



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:	10
Similarity cutoff >=	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_DM721.txt	16	1
MEME-ChIP_DM721.txt	11	2
PScanChIP_DM721.txt	37	3
RSAT_peak-motifs_DM721.txt	40	4

RESULTS

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

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

Original motif Consensus sequence: AMACA



Reverse complement motif Consensus sequence: TGTGT



Best Matches for Top Significant Motif ID 18 (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:	Backward
Position number:	1
Number of overlap:	5
Similarity score:	0

Alignment:
CACACACA
---AMACA

Original motif Consensus sequence: CACACACA

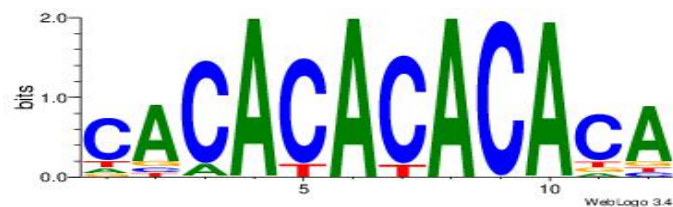
Reverse complement motif Consensus sequence: TGTGTGTG



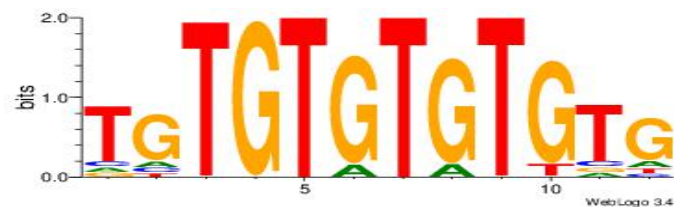
Dataset #: 4
 Motif ID: 79
 Motif name: CACACACACACA
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3
 Number of overlap: 5
 Similarity score: 0.0148279

Alignment:
 TGTGTGTGTGTG
 --TGTRT-----

Original motif Consensus sequence: CACACACACACA



Reverse complement motif Consensus sequence: TGTGTGTGTGTG



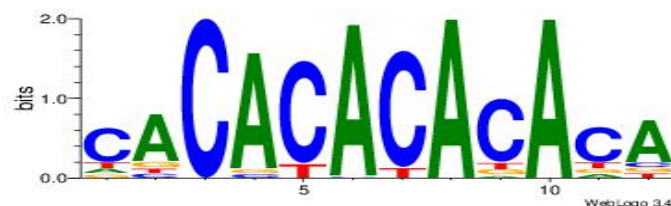
Dataset #: 4
 Motif ID: 95

Motif name:	CACACACACACA
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	4
Number of overlap:	5
Similarity score:	0.0228414

Alignment:

```
TGTGTGTGTGTG
----TGTRT----
```

Original motif Consensus sequence: CACACACACACA



Reverse complement motif Consensus sequence: TGTGTGTGTGTG



Dataset #:	4
Motif ID:	69
Motif name:	aaACAAAACaa
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	6
Number of overlap:	5
Similarity score:	0.0274014

Alignment:

AAACAAAACAA

-----AMACA--

Original motif Consensus sequence: AAACAAAACAA



Reverse complement motif Consensus sequence: TTGTTTTGTTT



Dataset #:	4
Motif ID:	86
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:	5
Similarity score:	0.0291354

Alignment:

HHCAAAAACAH

-----AMACA--

Original motif Consensus sequence: HHCAAAAACAH

Reverse complement motif Consensus sequence: HTGTTTTGHH

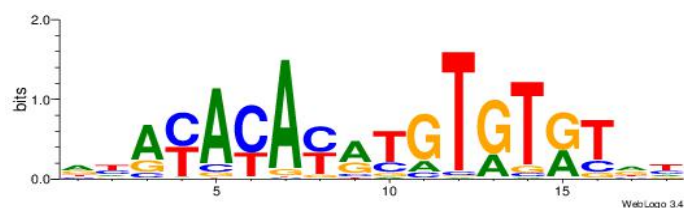


Dataset #: 4
 Motif ID: 97
 Motif name: ryayAyAyrTGTRTry
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 5
 Number of overlap: 5
 Similarity score: 0.0293401

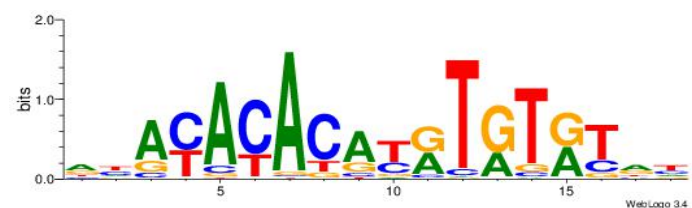
Alignment:

DHAYAYAYRTGTGTRTDH
 -----TGTRT-----

Original motif Consensus sequence: DHAYAYAYRTGTGTRTDH



Reverse complement motif Consensus sequence: HDAMACACAKKTKTKTHD

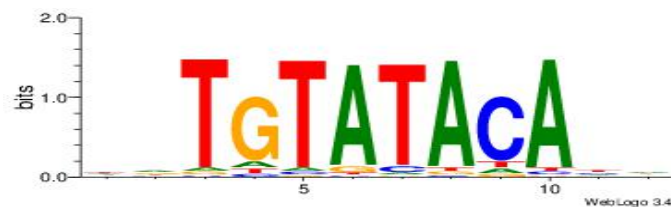


Dataset #: 4

Motif ID: 100
 Motif name: wrTGTATACAw
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 6
 Number of overlap: 5
 Similarity score: 0.0302831

Alignment:
 HDTGTATACAH
 --TGTRT-----

Original motif Consensus sequence: HDTGTATACAH



Reverse complement motif Consensus sequence: DHTGTATACADH



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: 3
 Number of overlap: 5
 Similarity score: 0.0378142

Alignment:
 AAAASAAA
 -AMACA--

Original motif Consensus sequence: AAAASAAA



Reverse complement motif Consensus sequence: TTTSTTTT

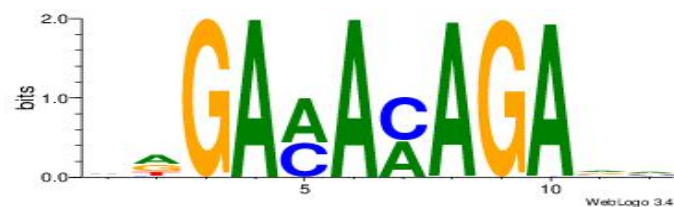
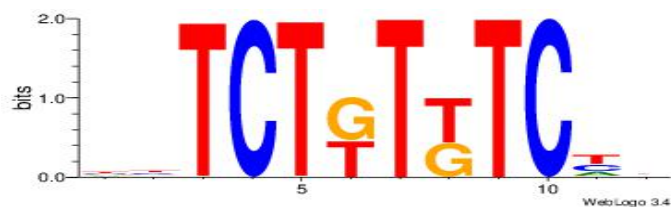


Dataset #:	4
Motif ID:	92
Motif name:	tyTCTkTCTCyy
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	4
Number of overlap:	5
Similarity score:	0.0390126

Alignment:
 VHGARAYAGAVV
 ---AMACA----

Original motif Consensus sequence: BBTCTKTKTCHB

Reverse complement motif Consensus sequence: VHGARAYAGAVV



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: 2
 Number of overlap: 5
 Similarity score: 0.042464

Alignment:
 GKGTGKGC
 -TGTRT--

Original motif Consensus sequence: GCRCACRC



Reverse complement motif Consensus sequence: GKGTGKGC



Dataset #: 3 Motif ID: 30 Motif name: ZEB1

Original motif Consensus sequence: CACCTD



Reverse complement motif Consensus sequence: HAGGTG



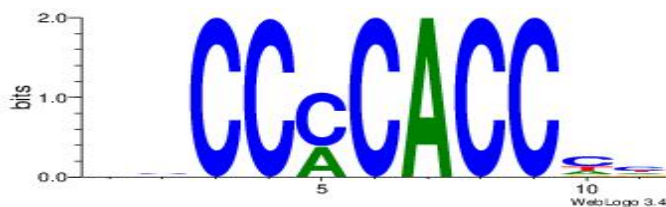
Best Matches for Top Significant Motif ID 30 (Highest to Lowest)

Dataset #: 4
 Motif ID: 89
 Motif name: ccCCmCACcc
 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: 0.0148347

Alignment:

HBCCMCACCHH
 -----CACCTD

Original motif Consensus sequence: HBCCMCACCHH



Reverse complement motif Consensus sequence: DDGGTGRGGBD



Dataset #: 4
 Motif ID: 93
 Motif name: rrAGGGGGArr
 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: 0.0194512

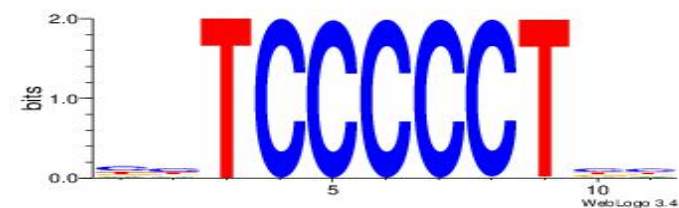
Alignment:

VVAGGGGGAVV
 -HAGGTG----

Original motif Consensus sequence: VVAGGGGGAVV



Reverse complement motif Consensus sequence: VVTCCCCCTVV

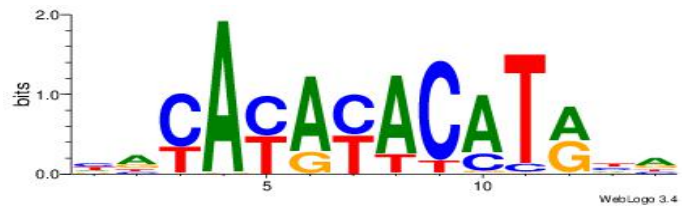


Dataset #: 4
 Motif ID: 75
 Motif name: yayAyAyACATrya
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 7
 Number of overlap: 6

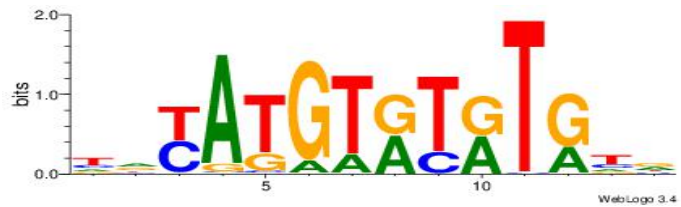
Similarity score: 0.0270731

Alignment:
HACAYAYACATRHD
-----CACCTD--

Original motif Consensus sequence: HACAYAYACATRHD



Reverse complement motif Consensus sequence: DHKATGTKTKTGT

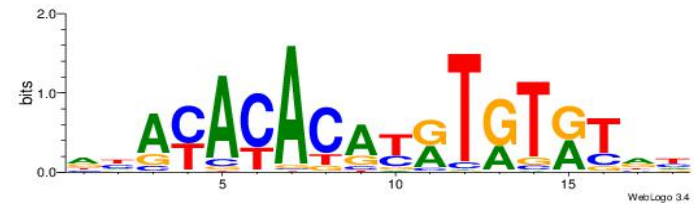
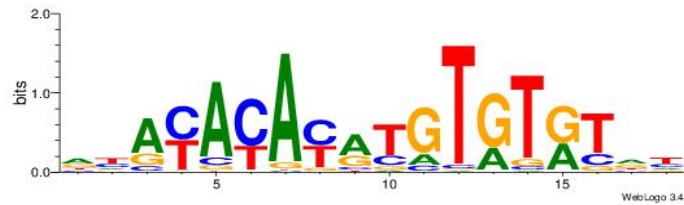


Dataset #: 4
Motif ID: 97
Motif name: ryayAyAyrTGTRTry
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 6
Number of overlap: 6
Similarity score: 0.0321302

Alignment:
HDAMACACAKKTKTKTHD
-----CACCTD-----

Original motif Consensus sequence: DHAYAYAYRTGTGTRTDH

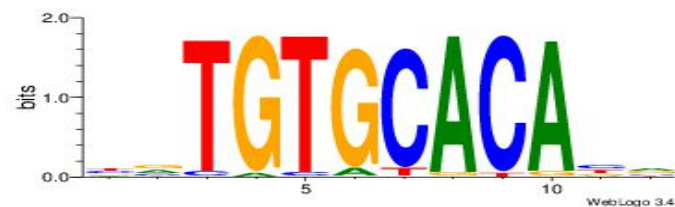
Reverse complement motif Consensus sequence:
HDAMACACAKKTKTKTHD



