



# 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

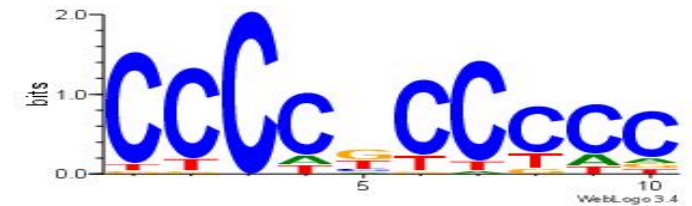
File name	Count of motifs	Dataset number
DREME_DM230.txt	1	1
MEME_DM230.txt	20	2
PScanChIP_DM230.txt	14	3
RSAT_peak-motifs_DM230.txt	10	4
W-ChIPMotifs_DM230.txt	11	5

## RESULTS

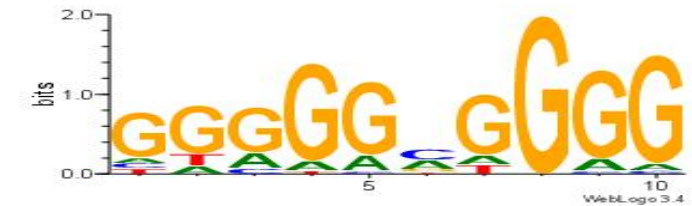
### Top 5 Significant Motifs - Global Matching (Highest to Lowest)

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)

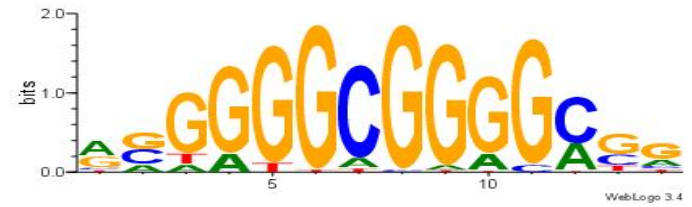
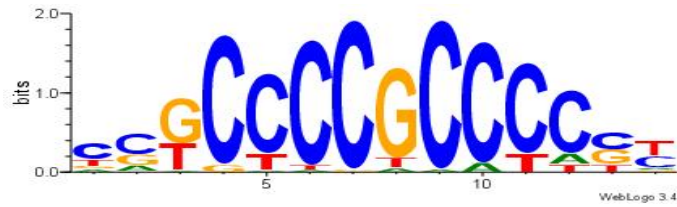
Dataset #:	2
Motif ID:	7
Motif name:	Motif 7
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	4
Number of overlap:	10
Similarity score:	0.00451594

Alignment:

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

Original motif      Consensus sequence: CSKCCCCGCCCSY

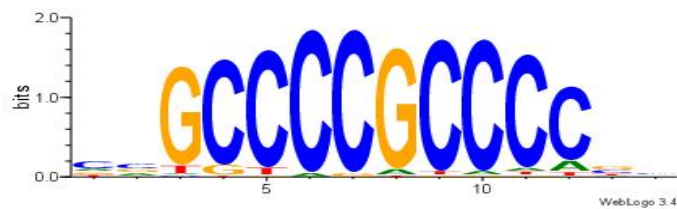
Reverse complement motif      Consensus sequence: MSGGGCGGGGY



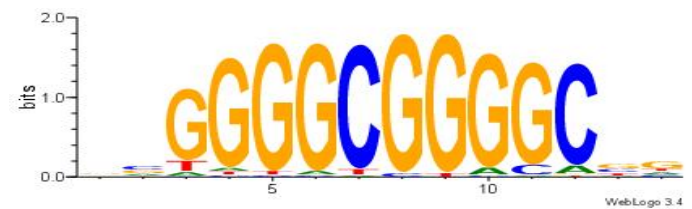
Dataset #: 4  
 Motif ID: 36  
 Motif name: csGCCCCGCCCCsc  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 4  
 Number of overlap: 10  
 Similarity score: 0.00965796

Alignment:  
 HVGCCCCGCCCCBB  
 ---CCCCKCCCC-

Original motif    Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif    Consensus sequence: BBGGGCGGGGC

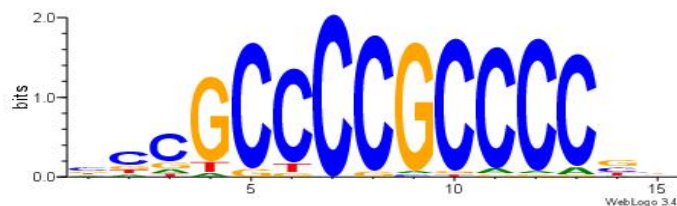


Dataset #: 4  
 Motif ID: 38

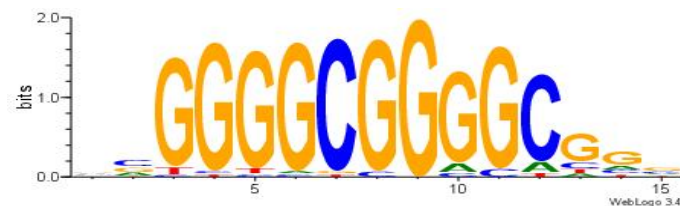
Motif name: cccGCCCCGCCCCsb  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 5  
 Number of overlap: 10  
 Similarity score: 0.0127292

Alignment:  
 BBGGGGCGGGGCGGB  
 -GGGGYGGGG-----

Original motif    Consensus sequence: BCCGCCCCGCCCCBB

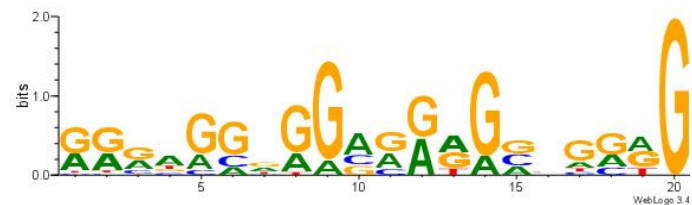
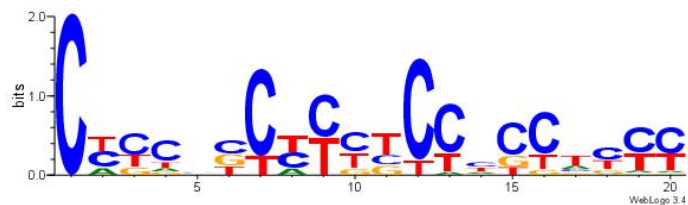


Reverse complement motif    Consensus sequence: BBGGGGCGGGGCGGB



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



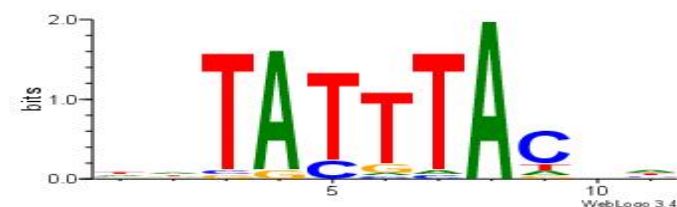


**Dataset #: 4      Motif ID: 45      Motif name: wbgTAAATAww**

Original motif      Consensus sequence: DBGTAATAHD



Reverse complement motif      Consensus sequence: DHTATTTACBD



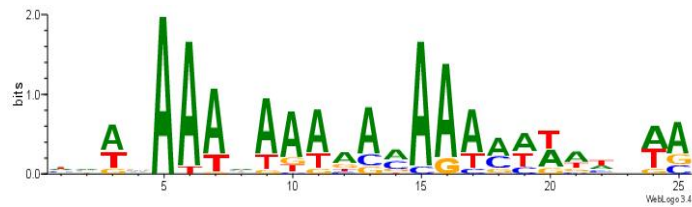
### Best Matches for Top Significant Motif ID 45 (Highest to Lowest)

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

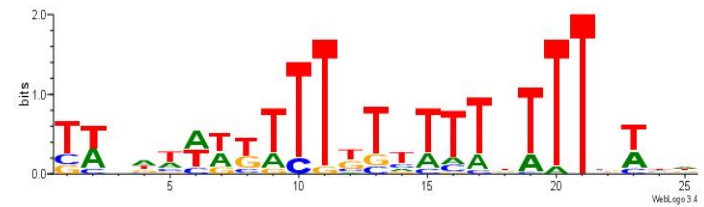
Alignment:

```
TWVHWWYTTTYTTTTHTTTVWBH
-----DHTATTTACBD
```

Original motif    Consensus sequence:  
 HDWVAAAHAAAAAMAAAMWWWHBWA



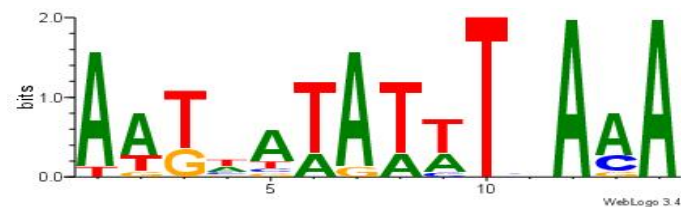
Reverse complement motif    Consensus sequence:  
 TWVHWWWYTTTTYTTTTHTTTTVWBH



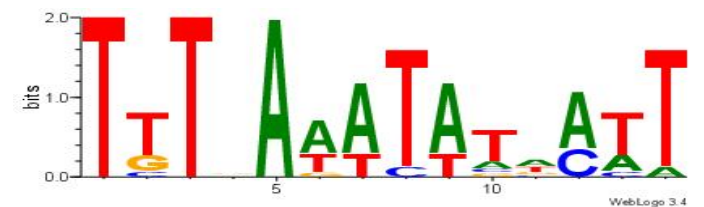
Dataset #: 2  
 Motif ID: 9  
 Motif name: Motif 9  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 4  
 Number of overlap: 11  
 Similarity score: 0.0250541

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

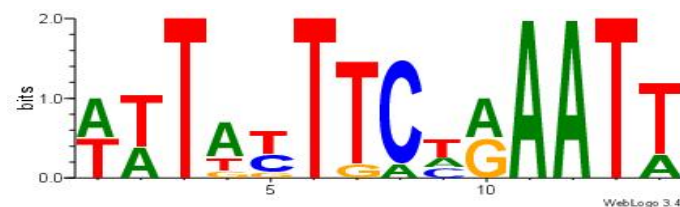
Alignment:

