



MOTIFSIM - MOTIF SIMilarity Detection Tool

Version 2.0

INPUT

Input Parameters

Number of files:	4
Number of top significant motifs:	10
Number of best matches:	10
Similarity cutoff $\geq$	0.75
Output file type:	All
Output file format:	All

Input files and motif counts

File name	Count of motifs	Dataset number
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: TGTRT

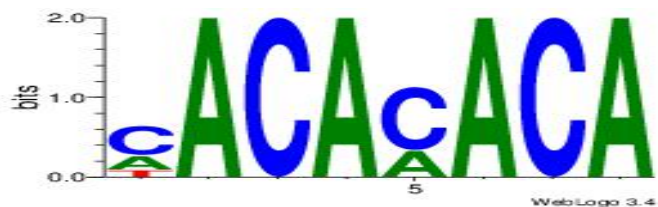


Best Matches for Top Significant Motif ID 18 (Highest to Lowest)

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

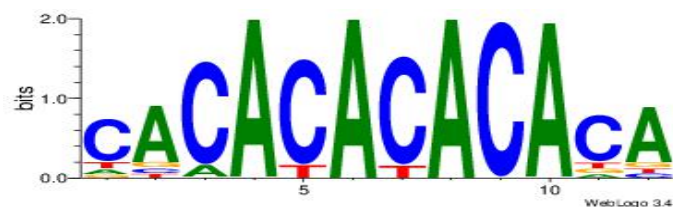


Dataset #: 4
 Motif ID: 79
 Motif name: CACACACACACA
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3
 Number of overlap: 5
 Similarity score: 0.0148279

Alignment:

TGTGTGTGTGTG
 --TGTRT-----

Original motif Consensus sequence: CACACACACACA



Reverse complement motif Consensus sequence: TGTGTGTGTGTG

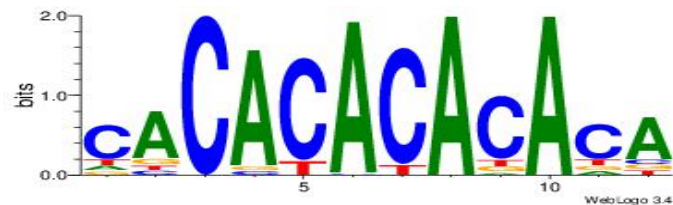


Dataset #: 4
 Motif ID: 95
 Motif name: CACACACACACA
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 4
 Number of overlap: 5

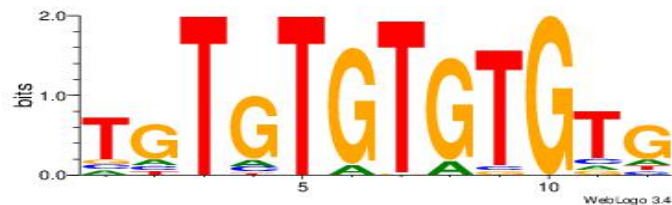
Similarity score: 0.0228414

Alignment:
TGTGTGTGTGTG
----TGTRT---

Original motif Consensus sequence: CACACACACACA



Reverse complement motif Consensus sequence: TGTGTGTGTGTG

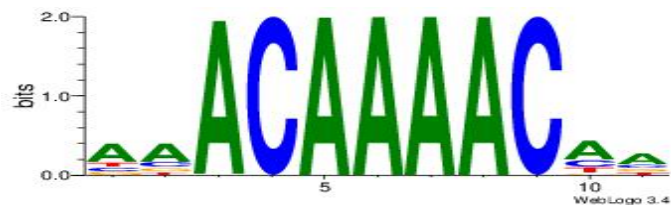


Dataset #: 4
Motif ID: 69
Motif name: aaACAAAACaa
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 6
Number of overlap: 5
Similarity score: 0.0274014

Alignment:
AAACAAAACAA
-----AMACA-

Original motif Consensus sequence: AAACAAAACAA

Reverse complement motif Consensus sequence: TTGTTTGTGTT



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



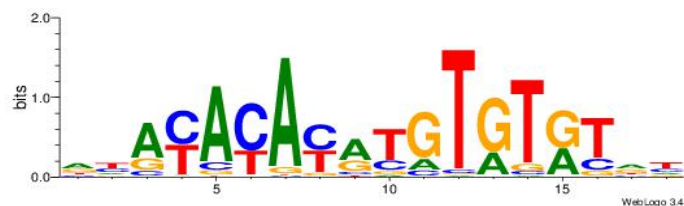
Dataset #: 4
 Motif ID: 97

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

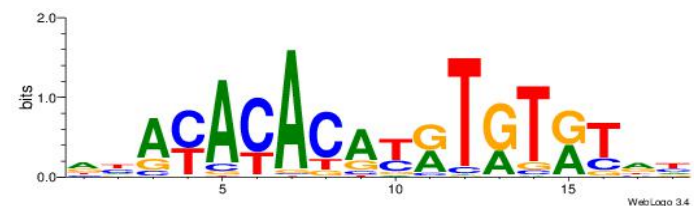
Alignment:

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

Original motif Consensus sequence: DHAYAYAYRTGTGTRTDH



Reverse complement motif Consensus sequence: HDAMACACAKKTKTKTHD



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

HDTGTATACAHD

--TGTRT-----

Original motif Consensus sequence: HDTGTATACAHD



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

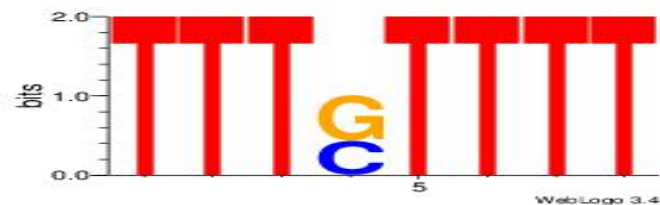
Alignment:

AAAASAAA

-AMACA--

Original motif Consensus sequence: AAAASAAA

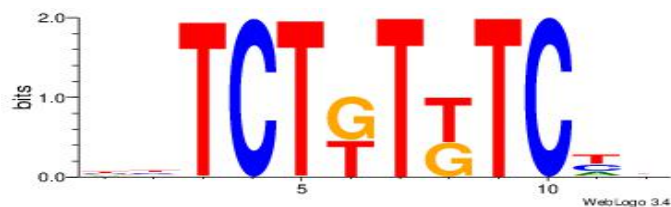
Reverse complement motif Consensus sequence: TTTSTTTT



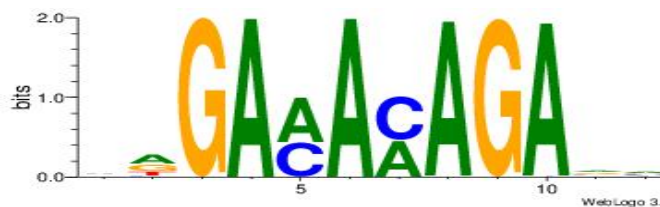
Dataset #: 4
 Motif ID: 92
 Motif name: tyTCTkTkTCyy
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 4
 Number of overlap: 5
 Similarity score: 0.0390126

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



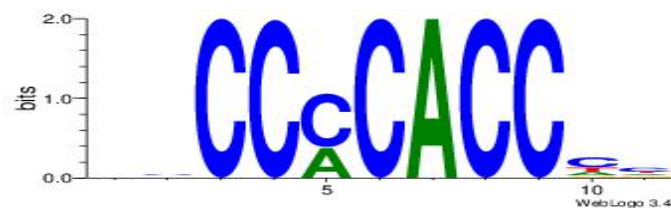
Best Matches for Top Significant Motif ID 30 (Highest to Lowest)

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

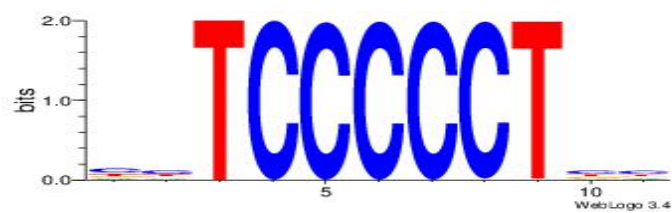
Similarity score: 0.0194512

Alignment:
VVAGGGGGAVV
-HAGGTG----

Original motif Consensus sequence: VVAGGGGGAVV



Reverse complement motif Consensus sequence: VVTCCCCCTVV

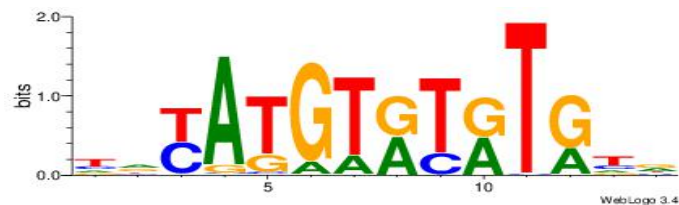


Dataset #: 4
Motif ID: 75
Motif name: yayAyAyACATrya
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 7
Number of overlap: 6
Similarity score: 0.0270731

Alignment:
HACAYAYACATRHD
-----CACCTD--

Original motif Consensus sequence: HACAYAYACATRHD

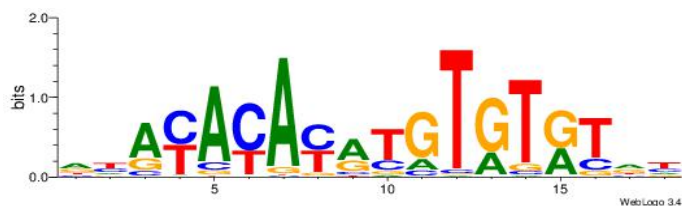
Reverse complement motif Consensus sequence: DHKATGTKTKGT



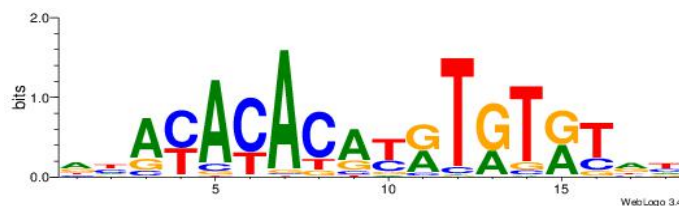
Dataset #: 4
 Motif ID: 97
 Motif name: ryayAyAyrTGTRTry
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 6
 Number of overlap: 6
 Similarity score: 0.0321302

