



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: 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 #: 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



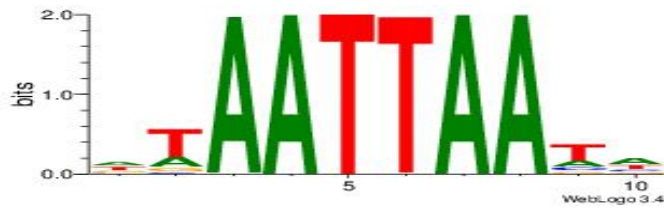
Dataset #:	4
Motif ID:	106
Motif name:	wtAATTAAtw
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	4
Number of overlap:	7
Similarity score:	0.0100679

Alignment:

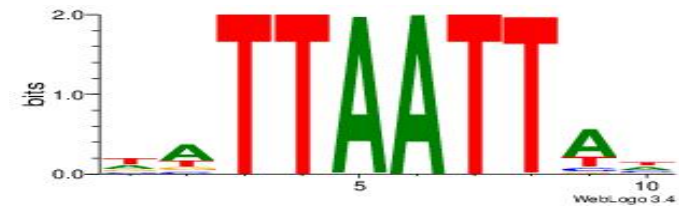
HATTAATTAD

---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

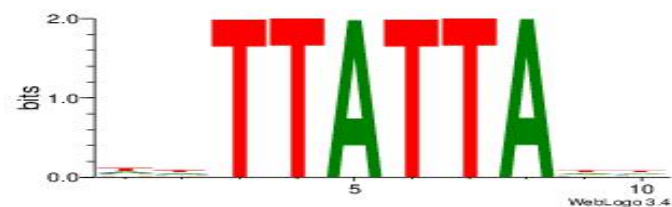
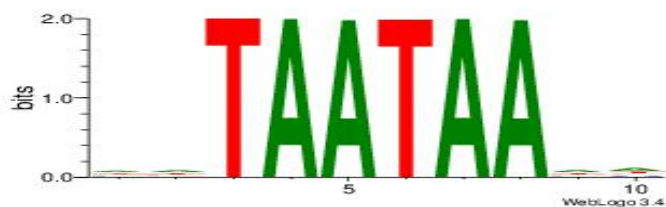
Alignment:

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



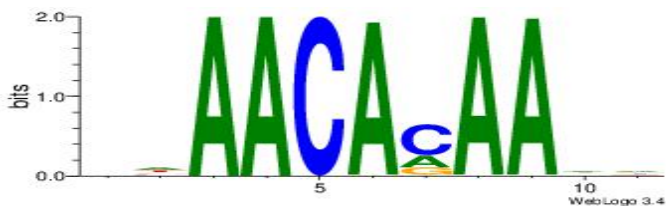
Dataset #: 4
Motif ID: 114
Motif name: awAACAcAAwa
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 4
Number of overlap: 6
Similarity score: 0.0122629

Alignment:

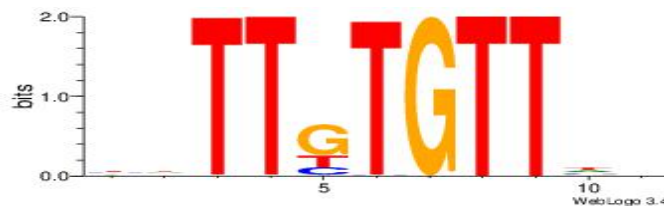
DDAACACAADV

--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:

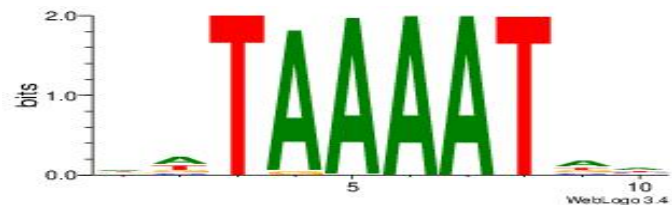
HWTAAAATHD

WWTAAA----

Original motif Consensus sequence: DHATTTTAWH



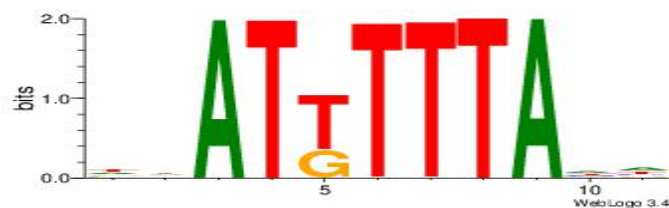
Reverse complement motif Consensus sequence: HWTAAAATHD



