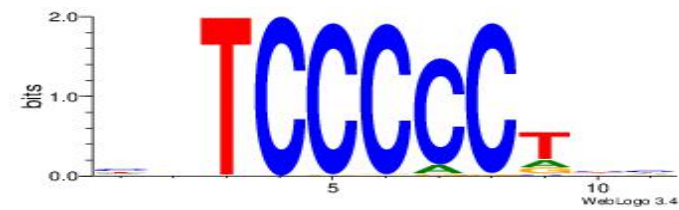
DVAGGGGGADD

-CAGGARGM--

Original motif Consensus sequence: DVAGGGGGADD



Reverse complement motif Consensus sequence: HDTCCCCCTVH



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

Original motif Consensus sequence: CTGWSCTC



Reverse complement motif Consensus sequence: GAGSWCAG



Best Matches for Motif ID 31 (Highest to Lowest)

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

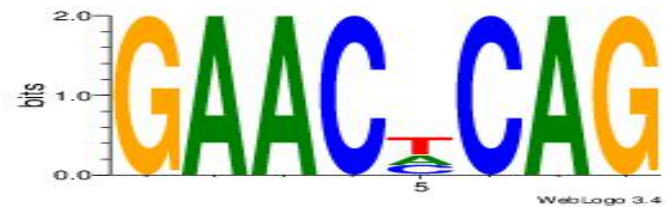
Number of overlap: 8
Similarity score: 0.023129

Alignment:
GAACDCAG
GAGSWCAG

Original motif Consensus sequence: CTGDGTTTC



Reverse complement motif Consensus sequence: GAACDCAG



Dataset #: 1
Motif ID: 8
Motif name: Motif 8
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 8
Similarity score: 0.0418605

Alignment:
KAKGCCAG
GAGSWCAG

Original motif Consensus sequence: CTGGCYTY

Reverse complement motif Consensus sequence: KAKGCCAG



Dataset #: 4
 Motif ID: 92
 Motif name: cgAKGyCAcg
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 8
 Similarity score: 0.0464751

Alignment:
 CGAGGYCACV
 -GAGSWCAG-

Original motif Consensus sequence: CGAGGYCACV



Reverse complement motif Consensus sequence: VGTGMCCTCG



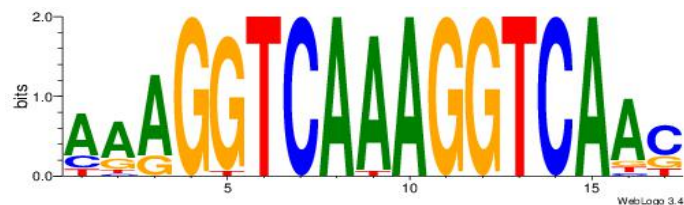
Dataset #: 3
 Motif ID: 84

Motif name:	NR1H2RXRA
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2
Number of overlap:	8
Similarity score:	0.0568298

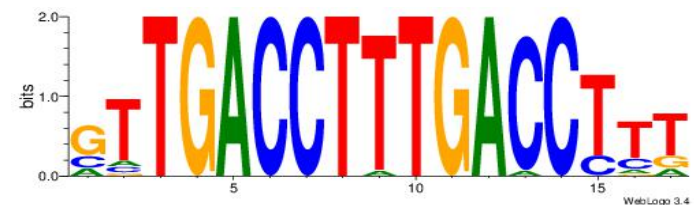
Alignment:

```
AAAGGTCAAAGGTCAAC
-----GAGSWCAG-
```

Original motif Consensus sequence: AAAGGTCAAAGGTCAAC



Reverse complement motif Consensus sequence: GTTGACCTTTGACCTT



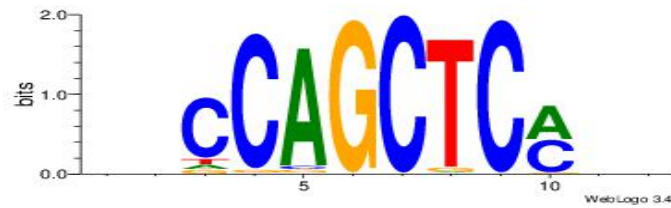
Dataset #:	4
Motif ID:	119
Motif name:	cbCCAGCTCmyk
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	2
Number of overlap:	8
Similarity score:	0.0705619

Alignment:

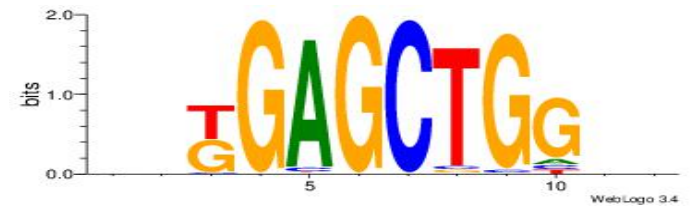
HBYGAGCTGGBB

-CTGWSCTC---

Original motif Consensus sequence: BBCCAGCTCMBD



Reverse complement motif Consensus sequence: HBYGAGCTGGBB



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

Original motif Consensus sequence: AVATGGC



Reverse complement motif Consensus sequence: GCCATVT



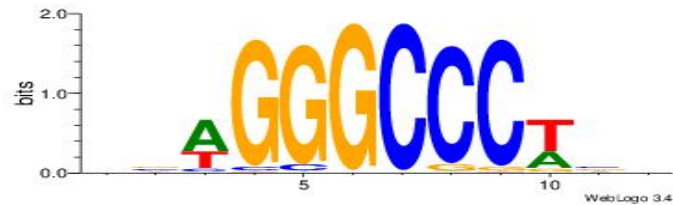
Best Matches for Motif ID 32 (Highest to Lowest)

Dataset #:	4
Motif ID:	124
Motif name:	cswGGGCCcswg
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	6

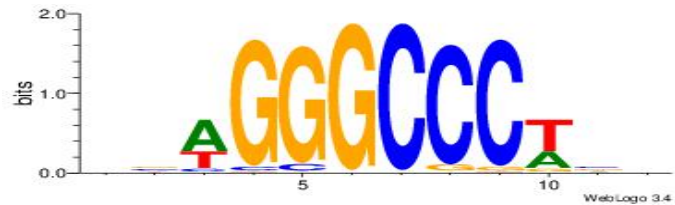
Number of overlap: 7
Similarity score: 0.0595251

Alignment:
VVGWGGCCWBB
AVATGGC-----

Original motif Consensus sequence: VVGWGGCCWBB



Reverse complement motif Consensus sequence: BBWGGCCWVV

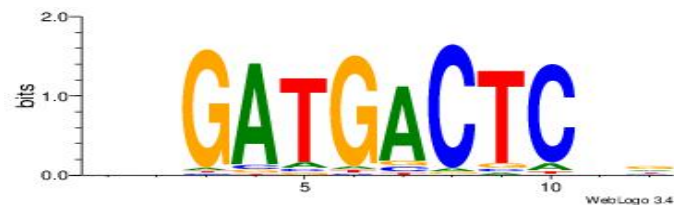
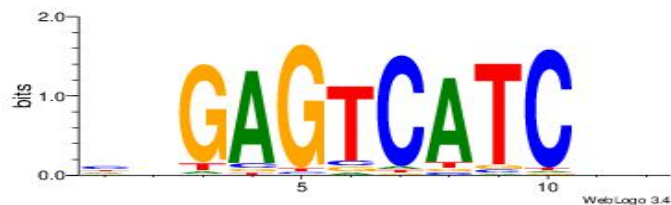


Dataset #: 4
Motif ID: 121
Motif name: ctGAGTCATCkb
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2
Number of overlap: 7
Similarity score: 0.0676952

Alignment:
HDGAGTCATCDB
----GCCATVT-

Original motif Consensus sequence: HDGAGTCATCDB

Reverse complement motif Consensus sequence: BHGATGACTCDD

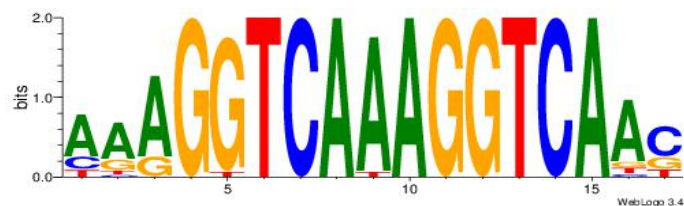


Dataset #: 3
 Motif ID: 84
 Motif name: NR1H2RXRA
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 8
 Number of overlap: 7
 Similarity score: 0.0701366

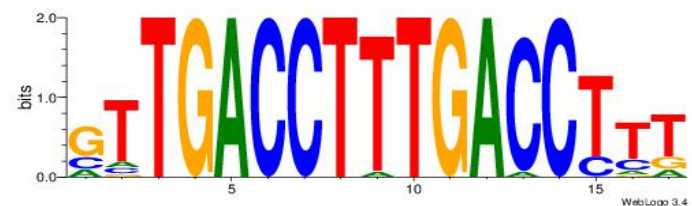
Alignment:

AAAGGTCAAAGGTCAAC
 -----AVATGGC----

Original motif Consensus sequence: AAAGGTCAAAGGTCAAC



Reverse complement motif Consensus sequence: GTTGACCTTTGACCTTT



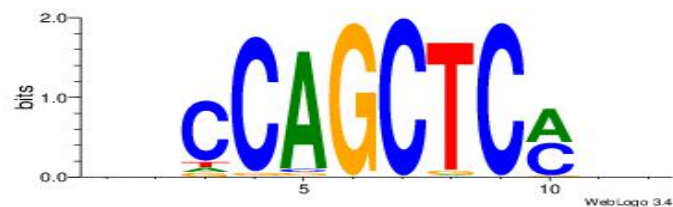
Dataset #: 4

Motif ID: 119
 Motif name: cbCCAGCTCmyk
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 5
 Number of overlap: 7
 Similarity score: 0.0704204

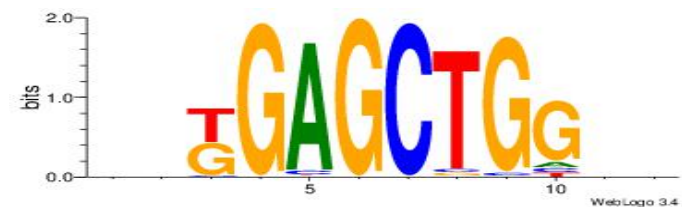
Alignment:

BBCCAGCTCMBD
 -GCCATVT-----

Original motif Consensus sequence: BBCCAGCTCMBD



Reverse complement motif Consensus sequence: HBYGAGCTGGBB



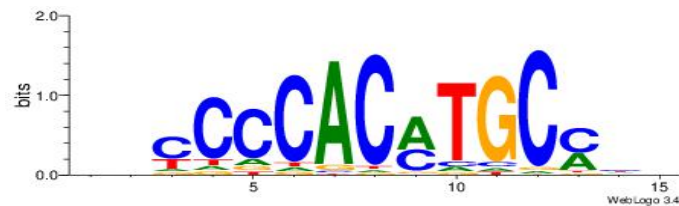
Dataset #: 4
 Motif ID: 98
 Motif name: myyCCCACmTGCmyr
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 7
 Similarity score: 0.0736077

Alignment:

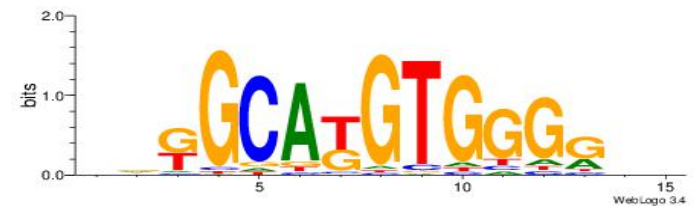
HBCCCCACMTGCMHV

-----AVATGGC--

Original motif Consensus sequence: HBCCCCACMTGCMHV



Reverse complement motif Consensus sequence: VDRGCAYGTGGGGVD



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

Original motif Consensus sequence: CMTTTCC



Reverse complement motif Consensus sequence: GGAAARG



Best Matches for Motif ID 33 (Highest to Lowest)

Dataset #:	1
Motif ID:	46
Motif name:	Motif 46
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward

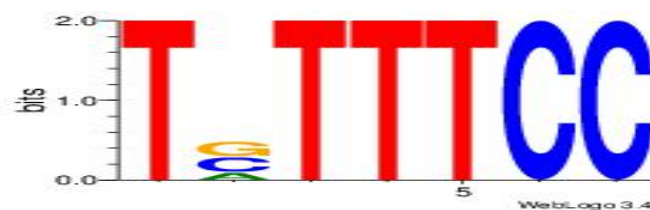
Position number: 1
Number of overlap: 7
Similarity score: 0.0542683

Alignment:
TSTTTCC
CMTTTCC

Original motif Consensus sequence: GGAAASA



Reverse complement motif Consensus sequence: TSTTTCC



Dataset #: 1
Motif ID: 44
Motif name: Motif 44
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 7
Similarity score: 0.0667064

Alignment:
CATTTCT
CMTTTCC

Original motif Consensus sequence: AGAAATG

Reverse complement motif Consensus sequence: CATTTCT

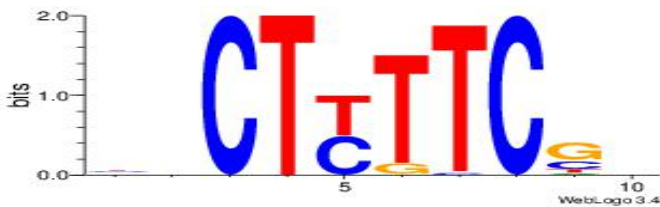


Dataset #: 4
 Motif ID: 88
 Motif name: ygCTyTTCsg
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 7
 Similarity score: 0.0693505

Alignment:

BCGAAMAGHH
 -GGAAARG--

Original motif Consensus sequence: HDCTYTTTCGB



Reverse complement motif Consensus sequence: BCGAAMAGHH

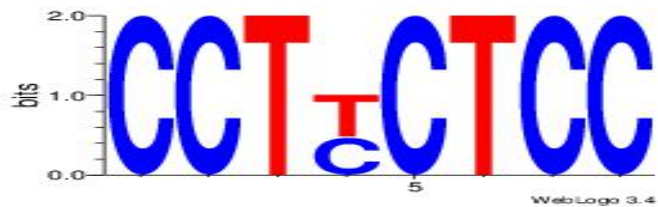


Dataset #: 1

Motif ID: 38
 Motif name: Motif 38
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 7
 Similarity score: 0.0734352

Alignment:
 GGAGMAGG
 GGAAARG-

Original motif Consensus sequence: CCTYCTCC



Reverse complement motif Consensus sequence: GGAGMAGG



Dataset #: 1
 Motif ID: 13
 Motif name: Motif 13
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 7
 Similarity score: 0.0861393

Alignment:
GGAAGSAR
-GGAAARG

Original motif Consensus sequence: GGAAGSAR



Reverse complement motif Consensus sequence: MTSCTTCC



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

Original motif Consensus sequence: ATATTTA



Reverse complement motif Consensus sequence: TAAATAT



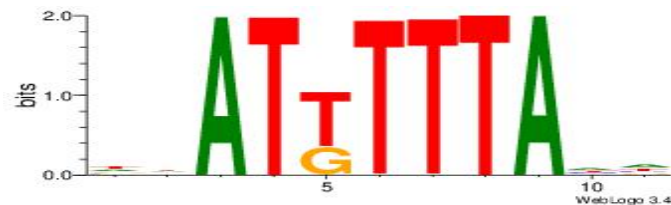
Best Matches for Motif ID 34 (Highest to Lowest)

Dataset #:	4
Motif ID:	108
Motif name:	wwATkTTTAww
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	3

Number of overlap: 7
 Similarity score: 0.0294375

Alignment:
 DHATKTTTAHH
 --ATATTTA--

Original motif Consensus sequence: DHATKTTTAHH



Reverse complement motif Consensus sequence: HHTAAARATHD

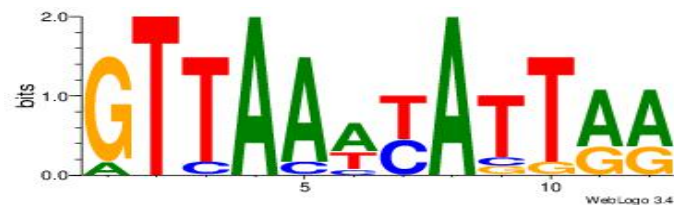
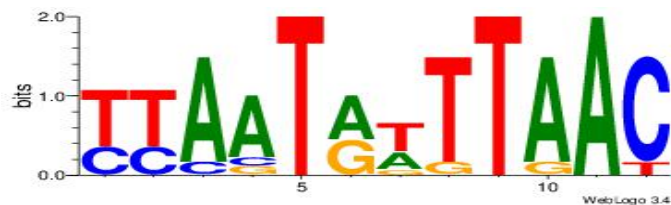


Dataset #: 3
 Motif ID: 82
 Motif name: HNF1B
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3
 Number of overlap: 7
 Similarity score: 0.033217

Alignment:
 GTTAAWKATTAA
 --TAAATAT---

Original motif Consensus sequence: TTAATRWTTAAC

Reverse complement motif Consensus sequence: GTTAAWKATTAA



Dataset #: 4
 Motif ID: 90
 Motif name: ymTACATAw
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 7
 Similarity score: 0.0399459

Alignment:

DBTATGTAHH

-ATATTTA--

Original motif Consensus sequence: HHTACATABD



Reverse complement motif Consensus sequence: DBTATGTAHH



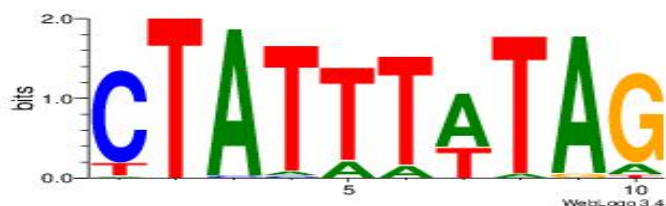
Dataset #: 3
 Motif ID: 61

Motif name: MEF2A
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 7
 Similarity score: 0.0440271

Alignment:

CTAWAAATAG
 ---TAAATAT

Original motif Consensus sequence: CTATTTWTAG



Reverse complement motif Consensus sequence: CTAWAAATAG



Dataset #: 3
 Motif ID: 69
 Motif name: NKX3-1
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 7
 Similarity score: 0.0453202

Alignment:

ATACTTA

ATATTTA

Original motif Consensus sequence: ATACTTA



Reverse complement motif Consensus sequence: TAAGTAT



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

Original motif Consensus sequence: KGCTGG



Reverse complement motif Consensus sequence: SCCAGCR



Best Matches for Motif ID 35 (Highest to Lowest)

Dataset #:	4
Motif ID:	115
Motif name:	ysCmAGCACwy
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	4

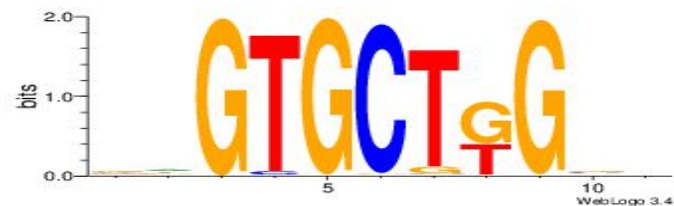
Number of overlap: 7
Similarity score: 0.0239923

Alignment:
DHGTGCTRGVH
---KGCTGGS-

Original motif Consensus sequence: HVCMAGCACHH



Reverse complement motif Consensus sequence: DHGTGCTRGVH



Dataset #: 1
Motif ID: 6
Motif name: Motif 6
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 2
Number of overlap: 7
Similarity score: 0.0288353

Alignment:
CCCASCMC
-SCCAGCR

Original motif Consensus sequence: CCCASCMC

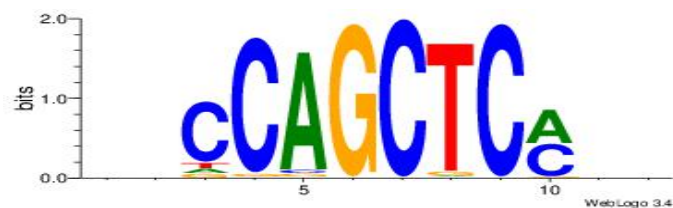
Reverse complement motif Consensus sequence: GYGSTGGG



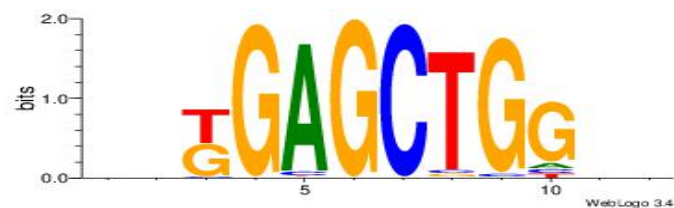
Dataset #: 4
 Motif ID: 119
 Motif name: cbCCAGCTCmyk
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 7
 Similarity score: 0.0386119

Alignment:
 HBYGAGCTGGBB
 ----KGCTGGS-

Original motif Consensus sequence: BBCCAGCTCMBD



Reverse complement motif Consensus sequence: HBYGAGCTGGBB

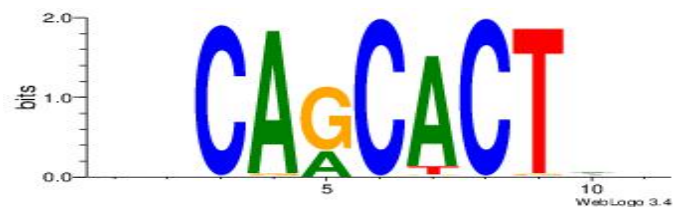


Dataset #: 4
 Motif ID: 93

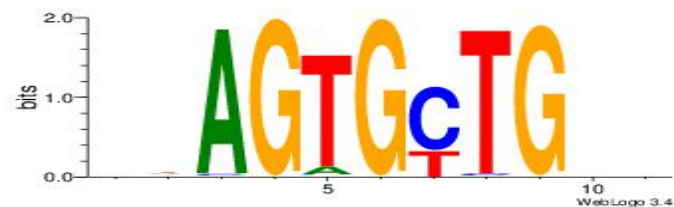
Motif name:	cmCARCACTwr
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	5
Number of overlap:	7
Similarity score:	0.0467269

Alignment:
BHCAGCACTHV
SCCAGCR----

Original motif Consensus sequence: BHCAGCACTHV



Reverse complement motif Consensus sequence: VHAGTGCTGHB



Dataset #:	1
Motif ID:	22
Motif name:	Motif 22
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	7
Similarity score:	0.04839

Alignment:
GTGGTGGY
-KGCTGGS

Original motif Consensus sequence: GTGGTGGY



Reverse complement motif Consensus sequence: MCCACCAC



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

Original motif Consensus sequence: CATGGTGG



Reverse complement motif Consensus sequence: CCACCATG



Best Matches for Motif ID 36 (Highest to Lowest)

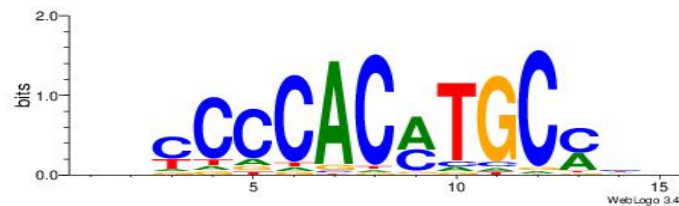
Dataset #:	4
Motif ID:	98
Motif name:	myyCCCACmTGCmyr
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	4

Number of overlap: 8
Similarity score: 0.0987507

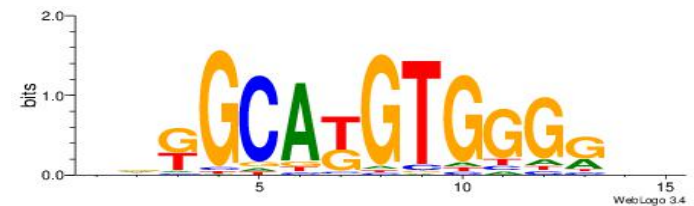
Alignment:

VDRGCAYGTGGGGVD
----CATGGTGG---

Original motif Consensus sequence: HBCCCCACMTGCMHV



Reverse complement motif Consensus sequence:
VDRGCAYGTGGGGVD



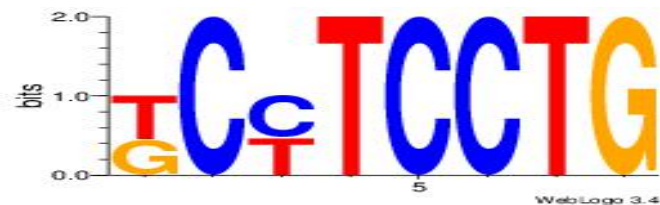
Dataset #: 1
Motif ID: 30
Motif name: Motif 30
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 8
Similarity score: 0.100683

Alignment:

YCMTCCCTG
CCACCATG

Original motif Consensus sequence: CAGGARGM

Reverse complement motif Consensus sequence: YCMTCCCTG



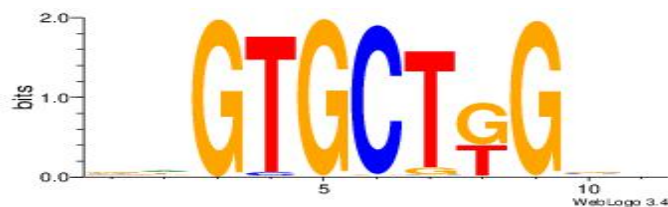
Dataset #: 4
 Motif ID: 115
 Motif name: ysCmAGCACwy
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 8
 Similarity score: 0.106759

Alignment:
 DHGTGCTRGVH
 -CATGGTGG--

Original motif Consensus sequence: HVCMAGCACHH



Reverse complement motif Consensus sequence: DHGTGCTRGVH

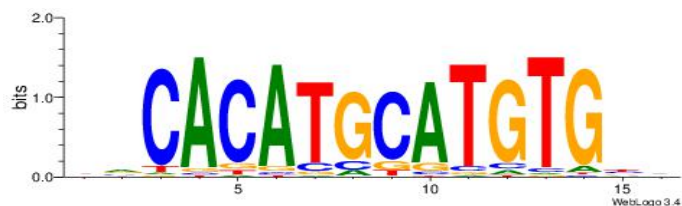


Dataset #: 4
 Motif ID: 118

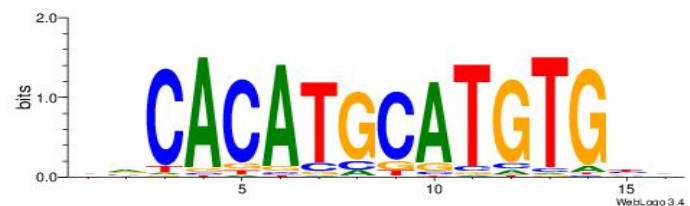
Motif name: yrCACATGCATGTGyr
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 5
 Number of overlap: 8
 Similarity score: 0.106836

Alignment:
 DVCACATGCATGTGBH
 ----CATGGTGG----

Original motif Consensus sequence: HVCACATGCATGTGBD



Reverse complement motif Consensus sequence: DVCACATGCATGTGBH



Dataset #: 4
 Motif ID: 101
 Motif name: csCACCCCgg
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 8
 Similarity score: 0.10804

Alignment:

BBGGGGTGVD

-CATGGTGG-

Original motif Consensus sequence: HVCACCCCB



Reverse complement motif Consensus sequence: BBGGGGTGVD



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

Original motif Consensus sequence: GYATGTGY



Reverse complement motif Consensus sequence: KCACATKC



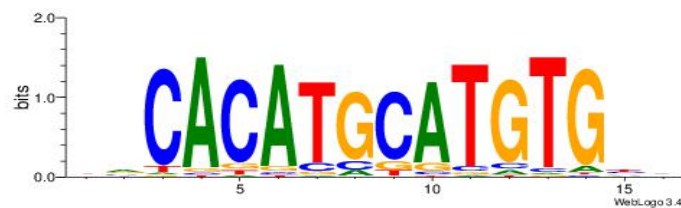
Best Matches for Motif ID 37 (Highest to Lowest)

Dataset #:	4
Motif ID:	118
Motif name:	yrCACATGCATGTGyr
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	8

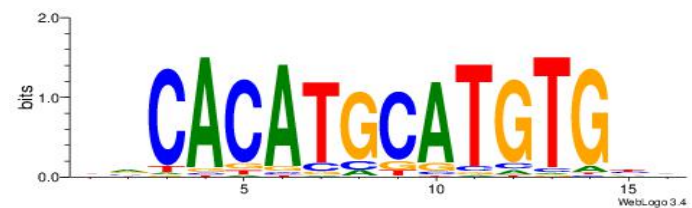
Number of overlap: 8
Similarity score: 0.0125979

Alignment:
HVCACATGCATGTGBD
-----GYATGTGY--

Original motif Consensus sequence: HVCACATGCATGTGBD



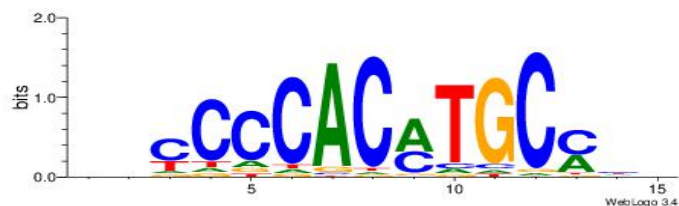
Reverse complement motif Consensus sequence:
DVCACATGCATGTGBH



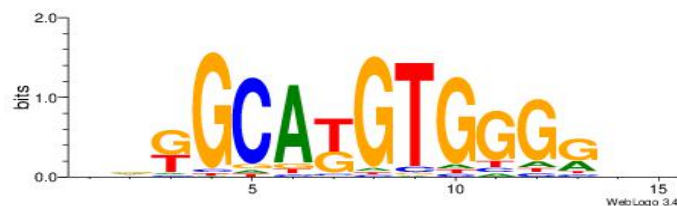
Dataset #: 4
Motif ID: 98
Motif name: myyCCCACmTGCmyr
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 5
Number of overlap: 8
Similarity score: 0.035887

Alignment:
VDRGCAYGTGGGGVD
---GYATGTGY----

Original motif Consensus sequence: HBCCCCACMTGCMHV



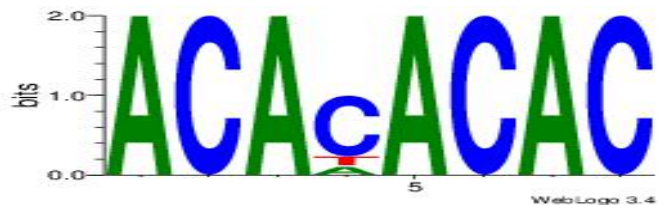
Reverse complement motif Consensus sequence: VDRGCAYGTGGGGVD



Dataset #: 1
Motif ID: 2
Motif name: Motif 2
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 8
Similarity score: 0.0415984

Alignment:
ACACACAC
KCACATKC

Original motif Consensus sequence: ACACACAC



Reverse complement motif Consensus sequence: GTGTGTGT

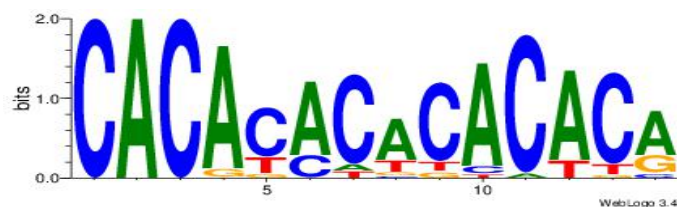


Dataset #: 2
 Motif ID: 58
 Motif name: Motif 58
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 8
 Similarity score: 0.0521491

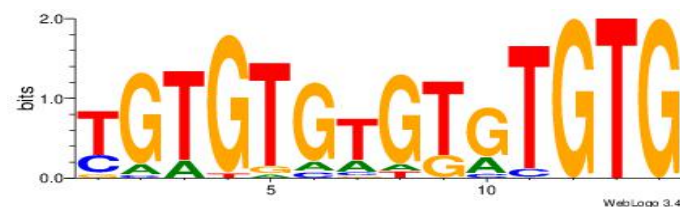
Alignment:

TGTGTGTGTGTGTG
 -GYATGTGY-----

Original motif Consensus sequence: CACACACACACA



Reverse complement motif Consensus sequence: TGTGTGTGTGTG

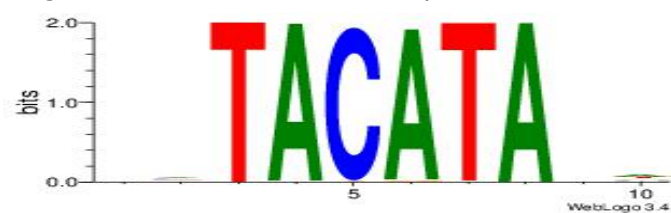


Dataset #: 4
 Motif ID: 90
 Motif name: ymTACATAyw
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 8

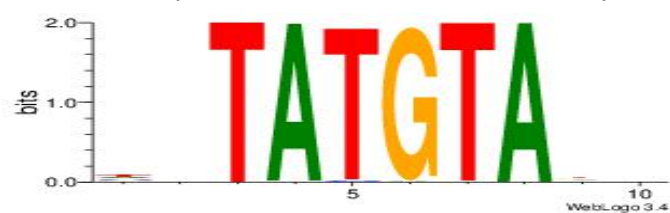
Similarity score: 0.0544369

Alignment:
DBTATGTAHH
-GYATGTGY-

Original motif Consensus sequence: HHTACATABD

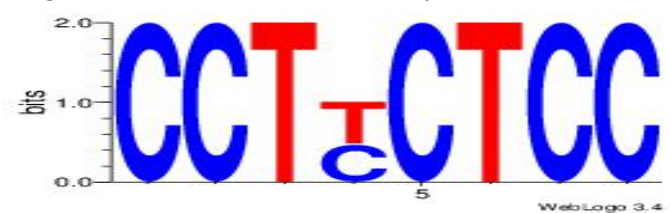


Reverse complement motif Consensus sequence: DBTATGTAHH



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

Original motif Consensus sequence: CCTYCTCC



Reverse complement motif Consensus sequence: GGAGMAGG



Best Matches for Motif ID 38 (Highest to Lowest)

Dataset #:	1
Motif ID:	51
Motif name:	Motif 51
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward

Position number: 1
Number of overlap: 8
Similarity score: 0.0329729

Alignment:
AGAGCWGG
GGAGMAGG

Original motif Consensus sequence: AGAGCWGG



Reverse complement motif Consensus sequence: CCWGCTCT

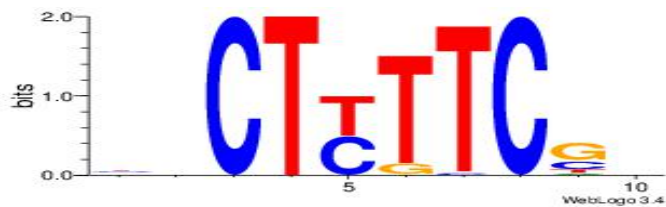


Dataset #: 4
Motif ID: 88
Motif name: ygCTyTTCsg
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 2
Number of overlap: 8
Similarity score: 0.0476921

Alignment:
BCGAAMAGHH
-GGAGMAGG-

Original motif Consensus sequence: HDCTYTTCGB

Reverse complement motif Consensus sequence: BCGAAMAGHH



Dataset #: 1
 Motif ID: 29
 Motif name: Motif 29
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 8
 Similarity score: 0.0493297

Alignment:
 GGGGCYGG
 GGAGMAGG

Original motif Consensus sequence: CCMGCCCC



Reverse complement motif Consensus sequence: GGGGCYGG



Dataset #: 4

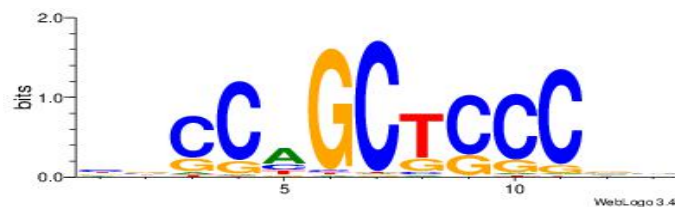
Motif ID: 103
 Motif name: csCCaGCTCCCgs
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 4
 Number of overlap: 8
 Similarity score: 0.0526885

Alignment:

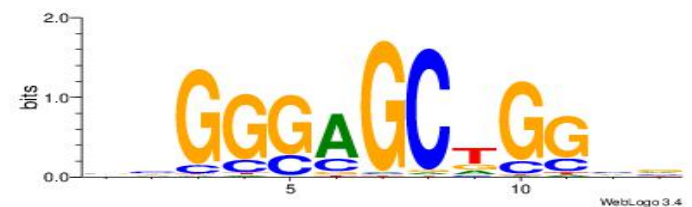
BVGGGAGCTGGBB

---GGAGMAGG---

Original motif Consensus sequence: BBCCAGCTCCCVB



Reverse complement motif Consensus sequence: BVGGGAGCTGGBB



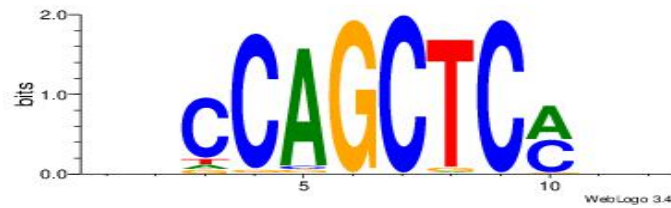
Dataset #: 4
 Motif ID: 119
 Motif name: cbCCAGCTCmyk
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3
 Number of overlap: 8
 Similarity score: 0.0576001

Alignment:

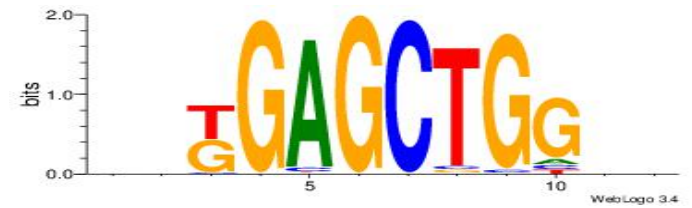
HBYGAGCTGGBB

--GGAGMAGG--

Original motif Consensus sequence: BBCCAGCTCMBD



Reverse complement motif Consensus sequence: HBYGAGCTGGBB

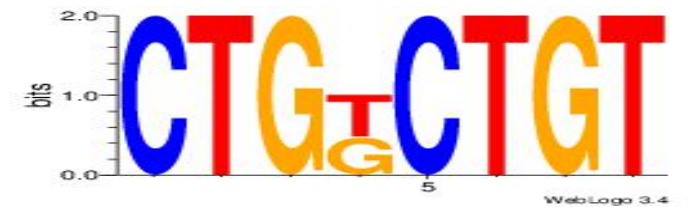


Dataset #: 1 Motif ID: 39 Motif name: Motif 39

Original motif Consensus sequence: ACAGMCAG



Reverse complement motif Consensus sequence: CTGYCTGT



Best Matches for Motif ID 39 (Highest to Lowest)

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

Number of overlap: 8
Similarity score: 0.0307023

Alignment:
KRAGGCAG
ACAGMCAG

Original motif Consensus sequence: CTGCCTKY



Reverse complement motif Consensus sequence: KRAGGCAG

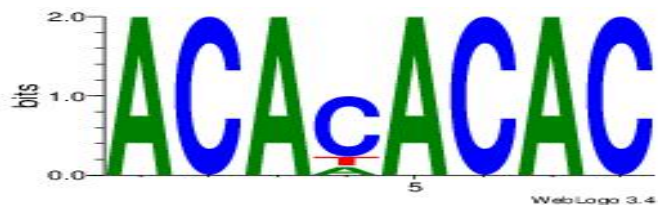


Dataset #: 1
Motif ID: 2
Motif name: Motif 2
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 8
Similarity score: 0.0593235

Alignment:
ACACACAC
ACAGMCAG

Original motif Consensus sequence: ACACACAC

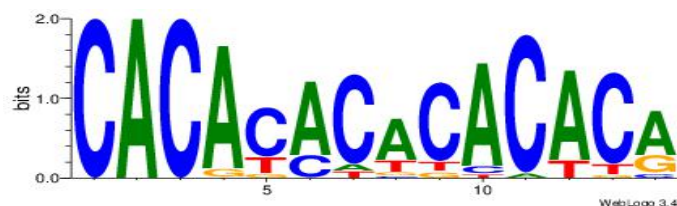
Reverse complement motif Consensus sequence: GTGTGTGT



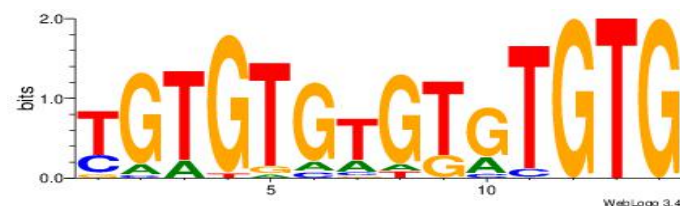
Dataset #: 2
 Motif ID: 58
 Motif name: Motif 58
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 6
 Number of overlap: 8
 Similarity score: 0.0634902

Alignment:
 TGTGTGTGTGTGTG
 -----CTGYCTGT-

Original motif Consensus sequence: CACACACACACA



Reverse complement motif Consensus sequence: TGTGTGTGTGTGT



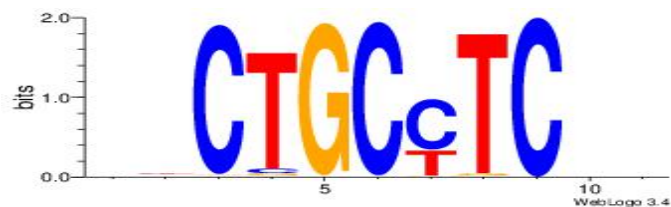
Dataset #: 4
 Motif ID: 116

Motif name:	dyCTGCyTCyc
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	3
Number of overlap:	8
Similarity score:	0.0653685

Alignment:

DHCTGCYTCHB
 --CTGYCTGT--

Original motif Consensus sequence: DHCTGCYTCHB



Reverse complement motif Consensus sequence: BHGAKGCAGHH



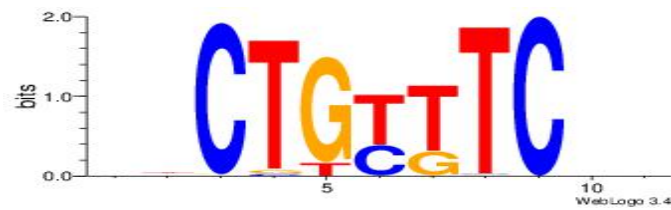
Dataset #:	4
Motif ID:	113
Motif name:	htCTGyKTCbt
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	2
Number of overlap:	8
Similarity score:	0.0674965

Alignment:

HVGAAMCAGVH

-ACAGMCAG--

Original motif Consensus sequence: HBCTGYTTCBH



Reverse complement motif Consensus sequence: HVGAAMCAGVH



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

Original motif Consensus sequence: CCACASC



Reverse complement motif Consensus sequence: GSTGTGG



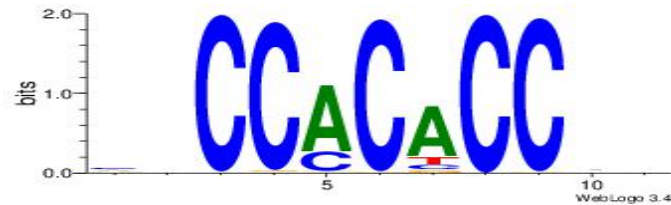
Best Matches for Motif ID 40 (Highest to Lowest)

Dataset #:	4
Motif ID:	110
Motif name:	cmCCACACCcm
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	3

Number of overlap: 7
Similarity score: 0.0381642

Alignment:
VBGGTGTGGBD
--GSTGTGG--

Original motif Consensus sequence: HVCCACACCBV



Reverse complement motif Consensus sequence: VBGGTGTGGBD

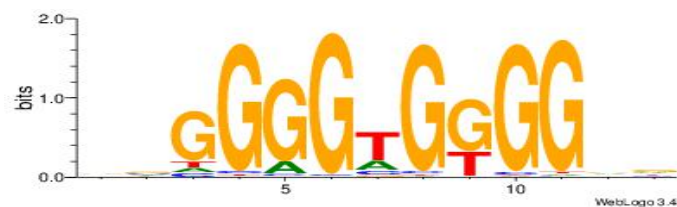
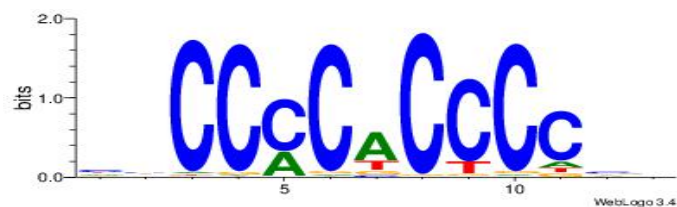


Dataset #: 4
Motif ID: 111
Motif name: ccCCmCaCCCCcc
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 5
Number of overlap: 7
Similarity score: 0.0665887

Alignment:
HBCCCCACCCCBH
--CCACASC----

Original motif Consensus sequence: HBCCCCACCCCBH

Reverse complement motif Consensus sequence: DBGGGGTGGGGB



Dataset #: 1
 Motif ID: 22
 Motif name: Motif 22
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 7
 Similarity score: 0.0714286

Alignment:
 GTGGTGGY
 -GSTGTGG

Original motif Consensus sequence: GTGGTGGY



Reverse complement motif Consensus sequence: MCCACCAC



Dataset #: 1
 Motif ID: 6

Motif name:	Motif 6
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	2
Number of overlap:	7
Similarity score:	0.0745048

Alignment:
 GYGSTGGG
 GSTGTGG-

Original motif Consensus sequence: CCCASCMC



Reverse complement motif Consensus sequence: GYGSTGGG



Dataset #:	1
Motif ID:	12
Motif name:	Motif 12
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	7
Similarity score:	0.0820312

Alignment:
MTGTGTGC
-GSTGTGG

Original motif Consensus sequence: GCACACAY



Reverse complement motif Consensus sequence: MTGTGTGC



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

Original motif Consensus sequence: CTCAGARA



Reverse complement motif Consensus sequence: TKTCTGAG



Best Matches for Motif ID 41 (Highest to Lowest)

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

Number of overlap: 8
Similarity score: 0.0342598

Alignment:
CACASASA
CTCAGARA

Original motif Consensus sequence: CACASASA



Reverse complement motif Consensus sequence: TSTSTGTG

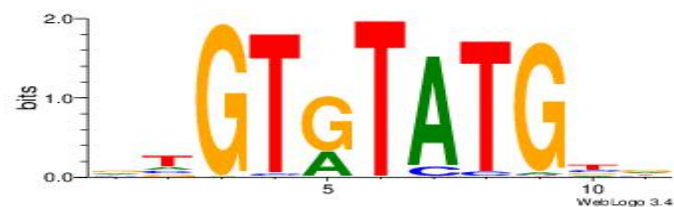
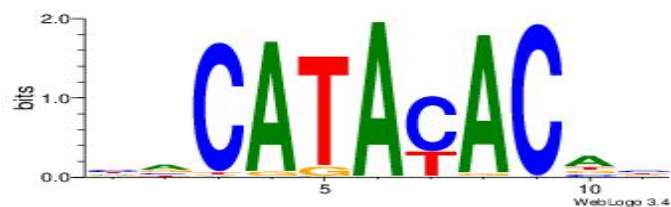


Dataset #: 4
Motif ID: 117
Motif name: yaCATAYACay
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 4
Number of overlap: 8
Similarity score: 0.0601983

Alignment:
DTGTGTATGBD
---TKTCTGAG

Original motif Consensus sequence: HVCATACACAH

Reverse complement motif Consensus sequence: DTGTGTATGBD



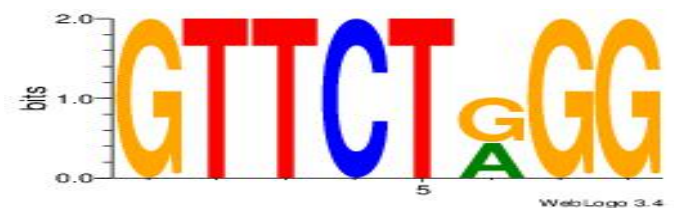
Dataset #: 1
 Motif ID: 42
 Motif name: Motif 42
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 8
 Similarity score: 0.0645699

Alignment:
 GTTCTKGG
 TKTCTGAG

Original motif Consensus sequence: CCYAGAAC



Reverse complement motif Consensus sequence: GTTCTKGG



Dataset #: 4
 Motif ID: 127

Motif name:	rryCAGGGAyw
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	3
Number of overlap:	8
Similarity score:	0.0655288

Alignment:

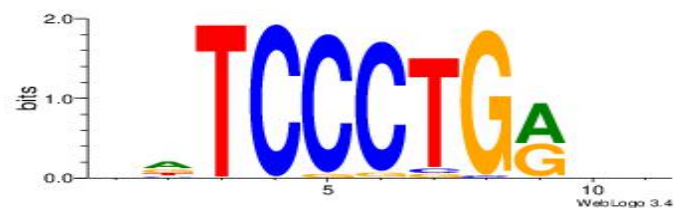
DDYCAGGGAHD

-CTCAGARA--

Original motif Consensus sequence: DDYCAGGGAHD



Reverse complement motif Consensus sequence: DHTCCCTGMDD



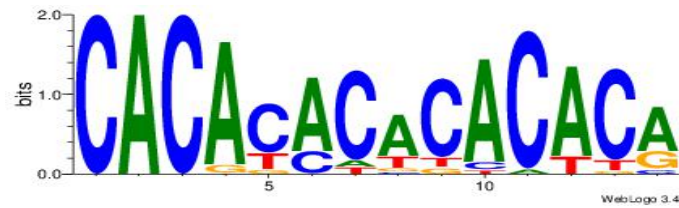
Dataset #:	2
Motif ID:	58
Motif name:	Motif 58
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	7
Number of overlap:	8
Similarity score:	0.0667371

Alignment:

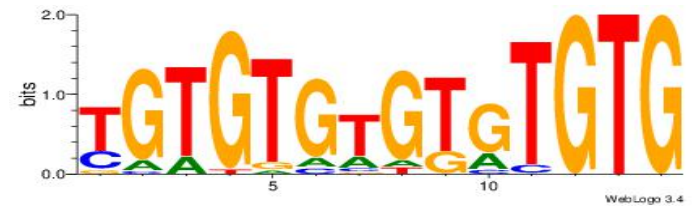
TGTGTGTGTGTGTG

-----TKTCTGAG

Original motif Consensus sequence: CACACACACACA



Reverse complement motif Consensus sequence: TGTGTGTGTGTGT

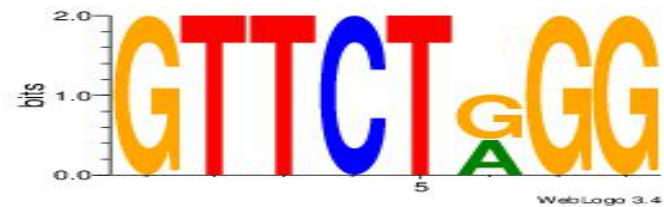


Dataset #: 1 Motif ID: 42 Motif name: Motif 42

Original motif Consensus sequence: CCYAGAAC



Reverse complement motif Consensus sequence: GTTCTKGG



Best Matches for Motif ID 42 (Highest to Lowest)

Dataset #:	1
Motif ID:	19
Motif name:	Motif 19
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: 0.0610815

Alignment:
CCTGGARC
CCYAGAAC

Original motif Consensus sequence: CCTGGARC



Reverse complement motif Consensus sequence: GKTCCAGG

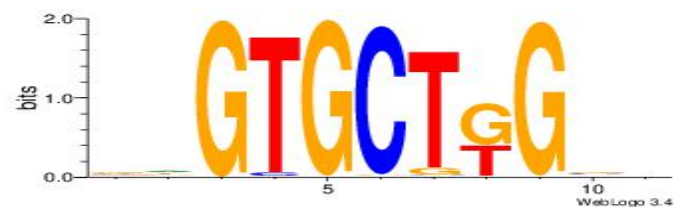


Dataset #: 4
Motif ID: 115
Motif name: ysCmAGCACwy
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 3
Number of overlap: 8
Similarity score: 0.0690213

Alignment:
HVCMAGCACHH
-CCYAGAAC--

Original motif Consensus sequence: HVCMAGCACHH

Reverse complement motif Consensus sequence: DHGTGCTRGVH



Dataset #: 1
 Motif ID: 6
 Motif name: Motif 6
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 8
 Similarity score: 0.0735374

Alignment:
 GYGSTGGG
 GTTCTKGG

Original motif Consensus sequence: CCCASCMC



Reverse complement motif Consensus sequence: GYGSTGGG



Dataset #: 4
 Motif ID: 109

Motif name: aaCAAAAACaa
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3
 Number of overlap: 8
 Similarity score: 0.0769138

Alignment:

HHGTTTTTGH
 --GTTCTKGG--

Original motif Consensus sequence: HHCAAAAACHH



Reverse complement motif Consensus sequence: HHGTTTTTGH



Dataset #: 1
 Motif ID: 41
 Motif name: Motif 41
 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: 0.0911976

Alignment:
CTCAGARA
CCYAGAAC

Original motif Consensus sequence: CTCAGARA

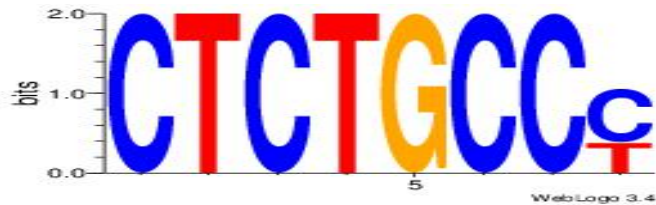


Reverse complement motif Consensus sequence: TKTCTGAG



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

Original motif Consensus sequence: CTCTGCCY



Reverse complement motif Consensus sequence: KGGCAGAG



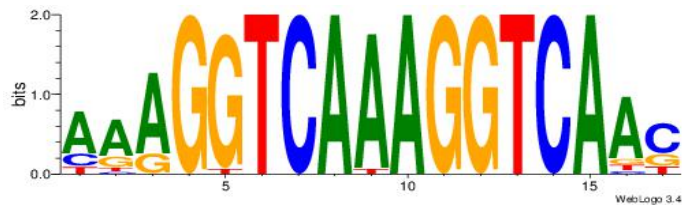
Best Matches for Motif ID 43 (Highest to Lowest)

Dataset #:	3
Motif ID:	84
Motif name:	NR1H2RXRA
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	7

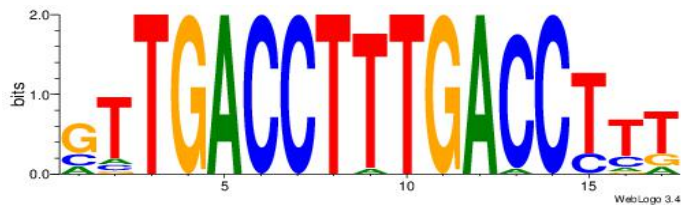
Number of overlap: 8
Similarity score: 0.0750223

Alignment:
GTTGACCTTTGACCTTT
-----CTCTGCCY---

Original motif Consensus sequence: AAAGGTCAAAGGTCAAC



Reverse complement motif Consensus sequence:
GTTGACCTTTGACCTTT

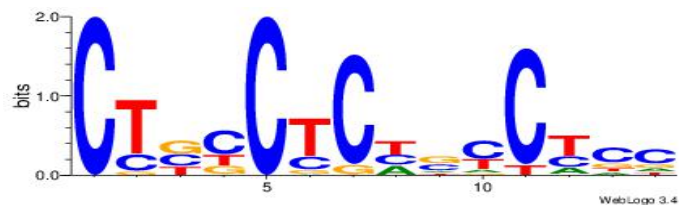


Dataset #: 2
Motif ID: 59
Motif name: Motif 59
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 5
Number of overlap: 8
Similarity score: 0.0776916

Alignment:
CTBCCTCHSYCYCC
-----CTCTGCCY--

Original motif Consensus sequence: CTBCCTCHSYCYCC

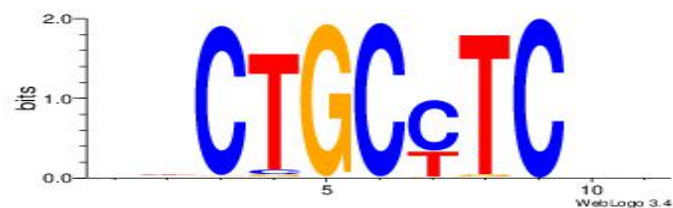
Reverse complement motif Consensus sequence: GGMGKSHGAGGB



Dataset #: 4
 Motif ID: 116
 Motif name: dyCTGCyTCyc
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 8
 Similarity score: 0.0799777

Alignment:
 DHCTGCTCHB
 CTCTGCCY---

Original motif Consensus sequence: DHCTGCTCHB



Reverse complement motif Consensus sequence: BHGAKGCAGHH



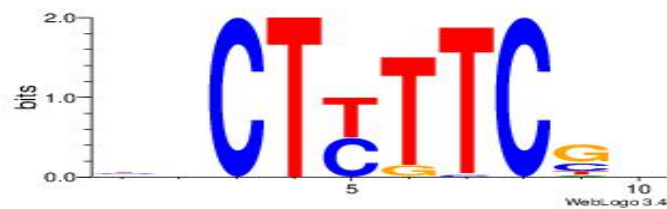
Dataset #: 4
 Motif ID: 88

Motif name: ygCTyTTCsg
 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: 0.0904749

Alignment:

HDCTYTTTCGB
 --CTCTGCCY

Original motif Consensus sequence: HDCTYTTTCGB



Reverse complement motif Consensus sequence: BCGAAMAGHH



Dataset #: 3
 Motif ID: 83
 Motif name: NR2F1
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 5
 Number of overlap: 8
 Similarity score: 0.0905992

Alignment:

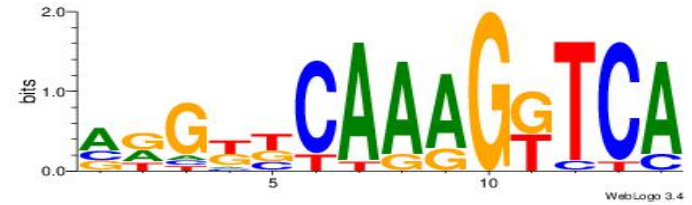
TGAMCTTTGMMCYT

----CTCTGCCY--

Original motif Consensus sequence: TGAMCTTTGMMCYT



Reverse complement motif Consensus sequence: AKGYCAAAGRTC



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

Original motif Consensus sequence: AGAAATG



Reverse complement motif Consensus sequence: CATTCT



Best Matches for Motif ID 44 (Highest to Lowest)

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

Number of overlap: 7
 Similarity score: 0.0447866

Alignment:
 MATTTTY
 CATTTCT

Original motif Consensus sequence: KAAAATR



Reverse complement motif Consensus sequence: MATTTTY

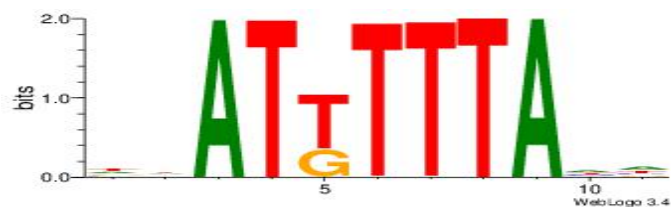


Dataset #: 4
 Motif ID: 108
 Motif name: wwATkTTTAww
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 4
 Number of overlap: 7
 Similarity score: 0.0513825

Alignment:
 DHATKTTTAHH
 -CATTTCT---

Original motif Consensus sequence: DHATKTTTAHH

Reverse complement motif Consensus sequence: HHTAAARATHD



Dataset #: 1
 Motif ID: 33
 Motif name: Motif 33
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 7
 Similarity score: 0.0527225

Alignment:
 GGAAARG
 AGAAATG

Original motif Consensus sequence: CMTTCC



Reverse complement motif Consensus sequence: GGAAARG



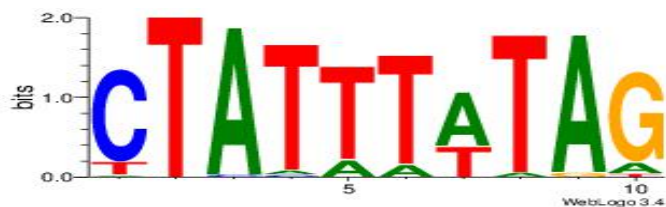
Dataset #: 3
 Motif ID: 61

Motif name:	MEF2A
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	7
Similarity score:	0.0603872

Alignment:

CTATTTWTAG
 -CATTCT--

Original motif Consensus sequence: CTATTTWTAG



Reverse complement motif Consensus sequence: CTAWAAATAG



Dataset #:	3
Motif ID:	71
Motif name:	Evi1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	2
Number of overlap:	7
Similarity score:	0.0740469

Alignment:

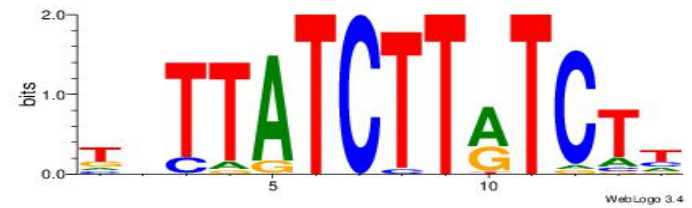
TBTTATCTTMTCTT

-----CATTTCT-

Original motif Consensus sequence: AAGAYAAGATAABA



Reverse complement motif Consensus sequence: TBTTATCTTMTCTT



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

Original motif Consensus sequence: ATTATTAW



Reverse complement motif Consensus sequence: WTAATAAT



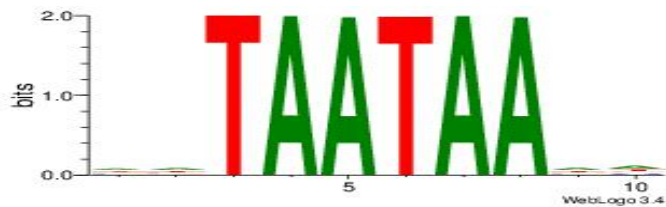
Best Matches for Motif ID 45 (Highest to Lowest)

Dataset #:	4
Motif ID:	100
Motif name:	wwTAATAAww
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	2

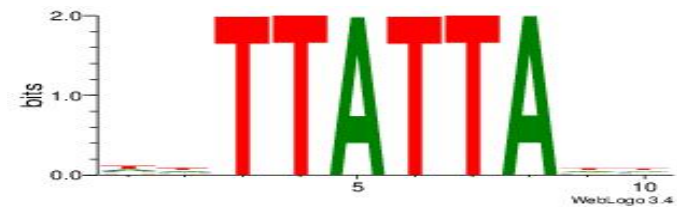
Number of overlap: 8
 Similarity score: 0.0312128

Alignment:
 DDTTATTAHD
 -ATTATTAW-

Original motif Consensus sequence: DHTAATAADD



Reverse complement motif Consensus sequence: DDTTATTAHD

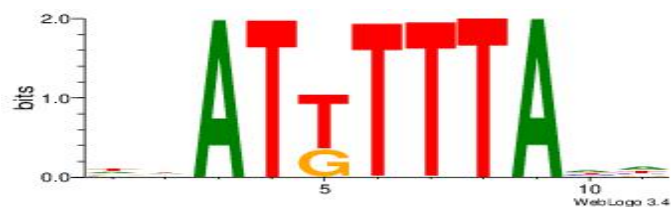


Dataset #: 4
 Motif ID: 108
 Motif name: wwATkTTTAww
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 8
 Similarity score: 0.0503721

Alignment:
 HHTAAARATHD
 -WTAATAAT--

Original motif Consensus sequence: DHATKTTTAHH

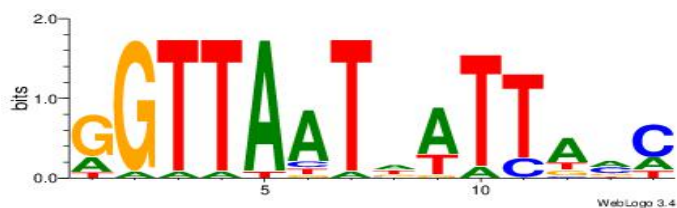
Reverse complement motif Consensus sequence: HHTAAARATHD



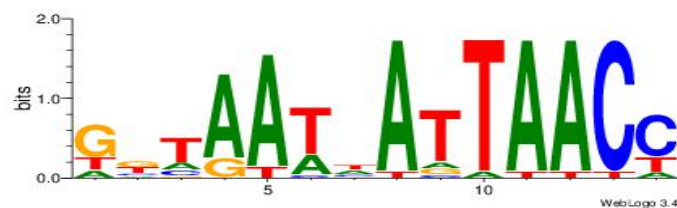
Dataset #: 3
 Motif ID: 68
 Motif name: HNF1A
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 8
 Similarity score: 0.0585066

Alignment:
 GYTAATDATTAAACC
 ----ATTATTAW--

Original motif Consensus sequence: GGTTAATDATTAMC



Reverse complement motif Consensus sequence: GYTAATDATTAAACC

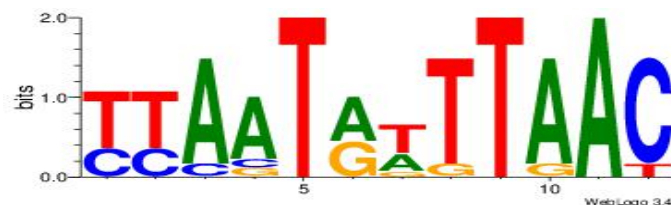


Dataset #: 3
 Motif ID: 82

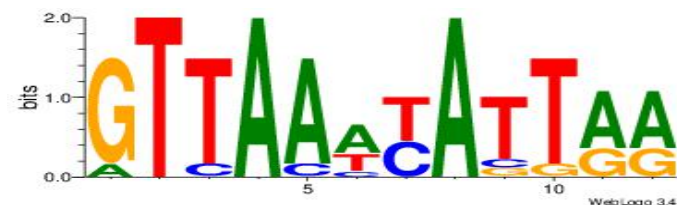
Motif name:	HNH1B
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	5
Number of overlap:	8
Similarity score:	0.0743796

Alignment:
TTAATRWTTAAC
WTAATAAT----

Original motif Consensus sequence: TTAATRWTTAAC



Reverse complement motif Consensus sequence: GTTAAWKATTAA



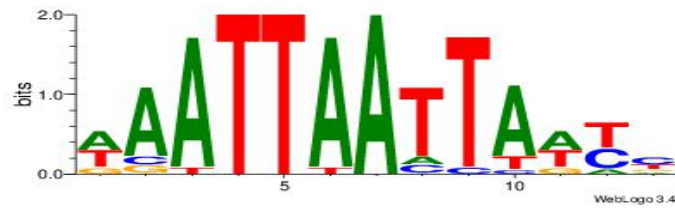
Dataset #:	3
Motif ID:	66
Motif name:	Lhx3
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	8
Similarity score:	0.0744439

Alignment:

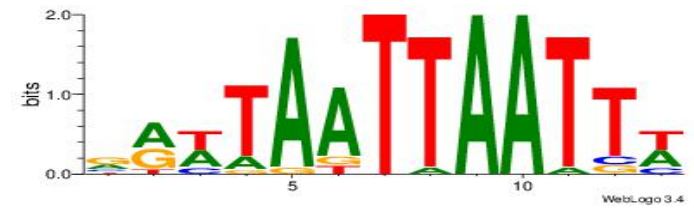
WAATTAATTAWYB

WTAATAAT-----

Original motif Consensus sequence: WAATTAATTAWYB



Reverse complement motif Consensus sequence: BMWTAATTAATTW



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

Original motif Consensus sequence: GGAAASA



Reverse complement motif Consensus sequence: TSTTTCC



Best Matches for Motif ID 46 (Highest to Lowest)

Dataset #:	1
Motif ID:	13
Motif name:	Motif 13
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1

Number of overlap: 7
Similarity score: 0.0428804

Alignment:
GGAAGSAR
GGAAASA-

Original motif Consensus sequence: GGAAGSAR



Reverse complement motif Consensus sequence: MTSCTTCC



Dataset #: 1
Motif ID: 33
Motif name: Motif 33
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 7
Similarity score: 0.0542683

Alignment:
GGAAARG
GGAAASA

Original motif Consensus sequence: CMTTTC

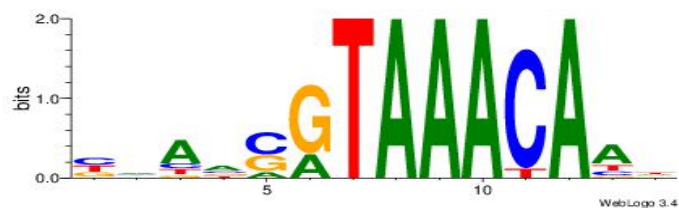
Reverse complement motif Consensus sequence: GGAAARG



Dataset #: 3
 Motif ID: 75
 Motif name: FOXF2
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 6
 Number of overlap: 7
 Similarity score: 0.0636714

Alignment:
 BHADSGTAAACAAD
 -----GGAAASA--

Original motif Consensus sequence: BHADSGTAAACAAD



Reverse complement motif Consensus sequence: DTTGTTACSBTBB



Dataset #: 3
 Motif ID: 86

Motif name:	FOXO3
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	7
Similarity score:	0.0652994

