



MOTIFSIM - MOTIF SIMilarity Detection Tool

Version 2.2

INPUT

Input Parameters

Number of files:	5
Number of top significant motifs:	5
Number of best matches:	5
Similarity cutoff \geq	0.75
Matching motif database:	UniProbe Mus Musculus
Motif tree:	Yes
Combined similar motifs:	Yes
Output file type:	All
Output file format:	All

Input files and motif counts

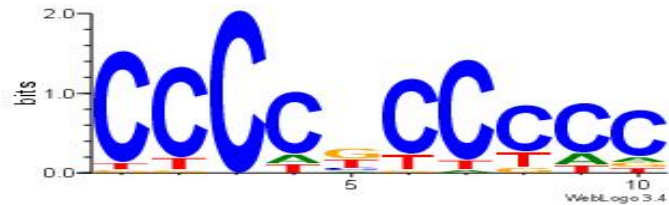
File name	Count of motifs	Dataset number
DREME_DM230.txt	1	1
MEME_DM230.txt	20	2
PScanChIP_DM230.txt	14	3
RSAT_peak-motifs_DM230.txt	10	4
W-ChIPMotifs_DM230.txt	11	5

RESULTS

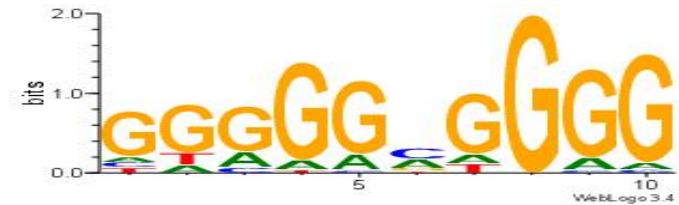
Top 5 Significant Motifs - Global Matching (Highest to Lowest)

Dataset #: 3 Motif ID: 24 Motif name: SP1

Original motif Consensus sequence: CCCCKCCCC



Reverse complement motif Consensus sequence: GGGGGYGGGG



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

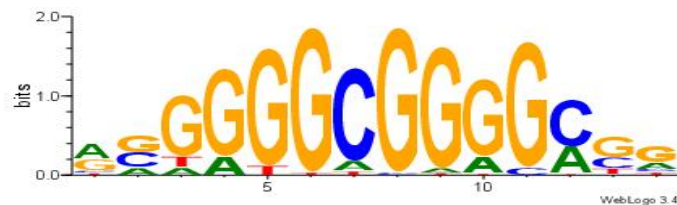
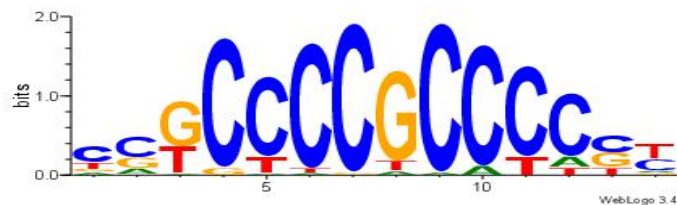
Dataset #:	2
Motif ID:	7
Motif name:	Motif 7
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2
Number of overlap:	10
Similarity score:	0.00451594

Alignment:

```
CSKCCCCGCCCSY  
---CCCCKCCCC-
```

Original motif Consensus sequence: CSKCCCCGCCCSY

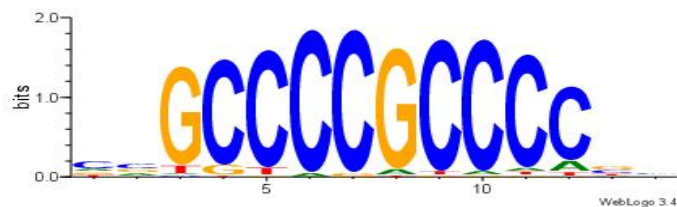
Reverse complement motif Consensus sequence: MSGGGCGGGGY



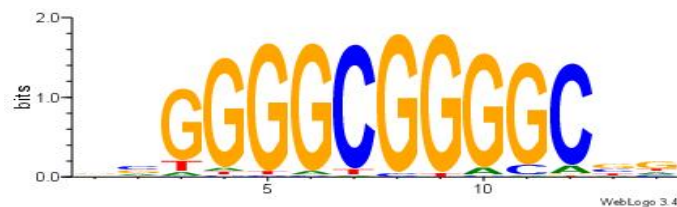
Dataset #: 4
 Motif ID: 36
 Motif name: csGCCCCGCCCCsc
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 10
 Similarity score: 0.00965796

Alignment:
 HVGCCCCGCCCCBB
 ---CCCCKCCCC-

Original motif Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGCGGGGC

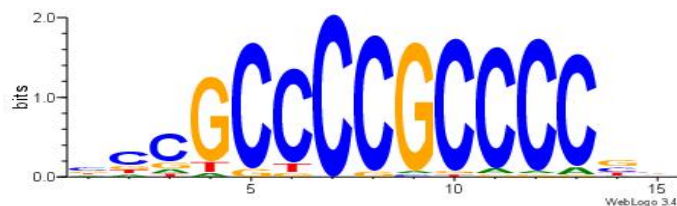


Dataset #: 4
 Motif ID: 38

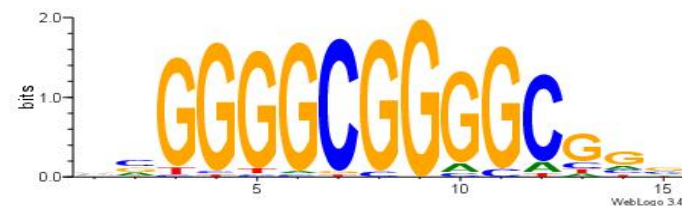
Motif name: cccGCCCCGCCCCsb
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 5
 Number of overlap: 10
 Similarity score: 0.0127292

Alignment:
 BCCGCCCCGCCCCBB
 ----CCCCKCCCC--

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB

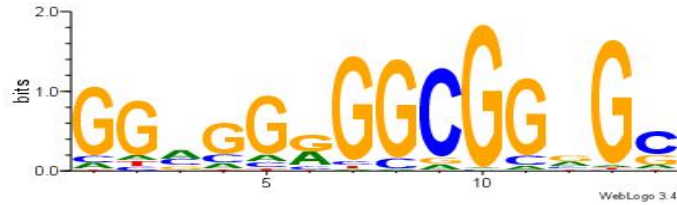


Dataset #: 5
 Motif ID: 50
 Motif name: TFF11
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 10
 Similarity score: 0.0174405

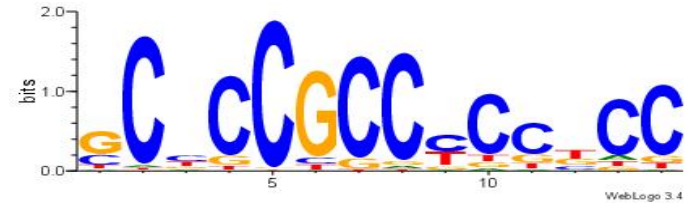
Alignment:

GGMGGRGGCGGVGC
---GGGGYGGGG---

Original motif Consensus sequence: GGMGGRGGCGGVGC



Reverse complement motif Consensus sequence: GCVCCGCCMCCYGC



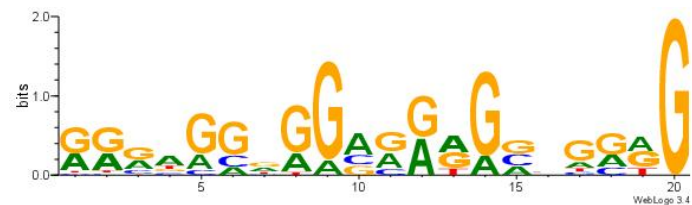
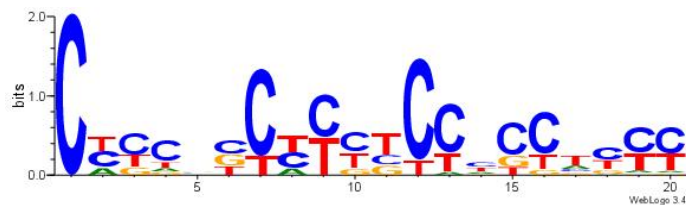
Dataset #: 5
Motif ID: 54
Motif name: TFM12
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 7
Number of overlap: 10
Similarity score: 0.0301548

Alignment:

CYCBBCYYYTCCHCCTYYY
-----CCCCKCCCC-----

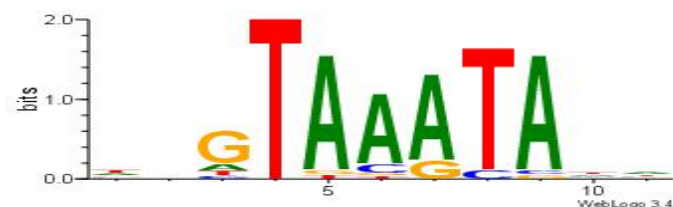
Original motif Consensus sequence: CYCBBCYYYTCCHCCTYYY

Reverse complement motif Consensus sequence:
KKKAGGDGGAKKMGBBGKMG

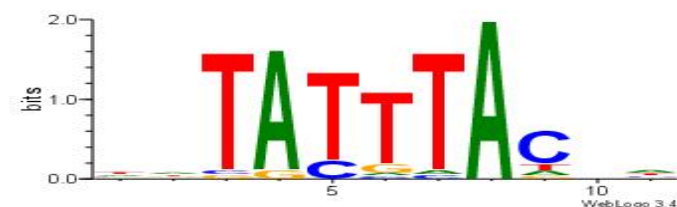


Dataset #: 4 Motif ID: 45 Motif name: wbgTAAATAww

Original motif Consensus sequence: DBGTAATAHD



Reverse complement motif Consensus sequence: DHTATTTACBD



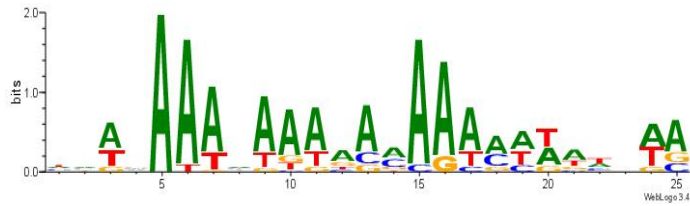
Best Matches for Top Significant Motif ID 45 (Highest to Lowest)

Dataset #:	5
Motif ID:	56
Motif name:	TFM11
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	15
Number of overlap:	11
Similarity score:	0.0192768

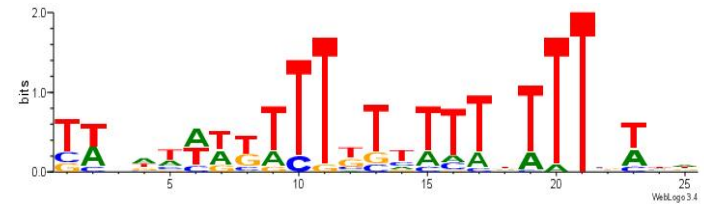
Alignment:

```
TWVHWWWYTTTYTTTTHTTTVWBH
-----DHTATTTACBD
```

Original motif Consensus sequence:
 HDWVAAAHAAAAAMAAAMWWWHBWA



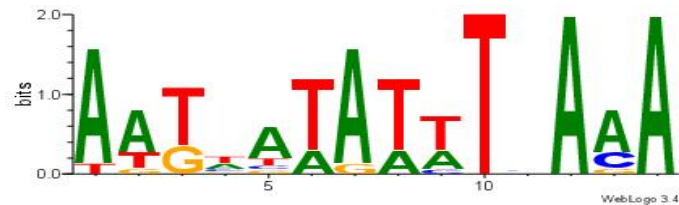
Reverse complement motif Consensus sequence:
 TWVHWWWYTTTTYTTTTHTTTTVWBH



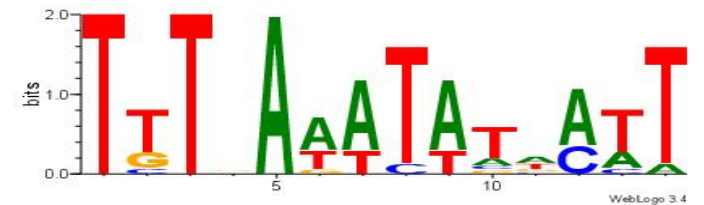
Dataset #: 2
 Motif ID: 9
 Motif name: Motif 9
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 4
 Number of overlap: 11
 Similarity score: 0.0250541

Alignment:
 AATHATATWTHAAA
 DHTATTTACBD---

Original motif Consensus sequence: AATHATATWTHAAA



Reverse complement motif Consensus sequence: TTTDAWATATHAT



Dataset #: 2
 Motif ID: 6
 Motif name: Motif 6
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.027895

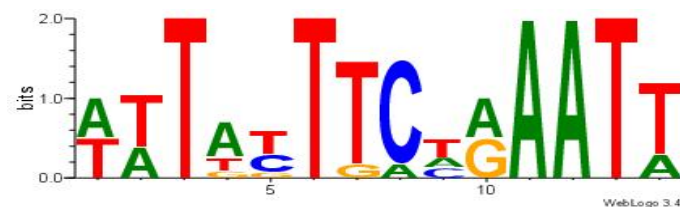
Alignment:

AATTYDGAARTAWW
 ---DBGTAAATAHD

Original motif Consensus sequence: AATTYDGAARTAWW



Reverse complement motif Consensus sequence: WWTAKTTCDKAAT



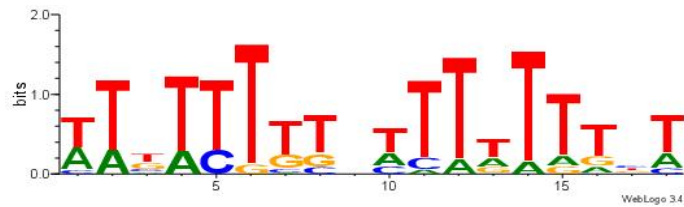
Dataset #: 5
 Motif ID: 52
 Motif name: TFM1
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 11

Similarity score: 0.0283217

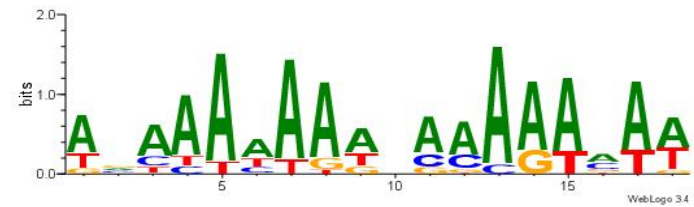
Alignment:

ABAAAAAWhAAAAARAW
DBGTAATAHD-----

Original motif Consensus sequence: WTKTTTTTHWTTTTTTBT



Reverse complement motif Consensus sequence:
ABAAAAAWhAAAAARAW



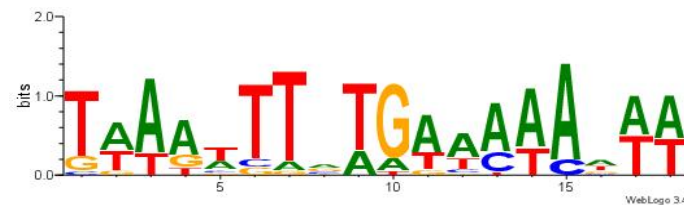
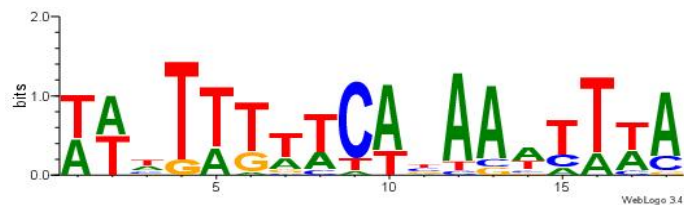
Dataset #: 5
Motif ID: 53
Motif name: TFM3
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 2
Number of overlap: 11
Similarity score: 0.0308097

Alignment:

TWAAWTTVTGAAAAHWW
-----DBGTAATAHD-

Original motif Consensus sequence: WWHTTTTTTCABAATTWA

Reverse complement motif Consensus sequence:
TWAAWTTVTGAAAAHWW

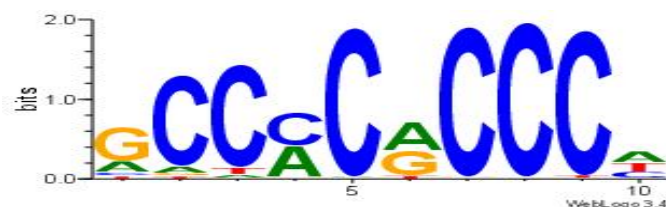


Dataset #: 3 Motif ID: 27 Motif name: Klf4

Original motif Consensus sequence: DGGYGKGGC



Reverse complement motif Consensus sequence: GCCYCMCCCD

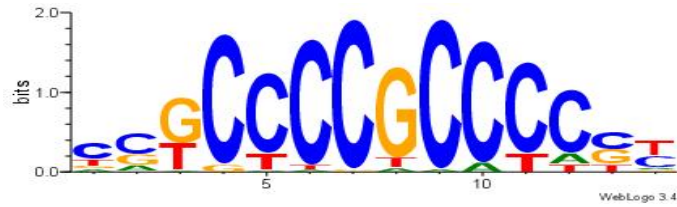


Best Matches for Top Significant Motif ID 27 (Highest to Lowest)

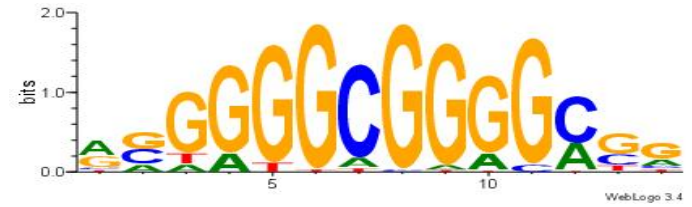
Dataset #:	2
Motif ID:	7
Motif name:	Motif 7
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	3
Number of overlap:	10
Similarity score:	0.0152457

Alignment:
 CSKCCCCGCCCSY
 --GCCYCMCCCD--

Original motif Consensus sequence: CSKCCCCGCCCCSY



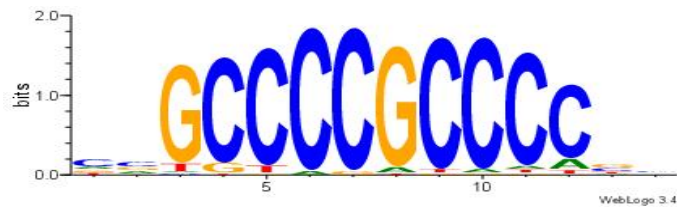
Reverse complement motif Consensus sequence: MSGGGCGGGGY



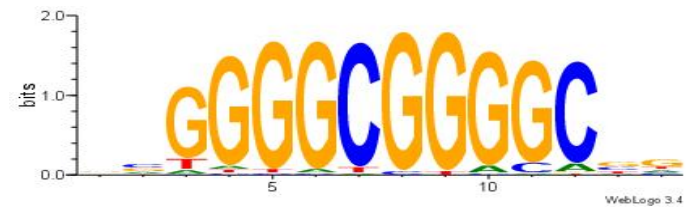
Dataset #: 4
Motif ID: 36
Motif name: csGCCCCGCCCCsc
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 3
Number of overlap: 10
Similarity score: 0.0160185

Alignment:
BBGGGGCGGGGCVD
--DGGGYGKGGC--

Original motif Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGC

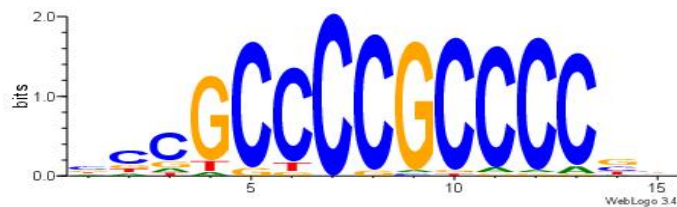


Dataset #: 4
 Motif ID: 38
 Motif name: cccGCCCCGCCCCsb
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3
 Number of overlap: 10
 Similarity score: 0.0194893

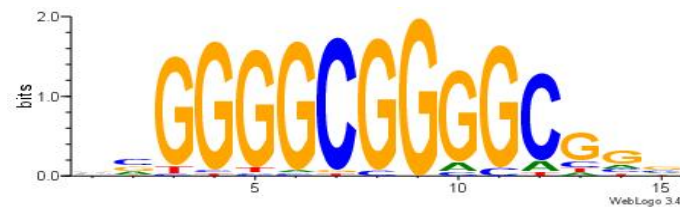
Alignment:

BBGGGGCGGGGCGGB
 --DGGGYGKGGC---

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB



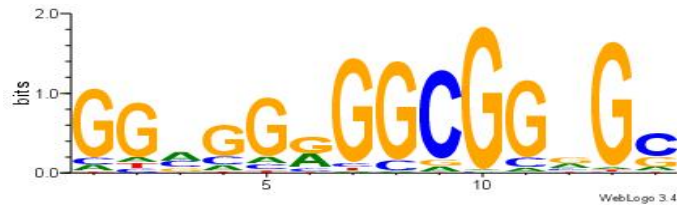
Dataset #: 5
 Motif ID: 50
 Motif name: TFF11
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 5

Number of overlap: 10
Similarity score: 0.0402906

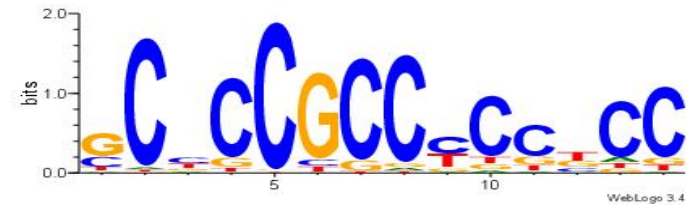
Alignment:

GGMGGRGGCGGVGC
----DGGGYGKGGC

Original motif Consensus sequence: GGMGGRGGCGGVGC



Reverse complement motif Consensus sequence: GCVCCGCCMCCYC



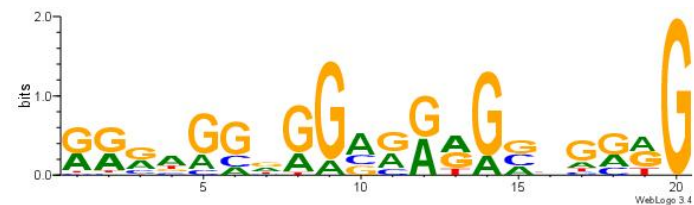
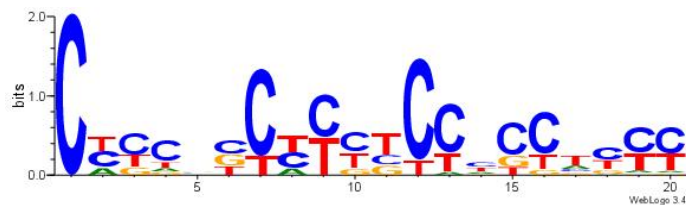
Dataset #: 5
Motif ID: 54
Motif name: TFM12
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 7
Number of overlap: 10
Similarity score: 0.0556427

Alignment:

CYCBBCYYYTCCHCCTYYY
----GCCYCMCCD-----

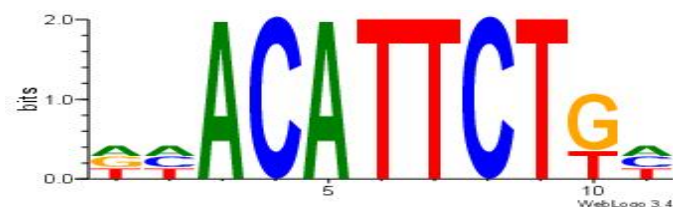
Original motif Consensus sequence: CYCBBCYYYTCCHCCTYYY

Reverse complement motif Consensus sequence:
KKKAGGDGGAKKMGBBGKMG



Dataset #: 4 Motif ID: 44 Motif name: dhACATTCTkh

Original motif Consensus sequence: DHACATTCTGH



Reverse complement motif Consensus sequence: HCAGAATGTHD



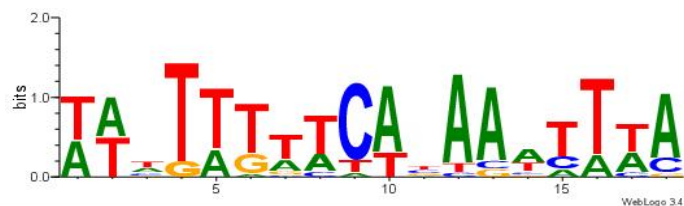
Best Matches for Top Significant Motif ID 44 (Highest to Lowest)

Dataset #:	5
Motif ID:	53
Motif name:	TFM3
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	8
Number of overlap:	11
Similarity score:	0.0217516

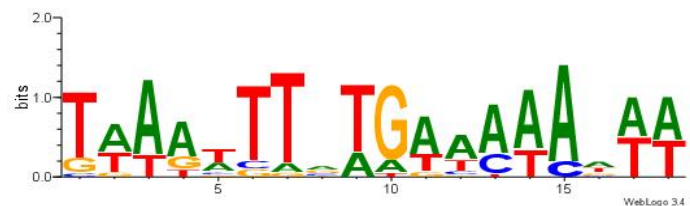
Alignment:

```
TWAAWTTVTGAAAAAHWW
DHACATTCTGH-----
```

Original motif Consensus sequence: WWHTTTTTTCABAAWTTWA



Reverse complement motif Consensus sequence: TWAAWTTVTGAAAAAHWW

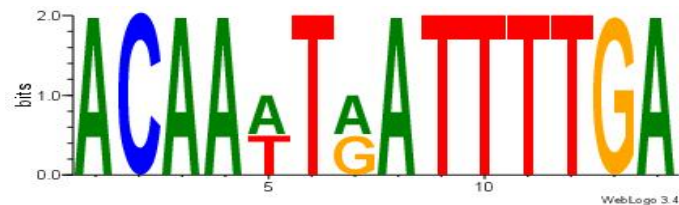


Dataset #: 2
Motif ID: 16
Motif name: Motif 16
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 4
Number of overlap: 11
Similarity score: 0.0258838

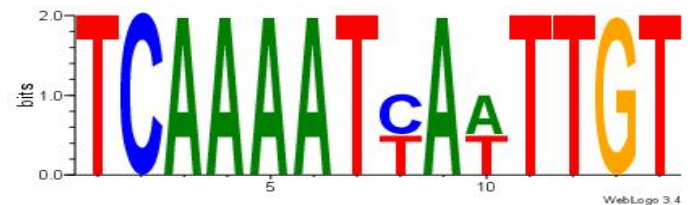
Alignment:

TCAAATKAWTTGT
HCAGAATGTHD---

Original motif Consensus sequence: ACAAWTRATTTTGA



Reverse complement motif Consensus sequence: TCAAATKAWTTG

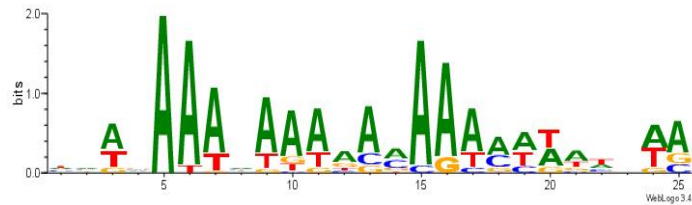


Dataset #: 5
 Motif ID: 56
 Motif name: TFM11
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 11
 Number of overlap: 11
 Similarity score: 0.0307858

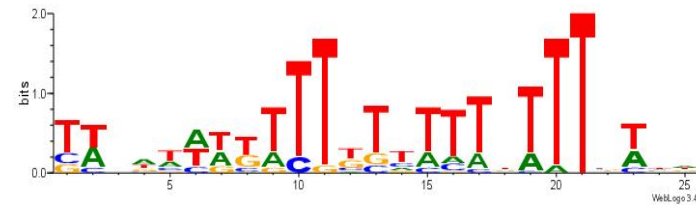
Alignment:

TWVHWWWYTTTYTTTTHTTTVWBH
 ----DHACATTCTGH-----

Original motif Consensus sequence:
 HDWVAAAHAAAAAMAAAMWWWHBWA



Reverse complement motif Consensus sequence:
 TWVHWWWYTTTYTTTTHTTTVWBH



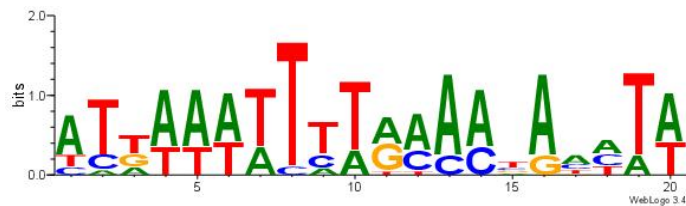
Dataset #: 5
 Motif ID: 55
 Motif name: TFM13
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 9

Number of overlap: 11
Similarity score: 0.0357323

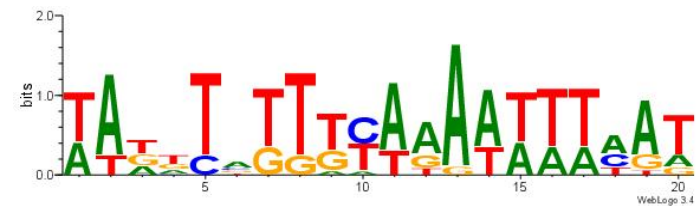
Alignment:

ATKAAWTTTTTRMAABAHTW
-DHACATTCTGH-----

Original motif Consensus sequence: ATKAAWTTTTTRMAABAHTW



Reverse complement motif Consensus sequence:
WAHHTVTTYKAAAATTRAT



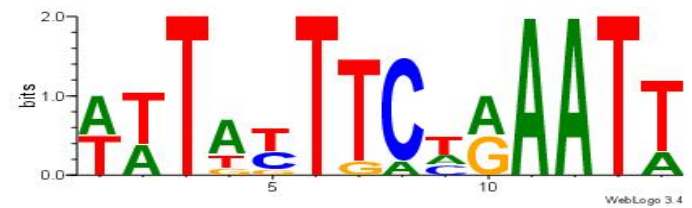
Dataset #: 2
Motif ID: 6
Motif name: Motif 6
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 4
Number of overlap: 11
Similarity score: 0.0400884

Alignment:

AATTYDGAARTAWW
HCAGAAATGTHD---

Original motif Consensus sequence: AATTYDGAARTAWW

Reverse complement motif Consensus sequence: WWTAKTTCDKAAT



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

Original motif Consensus sequence: GCGGGGC



Reverse complement motif Consensus sequence: GCCCGCC

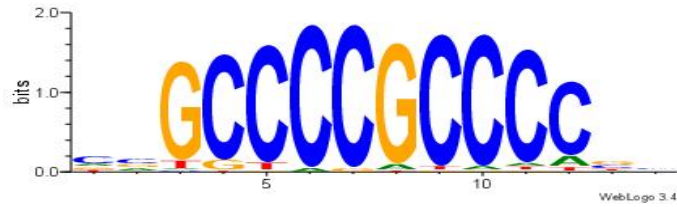


Best Matches for Top Significant Motif ID 1 (Highest to Lowest)

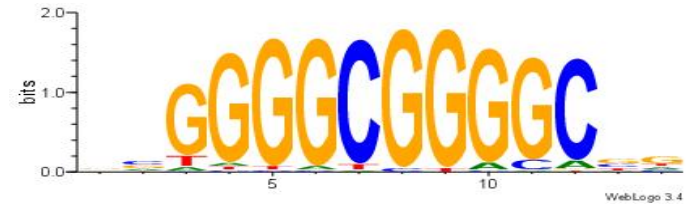
Dataset #:	4
Motif ID:	36
Motif name:	csGCCCCGCCCCsc
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	3
Number of overlap:	8
Similarity score:	0

Alignment:
 BBGGGGCGGGGCVD
 ----GGCGGGGC--

Original motif Consensus sequence: HVGCCCCGCCCCBB



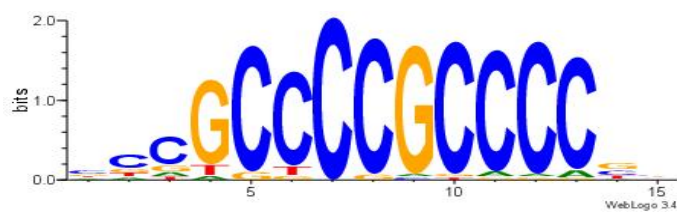
Reverse complement motif Consensus sequence: BBGGGGCGGGGC



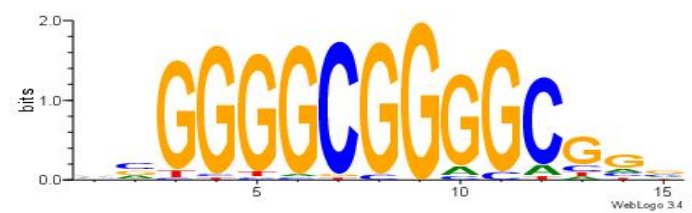
Dataset #: 4
 Motif ID: 38
 Motif name: cccGCCCCGCCCCsb
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 5
 Number of overlap: 8
 Similarity score: 0.00250079

Alignment:
 BBGGGGCGGGGCGGB
 ----GGCGGGGC----

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB

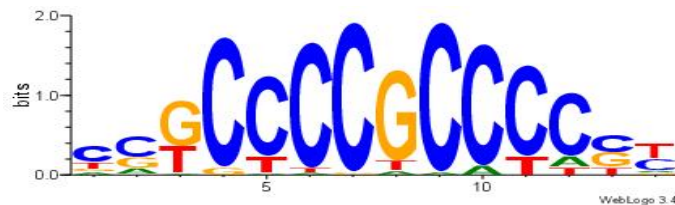


Dataset #: 2
 Motif ID: 7
 Motif name: Motif 7
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 5
 Number of overlap: 8
 Similarity score: 0.0149958

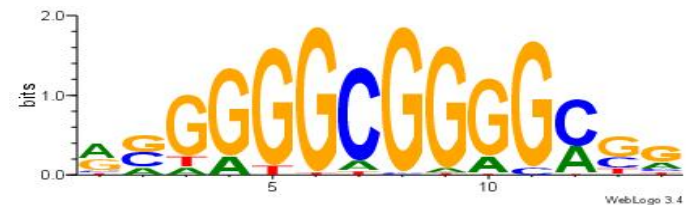
Alignment:

MSGGGGCGGGGYSG
 ----GGCGGGGC--

Original motif Consensus sequence: CSKCCCCGCCCSY



Reverse complement motif Consensus sequence: MSGGGGCGGGGY



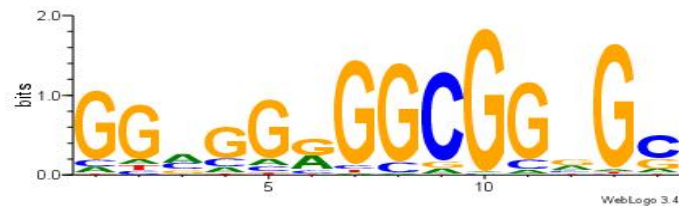
Dataset #: 5
 Motif ID: 50
 Motif name: TFF11
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 7
 Number of overlap: 8

Similarity score: 0.0348969

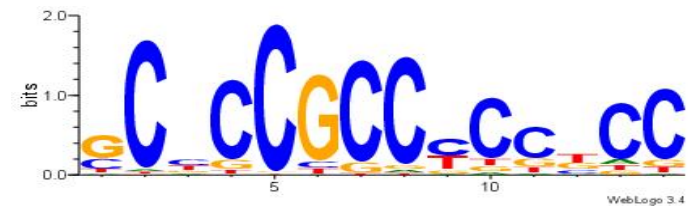
Alignment:

GCVCCGCCMCCYCC
GCCCCGCC-----

Original motif Consensus sequence: GGMGRRGGCGGVGC



Reverse complement motif Consensus sequence: GCVCCGCCMCCYCC



Dataset #: 3
Motif ID: 27
Motif name: Klf4
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: 0.0349983

Alignment:

DGGGYGKGGC
--GGCGGGC

Original motif Consensus sequence: DGGGYGKGGC

Reverse complement motif Consensus sequence: GCCYCMCCCD

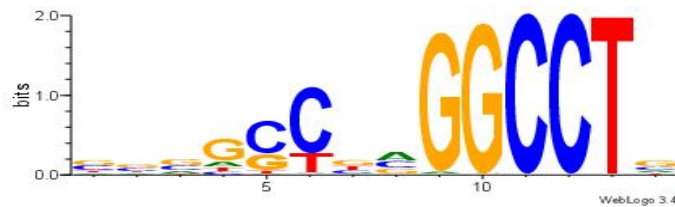


Dataset #: 3
 Motif ID: 22
 Motif name: Zfx
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 4
 Number of overlap: 8
 Similarity score: 0.0708224

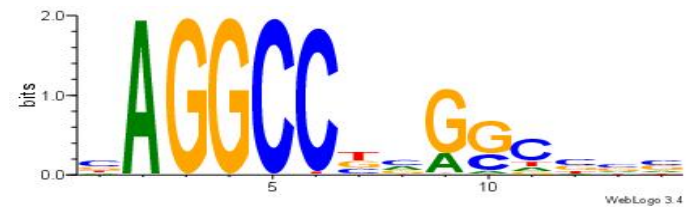
Alignment:

VAGGCCBBGGCVBB
 ---GCCCCGCC---

Original motif Consensus sequence: BBVGCCBVGCCCTV



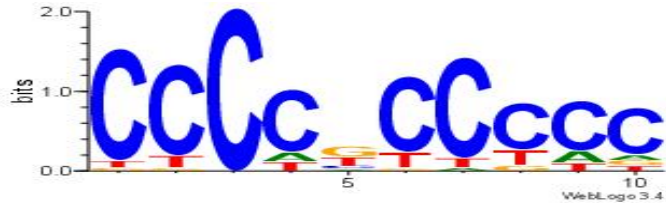
Reverse complement motif Consensus sequence: VAGGCCBBGGCVBB



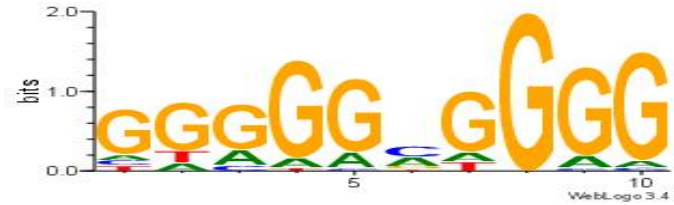
Significant Motifs - Global and Local Matching (Highest to Lowest)

Dataset #: 3 Motif ID: 24 Motif name: SP1

Original motif Consensus sequence: CCCCKCCCC



Reverse complement motif Consensus sequence: GGGGYGGGG



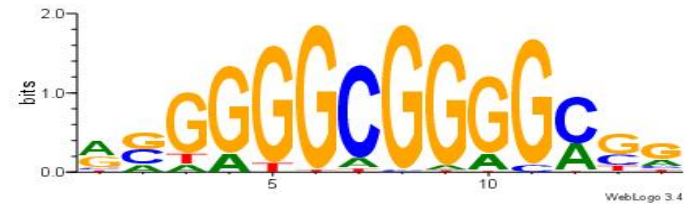
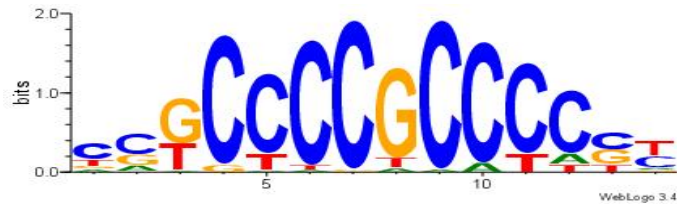
Best Matches for Significant Motif ID 24 (Highest to Lowest)

Dataset #:	2
Motif ID:	7
Motif name:	Motif 7
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	4
Number of overlap:	10
Similarity score:	0.00451594

Alignment:
 MSGGGGCGGGYSG
 -GGGGYGGGG---

Original motif Consensus sequence: CSKCCCCGCCCSY

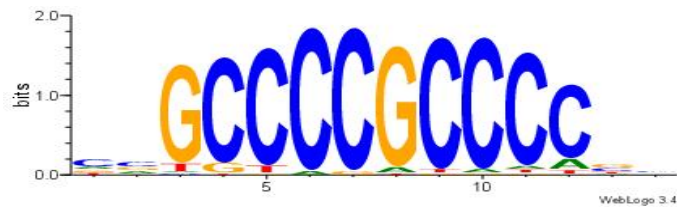
Reverse complement motif Consensus sequence: MSGGGGCGGGY



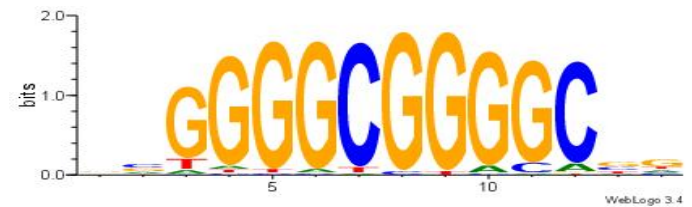
Dataset #: 4
 Motif ID: 36
 Motif name: csGCCCCGCCCCsc
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 4
 Number of overlap: 10
 Similarity score: 0.00965796

Alignment:
 BBGGGGCGGGGCVD
 -GGGGYGGGG---

Original motif Consensus sequence: HVGCCCCGCCCB



Reverse complement motif Consensus sequence: BBGGGGCGGGGC

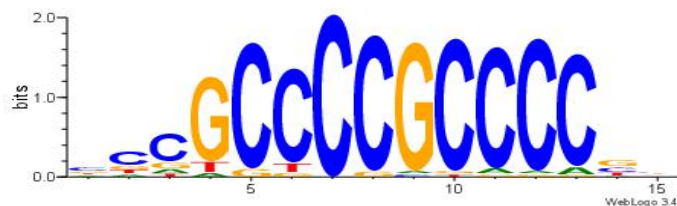


Dataset #: 4
 Motif ID: 38

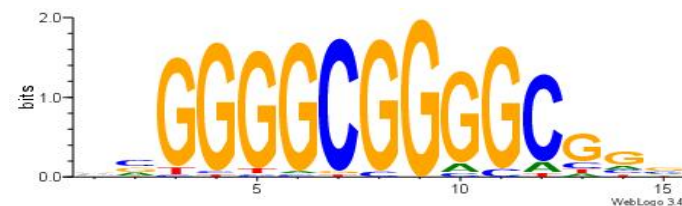
Motif name: cccGCCCCGCCCCsb
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 5
 Number of overlap: 10
 Similarity score: 0.0127292

Alignment:
 BCCGCCCCGCCCCBB
 ----CCCKCCCC--

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGCGGGGCGGB

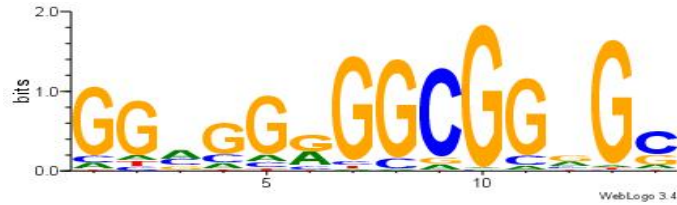


Dataset #: 5
 Motif ID: 50
 Motif name: TFF11
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 10
 Similarity score: 0.0174405

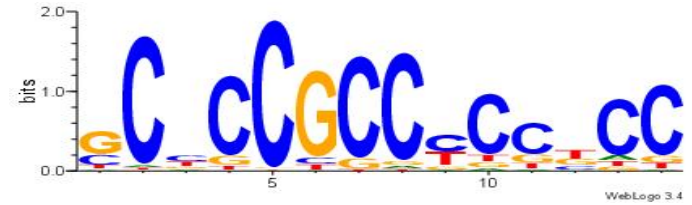
Alignment:

GGMGGRGGCGGVGC
---GGGGYGGGG---

Original motif Consensus sequence: GGMGGRGGCGGVGC



Reverse complement motif Consensus sequence: GCVCCGCCMCCYGC



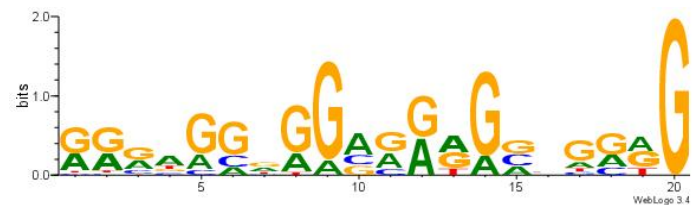
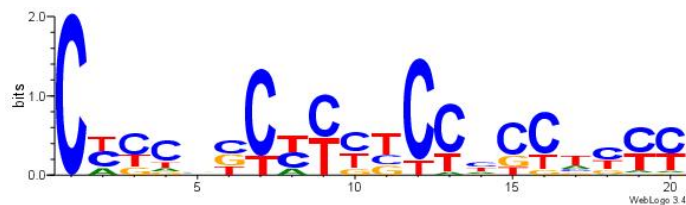
Dataset #: 5
Motif ID: 54
Motif name: TFM12
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 7
Number of overlap: 10
Similarity score: 0.0301548

Alignment:

CYCBBCYYYTCCHCCTYYY
-----CCCCKCCCC-----

Original motif Consensus sequence: CYCBBCYYYTCCHCCTYYY

Reverse complement motif Consensus sequence:
KKKAGGDGGAKKMGBBGKMG



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

Original motif Consensus sequence: ATAAAA



Reverse complement motif Consensus sequence: TTTTAT

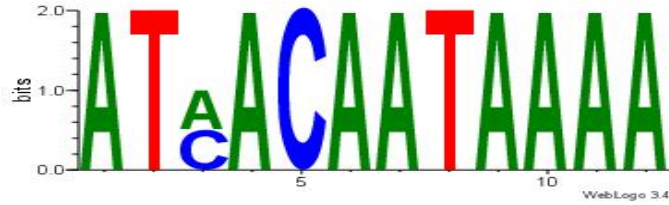


Best Matches for Significant Motif ID 21 (Highest to Lowest)

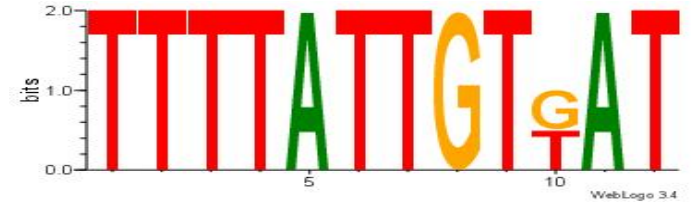
Dataset #:	2
Motif ID:	15
Motif name:	Motif 15
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	6
Similarity score:	0

Alignment:
 TTTTATTGTYAT
 TTTTAT-----

Original motif Consensus sequence: ATMACAATAAAA



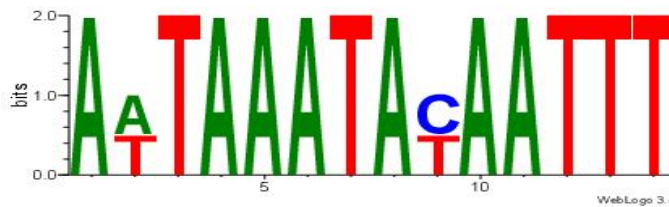
Reverse complement motif Consensus sequence: TTTTATTGTYAT



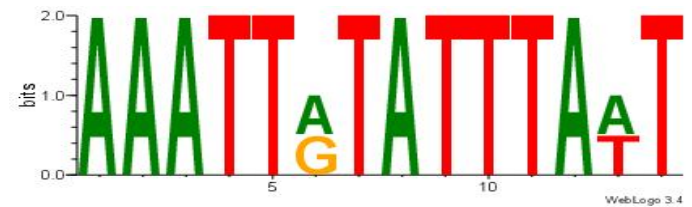
Dataset #: 2
Motif ID: 5
Motif name: Motif 5
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 6
Number of overlap: 6
Similarity score: 0.0208333

Alignment:
AAATTKTATTTAWT
---TTTTAT-----

Original motif Consensus sequence: AWTAAATAYAATTT



Reverse complement motif Consensus sequence: AAATTKTATTTAWT

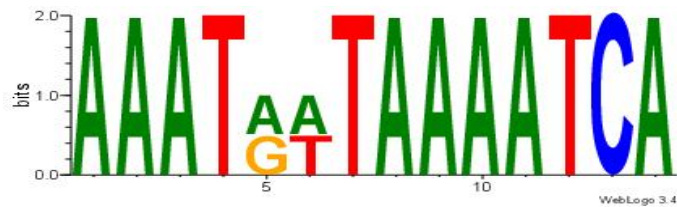


Dataset #: 2
 Motif ID: 8
 Motif name: Motif 8
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 4
 Number of overlap: 6
 Similarity score: 0.0208333

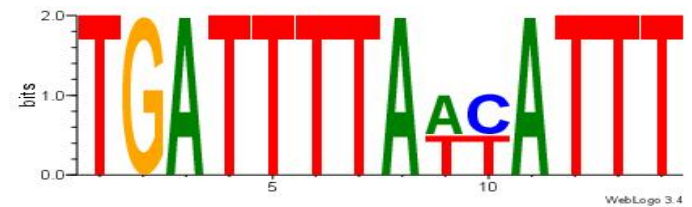
Alignment:

AAATRWTA~~AAA~~ATCA
 -----AT~~AAAA~~-----

Original motif Consensus sequence: AAATRWTA~~AAA~~ATCA



Reverse complement motif Consensus sequence: TGATTTTAWKATT



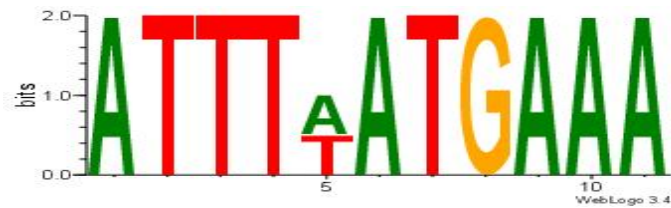
Dataset #: 2
 Motif ID: 11
 Motif name: Motif 11
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 6

Similarity score: 0.0208333

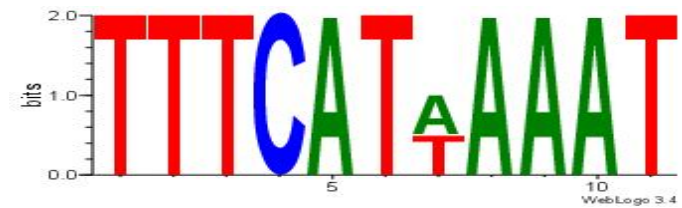
Alignment:

ATTTWATGAAA
----TTTTAT-

Original motif Consensus sequence: ATTTWATGAAA



Reverse complement motif Consensus sequence: TTTCATWAAAT



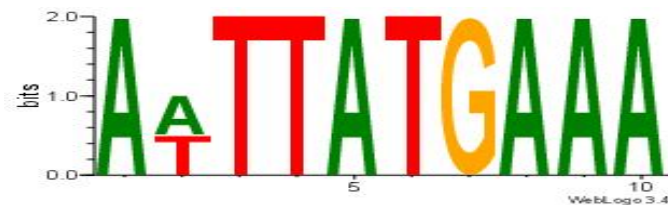
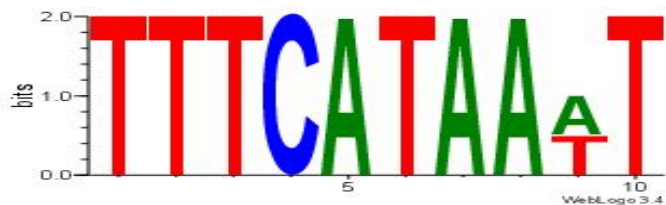
Dataset #: 2
Motif ID: 10
Motif name: Motif 10
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 6
Similarity score: 0.0416667

Alignment:

TTTCATAAWT
----TTTTAT

Original motif Consensus sequence: TTTCATAAWT

Reverse complement motif Consensus sequence: AWTTATGAAA

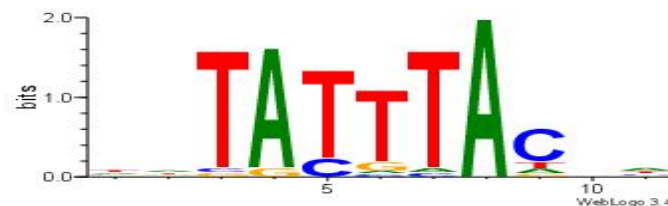


Dataset #: 4 Motif ID: 45 Motif name: wbgTAAATAww

Original motif Consensus sequence: DBGTAATAHD



Reverse complement motif Consensus sequence: DHTATTTACBD

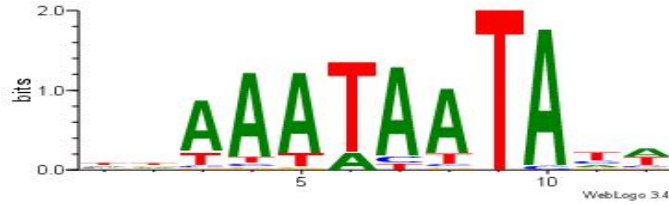


Best Matches for Significant Motif ID 45 (Highest to Lowest)

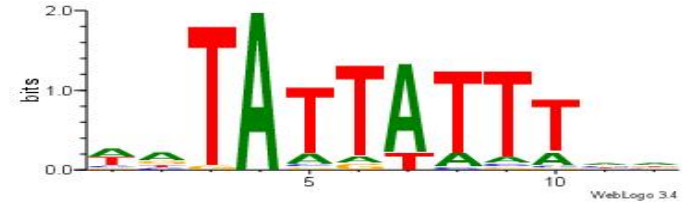
Dataset #:	4
Motif ID:	37
Motif name:	tkAAATAATAtw
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	11
Similarity score:	0.0162338

Alignment:
 HDAAATAATAHW
 -DBGTAATAAHD

Original motif Consensus sequence: HDAAATAATAHW



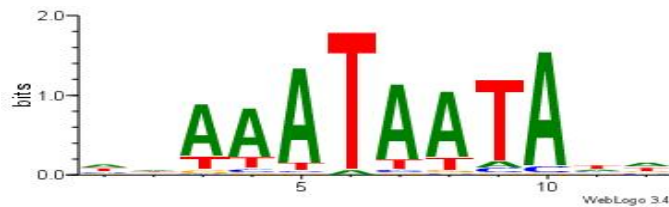
Reverse complement motif Consensus sequence: WHTATTATTTDH



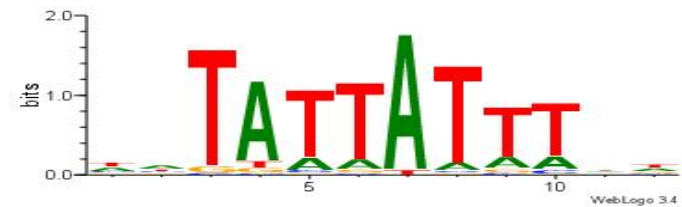
Dataset #: 4
Motif ID: 41
Motif name: wwAAATAATAtw
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 2
Number of overlap: 11
Similarity score: 0.0164863

Alignment:
DDTATTATTTDH
DHTATTTACBD-

Original motif Consensus sequence: HDAAATAATADD



Reverse complement motif Consensus sequence: DDTATTATTTDH

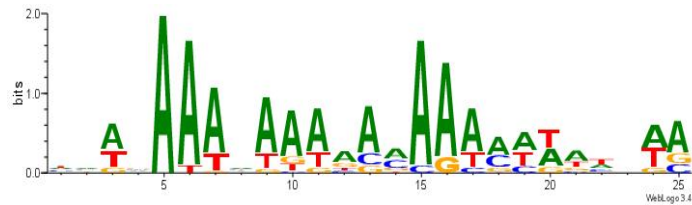


Dataset #: 5
 Motif ID: 56
 Motif name: TFM11
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 15
 Number of overlap: 11
 Similarity score: 0.0192768

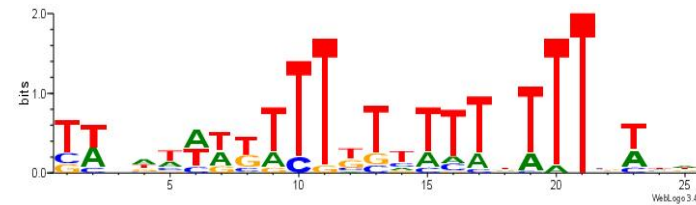
Alignment:

TWVHWWWYTTTYTTTTHTTTVWBH
 -----DHTATTTACBD

Original motif Consensus sequence:
 HDWVAAAHAAAAAMAAAMWWWHBWA



Reverse complement motif Consensus sequence:
 TWVHWWWYTTTYTTTTHTTTVWBH

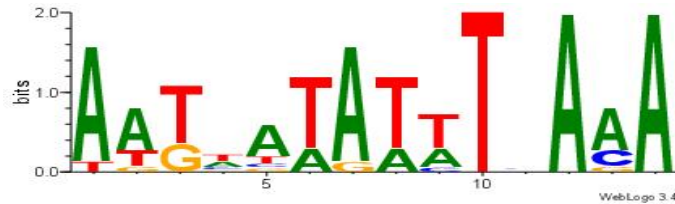


Dataset #: 2
 Motif ID: 9
 Motif name: Motif 9
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 4

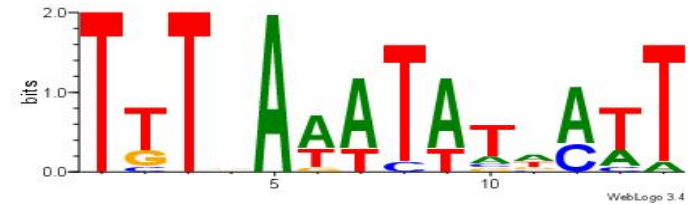
Number of overlap: 11
Similarity score: 0.0250541