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

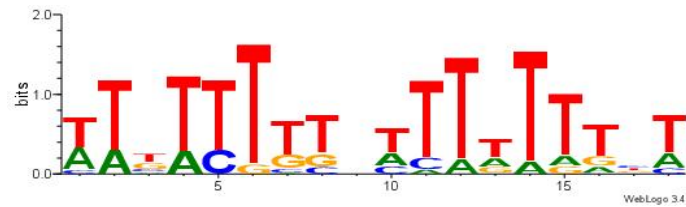


Similarity score: 0.0283217

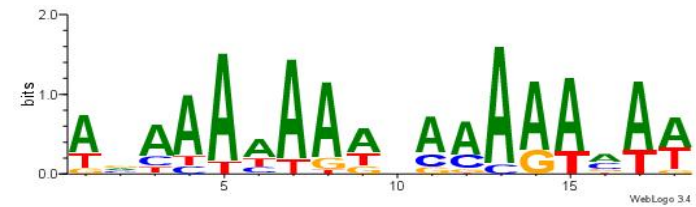
Alignment:

ABAAAAAWhAAAAARAW  
DBGTAATAHD-----

Original motif      Consensus sequence: WTKTTTTTHWTTTTTTBT



Reverse complement motif      Consensus sequence:  
ABAAAAAWhAAAAARAW



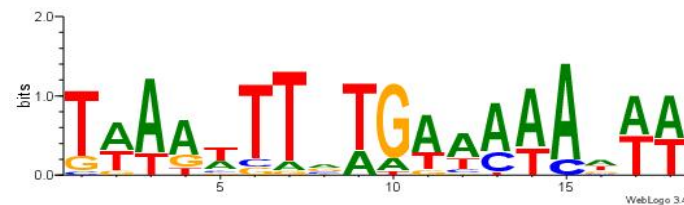
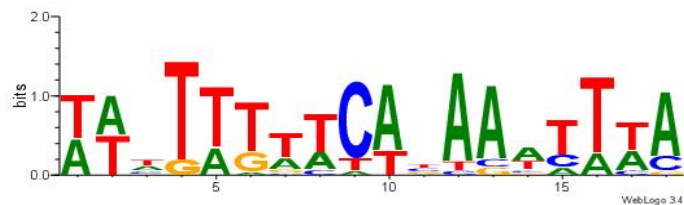
Dataset #: 5  
Motif ID: 53  
Motif name: TFM3  
Matching format of first motif: Original Motif  
Matching format of second motif: Reverse Complement  
Direction: Backward  
Position number: 2  
Number of overlap: 11  
Similarity score: 0.0308097

Alignment:

TWAAWTTVTGAAAAAHWW  
-----DBGTAATAHD-

Original motif      Consensus sequence: WWHTTTTTTCABAAWTTWA

Reverse complement motif      Consensus sequence:  
TWAAWTTVTGAAAAAHWW

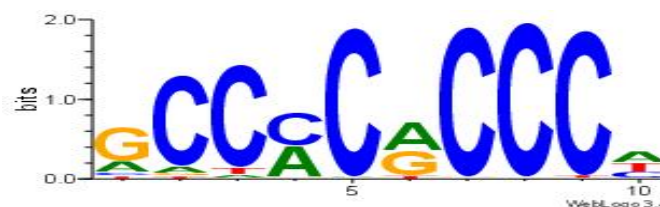


**Dataset #: 3      Motif ID: 27      Motif name: Klf4**

Original motif      Consensus sequence: DGGYGKGGC



Reverse complement motif      Consensus sequence: GCCYCMCCCD

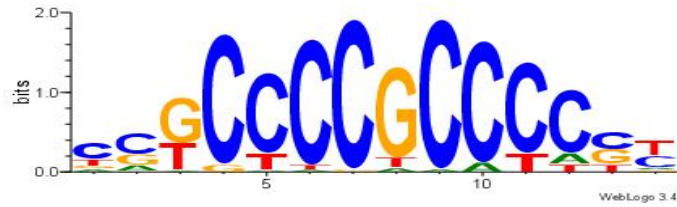


**Best Matches for Top Significant Motif ID 27 (Highest to Lowest)**

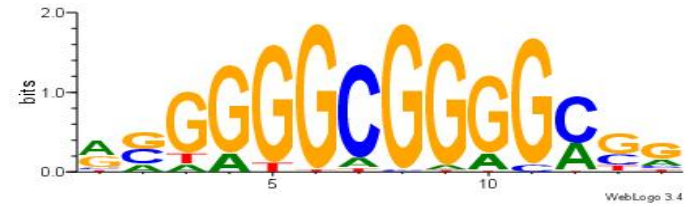
Dataset #:	2
Motif ID:	7
Motif name:	Motif 7
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	3
Number of overlap:	10
Similarity score:	0.0152457

Alignment:  
 CSKCCCCGCCCSY  
 --GCCYCMCCCD--

Original motif    Consensus sequence: CSKCCCCGCCCSY



Reverse complement motif    Consensus sequence: MSGGGCGGGGY

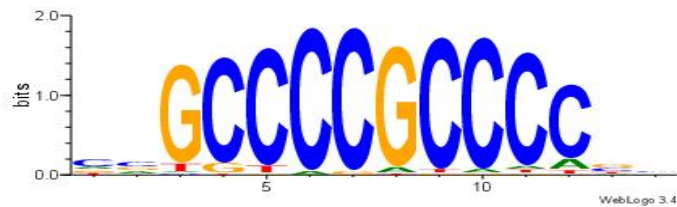


Dataset #: 4  
Motif ID: 36  
Motif name: csGCCCCGCCCSy  
Matching format of first motif: Original Motif  
Matching format of second motif: Reverse Complement  
Direction: Backward  
Position number: 3  
Number of overlap: 10  
Similarity score: 0.0160185

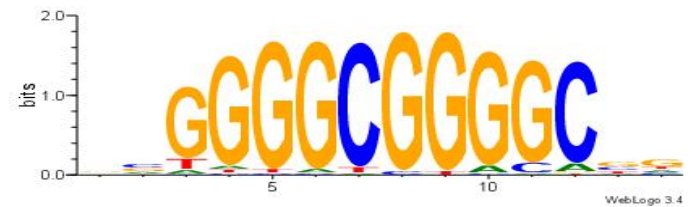
Alignment:

BBGGGGCGGGGCVD  
--DGGGYGKGGC--

Original motif    Consensus sequence: HVGCCCCGCCCB



Reverse complement motif    Consensus sequence: BBGGGGCGGGGC

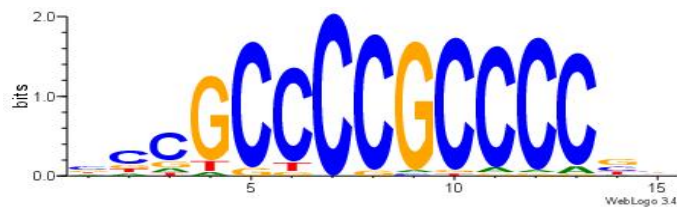


Dataset #: 4  
 Motif ID: 38  
 Motif name: cccGCCCCGCCCCsb  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 3  
 Number of overlap: 10  
 Similarity score: 0.0194893

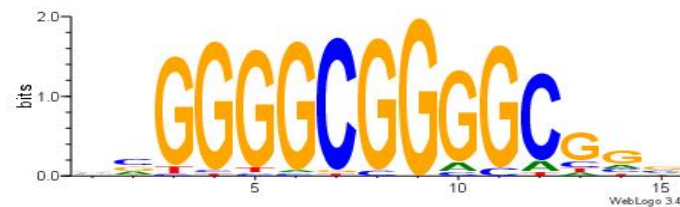
Alignment:

BBGGGGCGGGGCGGB  
 --DGGGYGKGGC---

Original motif      Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif      Consensus sequence: BBGGGGCGGGGCGGB

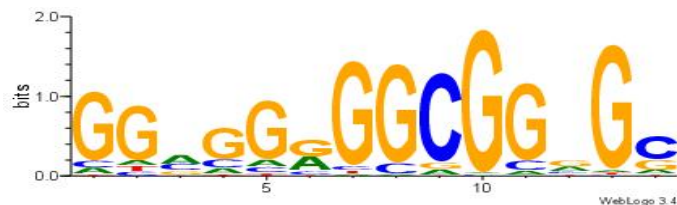


Dataset #: 5  
 Motif ID: 50  
 Motif name: TFF11  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 5

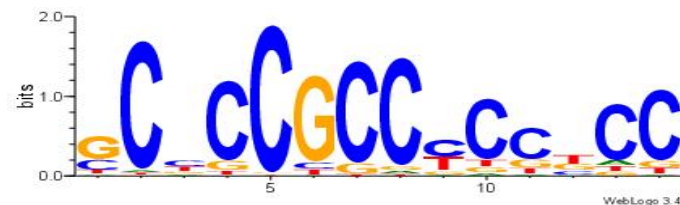
Number of overlap: 10  
Similarity score: 0.0402906

Alignment:  
GGMGGRGGCGGVGC  
----DGGGYGKGGC

Original motif      Consensus sequence: GGMGGRGGCGGVGC



Reverse complement motif      Consensus sequence: GCVCCGCCMCCYC

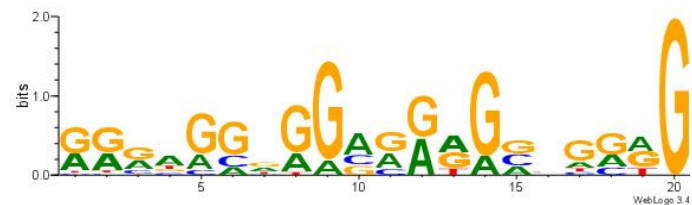
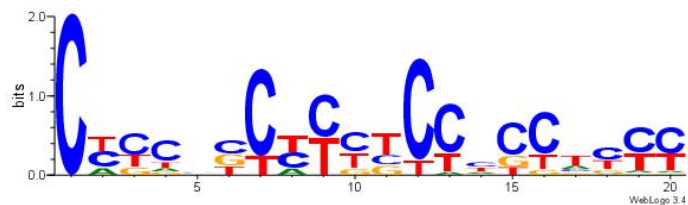


Dataset #: 5  
Motif ID: 54  
Motif name: TFM12  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Original Motif  
Direction: Backward  
Position number: 7  
Number of overlap: 10  
Similarity score: 0.0556427