Alignment:
 KGTAACA
 -GGAAASA

Original motif Consensus sequence: KGTAACA



Reverse complement motif Consensus sequence: TGTTTACR



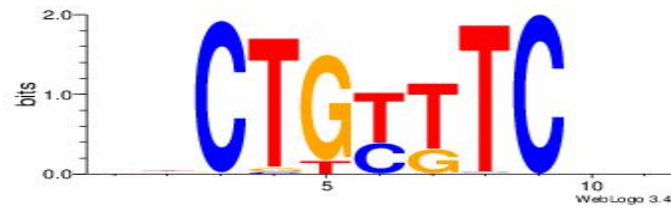
Dataset #:	4
Motif ID:	113
Motif name:	htCTGyKTCbt
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	4
Number of overlap:	7
Similarity score:	0.0693025

Alignment:

HBCTGYTTCBH

---TSTTTCC-

Original motif Consensus sequence: HBCTGYTTCBH



Reverse complement motif Consensus sequence: HVGAAMCAGVH



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

Original motif Consensus sequence: KGCTGCTG



Reverse complement motif Consensus sequence: CAGCAGCR



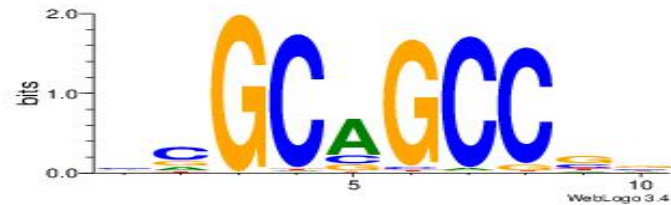
Best Matches for Motif ID 47 (Highest to Lowest)

Dataset #:	4
Motif ID:	105
Motif name:	ccGCAGCCss
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1

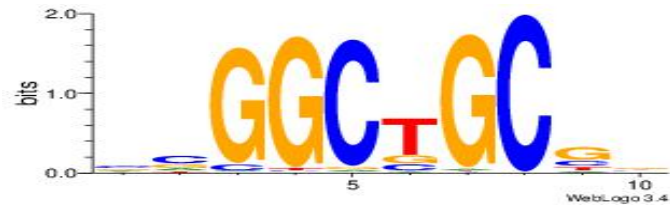
Number of overlap: 8
Similarity score: 0.0572744

Alignment:
BBGGCTGCGV
--KGCTGCTG

Original motif Consensus sequence: VCGCAGCCBB



Reverse complement motif Consensus sequence: BBGGCTGCGV

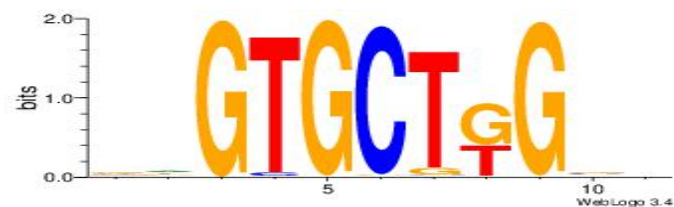


Dataset #: 4
Motif ID: 115
Motif name: ysCmAGCACwy
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 8
Similarity score: 0.0621107

Alignment:
DHGTGCTRGVH
KGCTGCTG---

Original motif Consensus sequence: HVCMAGCACHH

Reverse complement motif Consensus sequence: DHGTGCTRGVH



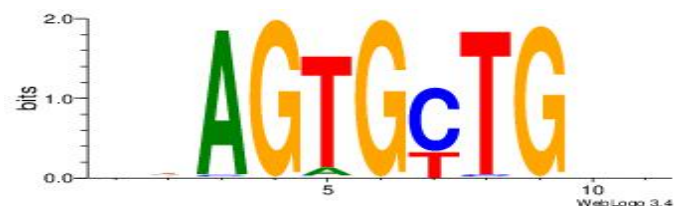
Dataset #: 4
 Motif ID: 93
 Motif name: cmCARCACTwr
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 8
 Similarity score: 0.0664426

Alignment:
 VHAGTGCTGHB
 -KGCTGCTG--

Original motif Consensus sequence: BHCAGCACTHV



Reverse complement motif Consensus sequence: VHAGTGCTGHB



Dataset #: 1
 Motif ID: 30

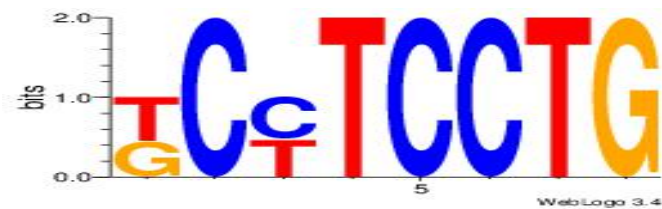
Motif name:	Motif 30
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	8
Similarity score:	0.0671183

Alignment:
 YCMTTCCTG
 KGCTGCTG

Original motif Consensus sequence: CAGGARGM



Reverse complement motif Consensus sequence: YCMTTCCTG



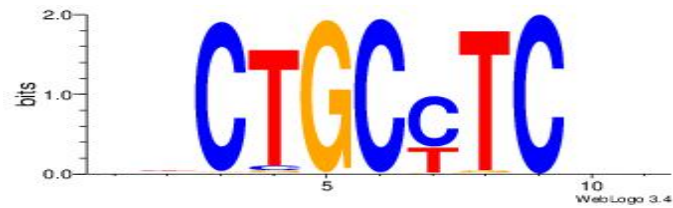
Dataset #:	4
Motif ID:	116
Motif name:	dyCTGCyTCyc
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	4
Number of overlap:	8
Similarity score:	0.0696714

Alignment:

DHCTGCYTCHB

KGCTGCTG---

Original motif Consensus sequence: DHCTGCYTCHB



Reverse complement motif Consensus sequence: BHGAKGCAGHH



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

Original motif Consensus sequence: ACACWG



Reverse complement motif Consensus sequence: CWGTGT



Best Matches for Motif ID 48 (Highest to Lowest)

Dataset #:	1
Motif ID:	12
Motif name:	Motif 12
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	3

Number of overlap: 6
Similarity score: 0.0450356

Alignment:
MTGTGTGC
CWGTGT--

Original motif Consensus sequence: GCACACAY



Reverse complement motif Consensus sequence: MTGTGTGC



Dataset #: 1
Motif ID: 11
Motif name: Motif 11
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 6
Similarity score: 0.0534035

Alignment:
CTGDGTTC
--CWGTGT

Original motif Consensus sequence: CTGDGTTC

Reverse complement motif Consensus sequence: GAACDCAG



Dataset #: 1
 Motif ID: 23
 Motif name: Motif 23
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 6
 Similarity score: 0.0615752

Alignment:
 MTSTGTA
 -CWGTGT

Original motif Consensus sequence: MTSTGTA



Reverse complement motif Consensus sequence: TACASAR



Dataset #: 1
 Motif ID: 7

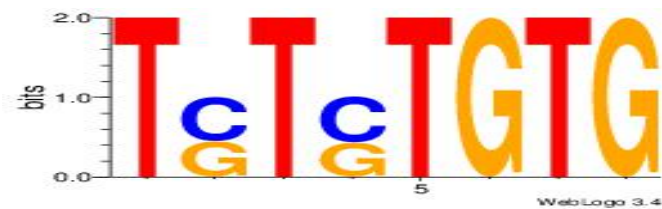
Motif name:	Motif 7
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	6
Similarity score:	0.065723

Alignment:
CACASASA
-ACACWG-

Original motif Consensus sequence: CACASASA



Reverse complement motif Consensus sequence: TSTSTGTG



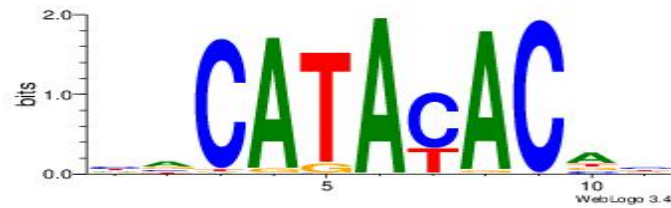
Dataset #:	4
Motif ID:	117
Motif name:	yaCATAYACay
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	6
Number of overlap:	6
Similarity score:	0.0663715

Alignment:

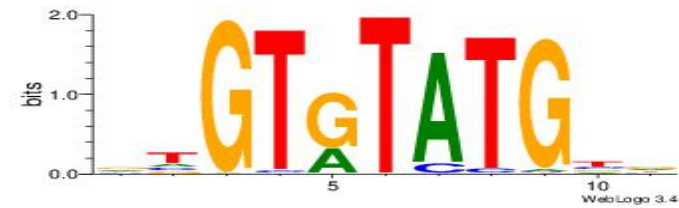
DTGTGTATGBD

CWGTGT-----

Original motif Consensus sequence: HVCATACACAH



Reverse complement motif Consensus sequence: DTGTGTATGBD



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

Original motif Consensus sequence: AGATAAAR



Reverse complement motif Consensus sequence: KTTTATCT



Best Matches for Motif ID 49 (Highest to Lowest)

Dataset #:	3
Motif ID:	71
Motif name:	Evi1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1

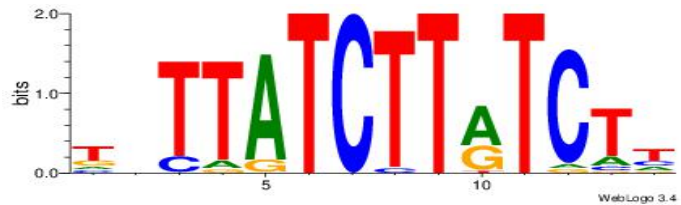
Number of overlap: 8
Similarity score: 0.0168651

Alignment:
TBTTATCTTMTCTT
KTTTATCT-----

Original motif Consensus sequence: AAGAYAAGATAABA



Reverse complement motif Consensus sequence: TBTTATCTTMTCTT

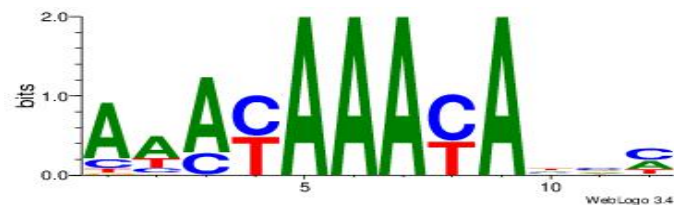
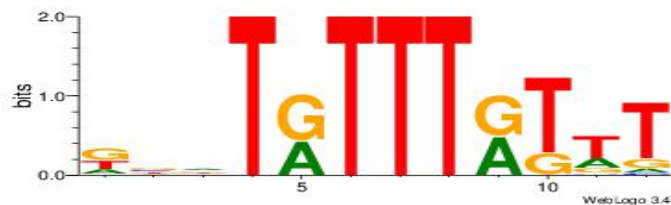


Dataset #: 3
Motif ID: 67
Motif name: FOXI1
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 8
Similarity score: 0.0451069

Alignment:
KBDTRTTTRTTT
----KTTTATCT

Original motif Consensus sequence: KBDTRTTTRTTT

Reverse complement motif Consensus sequence: AAAMAAAMADBY

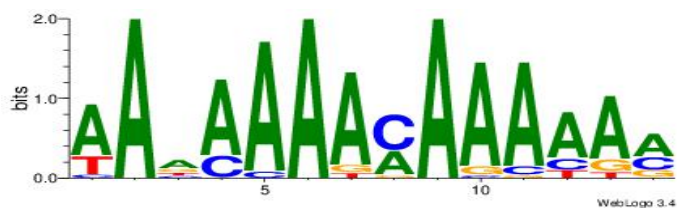


Dataset #: 2
 Motif ID: 60
 Motif name: Motif 60
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 5
 Number of overlap: 8
 Similarity score: 0.0469577

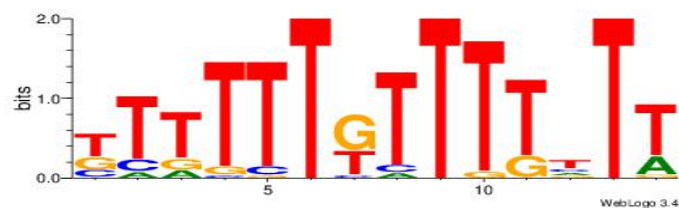
Alignment:

YTTTTTRTTTTDTT
 --KTTTATCT----

Original motif Consensus sequence: AADAAAAMAAAAAM



Reverse complement motif Consensus sequence: YTTTTTRTTTTDTT



Dataset #: 1
 Motif ID: 21

Motif name:	Motif 21
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	8
Similarity score:	0.0471231

Alignment:
GTTTGTTT
KTTTATCT

Original motif Consensus sequence: AAACAAAC



Reverse complement motif Consensus sequence: GTTTGTTT

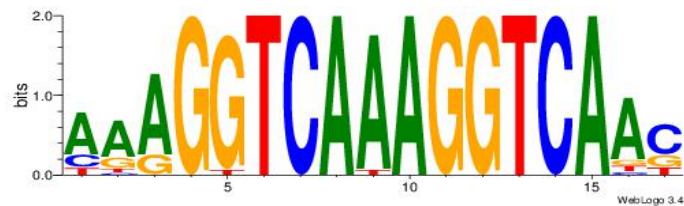


Dataset #:	3
Motif ID:	84
Motif name:	NR1H2RXRA
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	10
Number of overlap:	8
Similarity score:	0.0483731

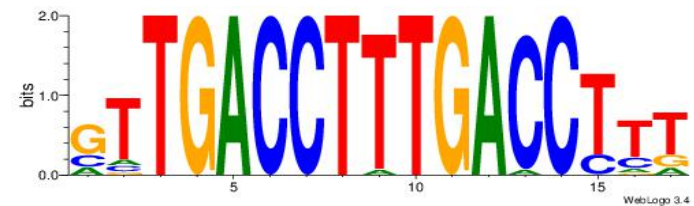
Alignment:

GTGACCTTTGACCTTT
KTTTATCT-----

Original motif Consensus sequence: AAAGGTCAAAGGTCAAC



Reverse complement motif Consensus sequence: GTTGACCTTTGACCTTT



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

Original motif Consensus sequence: GAAGAGCA



Reverse complement motif Consensus sequence: TGCTCTTC



Best Matches for Motif ID 50 (Highest to Lowest)

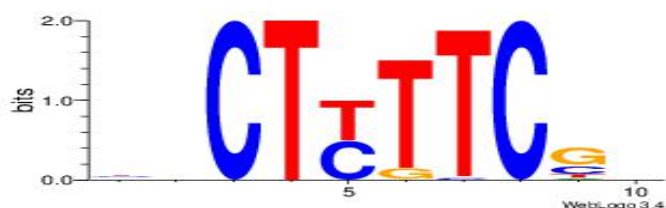
Dataset #:	4
Motif ID:	88
Motif name:	ygCTyTTCsg
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward

Position number: 3
 Number of overlap: 8
 Similarity score: 0.0206791

Alignment:

HDCTYTTTCGB
 TGCTCTTC--

Original motif Consensus sequence: HDCTYTTTCGB



Reverse complement motif Consensus sequence: BCGAAMAGHH



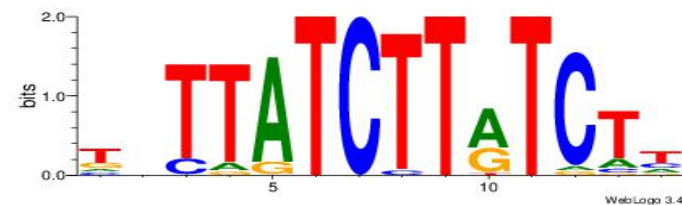
Dataset #: 3
 Motif ID: 71
 Motif name: Evi1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3
 Number of overlap: 8
 Similarity score: 0.0485428

Alignment:

TBTTATCTTMTCTT
 --TGCTCTTC----

Original motif Consensus sequence: AAGAYAAGATAABA

Reverse complement motif Consensus sequence: TBTTATCTTMTCTT



Dataset #: 3
 Motif ID: 83
 Motif name: NR2F1
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 8
 Similarity score: 0.0680446

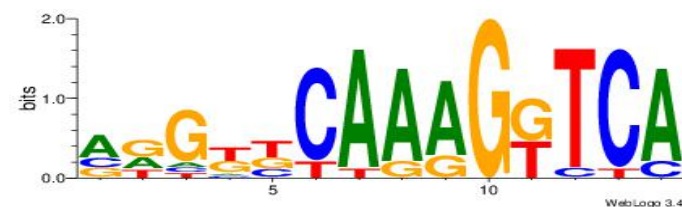
Alignment:

AKGYCAAAGRTCA
 -----GAAGAGCA

Original motif Consensus sequence: TGAMCTTTGMMCYT



Reverse complement motif Consensus sequence: AKGYCAAAGRTCA



Dataset #: 1

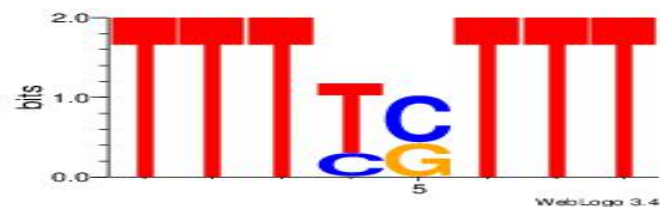
Motif ID:	5
Motif name:	Motif 5
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	8
Similarity score:	0.0707433

Alignment:
AAASAAAA
GAAGAGCA

Original motif Consensus sequence: AAASAAAA



Reverse complement motif Consensus sequence: TTTTSTTT



Dataset #:	4
Motif ID:	114
Motif name:	awAACAcAAwa
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	8
Similarity score:	0.0709876

Alignment:

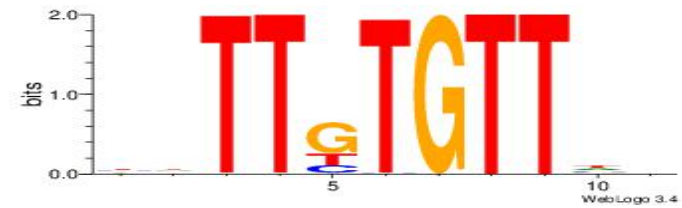
DDAACACAADV

-GAAGAGCA--

Original motif Consensus sequence: DDAACACAADV



Reverse complement motif Consensus sequence: BDTTGTGTTDD



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

Original motif Consensus sequence: AGAGCWGG



Reverse complement motif Consensus sequence: CCWGCTCT



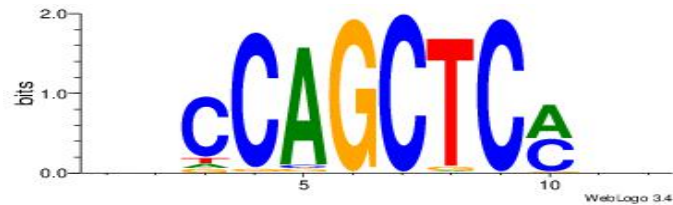
Best Matches for Motif ID 51 (Highest to Lowest)

Dataset #:	4
Motif ID:	119
Motif name:	cbCCAGCTCmyk
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	3

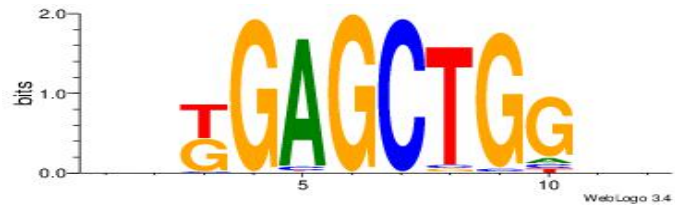
Number of overlap: 8
Similarity score: 0.0568763

Alignment:
BBCCAGCTCMBD
--CCWGCTCT--

Original motif Consensus sequence: BBCCAGCTCMBD



Reverse complement motif Consensus sequence: HBYGAGCTGGBB

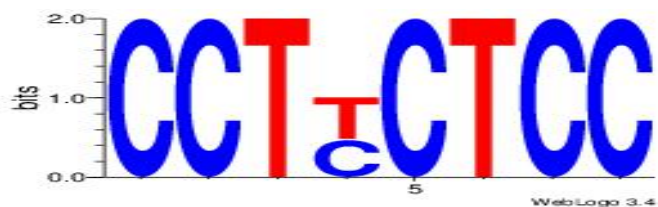


Dataset #: 1
Motif ID: 38
Motif name: Motif 38
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 8
Similarity score: 0.0627656

Alignment:
CCTYCTCC
CCWGCTCT

Original motif Consensus sequence: CCTYCTCC

Reverse complement motif Consensus sequence: GGAGMAGG



Dataset #: 1
 Motif ID: 15
 Motif name: Motif 15
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 8
 Similarity score: 0.0634208

Alignment:
 AGCCCWGG
 AGAGCWGG

Original motif Consensus sequence: AGCCCWGG



Reverse complement motif Consensus sequence: CCWGGGCT



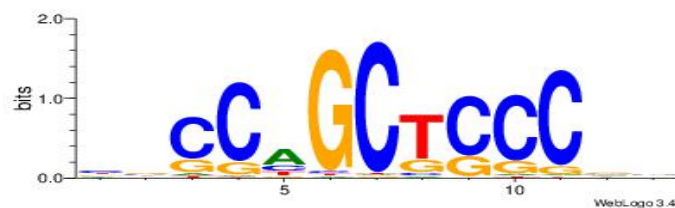
Dataset #: 4
 Motif ID: 103

Motif name:	csCCaGCTCCCgs
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	4
Number of overlap:	8
Similarity score:	0.0769435

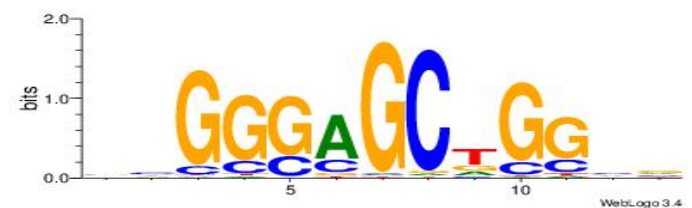
Alignment:

BVGGGAGCTGGBB
 ---AGAGCWGG--

Original motif Consensus sequence: BBCCAGCTCCCVB



Reverse complement motif Consensus sequence: BVGGGAGCTGGBB



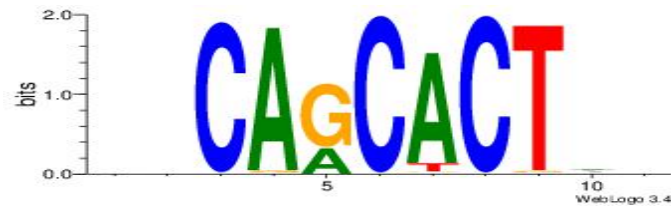
Dataset #:	4
Motif ID:	93
Motif name:	cmCARCACTwr
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	3
Number of overlap:	8
Similarity score:	0.0785511

Alignment:

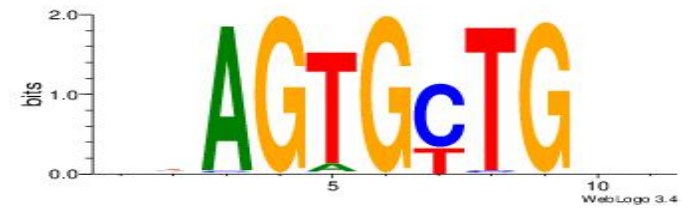
BHCAGCACTHV

-CCWGCTCT--

Original motif Consensus sequence: BHCAGCACTHV



Reverse complement motif Consensus sequence: VHAGTGCTGHB



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

Original motif Consensus sequence: AGVCAGG



Reverse complement motif Consensus sequence: CCTGVCT



Best Matches for Motif ID 52 (Highest to Lowest)

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

Number of overlap: 7
Similarity score: 0.0426638

Alignment:
GAGRMAGR
-AGVCAGG

Original motif Consensus sequence: GAGRMAGR



Reverse complement motif Consensus sequence: KCTRMCTC

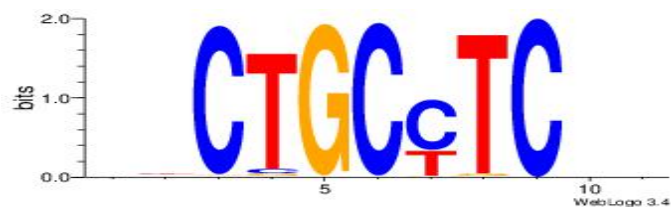


Dataset #: 4
Motif ID: 116
Motif name: dyCTGCyTCyc
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 4
Number of overlap: 7
Similarity score: 0.0621766

Alignment:
DHCTGCYTCHB
-CCTGVCT---

Original motif Consensus sequence: DHCTGCYTCHB

Reverse complement motif Consensus sequence: BHGAKGCAGHH



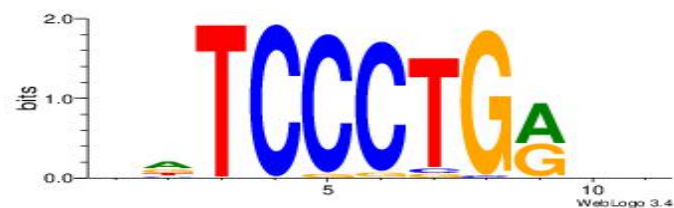
Dataset #: 4
 Motif ID: 127
 Motif name: rryCAGGGAyw
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 5
 Number of overlap: 7
 Similarity score: 0.0705096

Alignment:
 DHTCCCTGMDD
 ----CCTGVCT

Original motif Consensus sequence: DDYCAGGGAHD



Reverse complement motif Consensus sequence: DHTCCCTGMDD



Dataset #: 4
 Motif ID: 113

Motif name:	htCTGyKTCbt
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	4
Number of overlap:	7
Similarity score:	0.0753705

Alignment:

HVGAAMCAGVH

---AGVCAGG-

Original motif Consensus sequence: HBCTGYTTCBH



Reverse complement motif Consensus sequence: HVGAAMCAGVH



Dataset #:	4
Motif ID:	126
Motif name:	yvTGCAGsCAcg
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	7
Similarity score:	0.077286

Alignment:

BVTGCAGSCABV

-----AGVCAGG

Original motif Consensus sequence: BVTGCAGSCABV



Reverse complement motif Consensus sequence: VBTGSCTGCAVB



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

Original motif Consensus sequence: TSTGTR



Reverse complement motif Consensus sequence: MACASA



Best Matches for Motif ID 53 (Highest to Lowest)

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

Number of overlap: 6
Similarity score: 0.00228262

Alignment:
TSTSTGTG
TSTGTR--

Original motif Consensus sequence: CACASASA



Reverse complement motif Consensus sequence: TSTSTGTG

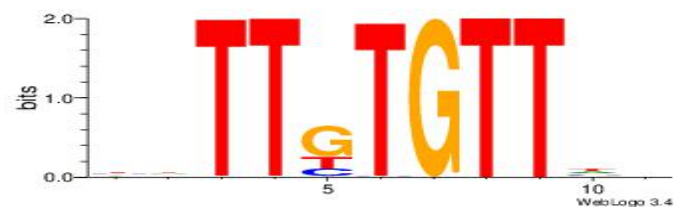


Dataset #: 4
Motif ID: 114
Motif name: awAACAcAAwa
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 4
Number of overlap: 6
Similarity score: 0.0122629

Alignment:
DDAACACAADV
--MACASA---

Original motif Consensus sequence: DDAACACAADV

Reverse complement motif Consensus sequence: BDTTGTGTTDD



Dataset #: 1
 Motif ID: 23
 Motif name: Motif 23
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 6
 Similarity score: 0.0137023

Alignment:
 MTSTGTA
 -TSTGTR

Original motif Consensus sequence: MTSTGTA



Reverse complement motif Consensus sequence: TACASAR

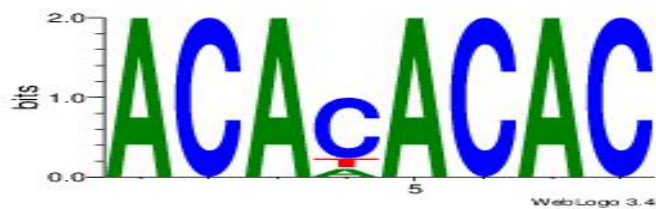


Dataset #: 1
 Motif ID: 2

Motif name:	Motif 2
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	2
Number of overlap:	6
Similarity score:	0.0252334

Alignment:
GTGTGTGT
-TSTGTR-

Original motif Consensus sequence: ACACACAC



Reverse complement motif Consensus sequence: GTGTGTGT



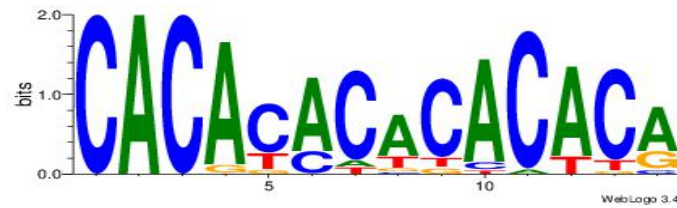
Dataset #:	2
Motif ID:	58
Motif name:	Motif 58
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	6
Similarity score:	0.025412

Alignment:

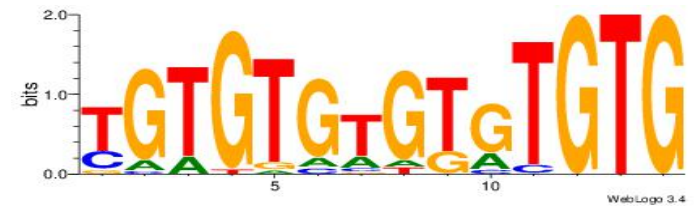
CACACACACACACA

MACASA-----

Original motif Consensus sequence: CACACACACACACA



Reverse complement motif Consensus sequence: TGTGTGTGTGTGT



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

Original motif Consensus sequence: RGAAA



Reverse complement motif Consensus sequence: TTTCK



Best Matches for Motif ID 54 (Highest to Lowest)

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

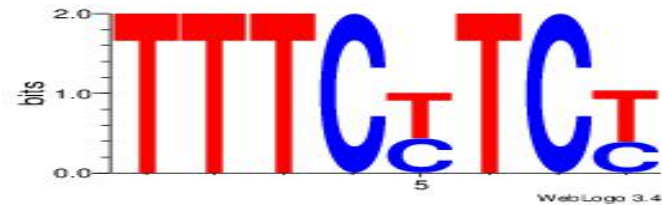
Number of overlap: 5
Similarity score: 0

Alignment:
TTTCKTCK
TTTCK---

Original motif Consensus sequence: RGARGAAA



Reverse complement motif Consensus sequence: TTTCKTCK



Dataset #: 1
Motif ID: 28
Motif name: Motif 28
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 3
Number of overlap: 5
Similarity score: 0.0199405

Alignment:
AVAGAAA
--RGAAA

Original motif Consensus sequence: AVAGAAA

Reverse complement motif Consensus sequence: TTTCTVT



Dataset #: 1
 Motif ID: 33
 Motif name: Motif 33
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 5
 Similarity score: 0.0284722

Alignment:
 CMTTTC
 TTTCT--

Original motif Consensus sequence: CMTTTC



Reverse complement motif Consensus sequence: GGAAAG



Dataset #: 1
 Motif ID: 46

Motif name:	Motif 46
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	3
Number of overlap:	5
Similarity score:	0.0284722

Alignment:
GGAAASA
RGAAA--

Original motif Consensus sequence: GGAAASA



Reverse complement motif Consensus sequence: TSTTTCC



Dataset #:	1
Motif ID:	44
Motif name:	Motif 44
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	3
Number of overlap:	5
Similarity score:	0.0339244

Alignment:

CATTTCT

--TTTCK

Original motif Consensus sequence: AGAAATG



Reverse complement motif Consensus sequence: CATTTCT



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

Original motif Consensus sequence: TTTAAA



Reverse complement motif Consensus sequence: TTTAAA



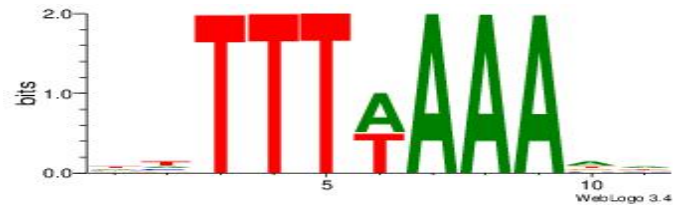
Best Matches for Motif ID 55 (Highest to Lowest)

Dataset #:	4
Motif ID:	120
Motif name:	wtTTTwAAAaw
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	3

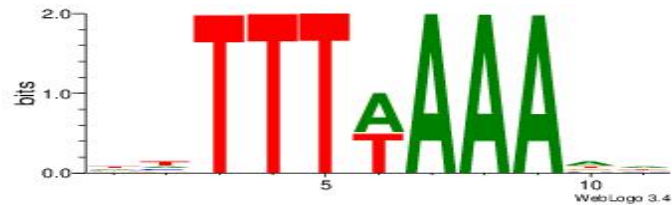
Number of overlap: 7
Similarity score: 0.00286145

Alignment:
HHTTTWAAADD
--TTTAAAA--

Original motif Consensus sequence: HHTTTWAAADD



Reverse complement motif Consensus sequence: DDTTTWAAAHH

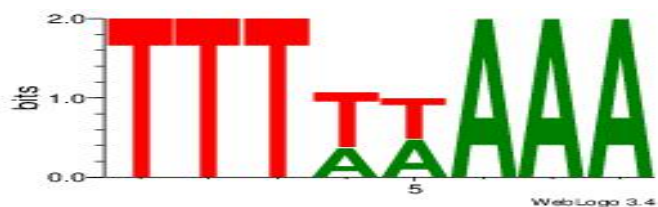


Dataset #: 1
Motif ID: 9
Motif name: Motif 9
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 7
Similarity score: 0.0142562

Alignment:
TTTWAAAA
-TTTAAAA

Original motif Consensus sequence: TTTWAAAA

Reverse complement motif Consensus sequence: TTTWAAAA



Dataset #: 4
 Motif ID: 91
 Motif name: wtATTTTaww
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 7
 Similarity score: 0.036821

Alignment:

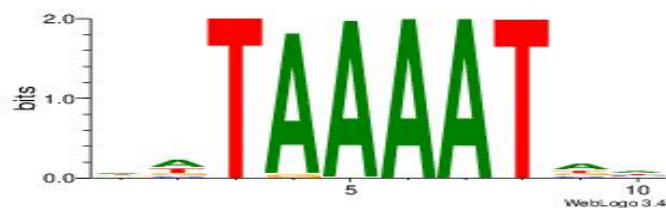
HWTAAAATHD

TTTAAAA---

Original motif Consensus sequence: DHATTTTAWH



Reverse complement motif Consensus sequence: HWTAAAATHD



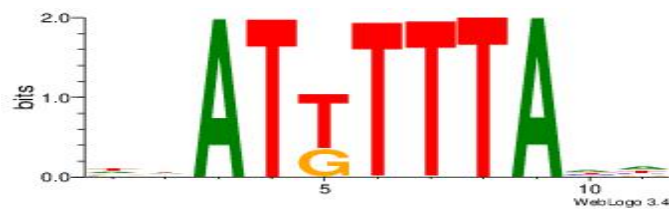
Dataset #: 4
 Motif ID: 108

Motif name: wwATkTTTAww
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 7
 Similarity score: 0.0428268

Alignment:

DHATKTTTAHH
 ----TTTTAAA

Original motif Consensus sequence: DHATKTTTAHH



Reverse complement motif Consensus sequence: HHTAAARATHD



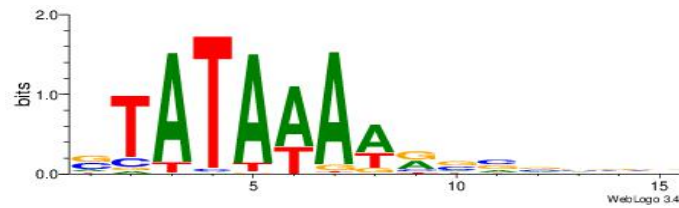
Dataset #: 3
 Motif ID: 62
 Motif name: TBP
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 8
 Number of overlap: 7
 Similarity score: 0.058454

Alignment:

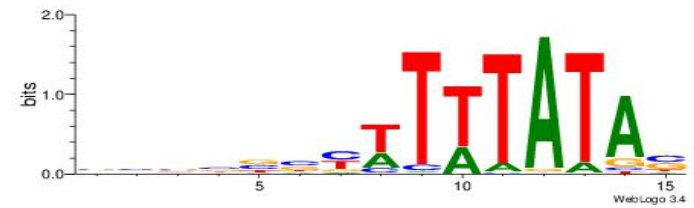
VBVVVVMWTTTATAS

-----TTTAAA-

Original motif Consensus sequence: STATAAWRVVVVBV



Reverse complement motif Consensus sequence: VBVVVVMWTTTAT



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

Original motif Consensus sequence: CACGGA



Reverse complement motif Consensus sequence: TCCGTG



Best Matches for Motif ID 56 (Highest to Lowest)

Dataset #:	4
Motif ID:	127
Motif name:	rryCAGGGAyw
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	3

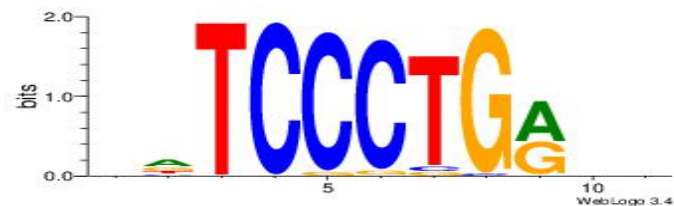
Number of overlap: 6
Similarity score: 0.0151346

Alignment:
DDYCAGGGAHD
---CACGGA--

Original motif Consensus sequence: DDYCAGGGAHD



Reverse complement motif Consensus sequence: DHTCCCTGMDD



Dataset #: 1
Motif ID: 7
Motif name: Motif 7
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 6
Similarity score: 0.0281094

Alignment:
CACASASA
CACGGA--

Original motif Consensus sequence: CACASASA

Reverse complement motif Consensus sequence: TSTSTGTG



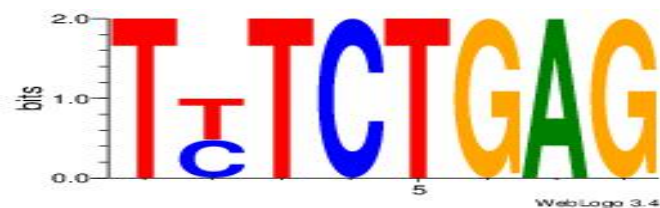
Dataset #: 1
 Motif ID: 41
 Motif name: Motif 41
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 6
 Similarity score: 0.051968

Alignment:
 TKTCTGAG
 --TCCGTG

Original motif Consensus sequence: CTCAGARA



Reverse complement motif Consensus sequence: TKTCTGAG



Dataset #: 1
 Motif ID: 19

Motif name:	Motif 19
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	6
Similarity score:	0.051968

Alignment:
CCTGGARC
CACGGA--

Original motif Consensus sequence: CCTGGARC



Reverse complement motif Consensus sequence: GKTCCAGG



Dataset #:	2
Motif ID:	53
Motif name:	Motif 53
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	6
Similarity score:	0.0528198

Alignment:

TSTGTR

TCCGTG

Original motif Consensus sequence: TSTGTR



Reverse complement motif Consensus sequence: MACASA



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

Original motif Consensus sequence: SAGGAA



Reverse complement motif Consensus sequence: TTCCTS



Best Matches for Motif ID 57 (Highest to Lowest)

Dataset #:	1
Motif ID:	30
Motif name:	Motif 30
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	3

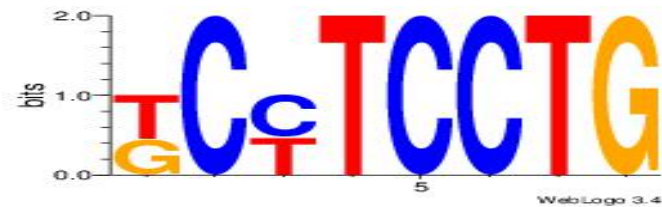
Number of overlap: 6
Similarity score: 0.0409967

Alignment:
CAGGARGM
SAGGAA--

Original motif Consensus sequence: CAGGARGM



Reverse complement motif Consensus sequence: YCMTCCCTG

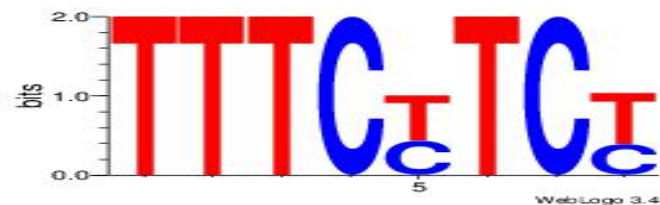


Dataset #: 1
Motif ID: 26
Motif name: Motif 26
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 2
Number of overlap: 6
Similarity score: 0.0466104

Alignment:
RGARGAAA
-SAGGAA-

Original motif Consensus sequence: RGARGAAA

Reverse complement motif Consensus sequence: TTTCKTCK



Dataset #: 1
 Motif ID: 28
 Motif name: Motif 28
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 6
 Similarity score: 0.0548389

Alignment:
 TTTCTVT
 TTCCTS-

Original motif Consensus sequence: AVAGAAA



Reverse complement motif Consensus sequence: TTTCTVT



Dataset #: 1
 Motif ID: 27

Motif name:	Motif 27
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	2
Number of overlap:	6
Similarity score:	0.0627861

Alignment:
KRAGGCAG
-SAGGAA-

Original motif Consensus sequence: CTGCCTKY



Reverse complement motif Consensus sequence: KRAGGCAG



Dataset #:	1
Motif ID:	4
Motif name:	Motif 4
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	6
Similarity score:	0.0659124

Alignment:
GAGRMAGR
SAGGAA--

Original motif Consensus sequence: GAGRMAGR

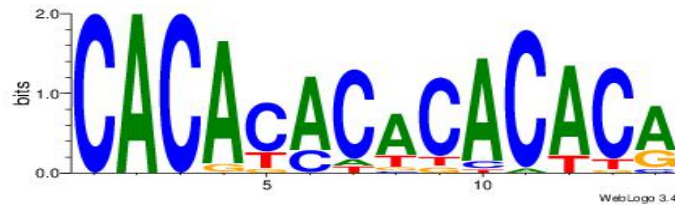


Reverse complement motif Consensus sequence: KCTRMCTC

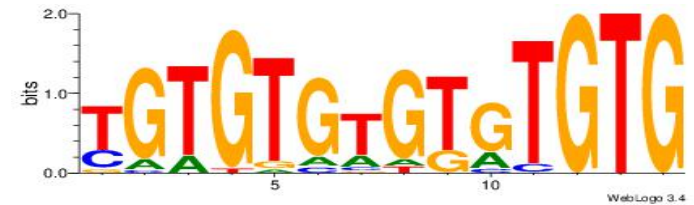


Dataset #: 2 Motif ID: 58 Motif name: Motif 58

Original motif Consensus sequence: CACACACACACA



Reverse complement motif Consensus sequence: TGTGTGTGTGT



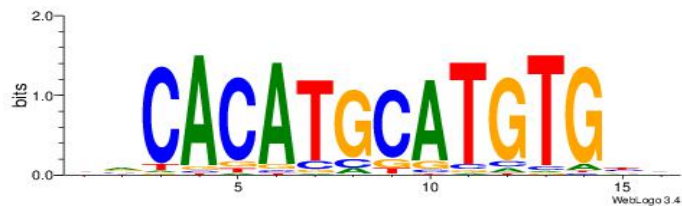
Best Matches for Motif ID 58 (Highest to Lowest)

Dataset #:	4
Motif ID:	118
Motif name:	yrCACATGCATGTGyr
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	3

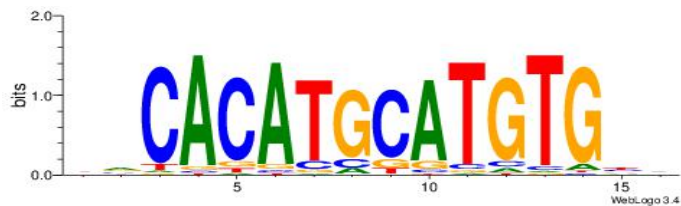
Number of overlap: 14
Similarity score: 0.0942589

Alignment:
HVCACATGCATGTGBD
--CACACACACACACA

Original motif Consensus sequence: HVCACATGCATGTGBD



Reverse complement motif Consensus sequence:
DVCACATGCATGTGBH

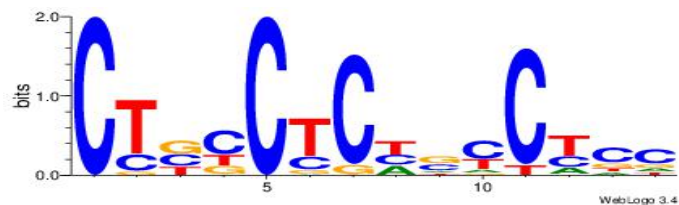


Dataset #: 2
Motif ID: 59
Motif name: Motif 59
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 14
Similarity score: 0.0950431

Alignment:
GGMGKSHGAGGBAG
TGTGTGTGTGTGTG

Original motif Consensus sequence: CTBCCTCHSYCYCC

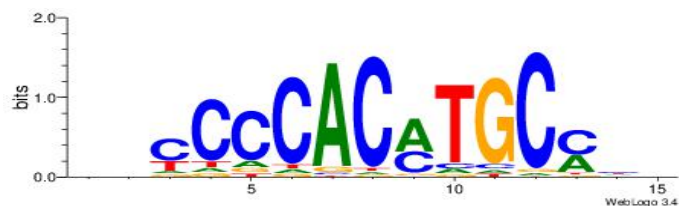
Reverse complement motif Consensus sequence: GGMGKSHGAGGB



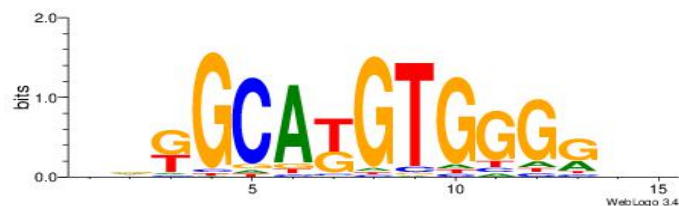
Dataset #: 4
 Motif ID: 98
 Motif name: myyCCCACmTGCmyr
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0.0967648

Alignment:
 HBCCCCACMTGCMHV
 -CACACACACACACA

Original motif Consensus sequence: HBCCCCACMTGCMHV



Reverse complement motif Consensus sequence: VDRGCAYGTGGGGVD



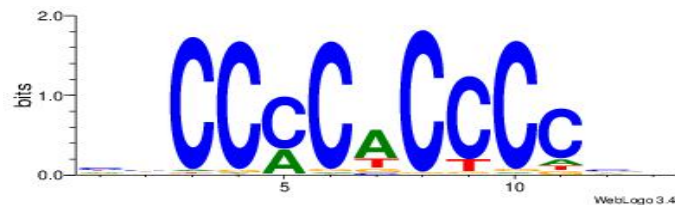
Dataset #: 4

Motif ID: 111
 Motif name: ccCCmCaCCCCcc
 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: 0.595051

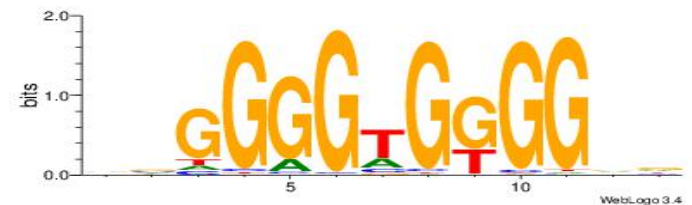
Alignment:

-HBCCCCACCCCBH
 CACACACACACA

Original motif Consensus sequence: HBCCCCACCCCBH



Reverse complement motif Consensus sequence: DBGGGGTGGGGB

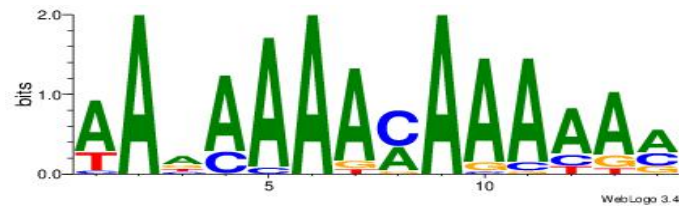


Dataset #: 2
 Motif ID: 60
 Motif name: Motif 60
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 13
 Similarity score: 0.597407

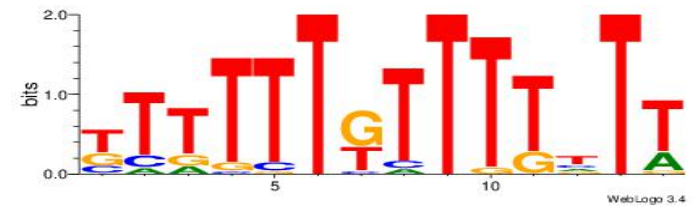
Alignment:

-AADAAAAMAAAAAM
CACACACACACACA-

Original motif Consensus sequence: AADAAAAMAAAAAM

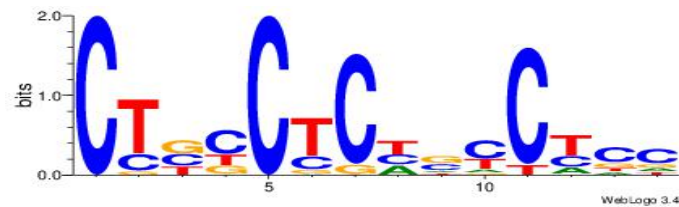


Reverse complement motif Consensus sequence: YTTTTTRTTTDTT



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

Original motif Consensus sequence: CTBCCTCHSYCYCC



Reverse complement motif Consensus sequence: GGMGKSHGAGGB



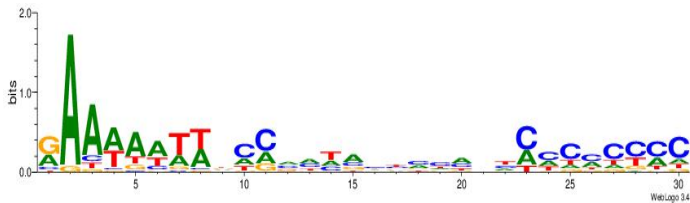
Best Matches for Motif ID 59 (Highest to Lowest)

Dataset #:	3
Motif ID:	81
Motif name:	Pax4
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	13

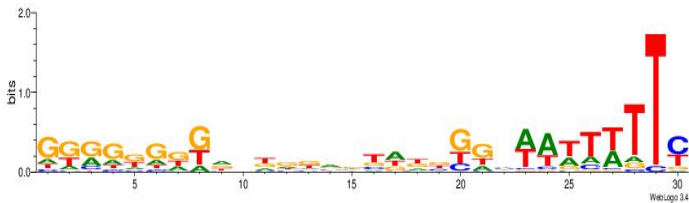
Number of overlap: 14
Similarity score: 0.0440476

Alignment:
RAAWAWTWDCMVHHVBBHHHVHMHCMCYMC
-----CTBCCTCHSYCYCC-----

Original motif Consensus sequence:
RAAWAWTWDCMVHHVBBHHHVHMHCMCYMC



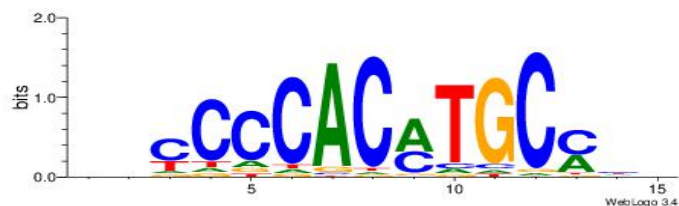
Reverse complement motif Consensus sequence:
GRKGRGDRHVHDDVBBHHBRGDWAWTWTTM



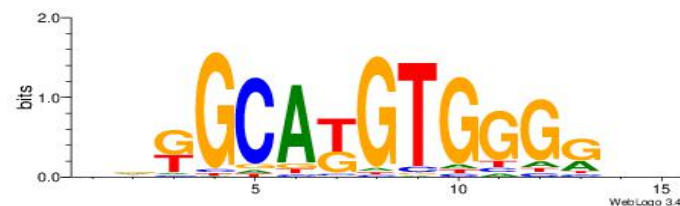
Dataset #: 4
Motif ID: 98
Motif name: myyCCCACmTGCmyr
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 14
Similarity score: 0.064469

Alignment:
HBCCCCACMTGCMHV
-CTBCCTCHSYCYCC

Original motif Consensus sequence: HBCCCCACMTGCMHV



Reverse complement motif Consensus sequence: VDRGCAYGTGGGGVD

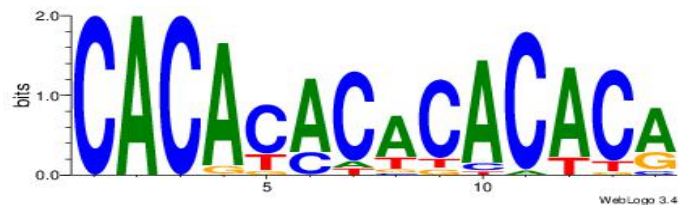


Dataset #: 2
Motif ID: 58
Motif name: Motif 58
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 14
Similarity score: 0.0727936

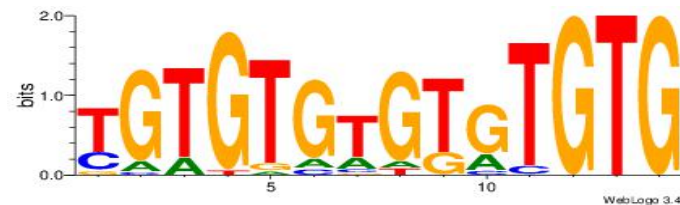
Alignment:

TGTGTGTGTGTGTG
GGMGKSHGAGGBAG

Original motif Consensus sequence: CACACACACACACA



Reverse complement motif Consensus sequence: TGTGTGTGTGTGTG

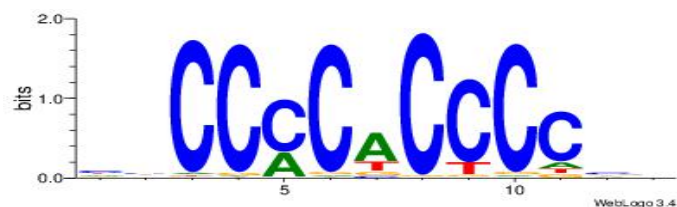


Dataset #: 4
 Motif ID: 111
 Motif name: ccCCmCaCCCCcc
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 13
 Similarity score: 0.53768

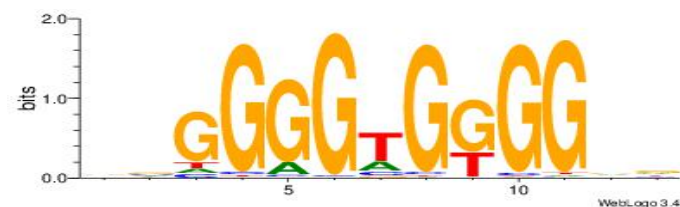
Alignment:

-HBCCCCACCCCBH
 CTBCCTCHSYCYCC

Original motif Consensus sequence: HBCCCCACCCCBH



Reverse complement motif Consensus sequence: DBGGGGTGGGGB

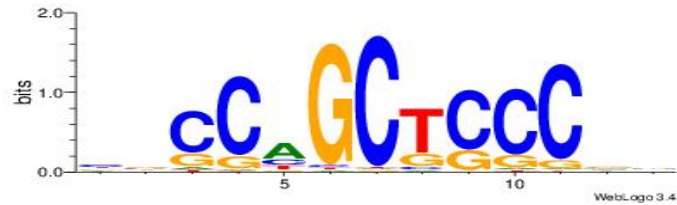


Dataset #: 4
 Motif ID: 103
 Motif name: csCCaGCTCCCgs
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 13

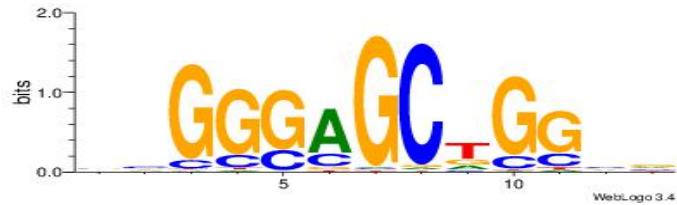
Similarity score: 0.558794

Alignment:
-BVGGGAGCTGGBB
GGMGKSHGAGGBAG

Original motif Consensus sequence: BBCCAGCTCCCVB

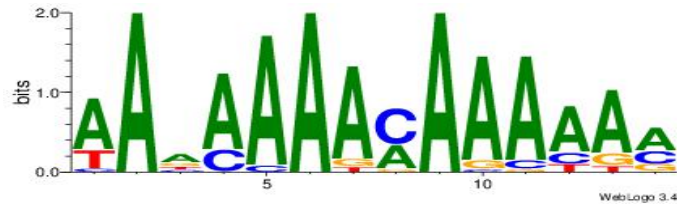


Reverse complement motif Consensus sequence: BVGGGAGCTGGBB

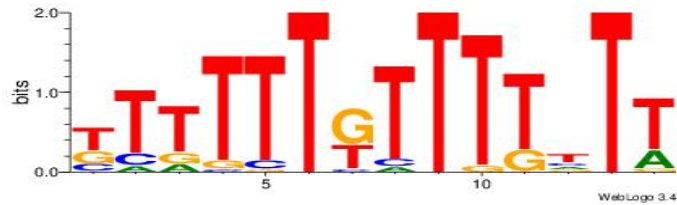


Dataset #: 2 Motif ID: 60 Motif name: Motif 60

Original motif Consensus sequence: AADAAAAMAAAAAM



Reverse complement motif Consensus sequence: YTTTTTRTTTDTT



Best Matches for Motif ID 60 (Highest to Lowest)

Dataset #:	3
Motif ID:	71
Motif name:	Evi1
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward

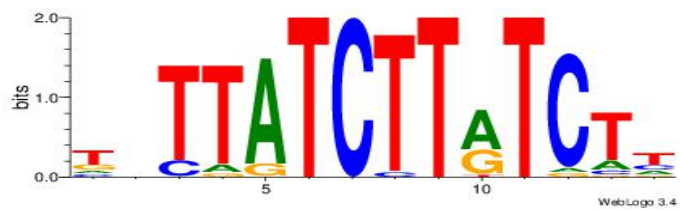
Position number: 1
Number of overlap: 14
Similarity score: 0.0695286

Alignment:
AAGAYAAGATAABA
AADAAAAMAAAAAM

Original motif Consensus sequence: AAGAYAAGATAABA



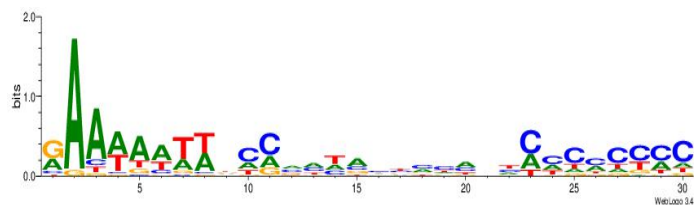
Reverse complement motif Consensus sequence: TBTTATCTTMTCTT



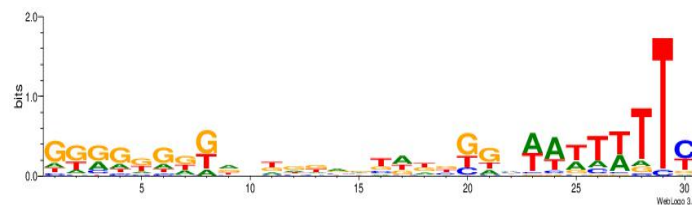
Dataset #: 3
Motif ID: 81
Motif name: Pax4
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 15
Number of overlap: 14
Similarity score: 0.0795461

Alignment:
RAAWAWTWDCMVHHVBBHHHVHMHCMCYMC
--AADAAAAMAAAAAM-----

Original motif Consensus sequence:
RAAWAWTWDCMVHHVBBHHHVHMHCMCYMC



Reverse complement motif Consensus sequence:
GRKGRGDRHVDHDDVBBHHBRGDWAWTWTTM

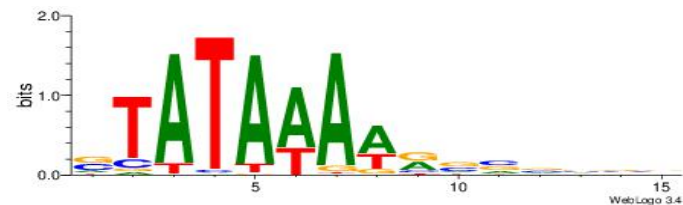


Dataset #: 3
Motif ID: 62
Motif name: TBP
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 14
Similarity score: 0.0901534

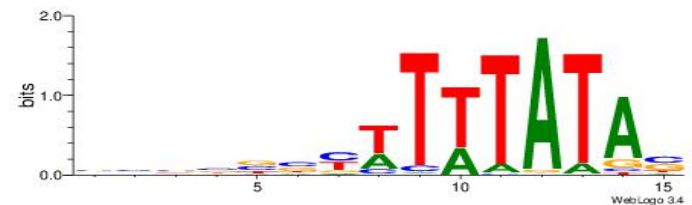
Alignment:

STATAAAWRVVVBV
-AADAAAAMAAAAM

Original motif Consensus sequence: STATAAAWRVVVBV



Reverse complement motif Consensus sequence: VBVVVMWTTTAT

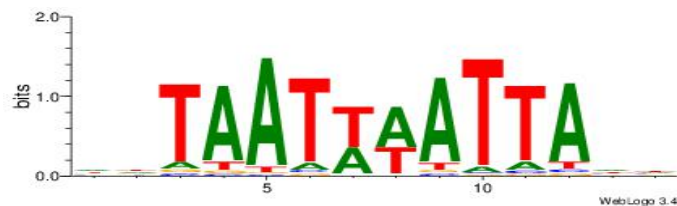


Dataset #: 4
 Motif ID: 125
 Motif name: wwTAATwwATTaww
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0.0954049

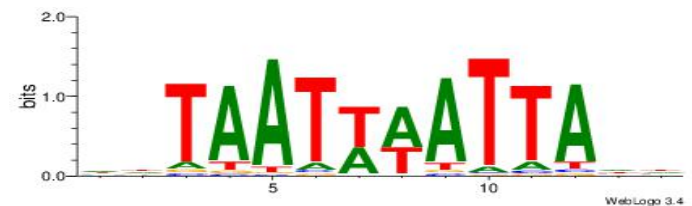
Alignment:

DDTAATWWATTAAHH
 AADAAAAMAAAAAM

Original motif Consensus sequence: DDTAATWWATTAAHH



Reverse complement motif Consensus sequence: HHTAATWWATTAAHH



Dataset #: 3
 Motif ID: 75
 Motif name: FOXF2
 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: 0.0959909

Alignment:
BHADSGTAAACAAD
AADAAAAMAAAAAM

Original motif Consensus sequence: BHADSGTAAACAAD

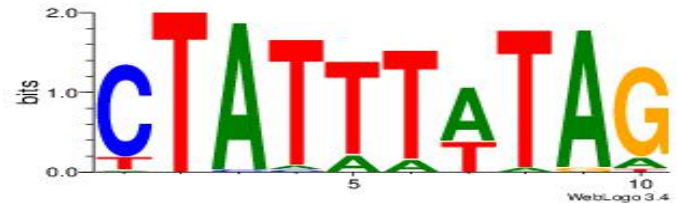


Reverse complement motif Consensus sequence: DTTGTTTACSBTBB



Dataset #: 3 Motif ID: 61 Motif name: MEF2A

Original motif Consensus sequence: CTATTTWTAG



Reverse complement motif Consensus sequence: CTAWAAATAG



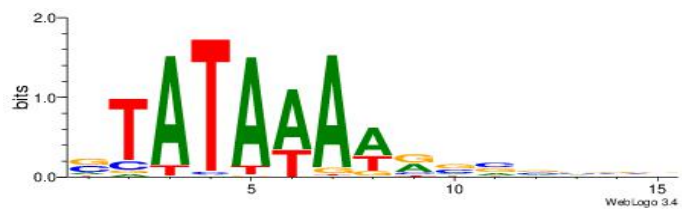
Best Matches for Motif ID 61 (Highest to Lowest)

Dataset #:	3
Motif ID:	62
Motif name:	TBP
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward

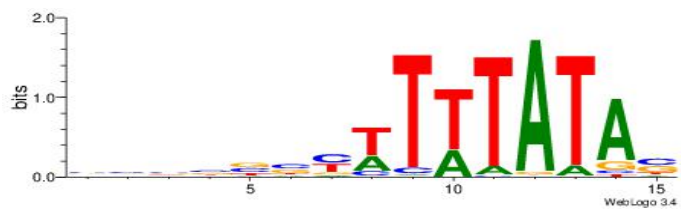
Position number: 6
Number of overlap: 10
Similarity score: 0.0368263

Alignment:
STATAAAWRVVVBV
CTAWAAATAG-----

Original motif Consensus sequence: STATAAAWRVVVBV



Reverse complement motif Consensus sequence: VBVVVMMWTTTAT

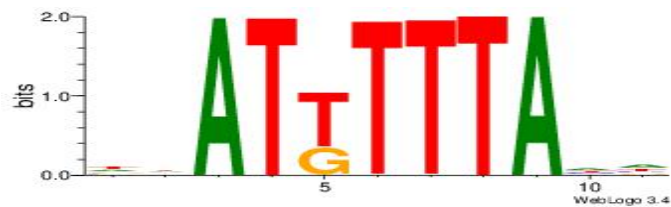


Dataset #: 4
Motif ID: 108
Motif name: wwATkTTTAww
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 2
Number of overlap: 10
Similarity score: 0.0401238

Alignment:
HHTAAARATHD
-CTAWAAATAG

Original motif Consensus sequence: DHATKTTTAHH

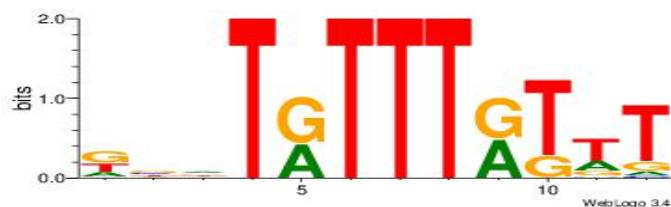
Reverse complement motif Consensus sequence: HHTAAARATHD



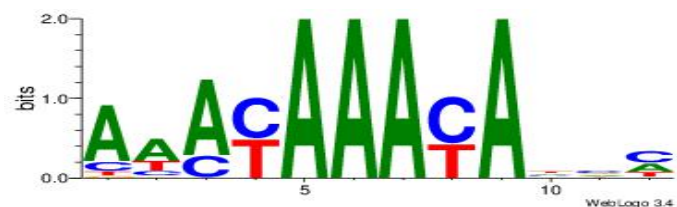
Dataset #: 3
 Motif ID: 67
 Motif name: FOXI1
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 10
 Similarity score: 0.056188

Alignment:
 KBDTRTTTTRTTT
 --CTATTTWTAG

Original motif Consensus sequence: KBDTRTTTTRTTT



Reverse complement motif Consensus sequence: AAAMAAAMADBY



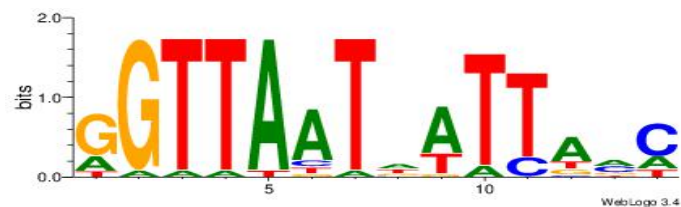
Dataset #: 3

Motif ID: 68
 Motif name: HNF1A
 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: 0.0684894

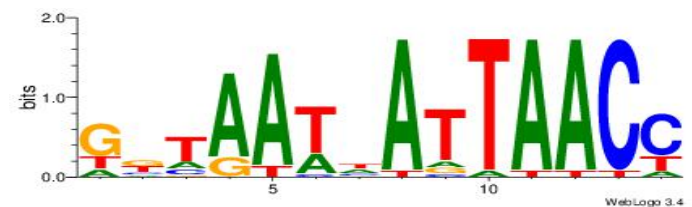
Alignment:

GGTTAATDATTAMC
 --CTATTTWTAG--

Original motif Consensus sequence: GGTTAATDATTAMC



Reverse complement motif Consensus sequence: GYTAATDATTAAC



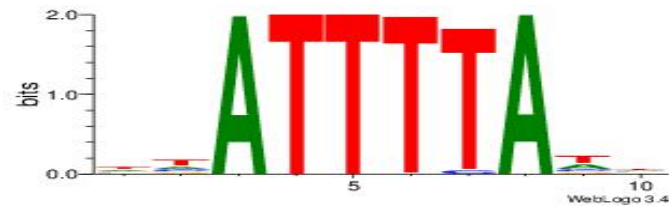
Dataset #: 4
 Motif ID: 91
 Motif name: wtATTTTAWW
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 10
 Similarity score: 0.0714984

Alignment:

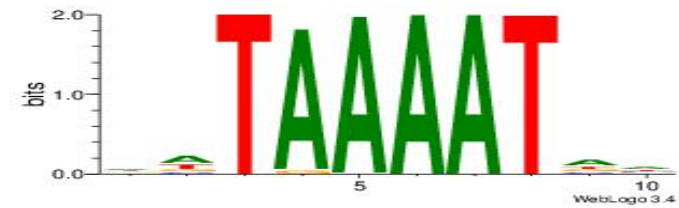
HWTAAAATHD

CTAWAAATAG

Original motif Consensus sequence: DHATTTTAWH



Reverse complement motif Consensus sequence: HWTAAAATHD

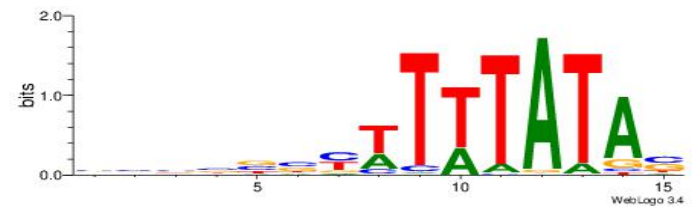


Dataset #: 3 Motif ID: 62 Motif name: TBP

Original motif Consensus sequence: STATAAWRVVVVBV



Reverse complement motif Consensus sequence: VBVVVVMWTTTAT



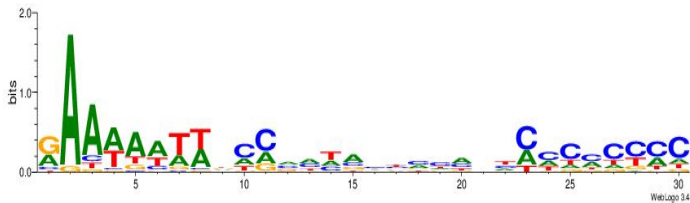
Best Matches for Motif ID 62 (Highest to Lowest)