Alignment:
AATHATATWTHAAA
DHTATTTACBD---

Original motif Consensus sequence: AATHATATWTHAAA



Reverse complement motif Consensus sequence: TTTDAWATATHAT

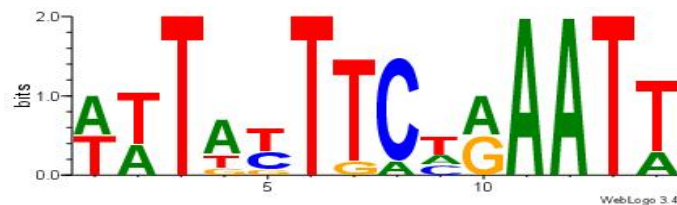


Dataset #: 2
Motif ID: 6
Motif name: Motif 6
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 11
Similarity score: 0.027895

Alignment:
AATTYDGAARTAWW
---DBGTAATAHD

Original motif Consensus sequence: AATTYDGAARTAWW

Reverse complement motif Consensus sequence: WWTAKTTCDKAAT



Dataset #: 3 Motif ID: 29 Motif name: HIF1AARNT

Original motif Consensus sequence: VBACGTGV



Reverse complement motif Consensus sequence: VCACGTBV

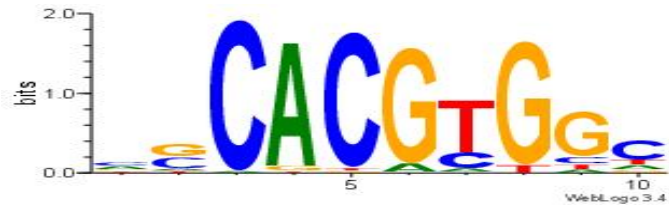


Best Matches for Significant Motif ID 29 (Highest to Lowest)

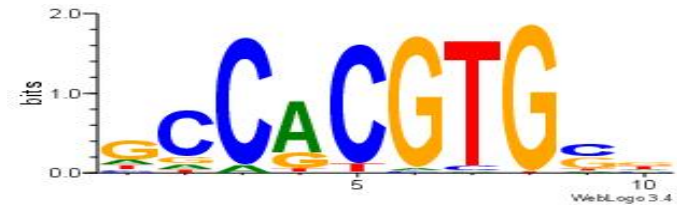
Dataset #:	3
Motif ID:	33
Motif name:	Mycn
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	2
Number of overlap:	8
Similarity score:	0.0123101

Alignment:
GCCACGTGSD
-VBACGTGV-

Original motif Consensus sequence: HSCACGTGGC



Reverse complement motif Consensus sequence: GCCACGTGSD

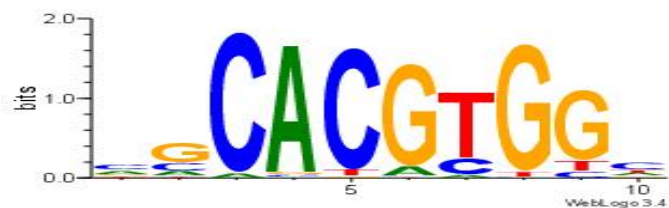


Dataset #: 3
Motif ID: 34
Motif name: Myc
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 2
Number of overlap: 8
Similarity score: 0.0144491

Alignment:

DCCACGTGCV
-VBACGTGV-

Original motif Consensus sequence: VGCACGTGGH



Reverse complement motif Consensus sequence: DCCACGTGCV



Dataset #: 4
 Motif ID: 40
 Motif name: kcACCTGCAGc
 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: 0.0295473

Alignment:

GBTGCAGGTGB
 ---VCACGTBV

Original motif Consensus sequence: BCACCTGCABC



Reverse complement motif Consensus sequence: GBTGCAGGTGB



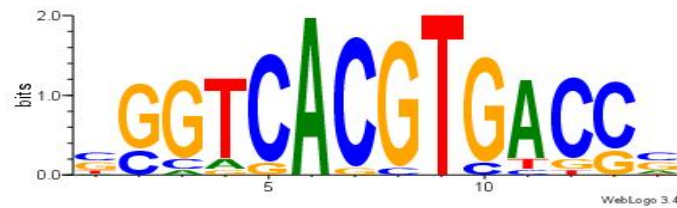
Dataset #: 4
 Motif ID: 42
 Motif name: sSGTCACGTGACSS
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 8

Similarity score: 0.0314837

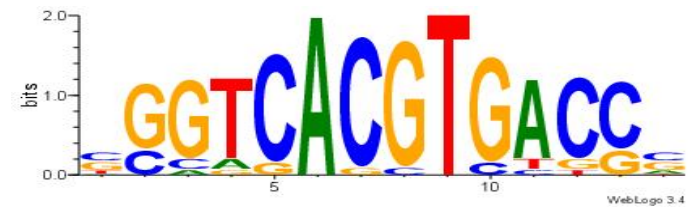
Alignment:

SGGTCACGTGACCS
---VCACGTBV---

Original motif Consensus sequence: SGGTCACGTGACCS



Reverse complement motif Consensus sequence: SGGTCACGTGACCS



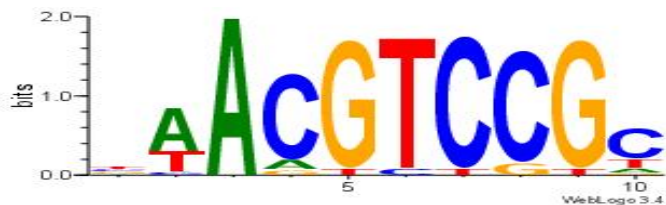
Dataset #: 3
Motif ID: 26
Motif name: MIZF
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 3
Number of overlap: 8
Similarity score: 0.0377204

Alignment:

GCGGACGTTV
--VCACGTBV

Original motif Consensus sequence: BAACGTCCGC

Reverse complement motif Consensus sequence: GCGGACGTTV



Dataset #: 3 Motif ID: 32 Motif name: ArntAhr

Original motif Consensus sequence: YGCGTG



Reverse complement motif Consensus sequence: CACGCM

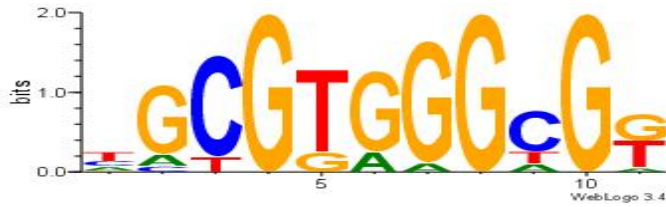


Best Matches for Significant Motif ID 32 (Highest to Lowest)

Dataset #:	3
Motif ID:	23
Motif name:	Egr1
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	6
Similarity score:	0

Alignment:
 HGCCTGGGCGK
 YGCGTG-----

Original motif Consensus sequence: HCGTGGGCGK



Reverse complement motif Consensus sequence: YCGCCACGCH



Dataset #: 3
Motif ID: 29
Motif name: HIF1AARNT
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: 0.0112447

Alignment:
VBACGTGV
-YCGGTG-

Original motif Consensus sequence: VBACGTGV



Reverse complement motif Consensus sequence: VCACGTBV

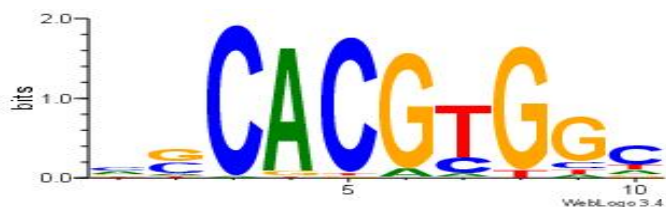


Dataset #: 3
 Motif ID: 33
 Motif name: Mycn
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3
 Number of overlap: 6
 Similarity score: 0.0377949

Alignment:

GCCACGTGSD
 --YGCGTG--

Original motif Consensus sequence: HSCACGTGGC



Reverse complement motif Consensus sequence: GCCACGTGSD



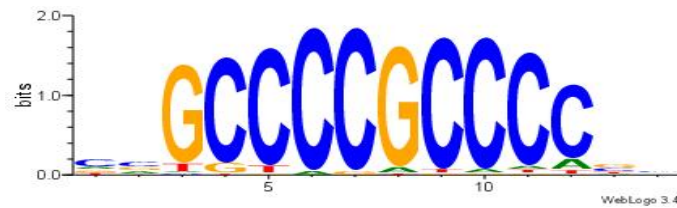
Dataset #: 4
 Motif ID: 36
 Motif name: csGCCCCGCCCCsc
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 5
 Number of overlap: 6

Similarity score: 0.0396403

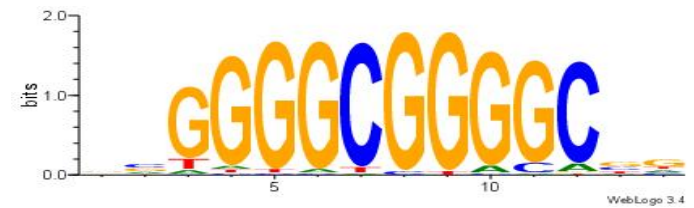
Alignment:

HVCCCCGCCCB
----CACGCM----

Original motif Consensus sequence: HVCCCCGCCCB



Reverse complement motif Consensus sequence: BBGGGCGGGGC



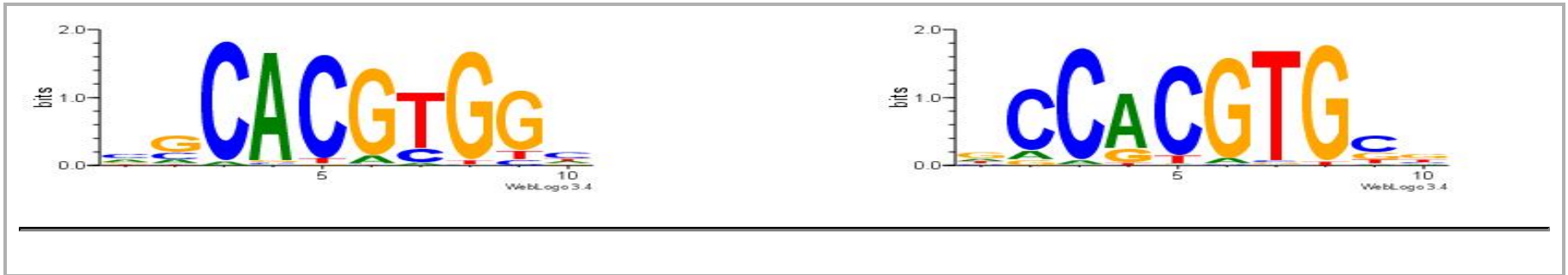
Dataset #: 3
Motif ID: 34
Motif name: Myc
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 3
Number of overlap: 6
Similarity score: 0.0399214

Alignment:

DCCACGTGCV
--YCCGTG--

Original motif Consensus sequence: VGCACGTGGH

Reverse complement motif Consensus sequence: DCCACGTGCV



Best Matches for Each Motif (Highest to Lowest)

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

Original motif Consensus sequence: GGCGGGGC



Reverse complement motif Consensus sequence: GCCCGGCC



Best Matches for Motif ID 1 (Highest to Lowest)

Dataset #:	4
Motif ID:	36
Motif name:	csGCCCCGCCCCsc
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	3
Number of overlap:	8

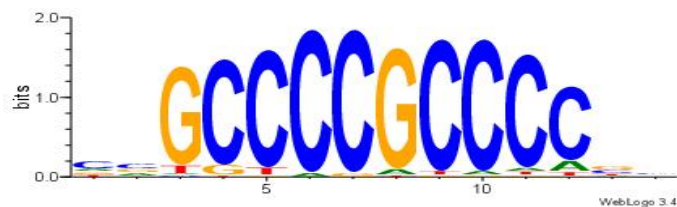
Similarity score: 0

Alignment:

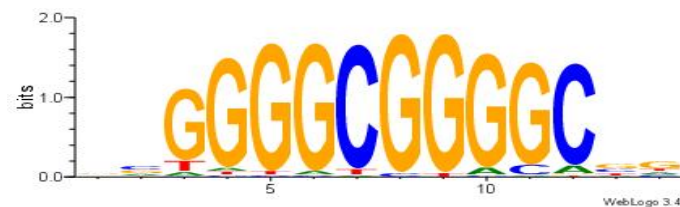
BBGGGGCGGGGCVD

----GGCGGGGC--

Original motif Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGC



Dataset #: 4
Motif ID: 38
Motif name: cccGCCCCGCCCCsb
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 5
Number of overlap: 8
Similarity score: 0.00250079

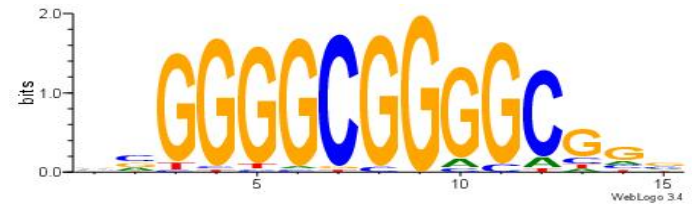
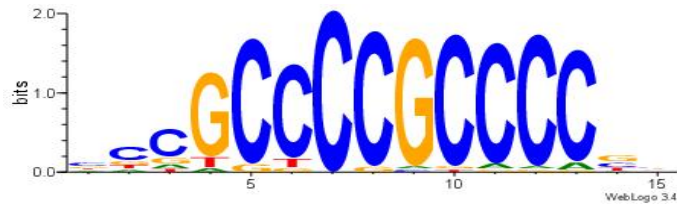
Alignment:

BBGGGGCGGGGCGB

----GGCGGGGC----

Original motif Consensus sequence: BCCGCCCCGCCCCBB

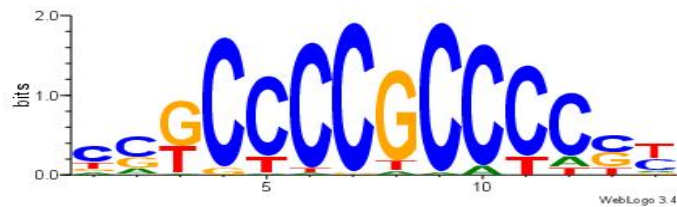
Reverse complement motif Consensus sequence:
BBGGGGCGGGGCGB



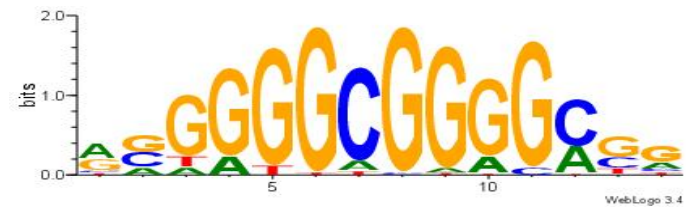
Dataset #: 2
 Motif ID: 7
 Motif name: Motif 7
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 5
 Number of overlap: 8
 Similarity score: 0.0149958

Alignment:
 MSGGGCGGGYSG
 ----GGCGGGC--

Original motif Consensus sequence: CSKCCCCGCCCSY



Reverse complement motif Consensus sequence: MSGGGCGGGY



Dataset #: 5
 Motif ID: 50

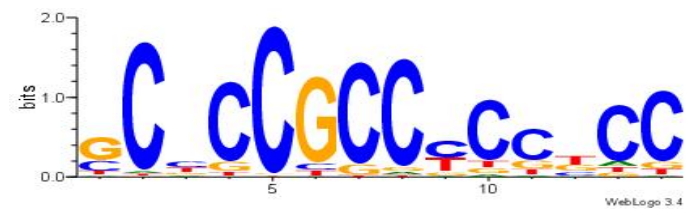
Motif name: TFF11
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 7
 Number of overlap: 8
 Similarity score: 0.0348969

Alignment:
 GCVCCGCCMCCYCC
 GCCCCGCC-----

Original motif Consensus sequence: GGMGRRGGCGGVGC



Reverse complement motif Consensus sequence: GCVCCGCCMCCYCC



Dataset #: 3
 Motif ID: 27
 Motif name: Klf4
 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: 0.0349983

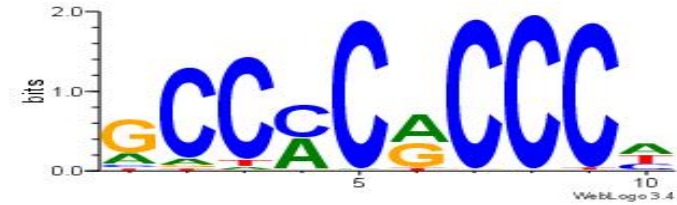
Alignment:

DGGGYGKGGC
--GGCGGGGC

Original motif Consensus sequence: DGGGYGKGGC



Reverse complement motif Consensus sequence: GCCYCMCCCD



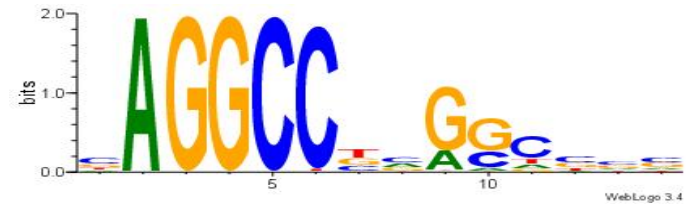
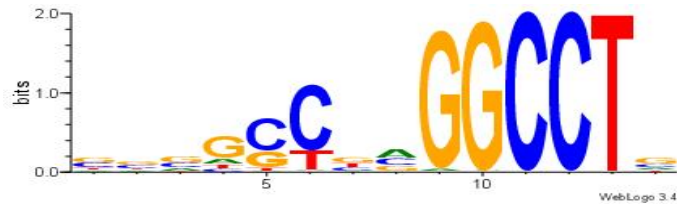
Dataset #: 3
Motif ID: 22
Motif name: Zfx
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 4
Number of overlap: 8
Similarity score: 0.0708224

Alignment:

VAGGCCBBGGCVBB
---GCCCGCC---

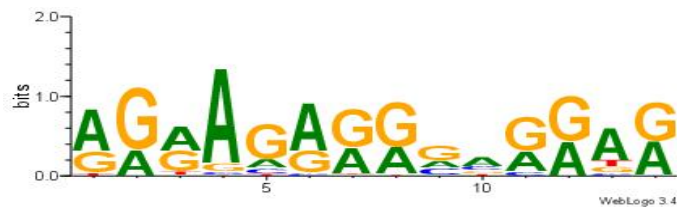
Original motif Consensus sequence: BBVGCCBVGGCCTV

Reverse complement motif Consensus sequence: VAGGCCBBGGCVBB

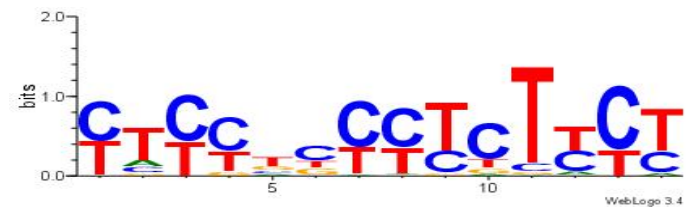


Dataset #: 2 Motif ID: 2 Motif name: Motif 2

Original motif Consensus sequence: RGRAGARRGARRAR



Reverse complement motif Consensus sequence: MTMMTCMMTCTK

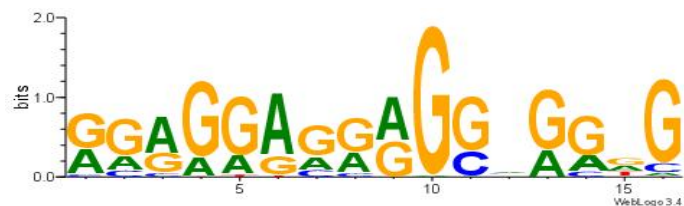


Best Matches for Motif ID 2 (Highest to Lowest)

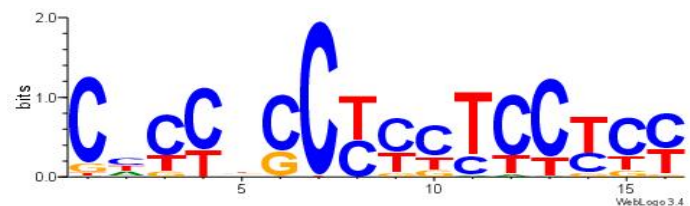
Dataset #:	5
Motif ID:	51
Motif name:	TFM2
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	14
Similarity score:	0.00948131

Alignment:
RGRGGAGRRGGHGGDG
--RGRAGARRGARRAR

Original motif Consensus sequence: RGRGGAGRRGGHGGDG



Reverse complement motif Consensus sequence: CHCCBCCKMCTCCKCM

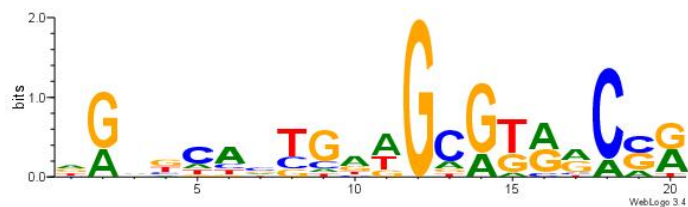


Dataset #: 3
Motif ID: 31
Motif name: Pax5
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 7
Number of overlap: 14
Similarity score: 0.047364

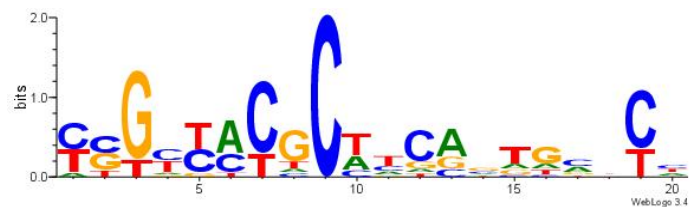
Alignment:

```
MSGKKRCGCWDCABTGBBCD  
-----MTMMTCMMTCTKCK
```

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD

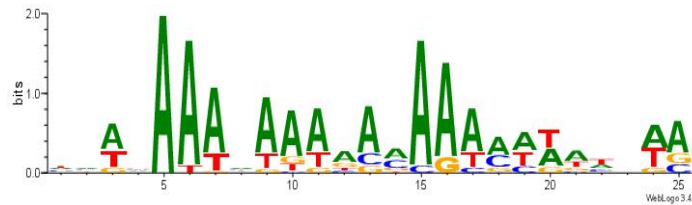


Dataset #: 5
 Motif ID: 56
 Motif name: TFM11
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 14
 Similarity score: 0.0541717

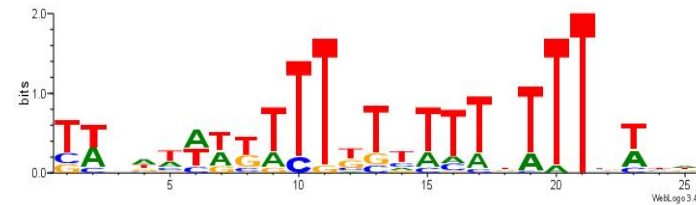
Alignment:

HDWVAAAHAAAAAMAAAMWWWHBWA
 -----RGRAGARRGARRAR--

Original motif Consensus sequence:
 HDWVAAAHAAAAAMAAAMWWWHBWA



Reverse complement motif Consensus sequence:
 TWVHWWWYTTTTTTTTHTTTVWBH



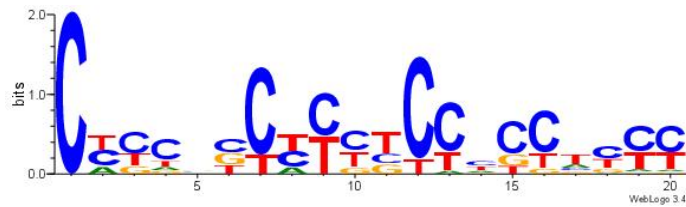
Dataset #: 5
 Motif ID: 54
 Motif name: TFM12
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 7

Number of overlap: 14
Similarity score: 0.0545069

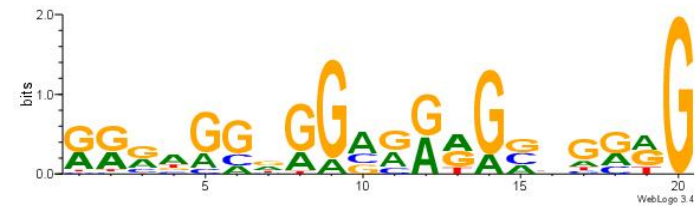
Alignment:

CYYCBBCYYYYTCCHCCTYYY
-----MTMMTCMMTCTKCK

Original motif Consensus sequence: CYYCBBCYYYYTCCHCCTYYY



Reverse complement motif Consensus sequence:
KKKAGGDGGAKKMGBBGKMG

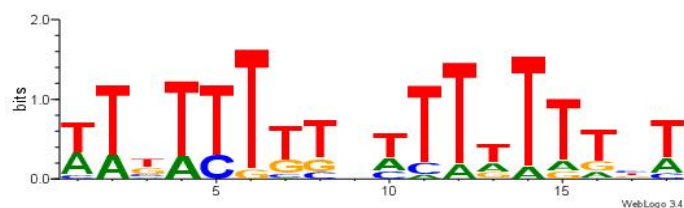


Dataset #: 5
Motif ID: 52
Motif name: TFM1
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 4
Number of overlap: 14
Similarity score: 0.0558935

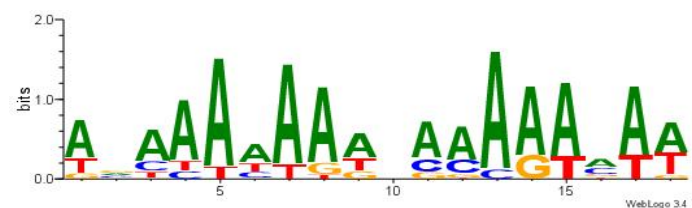
Alignment:

ABAAAAAWhAAAAARAW
-RGRAGARRGARRAR---

Original motif Consensus sequence: WTKTTTTTHWTTTTTBT

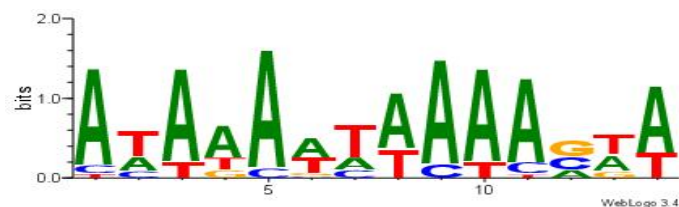


Reverse complement motif Consensus sequence: ABAAAAAWHAAAAARAW

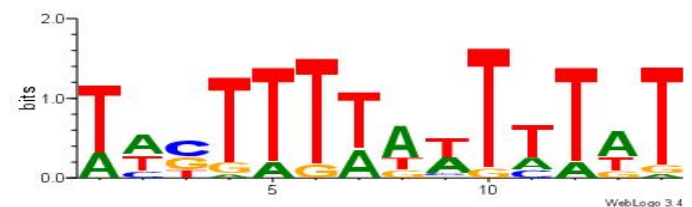


Dataset #: 2 Motif ID: 3 Motif name: Motif 3

Original motif Consensus sequence: AWAAAWTWAASWA



Reverse complement motif Consensus sequence: TWSTTTWAWTTT



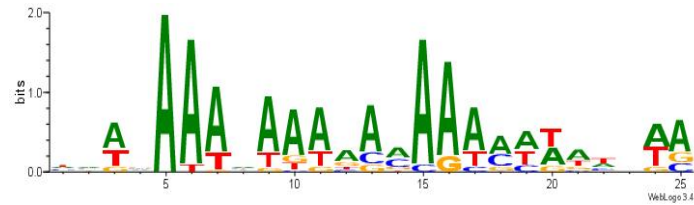
Best Matches for Motif ID 3 (Highest to Lowest)

Dataset #:	5
Motif ID:	56
Motif name:	TFM11
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	7
Number of overlap:	14
Similarity score:	0.0137914

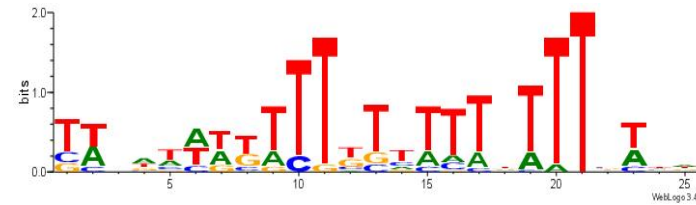
Alignment:

HDWVAAAHAAAAAMAAAMWWWHBWA
 -----AWAAAWTWAAASWA-----

Original motif Consensus sequence:
 HDWVAAAHAAAAAMAAAMWWWHBWA



Reverse complement motif Consensus sequence:
 TWVHWWWYTTTTYTTTTHTTTVWBH

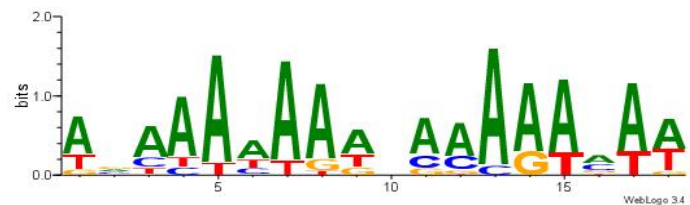
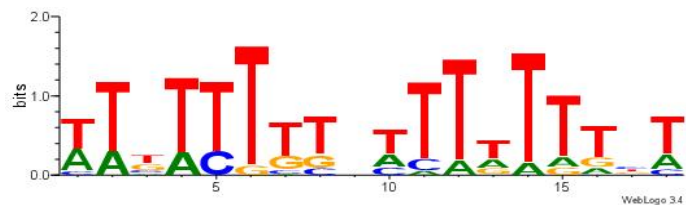


Dataset #: 5
 Motif ID: 52
 Motif name: TFM1
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0.0162962

Alignment:
 ABAAAAAWhAAAAARAW
 -----AWAAAWTWAAASWA

Original motif Consensus sequence: WTKTTTTTHWTTTTTBT

Reverse complement motif Consensus sequence:
 ABAAAAAWhAAAAARAW



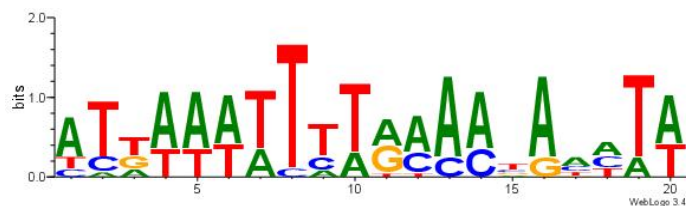
Dataset #: 5
 Motif ID: 55
 Motif name: TFM13
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 14
 Similarity score: 0.037679

Alignment:

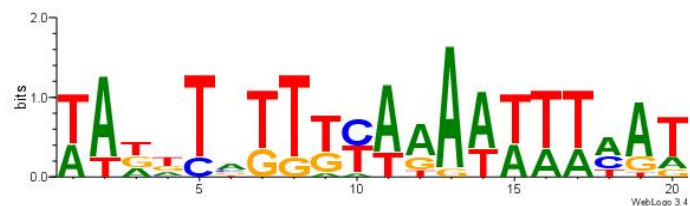
```

ATKAAWTTTTRMAABAHTW
--AWAAAWTWAAASWA----
  
```

Original motif Consensus sequence: ATKAAWTTTTRMAABAHTW



Reverse complement motif Consensus sequence: WAHHTVTTYKAAAATWTRAT



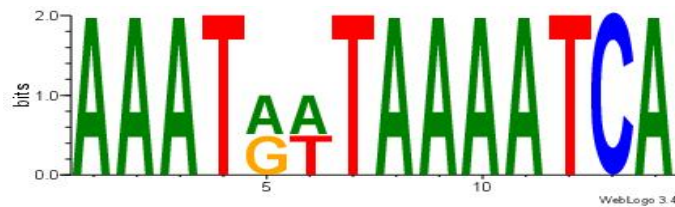
Dataset #: 2

Motif ID: 8
 Motif name: Motif 8
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0.0423952

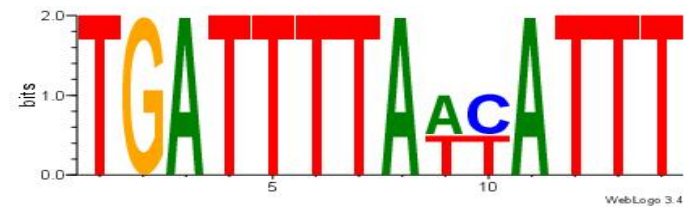
Alignment:

TGATTTTAWKATTT
 TWSTTTWAWTTTWT

Original motif Consensus sequence: AAATRWTAATCA



Reverse complement motif Consensus sequence: TGATTTTAWKATTT

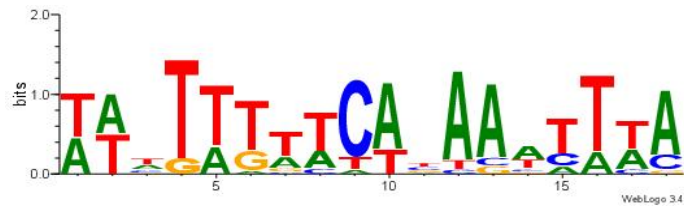


Dataset #: 5
 Motif ID: 53
 Motif name: TFM3
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 5
 Number of overlap: 14
 Similarity score: 0.0456419

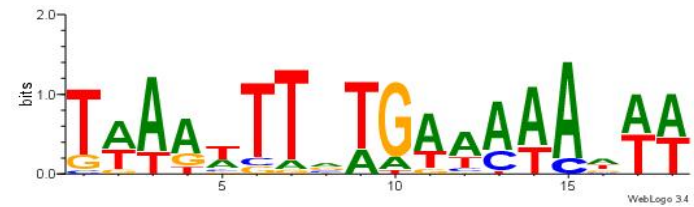
Alignment:

```
TWAAWTTVTGAAAAHWW  
----AWAAAWTWAAASWA
```

Original motif Consensus sequence: WWHTTTTTTCABAAWTTWA

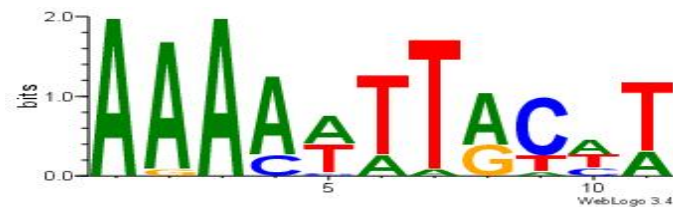


Reverse complement motif Consensus sequence: TWAAWTTVTGAAAAHWW



Dataset #: 2 Motif ID: 4 Motif name: Motif 4

Original motif Consensus sequence: AAAWTTTCWT



Reverse complement motif Consensus sequence: AWGKAAWTTTT



Best Matches for Motif ID 4 (Highest to Lowest)

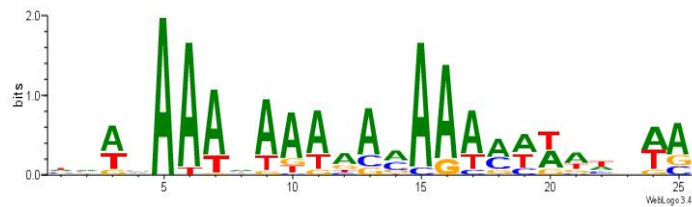
Dataset #:	5
Motif ID:	56
Motif name:	TFM11
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward

Position number: 14
 Number of overlap: 11
 Similarity score: 0.0718583

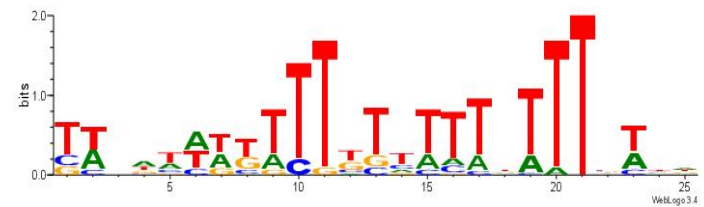
Alignment:

HDWVAAAHAAAAAMAAAMWWWHBWA
 -----AAAATTRCWT-

Original motif Consensus sequence:
 HDWVAAAHAAAAAMAAAMWWWHBWA



Reverse complement motif Consensus sequence:
 TWVHWWYTTTTTTTTTTTHTTTVWBH

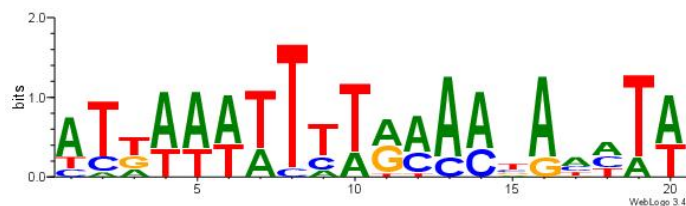


Dataset #: 5
 Motif ID: 55
 Motif name: TFM13
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 10
 Number of overlap: 11
 Similarity score: 0.0727073

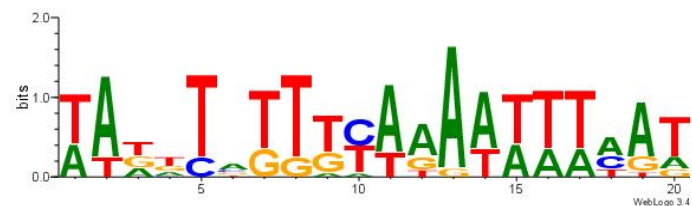
Alignment:

ATKAAWTTTTTRMAABAHHTW
 AWGKAAWTTTT-----

Original motif Consensus sequence: ATKAAWTTTTRMAABAHTW



Reverse complement motif Consensus sequence: WAHHTVTTYKAAAATTRAT

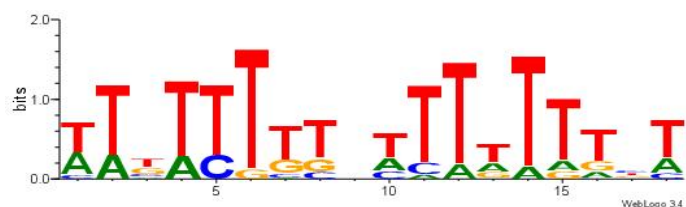


Dataset #: 5
Motif ID: 52
Motif name: TFM1
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 5
Number of overlap: 11
Similarity score: 0.0748297

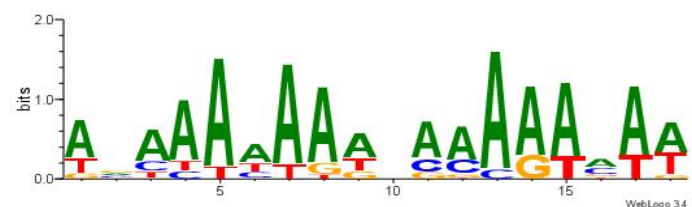
Alignment:

WTKTTTTTHWTTTTTTBT
---AWGKAAWTTTT-----

Original motif Consensus sequence: WTKTTTTTHWTTTTTTBT



Reverse complement motif Consensus sequence: ABAAAAAWHAAAAARAW

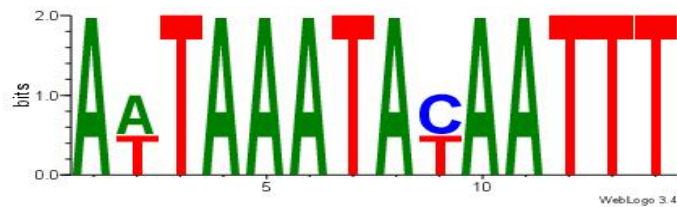


Dataset #: 2
 Motif ID: 5
 Motif name: Motif 5
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 4
 Number of overlap: 11
 Similarity score: 0.0786484

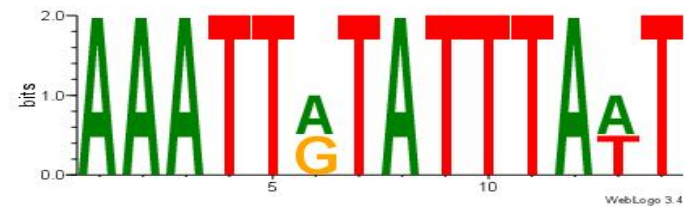
Alignment:

AAATTKTATTTAWT
 AAAAWTTRCWT---

Original motif Consensus sequence: AWTAAATAYAATTT



Reverse complement motif Consensus sequence: AAATTKTATTTAWT



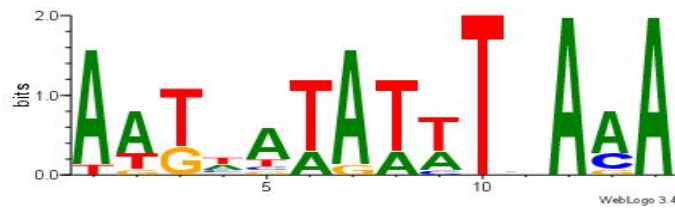
Dataset #: 2
 Motif ID: 9
 Motif name: Motif 9
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 4
 Number of overlap: 11

Similarity score: 0.0820375

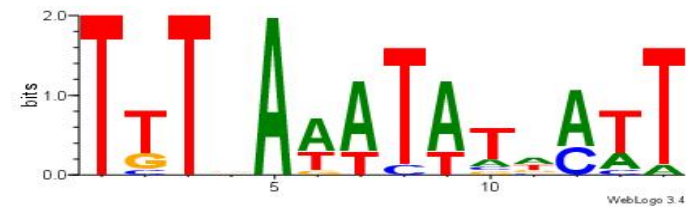
Alignment:

AATHATATWTHAAA
AWGKAAWTTTT---

Original motif Consensus sequence: AATHATATWTHAAA

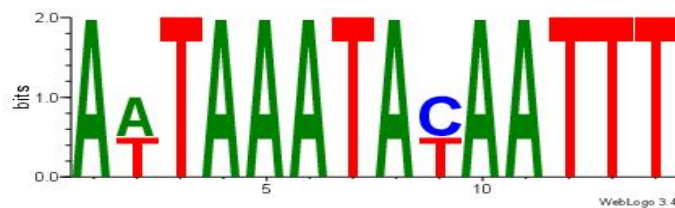


Reverse complement motif Consensus sequence: TTTDAWATATHAT

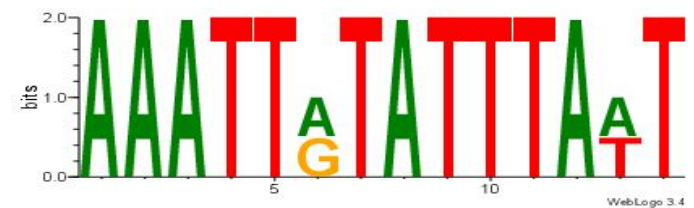


Dataset #: 2 Motif ID: 5 Motif name: Motif 5

Original motif Consensus sequence: AWTAAATAYAATTT



Reverse complement motif Consensus sequence: AAATTKTATTTAW



Best Matches for Motif ID 5 (Highest to Lowest)

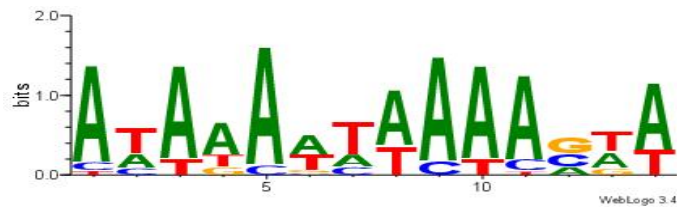
Dataset #:	2
Motif ID:	3
Motif name:	Motif 3
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward

Position number: 1
 Number of overlap: 14
 Similarity score: 0.101648

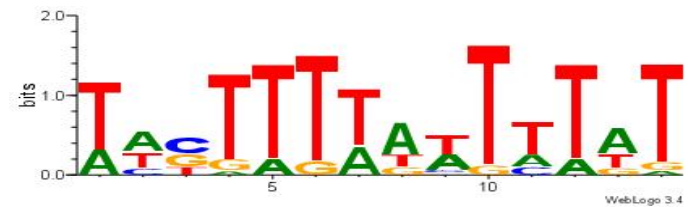
Alignment:

TWSTTTWAWTTTWT
 AAATTKTATTTAWT

Original motif Consensus sequence: AWAAAWTWAAASWA



Reverse complement motif Consensus sequence: TWSTTTWAWTTTWT



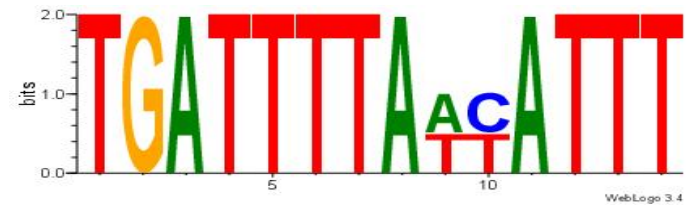
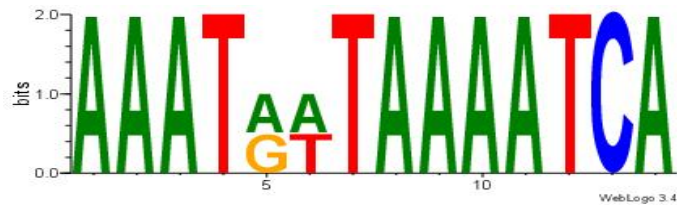
Dataset #: 2
 Motif ID: 8
 Motif name: Motif 8
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0.107143

Alignment:

TGATTTTAWKATTT
 AAATTKTATTTAWT

Original motif Consensus sequence: AAATRWAAAATCA

Reverse complement motif Consensus sequence: TGATTTTAWKATTT



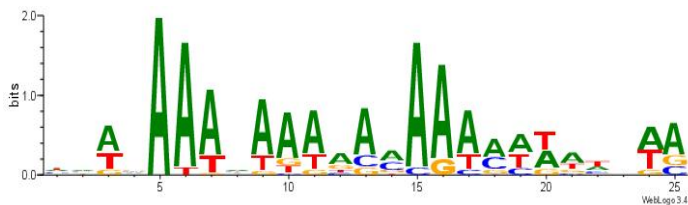
Dataset #: 5
 Motif ID: 56
 Motif name: TFM11
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 6
 Number of overlap: 14
 Similarity score: 0.109769

Alignment:

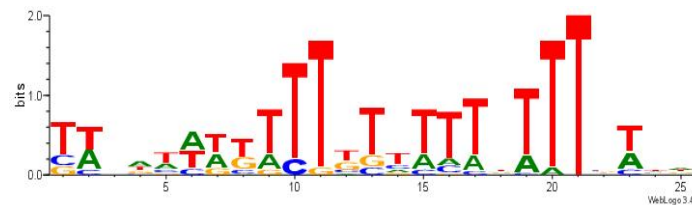
```

TWVHWWWYTTTYTTTTHTTTVWBH
-----AAATTKTATTTAWT-----
  
```

Original motif Consensus sequence:
 HDWVAAAHAAAAAMAAAMWWWHBWA



Reverse complement motif Consensus sequence:
 TWVHWWWYTTTYTTTTHTTTVWBH



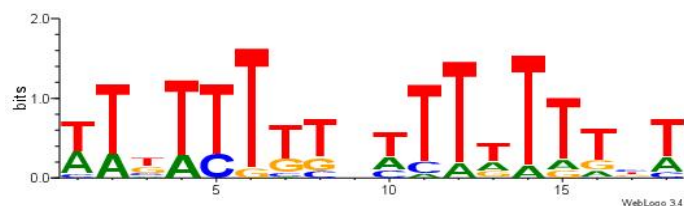
Dataset #: 5

Motif ID: 52
 Motif name: TFM1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 4
 Number of overlap: 14
 Similarity score: 0.110348

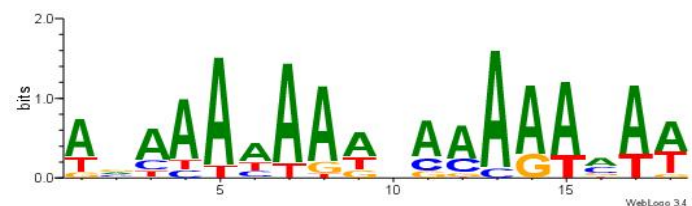
Alignment:

WTKTTTTTHWTTTTTBT
 -AAATTKTATTTAWT---

Original motif Consensus sequence: WTKTTTTTHWTTTTTBT



Reverse complement motif Consensus sequence: ABAAAAAWHAAAAARAW



Dataset #: 2
 Motif ID: 6
 Motif name: Motif 6
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 14

Similarity score: 0.111607

Alignment:

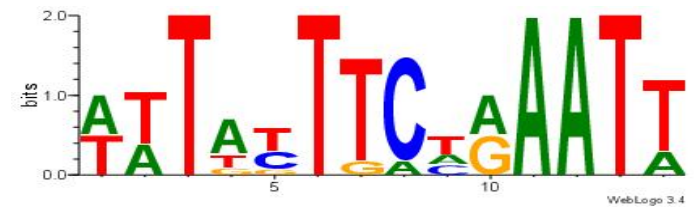
AATTYDGAARTAWW

AAATTKTATTTAWT

Original motif Consensus sequence: AATTYDGAARTAWW



Reverse complement motif Consensus sequence: WWTAKTTCDKAAAT

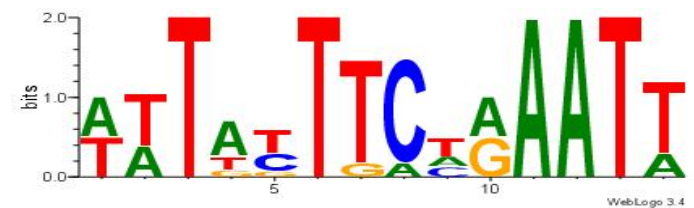


Dataset #: 2 Motif ID: 6 Motif name: Motif 6

Original motif Consensus sequence: AATTYDGAARTAWW



Reverse complement motif Consensus sequence: WWTAKTTCDKAAAT



Best Matches for Motif ID 6 (Highest to Lowest)

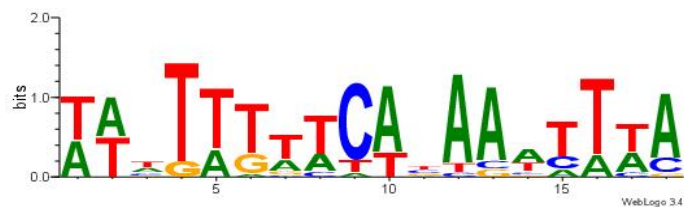
Dataset #:	5
Motif ID:	53
Motif name:	TFM3
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward

Position number: 4
Number of overlap: 14
Similarity score: 0.0325081

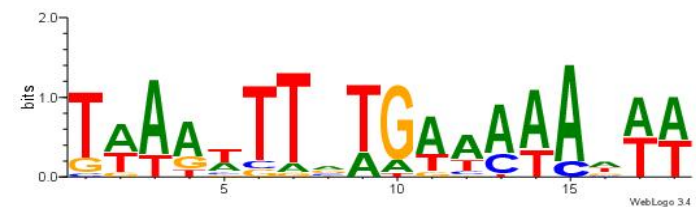
Alignment:

WWHTTTTTTCABAAWTTWA
-WWTAKTTCDKAATT---

Original motif Consensus sequence: WWHTTTTTTCABAAWTTWA



Reverse complement motif Consensus sequence: TWAAWTTVTGAAAAHWW

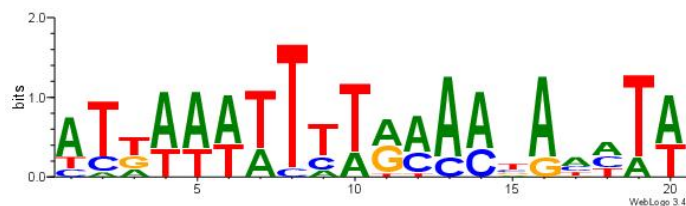


Dataset #: 5
Motif ID: 55
Motif name: TFM13
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 5
Number of overlap: 14
Similarity score: 0.0349702

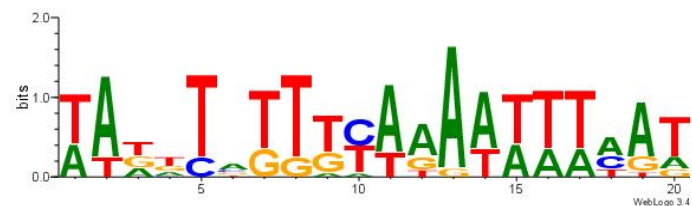
Alignment:

ATKAAWTTTTTRMAABAHHTW
-----AATTYDGAARTAWW--

Original motif Consensus sequence: ATKAAWTTTTRMAABAHTW



Reverse complement motif Consensus sequence: WAHHTVTTYKAAAATTRAT

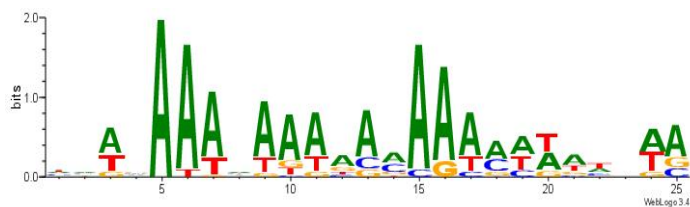


Dataset #: 5
 Motif ID: 56
 Motif name: TFM11
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 9
 Number of overlap: 14
 Similarity score: 0.0626838

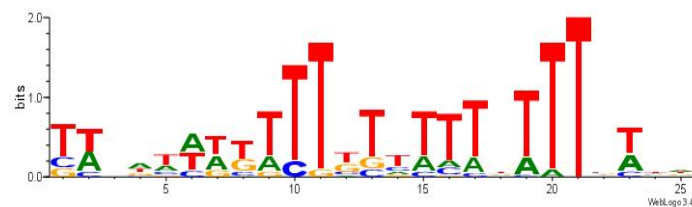
Alignment:

TWVHWWWYTTTTYTTTTTHTTTVWBH
 ---WWTAKTTCDKAATT-----

Original motif Consensus sequence: HDWVAAAHAAAAAMAAAMWWWHBWA



Reverse complement motif Consensus sequence: TWVHWWWYTTTTYTTTTTHTTTVWBH

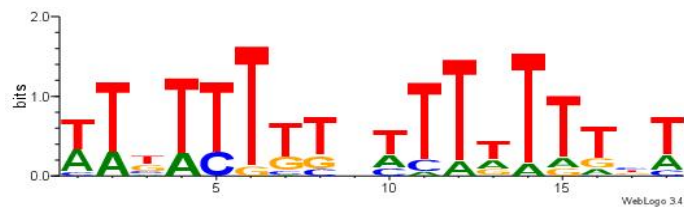


Dataset #: 5
 Motif ID: 52
 Motif name: TFM1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 14
 Similarity score: 0.0667239

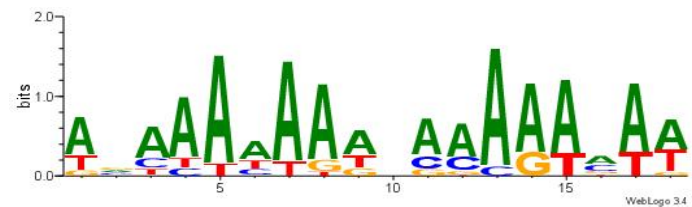
Alignment:

WKTTTTTHWTTTTTBT
 -WWTAKTTCDKAATT---

Original motif Consensus sequence: WKTTTTTHWTTTTTBT



Reverse complement motif Consensus sequence: ABAAAAAWHAAAAARAW

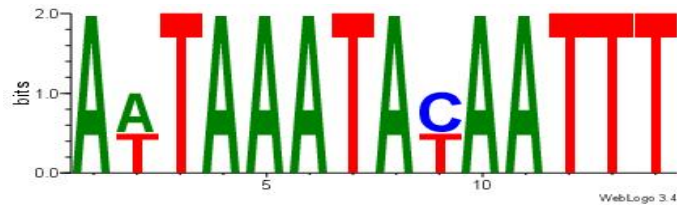


Dataset #: 2
 Motif ID: 5
 Motif name: Motif 5
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1

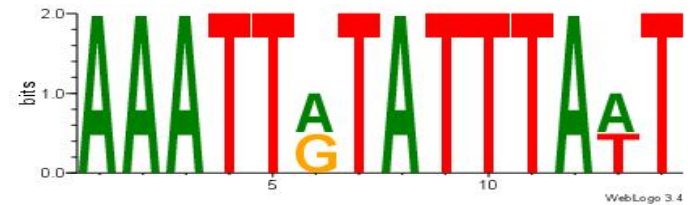
Number of overlap: 14
 Similarity score: 0.0741071

Alignment:
 AWTAAATAYAATTT
 WWTAKTTCDKAATT

Original motif Consensus sequence: AWTAAATAYAATTT

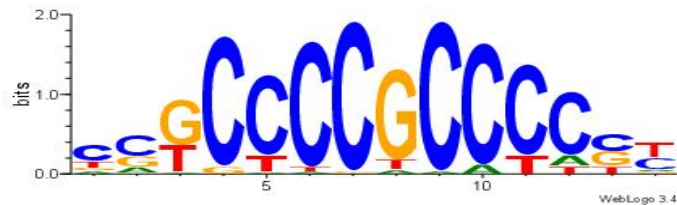


Reverse complement motif Consensus sequence: AAATTKTATTTAW

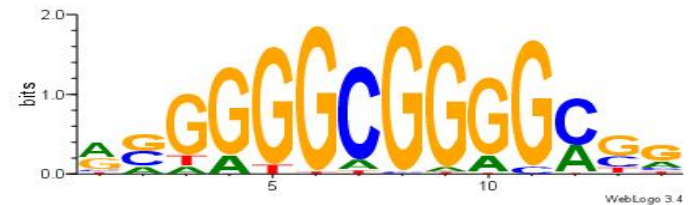


Dataset #: 2 Motif ID: 7 Motif name: Motif 7

Original motif Consensus sequence: CSKCCCCGCCCSY



Reverse complement motif Consensus sequence: MSGGGGCGGGY



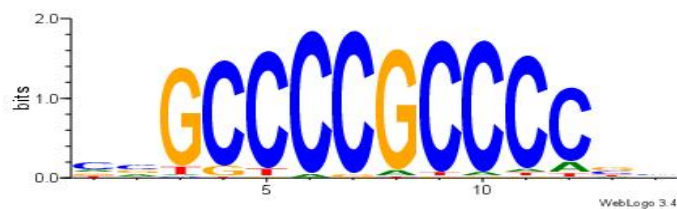
Best Matches for Motif ID 7 (Highest to Lowest)