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

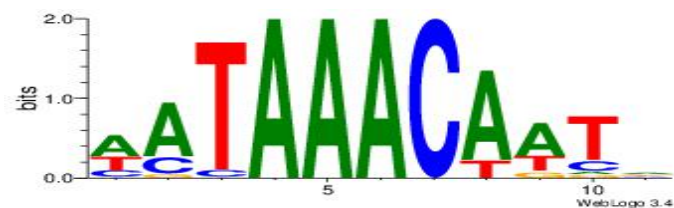
Alignment:

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: TTATAAA



Reverse complement motif Consensus sequence: TTTTAAA

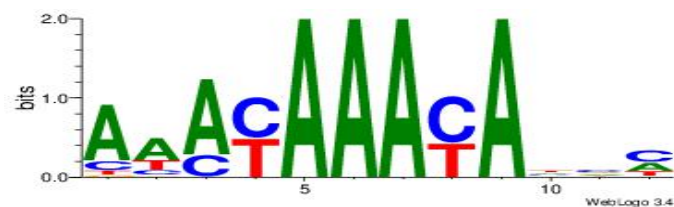
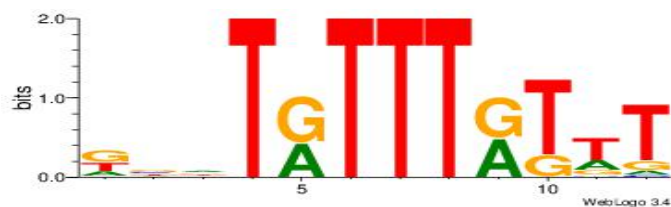


Dataset #: 3
Motif ID: 67
Motif name: FOXI1
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 6
Number of overlap: 6
Similarity score: 0.0347747

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:

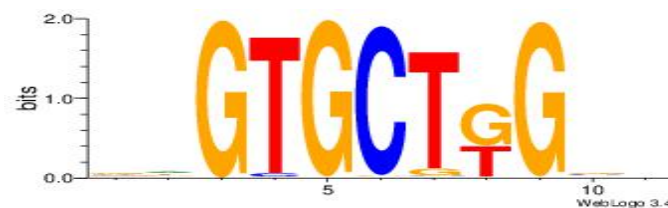
DHGTGCTRGVH

BCGTG-----

Original motif Consensus sequence: 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: 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

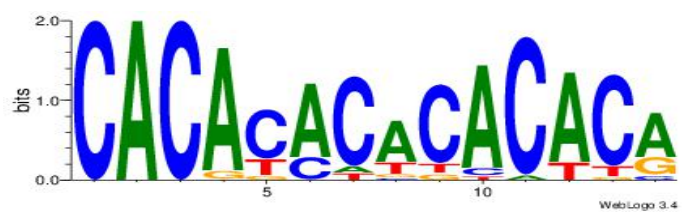


Dataset #: 2
 Motif ID: 58
 Motif name: Motif 58
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 5