Alignment:  
CYCBBCYYYTCCHCCTYYY  
----GCCYCMCCD-----

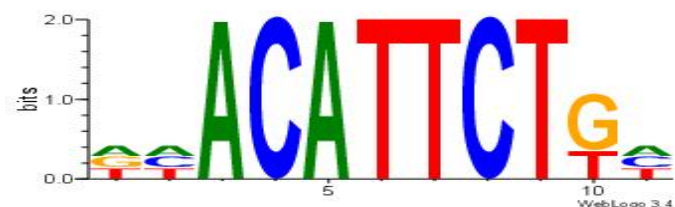
Original motif      Consensus sequence: CYCBBCYYYTCCHCCTYYY

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



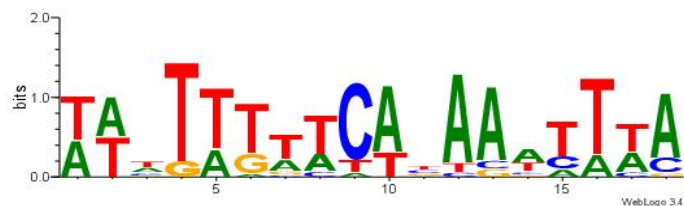
**Best Matches for Top Significant Motif ID 44 (Highest to Lowest)**

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

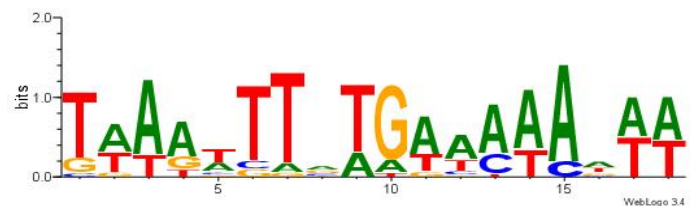
**Alignment:**

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

Original motif      Consensus sequence: WWHTTTTTTCABAAWTTWA



Reverse complement motif      Consensus sequence: TWAAWTTVTGAAAAHWW

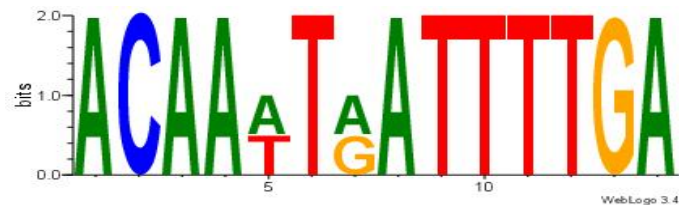


Dataset #: 2  
Motif ID: 16  
Motif name: Motif 16  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Reverse Complement  
Direction: Backward  
Position number: 4  
Number of overlap: 11  
Similarity score: 0.0258838

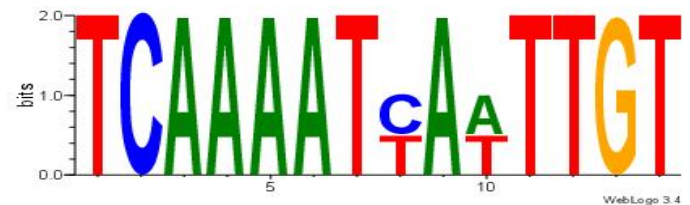
Alignment:

TCAAATKAWTTGT  
HCAGAATGTHD---

Original motif      Consensus sequence: ACAAWTRATTTTGA



Reverse complement motif      Consensus sequence: TCAAATKAWTTG

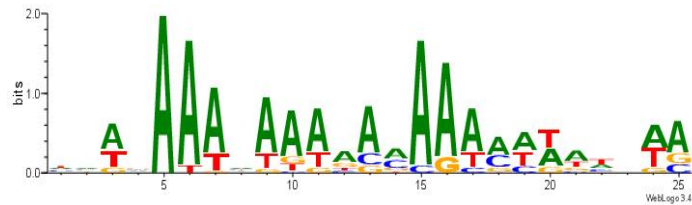


Dataset #: 5  
 Motif ID: 56  
 Motif name: TFM11  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 11  
 Number of overlap: 11  
 Similarity score: 0.0307858

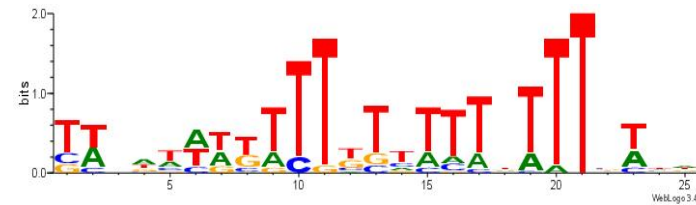
Alignment:

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

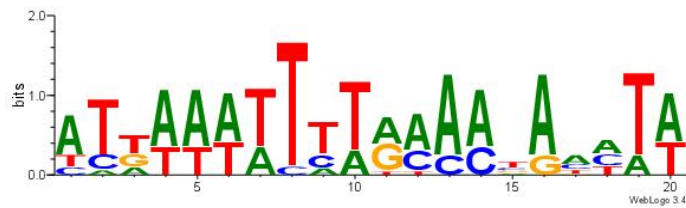


Number of overlap: 11  
Similarity score: 0.0357323

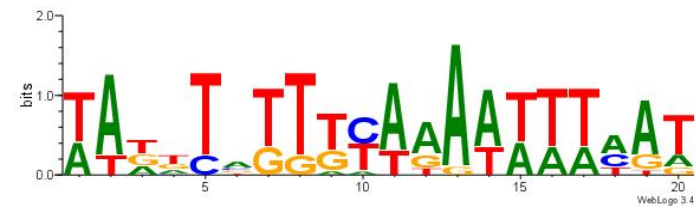
Alignment:

ATKAAWTTTTTRMAABAHTW  
-DHACATTCTGH-----

Original motif      Consensus sequence: ATKAAWTTTTTRMAABAHTW



Reverse complement motif      Consensus sequence:  
WAHHTVTTYKAAAATTRAT



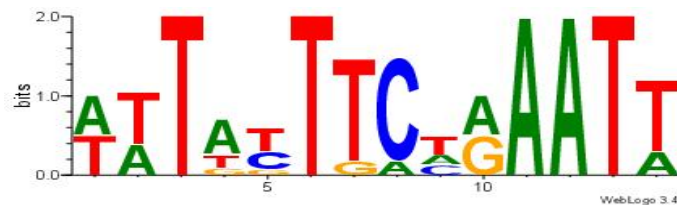
Dataset #: 2  
Motif ID: 6  
Motif name: Motif 6  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Original Motif  
Direction: Backward  
Position number: 4  
Number of overlap: 11  
Similarity score: 0.0400884

Alignment:

AATTYDGAARTAWW  
HCAGAAATGTHD---

Original motif      Consensus sequence: AATTYDGAARTAWW

Reverse complement motif      Consensus sequence: WWTAKTTCDKAAAT



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

Original motif      Consensus sequence: GCGGGGC



Reverse complement motif      Consensus sequence: GCCCGCC

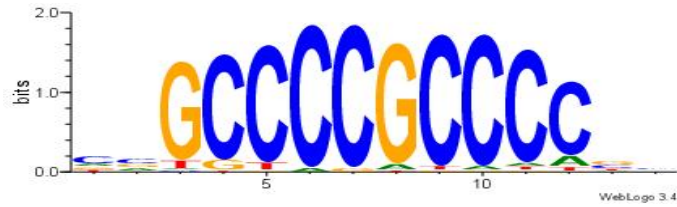


**Best Matches for Top Significant Motif ID 1 (Highest to Lowest)**

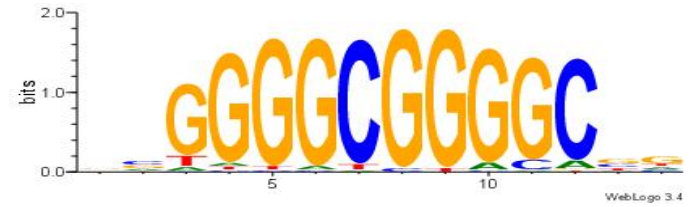
Dataset #:	4
Motif ID:	36
Motif name:	csGCCCCGCCCCsc
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	3
Number of overlap:	8
Similarity score:	0

Alignment:  
 BBGGGGCGGGGCVD  
 ----GGCGGGGC--

Original motif    Consensus sequence: HVGCCCCGCCCB



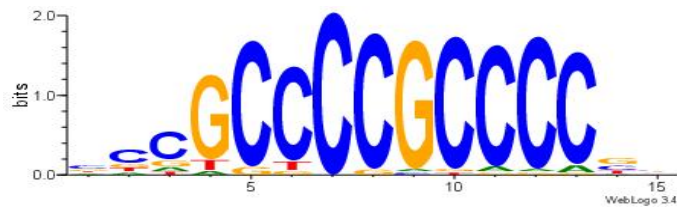
Reverse complement motif    Consensus sequence: BBGGGGCGGGGC



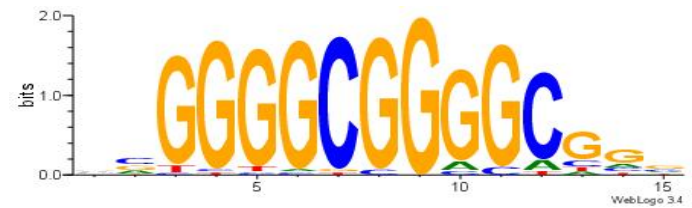
Dataset #: 4  
 Motif ID: 38  
 Motif name: cccGCCCCGCCCBsb  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 5  
 Number of overlap: 8  
 Similarity score: 0.00250079

Alignment:  
 BBGGGGCGGGGCGB  
 ----GGCGGGGC----

Original motif    Consensus sequence: BCCGCCCGCCCCBB



Reverse complement motif    Consensus sequence: BBGGGGCGGGGCGB

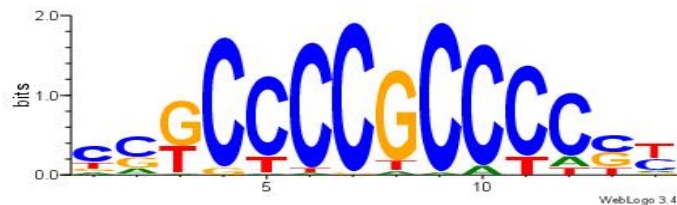


Dataset #: 2  
 Motif ID: 7  
 Motif name: Motif 7  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 5  
 Number of overlap: 8  
 Similarity score: 0.0149958