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

Original motif Consensus sequence: DHAYAYAYRTGTGTRTDH



Reverse complement motif Consensus sequence: HDAMACACAKKTKTKTHD



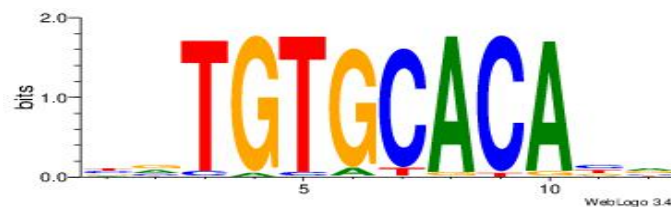
Dataset #: 4

Motif ID: 96
 Motif name: yrTGTGCACAr
 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

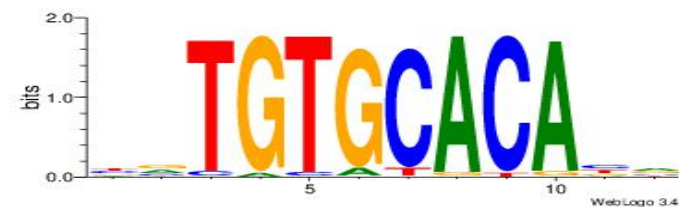
Alignment:

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:

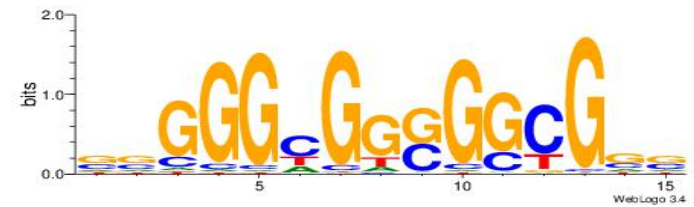
SSCGCCSCCGCCSS

-----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

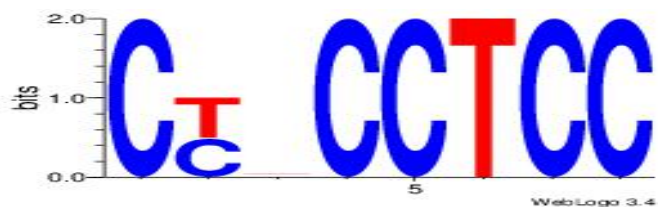
Alignment:

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

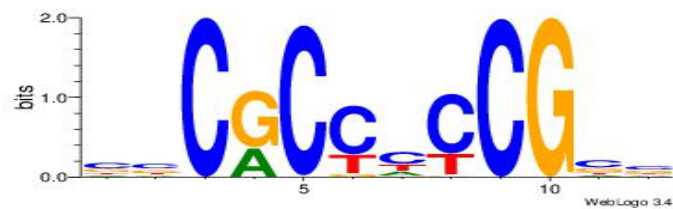


Dataset #: 4
 Motif ID: 88

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:
 BBCRCCYCCGGBB
 --CACCTD----

Original motif Consensus sequence: BBCRCCYCCGGBB



Reverse complement motif Consensus sequence: BBCGGKGGMGBB



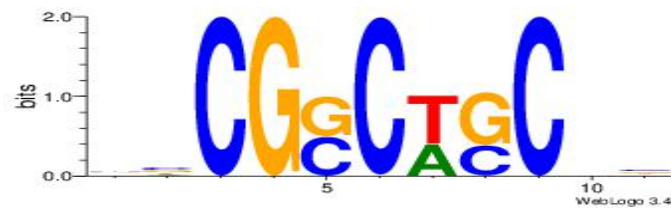
Dataset #: 4
 Motif ID: 90
 Motif name: ssCGsCwsCss
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 6
 Similarity score: 0.0564656

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



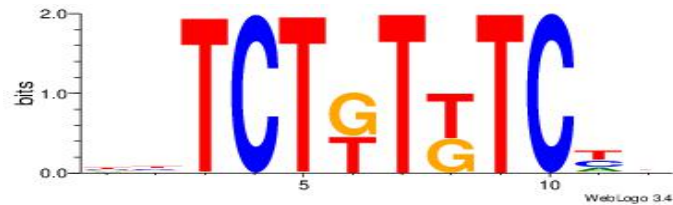
Best Matches for Top Significant Motif ID 7 (Highest to Lowest)

Dataset #:	4
Motif ID:	92
Motif name:	tyTCTkTKTCyy
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	4

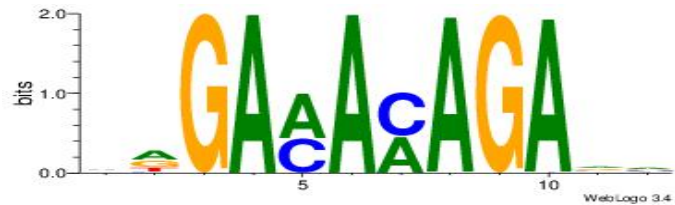
Number of overlap: 8
Similarity score: 0.00355249

Alignment:
BBTCTKTKTCHB
-TTCTSTST---

Original motif Consensus sequence: BBTCTKTKTCHB



Reverse complement motif Consensus sequence: VHGARAYAGAVV

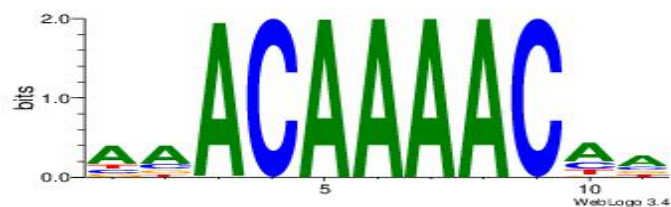


Dataset #: 4
Motif ID: 69
Motif name: aaACAAACaa
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 8
Similarity score: 0.0313478

Alignment:
AAACAAACAA
ASASAGAA---

Original motif Consensus sequence: AAACAAACAA

Reverse complement motif Consensus sequence: TTGTTTGT



Dataset #: 4
 Motif ID: 82
 Motif name: rmACAGCAGsr
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 8
 Similarity score: 0.0319191

Alignment:
 DVCTGCTGTVB
 ---TTCTSTST

Original motif Consensus sequence: VVACAGCAGVD



Reverse complement motif Consensus sequence: DVCTGCTGTVB



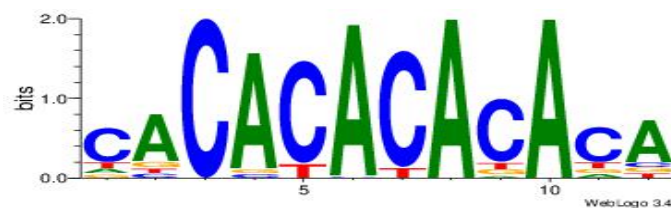
Dataset #: 4
 Motif ID: 95

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

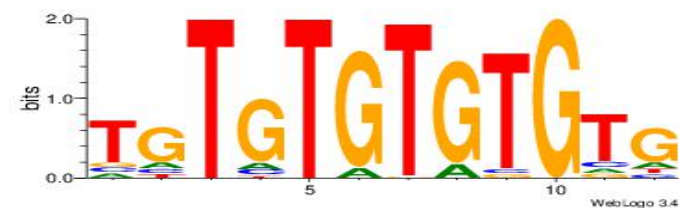
Alignment:

TGTGTGTGTGTG
 -TTCTSTST---

Original motif Consensus sequence: CACACACACACA



Reverse complement motif Consensus sequence: TGTGTGTGTGTG



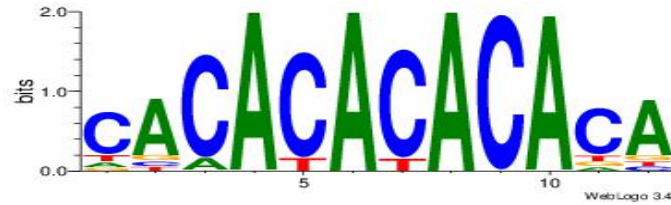
Dataset #:	4
Motif ID:	79
Motif name:	CACACACACACA
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	4
Number of overlap:	8
Similarity score:	0.0407034

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

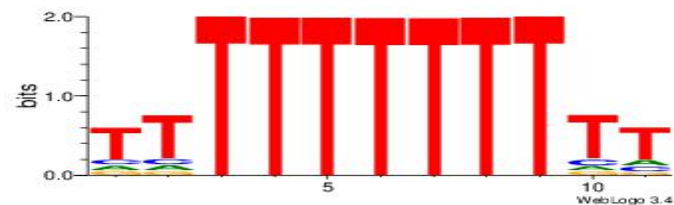
Alignment:

AAAAAAAAAAAA

ASASAGAA---

Original motif Consensus sequence: AAAAAAAAAA

Reverse complement motif Consensus sequence: TTTTTTTTTT

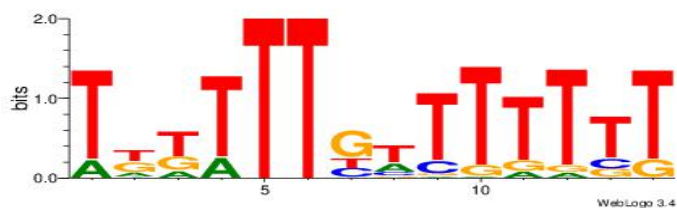


Dataset #: 2
 Motif ID: 26
 Motif name: Motif 26
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 5
 Number of overlap: 8
 Similarity score: 0.0451851

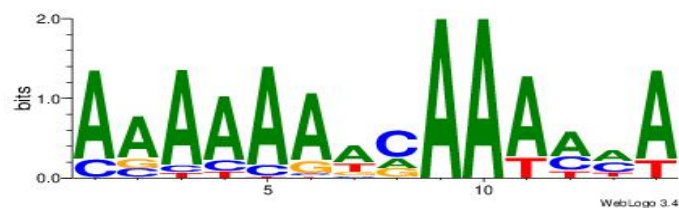
Alignment:

TKKTTTGTTTTTTT
 ----TTCTSTST--

Original motif Consensus sequence: TKKTTTGTTTTTTT



Reverse complement motif Consensus sequence: AAAAAACAAARR



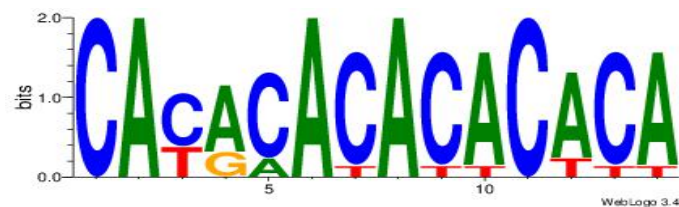
Dataset #: 2
 Motif ID: 27

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

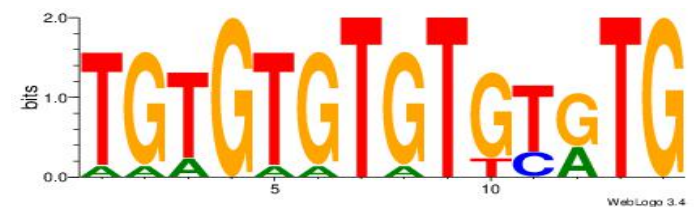
Alignment:

```
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:

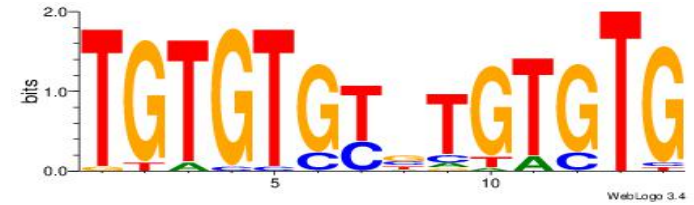
CACACAVRCACACA

-----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

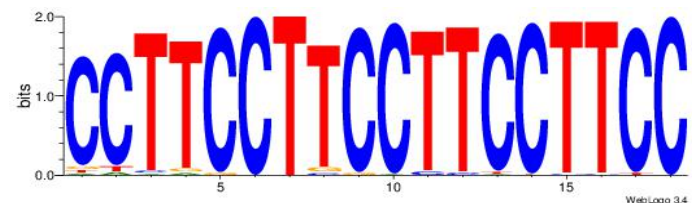
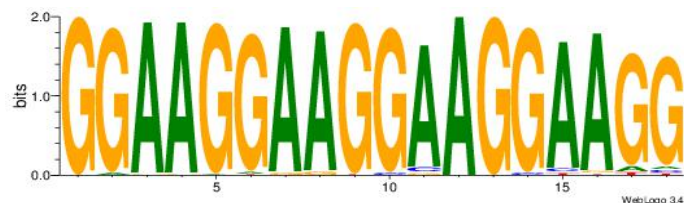
Alignment:

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



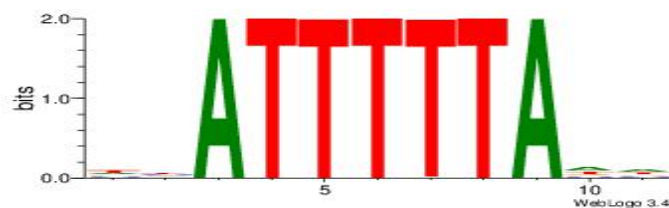
Reverse complement motif Consensus sequence: TATRTA



Dataset #: 4
 Motif ID: 85
 Motif name: wtATTTTAAww
 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: wyATTTTAAww
 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

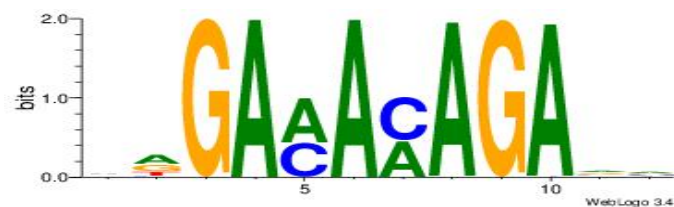
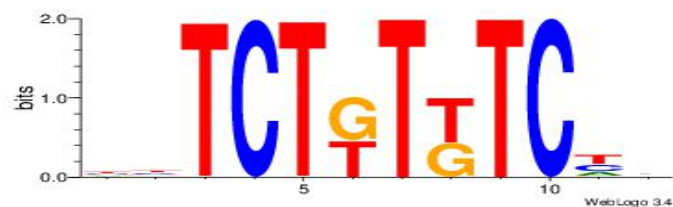


Dataset #: 4
Motif ID: 92
Motif name: tyTCTkTCTCyy
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 6
Number of overlap: 5
Similarity score: 0.0326182

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



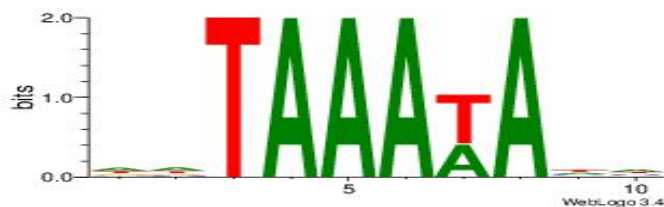
Dataset #: 4
 Motif ID: 83

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

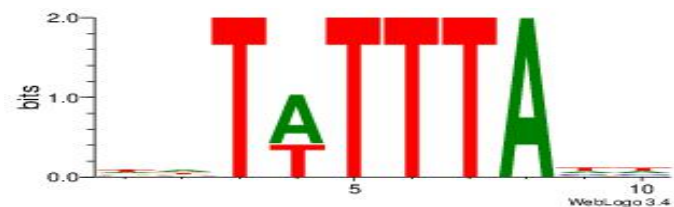
Alignment:

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:

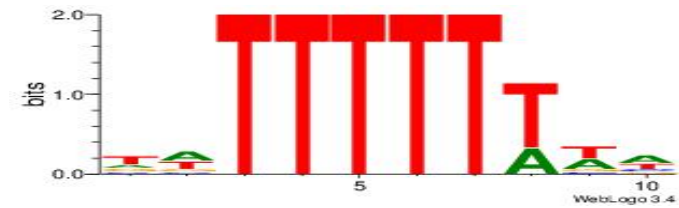
WWAAAAAAWH

-----RARAT-

Original motif Consensus sequence: WWAAAAAAWH



Reverse complement motif Consensus sequence: HWTTTTTTWW



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

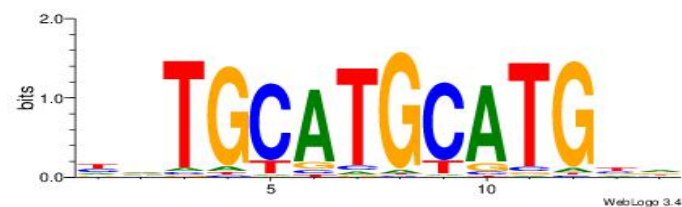
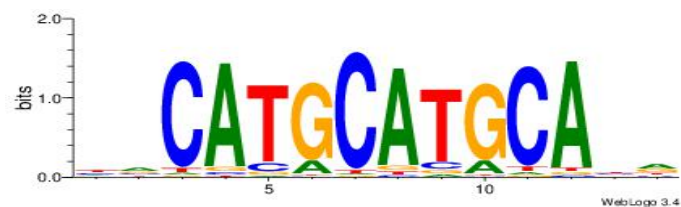
Alignment:

DVTGCATGCATGBH

-----ATKTM

Original motif Consensus sequence: HVCATGCATGCABD

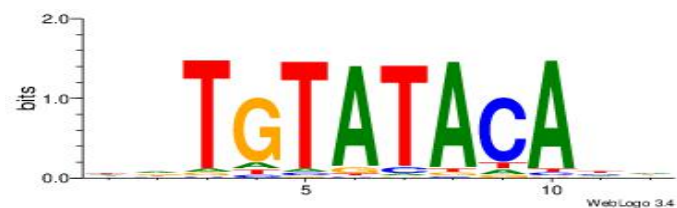
Reverse complement motif Consensus sequence: DVTGCATGCATGBH



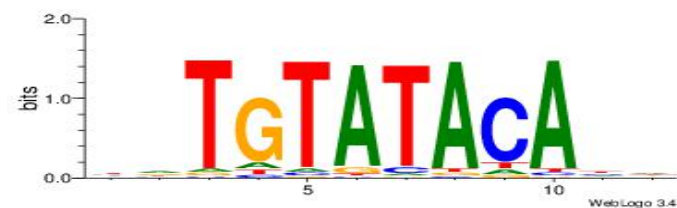
Dataset #: 4
 Motif ID: 100
 Motif name: wrTGTATACAw
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 5
 Similarity score: 0.0620607

Alignment:
 DHTGTATACADH
 -ATKTM-----

Original motif Consensus sequence: HDTGTATACAHD

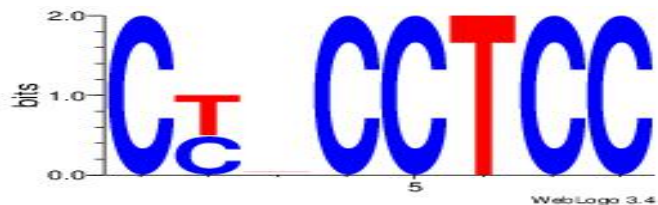


Reverse complement motif Consensus sequence: DHTGTATACADH



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)

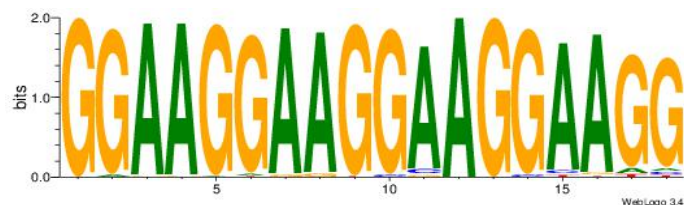
Dataset #: 3
 Motif ID: 48
 Motif name: EWSR1-FLI1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 6
 Number of overlap: 8
 Similarity score: 0.022644

Alignment:

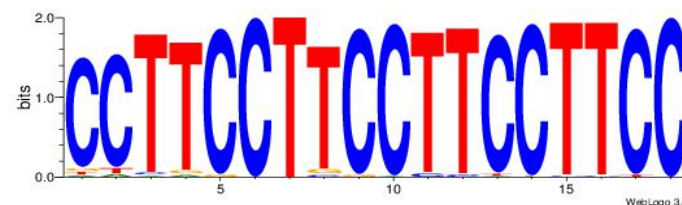
GGAAGGAAGGAAGGAAGG

-----GGAGGVMG-----

Original motif Consensus sequence: GGAAGGAAGGAAGGAAGG



Reverse complement motif Consensus sequence: CCTTCCTTCCTTCCTTC

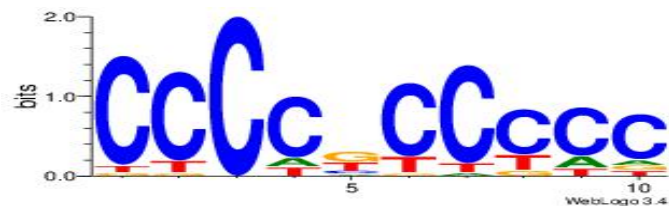


Dataset #: 3
 Motif ID: 32
 Motif name: SP1
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 8
 Similarity score: 0.0247246

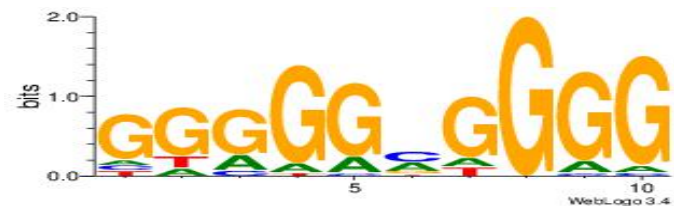
Alignment:

CCCCCKCCCC
 --CYBCCTCC

Original motif Consensus sequence: CCCCCKCCCC



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

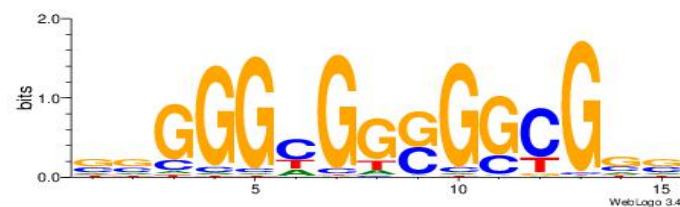
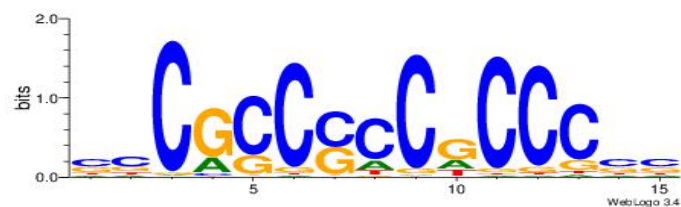


Dataset #: 4
Motif ID: 91
Motif name: ssCGCCsCCrCCCss
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 5
Number of overlap: 8
Similarity score: 0.0335629

Alignment:
SSCGCCSCCGCCSS
----CYBCCTCC----

Original motif Consensus sequence: SSCGCCSCCGCCSS

Reverse complement motif Consensus sequence:
SSGGGCGGSGGCGSS



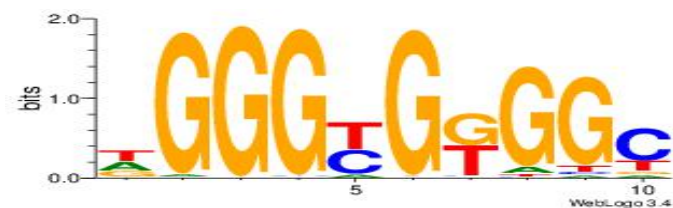
Dataset #: 3
 Motif ID: 52
 Motif name: Klf4
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 8