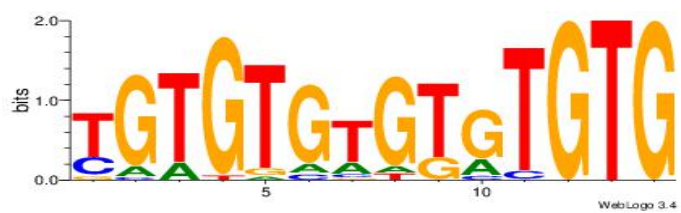
Similarity score: 0.0339655

Alignment:
CACACACACACACA
CACGB-----

Original motif Consensus sequence: CACACACACACACA



Reverse complement motif Consensus sequence: TGTGTGTGTGTGT

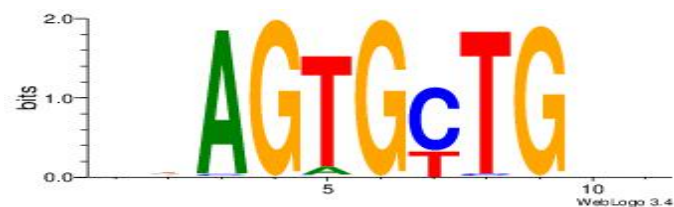
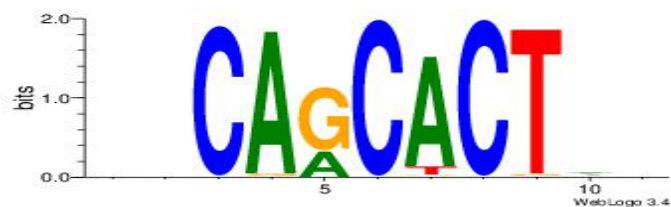


Dataset #: 4
Motif ID: 93
Motif name: cmCARCACTwr
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 6
Number of overlap: 5
Similarity score: 0.0385683

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

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: Forward
Position number: 1
Number of overlap: 5
Similarity score: 0.0199405

Alignment:
TTTCTVT
TTTCK--

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:
 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



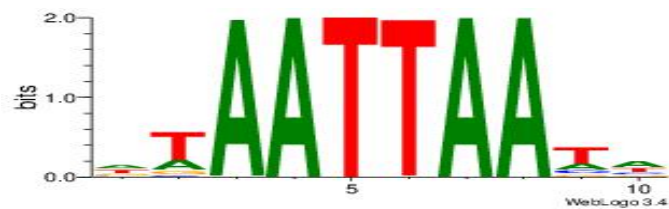
Best Matches for Top Significant Motif ID 64 (Highest to Lowest)