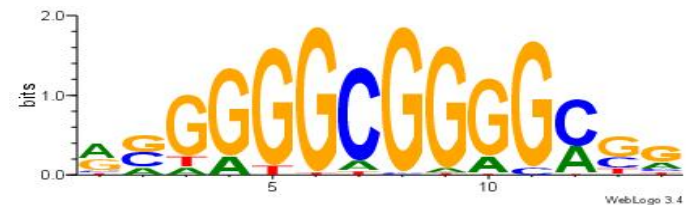
Alignment:

MSGGGGCGGGYSG  
 ----GGCGGGGC--

Original motif      Consensus sequence: CSKCCCCGCCCSY



Reverse complement motif      Consensus sequence: MSGGGGCGGGY



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

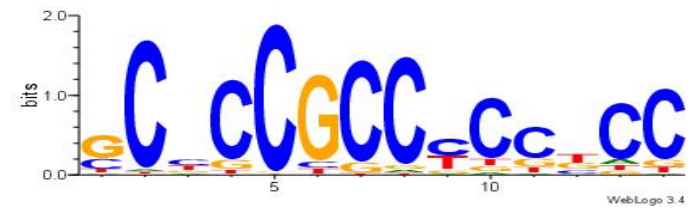
Alignment:

GCVCCGCCMCCYCC  
GCCCCGCC-----

Original motif    Consensus sequence: GGMGGRGGCGGVGC



Reverse complement motif    Consensus sequence: GCVCCGCCMCCYCC



---

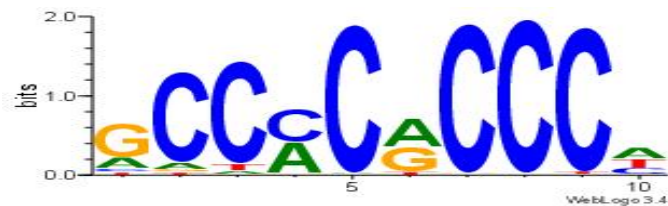
Dataset #: 3  
Motif ID: 27  
Motif name: Klf4  
Matching format of first motif: Original Motif  
Matching format of second motif: Original Motif  
Direction: Forward  
Position number: 3  
Number of overlap: 8  
Similarity score: 0.0349983

Alignment:

DGGGYGKGGC  
--GGCGGGC

Original motif    Consensus sequence: DGGGYGKGGC

Reverse complement motif    Consensus sequence: GCCYCMCCCD

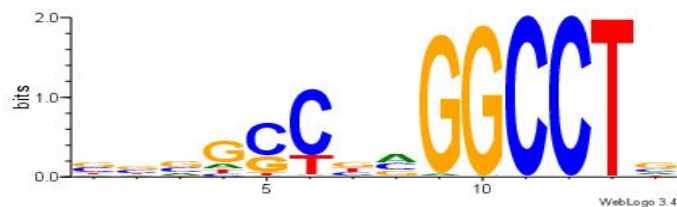


Dataset #: 3  
 Motif ID: 22  
 Motif name: Zfx  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 4  
 Number of overlap: 8  
 Similarity score: 0.0708224

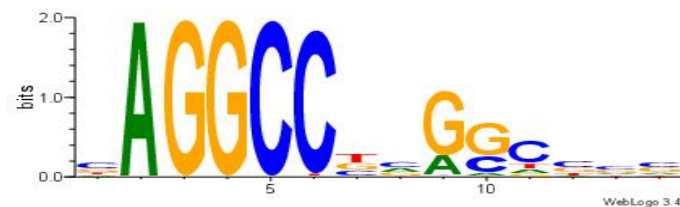
**Alignment:**

VAGGCCBBGGCVBB  
 ---GCCCCGCC---

Original motif      Consensus sequence: BBVGCCBVGGCCTV



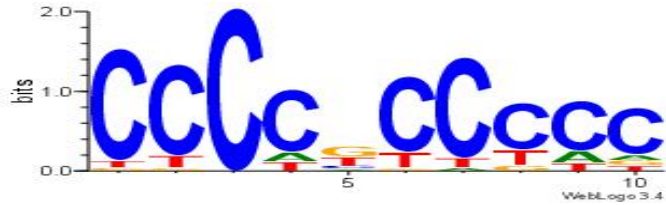
Reverse complement motif      Consensus sequence: VAGGCCBBGGCVBB



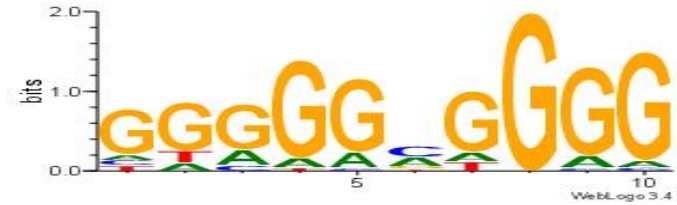
## Significant Motifs - Global and Local Matching (Highest to Lowest)

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

Original motif      Consensus sequence: CCCCKCCCC



Reverse complement motif      Consensus sequence: GGGGGYGGGG



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

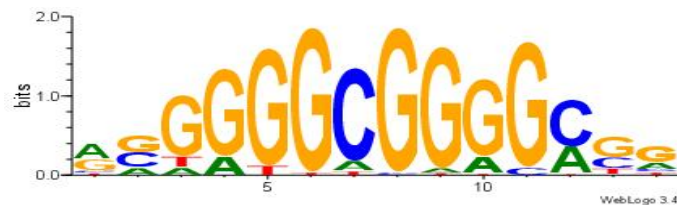
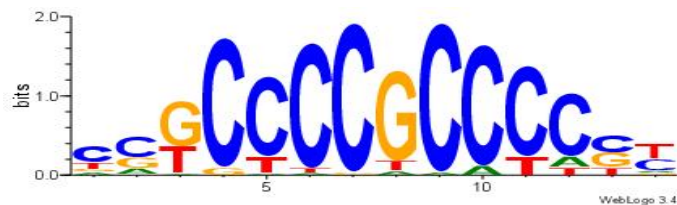
Dataset #:	2
Motif ID:	7
Motif name:	Motif 7
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2
Number of overlap:	10
Similarity score:	0.00451594

Alignment:

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

Original motif      Consensus sequence: CSKCCCCGCCCSY

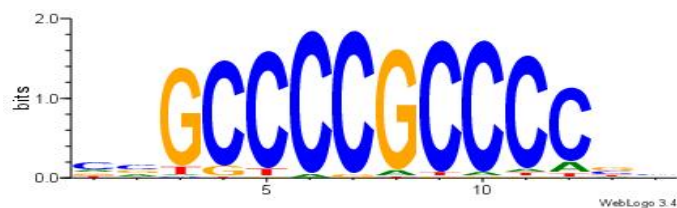
Reverse complement motif      Consensus sequence: MSGGGGCGGGGY



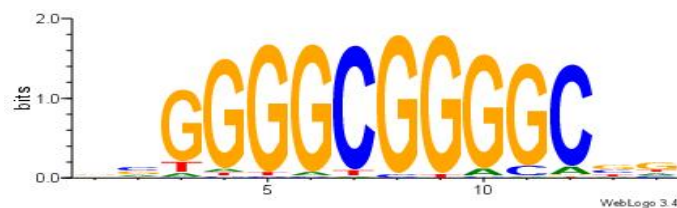
Dataset #: 4  
 Motif ID: 36  
 Motif name: csGCCCGCCCCsc  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 4  
 Number of overlap: 10  
 Similarity score: 0.00965796

Alignment:  
 BBGGGGCGGGGCVD  
 -GGGGYGGGG---

Original motif    Consensus sequence: HVGCCCGCCCCBB



Reverse complement motif    Consensus sequence: BBGGGGCGGGGC



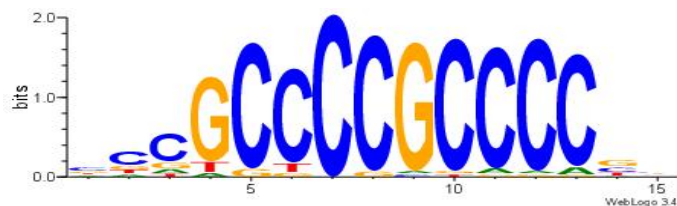
Dataset #: 4  
 Motif ID: 38



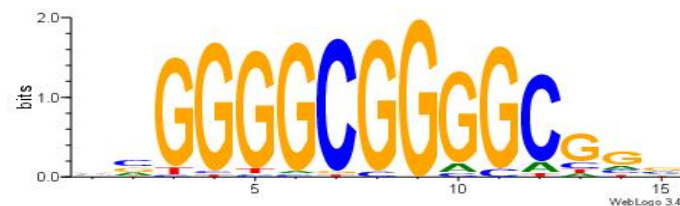
Motif name: cccGCCCCGCCCCsb  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 5  
 Number of overlap: 10  
 Similarity score: 0.0127292

Alignment:  
 BCCGCCCCGCCCCBB  
 ----CCCKCCCC-

Original motif    Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif    Consensus sequence: BBGGGCGGGGCGGB

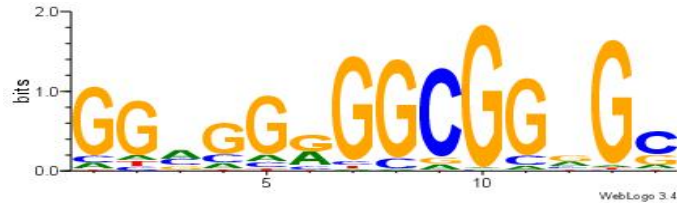


Dataset #: 5  
 Motif ID: 50  
 Motif name: TFF11  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 4  
 Number of overlap: 10  
 Similarity score: 0.0174405

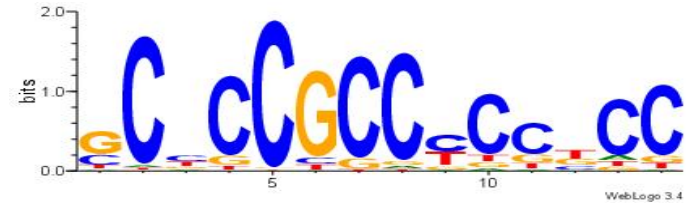
Alignment:

GGMGGRGGCGGVGC  
---GGGGYGGG---

Original motif    Consensus sequence: GGMGGRGGCGGVGC



Reverse complement motif    Consensus sequence: GCVCCGCCMCCYCC



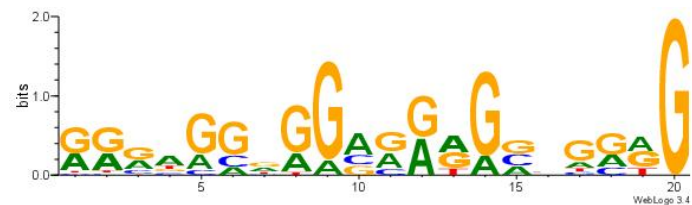
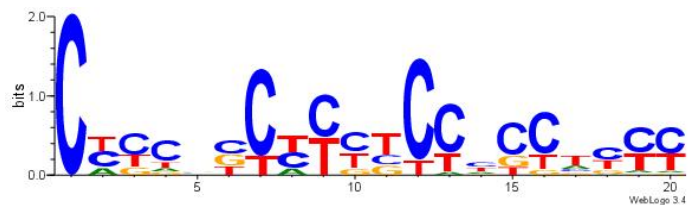
Dataset #: 5  
Motif ID: 54  
Motif name: TFM12  
Matching format of first motif: Original Motif  
Matching format of second motif: Original Motif  
Direction: Backward  
Position number: 5  
Number of overlap: 10  
Similarity score: 0.0301548

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

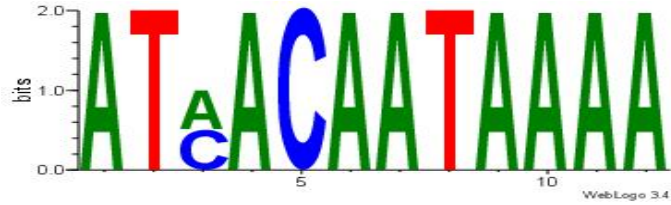


**Best Matches for Significant Motif ID 21 (Highest to Lowest)**

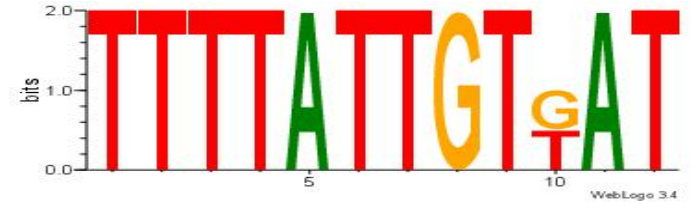
Dataset #:	2
Motif ID:	15
Motif name:	Motif 15
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	6
Similarity score:	0

Alignment:  
 TTTTATTGTYAT  
 TTTTAT-----

Original motif      Consensus sequence: ATMACAATAAAA



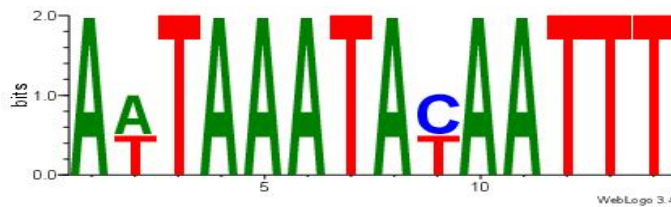
Reverse complement motif      Consensus sequence: TTTTATTGTYAT



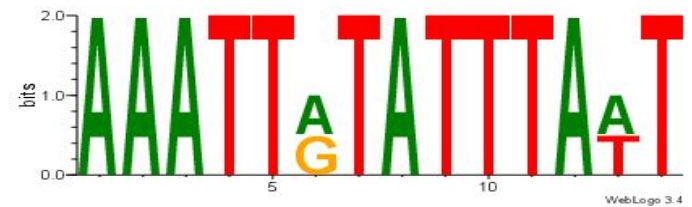
Dataset #: 2  
 Motif ID: 5  
 Motif name: Motif 5  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 6  
 Number of overlap: 6  
 Similarity score: 0.0208333

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

Original motif      Consensus sequence: AWTAAATAYAATTT



Reverse complement motif      Consensus sequence: AAATTKTATTTAWT

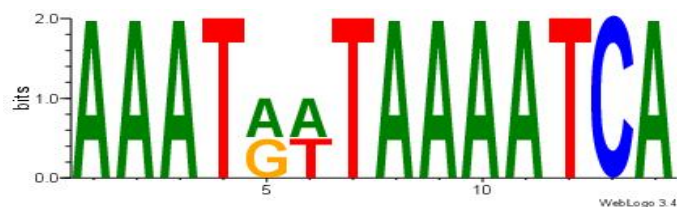


Dataset #: 2  
 Motif ID: 8  
 Motif name: Motif 8  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 4  
 Number of overlap: 6  
 Similarity score: 0.0208333

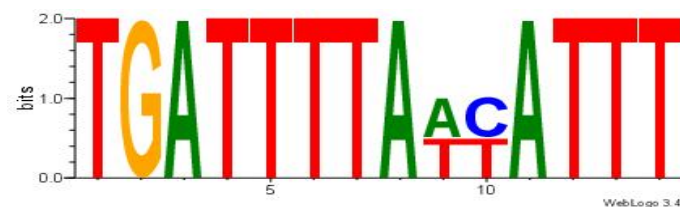
Alignment:

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

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



Reverse complement motif      Consensus sequence: TGATTTTAWKATT



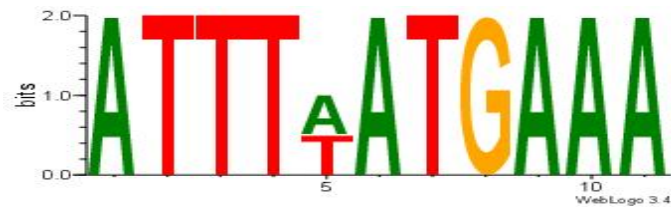
Dataset #: 2  
 Motif ID: 11  
 Motif name: Motif 11  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 2  
 Number of overlap: 6

Similarity score: 0.0208333

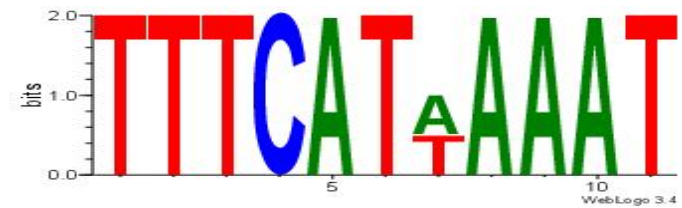
Alignment:

ATTTWATGAAA  
----TTTTAT-

Original motif      Consensus sequence: ATTTWATGAAA



Reverse complement motif      Consensus sequence: TTTCATWAAAT



---

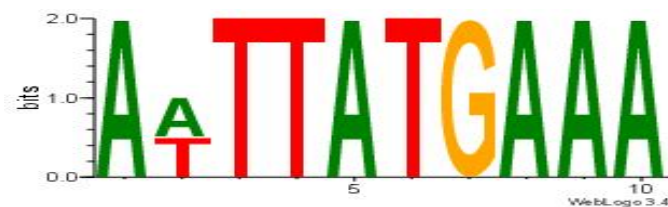
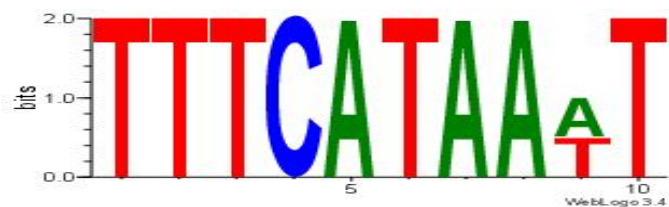
Dataset #: 2  
Motif ID: 10  
Motif name: Motif 10  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Original Motif  
Direction: Backward  
Position number: 1  
Number of overlap: 6  
Similarity score: 0.0416667

Alignment:

TTTCATAAWT  
----TTTTAT

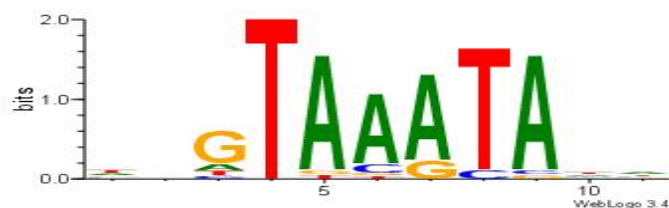
Original motif      Consensus sequence: TTTCATAAWT

Reverse complement motif      Consensus sequence: AWTTATGAAA

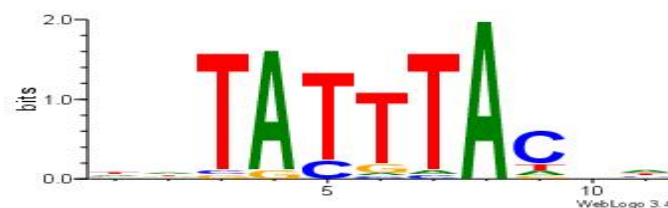


**Dataset #: 4      Motif ID: 45      Motif name: wbgTAAATAww**

Original motif      Consensus sequence: DBGTAATAHD



Reverse complement motif      Consensus sequence: DHTATTTACBD

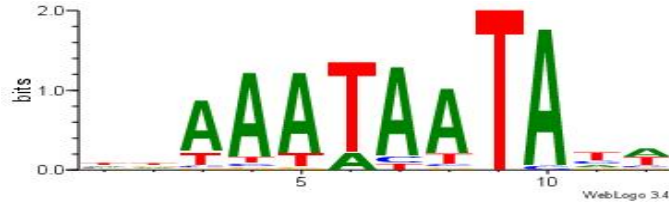


### Best Matches for Significant Motif ID 45 (Highest to Lowest)

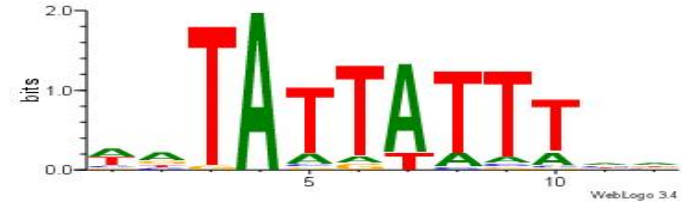
Dataset #:	4
Motif ID:	37
Motif name:	tkAAATAATAtw
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	11
Similarity score:	0.0162338