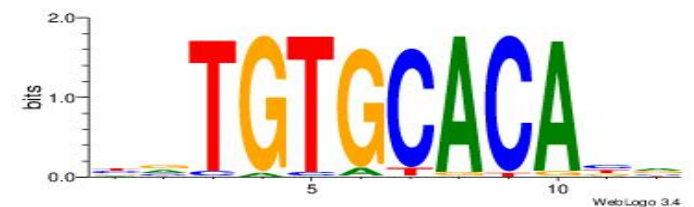
Dataset #: 4
 Motif ID: 96
 Motif name: yrTGTGCACAYr
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 6
 Similarity score: 0.0342918

Alignment:
 BVTGTGCACABV
 HAGGTG-----

Original motif Consensus sequence: BVTGTGCACABV



Reverse complement motif Consensus sequence: BBTGTGCACAVV

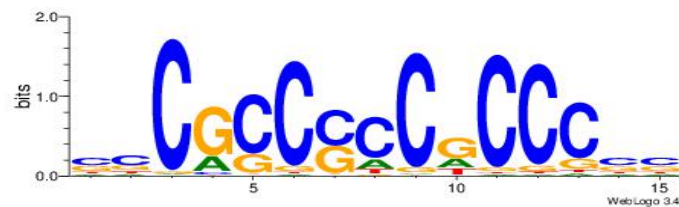


Dataset #: 4
 Motif ID: 91

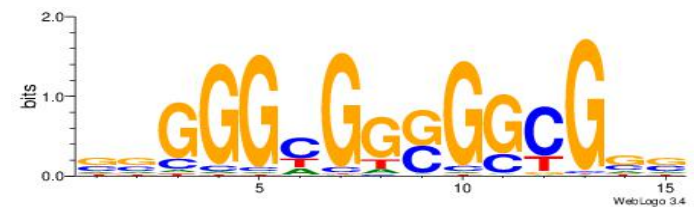
Motif name:	ssCGCCsCCrCCCss
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	9
Number of overlap:	6
Similarity score:	0.0456166

Alignment:
SSCGCCSCCGCCSS
-----CACCTD-

Original motif Consensus sequence: SSCGCCSCCGCCSS



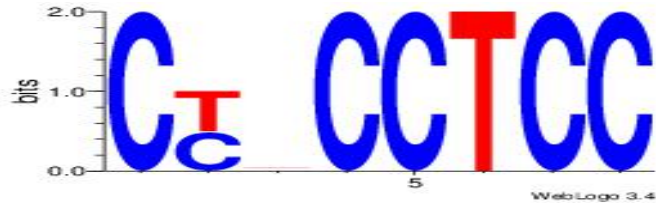
Reverse complement motif Consensus sequence: SSGGGCGGSGGCGSS



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:	6
Similarity score:	0.0458702

Alignment:
CYBCCTCC
-CACCTD-

Original motif Consensus sequence: CYBCCTCC



Reverse complement motif Consensus sequence: GGAGGVMG



Dataset #:	4
Motif ID:	84
Motif name:	wsAGCTACwy
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	4
Number of overlap:	6
Similarity score:	0.0461351

Alignment:
VHGTAGCTVD
---CACCTD-

Original motif Consensus sequence: DVAGCTACHB

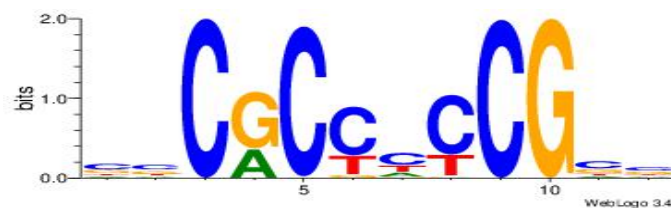
Reverse complement motif Consensus sequence: VHGTAGCTVD



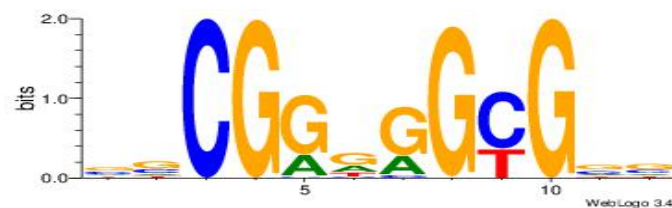
Dataset #: 4
 Motif ID: 88
 Motif name: ssCrCYyYCGss
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 5
 Number of overlap: 6
 Similarity score: 0.0554152

Alignment:
 BBCRCCYCCGBB
 --CACCTD----

Original motif Consensus sequence: BBCRCCYCCGBB



Reverse complement motif Consensus sequence: BBCGGKGGMGBB

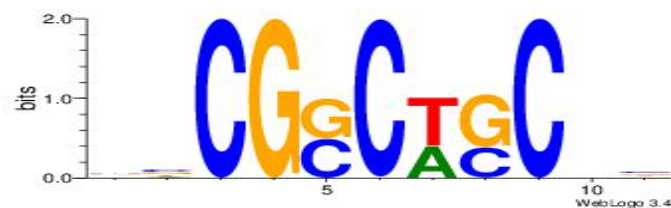


Dataset #: 4
 Motif ID: 90

Motif name: ssCGsCwsCss
 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: 0.0564656

Alignment:
 BBCGSCWSCBB
 -----CACCTD

Original motif Consensus sequence: BBCGSCWSCBB



Reverse complement motif Consensus sequence: BBGSWGSCGBB



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

Original motif Consensus sequence: ASASAGAA



Reverse complement motif Consensus sequence: TTCTSTST



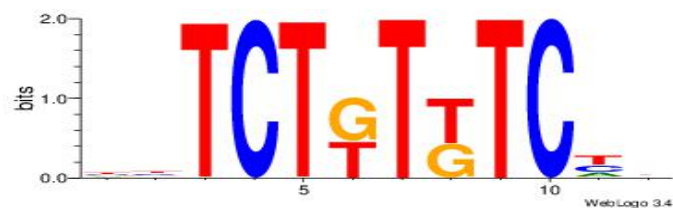
Best Matches for Top Significant Motif ID 7 (Highest to Lowest)

Dataset #: 4
 Motif ID: 92
 Motif name: tyTCTkTTCyy
 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: 0.00355249

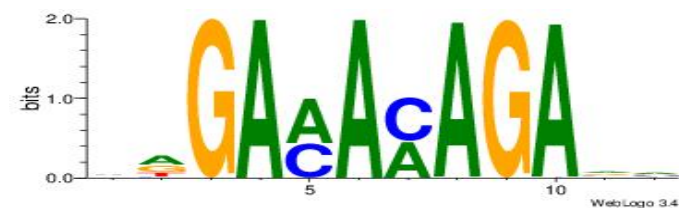
Alignment:

BBTCTKTKTCHB
 -TTCTSTST---

Original motif Consensus sequence: BBTCTKTKTCHB



Reverse complement motif Consensus sequence: VHGARAYAGAVV



Dataset #: 4
 Motif ID: 69
 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: 8

Alignment:

```
AAACAAACAA
ASASAGAA---
```

Alignment:

```
DVCTGCTGTVB
---TTCTSTST
```

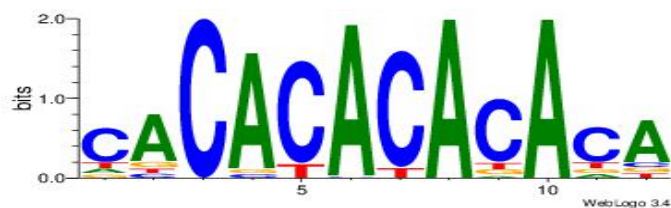
Reverse complement motif Consensus sequence: DVCTGCTGTVB



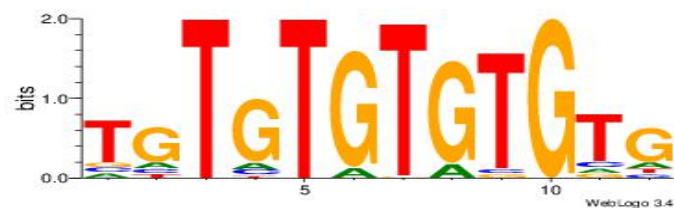
Dataset #: 4
 Motif ID: 95
 Motif name: CACACACACACA
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 4
 Number of overlap: 8
 Similarity score: 0.0398795

Alignment:
 TGTGTGTGTGTG
 -TTCTSTST---

Original motif Consensus sequence: CACACACACACA



Reverse complement motif Consensus sequence: TGTGTGTGTGTG

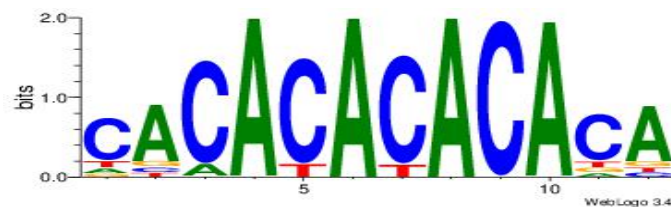


Dataset #: 4
 Motif ID: 79

Motif name:	CACACACACACA
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:	0.0407034

Alignment:
TGTGTGTGTGTG
-TTCTSTST---

Original motif Consensus sequence: CACACACACACA



Reverse complement motif Consensus sequence: TGTGTGTGTGTG



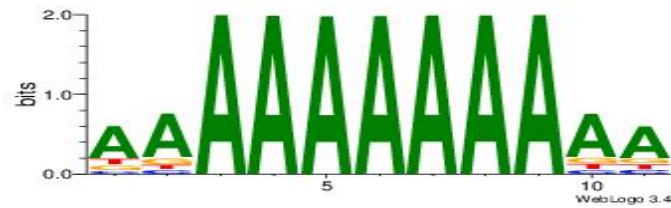
Dataset #:	4
Motif ID:	102
Motif name:	AAAAAAAAAAAA
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	8
Similarity score:	0.0441956

Alignment:

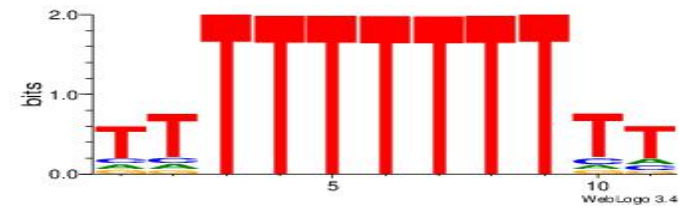
AAAAAAAAAA

ASASAGAA---

Original motif Consensus sequence: AAAAAAAAAA



Reverse complement motif Consensus sequence: TTTTTTTTTT



Dataset #:	2
Motif ID:	26
Motif name:	Motif 26
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	5
Number of overlap:	8
Similarity score:	0.0451851

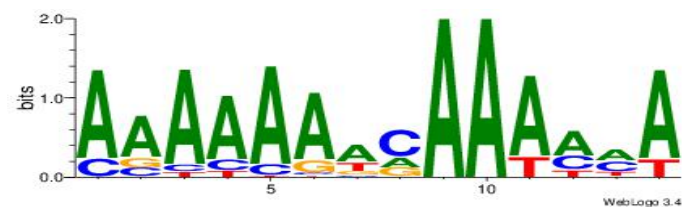
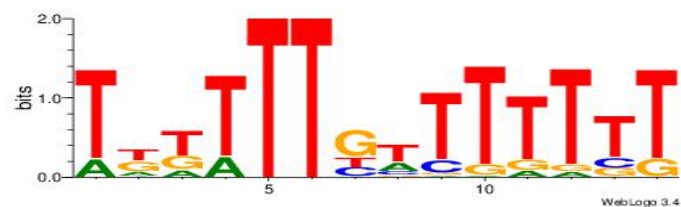
Alignment:

TKKTTTGTTTTTTT

----TTCTSTST--

Original motif Consensus sequence: TKKTTTGTTTTTTT

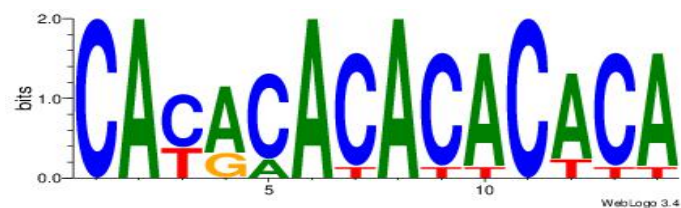
Reverse complement motif Consensus sequence: AAAAAACAAARR