Dataset #:	3
Motif ID:	81
Motif name:	Pax4
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1

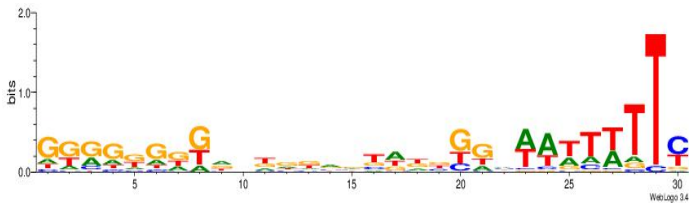
Number of overlap: 15
Similarity score: 0.050528

Alignment:
RAAWAWTWDCMVHHVBBHHHVHMHCMCYMC
STATAAAWRVVVVBV-----

Original motif Consensus sequence:
RAAWAWTWDCMVHHVBBHHHVHMHCMCYMC



Reverse complement motif Consensus sequence:
GRKGRGDRHVHDDVBBHHBRGDWAWTWTTM

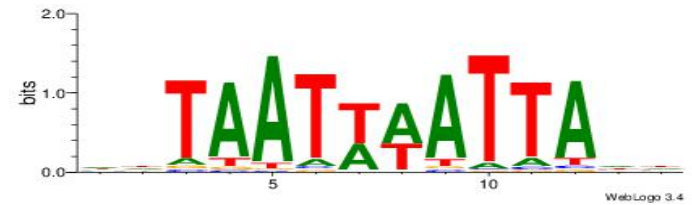
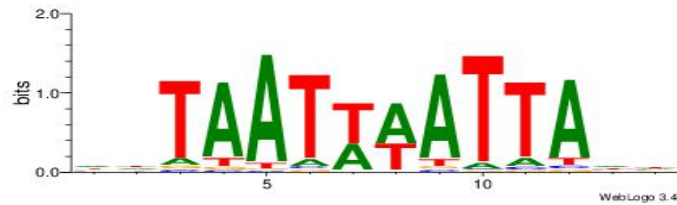


Dataset #: 4
Motif ID: 125
Motif name: wwTAATwwATTaww
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 14
Similarity score: 0.581919

Alignment:
DDTAATWWATTAAH-
VBVVVVMWTTTATAS

Original motif Consensus sequence: DDTAATWWATTAAH

Reverse complement motif Consensus sequence: HHTAATWWATTAAH

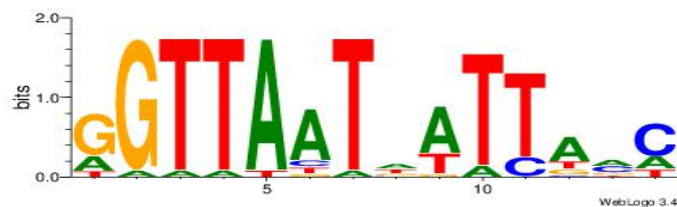


Dataset #: 3
 Motif ID: 68
 Motif name: HNF1A
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0.583461

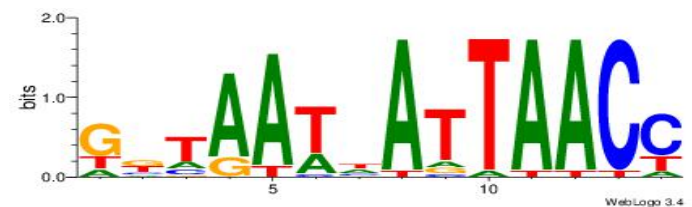
Alignment:

-GYTAATDATTAAACC
 VBVVVVMWTTTATAS

Original motif Consensus sequence: GGTTAATDATTAMC



Reverse complement motif Consensus sequence: GYTAATDATTAAACC



Dataset #: 2
 Motif ID: 60

Motif name:	Motif 60
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	14
Similarity score:	0.58354

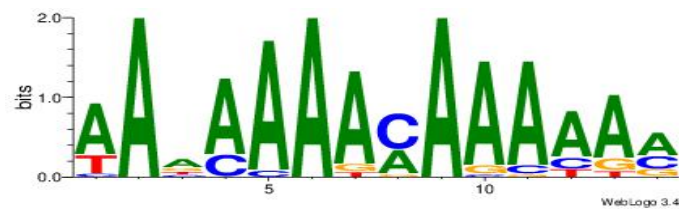
Alignment:

```

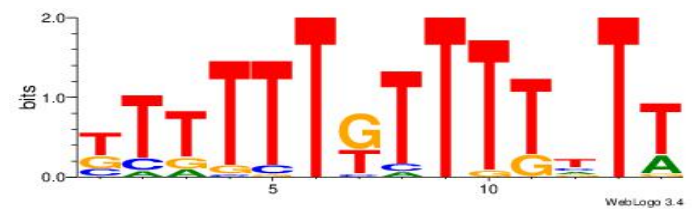
-AADAAAAMAAAAAM
STATAAAWRVVVBV

```

Original motif Consensus sequence: AADAAAAMAAAAAM



Reverse complement motif Consensus sequence: YTTTTTRTTTTDTT

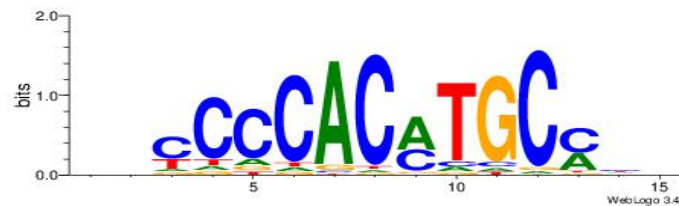


Dataset #:	4
Motif ID:	98
Motif name:	myyCCCACmTGCmyr
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2
Number of overlap:	14
Similarity score:	0.587864

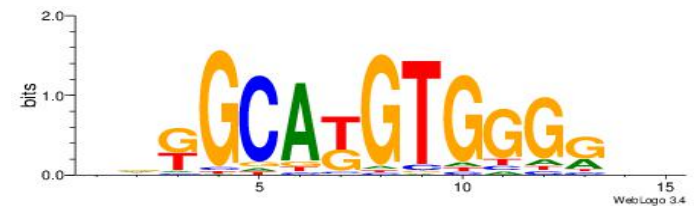
Alignment:

-HBCCCCACMTGCMHV
VBVVVVMWTTTATAS-

Original motif Consensus sequence: HBCCCCACMTGCMHV

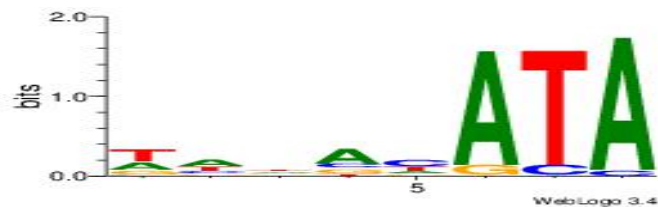


Reverse complement motif Consensus sequence: VDRGCAYGTGGGGVD

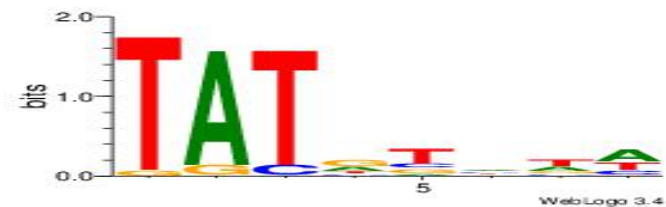


Dataset #: 3 Motif ID: 63 Motif name: FOXL1

Original motif Consensus sequence: WHDAHATA



Reverse complement motif Consensus sequence: TATDTHW



Best Matches for Motif ID 63 (Highest to Lowest)

Dataset #:	3
Motif ID:	75
Motif name:	FOXF2
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward

Position number: 7
Number of overlap: 8
Similarity score: 0.0287322

Alignment:
BHADSGTAAACAAD
WHDAAHATA-----

Original motif Consensus sequence: BHADSGTAAACAAD



Reverse complement motif Consensus sequence: DTTGTTTACSBTBB

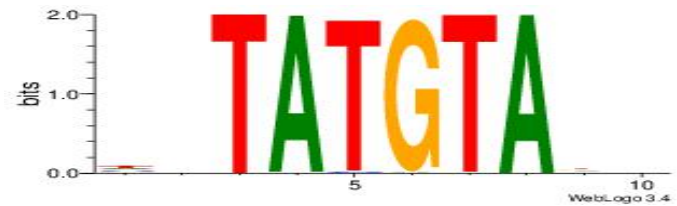


Dataset #: 4
Motif ID: 90
Motif name: ymTACATAw
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 3
Number of overlap: 8
Similarity score: 0.0294054

Alignment:
DBTATGTAHH
--TATDTHW

Original motif Consensus sequence: HHTACATABD

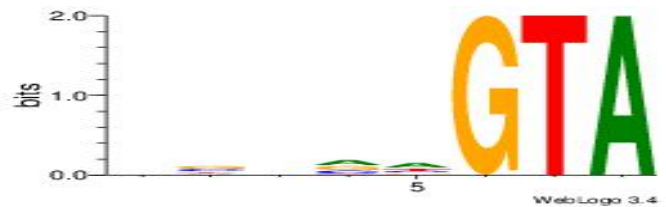
Reverse complement motif Consensus sequence: DBTATGTAHH



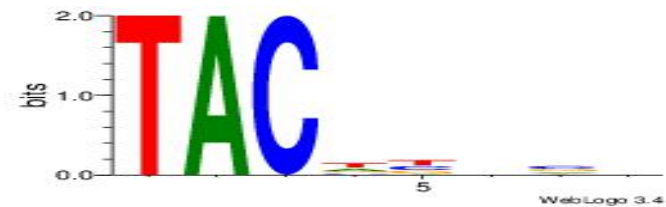
Dataset #: 3
 Motif ID: 74
 Motif name: FOXC1
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 8
 Similarity score: 0.036287

Alignment:
 VBHVHGTA
 WHDAHATA

Original motif Consensus sequence: VBHVHGTA



Reverse complement motif Consensus sequence: TACHBHBV



Dataset #: 3

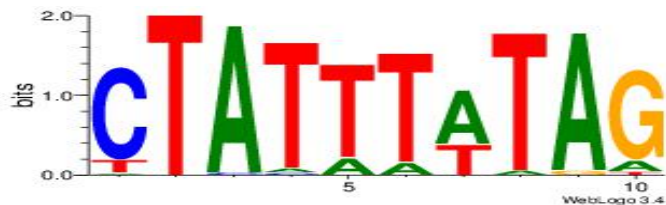
Motif ID:	61
Motif name:	MEF2A
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	2
Number of overlap:	8
Similarity score:	0.0377453

Alignment:

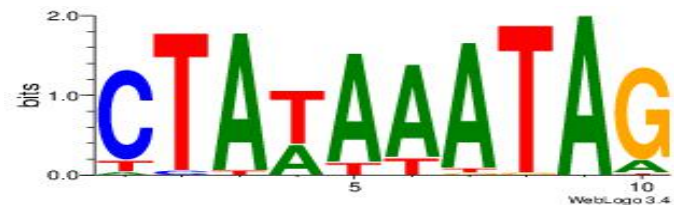
CTAWAAATAG

-WHDAHATA-

Original motif Consensus sequence: CTATTTWTAG



Reverse complement motif Consensus sequence: CTAWAAATAG



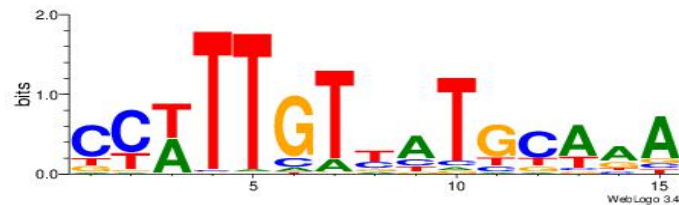
Dataset #:	3
Motif ID:	76
Motif name:	Sox2
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	8
Similarity score:	0.0399271

Alignment:

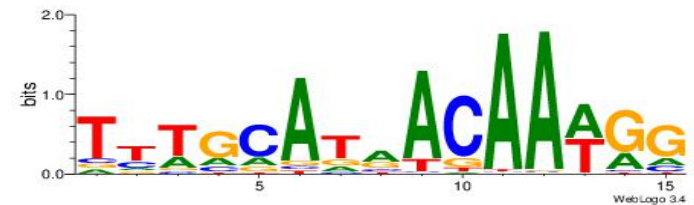
CCWTTGTYATGCAAA

-----TATDTHW

Original motif Consensus sequence: CCWTTGTYATGCAAA



Reverse complement motif Consensus sequence: TTTGCATMACAAWGG



Dataset #: 3 Motif ID: 64 Motif name: ARID3A

Original motif Consensus sequence: ATYAAA



Reverse complement motif Consensus sequence: TTTMAT



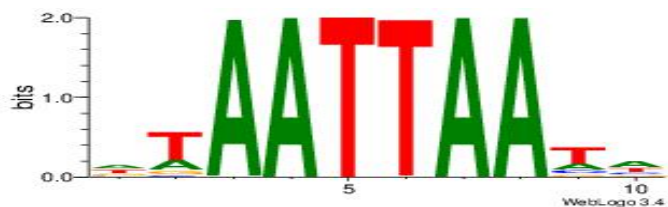
Best Matches for Motif ID 64 (Highest to Lowest)

Dataset #:	4
Motif ID:	106
Motif name:	wtAATTAAtw
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward

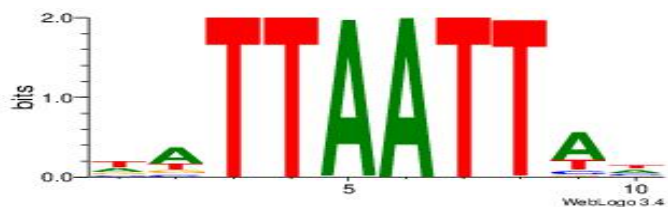
Position number: 4
Number of overlap: 6
Similarity score: 0.0114914

Alignment:
DTAATTAATH
---ATYAAA-

Original motif Consensus sequence: DTAATTAATH



Reverse complement motif Consensus sequence: HATTAATTAD



Dataset #: 1
Motif ID: 20
Motif name: Motif 20
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 6
Similarity score: 0.015396

Alignment:
ATTAMAGG
ATYAAA--

Original motif Consensus sequence: ATTAMAGG

Reverse complement motif Consensus sequence: CCTYTAAT

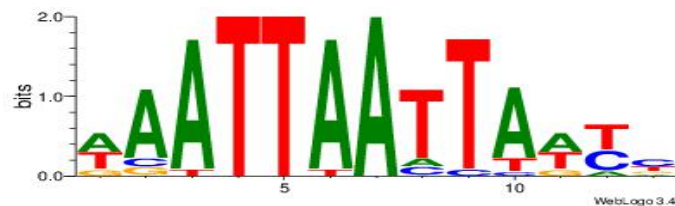


Dataset #: 3
 Motif ID: 66
 Motif name: Lhx3
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 6
 Number of overlap: 6
 Similarity score: 0.0225727

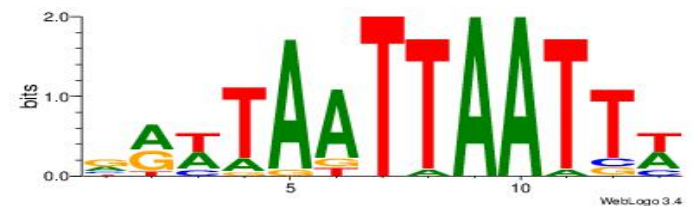
Alignment:

BMWTAATTAATTW
 -----TTMAT--

Original motif Consensus sequence: WAATTAATTAWYB



Reverse complement motif Consensus sequence: BMWTAATTAATTW



Dataset #: 1

Motif ID: 49
 Motif name: Motif 49
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 6
 Similarity score: 0.0340365

Alignment:
 AGATAAAR
 --ATYAAA

Original motif Consensus sequence: AGATAAAR



Reverse complement motif Consensus sequence: KTTTATCT



Dataset #: 1
 Motif ID: 25
 Motif name: Motif 25
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 6
 Similarity score: 0.0368439

Alignment:

WWTAAA

ATYAAA

Original motif Consensus sequence: TTTAWW

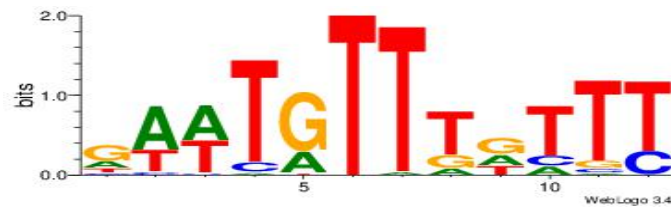


Reverse complement motif Consensus sequence: WWTAAA

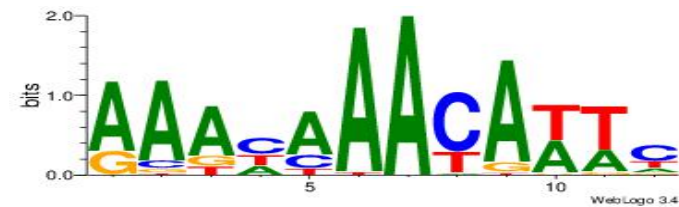


Dataset #: 3 Motif ID: 65 Motif name: Foxd3

Original motif Consensus sequence: GAWTGTTTDTTT



Reverse complement motif Consensus sequence: AAAHAAACAWTC



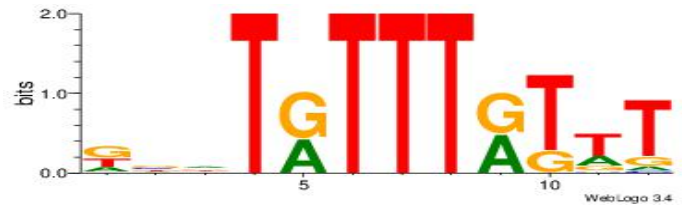
Best Matches for Motif ID 65 (Highest to Lowest)

Dataset #:	3
Motif ID:	67
Motif name:	FOX11
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1

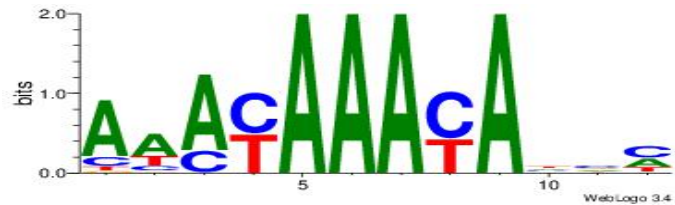
Number of overlap: 12
Similarity score: 0.00335618

Alignment:
AAAMAAAMADBY
AAAHAAACAWTC

Original motif Consensus sequence: KBDTRTTTTRTTT



Reverse complement motif Consensus sequence: AAAMAAAMADBY

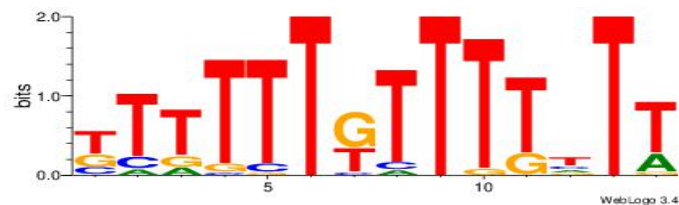
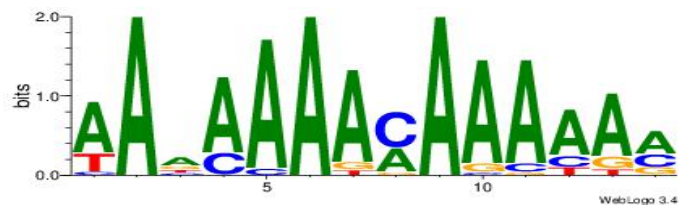


Dataset #: 2
Motif ID: 60
Motif name: Motif 60
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 12
Similarity score: 0.0177558

Alignment:
YTTTTTRTTTDTT
GAWTGTTTDTT--

Original motif Consensus sequence: AADAAAAMAAAAAM

Reverse complement motif Consensus sequence: YTTTTTRTTTDTT



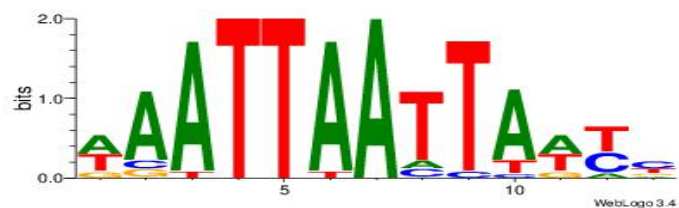
Dataset #: 3
 Motif ID: 66
 Motif name: Lhx3
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 12
 Similarity score: 0.0424677

Alignment:

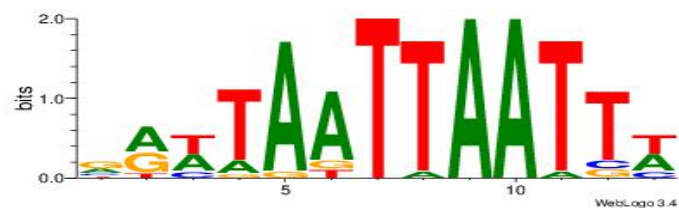
BMWTAATTAATTW

GAWTGTTTDTTT-

Original motif Consensus sequence: WAATTAATTAWYB



Reverse complement motif Consensus sequence: BMWTAATTAATTW



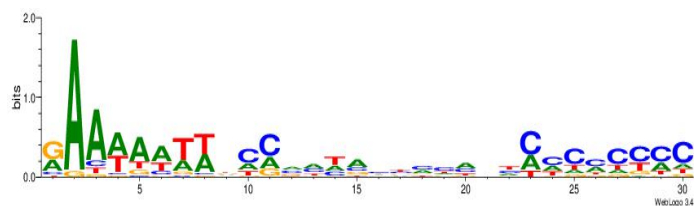
Dataset #: 3
 Motif ID: 81

Motif name:	Pax4
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	16
Number of overlap:	12
Similarity score:	0.0493847

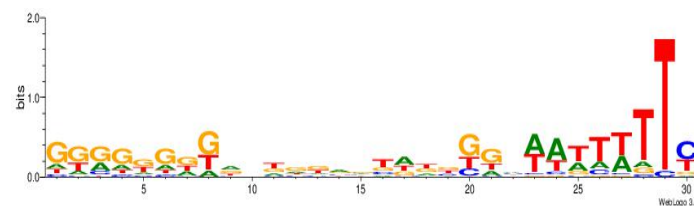
Alignment:

```
RAAWAWTWDCMVHHVBBHHHVHMHCMCYMC
---AAAHAAACAWTC-----
```

Original motif Consensus sequence:
RAAWAWTWDCMVHHVBBHHHVHMHCMCYMC



Reverse complement motif Consensus sequence:
GRKGRGDRHVDDBBHHBRGDWAWTWTTM



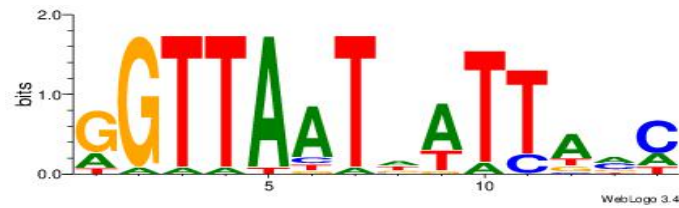
Dataset #:	3
Motif ID:	68
Motif name:	HNF1A
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	3
Number of overlap:	12
Similarity score:	0.0526352

Alignment:

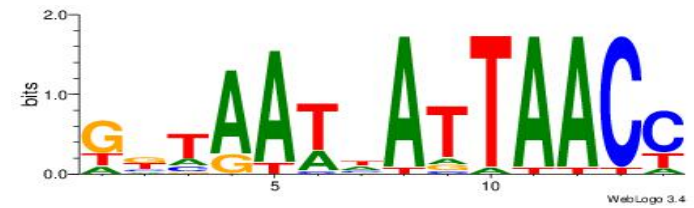
GGTTAATDATTAMC

GAWTGTTTDTTT--

Original motif Consensus sequence: GGTTAATDATTAMC

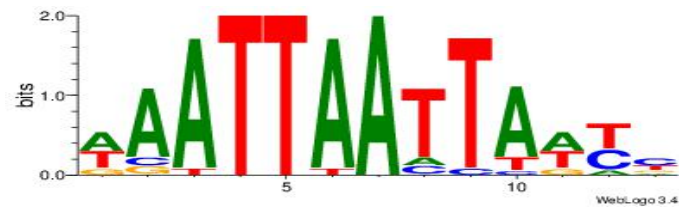


Reverse complement motif Consensus sequence: GYTAATDATTAAAC

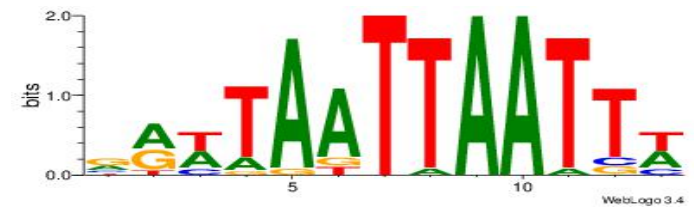


Dataset #: 3 Motif ID: 66 Motif name: Lhx3

Original motif Consensus sequence: WAATTAATTAWYB



Reverse complement motif Consensus sequence: BMWTAATTAATTW



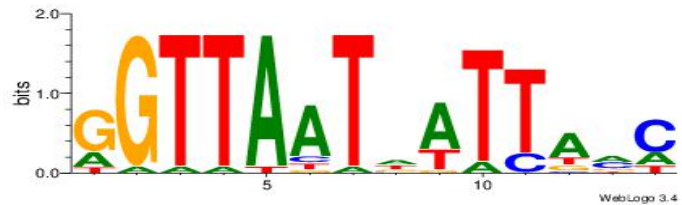
Best Matches for Motif ID 66 (Highest to Lowest)

Dataset #:	3
Motif ID:	68
Motif name:	HNF1A
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1

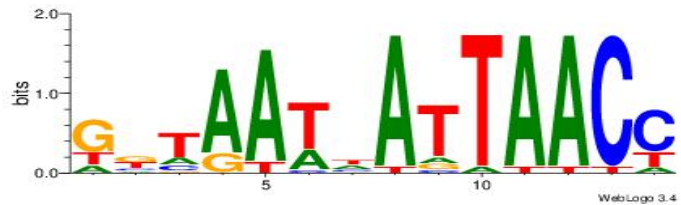
Number of overlap: 13
Similarity score: 0.0814534

Alignment:
GYTAATDATTAAACC
-WAATTAATTAWYB

Original motif Consensus sequence: GGTTAATDATTAMC



Reverse complement motif Consensus sequence: GYTAATDATTAAACC

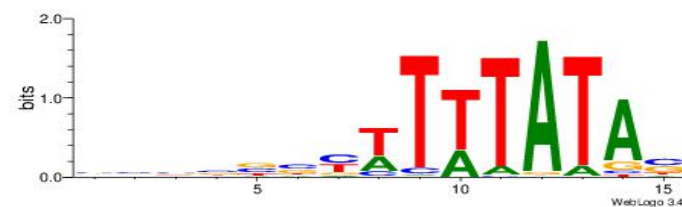


Dataset #: 3
Motif ID: 62
Motif name: TBP
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 3
Number of overlap: 13
Similarity score: 0.100645

Alignment:
VBVVVVMWTTTATAS
--BMWTAATTAATTW

Original motif Consensus sequence: STATAAWRVVVVBV

Reverse complement motif Consensus sequence: VBVVVVMWTTTAT



Alignment:

```
TBTTATCTTMTCTT
BMWTAATTAATTW-
```

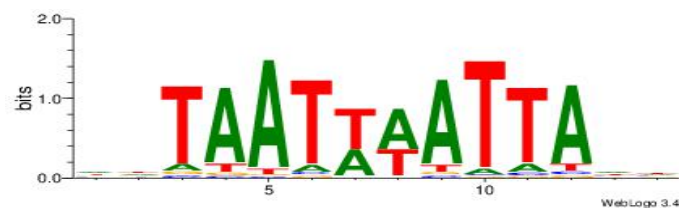
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Motif name: wwTAATwwATTaww
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 13
 Similarity score: 0.102843

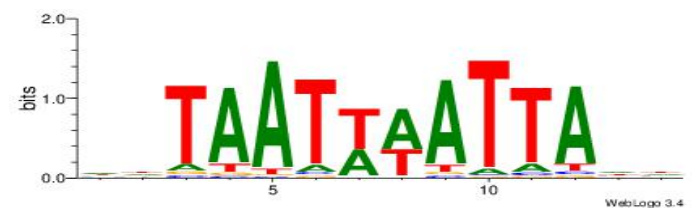
Alignment:

DDTAATWWATTAAHH
 -WAATTAATTAWYB

Original motif Consensus sequence: DDTAATWWATTAAHH



Reverse complement motif Consensus sequence: HHTAATWWATTAA



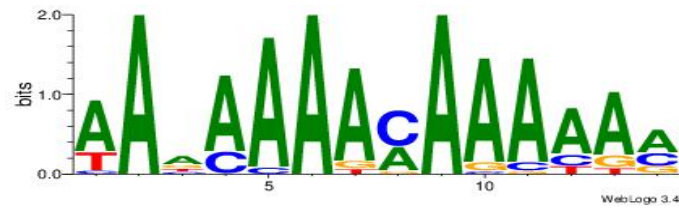
Dataset #: 2
 Motif ID: 60
 Motif name: Motif 60
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 13
 Similarity score: 0.106545

Alignment:

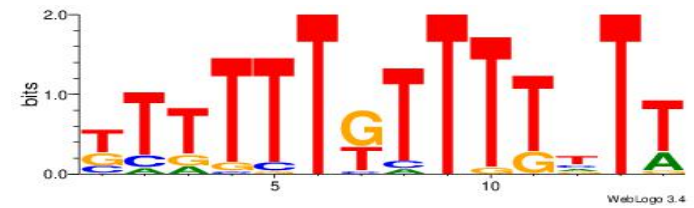
AADAAAAMAAAAAM

-BMWTAATTAATTW

Original motif Consensus sequence: AADAAAAMAAAAAM

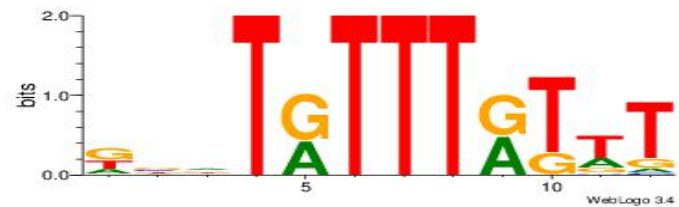


Reverse complement motif Consensus sequence: YTTTTTRTTTDTT



Dataset #: 3 Motif ID: 67 Motif name: FOXI1

Original motif Consensus sequence: KBDTRTTTTRTT



Reverse complement motif Consensus sequence: AAAMAAAMADBY



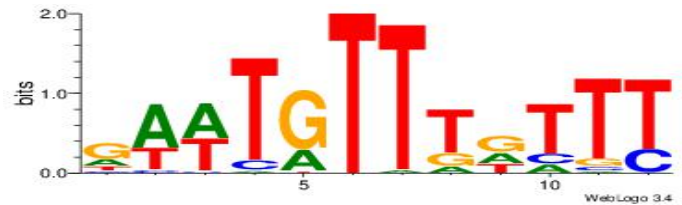
Best Matches for Motif ID 67 (Highest to Lowest)

Dataset #:	3
Motif ID:	65
Motif name:	Foxd3
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1

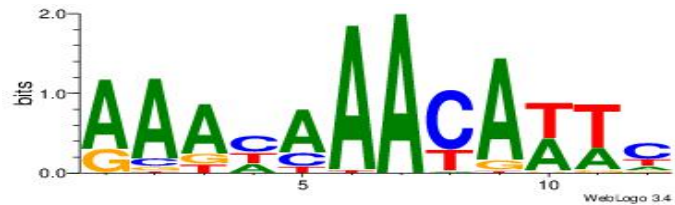
Number of overlap: 12
Similarity score: 0.0238603

Alignment:
AAAHAAACAWTC
AAAMAAAMADBY

Original motif Consensus sequence: GAWTGTTTDTTT



Reverse complement motif Consensus sequence: AAAHAAACAWTC

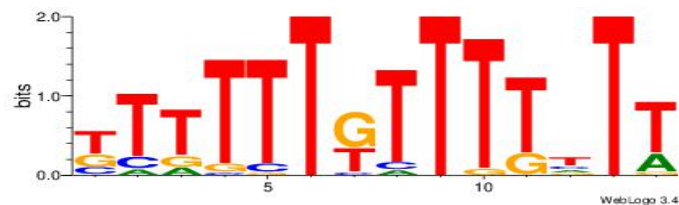
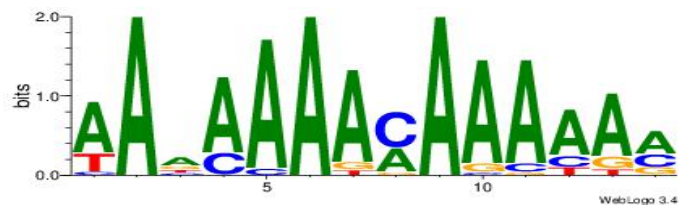


Dataset #: 2
Motif ID: 60
Motif name: Motif 60
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 12
Similarity score: 0.035724

Alignment:
YTTTTTRTTTTDTT
KBDTRTTTTRTTT--

Original motif Consensus sequence: AADAAAAMAAAAAM

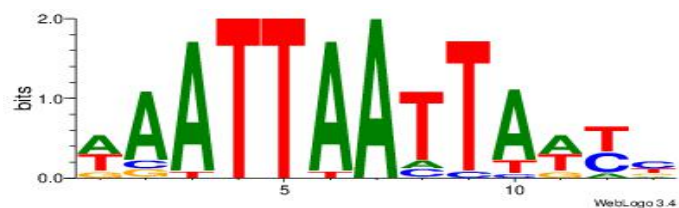
Reverse complement motif Consensus sequence: YTTTTTRTTTTDTT



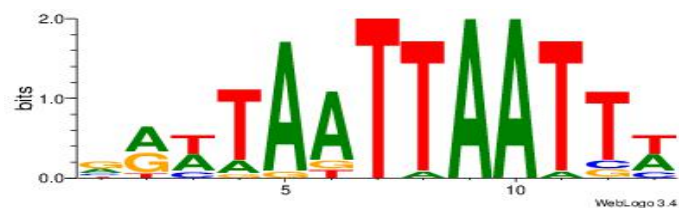
Dataset #: 3
 Motif ID: 66
 Motif name: Lhx3
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 12
 Similarity score: 0.0611272

Alignment:
 WAATTAATTAWYB
 AAAMAAAMADBY-

Original motif Consensus sequence: WAATTAATTAWYB



Reverse complement motif Consensus sequence: BMWTAATTAATTW



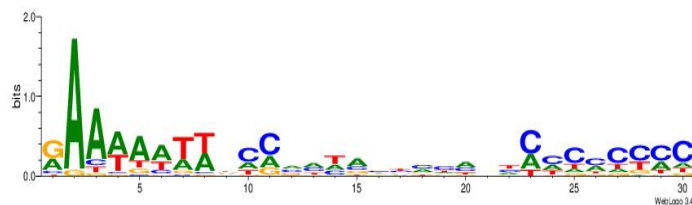
Dataset #: 3
 Motif ID: 81

Motif name:	Pax4
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	3
Number of overlap:	12
Similarity score:	0.0613545

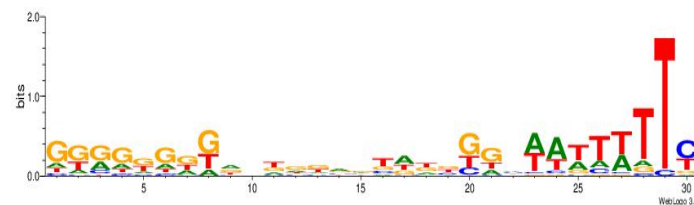
Alignment:

```
RAAWAWTWDCMVHHVBBHHHVHMHCMCYMC
--AAAMAAAMADBY-----
```

Original motif Consensus sequence:
RAAWAWTWDCMVHHVBBHHHVHMHCMCYMC



Reverse complement motif Consensus sequence:
GRKGRGDRHVDHBBHHBRGDWAWTWTTM



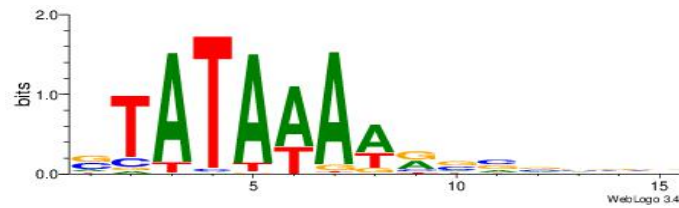
Dataset #:	3
Motif ID:	62
Motif name:	TBP
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	2
Number of overlap:	12
Similarity score:	0.0644285

Alignment:

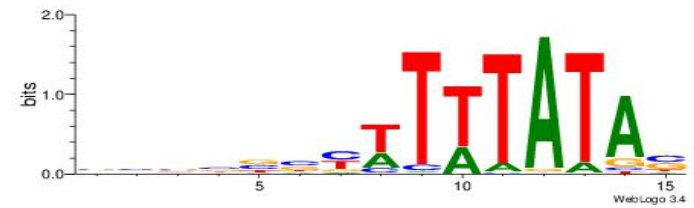
VBVVVVMWTTTATAS

--KBDTRTTTTRTTT--

Original motif Consensus sequence: STATAAAWRVVVBV

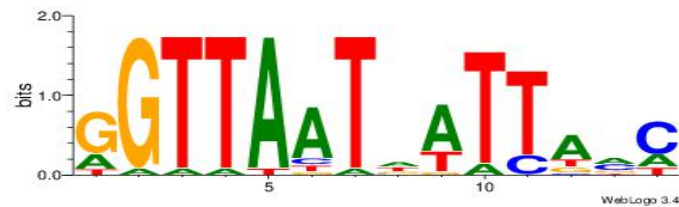


Reverse complement motif Consensus sequence: VBVVVVMWTTTATAS

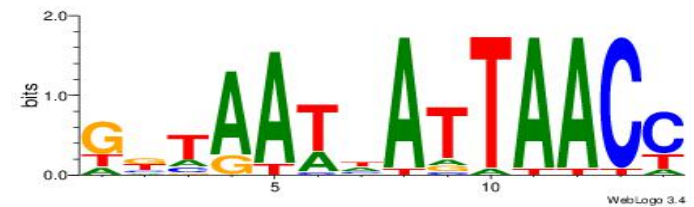


Dataset #: 3 Motif ID: 68 Motif name: HNF1A

Original motif Consensus sequence: GGTTAATDATTAMC



Reverse complement motif Consensus sequence: GYTAATDATTAAAC



Best Matches for Motif ID 68 (Highest to Lowest)

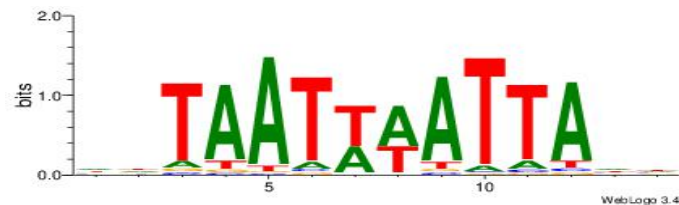
Dataset #:	4
Motif ID:	125
Motif name:	wwTAATwwATTaww
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1

Number of overlap: 14
Similarity score: 0.0430148

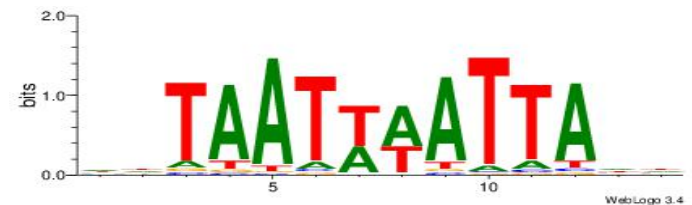
Alignment:

DDTAATWWATTAHH
GGTTAATDATTAMC

Original motif Consensus sequence: DDTAATWWATTAHH



Reverse complement motif Consensus sequence: HHTAATWWATTAA



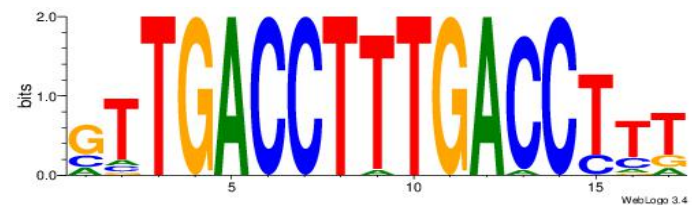
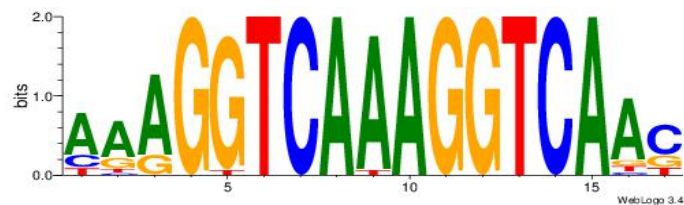
Dataset #: 3
Motif ID: 84
Motif name: NR1H2RXRA
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 14
Similarity score: 0.0678001

Alignment:

AAAGGTCAAAGGTCAAC
---GGTTAATDATTAMC

Original motif Consensus sequence: AAAGGTCAAAGGTCAAC

Reverse complement motif Consensus sequence:
GTTGACCTTTGACCTT

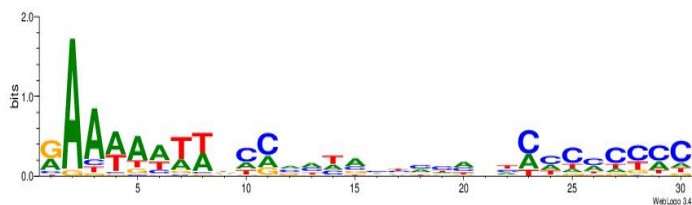


Dataset #: 3
 Motif ID: 81
 Motif name: Pax4
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 17
 Number of overlap: 14
 Similarity score: 0.0691946

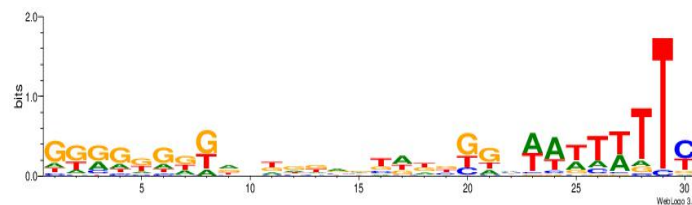
Alignment:

GRKGRGDRHVHDDVBBHHBRGDWAWTWTTM
 -----GYTAATDATTAACC

Original motif Consensus sequence:
 RAAWAWTWDCMVHHVBBHHHVHMHCMCYMC



Reverse complement motif Consensus sequence:
 GRKGRGDRHVHDDVBBHHBRGDWAWTWTTM



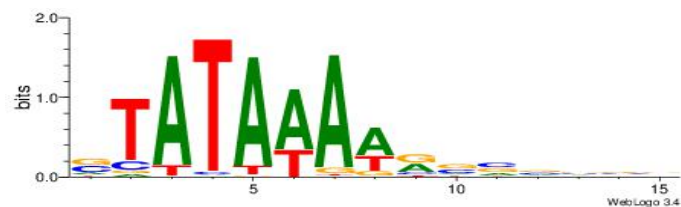
Dataset #: 3

Motif ID: 62
 Motif name: TBP
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0.0722834

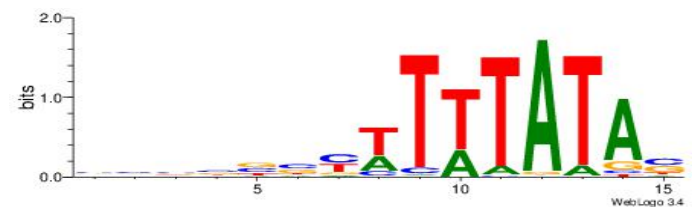
Alignment:

VBVVVVMWTTTATAS
 -GYTAATDATTAACC

Original motif Consensus sequence: STATAAWRVVVVBV



Reverse complement motif Consensus sequence: VBVVVVMWTTTAT



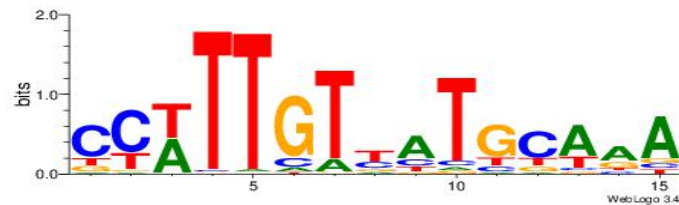
Dataset #: 3
 Motif ID: 76
 Motif name: Sox2
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 14
 Similarity score: 0.077247

Alignment:

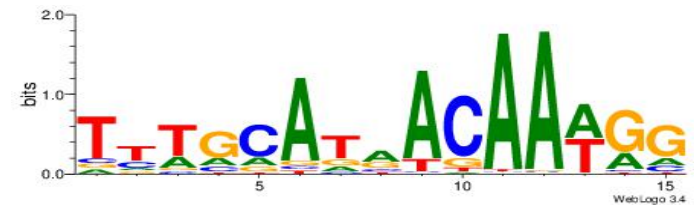
CCWTTGTYATGCAAA

GGTTAATDATTAMC-

Original motif Consensus sequence: CCWTTGTYATGCAAA



Reverse complement motif Consensus sequence: TTTGCATMACAAWGG



Dataset #: 3 Motif ID: 69 Motif name: NKX3-1

Original motif Consensus sequence: A T A C T T A



Reverse complement motif Consensus sequence: T A A G T A T



Best Matches for Motif ID 69 (Highest to Lowest)

Dataset #:	4
Motif ID:	90
Motif name:	ymTACATAyw
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward

Position number: 2
Number of overlap: 7
Similarity score: 0

Alignment:

HHTACATABD
-ATACTTA--

Original motif Consensus sequence: HHTACATABD



Reverse complement motif Consensus sequence: DBTATGTAHH



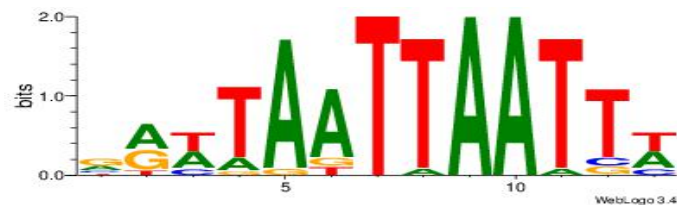
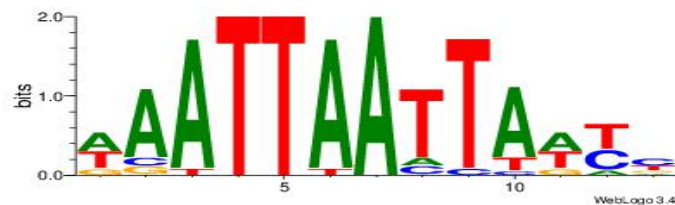
Dataset #: 3
Motif ID: 66
Motif name: Lhx3
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 5
Number of overlap: 7
Similarity score: 0.000214177

Alignment:

WAATTAATTAWYB
--TAAGTAT----

Original motif Consensus sequence: WAATTAATTAWYB

Reverse complement motif Consensus sequence: BMWTAATTAATTW



Dataset #: 1
 Motif ID: 10
 Motif name: Motif 10
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 7
 Similarity score: 0.00274846

Alignment:
 TATGTAD
 TAAGTAT

Original motif Consensus sequence: HTACATA



Reverse complement motif Consensus sequence: TATGTAD



Dataset #: 1

Motif ID:	34
Motif name:	Motif 34
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	7
Similarity score:	0.00883486

Alignment:
ATATTTA
ATACTTA

Original motif Consensus sequence: ATATTTA



Reverse complement motif Consensus sequence: TAAATAT



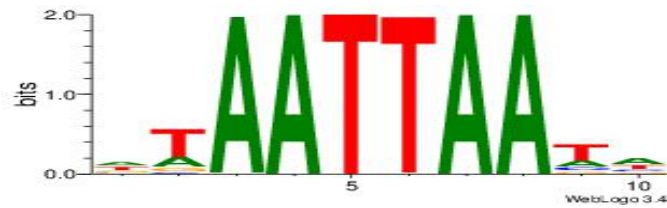
Dataset #:	4
Motif ID:	106
Motif name:	wtAATTAAtw
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	4
Number of overlap:	7
Similarity score:	0.0100679

Alignment:

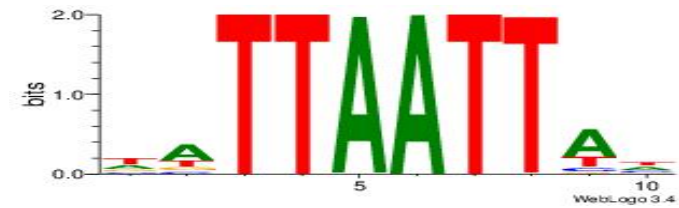
HATTAATTAD

---TAAGTAT

Original motif Consensus sequence: DTAATTAATH



Reverse complement motif Consensus sequence: HATTAATTAD

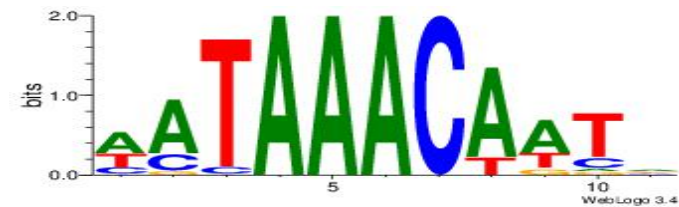


Dataset #: 3 Motif ID: 70 Motif name: Foxq1

Original motif Consensus sequence: HATTGTTTATW



Reverse complement motif Consensus sequence: WATAACAATH



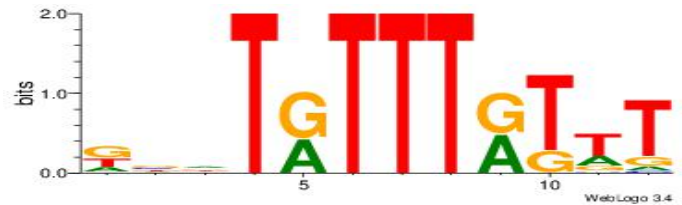
Best Matches for Motif ID 70 (Highest to Lowest)

Dataset #:	3
Motif ID:	67
Motif name:	FOXI1
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2

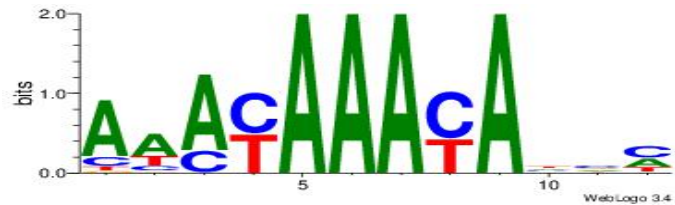
Number of overlap: 11
Similarity score: 0.0247019

Alignment:
KBDTRTTTTRTTT
HATTGTTTATW-

Original motif Consensus sequence: KBDTRTTTTRTTT



Reverse complement motif Consensus sequence: AAAMAAAMADBY

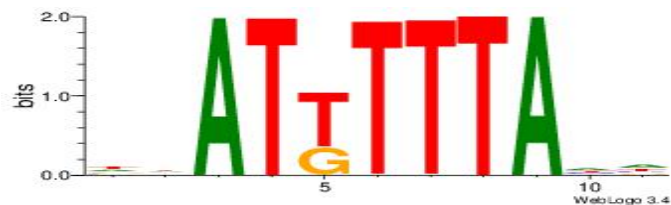


Dataset #: 4
Motif ID: 108
Motif name: wwATkTTTAww
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 11
Similarity score: 0.0341803

Alignment:
DHATKTTTAHH
HATTGTTTATW

Original motif Consensus sequence: DHATKTTTAHH

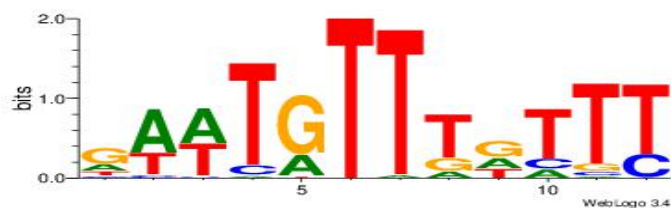
Reverse complement motif Consensus sequence: HHTAAARATHD



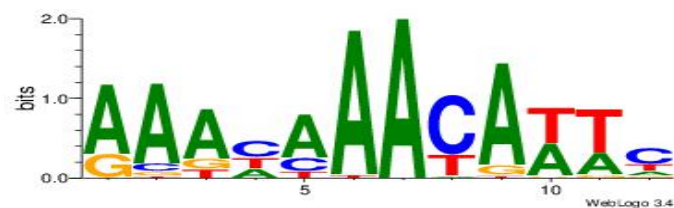
Dataset #: 3
 Motif ID: 65
 Motif name: Foxd3
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.0354607

Alignment:
 GAWTGTTTDTTT
 HATTGTTTATW-

Original motif Consensus sequence: GAWTGTTTDTTT



Reverse complement motif Consensus sequence: AAAHAAACAWTC



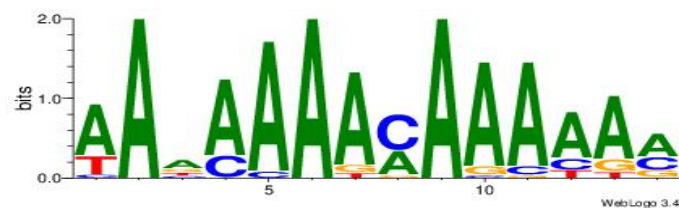
Dataset #: 2
 Motif ID: 60

Motif name:	Motif 60
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	3
Number of overlap:	11
Similarity score:	0.0611511

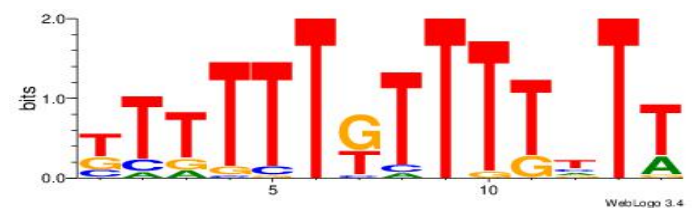
Alignment:

```
YTTTTTRTTTDTT
-HATTGTTTATW--
```

Original motif Consensus sequence: AADAAAAMAAAAAM



Reverse complement motif Consensus sequence: YTTTTTRTTTDTT



Dataset #:	4
Motif ID:	114
Motif name:	awAACAcAAwa
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	11
Similarity score:	0.0621125

Alignment:

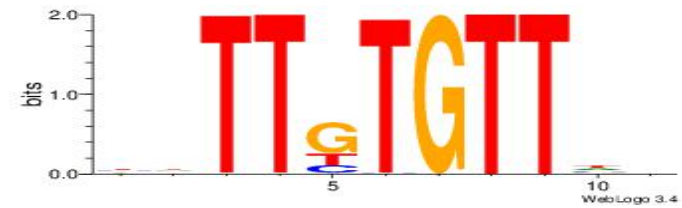
BDTTGTGTTDD

HATTGTTTATW

Original motif Consensus sequence: DDAACACAADV



Reverse complement motif Consensus sequence: BDTTGTGTTDD

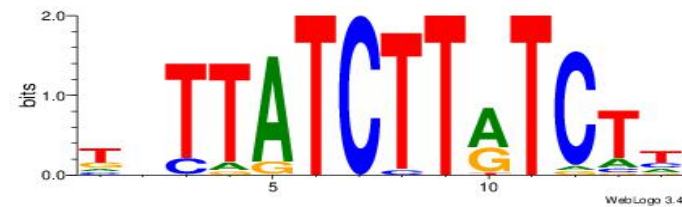


Dataset #: 3 Motif ID: 71 Motif name: Evi1

Original motif Consensus sequence: AAGAYAAGATAABA



Reverse complement motif Consensus sequence: TBTTATCTTMTCTT



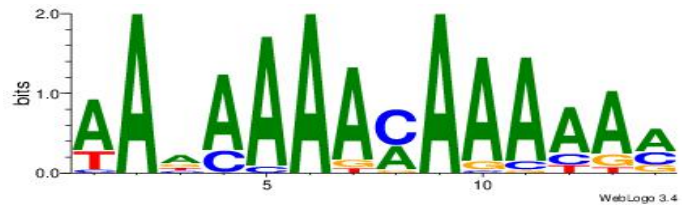
Best Matches for Motif ID 71 (Highest to Lowest)

Dataset #:	2
Motif ID:	60
Motif name:	Motif 60
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1

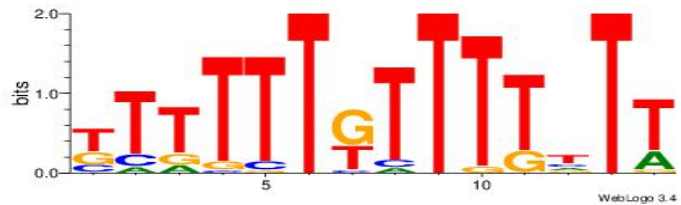
Number of overlap: 14
Similarity score: 0.0493882

Alignment:
AADAAAAMAAAAAM
AAGAYAAGATAABA

Original motif Consensus sequence: AADAAAAMAAAAAM



Reverse complement motif Consensus sequence: YTTTTTRTTTTDTT

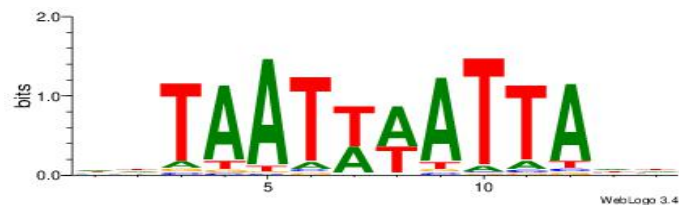
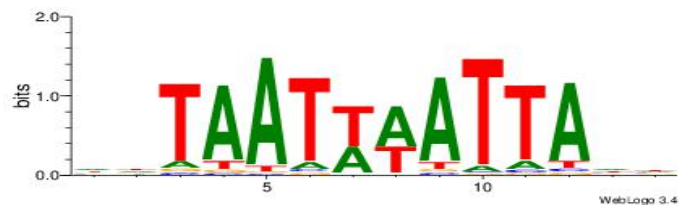


Dataset #: 4
Motif ID: 125
Motif name: wwTAATwwATTaww
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 14
Similarity score: 0.072295

Alignment:
DDTAATWWATTAAH
AAGAYAAGATAABA

Original motif Consensus sequence: DDTAATWWATTAAH

Reverse complement motif Consensus sequence: HHTAATWWATTAAH

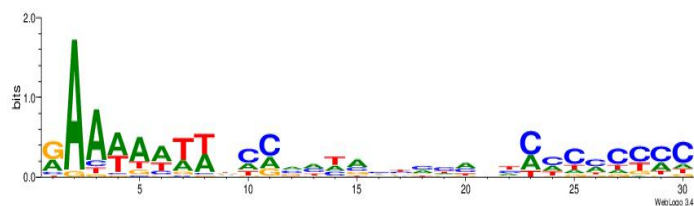


Dataset #: 3
 Motif ID: 81
 Motif name: Pax4
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 5
 Number of overlap: 14
 Similarity score: 0.0763889

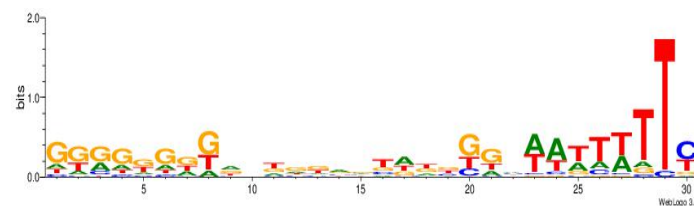
Alignment:

RAAWAWTWDCMVHHVBBHHHVHMHCMCYMC
 ----AAGAYAAGATAABA-----

Original motif Consensus sequence:
 RAAWAWTWDCMVHHVBBHHHVHMHCMCYMC



Reverse complement motif Consensus sequence:
 GRKGRGDRHVHDDVBBHHBRGDWAWTWTTM



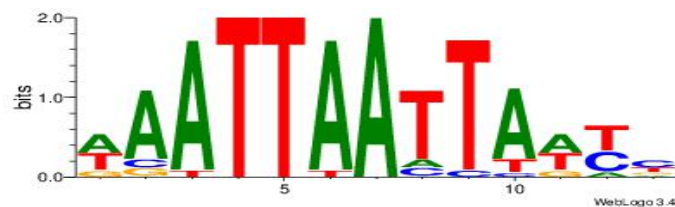
Dataset #: 3

Motif ID: 66
 Motif name: Lhx3
 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: 0.564942

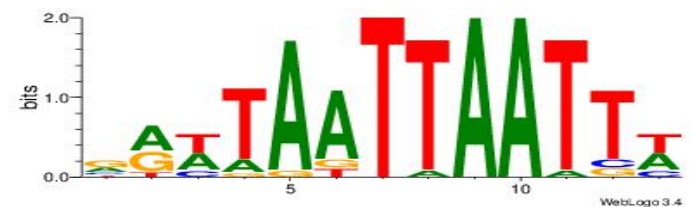
Alignment:

BMWTAATTAATTW-
 TBTATCTTMTCTT

Original motif Consensus sequence: WAATTAATTAWYB



Reverse complement motif Consensus sequence: BMWTAATTAATTW



Dataset #: 3
 Motif ID: 75
 Motif name: FOXF2
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 13
 Similarity score: 0.568274

Alignment:

-DTTGTTTACSBTBB
TBTTATCTTMTCTT-

Original motif Consensus sequence: BHADSGTAAACAAD



Reverse complement motif Consensus sequence: DTTGTTTACSBTBB



Dataset #: 3 Motif ID: 72 Motif name: Nkx2-5

Original motif Consensus sequence: WTAAKTG



Reverse complement motif Consensus sequence: CARTTAW



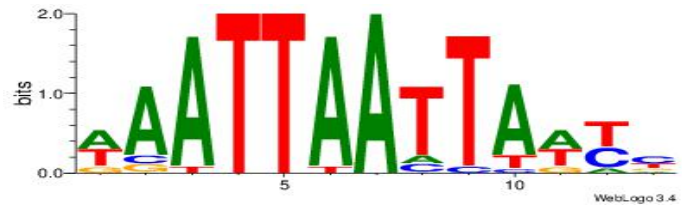
Best Matches for Motif ID 72 (Highest to Lowest)

Dataset #:	3
Motif ID:	66
Motif name:	Lhx3
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	7

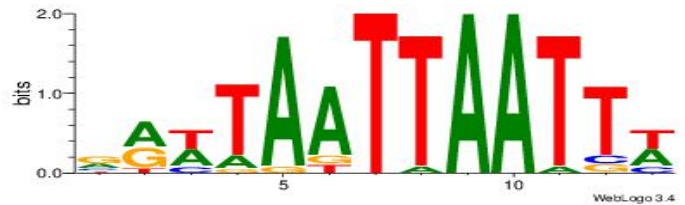
Number of overlap: 7
Similarity score: 0.0204974

Alignment:
WAATTAATTAWYB
-----CARTTAW

Original motif Consensus sequence: WAATTAATTAWYB



Reverse complement motif Consensus sequence: BMWTAATTAATTW

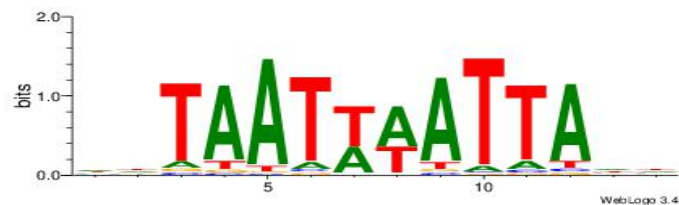
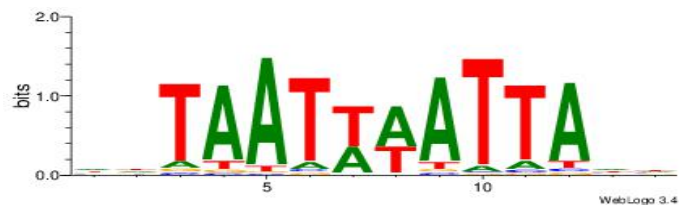


Dataset #: 4
Motif ID: 125
Motif name: wwTAATwwATTaww
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 2
Number of overlap: 7
Similarity score: 0.021519

Alignment:
HHTAATWWATTADD
-WTAAKTG-----

Original motif Consensus sequence: DDTAATWWATTAAHH

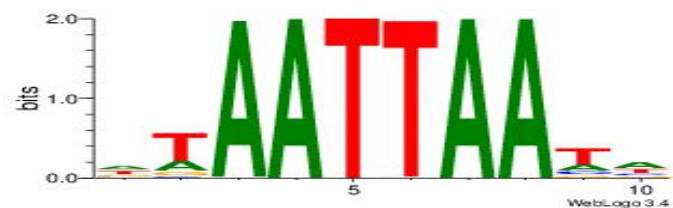
Reverse complement motif Consensus sequence: HHTAATWWATTAD



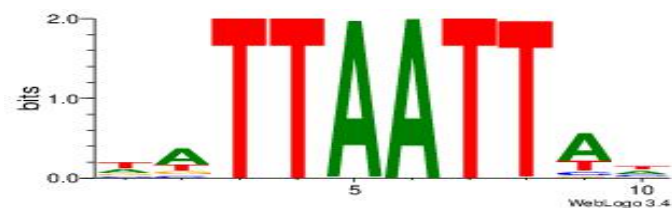
Dataset #: 4
 Motif ID: 106
 Motif name: wtAATTAAtw
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3
 Number of overlap: 7
 Similarity score: 0.0245852

Alignment:
 HATTAATTAD
 --WTAAKTG--

Original motif Consensus sequence: DTAATTAATH



Reverse complement motif Consensus sequence: HATTAATTAD



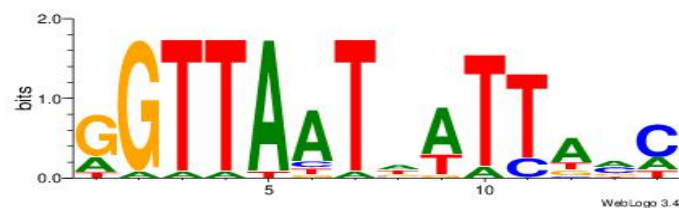
Dataset #: 3
 Motif ID: 68

Motif name:	HNF1A
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	6
Number of overlap:	7
Similarity score:	0.0356285

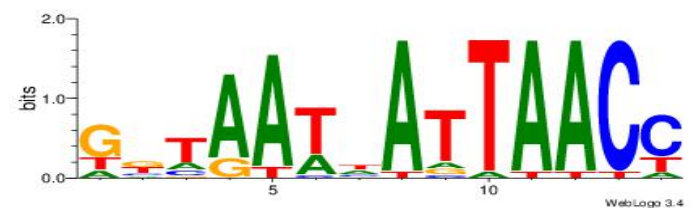
Alignment:

```
GGTTAATDATTAMC
--WTAAKTG-----
```

Original motif Consensus sequence: GGTTAATDATTAMC



Reverse complement motif Consensus sequence: GYTAATDATTAAC



Dataset #:	1
Motif ID:	45
Motif name:	Motif 45
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	2
Number of overlap:	7
Similarity score:	0.0367872

Alignment:

WTAATAAT

-WTAAKTG

Original motif Consensus sequence: ATTATTAW

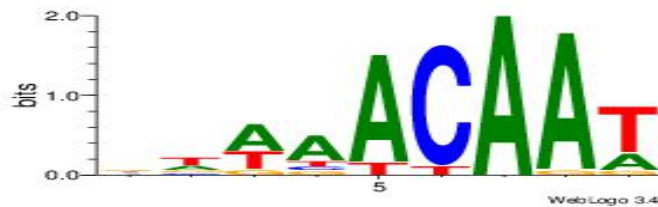


Reverse complement motif Consensus sequence: WTAATAAT

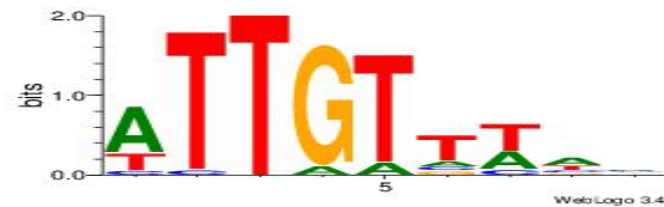


Dataset #: 3 Motif ID: 73 Motif name: SRY

Original motif Consensus sequence: BDWAACAAT



Reverse complement motif Consensus sequence: ATTGTTWDB



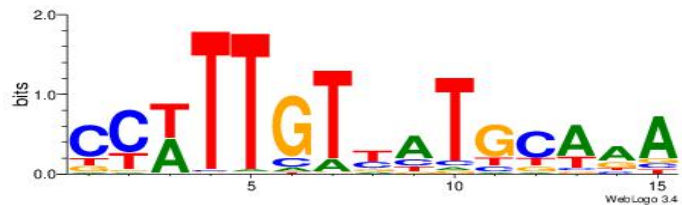
Best Matches for Motif ID 73 (Highest to Lowest)