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

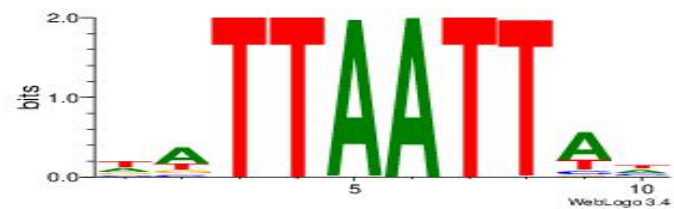
Alignment:

```
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

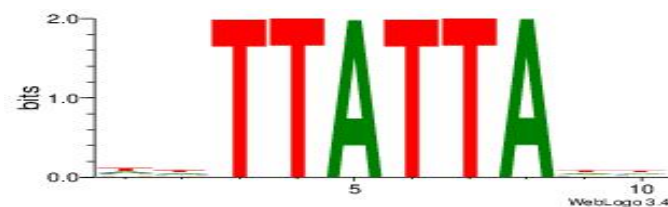
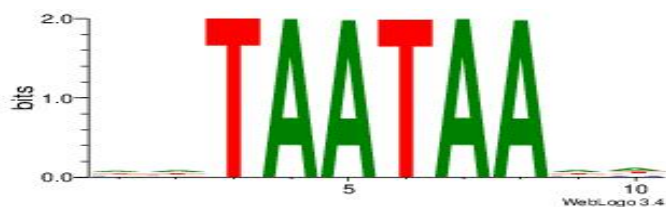
Alignment:

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)

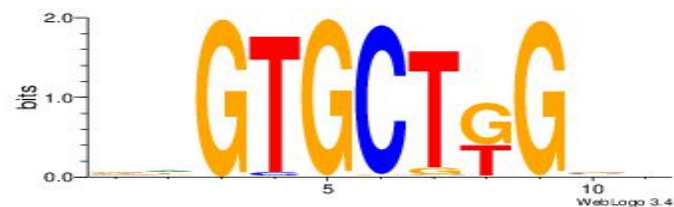
Dataset #:	4
Motif ID:	115
Motif name:	ysCmAGCACwy
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	3
Number of overlap:	8
Similarity score:	0.0212781

Alignment:
 DHGTGCTRGVH
 --GYGSTGGG--

Original motif Consensus sequence: HVCMAGCACHH



Reverse complement motif Consensus sequence: DHGTGCTRGVH

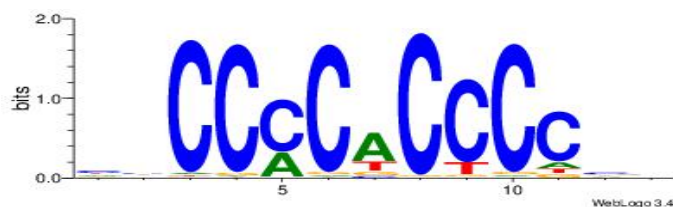


Dataset #: 4
 Motif ID: 111
 Motif name: ccCCmCaCCCCcc
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 8
 Similarity score: 0.0266863

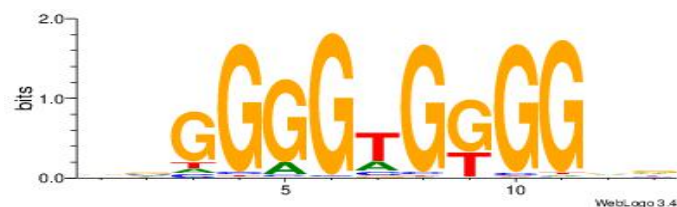
Alignment:

HBCCCCACCCCBH
 ---CCASC MC---

Original motif Consensus sequence: HBCCCCACCCCBH



Reverse complement motif Consensus sequence: DBGGGTGGGGB

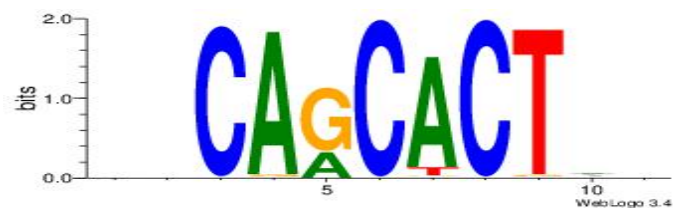


Dataset #: 4
 Motif ID: 93
 Motif name: cmCARCACTwr
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 4
 Number of overlap: 8
 Similarity score: 0.030511

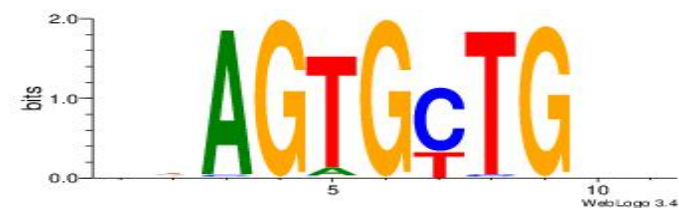
Alignment:

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

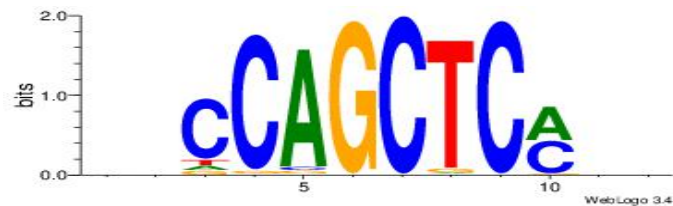
Similarity score: 0.0322039

Alignment:

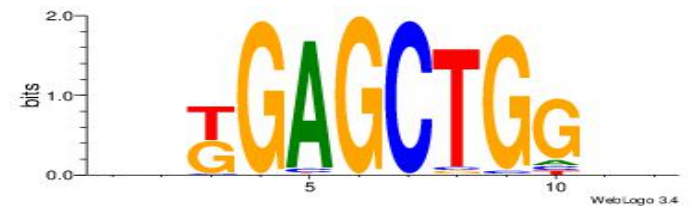
HBYGAGCTGGBB

---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--

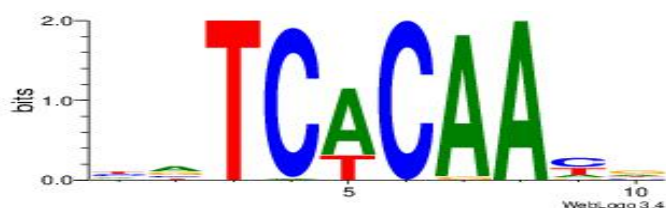
Original motif Consensus sequence: HVCACCCCB

Reverse complement motif Consensus sequence: BBGGGTGVD

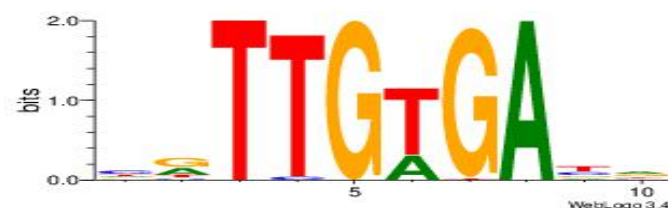


Dataset #: 4 **Motif ID: 94** **Motif name: yrTCWCAAyr**

Original motif Consensus sequence: HVTCAAAyD



Reverse complement motif Consensus sequence: HKTTGTGABH



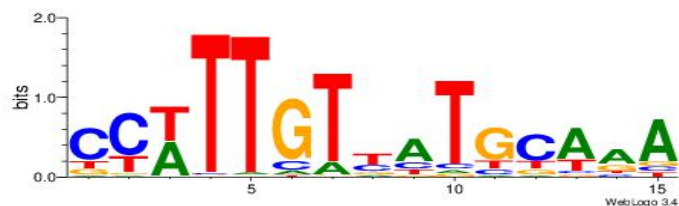
Best Matches for Top Significant Motif ID 94 (Highest to Lowest)

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

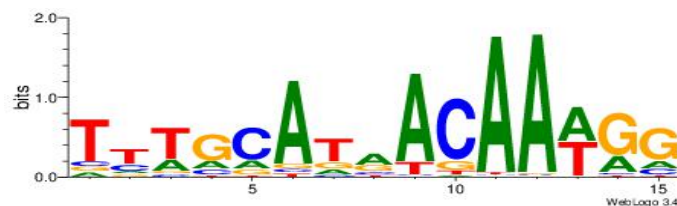
Alignment:

```
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

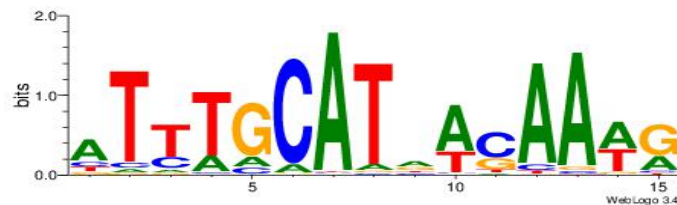
Alignment:

CWTTGTHATGCAAAT
-----HKTGTGABH

Original motif Consensus sequence: CWTTGTHATGCAAAT



Reverse complement motif Consensus sequence: ATTTGCATHACAAV

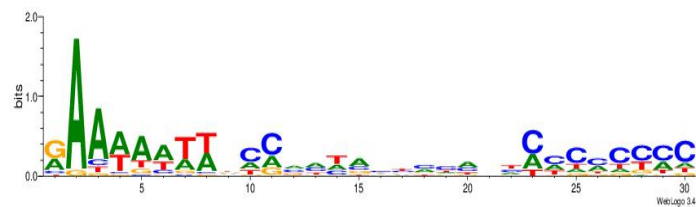


Dataset #: 3
 Motif ID: 81
 Motif name: Pax4
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 20
 Number of overlap: 10
 Similarity score: 0.0426407

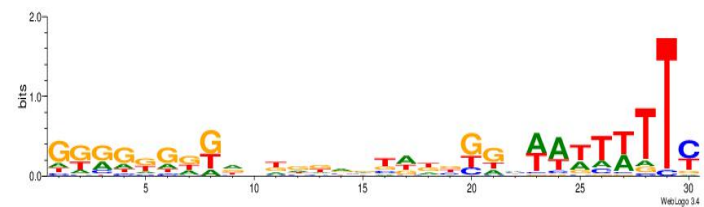
Alignment:

RAAAWATWDCMVHHVBBHHHVHMHCMCYMC
 -----HVTCAAAAYD-

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

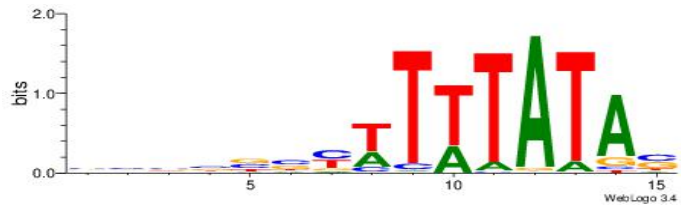
Number of overlap: 10
Similarity score: 0.0429648