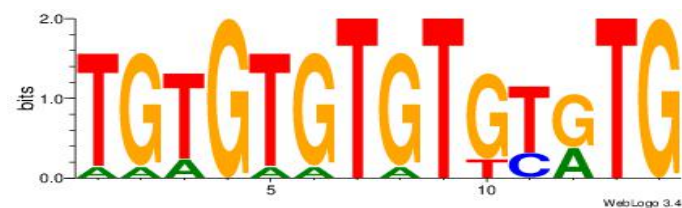
Dataset #: 2
 Motif ID: 27
 Motif name: Motif 27
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 6
 Number of overlap: 8
 Similarity score: 0.0493389

Alignment:
 TGTGTGTGTGKTG
 -----TTCTSTST-

Original motif Consensus sequence: CAYACACACACACA



Reverse complement motif Consensus sequence: TGTGTGTGTGKTG



Dataset #: 2
 Motif ID: 25

Motif name:	Motif 25
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	6
Number of overlap:	8
Similarity score:	0.0494079

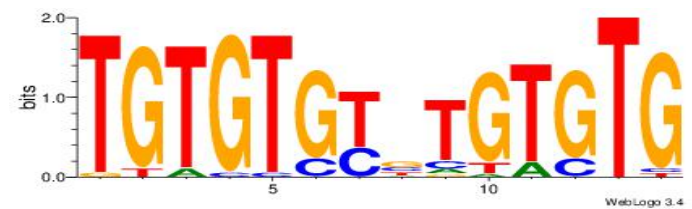
Alignment:

CACACAVRCACACA
 -----ASASAGAA-

Original motif Consensus sequence: CACACAVRCACACA



Reverse complement motif Consensus sequence: TGTGTGKVTGTGT



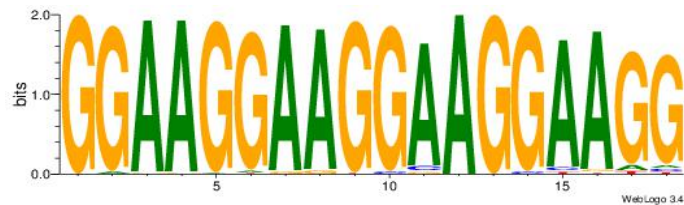
Dataset #:	3
Motif ID:	48
Motif name:	EWSR1-FLI1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	4
Number of overlap:	8
Similarity score:	0.0559328

Alignment:

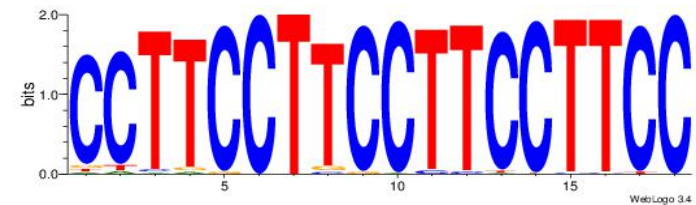
CCTTCCTTCCTTCCTTCC

---TTCTSTST-----

Original motif Consensus sequence: GGAAGGAAGGAAGGAAGG



Reverse complement motif Consensus sequence: CCTTCCTTCCTTCCTTCC



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

Original motif Consensus sequence: ATKTM



Reverse complement motif Consensus sequence: RARAT



Best Matches for Top Significant Motif ID 21 (Highest to Lowest)

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: 2
Number of overlap: 5
Similarity score: 0.0065927

Alignment:
CATTTKC
-ATKTM-

Original motif Consensus sequence: GRAAATG



Reverse complement motif Consensus sequence: CATTTKC



Dataset #: 1
Motif ID: 10
Motif name: Motif 10
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: 0.0217628

Alignment:
TAMATA
-RARAT

Original motif Consensus sequence: TAMATA

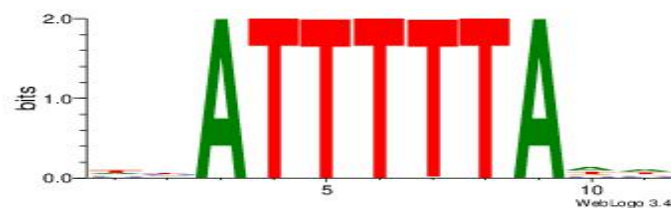
Reverse complement motif Consensus sequence: TATRTA



Dataset #: 4
 Motif ID: 85
 Motif name: wtATTTTAAw
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 5
 Number of overlap: 5
 Similarity score: 0.0314602

Alignment:
 DDTAAAAATHD
 ----RARAT--

Original motif Consensus sequence: DHATTTTADD



Reverse complement motif Consensus sequence: DDTAAAAATHD



Dataset #: 4

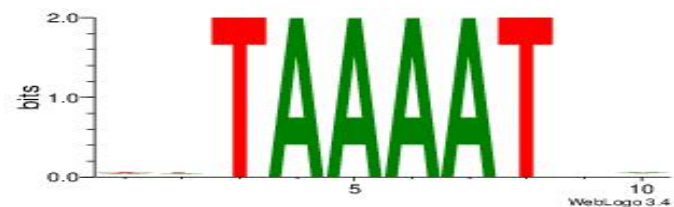
Motif ID: 71
 Motif name: wyATTTTAww
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 5
 Similarity score: 0.0314958

Alignment:
 DDTAAAATHD
 ---RARAT--

Original motif Consensus sequence: DHATTTTADD



Reverse complement motif Consensus sequence: DDTAAAATHD



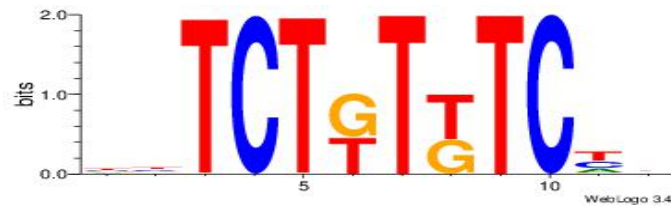
Dataset #: 4
 Motif ID: 92
 Motif name: tyTCTkTCTCyy
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 6
 Number of overlap: 5
 Similarity score: 0.0326182

Alignment:

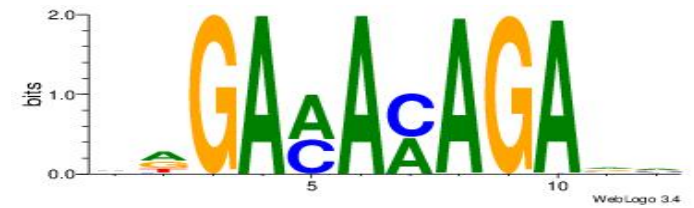
VHGARAYAGAVV

--RARAT-----

Original motif Consensus sequence: BBTCTKTKTCHB



Reverse complement motif Consensus sequence: VHGARAYAGAVV



Dataset #:	4
Motif ID:	74
Motif name:	twTACATAvw
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:	0.0335447

Alignment:

DBTATGTAHH

---ATKTM--

Original motif Consensus sequence: HHTACATAVD

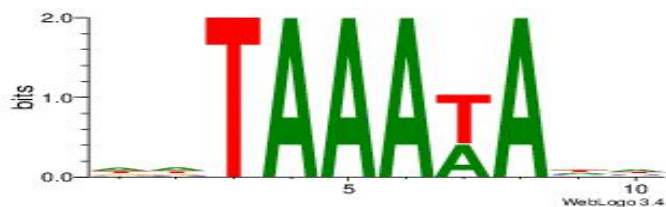
Reverse complement motif Consensus sequence: DBTATGTAHH



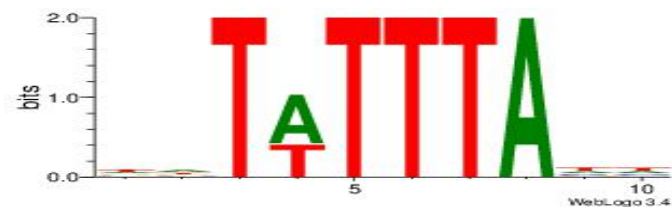
Dataset #: 4
 Motif ID: 83
 Motif name: wwTAAAwAww
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 4
 Number of overlap: 5
 Similarity score: 0.0514182

Alignment:
 HHTWTTTADD
 ---ATKTM--

Original motif Consensus sequence: DDTAAAWAHH



Reverse complement motif Consensus sequence: HHTWTTTADD



Dataset #: 4
 Motif ID: 76

Motif name: wwWAAAAAwa
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 5
 Number of overlap: 5
 Similarity score: 0.0597589

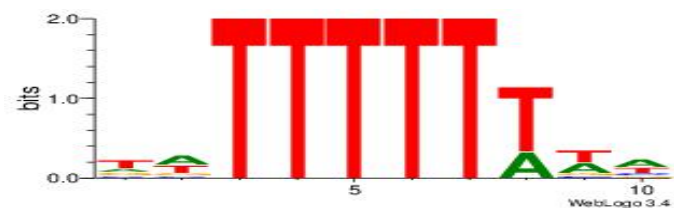
Alignment:

WWAAAAAAWH
 ----RARAT-

Original motif Consensus sequence: WWAAAAAAWH



Reverse complement motif Consensus sequence: HWTTTTTTTW

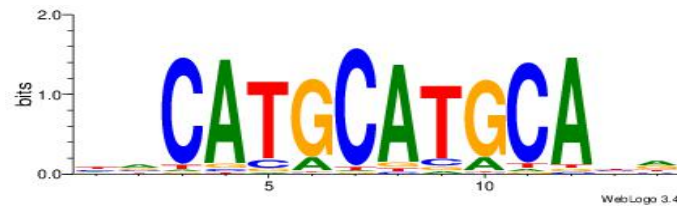


Dataset #: 4
 Motif ID: 101
 Motif name: AAAAAAAAAA
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 10
 Number of overlap: 5
 Similarity score: 0.0609742

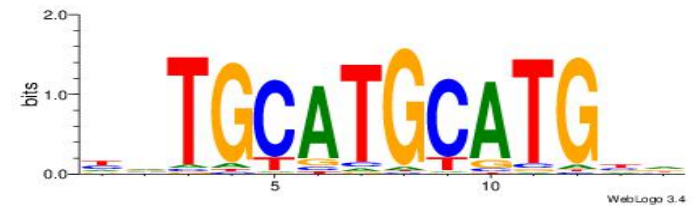
Alignment:

DVTGCATGCATGBH
-----ATKTM

Original motif Consensus sequence: HVCATGCATGCABD



Reverse complement motif Consensus sequence: DVTGCATGCATGBH



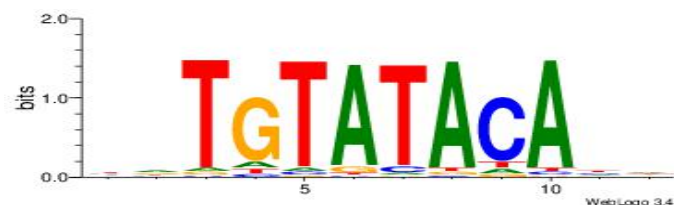
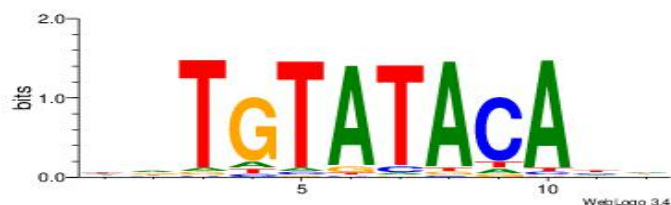
Dataset #:	4
Motif ID:	100
Motif name:	wrTGTATACAw
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	2
Number of overlap:	5
Similarity score:	0.0620607

Alignment:

DHTGTATACADH
-ATKTM-----

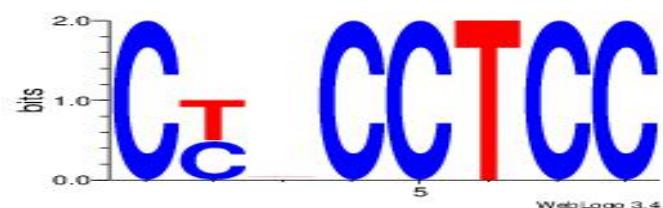
Original motif Consensus sequence: HDTGTATACAHD