Dataset #:	3
Motif ID:	76
Motif name:	Sox2
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	5

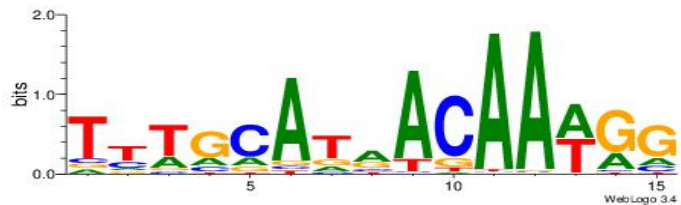
Number of overlap: 9
Similarity score: 0.0274533

Alignment:
TTTGCATMACAAWGG
----BDWAACAAT--

Original motif Consensus sequence: CCWTTGTYATGCAAA



Reverse complement motif Consensus sequence: TTTGCATMACAAWGG

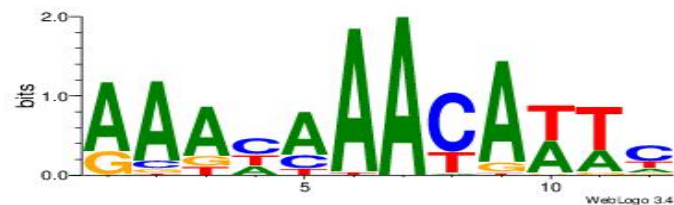
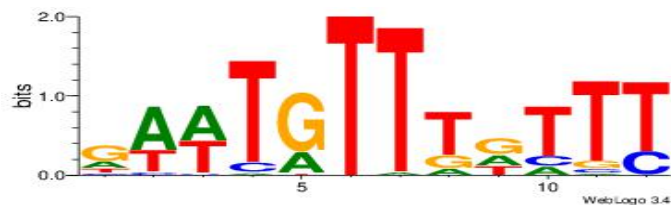


Dataset #: 3
Motif ID: 65
Motif name: Foxd3
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 2
Number of overlap: 9
Similarity score: 0.0332484

Alignment:
AAAHAAACAWTC
-BDWAACAAT--

Original motif Consensus sequence: GAWTGTTTDTTT

Reverse complement motif Consensus sequence: AAAHAAACAWTC



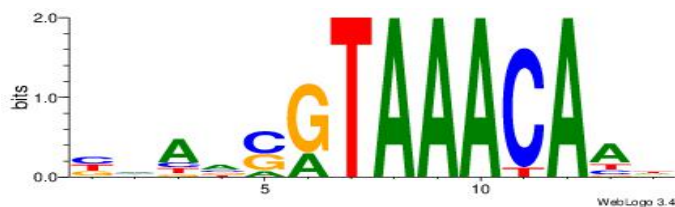
Dataset #: 3
 Motif ID: 75
 Motif name: FOXF2
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 9
 Similarity score: 0.0379812

Alignment:

DTTGTTTACSBTBB

ATTGTTWDB-----

Original motif Consensus sequence: BHADSGTAAACAAD



Reverse complement motif Consensus sequence: DTTGTTTACSBTBB



Dataset #: 3
 Motif ID: 70

Motif name:	Foxq1
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	2
Number of overlap:	9
Similarity score:	0.0407369

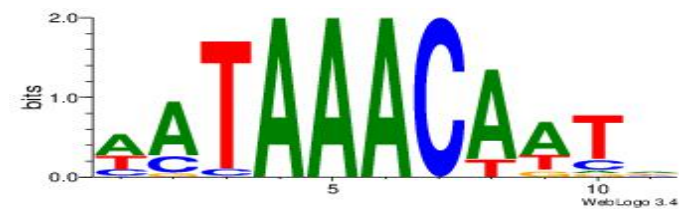
Alignment:

WATAACAATH
 -BDWAACAAT-

Original motif Consensus sequence: HATTGTTTATW



Reverse complement motif Consensus sequence: WATAACAATH



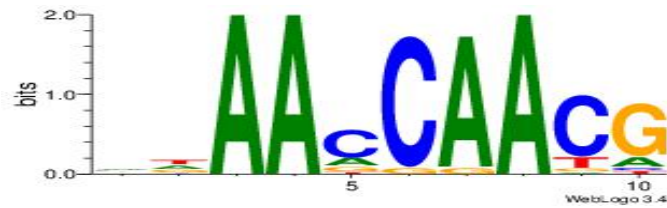
Dataset #:	4
Motif ID:	96
Motif name:	mdAAcCAACG
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	9
Similarity score:	0.044154

Alignment:

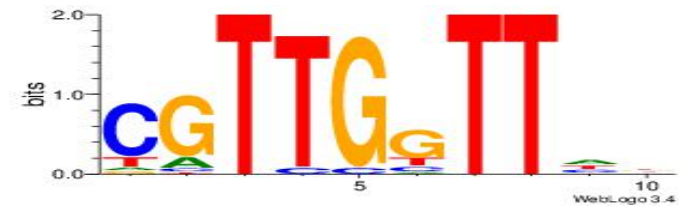
CGTTGGTTDB

-ATTGTTWDB

Original motif Consensus sequence: VDAACCAACG

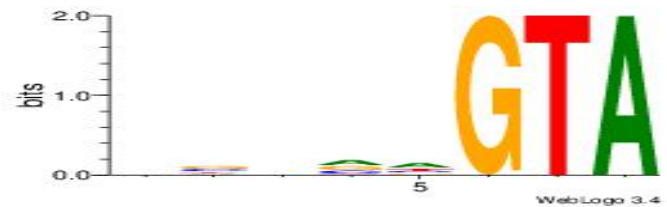


Reverse complement motif Consensus sequence: CGTTGGTTDB

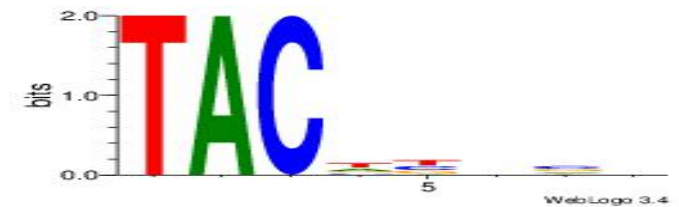


Dataset #: 3 Motif ID: 74 Motif name: FOXC1

Original motif Consensus sequence: VBHVHGTA



Reverse complement motif Consensus sequence: TACHBHBV



Best Matches for Motif ID 74 (Highest to Lowest)

Dataset #:	3
Motif ID:	75
Motif name:	FOXF2
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1

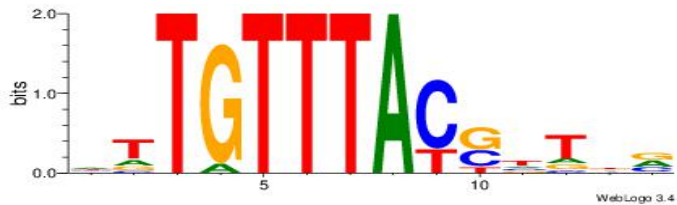
Number of overlap: 8
Similarity score: 0.0250969

Alignment:
DTTGTTTACSBTB
-----TACHBHBV

Original motif Consensus sequence: BHADSGTAAACAAD



Reverse complement motif Consensus sequence: DTTGTTTACSBTB

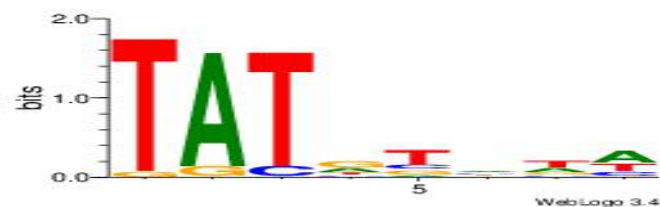
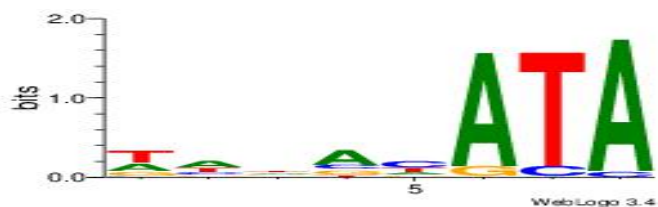


Dataset #: 3
Motif ID: 63
Motif name: FOXL1
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 8
Similarity score: 0.0421733

Alignment:
WHD AHATA
VBHVHGTA

Original motif Consensus sequence: WHDAHATA

Reverse complement motif Consensus sequence: TATD TDHW



Dataset #: 4
 Motif ID: 90
 Motif name: ymTACATayw
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 8
 Similarity score: 0.0422828

Alignment:
 HHTACATABD
 --TACHBHBV

Original motif Consensus sequence: HHTACATABD



Reverse complement motif Consensus sequence: DBTATGTAHH



Dataset #: 3
 Motif ID: 62

Motif name:	TBP
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	3
Number of overlap:	8
Similarity score:	0.0452131

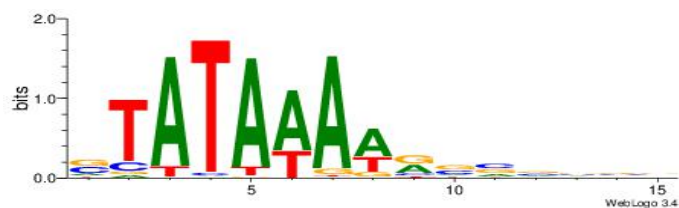
Alignment:

```

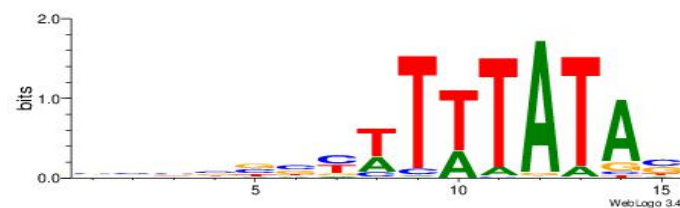
STATAAWRVVVBV
--TACHBHBV-----

```

Original motif Consensus sequence: STATAAWRVVVBV



Reverse complement motif Consensus sequence: VBVVVMWTTTAT



Dataset #:	3
Motif ID:	81
Motif name:	Pax4
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	14
Number of overlap:	8
Similarity score:	0.046771

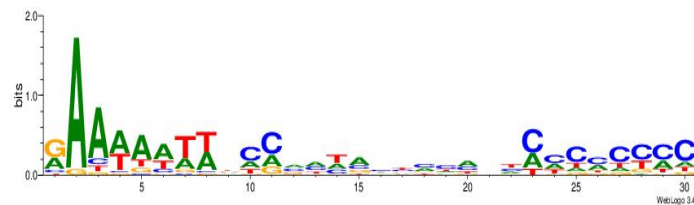
Alignment:

GRKGRGDRHVVHDDVBBHHBRGDWAWTWTTM

-----VBHVHGTA-----

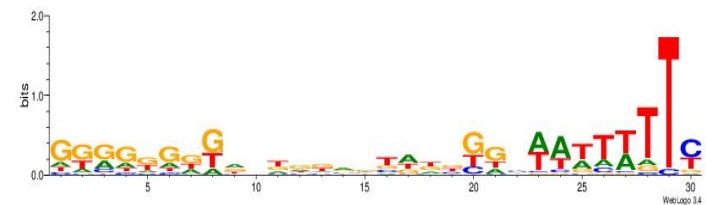
Original motif Consensus sequence:

RAAWAWTWDCMVHHVBBHHHVHMHCMCYMC



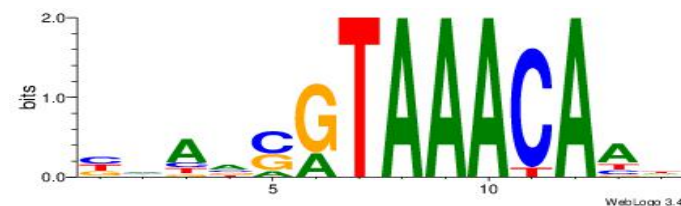
Reverse complement motif Consensus sequence:

GRKGRGDRHVVHDDVBBHHBRGDWAWTWTTM



Dataset #: 3 Motif ID: 75 Motif name: FOXF2

Original motif Consensus sequence: BHADSGTAAACAAD



Reverse complement motif Consensus sequence: DTTGTTTACSBTBB



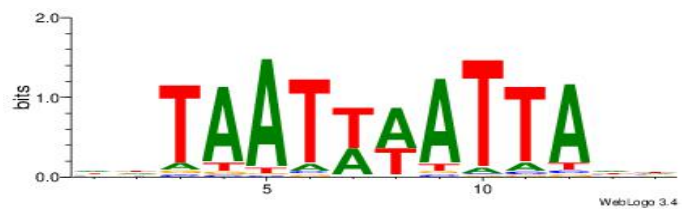
Best Matches for Motif ID 75 (Highest to Lowest)

Dataset #:	4
Motif ID:	125
Motif name:	wwTAATwwATTaww
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward

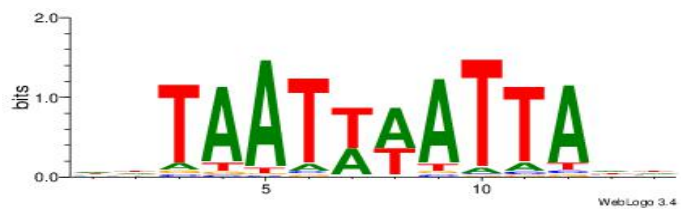
Position number: 1
Number of overlap: 14
Similarity score: 0.0789966

Alignment:
DDTAATWWATTAHH
DTTGTTTACSBTBB

Original motif Consensus sequence: DDTAATWWATTAHH



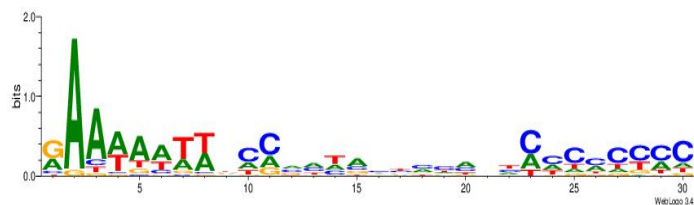
Reverse complement motif Consensus sequence: HHTAATWWATTAD



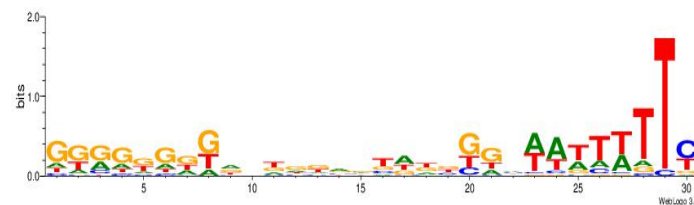
Dataset #: 3
Motif ID: 81
Motif name: Pax4
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 3
Number of overlap: 14
Similarity score: 0.0801361

Alignment:
GRKGRGDRHVVHDDVBBHHBRGDWAWTWTM
-----BHADSGTAAACAAD--

Original motif Consensus sequence:
RAAWAWTWDCMVHHVBBHHHVHMHCMCYMC



Reverse complement motif Consensus sequence:
GRKGRGDRHVDVBBHHBRGDWAWTWTTM

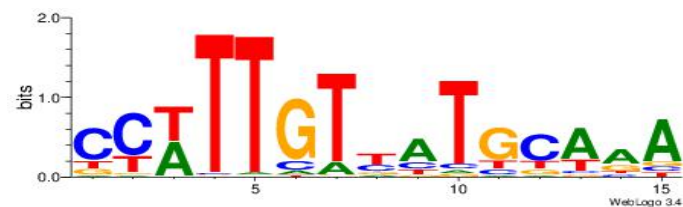


Dataset #: 3
Motif ID: 76
Motif name: Sox2
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 14
Similarity score: 0.0829475

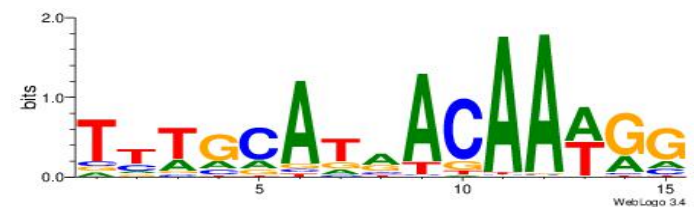
Alignment:

TTTGCATMACAAWGG
BHADSGTAAACAAD-

Original motif Consensus sequence: CCWTTGTYATGCAAA



Reverse complement motif Consensus sequence:
TTTGCATMACAAWGG

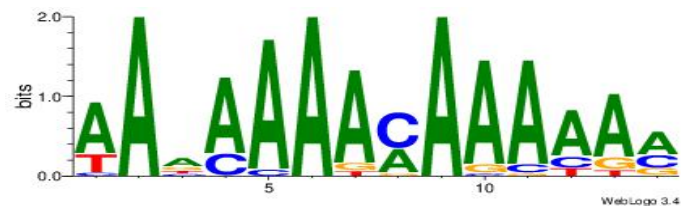


Dataset #: 2
 Motif ID: 60
 Motif name: Motif 60
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0.0886208

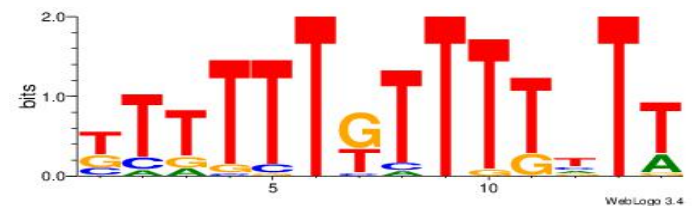
Alignment:

AADAAAAMAAAAAM
 BHADSGTAAACAAD

Original motif Consensus sequence: AADAAAAMAAAAAM



Reverse complement motif Consensus sequence: YTTTTTRTTTTDTT



Dataset #: 3
 Motif ID: 80
 Motif name: Pou5f1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 14

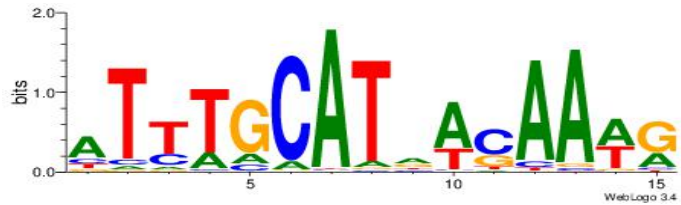
Similarity score: 0.0891042

Alignment:
ATTTCATHACAAWG
-DTTGTTTACSBTBB

Original motif Consensus sequence: CWTGTHATGCAAAT

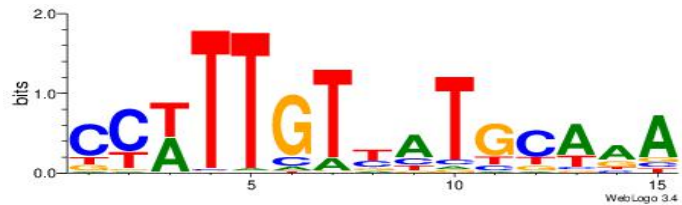


Reverse complement motif Consensus sequence: ATTTGCATHACAA

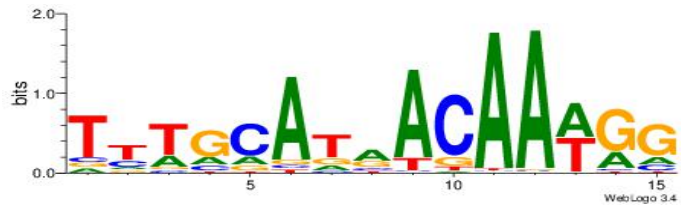


Dataset #: 3 Motif ID: 76 Motif name: Sox2

Original motif Consensus sequence: CCWTTGTYATGCAAA



Reverse complement motif Consensus sequence: TTTGCATMACAAWGG



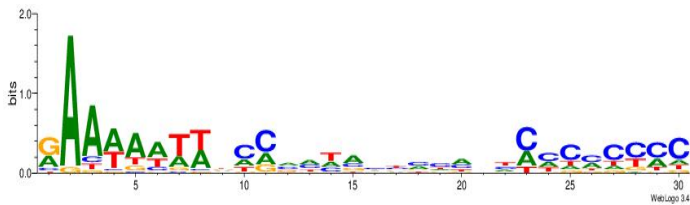
Best Matches for Motif ID 76 (Highest to Lowest)

Dataset #:	3
Motif ID:	81
Motif name:	Pax4
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif

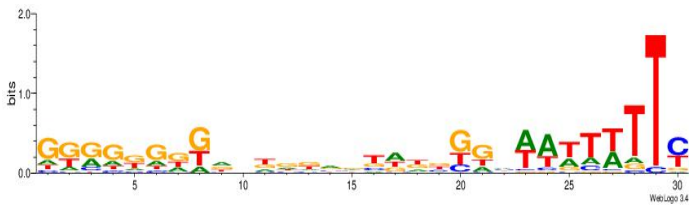
Direction: Forward
Position number: 8
Number of overlap: 15
Similarity score: 0.0816521

Alignment:
RAAWAWTWDCMVHHVBBHHHVHMHCMCYMC
-----TTTGCATMACAAWGG-----

Original motif Consensus sequence:
RAAWAWTWDCMVHHVBBHHHVHMHCMCYMC



Reverse complement motif Consensus sequence:
GRKGRGDRHVHDDVBBHHBRGDWAWTWTTM



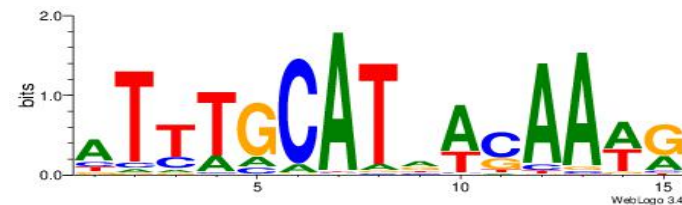
Dataset #: 3
Motif ID: 80
Motif name: Pou5f1
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 2
Number of overlap: 14
Similarity score: 0.5

Alignment:
ATTTGCATHACAAG-
-TTTGCATMACAAWGG

Original motif Consensus sequence: CWTGTHATGCAAAT



Reverse complement motif Consensus sequence: ATTTGCATHACAAAT

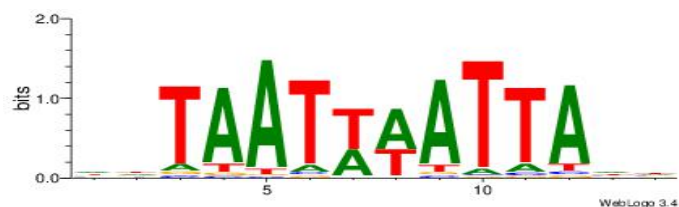


Dataset #: 4
 Motif ID: 125
 Motif name: wwTAATwwATTaww
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0.584157

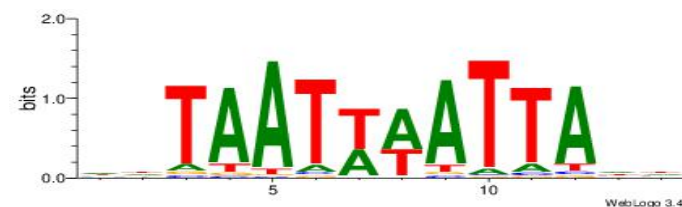
Alignment:

-HHTAATWWATTADD
 CCWTTGTYATGCAA

Original motif Consensus sequence: DDTAATWWATTAAH



Reverse complement motif Consensus sequence: HHTAATWWATTAA

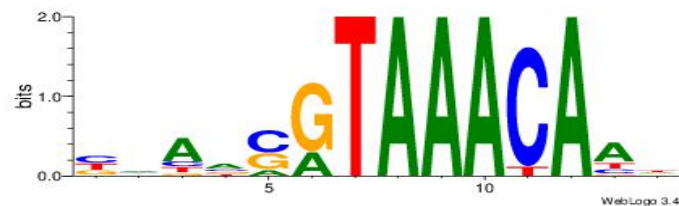


Dataset #: 3
 Motif ID: 75
 Motif name: FOXF2
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0.585609

Alignment:

DTTGTTTACSBTBB-
 CCWTTGTATGCAAA

Original motif Consensus sequence: BHADSGTAAACAAD



Reverse complement motif Consensus sequence: DTTGTTTACSBTBB

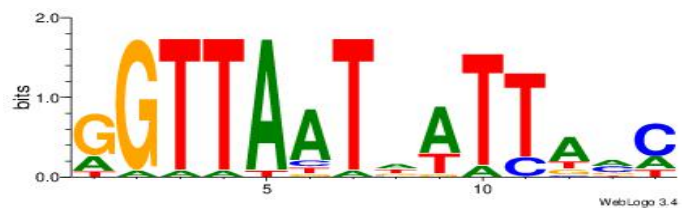


Dataset #: 3
 Motif ID: 68
 Motif name: HNF1A
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 14

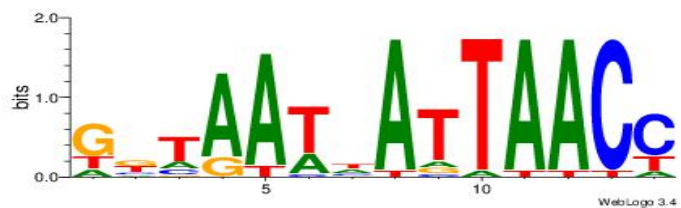
Similarity score: 0.59033

Alignment:
GGTTAATDATTAMC-
CCWTTGTYATGCAAA

Original motif Consensus sequence: GGTTAATDATTAMC



Reverse complement motif Consensus sequence: GYTAATDATTAAAC



Dataset #: 3 Motif ID: 77 Motif name: Sox5

Original motif Consensus sequence: HAACAAT



Reverse complement motif Consensus sequence: ATTGTH



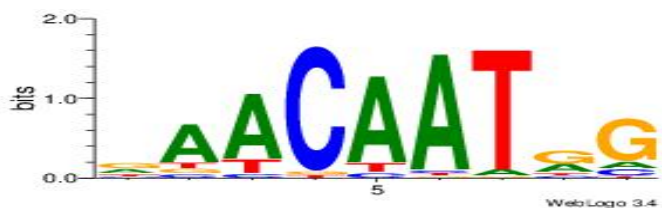
Best Matches for Motif ID 77 (Highest to Lowest)

Dataset #:	3
Motif ID:	87
Motif name:	SOX9
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward

Position number: 3
 Number of overlap: 7
 Similarity score: 0

Alignment:
 CMATTGTTH
 --ATTGTTH

Original motif Consensus sequence: DAACAATRG



Reverse complement motif Consensus sequence: CMATTGTTH

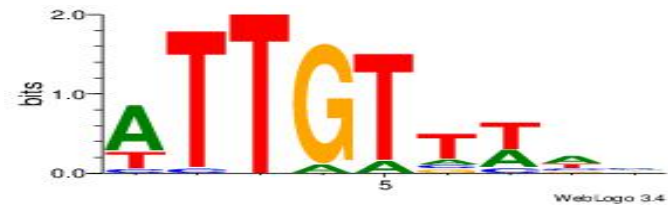
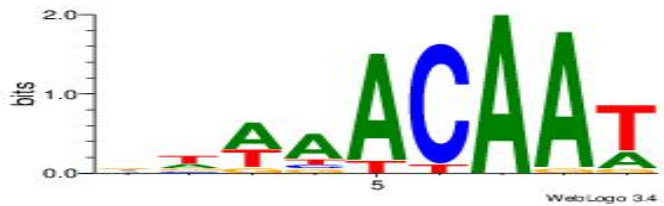


Dataset #: 3
 Motif ID: 73
 Motif name: SRY
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 7
 Similarity score: 0.0011033

Alignment:
 ATTGTTWDB
 ATTGTTH--

Original motif Consensus sequence: BDWAACAAT

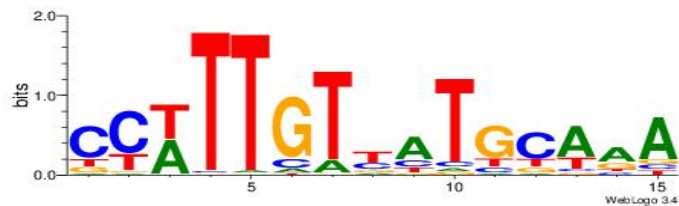
Reverse complement motif Consensus sequence: ATTGTTWDB



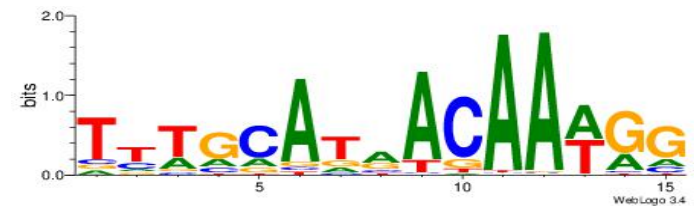
Dataset #: 3
 Motif ID: 76
 Motif name: Sox2
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 7
 Number of overlap: 7
 Similarity score: 0.022869

Alignment:
 CCWTTGTYATGCAAA
 -----ATTGTTH--

Original motif Consensus sequence: CCWTTGTYATGCAAA



Reverse complement motif Consensus sequence: TTTGCATMACAAWGG



Dataset #: 3

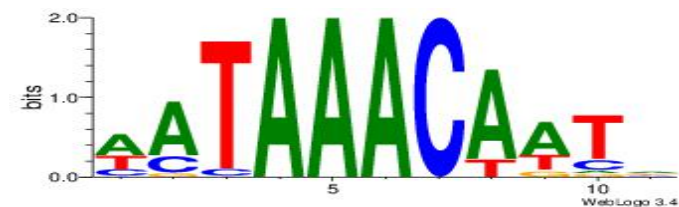
Motif ID:	70
Motif name:	Foxq1
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	4
Number of overlap:	7
Similarity score:	0.0242658

Alignment:
WATAACAATH
-HACAAT---

Original motif Consensus sequence: HATTGTTTATW



Reverse complement motif Consensus sequence: WATAACAATH



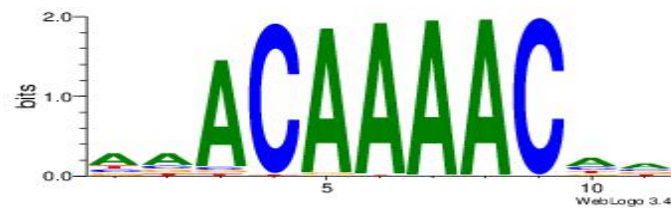
Dataset #:	4
Motif ID:	89
Motif name:	aaACAAAACaa
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	7
Similarity score:	0.0278776

Alignment:

AAACAAAACHV

HAACAAT----

Original motif Consensus sequence: AAACAAAACHV



Reverse complement motif Consensus sequence: BHGTTTTGTTT



Dataset #: 3 Motif ID: 78 Motif name: RORA_1

Original motif Consensus sequence: AWVDAGGTCA



Reverse complement motif Consensus sequence: TGACCTDVWT



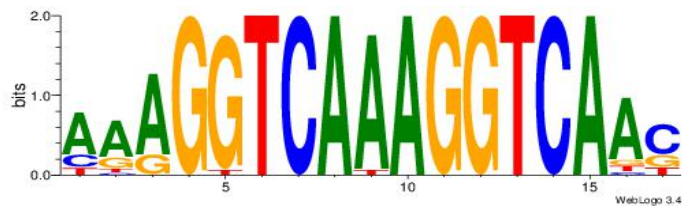
Best Matches for Motif ID 78 (Highest to Lowest)

Dataset #:	3
Motif ID:	84
Motif name:	NR1H2RXRA
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	3

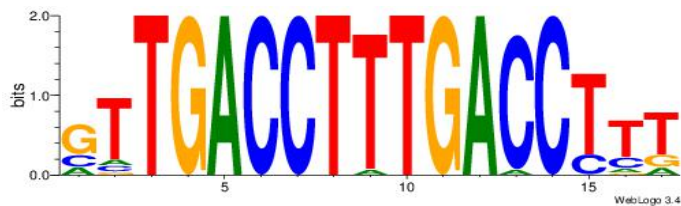
Number of overlap: 10
Similarity score: 0.05425

Alignment:
AAAGGTCAAAGGTCAAC
-----AWVDAGGTCA--

Original motif Consensus sequence: AAAGGTCAAAGGTCAAC



Reverse complement motif Consensus sequence:
GTTGACCTTTGACCTTT

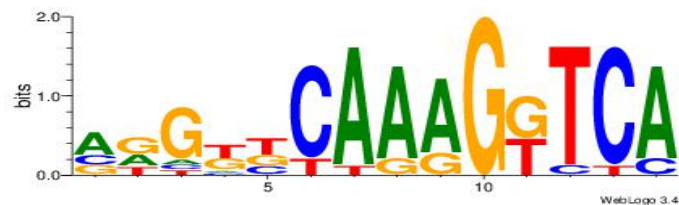


Dataset #: 3
Motif ID: 83
Motif name: NR2F1
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 5
Number of overlap: 10
Similarity score: 0.0654808

Alignment:
AKGY YCAAAGRTCA
-----AWVDAGGTCA

Original motif Consensus sequence: TGAMCTTTGMMCYT

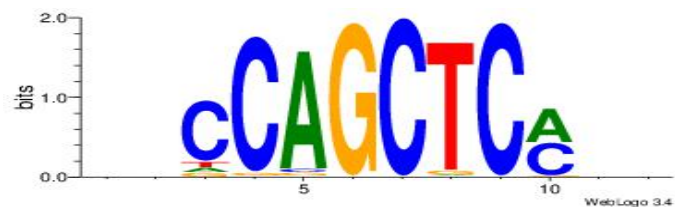
Reverse complement motif Consensus sequence: AKGY YCAAAGRTC



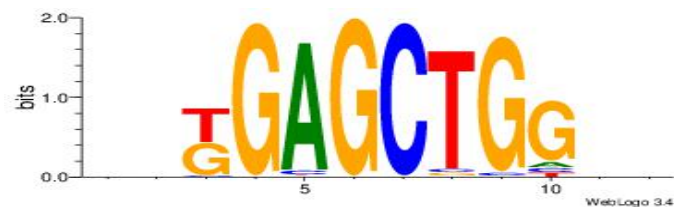
Dataset #: 4
 Motif ID: 119
 Motif name: cbCCAGCTCmyk
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 10
 Similarity score: 0.0688859

Alignment:
 HBYGAGCTGGBB
 --TGACCTDVWT

Original motif Consensus sequence: BBCCAGCTCMBD



Reverse complement motif Consensus sequence: HBYGAGCTGGBB



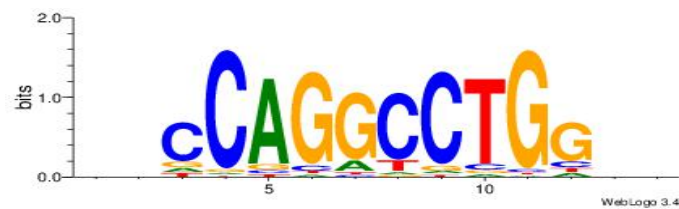
Dataset #: 4
 Motif ID: 122

Motif name:	hsCCAGGCCTGGsr
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	5
Number of overlap:	10
Similarity score:	0.0826087

Alignment:

HVCCAGGCCTGGBD
 ----TGACCTDVWT

Original motif Consensus sequence: HVCCAGGCCTGGBD



Reverse complement motif Consensus sequence: HBCCAGGCCTGGV



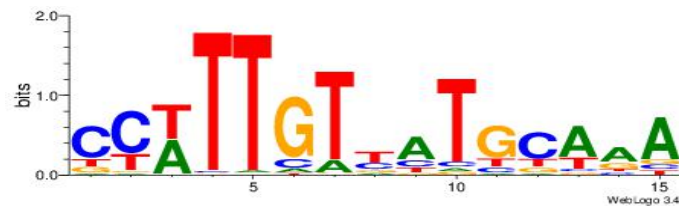
Dataset #:	3
Motif ID:	76
Motif name:	Sox2
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	2
Number of overlap:	10
Similarity score:	0.0865719

Alignment:

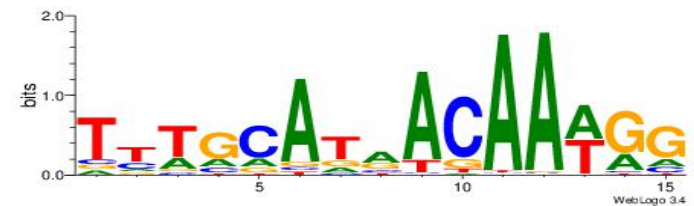
TTTGCATMACAAWGG

----AWVDAGGTCA-

Original motif Consensus sequence: CCWTTGTYATGCAAA



Reverse complement motif Consensus sequence: TTTGCATMACAAWGG



Dataset #: 3 Motif ID: 79 Motif name: Prrx2

Original motif Consensus sequence: AATTA



Reverse complement motif Consensus sequence: TAATT



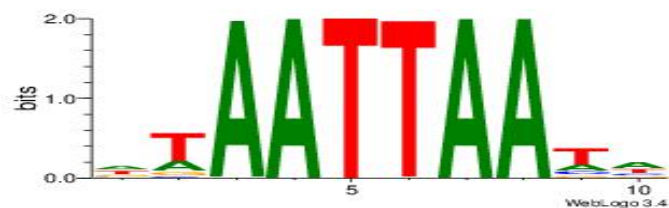
Best Matches for Motif ID 79 (Highest to Lowest)

Dataset #:	4
Motif ID:	106
Motif name:	wtAATTAAtw
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward

Position number: 3
 Number of overlap: 5
 Similarity score: 0.00550847

Alignment:
 HATTAATTAD
 ----TAATT--

Original motif Consensus sequence: DTAATTAATH



Reverse complement motif Consensus sequence: HATTAATTAD

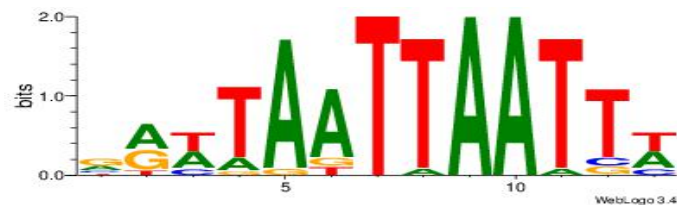
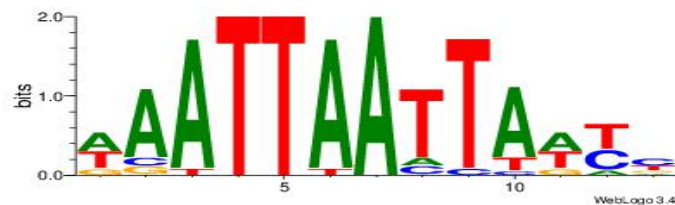


Dataset #: 3
 Motif ID: 66
 Motif name: Lhx3
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 5
 Similarity score: 0.00864407

Alignment:
 BMWTAATTAATTW
 -----TAATT-

Original motif Consensus sequence: WAATTAATTAWYB

Reverse complement motif Consensus sequence: BMWTAATTAATTW



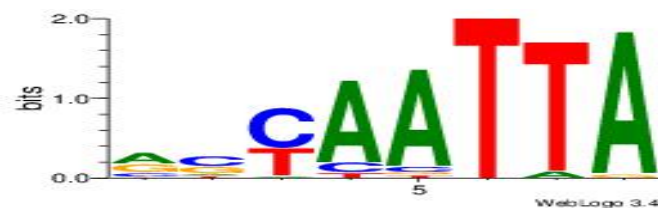
Dataset #: 3
 Motif ID: 85
 Motif name: Nobox
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 5
 Similarity score: 0.0115968

Alignment:
 TAATTRSY
 TAATT---

Original motif Consensus sequence: TAATTRSY



Reverse complement motif Consensus sequence: MSMAATTA

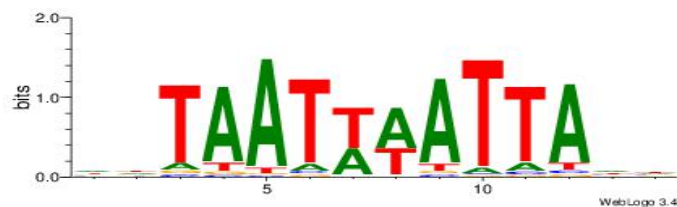


Dataset #: 4

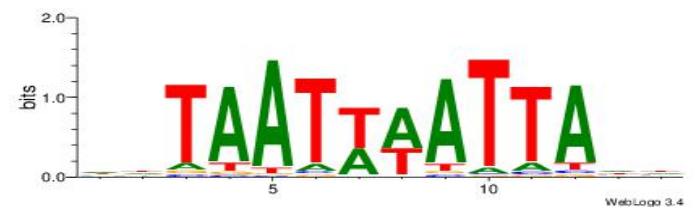
Motif ID: 125
 Motif name: wwTAATwwATTaww
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 8
 Number of overlap: 5
 Similarity score: 0.0417489

Alignment:
 HHTAATWWATTADD
 --TAATT-----

Original motif Consensus sequence: DDTAATWWATTAAH



Reverse complement motif Consensus sequence: HHTAATWWATTAD



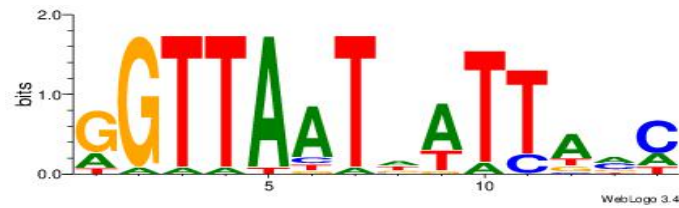
Dataset #: 3
 Motif ID: 68
 Motif name: HNF1A
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 4
 Number of overlap: 5
 Similarity score: 0.0434826

Alignment:

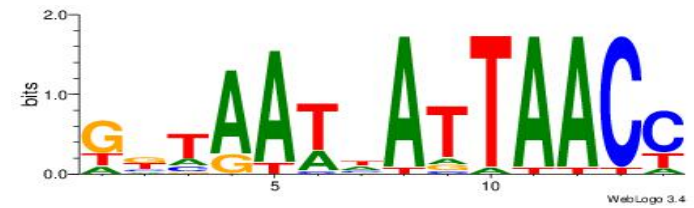
GYTAATDATTAAACC

---AATTA-----

Original motif Consensus sequence: GGTTAATDATTAMC



Reverse complement motif Consensus sequence: GYTAATDATTAAACC

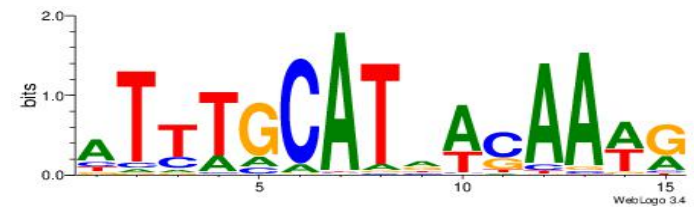


Dataset #: 3 Motif ID: 80 Motif name: Pou5f1

Original motif Consensus sequence: CWTGTHATGCAAAT



Reverse complement motif Consensus sequence: ATTTGCATHACAAV



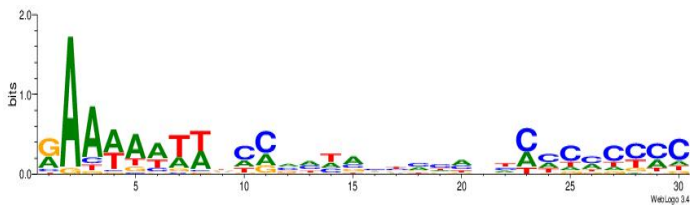
Best Matches for Motif ID 80 (Highest to Lowest)

Dataset #:	3
Motif ID:	81
Motif name:	Pax4
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	5

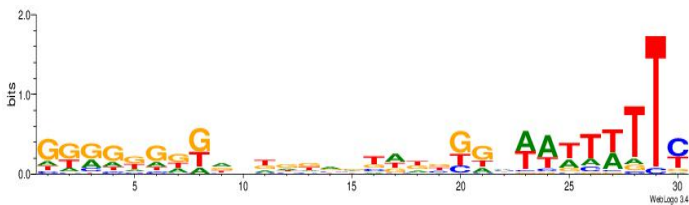
Number of overlap: 15
Similarity score: 0.0828317

Alignment:
RAAWAWTWDCMVHHVBBHHHVHMHCMCYMC
-----ATTTGCATHACAAWG-----

Original motif Consensus sequence:
RAAWAWTWDCMVHHVBBHHHVHMHCMCYMC



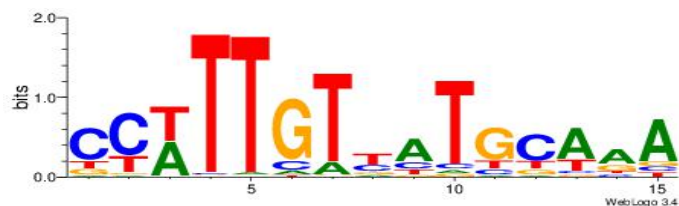
Reverse complement motif Consensus sequence:
GRKGRGDRHVHDDVBBHHBRGDWAWTWTTM



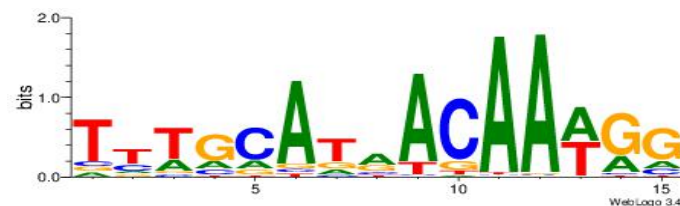
Dataset #: 3
Motif ID: 76
Motif name: Sox2
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 2
Number of overlap: 14
Similarity score: 0.5

Alignment:
CCWTTGTYATGCAA-
-CWTTGTHATGCAAAT

Original motif Consensus sequence: CCWTTGTYATGCAAA



Reverse complement motif Consensus sequence: TTTGCATMACAAWGG



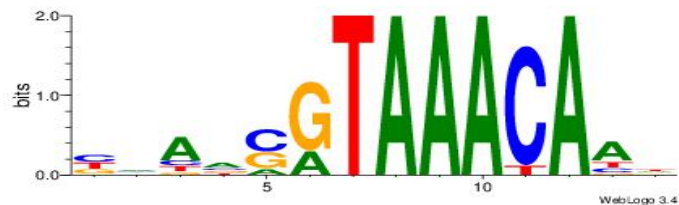
Dataset #: 3
Motif ID: 75
Motif name: FOXF2
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 14
Similarity score: 0.591766

Alignment:

-DTTGTTTACSBTBB

ATTTGCATHACAAWG

Original motif Consensus sequence: BHADSGTAAACAAD



Reverse complement motif Consensus sequence: DTTGTTTACSBTBB

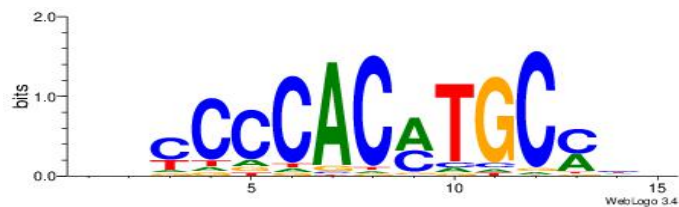


Dataset #: 4
 Motif ID: 98
 Motif name: myyCCCACmTGCmyr
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 14
 Similarity score: 0.592463

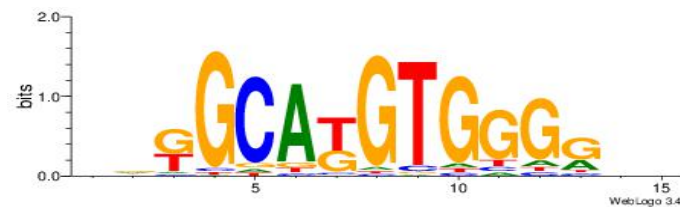
Alignment:

HBCCCCACMTGCMHV-
 -CWTGTGTHATGCAAAT

Original motif Consensus sequence: HBCCCCACMTGCMHV



Reverse complement motif Consensus sequence: VDRGCAYGTGGGGVD



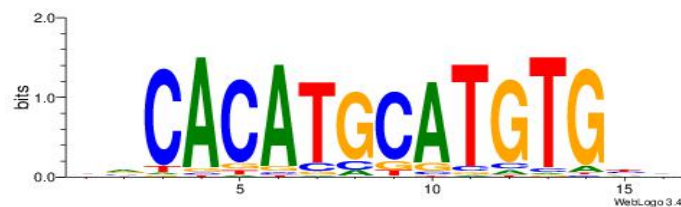
Dataset #: 4
 Motif ID: 118
 Motif name: yrCACATGCATGTGyr
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 4

Number of overlap: 13
Similarity score: 1.07966

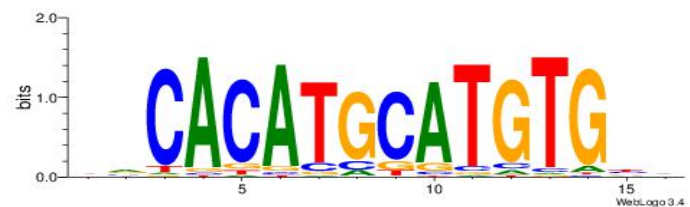
Alignment:

--DVCACATGCATGTGBH
CWTGTGTHATGCAAAT---

Original motif Consensus sequence: HVCACATGCATGTGBD

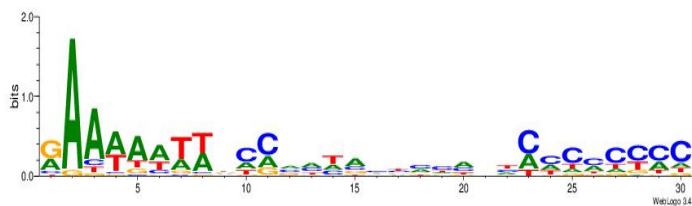


Reverse complement motif Consensus sequence: DVCACATGCATGTGBH

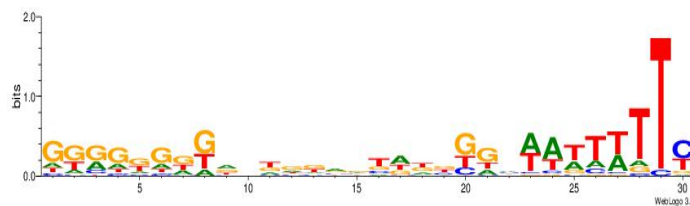


Dataset #: 3 Motif ID: 81 Motif name: Pax4

Original motif Consensus sequence: RAAWAWTWDCMVHHVBBHHHVHMHCMCYMC



Reverse complement motif Consensus sequence: GRKGRGDRHVDHDDVBBHHBRGDWAWTWTTM



Best Matches for Motif ID 81 (Highest to Lowest)

Dataset #: 3
Motif ID: 62
Motif name: TBP

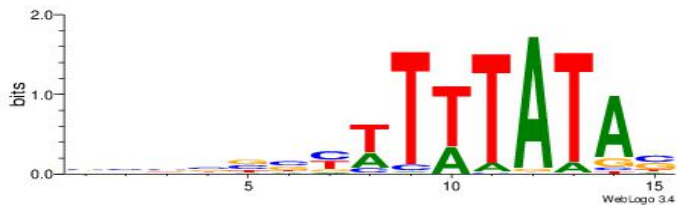
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 15
Similarity score: 0.0350174

Alignment:
STATAAAWRVVVBV-----
RAAWAWTWDCMVHHVBHHHVHMHCMCYMC

Original motif Consensus sequence: STATAAAWRVVVBV



Reverse complement motif Consensus sequence: VBVVVMWTTTAT

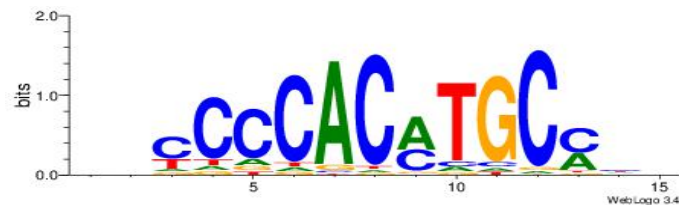


Dataset #: 4
Motif ID: 98
Motif name: myyCCCACmTGCmyr
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 15
Similarity score: 0.0514106

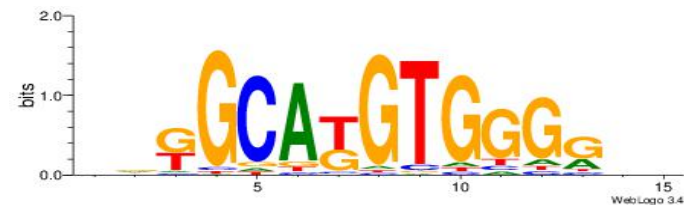
Alignment:

-----HBCCCCACMTGCMHV
RAAWAWTWDCMVHHVBBHHHVHMHCMCYMC

Original motif Consensus sequence: HBCCCCACMTGCMHV



Reverse complement motif Consensus sequence: VDRGCAYGTGGGGVD



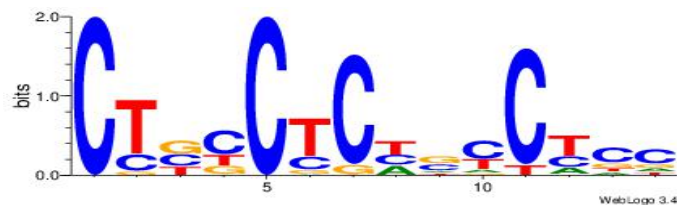
Dataset #:	2
Motif ID:	59
Motif name:	Motif 59
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	14
Similarity score:	0.542018

Alignment:

-----CTBCCTCHSYCYCC
RAAWAWTWDCMVHHVBBHHHVHMHCMCYMC

Original motif Consensus sequence: CTBCCTCHSYCYCC

Reverse complement motif Consensus sequence: GGMGKSHGAGGB

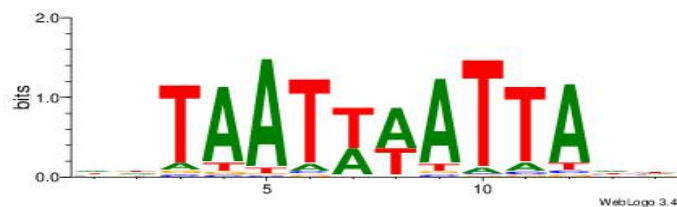


Dataset #: 4
 Motif ID: 125
 Motif name: wwTAATwwATTaww
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0.557646

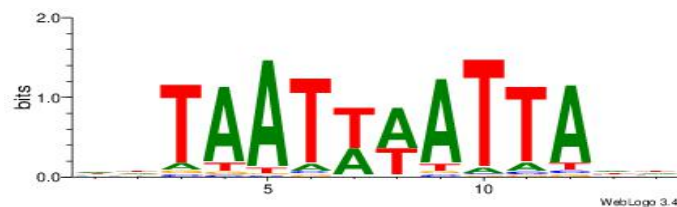
Alignment:

-----HHTAATWWATTADD
 GRKGRGDRHVVHDDVBBHHBRGDWAWTWTTM

Original motif Consensus sequence: DDTAATWWATTAAH



Reverse complement motif Consensus sequence: HHTAATWWATTAAH

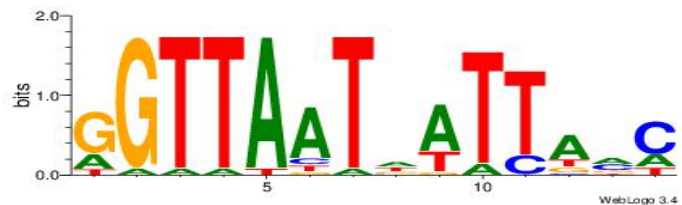


Dataset #: 3
 Motif ID: 68

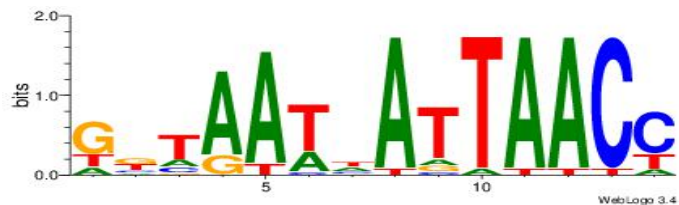
Motif name: HNF1A
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 14
Similarity score: 0.564862

Alignment:
-----GYTAATDATTAACC
GRKGRGDRHVVHDDVBBHHBRGDWAWTWTTM

Original motif Consensus sequence: GGTTAATDATTAMC

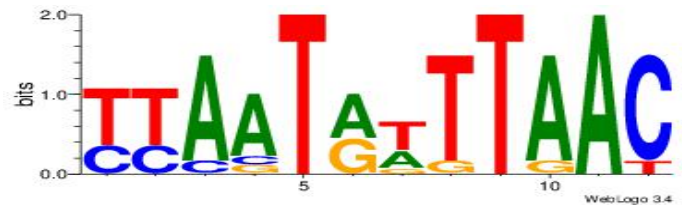


Reverse complement motif Consensus sequence: GYTAATDATTAAC

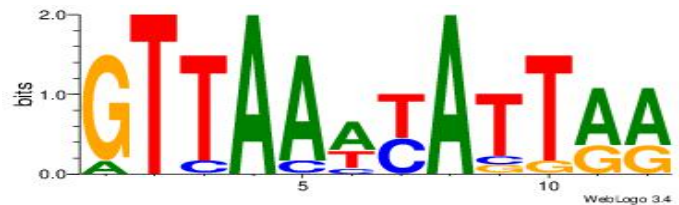


Dataset #: 3 Motif ID: 82 Motif name: HNF1B

Original motif Consensus sequence: TTAATRWTTAAC



Reverse complement motif Consensus sequence: GTTAAWKATTAA



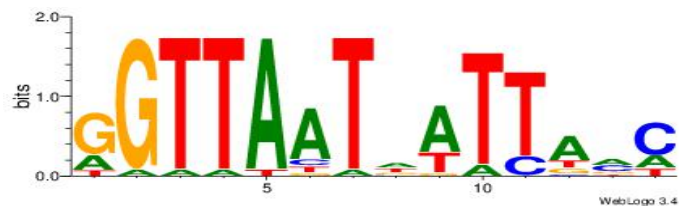
Best Matches for Motif ID 82 (Highest to Lowest)

Dataset #: 3
 Motif ID: 68
 Motif name: HNF1A
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 12
 Similarity score: 0.0255432

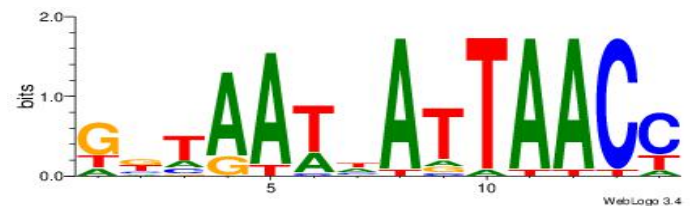
Alignment:

GYTAATDATTAAACC
 -TTAATRWTTAAC-

Original motif Consensus sequence: GGTTAATDATTAMC



Reverse complement motif Consensus sequence: GYTAATDATTAAACC

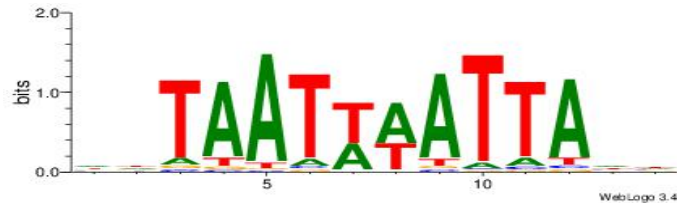


Dataset #: 4
 Motif ID: 125
 Motif name: wwTAATwwATTaww
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 12

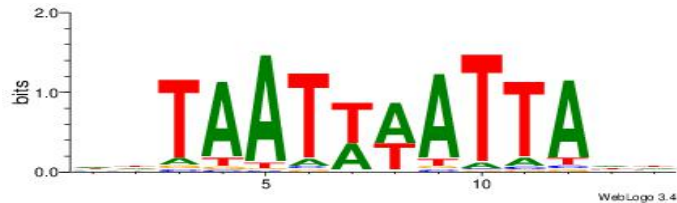
Similarity score: 0.0657822

Alignment:
DDTAATWWATTAHH
-GTTAAWKATTAA-

Original motif Consensus sequence: DDTAATWWATTAHH



Reverse complement motif Consensus sequence: HHTAATWWATTAA

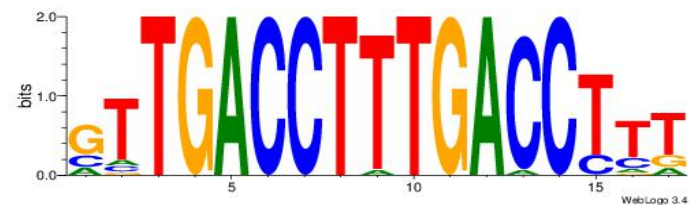
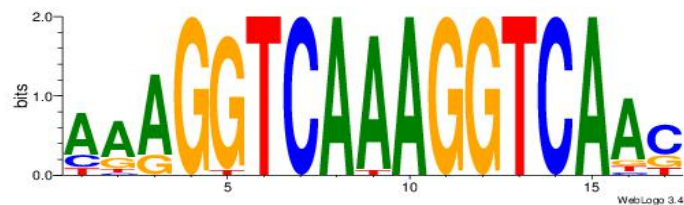


Dataset #: 3
Motif ID: 84
Motif name: NR1H2RXRA
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2
Number of overlap: 12
Similarity score: 0.0685194

Alignment:
AAAGGTCAAAGGTCAAC
----GTTAAWKATTAA-

Original motif Consensus sequence: AAAGGTCAAAGGTCAAC

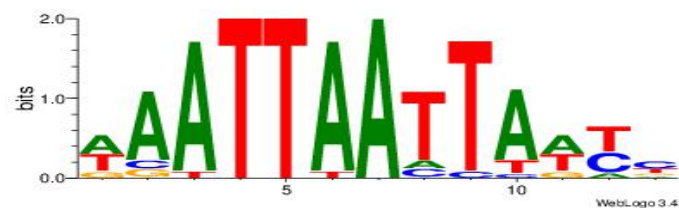
Reverse complement motif Consensus sequence:
GTTGACCTTTGACCTTT



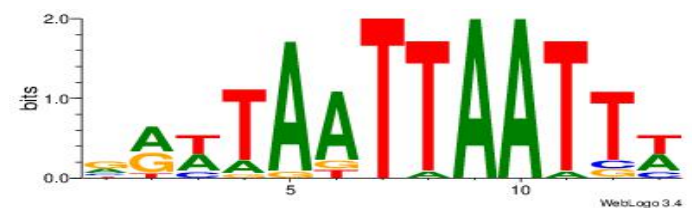
Dataset #: 3
 Motif ID: 66
 Motif name: Lhx3
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 12
 Similarity score: 0.0745842

Alignment:
 WAATTAATTAWYB
 TTAATRWTTAAC-

Original motif Consensus sequence: WAATTAATTAWYB



Reverse complement motif Consensus sequence: BMWTAATTAATTW



Dataset #: 2
 Motif ID: 60

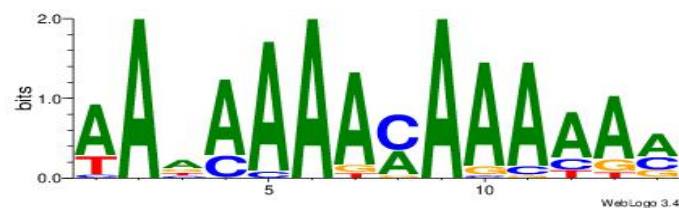
Motif name:	Motif 60
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	12
Similarity score:	0.0845958

Alignment:

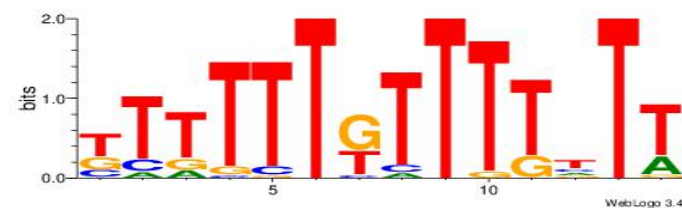
AADAAAAMAAAAAM

-GTTAAWKATTAA-

Original motif Consensus sequence: AADAAAAMAAAAAM



Reverse complement motif Consensus sequence: YTTTTTRTTTDDTT

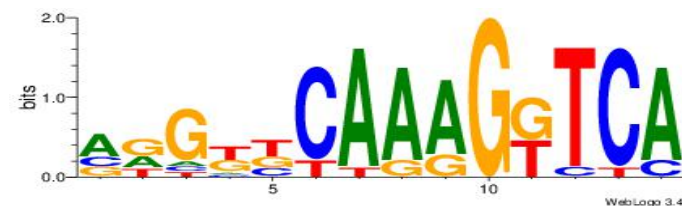


Dataset #: 3 Motif ID: 83 Motif name: NR2F1

Original motif Consensus sequence: TGAMCTTTGMMCYT



Reverse complement motif Consensus sequence: AKGYCAAAGRTCA



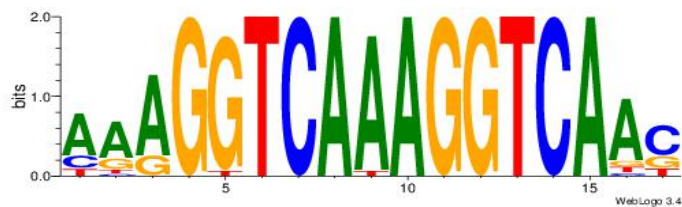
Best Matches for Motif ID 83 (Highest to Lowest)

Dataset #: 3
 Motif ID: 84
 Motif name: NR1H2RXRA
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 14
 Similarity score: 0.0174588

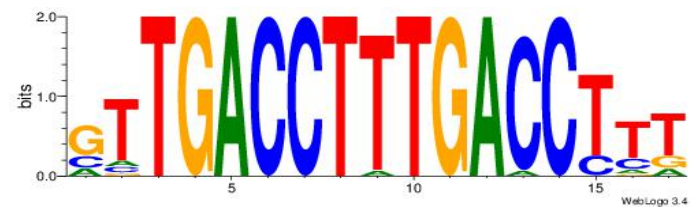
Alignment:

GTTGACCTTTGACCTTT
 --TGAMCTTTGMMCYT-

Original motif Consensus sequence: AAAGGTCAAAGGTCAAC



Reverse complement motif Consensus sequence: GTTGACCTTTGACCTTT



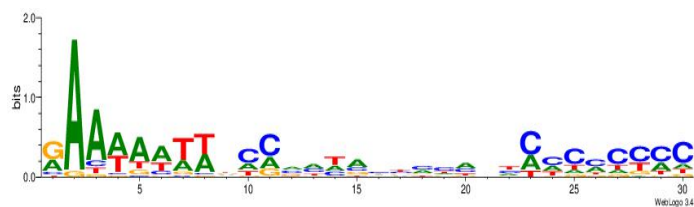
Dataset #: 3
 Motif ID: 81
 Motif name: Pax4
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 8

Number of overlap: 14
Similarity score: 0.0713206

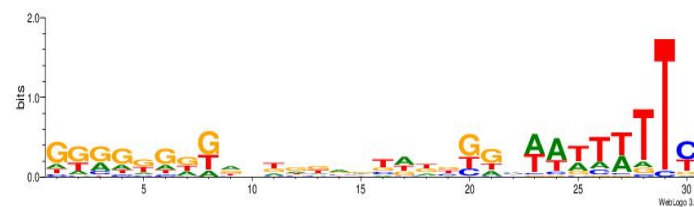
Alignment:

RAAWAWTWDCMVHHVBBHHHVHMHCMCYMC
-----TGAMCTTTGMMCYT-----

Original motif Consensus sequence:
RAAWAWTWDCMVHHVBBHHHVHMHCMCYMC



Reverse complement motif Consensus sequence:
GRKGRGDRHVHDDVBBHHBRGDWAWTWTTM

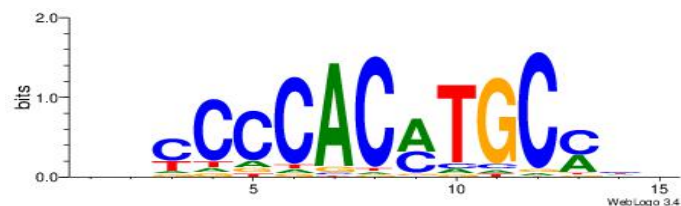


Dataset #: 4
Motif ID: 98
Motif name: myyCCCACmTGCmyr
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 14
Similarity score: 0.0745302

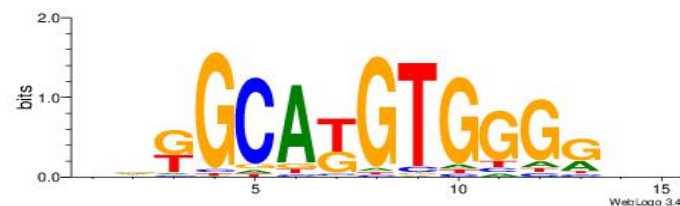
Alignment:

HBCCCCACMTGCMHV
AKGY YCAAAGRTCA-

Original motif Consensus sequence: HBCCCCACMTGCMHV



Reverse complement motif Consensus sequence: VDRGCAYGTGGGGVD



Dataset #: 3
Motif ID: 71
Motif name: Evi1
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 3
Number of overlap: 12
Similarity score: 1.06838