Alignment:
STATAAWRVVVBV
-HVTCAAYD----

Original motif Consensus sequence: STATAAWRVVVBV



Reverse complement motif Consensus sequence: VBVVVMWTTTAT

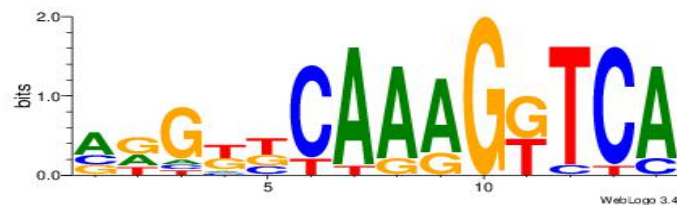


Dataset #: 3
Motif ID: 83
Motif name: NR2F1
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 10
Similarity score: 0.0463536

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

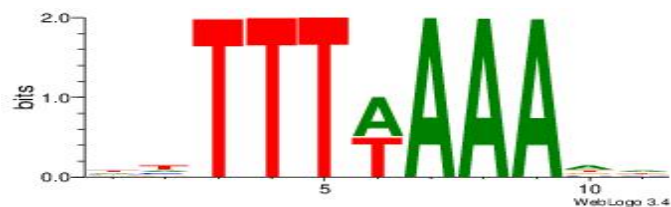


Best Matches for Top Significant Motif ID 55 (Highest to Lowest)

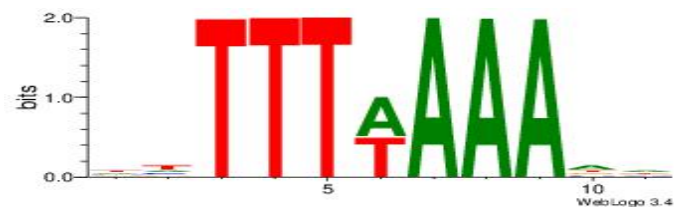
Dataset #:	4
Motif ID:	120
Motif name:	wtTTTwAAAaw
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	3
Number of overlap:	7
Similarity score:	0.00286145

Alignment:
 HHTTTWAAADD
 --TTTAAAA--

Original motif Consensus sequence: HHTTTWAAADD



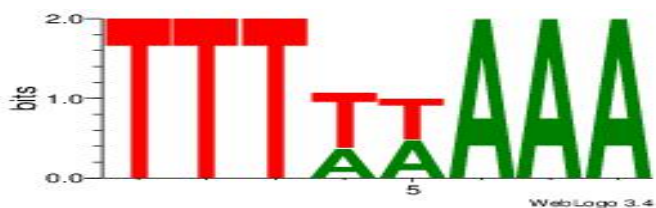
Reverse complement motif Consensus sequence: DDTTTWAAAH



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



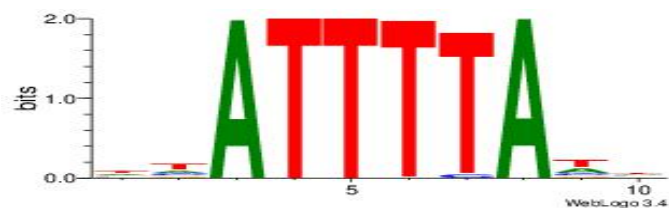
Dataset #: 4
 Motif ID: 91
 Motif name: wtATTTTAAww
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 7
 Similarity score: 0.036821

Alignment:

HWTAAAATHD

TTTAAAA---

Original motif Consensus sequence: DHATTTTAAWH



Reverse complement motif Consensus sequence: HWTAAAATHD

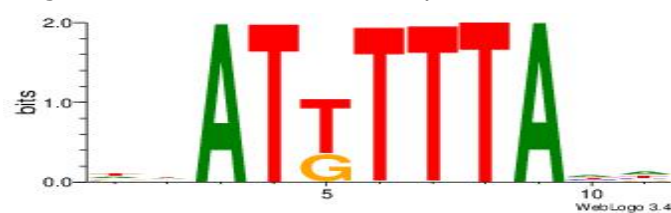


Dataset #: 4
 Motif ID: 108
 Motif name: wwATkTTTAww
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 7