Reverse complement motif Consensus sequence: DHTGTATACADH



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

Original motif Consensus sequence: CYBCCTCC



Reverse complement motif Consensus sequence: GGAGGVMG



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

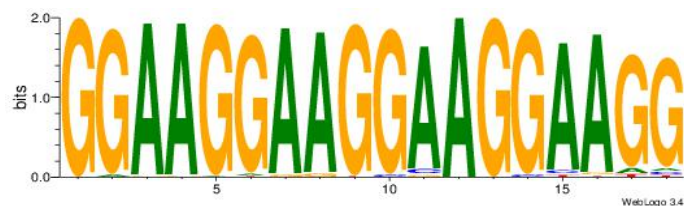
Dataset #:	3
Motif ID:	48
Motif name:	EWSR1-FLI1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	6
Number of overlap:	8
Similarity score:	0.022644

Alignment:

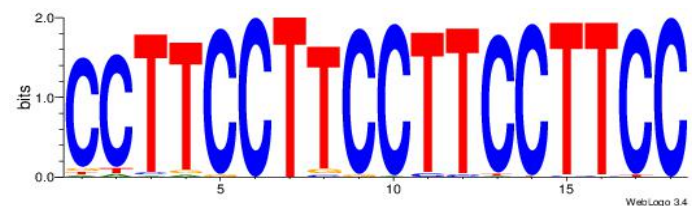
GGAAGGAAGGAAGGAAGG

-----GGAGGVMG-----

Original motif Consensus sequence: GGAAGGAAGGAAGGAAGG



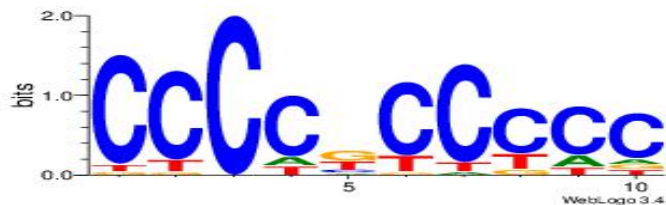
Reverse complement motif Consensus sequence: CCTTCCTTCCTTCCTTCC



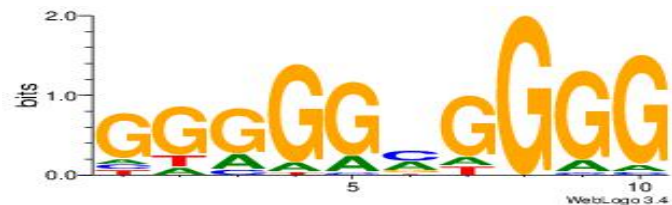
Dataset #: 3
Motif ID: 32
Motif name: SP1
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 3
Number of overlap: 8
Similarity score: 0.0247246

Alignment:
CCCCKCCCCC
--CYBCCTCC

Original motif Consensus sequence: CCCCCKCCCCC



Reverse complement motif Consensus sequence: GGGGGYGGGG



Dataset #: 4
 Motif ID: 93
 Motif name: rrAGGGGGArr
 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: 0.0300296

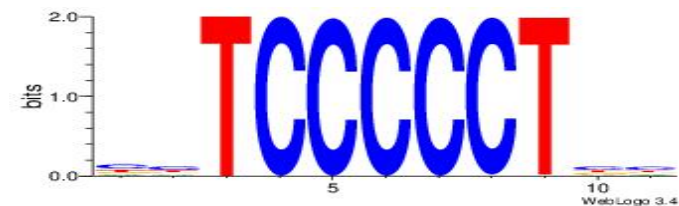
Alignment:

VVTCCCCCTVV
 ---CYBCCTCC

Original motif Consensus sequence: VVAGGGGGAVV



Reverse complement motif Consensus sequence: VVTCCCCCTVV



Dataset #: 4
 Motif ID: 91
 Motif name: ssCGCCsCCrCCCss
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 5
 Number of overlap: 8

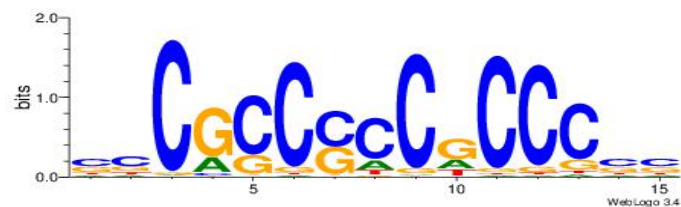
Similarity score: 0.0335629

Alignment:

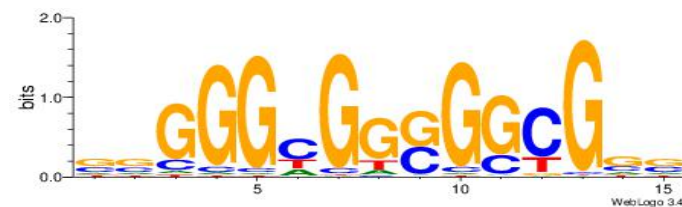
SSCGCCSCCGCCSS

----CYBCCTCC---

Original motif Consensus sequence: SSCGCCSCCGCCSS



Reverse complement motif Consensus sequence: SSGGGCGGSGGCGSS



Dataset #: 3
Motif ID: 52
Motif name: Klf4
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: 0.0354458

Alignment:

GCCYCMCCCD

-CYBCCTCC-

Original motif Consensus sequence: DGGYGKGGC

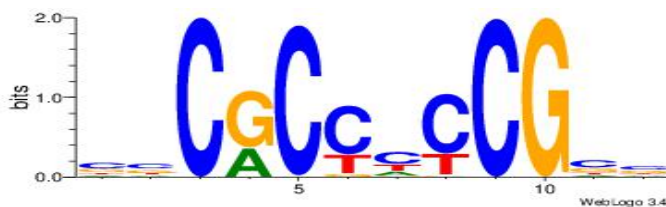
Reverse complement motif Consensus sequence: GCCYCMCCCD



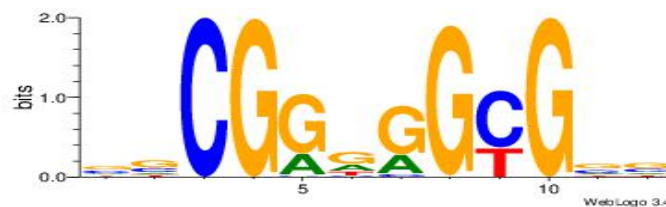
Dataset #: 4
 Motif ID: 88
 Motif name: ssCrCYyYCGss
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 8
 Similarity score: 0.045829

Alignment:
 BBCRCCYCCGBB
 ----CYBCCTCC

Original motif Consensus sequence: BBCRCCYCCGBB



Reverse complement motif Consensus sequence: BBCGGKGGMGBB



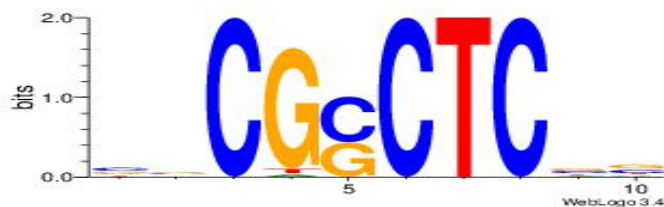
Dataset #: 4
 Motif ID: 73

Motif name:	ssCGsCTC _{ss}
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:	0.0472644

Alignment:

VVCGSCTCBB
 -CYBCCTCC-

Original motif Consensus sequence: VVCGSCTCBB



Reverse complement motif Consensus sequence: BBGAGSCGVV



Dataset #:	3
Motif ID:	57
Motif name:	MZF1_5-13
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:	0.049303

Alignment:

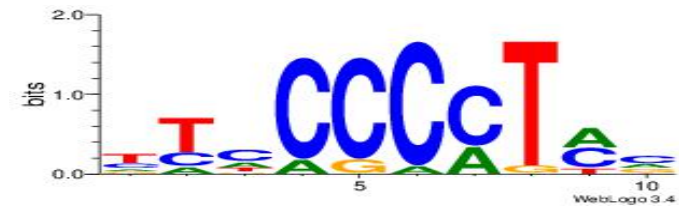
BTHCCCCTYB

--CYBCCTCC

Original motif Consensus sequence: BKAGGGGDAD



Reverse complement motif Consensus sequence: BTHCCCCTYB



Dataset #:	3
Motif ID:	34
Motif name:	RREB1
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:	0.0528666

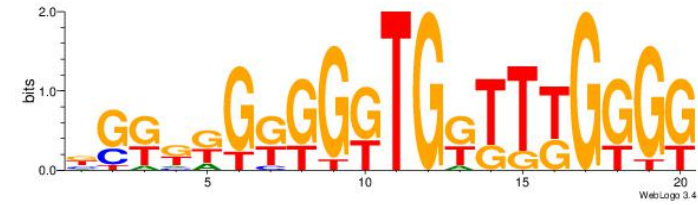
Alignment:

BGRRRGRGGRTGRTTYGGGG

----GGAGGVMG-----

Original motif Consensus sequence: CCCMAAMCAMCCMCMMMC

Reverse complement motif Consensus sequence:
BGRRRGRGGRTGRTTYGGGG



Alignment:

```
HBCCMCACCHH
-CYBCCTCC--
```


Original motif Consensus sequence: CACACACA



Reverse complement motif Consensus sequence: TGTGTGTG



Best Matches for Top Significant Motif ID 2 (Highest to Lowest)

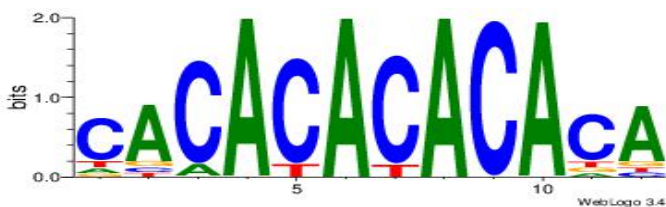
Dataset #:	4
Motif ID:	79
Motif name:	CACACACACA
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	3
Number of overlap:	8
Similarity score:	0.00486551

Alignment:

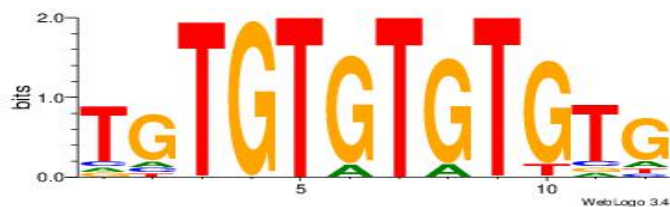
CACACACACA

--CACACACA--

Original motif Consensus sequence: CACACACACA



Reverse complement motif Consensus sequence: TGTGTGTGTG

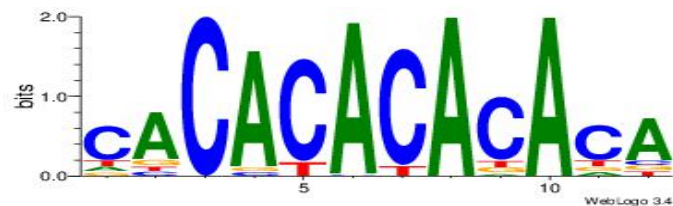


Dataset #: 4
 Motif ID: 95
 Motif name: CACACACACACA
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 5
 Number of overlap: 8
 Similarity score: 0.0100991

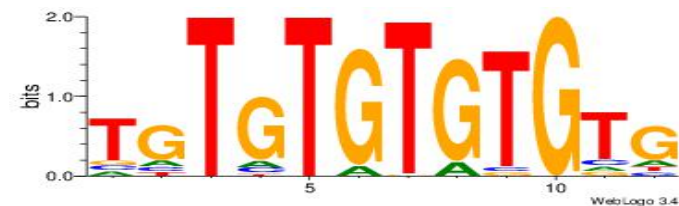
Alignment:

TGTGTGTGTGTG
 ----TGTGTGTG

Original motif Consensus sequence: CACACACACACA



Reverse complement motif Consensus sequence: TGTGTGTGTGTG

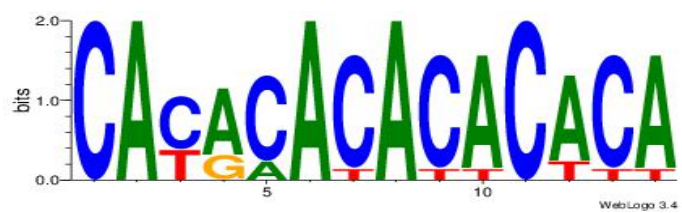


Dataset #: 2
 Motif ID: 27
 Motif name: Motif 27
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3
 Number of overlap: 8