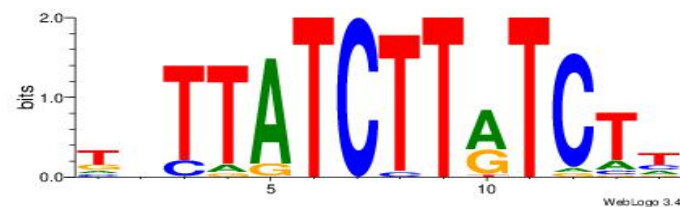
Alignment:

--TBTTATCTTMTCTT
TGAMCTTTGMMCYT--

Original motif Consensus sequence: AAGAYAAGATAABA



Reverse complement motif Consensus sequence: TBTTATCTTMTCTT

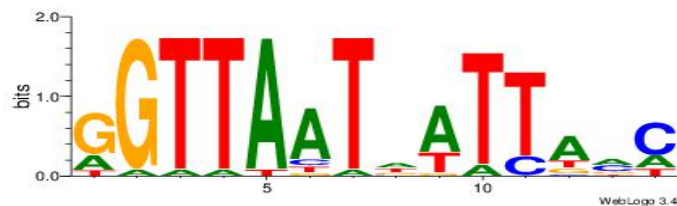


Dataset #: 3
 Motif ID: 68
 Motif name: HNF1A
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 12
 Similarity score: 1.06886

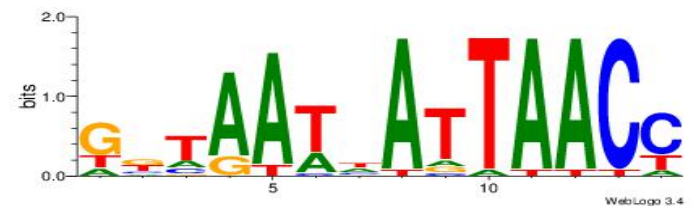
Alignment:

GGTAAATDATTAMC--
 --TGAMCTTTGMMCYT

Original motif Consensus sequence: GGTAAATDATTAMC



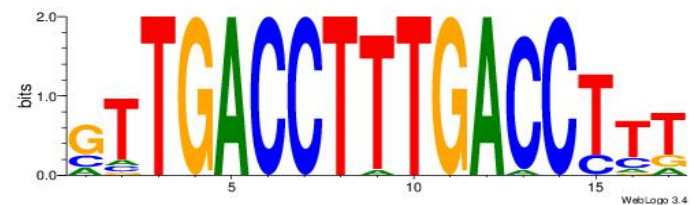
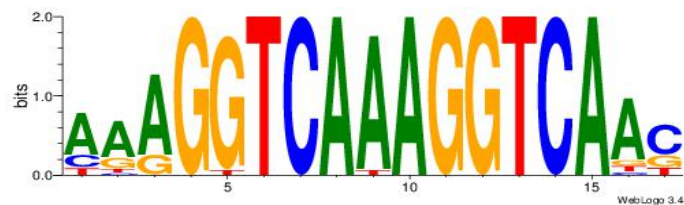
Reverse complement motif Consensus sequence: GYTAATDATTAAAC



Dataset #: 3 Motif ID: 84 Motif name: NR1H2RXRA

Original motif Consensus sequence: AAAGGTCAAAGGTCAAC

Reverse complement motif Consensus sequence:
GTTGACCTTTGACCTT



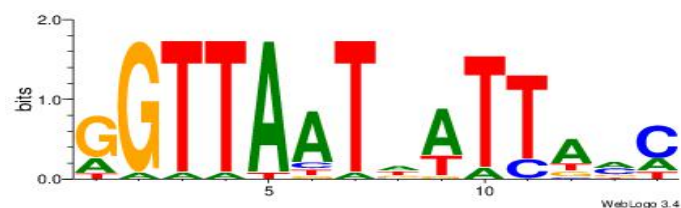
Best Matches for Motif ID 84 (Highest to Lowest)

Dataset #: 3
 Motif ID: 68
 Motif name: HNF1A
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0.0896514

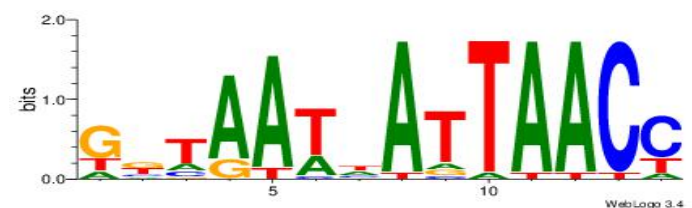
Alignment:

---GGTTAATDATTAMC
 AAAGGTCAAAGGTCAAC

Original motif Consensus sequence: GGTTAATDATTAMC



Reverse complement motif Consensus sequence: GYTAATDATTAAAC



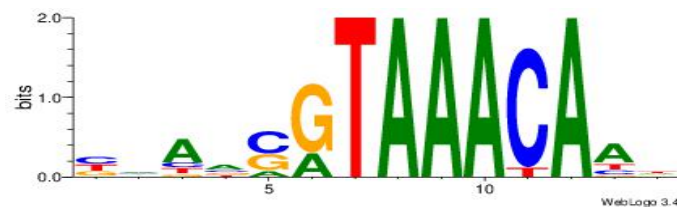
Dataset #: 3

Motif ID: 75
 Motif name: FOXF2
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 13
 Similarity score: 0.595213

Alignment:

----DTTGTTTACSBTBB
 GTTGACCTTTGACCTTT-

Original motif Consensus sequence: BHADSGTAAACAAD



Reverse complement motif Consensus sequence: DTTGTTTACSBTBB

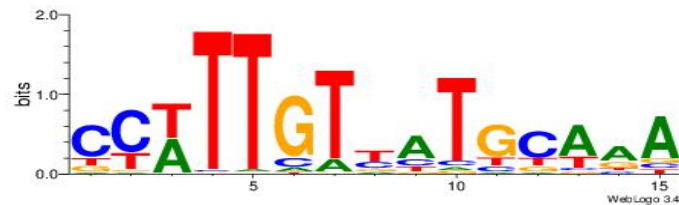


Dataset #: 3
 Motif ID: 76
 Motif name: Sox2
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 4
 Number of overlap: 12
 Similarity score: 1.0817

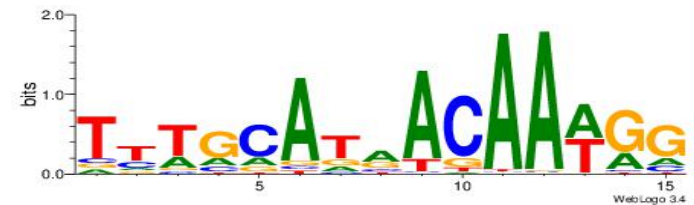
Alignment:

```
-----TTTGCATMACAAWGG
AAAGGTCAAAGGTCAAC----
```

Original motif Consensus sequence: CCWTTGTYATGCAAA



Reverse complement motif Consensus sequence:
TTTGCATMACAAWGG



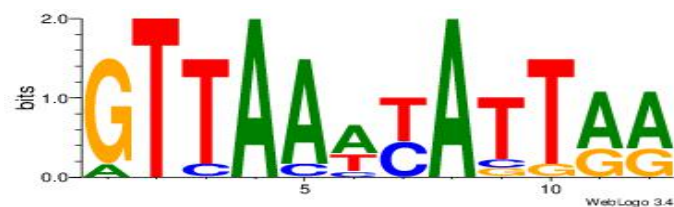
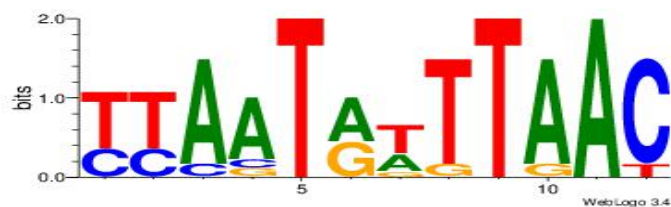
Dataset #:	3
Motif ID:	82
Motif name:	HNF1B
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	12
Similarity score:	1.0906

Alignment:

```
-----TTAATRWTTAAC
AAAGGTCAAAGGTCAAC
```

Original motif Consensus sequence: TTAATRWTTAAC

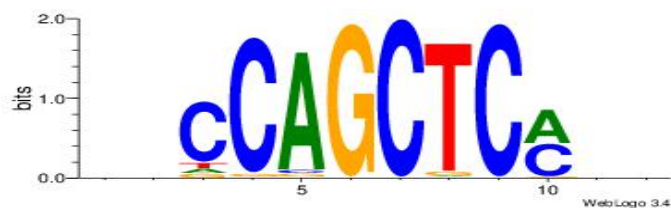
Reverse complement motif Consensus sequence: GTTAAWKATTAA



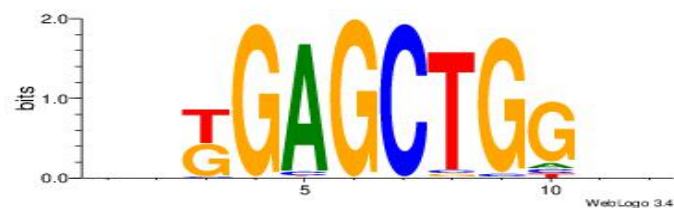
Dataset #: 4
 Motif ID: 119
 Motif name: cbCCAGCTCmyk
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 12
 Similarity score: 1.09978

Alignment:
 HBYGAGCTGGBB-----
 GTTGACCTTTGACCTTT

Original motif Consensus sequence: BBCCAGCTCMBD



Reverse complement motif Consensus sequence: HBYGAGCTGGBB

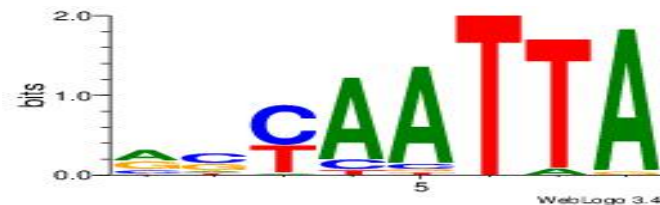


Dataset #: 3 Motif ID: 85 Motif name: Nobox

Original motif Consensus sequence: TAATRSY



Reverse complement motif Consensus sequence: MSMAATTA



Best Matches for Motif ID 85 (Highest to Lowest)

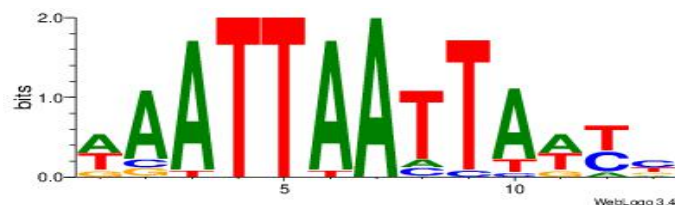
Dataset #:	3
Motif ID:	66
Motif name:	Lhx3
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	5
Number of overlap:	8
Similarity score:	0.0419408

Alignment:

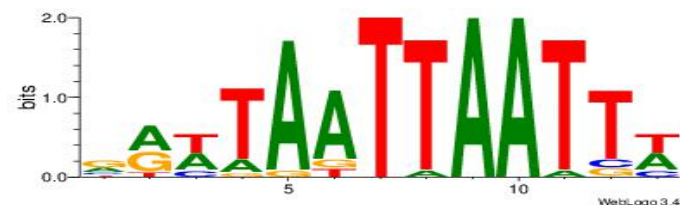
WAATTAATTAWYB

----TAATRSY-

Original motif Consensus sequence: WAATTAATTAWYB



Reverse complement motif Consensus sequence: BMWTAATTAATTW

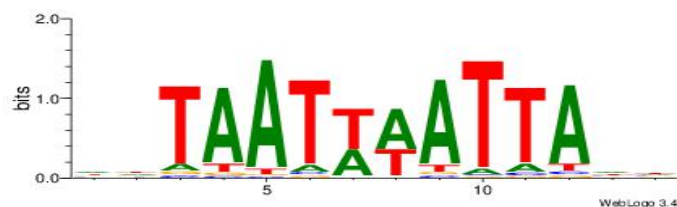


Dataset #: 4
 Motif ID: 125
 Motif name: wwTAATwwATTaww
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 7
 Number of overlap: 8
 Similarity score: 0.0591612

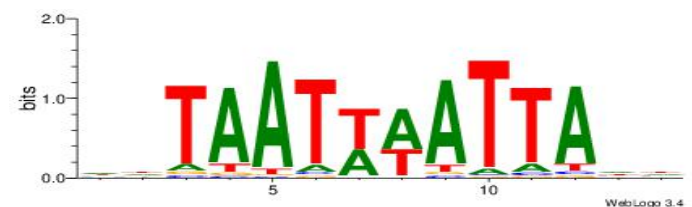
Alignment:

HHTAATWWATTADD
 -----TAATTRS Y

Original motif Consensus sequence: DDTAATWWATTAAH



Reverse complement motif Consensus sequence: HHTAATWWATTAD

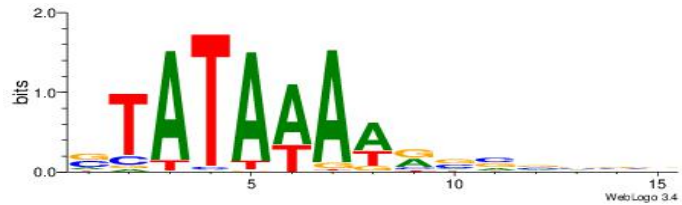


Dataset #: 3
 Motif ID: 62
 Motif name: TBP
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 5
 Number of overlap: 8

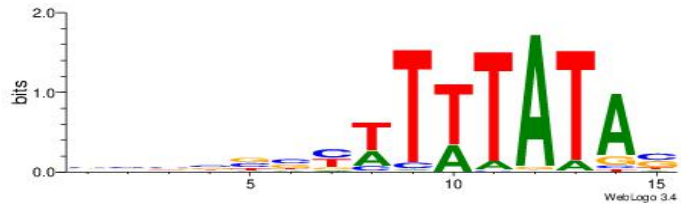
Similarity score: 0.0604219

Alignment:
VBVVVMWTTTATAS
----MSMAATTA----

Original motif Consensus sequence: STATAAAWRVVVBV



Reverse complement motif Consensus sequence: VBVVVMWTTTAT

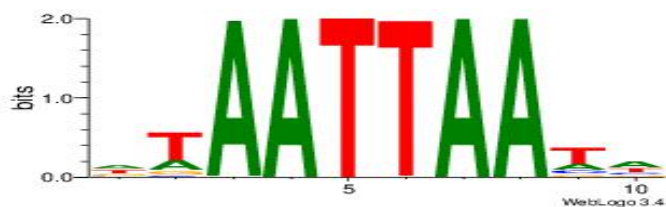


Dataset #: 4
Motif ID: 106
Motif name: wtAATTAAtw
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2
Number of overlap: 8
Similarity score: 0.0649275

Alignment:
DTAATTAATH
-TAATTRSY-

Original motif Consensus sequence: DTAATTAATH

Reverse complement motif Consensus sequence: HATTAATTAD

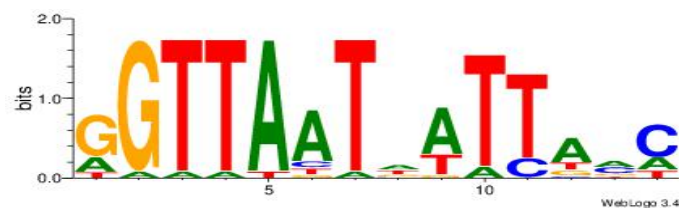


Dataset #: 3
 Motif ID: 68
 Motif name: HNF1A
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 8
 Similarity score: 0.0652412

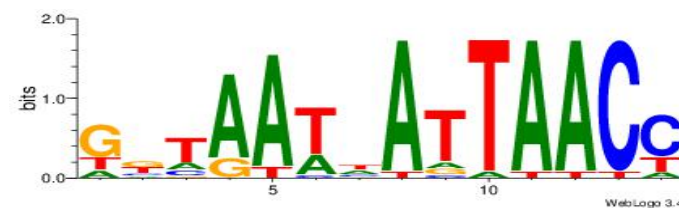
Alignment:

GGTTAATDATTAMC
 -----TAATTSY

Original motif Consensus sequence: GGTTAATDATTAMC



Reverse complement motif Consensus sequence: GYTAATDATTAAAC



Dataset #: 3 Motif ID: 86 Motif name: FOXO3

Original motif Consensus sequence: KGTAACA



Reverse complement motif Consensus sequence: TGTTTACR



Best Matches for Motif ID 86 (Highest to Lowest)

Dataset #:	3
Motif ID:	75
Motif name:	FOXF2
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	5
Number of overlap:	8
Similarity score:	0.0236411

Alignment:

DTTGTTTACSBTBB

--TGTTTACR----

Original motif Consensus sequence: BHADSGTAAACAAD



Reverse complement motif Consensus sequence: DTTGTTTACSBTBB



Dataset #: 3
 Motif ID: 70
 Motif name: Foxq1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 4
 Number of overlap: 8
 Similarity score: 0.0397436

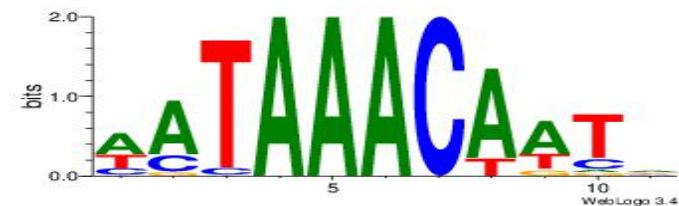
Alignment:

HATTGTTTATW
 TGTTTACR---

Original motif Consensus sequence: HATTGTTTATW



Reverse complement motif Consensus sequence: WATAACAATH

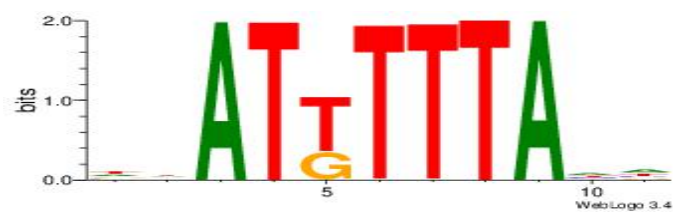


Dataset #: 4
 Motif ID: 108
 Motif name: wwATkTTTAww
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 8

Similarity score: 0.054763

Alignment:
DHATKTTTAHH
---TGTTTACR

Original motif Consensus sequence: DHATKTTTAHH



Reverse complement motif Consensus sequence: HHTAAARATHD

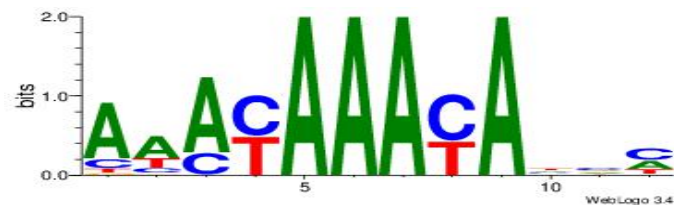
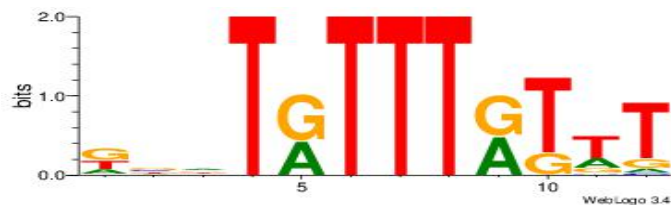


Dataset #: 3
Motif ID: 67
Motif name: FOXI1
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 2
Number of overlap: 8
Similarity score: 0.0656948

Alignment:
AAAMAAAMADBY
---KGTAACA-

Original motif Consensus sequence: KBDTRTTTTRTTT

Reverse complement motif Consensus sequence: AAAMAAAMADBY



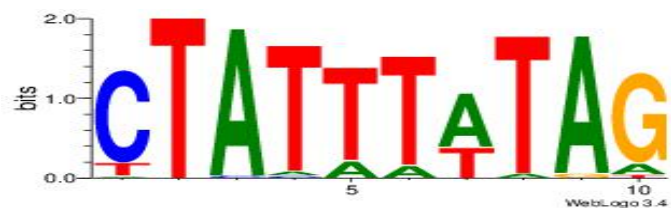
Dataset #: 3
 Motif ID: 61
 Motif name: MEF2A
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 8
 Similarity score: 0.0727619

Alignment:

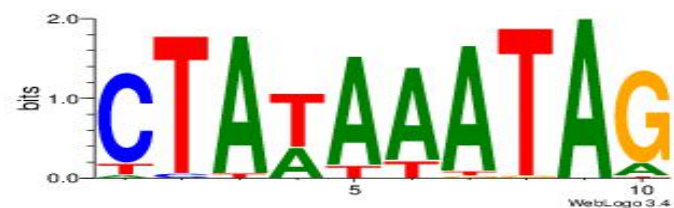
CTATTTWTAG

-TGTTTACR-

Original motif Consensus sequence: CTATTTWTAG

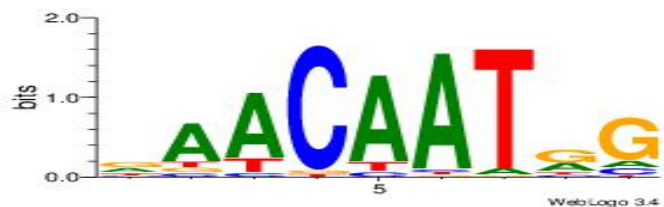


Reverse complement motif Consensus sequence: CTAWAAATAG



Dataset #: 3 Motif ID: 87 Motif name: SOX9

Original motif Consensus sequence: DAACAATRG



Reverse complement motif Consensus sequence: CMATTGTTH



Best Matches for Motif ID 87 (Highest to Lowest)

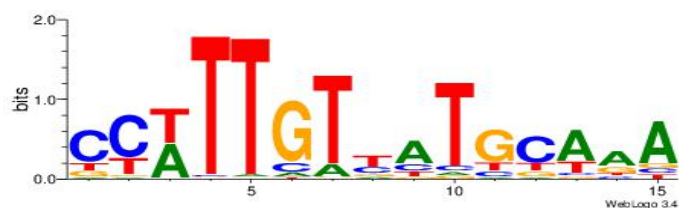
Dataset #:	3
Motif ID:	76
Motif name:	Sox2
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	7
Number of overlap:	9
Similarity score:	0.018186

Alignment:

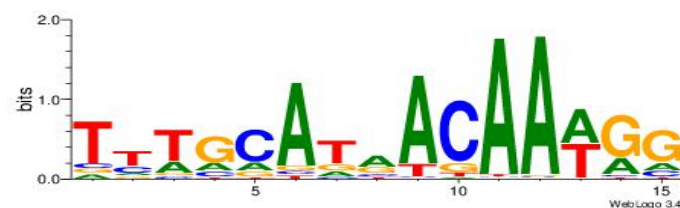
TTTGCATMACAAWGG

DAACAATRG-----

Original motif Consensus sequence: CCWTTGTYATGCAAA



Reverse complement motif Consensus sequence:
TTTGCATMACAAWGG

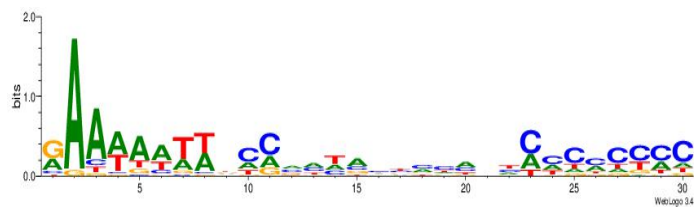


Dataset #: 3
 Motif ID: 81
 Motif name: Pax4
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 9
 Similarity score: 0.0583456

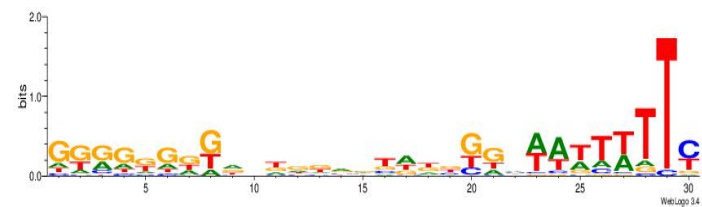
Alignment:

RAAWAWTWDCMVHHVBBHHHVHMHCMCYMC
 DAACAATRG-----

Original motif Consensus sequence:
 RAAWAWTWDCMVHHVBBHHHVHMHCMCYMC



Reverse complement motif Consensus sequence:
 GRKGRGDRHVHDDVBBHHBRGDWAWTWTTM

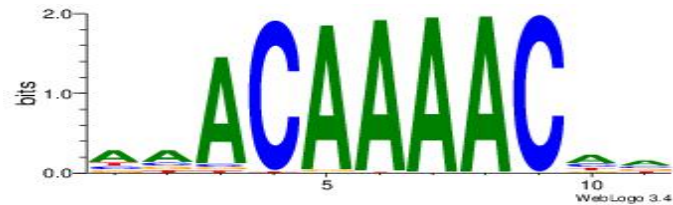


Dataset #: 4
 Motif ID: 89
 Motif name: aaACAAAACaa
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1

Number of overlap: 9
Similarity score: 0.0599655

Alignment:
AAACAAAACHV
DAACAATRG--

Original motif Consensus sequence: AAACAAAACHV



Reverse complement motif Consensus sequence: BHGTTTTGTTT

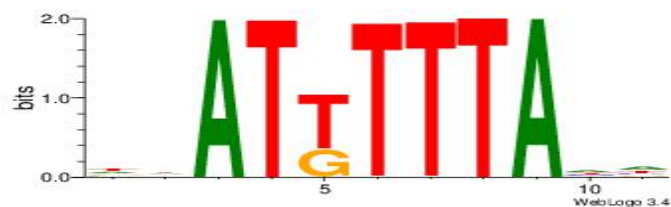


Dataset #: 4
Motif ID: 108
Motif name: wwATkTTTAww
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 3
Number of overlap: 9
Similarity score: 0.0642936

Alignment:
DHATKTTTAHH
CMATTGTTH--

Original motif Consensus sequence: DHATKTTTAHH

Reverse complement motif Consensus sequence: HHTAAARATHD



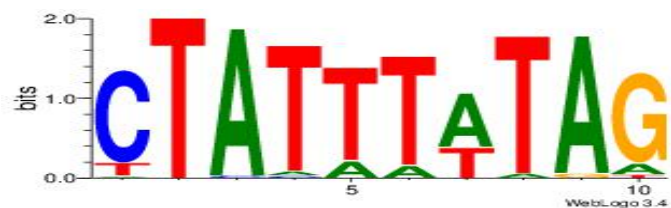
Dataset #: 3
 Motif ID: 61
 Motif name: MEF2A
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 9
 Similarity score: 0.0646581

Alignment:

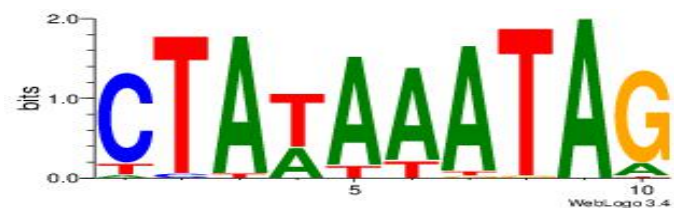
CTATTTWTAG

-CMATTGTH

Original motif Consensus sequence: CTATTTWTAG

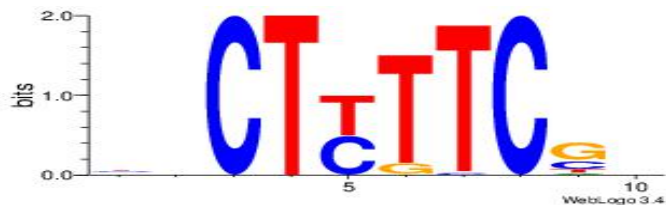


Reverse complement motif Consensus sequence: CTAWAAATAG



Dataset #: 4 **Motif ID: 88** **Motif name: ygCTyTTCsg**

Original motif Consensus sequence: HDCTYTTTCGB



Reverse complement motif Consensus sequence: BCGAAMAGHH



Best Matches for Motif ID 88 (Highest to Lowest)

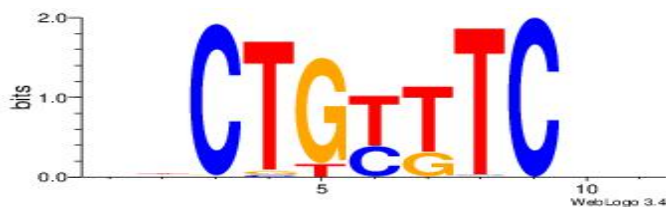
Dataset #: 4
 Motif ID: 113
 Motif name: htCTGyKTCbt
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 10
 Similarity score: 0.0278763

Alignment:

HVGAAMCAGVH

-BCGAAMAGHH

Original motif Consensus sequence: HBCTGYTTTCBH



Reverse complement motif Consensus sequence: HVGAAMCAGVH

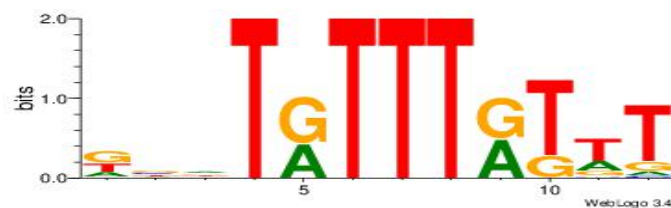


Dataset #: 3
 Motif ID: 67
 Motif name: FOXI1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 10
 Similarity score: 0.0294361

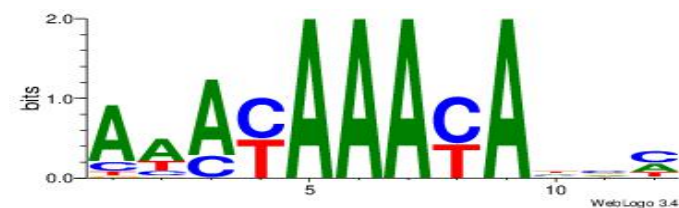
Alignment:

AAAMAAAMADBY
 --BCGAAMAGHH

Original motif Consensus sequence: KBDTRTTTTRTT



Reverse complement motif Consensus sequence: AAAMAAAMADBY

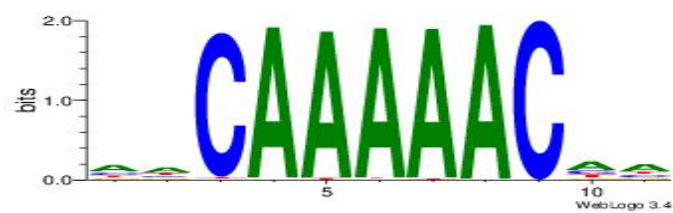


Dataset #: 4
 Motif ID: 109
 Motif name: aaCAAAAACaa
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 10

Similarity score: 0.0382901

Alignment:
HHCAAAAACHH
-BCGAAMAGHH

Original motif Consensus sequence: HHCAAAAACHH



Reverse complement motif Consensus sequence: HHGTTTTTGHH



Dataset #: 4
Motif ID: 91
Motif name: wtATTTTAWw
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: 0.0393404

Alignment:
HWTAAAATHD
BCGAAMAGHH

Original motif Consensus sequence: DHATTTTAWH

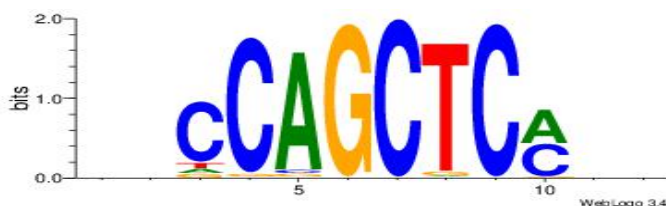
Reverse complement motif Consensus sequence: HWTAAAATHD



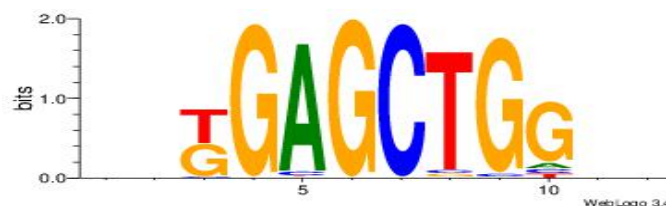
Dataset #: 4
 Motif ID: 119
 Motif name: cbCCAGCTCmyk
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 10
 Similarity score: 0.0400249

Alignment:
 HBYGAGCTGGBB
 -BCGAAMAGHH-

Original motif Consensus sequence: BBCCAGCTCMBD

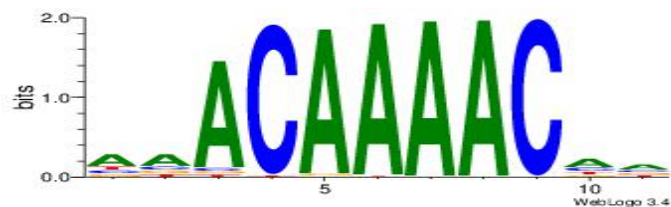


Reverse complement motif Consensus sequence: HBYGAGCTGGBB

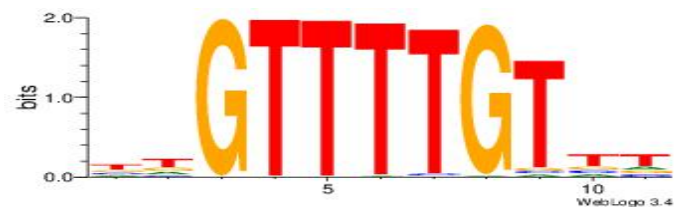


Dataset #: 4 Motif ID: 89 Motif name: aaACAAAACaa

Original motif Consensus sequence: AAACAAAACHV



Reverse complement motif Consensus sequence: BHGTTTTGTTT



Best Matches for Motif ID 89 (Highest to Lowest)

Dataset #:	4
Motif ID:	109
Motif name:	aaCAAAAACaa
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:	0.00582159

Alignment:

HHGTTTTTGHH

BHGTTTTGTTT

Original motif Consensus sequence: HHCAAAAACHH



Reverse complement motif Consensus sequence: HHGTTTTGHH

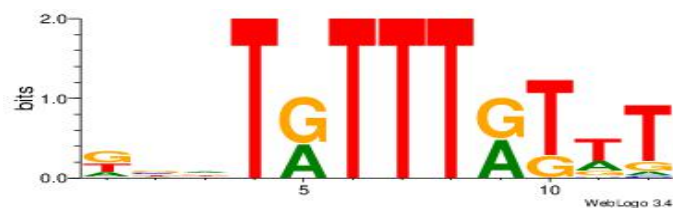


Dataset #: 3
 Motif ID: 67
 Motif name: FOXI1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 11
 Similarity score: 0.0320461

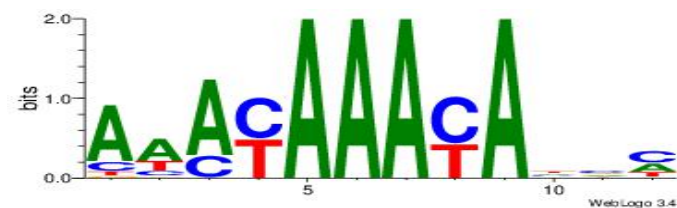
Alignment:

KBDTRTTTTRTTT
 BHGTTTTGTTT-

Original motif Consensus sequence: KBDTRTTTTRTTT



Reverse complement motif Consensus sequence: AAAMAAAMADBY

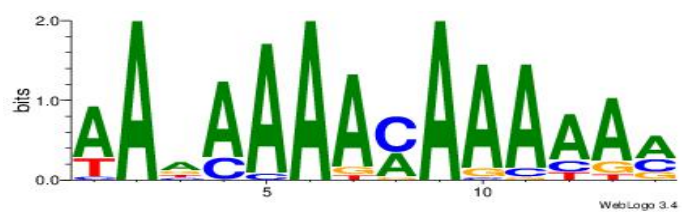


Dataset #: 2
 Motif ID: 60
 Motif name: Motif 60
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 11

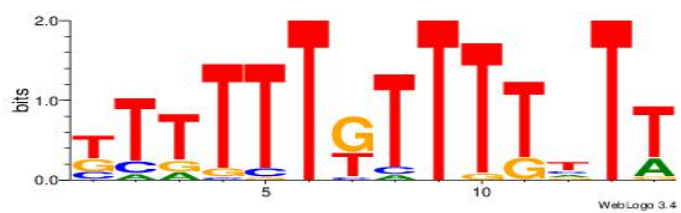
Similarity score: 0.039575

Alignment:
AADAAAAMAAAAAM
--AAACAAAACHV--

Original motif Consensus sequence: AADAAAAMAAAAAM



Reverse complement motif Consensus sequence: YTTTTTRTTTTDTT

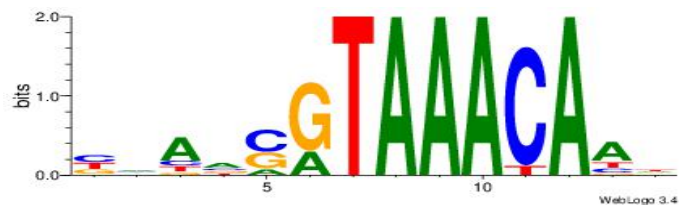


Dataset #: 3
Motif ID: 75
Motif name: FOXF2
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 3
Number of overlap: 11
Similarity score: 0.0401124

Alignment:
BHADSGTAAACAAD
--AAACAAAACHV--

Original motif Consensus sequence: BHADSGTAAACAAD

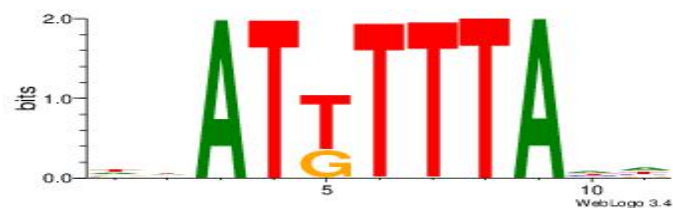
Reverse complement motif Consensus sequence: DTTGTTTACSBTBE



Dataset #: 4
 Motif ID: 108
 Motif name: wwATkTTTAww
 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: 0.0486334

Alignment:
 DHATKTTTAHH
 BHGTTTTGTTT

Original motif Consensus sequence: DHATKTTTAHH



Reverse complement motif Consensus sequence: HHTAAARATHD

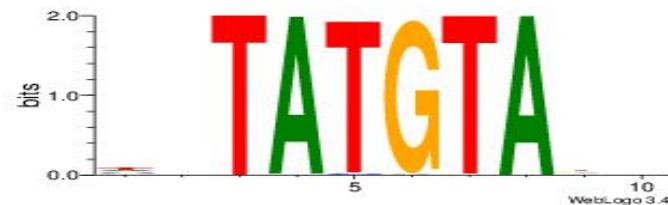


Dataset #: 4 Motif ID: 90 Motif name: ymTACATAyw

Original motif Consensus sequence: HHTACATABD



Reverse complement motif Consensus sequence: DBTATGTAHH



Best Matches for Motif ID 90 (Highest to Lowest)

Dataset #: 4
 Motif ID: 114
 Motif name: awAACAcAAwa
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 10
 Similarity score: 0.0626629

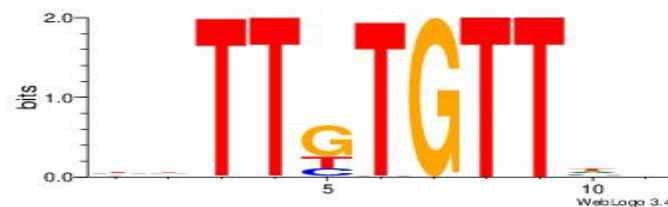
Alignment:

BDTTGTGTTDD
 -DBTATGTAHH

Original motif Consensus sequence: DDAACACAADV



Reverse complement motif Consensus sequence: BDTTGTGTTDD

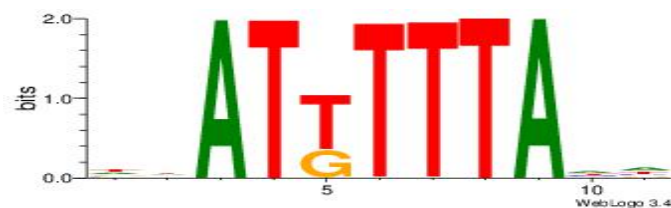


Dataset #: 4
 Motif ID: 108
 Motif name: wwATkTTTAww
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 10
 Similarity score: 0.0690336

Alignment:

HHTAAARATHD
 HHTACATABD-

Original motif Consensus sequence: DHATKTTTAHH



Reverse complement motif Consensus sequence: HHTAAARATHD

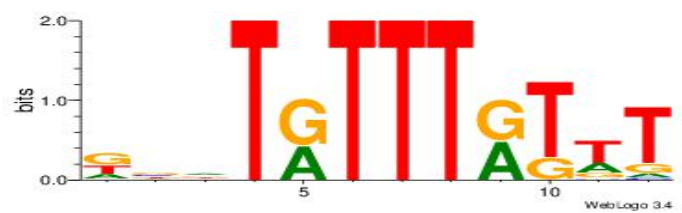


Dataset #: 3
 Motif ID: 67
 Motif name: FOXI1
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 10

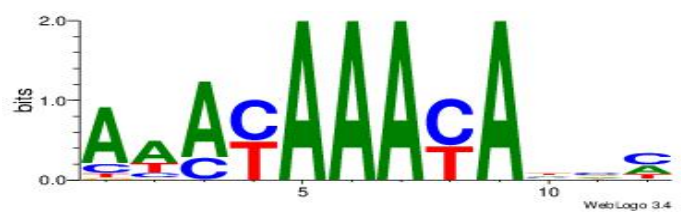
Similarity score: 0.0763781

Alignment:
AAAMAAAMADBY
-HHTACATABD-

Original motif Consensus sequence: KBDTRTTTTRTTT



Reverse complement motif Consensus sequence: AAAMAAAMADBY

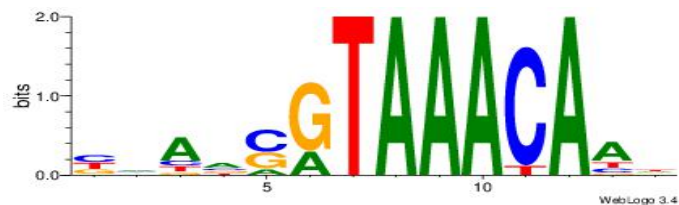


Dataset #: 3
Motif ID: 75
Motif name: FOXF2
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 5
Number of overlap: 10
Similarity score: 0.0772253

Alignment:
DTTGTTTACSBTBB
DBTATGTAHH----

Original motif Consensus sequence: BHADSGTAAACAAD

Reverse complement motif Consensus sequence: DTTGTTTACSBTBB



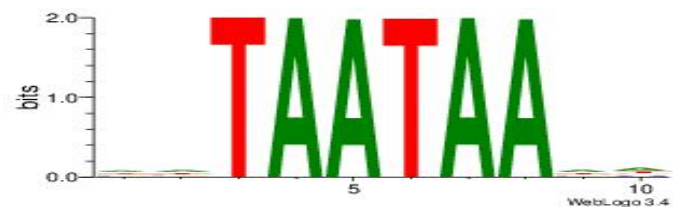
Dataset #: 4
 Motif ID: 100
 Motif name: wwTAATAAww
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 10
 Similarity score: 0.0773471

Alignment:

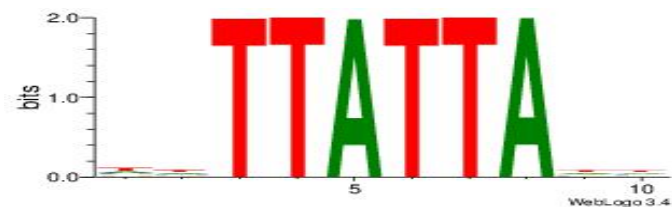
DDTTATTAHD

DBTATGTAHH

Original motif Consensus sequence: DHTAATAADD



Reverse complement motif Consensus sequence: DDTTATTAHD

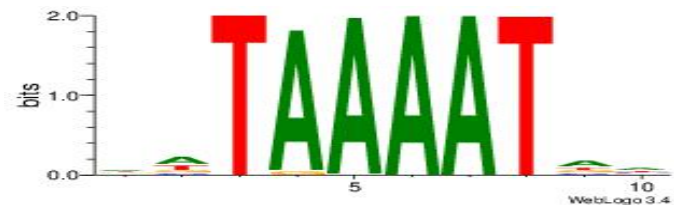


Dataset #: 4 Motif ID: 91 Motif name: wtATTTTAww

Original motif Consensus sequence: DHATTTTAWH



Reverse complement motif Consensus sequence: HWTAAAATHD



Best Matches for Motif ID 91 (Highest to Lowest)

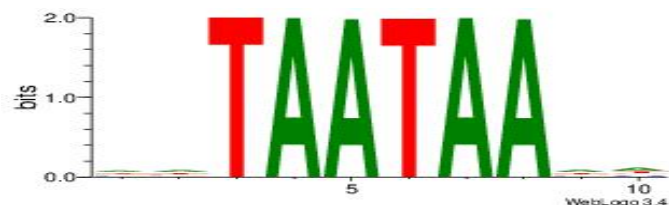
Dataset #: 4
 Motif ID: 100
 Motif name: wwTAATAAww
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 10
 Similarity score: 0.0307554

Alignment:

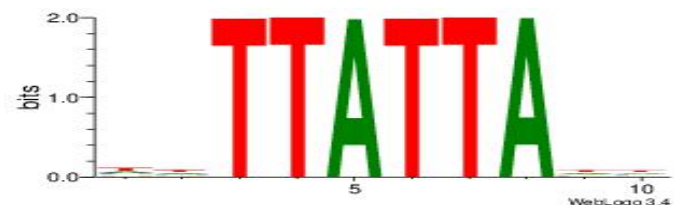
DHTAATAADD

HWTAAAATHD

Original motif Consensus sequence: DHTAATAADD



Reverse complement motif Consensus sequence: DDTTATTAHD



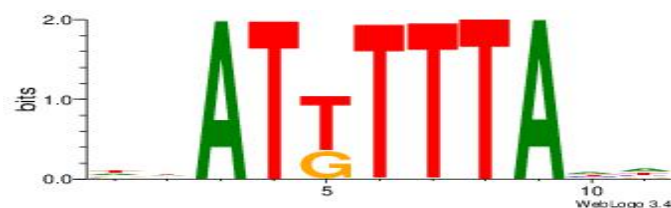
Dataset #: 4
 Motif ID: 108
 Motif name: wwATkTTTAww
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 10
 Similarity score: 0.031047

Alignment:

HHTAAARATHD

-HWTAAAATHD

Original motif Consensus sequence: DHATKTTTAHH



Reverse complement motif Consensus sequence: HHTAAARATHD

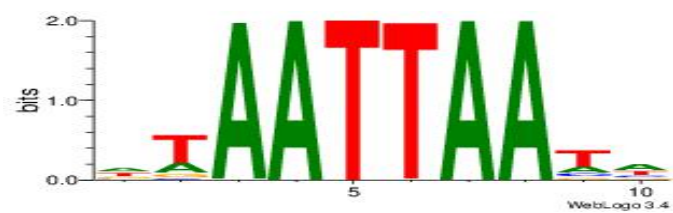


Dataset #: 4
 Motif ID: 106
 Motif name: wtAATTAAtw
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 10

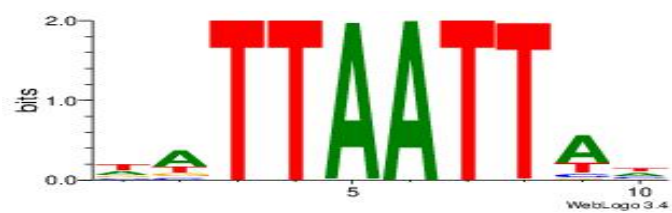
Similarity score: 0.0371798

Alignment:
DTAATTAATH
DHATTTTAWH

Original motif Consensus sequence: DTAATTAATH



Reverse complement motif Consensus sequence: HATTAATTAD



Dataset #: 4
Motif ID: 95
Motif name: rmATGCTAww
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: 0.0404266

Alignment:
DHATGCTADH
DHATTTTAWH

Original motif Consensus sequence: DHATGCTADH

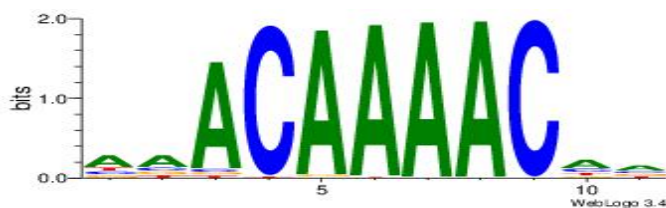
Reverse complement motif Consensus sequence: HDTAGCATHD



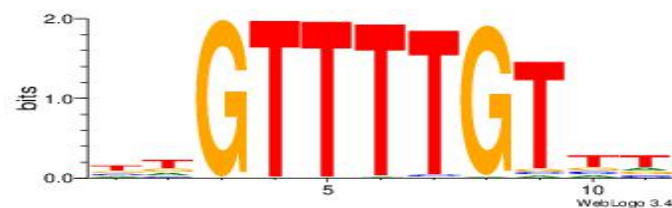
Dataset #: 4
 Motif ID: 89
 Motif name: aaACAAACaa
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 10
 Similarity score: 0.0448101

Alignment:
 BHGTTTTGTTT
 -DHATTTTAWH

Original motif Consensus sequence: AAACAAACHV



Reverse complement motif Consensus sequence: BHGTTTTGTTT



Dataset #: 4 Motif ID: 92 Motif name: cgAKGyCAcg

Original motif Consensus sequence: CGAGGYCACV



Reverse complement motif Consensus sequence: VGTGMCCTCG



Best Matches for Motif ID 92 (Highest to Lowest)

Dataset #:	4
Motif ID:	97
Motif name:	sgArGCCACg
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:	0.00323214

Alignment:

SGARGCCACG

CGAGGYCACV

Original motif Consensus sequence: SGARGCCACG



Reverse complement motif Consensus sequence: CGTGGCKTCS



Dataset #: 4
 Motif ID: 107
 Motif name: crCGyGCRcg
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 10
 Similarity score: 0.039949

Alignment:

CGTGCACGCG
 VGTGMCCTCG

Original motif Consensus sequence: CGCGTGCACG



Reverse complement motif Consensus sequence: CGTGCACGCG

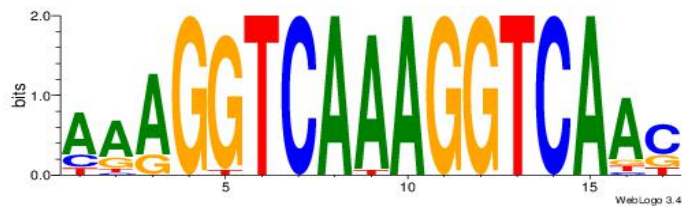


Dataset #: 3
 Motif ID: 84
 Motif name: NR1H2RXRA
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 8
 Number of overlap: 10

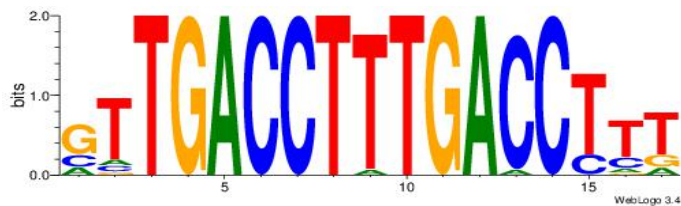
Similarity score: 0.0444539

Alignment:
GTTGACCTTTGACCTTT
VGTGMCCTCG-----

Original motif Consensus sequence: AAAGGTCAAAGGTCAAC



Reverse complement motif Consensus sequence: GTTGACCTTTGACCTTT



Dataset #: 4
Motif ID: 95
Motif name: rmATGCTAww
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: 0.0540906

Alignment:
DHATGCTADH
CGAGGYCACV

Original motif Consensus sequence: DHATGCTADH

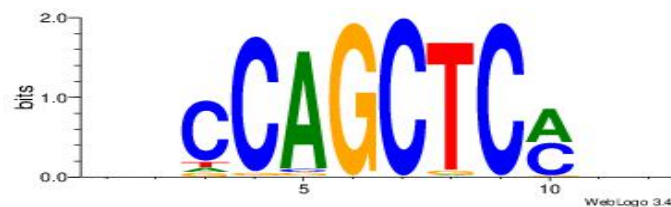
Reverse complement motif Consensus sequence: HDTAGCATHD



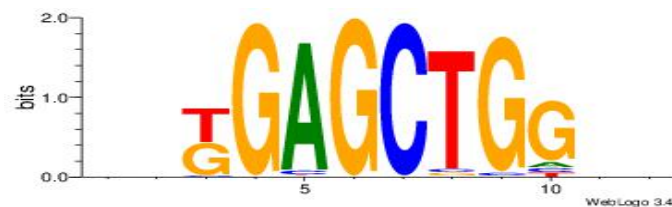
Dataset #: 4
 Motif ID: 119
 Motif name: cbCCAGCTCmyk
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 10
 Similarity score: 0.0546695

Alignment:
 HBYGAGCTGGBB
 VGTGMCCTCG--

Original motif Consensus sequence: BBCCAGCTCMBD

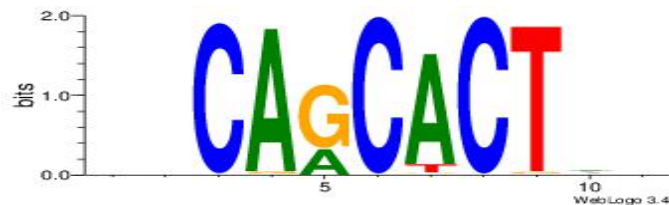


Reverse complement motif Consensus sequence: HBYGAGCTGGBB

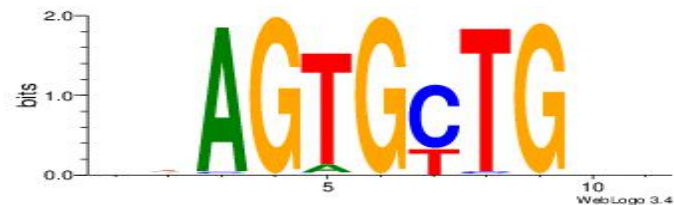


Dataset #: 4 Motif ID: 93 Motif name: cmCARCACTwr

Original motif Consensus sequence: BHCAGCACTHV



Reverse complement motif Consensus sequence: VHAGTGCTGHB

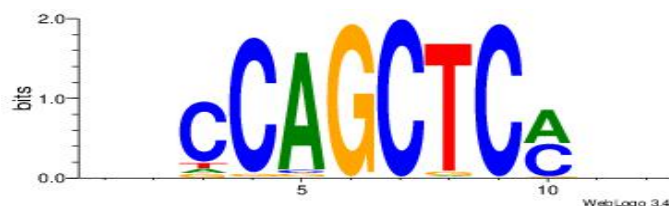


Best Matches for Motif ID 93 (Highest to Lowest)

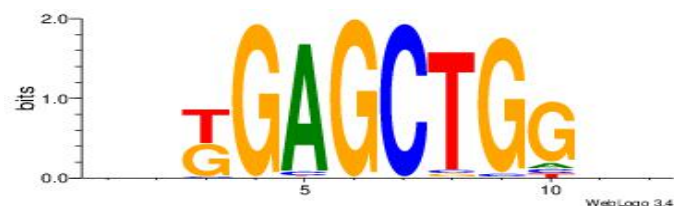
Dataset #: 4
 Motif ID: 119
 Motif name: cbCCAGCTCmyk
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.00936148

Alignment:
 BBCCAGCTCMBD
 -BHCAGCACTHV

Original motif Consensus sequence: BBCCAGCTCMBD



Reverse complement motif Consensus sequence: HBYGAGCTGGBB



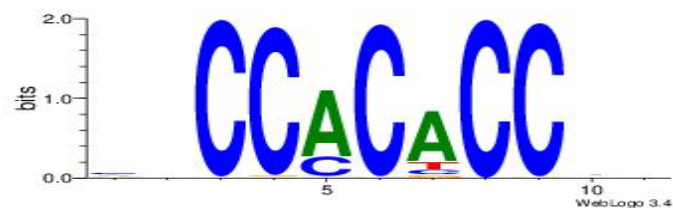
Dataset #: 4
 Motif ID: 110
 Motif name: cmCCACACCcm
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.0121475

Alignment:

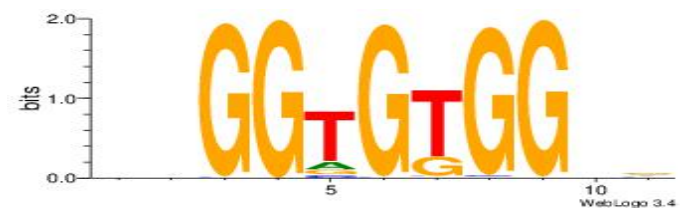
HVCCACACCBV

BHCAGCACTHV

Original motif Consensus sequence: HVCCACACCBV



Reverse complement motif Consensus sequence: VBGGTGTGGBD

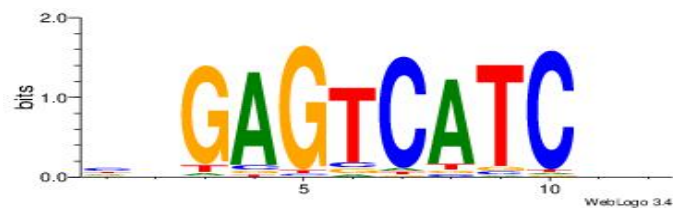


Dataset #: 4
 Motif ID: 121
 Motif name: ctGAGTCATCkb
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 11

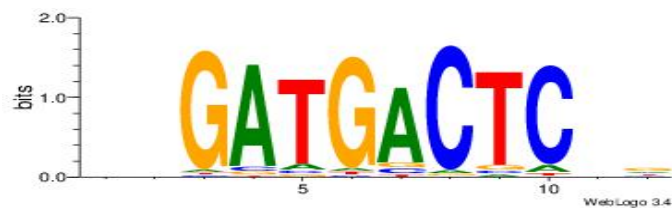
Similarity score: 0.0295417

Alignment:
HDGAGTCATCDB
-VHAGTGCTGHB

Original motif Consensus sequence: HDGAGTCATCDB



Reverse complement motif Consensus sequence: BHGATGACTCDD

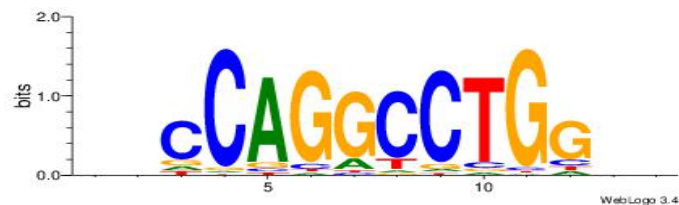
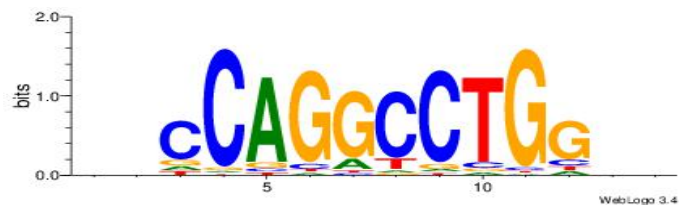


Dataset #: 4
Motif ID: 122
Motif name: hsCCAGGCCTGGsr
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 2
Number of overlap: 11
Similarity score: 0.0336897

Alignment:
HBCCAGGCCTGGVD
--VHAGTGCTGHB-

Original motif Consensus sequence: HVCCAGGCCTGGBD

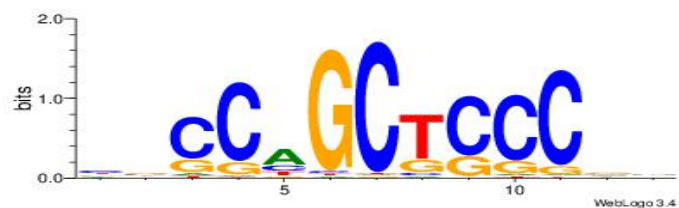
Reverse complement motif Consensus sequence: HBCCAGGCCTGGV



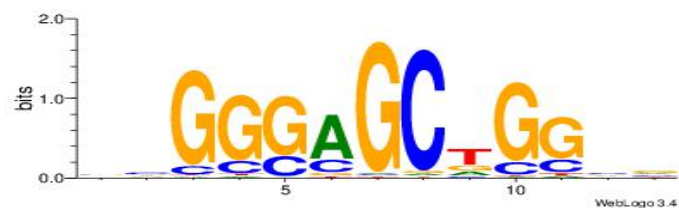
Dataset #: 4
 Motif ID: 103
 Motif name: csCCaGCTCCCgs
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 11
 Similarity score: 0.0373286

Alignment:
 BBCCAGCTCCCVB
 -BHCAGCACTHV-

Original motif Consensus sequence: BBCCAGCTCCCVB

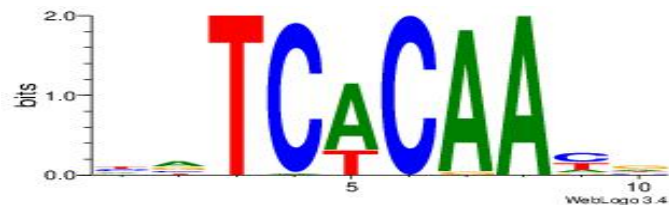


Reverse complement motif Consensus sequence: BVGGGAGCTGGBB

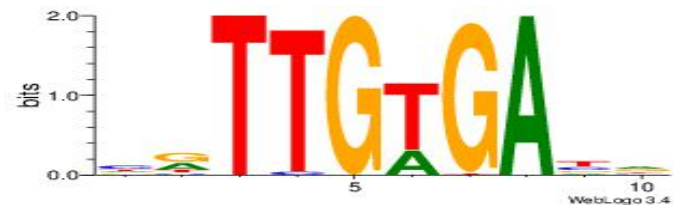


Dataset #: 4 **Motif ID: 94** **Motif name: yrTCWCAAyr**

Original motif Consensus sequence: HVTCACAAAYD



Reverse complement motif Consensus sequence: HKTTGTGABH



Best Matches for Motif ID 94 (Highest to Lowest)

Dataset #:	4
Motif ID:	114
Motif name:	awAACAcAAwa
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	10
Similarity score:	0.00495535

Alignment:

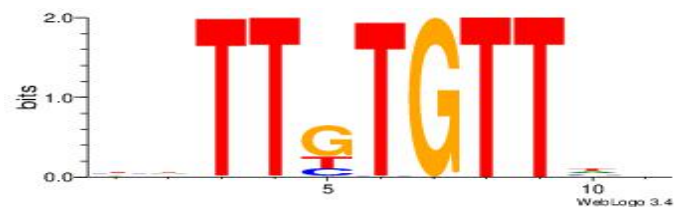
BDTTGTGTTDD

HKTTGTGABH-

Original motif Consensus sequence: DDAACACAADV



Reverse complement motif Consensus sequence: BDTTGTGTTDD

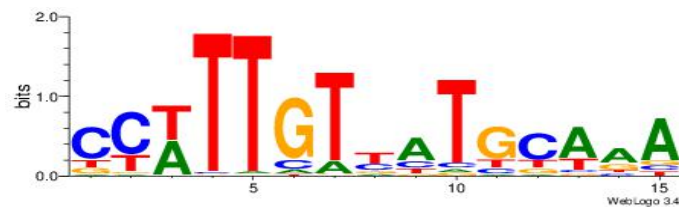


Dataset #: 3
 Motif ID: 76
 Motif name: Sox2
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 10
 Similarity score: 0.00762497

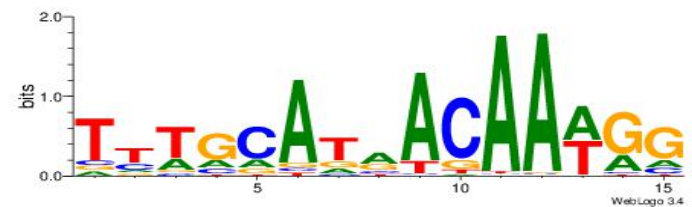
Alignment:

CCWTTGTYATGCAAA
 ----HKTGTGABH-

Original motif Consensus sequence: CCWTTGTYATGCAAA



Reverse complement motif Consensus sequence: TTTGCATMACAAWGG



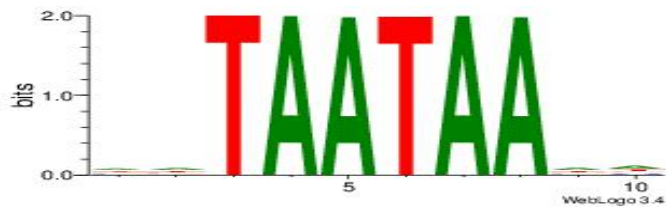
Dataset #: 4
 Motif ID: 100
 Motif name: wwTAATAAww
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1

Number of overlap: 10
Similarity score: 0.0114769

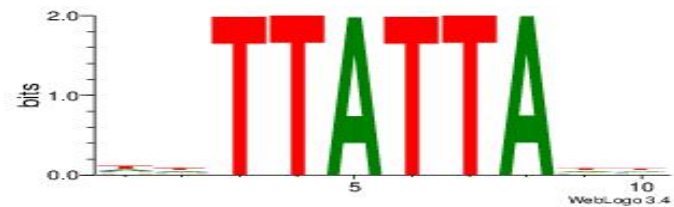
Alignment:

DDTTATTAHD
HKTTGTGABH

Original motif Consensus sequence: DHTAATAADD



Reverse complement motif Consensus sequence: DDTTATTAHD



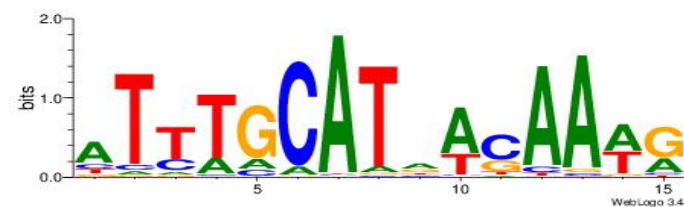
Dataset #: 3
Motif ID: 80
Motif name: Pou5f1
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 6
Number of overlap: 10
Similarity score: 0.0127574

Alignment:

CWTTGTHATGCAAAT
-----HKTTGTGABH

Original motif Consensus sequence: CWTTGTHATGCAAAT

Reverse complement motif Consensus sequence: ATTTGCATHACAAAT



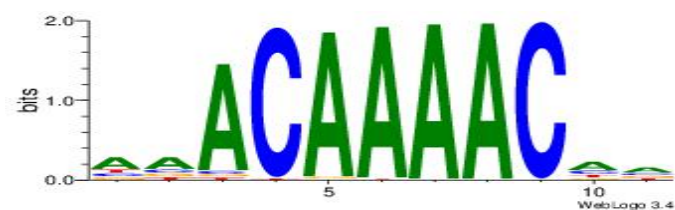
Dataset #: 4
 Motif ID: 89
 Motif name: aaACAAACaa
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 10
 Similarity score: 0.0208363

Alignment:

AAACAAACHV

HVTCACAAYD-

Original motif Consensus sequence: AAACAAACHV



Reverse complement motif Consensus sequence: BHGTTTTGTTT



Dataset #: 4 Motif ID: 95 Motif name: rmATGCTAww

Original motif Consensus sequence: DHATGCTADH



Reverse complement motif Consensus sequence: HDTAGCATHD



Best Matches for Motif ID 95 (Highest to Lowest)

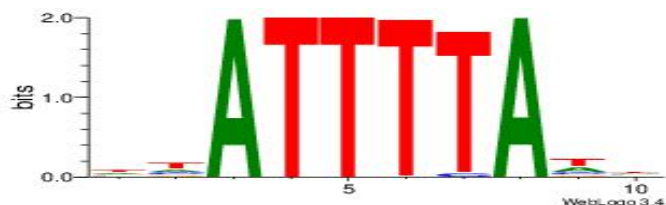
Dataset #:	4
Motif ID:	91
Motif name:	wtATTTTAWw
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	10
Similarity score:	0.00863735

Alignment:

DHATTTTAWH

DHATGCTADH

Original motif Consensus sequence: DHATTTTAWH



Reverse complement motif Consensus sequence: HWTAAAATHD



Dataset #: 4
 Motif ID: 115
 Motif name: ysCmAGCACwy
 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: 0.0142021

Alignment:

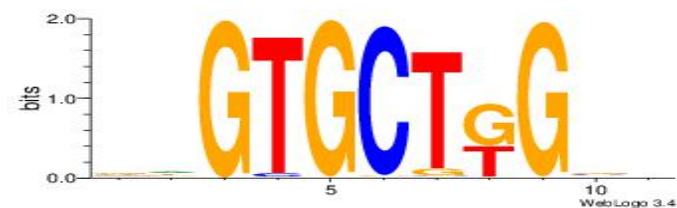
DHGTGCTRGVH

DHATGCTADH-

Original motif Consensus sequence: HVCMAGCACHH



Reverse complement motif Consensus sequence: DHGTGCTRGVH



Dataset #: 3
 Motif ID: 80
 Motif name: Pou5f1
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 10