Similarity score: 0.0428268

Alignment:
DHATKTTTAHH
----TTTTAAA

Original motif Consensus sequence: DHATKTTTAHH



Reverse complement motif Consensus sequence: HHTAAARATHD

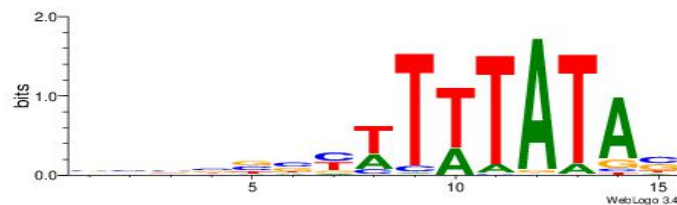
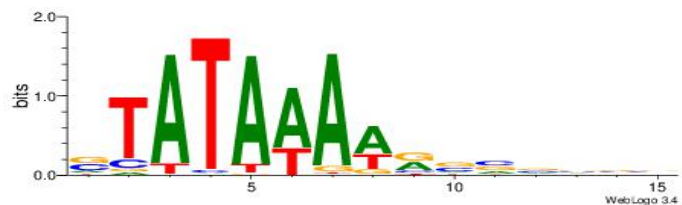


Dataset #: 3
Motif ID: 62
Motif name: TBP
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 8
Number of overlap: 7
Similarity score: 0.058454

Alignment:
VBVVVVMWTTTATAS
-----TTTTAAA-

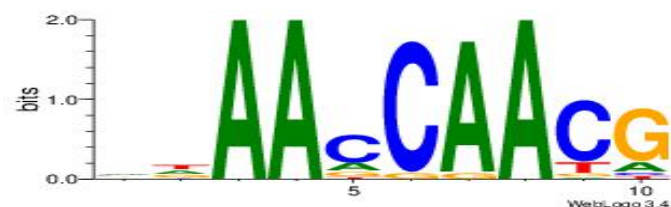
Original motif Consensus sequence: STATAAAWRVVVBV

Reverse complement motif Consensus sequence: VBVVVVMWTTTAT

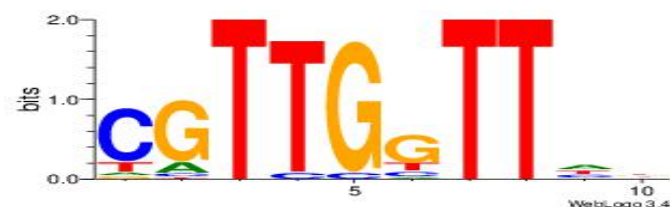


Dataset #: 4 Motif ID: 96 Motif name: mdAAcCAACG

Original motif Consensus sequence: VDAACCAACG



Reverse complement motif Consensus sequence: CGTTGGTTDB



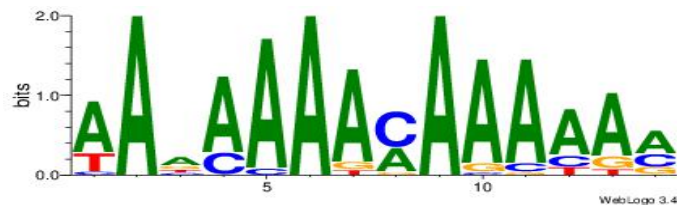
Best Matches for Top Significant Motif ID 96 (Highest to Lowest)