 Similarity score: 0.0354458

Alignment:

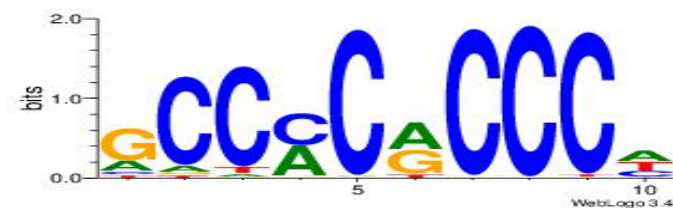
GCCYCMCCCD

-CYBCCTCC-

Original motif Consensus sequence: DGGGYGKGGC



Reverse complement motif Consensus sequence: GCCYCMCCCD

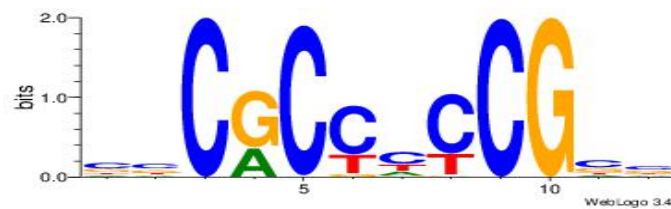


Dataset #: 4
 Motif ID: 88

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



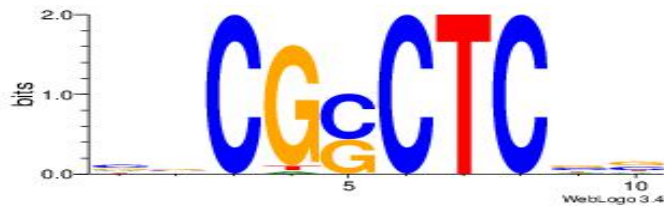
Dataset #: 4
 Motif ID: 73
 Motif name: ssCGsCTCcss
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 8
 Similarity score: 0.0472644

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

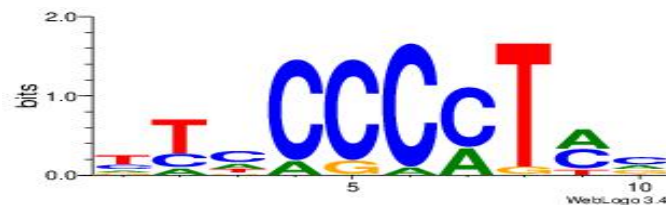
Alignment:

BTHCCCCTYB

--CYBCCTCC

Original motif Consensus sequence: BKAGGGGDAD

Reverse complement motif Consensus sequence: BTHCCCCTYB

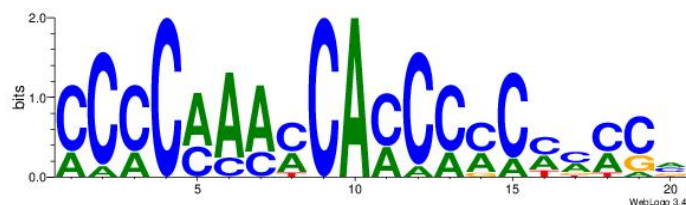


Dataset #: 3
 Motif ID: 34
 Motif name: RREB1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 5
 Number of overlap: 8
 Similarity score: 0.0528666

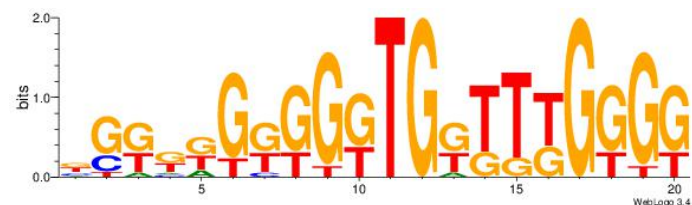
Alignment:

BGRRRGRGGRTGRTTYGGGG
 ----GGAGGVMG-----

Original motif Consensus sequence: CCCMAAMCAMCCMCMMMCV



Reverse complement motif Consensus sequence: BGRRRGRGGRTGRTTYGGGG

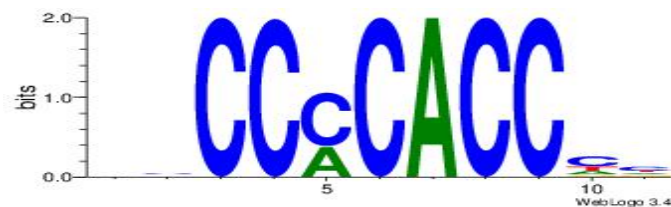


Dataset #: 4

Motif ID: 89
 Motif name: ccCCmCACcc
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 8
 Similarity score: 0.0549805

Alignment:
 HBCCMCACCHH
 -CYBCCTCC--

Original motif Consensus sequence: HBCCMCACCHH



Reverse complement motif Consensus sequence: DDGGTGRGGBD



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

Original motif Consensus sequence: CACACACA



Reverse complement motif Consensus sequence: TGTGTGTG

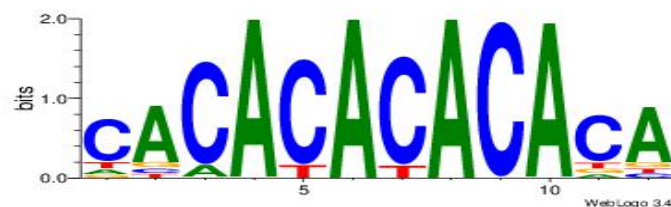


Best Matches for Top Significant Motif ID 2 (Highest to Lowest)

Dataset #: 4
 Motif ID: 79
 Motif name: CACACACACACA
 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:
 CACACACACACA
 --CACACACA--

Original motif Consensus sequence: CACACACACACA



Reverse complement motif Consensus sequence: TGTGTGTGTGTG

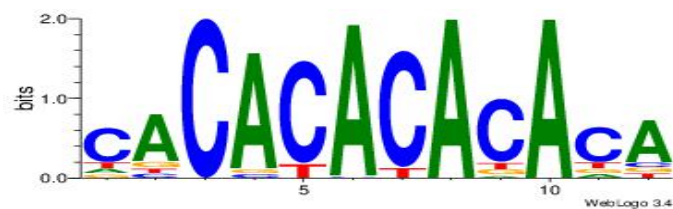


Dataset #: 4
 Motif ID: 95
 Motif name: CACACACACACA
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement

Direction: Forward
 Position number: 5
 Number of overlap: 8
 Similarity score: 0.0100991

Alignment:
 TGTGTGTGTGTG
 ----TGTGTGTG

Original motif Consensus sequence: CACACACACA



Reverse complement motif Consensus sequence: TGTGTGTGTG



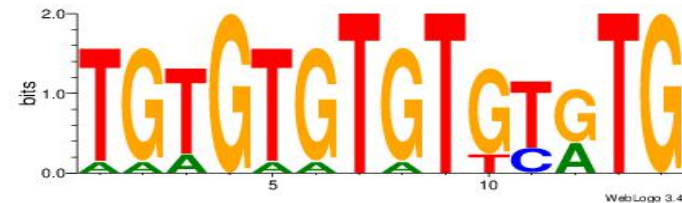
Dataset #: 2
 Motif ID: 27
 Motif name: Motif 27
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3
 Number of overlap: 8
 Similarity score: 0.0101254

Alignment:
 TGTGTGTGTGKTG
 --TGTGTGTG----

Original motif Consensus sequence: CAYACACACACACA



Reverse complement motif Consensus sequence: TGTGTGTGTGKT



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

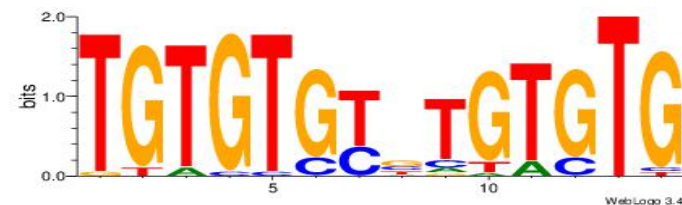
Alignment:

TGTGTGKVTGTGTG
TGTGTGTG-----

Original motif Consensus sequence: CACACAVRCACACA



Reverse complement motif Consensus sequence: TGTGTGKVTGTGT

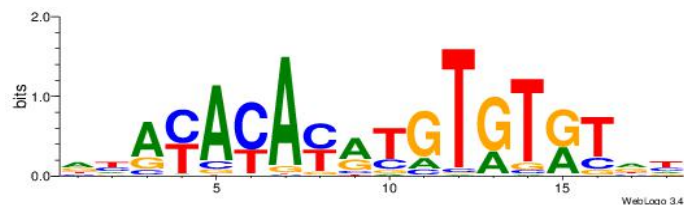


Dataset #: 4
 Motif ID: 97
 Motif name: ryayAyAyrTGTRTry
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 8
 Similarity score: 0.0393219

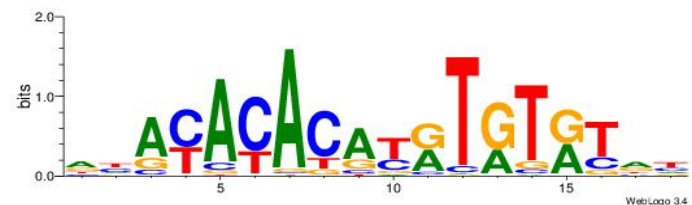
Alignment:

DHAYAYAYRTGTGTRTDH
 -----TGTGTGTG--

Original motif Consensus sequence: DHAYAYAYRTGTGTRTDH



Reverse complement motif Consensus sequence: HDAMACACAKKTKTKTHD

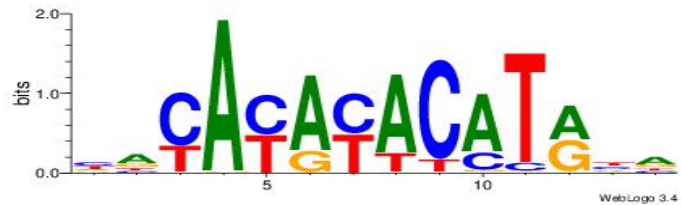


Dataset #: 4
 Motif ID: 75
 Motif name: yayAyAyACATrya
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3

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

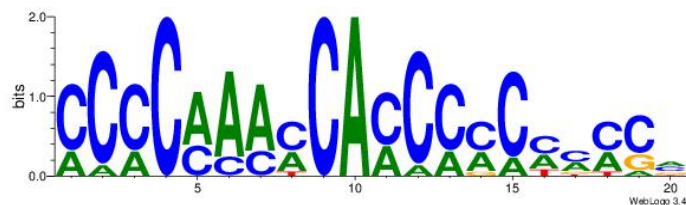
Alignment:

```

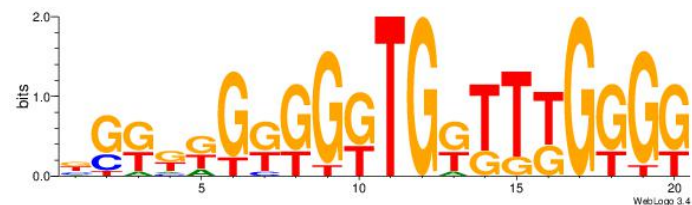
CCCCMAAMCAMCCMCMMMC
-----CACACACA-----

```

Original motif Consensus sequence: CCCCMAAMCAMCCMCMMMC



Reverse complement motif Consensus sequence: BGRRRGRGGRTGRTTYGGGG



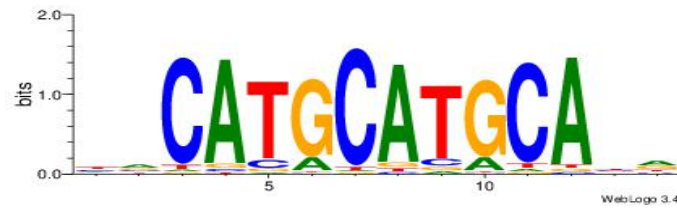
Dataset #:	4
Motif ID:	101
Motif name:	AAAAAAAAAA
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	7
Number of overlap:	8
Similarity score:	0.0764586

Alignment:

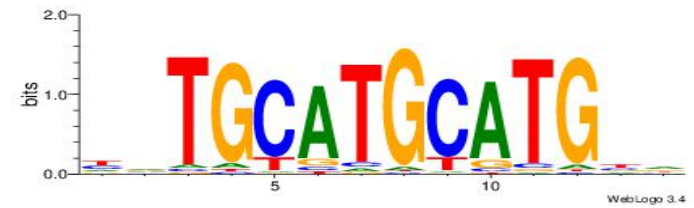
DVTGCATGCATGBH

-----TGTGTGTG

Original motif Consensus sequence: HVCATGCATGCABD



Reverse complement motif Consensus sequence: DVTGCATGCATGB



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

Original motif Consensus sequence: CTCTGY



Reverse complement motif Consensus sequence: KCAGAG



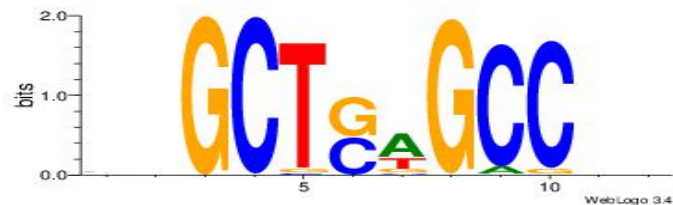
Best Matches for Top Significant Motif ID 20 (Highest to Lowest)

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

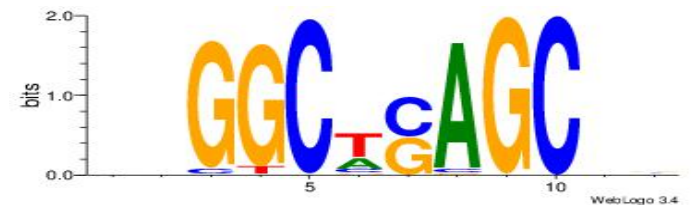
Number of overlap: 6
Similarity score: 0.0323407

Alignment:
VBGCTSAGCCHB
---CTCTGY---

Original motif Consensus sequence: VBGCTSAGCCHB



Reverse complement motif Consensus sequence: BDGGCTSAGCBV

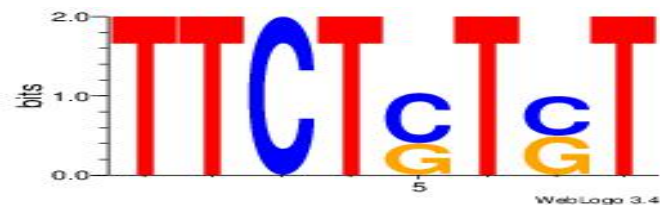


Dataset #: 1
Motif ID: 7
Motif name: Motif 7
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 6
Similarity score: 0.0352938

Alignment:
ASASAGAA
--KCAGAG

Original motif Consensus sequence: ASASAGAA

Reverse complement motif Consensus sequence: TTCTSTST

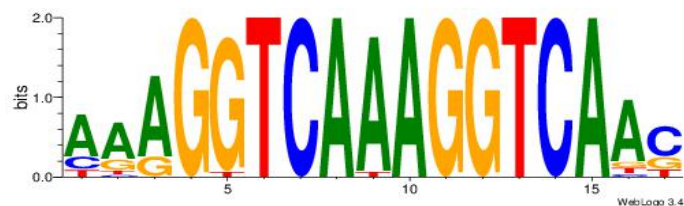


Dataset #: 3
 Motif ID: 59
 Motif name: NR1H2RXRA
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 7
 Number of overlap: 6
 Similarity score: 0.0398495

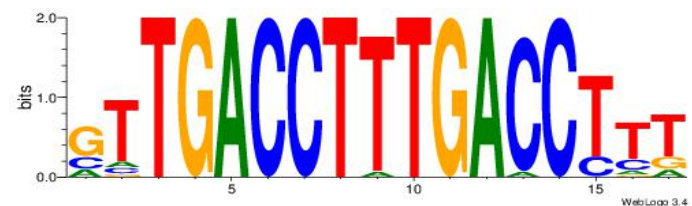
Alignment:

AAAGGTCAAAGGTCAAC
 -----KCAGAG-----

Original motif Consensus sequence: AAAGGTCAAAGGTCAAC



Reverse complement motif Consensus sequence: GTTGACCTTTGACCTT



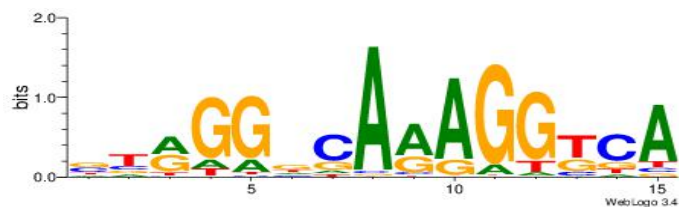
Dataset #: 3

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

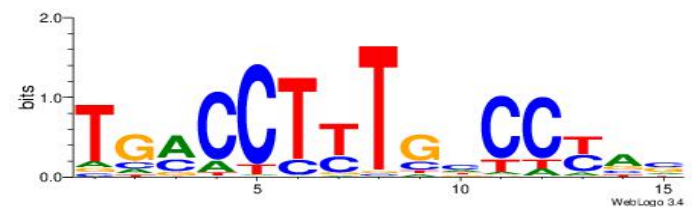
Alignment:

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

Original motif Consensus sequence: BTRGGDCARAGGKCA



Reverse complement motif Consensus sequence: TGRCCCTKGHCCK



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

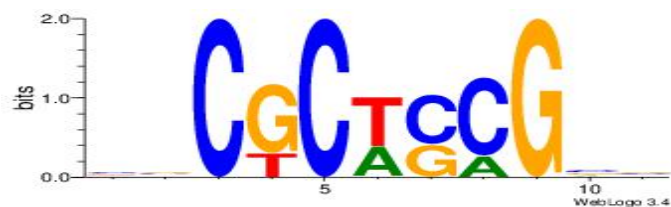


Dataset #:	4
Motif ID:	72
Motif name:	ssCKCwsCGss
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2
Number of overlap:	6
Similarity score:	0.0439226

Alignment:
BVCGCWSCGBV
----CTCTGY-

Original motif Consensus sequence: BVCGCWSCGBV

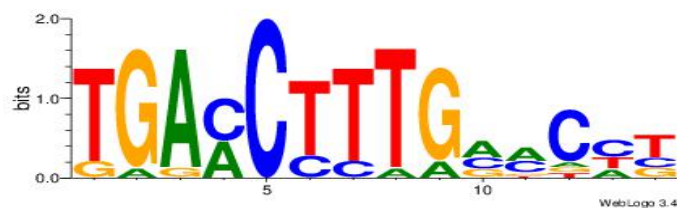
Reverse complement motif Consensus sequence: VBCGSWGCGVB



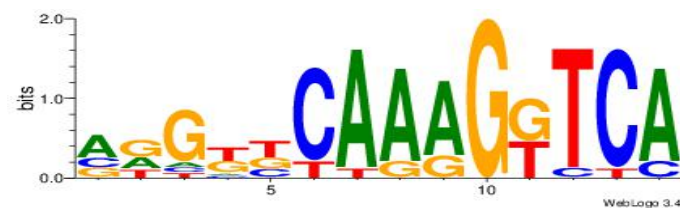
Dataset #: 3
 Motif ID: 38
 Motif name: NR2F1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 5
 Number of overlap: 6
 Similarity score: 0.0462597

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

Original motif Consensus sequence: TGAMCTTTGMMCYT



Reverse complement motif Consensus sequence: AKGYCAAAGRTCA

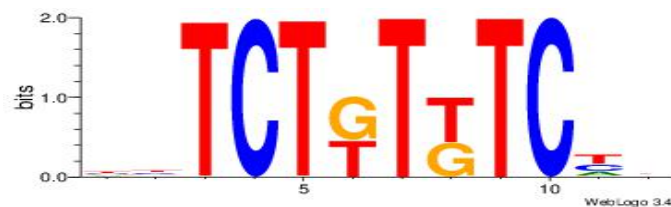


Dataset #: 4
 Motif ID: 92

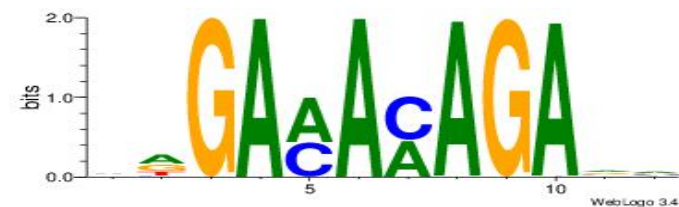
Motif name: tyTCTkTkTCyy
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 6
 Similarity score: 0.0467436

Alignment:
 BBTCTKTKTCHB
 -CTCTGY-----

Original motif Consensus sequence: BBTCTKTKTCHB



Reverse complement motif Consensus sequence: VHGARAYAGAVV



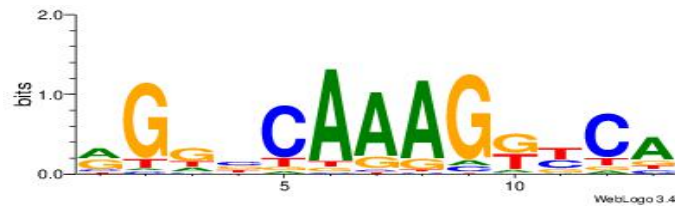
Dataset #: 3
 Motif ID: 50
 Motif name: HNF4A
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 6
 Similarity score: 0.0481824

Alignment:

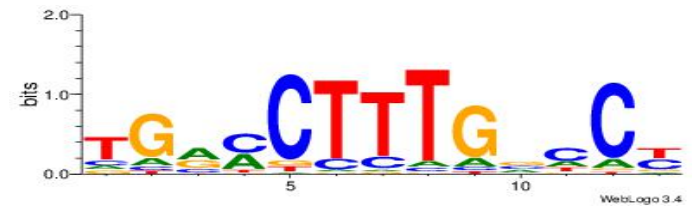
RGGBCAAAGKYCA

---KCAGAG----

Original motif Consensus sequence: RGGBCAAAGKYCA



Reverse complement motif Consensus sequence: TGM YCTTTGBCK



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: GCGGACGTTV



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

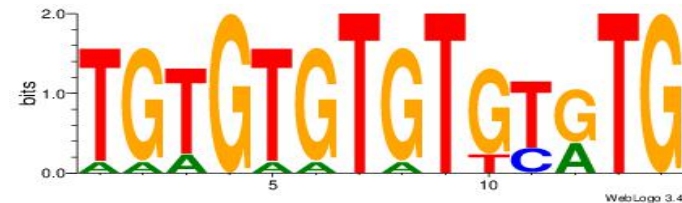
Alignment:

```
TGTGTGTGTTKTG
-----YGCGTG--
```


Original motif Consensus sequence: CAYACACACACACA



Reverse complement motif Consensus sequence: TGTGTGTGTGKT

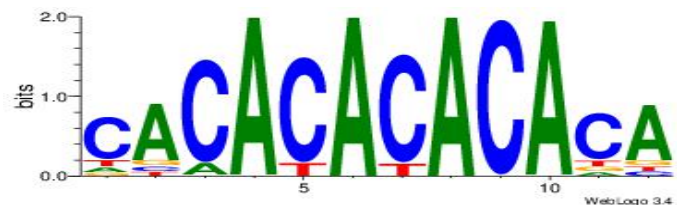


Dataset #: 4
 Motif ID: 79
 Motif name: CACACACACACA
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 7
 Number of overlap: 6
 Similarity score: 0.0420782

Alignment:

TGTGTGTGTGTG
 YGCGTG-----

Original motif Consensus sequence: CACACACACACA



Reverse complement motif Consensus sequence: TGTGTGTGTGTG

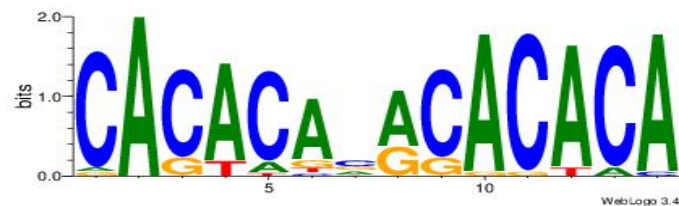


Dataset #: 2
 Motif ID: 25
 Motif name: Motif 25
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 6
 Similarity score: 0.0430749

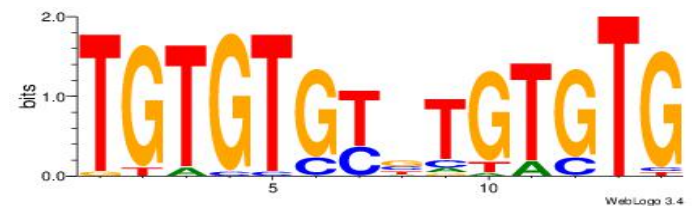
Alignment:

CACACAVRCACACA
 -----CACGCM

Original motif Consensus sequence: CACACAVRCACACA



Reverse complement motif Consensus sequence: TGTGTGKVTGTGT



Dataset #: 4
 Motif ID: 101
 Motif name: AAAAAAAAAA
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 6

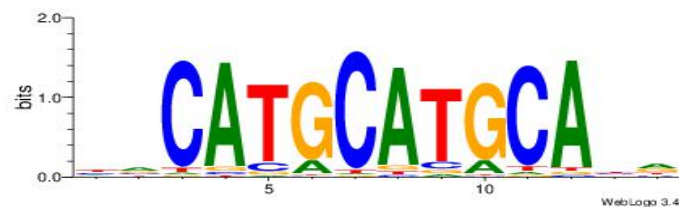
Similarity score: 0.043218

Alignment:

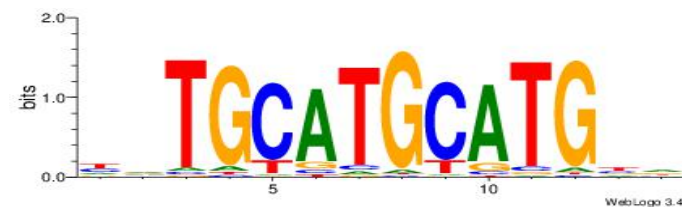
HVCATGCATGCABD

--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

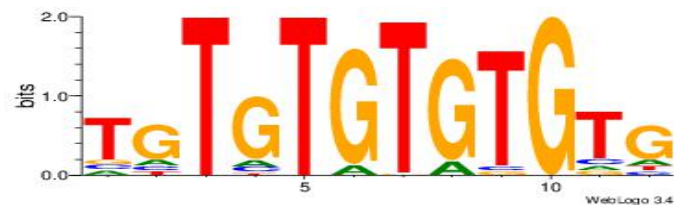
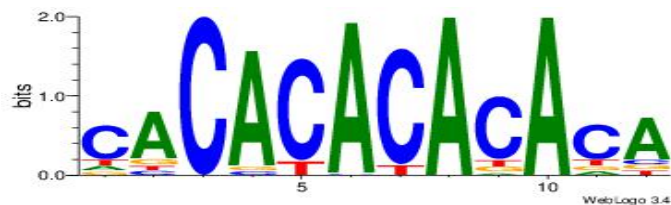
Alignment:

TGTGTGTGTGTG

----YGCGTG--

Original motif Consensus sequence: CACACACACACA

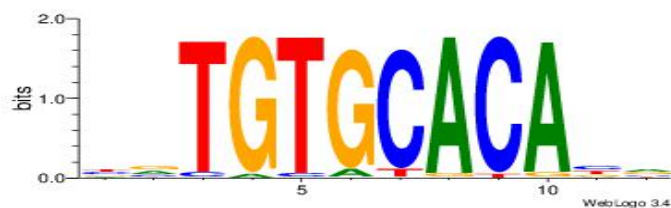
Reverse complement motif Consensus sequence: TGTGTGTGTGTG



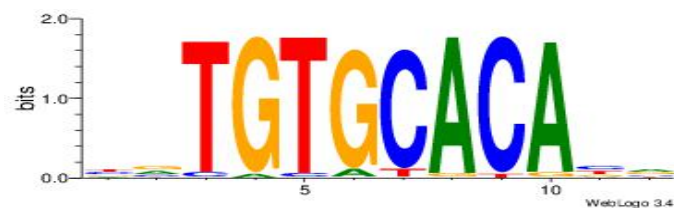
Dataset #: 4
 Motif ID: 96
 Motif name: yrTGTGCACAYr
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 7
 Number of overlap: 6
 Similarity score: 0.0477579

Alignment:
 BVTGTGCACABV
 YGCGTG-----

Original motif Consensus sequence: BVTGTGCACABV



Reverse complement motif Consensus sequence: BBTGTGCACAVV



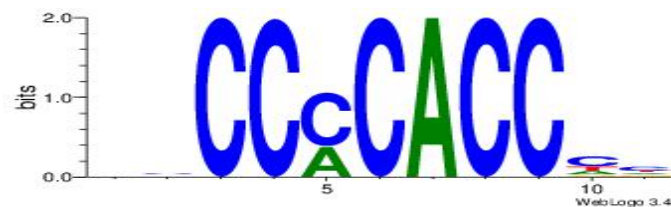
Dataset #: 4
 Motif ID: 89

Motif name:	ccCCmCACcc
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:

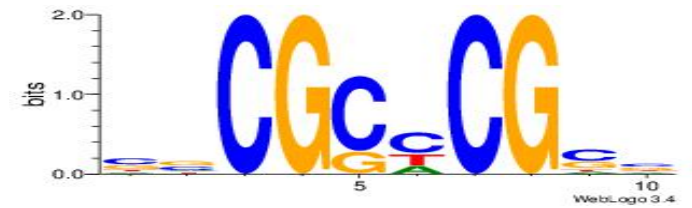
VBCGCMCGSV

----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

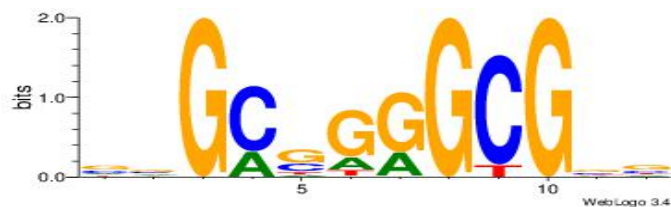
Reverse complement motif Consensus sequence: TGTGTGTG



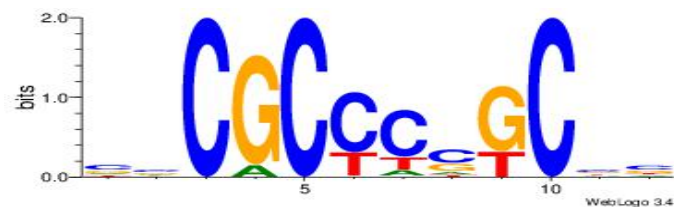
Dataset #: 4
 Motif ID: 67
 Motif name: ssGMsGRGCGss
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 7
 Number of overlap: 6
 Similarity score: 0.0538134

Alignment:
 BBCGCCSGCVV
 CACGCM-----

Original motif Consensus sequence: VVGCSGGGCGBB



Reverse complement motif Consensus sequence: BBCGCCSGCVV



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)

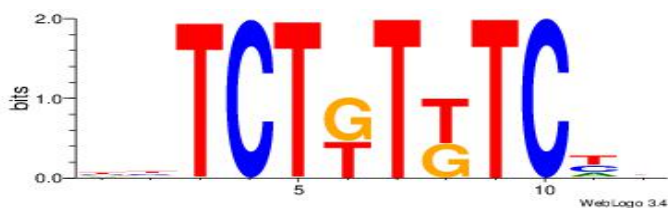
Dataset #: 4
 Motif ID: 92
 Motif name: tyTCTkTKTCyy
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3
 Number of overlap: 8
 Similarity score: 0.0131318

Alignment:

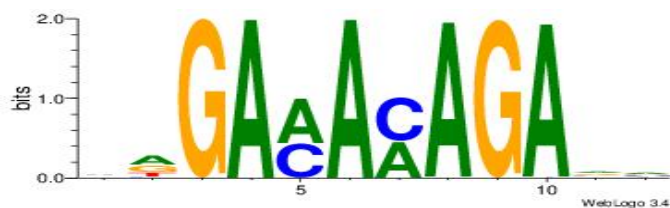
VHGARAYAGAVV

--GAGRCAGR--

Original motif Consensus sequence: BBTCTKTKTCHB



Reverse complement motif Consensus sequence: VHGARAYAGAVV



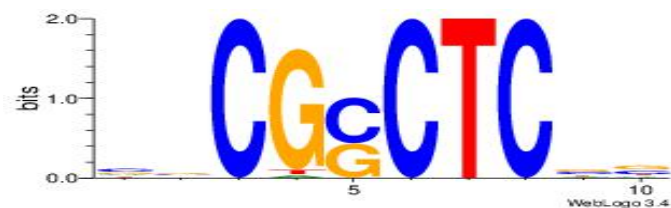