Alignment:  
 HDAAATAATAHW  
 -DBGTAATAHD

Original motif      Consensus sequence: HDAAATAATAHW



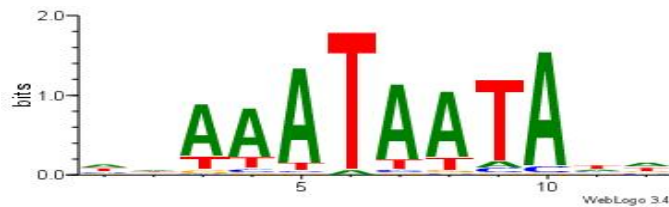
Reverse complement motif      Consensus sequence: WHTATTATTTDH



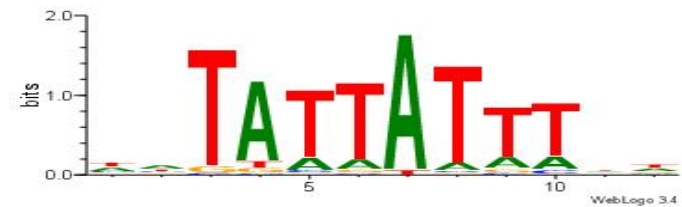
Dataset #: 4  
Motif ID: 41  
Motif name: wwAAATAATAtw  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Reverse Complement  
Direction: Backward  
Position number: 2  
Number of overlap: 11  
Similarity score: 0.0164863

Alignment:  
DDTATTATTTDH  
DHTATTTACBD-

Original motif      Consensus sequence: HDAAATAATADD



Reverse complement motif      Consensus sequence: DDTATTATTTDH



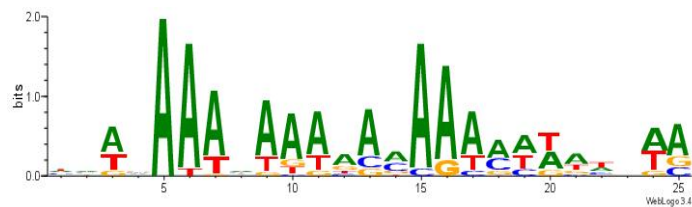


Dataset #: 5  
 Motif ID: 56  
 Motif name: TFM11  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 15  
 Number of overlap: 11  
 Similarity score: 0.0192768

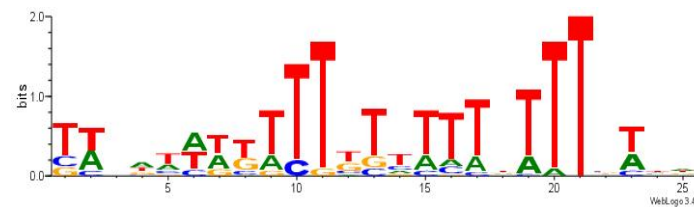
Alignment:

TWVHWWWYTTTYTTTTTHTTTVWBH  
 -----DHTATTTACBD

Original motif    Consensus sequence:  
 HDWVAAAHAAAAAMAAAMWWWHBWA



Reverse complement motif    Consensus sequence:  
 TWVHWWWYTTTYTTTTTHTTTVWBH

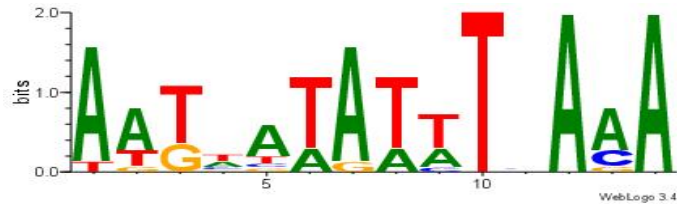


Dataset #: 2  
 Motif ID: 9  
 Motif name: Motif 9  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 4

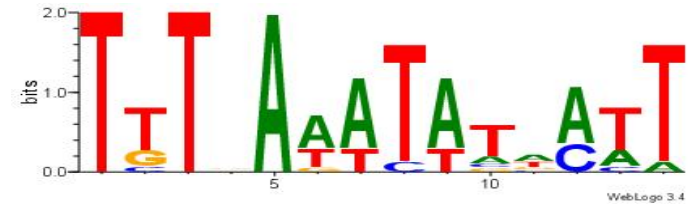
Number of overlap: 11  
Similarity score: 0.0250541

Alignment:  
AATHATATWTHAAA  
DHTATTTACBD---

Original motif      Consensus sequence: AATHATATWTHAAA



Reverse complement motif      Consensus sequence: TTTDAWATATHAT

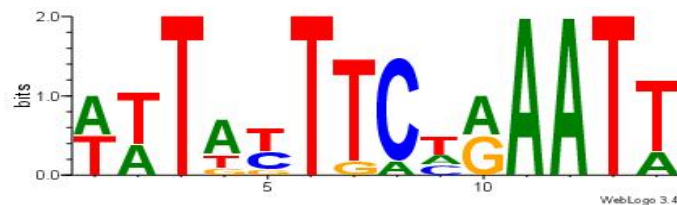


Dataset #: 2  
Motif ID: 6  
Motif name: Motif 6  
Matching format of first motif: Original Motif  
Matching format of second motif: Original Motif  
Direction: Backward  
Position number: 1  
Number of overlap: 11  
Similarity score: 0.027895

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)**

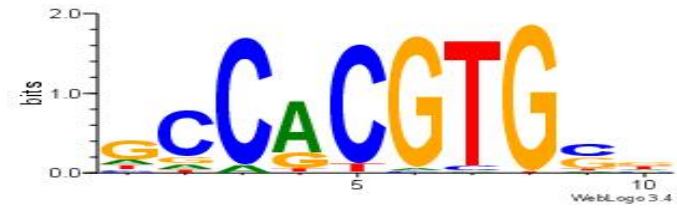
Dataset #:	3
Motif ID:	33
Motif name:	Mycn
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	2
Number of overlap:	8
Similarity score:	0.0123101

Alignment:  
GCCACGTGSD  
-VBACGTGV-

Original motif      Consensus sequence: HSCACGTGGC



Reverse complement motif      Consensus sequence: GCCACGTGSD

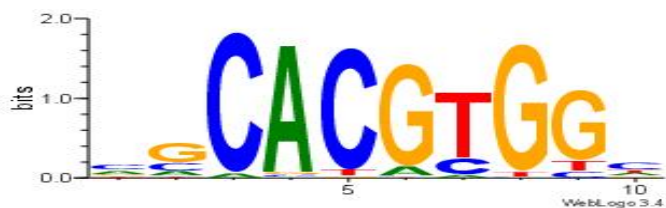


Dataset #: 3  
Motif ID: 34  
Motif name: Myc  
Matching format of first motif: Original Motif  
Matching format of second motif: Reverse Complement  
Direction: Backward  
Position number: 2  
Number of overlap: 8  
Similarity score: 0.0144491

Alignment:

DCCACGTGCV  
-VBACGTGV-

Original motif      Consensus sequence: VGCACGTGGH



Reverse complement motif      Consensus sequence: DCCACGTGCV

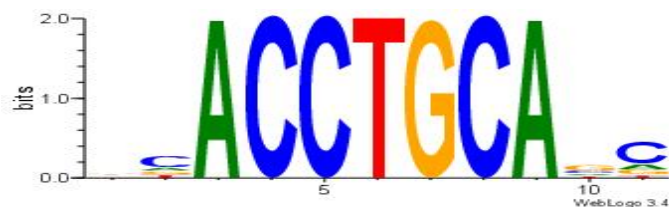


Dataset #: 4  
 Motif ID: 40  
 Motif name: kcACCTGCAGc  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 8  
 Similarity score: 0.0295473

Alignment:

GBTGCAGGTGB  
 ---VCACGTBV

Original motif      Consensus sequence: BCACCTGCABC



Reverse complement motif      Consensus sequence: GBTGCAGGTGB



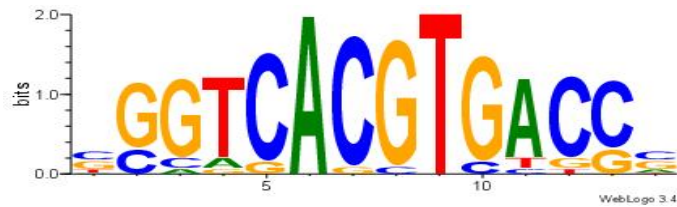
Dataset #: 4  
 Motif ID: 42  
 Motif name: sSGTCACGTGACSS  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 4  
 Number of overlap: 8

Similarity score: 0.0314837

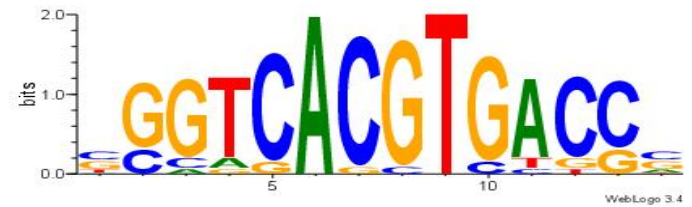
Alignment:

SGGTCACGTGACCS  
---VCACGTBV---

Original motif    Consensus sequence: SGGTCACGTGACCS



Reverse complement motif    Consensus sequence: SGGTCACGTGACCS



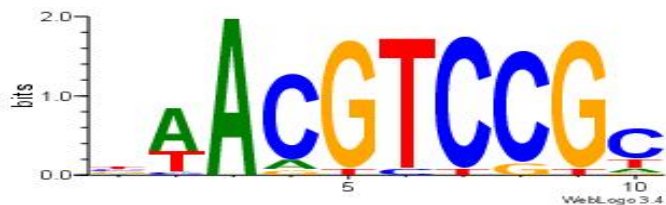
Dataset #: 3  
Motif ID: 26  
Motif name: MIZF  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Reverse Complement  
Direction: Forward  
Position number: 3  
Number of overlap: 8  
Similarity score: 0.0377204