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

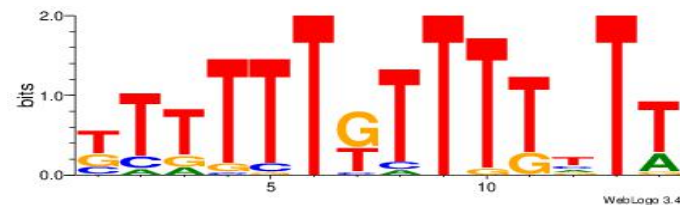
Alignment:

```
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

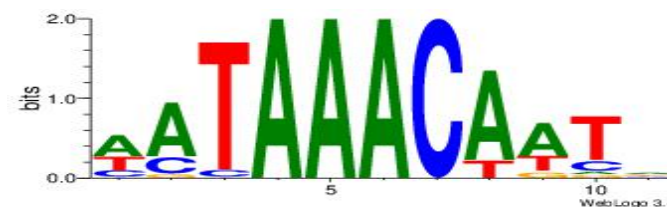
Alignment:

HATTGTTTATW
 -CGTTGGTTDB

Original motif Consensus sequence: HATTGTTTATW



Reverse complement motif Consensus sequence: WATAACAATH

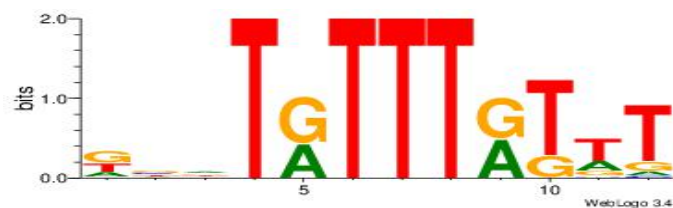


Dataset #: 3
 Motif ID: 67
 Motif name: FOXI1
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 10
 Similarity score: 0.036655

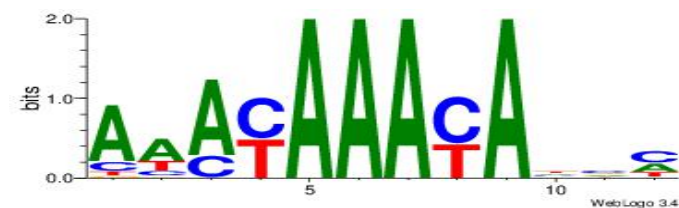
Alignment:

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

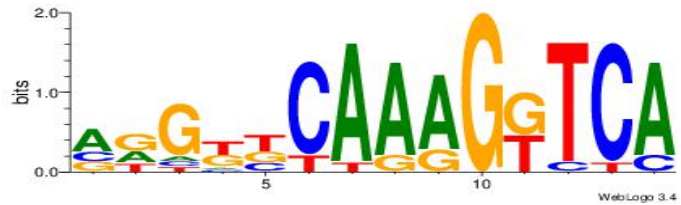
Similarity score: 0.0376121

Alignment:
TGAMCTTTGMMCYT
CGTTGGTTDB-----

Original motif Consensus sequence: TGAMCTTTGMMCYT



Reverse complement motif Consensus sequence: AKGYCAAAGRTC

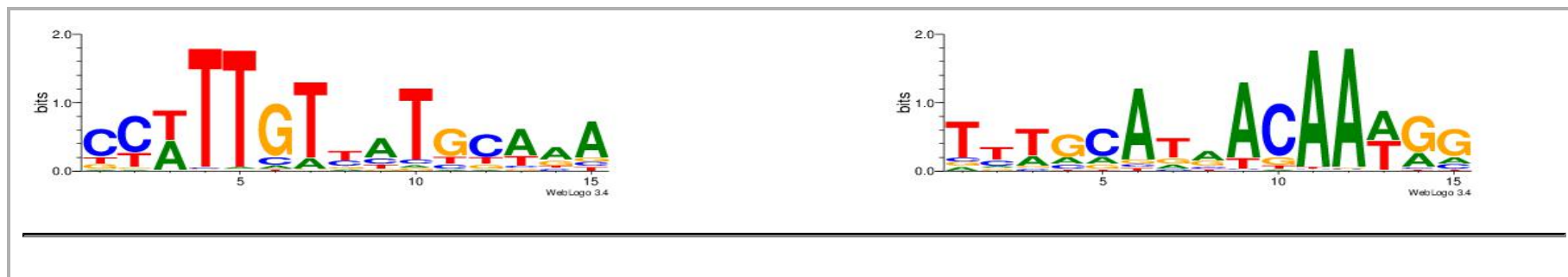


Dataset #: 3
Motif ID: 76
Motif name: Sox2
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 6
Number of overlap: 10
Similarity score: 0.0382008

Alignment:
TTTGCATMACAAWGG
VDAACCAACG-----

Original motif Consensus sequence: CCWTTGTYATGCAAA

Reverse complement motif Consensus sequence:
TTTGCATMACAAWGG



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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