Dataset #: 4
 Motif ID: 73
 Motif name: ssCGsCTC_{ss}
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3
 Number of overlap: 8
 Similarity score: 0.0334555

Alignment:

BBGAGSCGVV

--GAGRCAGR

Original motif Consensus sequence: VVCGSCTCBB



Reverse complement motif Consensus sequence: BBGAGSCGVV

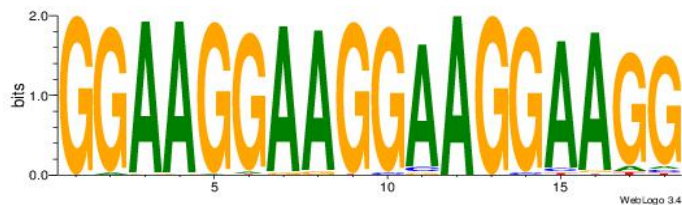


Dataset #: 3
 Motif ID: 48
 Motif name: EWSR1-FLI1
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 7
 Number of overlap: 8

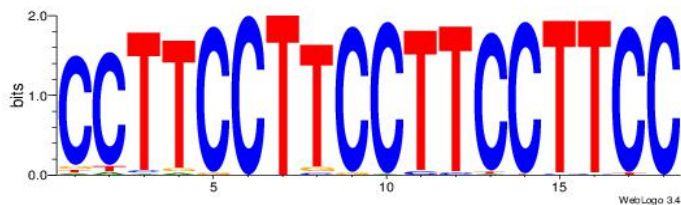
Similarity score: 0.0397014

Alignment:
GGAAGGAAGGAAGGAAGG
-----GAGRCAGR-----

Original motif Consensus sequence: GGAAGGAAGGAAGGAAGG



Reverse complement motif Consensus sequence:
CCTTCCTTCCTTCCTTCC

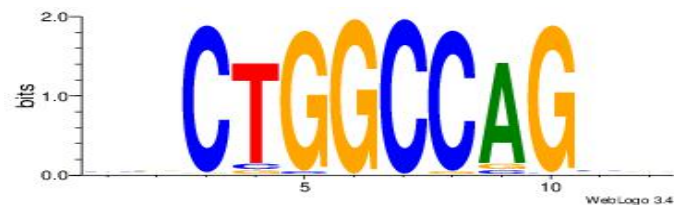
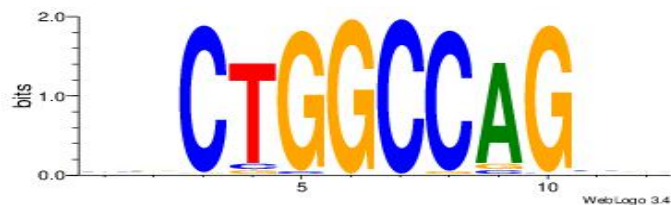


Dataset #: 4
Motif ID: 99
Motif name: sgCTGGCCAGcs
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 2
Number of overlap: 8
Similarity score: 0.0475948

Alignment:
VVCTGGCCAGBB
-MCTGKCTC---

Original motif Consensus sequence: BBCTGGCCAGVV

Reverse complement motif Consensus sequence: VVCTGGCCAGBB

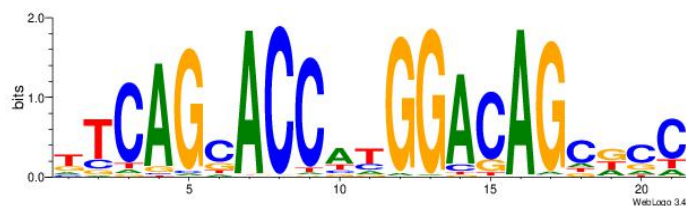


Dataset #: 3
 Motif ID: 35
 Motif name: REST
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 4
 Number of overlap: 8
 Similarity score: 0.049302

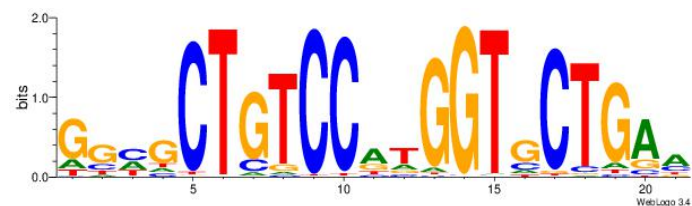
Alignment:

GYGCTGTCCATGGTGCTGAA
 ---MCTGKCTC-----

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC



Reverse complement motif Consensus sequence: GYGCTGTCCATGGTGCTGAA



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:

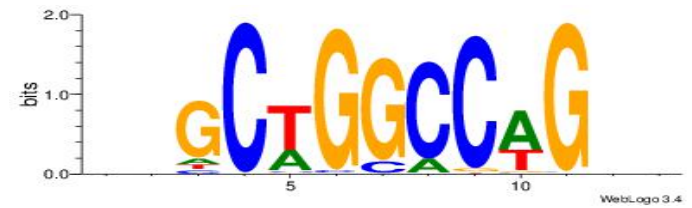
BBCWGGCCAGCBB

-MCTGKCTC-----

Original motif Consensus sequence: BBCWGGCCAGCBB



Reverse complement motif Consensus sequence: BBGCTGGCCWGB



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

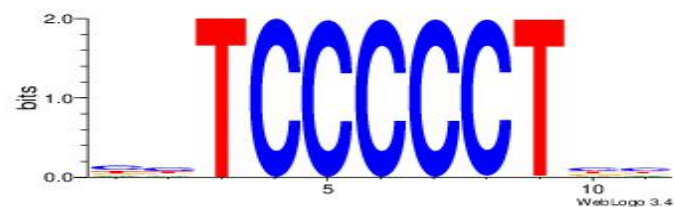
Alignment:

VVAGGGGGAVV

---GAGRCAGR

Original motif Consensus sequence: VVAGGGGGAVV

Reverse complement motif Consensus sequence: VVCCCCCTVV

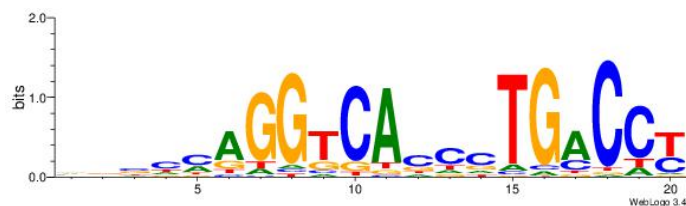


Dataset #: 3
 Motif ID: 45
 Motif name: ESR1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 13
 Number of overlap: 8
 Similarity score: 0.055859

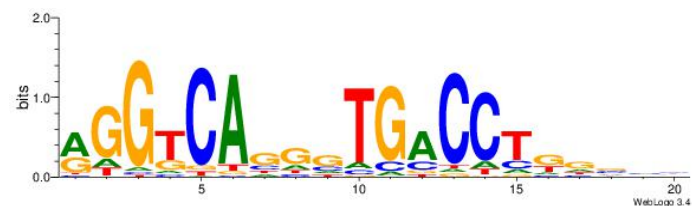
Alignment:

VDBHMAGGTCACCCTGACCY
 -----MCTGKCTC

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV

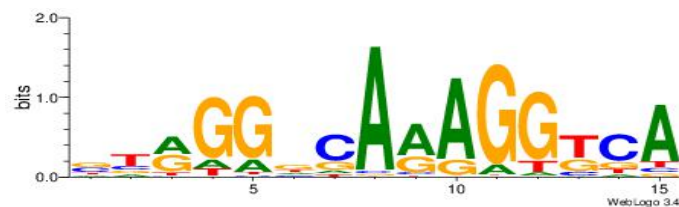


Dataset #: 3

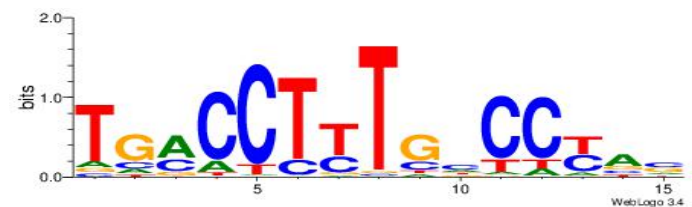
Motif ID: 36
 Motif name: PPARGRXRA
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 4
 Number of overlap: 8
 Similarity score: 0.0596402

Alignment:
 TGRCCCTKTGHCCKAB
 ---MCTGKCTC----

Original motif Consensus sequence: BTRGGDCARAGGKCA



Reverse complement motif Consensus sequence: TGRCCCTKTGHCCK



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

Original motif Consensus sequence: GCRCACRC



Reverse complement motif Consensus sequence: GKG TGKGC



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