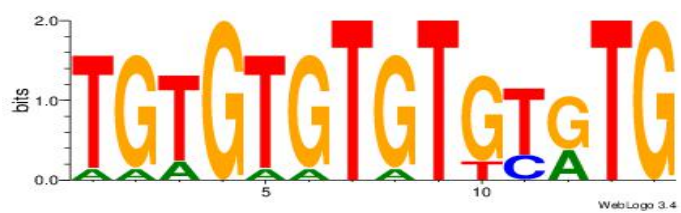
Similarity score: 0.0101254

Alignment:
TGTGTGTGTGKTG
--TGTGTGTG----

Original motif Consensus sequence: CAYACACACACACA



Reverse complement motif Consensus sequence: TGTGTGTGTGKTG

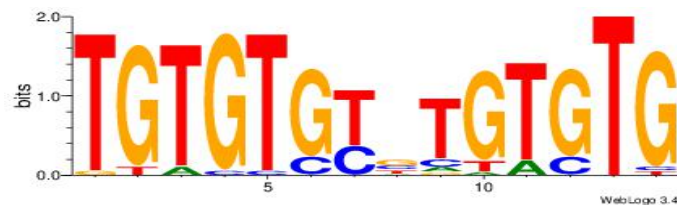


Dataset #: 2
Motif ID: 25
Motif name: Motif 25
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 7
Number of overlap: 8
Similarity score: 0.0226631

Alignment:
TGTGTGKVTGTGTG
TGTGTGTG-----

Original motif Consensus sequence: CACACAVRCACACA

Reverse complement motif Consensus sequence: TGTGTGKVTGTGTG

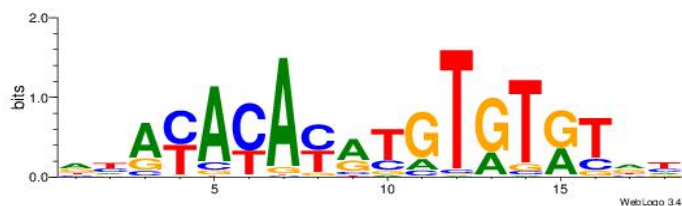


Dataset #: 4
 Motif ID: 97
 Motif name: ryayAyAyrTGTRTry
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 8
 Similarity score: 0.0393219

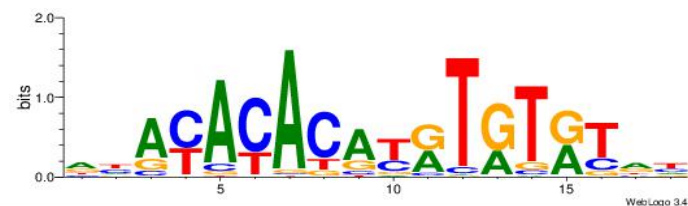
Alignment:

DHAYAYAYRTGTGTRTDH
 -----TGTGTGTG-

Original motif Consensus sequence: DHAYAYAYRTGTGTRTDH



Reverse complement motif Consensus sequence: HDAMACACAKKTKTKTHD

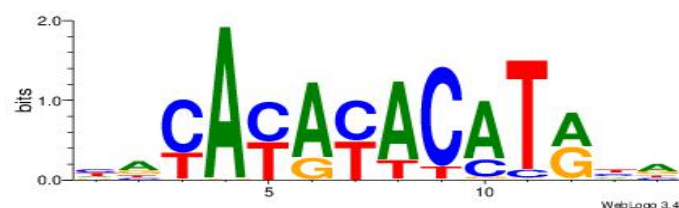


Dataset #: 4

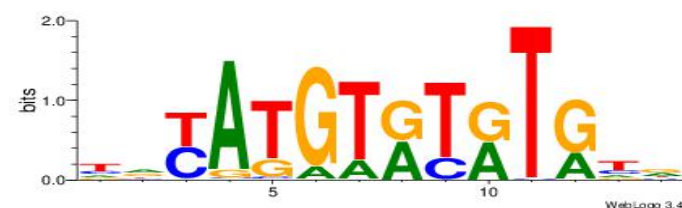
Motif ID: 75
 Motif name: yayAyAyACATrya
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 8
 Similarity score: 0.0468047

Alignment:
 HACAYAYACATRHD
 --CACACACA-----

Original motif Consensus sequence: HACAYAYACATRHD



Reverse complement motif Consensus sequence: DHKATGTKTKTGT



Dataset #: 4
 Motif ID: 86
 Motif name: aaCAAAAACaa
 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: 0.0633924

Alignment:

HHCAAAAACAH

--CACACACA--

Original motif Consensus sequence: HHCAAAAACAH



Reverse complement motif Consensus sequence: HTGTTTTTGHH



Dataset #:	4
Motif ID:	74
Motif name:	twTACATAvw
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:	0.0691437

Alignment:

DBTATGTAHH

TGTGTGTG--

Original motif Consensus sequence: HHTACATAVD

Reverse complement motif Consensus sequence: DBTATGTAHH

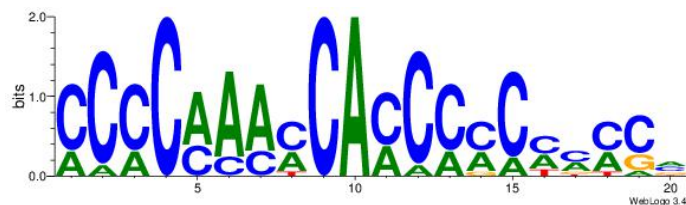


Dataset #: 3
 Motif ID: 34
 Motif name: RREB1
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 7
 Number of overlap: 8
 Similarity score: 0.0752394

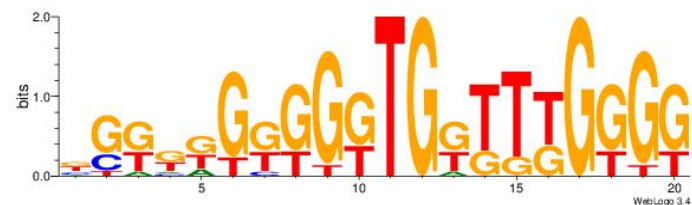
Alignment:

CCCCMAAMCAMECCMMMCV
 -----CACACACA-----

Original motif Consensus sequence: CCCCMAAMCAMECCMMMCV



Reverse complement motif Consensus sequence: BGRRRGRGGRTGRTTYGGGG



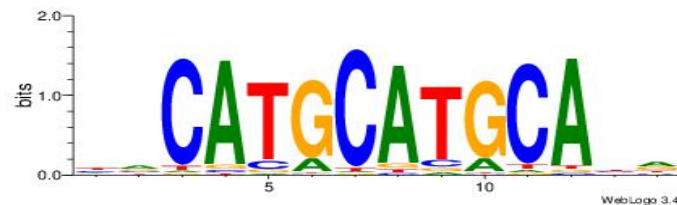
Dataset #: 4

Motif ID: 101
 Motif name: AAAAAAAAAA
 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: 0.0764586

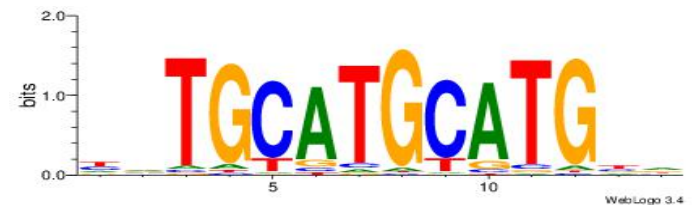
Alignment:

DVTGCATGCATGBH
 -----TGTGTGTG

Original motif Consensus sequence: HVCATGCATGCABD



Reverse complement motif Consensus sequence: DVTGCATGCATGBH



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

Original motif Consensus sequence: CTCTGY



Reverse complement motif Consensus sequence: KCAGAG

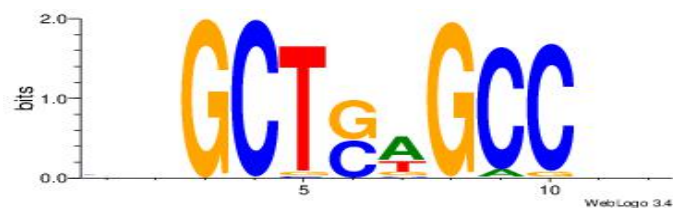


Best Matches for Top Significant Motif ID 20 (Highest to Lowest)

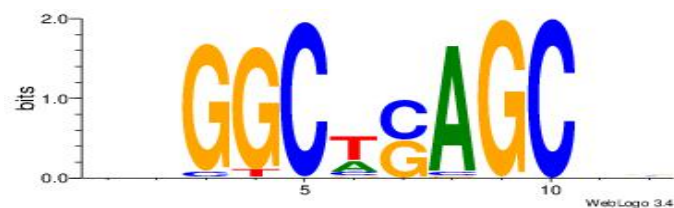
Dataset #: 4
 Motif ID: 77
 Motif name: ssGCTswGCCms
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 6
 Similarity score: 0.0323407

Alignment:
 VBGCTSAGCCHB
 ---CTCTGY---

Original motif Consensus sequence: VBGCTSAGCCHB



Reverse complement motif Consensus sequence: BDGGCTSAGCBV



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: 0.0352938

Alignment:
 ASASAGAA
 --KCAGAG

Original motif Consensus sequence: ASASAGAA



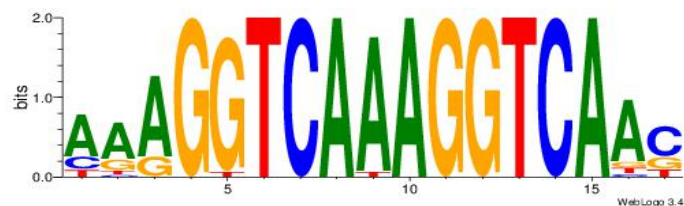
Reverse complement motif Consensus sequence: TTCTSTST



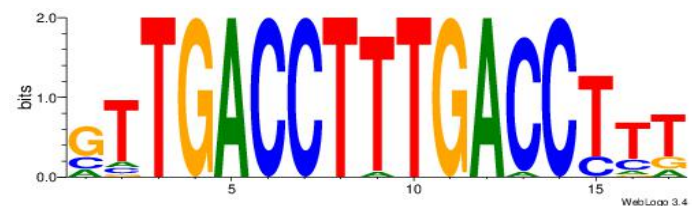
Dataset #: 3
 Motif ID: 59
 Motif name: NR1H2RXRA
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 7
 Number of overlap: 6
 Similarity score: 0.0398495

Alignment:
 AAAGGTCAAAGGTCAAC
 -----KCAGAG-----

Original motif Consensus sequence: AAAGGTCAAAGGTCAAC



Reverse complement motif Consensus sequence: GTTGACCTTTGACCTT

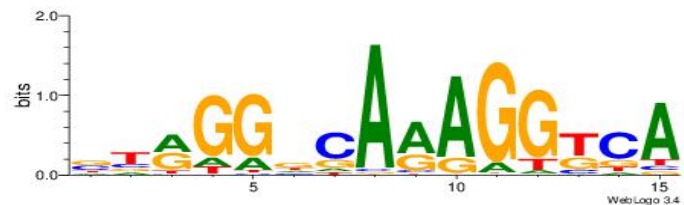


Dataset #: 3
 Motif ID: 36
 Motif name: PPARGRXRA
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 6
 Number of overlap: 6
 Similarity score: 0.0415907

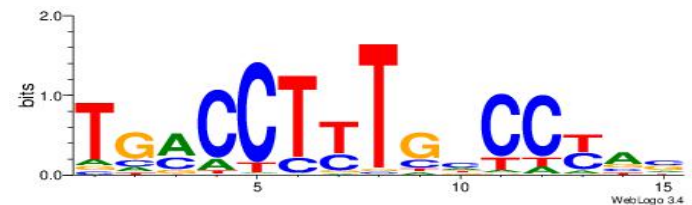
Alignment:

BTRGGDCARAGGKCA
 -----KCAGAG-----

Original motif Consensus sequence: BTRGGDCARAGGKCA



Reverse complement motif Consensus sequence: TGRCCCTKTGHCCCK



Dataset #: 1
 Motif ID: 11
 Motif name: Motif 11
 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: 0.0430865