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

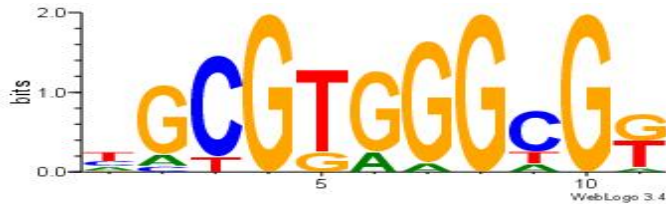


**Best Matches for Significant Motif ID 32 (Highest to Lowest)**

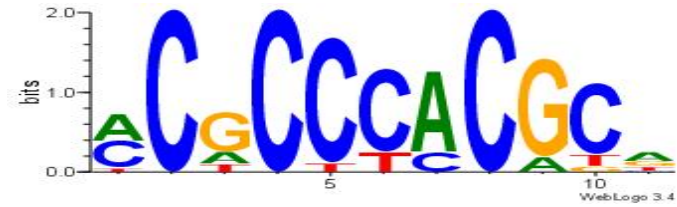
Dataset #:	3
Motif ID:	23
Motif name:	Egr1
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	6
Similarity score:	0

Alignment:  
 HGC GTGGGCGK  
 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



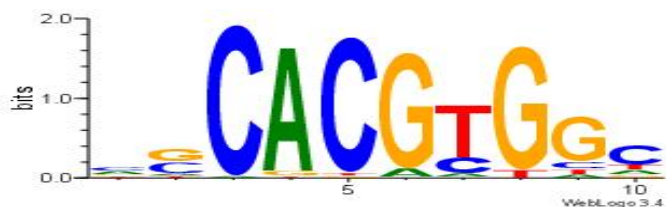


Dataset #: 3  
 Motif ID: 33  
 Motif name: Mycn  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 3  
 Number of overlap: 6  
 Similarity score: 0.0377949

Alignment:

GCCACGTGSD  
 --YGCGTG--

Original motif      Consensus sequence: HSCACGTGGC



Reverse complement motif      Consensus sequence: GCCACGTGSD



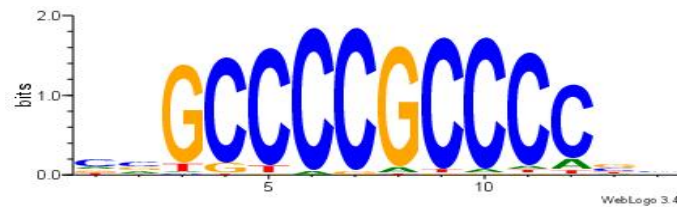
Dataset #: 4  
 Motif ID: 36  
 Motif name: csGCCCCGCCCCsc  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 5  
 Number of overlap: 6

Similarity score: 0.0396403

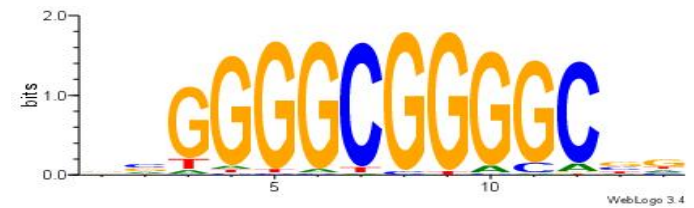
Alignment:

HVCCCCGCCCCBB  
----CACGCM----

Original motif    Consensus sequence: HVCCCCGCCCCBB



Reverse complement motif    Consensus sequence: BBGGGCGGGGC



---

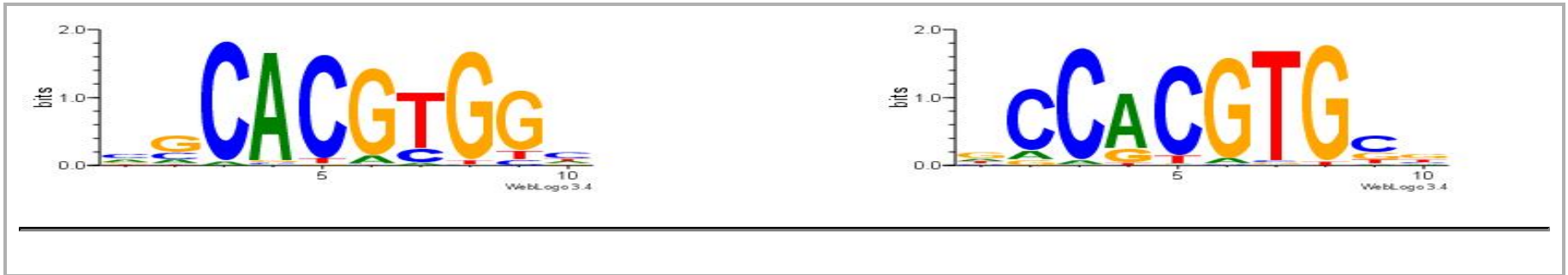
Dataset #: 3  
Motif ID: 34  
Motif name: Myc  
Matching format of first motif: Original Motif  
Matching format of second motif: Reverse Complement  
Direction: Backward  
Position number: 3  
Number of overlap: 6  
Similarity score: 0.0399214

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)

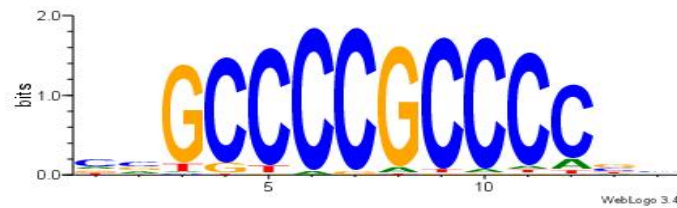
Dataset #:	4
Motif ID:	36
Motif name:	csGCCCCGCCCCsc
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	3
Number of overlap:	8

Similarity score: 0

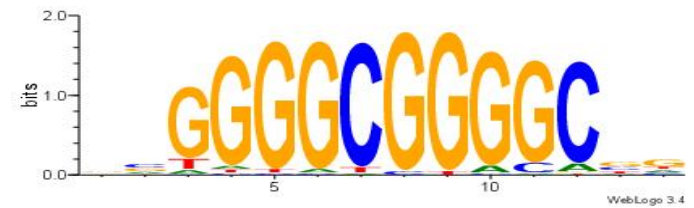
Alignment:

BBGGGGCGGGGCVD  
----GGCGGGGC--

Original motif      Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif      Consensus sequence: BBGGGGCGGGGC



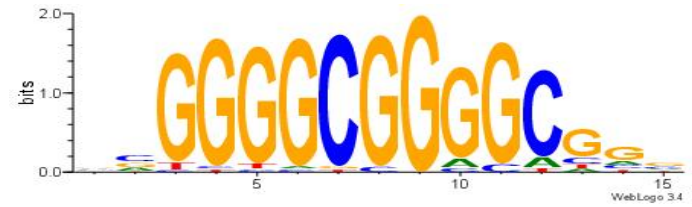
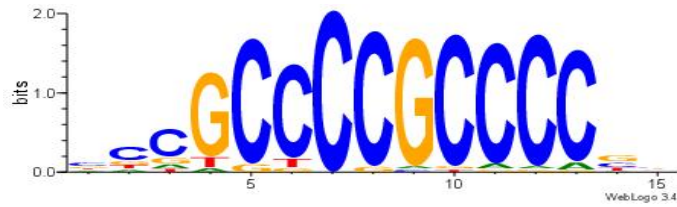
Dataset #: 4  
Motif ID: 38  
Motif name: cccGCCCCGCCCCsb  
Matching format of first motif: Original Motif  
Matching format of second motif: Reverse Complement  
Direction: Forward  
Position number: 5  
Number of overlap: 8  
Similarity score: 0.00250079

Alignment:

BBGGGGCGGGGCGB  
----GGCGGGGC---

Original motif      Consensus sequence: BCCGCCCCGCCCCBB

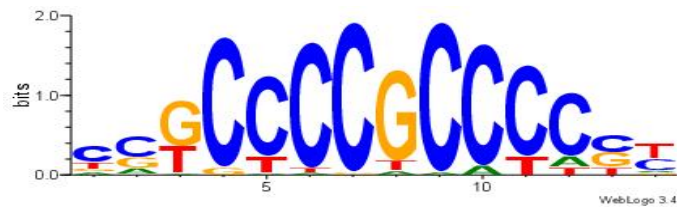
Reverse complement motif      Consensus sequence:  
BBGGGGCGGGGCGB



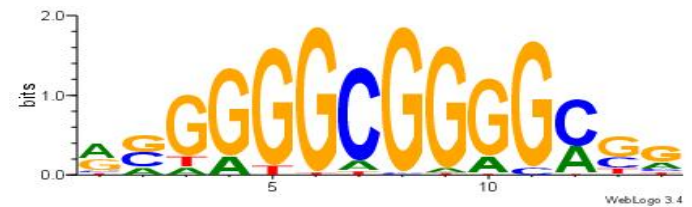
Dataset #: 2  
 Motif ID: 7  
 Motif name: Motif 7  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 5  
 Number of overlap: 8  
 Similarity score: 0.0149958

Alignment:  
 MSGGGCGGGYSG  
 ----GGCGGGC--

Original motif    Consensus sequence: CSKCCCCGCCCSY



Reverse complement motif    Consensus sequence: MSGGGCGGGYSG



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

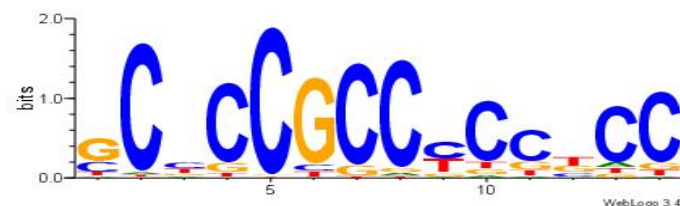
Alignment:

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



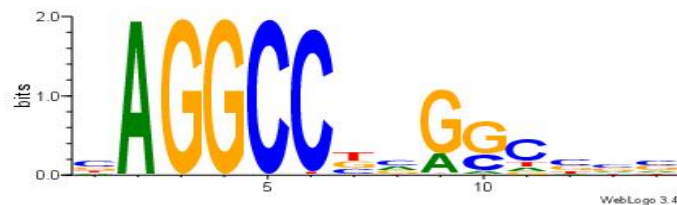
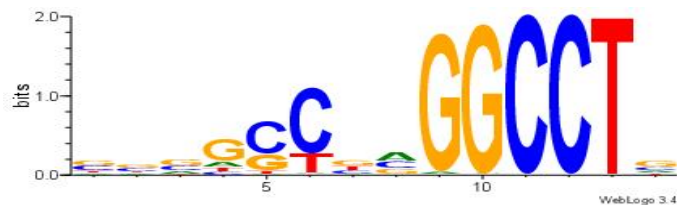
Dataset #: 3  
Motif ID: 22  
Motif name: Zfx  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Reverse Complement  
Direction: Forward  
Position number: 4  
Number of overlap: 8  
Similarity score: 0.0708224