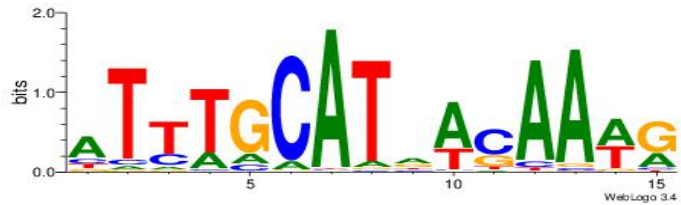
Similarity score: 0.0215325

Alignment:
CWTGTHATGCAAAT
-----DHATGCTADH

Original motif Consensus sequence: CWTGTHATGCAAAT



Reverse complement motif Consensus sequence: ATTTGCATHACAAAT

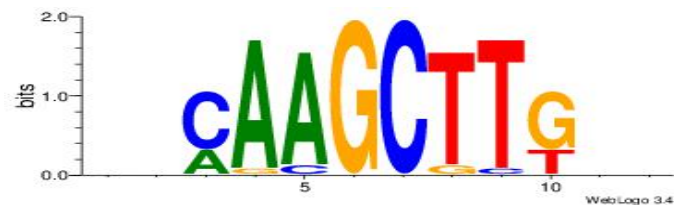
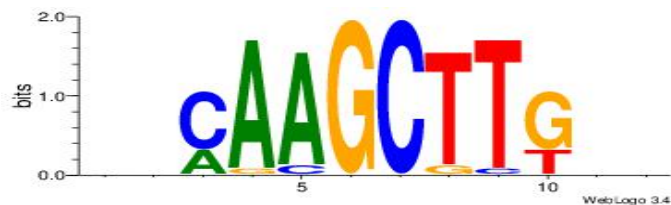


Dataset #: 4
Motif ID: 123
Motif name: asMAAGCTTKst
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 2
Number of overlap: 10
Similarity score: 0.0234838

Alignment:
HBCAAGCTTGVD
-DHATGCTADH-

Original motif Consensus sequence: HBCAAGCTTGVD

Reverse complement motif Consensus sequence: DVCAAGCTTGBH



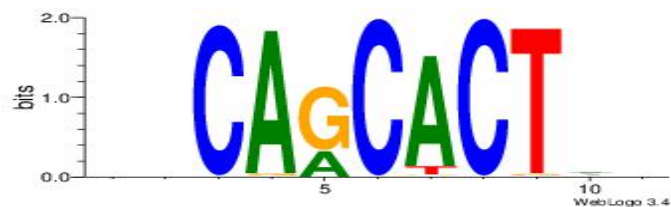
Dataset #: 4
 Motif ID: 93
 Motif name: cmCARCACTwr
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 10
 Similarity score: 0.0266703

Alignment:

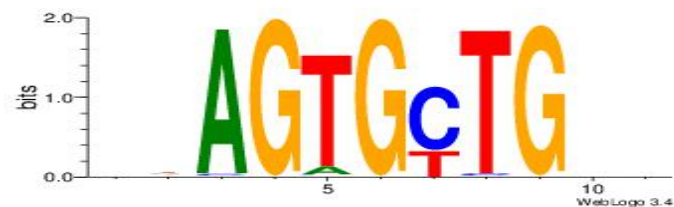
VHAGTGCTGHB

DHATGCTADH-

Original motif Consensus sequence: BHCAGCACTHV

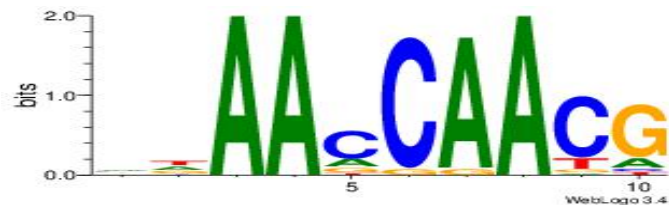


Reverse complement motif Consensus sequence: VHAGTGCTGHB

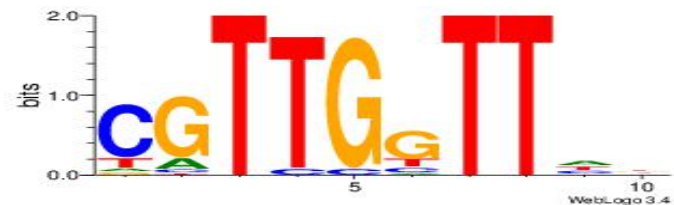


Dataset #: 4 **Motif ID: 96** **Motif name: mdAAcCAACG**

Original motif Consensus sequence: VDAACCAACG



Reverse complement motif Consensus sequence: CGTTGGTTDB



Best Matches for Motif ID 96 (Highest to Lowest)

Dataset #:	4
Motif ID:	97
Motif name:	sgArGCCACg
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:	0.0161902

Alignment:

SGARGCCACG

VDAACCAACG

Original motif Consensus sequence: SGARGCCACG



Reverse complement motif Consensus sequence: CGTGGCKTCS



Dataset #: 2
 Motif ID: 60
 Motif name: Motif 60
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 10
 Similarity score: 0.0244161

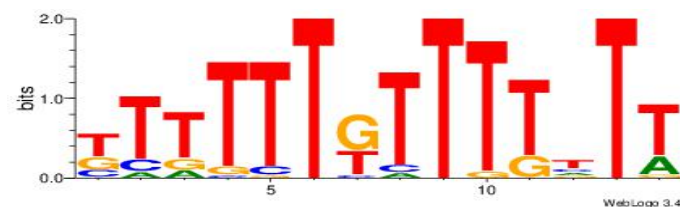
Alignment:

YTTTTTRTTTTDTT
 --CGTTGGTTDB--

Original motif Consensus sequence: AADAAAAMAAAAAM



Reverse complement motif Consensus sequence: YTTTTTRTTTTDTT

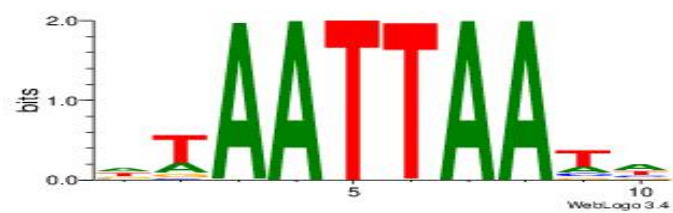


Dataset #: 4
 Motif ID: 106
 Motif name: wtAATTAAtw
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 10

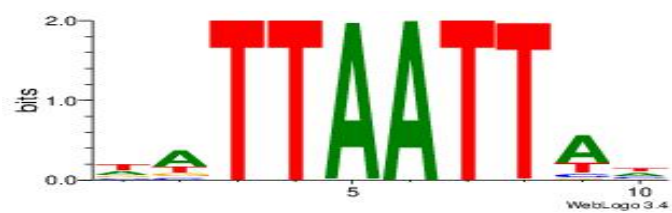
Similarity score: 0.0244247

Alignment:
HATTAATTAD
CGTTGGTTDB

Original motif Consensus sequence: DTAATTAATH



Reverse complement motif Consensus sequence: HATTAATTAD

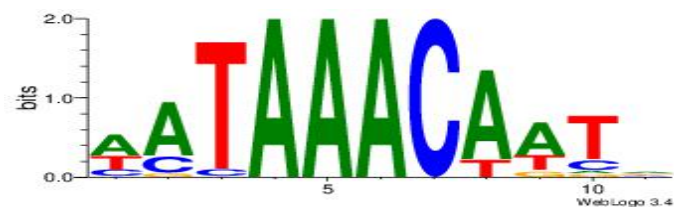


Dataset #: 3
Motif ID: 70
Motif name: Foxq1
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 10
Similarity score: 0.0266383

Alignment:
HATTGTTTATW
-CGTTGGTTDB

Original motif Consensus sequence: HATTGTTTATW

Reverse complement motif Consensus sequence: WATAACAATH



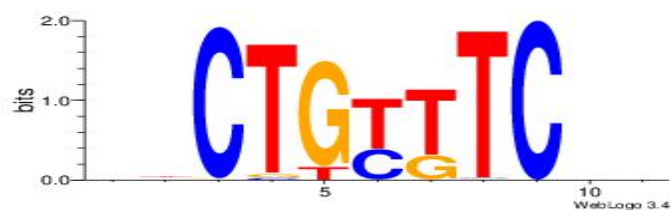
Dataset #: 4
 Motif ID: 113
 Motif name: htCTGyKTCbt
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 10
 Similarity score: 0.0296542

Alignment:

HVGAAMCAGVH

-VDAACCAACG

Original motif Consensus sequence: HBCTGYTTCBH



Reverse complement motif Consensus sequence: HVGAAMCAGVH



Dataset #: 4 Motif ID: 97 Motif name: sgArGCCACg

Original motif Consensus sequence: SGARGCCACG



Reverse complement motif Consensus sequence: CGTGGCKTCS



Best Matches for Motif ID 97 (Highest to Lowest)

Dataset #:	4
Motif ID:	92
Motif name:	cgAKGyCAcg
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:	0.0020736

Alignment:

CGAGGYCACV

SGARGCCACG

Original motif Consensus sequence: CGAGGYCACV



Reverse complement motif Consensus sequence: VGTGMCCTCG



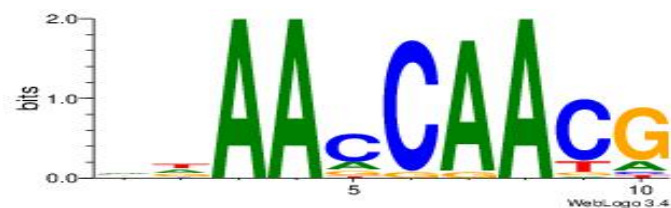
Dataset #: 4
 Motif ID: 96
 Motif name: mdAAcCAACG
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 10
 Similarity score: 0.0408537

Alignment:

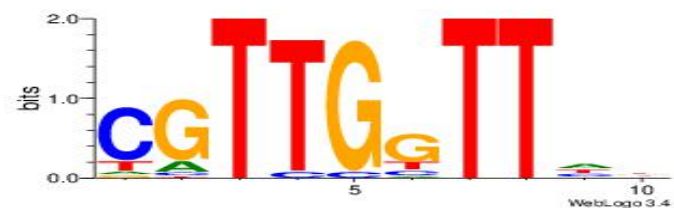
VDAACCAACG

SGARGCCACG

Original motif Consensus sequence: VDAACCAACG



Reverse complement motif Consensus sequence: CGTTGGTTDB



Dataset #: 4
 Motif ID: 95
 Motif name: rmATGCTAww
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 10

Similarity score: 0.0472561

Alignment:

HDTAGCATHD

CGTGGCKTCS

Original motif Consensus sequence: DHATGCTADH



Reverse complement motif Consensus sequence: HDTAGCATHD



Dataset #: 4
Motif ID: 126
Motif name: yvTGCAGsCAcg
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 10
Similarity score: 0.057998

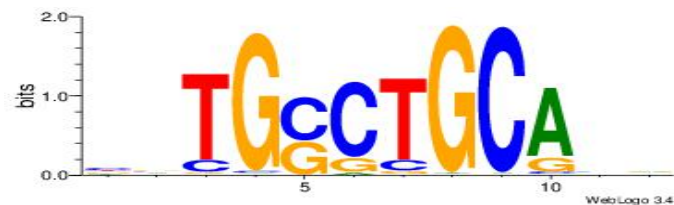
Alignment:

VB TG S CT GCAVB

CGTGGCKTCS--

Original motif Consensus sequence: BVTGCAGSCABV

Reverse complement motif Consensus sequence: VBTGSCTGCAVB



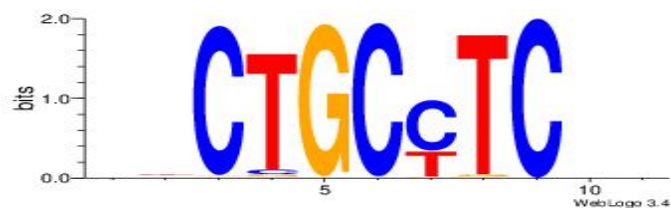
Dataset #: 4
 Motif ID: 116
 Motif name: dyCTGCyTCyc
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 10
 Similarity score: 0.0617012

Alignment:

BHGAKGCAGHH

-SGARGCCACG

Original motif Consensus sequence: DHCTGCYCHB

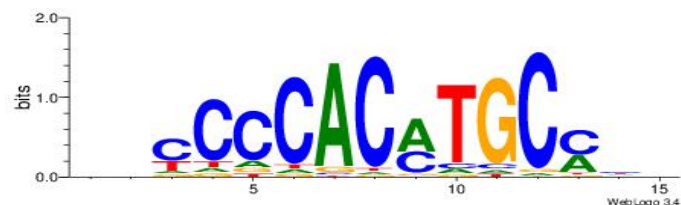


Reverse complement motif Consensus sequence: BHGAKGCAGHH

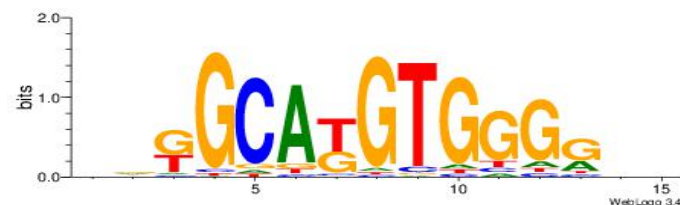


Dataset #: 4 Motif ID: 98 Motif name: myyCCCACmTGCmyr

Original motif Consensus sequence: HBCCCCACMTGCMHV



Reverse complement motif Consensus sequence: VDRGCAYGTGGGGVD



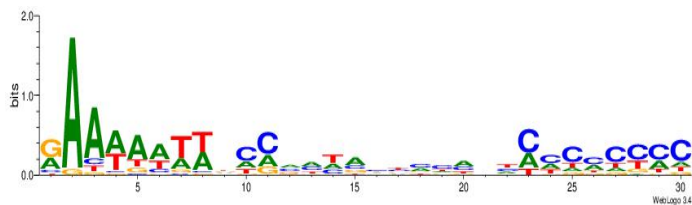
Best Matches for Motif ID 98 (Highest to Lowest)

Dataset #:	3
Motif ID:	81
Motif name:	Pax4
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	8
Number of overlap:	15
Similarity score:	0.0499349

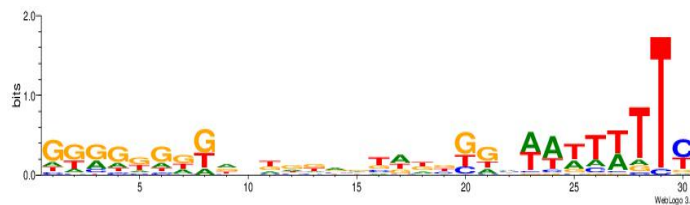
Alignment:

```
RAAWAWTWDCMVHHVBBHHHVHMHCMCYMC
-----HBCCCCACMTGCMHV-----
```

Original motif Consensus sequence:
RAAWAWTWDCMVHHVBBHHHVHMHCMCYMC



Reverse complement motif Consensus sequence:
GRKGRGDRHVHDDVBBHHBRGDWAWTWTTM

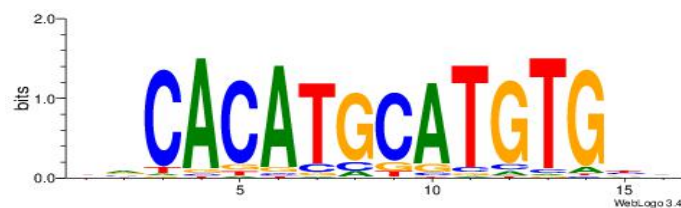


Dataset #: 4
 Motif ID: 118
 Motif name: yrCACATGCATGTGyr
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 15
 Similarity score: 0.0613869

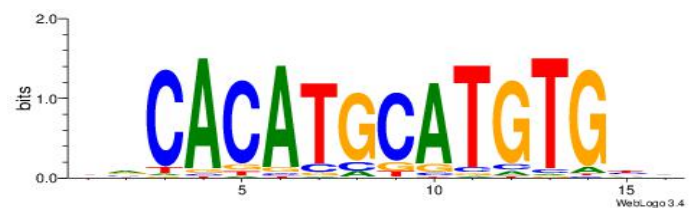
Alignment:

HVCACATGCATGTGBD
 -HBCCCCACMTGCMHV

Original motif Consensus sequence: HVCACATGCATGTGBD



Reverse complement motif Consensus sequence: DVCACATGCATGTGBH

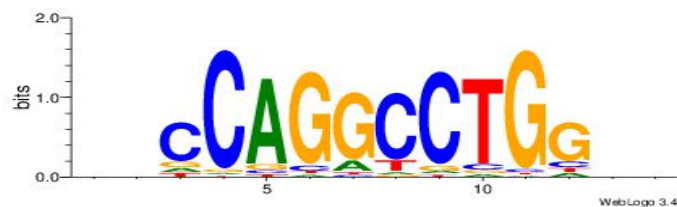


Dataset #: 4
 Motif ID: 122
 Motif name: hsCCAGGCCTGGsr
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward

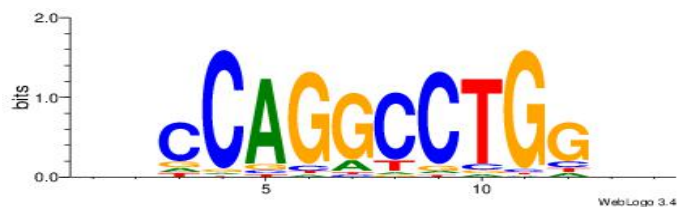
Position number: 1
Number of overlap: 14
Similarity score: 0.538726

Alignment:
HVCCAGGCCTGGBD-
HBCCCCACMTGCMHV

Original motif Consensus sequence: HVCCAGGCCTGGBD



Reverse complement motif Consensus sequence: HBCCAGGCCTGGV

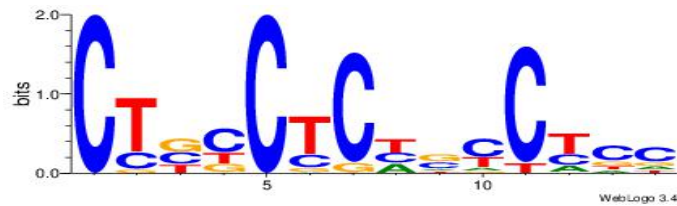


Dataset #: 2
Motif ID: 59
Motif name: Motif 59
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 14
Similarity score: 0.560094

Alignment:
-CTBCCTCHSYCYCC
HBCCCCACMTGCMHV

Original motif Consensus sequence: CTBCCTCHSYCYCC

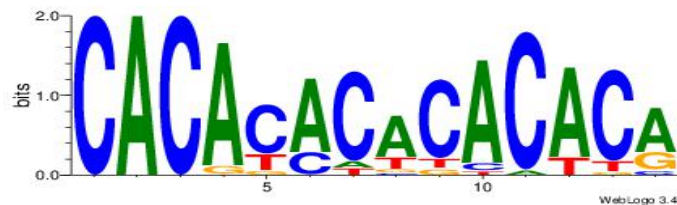
Reverse complement motif Consensus sequence: GGMGKSHGAGGB



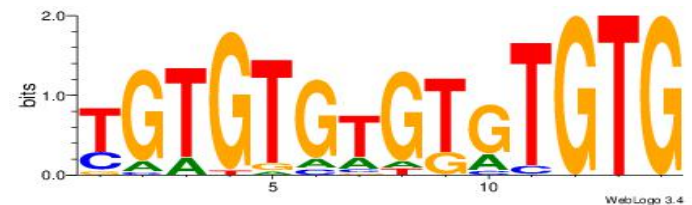
Dataset #: 2
 Motif ID: 58
 Motif name: Motif 58
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0.57014

Alignment:
 -CACACACACACACA
 HBCCCCACMTGCMHV

Original motif Consensus sequence: CACACACACACACA



Reverse complement motif Consensus sequence: TGTGTGTGTGTGT

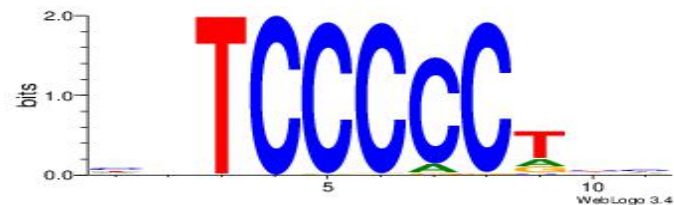


Dataset #: 4 Motif ID: 99 Motif name: graGGGGGArr

Original motif Consensus sequence: DVAGGGGGADD



Reverse complement motif Consensus sequence: HDTCCCCCTVH



Best Matches for Motif ID 99 (Highest to Lowest)

Dataset #:	4
Motif ID:	127
Motif name:	rryCAGGGAyw
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	11
Similarity score:	0.0288287

Alignment:

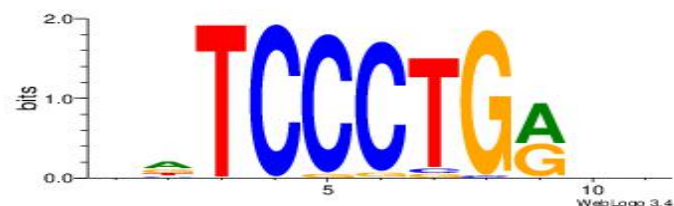
DDYCAGGGAHD

DVAGGGGGADD

Original motif Consensus sequence: DDYCAGGGAHD



Reverse complement motif Consensus sequence: DHTCCCTGMDD

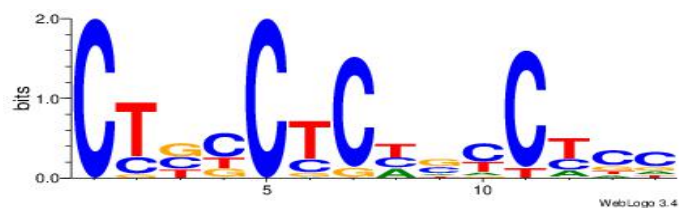


Dataset #: 2
 Motif ID: 59
 Motif name: Motif 59
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 4
 Number of overlap: 11
 Similarity score: 0.0416239

Alignment:

GGMGKSHGAGGBAG
 ---DVAGGGGGADD

Original motif Consensus sequence: CTBCCTCHSYCYCC



Reverse complement motif Consensus sequence: GGMGKSHGAGGB

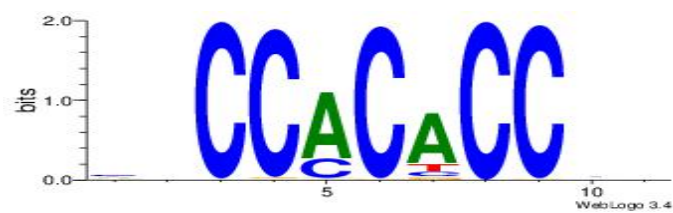


Dataset #: 4
 Motif ID: 110
 Motif name: cmCCACACCcm
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 11

Similarity score: 0.0422985

Alignment:
HVCCACACCBV
HDTCCCCCTVH

Original motif Consensus sequence: HVCCACACCBV



Reverse complement motif Consensus sequence: VBGGTGTGGBD

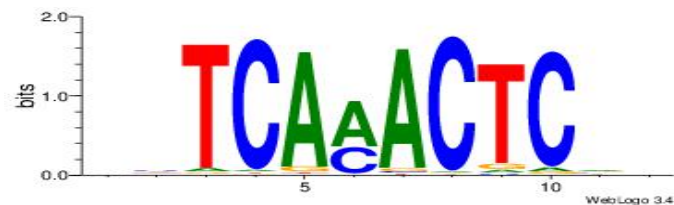
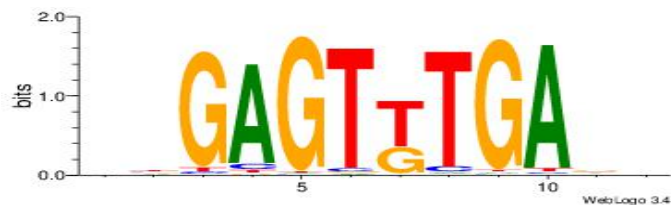


Dataset #: 4
Motif ID: 112
Motif name: ctGAGTkTGAgg
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 11
Similarity score: 0.042367

Alignment:
VBGAGTKTGADD
-DVAGGGGGADD

Original motif Consensus sequence: VBGAGTKTGADD

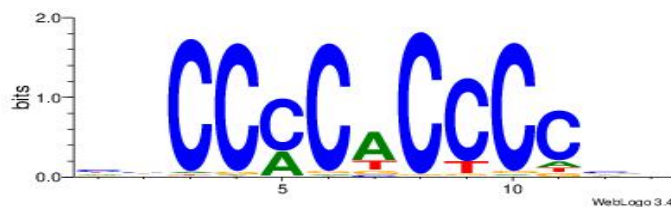
Reverse complement motif Consensus sequence: HHTCARACTCVV



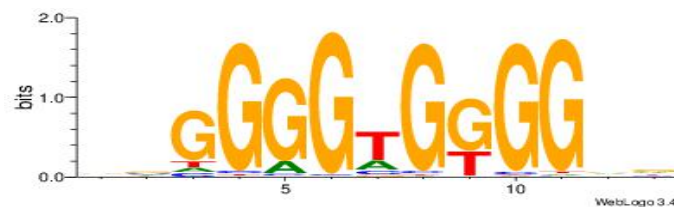
Dataset #: 4
 Motif ID: 111
 Motif name: ccCCmCaCCCCcc
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.0428468

Alignment:
 DBGGGGTGGGGBD
 DVAGGGGGADD--

Original motif Consensus sequence: HBCCCCACCCCBH

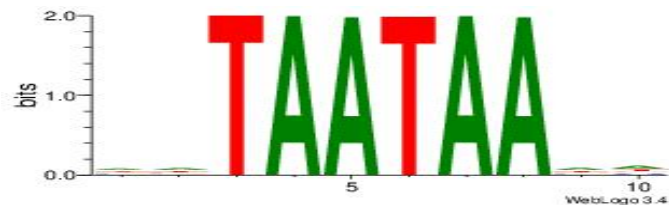


Reverse complement motif Consensus sequence: DBGGGGTGGGGB

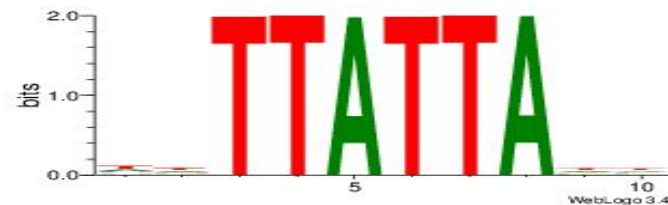


Dataset #: 4 Motif ID: 100 Motif name: wwTAATAAww

Original motif Consensus sequence: DHTAATAADD



Reverse complement motif Consensus sequence: DDTTATT AHD



Best Matches for Motif ID 100 (Highest to Lowest)

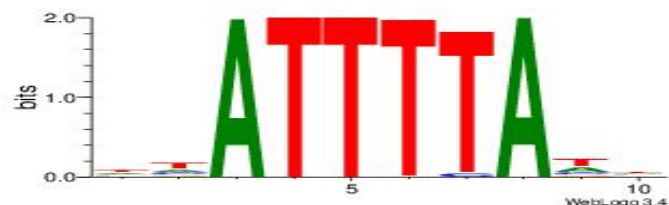
Dataset #:	4
Motif ID:	91
Motif name:	wtATTTTAww
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	10
Similarity score:	0.0241522

Alignment:

HWTAAAATHD

DHTAATAADD

Original motif Consensus sequence: DHATTTTAWH



Reverse complement motif Consensus sequence: HWTAAAATHD

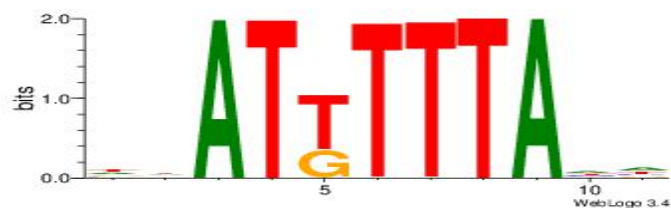


Dataset #: 4
 Motif ID: 108
 Motif name: wwATkTTTAww
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 10
 Similarity score: 0.0255442

Alignment:

DHATKTTTAHH
 -DDTTATTAHD

Original motif Consensus sequence: DHATKTTTAHH



Reverse complement motif Consensus sequence: HHTAAARATHD

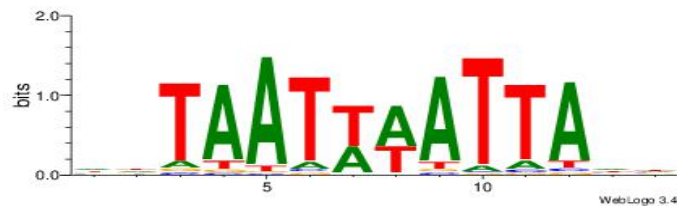


Dataset #: 4
 Motif ID: 125
 Motif name: wwTAATwwATTAWw
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 10

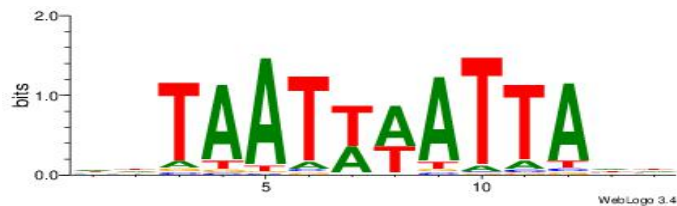
Similarity score: 0.0362107

Alignment:
HHTAATWWATTADD
DHTAATAADD-----

Original motif Consensus sequence: DDTAATWWATTAHH



Reverse complement motif Consensus sequence: HHTAATWWATTAD

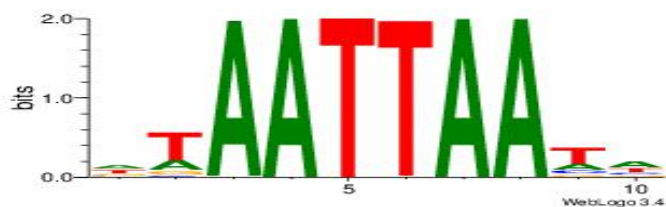


Dataset #: 4
Motif ID: 106
Motif name: wtAATTAAtw
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 10
Similarity score: 0.0364833

Alignment:
HATTAATTAD
DDTTATTAHD

Original motif Consensus sequence: DTAATTAATH

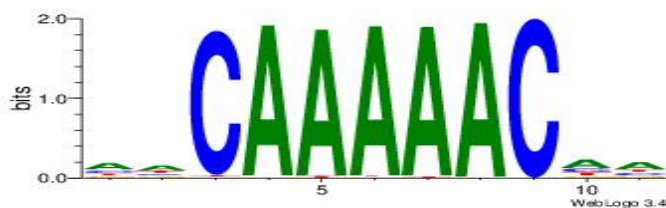
Reverse complement motif Consensus sequence: HATTAATTAD



Dataset #: 4
 Motif ID: 109
 Motif name: aaCAAAAACaa
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 10
 Similarity score: 0.0471554

Alignment:
 HHCAAAAACHH
 DHTAATAADD-

Original motif Consensus sequence: HHCAAAAACHH



Reverse complement motif Consensus sequence: HHGTTTTTGHH



Dataset #: 4 Motif ID: 101 Motif name: csCACCCCgg

Original motif Consensus sequence: HVCACCCCB



Reverse complement motif Consensus sequence: BBGGGGTGVD



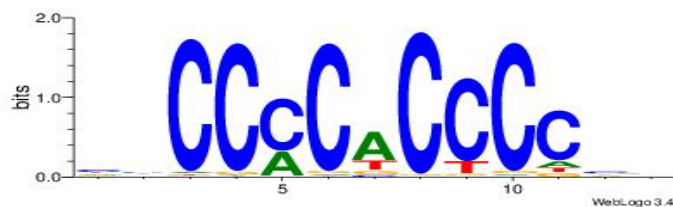
Best Matches for Motif ID 101 (Highest to Lowest)

Dataset #:	4
Motif ID:	111
Motif name:	ccCCmCaCCCCcc
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

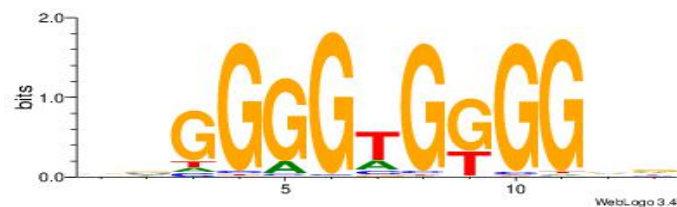
Alignment:

```
HBCCCCACCCCBH
---HVCACCCCB
```

Original motif Consensus sequence: HBCCCCACCCCBH



Reverse complement motif Consensus sequence: DBGGGGTGGGB



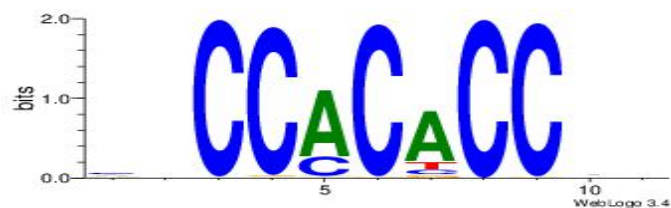
Dataset #: 4
 Motif ID: 110
 Motif name: cmCCACACCcm
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 10
 Similarity score: 0.00930301

Alignment:

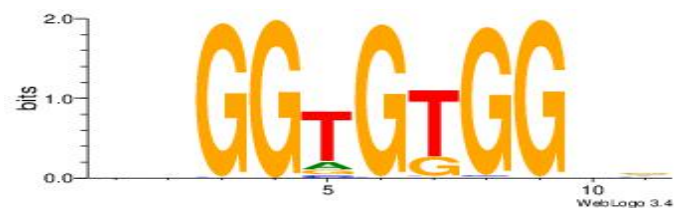
HVCCACACCBV

-HVCACCCCB

Original motif Consensus sequence: HVCCACACCBV



Reverse complement motif Consensus sequence: VBGGTGTGGBD



Dataset #: 4
 Motif ID: 99
 Motif name: graGGGGGArr
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 10

Similarity score: 0.0256956

Alignment:

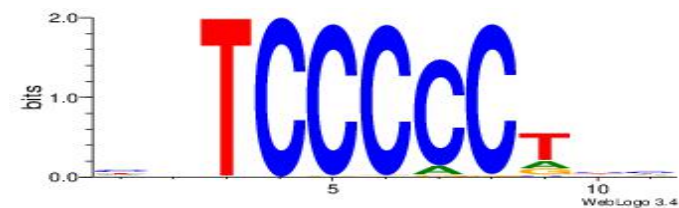
HDTCCCCCTVH

-HVCACCCCB

Original motif Consensus sequence: DVAGGGGGADD



Reverse complement motif Consensus sequence: HDTCCCCCTVH



Dataset #: 4
Motif ID: 119
Motif name: cbCCAGCTCmyk
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: 0.033038

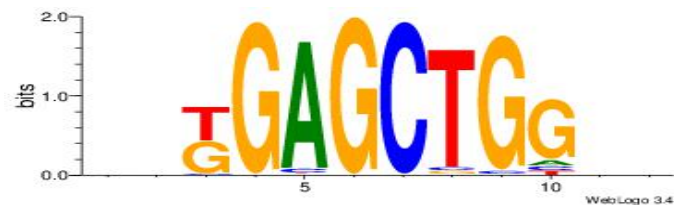
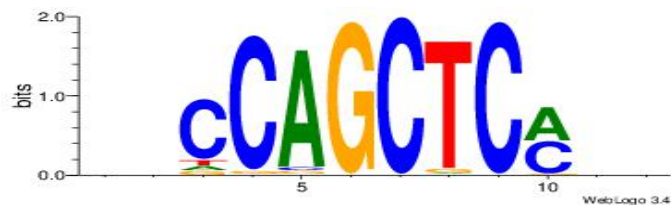
Alignment:

HBYGAGCTGGBB

-BBGGGGTGVD-

Original motif Consensus sequence: BBCCAGCTCMBD

Reverse complement motif Consensus sequence: HBYGAGCTGGBB



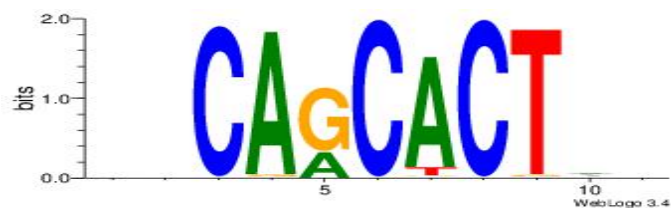
Dataset #: 4
 Motif ID: 93
 Motif name: cmCARCACTwr
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 10
 Similarity score: 0.0377738

Alignment:

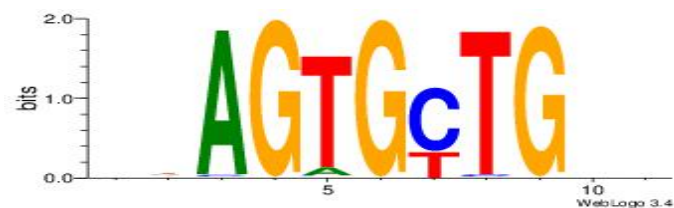
BHCAGCACTHV

HVCACCCBB-

Original motif Consensus sequence: BHCAGCACTHV

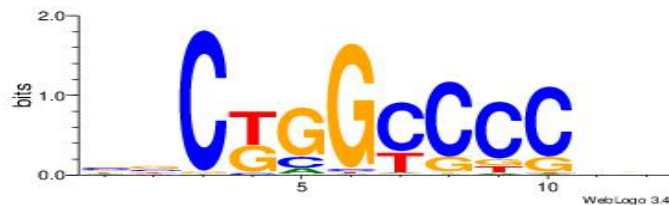


Reverse complement motif Consensus sequence: VHAGTGCTGHB



Dataset #: 4 Motif ID: 102 Motif name: ssCkGGYCCCsg

Original motif Consensus sequence: BBCKGGCCCCV



Reverse complement motif Consensus sequence: VVGGGGCCCRBB



Best Matches for Motif ID 102 (Highest to Lowest)

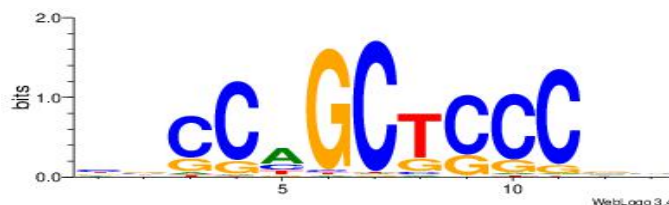
Dataset #:	4
Motif ID:	103
Motif name:	csCCaGCTCCCgs
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	2
Number of overlap:	12
Similarity score:	0.00699729

Alignment:

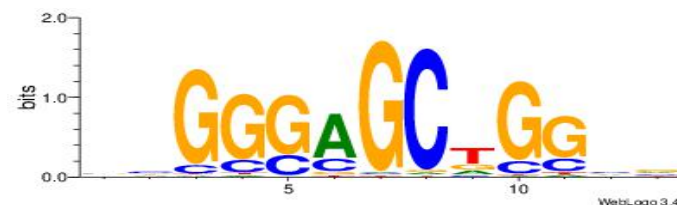
BVGGGAGCTGGBB

-VVGGGGCCCRBB

Original motif Consensus sequence: BBCCAGCTCCCVB



Reverse complement motif Consensus sequence: BVGGGAGCTGGBB

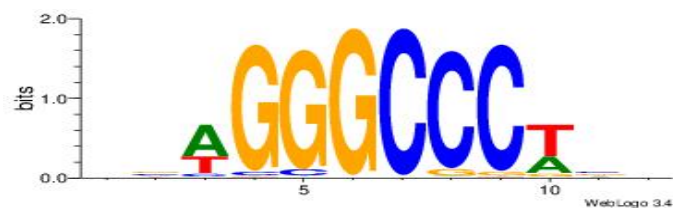


Dataset #: 4
 Motif ID: 124
 Motif name: cswGGGCCCwsg
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 12
 Similarity score: 0.00901563

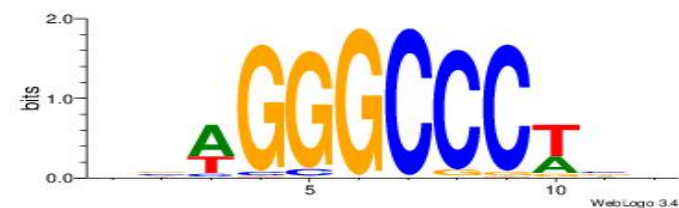
Alignment:

VVWGGGCCCWBB
 BBCKGGCCCCVV

Original motif Consensus sequence: VVWGGGCCCWBB



Reverse complement motif Consensus sequence: BBWGGGCCCWVV



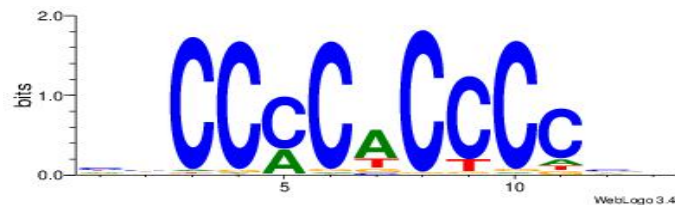
Dataset #: 4
 Motif ID: 111
 Motif name: ccCCmCaCCCCcc
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 12

Similarity score: 0.015463

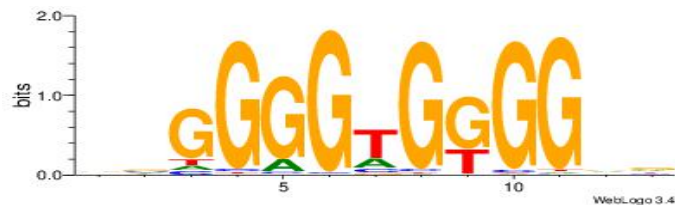
Alignment:

DBGGGGTGGGGBD
VVGGGGCCRGBB-

Original motif Consensus sequence: HBCCCCACCCCBH



Reverse complement motif Consensus sequence: DBGGGGTGGGGB



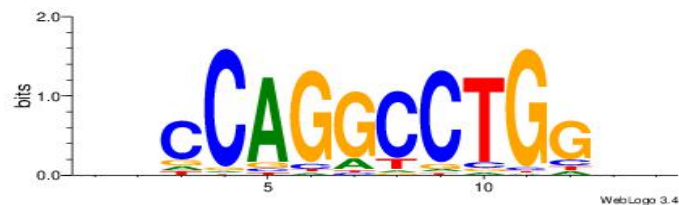
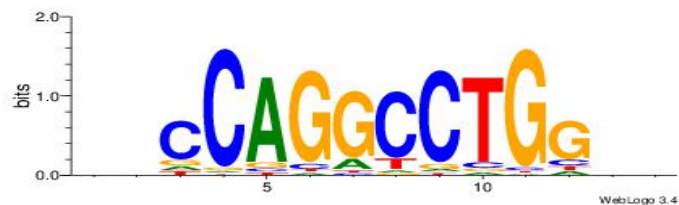
Dataset #: 4
Motif ID: 122
Motif name: hsCCAGGCCTGGsr
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2
Number of overlap: 12
Similarity score: 0.0222107

Alignment:

HVCCAGGCCTGGBD
-BBCKGGCCCCVV-

Original motif Consensus sequence: HVCCAGGCCTGGBD

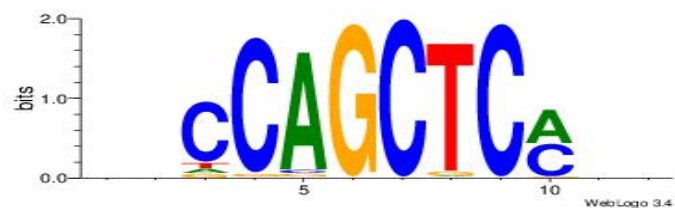
Reverse complement motif Consensus sequence: HBCCAGGCCTGGV



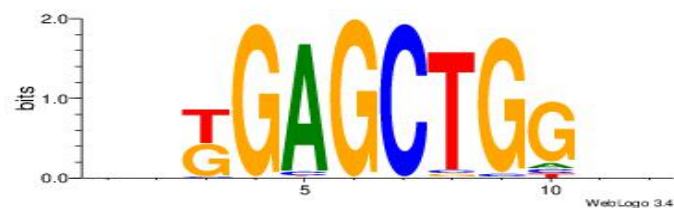
Dataset #: 4
 Motif ID: 119
 Motif name: cbCCAGCTCmyk
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 12
 Similarity score: 0.0277516

Alignment:
 BBCCAGCTCMBD
 BBCKGGCCCCVV

Original motif Consensus sequence: BBCCAGCTCMBD

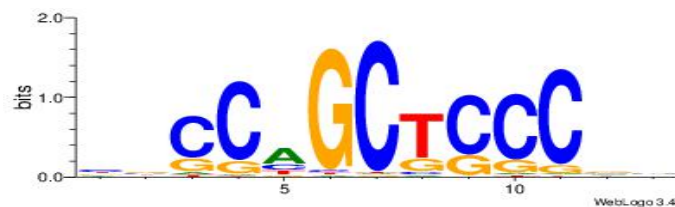


Reverse complement motif Consensus sequence: HBYGAGCTGGBB

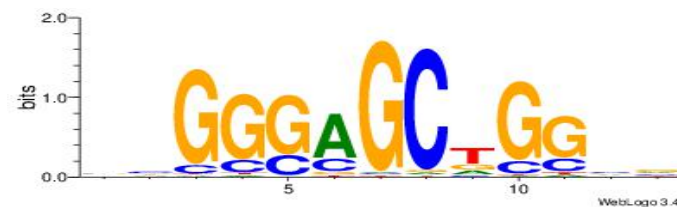


Dataset #: 4 Motif ID: 103 Motif name: csCCaGCTCCCgs

Original motif Consensus sequence: BBCCAGCTCCCVB



Reverse complement motif Consensus sequence: BVGGGAGCTGGBB



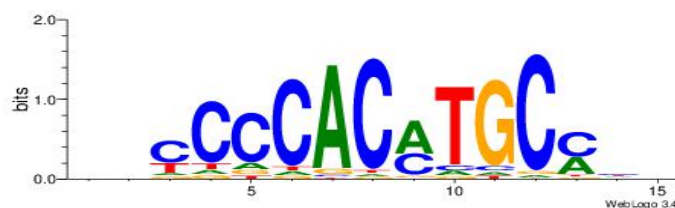
Best Matches for Motif ID 103 (Highest to Lowest)

Dataset #:	4
Motif ID:	98
Motif name:	myyCCCACmTGCmyr
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	3
Number of overlap:	13
Similarity score:	0.0331906

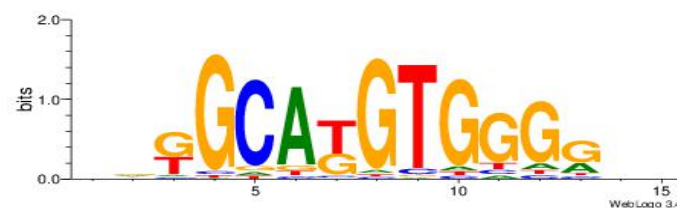
Alignment:

```
HBCCCCACMTGCMHV
--BBCCAGCTCCCVB
```

Original motif Consensus sequence: HBCCCCACMTGCMHV



Reverse complement motif Consensus sequence: VDRGCAYGTGGGGVD

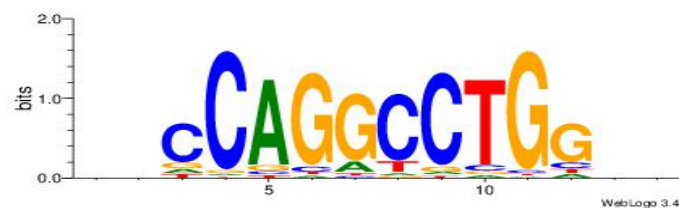


Dataset #: 4
 Motif ID: 122
 Motif name: hsCCAGGCCTGGsr
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 13
 Similarity score: 0.033684

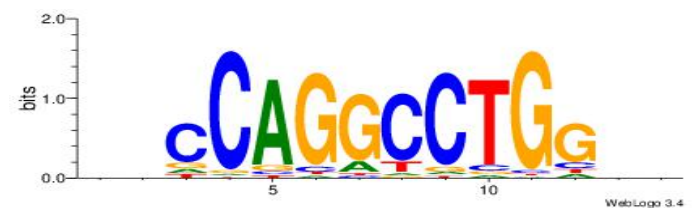
Alignment:

HVCCAGGCCTGGBD
 -BVGGGAGCTGGBB

Original motif Consensus sequence: HVCCAGGCCTGGBD



Reverse complement motif Consensus sequence: HBCCAGGCCTGGV



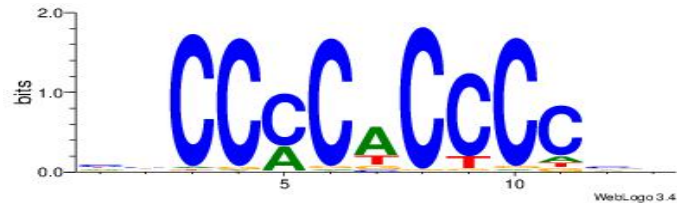
Dataset #: 4
 Motif ID: 111
 Motif name: ccCCmCaCCCCcc
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 13

Similarity score: 0.0344113

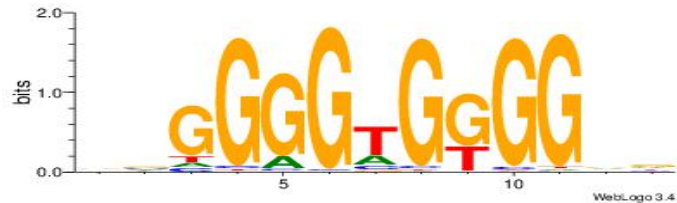
Alignment:

HBCCCCACCCCBH
BBCCAGCTCCCVB

Original motif Consensus sequence: HBCCCCACCCCBH



Reverse complement motif Consensus sequence: DBGGGGTGGGGB



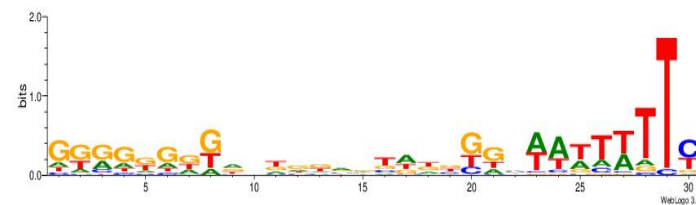
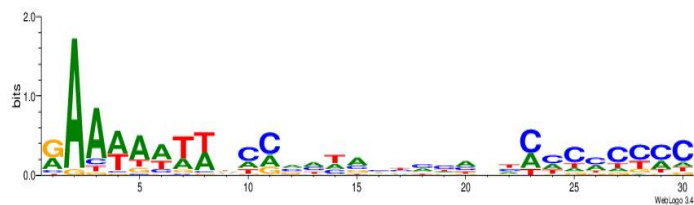
Dataset #: 3
Motif ID: 81
Motif name: Pax4
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 3
Number of overlap: 13
Similarity score: 0.0424871

Alignment:

GRKGRGDRHVHDDVBBHHBRGDWAWTWTTM
--BVGGGAGCTGGBB-----

Original motif Consensus sequence:
RAAWAWTWDCMVHHVBBHHVHMHCMCYMC

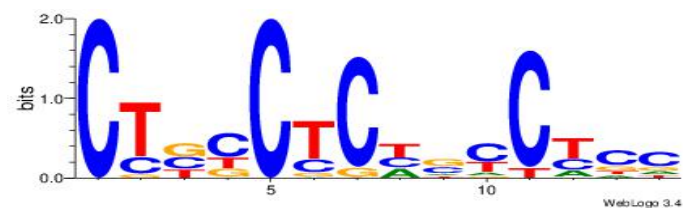
Reverse complement motif Consensus sequence:
GRKGRGDRHVHDDVBBHHBRGDWAWTWTTM



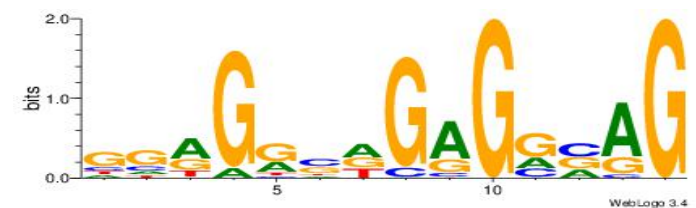
Dataset #: 2
 Motif ID: 59
 Motif name: Motif 59
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 13
 Similarity score: 0.0502084

Alignment:
 GGMGKSHGAGGBAG
 -BVGGGAGCTGGBB

Original motif Consensus sequence: CTBCCTCHSYCYCC

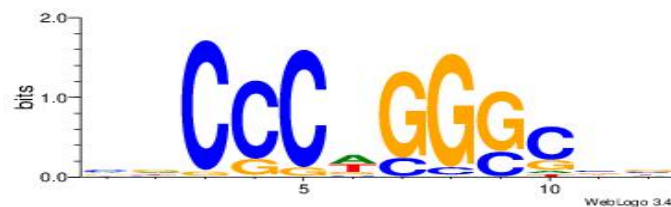


Reverse complement motif Consensus sequence: GGMGKSHGAGGB

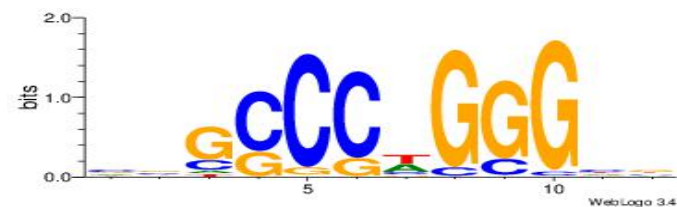


Dataset #: 4 Motif ID: 104 Motif name: cgCCCwGGScsg

Original motif Consensus sequence: VDCCCWGGGCBB



Reverse complement motif Consensus sequence: BBGCCCWGGGHV



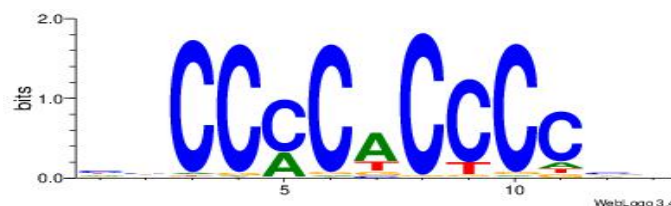
Best Matches for Motif ID 104 (Highest to Lowest)

Dataset #:	4
Motif ID:	111
Motif name:	ccCCmCaCCCCcc
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	12
Similarity score:	0.0295528

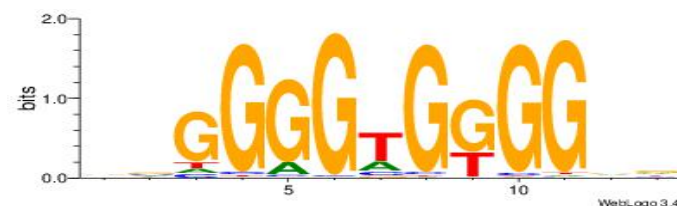
Alignment:

HBCCCCACCCCBH
 -VDCCCWGGGCBB

Original motif Consensus sequence: HBCCCCACCCCBH



Reverse complement motif Consensus sequence: DBGGGGTGGGGB



Dataset #: 4
 Motif ID: 126
 Motif name: yvTGCAGsCAcg
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 12
 Similarity score: 0.0306486

Alignment:

BVTGCAGSCABV

VDCCCWGGGCBB

Original motif Consensus sequence: BVTGCAGSCABV



Reverse complement motif Consensus sequence: VBTGSCCTGCAVB



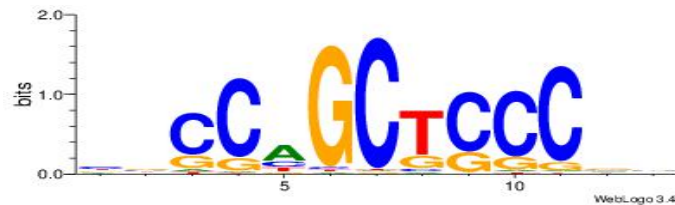
Dataset #: 4
 Motif ID: 103
 Motif name: csCCaGCTCCCgs
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 12

Similarity score: 0.0384576

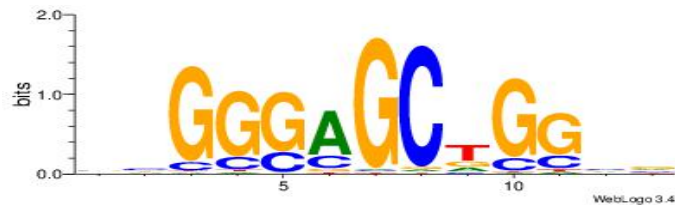
Alignment:

BBCCAGCTCCCVB
VDCCCWGGGCBB-

Original motif Consensus sequence: BBCCAGCTCCCVB



Reverse complement motif Consensus sequence: BVGGGAGCTGGBE



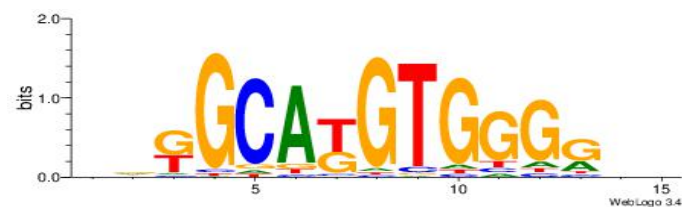
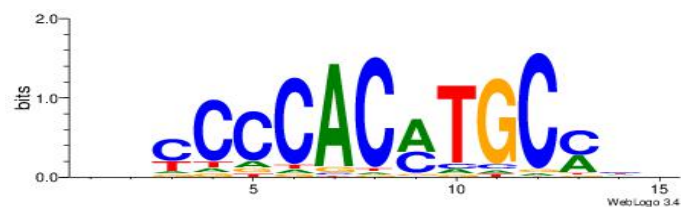
Dataset #: 4
Motif ID: 98
Motif name: myyCCCACmTGCmyr
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 4
Number of overlap: 12
Similarity score: 0.0393753

Alignment:

HBCCCCACMTGCMHV
---VDCCCWGGGCBB

Original motif Consensus sequence: HBCCCCACMTGCMHV

Reverse complement motif Consensus sequence:
VDRGCAYGTGGGGVD

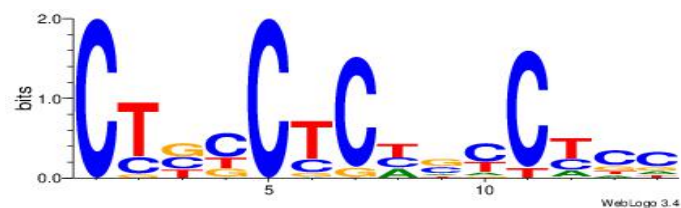


Dataset #: 2
 Motif ID: 59
 Motif name: Motif 59
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 12
 Similarity score: 0.0399857

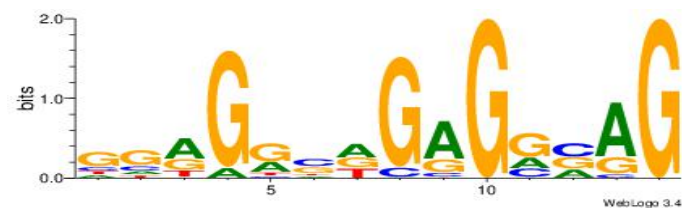
Alignment:

CTBCCTCHSYCYCC
 --VDCCCWGGGCBB

Original motif Consensus sequence: CTBCCTCHSYCYCC

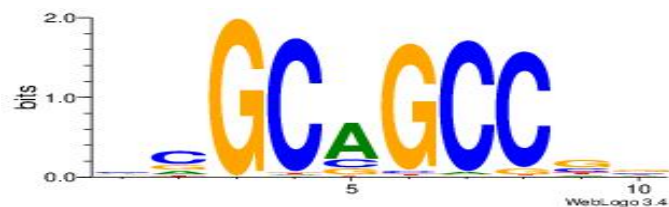


Reverse complement motif Consensus sequence: GGMGKSHGAGGB

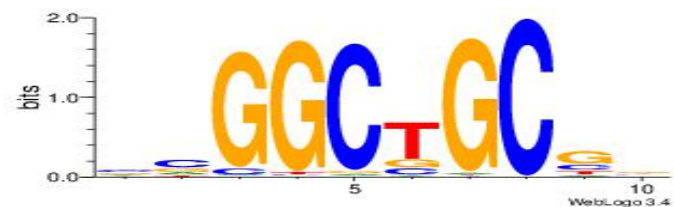


Dataset #: 4 Motif ID: 105 Motif name: ccGCAGCCss

Original motif Consensus sequence: VCGCAGCCBB



Reverse complement motif Consensus sequence: BBGGCTGCGV



Best Matches for Motif ID 105 (Highest to Lowest)

Dataset #:	4
Motif ID:	126
Motif name:	yvTGCAGsCAcg
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

Alignment:

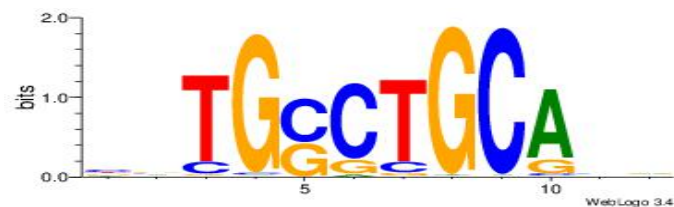
VBTGsCTGCAVB

-BBGGCTGCGV-

Original motif Consensus sequence: BVTGCAGSCABV



Reverse complement motif Consensus sequence: VBTGSCTGCAVB



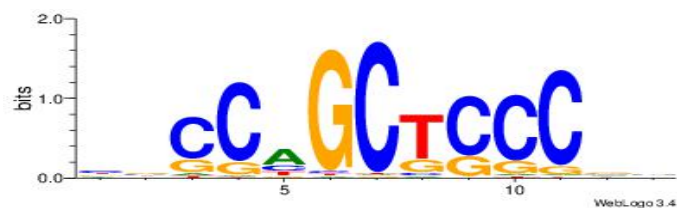
Dataset #: 4
 Motif ID: 103
 Motif name: csCCaGCTCCCgs
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 10
 Similarity score: 0.0101194

Alignment:

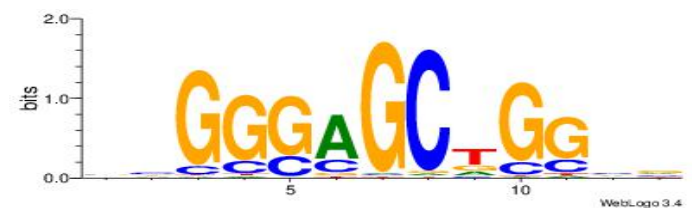
BVGGGAGCTGGBB

BBGGCTGCGV---

Original motif Consensus sequence: BBCCAGCTCCCVB



Reverse complement motif Consensus sequence: BVGGGAGCTGGBB

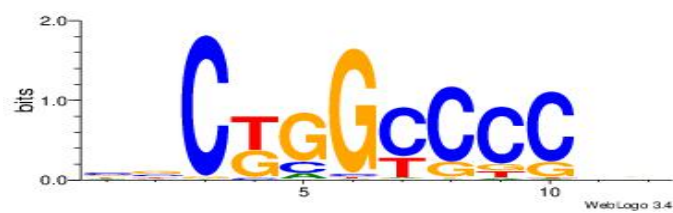


Dataset #: 4
 Motif ID: 102
 Motif name: ssCkGGYCCCsg
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 10

Similarity score: 0.0260007

Alignment:
BBCKGGCCCCVV
BBGGCTGCGV--

Original motif Consensus sequence: BBCKGGCCCCVV



Reverse complement motif Consensus sequence: VVGGGGCCCRGBB

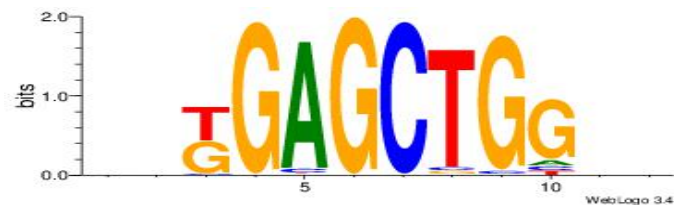
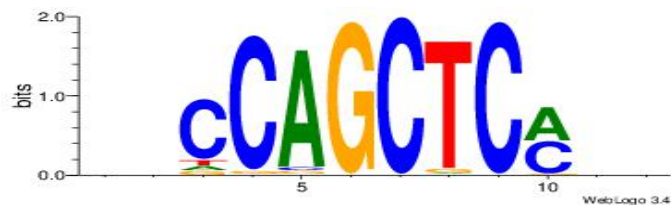


Dataset #: 4
Motif ID: 119
Motif name: cbCCAGCTCmyk
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 3
Number of overlap: 10
Similarity score: 0.0296738

Alignment:
HBYGAGCTGGBB
--BBGGCTGCGV

Original motif Consensus sequence: BBCCAGCTCMBD

Reverse complement motif Consensus sequence: HBYGAGCTGGBB



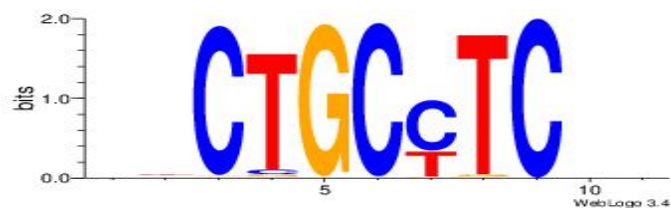
Dataset #: 4
 Motif ID: 116
 Motif name: dyCTGCyTCyc
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 10
 Similarity score: 0.0303133

Alignment:

DHCTGCYTCHB

-BBGGCTGCGV

Original motif Consensus sequence: DHCTGCYTCHB

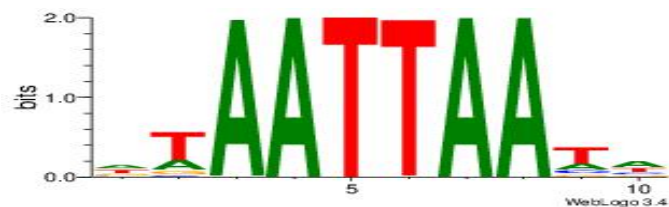


Reverse complement motif Consensus sequence: BHGAKGCAGHH

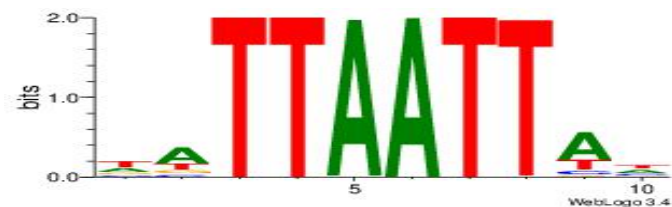


Dataset #: 4 Motif ID: 106 Motif name: wtAATTAAtw

Original motif Consensus sequence: DTAATTAATH



Reverse complement motif Consensus sequence: HATTAATTAD



Best Matches for Motif ID 106 (Highest to Lowest)

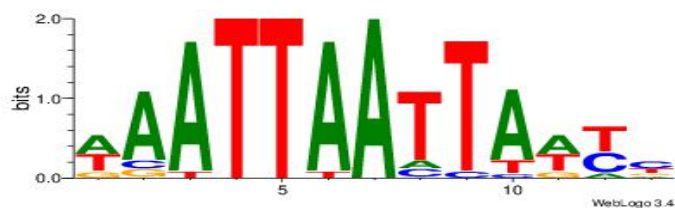
Dataset #:	3
Motif ID:	66
Motif name:	Lhx3
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	3
Number of overlap:	10
Similarity score:	0.0302494

Alignment:

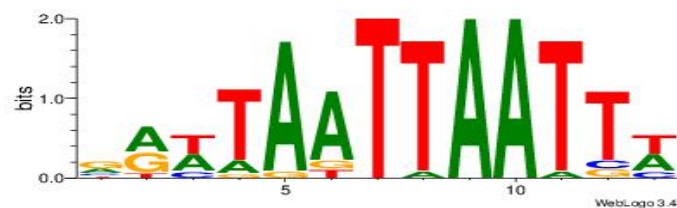
BMWTAATTAATTW

-DTAATTAATH--

Original motif Consensus sequence: WAATTAATTAWYB



Reverse complement motif Consensus sequence: BMWTAATTAATTW

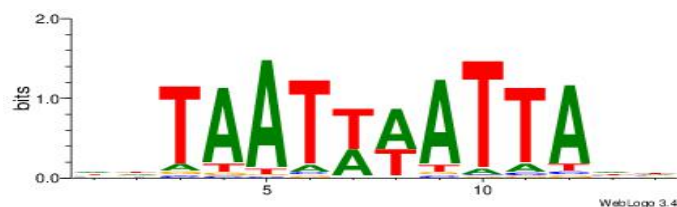


Dataset #: 4
 Motif ID: 125
 Motif name: wwTAATwwATTaww
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 10
 Similarity score: 0.0551105

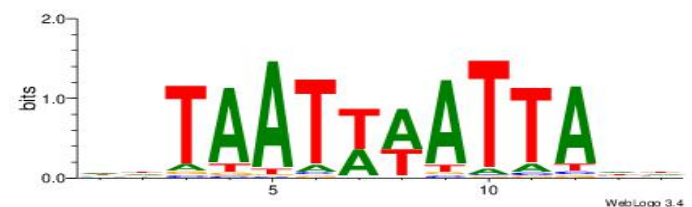
Alignment:

HHTAATWWATTADD
 ---HATTAATTAD-

Original motif Consensus sequence: DDTAATWWATTAAH



Reverse complement motif Consensus sequence: HHTAATWWATTAD

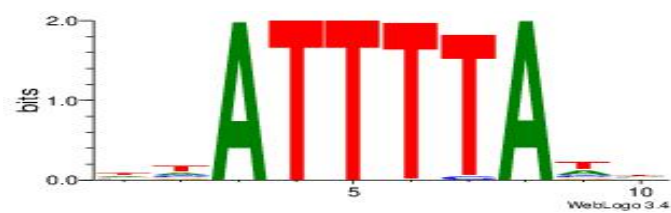


Dataset #: 4
 Motif ID: 91
 Motif name: wtATTTTAww
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 10