Alignment:
 CCGCCGCC
 -CTCTGY-

Original motif Consensus sequence: CCGCCGCC



Reverse complement motif Consensus sequence: GGCGGCGG

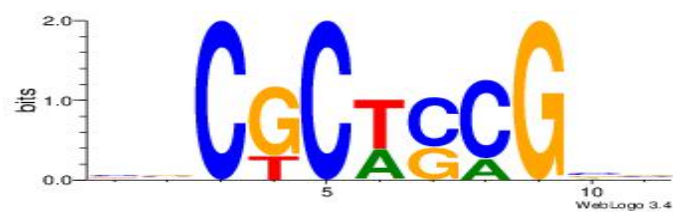


Dataset #: 4
 Motif ID: 72
 Motif name: ssCKCwsCGss
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 6

Similarity score: 0.0439226

Alignment:
BVCGCWSCGBV
----CTCTGY--

Original motif Consensus sequence: BVCGCWSCGBV



Reverse complement motif Consensus sequence: VBCGSWGCGVB

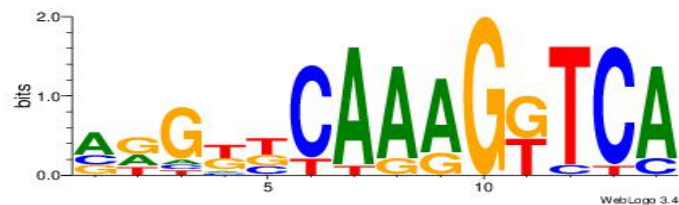


Dataset #: 3
Motif ID: 38
Motif name: NR2F1
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 5
Number of overlap: 6
Similarity score: 0.0462597

Alignment:
AKGYCAAAGRTCA
----KCAGAG----

Original motif Consensus sequence: TGAMCTTTGMMCYT

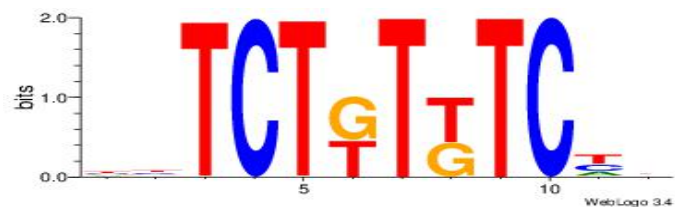
Reverse complement motif Consensus sequence: AKGYCAAAGRTCA



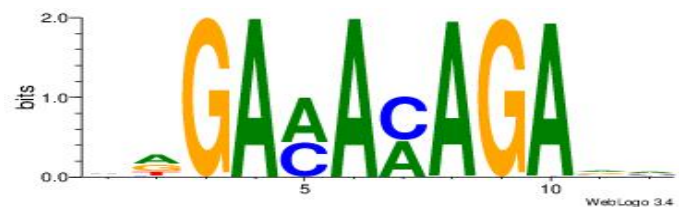
Dataset #: 4
 Motif ID: 92
 Motif name: tyTCTkTkTCyy
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 6
 Similarity score: 0.0467436

Alignment:
 BBTCTKTKTCHB
 -CTCTGY-----

Original motif Consensus sequence: BBTCTKTKTCHB



Reverse complement motif Consensus sequence: VHGARAYAGAVV

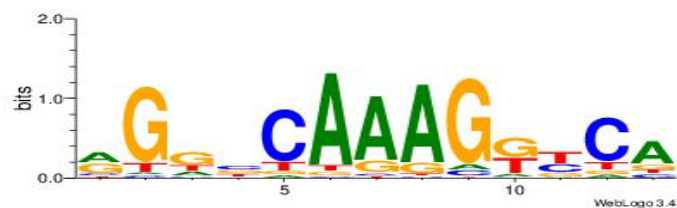


Dataset #: 3
 Motif ID: 50

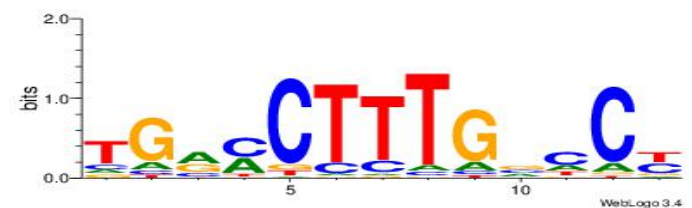
Motif name:	HNH4A
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	4
Number of overlap:	6
Similarity score:	0.0481824

Alignment:
RGGBCAAAGKYCA
---KCAGAG----

Original motif Consensus sequence: RGGBCAAAGKYCA



Reverse complement motif Consensus sequence: TGMYCTTTGBCCK



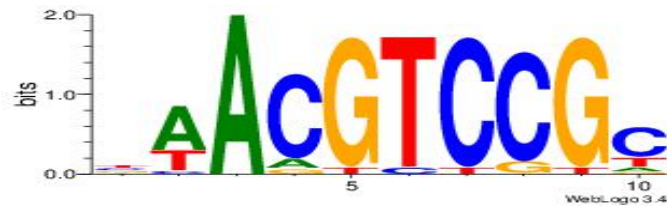
Dataset #:	3
Motif ID:	53
Motif name:	MIZF
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	5
Number of overlap:	6
Similarity score:	0.049747

Alignment:

BAACGTCCGC

----CTCTGY

Original motif Consensus sequence: BAACGTCCGC



Reverse complement motif Consensus sequence: GCGGACGTTT



Dataset #: 3 Motif ID: 42 Motif name: ArntAhr

Original motif Consensus sequence: YGCGTG



Reverse complement motif Consensus sequence: CACGCM



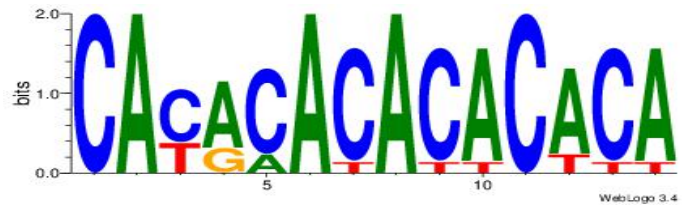
Best Matches for Top Significant Motif ID 42 (Highest to Lowest)

Dataset #:	2
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:	7

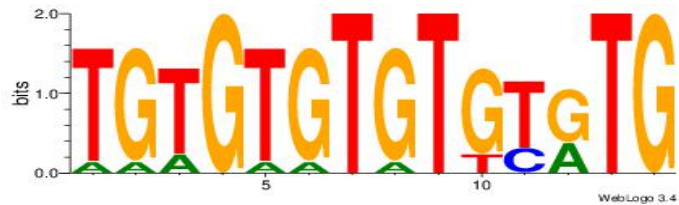
Number of overlap: 6
Similarity score: 0.0388571

Alignment:
TGTGTGTGTGKTG
-----YGCGTG--

Original motif Consensus sequence: CAYACACACACACA



Reverse complement motif Consensus sequence: TGTGTGTGTGKTG

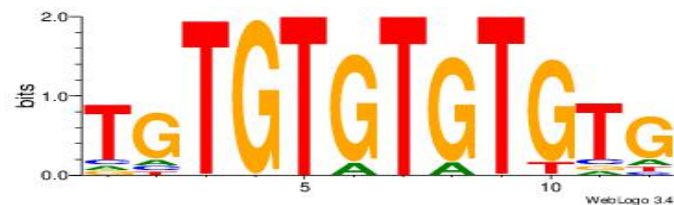
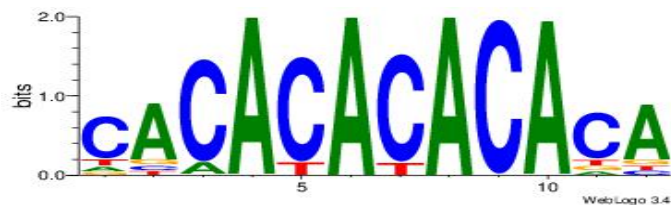


Dataset #: 4
Motif ID: 79
Motif name: CACACACACACA
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 7
Number of overlap: 6
Similarity score: 0.0420782

Alignment:
TGTGTGTGTGTG
YGCGTG-----

Original motif Consensus sequence: CACACACACACA

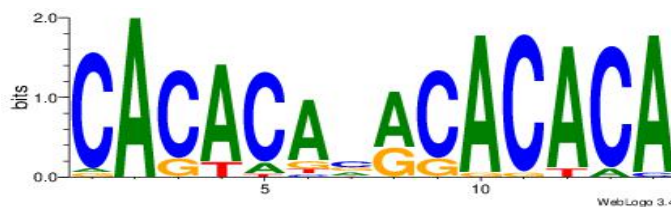
Reverse complement motif Consensus sequence: TGTGTGTGTGTG



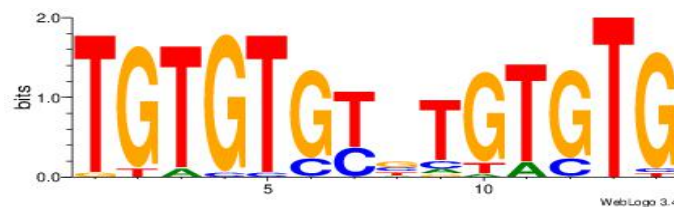
Dataset #: 2
 Motif ID: 25
 Motif name: Motif 25
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 6
 Similarity score: 0.0430749

Alignment:
 CACACAVRCACACA
 -----CACGCM

Original motif Consensus sequence: CACACAVRCACACA



Reverse complement motif Consensus sequence: TGTGTGKVTGTGT



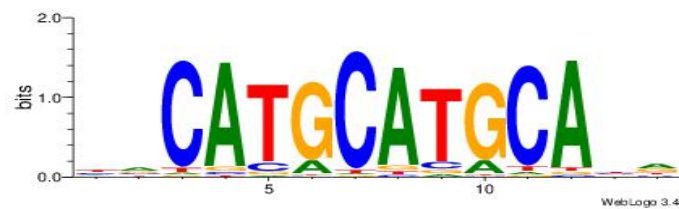
Dataset #: 4
 Motif ID: 101

Motif name:	AAAAAAAAAAAA
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	3
Number of overlap:	6
Similarity score:	0.043218

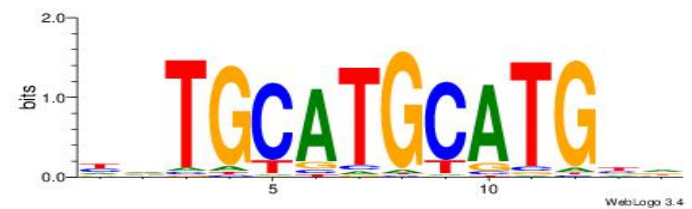
Alignment:

```
HVCATGCATGCABD
--CACGCM-----
```

Original motif Consensus sequence: HVCATGCATGCABD



Reverse complement motif Consensus sequence: DVTGCATGCATGB



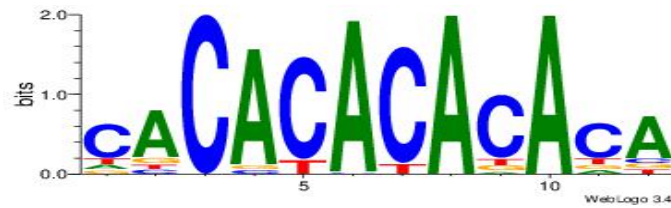
Dataset #:	4
Motif ID:	95
Motif name:	CACACACACACA
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	5
Number of overlap:	6
Similarity score:	0.0440329

Alignment:

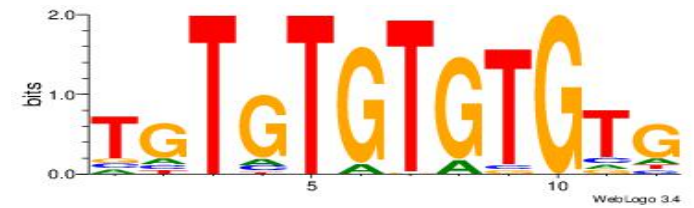
TGTGTGTGTGTG

----YGCGTG--

Original motif Consensus sequence: CACACACACACA



Reverse complement motif Consensus sequence: TGTGTGTGTGTG



Dataset #:	4
Motif ID:	96
Motif name:	yrTGTGCACAYr
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	7
Number of overlap:	6
Similarity score:	0.0477579