Dataset #: 4
 Motif ID: 36
 Motif name: csGCCCCGCCCSy
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif

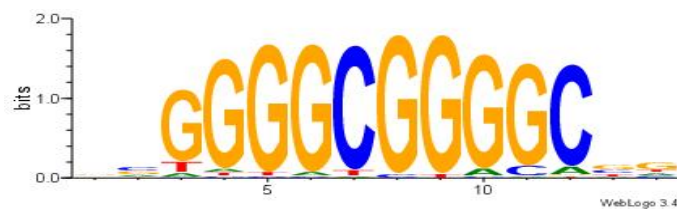
Direction: Forward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0

Alignment:
 HVGCCCGCCCCBB
 CSKCCCGCCCCSY

Original motif Consensus sequence: HVGCCCGCCCCBB



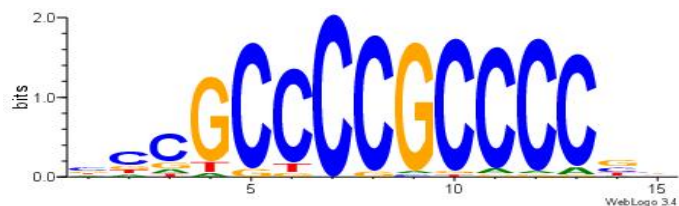
Reverse complement motif Consensus sequence: BBGGGGCGGGGC



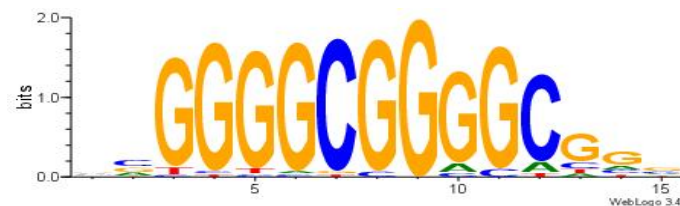
Dataset #: 4
 Motif ID: 38
 Motif name: cccGCCCCGCCCCsb
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0.0012818

Alignment:
 BCCGCCCCGCCCCBB
 -CSKCCCGCCCCSY

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB

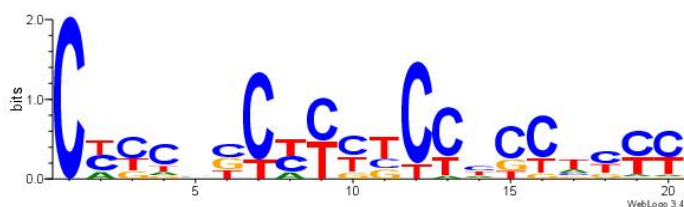


Dataset #: 5
Motif ID: 54
Motif name: TFM12
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 4
Number of overlap: 14
Similarity score: 0.0537802

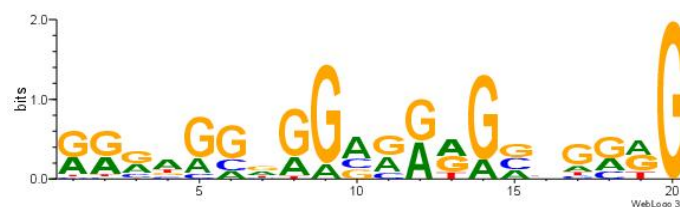
Alignment:

```
CYYCBBBCYYYTCCHCCTYYY  
---CSKCCCCGCCCSY---
```

Original motif Consensus sequence: CYYCBBBCYYYTCCHCCTYYY



Reverse complement motif Consensus sequence: KKKAGGDGGAKKMGBBGKMG

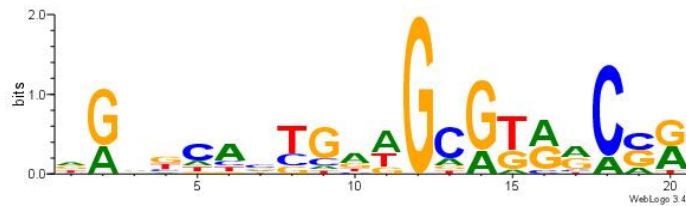


Dataset #: 3
 Motif ID: 31
 Motif name: Pax5
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 7
 Number of overlap: 14
 Similarity score: 0.0662825

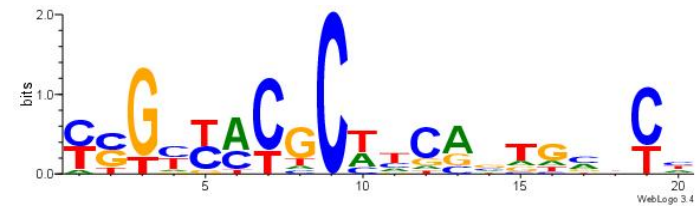
Alignment:

DGVBCABTGDWGCGRRCR
 -----MSGGGGCGGGYSG

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBCD

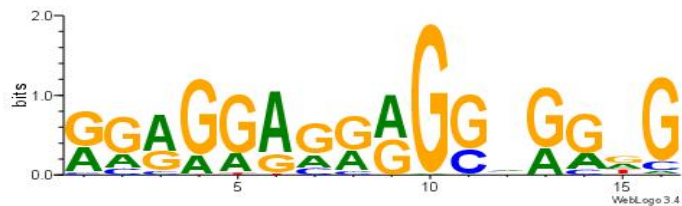


Dataset #: 5
 Motif ID: 51
 Motif name: TFM2
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1

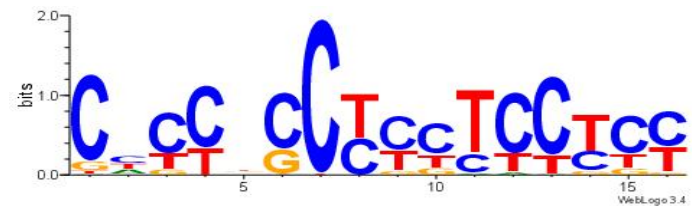
Number of overlap: 14
 Similarity score: 0.0758609

Alignment:
 CHCCBCKMCTCCKCM
 CSKCCCCGCCCSY--

Original motif Consensus sequence: RGRGGAGRRGGHGGDG

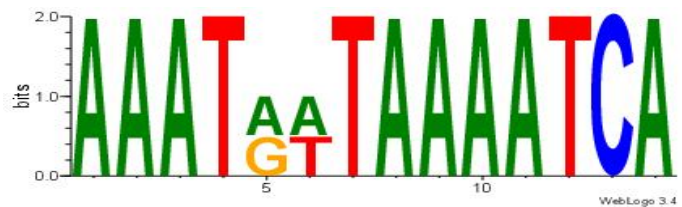


Reverse complement motif Consensus sequence:
 CHCCBCKMCTCCKCM

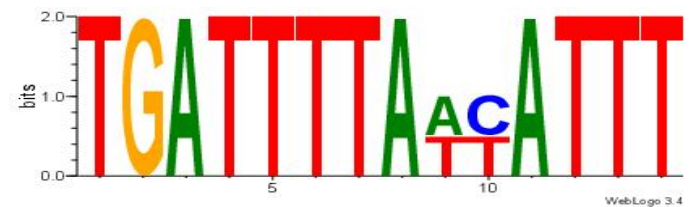


Dataset #: 2 Motif ID: 8 Motif name: Motif 8

Original motif Consensus sequence: AAATRWATAAATCA



Reverse complement motif Consensus sequence: TGATTTAWKATT



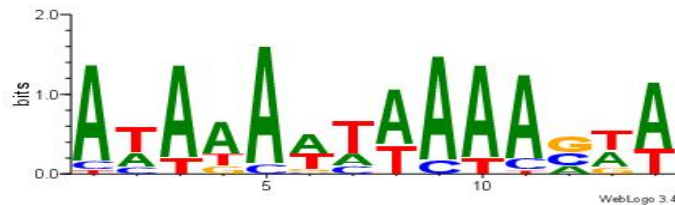
Best Matches for Motif ID 8 (Highest to Lowest)

Dataset #: 2
 Motif ID: 3
 Motif name: Motif 3
 Matching format of first motif: Reverse Complement

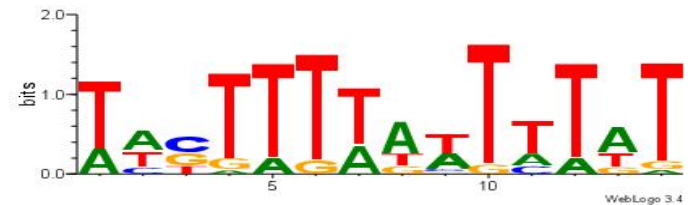
Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0.0961539

Alignment:
 TWSTTTWAWTTTWT
 TGATTTTAWKATTT

Original motif Consensus sequence: AWAAAWTWAAASWA



Reverse complement motif Consensus sequence: TWSTTTWAWTTTWT

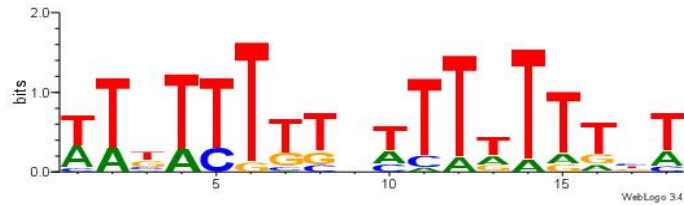


Dataset #: 5
 Motif ID: 52
 Motif name: TFM1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 4
 Number of overlap: 14
 Similarity score: 0.10348

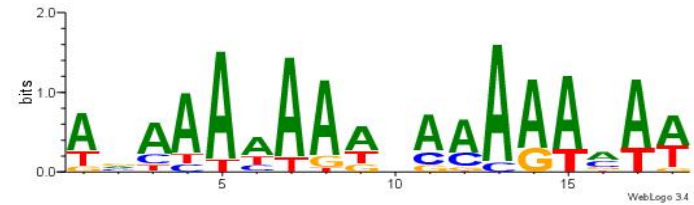
Alignment:

WKTTTTTHWTTTTTBT
-TGATTTTAWKATTT---

Original motif Consensus sequence: WKTTTTTHWTTTTTBT



Reverse complement motif Consensus sequence:
ABAAAAAWHAAAAARAW



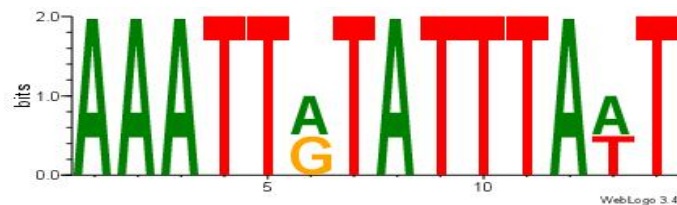
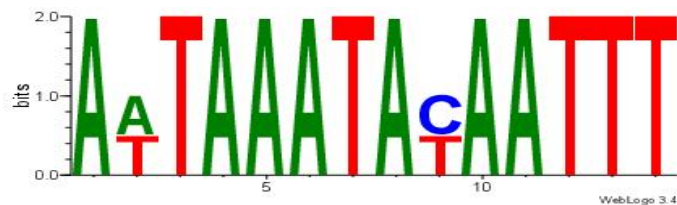
Dataset #: 2
Motif ID: 5
Motif name: Motif 5
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 14
Similarity score: 0.107143

Alignment:

AAATTKTATTTAWT
TGATTTTAWKATTT

Original motif Consensus sequence: AWTAAATAYAATTT

Reverse complement motif Consensus sequence: AAATTKTATTTAWT



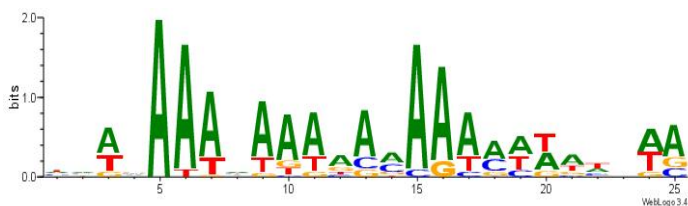
Dataset #: 5
 Motif ID: 56
 Motif name: TFM11
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 7
 Number of overlap: 14
 Similarity score: 0.111345

Alignment:

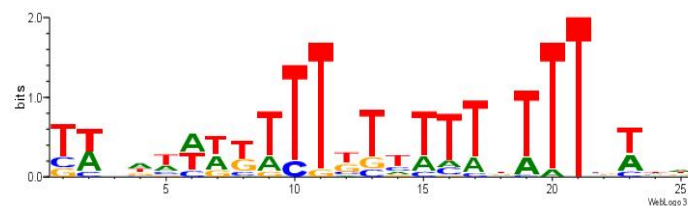
```

HDWVAAAHAAAAAMAAAMWWWHBWA
-----AAATRWTAATAATCA-----
  
```

Original motif Consensus sequence:
 HDWVAAAHAAAAAMAAAMWWWHBWA



Reverse complement motif Consensus sequence:
 TWVHWWYTTTTTTTTTTTTHTTTWWBH



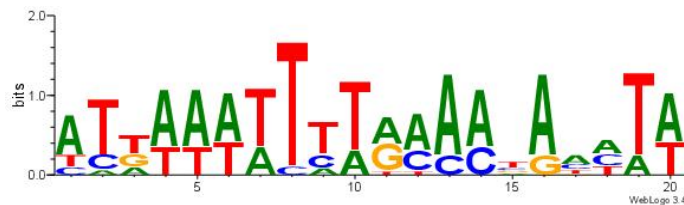
Dataset #: 5

Motif ID: 55
 Motif name: TFM13
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 4
 Number of overlap: 14
 Similarity score: 0.11369

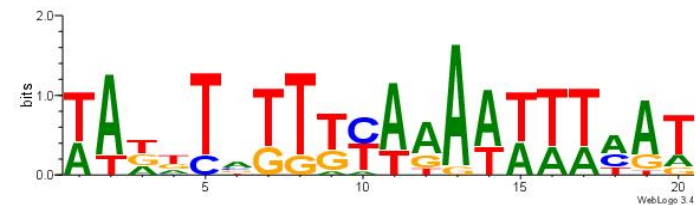
Alignment:

WAHHTVTTYKAAAATTRAT
 ---TGATTTTAWKATTT---

Original motif Consensus sequence: ATKAAWTTTTRMAABAHTW

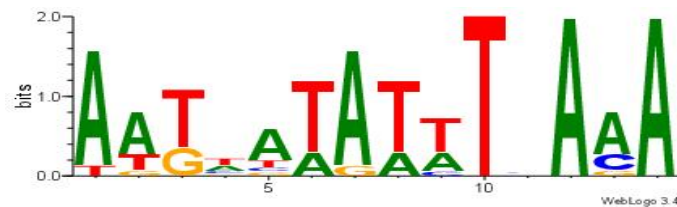


Reverse complement motif Consensus sequence: WAHHTVTTYKAAAATTRAT

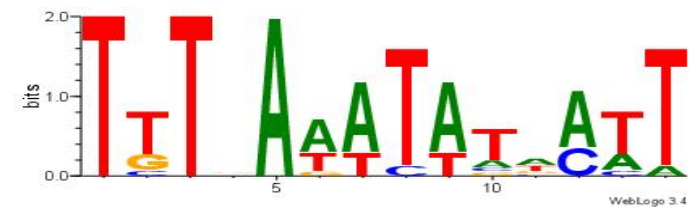


Dataset #: 2 Motif ID: 9 Motif name: Motif 9

Original motif Consensus sequence: AATHATATWTHAAA



Reverse complement motif Consensus sequence: TTTDAWATATHAT



Best Matches for Motif ID 9 (Highest to Lowest)

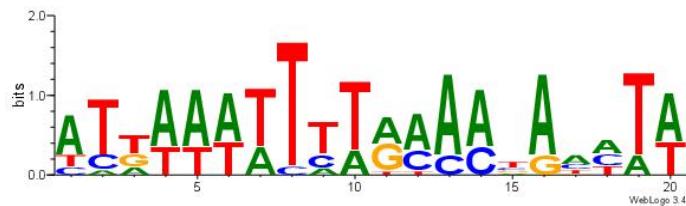
Dataset #: 5
 Motif ID: 55
 Motif name: TFM13
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0.0332341

Alignment:

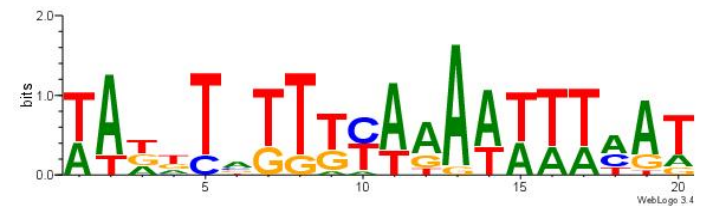
```

WAHHTVTTYKAAAATTRAT
-----TTTDAWATATHATT
  
```

Original motif Consensus sequence: ATKAAWTTTTRMAABAHTW



Reverse complement motif Consensus sequence: WAHHTVTTYKAAAATTRAT

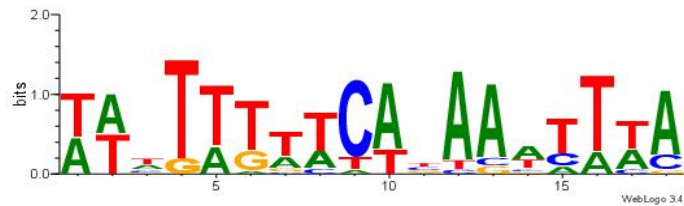


Dataset #: 5
 Motif ID: 53
 Motif name: TFM3
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif

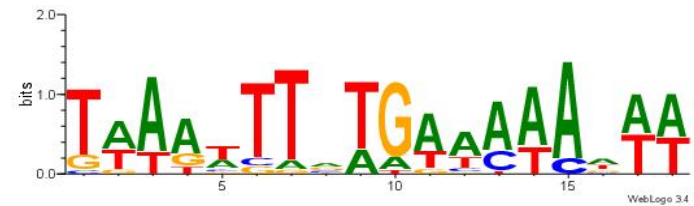
Direction: Backward
 Position number: 2
 Number of overlap: 14
 Similarity score: 0.0486562

Alignment:
 WWHTTTTTTCABAAWTTWA
 ---TTTDAWATATHATT-

Original motif Consensus sequence: WWHTTTTTTCABAAWTTWA



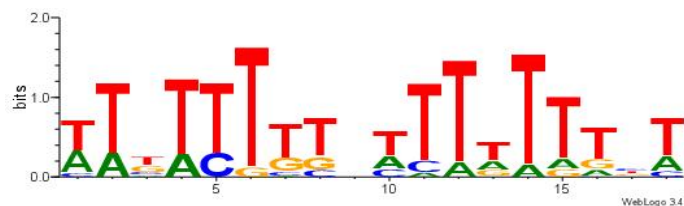
Reverse complement motif Consensus sequence: TWAAWTTVTGAAAAHWW



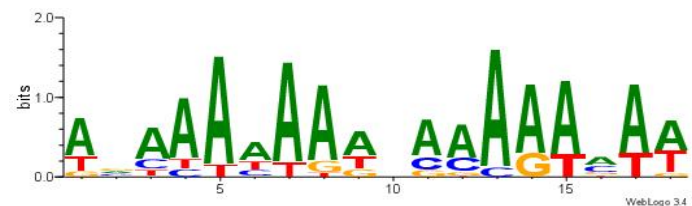
Dataset #: 5
 Motif ID: 52
 Motif name: TFM1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 14
 Similarity score: 0.0528083

Alignment:
 WKTTTTTTHWTTTTTTBT
 ---TTTDAWATATHATT-

Original motif Consensus sequence: WTKTTTTTHWTTTTTBT



Reverse complement motif Consensus sequence: ABAAAAAWHAAAAARAW

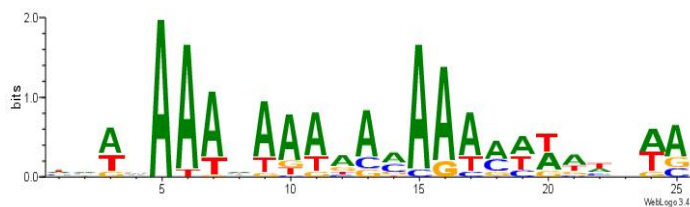


Dataset #: 5
Motif ID: 56
Motif name: TFM11
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 14
Similarity score: 0.054155

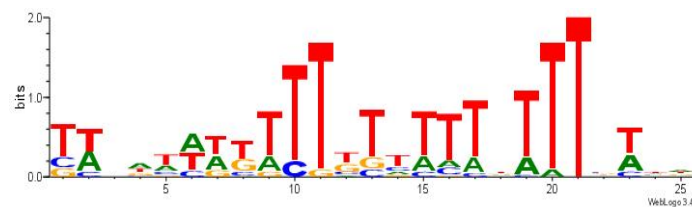
Alignment:

HDWVAAAHAAAAAMAAAMWWWHBWA
TTTDAWATATHATT-----

Original motif Consensus sequence: HDWVAAAHAAAAAMAAAMWWWHBWA



Reverse complement motif Consensus sequence: TWVHWWWYTTTTYTTTTTHTTTTVWBH

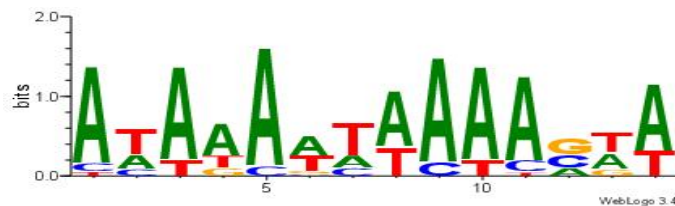


Dataset #: 2
 Motif ID: 3
 Motif name: Motif 3
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0.0675748

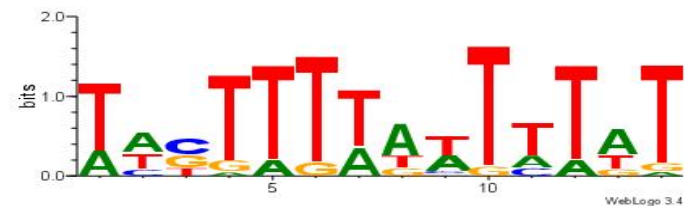
Alignment:

TWSTTTWAWTTTWT
 AATHATATWTHAAA

Original motif Consensus sequence: AWAAAWTWAASWA

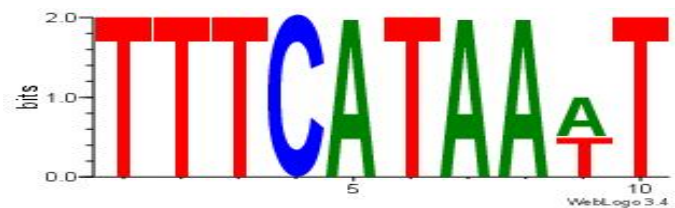


Reverse complement motif Consensus sequence: TWSTTTWAWTTTWT

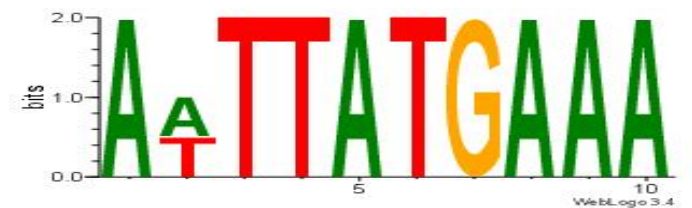


Dataset #: 2 Motif ID: 10 Motif name: Motif 10

Original motif Consensus sequence: TTCATAAWT



Reverse complement motif Consensus sequence: AWTTATGAAA



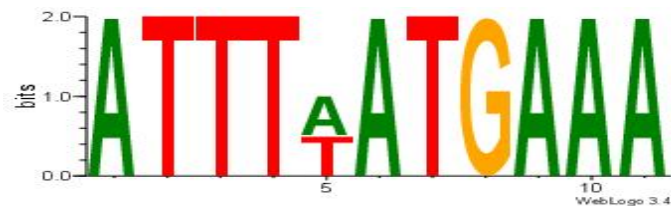
Best Matches for Motif ID 10 (Highest to Lowest)

Dataset #: 2
Motif ID: 11
Motif name: Motif 11
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 2
Number of overlap: 10
Similarity score: 0.01875

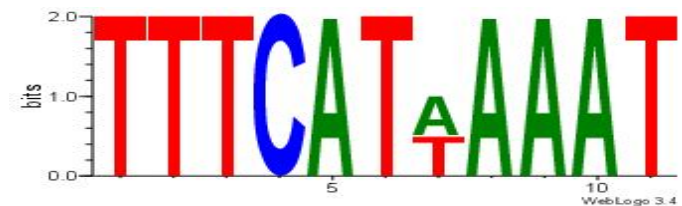
Alignment:

ATTTWATGAAA
-AWTTATGAAA

Original motif Consensus sequence: ATTTWATGAAA



Reverse complement motif Consensus sequence: TTTTCATWAAAT



Dataset #: 2
Motif ID: 6
Motif name: Motif 6
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif

Direction: Forward
 Position number: 5
 Number of overlap: 10
 Similarity score: 0.0375

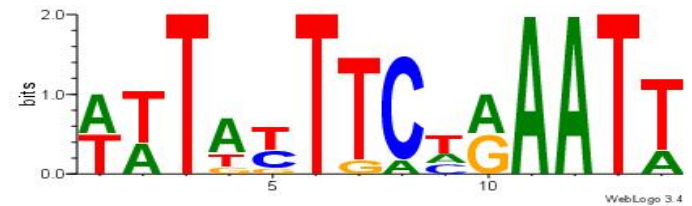
Alignment:

AATTYDGAARTAWW
 ----AWTTATGAAA

Original motif Consensus sequence: AATTYDGAARTAWW



Reverse complement motif Consensus sequence: WWTAKTTCDKAAT

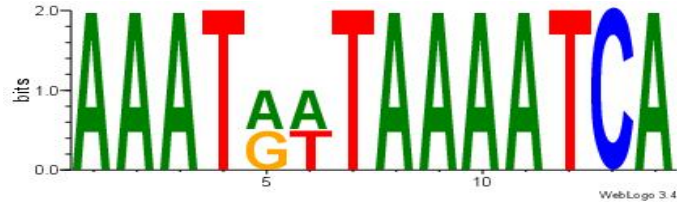


Dataset #: 2
 Motif ID: 8
 Motif name: Motif 8
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 4
 Number of overlap: 10
 Similarity score: 0.04375

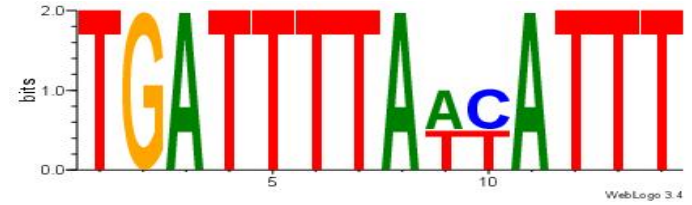
Alignment:

TGATTTTAWKATTT
 -TTTCATAAWT---

Original motif Consensus sequence: AAATRWTAATCA



Reverse complement motif Consensus sequence: TGATTTAWKATT

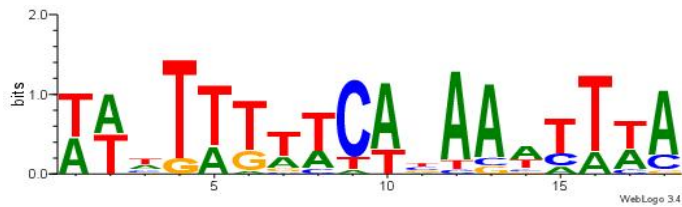


Dataset #: 5
 Motif ID: 53
 Motif name: TFM3
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 6
 Number of overlap: 10
 Similarity score: 0.0448864

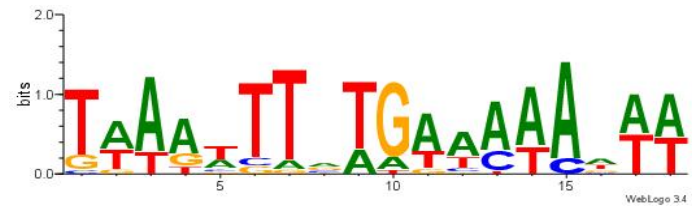
Alignment:

TWAAWTTVTGAAAAHWW
 ---AWTTATGAAA-----

Original motif Consensus sequence: WWHTTTTTCABAATTWA



Reverse complement motif Consensus sequence: TWAAWTTVTGAAAAHWW

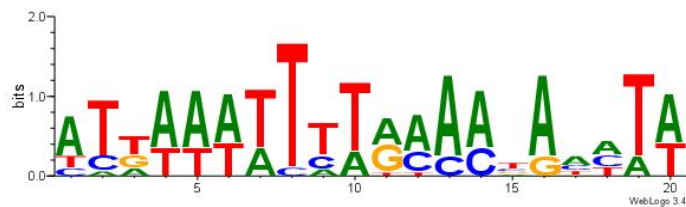


Dataset #: 5
 Motif ID: 55
 Motif name: TFM13
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 5
 Number of overlap: 10
 Similarity score: 0.0545833

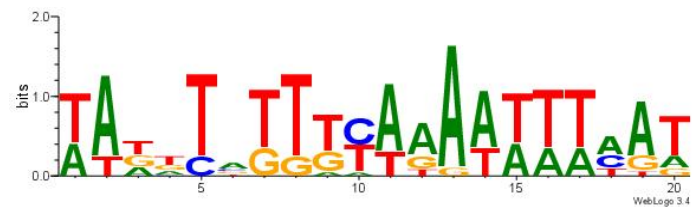
Alignment:

ATKAAWTTTTRMAABAHTW
 ----AWTTATGAAA-----

Original motif Consensus sequence: ATKAAWTTTTRMAABAHTW



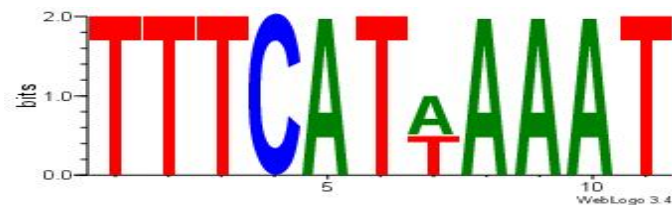
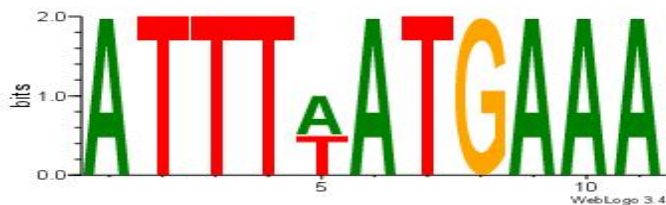
Reverse complement motif Consensus sequence: WAHHTVTTYKAAAATTRAT



Dataset #: 2 Motif ID: 11 Motif name: Motif 11

Original motif Consensus sequence: ATTTWATGAAA

Reverse complement motif Consensus sequence: TTTCATWAAAT

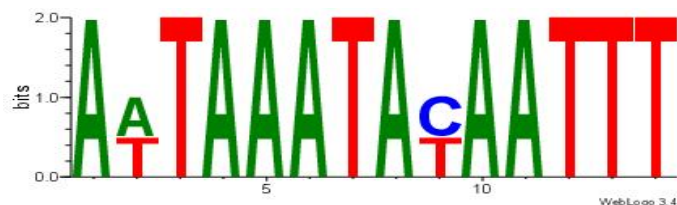


Best Matches for Motif ID 11 (Highest to Lowest)

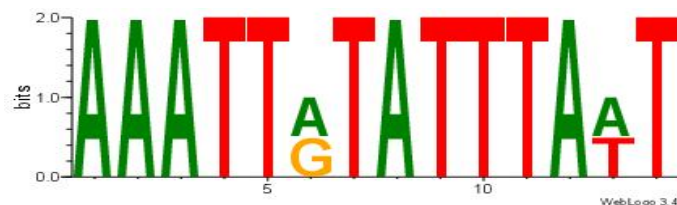
Dataset #: 2
 Motif ID: 5
 Motif name: Motif 5
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 4
 Number of overlap: 11
 Similarity score: 0.0795455

Alignment:
 AAATTKTATTTAWT
 ---TTTCATWAAAT

Original motif Consensus sequence: AWTAAATAYAATTT



Reverse complement motif Consensus sequence: AAATTKTATTTAWT



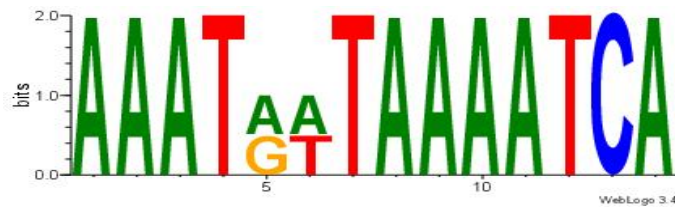
Dataset #: 2

Motif ID: 8
 Motif name: Motif 8
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 11
 Similarity score: 0.0795455

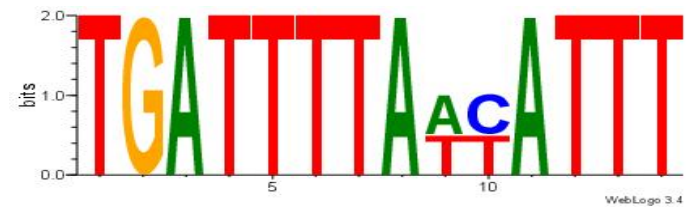
Alignment:

AAATRWATAAATCA
 --TTTCATWAAAT--

Original motif Consensus sequence: AAATRWATAAATCA



Reverse complement motif Consensus sequence: TGATTTTAWKATT

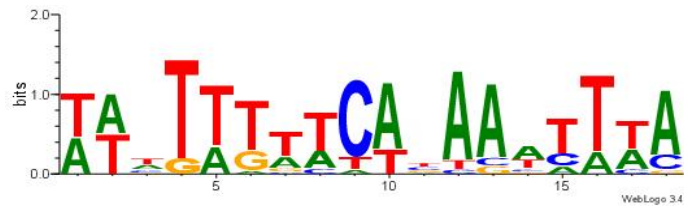


Dataset #: 5
 Motif ID: 53
 Motif name: TFM3
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 6
 Number of overlap: 11
 Similarity score: 0.0991736

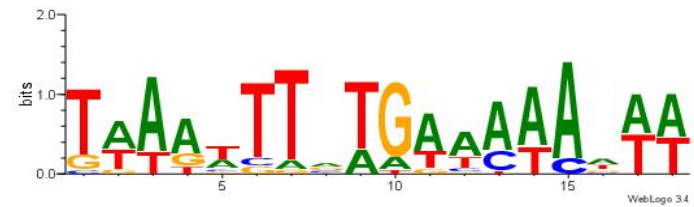
Alignment:

```
WWHTTTTTTCABAAWTTWA  
-----TTCATWAAAT--
```

Original motif Consensus sequence: WWHTTTTTTCABAAWTTWA



Reverse complement motif Consensus sequence:
TAAWTTTGTGAAAAHWW



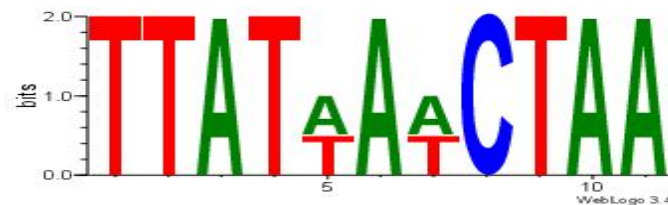
Dataset #:	2
Motif ID:	18
Motif name:	Motif 18
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	11
Similarity score:	0.102273

Alignment:

```
TTATWAWCTAA  
ATTTWATGAAA
```

Original motif Consensus sequence: TTAGWTWATAA

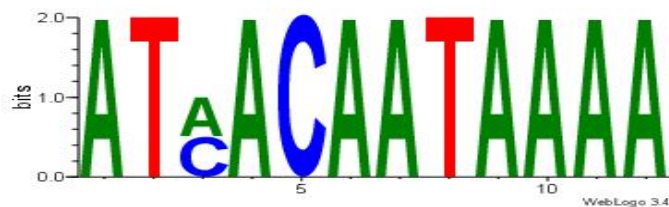
Reverse complement motif Consensus sequence: TTATWAWCTAA



Dataset #: 2
 Motif ID: 15
 Motif name: Motif 15
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.102273

Alignment:
 TTTTATTGTYAT
 ATTTWATGAAA-

Original motif Consensus sequence: ATMACAATAAAA



Reverse complement motif Consensus sequence: TTTTATTGTYAT



Dataset #: 2 Motif ID: 12 Motif name: Motif 12

Original motif Consensus sequence: AAAACAAA



Reverse complement motif Consensus sequence: TTTGTTTT



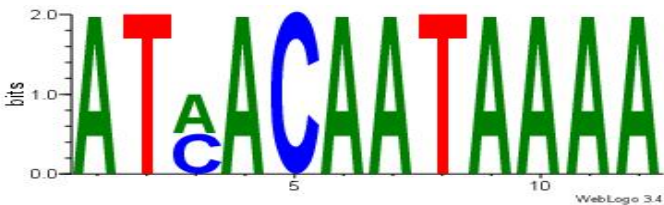
Best Matches for Motif ID 12 (Highest to Lowest)

Dataset #:	2
Motif ID:	15
Motif name:	Motif 15
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:	0.0625

Alignment:

```
TTTTATTGTYAT
- TTTGTTTT---
```

Original motif Consensus sequence: ATMACAATAAAA



Reverse complement motif Consensus sequence: TTTTATTGTYAT

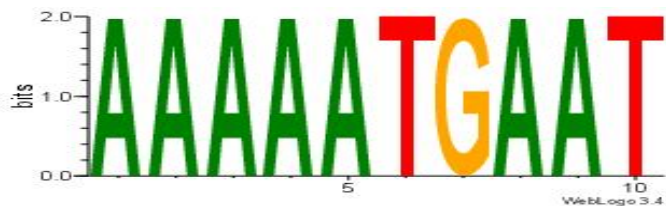


Dataset #: 2
 Motif ID: 17
 Motif name: Motif 17
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 8
 Similarity score: 0.0625

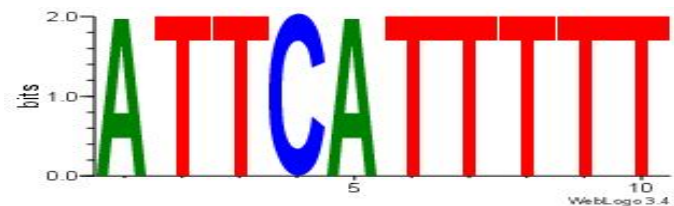
Alignment:

AAAAATGAAT
 -AAAACAAA-

Original motif Consensus sequence: AAAAATGAAT



Reverse complement motif Consensus sequence: ATTCA TTTT



Dataset #: 2
 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: 8

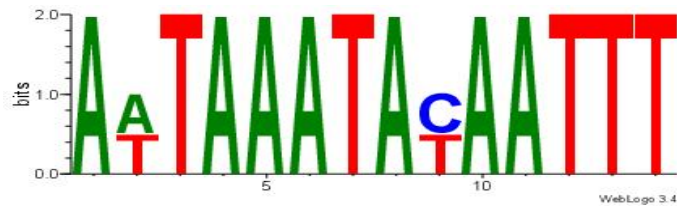
Similarity score: 0.078125

Alignment:

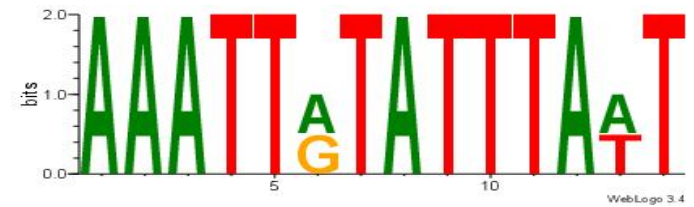
AWTAAATAYAATTT

----AAAACAAA--

Original motif Consensus sequence: AWTAAATAYAATTT



Reverse complement motif Consensus sequence: AAATTKTATTTAW



Dataset #: 2
Motif ID: 14
Motif name: Motif 14
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: 0.078125

Alignment:

AWAAATAA

AAAACAAA

Original motif Consensus sequence: AWAAATAA

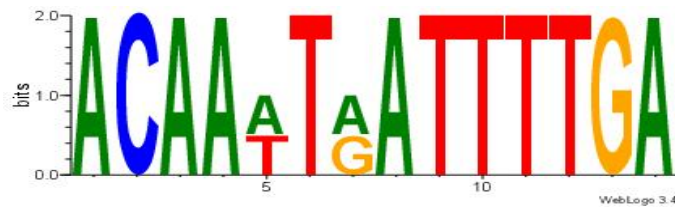
Reverse complement motif Consensus sequence: TTATTTWT



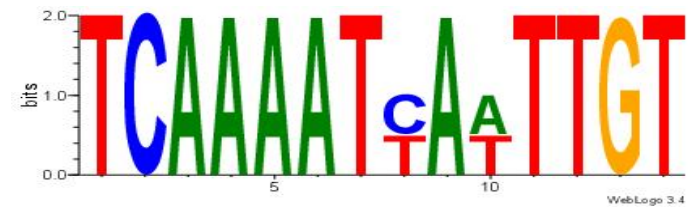
Dataset #: 2
 Motif ID: 16
 Motif name: Motif 16
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 5
 Number of overlap: 8
 Similarity score: 0.078125

Alignment:
 TCAAAATKAWTTGT
 --AAAACAAA----

Original motif Consensus sequence: ACAAWTRATTTTGA



Reverse complement motif Consensus sequence: TCAAAATKAWTTG



Dataset #: 2 Motif ID: 13 Motif name: Motif 13

Original motif Consensus sequence: AAAGATTT



Reverse complement motif Consensus sequence: AAATCTTT



Best Matches for Motif ID 13 (Highest to Lowest)

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

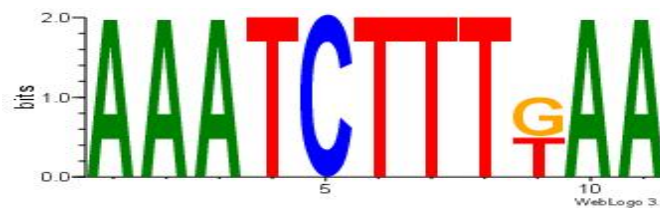
Alignment:

```
AAATCTTTYAA  
AAATCTTT---
```

Original motif Consensus sequence: TTMAAGATTT



Reverse complement motif Consensus sequence: AAATCTTTYAA

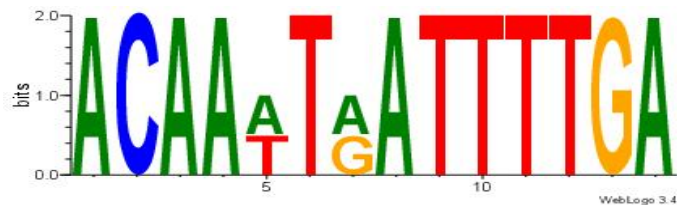


Dataset #: 2
 Motif ID: 16
 Motif name: Motif 16
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 5
 Number of overlap: 8
 Similarity score: 0.0625

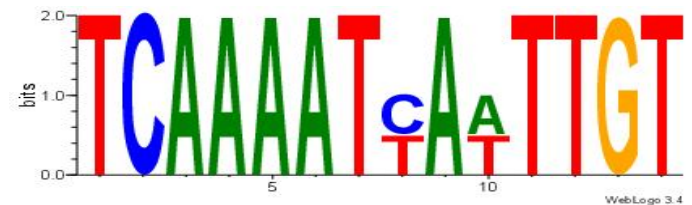
Alignment:

TCAAAATKAWTTGT
 ----AAAGATTT--

Original motif Consensus sequence: ACAAWTRATTTTGA



Reverse complement motif Consensus sequence: TCAAAATKAWTTG



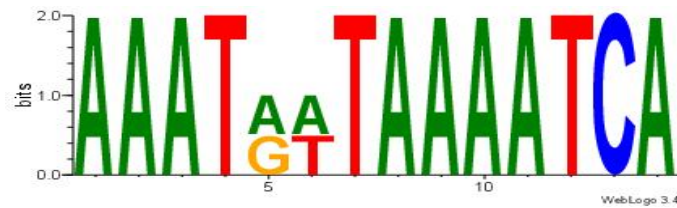
Dataset #: 2
 Motif ID: 8
 Motif name: Motif 8
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 8

Similarity score: 0.0625

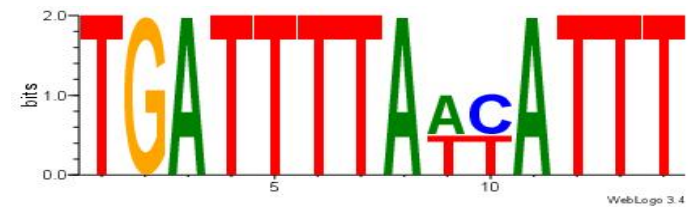
Alignment:

AAATRWTA~~AA~~ATCA
-----AAATCTTT

Original motif Consensus sequence: AAATRWTA~~AA~~ATCA



Reverse complement motif Consensus sequence: TGATTTTAWKATT



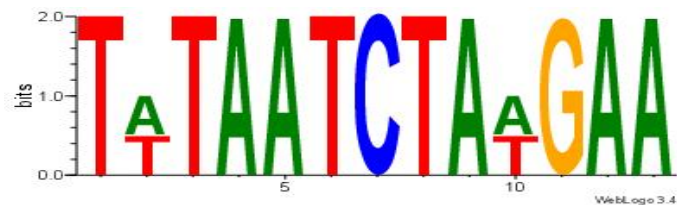
Dataset #: 2
Motif ID: 19
Motif name: Motif 19
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 3
Number of overlap: 8
Similarity score: 0.078125

Alignment:

TTCWTAGATTAWA
---AAAGATTT--

Original motif Consensus sequence: TTCWTAGATTAWA

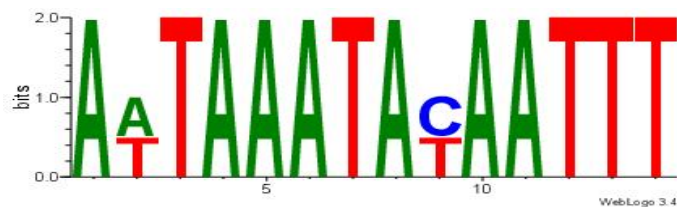
Reverse complement motif Consensus sequence: TWTAATCTAWGAA



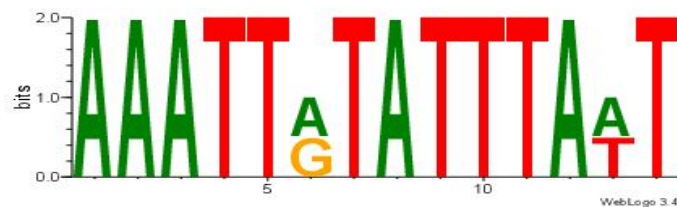
Dataset #: 2
 Motif ID: 5
 Motif name: Motif 5
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 8
 Similarity score: 0.078125

Alignment:
 AAATTKTATTTAWT
 AAATCTTT-----

Original motif Consensus sequence: AWTAAATAYAATTT



Reverse complement motif Consensus sequence: AAATTKTATTTAWT



Dataset #: 2 Motif ID: 14 Motif name: Motif 14

Original motif Consensus sequence: AWAAATAA



Reverse complement motif Consensus sequence: TTATTTWT



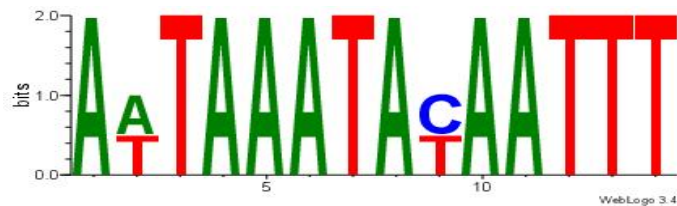
Best Matches for Motif ID 14 (Highest to Lowest)

Dataset #: 2
 Motif ID: 5
 Motif name: Motif 5
 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: 0.046875

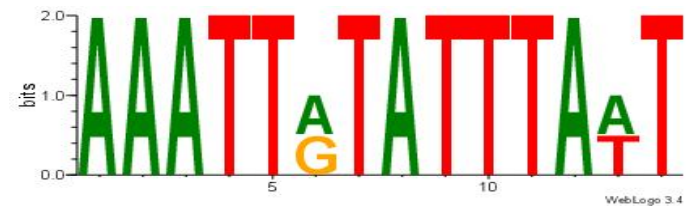
Alignment:

```
AAATTKTATTTAWT
-----TTATTTWT-
```

Original motif Consensus sequence: AWTAAATAYAATTT



Reverse complement motif Consensus sequence: AAATTKTATTTAW

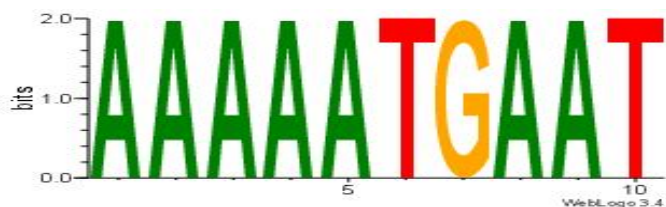


Dataset #: 2
 Motif ID: 17
 Motif name: Motif 17
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 8
 Similarity score: 0.046875

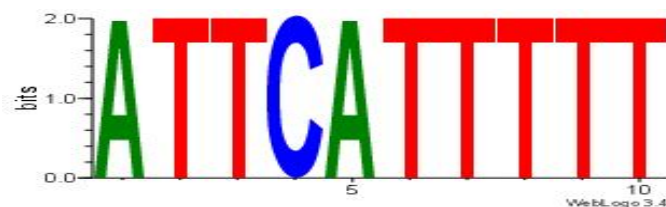
Alignment:

AAAAATGAAT
 AWAAATAA--

Original motif Consensus sequence: AAAAATGAAT



Reverse complement motif Consensus sequence: ATTCA TTTT



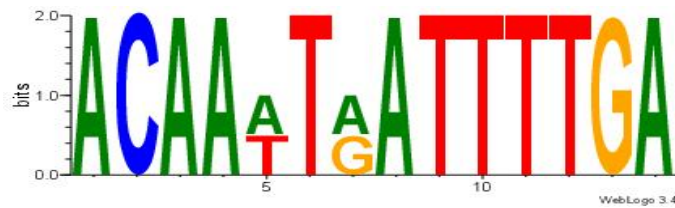
Dataset #: 2
 Motif ID: 16
 Motif name: Motif 16
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 8

Similarity score: 0.0625

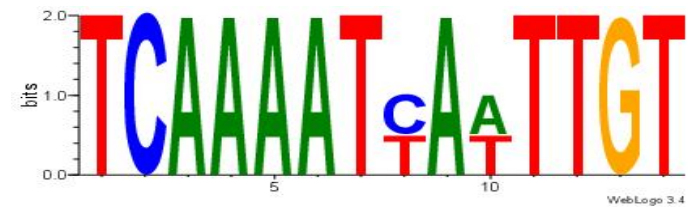
Alignment:

TCAAAATKAWTTGT
-----TTATTTWT

Original motif Consensus sequence: ACAAWTRATTTTGA



Reverse complement motif Consensus sequence: TCAAAATKAWTTG



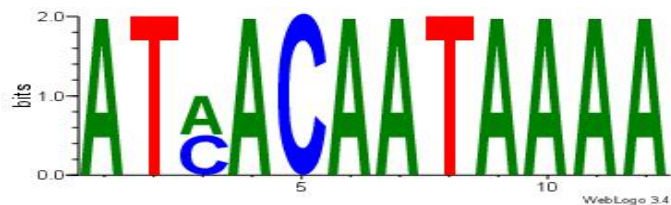
Dataset #: 2
Motif ID: 15
Motif name: Motif 15
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 3
Number of overlap: 8
Similarity score: 0.0625

Alignment:

ATMACAATAAAA
--AWAAATAA--

Original motif Consensus sequence: ATMACAATAAAA

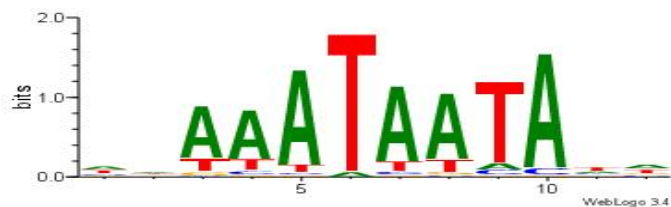
Reverse complement motif Consensus sequence: TTTTATTGTYAT



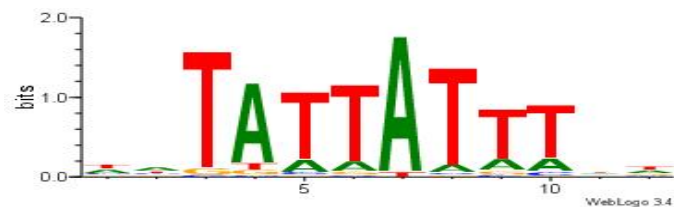
Dataset #: 4
 Motif ID: 41
 Motif name: wwAAATAATAtw
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 5
 Number of overlap: 8
 Similarity score: 0.0636574

Alignment:
 HDAAATAATADD
 AWAAATAA----

Original motif Consensus sequence: HDAAATAATADD

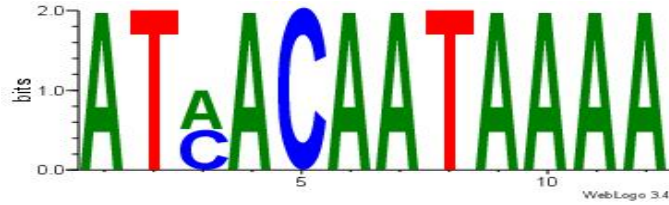


Reverse complement motif Consensus sequence: DDTATTATTDH

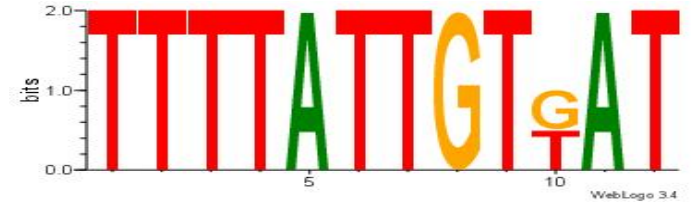


Dataset #: 2 Motif ID: 15 Motif name: Motif 15

Original motif Consensus sequence: ATMACAATAAAA



Reverse complement motif Consensus sequence: TTTATTGTYAT



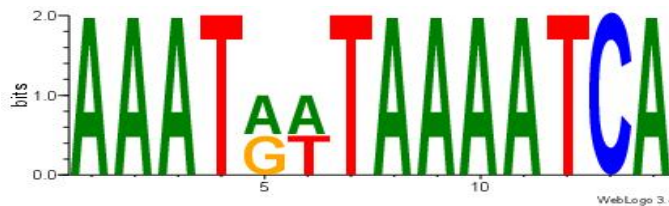
Best Matches for Motif ID 15 (Highest to Lowest)

Dataset #:	2
Motif ID:	8
Motif name:	Motif 8
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	12
Similarity score:	0.104167

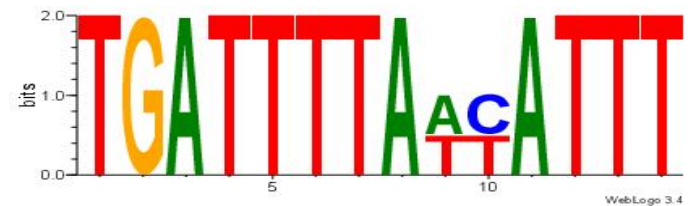
Alignment:

```
AAATRWTAATCA  
--ATMACAATAAAA
```

Original motif Consensus sequence: AAATRWTAATCA



Reverse complement motif Consensus sequence: TGATTTAWKATT

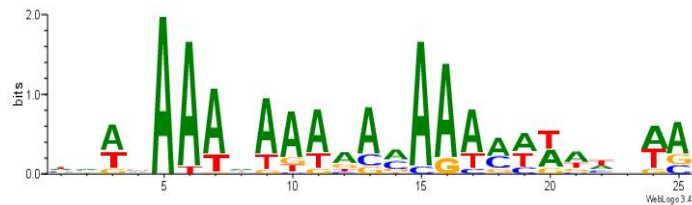


Dataset #: 5
 Motif ID: 56
 Motif name: TFM11
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 6
 Number of overlap: 12
 Similarity score: 0.109681

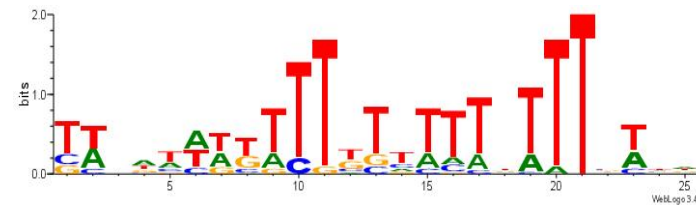
Alignment:

TWVHWWWYTTTYTTTTHTTTVWBH
 -----TTTTATTGTYAT-----

Original motif Consensus sequence:
 HDWVAAAHAAAAAMAAAMWWWHBWA



Reverse complement motif Consensus sequence:
 TWVHWWWYTTTYTTTTHTTTVWBH

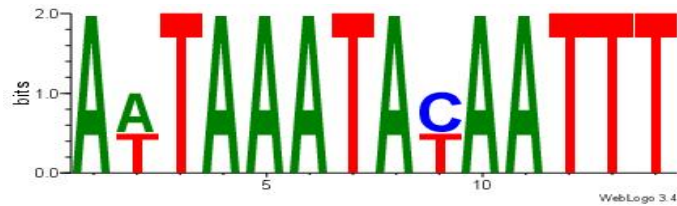


Dataset #: 2
 Motif ID: 5
 Motif name: Motif 5
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2

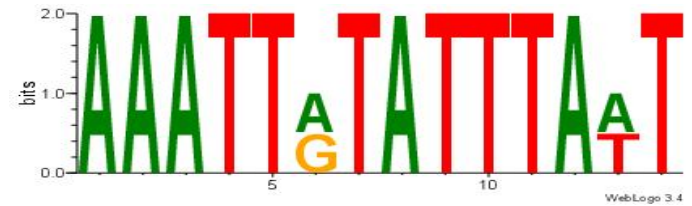
Number of overlap: 12
 Similarity score: 0.114583

Alignment:
 AWTAAATAYAATTT
 -ATMACAATAAAA-

Original motif Consensus sequence: AWTAAATAYAATTT



Reverse complement motif Consensus sequence: AAATTKTATTTAW

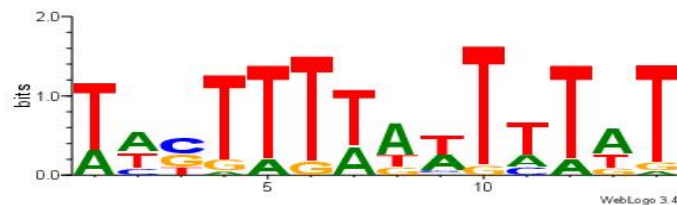
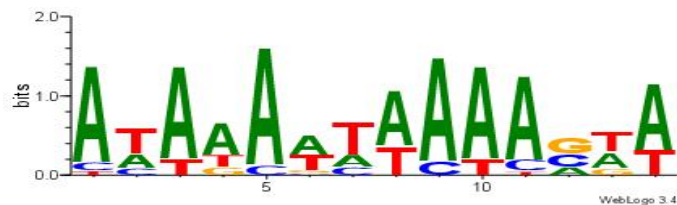


Dataset #: 2
 Motif ID: 3
 Motif name: Motif 3
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 12
 Similarity score: 0.114583

Alignment:
 AWAAAWTWAAASWA
 ATMACAATAAAA--

Original motif Consensus sequence: AWAAAWTWAAASWA

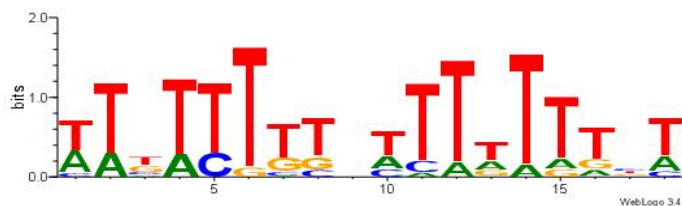
Reverse complement motif Consensus sequence: TWSTTTWAWTTT



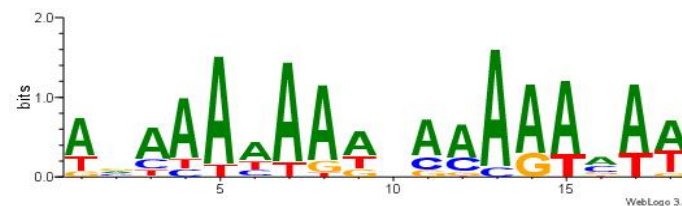
Dataset #: 5
 Motif ID: 52
 Motif name: TFM1
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3
 Number of overlap: 12
 Similarity score: 0.115652

Alignment:
 ABAAAAA WHAAAAA RAW
 --ATMACAATAAAA----

Original motif Consensus sequence: WTKTTTTTHWTTTTTTBT

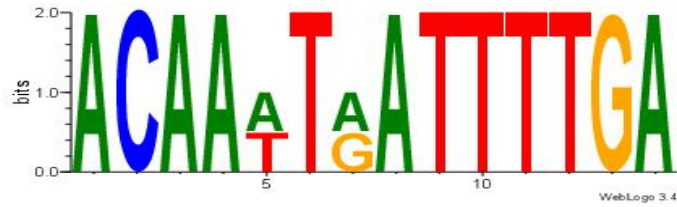


Reverse complement motif Consensus sequence: ABAAAAA WHAAAAA RAW

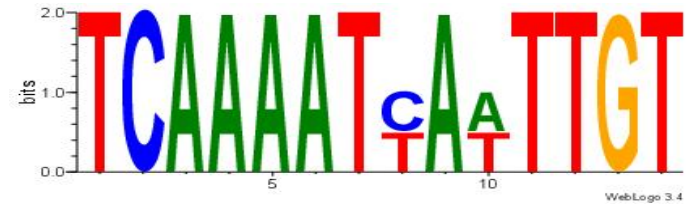


Dataset #: 2 Motif ID: 16 Motif name: Motif 16

Original motif Consensus sequence: ACAAWTRATTTTGA



Reverse complement motif Consensus sequence: TCAAAAATKAWTTG



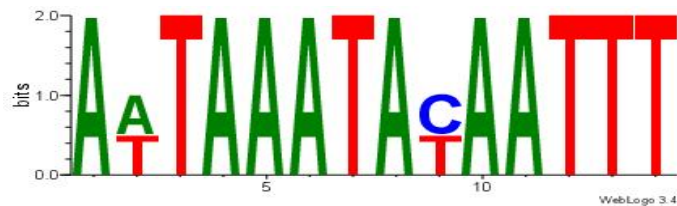
Best Matches for Motif ID 16 (Highest to Lowest)

Dataset #:	2
Motif ID:	5
Motif name:	Motif 5
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	14
Similarity score:	0.1

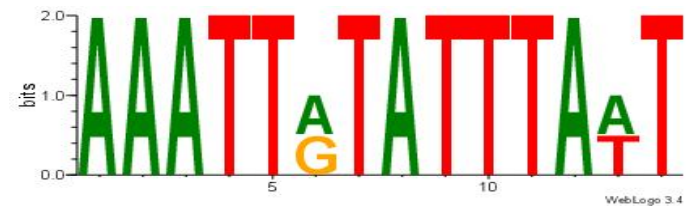
Alignment:

```
AWTAAATAYAATTT
TCAAAAATKAWTTGT
```

Original motif Consensus sequence: AWTAAATAYAATTT



Reverse complement motif Consensus sequence: AAATTKATTTAW

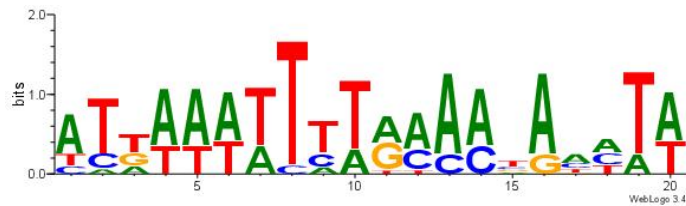


Dataset #: 5
 Motif ID: 55
 Motif name: TFM13
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 8
 Number of overlap: 13
 Similarity score: 0.599359

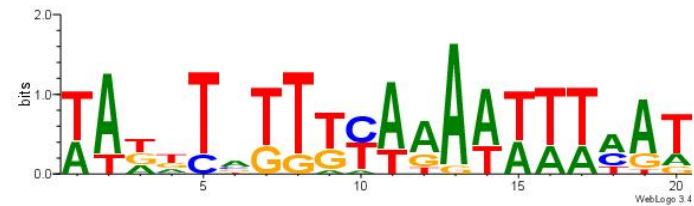
Alignment:

ATKAAWTTTTRMAABAHTW-
 -----TCAAATKAWTTGT

Original motif Consensus sequence: ATKAAWTTTTRMAABAHTW



Reverse complement motif Consensus sequence: WAHHTVTTYKAAAATTRAT



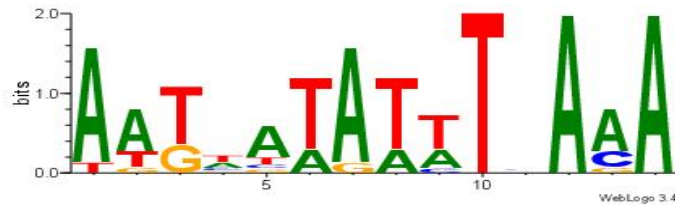
Dataset #: 2
 Motif ID: 9
 Motif name: Motif 9
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3

Number of overlap: 12
Similarity score: 1.08264

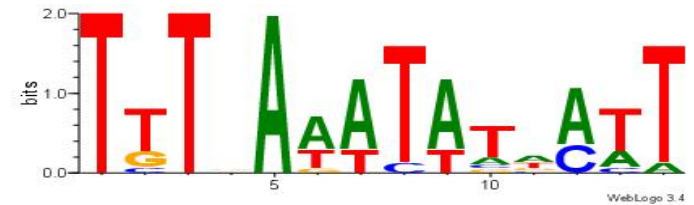
Alignment:

--AATHATATWTHAAA
ACAAWTRATTTTGA--

Original motif Consensus sequence: AATHATATWTHAAA



Reverse complement motif Consensus sequence: TTTDAWATATHAT



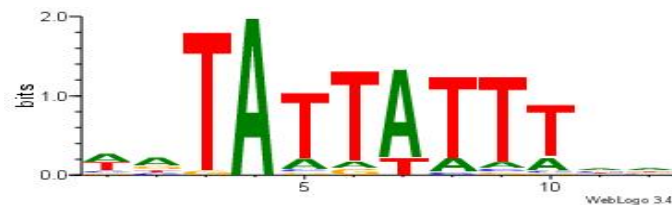
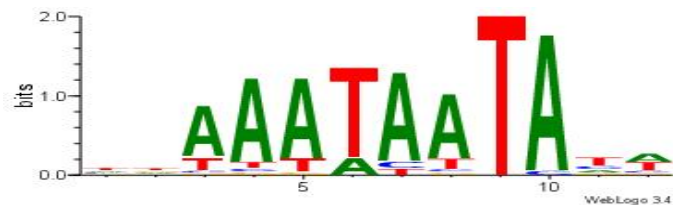
Dataset #: 4
Motif ID: 37
Motif name: tkAAATAATAtw
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 12
Similarity score: 1.08403

Alignment:

--WHTATTATTTDH
TCAAATKAWTTGT

Original motif Consensus sequence: HDAAATAATAHW

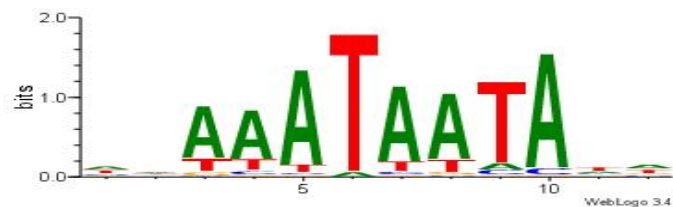
Reverse complement motif Consensus sequence: WHTATTATTTDH



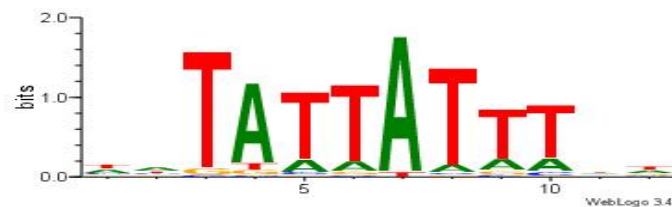
Dataset #: 4
 Motif ID: 41
 Motif name: wwAAATAATAtw
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 12
 Similarity score: 1.08881

Alignment:
 --DDTATTATTTDH
 TCAAATKAWTTGT

Original motif Consensus sequence: HDAAATAATADD



Reverse complement motif Consensus sequence: DDTATTATTTDH

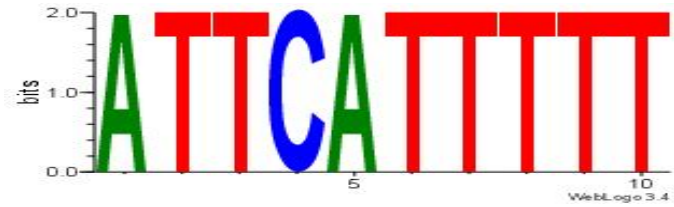


Dataset #: 2 Motif ID: 17 Motif name: Motif 17

Original motif Consensus sequence: AAAAATGAAT



Reverse complement motif Consensus sequence: ATTCATTTTT



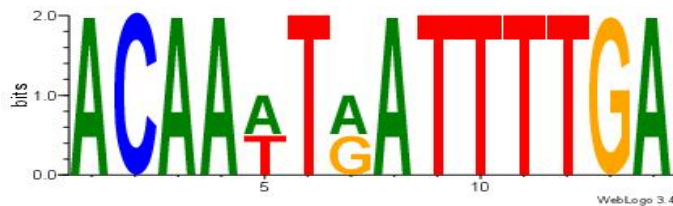
Best Matches for Motif ID 17 (Highest to Lowest)

Dataset #:	2
Motif ID:	16
Motif name:	Motif 16
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	4
Number of overlap:	10
Similarity score:	0.05

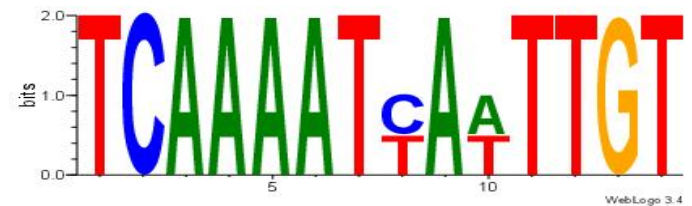
Alignment:

```
ACAAWTRATTTTGA
-ATTCATTTTT---
```

Original motif Consensus sequence: ACAAWTRATTTTGA



Reverse complement motif Consensus sequence: TCAAATKAWTTG

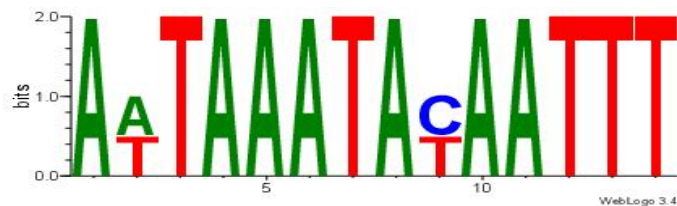


Dataset #: 2
 Motif ID: 5
 Motif name: Motif 5
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 10
 Similarity score: 0.0875

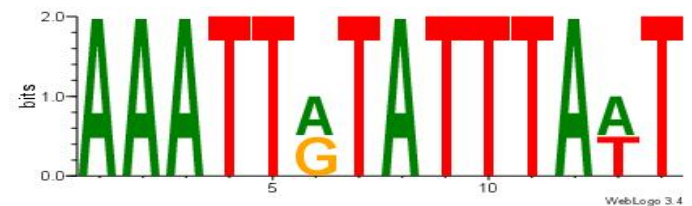
Alignment:

AWTAAATAYAATTT
 ---AAAAATGAAT-

Original motif Consensus sequence: AWTAAATAYAATTT



Reverse complement motif Consensus sequence: AAATTKTATTTAW



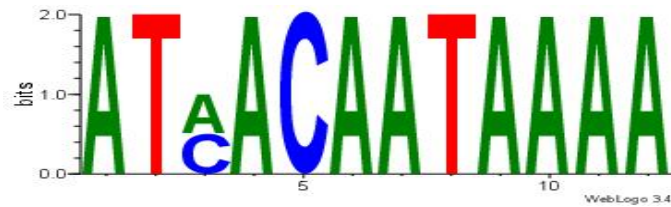
Dataset #: 2
 Motif ID: 15
 Motif name: Motif 15
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 10

Similarity score: 0.0875

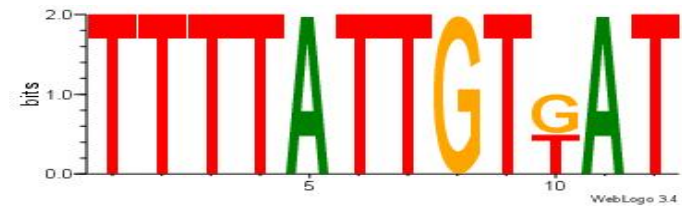
Alignment:

ATMACAATAAAA
--AAAAATGAAT

Original motif Consensus sequence: ATMACAATAAAA



Reverse complement motif Consensus sequence: TTTTATTGTYAT



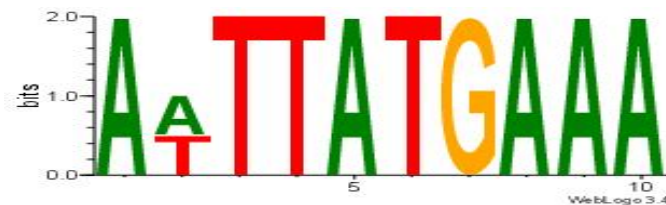
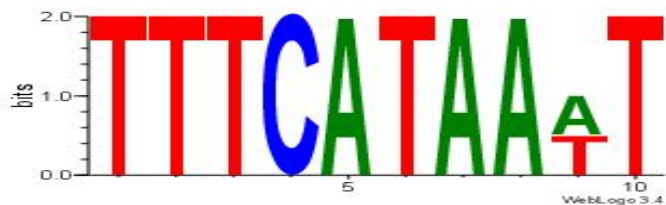
Dataset #: 2
Motif ID: 10
Motif name: Motif 10
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 10
Similarity score: 0.0875

Alignment:

AWTTATGAAA
AAAAATGAAT

Original motif Consensus sequence: TTTCATAAWT

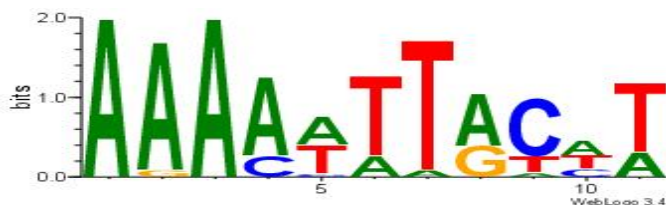
Reverse complement motif Consensus sequence: AWTTATGAAA



Dataset #: 2
 Motif ID: 4
 Motif name: Motif 4
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 10
 Similarity score: 0.0947369

Alignment:
 AWGKAAWTTTT
 -ATTCATTTTT

Original motif Consensus sequence: AAAAWTTRCWT



Reverse complement motif Consensus sequence: AWGKAAWTTTT

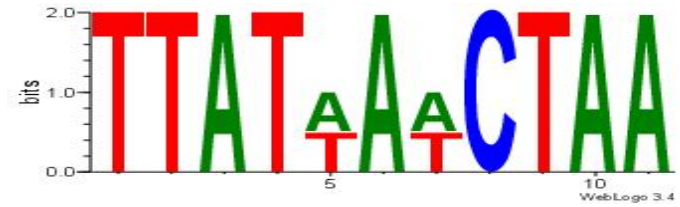


Dataset #: 2 Motif ID: 18 Motif name: Motif 18

Original motif Consensus sequence: TTAGWTWATAA



Reverse complement motif Consensus sequence: TTATWAWCTAA



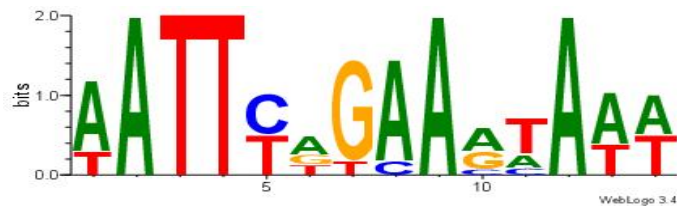
Best Matches for Motif ID 18 (Highest to Lowest)

Dataset #:	2
Motif ID:	6
Motif name:	Motif 6
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	11
Similarity score:	0.09375

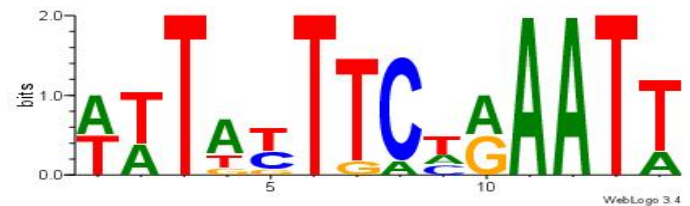
Alignment:

```
AATTYDGAARTAWW
-TTATWAWCTAA--
```

Original motif Consensus sequence: AATTYDGAARTAWW



Reverse complement motif Consensus sequence: WWTAKTTCDKAAT

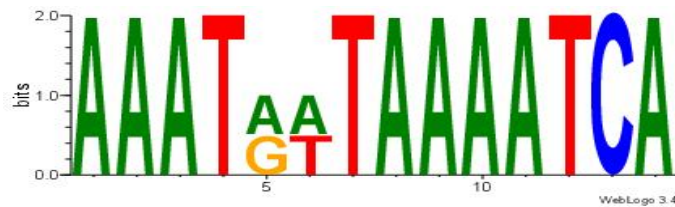


Dataset #: 2
 Motif ID: 8
 Motif name: Motif 8
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 4
 Number of overlap: 11
 Similarity score: 0.102273

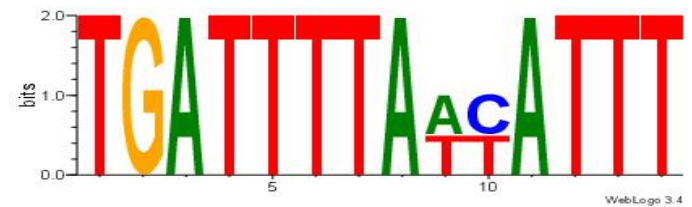
Alignment:

AAATRWTA~~AA~~ATCA
 TTATWAWCTAA---

Original motif Consensus sequence: AAATRWTA~~AA~~ATCA



Reverse complement motif Consensus sequence: TGATTTAWKATT



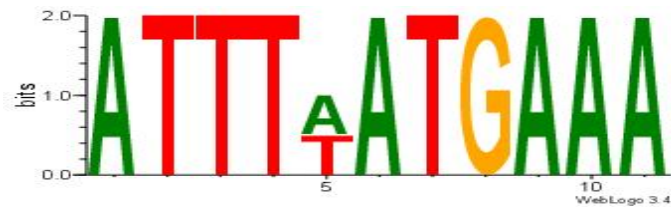
Dataset #: 2
 Motif ID: 11
 Motif name: Motif 11
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 11

Similarity score: 0.102273

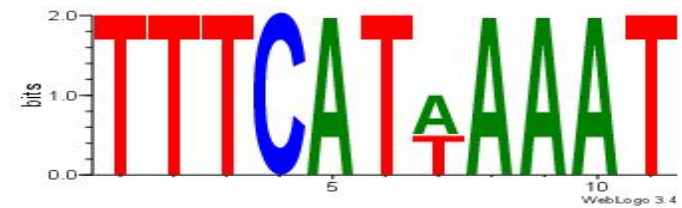
Alignment:

TTTCATWAAAT
TTAGWTWATAA

Original motif Consensus sequence: ATTTWATGAAA



Reverse complement motif Consensus sequence: TTTCATWAAAT



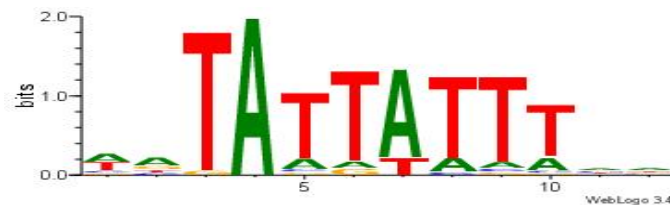
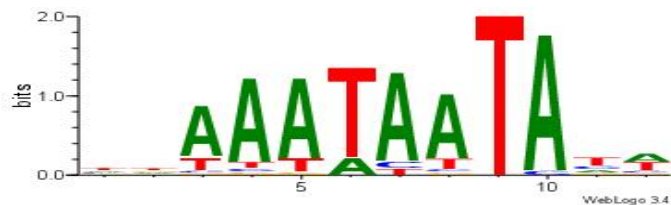
Dataset #: 4
Motif ID: 37
Motif name: tkAAATAATAtw
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2
Number of overlap: 11
Similarity score: 0.102273

Alignment:

HDAAATAATAHW
TTAGWTWATAA-

Original motif Consensus sequence: HDAAATAATAHW

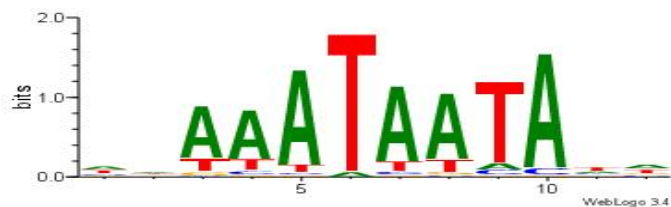
Reverse complement motif Consensus sequence: WHTATTATTTDH



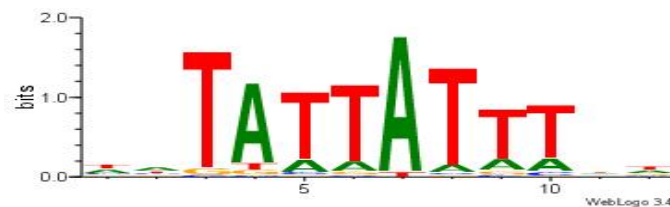
Dataset #: 4
 Motif ID: 41
 Motif name: wwAAATAATAtw
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.104798

Alignment:
 DDTATTATTTDH
 -TTATWAWCTAA

Original motif Consensus sequence: HDAAATAATADD



Reverse complement motif Consensus sequence: DDTATTATTTDH

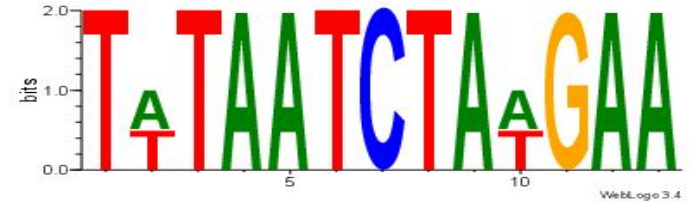


Dataset #: 2 Motif ID: 19 Motif name: Motif 19

Original motif Consensus sequence: TTCWTAGATTAWA



Reverse complement motif Consensus sequence: TWTAACTAWGAA



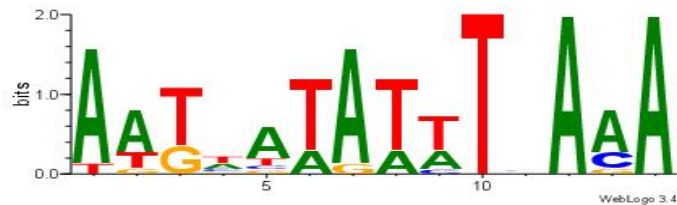
Best Matches for Motif ID 19 (Highest to Lowest)

Dataset #:	2
Motif ID:	9
Motif name:	Motif 9
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	13
Similarity score:	0.0641025

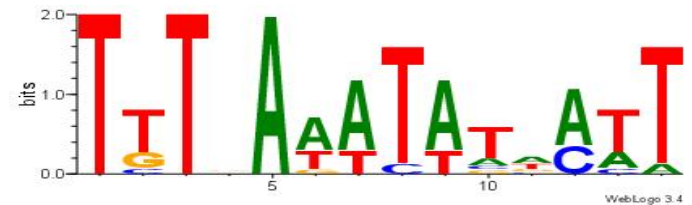
Alignment:

AATHATATWTHAAA
 -TTCWTAGATTAWA

Original motif Consensus sequence: AATHATATWTHAAA



Reverse complement motif Consensus sequence: TTTDAWATATHAT

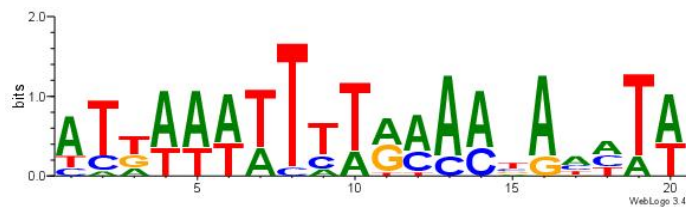


Dataset #: 5
 Motif ID: 55
 Motif name: TFM13
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 7
 Number of overlap: 13
 Similarity score: 0.0762821

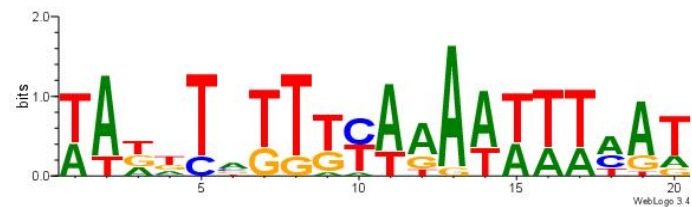
Alignment:

WAHHTVTTYKAAAATTRAT
 -----TTCWTAGATTAWA-

Original motif Consensus sequence: ATKAAWTTTTRMAABAHTW



Reverse complement motif Consensus sequence: WAHHTVTTYKAAAATTRAT



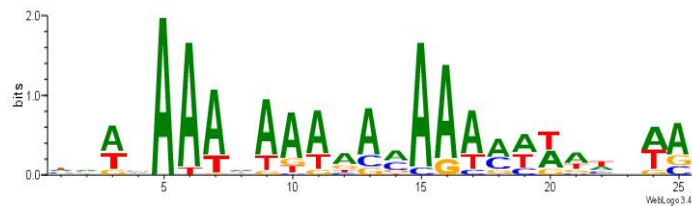
Dataset #: 5
 Motif ID: 56
 Motif name: TFM11
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 12

Number of overlap: 13
 Similarity score: 0.0810709

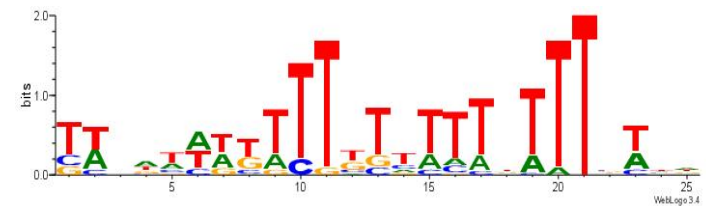
Alignment:

HDWVAAAHA AAAA MAAA MWWW HBWA
 -TWTAATCTAWGAA-----

Original motif Consensus sequence:
 HDWVAAAHA AAAA MAAA MWWW HBWA



Reverse complement motif Consensus sequence:
 TWVHWWWYTTTTTTTTTHTTTVWBH

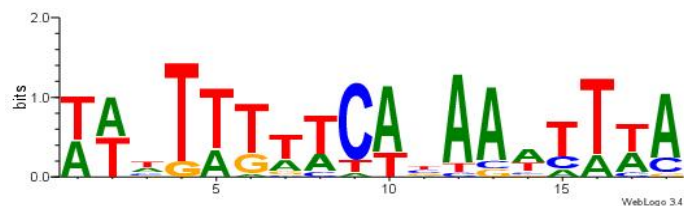


Dataset #: 5
 Motif ID: 53
 Motif name: TFM3
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 13
 Similarity score: 0.0815851

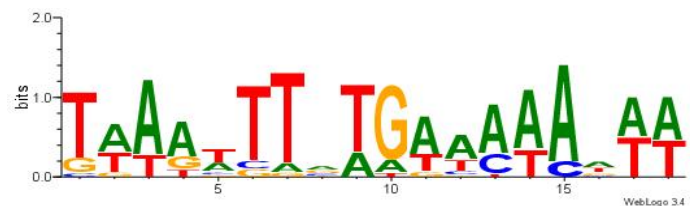
Alignment:

TWAAWTTVTGAAAAAHWW
 -----TTCWTAGATTAWA

Original motif Consensus sequence: WWHTTTTTTCABAAWTTWA



Reverse complement motif Consensus sequence: TWAAWTTVTGAAAAHWW



Dataset #: 2
 Motif ID: 6
 Motif name: Motif 6
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 12
 Similarity score: 0.5625

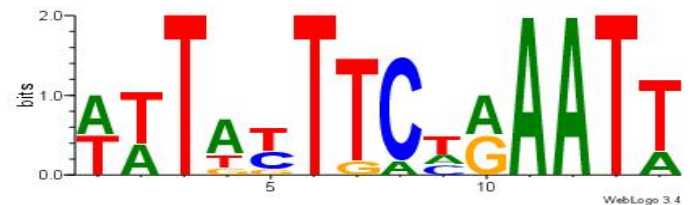
Alignment:

AATTYDGAARTAWW-
 --TTCWTAGATTAWA

Original motif Consensus sequence: AATTYDGAARTAWW



Reverse complement motif Consensus sequence: WWTAKTTCDKAAAT

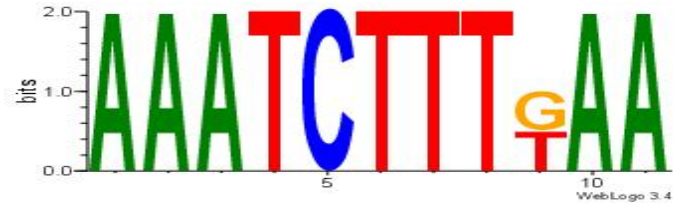


Dataset #: 2 Motif ID: 20 Motif name: Motif 20

Original motif Consensus sequence: TTMAAAGATTT



Reverse complement motif Consensus sequence: AAATCTTTYAA



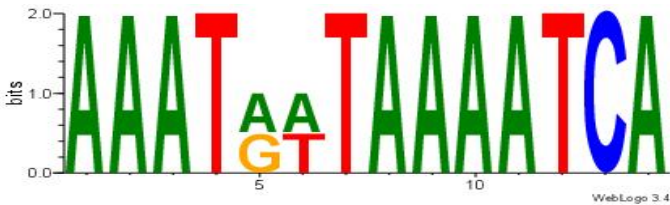
Best Matches for Motif ID 20 (Highest to Lowest)

Dataset #:	2
Motif ID:	8
Motif name:	Motif 8
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	4
Number of overlap:	11
Similarity score:	0.0681818

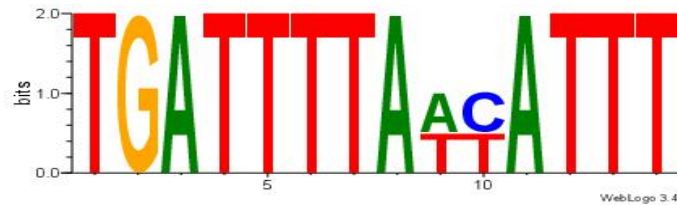
Alignment:

```
AAATRWTAAAATCA
---AAATCTTTYAA
```

Original motif Consensus sequence: AAATRWTAAAATCA



Reverse complement motif Consensus sequence: TGATTTTAWKATT



Dataset #: 2
 Motif ID: 19
 Motif name: Motif 19
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.0681818

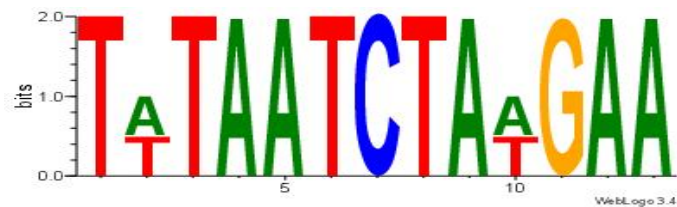
Alignment:

TTCWTAGATTAWA
 TTMAAAGATTT--

Original motif Consensus sequence: TTCWTAGATTAWA



Reverse complement motif Consensus sequence: TWTAATCTAWGAA

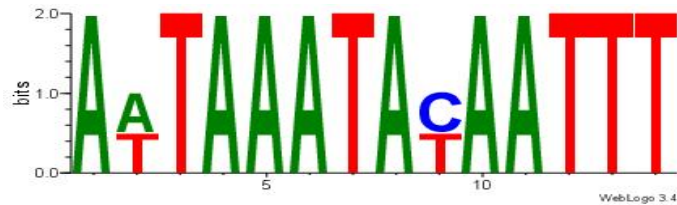


Dataset #: 2
 Motif ID: 5
 Motif name: Motif 5
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2

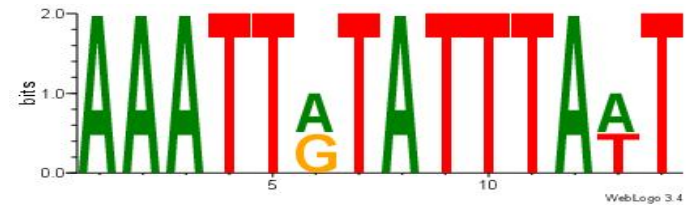
Number of overlap: 11
 Similarity score: 0.102273

Alignment:
 AAATTKTATTTAWT
 -AAATCTTTYAA--

Original motif Consensus sequence: AWTAAATAYAATTT



Reverse complement motif Consensus sequence: AAATTKTATTTAWT

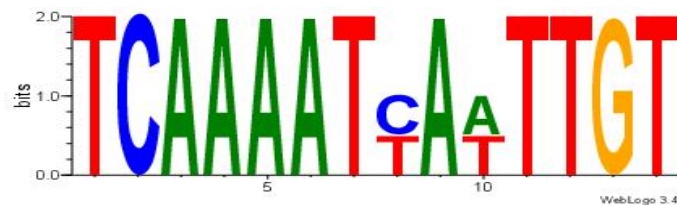
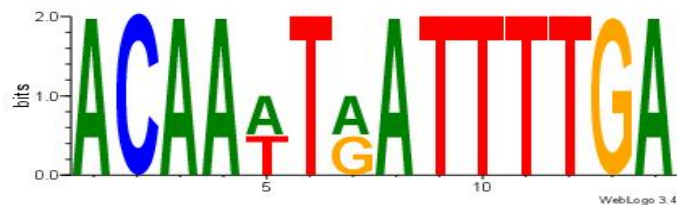


Dataset #: 2
 Motif ID: 16
 Motif name: Motif 16
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.102273

Alignment:
 ACAAWTRATTTTGA
 TTMAAAGATTT---

Original motif Consensus sequence: ACAAWTRATTTTGA

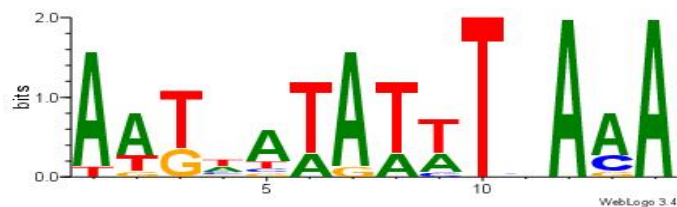
Reverse complement motif Consensus sequence: TCAAAATKAWTTG



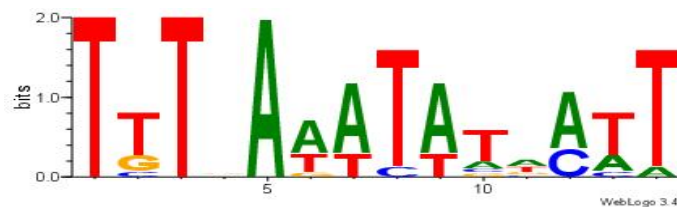
Dataset #: 2
 Motif ID: 9
 Motif name: Motif 9
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 11
 Similarity score: 0.106061

Alignment:
 TTTDAWATATHATT
 --TTMAAAGATTT-

Original motif Consensus sequence: AATHATATWTHAAA



Reverse complement motif Consensus sequence: TTTDAWATATHATT



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

Original motif Consensus sequence: ATAAAA



Reverse complement motif Consensus sequence: TTTTAT



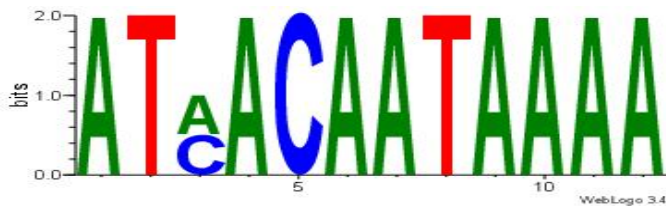
Best Matches for Motif ID 21 (Highest to Lowest)

Dataset #:	2
Motif ID:	15
Motif name:	Motif 15
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	6
Similarity score:	0

Alignment:

```
TTTTATTGTYAT
TTTTAT-----
```

Original motif Consensus sequence: ATMACAATAAAA



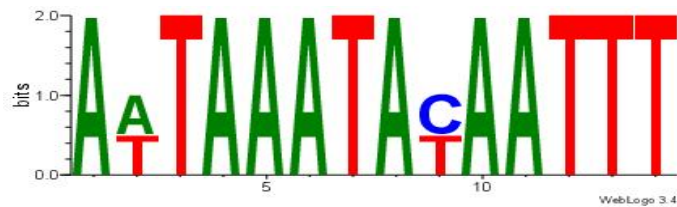
Reverse complement motif Consensus sequence: TTTTATTGTYAT



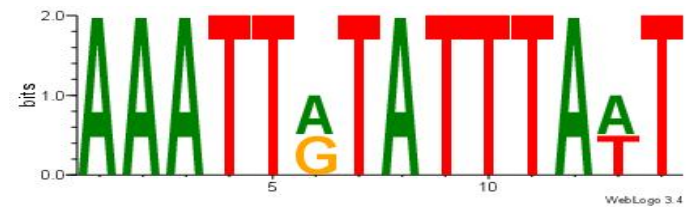
Dataset #: 2
 Motif ID: 5
 Motif name: Motif 5
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 6
 Number of overlap: 6
 Similarity score: 0.0208333

Alignment:
 AAATTKTATTTAWT
 ---TTTTAT-----

Original motif Consensus sequence: AWTAAATAYAATTT



Reverse complement motif Consensus sequence: AAATTKTATTTAWT



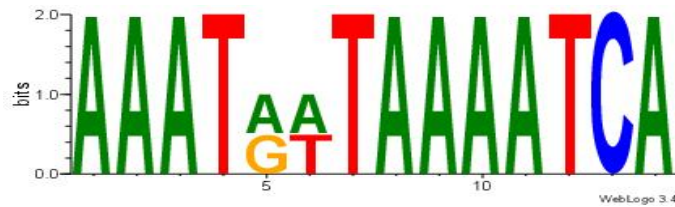
Dataset #: 2
 Motif ID: 8
 Motif name: Motif 8
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 4
 Number of overlap: 6

Similarity score: 0.0208333

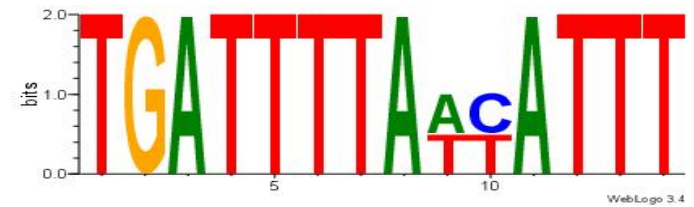
Alignment:

AAATRWATAAATCA
-----ATAAAA---

Original motif Consensus sequence: AAATRWATAAATCA



Reverse complement motif Consensus sequence: TGATTTAWKATT



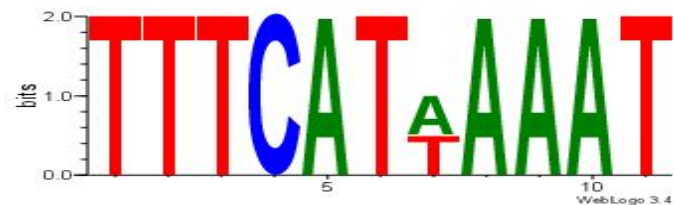
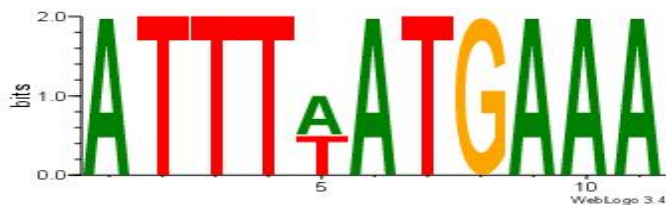
Dataset #: 2
Motif ID: 11
Motif name: Motif 11
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2
Number of overlap: 6
Similarity score: 0.0208333

Alignment:

ATTTWATGAAA
-----TTTAT-

Original motif Consensus sequence: ATTTWATGAAA

Reverse complement motif Consensus sequence: TTTATWAAAT

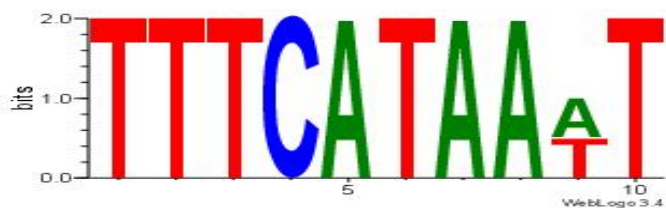


Dataset #: 2
 Motif ID: 10
 Motif name: Motif 10
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 6
 Similarity score: 0.0416667

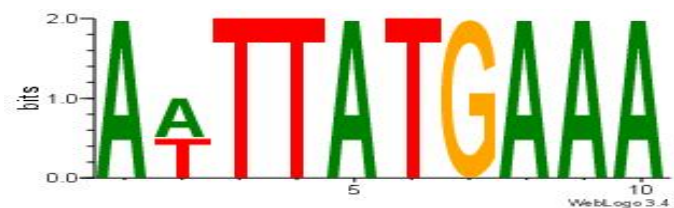
Alignment:

TTTCATAAWT
 ----TTTTAT

Original motif Consensus sequence: TTTCATAAWT

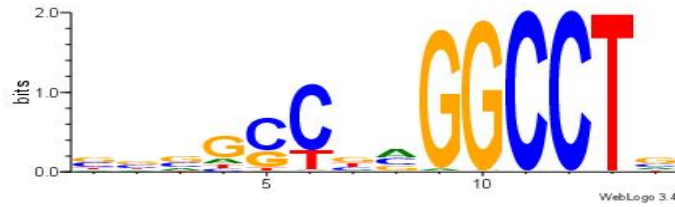


Reverse complement motif Consensus sequence: AWTTATGAAA

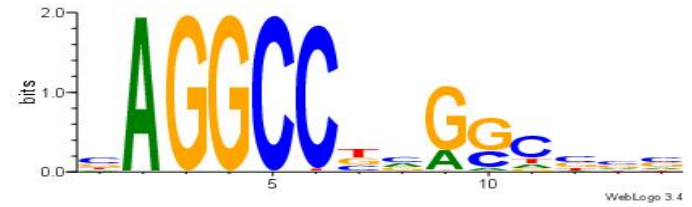


Dataset #: 3 Motif ID: 22 Motif name: Zfx

Original motif Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif Consensus sequence: VAGGCCBBGGCV



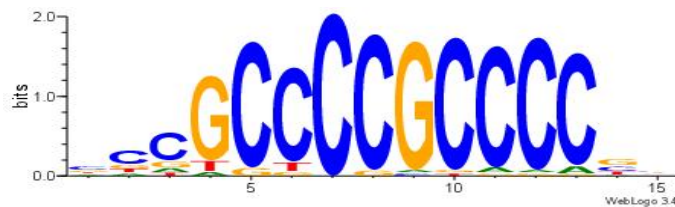
Best Matches for Motif ID 22 (Highest to Lowest)

Dataset #: 4
Motif ID: 38
Motif name: cccGCCCCGCCCCsb
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 14
Similarity score: 0.0514008

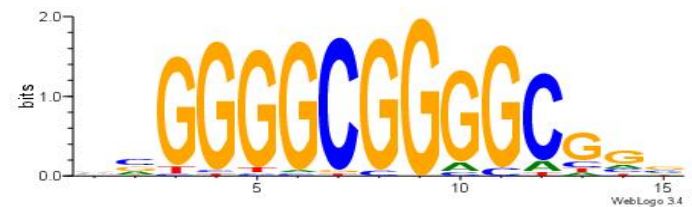
Alignment:

```
BCCGCCCCGCCCCBB  
BBVGCCBVGGCCTV-
```

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB

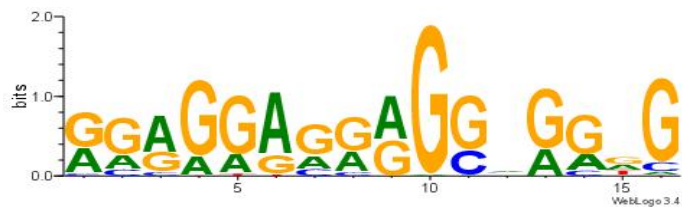


Dataset #: 5
 Motif ID: 51
 Motif name: TFM2
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 14
 Similarity score: 0.0590031

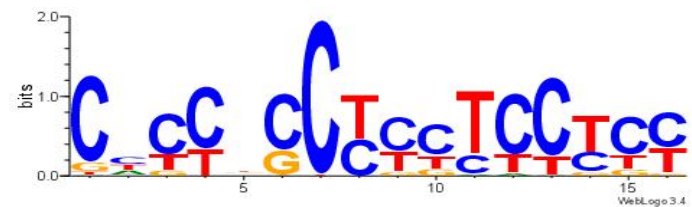
Alignment:

CHCCBCKMCTCCKCM
 -BBVGCCBVGGCCTV-

Original motif Consensus sequence: RGRGGAGRRGGHGGDG



Reverse complement motif Consensus sequence: CHCCBCKMCTCCKCM



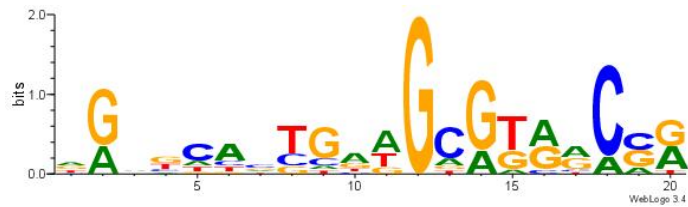
Dataset #: 3
 Motif ID: 31
 Motif name: Pax5
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 5

Number of overlap: 14
Similarity score: 0.0611182

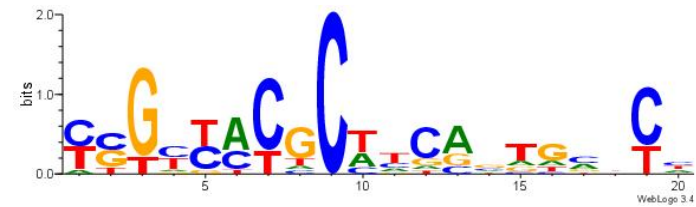
Alignment:

DGVBCABTGDWGCGRRCR
--BBVGCCBVGGCCTV----

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR



Reverse complement motif Consensus sequence:
MSGKKRCGCWDCABTGBBCD

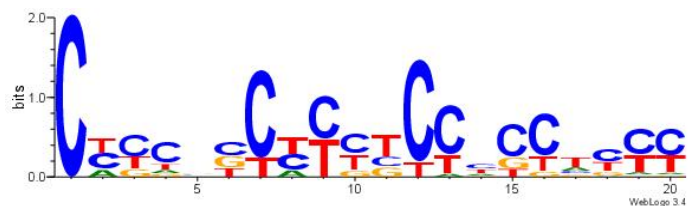


Dataset #: 5
Motif ID: 54
Motif name: TFM12
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 6
Number of overlap: 14
Similarity score: 0.0629383

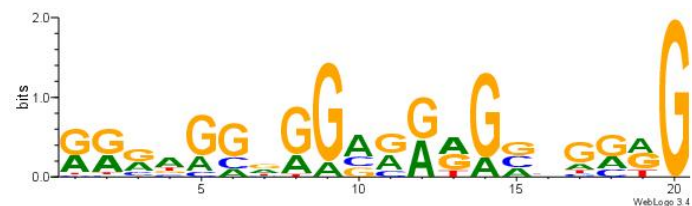
Alignment:

KKKAGGDGGAKKMGBBGKMG
-----VAGGCCBBGGCVBB-

Original motif Consensus sequence: CYCBBYYYTCCHCCTYYY



Reverse complement motif Consensus sequence: KKKAGGDGGAKKMGBBGKMG

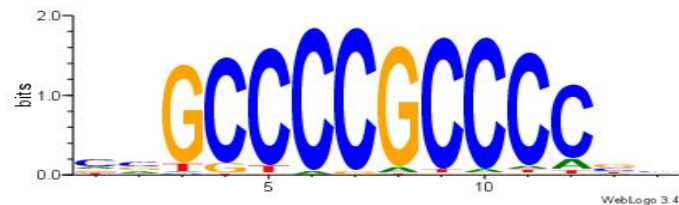


Dataset #: 4
Motif ID: 36
Motif name: csGCCCCGCCCCsc
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 14
Similarity score: 0.0654514

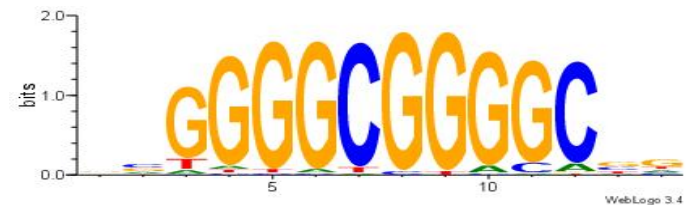
Alignment:

HVCCCCGCCCCBB
VAGGCCBBGGCVBB

Original motif Consensus sequence: HVCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGCGGGGC

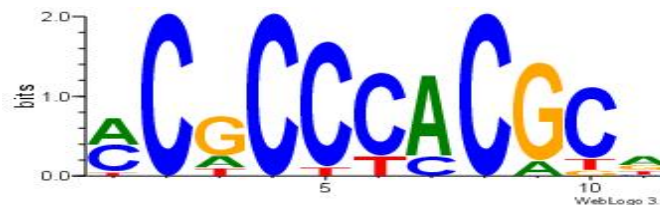


Dataset #: 3 Motif ID: 23 Motif name: Egr1

Original motif Consensus sequence: HCGTGGGCGK



Reverse complement motif Consensus sequence: YCGCCACGCH



Best Matches for Motif ID 23 (Highest to Lowest)

Dataset #:	5
Motif ID:	50
Motif name:	TFF11
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	4
Number of overlap:	11
Similarity score:	0.0514701

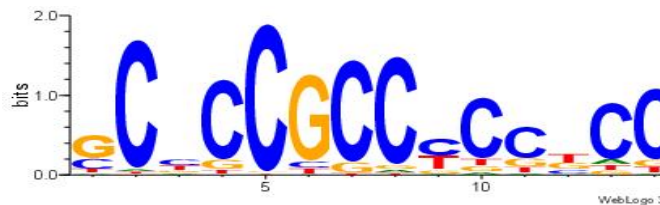
Alignment:

```
GCVCCGCCMCCYCC
---YCGCCACGCH
```

Original motif Consensus sequence: GGMGRRGGCGGVGC



Reverse complement motif Consensus sequence: GCVCCGCCMCCYCC

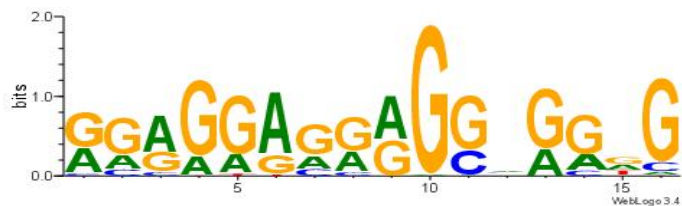


Dataset #: 5
 Motif ID: 51
 Motif name: TFM2
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 6
 Number of overlap: 11
 Similarity score: 0.0698683

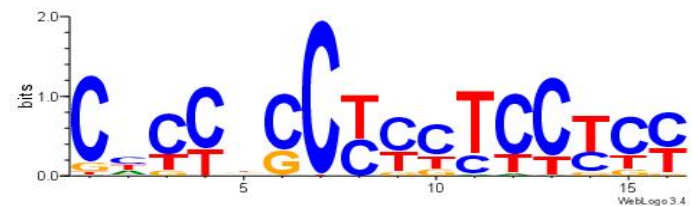
Alignment:

CHCCBCKMCTCCKCM
 -----YCGCCACGCH

Original motif Consensus sequence: RGRGGAGRRGGHGGDG



Reverse complement motif Consensus sequence: CHCCBCKMCTCCKCM



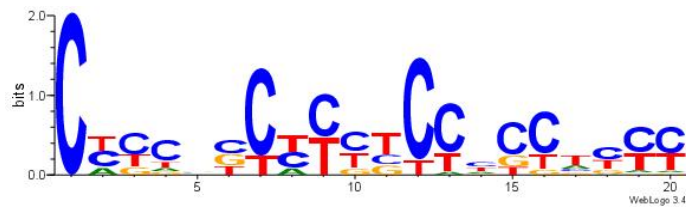
Dataset #: 5
 Motif ID: 54
 Motif name: TFM12
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward

Position number: 9
 Number of overlap: 11
 Similarity score: 0.0718056

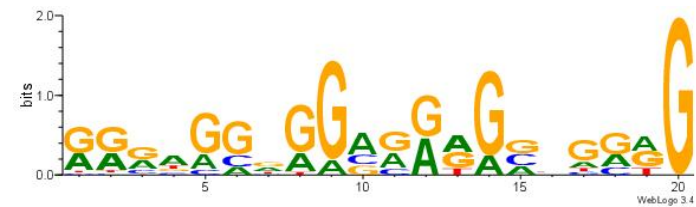
Alignment:

KKKAGGDGGAKKMGBBGKMG
 -HGCGTGGGCGK-----

Original motif Consensus sequence: CYCBBYYYTCCHCCTYYY



Reverse complement motif Consensus sequence: KKKAGGDGGAKKMGBBGKMG

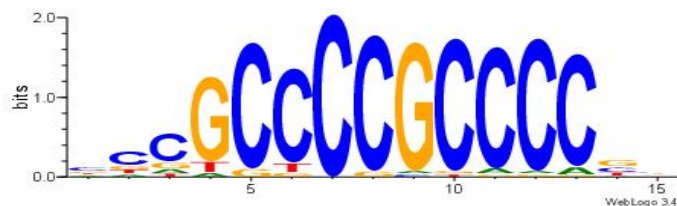


Dataset #: 4
 Motif ID: 38
 Motif name: cccGCCCCGCCCCsb
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 5
 Number of overlap: 11
 Similarity score: 0.0730967

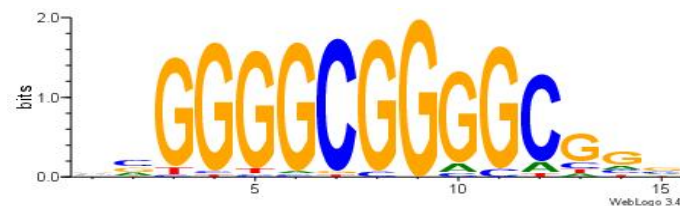
Alignment:

BBGGGGCGGGGCGGB
 ----HGCGTGGGCGK

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB

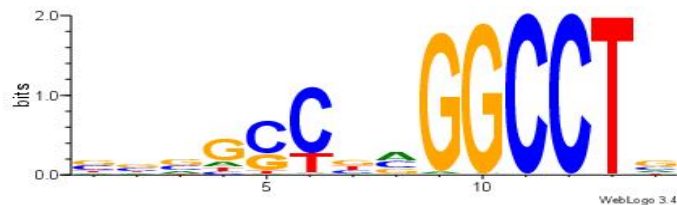


Dataset #: 3
Motif ID: 22
Motif name: Zfx
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2
Number of overlap: 11
Similarity score: 0.0764878

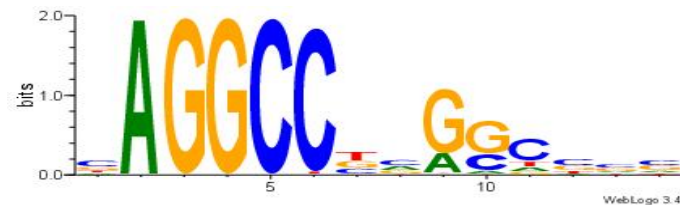
Alignment:

BBVGCCBVGGCCTV
--HGCGTGGGCGK-

Original motif Consensus sequence: BBVGCCBVGGCCTV

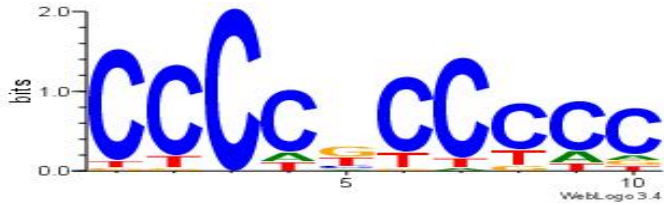


Reverse complement motif Consensus sequence: VAGGCCBBGGCV

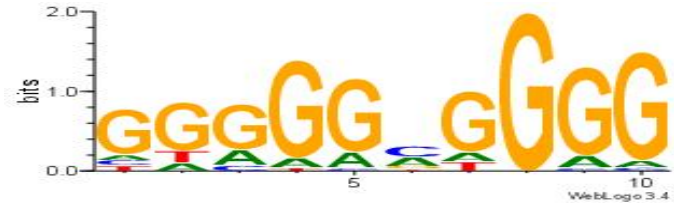


Dataset #: 3 Motif ID: 24 Motif name: SP1

Original motif Consensus sequence: CCCCKCCCC



Reverse complement motif Consensus sequence: GGGGYGGGG



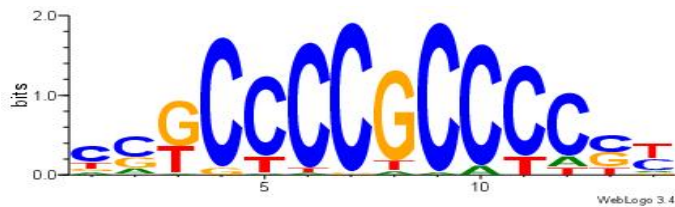
Best Matches for Motif ID 24 (Highest to Lowest)

Dataset #:	2
Motif ID:	7
Motif name:	Motif 7
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	4
Number of overlap:	10
Similarity score:	0.00451594

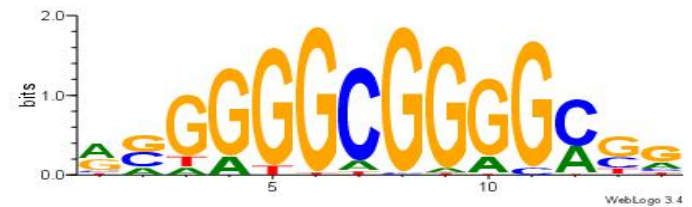
Alignment:

MSGGGGCGGGYSG
-GGGGYGGGG---

Original motif Consensus sequence: CSKCCCCGCCCSY



Reverse complement motif Consensus sequence: MSGGGGCGGGY

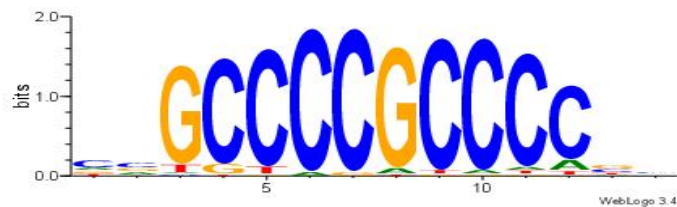


Dataset #: 4
 Motif ID: 36
 Motif name: csGCCCCGCCCCsc
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 4
 Number of overlap: 10
 Similarity score: 0.00965796

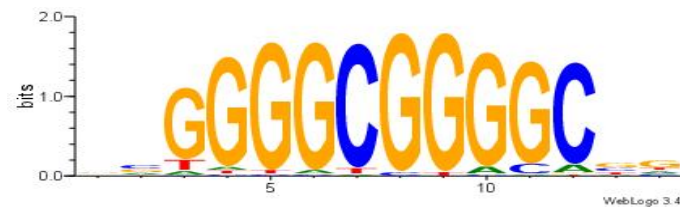
Alignment:

BBGGGGCGGGGCVD
 -GGGGYGGGG---

Original motif Consensus sequence: HVGCCCCGCCCB



Reverse complement motif Consensus sequence: BBGGGGCGGGGC

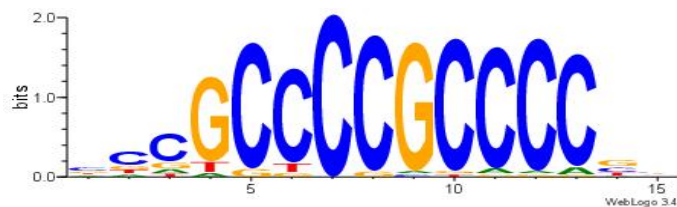


Dataset #: 4
 Motif ID: 38
 Motif name: cccGCCCCGCCCSb
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 5

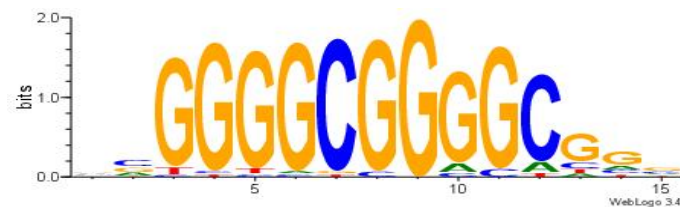
Number of overlap: 10
Similarity score: 0.0127292

Alignment:
BCCGCCCCGCCCCBB
----CCCCKCCCC--

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence:
BBGGGGCGGGGCGGB

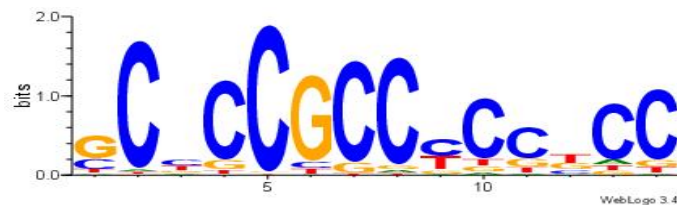


Dataset #: 5
Motif ID: 50
Motif name: TFF11
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 4
Number of overlap: 10
Similarity score: 0.0174405

Alignment:
GGMGGRGGCGGVGC
---GGGGYGGGG--

Original motif Consensus sequence: GGMGGRGGCGGVGC

Reverse complement motif Consensus sequence: GCVCCGCCMCCYC

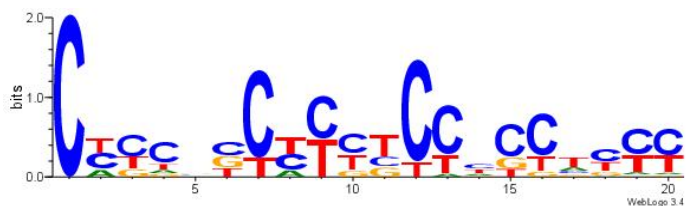


Dataset #: 5
 Motif ID: 54
 Motif name: TFM12
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 7
 Number of overlap: 10
 Similarity score: 0.0301548

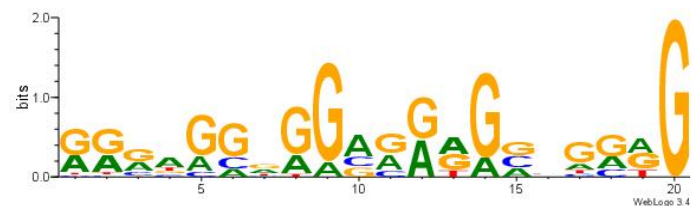
Alignment:

CYCBBCYYYTCCHCCTYYY
 -----CCCCKCCCC-----

Original motif Consensus sequence: CYCBBCYYYTCCHCCTYYY

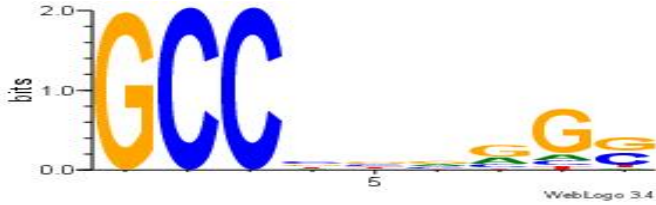


Reverse complement motif Consensus sequence: KKKAGGDGGAKKMGBBGKMG

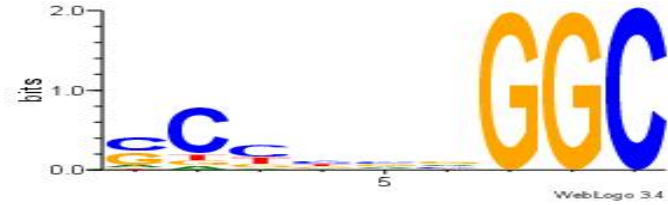


Dataset #: 3 Motif ID: 25 Motif name: TFAP2A

Original motif Consensus sequence: GCCBBVRGS



Reverse complement motif Consensus sequence: SCMVBGGC



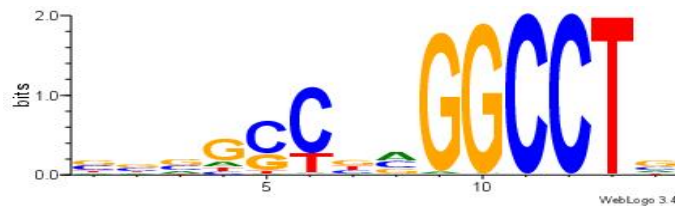
Best Matches for Motif ID 25 (Highest to Lowest)

Dataset #:	3
Motif ID:	22
Motif name:	Zfx
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	3
Number of overlap:	9
Similarity score:	0.0131247

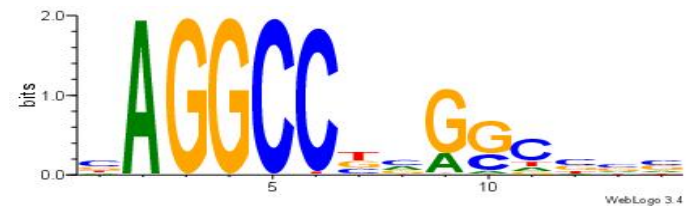
Alignment:

```
BBVGCCBVGGCCTV  
---SCMVBBGGC---
```

Original motif Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif Consensus sequence: VAGGCCBBGGCV

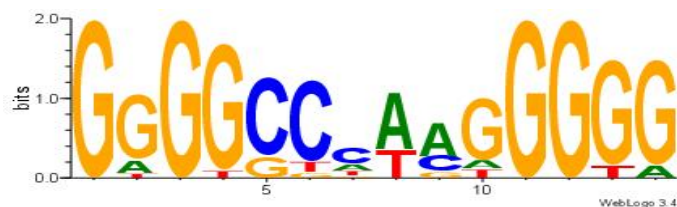


Dataset #: 3
 Motif ID: 30
 Motif name: PLAG1
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 9
 Similarity score: 0.0414588

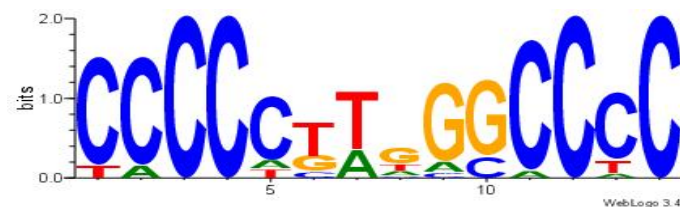
Alignment:

GGGGCCCAAGGGG
 ---GCCBBVRGS--

Original motif Consensus sequence: GGGGCCCAAGGGG



Reverse complement motif Consensus sequence: CCCCTTGGGCC



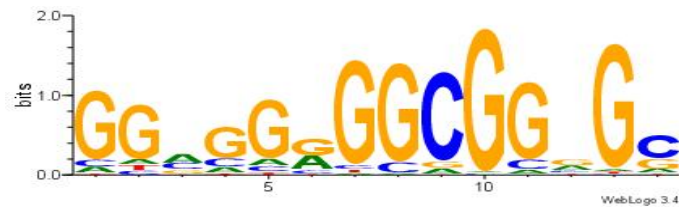
Dataset #: 5
 Motif ID: 50
 Motif name: TFF11
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 9

Similarity score: 0.0415732

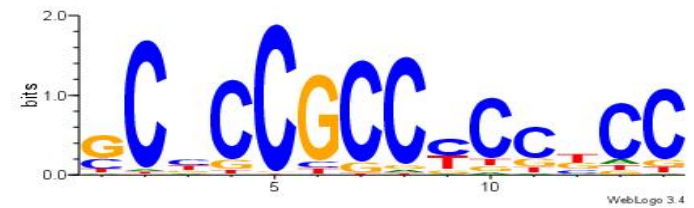
Alignment:

GGMGGRGGCGGVGC
SCMVBBGGC-----

Original motif Consensus sequence: GGMGGRGGCGGVGC



Reverse complement motif Consensus sequence: GCVCCGCCMCCYC



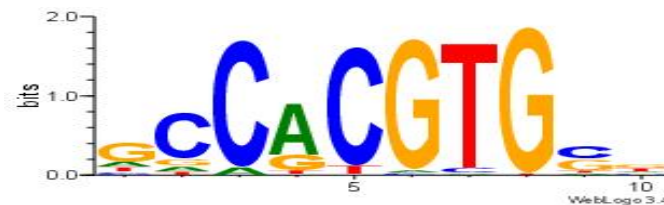
Dataset #: 3
Motif ID: 33
Motif name: Mycn
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 2
Number of overlap: 9
Similarity score: 0.0550803

Alignment:

HSCACGTGGC
-SCMVBBGGC

Original motif Consensus sequence: HSCACGTGGC

Reverse complement motif Consensus sequence: GCCACGTGSD



Dataset #: 5
 Motif ID: 48
 Motif name: TFW3
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 9
 Similarity score: 0.0552877

Alignment:

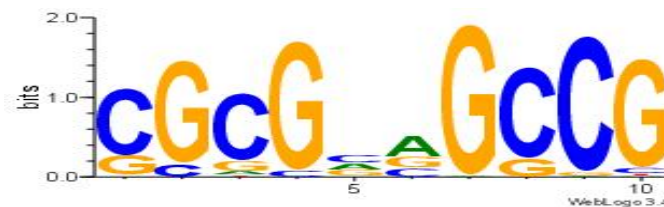
CGGCYBCGCG

-GCCBBVRGS

Original motif Consensus sequence: CGGCYBCGCG

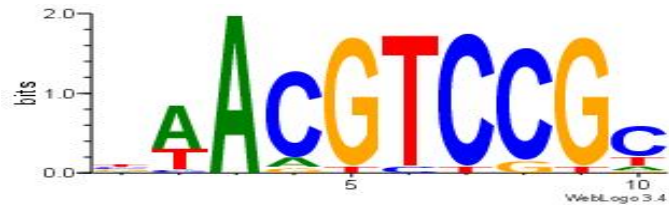


Reverse complement motif Consensus sequence: CGCGBMGCCG

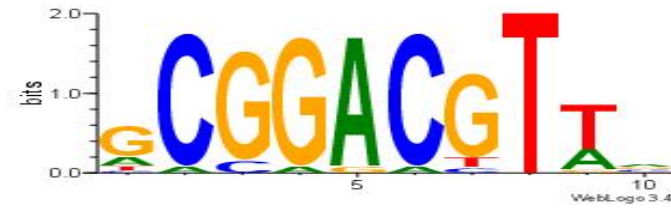


Dataset #: 3 Motif ID: 26 Motif name: MIZF

Original motif Consensus sequence: BAACGTCCGC



Reverse complement motif Consensus sequence: GCGGACGTTT



Best Matches for Motif ID 26 (Highest to Lowest)

Dataset #:	3
Motif ID:	35
Motif name:	GABPA
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	10
Similarity score:	0.0459305

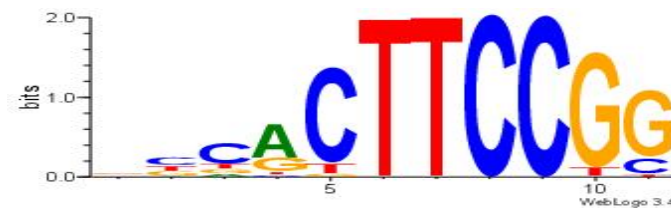
Alignment:

```
CCGGAAGTGVV  
GCGGACGTTV-
```

Original motif Consensus sequence: CCGGAAGTG



Reverse complement motif Consensus sequence: VVCACTCCGG



Dataset #: 4
 Motif ID: 40
 Motif name: kcACCTGCAGc
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 10
 Similarity score: 0.0778314

Alignment:

BCACCTGCABC
 BAACGTCCGC-

Original motif Consensus sequence: BCACCTGCABC



Reverse complement motif Consensus sequence: GBTGCAGGTGB



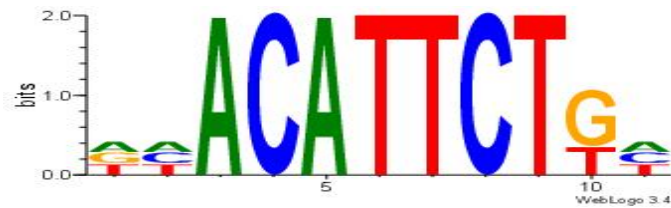
Dataset #: 4
 Motif ID: 44
 Motif name: dhACATTCTkh
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 10

Similarity score: 0.0794339

Alignment:

DHACATTCTGH
BAACGTCCGC-

Original motif Consensus sequence: DHACATTCTGH



Reverse complement motif Consensus sequence: HCAGAATGTHD



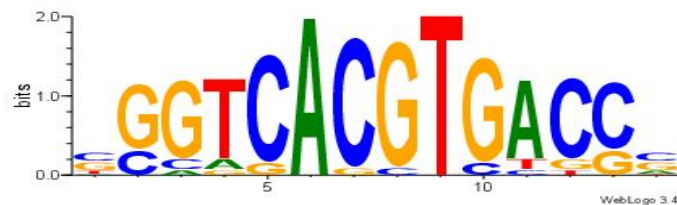
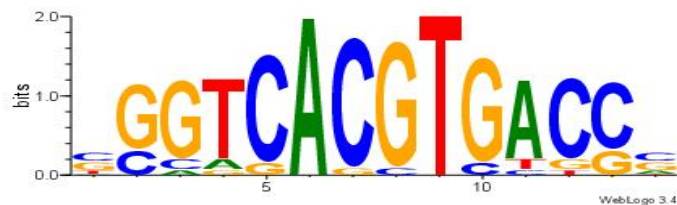
Dataset #: 4
Motif ID: 42
Motif name: sSGTCACGTGACSS
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2
Number of overlap: 10
Similarity score: 0.0804061

Alignment:

SGGTCACGTGACCS
---BAACGTCCGC-

Original motif Consensus sequence: SGGTCACGTGACCS

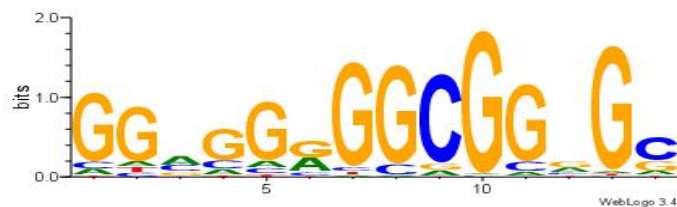
Reverse complement motif Consensus sequence: SGGTCACGTGACCS



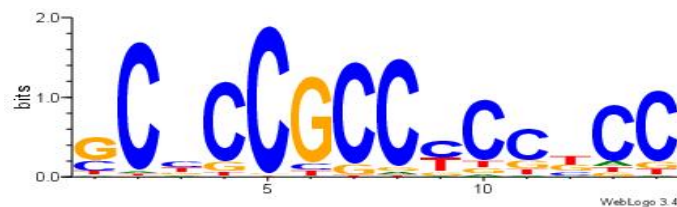
Dataset #: 5
 Motif ID: 50
 Motif name: TFF11
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 10
 Similarity score: 0.0861006

Alignment:
 GCVCCGCCMCCYCC
 -BAACGTCCGC---

Original motif Consensus sequence: GGMGRRGGCGGVGC



Reverse complement motif Consensus sequence: GCVCCGCCMCCYCC



Dataset #: 3 Motif ID: 27 Motif name: Klf4

Original motif Consensus sequence: DGGGYGKGGC



Reverse complement motif Consensus sequence: GCCYCMCCCD



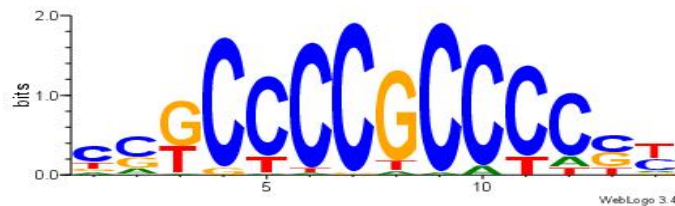
Best Matches for Motif ID 27 (Highest to Lowest)

Dataset #:	2
Motif ID:	7
Motif name:	Motif 7
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	3
Number of overlap:	10
Similarity score:	0.0152457

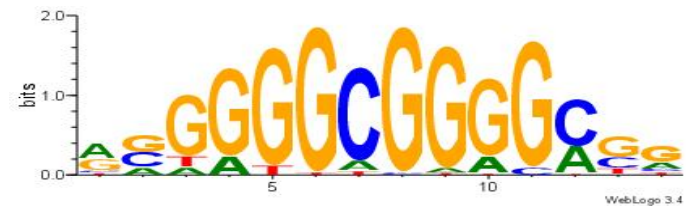
Alignment:

```
CSKCCCCGCCCSY
--GCCYCMCCCD--
```

Original motif Consensus sequence: CSKCCCCGCCCSY



Reverse complement motif Consensus sequence: MSGGGCGGGGY

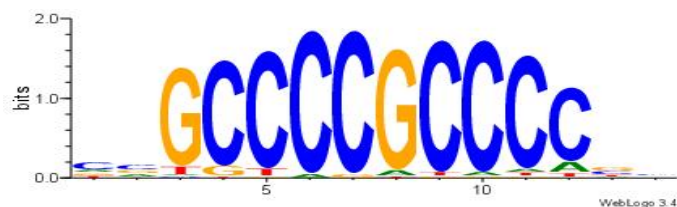


Dataset #: 4
 Motif ID: 36
 Motif name: csGCCCCGCCCCsc
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3
 Number of overlap: 10
 Similarity score: 0.0160185

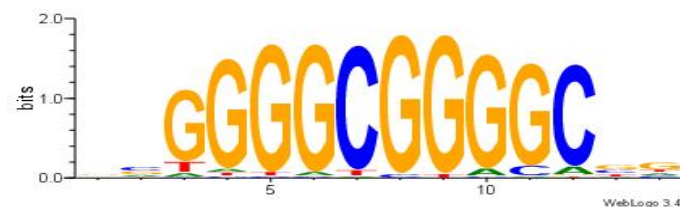
Alignment:

BBGGGGCGGGGCVD
 --DGGGYGKGGC--

Original motif Consensus sequence: HVGCCCCGCCCB



Reverse complement motif Consensus sequence: BBGGGGCGGGGC



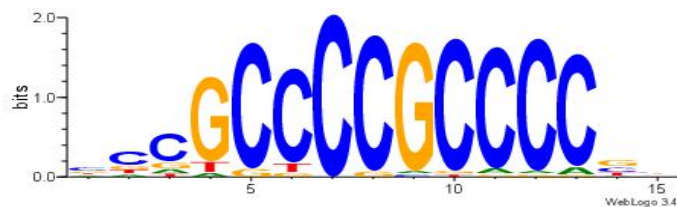
Dataset #: 4
 Motif ID: 38
 Motif name: cccGCCCCGCCCCsb
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3
 Number of overlap: 10

Similarity score: 0.0194893

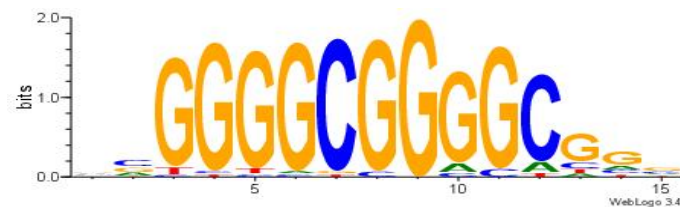
Alignment:

BBGGGGCGGGGCGGB
--DGGGYGKGGC---

Original motif Consensus sequence: BCCGCCCCGCCCCB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB



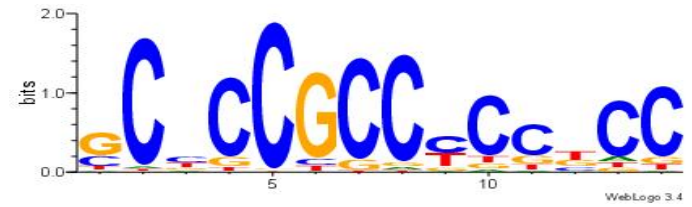
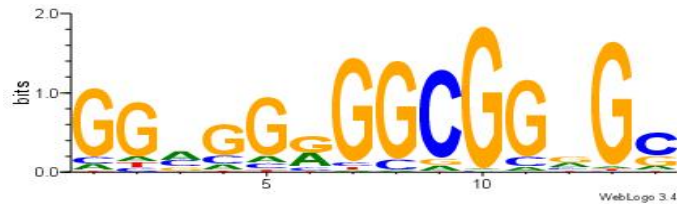
Dataset #: 5
Motif ID: 50
Motif name: TFF11
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 5
Number of overlap: 10
Similarity score: 0.0402906

Alignment:

GGMGGRGGCGGVGC
----DGGGYGKGGC

Original motif Consensus sequence: GGMGGRGGCGGVGC

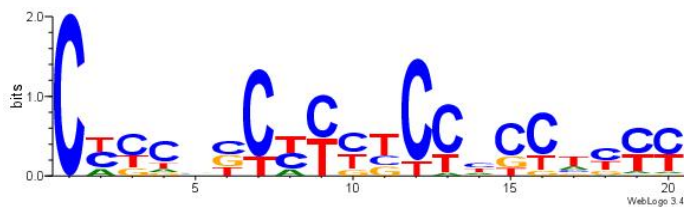
Reverse complement motif Consensus sequence: GCVCCGCCMCCYC



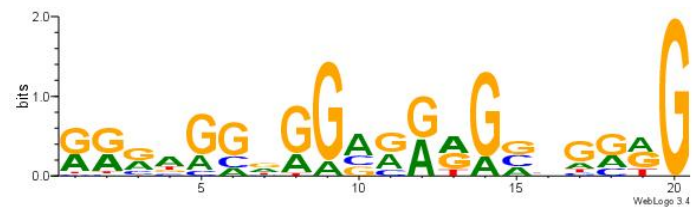
Dataset #: 5
 Motif ID: 54
 Motif name: TFM12
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 7
 Number of overlap: 10
 Similarity score: 0.0556427

Alignment:
 CYCBBCYYYTCCHCCTYYY
 ----GCCYCMCCCD-----

Original motif Consensus sequence: CYCBBCYYYTCCHCCTYYY



Reverse complement motif Consensus sequence: KKKAGGDGGAKKMGBBGKMG



Dataset #: 3 Motif ID: 28 Motif name: E2F1

Original motif Consensus sequence: TTTSGCGC



Reverse complement motif Consensus sequence: GCGCSAAA



Best Matches for Motif ID 28 (Highest to Lowest)

Dataset #: 3
 Motif ID: 30
 Motif name: PLAG1
 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: 0.0568827

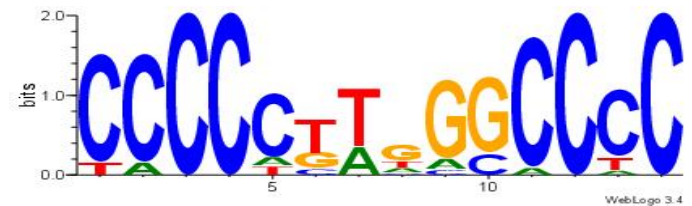
Alignment:

GGGGCCCAAGGGGG
 -GCGCSAAA-----

Original motif Consensus sequence: GGGGCCCAAGGGGG



Reverse complement motif Consensus sequence: CCCCTTGGGCC



Dataset #: 4
 Motif ID: 39
 Motif name: kCAGCCAATmr
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 8
 Similarity score: 0.0624791

Alignment:
 DCAGCCAATVR
 -GCGCSAAA--

Original motif Consensus sequence: DCAGCCAATVR



Reverse complement motif Consensus sequence: MBATTGGCTGH



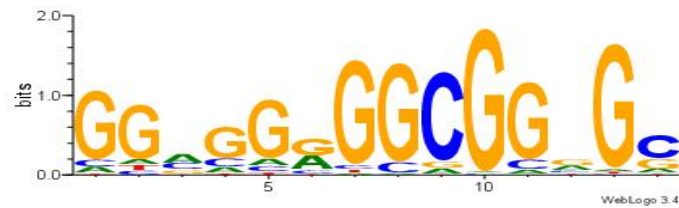
Dataset #: 5
 Motif ID: 50
 Motif name: TFF11
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 4
 Number of overlap: 8

Similarity score: 0.0781129

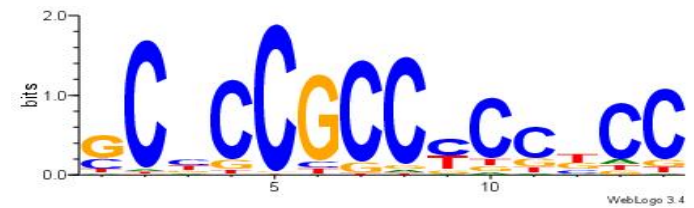
Alignment:

GCVCCGCCMCCYCC
---GCGCSAAA---

Original motif Consensus sequence: GGMGRRGGCGGVGC



Reverse complement motif Consensus sequence: GCVCCGCCMCCYCC



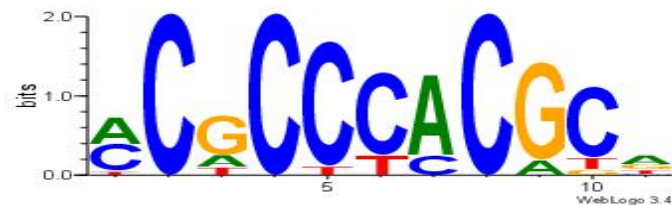
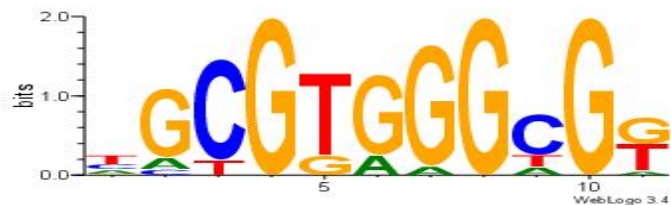
Dataset #: 3
Motif ID: 23
Motif name: Egr1
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 4
Number of overlap: 8
Similarity score: 0.0784105

Alignment:

YCGCCCACGCH
GCGCSAAA---

Original motif Consensus sequence: HGCGTGGGCGK

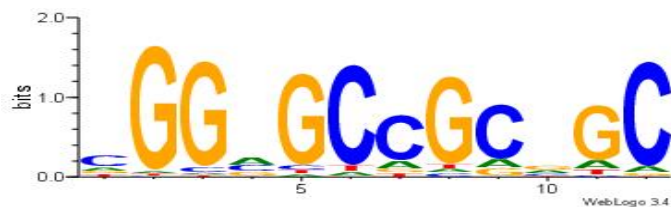
Reverse complement motif Consensus sequence: YCGCCCACGCH



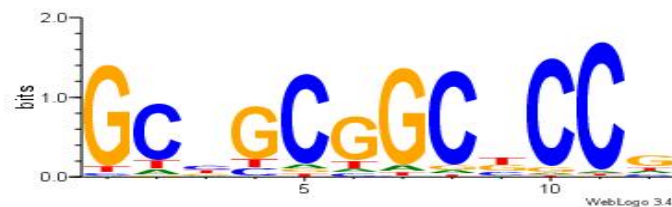
Dataset #: 5
 Motif ID: 49
 Motif name: TFF1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 8
 Similarity score: 0.0798986

Alignment:
 CGGVGCCGCVGC
 --GCGCSAAA--

Original motif Consensus sequence: CGGVGCCGCVGC



Reverse complement motif Consensus sequence: GCVGCCGCBCCG



Dataset #: 3 Motif ID: 29 Motif name: HIF1AARNT

Original motif Consensus sequence: VBACGTGV



Reverse complement motif Consensus sequence: VCACGTBV



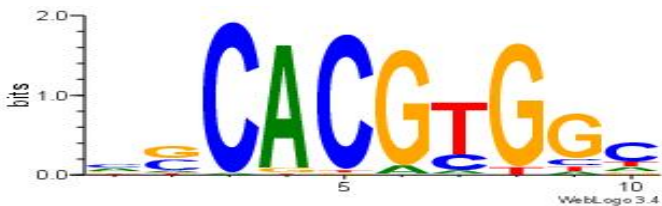
Best Matches for Motif ID 29 (Highest to Lowest)

Dataset #:	3
Motif ID:	33
Motif name:	Mycn
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:	0.0123101

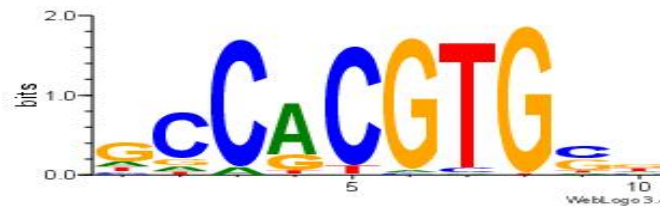
Alignment:

```
GCCACGTGSD  
-VBACGTGV-
```

Original motif Consensus sequence: HSCACGTGGC



Reverse complement motif Consensus sequence: GCCACGTGSD

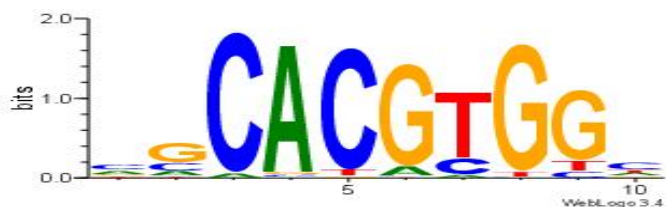


Dataset #: 3
 Motif ID: 34
 Motif name: Myc
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 8
 Similarity score: 0.0144491

Alignment:

DCCACGTGCV
 -VBACGTGV-

Original motif Consensus sequence: VGCACGTGGH



Reverse complement motif Consensus sequence: DCCACGTGCV



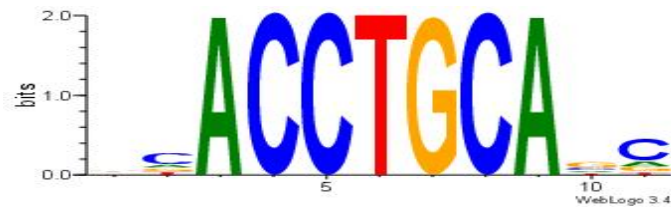
Dataset #: 4
 Motif ID: 40
 Motif name: kcACCTGCAGc
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 8

Similarity score: 0.0295473

Alignment:

GBTGCAGGTGB
---VCACGTBV

Original motif Consensus sequence: BCACCTGCABC



Reverse complement motif Consensus sequence: GBTGCAGGTGB



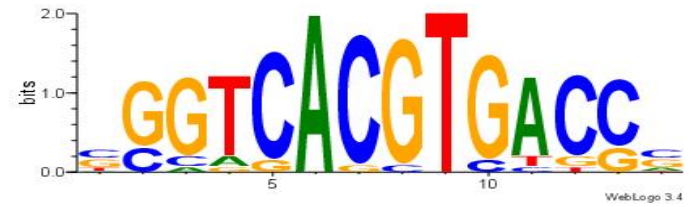
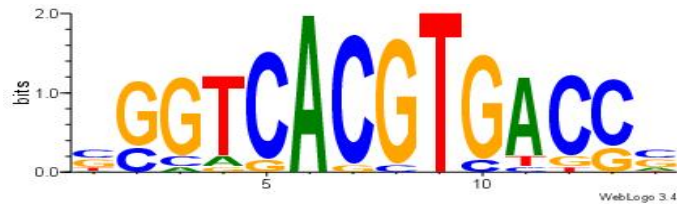
Dataset #: 4
Motif ID: 42
Motif name: sSGTCACGTGACSS
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 4
Number of overlap: 8
Similarity score: 0.0314837

Alignment:

SGGTCACGTGACCS
---VCACGTBV---

Original motif Consensus sequence: SGGTCACGTGACCS

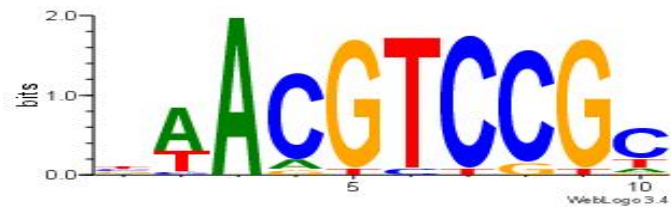
Reverse complement motif Consensus sequence: SGGTCACGTGACCS



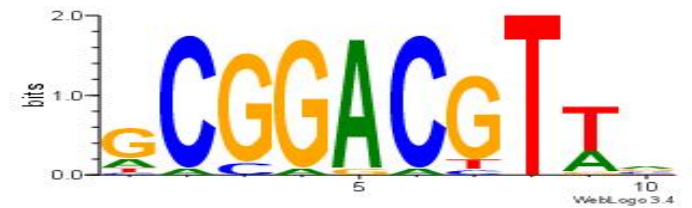
Dataset #: 3
 Motif ID: 26
 Motif name: MIZF
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3
 Number of overlap: 8
 Similarity score: 0.0377204

Alignment:
 GCGGACGTTV
 --VCACGTBV

Original motif Consensus sequence: BAACGTCCGC

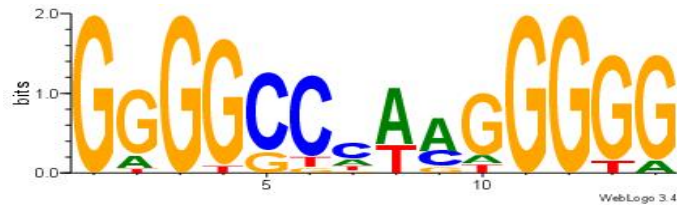


Reverse complement motif Consensus sequence: GCGGACGTTV

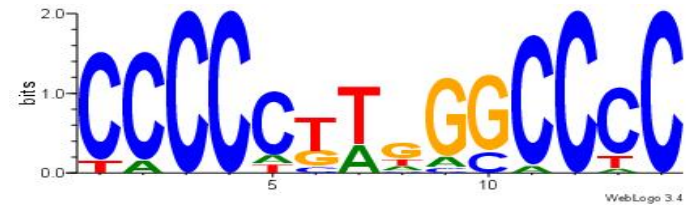


Dataset #: 3 Motif ID: 30 Motif name: PLAG1

Original motif Consensus sequence: GGGCCCAAGGGG



Reverse complement motif Consensus sequence: CCCCTTGGCC



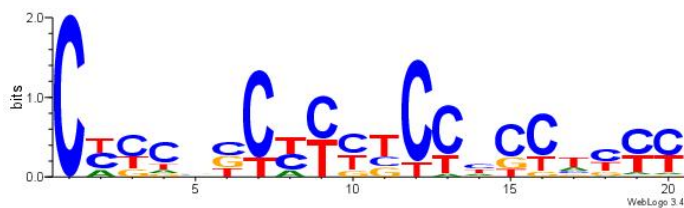
Best Matches for Motif ID 30 (Highest to Lowest)

Dataset #: 5
 Motif ID: 54
 Motif name: TFM12
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 6
 Number of overlap: 14
 Similarity score: 0.0876918

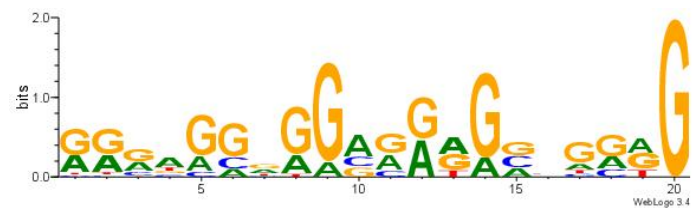
Alignment:

CYCBBCYYYTCCHCCTYYY
 -CCCCCTGGGCC--

Original motif Consensus sequence: CYCBBCYYYTCCHCCTYYY



Reverse complement motif Consensus sequence: KKKAGGDGGAKKMGBBGKMG

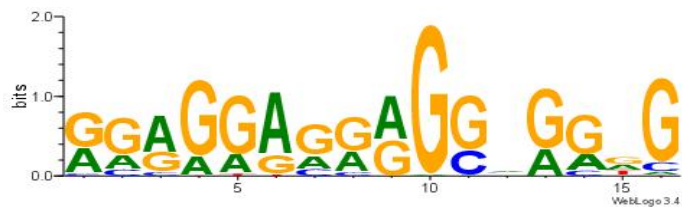


Dataset #: 5
 Motif ID: 51
 Motif name: TFM2
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3
 Number of overlap: 14
 Similarity score: 0.0880716

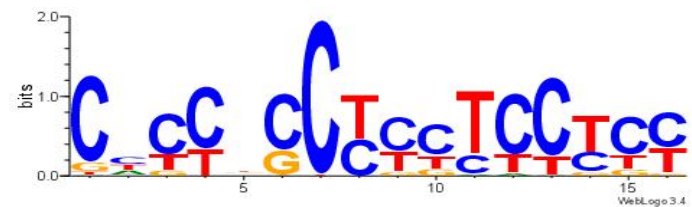
Alignment:

CHCCBCKMCTCCKCM
 --CCCCCTGGGCCCC

Original motif Consensus sequence: RGRGGAGRRGGHGGDG



Reverse complement motif Consensus sequence: CHCCBCKMCTCCKCM



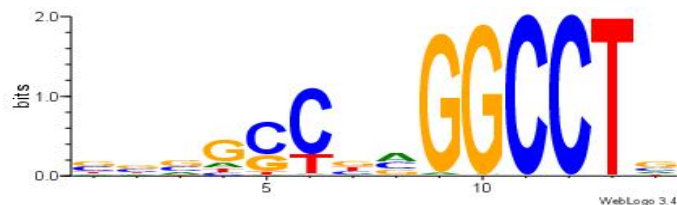
Dataset #: 3
 Motif ID: 22
 Motif name: Zfx
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1

Number of overlap: 14
Similarity score: 0.0886295

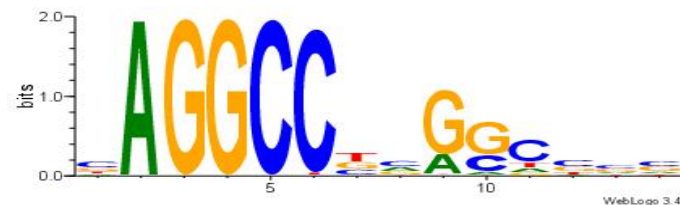
Alignment:

VAGGCCBBGGCVBB
GGGGCCCAAGGGGG

Original motif Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif Consensus sequence: VAGGCCBBGGCVBB



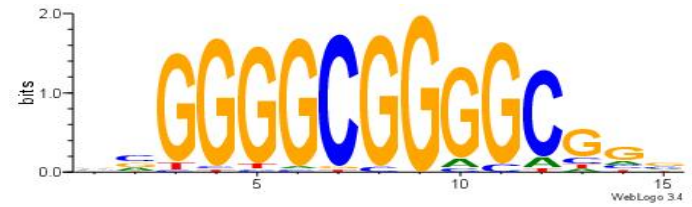
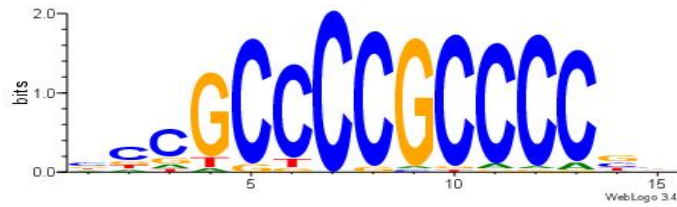
Dataset #: 4
Motif ID: 38
Motif name: cccGCCCCGCCCCsb
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2
Number of overlap: 14
Similarity score: 0.0904945

Alignment:

BCCGCCCCGCCCCBB
CCCCCTTGGGCCCC-

Original motif Consensus sequence: BCCGCCCCGCCCCBB

Reverse complement motif Consensus sequence:
BBGGGGCGGGGCGGB

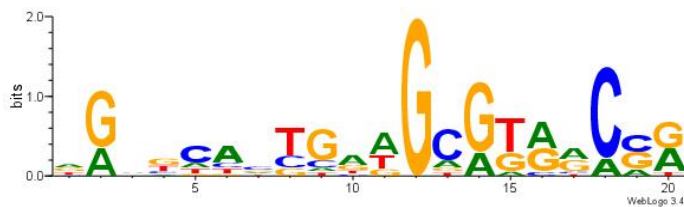


Dataset #: 3
 Motif ID: 31
 Motif name: Pax5
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0.0943783

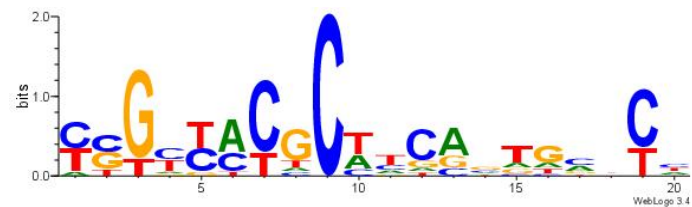
Alignment:

DGVCABTGDWCGKRRCSR
 GGGGCCCAAGGGG-----

Original motif Consensus sequence: DGVCABTGDWCGKRRCSR

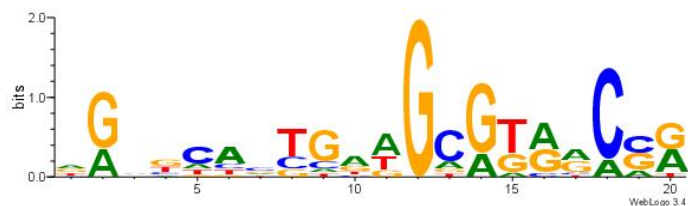


Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD

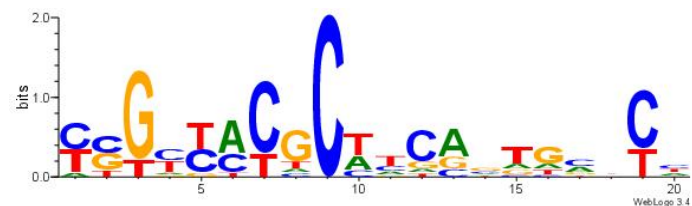


Dataset #: 3 Motif ID: 31 Motif name: Pax5

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGGBCD



Best Matches for Motif ID 31 (Highest to Lowest)

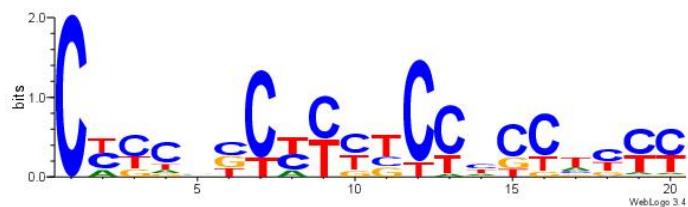
Dataset #:	5
Motif ID:	54
Motif name:	TFM12
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	20
Similarity score:	0.0373929

Alignment:

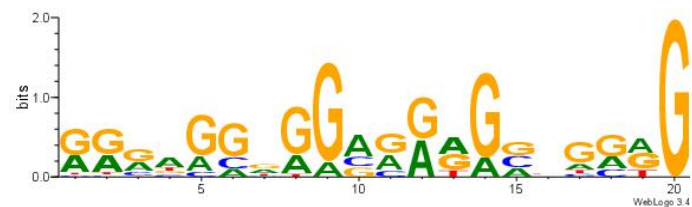
```

KKKAGGDGGAKKMGBBGKMG
DGVBCABTGDWGCGRRCR
  
```

Original motif Consensus sequence: CYYCBCYYYTCCHCCTYYY



Reverse complement motif Consensus sequence: KKKAGGDGGAKKMGBBGKMG

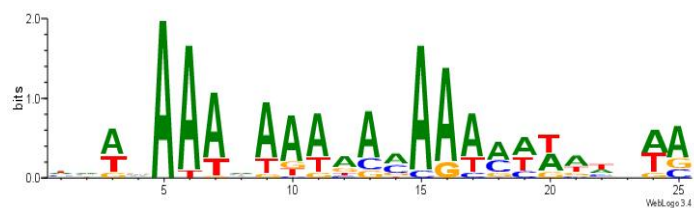


Dataset #: 5
 Motif ID: 56
 Motif name: TFM11
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 6
 Number of overlap: 20
 Similarity score: 0.0546306

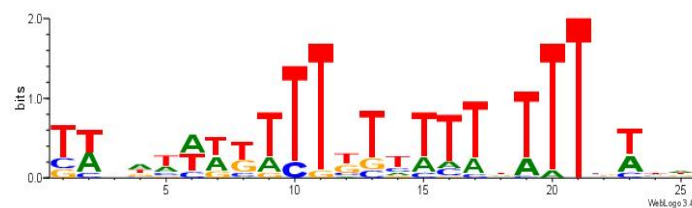
Alignment:

HDWVAAAHA AAAA MAAA MWWW HBWA
 DGVBCABTGDWGCGRRC SR-----

Original motif Consensus sequence:
 HDWVAAAHA AAAA MAAA MWWW HBWA



Reverse complement motif Consensus sequence:
 TWVHWWWYTTTTTTTTTHTTTVWBH



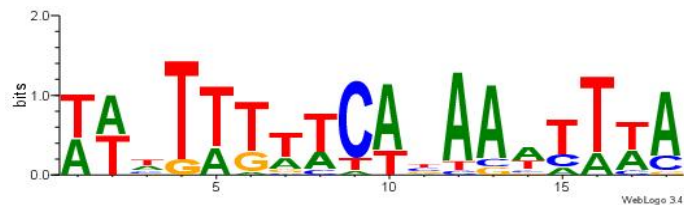
Dataset #: 5
 Motif ID: 53
 Motif name: TFM3
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward

Position number: 2
 Number of overlap: 17
 Similarity score: 1.5457

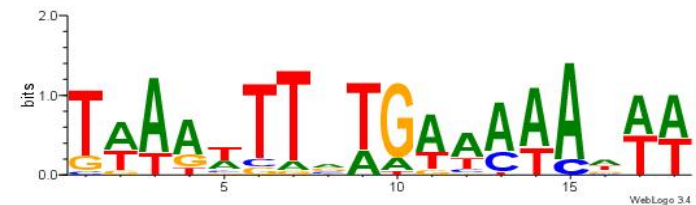
Alignment:

TWAAWTTVTGAAAAAHWW---
 -DGVBCABTGDWGCGRRCR

Original motif Consensus sequence: WWHTTTTTTCABAAWTTWA



Reverse complement motif Consensus sequence: TWAAWTTVTGAAAAAHWW

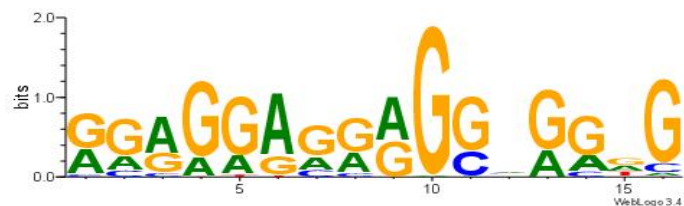


Dataset #: 5
 Motif ID: 51
 Motif name: TFM2
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 16
 Similarity score: 2.0519

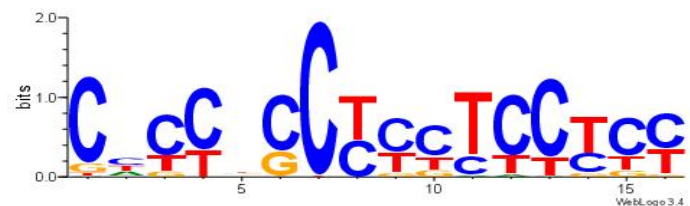
Alignment:

RGRGGAGRRGGHGGDG----
 MSGKKRCGCWDCABTGBBCD

Original motif Consensus sequence: RGRGGAGRRGGHGGDG



Reverse complement motif Consensus sequence: CHCCBCCKMCTCCKCM

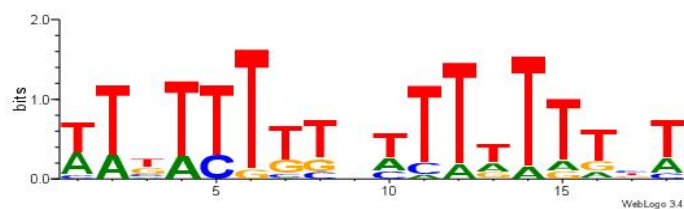


Dataset #: 5
Motif ID: 52
Motif name: TFM1
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 3
Number of overlap: 16
Similarity score: 2.05456

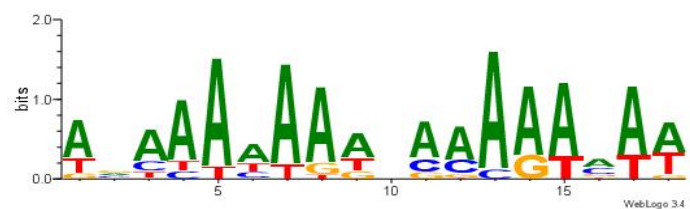
Alignment:

ABAAAAAWhAAAAARAW----
--DGVBCABTGDWGCGRRCsr

Original motif Consensus sequence: WTKTTTTTHWTTTTTTBT



Reverse complement motif Consensus sequence: ABAAAAAWhAAAAARAW



Dataset #: 3 **Motif ID: 32** **Motif name: ArntAhr**

Original motif Consensus sequence: YGCGTG



Reverse complement motif Consensus sequence: CACGCM



Best Matches for Motif ID 32 (Highest to Lowest)

Dataset #:	3
Motif ID:	23
Motif name:	Egr1
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	6
Similarity score:	0

Alignment:

```
HGCGTGGGCGK  
YGCGTG-----
```

Original motif Consensus sequence: HGCGTGGGCGK



Reverse complement motif Consensus sequence: YGCCACGCH



Dataset #: 3
Motif ID: 29
Motif name: HIF1AARNT
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: 0.0112447

Alignment:
VBACGTGV
-YGCGTG-

Original motif Consensus sequence: VBACGTGV



Reverse complement motif Consensus sequence: VCACGTBV



Dataset #: 3
Motif ID: 33
Motif name: Mycn
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 3