Similarity score: 0.0562809

Alignment:
DHATTTTAWH
DTAATTAATH

Original motif Consensus sequence: DHATTTTAWH



Reverse complement motif Consensus sequence: HWTAAAATHD

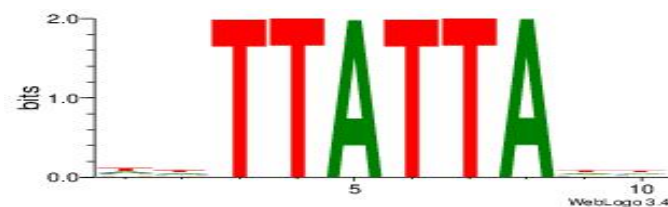
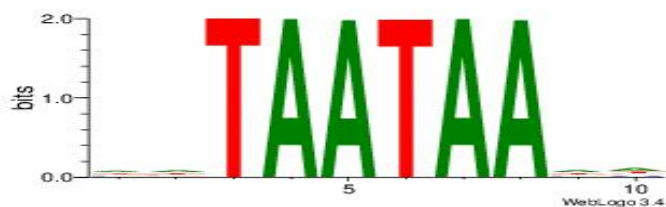


Dataset #: 4
Motif ID: 100
Motif name: wwTAATAAww
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 10
Similarity score: 0.0621876

Alignment:
DDTTATTAHD
HATTAATTAD

Original motif Consensus sequence: DHTAATAADD

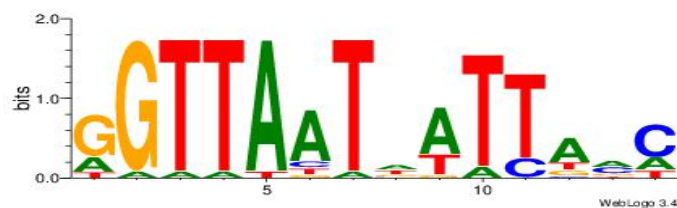
Reverse complement motif Consensus sequence: DDTTATTAHD



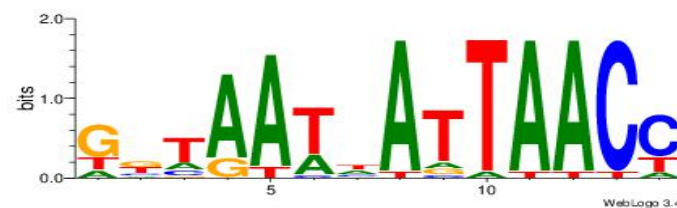
Dataset #: 3
 Motif ID: 68
 Motif name: HNF1A
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 10
 Similarity score: 0.0690833

Alignment:
 GGTTAATDATTAMC
 ----HATTAATTAD

Original motif Consensus sequence: GGTTAATDATTAMC



Reverse complement motif Consensus sequence: GYTAATDATTAAAC



Dataset #: 4 Motif ID: 107 Motif name: crCGyGCRcg

Original motif Consensus sequence: CGCGTGCACG



Reverse complement motif Consensus sequence: CGTGCACGCG



Best Matches for Motif ID 107 (Highest to Lowest)

Dataset #:	4
Motif ID:	92
Motif name:	cgAKGyCAcg
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	10
Similarity score:	0.0293056

Alignment:

VGTGMCCTCG

CGTGCACGCG

Original motif Consensus sequence: CGAGGYCACV



Reverse complement motif Consensus sequence: VGTGMCCTCG



Dataset #: 4
 Motif ID: 115
 Motif name: ysCmAGCACwy
 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: 0.0326988

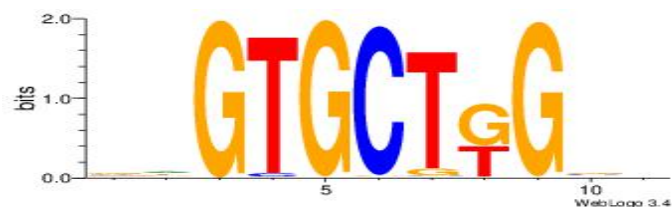
Alignment:

DHGTGCTRGVH
 -CGTGCACGCG

Original motif Consensus sequence: HVCMAGCACHH



Reverse complement motif Consensus sequence: DHGTGCTRGVH

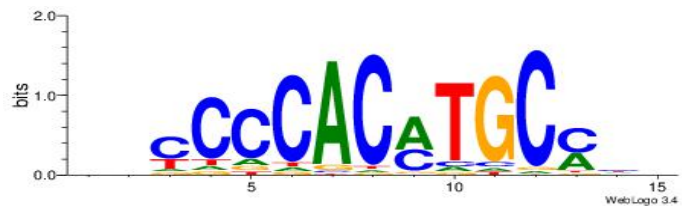


Dataset #: 4
 Motif ID: 98
 Motif name: myyCCCACmTGCmyr
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 10

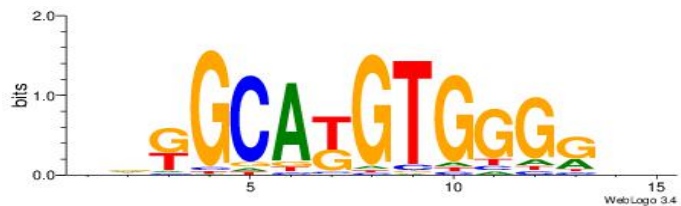
Similarity score: 0.033442

Alignment:
HBCCCCACMTGCMHV
-----CGCGTGCACG

Original motif Consensus sequence: HBCCCCACMTGCMHV



Reverse complement motif Consensus sequence: VDRGCAYGTGGGGVD

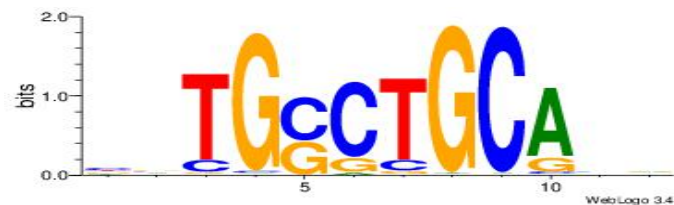


Dataset #: 4
Motif ID: 126
Motif name: yvTGCAGsCAcg
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 3
Number of overlap: 10
Similarity score: 0.0362108

Alignment:
VBTGSCTGCAVB
--CGCGTGCACG

Original motif Consensus sequence: BVTGCAGSCABV

Reverse complement motif Consensus sequence: VBTGSCTGCAVB



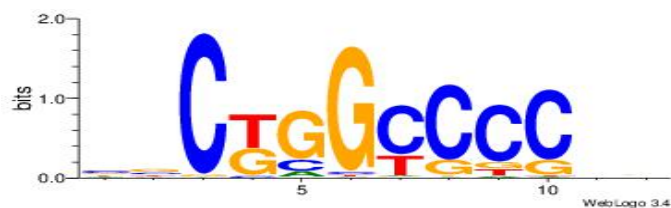
Dataset #: 4
 Motif ID: 102
 Motif name: ssCkGGYCCCsg
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 10
 Similarity score: 0.0421604

Alignment:

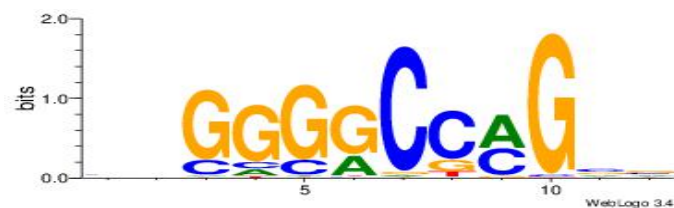
VVGGGGCCRBBB

--CGTGCACGCG

Original motif Consensus sequence: BBCKGGCCCCVV

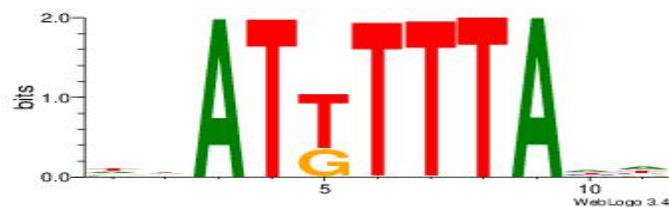


Reverse complement motif Consensus sequence: VVGGGGCCRBBB



Dataset #: 4 Motif ID: 108 Motif name: wwATkTTTAww

Original motif Consensus sequence: DHATKTTTAHH



Reverse complement motif Consensus sequence: HHTAAARATHD



Best Matches for Motif ID 108 (Highest to Lowest)

Dataset #:	3
Motif ID:	70
Motif name:	Foxq1
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	11
Similarity score:	0.0381631

Alignment:

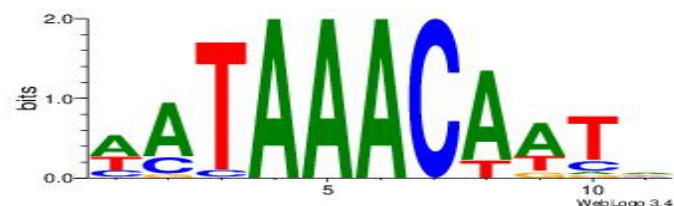
HATTGTTTATW

DHATKTTTAHH

Original motif Consensus sequence: HATTGTTTATW



Reverse complement motif Consensus sequence: WATAACAATH



Dataset #: 4
 Motif ID: 109
 Motif name: aaCAAAAACaa
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.0416262

Alignment:

HHCAAAAACHH

HHTAAARATHD

Original motif Consensus sequence: HHCAAAAACHH



Reverse complement motif Consensus sequence: HHGTTTTTGHH

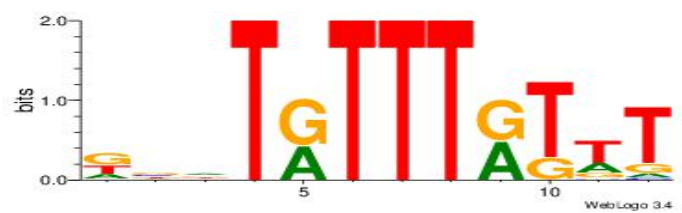


Dataset #: 3
 Motif ID: 67
 Motif name: FOXI1
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 11

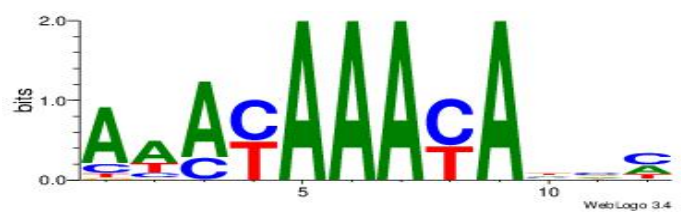
Similarity score: 0.0453405

Alignment:
KBDTRTTTTRTTT
DHATKTTTAHH-

Original motif Consensus sequence: KBDTRTTTTRTTT



Reverse complement motif Consensus sequence: AAAMAAAMADBY



Dataset #: 4
Motif ID: 113
Motif name: htCTGyKTCbt
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 11
Similarity score: 0.0594403

Alignment:
HBCTGYTTCBH
DHATKTTTAHH

Original motif Consensus sequence: HBCTGYTTCBH

Reverse complement motif Consensus sequence: HVGAAMCAGVH



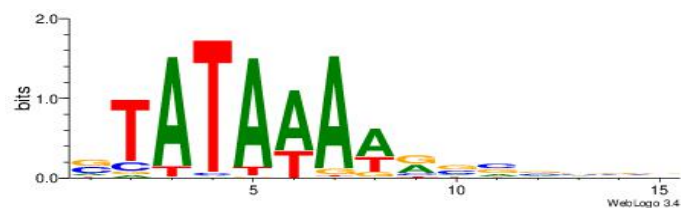
Dataset #: 3
 Motif ID: 62
 Motif name: TBP
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 4
 Number of overlap: 11
 Similarity score: 0.0630171

Alignment:

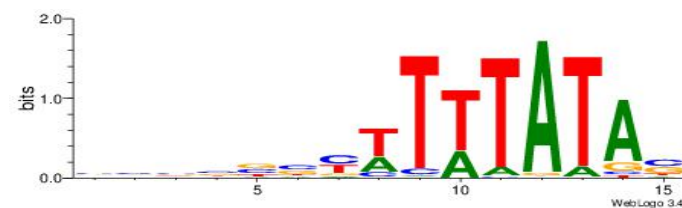
VBVVVMWTTTATAS

-DHATKTTTAHH---

Original motif Consensus sequence: STATAAWRVVVVBV



Reverse complement motif Consensus sequence: VBVVVMWTTTATAS



Dataset #: 4 Motif ID: 109 Motif name: aaCAAAAACaa

Original motif Consensus sequence: HHCAAAAACHH



Reverse complement motif Consensus sequence: HHGTTTTTGHH



Best Matches for Motif ID 109 (Highest to Lowest)

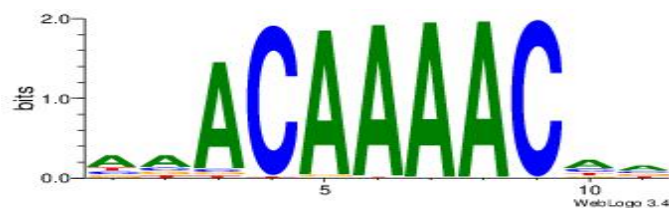
Dataset #:	4
Motif ID:	89
Motif name:	aaACAAACaa
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	11
Similarity score:	0.00652588

Alignment:

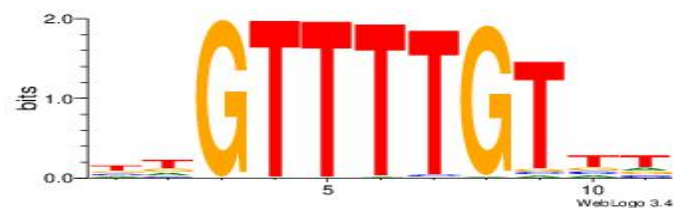
BHGTTTTGTTT

HHGTTTTTGHH

Original motif Consensus sequence: AAACAAAACHV



Reverse complement motif Consensus sequence: BHGTTTTGTTT



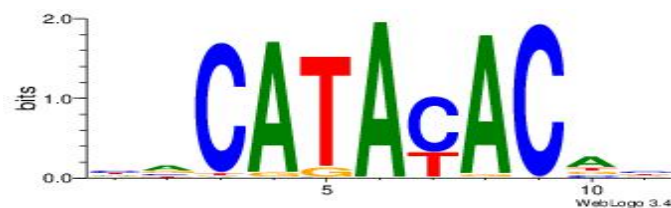
Dataset #: 4
 Motif ID: 117
 Motif name: yaCATAYACay
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.0113253

Alignment:

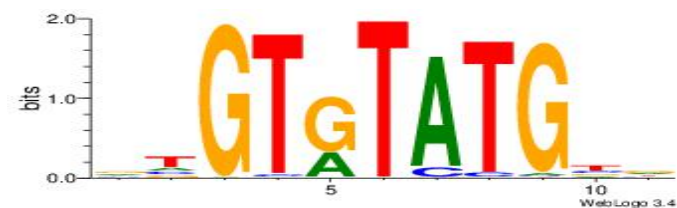
DTGTGTATGBD

HHGTTTTTGH

Original motif Consensus sequence: HVCATACACAH



Reverse complement motif Consensus sequence: DTGTGTATGBD

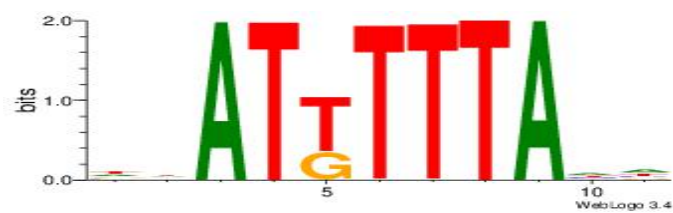


Dataset #: 4
 Motif ID: 108
 Motif name: wwATkTTTAww
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 11

Similarity score: 0.0251184

Alignment:
DHATKTTTAHH
HHGTTTTTGH

Original motif Consensus sequence: DHATKTTTAHH



Reverse complement motif Consensus sequence: HHTAAARATHD

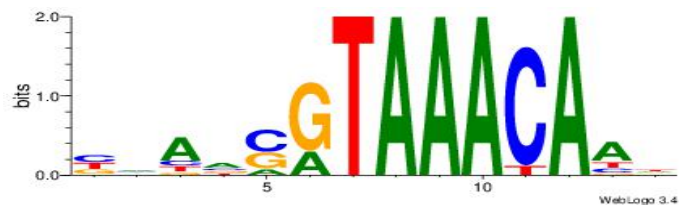


Dataset #: 3
Motif ID: 75
Motif name: FOXF2
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2
Number of overlap: 11
Similarity score: 0.0278186

Alignment:
BHADSGTAAACAAD
--HHCAAAAACHH--

Original motif Consensus sequence: BHADSGTAAACAAD

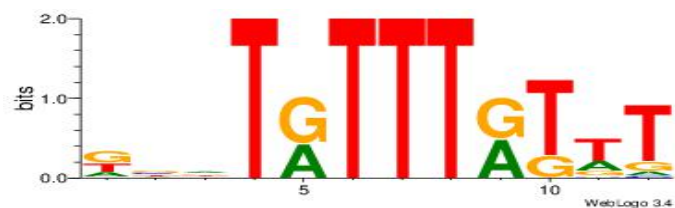
Reverse complement motif Consensus sequence: DTTGTTTACSBTBE



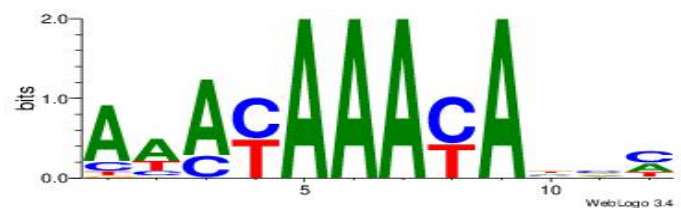
Dataset #: 3
 Motif ID: 67
 Motif name: FOXI1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 11
 Similarity score: 0.0320335

Alignment:
 KBDTRTTTRTTT
 -HHGTTTTTGH

Original motif Consensus sequence: KBDTRTTTRTTT

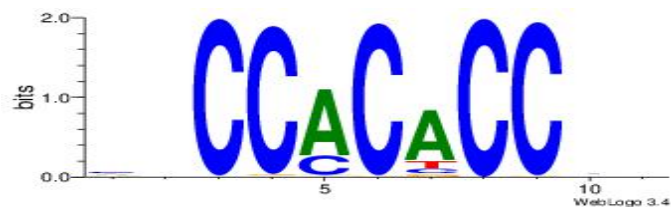


Reverse complement motif Consensus sequence: AAAMAAAMADBY

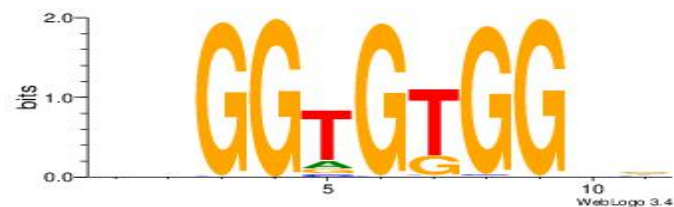


Dataset #: 4 Motif ID: 110 Motif name: cmCCACACCcm

Original motif Consensus sequence: HVCCACACCBV



Reverse complement motif Consensus sequence: VBGGTGTGGBD



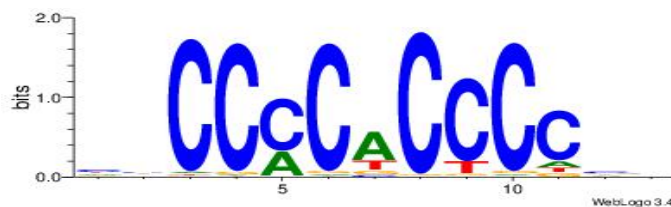
Best Matches for Motif ID 110 (Highest to Lowest)

Dataset #: 4
 Motif ID: 111
 Motif name: ccCCmCaCCCCcc
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 11
 Similarity score: 0.00944953

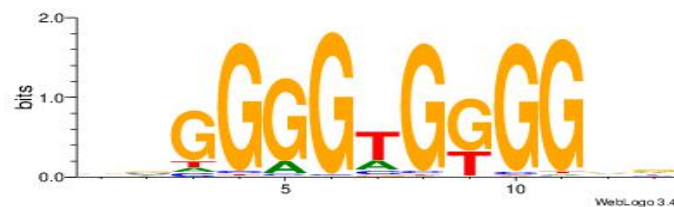
Alignment:

HBCCCCACCCCBH
 HVCCACACCBV--

Original motif Consensus sequence: HBCCCCACCCCBH



Reverse complement motif Consensus sequence: DBGGGGTGGGGB



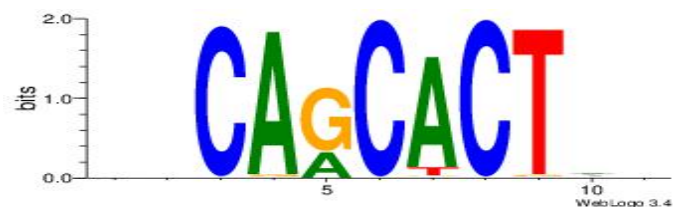
Dataset #: 4
 Motif ID: 93
 Motif name: cmCARCACTwr
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.0342522

Alignment:

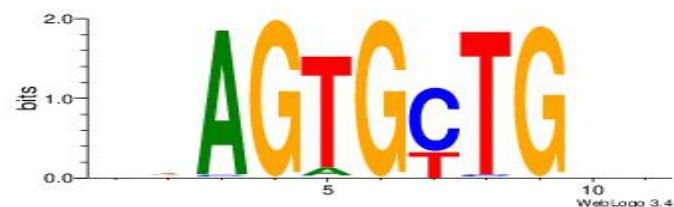
BHCAGCACTHV

HVCCACACCBV

Original motif Consensus sequence: BHCAGCACTHV



Reverse complement motif Consensus sequence: VHAGTGCTGHB

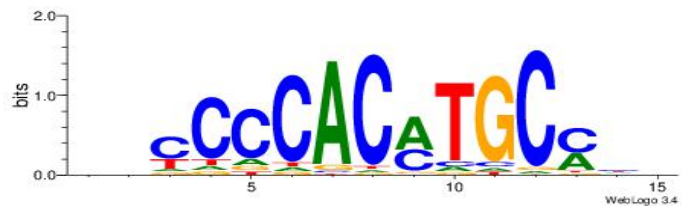


Dataset #: 4
 Motif ID: 98
 Motif name: myyCCCACmTGCmyr
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 11

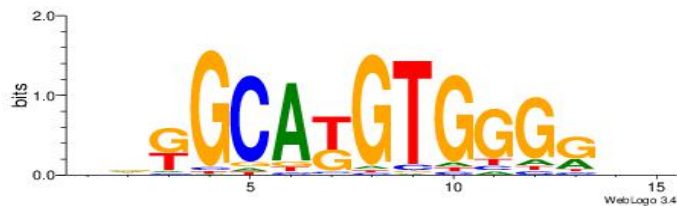
Similarity score: 0.0444

Alignment:
HBCCCCACMTGCMHV
HVCCACACCBV----

Original motif Consensus sequence: HBCCCCACMTGCMHV



Reverse complement motif Consensus sequence: VDRGCAYGTGGGGVD

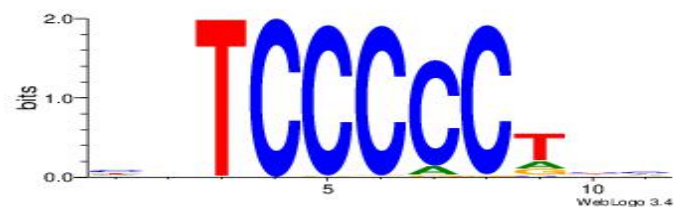


Dataset #: 4
Motif ID: 99
Motif name: graGGGGGArr
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 11
Similarity score: 0.0501309

Alignment:
DVAGGGGGADD
VBGGTGTGGBD

Original motif Consensus sequence: DVAGGGGGADD

Reverse complement motif Consensus sequence: HDTCCCCCTVH



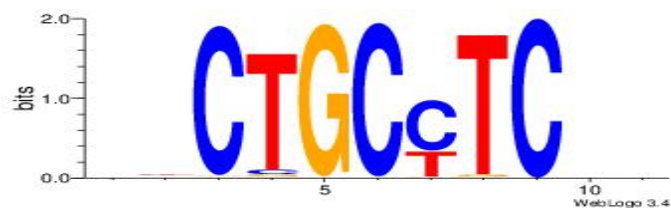
Dataset #: 4
 Motif ID: 116
 Motif name: dyCTGCyTCyc
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.0510757

Alignment:

BHGA KGCAGHH

VBGGTGTGGBD

Original motif Consensus sequence: DHCTGCYTCHB

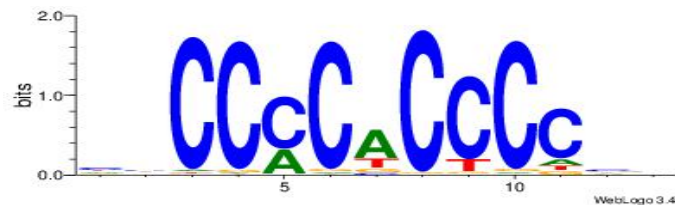


Reverse complement motif Consensus sequence: BHGA KGCAGHH

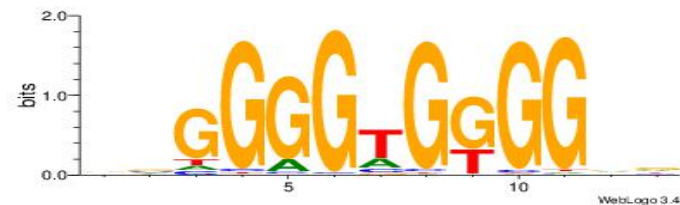


Dataset #: 4 Motif ID: 111 Motif name: ccCCmCaCCCCcc

Original motif Consensus sequence: HBCCCCACCCCBH



Reverse complement motif Consensus sequence: DBGGGGTGGGGB



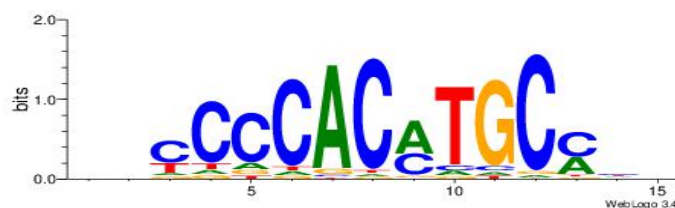
Best Matches for Motif ID 111 (Highest to Lowest)

Dataset #:	4
Motif ID:	98
Motif name:	myyCCCACmTGCmyr
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:	0.0348277

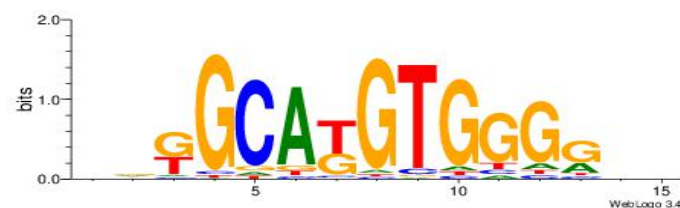
Alignment:

```
HBCCCCACMTGCMHV
--HBCCCCACCCCBH
```

Original motif Consensus sequence: HBCCCCACMTGCMHV



Reverse complement motif Consensus sequence: VDRGCAYGTGGGGVD

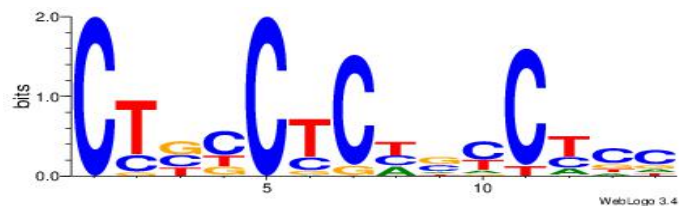


Dataset #: 2
 Motif ID: 59
 Motif name: Motif 59
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 13
 Similarity score: 0.0360633

Alignment:

CTBCCTCHSYCYCC
 -HBCCCCACCCCBH

Original motif Consensus sequence: CTBCCTCHSYCYCC



Reverse complement motif Consensus sequence: GGMGKSHGAGGB



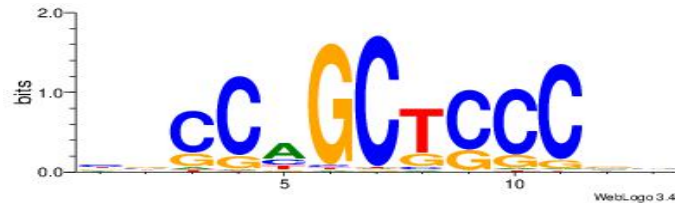
Dataset #: 4
 Motif ID: 103
 Motif name: csCCaGCTCCCgs
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 13

Similarity score: 0.0413801

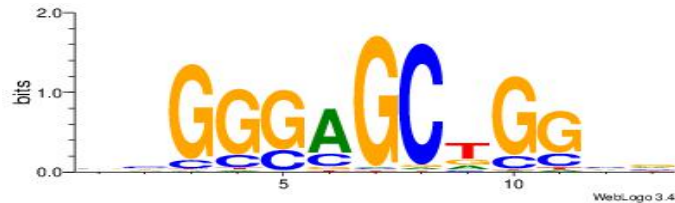
Alignment:

BBCCAGCTCCCVB
HBCCCCACCCCBH

Original motif Consensus sequence: BBCCAGCTCCCVB



Reverse complement motif Consensus sequence: BVGGGAGCTGGBB



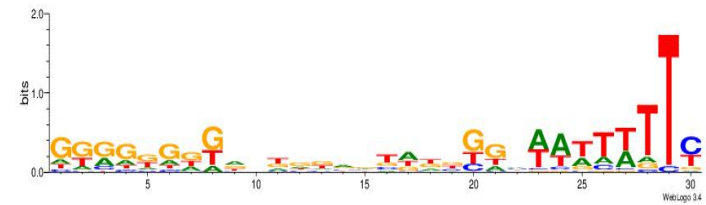
Dataset #: 3
Motif ID: 81
Motif name: Pax4
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 3
Number of overlap: 13
Similarity score: 0.0432691

Alignment:

RAAWAWTWDCMVHHVBBHHHVHMHCMCYMC
-----HBCCCCACCCCBH--

Original motif Consensus sequence:
RAAWAWTWDCMVHHVBBHHHVHMHCMCYMC

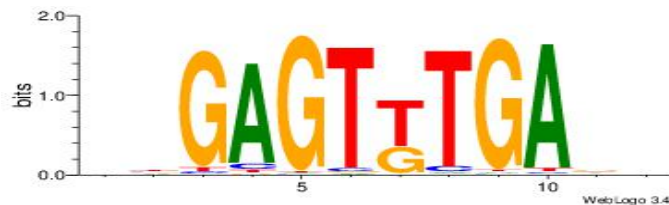
Reverse complement motif Consensus sequence:
GRKGRGDRHVHDDVBBHHBRGDWAWTWTTM



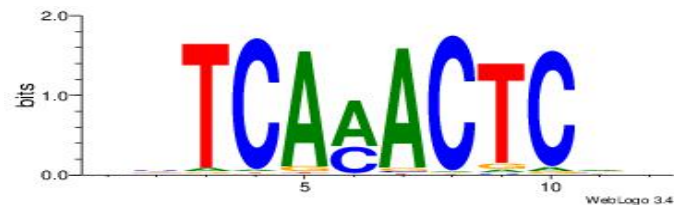
Alignment:

```
HBCCAGGCCTGGVD
HBCCCCACCCCBH-
```

Original motif Consensus sequence: VBGAGTKTGADD



Reverse complement motif Consensus sequence: HHTCARACTCVV



Best Matches for Motif ID 112 (Highest to Lowest)

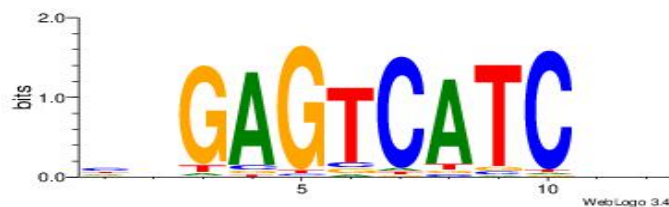
Dataset #:	4
Motif ID:	121
Motif name:	ctGAGTCATCkb
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	12
Similarity score:	0.00842365

Alignment:

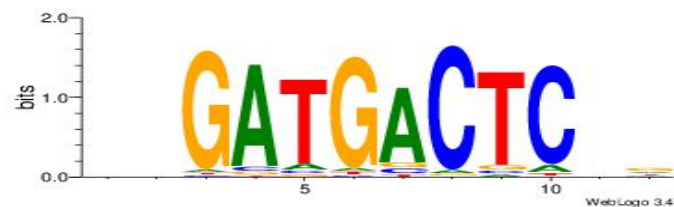
BHGATGACTCDD

HHTCARACTCVV

Original motif Consensus sequence: HDGAGTCATCDB



Reverse complement motif Consensus sequence: BHGATGACTCDD



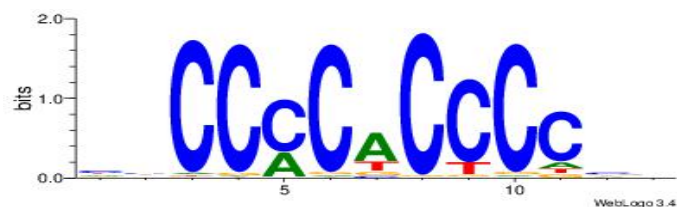
Dataset #: 4
 Motif ID: 111
 Motif name: ccCCmCaCCCCcc
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 12
 Similarity score: 0.0219353

Alignment:

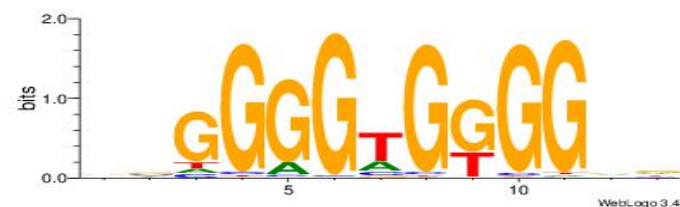
DBGGGGTGGGGBD

VBGAGTKTGADD-

Original motif Consensus sequence: HBCCCCACCCCBH



Reverse complement motif Consensus sequence: DBGGGGTGGGGB

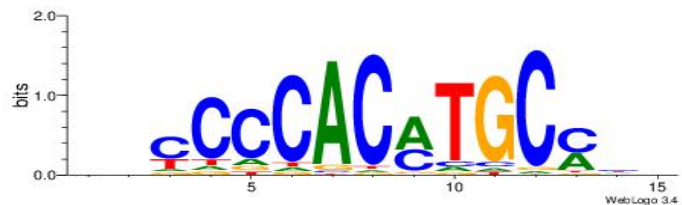


Dataset #: 4
 Motif ID: 98
 Motif name: myyCCCACmTGCmyr
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 12

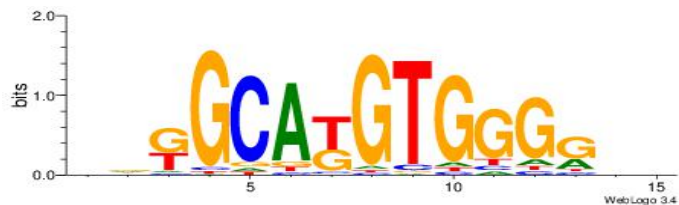
Similarity score: 0.0363368

Alignment:
HBCCCCACMTGCMHV
-HHTCARACTCVV--

Original motif Consensus sequence: HBCCCCACMTGCMHV



Reverse complement motif Consensus sequence: VDRGCAYGTGGGGVD

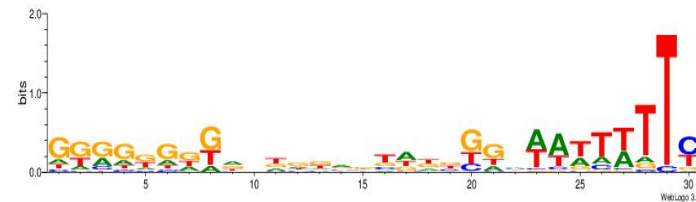
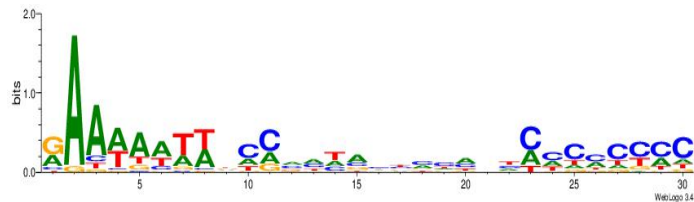


Dataset #: 3
Motif ID: 81
Motif name: Pax4
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 16
Number of overlap: 12
Similarity score: 0.0370187

Alignment:
RAAWAWTWDCMVHHVBBHHHVHMHCMCYMC
---HHTCARACTCVV-----

Original motif Consensus sequence:
RAAWAWTWDCMVHHVBBHHHVHMHCMCYMC

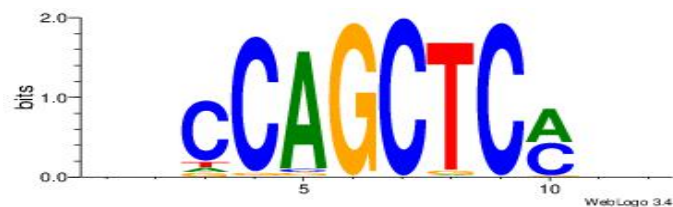
Reverse complement motif Consensus sequence:
GRKGRGDRHVHDDVBBHHBRGDWAWTWTTM



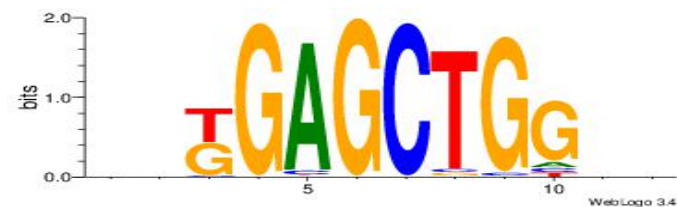
Dataset #: 4
 Motif ID: 119
 Motif name: cbCCAGCTCmyk
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 12
 Similarity score: 0.0389051

Alignment:
 BBCCAGCTCMBD
 HHTCARACTCVV

Original motif Consensus sequence: BBCCAGCTCMBD



Reverse complement motif Consensus sequence: HBYGAGCTGGBB



Dataset #: 4 Motif ID: 113 Motif name: htCTGyKTCbt

Original motif Consensus sequence: HBCTGYTTCBH



Reverse complement motif Consensus sequence: HVGAAMCAGVH



Best Matches for Motif ID 113 (Highest to Lowest)

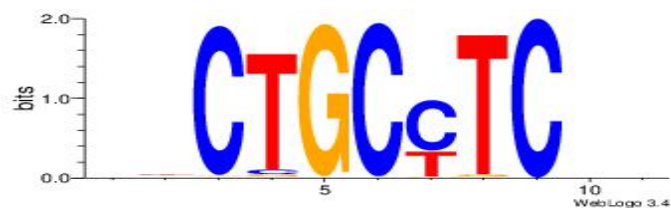
Dataset #: 4
Motif ID: 116
Motif name: dyCTGCyTCyc
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 11
Similarity score: 0

Alignment:

DHCTGCYTCHB

HBCTGYTTCBH

Original motif Consensus sequence: DHCTGCYTCHB



Reverse complement motif Consensus sequence: BHGAKGCAGHH

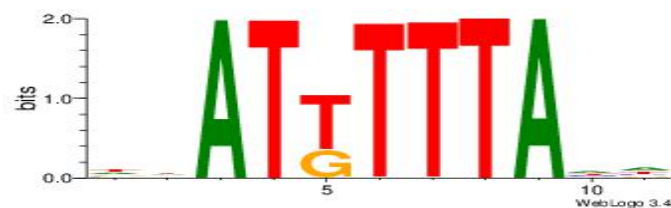


Dataset #: 4
 Motif ID: 108
 Motif name: wwATkTTTAww
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.0453878

Alignment:

DHATKTTTAHH
 HBCTGYTTCBH

Original motif Consensus sequence: DHATKTTTAHH



Reverse complement motif Consensus sequence: HHTAAARATHD



Dataset #: 4
 Motif ID: 114
 Motif name: awAACAcAAwa
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 11

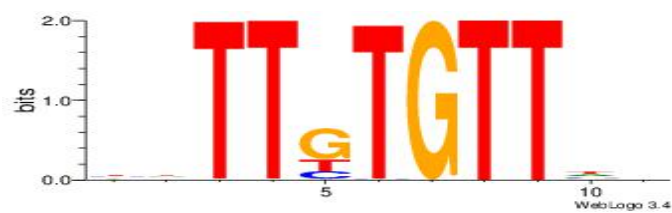
Similarity score: 0.0496817

Alignment:
BDTTGTGTTDD
HBCTGYTTCBH

Original motif Consensus sequence: DDAACACAADV



Reverse complement motif Consensus sequence: BDTTGTGTTDD

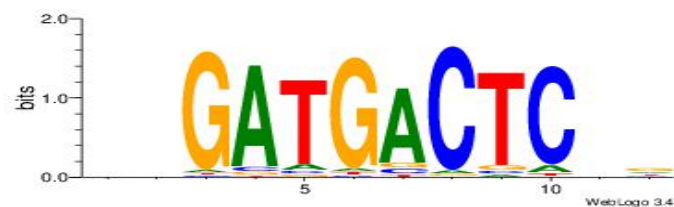
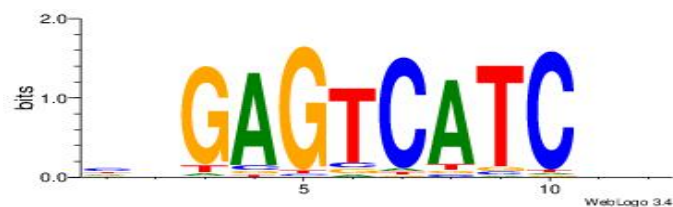


Dataset #: 4
Motif ID: 121
Motif name: ctGAGTCATCkb
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2
Number of overlap: 11
Similarity score: 0.0512287

Alignment:
HDGAGTCATCDB
HVGAAACAGVH-

Original motif Consensus sequence: HDGAGTCATCDB

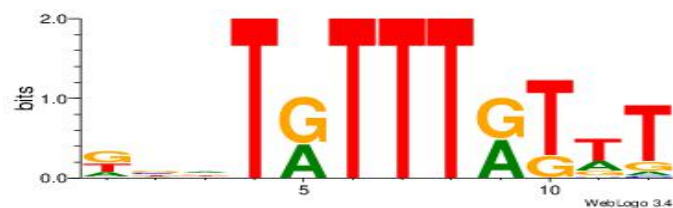
Reverse complement motif Consensus sequence: BHGATGACTCDD



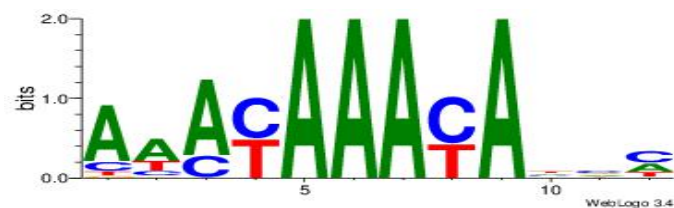
Dataset #: 3
 Motif ID: 67
 Motif name: FOXI1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.0525328

Alignment:
 AAAMAAAMADBY
 -HVGAAAMCAGVH

Original motif Consensus sequence: KBDTRTTTTRTT



Reverse complement motif Consensus sequence: AAAMAAAMADBY

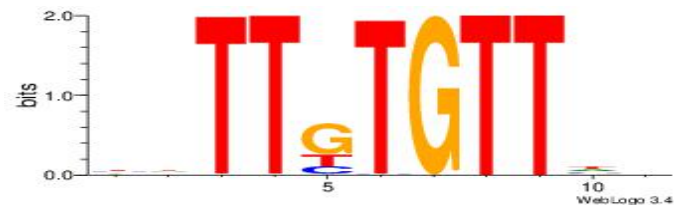


Dataset #: 4 Motif ID: 114 Motif name: awAACAcAAwa

Original motif Consensus sequence: DDAACACAADV



Reverse complement motif Consensus sequence: BDTTGTGTTDD



Best Matches for Motif ID 114 (Highest to Lowest)

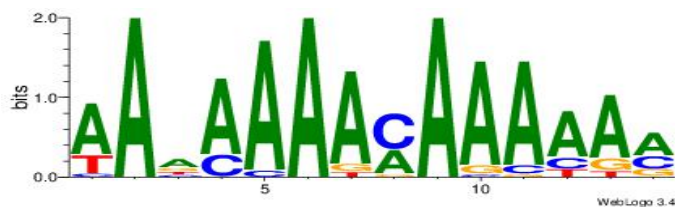
Dataset #:	2
Motif ID:	60
Motif name:	Motif 60
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	11
Similarity score:	0.0409581

Alignment:

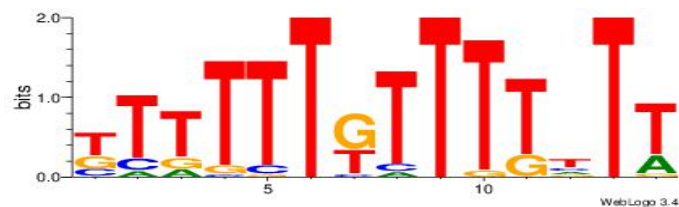
AADAAAAMAAAAAM

-DDAACACAADV--

Original motif Consensus sequence: AADAAAAMAAAAAM



Reverse complement motif Consensus sequence: YTTTTTRTTTDDT



Dataset #: 3
 Motif ID: 71
 Motif name: Evi1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 4
 Number of overlap: 11
 Similarity score: 0.0441291

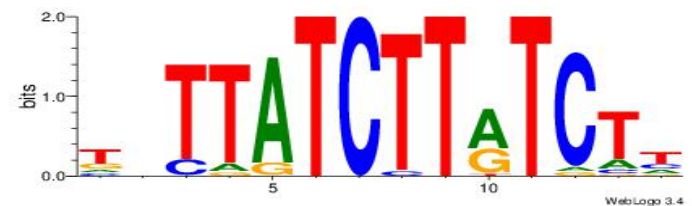
Alignment:

TBTTATCTTMTCTT
 BDTTGTGTTDD---

Original motif Consensus sequence: AAGAYAAGATAABA



Reverse complement motif Consensus sequence: TBTTATCTTMTCTT

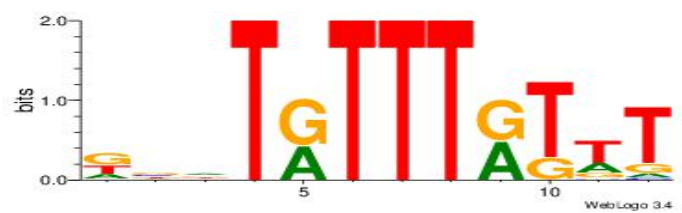


Dataset #: 3
 Motif ID: 67
 Motif name: FOXI1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 11

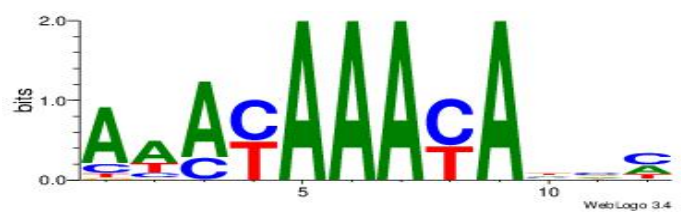
Similarity score: 0.0515608

Alignment:
KBDTRTTTTRTTT
-BDTTGTGTTDD

Original motif Consensus sequence: KBDTRTTTTRTTT



Reverse complement motif Consensus sequence: AAAMAAAMADBY

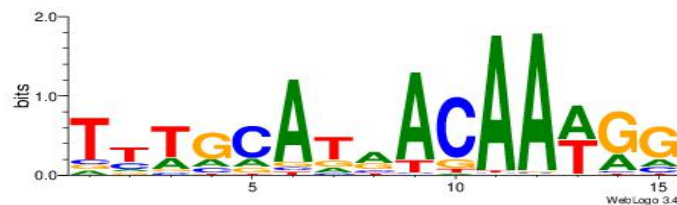
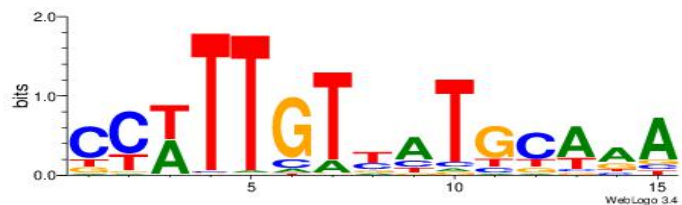


Dataset #: 3
Motif ID: 76
Motif name: Sox2
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2
Number of overlap: 11
Similarity score: 0.0542339

Alignment:
CCWTTGTYATGCAAA
---BDTTGTGTTDD-

Original motif Consensus sequence: CCWTTGTYATGCAAA

Reverse complement motif Consensus sequence:
TTTGCATMACAAWGG



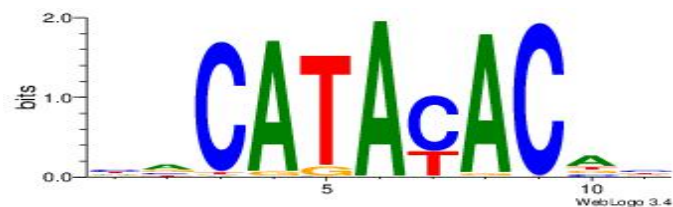
Dataset #: 4
 Motif ID: 117
 Motif name: yaCATAYACay
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.0554944

Alignment:

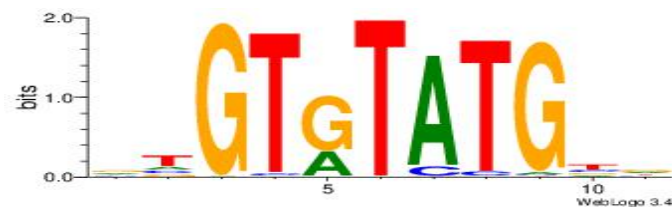
DTGTGTATGBD

BDTTGTGTTDD

Original motif Consensus sequence: HVCATACACAH



Reverse complement motif Consensus sequence: DTGTGTATGBD

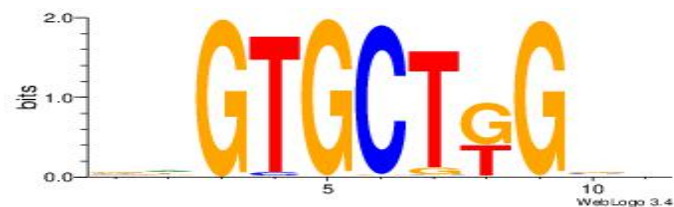


Dataset #: 4 Motif ID: 115 Motif name: ysCmAGCACwy

Original motif Consensus sequence: HVCMAGCACHH



Reverse complement motif Consensus sequence: DHGTGCTRGVH

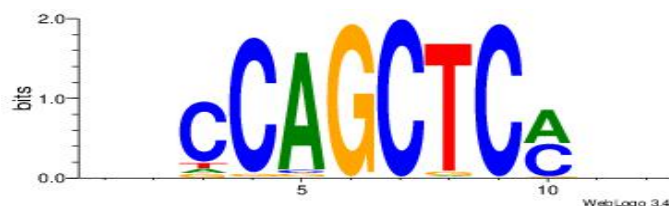


Best Matches for Motif ID 115 (Highest to Lowest)

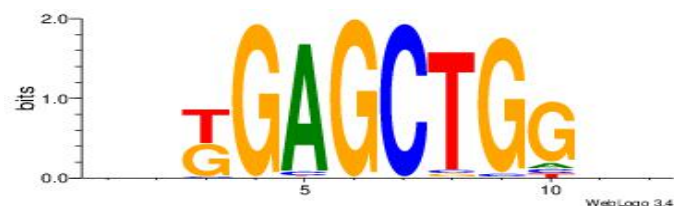
Dataset #: 4
Motif ID: 119
Motif name: cbCCAGCTCmyk
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2
Number of overlap: 11
Similarity score: 0.00720731

Alignment:
BCCAGCTCMBD
HVCMAGCACHH-

Original motif Consensus sequence: BCCAGCTCMBD



Reverse complement motif Consensus sequence: HBYGAGCTGGBB



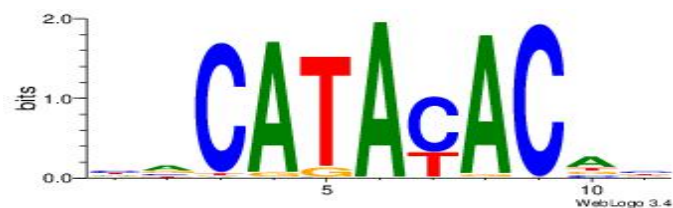
Dataset #: 4
 Motif ID: 117
 Motif name: yaCATAYACay
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.0367273

Alignment:

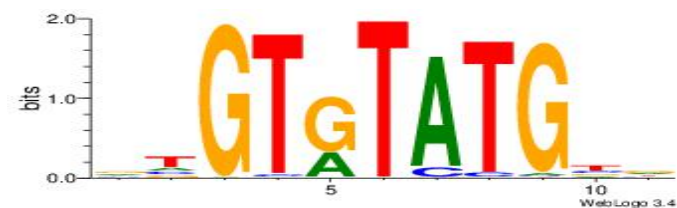
HVCATACACAH

HVCMAGCACHH

Original motif Consensus sequence: HVCATACACAH



Reverse complement motif Consensus sequence: DTGTGTATGBD



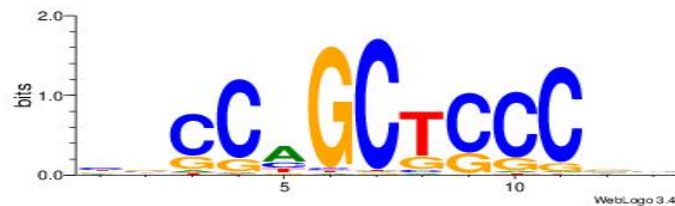
Dataset #: 4
 Motif ID: 103
 Motif name: csCCaGCTCCCgs
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 11

Similarity score: 0.0374067

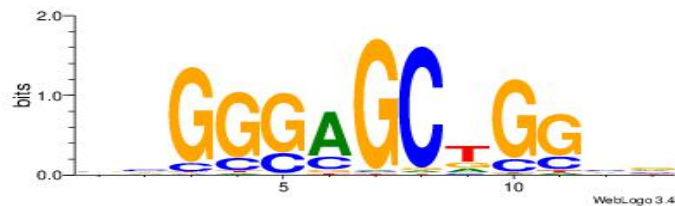
Alignment:

BBCCAGCTCCCVB
HVCMAGCACHH--

Original motif Consensus sequence: BBCCAGCTCCCVB



Reverse complement motif Consensus sequence: BVGGGAGCTGGBB



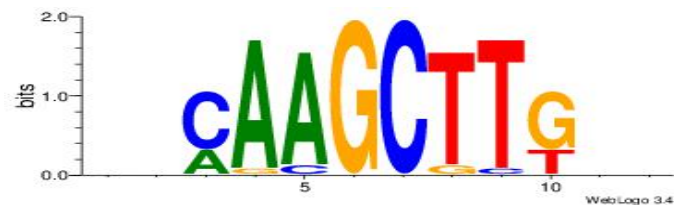
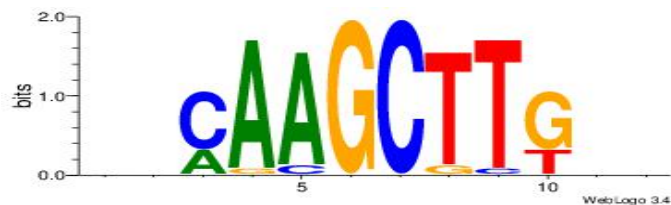
Dataset #: 4
Motif ID: 123
Motif name: asMAAGCTTKst
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 11
Similarity score: 0.0385747

Alignment:

HBCAAGCTTGVD
HVCMAGCACHH-

Original motif Consensus sequence: HBCAAGCTTGVD

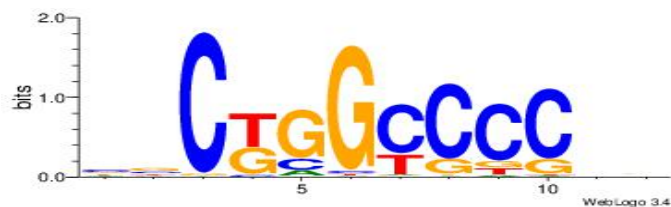
Reverse complement motif Consensus sequence: DVCAAGCTTGBH



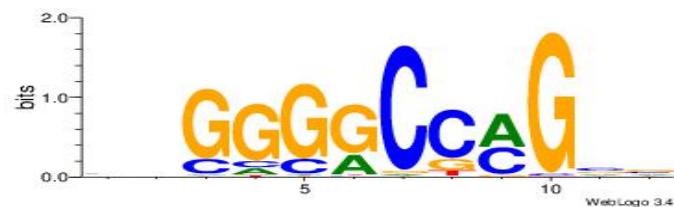
Dataset #: 4
 Motif ID: 102
 Motif name: ssCkGGYCCCsg
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.0395809

Alignment:
 VVGGGGCCRGBB
 -DHGTGCTRGVH

Original motif Consensus sequence: BBCKGGCCCCVV

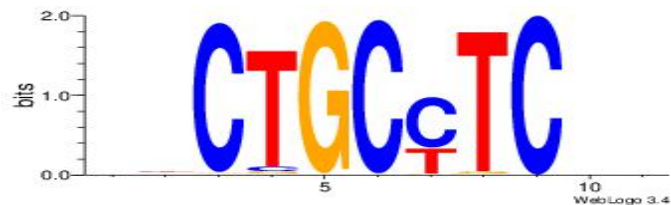


Reverse complement motif Consensus sequence: VVGGGGCCRGBB



Dataset #: 4 Motif ID: 116 Motif name: dyCTGCyTCyc

Original motif Consensus sequence: DHCTGCYTCHB



Reverse complement motif Consensus sequence: BHGAKGCAGHH



Best Matches for Motif ID 116 (Highest to Lowest)

Dataset #:	4
Motif ID:	113
Motif name:	htCTGyKTCbt
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	11
Similarity score:	0

Alignment:

HBCTGYTTCBH

DHCTGCYTCHB

Original motif Consensus sequence: HBCTGYTTCBH



Reverse complement motif Consensus sequence: HVGAAMCAGVH



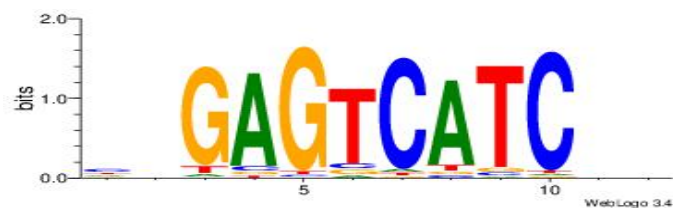
Dataset #: 4
 Motif ID: 121
 Motif name: ctGAGTCATCkb
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 11
 Similarity score: 0.0409177

Alignment:

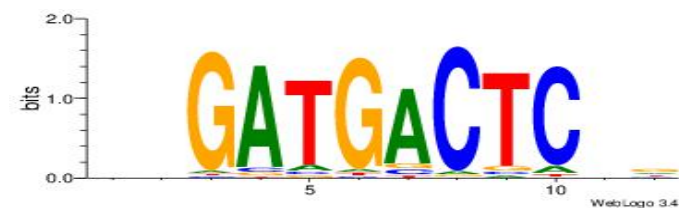
HDGAGTCATCDB

BHGAKGCAGHH-

Original motif Consensus sequence: HDGAGTCATCDB



Reverse complement motif Consensus sequence: BHGATGACTCDD

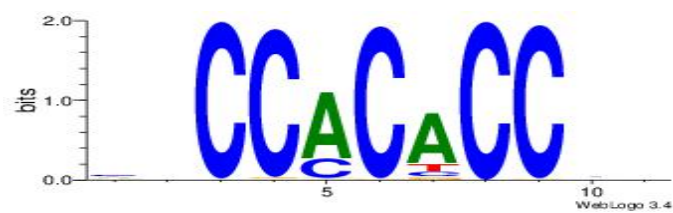


Dataset #: 4
 Motif ID: 110
 Motif name: cmCCACACCcm
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 11

Similarity score: 0.0482758

Alignment:
VBGGTGTGGBD
BHGA KGCAGHH

Original motif Consensus sequence: HVCCACACCBV



Reverse complement motif Consensus sequence: VBGGTGTGGBD

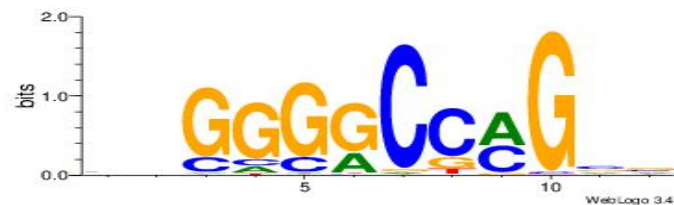
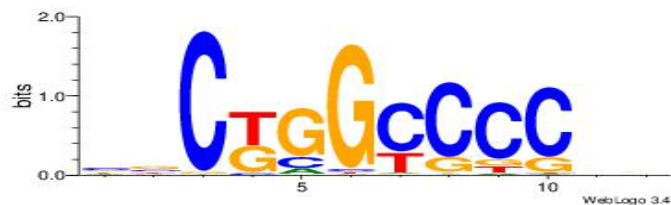


Dataset #: 4
Motif ID: 102
Motif name: ssCkGGYCCCsg
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 11
Similarity score: 0.0492303

Alignment:
BBCKGGCCCCVV
DHCTG C Y T C H B -

Original motif Consensus sequence: BBCKGGCCCCVV

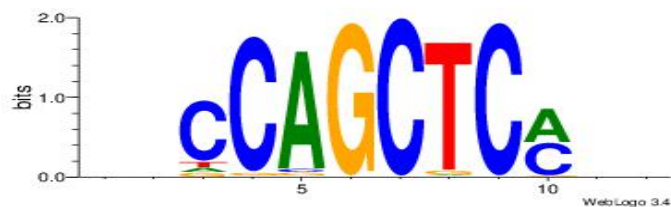
Reverse complement motif Consensus sequence: VVGGGGCCCRBB



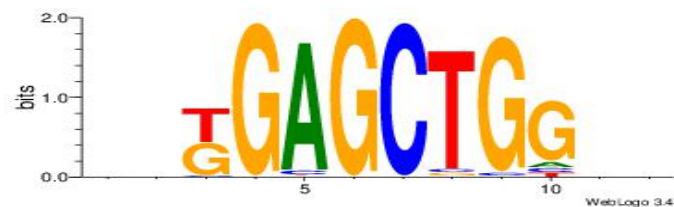
Dataset #: 4
 Motif ID: 119
 Motif name: cbCCAGCTCmyk
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.0496606

Alignment:
 BBCCAGCTCMBD
 -DHCTGCTCHB

Original motif Consensus sequence: BBCCAGCTCMBD

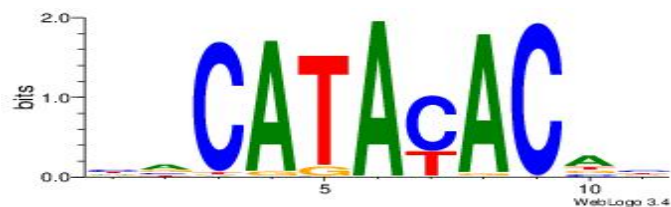


Reverse complement motif Consensus sequence: HBYGAGCTGGBB

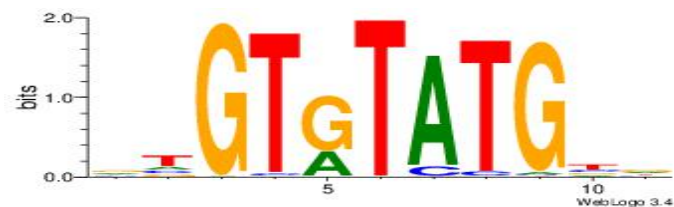


Dataset #: 4 **Motif ID: 117** **Motif name: yaCATAYACay**

Original motif Consensus sequence: HVCATACACAH



Reverse complement motif Consensus sequence: DTGTGTATGBD



Best Matches for Motif ID 117 (Highest to Lowest)

Dataset #:	4
Motif ID:	109
Motif name:	aaCAAAAACaa
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:	0.0144352

Alignment:

HHGTTTTTGHH

DTGTGTATGBD

Original motif Consensus sequence: HHCAAAAACHH



Reverse complement motif Consensus sequence: HHGTTTTTGHH

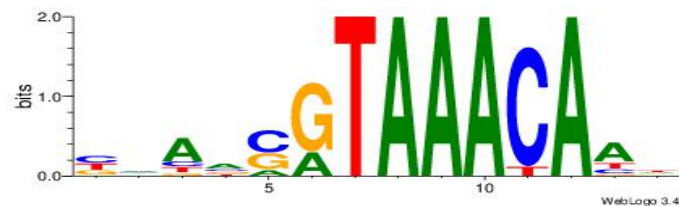


Dataset #: 3
 Motif ID: 75
 Motif name: FOXF2
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 11
 Similarity score: 0.0390604

Alignment:

DTTGTTTACSBTBB
 -DTGTGTATGBD--

Original motif Consensus sequence: BHADSGTAAACAAD



Reverse complement motif Consensus sequence: DTTGTTTACSBTBB



Dataset #: 4
 Motif ID: 112
 Motif name: ctGAGTkTGAgg
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 11

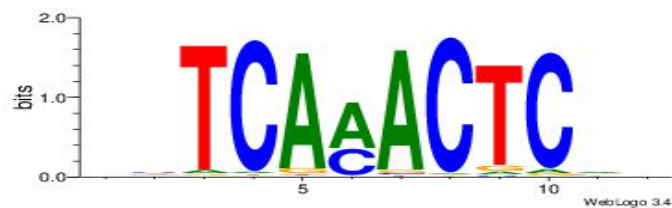
Similarity score: 0.0405823

Alignment:
HHTCARACTCVV
HVCATACACAH-

Original motif Consensus sequence: VBGAGTKTGADD



Reverse complement motif Consensus sequence: HHTCARACTCVV

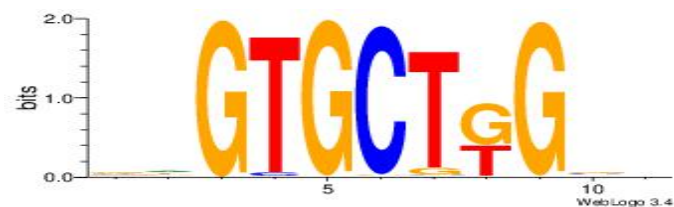


Dataset #: 4
Motif ID: 115
Motif name: ysCmAGCACwy
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 11
Similarity score: 0.0423793

Alignment:
HVCMAGCACHH
HVCATACACAH

Original motif Consensus sequence: HVCMAGCACHH

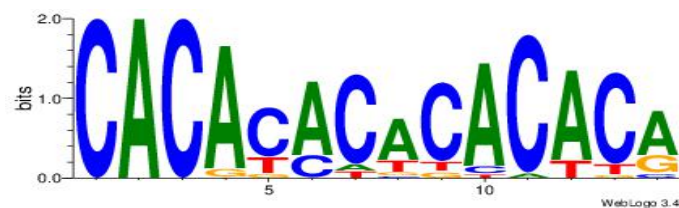
Reverse complement motif Consensus sequence: DHGTGCTRGVH



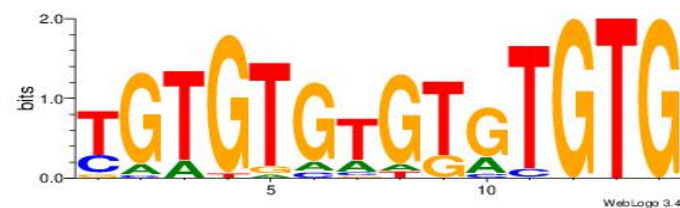
Dataset #: 2
 Motif ID: 58
 Motif name: Motif 58
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.0462842

Alignment:
 CACACACACACA
 HVCATACACAH---

Original motif Consensus sequence: CACACACACACA

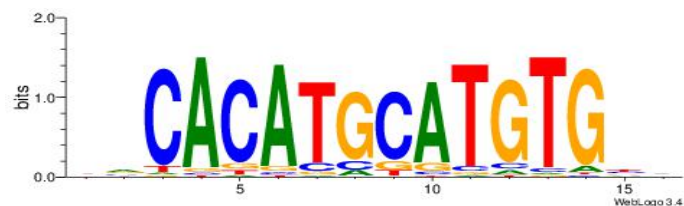


Reverse complement motif Consensus sequence: TGTGTGTGTGTGT

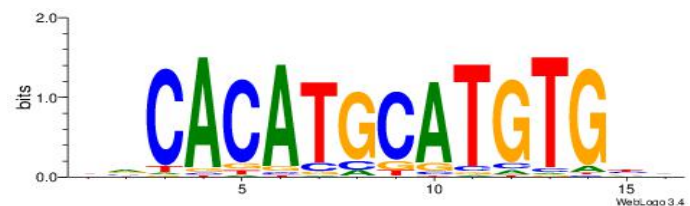


Dataset #: 4 **Motif ID: 118** **Motif name: yrCACATGCATGTGyr**

Original motif Consensus sequence: HVCACATGCATGTGBD



Reverse complement motif Consensus sequence: DVCACATGCATGTGBH



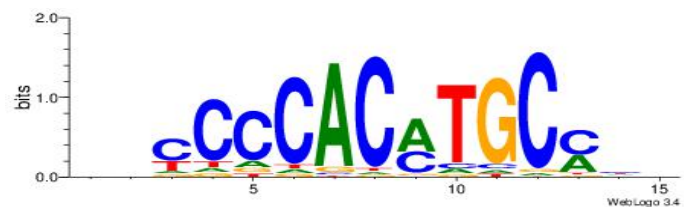
Best Matches for Motif ID 118 (Highest to Lowest)