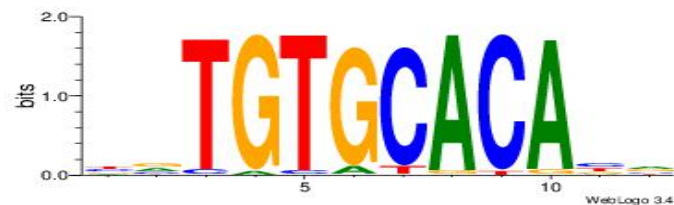
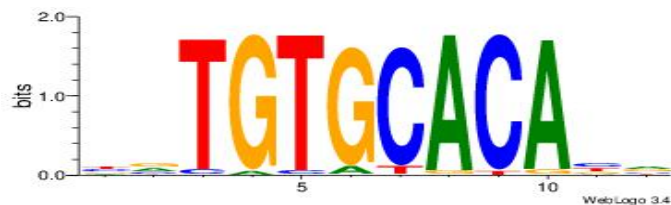
Alignment:

BVTGTGCACABV

YGCGTG-----

Original motif Consensus sequence: BVTGTGCACABV

Reverse complement motif Consensus sequence: BBTGTGCACAVV

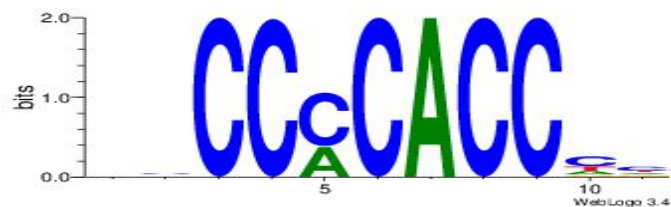


Dataset #: 4
 Motif ID: 89
 Motif name: ccCCmCACCCc
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 6
 Similarity score: 0.0479115

Alignment:

HBCCMCACCHH
 -----CACGCM

Original motif Consensus sequence: HBCCMCACCHH



Reverse complement motif Consensus sequence: DDGGTGRGGBD



Dataset #: 4
 Motif ID: 65

Motif name: ssCGrGCGss
 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: 0.0487655

Alignment:

VBCGCMCGSV
 ----CACGCM

Original motif Consensus sequence: VSCGRGCGBV



Reverse complement motif Consensus sequence: VBCGCMCGSV



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: 6
 Similarity score: 0.0505006

Alignment:
CACACACA
CACGCM--

Original motif Consensus sequence: CACACACA



Reverse complement motif Consensus sequence: TGTGTGTG

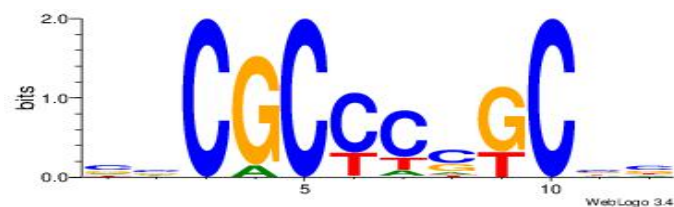
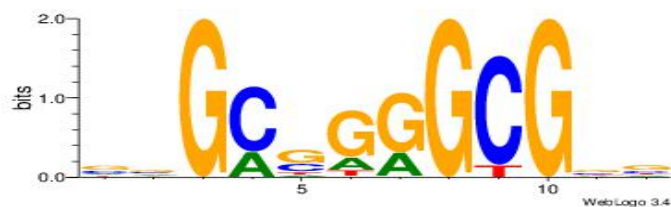


Dataset #:	4
Motif ID:	67
Motif name:	ssGMsGRGCGss
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	7
Number of overlap:	6
Similarity score:	0.0538134

Alignment:
BBCGCCCCSGCVV
CACGCM-----

Original motif Consensus sequence: VVGCSGGGCGBB

Reverse complement motif Consensus sequence: BBCGCCCCSGCVV



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

Original motif Consensus sequence: GAGRCAGR



Reverse complement motif Consensus sequence: MCTGKCTC

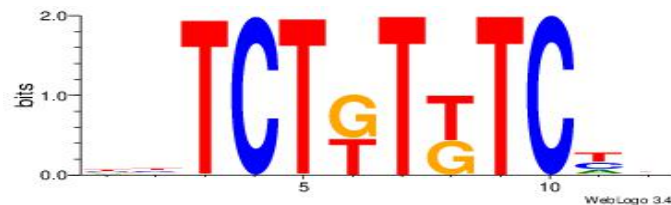


Best Matches for Top Significant Motif ID 13 (Highest to Lowest)

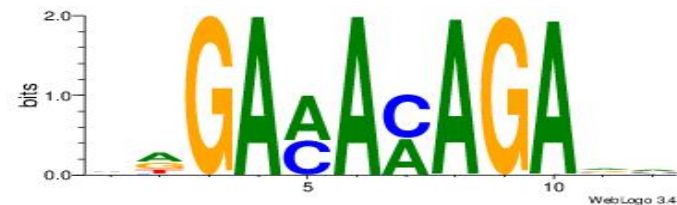
Dataset #:	4
Motif ID:	92
Motif name:	tyTCTkTCTCyy
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	3
Number of overlap:	8
Similarity score:	0.0131318

Alignment:
 VHGARAYAGAVV
 --GAGRCAGR--

Original motif Consensus sequence: BBTCTKTKTCHB



Reverse complement motif Consensus sequence: VHGARAYAGAVV

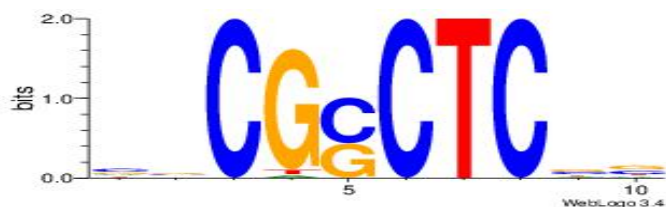


Dataset #: 4
 Motif ID: 73
 Motif name: ssCGsCTC
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3
 Number of overlap: 8
 Similarity score: 0.0334555

Alignment:

BBGAGSCGVV
 --GAGRCAGR

Original motif Consensus sequence: VVCGSCTCBB



Reverse complement motif Consensus sequence: BBGAGSCGVV

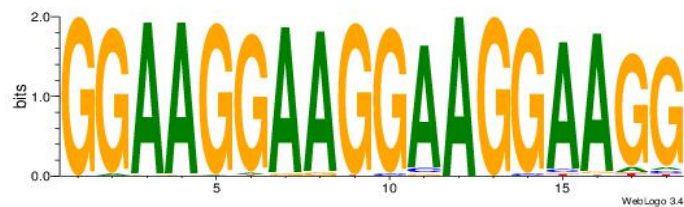


Dataset #: 3
 Motif ID: 48
 Motif name: EWSR1-FLI1
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 7
 Number of overlap: 8
 Similarity score: 0.0397014

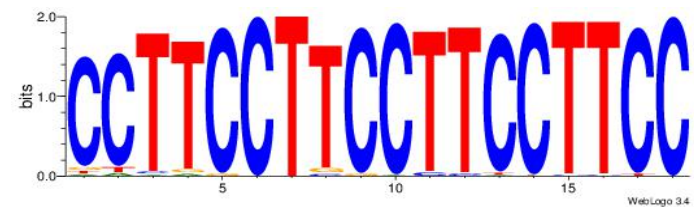
Alignment:

GGAAGGAAGGAAGGAAGG
 -----GAGRCAGR-----

Original motif Consensus sequence: GGAAGGAAGGAAGGAAGG



Reverse complement motif Consensus sequence: CCTTCCTTCCTTCCTTCC

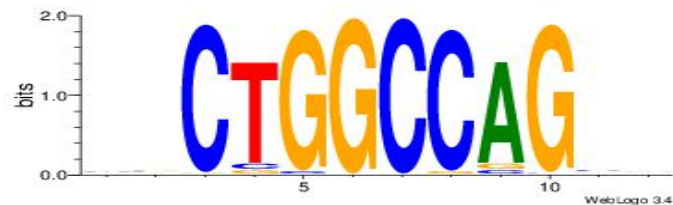


Dataset #: 4
 Motif ID: 99
 Motif name: sgCTGGCCAGcs
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2

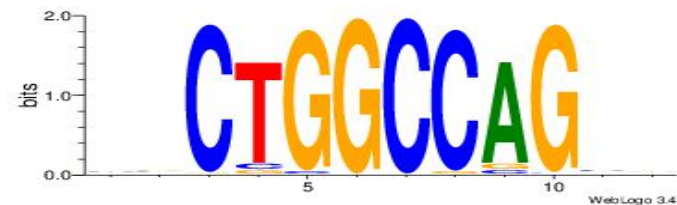
Number of overlap: 8
Similarity score: 0.0475948

Alignment:
VVCTGGCCAGBB
-MCTGKCTC---

Original motif Consensus sequence: BBCTGGCCAGVV



Reverse complement motif Consensus sequence: VVCTGGCCAGBB

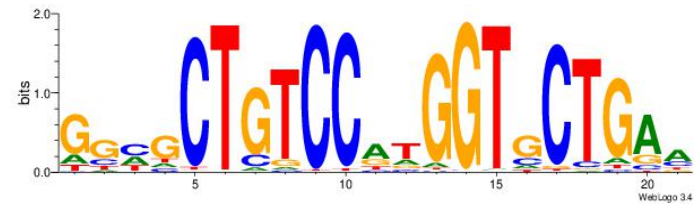
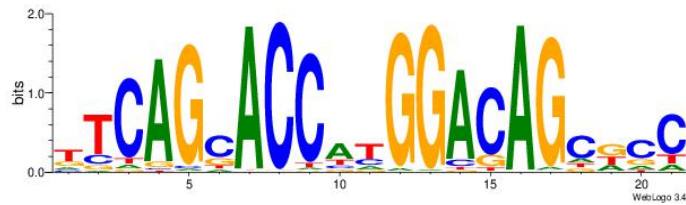


Dataset #: 3
Motif ID: 35
Motif name: REST
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 4
Number of overlap: 8
Similarity score: 0.049302

Alignment:
GGYGCTGTCCATGGTGCTGAA
---MCTGKCTC-----

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC

Reverse complement motif Consensus sequence:
GGYGCTGTCCATGGTGCTGAA



Dataset #: 2
 Motif ID: 23
 Motif name: Motif 23
 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: 0.0551203

Alignment:
 GGGGMGGG
 GAGRCAGR

Original motif Consensus sequence: CCCRCCCC



Reverse complement motif Consensus sequence: GGGGMGGG



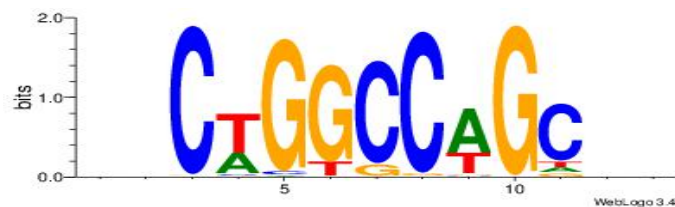
Dataset #: 4
 Motif ID: 80

Motif name:	ssCwGGCCwGCss
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:	0.055328

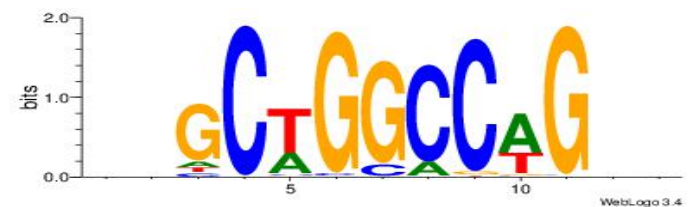
Alignment:

BBCWGGCCAGCBB
 -MCTGKCTC-----

Original motif Consensus sequence: BBCWGGCCAGCBB



Reverse complement motif Consensus sequence: BBGCTGGCCWGBB



Dataset #:	4
Motif ID:	93
Motif name:	rrAGGGGGArr
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:	0.0555608

Alignment:

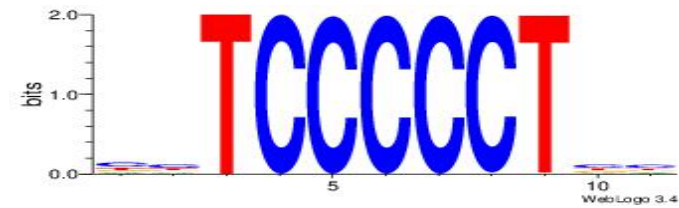
VVAGGGGGAVV

---GAGRCAGR

Original motif Consensus sequence: VVAGGGGGAVV



Reverse complement motif Consensus sequence: VVTCCCCCTVV



Dataset #:	3
Motif ID:	45
Motif name:	ESR1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	13
Number of overlap:	8
Similarity score:	0.055859