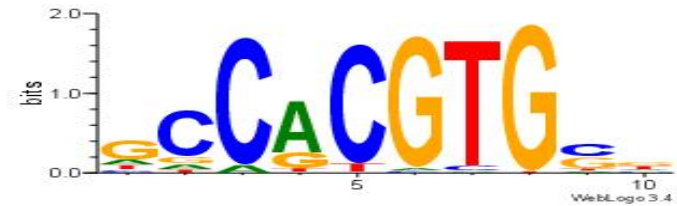
Number of overlap: 6
Similarity score: 0.0377949

Alignment:
GCCACGTGSD
--YGCGTG--

Original motif Consensus sequence: HSCACGTGGC



Reverse complement motif Consensus sequence: GCCACGTGSD

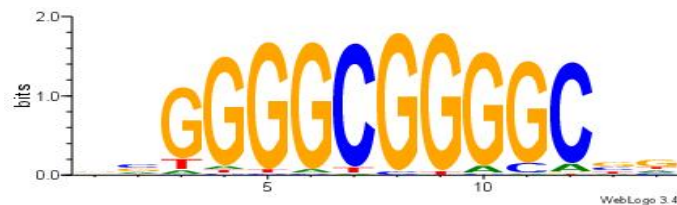
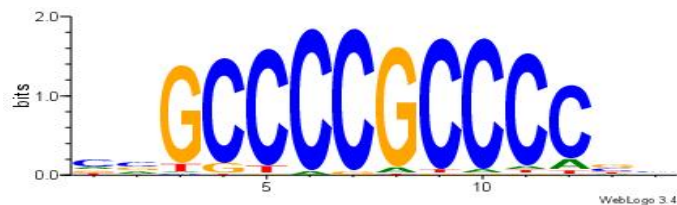


Dataset #: 4
Motif ID: 36
Motif name: csGCCCCGCCCCsc
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 5
Number of overlap: 6
Similarity score: 0.0396403

Alignment:
HVGCCCCGCCCCBB
----CACGCM----

Original motif Consensus sequence: HVGCCCCGCCCCBB

Reverse complement motif Consensus sequence: BBGGGCGGGGC



Dataset #: 3
 Motif ID: 34
 Motif name: Myc
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 6
 Similarity score: 0.0399214

Alignment:
 DCCACGTGCV
 --YGCCGTG--

Original motif Consensus sequence: VGCACGTGGH

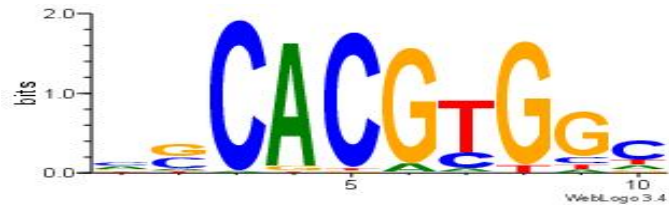


Reverse complement motif Consensus sequence: DCCACGTGCV

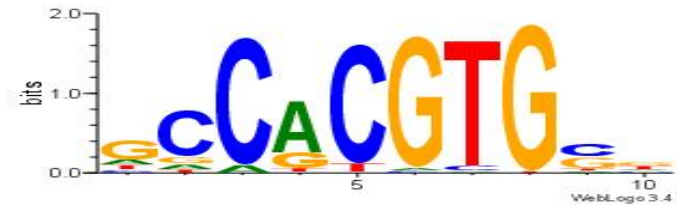


Dataset #: 3 Motif ID: 33 Motif name: Mycn

Original motif Consensus sequence: HSCACGTGGC



Reverse complement motif Consensus sequence: GCCACGTGSD



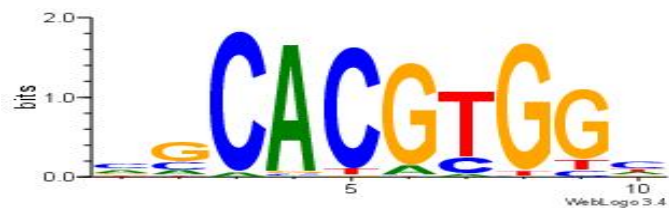
Best Matches for Motif ID 33 (Highest to Lowest)

Dataset #: 3
Motif ID: 34
Motif name: Myc
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 10
Similarity score: 0

Alignment:

DCCACGTGCV
GCCACGTGSD

Original motif Consensus sequence: VGCACGTGGH



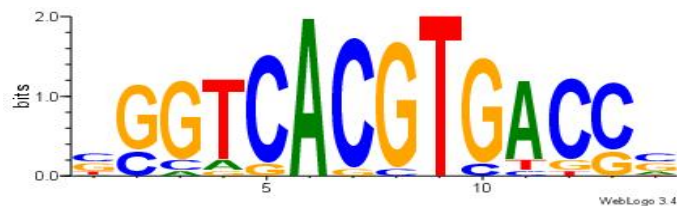
Reverse complement motif Consensus sequence: DCCACGTGCV



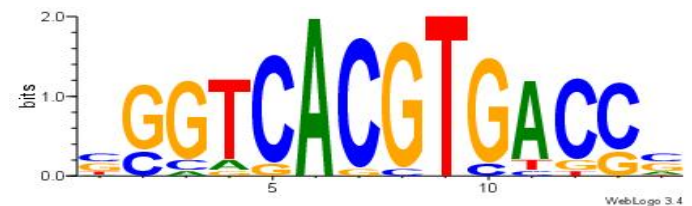
Dataset #: 4
 Motif ID: 42
 Motif name: sSGTCACGTGACSS
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 10
 Similarity score: 0.0628441

Alignment:
 SGGTCACGTGACCS
 --HSCACGTGGC--

Original motif Consensus sequence: SGGTCACGTGACCS



Reverse complement motif Consensus sequence: SGGTCACGTGACCS



Dataset #: 3
 Motif ID: 35
 Motif name: GABPA
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 10

Similarity score: 0.0884396

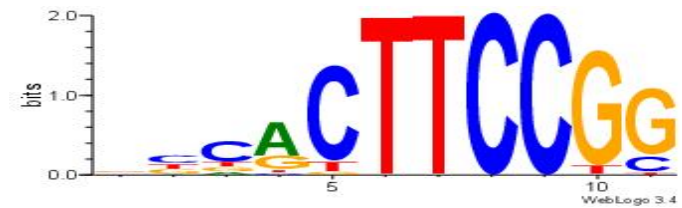
Alignment:

VVCACTTCCGG
GCCACGTGSD-

Original motif Consensus sequence: CCGGAAGTGVV



Reverse complement motif Consensus sequence: VVCACTTCCGG



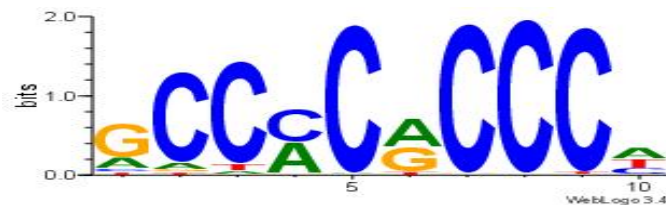
Dataset #: 3
Motif ID: 27
Motif name: Klf4
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 10
Similarity score: 0.0893272

Alignment:

DGGGYGKGGC
HSCACGTGGC

Original motif Consensus sequence: DGGGYGKGGC

Reverse complement motif Consensus sequence: GCCYCMCCCD

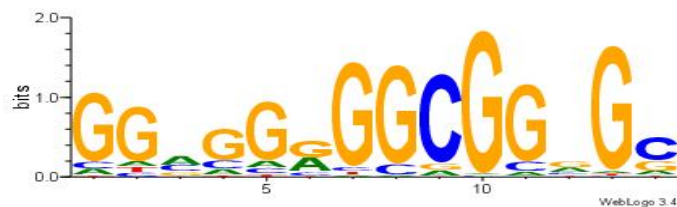


Dataset #: 5
 Motif ID: 50
 Motif name: TFF11
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 10
 Similarity score: 0.0895444

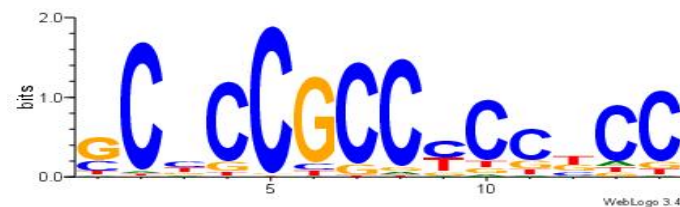
Alignment:

GGMGRRGGCGGVGC
 --HSCACGTGGC--

Original motif Consensus sequence: GGMGRRGGCGGVGC

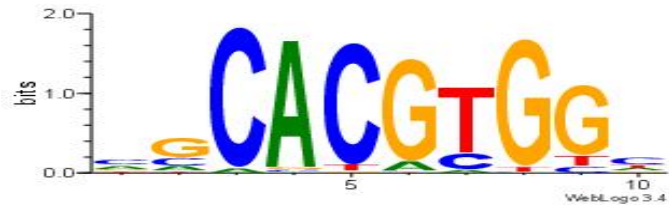


Reverse complement motif Consensus sequence: GCVCCGCCMCCYC

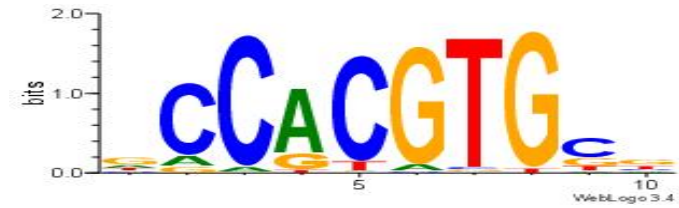


Dataset #: 3 Motif ID: 34 Motif name: Myc

Original motif Consensus sequence: VGCACGTGGH



Reverse complement motif Consensus sequence: DCCACGTGCV



Best Matches for Motif ID 34 (Highest to Lowest)

Dataset #:	3
Motif ID:	33
Motif name:	Mycn
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	10
Similarity score:	0

Alignment:

```
GCCACGTGSD  
DCCACGTGCV
```

Original motif Consensus sequence: HSCACGTGGC



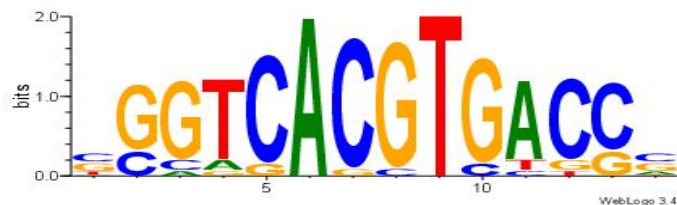
Reverse complement motif Consensus sequence: GCCACGTGSD



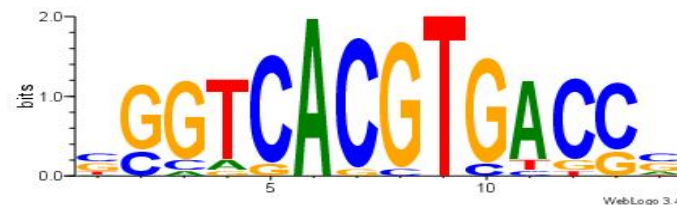
Dataset #: 4
 Motif ID: 42
 Motif name: sSGTCACGTGACsS
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 10
 Similarity score: 0.0646601

Alignment:
 SGGTCACGTGACCS
 --DCCACGTGCV--

Original motif Consensus sequence: SGGTCACGTGACCS



Reverse complement motif Consensus sequence: SGGTCACGTGACCS



Dataset #: 3
 Motif ID: 35
 Motif name: GABPA
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 10

Similarity score: 0.0840341

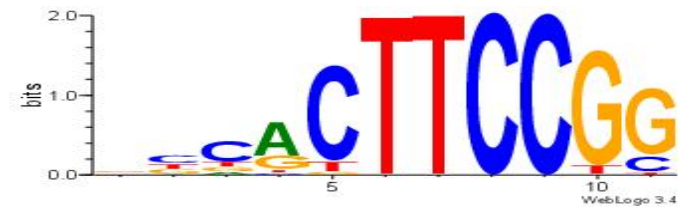
Alignment:

VVCACTTCCGG
DCCACGTGCV-

Original motif Consensus sequence: CCGGAAGTGVV



Reverse complement motif Consensus sequence: VVCACTTCCGG



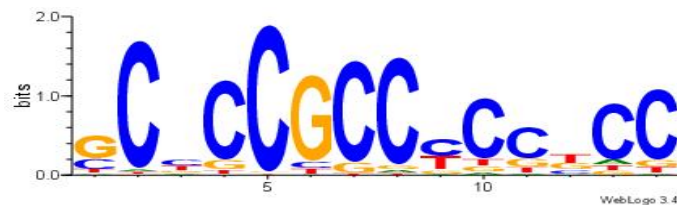
Dataset #: 5
Motif ID: 50
Motif name: TFF11
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 3
Number of overlap: 10
Similarity score: 0.0851555

Alignment:

GGMGRRGGCGGVGC
--VGCACGTGGH--

Original motif Consensus sequence: GGMGRRGGCGGVGC

Reverse complement motif Consensus sequence: GCVCCGCCMCCYCG



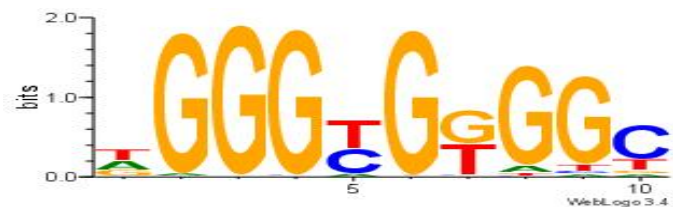
Dataset #: 3
 Motif ID: 27
 Motif name: Klf4
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 10
 Similarity score: 0.0883745

Alignment:

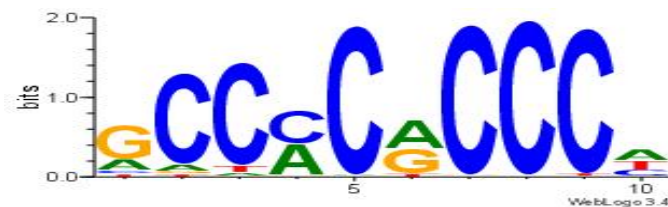
DGGGYGKGGC

VGCACGTGGH

Original motif Consensus sequence: DGGGYGKGGC



Reverse complement motif Consensus sequence: GCCYCMCCCD

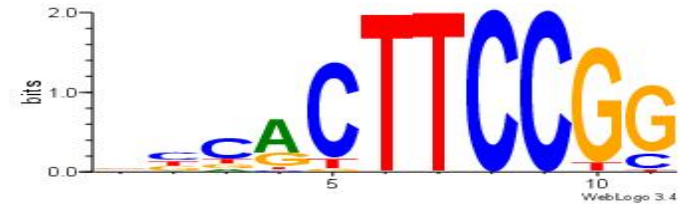


Dataset #: 3 Motif ID: 35 Motif name: GABPA

Original motif Consensus sequence: CCGGAAGTGVV



Reverse complement motif Consensus sequence: VVCACTTCCGG



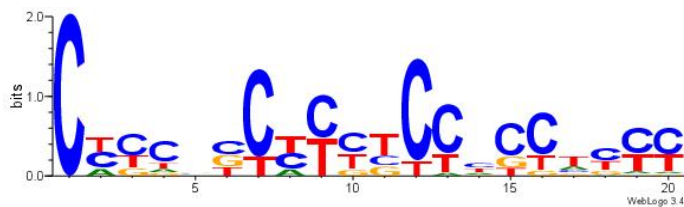
Best Matches for Motif ID 35 (Highest to Lowest)

Dataset #: 5
 Motif ID: 54
 Motif name: TFM12
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 5
 Number of overlap: 11
 Similarity score: 0.0360984

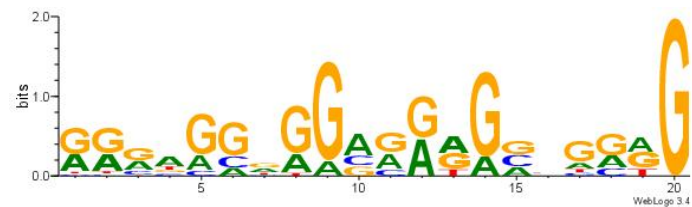
Alignment:

```
CYVCBBCYYYTCCHCCTYYY
-----VVCACTTCCGG-----
```

Original motif Consensus sequence: CYVCBBCYYYTCCHCCTYYY



Reverse complement motif Consensus sequence: KKKAGGDGGAKKMGBBGKMG

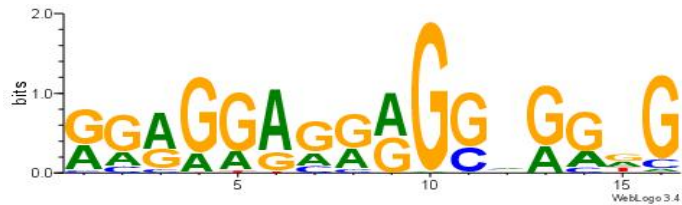


Dataset #: 5
 Motif ID: 51
 Motif name: TFM2
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 5
 Number of overlap: 11
 Similarity score: 0.0445566

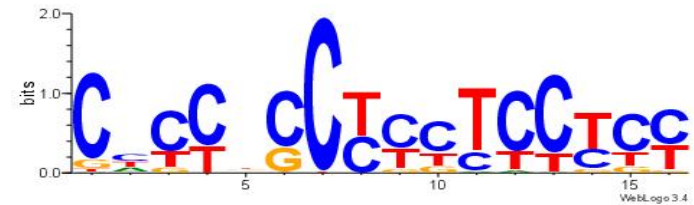
Alignment:

RGRGGAGRRGGHGGDG
 -CCGGAAGTGVV-----

Original motif Consensus sequence: RGRGGAGRRGGHGGDG



Reverse complement motif Consensus sequence: CHCCBCKMCTCCKCM



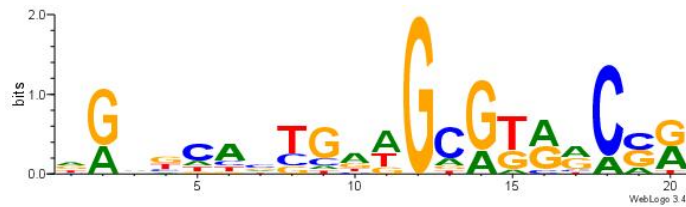
Dataset #: 3
 Motif ID: 31
 Motif name: Pax5
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3

Number of overlap: 11
Similarity score: 0.0446257

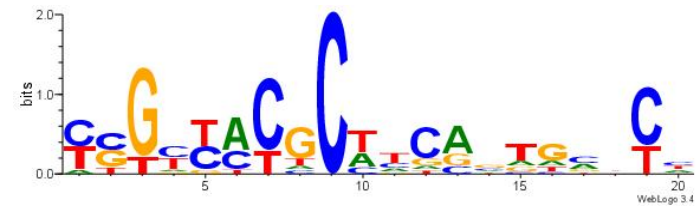
Alignment:

DGVBCABTGDWGCGRRCR
-----VVCACTTCCGG--

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR



Reverse complement motif Consensus sequence:
MSGKKRCGCWDCABTGBBCD



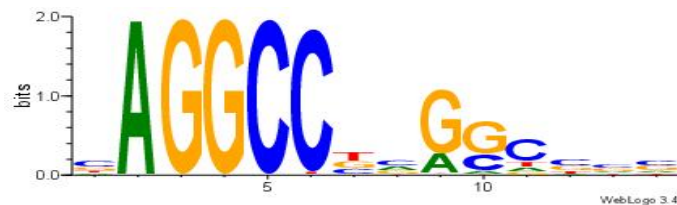
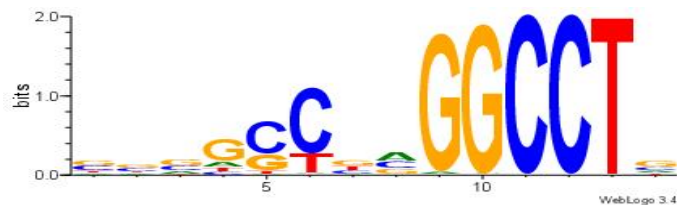
Dataset #: 3
Motif ID: 22
Motif name: Zfx
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 4
Number of overlap: 11
Similarity score: 0.0457327

Alignment:

BBVGCCBVGGCCTV
VVCACTTCCGG---

Original motif Consensus sequence: BBVGCCBVGGCCTV

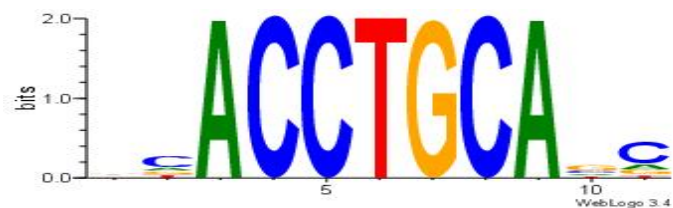
Reverse complement motif Consensus sequence: VAGGCCBBGGCV



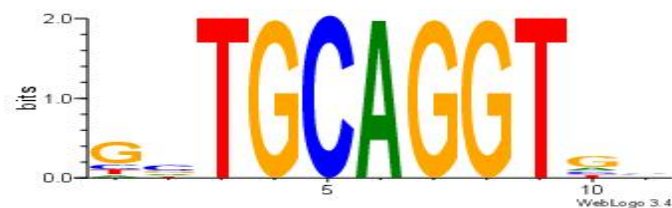
Dataset #: 4
 Motif ID: 40
 Motif name: kcACCTGCAGc
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.0483841

Alignment:
 BCACCTGCABC
 VVCACTTCCGG

Original motif Consensus sequence: BCACCTGCABC

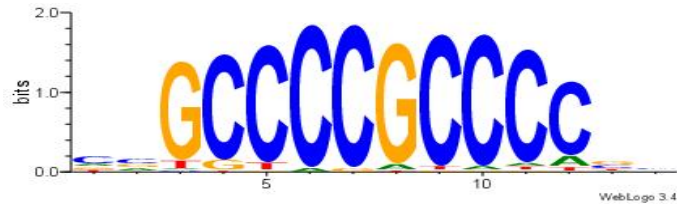


Reverse complement motif Consensus sequence: GBTGCAGGTGB

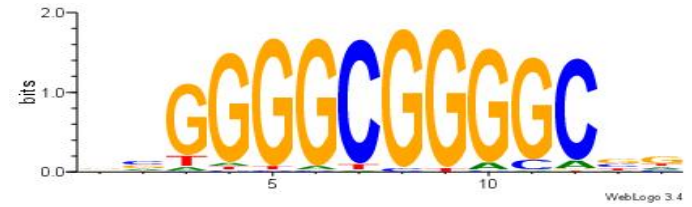


Dataset #: 4 Motif ID: 36 Motif name: csGCCCCGCCCCsc

Original motif Consensus sequence: HVGCCCCGCCCB



Reverse complement motif Consensus sequence: BBGGGCGGGGC



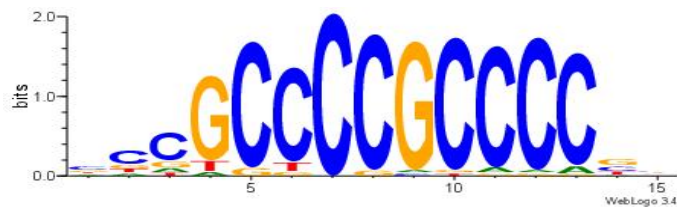
Best Matches for Motif ID 36 (Highest to Lowest)

Dataset #: 4
 Motif ID: 38
 Motif name: cccGCCCCGCCCBsb
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0

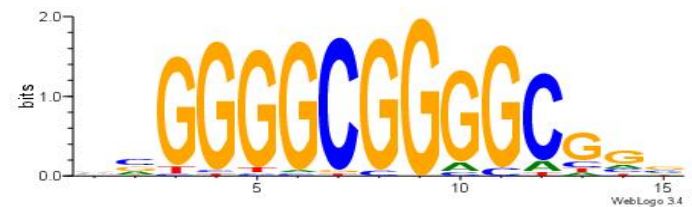
Alignment:

BBGGGCGGGGCGGB
 BBGGGCGGGGCVD-

Original motif Consensus sequence: BCCGCCCGCCCCB



Reverse complement motif Consensus sequence: BBGGGCGGGGCGGB

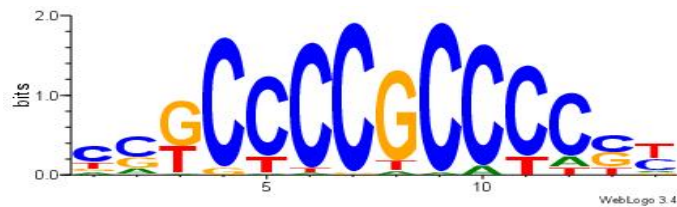


Dataset #: 2
 Motif ID: 7
 Motif name: Motif 7
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0.0117332

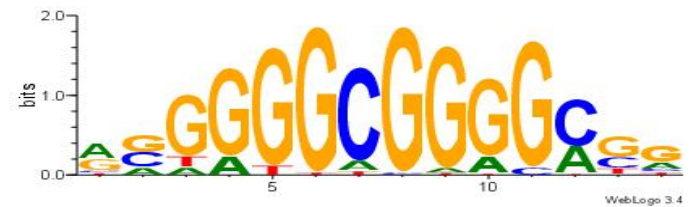
Alignment:

CSKCCCCGCCCSY
 HVGCCCCGCCCB

Original motif Consensus sequence: CSKCCCCGCCCSY



Reverse complement motif Consensus sequence: MSGGGCGGGY



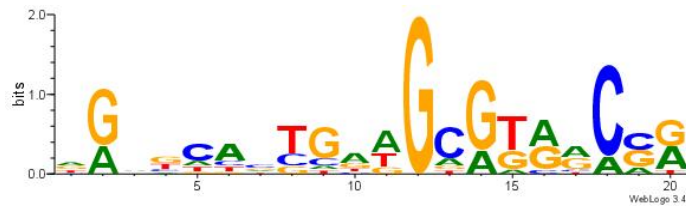
Dataset #: 3
 Motif ID: 31
 Motif name: Pax5
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 14

Similarity score: 0.0747029

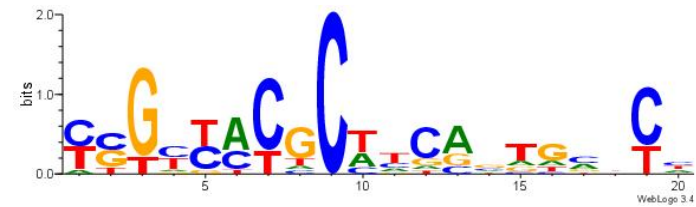
Alignment:

```
MSGKKRCGCWDCABTGBBCD  
-----HVGCCCCGCCCCBB
```

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR



Reverse complement motif Consensus sequence:
MSGKKRCGCWDCABTGBBCD



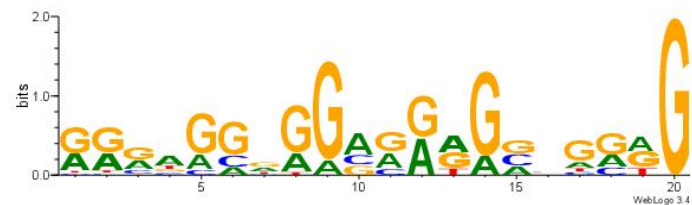
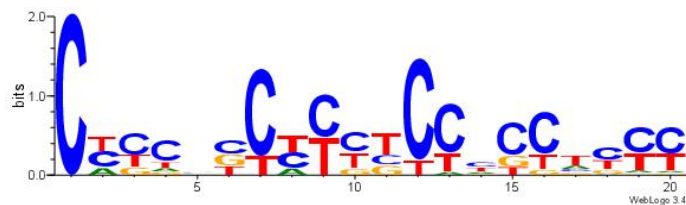
Dataset #: 5
Motif ID: 54
Motif name: TFM12
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 4
Number of overlap: 14
Similarity score: 0.0777991

Alignment:

```
CYYCBBCYYYYTCCHCCTYYY  
---HVGCCCCGCCCCBB---
```

Original motif Consensus sequence: CYYCBBCYYYYTCCHCCTYYY

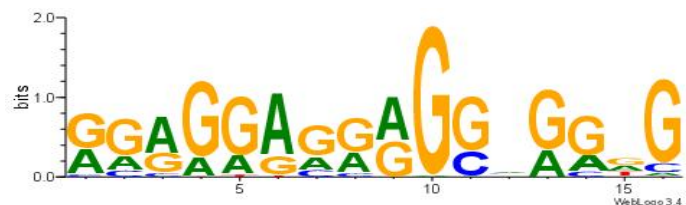
Reverse complement motif Consensus sequence:
KKKAGGDGGAKKMGBBGKMG



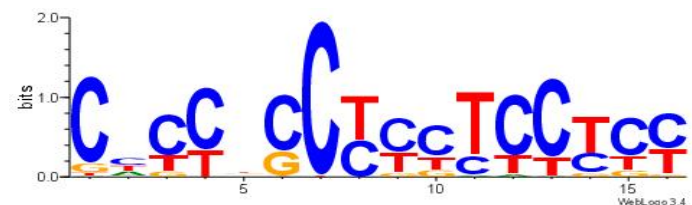
Dataset #: 5
 Motif ID: 51
 Motif name: TFM2
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 14
 Similarity score: 0.0880609

Alignment:
 RGRGGAGRRGGHGGDG
 BBGGGGCGGGCVD--

Original motif Consensus sequence: RGRGGAGRRGGHGGDG

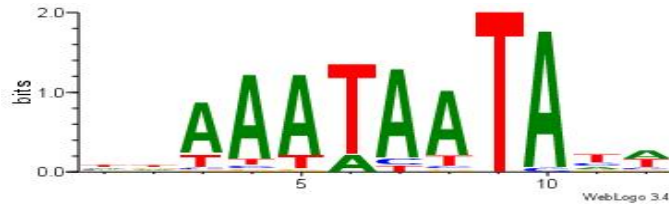


Reverse complement motif Consensus sequence: CHCCBCKMCTCCKCM

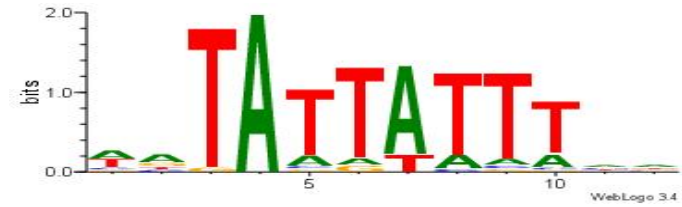


Dataset #: 4 Motif ID: 37 Motif name: tkAAATAATatw

Original motif Consensus sequence: HDAAATAATAHW



Reverse complement motif Consensus sequence: WHTATTATTTDH



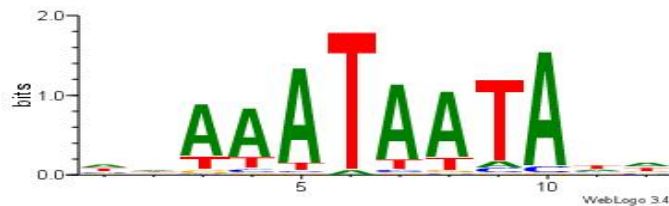
Best Matches for Motif ID 37 (Highest to Lowest)

Dataset #:	4
Motif ID:	41
Motif name:	wwAAATAATAtw
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	12
Similarity score:	0

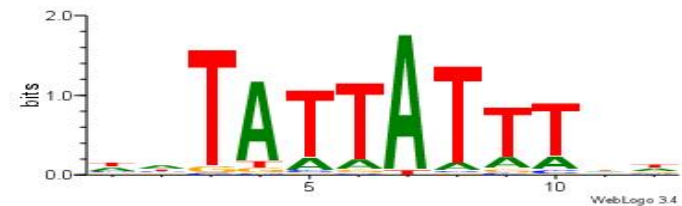
Alignment:

```
HDAAATAATADD  
HDAAATAATAHW
```

Original motif Consensus sequence: HDAAATAATADD



Reverse complement motif Consensus sequence: DDTATTATTTDH

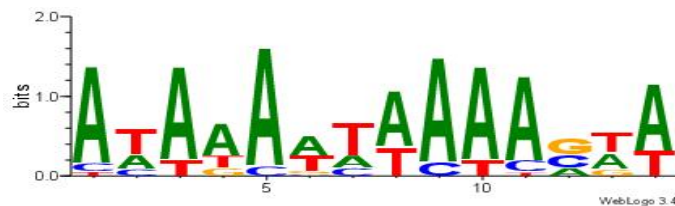


Dataset #: 2
 Motif ID: 3
 Motif name: Motif 3
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 12
 Similarity score: 0.0522317

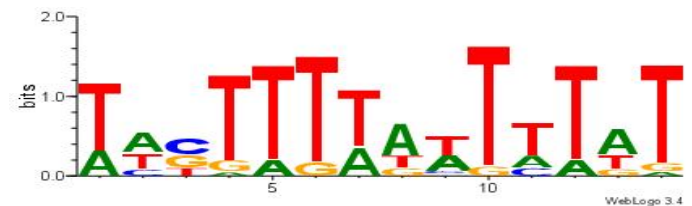
Alignment:

TWSTTTWAWTTTWT
 -WHTATTATTTDH-

Original motif Consensus sequence: AWAAAWTWAAASWA



Reverse complement motif Consensus sequence: TWSTTTWAWTTTWT



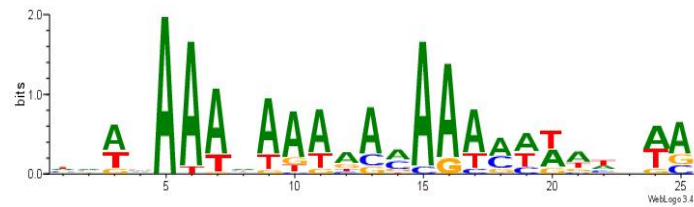
Dataset #: 5
 Motif ID: 56
 Motif name: TFM11
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 12

Similarity score: 0.0590505

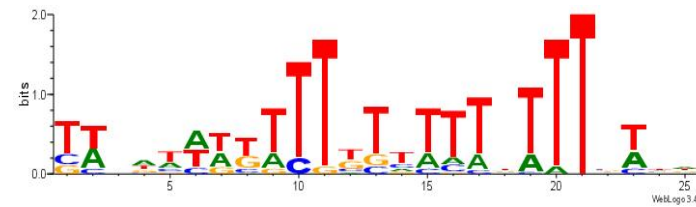
Alignment:

```
TWVHWWYTTTYTTTTHTTTVWBH  
-----WHTATTATTTDH--
```

Original motif Consensus sequence:
HDWVAAAHAAAAAMAAAMWWWHBWA



Reverse complement motif Consensus sequence:
TWVHWWYTTTYTTTTHTTTVWBH



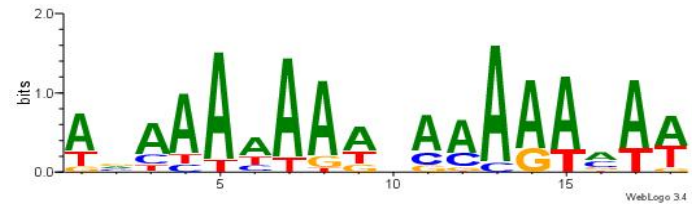
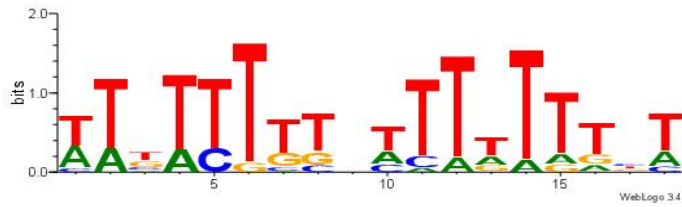
Dataset #: 5
Motif ID: 52
Motif name: TFM1
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 12
Similarity score: 0.0637702

Alignment:

```
ABAAAAAWhAAAAARAW  
HDAAATAATAHW-----
```

Original motif Consensus sequence: WTKTTTTTHWTTTTTTTBT

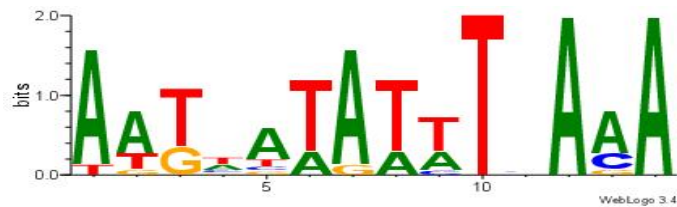
Reverse complement motif Consensus sequence:
ABAAAAAWhAAAAARAW



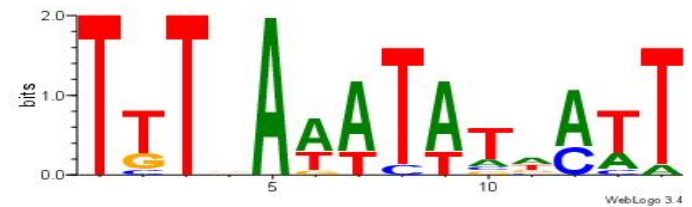
Dataset #: 2
 Motif ID: 9
 Motif name: Motif 9
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 12
 Similarity score: 0.0641975

Alignment:
 AATHATATWTHAAA
 --WHTATTATTTDH

Original motif Consensus sequence: AATHATATWTHAAA

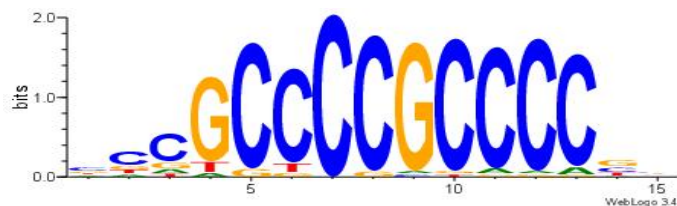


Reverse complement motif Consensus sequence: TTTDAWATATHAT

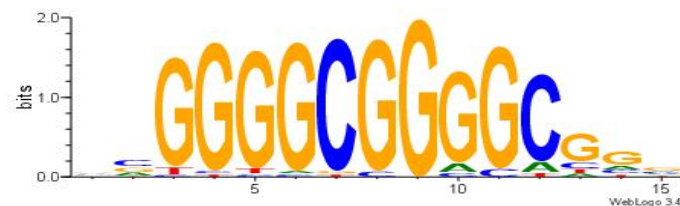


Dataset #: 4 Motif ID: 38 Motif name: cccGCCCGCCCCsb

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB



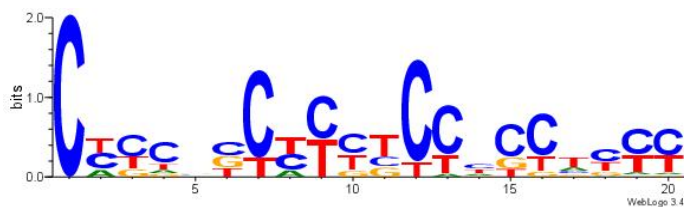
Best Matches for Motif ID 38 (Highest to Lowest)

Dataset #:	5
Motif ID:	54
Motif name:	TFM12
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	3
Number of overlap:	15
Similarity score:	0.0773345

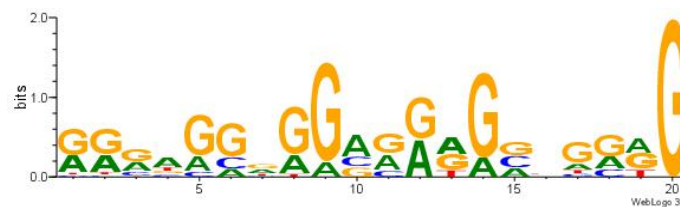
Alignment:

```
CYYCBBBCYYYTCCHCCTYYY
--BCCGCCCCGCCCCBB---
```

Original motif Consensus sequence: CYYCBBBCYYYTCCHCCTYYY



Reverse complement motif Consensus sequence: KKKAGGDGGAKKMGBBGKMG

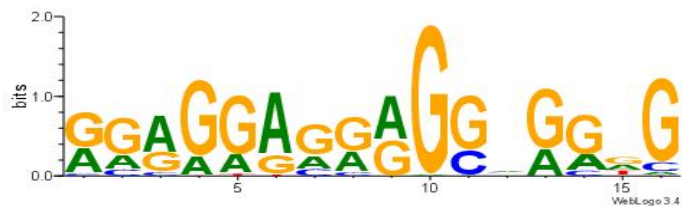


Dataset #: 5
 Motif ID: 51
 Motif name: TFM2
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 15
 Similarity score: 0.0869149

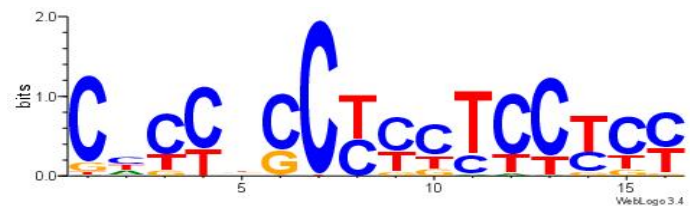
Alignment:

RGRGGAGRRGGHGGDG
 BBGGGGCGGGGCGGB-

Original motif Consensus sequence: RGRGGAGRRGGHGGDG



Reverse complement motif Consensus sequence: CHCCBCKMCTCKCM



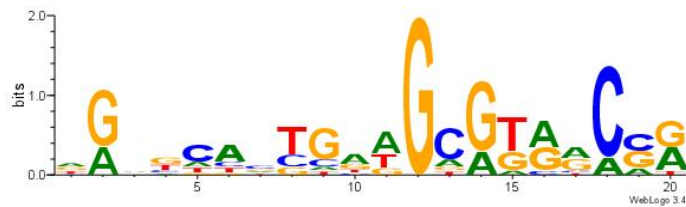
Dataset #: 3
 Motif ID: 31
 Motif name: Pax5
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward

Position number: 1
 Number of overlap: 15
 Similarity score: 0.0992376

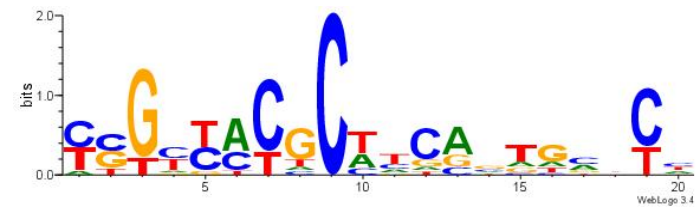
Alignment:

MSGKKRCGCWDCABTGBBCD
 BBGGGGCGGGGCGGB-----

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD

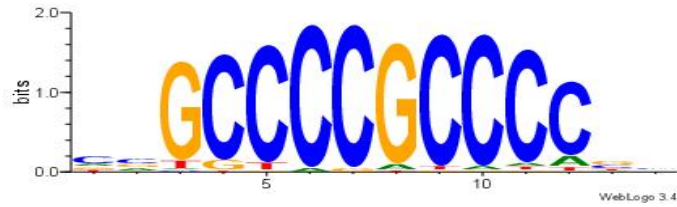


Dataset #: 4
 Motif ID: 36
 Motif name: csGCCCCGCCCCsc
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0.5

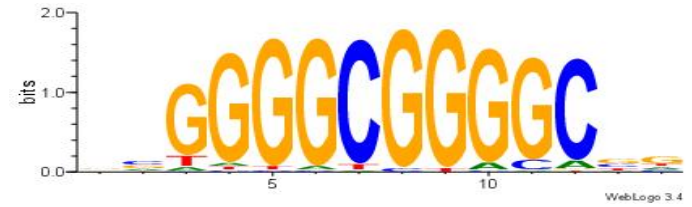
Alignment:

-HVGCCCCGCCCCBB
 BCCGCCCCGCCCCBB

Original motif Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGC

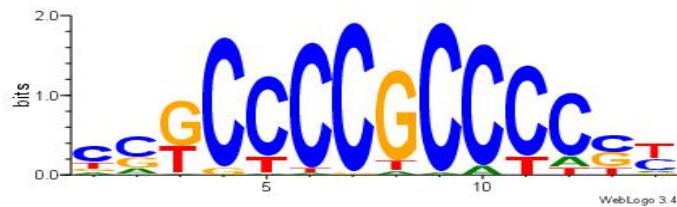


Dataset #: 2
Motif ID: 7
Motif name: Motif 7
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 14
Similarity score: 0.513015

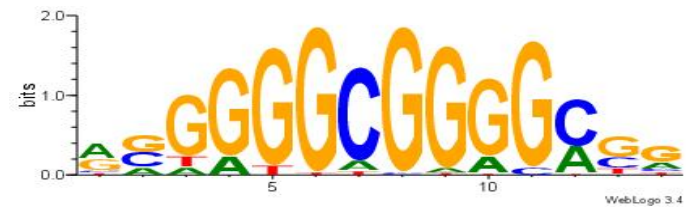
Alignment:

-CSKCCCCGCCCCSY
BCCGCCCGCCCCBB

Original motif Consensus sequence: CSKCCCCGCCCCSY



Reverse complement motif Consensus sequence: MSGGGGCGGGGY



Dataset #: 4 **Motif ID: 39** **Motif name: kCAGCCAATmr**

Original motif Consensus sequence: DCAGCCAATVR



Reverse complement motif Consensus sequence: MBATTGGCTGH



Best Matches for Motif ID 39 (Highest to Lowest)

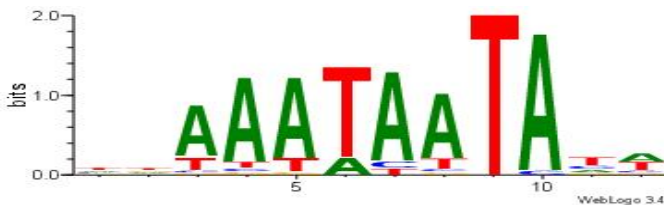
Dataset #:	4
Motif ID:	37
Motif name:	tkAAATAATAtw
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	2
Number of overlap:	11
Similarity score:	0.0559269

Alignment:

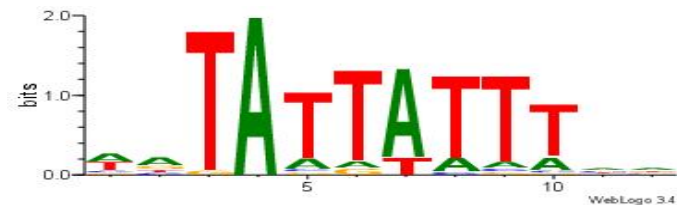
WHTATTATTTDH

-MBATTGGCTGH

Original motif Consensus sequence: HDAAATAATAHW



Reverse complement motif Consensus sequence: WHTATTATTTDH

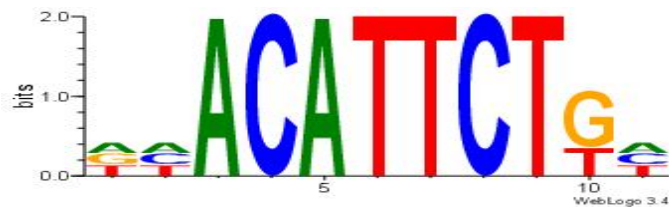


Dataset #: 4
 Motif ID: 44
 Motif name: dhACATTCTkh
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.0588235

Alignment:

HCAGAATGTHD
 DCAGCCAATVR

Original motif Consensus sequence: DHACATTCTGH



Reverse complement motif Consensus sequence: HCAGAATGTHD

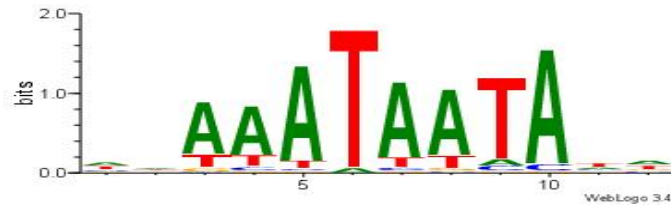


Dataset #: 4
 Motif ID: 41
 Motif name: wwAAATAATAtw
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1

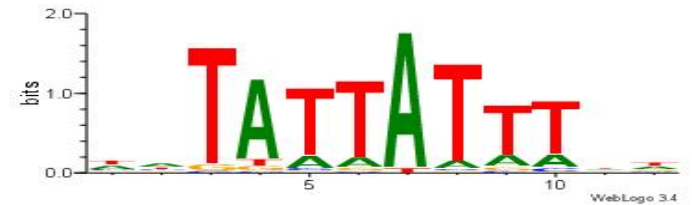
Number of overlap: 11
Similarity score: 0.0597643

Alignment:
DDTATTATTTDH
-MBATTGGCTGH

Original motif Consensus sequence: HDAAATAATADD



Reverse complement motif Consensus sequence: DDTATTATTTDH

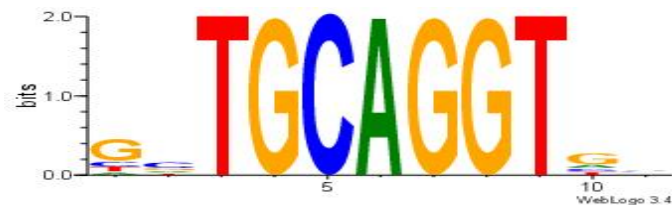
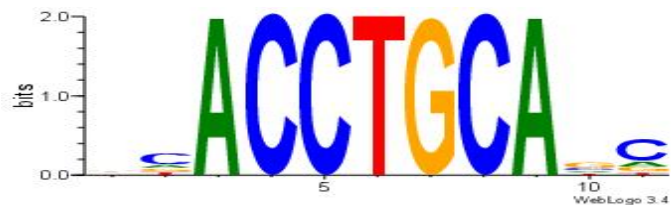


Dataset #: 4
Motif ID: 40
Motif name: kcACCTGCAGc
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 11
Similarity score: 0.0599548

Alignment:
BCACCTGCABC
MBATTGGCTGH

Original motif Consensus sequence: BCACCTGCABC

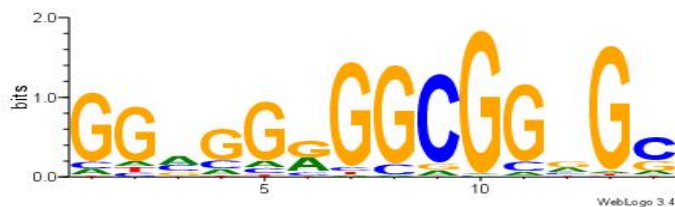
Reverse complement motif Consensus sequence: GBTGCAGGTGB



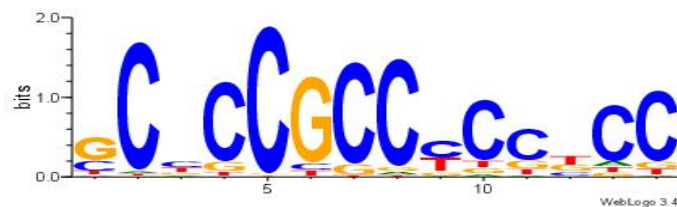
Dataset #: 5
 Motif ID: 50
 Motif name: TFF11
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 11
 Similarity score: 0.0614719

Alignment:
 GCVCCGCCMCCYCC
 --DCAGCCAATVR--

Original motif Consensus sequence: GGMGRRGGCGGVGC

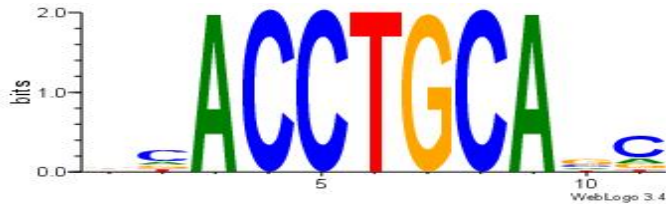


Reverse complement motif Consensus sequence: GCVCCGCCMCCYCC



Dataset #: 4 Motif ID: 40 Motif name: kcACCTGCAgc

Original motif Consensus sequence: BCACCTGCABC



Reverse complement motif Consensus sequence: GBTGCAGGTGB



Best Matches for Motif ID 40 (Highest to Lowest)

Dataset #:	4
Motif ID:	43
Motif name:	wsTACwGTAsw
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	11
Similarity score:	0.0215284

Alignment:

DBTACWGTA VH
BCACCTGCABC

Original motif Consensus sequence: HVTACWGTA BD



Reverse complement motif Consensus sequence: DBTACWGTA VH

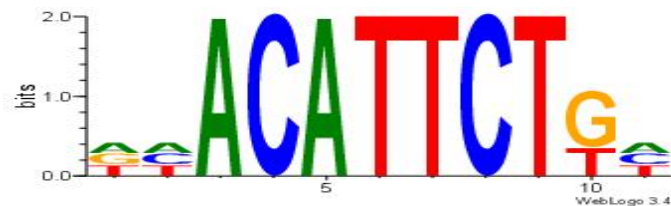


Dataset #: 4
 Motif ID: 44
 Motif name: dhACATTCTkh
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.0254134

Alignment:

DHACATTCTGH
 BCACCTGCABC

Original motif Consensus sequence: DHACATTCTGH



Reverse complement motif Consensus sequence: HCAGAATGTHD



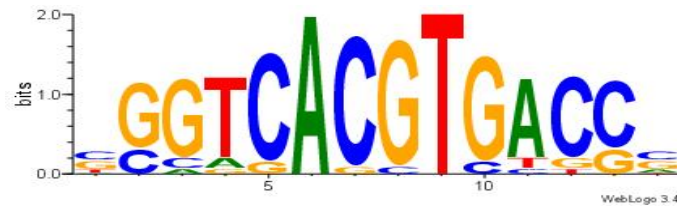
Dataset #: 4
 Motif ID: 42
 Motif name: sSGTCACGTGACSS
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 11

Similarity score: 0.031338

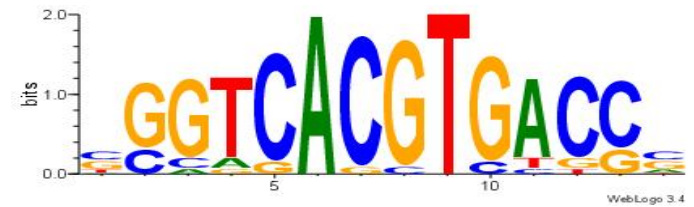
Alignment:

SGGTCACGTGACCS
---BCACCTGCABC

Original motif Consensus sequence: SGGTCACGTGACCS



Reverse complement motif Consensus sequence: SGGTCACGTGACCS



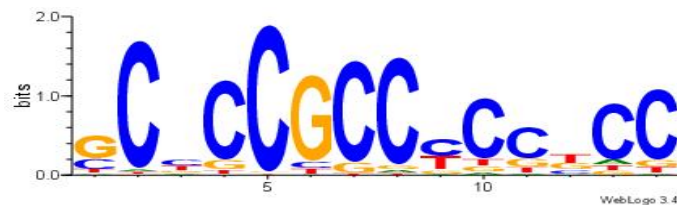
Dataset #: 5
Motif ID: 50
Motif name: TFF11
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 4
Number of overlap: 11
Similarity score: 0.034471

Alignment:

GCVCCGCCMCCYCC
BCACCTGCABC---

Original motif Consensus sequence: GGMGRRGGCGGVGC

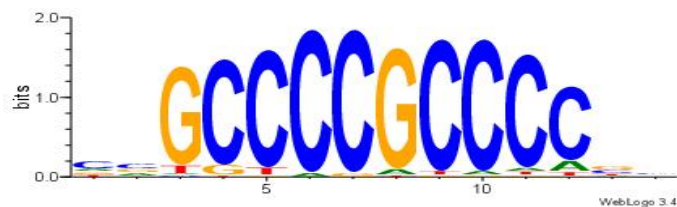
Reverse complement motif Consensus sequence: GCVCCGCCMCCYCC



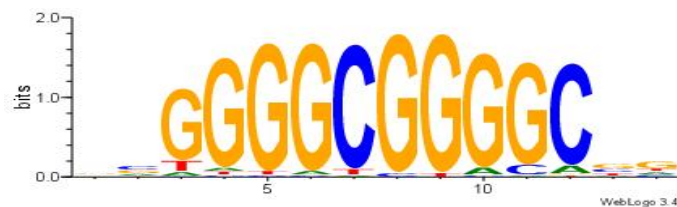
Dataset #: 4
 Motif ID: 36
 Motif name: csGCCCCGCCCCsc
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 11
 Similarity score: 0.0402518

Alignment:
 HVGCCCCGCCCCBB
 -BCACCTGCABC--

Original motif Consensus sequence: HVGCCCCGCCCCBB

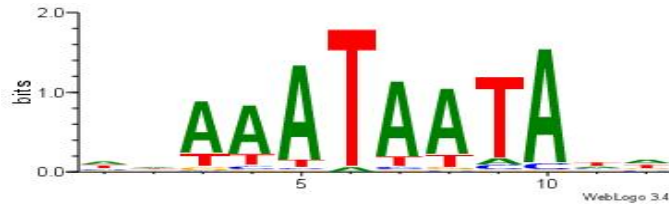


Reverse complement motif Consensus sequence: BBGGGCGGGGC

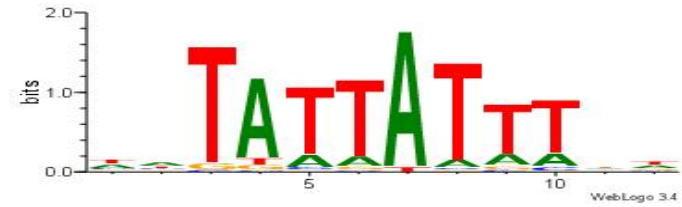


Dataset #: 4 Motif ID: 41 Motif name: wwAAATAATAtw

Original motif Consensus sequence: HDAAATAATADD



Reverse complement motif Consensus sequence: DDTATTATTTDH



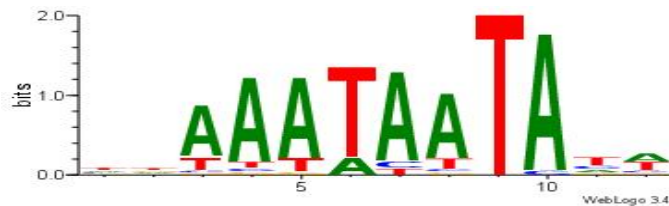
Best Matches for Motif ID 41 (Highest to Lowest)