Dataset #:	4
Motif ID:	98
Motif name:	myyCCCACmTGCmyr
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:	0.0676289

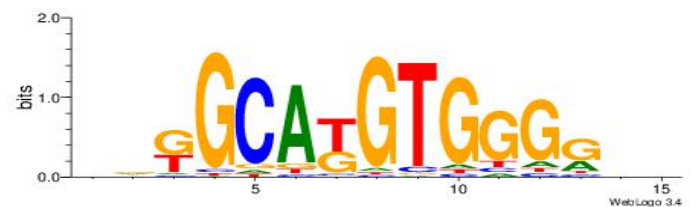
Alignment:

–HBCCCCACMTGCMHV
HVCACATGCATGTGBD

Original motif Consensus sequence: HBCCCCACMTGCMHV



Reverse complement motif Consensus sequence: VDRGCAYGTGGGGVD

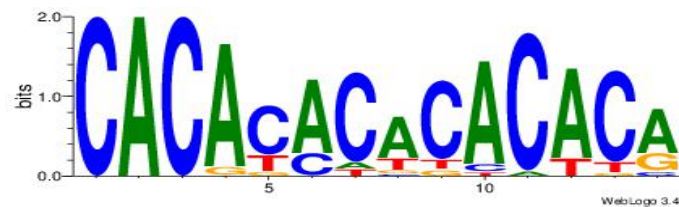


Dataset #: 2
 Motif ID: 58
 Motif name: Motif 58
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0.573876

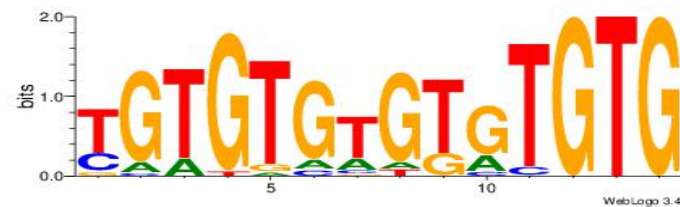
Alignment:

--CACACACACACACA
 HVCACATGCATGTGBD

Original motif Consensus sequence: CACACACACACACA



Reverse complement motif Consensus sequence: TGTGTGTGTGTGT



Dataset #: 3
 Motif ID: 80
 Motif name: Pou5f1
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3

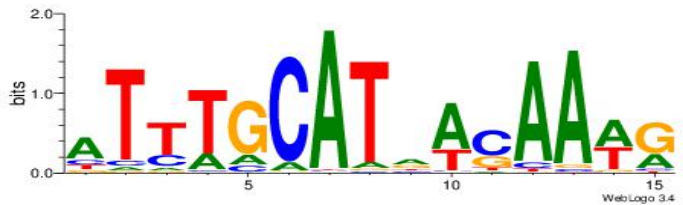
Number of overlap: 13
Similarity score: 1.06805

Alignment:
ATTTGCATHACAAG---
--HVCACATGCATGTGBD

Original motif Consensus sequence: CWTGTHATGCAAAT



Reverse complement motif Consensus sequence: ATTTGCATHACAAG

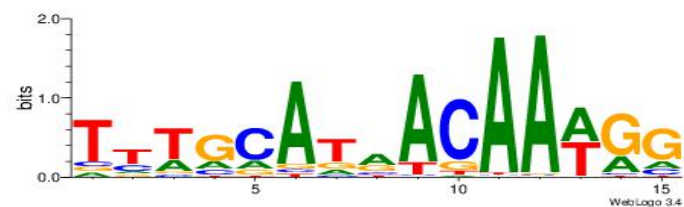
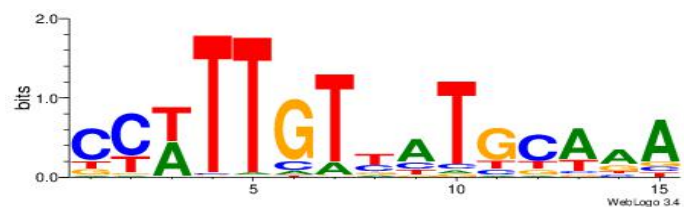


Dataset #: 3
Motif ID: 76
Motif name: Sox2
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 3
Number of overlap: 13
Similarity score: 1.07558

Alignment:
CCWTTGTYATGCAAA---
--DVCACATGCATGTGBH

Original motif Consensus sequence: CCWTTGTYATGCAAA

Reverse complement motif Consensus sequence:
TTTGCATMACAAWGG



Dataset #: 4
 Motif ID: 126
 Motif name: yVTGCAGsCAcg
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 12
 Similarity score: 1.55231

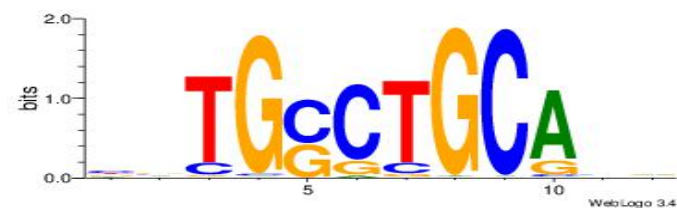
Alignment:

BVTGCAGSCABV----
 HVCACATGCATGTGBD

Original motif Consensus sequence: BVTGCAGSCABV

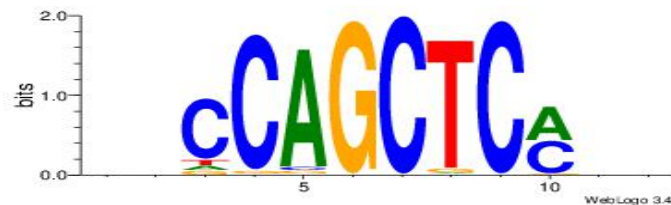


Reverse complement motif Consensus sequence: VBTGSCCTGCAVB

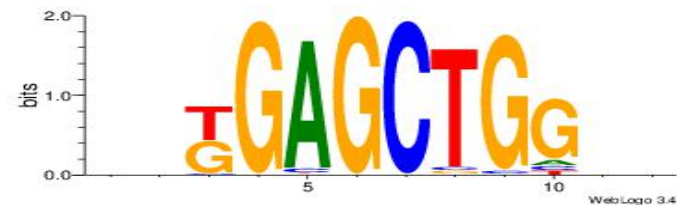


Dataset #: 4 Motif ID: 119 Motif name: cbCCAGCTCmyk

Original motif Consensus sequence: BBCCAGCTCMBD



Reverse complement motif Consensus sequence: HBYGAGCTGGBB



Best Matches for Motif ID 119 (Highest to Lowest)

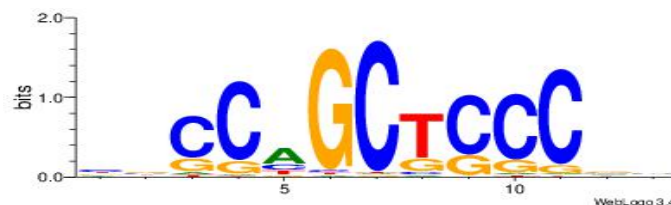
Dataset #:	4
Motif ID:	103
Motif name:	csCCaGCTCCCgs
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2
Number of overlap:	12
Similarity score:	0.00141375

Alignment:

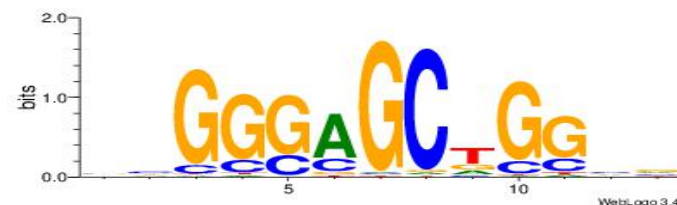
BBCCAGCTCCCVB

BBCCAGCTCMBD-

Original motif Consensus sequence: BBCCAGCTCCCVB



Reverse complement motif Consensus sequence: BVGGGAGCTGGBB



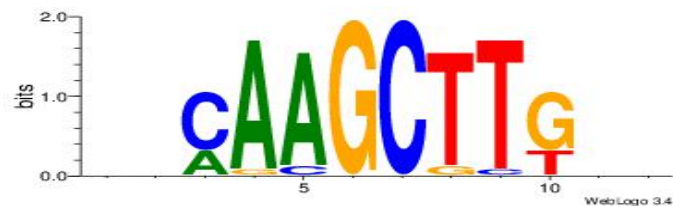
Dataset #: 4
 Motif ID: 123
 Motif name: asMAAGCTTKst
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 12
 Similarity score: 0.0040263

Alignment:

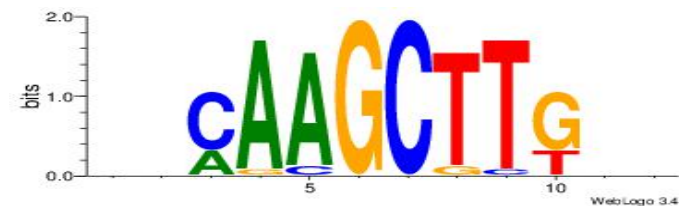
DVCAAGCTTGBH

HBYGAGCTGGBB

Original motif Consensus sequence: HBCAAGCTTGVD



Reverse complement motif Consensus sequence: DVCAAGCTTGBH

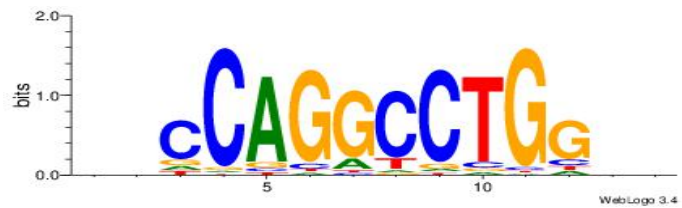


Dataset #: 4
 Motif ID: 122
 Motif name: hsCCAGGCCTGGsr
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 12

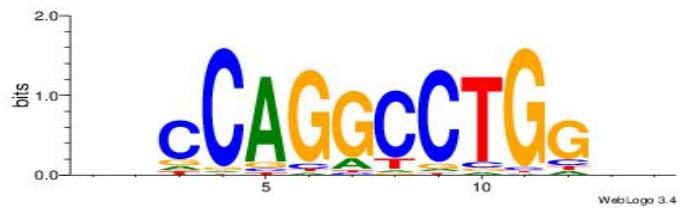
Similarity score: 0.0363393

Alignment:
HVCCAGGCCTGGBD
BBCCAGCTCMBD--

Original motif Consensus sequence: HVCCAGGCCTGGBD



Reverse complement motif Consensus sequence: HBCCAGGCCTGGV

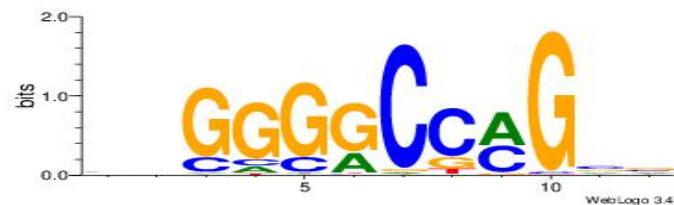
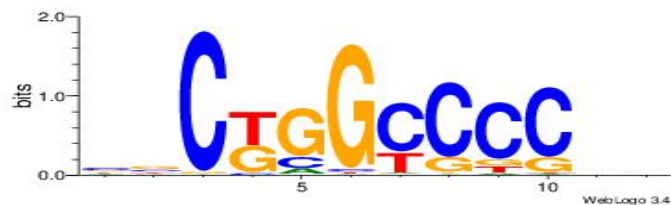


Dataset #: 4
Motif ID: 102
Motif name: ssCkGGYCCCsg
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 12
Similarity score: 0.0378472

Alignment:
BBCKGGCCCCVV
BBCCAGCTCMBD

Original motif Consensus sequence: BBCKGGCCCCVV

Reverse complement motif Consensus sequence: VVGGGGCCRGBB

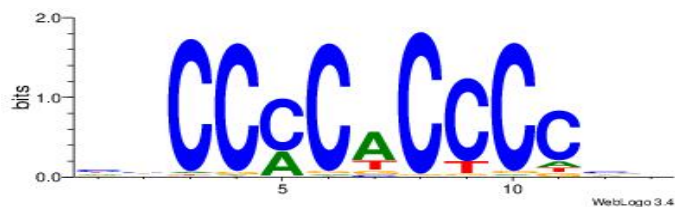


Dataset #: 4
 Motif ID: 111
 Motif name: ccCCmCaCCCCcc
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 12
 Similarity score: 0.0419313

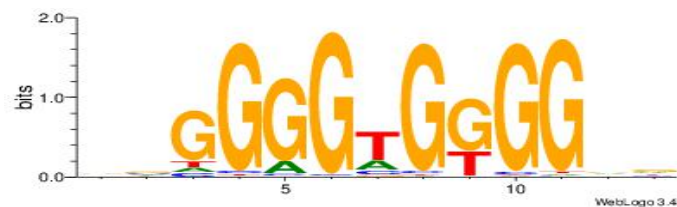
Alignment:

HBCCCCACCCCBH
 -BBCCAGCTCMBD

Original motif Consensus sequence: HBCCCCACCCCBH

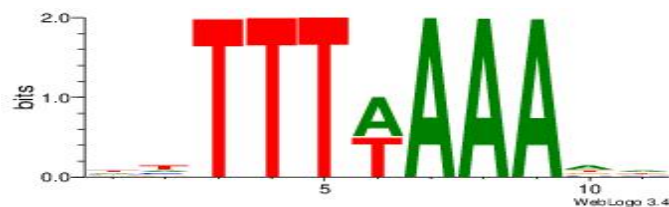


Reverse complement motif Consensus sequence: DBGGGGTGGGGB

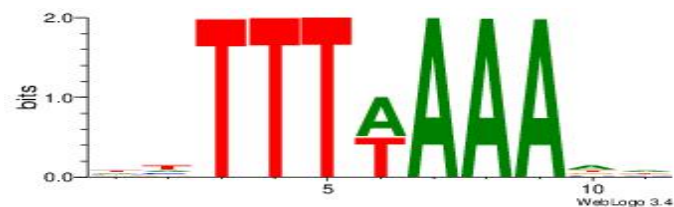


Dataset #: 4 Motif ID: 120 Motif name: wtTTTwAAAaw

Original motif Consensus sequence: HHTTTWAAADD



Reverse complement motif Consensus sequence: DDTTTWAAAHH



Best Matches for Motif ID 120 (Highest to Lowest)

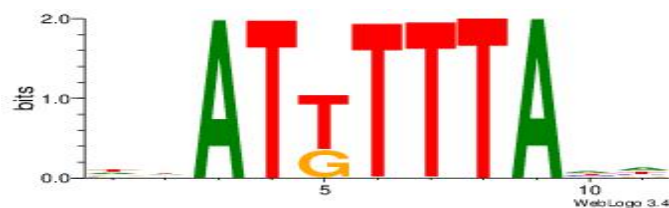
Dataset #:	4
Motif ID:	108
Motif name:	wwATkTTTAww
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	11
Similarity score:	0.0769117

Alignment:

HHTAAARATHD

HHTTTWAAADD

Original motif Consensus sequence: DHATKTTTAHH



Reverse complement motif Consensus sequence: HHTAAARATHD



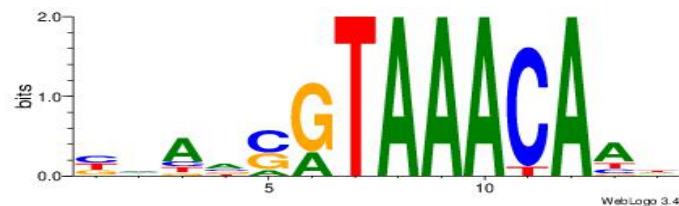
Dataset #: 3
 Motif ID: 75
 Motif name: FOXF2
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.0772648

Alignment:

DTTGTTTACSBTBB

DDTTTWAAAH---

Original motif Consensus sequence: BHADSGTAAACAAD



Reverse complement motif Consensus sequence: DTTGTTTACSBTBB



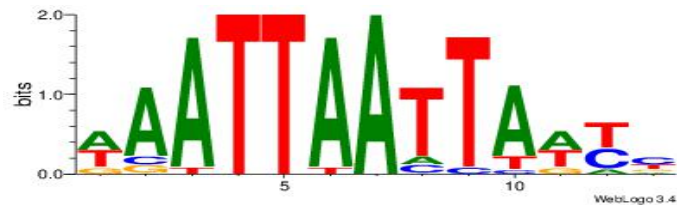
Dataset #: 3
 Motif ID: 66
 Motif name: Lhx3
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3
 Number of overlap: 11

Similarity score: 0.0876632

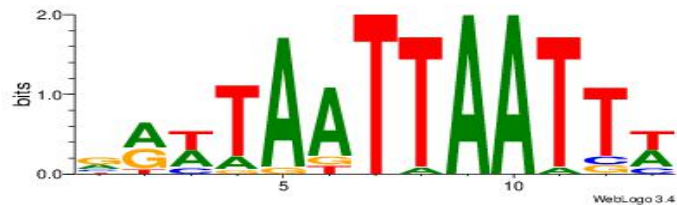
Alignment:

BMWTAATTAATTW
--DDTTTWAAAHH

Original motif Consensus sequence: WAATTAATTAWYB



Reverse complement motif Consensus sequence: BMWTAATTAATTW



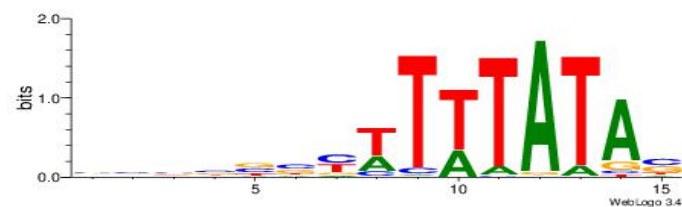
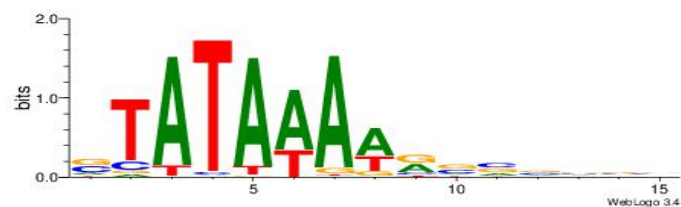
Dataset #: 3
Motif ID: 62
Motif name: TBP
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 11
Similarity score: 0.0881502

Alignment:

STATAAAWRVVVBV
HHTTTWAAADD----

Original motif Consensus sequence: STATAAAWRVVVBV

Reverse complement motif Consensus sequence: VBVVVMWTTTAT



Dataset #: 4
 Motif ID: 114
 Motif name: awAACAcAAwa
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.090069

Alignment:

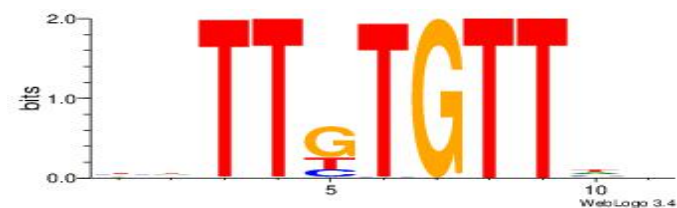
BDTTGTGTTDD

HHTTTWAAADD

Original motif Consensus sequence: DDAACACAADV

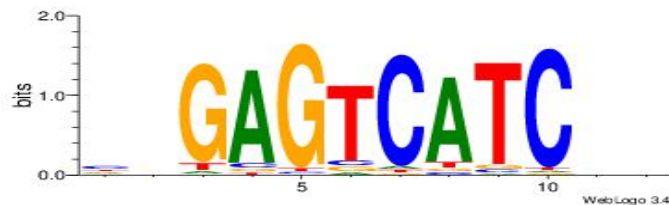


Reverse complement motif Consensus sequence: BDTTGTGTTDD

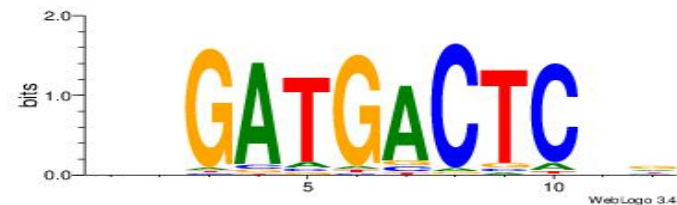


Dataset #: 4 Motif ID: 121 Motif name: ctGAGTCATCkb

Original motif Consensus sequence: HDGAGTCATCDB



Reverse complement motif Consensus sequence: BHGATGACTCDD



Best Matches for Motif ID 121 (Highest to Lowest)

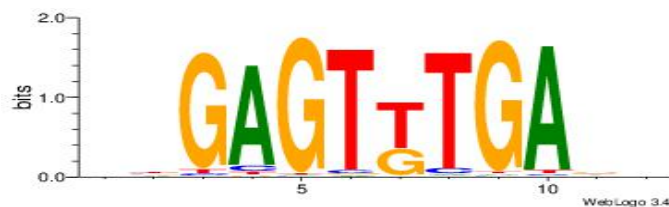
Dataset #:	4
Motif ID:	112
Motif name:	ctGAGTkTGAgg
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	12
Similarity score:	0.0322402

Alignment:

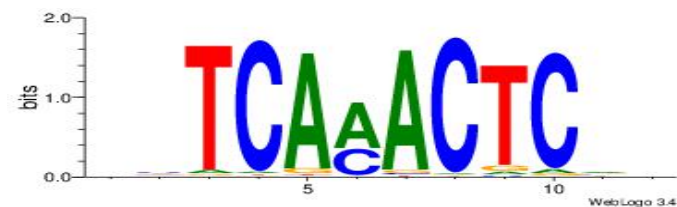
HHTCARACTCVV

BHGATGACTCDD

Original motif Consensus sequence: VBGAGTKTGADD



Reverse complement motif Consensus sequence: HHTCARACTCVV

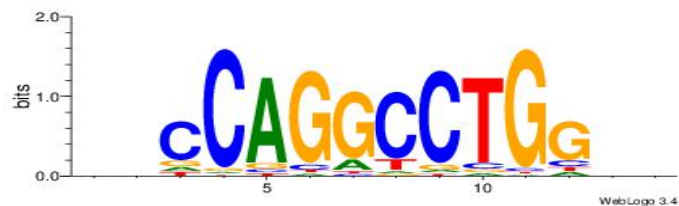


Dataset #: 4
 Motif ID: 122
 Motif name: hsCCAGGCCTGGsr
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 12
 Similarity score: 0.0510995

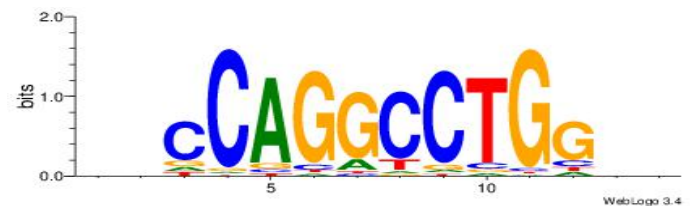
Alignment:

HBCCAGGCCTGGVD
 -HDGAGTCATCDB-

Original motif Consensus sequence: HVCCAGGCCTGGBD



Reverse complement motif Consensus sequence: HBCCAGGCCTGGV



Dataset #: 4
 Motif ID: 102
 Motif name: ssCkGGYCCCsg
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 12

Similarity score: 0.0569923

Alignment:

BBCKGGCCCCVV
BHGATGACTCDD

Original motif Consensus sequence: BBCKGGCCCCV



Reverse complement motif Consensus sequence: VVGGGGCCCRGBB



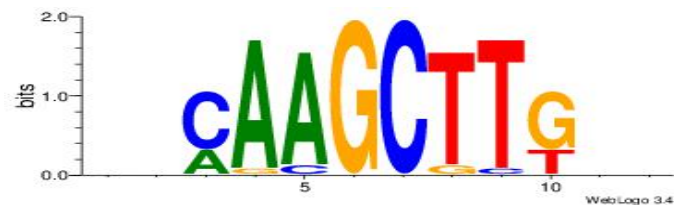
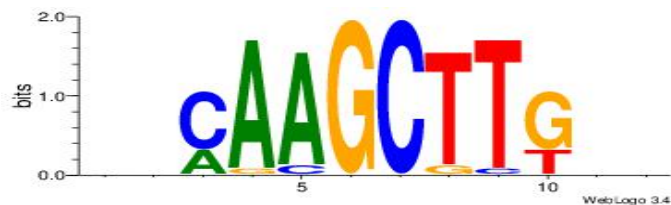
Dataset #: 4
Motif ID: 123
Motif name: asMAAGCTTKst
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 12
Similarity score: 0.0601978

Alignment:

DVCAAGCTTGBH
HDGAGTCATCDB

Original motif Consensus sequence: HBCAAGCTTGVD

Reverse complement motif Consensus sequence: DVCAAGCTTGBH

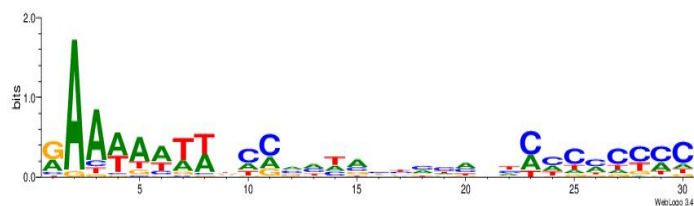


Dataset #: 3
 Motif ID: 81
 Motif name: Pax4
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 11
 Number of overlap: 12
 Similarity score: 0.0641337

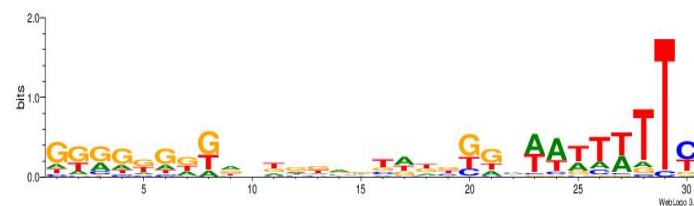
Alignment:

RAAWAWTWDCMVHHVBBHHHVHMHCMCYMC
 -----BHGATGACTCDD-----

Original motif Consensus sequence:
 RAAWAWTWDCMVHHVBBHHHVHMHCMCYMC

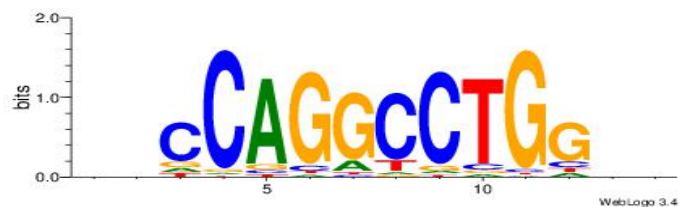


Reverse complement motif Consensus sequence:
 GRKGRGDRHVHDDVBBHHBRGDWAWTWTTM

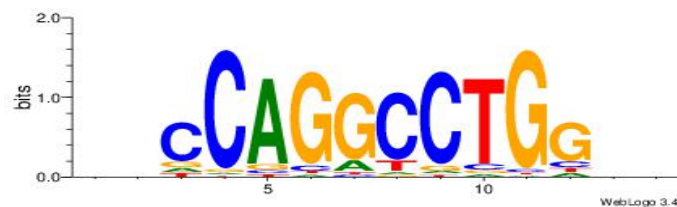


Dataset #: 4 Motif ID: 122 Motif name: hsCCAGGCCTGGsr

Original motif Consensus sequence: HVCCAGGCCTGGBD



Reverse complement motif Consensus sequence: HBCCAGGCCTGGV



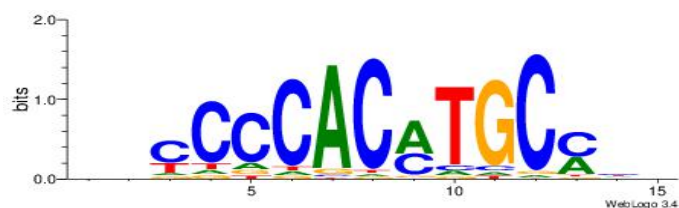
Best Matches for Motif ID 122 (Highest to Lowest)

Dataset #:	4
Motif ID:	98
Motif name:	myyCCCACmTGCmyr
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:	0.0170832

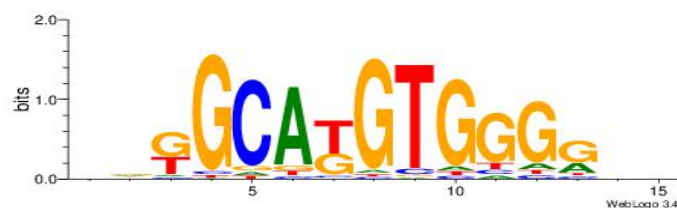
Alignment:

```
HBCCCCACMTGCMHV
HVCCAGGCCTGGBD-
```

Original motif Consensus sequence: HBCCCCACMTGCMHV



Reverse complement motif Consensus sequence: VDRGCAYGTGGGGVD

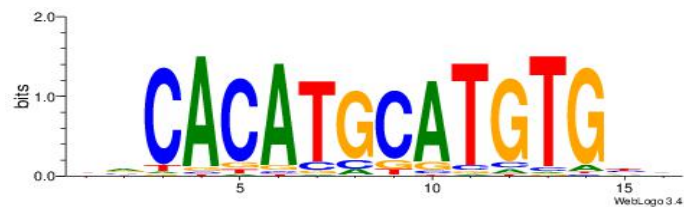


Dataset #: 4
 Motif ID: 118
 Motif name: yrCACATGCATGTGyr
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 14
 Similarity score: 0.0217283

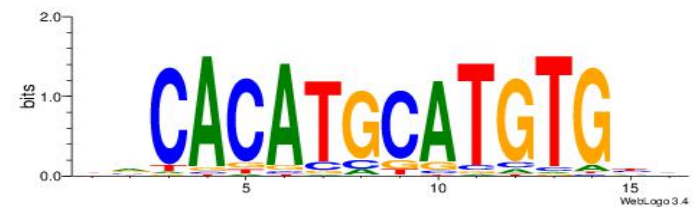
Alignment:

DVCACATGCATGTGBH
 -HBCCAGGCCTGGVD-

Original motif Consensus sequence: HVCACATGCATGTGBD



Reverse complement motif Consensus sequence: DVCACATGCATGTGBH

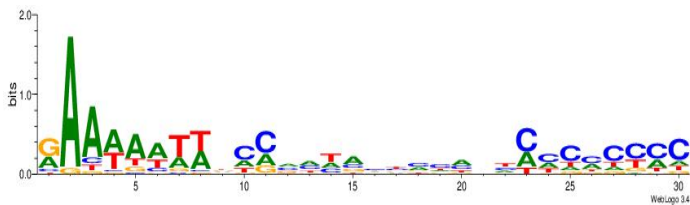


Dataset #: 3
 Motif ID: 81
 Motif name: Pax4
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 9

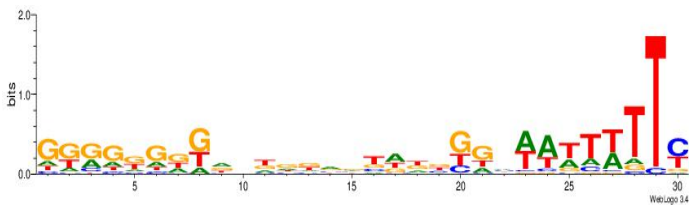
Number of overlap: 14
Similarity score: 0.0375854

Alignment:
RAAWAWTWDCMVHHVBBHHHVHMHCMCYMC
-----HBCCAGGCCTGGVD-----

Original motif Consensus sequence:
RAAWAWTWDCMVHHVBBHHHVHMHCMCYMC



Reverse complement motif Consensus sequence:
GRKGRGDRHVHDDVBBHHBRGDWAWTWTTM

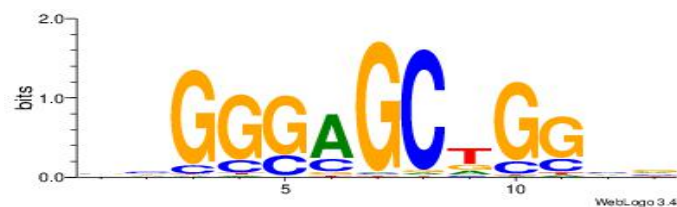
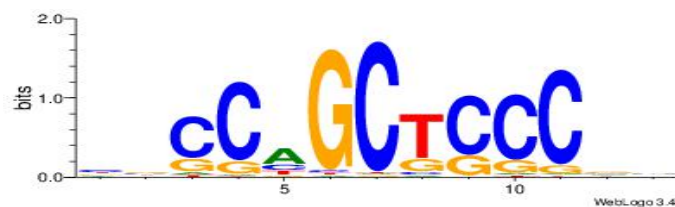


Dataset #: 4
Motif ID: 103
Motif name: csCCaGCTCCCgs
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 13
Similarity score: 0.516252

Alignment:
-BBCCAGCTCCCVB
HBCCAGGCCTGGVD

Original motif Consensus sequence: BBCCAGCTCCCVB

Reverse complement motif Consensus sequence: BVGGGAGCTGGBB

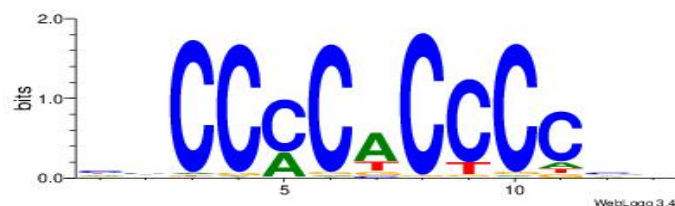


Dataset #: 4
 Motif ID: 111
 Motif name: ccCCmCaCCCCcc
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 13
 Similarity score: 0.531063

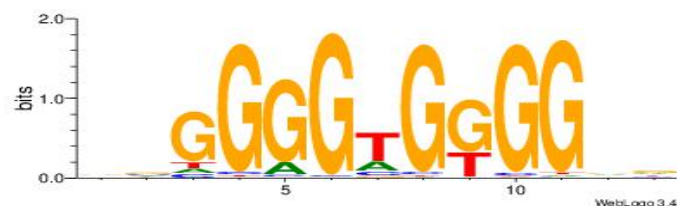
Alignment:

DBGGGGTGGGGBD-
 HVCCAGGCCTGGBD

Original motif Consensus sequence: HBCCCCACCCCBH

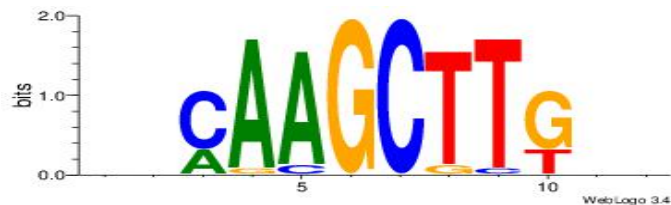


Reverse complement motif Consensus sequence: DBGGGGTGGGGB

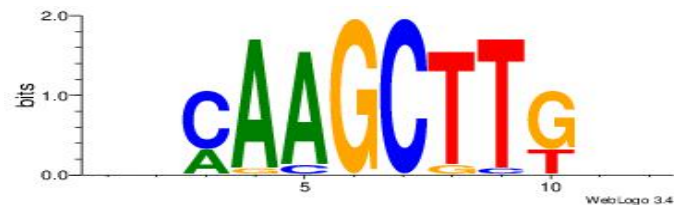


Dataset #: 4 Motif ID: 123 Motif name: asMAAGCTTKst

Original motif Consensus sequence: HBCAAGCTTGVD



Reverse complement motif Consensus sequence: DVCAAGCTTGBH



Best Matches for Motif ID 123 (Highest to Lowest)

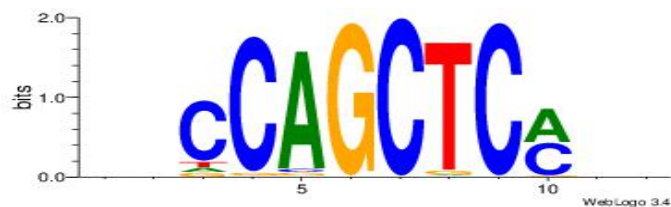
Dataset #: 4
Motif ID: 119
Motif name: cbCCAGCTCmyk
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 12
Similarity score: 0

Alignment:

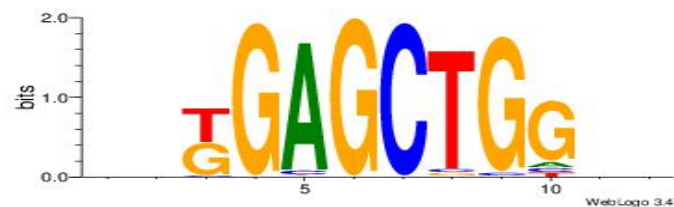
HBYGAGCTGGBB

DVCAAGCTTGBH

Original motif Consensus sequence: BBCCAGCTCMBD



Reverse complement motif Consensus sequence: HBYGAGCTGGBB

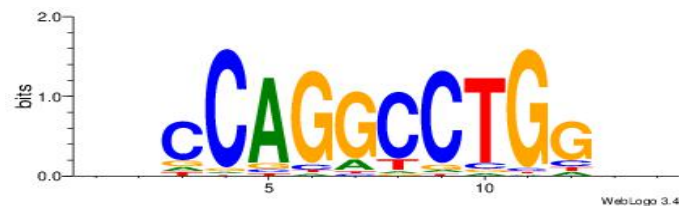


Dataset #: 4
 Motif ID: 122
 Motif name: hsCCAGGCCTGGsr
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 12
 Similarity score: 0.025923

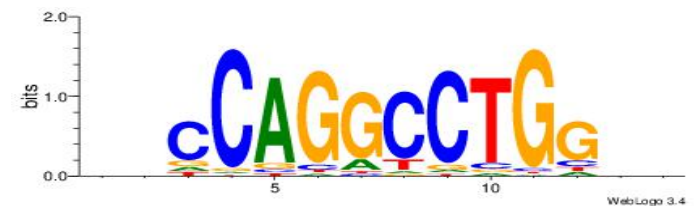
Alignment:

HBCCAGGCCTGGVD
 -DVCAAGCTTGBH-

Original motif Consensus sequence: HVCCAGGCCTGGBD



Reverse complement motif Consensus sequence: HBCCAGGCCTGGV



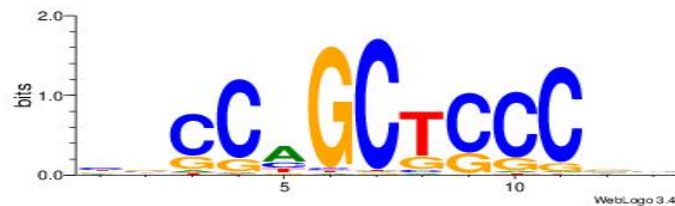
Dataset #: 4
 Motif ID: 103
 Motif name: csCCaGCTCCCgs
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 12

Similarity score: 0.0387894

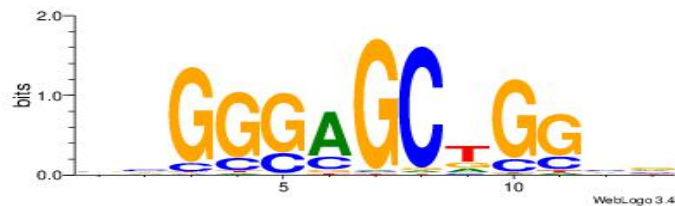
Alignment:

BBCCAGCTCCCVB
HBCAAGCTTGVD-

Original motif Consensus sequence: BBCCAGCTCCCVB



Reverse complement motif Consensus sequence: BVGGGAGCTGGBE



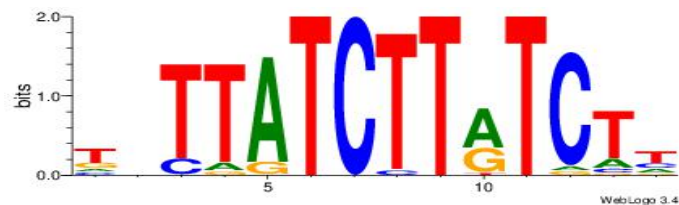
Dataset #: 3
Motif ID: 71
Motif name: Evi1
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 3
Number of overlap: 12
Similarity score: 0.0417163

Alignment:

TBTTATCTTMTCTT
--HBCAAGCTTGVD

Original motif Consensus sequence: AAGAYAAGATAABA

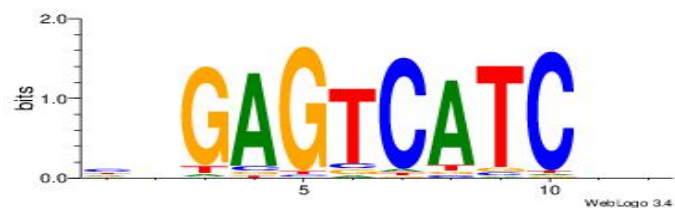
Reverse complement motif Consensus sequence: TBTTATCTTMTCTT



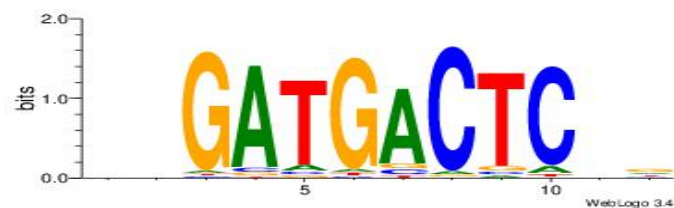
Dataset #: 4
 Motif ID: 121
 Motif name: ctGAGTCATCkb
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 12
 Similarity score: 0.0518025

Alignment:
 BHGATGACTCDD
 HBCAAGCTTGVD

Original motif Consensus sequence: HDGAGTCATCDB

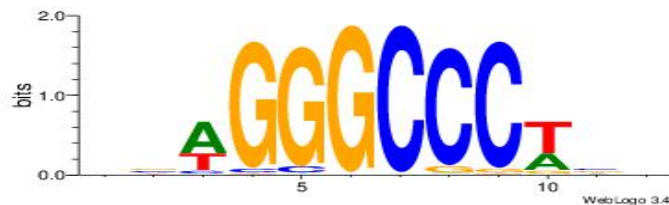


Reverse complement motif Consensus sequence: BHGATGACTCDD

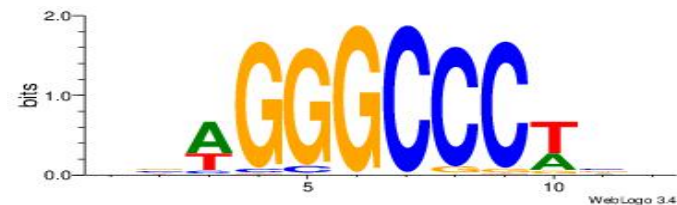


Dataset #: 4 Motif ID: 124 Motif name: cswGGGCCcwsg

Original motif Consensus sequence: VVWGGGCCCWBB



Reverse complement motif Consensus sequence: BBWGGGCCCWVV



Best Matches for Motif ID 124 (Highest to Lowest)

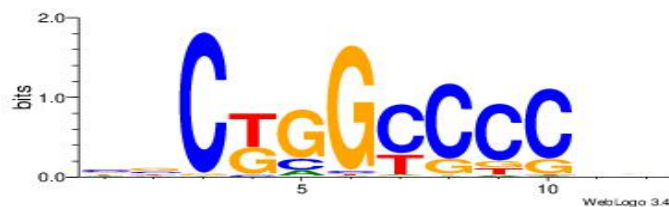
Dataset #:	4
Motif ID:	102
Motif name:	ssCkGGYCCCsg
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	12
Similarity score:	0.0170635

Alignment:

BBCKGGCCCCVV

VVWGGGCCCWBB

Original motif Consensus sequence: BBCKGGCCCCVV



Reverse complement motif Consensus sequence: VVGGGGCCRGBB



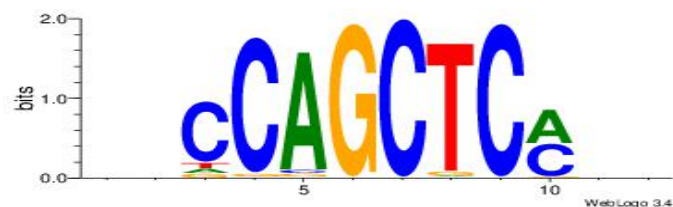
Dataset #: 4
 Motif ID: 119
 Motif name: cbCCAGCTCmyk
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 12
 Similarity score: 0.0400014

Alignment:

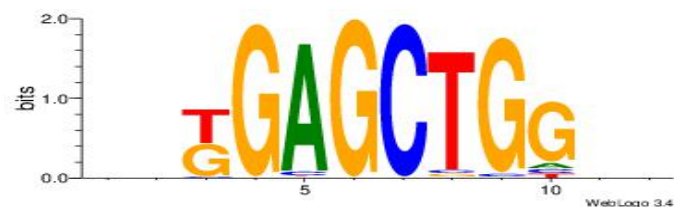
HBYGAGCTGGBB

VVWGGGCCCWBB

Original motif Consensus sequence: BBCCAGCTCMBD



Reverse complement motif Consensus sequence: HBYGAGCTGGBB



Dataset #: 4
 Motif ID: 126
 Motif name: yvTGCAGsCAcg
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 12

Similarity score: 0.0429334

Alignment:
BVTGCAGSCABV
VVGWGGCCCCWBB

Original motif Consensus sequence: BVTGCAGSCABV



Reverse complement motif Consensus sequence: VBTGSCCTGCAVB

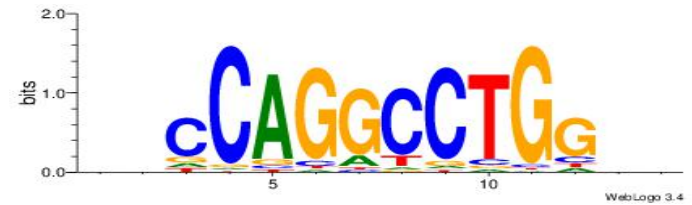
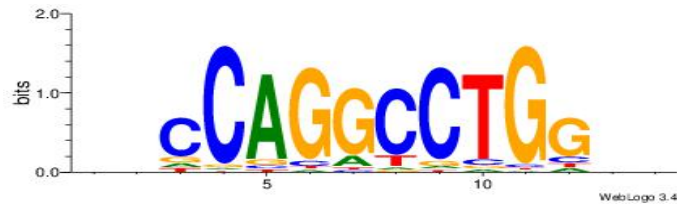


Dataset #: 4
Motif ID: 122
Motif name: hsCCAGGCCTGGsr
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2
Number of overlap: 12
Similarity score: 0.0467887

Alignment:
HVCCAGGCCTGGBD
-VVGWGGCCCCWBB-

Original motif Consensus sequence: HVCCAGGCCTGGBD

Reverse complement motif Consensus sequence: HBCCAGGCCTGGV



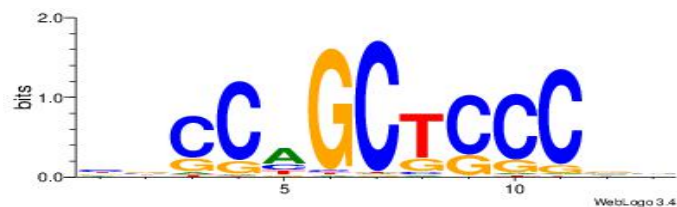
Dataset #: 4
 Motif ID: 103
 Motif name: csCCaGCTCCCgs
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 12
 Similarity score: 0.0482771

Alignment:

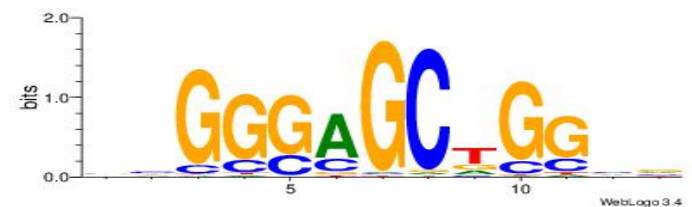
BBCCAGCTCCCVB

-BBWGGGCCCWVV

Original motif Consensus sequence: BBCCAGCTCCCVB

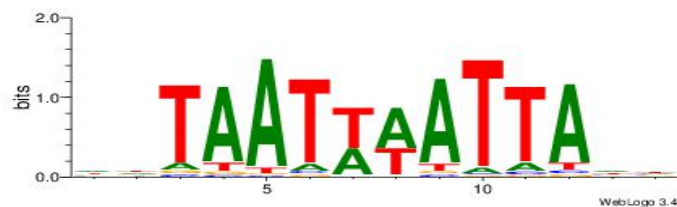


Reverse complement motif Consensus sequence: BVGGGAGCTGGBB

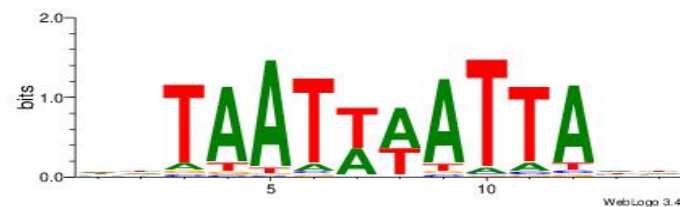


Dataset #: 4 Motif ID: 125 Motif name: wwTAATwwATTaww

Original motif Consensus sequence: DDTAATWWATTAHH



Reverse complement motif Consensus sequence: HHTAATWWATTAD



Best Matches for Motif ID 125 (Highest to Lowest)

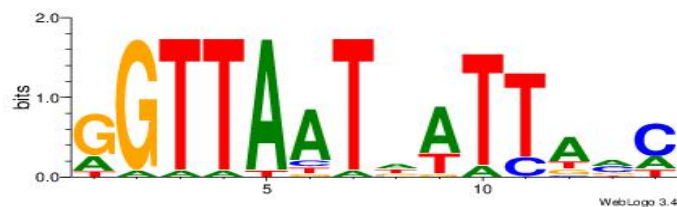
Dataset #:	3
Motif ID:	68
Motif name:	HNF1A
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	14
Similarity score:	0.0447485

Alignment:

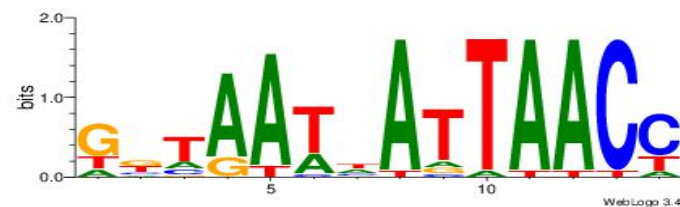
GGTTAATDATTAMC

DDTAATWWATTAHH

Original motif Consensus sequence: GGTTAATDATTAMC



Reverse complement motif Consensus sequence: GYTAATDATTAAAC

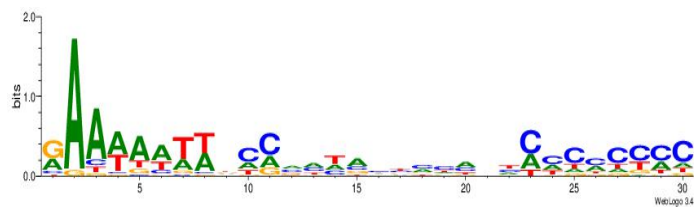


Dataset #: 3
 Motif ID: 81
 Motif name: Pax4
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 14
 Similarity score: 0.0620115

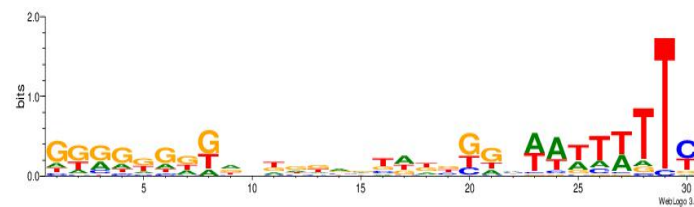
Alignment:

GRKGRGDRHVHDDVBBHHBRGDWAWTWTTM
 -----HHTAATWWATTADD-

Original motif Consensus sequence:
 RAAWAWTWDCMVHHVBBHHVHMHCMCYMC



Reverse complement motif Consensus sequence:
 GRKGRGDRHVHDDVBBHHBRGDWAWTWTTM



Dataset #: 3
 Motif ID: 75
 Motif name: FOXF2
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1

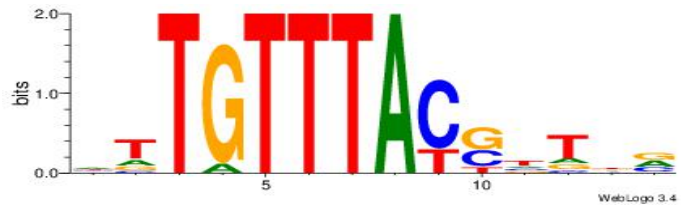
Number of overlap: 14
Similarity score: 0.0703085

Alignment:
BHADSGTAAACAAD
HHTAATWWATTADD

Original motif Consensus sequence: BHADSGTAAACAAD



Reverse complement motif Consensus sequence: DTTGTTTACSBTBE

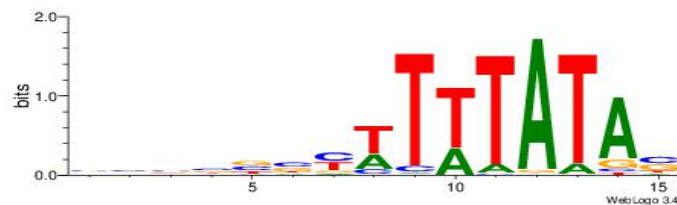
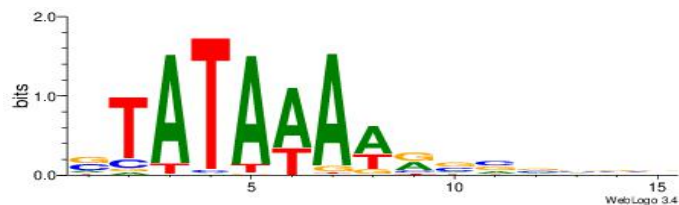


Dataset #: 3
Motif ID: 62
Motif name: TBP
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2
Number of overlap: 14
Similarity score: 0.0724742

Alignment:
STATAAWRVVVBV
HHTAATWWATTADD-

Original motif Consensus sequence: STATAAWRVVVBV

Reverse complement motif Consensus sequence: VBVVVVMWTTTAT

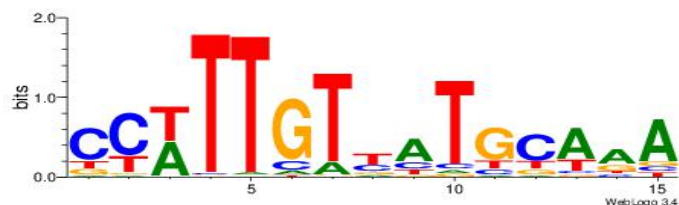


Dataset #: 3
 Motif ID: 76
 Motif name: Sox2
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0.0728076

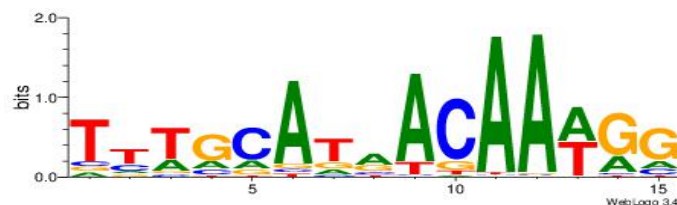
Alignment:

TTTGCATMACAAWGG
 -DDTAATWWATTAHH

Original motif Consensus sequence: CCWTTGTATGCAAA



Reverse complement motif Consensus sequence: TTTGCATMACAAWGG

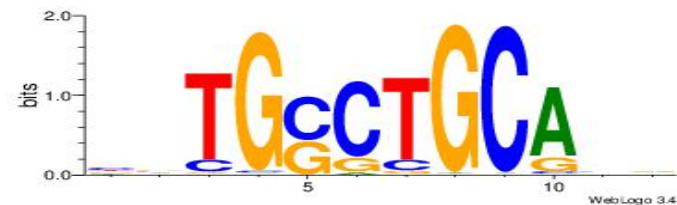


Dataset #: 4 Motif ID: 126 Motif name: yvTGCAGsCAcg

Original motif Consensus sequence: BVTGCAGSCABV



Reverse complement motif Consensus sequence: VBTGSCGTGCAVB



Best Matches for Motif ID 126 (Highest to Lowest)

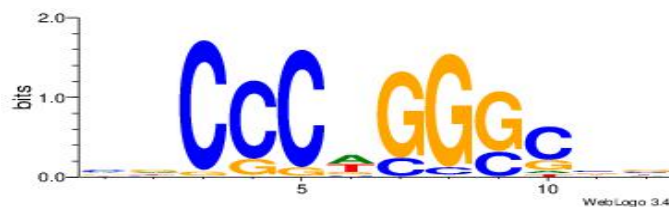
Dataset #:	4
Motif ID:	104
Motif name:	cgCCCwGGScsg
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	12
Similarity score:	0.0284753

Alignment:

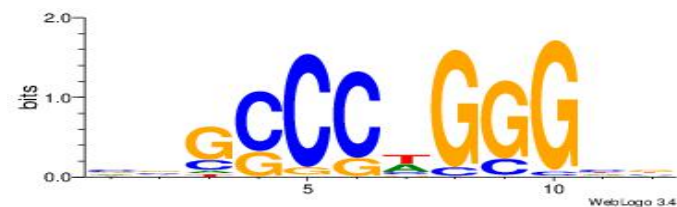
VDCCCWGGGCBB

BVTGCAGSCABV

Original motif Consensus sequence: VDCCCWGGGCBB



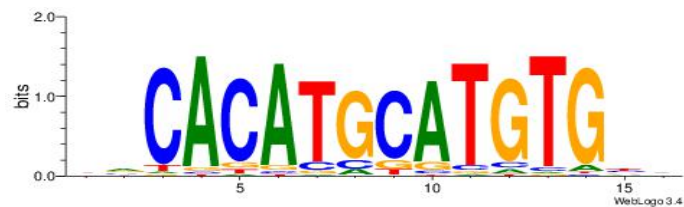
Reverse complement motif Consensus sequence: BBGCCCWGGGHV



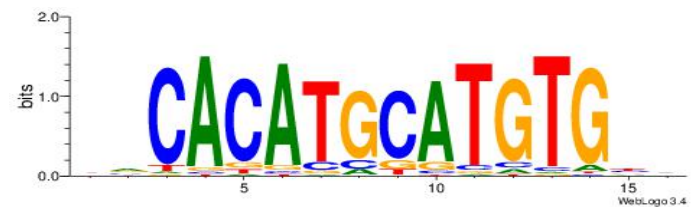
Dataset #: 4
 Motif ID: 118
 Motif name: yrCACATGCATGTGyr
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 12
 Similarity score: 0.0340354

Alignment:
 HVCACATGCATGTGBD
 BVTGCAGSCABV-----

Original motif Consensus sequence: HVCACATGCATGTGBD



Reverse complement motif Consensus sequence: DVCACATGCATGTGBH

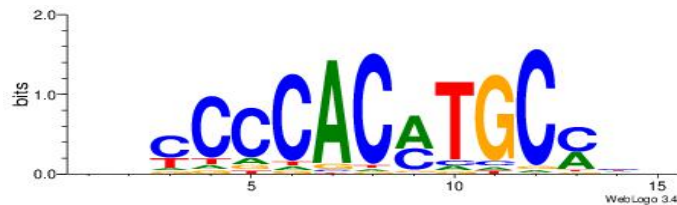


Dataset #: 4
 Motif ID: 98
 Motif name: myyCCCACmTGCmyr
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1

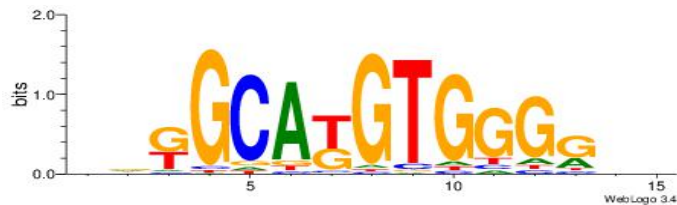
Number of overlap: 12
Similarity score: 0.0351986

Alignment:
VDRGCAYGTGGGGVD
---BVTGCAGSCABV

Original motif Consensus sequence: HBCCCCACMTGCMHV



Reverse complement motif Consensus sequence: VDRGCAYGTGGGGVD

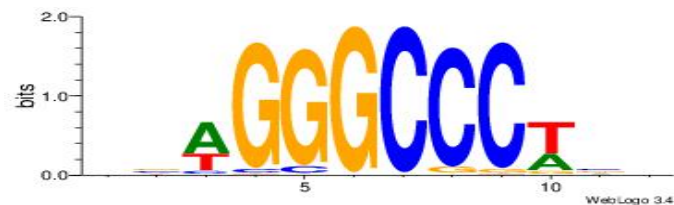
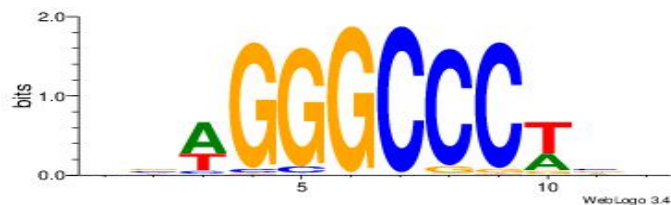


Dataset #: 4
Motif ID: 124
Motif name: cswGGGCCCwsg
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 12
Similarity score: 0.0357442

Alignment:
VVGGGCCCWBB
BVTGCAGSCABV

Original motif Consensus sequence: VVGGGCCCWBB

Reverse complement motif Consensus sequence: BBWGGGCCWVV



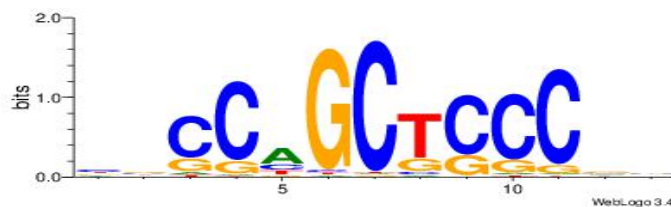
Dataset #: 4
 Motif ID: 103
 Motif name: csCCaGCTCCCgs
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 12
 Similarity score: 0.0445722

Alignment:

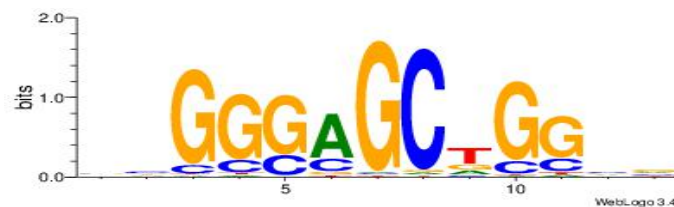
BBCCAGCTCCCVB

VB TG SCTGCAVB-

Original motif Consensus sequence: BBCCAGCTCCCVB



Reverse complement motif Consensus sequence: BVGGGAGCTGGBB

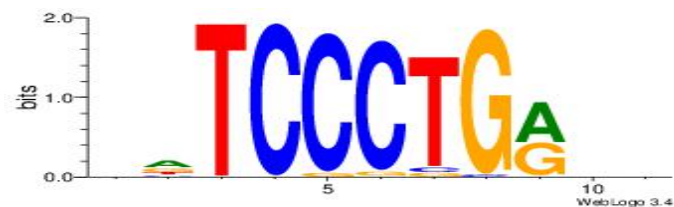


Dataset #: 4 Motif ID: 127 Motif name: rryCAGGGAyw

Original motif Consensus sequence: DDYCAGGGAHD



Reverse complement motif Consensus sequence: DHTCCCTGMDD



Best Matches for Motif ID 127 (Highest to Lowest)

Dataset #:	4
Motif ID:	99
Motif name:	graGGGGGArr
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	11
Similarity score:	0.0283253

Alignment:

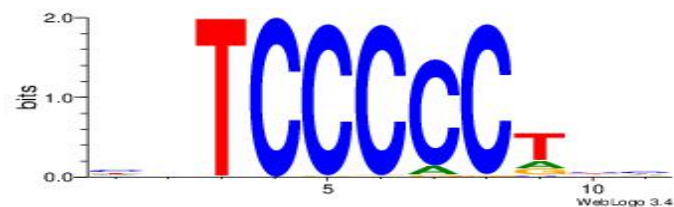
DVAGGGGGADD

DDYCAGGGAHD

Original motif Consensus sequence: DVAGGGGGADD



Reverse complement motif Consensus sequence: HDTCCCCCTVH



Dataset #: 4
 Motif ID: 126
 Motif name: yvTGCAGsCAcg
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.0326364

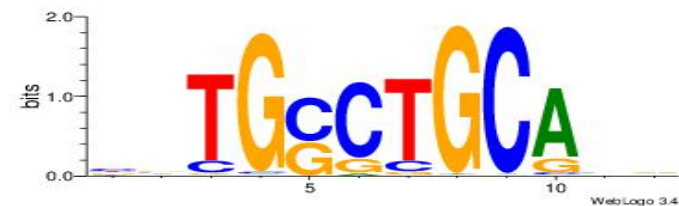
Alignment:

VBTGSCTGCAVB
 DHTCCCTGMDD-

Original motif Consensus sequence: BVTGCAGSCABV



Reverse complement motif Consensus sequence: VBTGSCTGCAVB



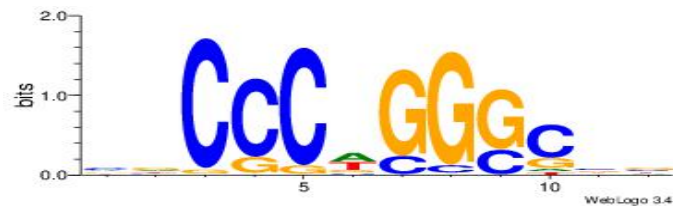
Dataset #: 4
 Motif ID: 104
 Motif name: cgCCCwGGScsg
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 11

Similarity score: 0.0424475

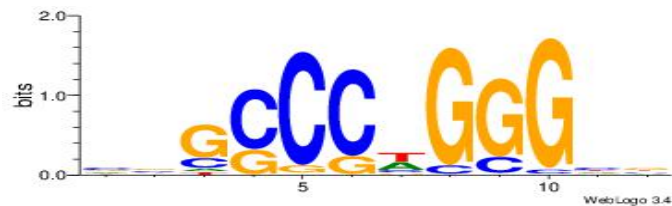
Alignment:

VDCCCWGGGCBB
-DDYCAGGGAHD

Original motif Consensus sequence: VDCCCWGGGCBB



Reverse complement motif Consensus sequence: BBGCCCWGGGHV



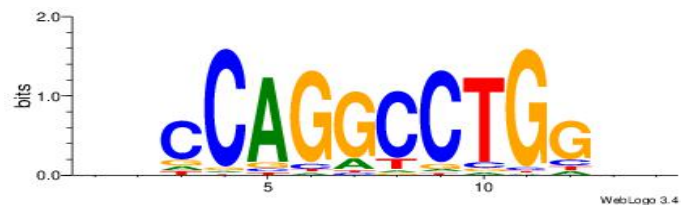
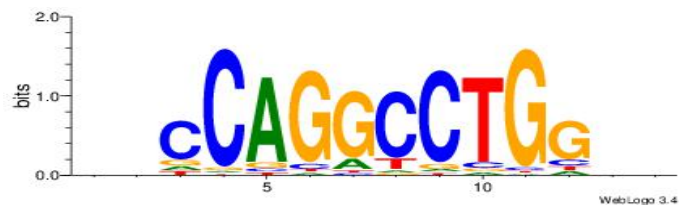
Dataset #: 4
Motif ID: 122
Motif name: hsCCAGGCCTGGsr
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 4
Number of overlap: 11
Similarity score: 0.0451737

Alignment:

HVCCAGGCCTGGBD
DDYCAGGGAHD---

Original motif Consensus sequence: HVCCAGGCCTGGBD

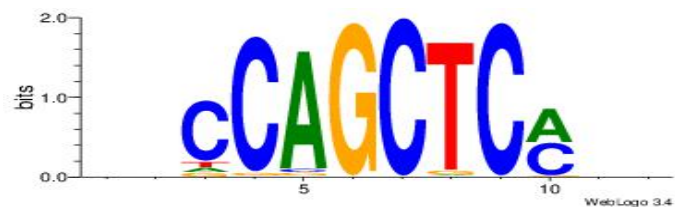
Reverse complement motif Consensus sequence: HBCCAGGCCTGGV



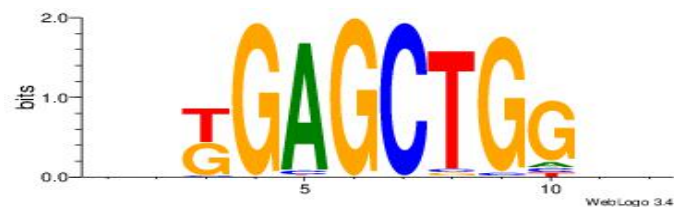
Dataset #: 4
 Motif ID: 119
 Motif name: cbCCAGCTCmyk
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.0514394

Alignment:
 BBCCAGCTCMBD
 DDYCAGGGAHD-

Original motif Consensus sequence: BBCCAGCTCMBD



Reverse complement motif Consensus sequence: HBYGAGCTGGBB



Results created by MOTIFSIM on 06-18-2018 16:26:48
Runtime: 858.069 seconds

MOTIFSIM is written by Ngoc Tam L. Tran
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