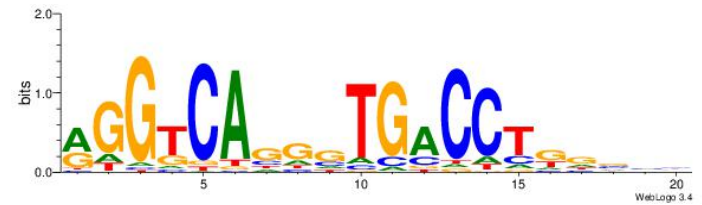
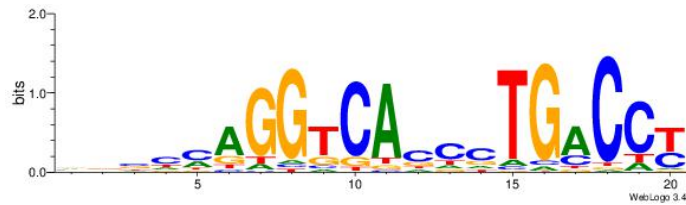
Alignment:

VDBHMAGGTCACCCTGACCY

-----MCTGKCTC

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY

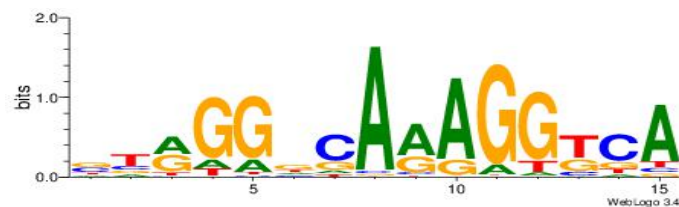
Reverse complement motif Consensus sequence:
MGGTCAGGGTGACCTRDBHV



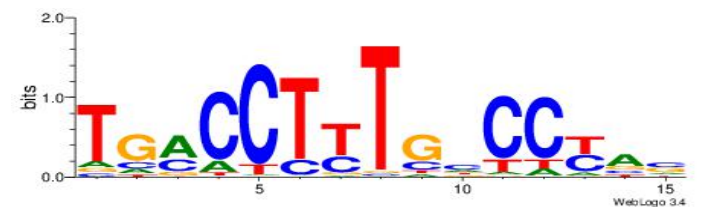
Dataset #: 3
 Motif ID: 36
 Motif name: PPARGRXRA
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 4
 Number of overlap: 8
 Similarity score: 0.0596402

Alignment:
 TGRCCCTKTGHCCCKAB
 ---MCTGKCTC----

Original motif Consensus sequence: BTRGGDCARAGGKCA



Reverse complement motif Consensus sequence: TGRCCCTKTGHCCCKAB



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

Original motif Consensus sequence: GCRCACRC



Reverse complement motif Consensus sequence: GKGTGKGC



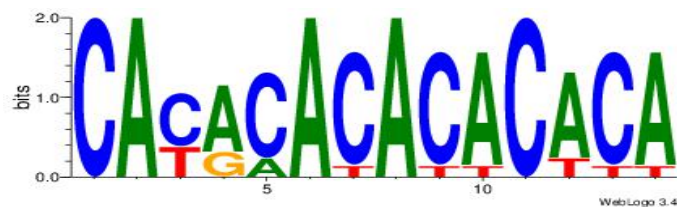
Best Matches for Top Significant Motif ID 14 (Highest to Lowest)

Dataset #:	2
Motif ID:	27
Motif name:	Motif 27
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:	0.0307099

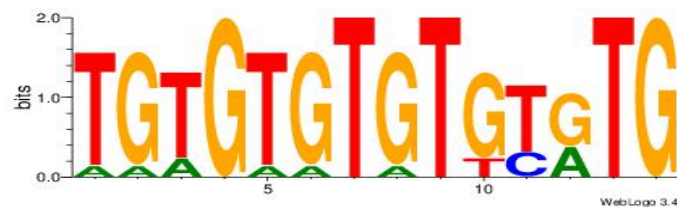
Alignment:

CAYACACACACACA
 ---GCRCACRC---

Original motif Consensus sequence: CAYACACACACACA



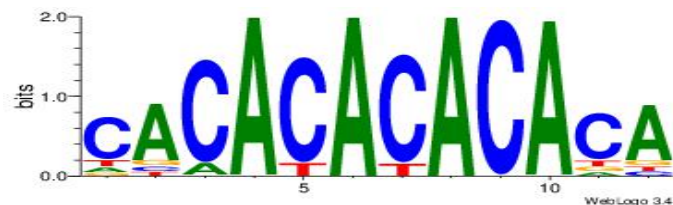
Reverse complement motif Consensus sequence: TGTGTGTGTGKT



Dataset #: 4
 Motif ID: 79
 Motif name: CACACACACACA
 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: 0.0357914

Alignment:
 CACACACACACA
 -GCRACACRC---

Original motif Consensus sequence: CACACACACACA



Reverse complement motif Consensus sequence: TGTGTGTGTGTG

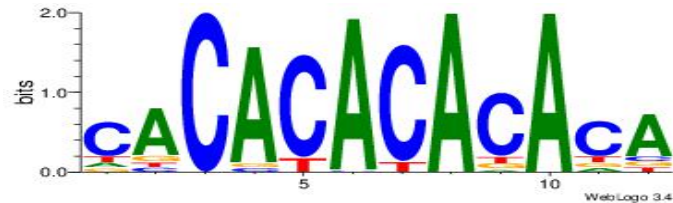


Dataset #: 4
 Motif ID: 95
 Motif name: CACACACACACA
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 4
 Number of overlap: 8

Similarity score: 0.0366948

Alignment:
CACACACACACA
-GCRCACRC---

Original motif Consensus sequence: CACACACACACA



Reverse complement motif Consensus sequence: TGTGTGTGTGTG



Dataset #: 3
Motif ID: 52
Motif name: Klf4
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: 0.03983

Alignment:
DGGGYGKGGC
-GKGTGKGC-

Original motif Consensus sequence: DGGGYGKGGC

Reverse complement motif Consensus sequence: GCCYCMCCCD

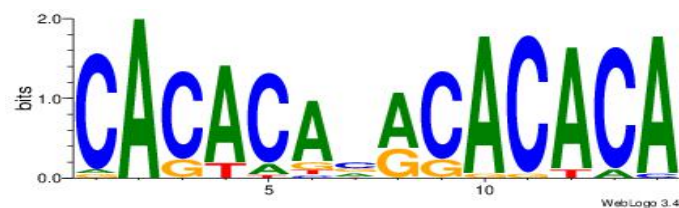


Dataset #: 2
 Motif ID: 25
 Motif name: Motif 25
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 8
 Similarity score: 0.0418776

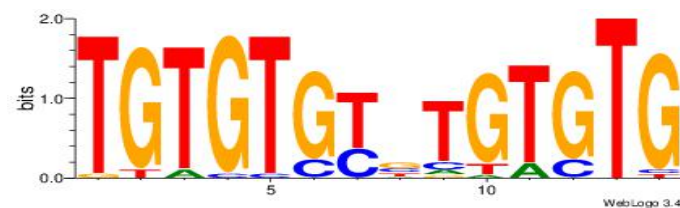
Alignment:

CACACAVRCACACA
 -----GCRACRC-

Original motif Consensus sequence: CACACAVRCACACA



Reverse complement motif Consensus sequence: TGTGTGKVTGTGT



Dataset #: 3
 Motif ID: 44

Motif name:	Egr1
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:	0.0429433

Alignment:

HGCGTGGGCGK
 -GKGTGKGC--

Original motif Consensus sequence: HGCGTGGGCGK



Reverse complement motif Consensus sequence: YGCCCCACGCH



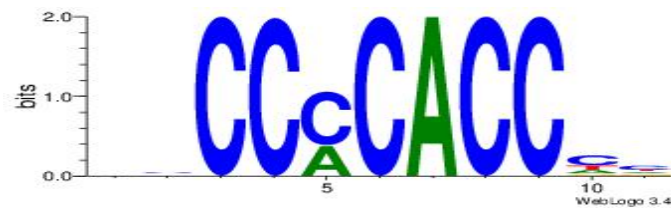
Dataset #:	4
Motif ID:	89
Motif name:	ccCCmCACCCc
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	2
Number of overlap:	8
Similarity score:	0.0505252

Alignment:

DDGGTGRGGBD

-GKGTGKGC--

Original motif Consensus sequence: HBCCMCACCHH



Reverse complement motif Consensus sequence: DDGGTGRGGBD



Dataset #:	4
Motif ID:	96
Motif name:	yrTGTGCACAYr
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:	0.0537384

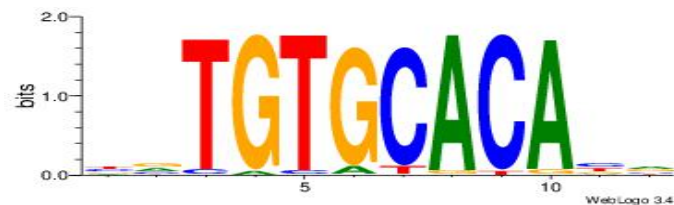
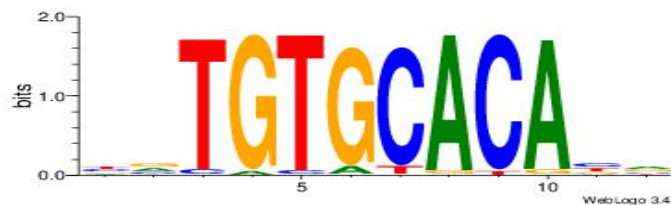
Alignment:

BVTGTGCACABV

---GCRCACRC-

Original motif Consensus sequence: BVTGTGCACABV

Reverse complement motif Consensus sequence: BBTGTGCACAVV



Dataset #: 4
 Motif ID: 65
 Motif name: ssCGrGCGss
 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: 0.067702

Alignment:

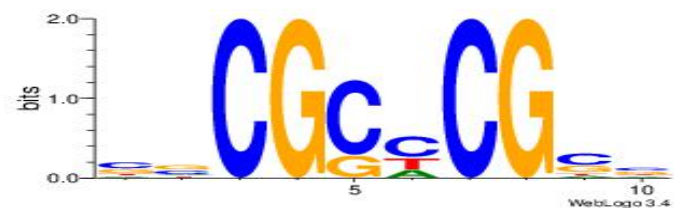
VBCGCMCGSV

-GCRCACRC-

Original motif Consensus sequence: VSCGRGCGBV



Reverse complement motif Consensus sequence: VBCGCMCGSV



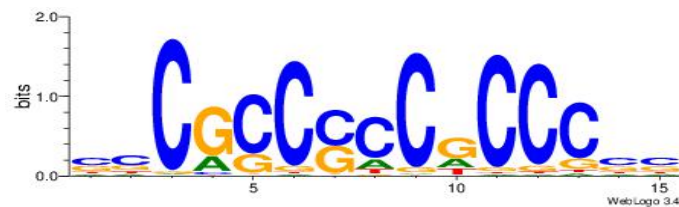
Dataset #: 4
 Motif ID: 91

Motif name: ssCGCCsCCrCCCss
 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: 0.0685867

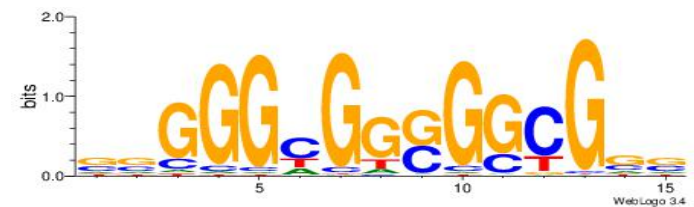
Alignment:

SSCGCCSCCGCCSS
 ---GCRCACRC----

Original motif Consensus sequence: SSCGCCSCCGCCSS



Reverse complement motif Consensus sequence: SSGGGCGGSGGCGSS



Results created by MOTIFSIM on 06-19-2018 09:49:23

Runtime: 1032.94 seconds

MOTIFSIM is written by Ngoc Tam L. Tran

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