Dataset #:	4
Motif ID:	37
Motif name:	tkAAATAATAtw
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	12
Similarity score:	0

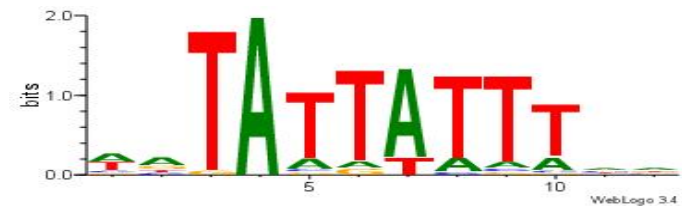
Alignment:

HDAAATAATAHW
HDAAATAATADD

Original motif Consensus sequence: HDAAATAATAHW



Reverse complement motif Consensus sequence: WHTATTATTTDH

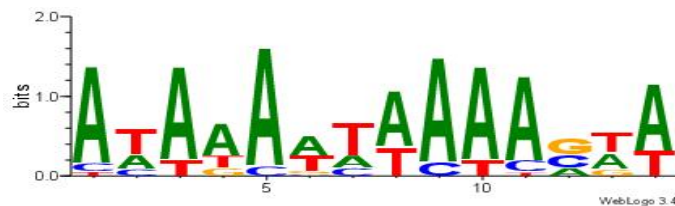


Dataset #: 2
 Motif ID: 3
 Motif name: Motif 3
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 12
 Similarity score: 0.0536028

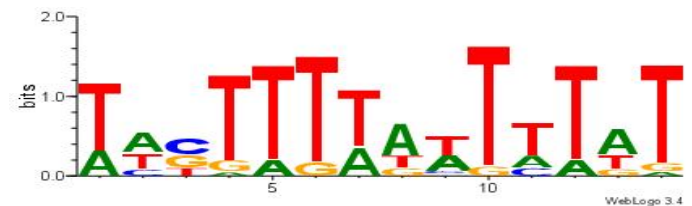
Alignment:

AWAAAWTWAAASWA
 -HDAAATAATADD-

Original motif Consensus sequence: AWAAAWTWAAASWA



Reverse complement motif Consensus sequence: TWSTTTWAWTTT



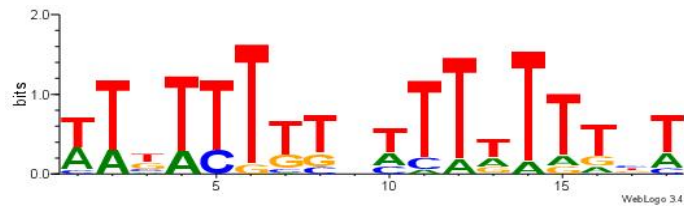
Dataset #: 5
 Motif ID: 52
 Motif name: TFM1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 7
 Number of overlap: 12

Similarity score: 0.0565705

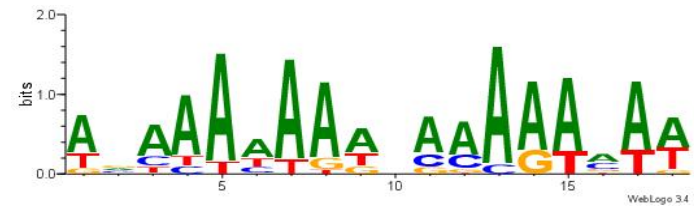
Alignment:

```
WKTTTTTHWTTTTTBT  
-----DDTATTATTDH
```

Original motif Consensus sequence: WKTTTTTHWTTTTTBT



Reverse complement motif Consensus sequence:
ABAAAAAWhAAAAARAW



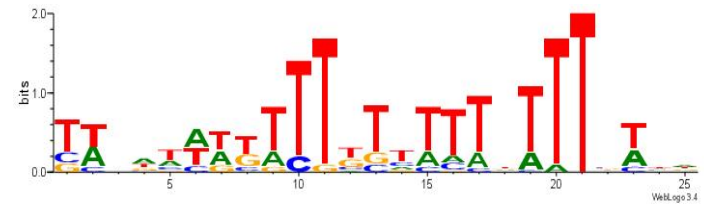
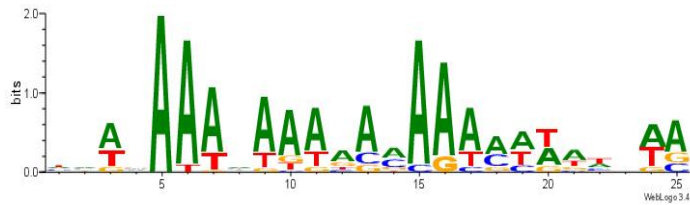
Dataset #: 5
Motif ID: 56
Motif name: TFM11
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 3
Number of overlap: 12
Similarity score: 0.0575935

Alignment:

```
HDWVAAAHAAAAAMAAAMWWWHBWA  
--HDAAATAATADD-----
```

Original motif Consensus sequence:
HDWVAAAHAAAAAMAAAMWWWHBWA

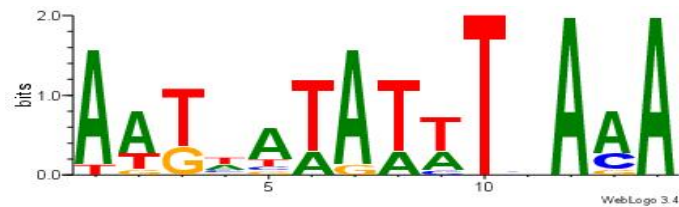
Reverse complement motif Consensus sequence:
TWVHWWWYTTTTYTTTTTHTTTVWBH



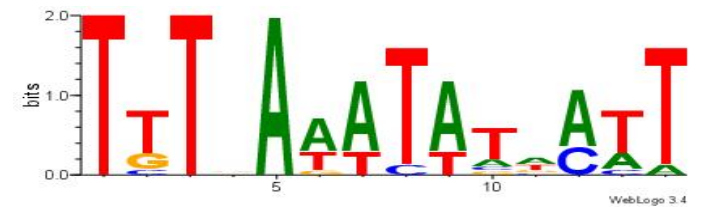
Dataset #: 2
 Motif ID: 9
 Motif name: Motif 9
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 12
 Similarity score: 0.0591821

Alignment:
 AATHATATWTHAAA
 --DDTATTATTTDH

Original motif Consensus sequence: AATHATATWTHAAA

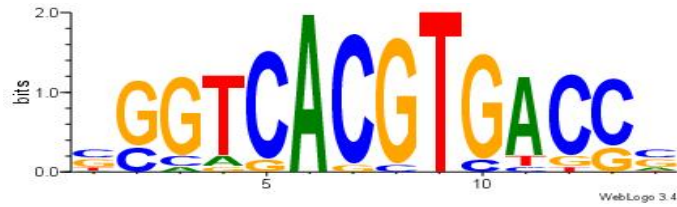


Reverse complement motif Consensus sequence: TTTDAWATATHAT

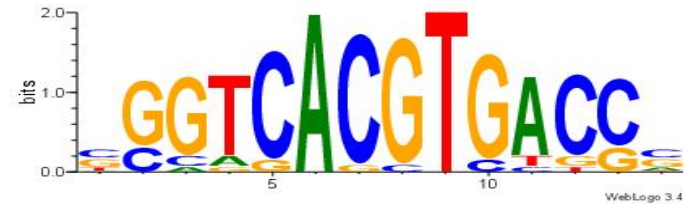


Dataset #: 4 Motif ID: 42 Motif name: sSGTCACGTGACs

Original motif Consensus sequence: SGGTCACGTGACCS



Reverse complement motif Consensus sequence: SGGTCACGTGACCS



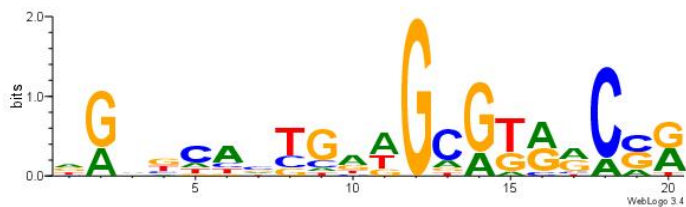
Best Matches for Motif ID 42 (Highest to Lowest)

Dataset #:	3
Motif ID:	31
Motif name:	Pax5
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	7
Number of overlap:	14
Similarity score:	0.0518737

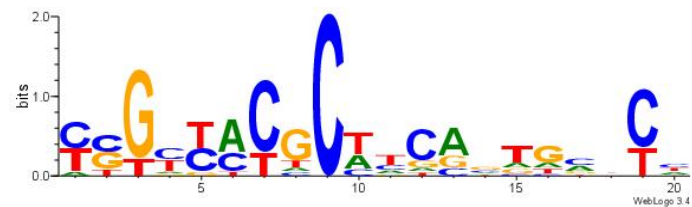
Alignment:

```
DGVBCABTGDWGCGRCSR
-----SSGGTCACGTGACCS
```

Original motif Consensus sequence: DGVBCABTGDWGCGRCSR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBCD

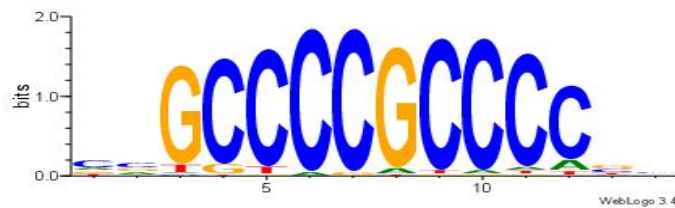


Dataset #: 4
 Motif ID: 36
 Motif name: csGCCCCGCCCCsc
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0.0539097

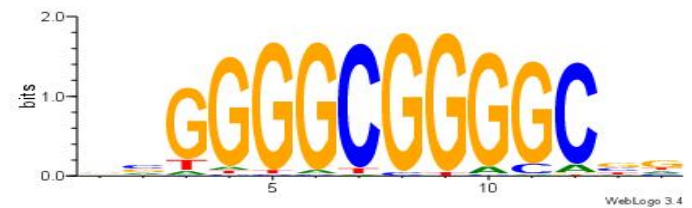
Alignment:

BBGGGGCGGGGCVD
 SGGTCACGTGACCS

Original motif Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGC



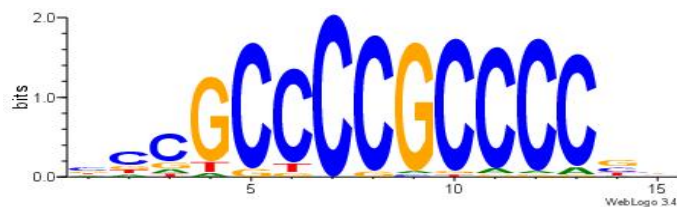
Dataset #: 4
 Motif ID: 38
 Motif name: cccGCCCCGCCCCsb
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 14

Similarity score: 0.0581955

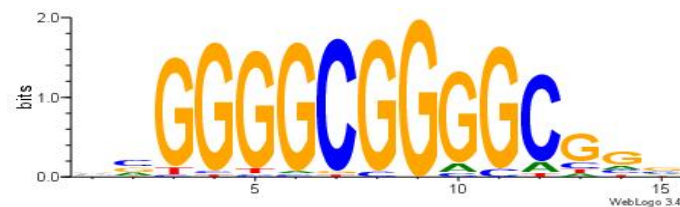
Alignment:

BCCGCCCCGCCCCBB
SGGTCACGTGACCS-

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB



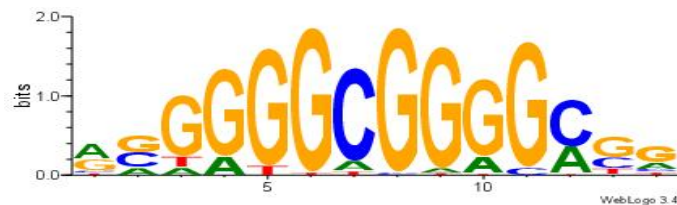
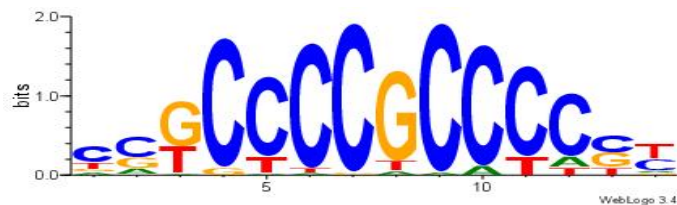
Dataset #: 2
Motif ID: 7
Motif name: Motif 7
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 14
Similarity score: 0.0634135

Alignment:

MSGGGGCGGGGYSG
SGGTCACGTGACCS

Original motif Consensus sequence: CSKCCCCGCCCSY

Reverse complement motif Consensus sequence: MSGGGGCGGGGY



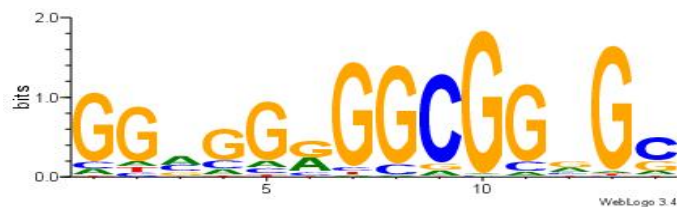
Dataset #: 5
 Motif ID: 50
 Motif name: TFF11
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 12
 Similarity score: 1.05855

Alignment:

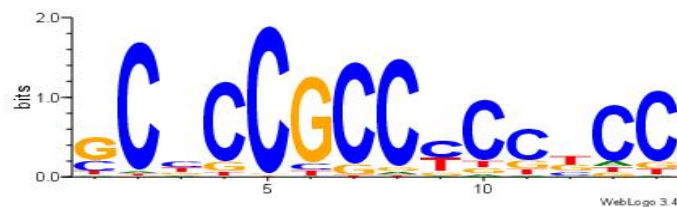
```

--GCVCCGCCMCCYCC
SGGTCACGTGACCS--
  
```

Original motif Consensus sequence: GGMGRRGGCGGVGC



Reverse complement motif Consensus sequence: GCVCCGCCMCCYCC



Dataset #: 4 Motif ID: 43 Motif name: wsTACwGTAsw

Original motif Consensus sequence: HVTACWG TABD



Reverse complement motif Consensus sequence: DBTACWG TAVH



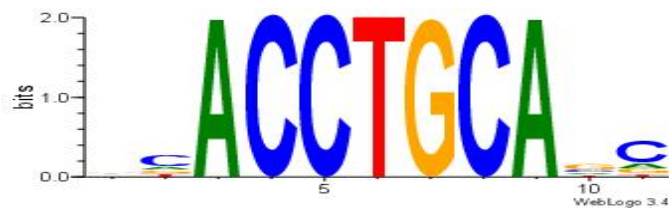
Best Matches for Motif ID 43 (Highest to Lowest)

Dataset #:	4
Motif ID:	40
Motif name:	kcACCTGC Agc
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	11
Similarity score:	0.0199592

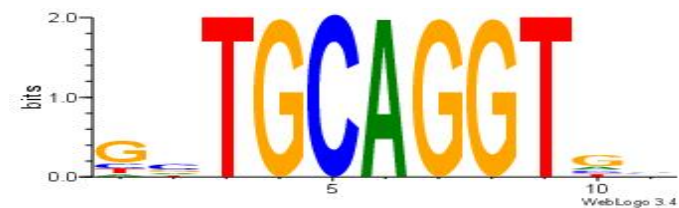
Alignment:

GBTGCAGGTGB
HVTACWG TABD

Original motif Consensus sequence: BCACCTGC ABC



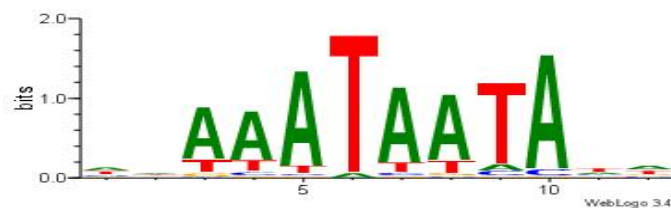
Reverse complement motif Consensus sequence: GBTGCAGGTGB



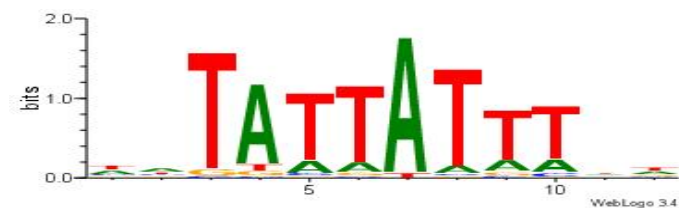
Dataset #: 4
 Motif ID: 41
 Motif name: wwAAATAATAtw
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 11
 Similarity score: 0.0309343

Alignment:
 DDTATTATTTDH
 -HVTACWGTABD

Original motif Consensus sequence: HDAAATAATADD



Reverse complement motif Consensus sequence: DDTATTATTTDH



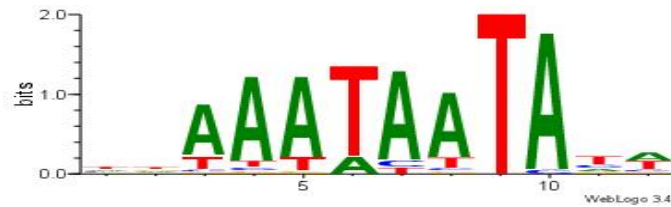
Dataset #: 4
 Motif ID: 37
 Motif name: tkAAATAATAtw
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 11

Similarity score: 0.0337121

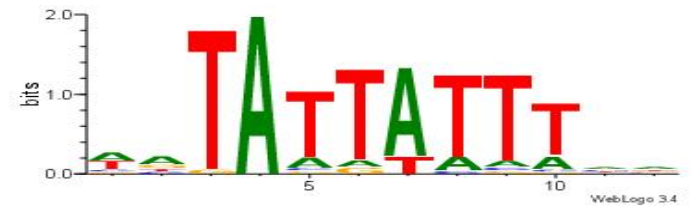
Alignment:

HDAAATAATAHW
DBTACWGTAVH-

Original motif Consensus sequence: HDAAATAATAHW



Reverse complement motif Consensus sequence: WHTATTATTTDH



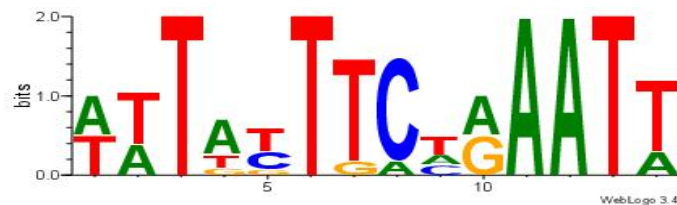
Dataset #: 2
Motif ID: 6
Motif name: Motif 6
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 4
Number of overlap: 11
Similarity score: 0.0353535

Alignment:

AATTYDGAARTAWW
HVTACWGTABD---

Original motif Consensus sequence: AATTYDGAARTAWW

Reverse complement motif Consensus sequence: WWTAKTTCDKAAAT



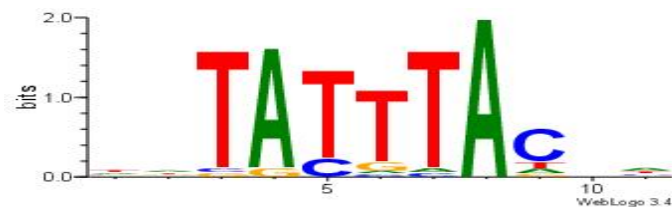
Dataset #: 4
 Motif ID: 45
 Motif name: wbgTAAATAww
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.037518

Alignment:
 DBGTAATAHD
 DBTACWGTAVH

Original motif Consensus sequence: DBGTAATAHD

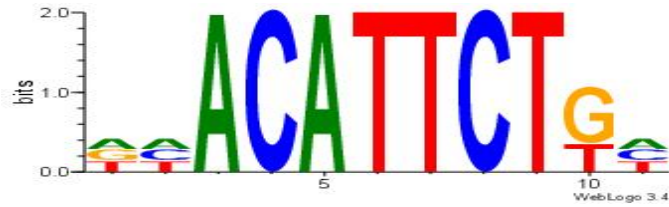


Reverse complement motif Consensus sequence: DHTATTTACBD



Dataset #: 4 Motif ID: 44 Motif name: dhACATTCTkh

Original motif Consensus sequence: DHACATTCTGH



Reverse complement motif Consensus sequence: HCAGAATGTHD



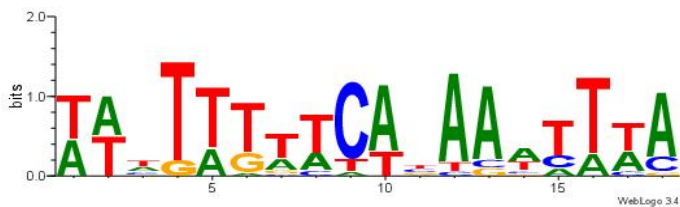
Best Matches for Motif ID 44 (Highest to Lowest)

Dataset #:	5
Motif ID:	53
Motif name:	TFM3
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	8
Number of overlap:	11
Similarity score:	0.0217516

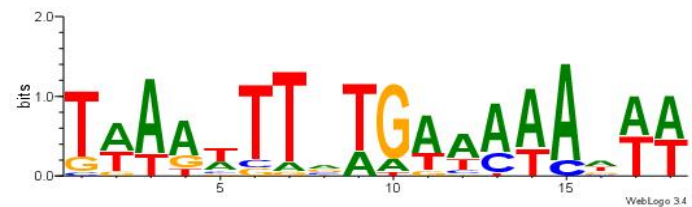
Alignment:

```
TWAAWTTVTGAAAAHWW
DHACATTCTGH-----
```

Original motif Consensus sequence: WWHTTTTTCABAATTWA



Reverse complement motif Consensus sequence: TAAWTTVTGAAAAHWW

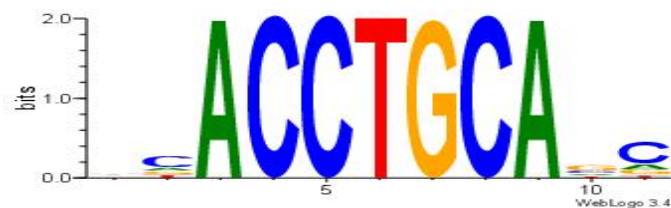


Dataset #: 4
 Motif ID: 40
 Motif name: kcACCTGCAGc
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.0238442

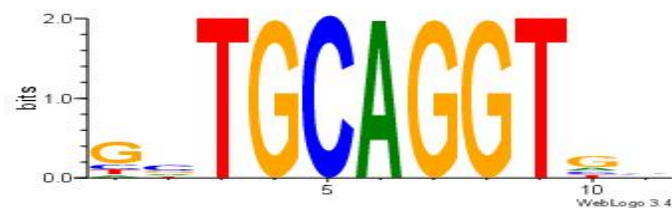
Alignment:

BCACCTGCABC
 DHACATTCTGH

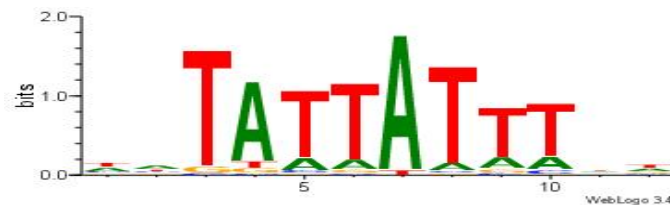
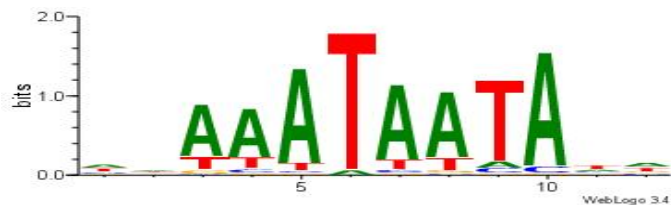
Original motif Consensus sequence: BCACCTGCABC



Reverse complement motif Consensus sequence: GBTGCAGGTGB



Dataset #: 2
 Motif ID: 16
 Motif name: Motif 16
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 11



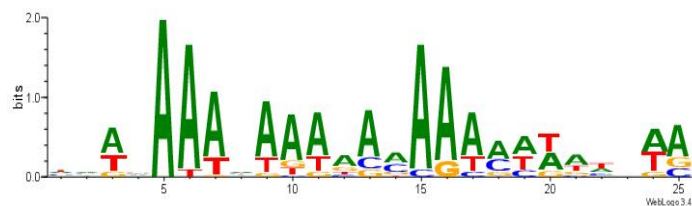
Dataset #: 5
 Motif ID: 56
 Motif name: TFM11
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 11
 Number of overlap: 11
 Similarity score: 0.0307858

Alignment:

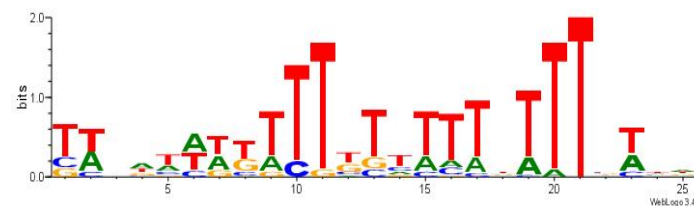
```

TWVHWWYTTTYYTTTTHTTTVWBH
----DHACATTCTGH-----
  
```

Original motif Consensus sequence:
 HDWVAAAHAAAAAMAAAMWWWHBWA

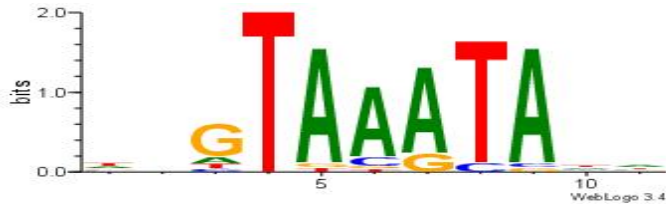


Reverse complement motif Consensus sequence:
 TWVHWWYTTTYYTTTTHTTTVWBH



Dataset #: 4 Motif ID: 45 Motif name: wbgTAAATAww

Original motif Consensus sequence: DBGTAATAHD



Reverse complement motif Consensus sequence: DHTATTTACBD



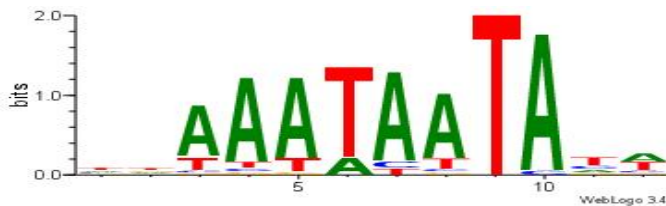
Best Matches for Motif ID 45 (Highest to Lowest)

Dataset #:	4
Motif ID:	37
Motif name:	tkAAATAATAtw
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	11
Similarity score:	0.0162338

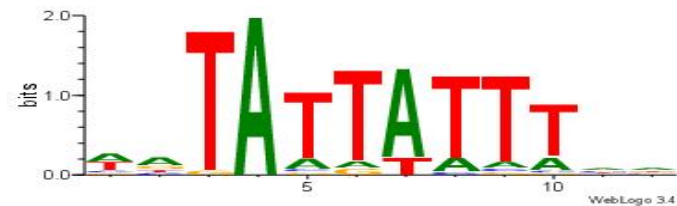
Alignment:

```
HDAAATAATAHW  
-DBGTAATAAHD
```

Original motif Consensus sequence: HDAAATAATAHW



Reverse complement motif Consensus sequence: WHTATTATTTDH

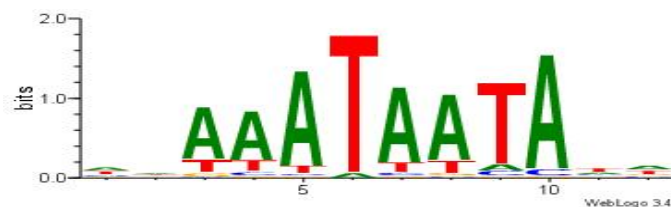


Dataset #: 4
 Motif ID: 41
 Motif name: wwAAATAATAtw
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 11
 Similarity score: 0.0164863

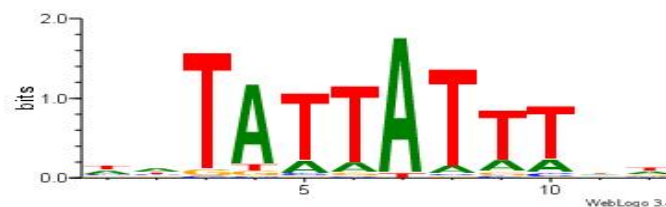
Alignment:

DDTATTATTTDH
 DHTATTTACBD-

Original motif Consensus sequence: HDAAATAATADD



Reverse complement motif Consensus sequence: DDTATTATTTDH



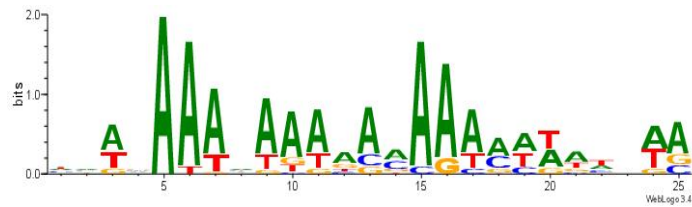
Dataset #: 5
 Motif ID: 56
 Motif name: TFM11
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 15
 Number of overlap: 11

Similarity score: 0.0192768

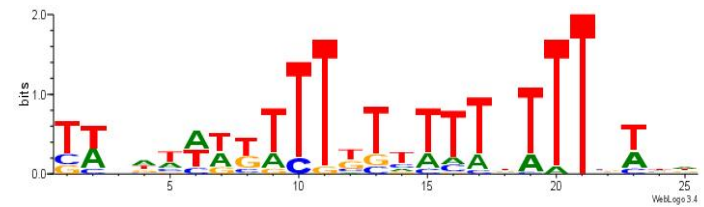
Alignment:

```
TWVHWWWYTTTYTTTTHTTTVWBH  
-----DHTATTTACBD
```

Original motif Consensus sequence:
HDWVAAAHAAAAAMAAAMWWWHBWA



Reverse complement motif Consensus sequence:
TWVHWWWYTTTYTTTTHTTTVWBH



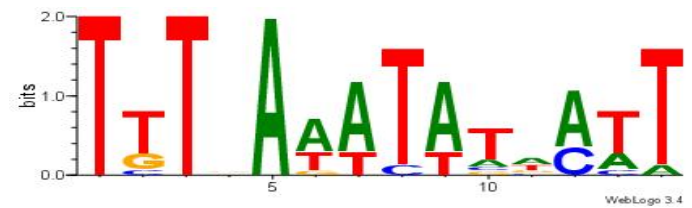
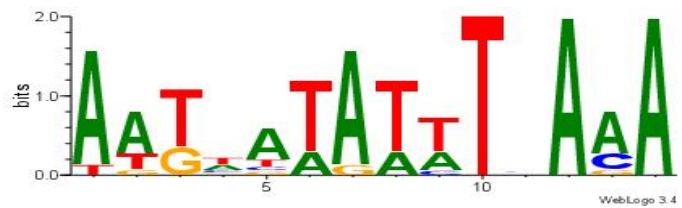
Dataset #: 2
Motif ID: 9
Motif name: Motif 9
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 4
Number of overlap: 11
Similarity score: 0.0250541

Alignment:

```
AATHATATWTHAAA  
DHTATTTACBD---
```

Original motif Consensus sequence: AATHATATWTHAAA

Reverse complement motif Consensus sequence: TTTDAWATATHAT



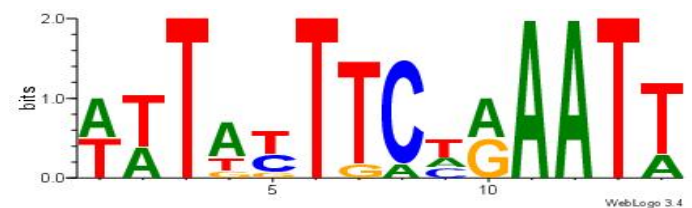
Dataset #: 2
 Motif ID: 6
 Motif name: Motif 6
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.027895

Alignment:
 AATTYDGAARTAWW
 ---DBGTAAATAHD

Original motif Consensus sequence: AATTYDGAARTAWW



Reverse complement motif Consensus sequence: WWTAKTTCDKAAAT



Dataset #: 5 Motif ID: 46 Motif name: TFW1

Original motif Consensus sequence: GTCGCG



Reverse complement motif Consensus sequence: CGCGAC



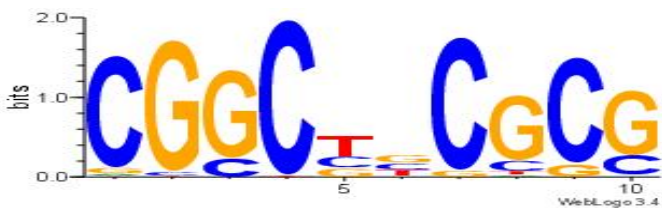
Best Matches for Motif ID 46 (Highest to Lowest)

Dataset #:	5
Motif ID:	48
Motif name:	TFW3
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:	0.0350356

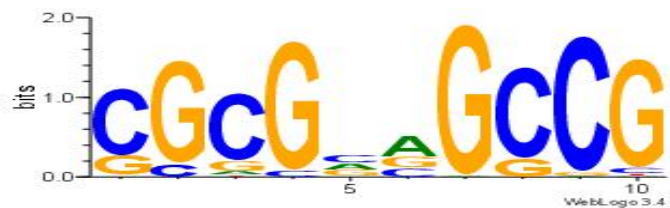
Alignment:

```
CGGCYBCGCG  
----GTCGCG
```

Original motif Consensus sequence: CGGCYBCGCG



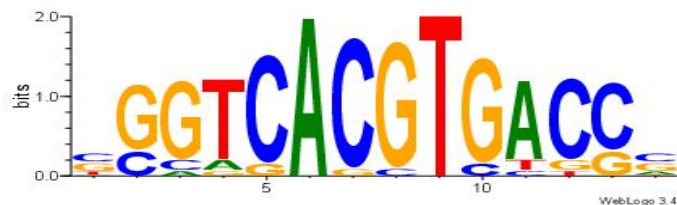
Reverse complement motif Consensus sequence: CGCGBMGCCG



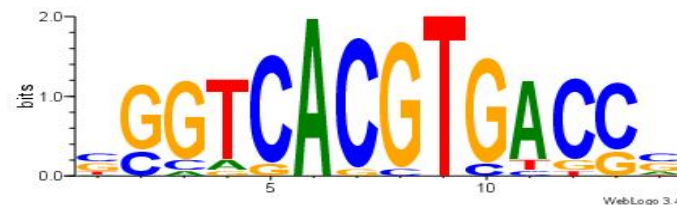
Dataset #: 4
 Motif ID: 42
 Motif name: sSGTCACGTGACSSs
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 6
 Similarity score: 0.0375102

Alignment:
 SGGTCACGTGACCS
 --GTCGCG-----

Original motif Consensus sequence: SGGTCACGTGACCS



Reverse complement motif Consensus sequence: SGGTCACGTGACCS



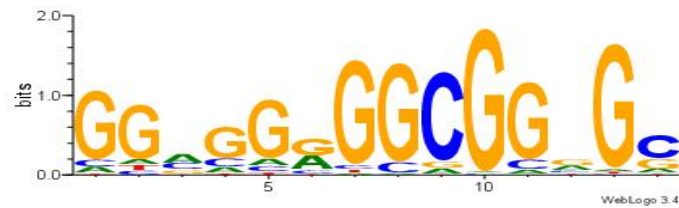
Dataset #: 5
 Motif ID: 50
 Motif name: TFF11
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 5
 Number of overlap: 6

Similarity score: 0.0381641

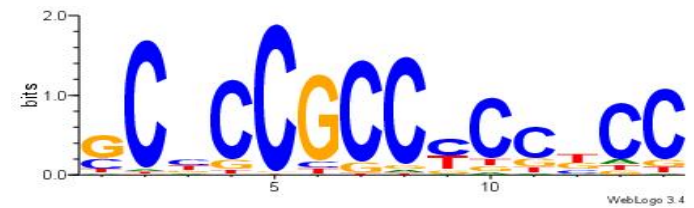
Alignment:

GCVCCGCCMCCYCC
-----CGCGAC-----

Original motif Consensus sequence: GGMGRRGGCGGVGC



Reverse complement motif Consensus sequence: GCVCCGCCMCCYCC



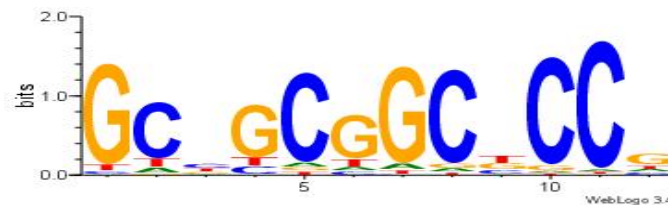
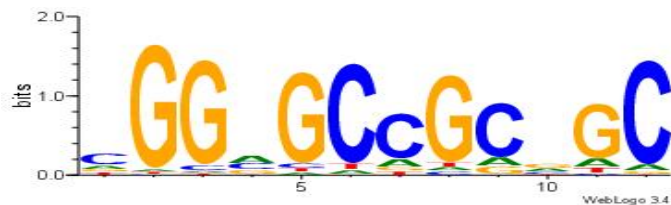
Dataset #: 5
Motif ID: 49
Motif name: TFF1
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 6
Similarity score: 0.0431161

Alignment:

CGGVGCCGCVGC
-----CGCGAC

Original motif Consensus sequence: CGGVGCCGCVGC

Reverse complement motif Consensus sequence: GCVCCGCCMCCYCC



Dataset #: 5
 Motif ID: 47
 Motif name: TFW2
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 6
 Similarity score: 0.052047

Alignment:
 CCGCGCGS
 -CGCGAC-

Original motif Consensus sequence: SCGCGCGG



Reverse complement motif Consensus sequence: CCGCGCGS



Dataset #: 5 Motif ID: 47 Motif name: TFW2

Original motif Consensus sequence: SCGCGCGG



Reverse complement motif Consensus sequence: CCGCGCGS



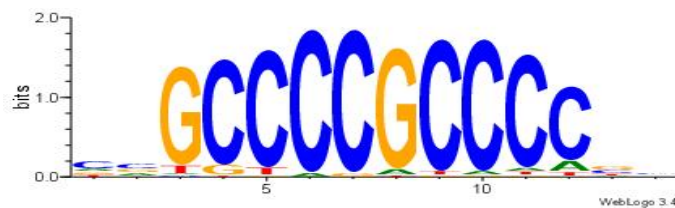
Best Matches for Motif ID 47 (Highest to Lowest)

Dataset #:	4
Motif ID:	36
Motif name:	csGCCCCGCCCCsc
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:	0.0456233

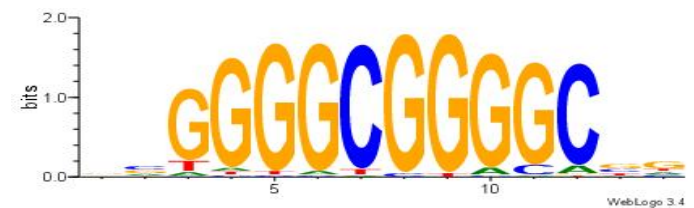
Alignment:

```
HVGCCCCGCCCCBB  
-CCGCGCGS-----
```

Original motif Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGC

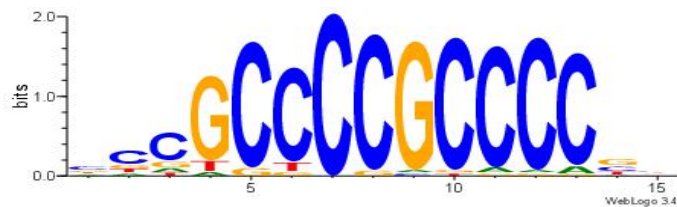


Dataset #: 4
 Motif ID: 38
 Motif name: cccGCCCCGCCCCsb
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 7
 Number of overlap: 8
 Similarity score: 0.045686

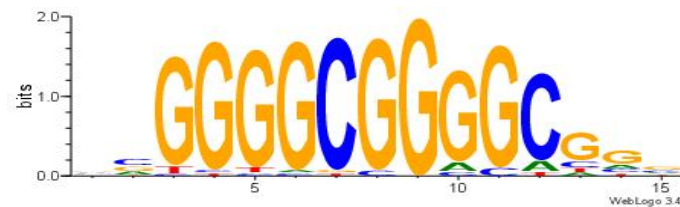
Alignment:

BBGGGGCGGGGCGGB
 -----SCGCGCGG-

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB



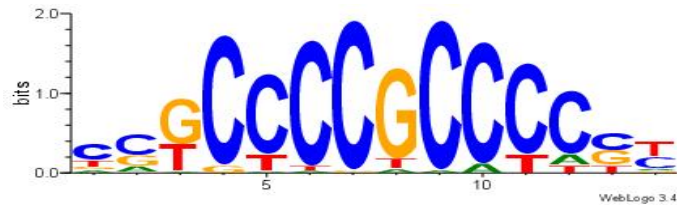
Dataset #: 2
 Motif ID: 7
 Motif name: Motif 7
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 6

Number of overlap: 8
Similarity score: 0.0504058

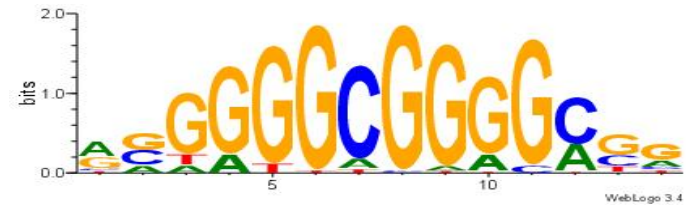
Alignment:

CSKCCCCGCCCCSY
-CCGCGCGS-----

Original motif Consensus sequence: CSKCCCCGCCCCSY



Reverse complement motif Consensus sequence: MSGGGGCGGGGY



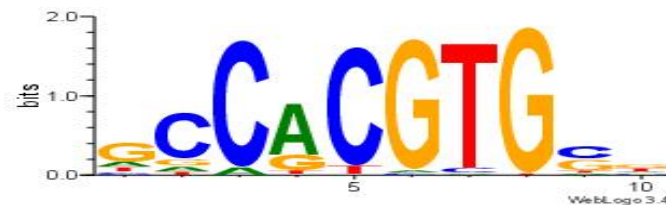
Dataset #: 3
Motif ID: 33
Motif name: Mycn
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 2
Number of overlap: 8
Similarity score: 0.0527532

Alignment:

HSCACGTGGC
-SCGCGCGG-

Original motif Consensus sequence: HSCACGTGGC

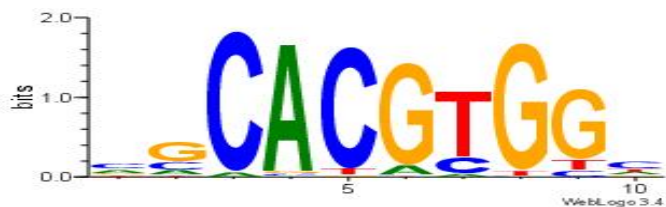
Reverse complement motif Consensus sequence: GCCACGTGSD



Dataset #: 3
 Motif ID: 34
 Motif name: Myc
 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: 0.0574543

Alignment:
 VGCACGTGGH
 -SCGCGCGG-

Original motif Consensus sequence: VGCACGTGGH

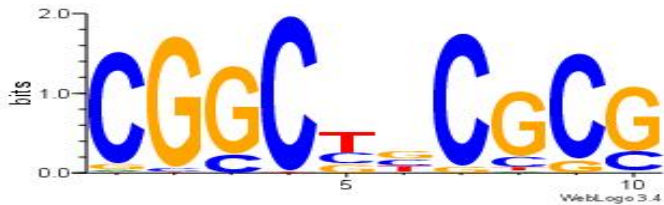


Reverse complement motif Consensus sequence: DCCACGTGCV

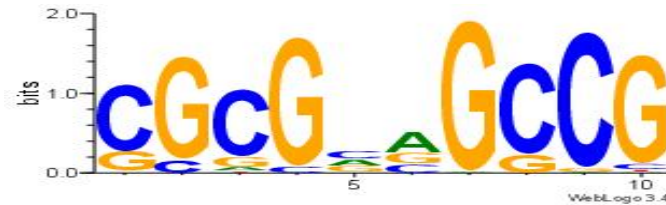


Dataset #: 5 Motif ID: 48 Motif name: TFW3

Original motif Consensus sequence: CGGCYBCGCG



Reverse complement motif Consensus sequence: CGCGBMGCCG

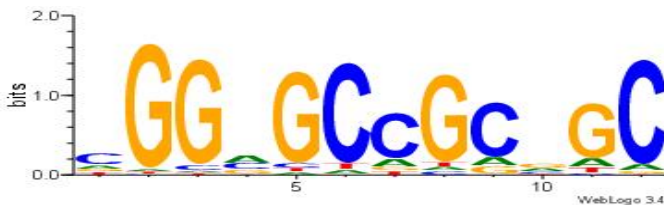


Best Matches for Motif ID 48 (Highest to Lowest)

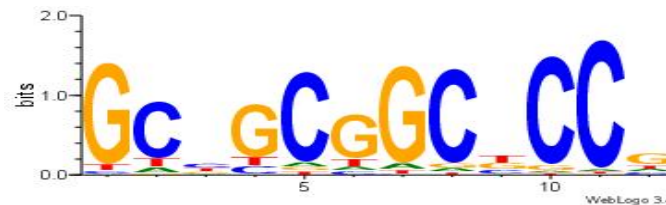
Dataset #:	5
Motif ID:	49
Motif name:	TFF1
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	3
Number of overlap:	10
Similarity score:	0.0623879

Alignment:
CGGVGCCGCVGC
CGGCYBCGCG--

Original motif Consensus sequence: CGGVGCCGCVGC



Reverse complement motif Consensus sequence: GCVGCGGCBCCG

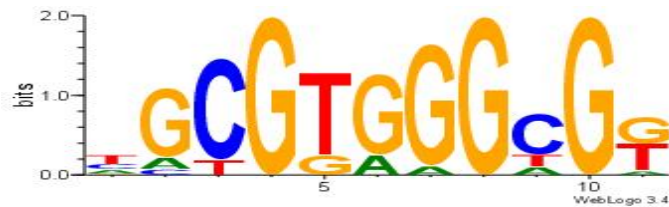


Dataset #: 3
 Motif ID: 23
 Motif name: Egr1
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 10
 Similarity score: 0.0630189

Alignment:

YGCCCCACGCH
 CGGCYBCGCG-

Original motif Consensus sequence: HGCGTGGGCGK



Reverse complement motif Consensus sequence: YGCCCCACGCH



Dataset #: 5
 Motif ID: 50
 Motif name: TFF11
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 10

Similarity score: 0.0645308

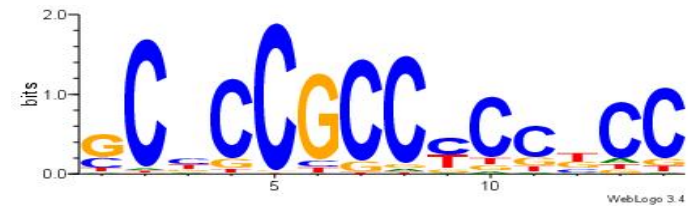
Alignment:

GGMGGRGGCGGVGC
CGCGBMGCCG-----

Original motif Consensus sequence: GGMGGRGGCGGVGC



Reverse complement motif Consensus sequence: GCVCCGCCMCCYC



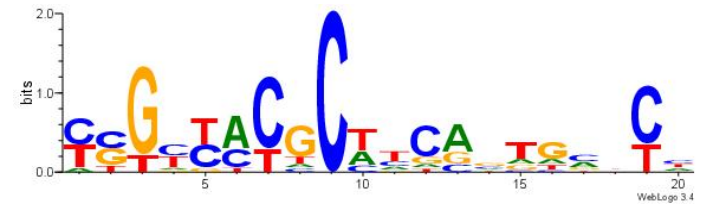
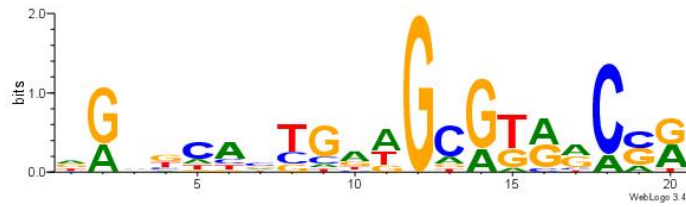
Dataset #: 3
Motif ID: 31
Motif name: Pax5
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 11
Number of overlap: 10
Similarity score: 0.0714355

Alignment:

MSGKKRCGCWDCABTGBCD
-----CGGCYBCGCG

Original motif Consensus sequence: DGVBCABTDWGCGKRRCSR

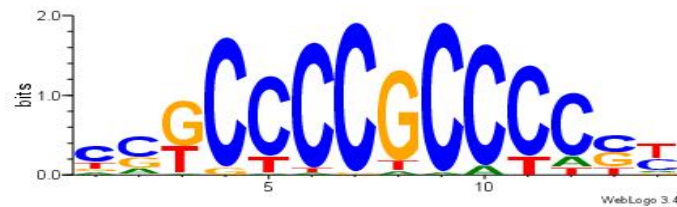
Reverse complement motif Consensus sequence:
MSGKKRCGCWDCABTGBCD



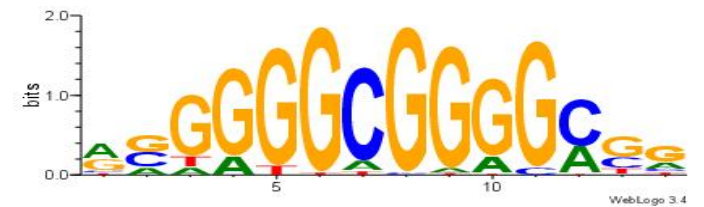
Dataset #: 2
 Motif ID: 7
 Motif name: Motif 7
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 10
 Similarity score: 0.0717594

Alignment:
 CSKCCCCGCCCSY
 CGGCYBCGCG----

Original motif Consensus sequence: CSKCCCCGCCCSY

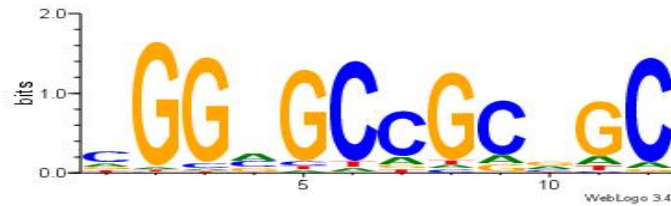


Reverse complement motif Consensus sequence: MSGGGCGGGY

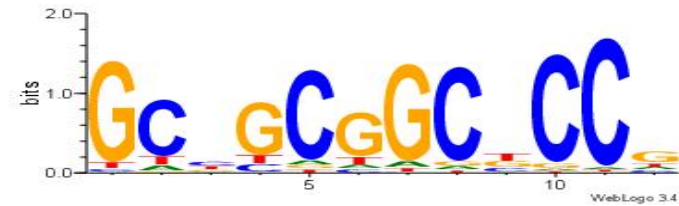


Dataset #: 5 Motif ID: 49 Motif name: TFF1

Original motif Consensus sequence: CGGVGCCGCVGC



Reverse complement motif Consensus sequence: GCVGCCGCBCCG



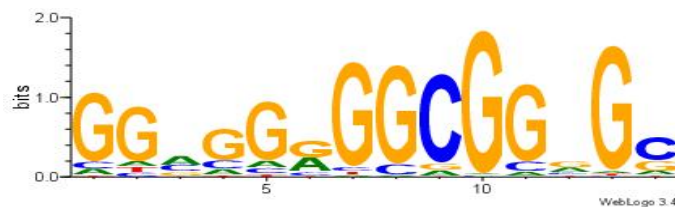
Best Matches for Motif ID 49 (Highest to Lowest)

Dataset #:	5
Motif ID:	50
Motif name:	TFF11
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	12
Similarity score:	0.0292081

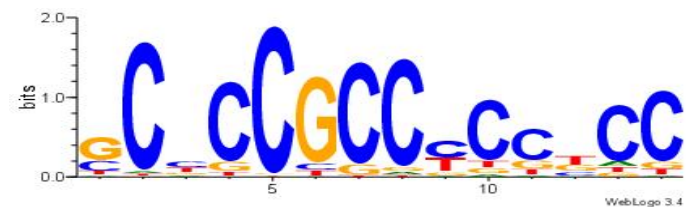
Alignment:

```
GGMGGRGGCGGVGC  
--CGGVGCCGCVGC
```

Original motif Consensus sequence: GGMGGRGGCGGVGC



Reverse complement motif Consensus sequence: GCVCCGCCMCCYC

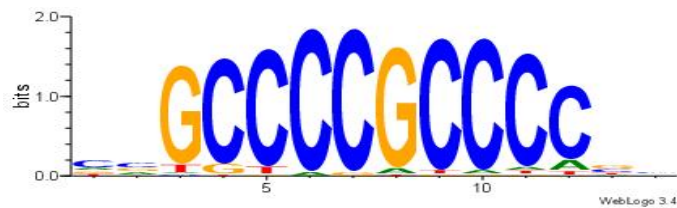


Dataset #: 4
 Motif ID: 36
 Motif name: csGCCCCGCCCCsc
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 12
 Similarity score: 0.0542674

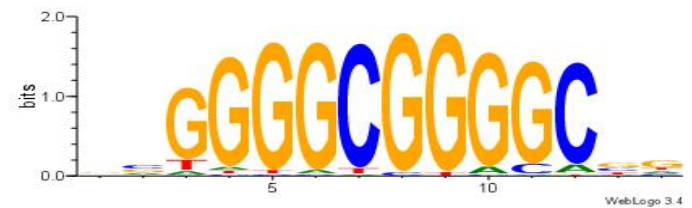
Alignment:

HVGCCCCGCCCCBB
 CGGVGCCGCVGC--

Original motif Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGC



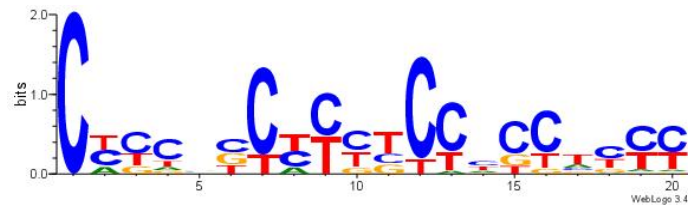
Dataset #: 5
 Motif ID: 54
 Motif name: TFM12
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 12

Similarity score: 0.0543272

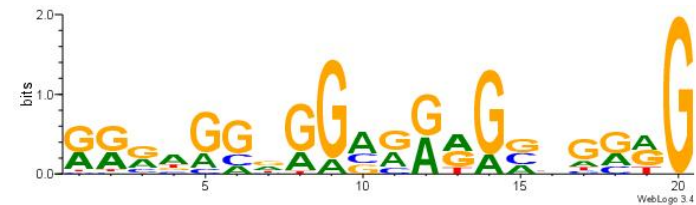
Alignment:

KKKAGGDGGAKKMGBBGKMG
-----CGGVGCCGCVGC--

Original motif Consensus sequence: CYCBBYYYTCCHCCTYYY



Reverse complement motif Consensus sequence:
KKKAGGDGGAKKMGBBGKMG



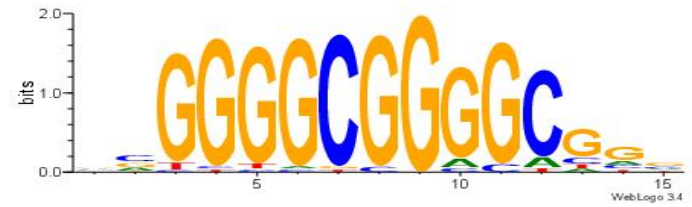
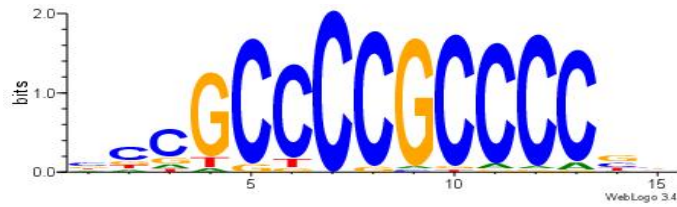
Dataset #: 4
Motif ID: 38
Motif name: cccGCCCCGCCCCsb
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 4
Number of overlap: 12
Similarity score: 0.0548371

Alignment:

BBGGGGCGGGGCGGB
---CGGVGCCGCVGC

Original motif Consensus sequence: BCCGCCCCGCCCCBB

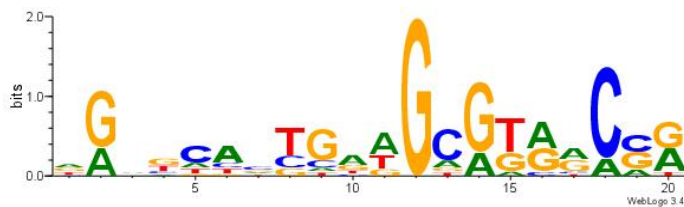
Reverse complement motif Consensus sequence:
BBGGGGCGGGGCGGB