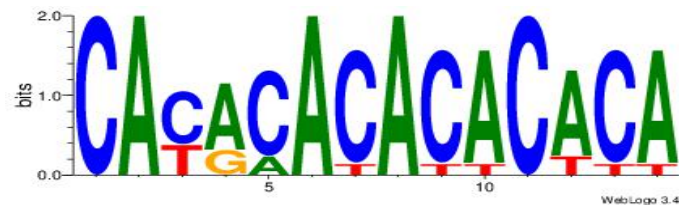
Dataset #: 2
 Motif ID: 27
 Motif name: Motif 27
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 8
 Similarity score: 0.0307099

Alignment:

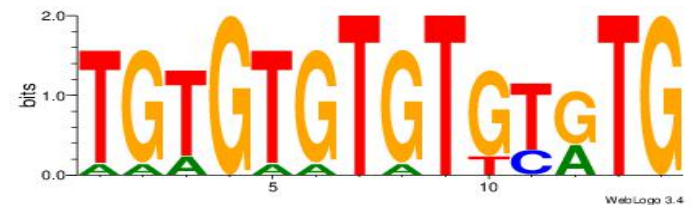
CAYACACACACACA

---GCRACACRC---

Original motif Consensus sequence: CAYACACACACACA



Reverse complement motif Consensus sequence: TGTGTGTGTGKT

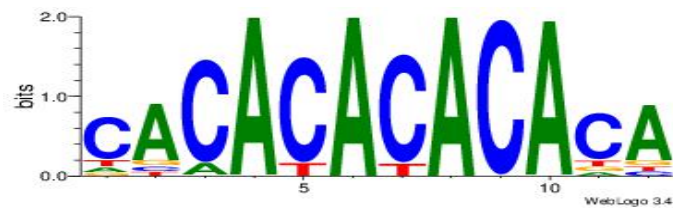


Dataset #: 4
 Motif ID: 79
 Motif name: CACACACACACA
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif

Direction: Backward
Position number: 4
Number of overlap: 8
Similarity score: 0.0357914

Alignment:
CACACACACACA
-GCRCACRC---

Original motif Consensus sequence: CACACACACACA



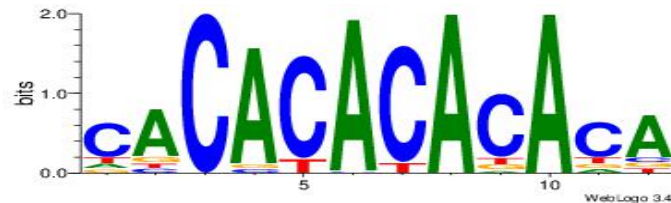
Reverse complement motif Consensus sequence: TGTGTGTGTG



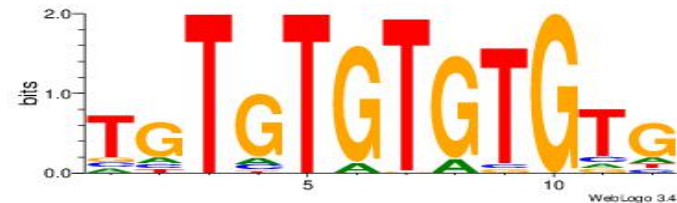
Dataset #: 4
Motif ID: 95
Motif name: CACACACACACA
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 4
Number of overlap: 8
Similarity score: 0.0366948

Alignment:
CACACACACACA
-GCRCACRC---

Original motif Consensus sequence: CACACACACA



Reverse complement motif Consensus sequence: TGTGTGTGTG

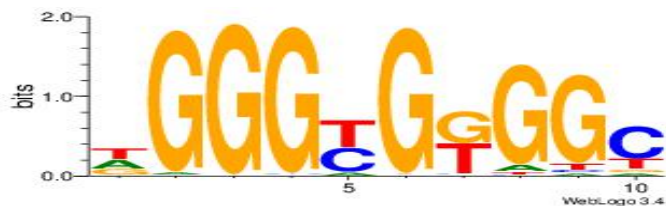


Dataset #: 3
 Motif ID: 52
 Motif name: Klf4
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 8
 Similarity score: 0.03983

Alignment:

DGGGYGKGGC
 -GKGTGKGC-

Original motif Consensus sequence: DGGGYGKGGC



Reverse complement motif Consensus sequence: GCCYCMCCCD

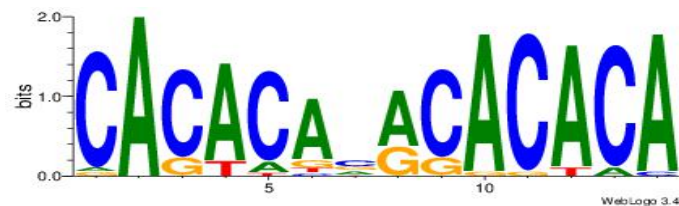


Dataset #: 2
 Motif ID: 25
 Motif name: Motif 25
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 8
 Similarity score: 0.0418776

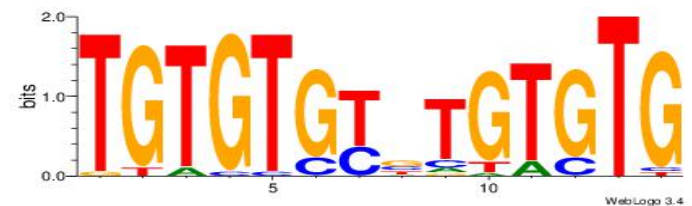
Alignment:

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:
HCGGTGGGCGK
-GKGTGKGC--

Original motif Consensus sequence: HCGGTGGGCGK



Reverse complement motif Consensus sequence: YCGCCACGCH

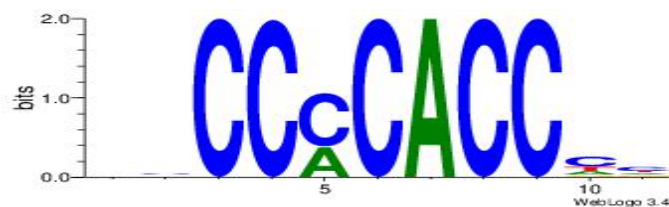


Dataset #: 4
Motif ID: 89
Motif name: ccCCmCACcc
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 2
Number of overlap: 8
Similarity score: 0.0505252

Alignment:
DDGGTGRGGBD
-GKGTGKGC--

Original motif Consensus sequence: HBCCMCACCHH

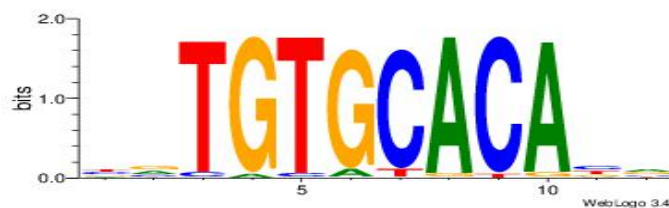
Reverse complement motif Consensus sequence: DDGGTGRGGBD



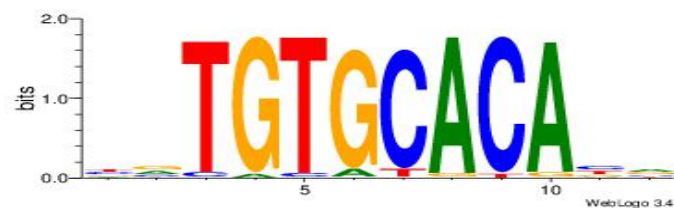
Dataset #: 4
 Motif ID: 96
 Motif name: yrTGTGCACAYr
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 8
 Similarity score: 0.0537384

Alignment:
 BVTGTGCACABV
 ---GCRRCACRC-

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

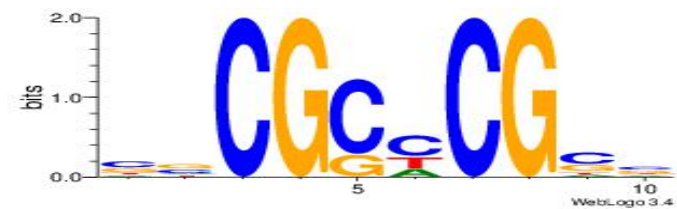
Alignment:

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:

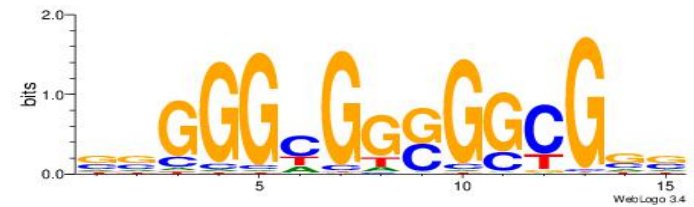
SSCGCCSCCGCCSS

---GCRACRC----

Original motif Consensus sequence: SSCGCCSCCGCCSS



Reverse complement motif Consensus sequence: SSGGGCGGSGGCGSS



Results created by MOTIFSIM on 09-23-2015 13:07:14

Runtime: 146.584 seconds.

MOTIFSIM is written by Ngoc Tam L. Tran

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