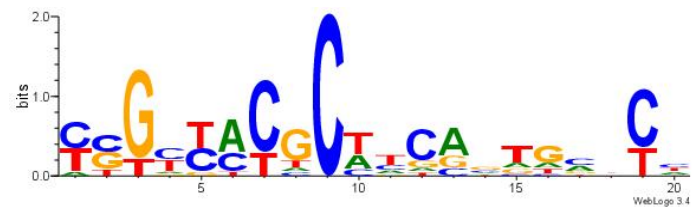
Dataset #: 3
 Motif ID: 31
 Motif name: Pax5
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 12
 Similarity score: 0.0556962

Alignment:
 DGVCABTGDWCGKRRCSR
 GCVGCGGCBCCG-----

Original motif Consensus sequence: DGVCABTGDWCGKRRCSR

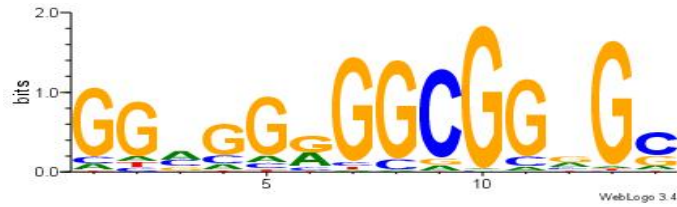


Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD

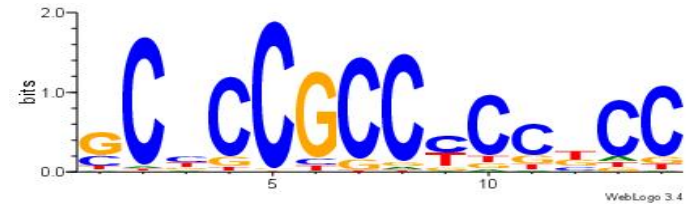


Dataset #: 5 Motif ID: 50 Motif name: TFF11

Original motif Consensus sequence: GGMGRRGGCGGVGC



Reverse complement motif Consensus sequence: GCVCCGCCMCCYCC



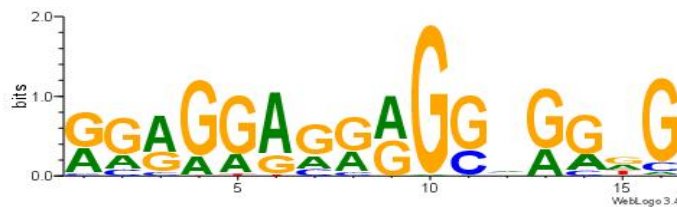
Best Matches for Motif ID 50 (Highest to Lowest)

Dataset #:	5
Motif ID:	51
Motif name:	TFM2
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	14
Similarity score:	0.033716

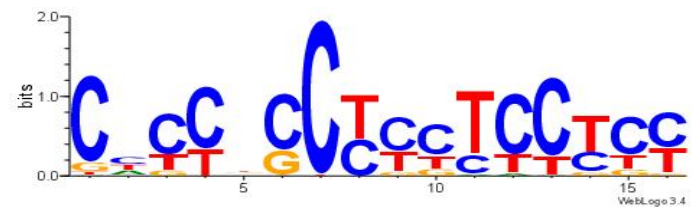
Alignment:

```
RGRGGAGRRGGHGGDG  
GGMGRRGGCGGVGC--
```

Original motif Consensus sequence: RGRGGAGRRGGHGGDG



Reverse complement motif Consensus sequence: CHCCBCCKMCTCCKCM

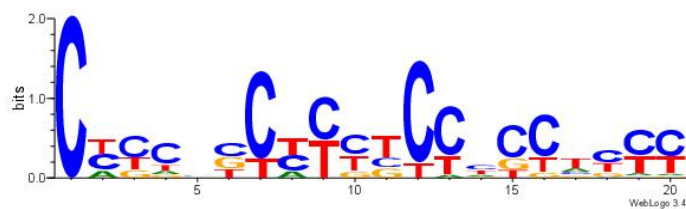


Dataset #: 5
 Motif ID: 54
 Motif name: TFM12
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 6
 Number of overlap: 14
 Similarity score: 0.0386905

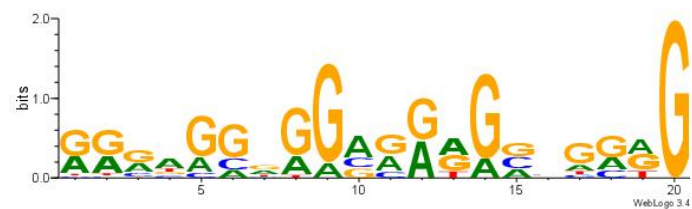
Alignment:

CYYCBBCYYYTCCHCCTYYY
 -----GCVCCGCCMCCYCC-

Original motif Consensus sequence: CYYCBBCYYYTCCHCCTYYY



Reverse complement motif Consensus sequence: KKKAGGDGGAKKMGBBGKMG



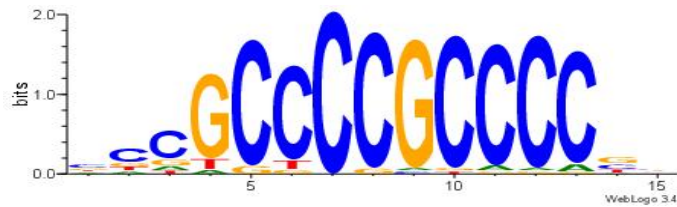
Dataset #: 4
 Motif ID: 38
 Motif name: cccGCCCCGCCCCsb
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2

Number of overlap: 14
Similarity score: 0.0548198

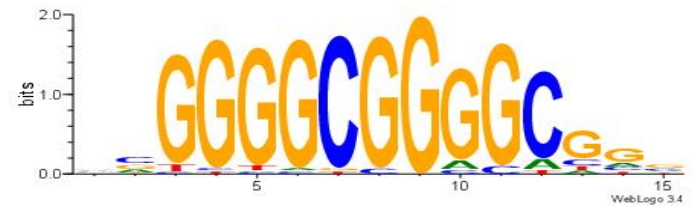
Alignment:

BBGGGGCGGGGCGGB
GGMGRRGGCGGVGC-

Original motif Consensus sequence: BCCGCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB

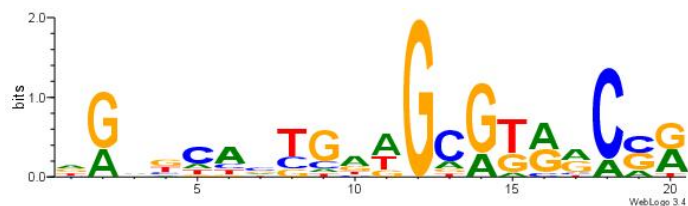


Dataset #: 3
Motif ID: 31
Motif name: Pax5
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 3
Number of overlap: 14
Similarity score: 0.0573129

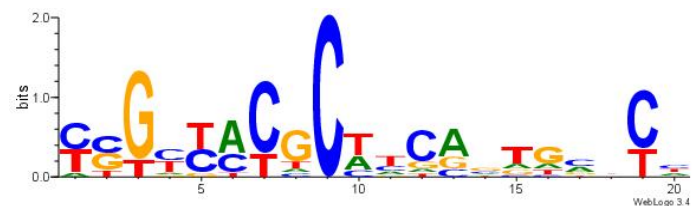
Alignment:

DGVBCABTGDWCGKRRCSR
----GGMGRRGGCGGVGC--

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBCD

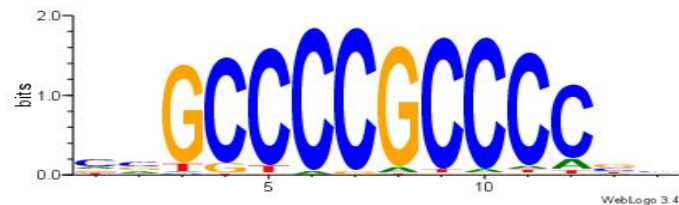


Dataset #: 4
Motif ID: 36
Motif name: csGCCCCGCCCCsc
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 14
Similarity score: 0.0652173

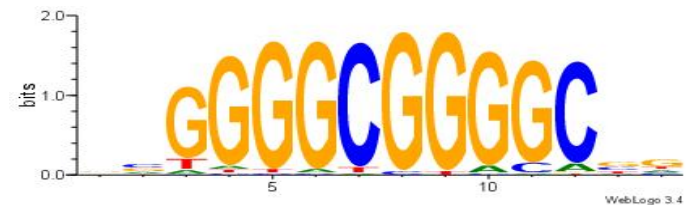
Alignment:

BBGGGGCGGGGCVD
GGMGGRGGCGGVGC

Original motif Consensus sequence: HVGCCCCGCCCCBB

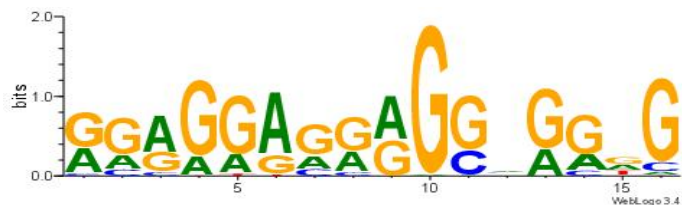


Reverse complement motif Consensus sequence: BBGGGGCGGGGC

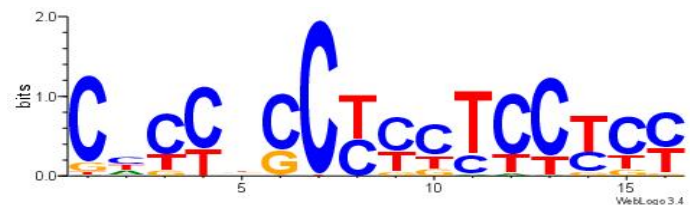


Dataset #: 5 Motif ID: 51 Motif name: TFM2

Original motif Consensus sequence: RGRGGAGRRGGHGGDG



Reverse complement motif Consensus sequence: CHCCBCKMCTCCKCM



Best Matches for Motif ID 51 (Highest to Lowest)

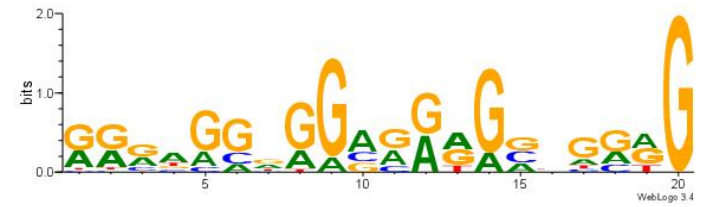
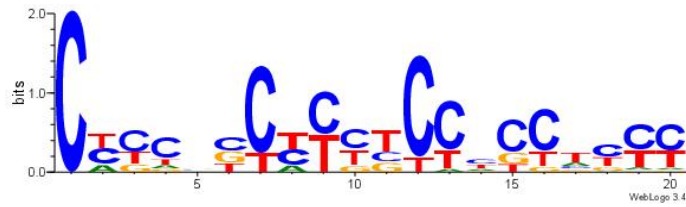
Dataset #:	5
Motif ID:	54
Motif name:	TFM12
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	16
Similarity score:	0.0331473

Alignment:

```
CYYCBBCYYYTCCHCCTYYY  
CHCCBCKMCTCCKCM-----
```

Original motif Consensus sequence: CYYCBBCYYYTCCHCCTYYY

Reverse complement motif Consensus sequence: KKKAGGDGGAKKMGBBGKMG

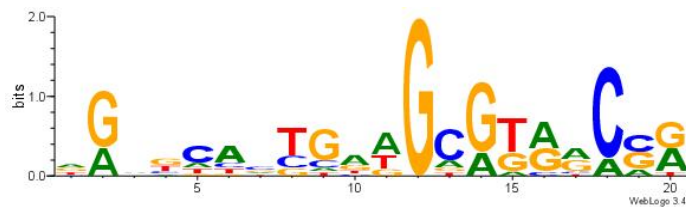


Dataset #: 3
 Motif ID: 31
 Motif name: Pax5
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 16
 Similarity score: 0.0668155

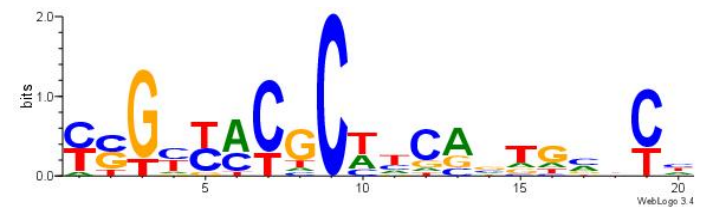
Alignment:

DGVCABTGDWGCGRRCR
 -RGRGGAGRRGGHGGD-

Original motif Consensus sequence: DGVCABTGDWGCGRRCR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBCD



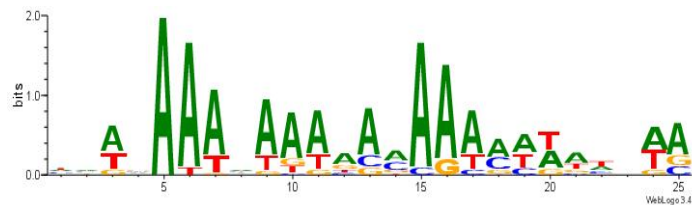
Dataset #: 5

Motif ID: 56
 Motif name: TFM11
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 8
 Number of overlap: 16
 Similarity score: 0.0794752

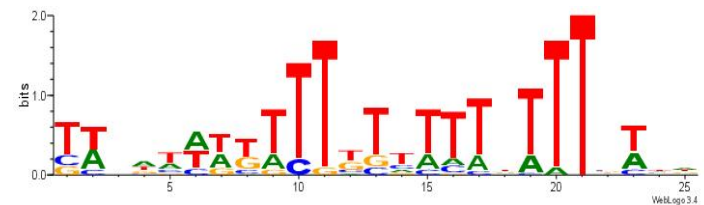
Alignment:

HDWVAAAHAAAAAAMAAAMWWWHBWA
 -----RGRGGAGRRGGHGGDG--

Original motif Consensus sequence:
 HDWVAAAHAAAAAAMAAAMWWWHBWA



Reverse complement motif Consensus sequence:
 TWVHWWWYTTTTTTTTTHTTTVWBH



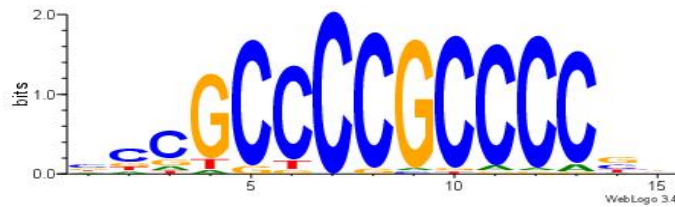
Dataset #: 4
 Motif ID: 38
 Motif name: cccGCCCCGCCCCsb
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 15

Similarity score: 0.558405

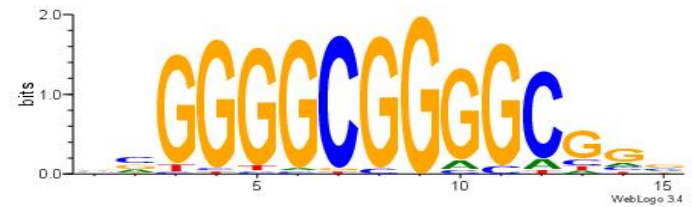
Alignment:

BCCGCCCCGCCCCBB-
CHCCBCKMCTCCKCM

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB



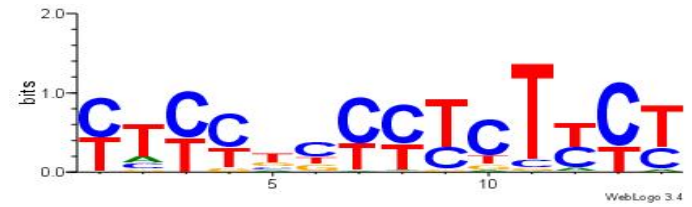
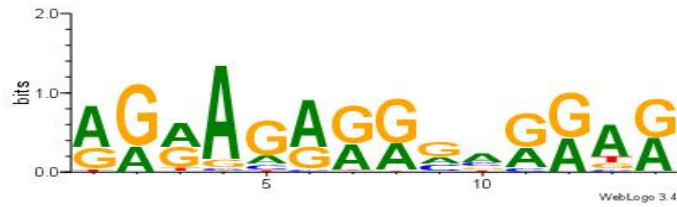
Dataset #: 2
Motif ID: 2
Motif name: Motif 2
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 14
Similarity score: 1.01195

Alignment:

--RGRAGARRGARRAR
RGRGGAGRRGGHGGDG

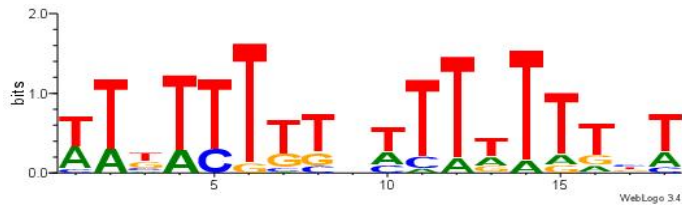
Original motif Consensus sequence: RGRAGARRGARRAR

Reverse complement motif Consensus sequence: MTMMTCMMTCTK

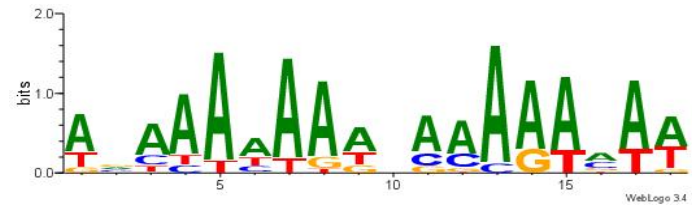


Dataset #: 5 Motif ID: 52 Motif name: TFM1

Original motif Consensus sequence: WTKTTTTTHWTTTTTTBT



Reverse complement motif Consensus sequence: ABAAAAA WHAAAAARAW



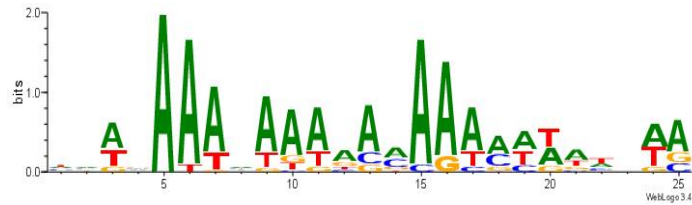
Best Matches for Motif ID 52 (Highest to Lowest)

Dataset #:	5
Motif ID:	56
Motif name:	TFM11
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	6
Number of overlap:	18
Similarity score:	0

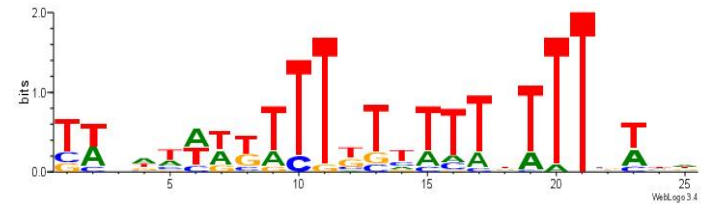
Alignment:

TWVHWWYTTTYTTTTHTTTVWBH
 -----WTKTTTTTHWTTTTTTBT--

Original motif Consensus sequence:
 HDWVAAAHAAAAAMAAAMWWWHBWA



Reverse complement motif Consensus sequence:
 TWVHWWYTTTYTTTTHTTTVWBH

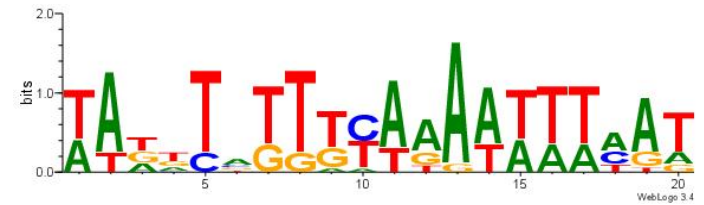
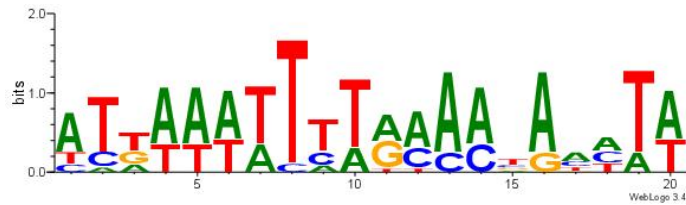


Dataset #: 5
 Motif ID: 55
 Motif name: TFM13
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 18
 Similarity score: 0.0364672

Alignment:
 ATKAAWTTTTRMAABAHTW
 ABAAAAAWhAAAAARAW--

Original motif Consensus sequence: ATKAAWTTTTRMAABAHTW

Reverse complement motif Consensus sequence:
 WAHHTVTTYKAAAATTRAT

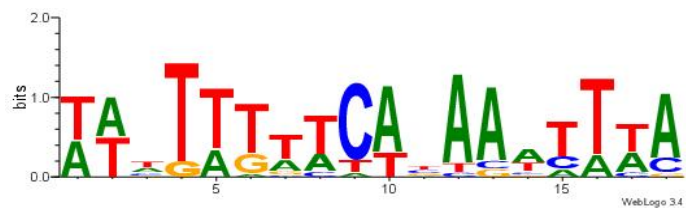


Dataset #: 5
 Motif ID: 53
 Motif name: TFM3
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 18
 Similarity score: 0.0456974

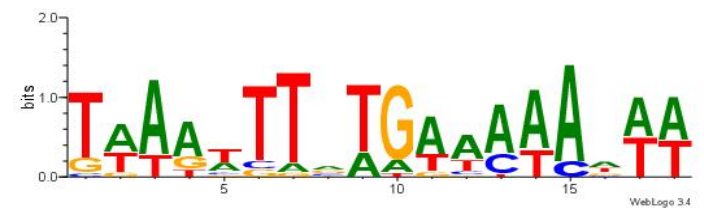
Alignment:

WWHTTTTTTCABAAWTTWA
 WKTTTTTTHWTTTTTTBT

Original motif Consensus sequence: WWHTTTTTTCABAAWTTWA



Reverse complement motif Consensus sequence: TAAWTTVTGAAAAHWW



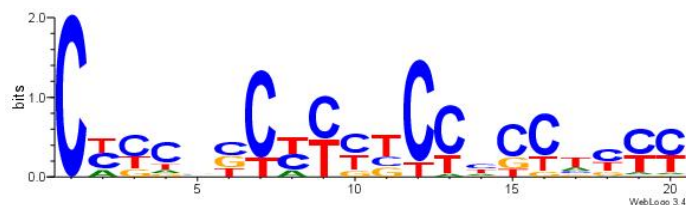
Dataset #: 5

Motif ID: 54
 Motif name: TFM12
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 17
 Similarity score: 0.572783

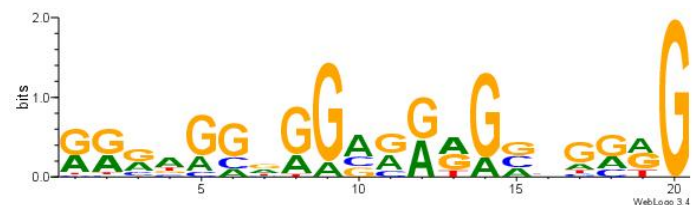
Alignment:

CYYCBBCYYYTCCHCCTYYY-
 ---WTKTTTTTTHWTTTTTBT

Original motif Consensus sequence: CYYCBBCYYYTCCHCCTYYY



Reverse complement motif Consensus sequence: KKKAGGDGGAKKMGBBGKMG



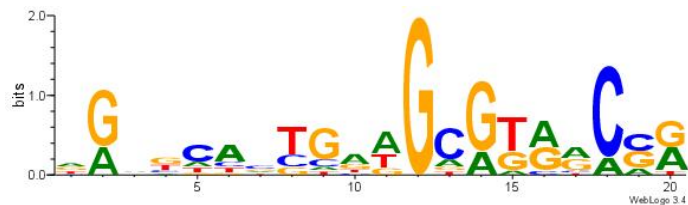
Dataset #: 3
 Motif ID: 31
 Motif name: Pax5
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 5
 Number of overlap: 16

Similarity score: 1.07322

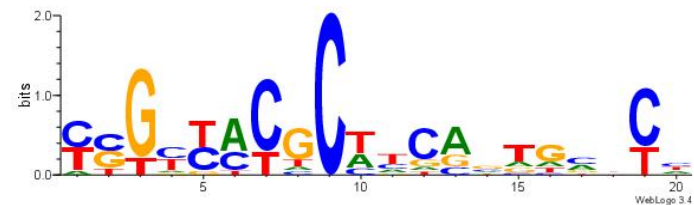
Alignment:

```
--MSGKKRCGCWDCABTGBBCD  
WKTTTTTTHWTTTTTTTBT----
```

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR

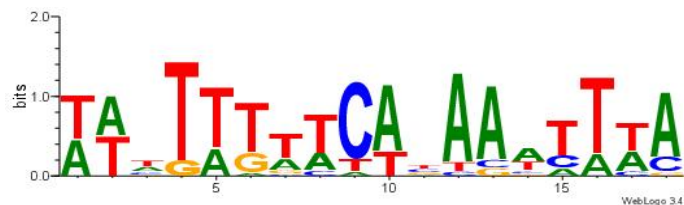


Reverse complement motif Consensus sequence:
MSGKKRCGCWDCABTGBBCD

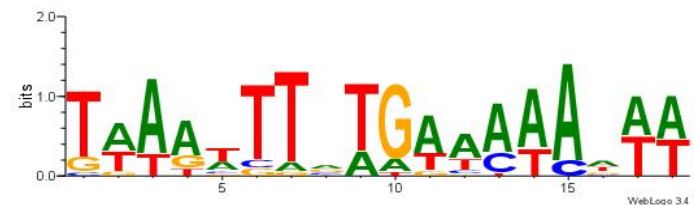


Dataset #: 5 Motif ID: 53 Motif name: TFM3

Original motif Consensus sequence: WWHTTTTTCABAATTWA



Reverse complement motif Consensus sequence:
TWAATTTVTGAAAAHWW



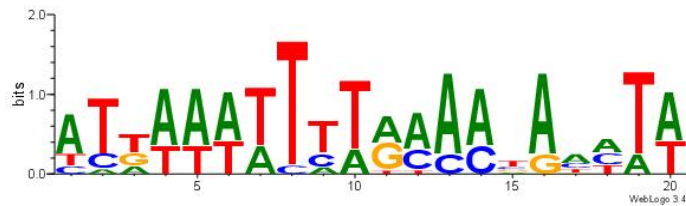
Best Matches for Motif ID 53 (Highest to Lowest)

Dataset #:	5
Motif ID:	55
Motif name:	TFM13
Matching format of first motif:	Reverse Complement

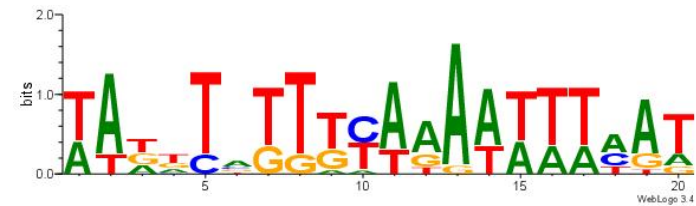
Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 18
 Similarity score: 0.013876

Alignment:
 ATKAAWTTTTRMAABAHTW
 -TWAAWTTVTGAAAAHWW-

Original motif Consensus sequence: ATKAAWTTTTRMAABAHTW



Reverse complement motif Consensus sequence:
 WAHHTVTTYKAAAATTRAT

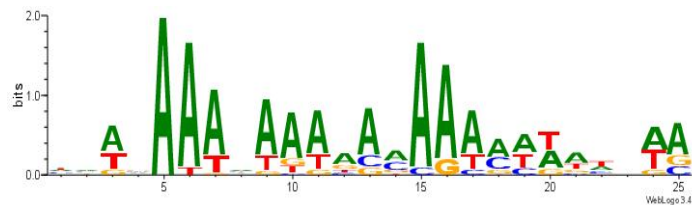


Dataset #: 5
 Motif ID: 56
 Motif name: TFM11
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 5
 Number of overlap: 18
 Similarity score: 0.0402327

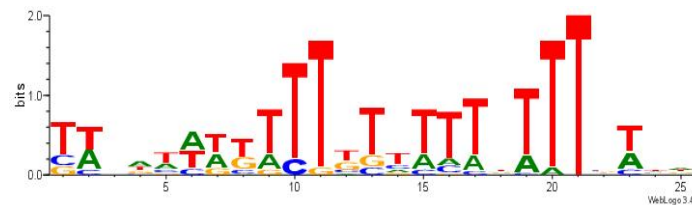
Alignment:

TWVHWWYTTTYTTTTHTTTVWBH
 ---WWHTTTTTCABAAWTTWA---

Original motif Consensus sequence:
 HDWVAAAHAAAAAMAAAMWWWHBWA



Reverse complement motif Consensus sequence:
 TWVHWWYTTTYTTTTHTTTVWBH

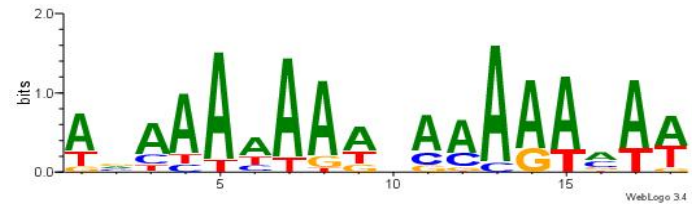
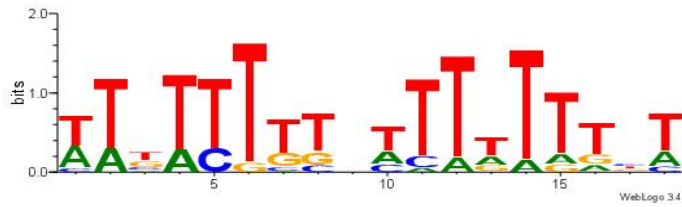


Dataset #: 5
 Motif ID: 52
 Motif name: TFM1
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 18
 Similarity score: 0.0432207

Alignment:
 WKTTTTTHWTTTTTBT
 WWHTTTTTCABAAWTTWA

Original motif Consensus sequence: WKTTTTTHWTTTTTBT

Reverse complement motif Consensus sequence:
 ABAAAAAWHAAAAARAW



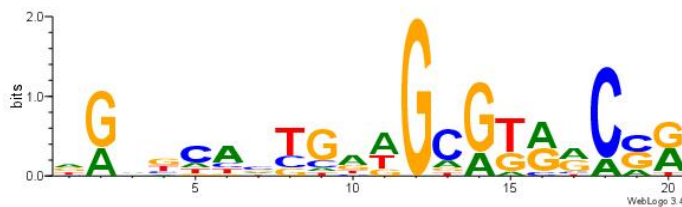
Dataset #: 3
 Motif ID: 31
 Motif name: Pax5
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 4
 Number of overlap: 17
 Similarity score: 0.561883

Alignment:

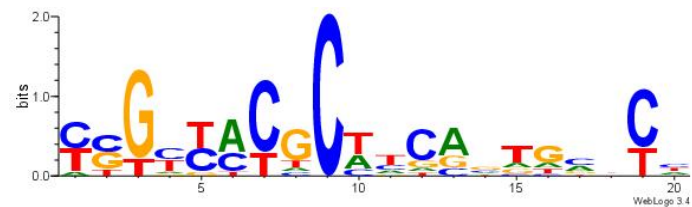
```

-MSGKKRCGCWDCABTGBBCD
WWHTTTTTTCABAAWTTWA---
  
```

Original motif Consensus sequence: DGVCABTGDWGCGRCSR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD



Dataset #: 2

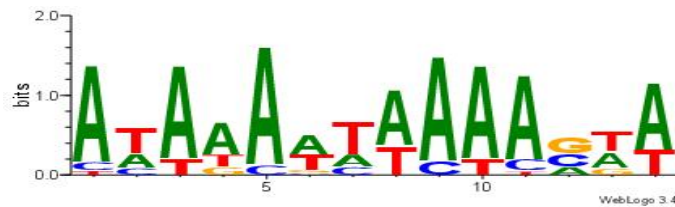
Motif ID: 3
 Motif name: Motif 3
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 14
 Similarity score: 2.04564

Alignment:

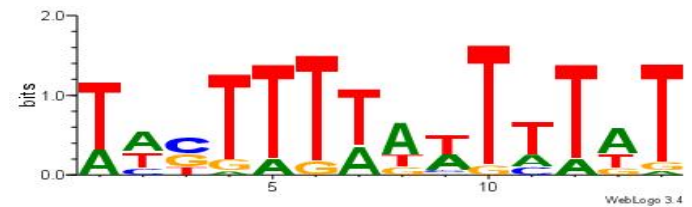
```

----TWSTTTWAWTTTWT
WWHTTTTTTCABAAWTTWA
  
```

Original motif Consensus sequence: AWAAAWTWAAASWA

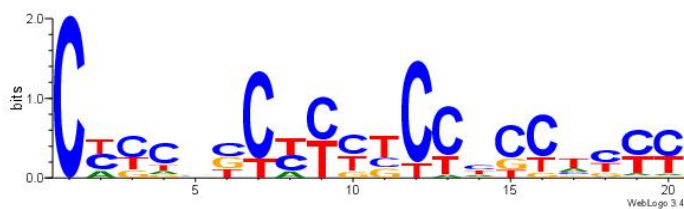


Reverse complement motif Consensus sequence: TWSTTTWAWTTTWT

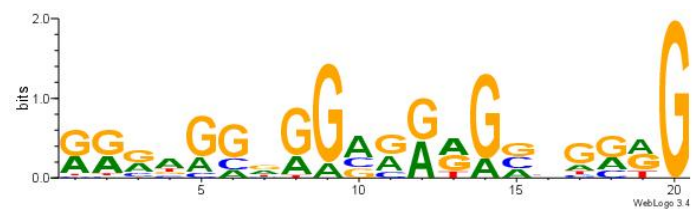


Dataset #: 5 Motif ID: 54 Motif name: TFM12

Original motif Consensus sequence: CYCBBCYYYTCCHCCTYYY



Reverse complement motif Consensus sequence: KKKAGGDGGAKKMGBBGKMG



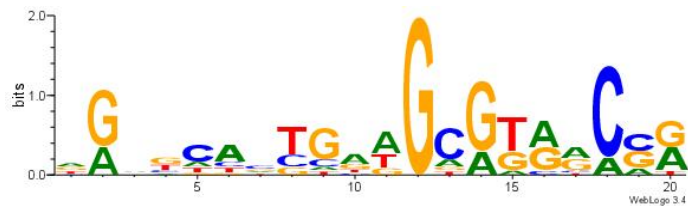
Best Matches for Motif ID 54 (Highest to Lowest)

Dataset #: 3
Motif ID: 31
Motif name: Pax5
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 20
Similarity score: 0.0458155

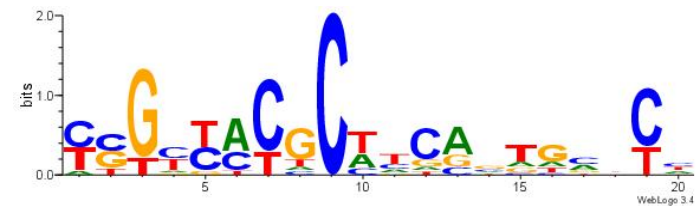
Alignment:

```
MSGKKRCGCWDCABTGBBBCD  
CYVCBBCYYYTCCHCCTYYY
```

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBBCD



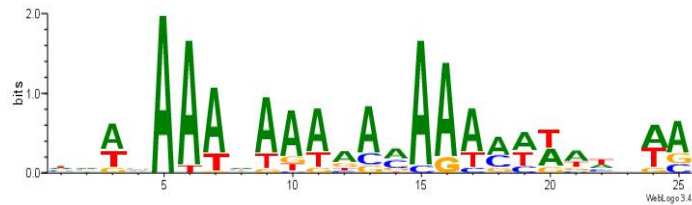
Dataset #: 5
Motif ID: 56
Motif name: TFM11
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement

Direction: Backward
 Position number: 6
 Number of overlap: 20
 Similarity score: 0.0573204

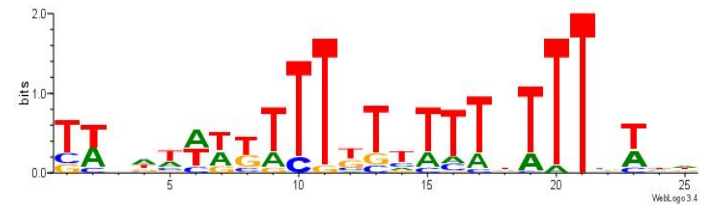
Alignment:

TWVHWWYTTTYTTTTHTTTVWBH
 CYVCBBCYYYTCCHCCTYYY-----

Original motif Consensus sequence:
 HDWVAAAHAAAAAMAAAMWWWHBWA



Reverse complement motif Consensus sequence:
 TWVHWWYTTTYTTTTHTTTVWBH

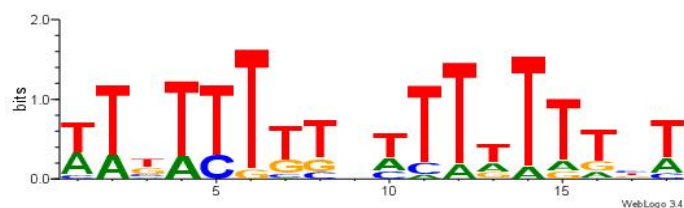


Dataset #: 5
 Motif ID: 52
 Motif name: TFM1
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 17
 Similarity score: 1.56255

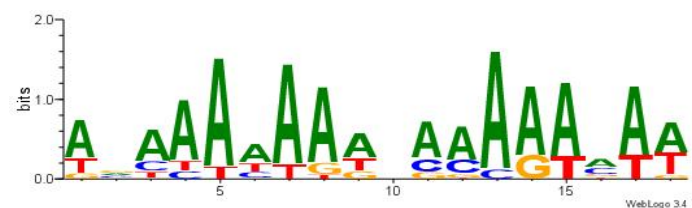
Alignment:

---WTKTTTTTHWTTTTTTBT
 CYVCBBCYYYTCCHCCTYYY-

Original motif Consensus sequence: WTKTTTTTHWTTTTTTBT



Reverse complement motif Consensus sequence: ABAAAAAWhAAAAARAW

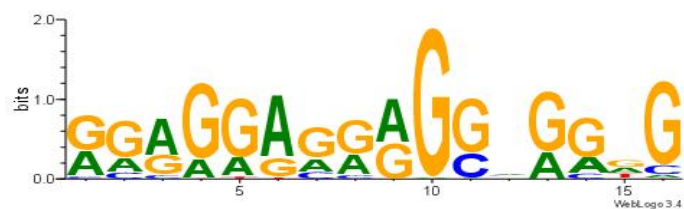


Dataset #: 5
Motif ID: 51
Motif name: TFM2
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 16
Similarity score: 2.01568

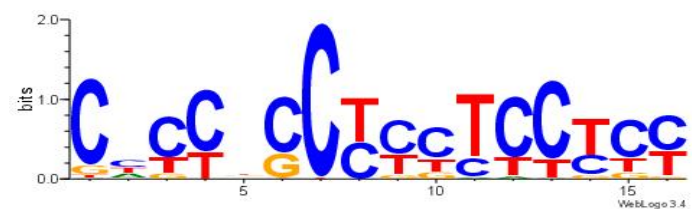
Alignment:

RGRGGAGRRGGHGGDG-----
KKKAGGDGGAKKMGBBGKMG

Original motif Consensus sequence: RGRGGAGRRGGHGGDG



Reverse complement motif Consensus sequence: CHCCBCKMCTCCKCM

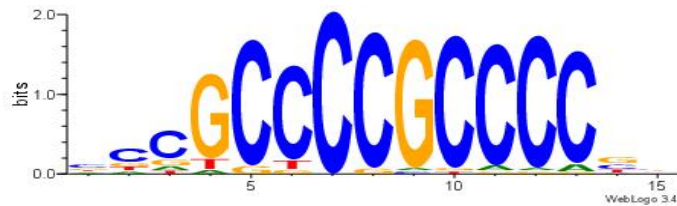


Dataset #: 4
 Motif ID: 38
 Motif name: cccGCCCCGCCCCsb
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 15
 Similarity score: 2.55221

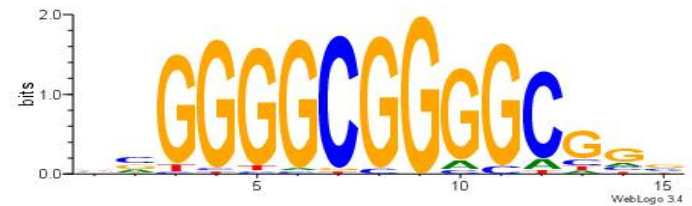
Alignment:

-----BCCGCCCCGCCCCBB
 CYYCBBCYYYTCCHCCTYYY

Original motif Consensus sequence: BCCGCCCCGCCCCBB



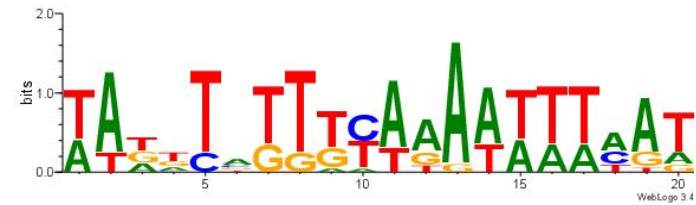
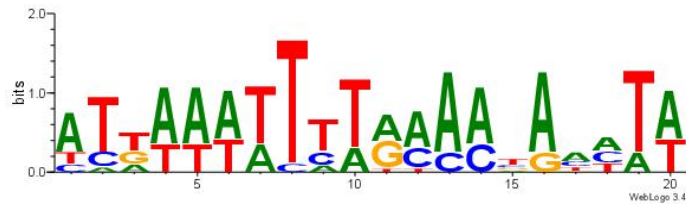
Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB



Dataset #: 5 Motif ID: 55 Motif name: TFM13

Original motif Consensus sequence: ATKAAWTTTTTRMAABAHTW

Reverse complement motif Consensus sequence: WAHHTVTTYKAAAATTRAT



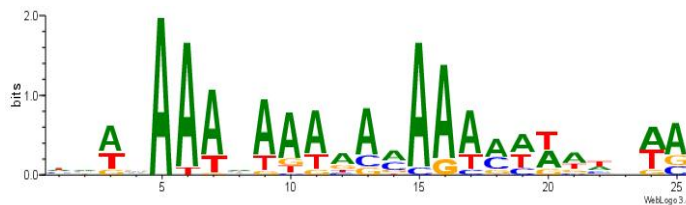
Best Matches for Motif ID 55 (Highest to Lowest)

Dataset #: 5
 Motif ID: 56
 Motif name: TFM11
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 5
 Number of overlap: 20
 Similarity score: 0.0352451

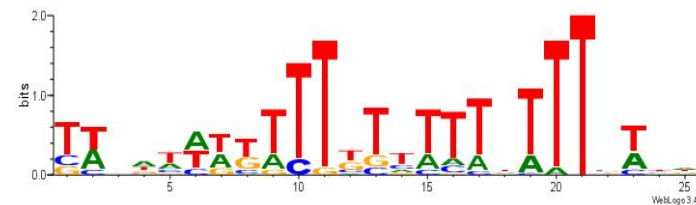
Alignment:

```
TWVHWWWYTTTTYTTTTHTTTVWBH
----WAHHTVTTYKAAAATTRAT-
```

Original motif Consensus sequence:
 HDWVAAAHAAAAAMAAAMWWWHBWA



Reverse complement motif Consensus sequence:
 TWVHWWWYTTTTYTTTTHTTTVWBH

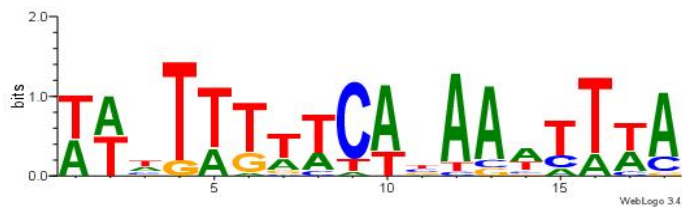


Dataset #: 5
 Motif ID: 53
 Motif name: TFM3
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 18
 Similarity score: 1.02254

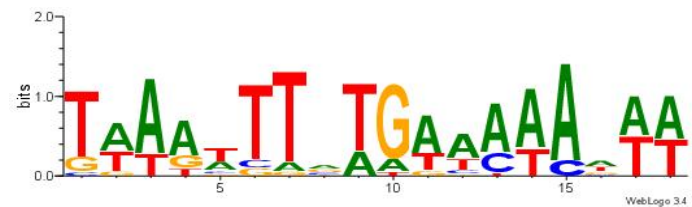
Alignment:

TWAAWTTVTGAAAAHWW--
 ATKAAWTTTTRMAABAHHTW

Original motif Consensus sequence: WWHTTTTTTCABAAWTTWA



Reverse complement motif Consensus sequence: TWAAWTTVTGAAAAHWW



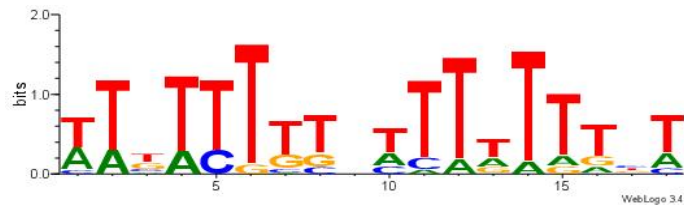
Dataset #: 5
 Motif ID: 52
 Motif name: TFM1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1

Number of overlap: 18
Similarity score: 1.02868

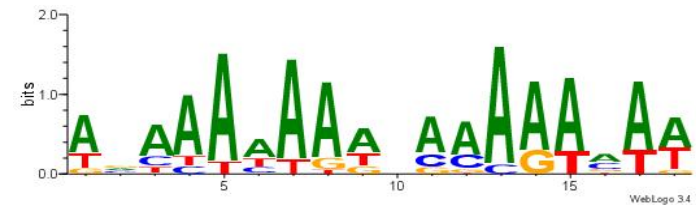
Alignment:

WKTTTTTTHWTTTTTTBT--
WAHHTVTTYKAAAATTRAT

Original motif Consensus sequence: WTKTTTTTHWTTTTTTBT



Reverse complement motif Consensus sequence:
ABAAAAAWHAAAAARAW

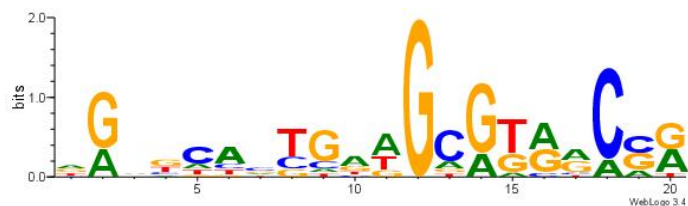


Dataset #: 3
Motif ID: 31
Motif name: Pax5
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 6
Number of overlap: 15
Similarity score: 2.56565

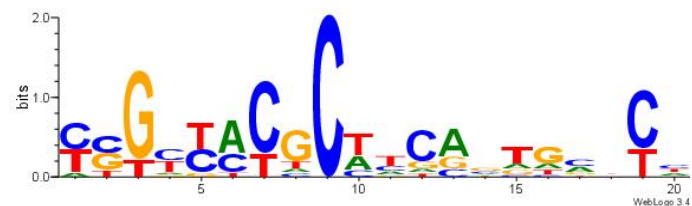
Alignment:

-----MSGKKRCGCWDCABTGBBCD
WAHHTVTTYKAAAATTRAT-----

Original motif Consensus sequence: DGVBCABTGDWGCGRCSR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBCD

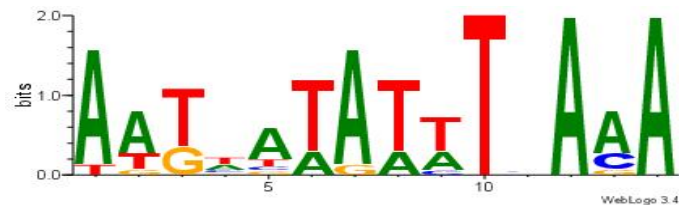


Dataset #: 2
 Motif ID: 9
 Motif name: Motif 9
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 14
 Similarity score: 3.02278

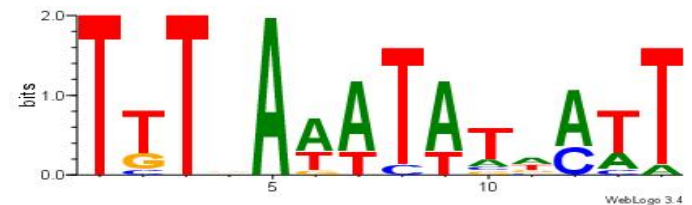
Alignment:

```
-----TTTDAWATATHATT
WAHHTVTTYKAAAATTRAT
```

Original motif Consensus sequence: AATHATWTHAAA

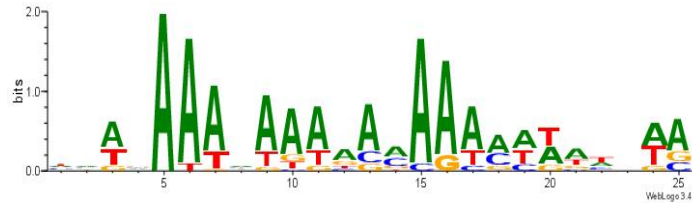


Reverse complement motif Consensus sequence: TTTDAWATATHATT

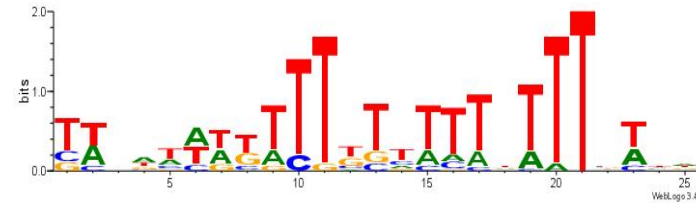


Dataset #: 5 **Motif ID: 56** **Motif name: TFM11**

Original motif Consensus sequence:
HDWVAAAHAAAAAMAAAMWWWHBWA



Reverse complement motif Consensus sequence:
TWVHWWWYTTTTYTTTTTHTTTVWBH



Best Matches for Motif ID 56 (Highest to Lowest)

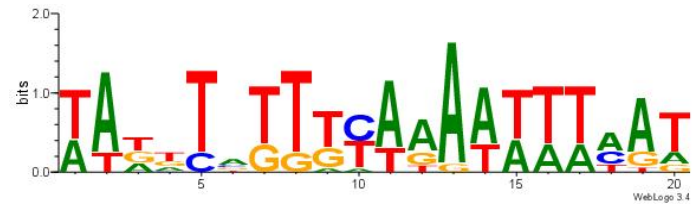
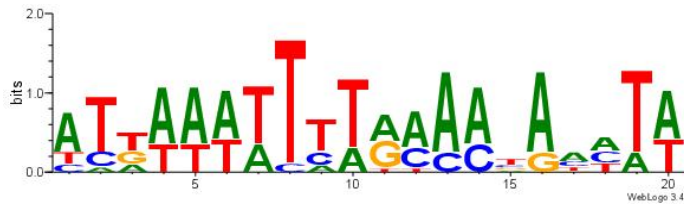
Dataset #:	5
Motif ID:	55
Motif name:	TFM13
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	20
Similarity score:	0.0486765

Alignment:

```
WAHHTVTTYKAAAATTRAT-----  
TWVHWWWYTTTTYTTTTTHTTTVWBH
```

Original motif Consensus sequence: ATKAAWTTTTRMAABAHTW

Reverse complement motif Consensus sequence:
WAHHTVTTYKAAAATTRAT

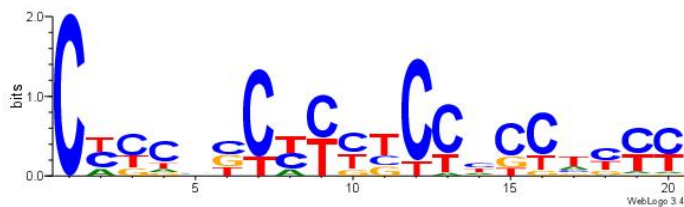


Dataset #: 5
 Motif ID: 54
 Motif name: TFM12
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.0693284

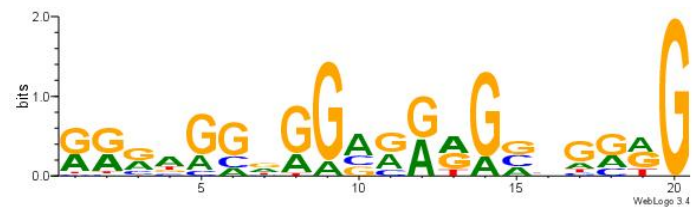
Alignment:

KKKAGGDGGAKKMGBBGKMG-----
 HDWVAAAHAAAAAMAAAMWWWHBWA

Original motif Consensus sequence: CYCBCYYYTCCHCCTYYY



Reverse complement motif Consensus sequence: KKKAGGDGGAKKMGBBGKMG



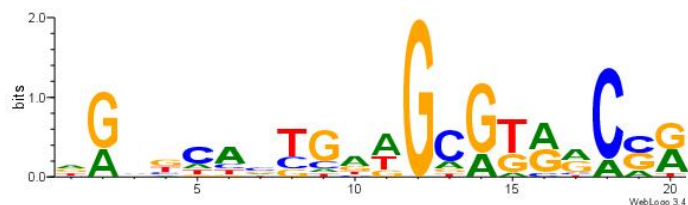
Dataset #: 3

Motif ID: 31
 Motif name: Pax5
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.0750613

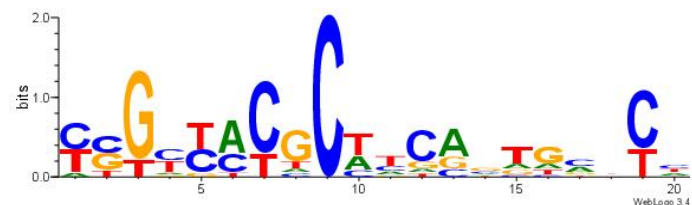
Alignment:

DGVBCABTGDWGCGRRCR-----
 HDWVAAAHA AAAAAMAAAMWWWHBWA

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGGBCD



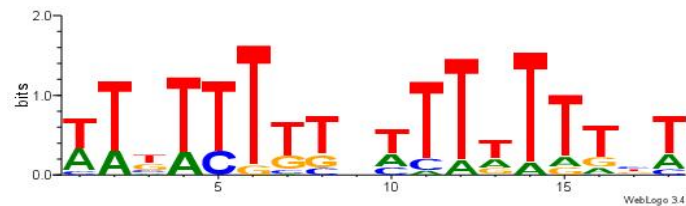
Dataset #: 5
 Motif ID: 52
 Motif name: TFM1
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 18

Similarity score: 1.0232

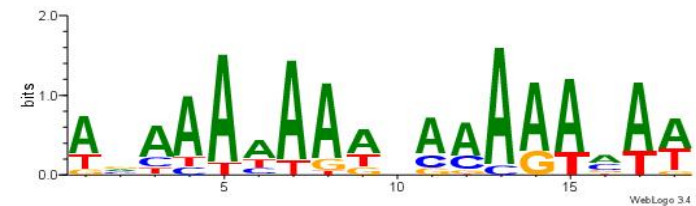
Alignment:

-----ABAAAAAWHAAAAARAW
HDWVAAAHAAAAAMAAAMWWWHBWA

Original motif Consensus sequence: WTKTTTTTHWTTTTTBT



Reverse complement motif Consensus sequence:
ABAAAAAWHAAAAARAW



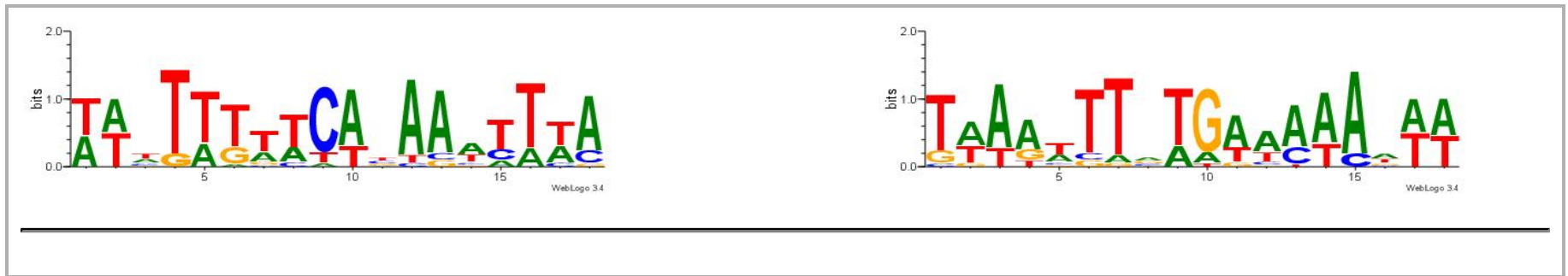
Dataset #: 5
Motif ID: 53
Motif name: TFM3
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 18
Similarity score: 1.05388

Alignment:

WWHTTTTTCABAAWTTWA-----
TWVHWWWYTTTYTTTTTHTTTVWBH

Original motif Consensus sequence: WWHTTTTTCABAAWTTWA

Reverse complement motif Consensus sequence:
TAAWTTVTGAAAAAHWW



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 Runtime: 360.893 seconds

MOTIFSIM is written by Ngoc Tam L. Tran
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