Alignment:

VAGGCCBBGGCVBB  
---GCCCGCC---

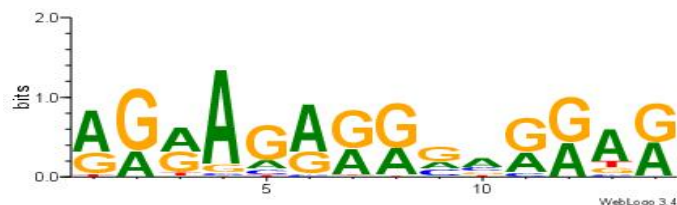
Original motif      Consensus sequence: BBVGCCBVGGCCTV

Reverse complement motif      Consensus sequence: VAGGCCBBGGCVBB

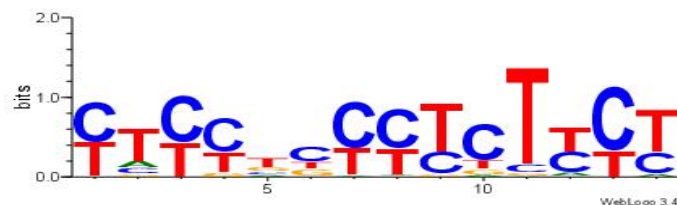


**Dataset #: 2      Motif ID: 2      Motif name: Motif 2**

Original motif      Consensus sequence: RGRAGARRGARRAR



Reverse complement motif      Consensus sequence: MTMMTCMMTCTK



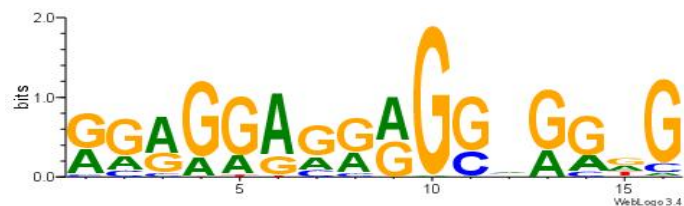
**Best Matches for Motif ID 2 (Highest to Lowest)**

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

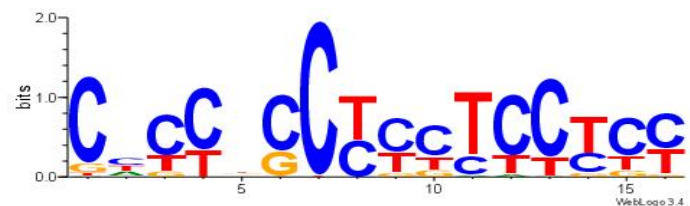
Alignment:  
RGRGGAGRRGGHGGDG  
--RGRAGARRGARRAR



Original motif      Consensus sequence: RGRGGAGRRGGHGGDG



Reverse complement motif      Consensus sequence: CHCCBCCKMCTCCKCM

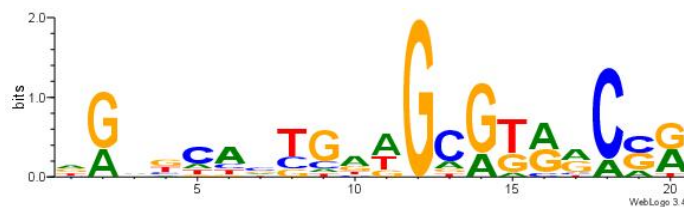


Dataset #: 3  
Motif ID: 31  
Motif name: Pax5  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Reverse Complement  
Direction: Forward  
Position number: 7  
Number of overlap: 14  
Similarity score: 0.047364

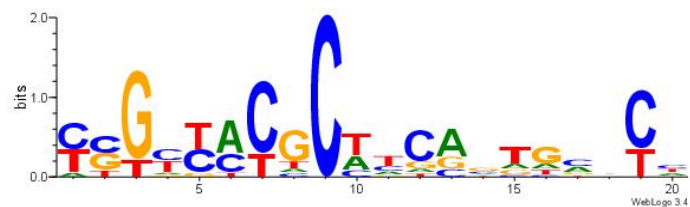
Alignment:

```
MSGKKRCGCWDCABTG B B C D  
-----MTMMTCMMTCTKCK
```

Original motif      Consensus sequence: DGVBCABTGDWGCGRRCRCSR



Reverse complement motif      Consensus sequence: MSGKKRCGCWDCABTG B B C D

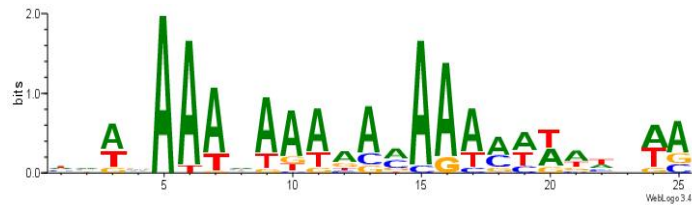


Dataset #: 5  
 Motif ID: 56  
 Motif name: TFM11  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 3  
 Number of overlap: 14  
 Similarity score: 0.0541717

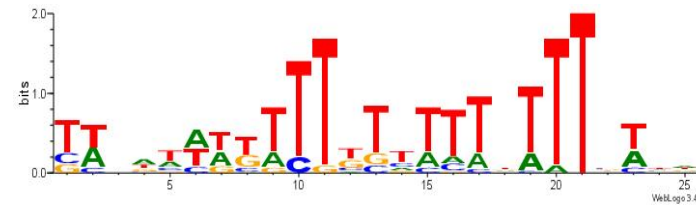
Alignment:

HDWVAAAHAAAAAMAAAMWWWHBWA  
 -----RGRAGARRGARRAR--

Original motif    Consensus sequence:  
 HDWVAAAHAAAAAMAAAMWWWHBWA



Reverse complement motif    Consensus sequence:  
 TWVHWWWYTTTTTTTTHTTTVWBH



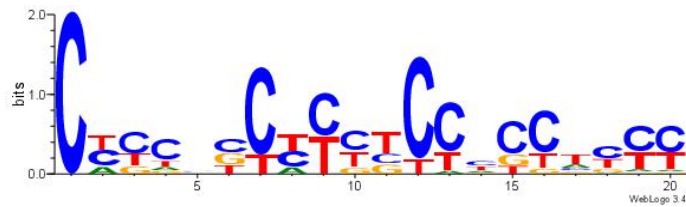
Dataset #: 5  
 Motif ID: 54  
 Motif name: TFM12  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 7

Number of overlap: 14  
Similarity score: 0.0545069

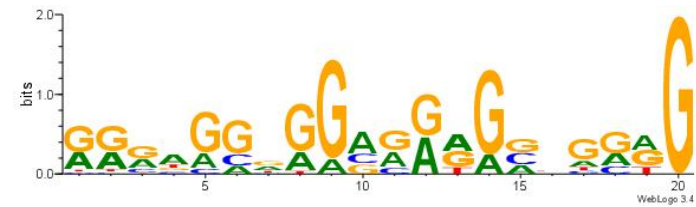
Alignment:

CYYCBBCYYYYTCCHCCTYYY  
-----MTMMTCMMTCTKCK

Original motif    Consensus sequence: CYYCBBCYYYYTCCHCCTYYY



Reverse complement motif    Consensus sequence: KKKAGGDGGAKKMGBBGKMG

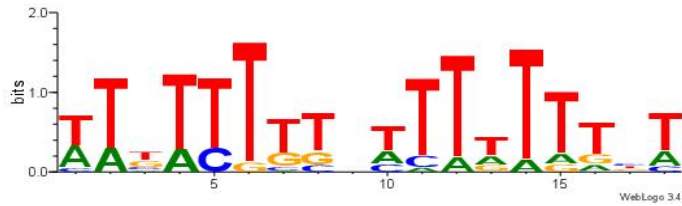


Dataset #: 5  
Motif ID: 52  
Motif name: TFM1  
Matching format of first motif: Original Motif  
Matching format of second motif: Reverse Complement  
Direction: Backward  
Position number: 4  
Number of overlap: 14  
Similarity score: 0.0558935

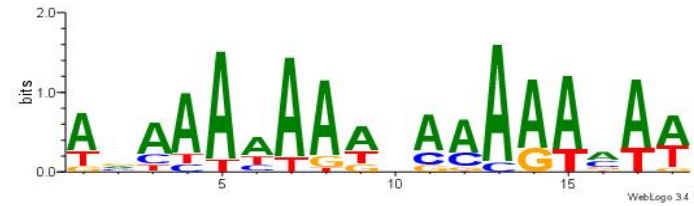
Alignment:

ABAAAAAWhAAAAARAW  
-RGRAGARRGARRAR---

Original motif      Consensus sequence: WTKTTTTTHWTTTTTTBT

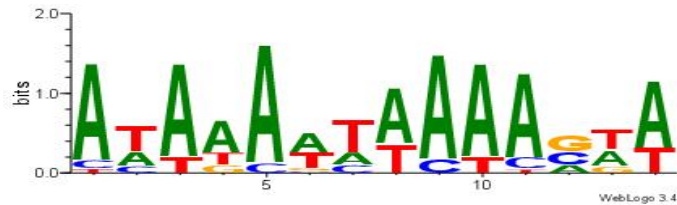


Reverse complement motif      Consensus sequence: ABAAAAAWHAAAAARAW

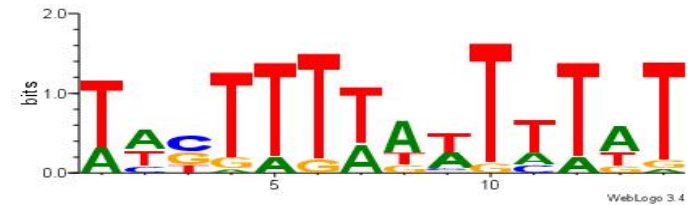


**Dataset #: 2      Motif ID: 3      Motif name: Motif 3**

Original motif      Consensus sequence: AWAAAWTWAASWA



Reverse complement motif      Consensus sequence: TWSTTTWAWTTT



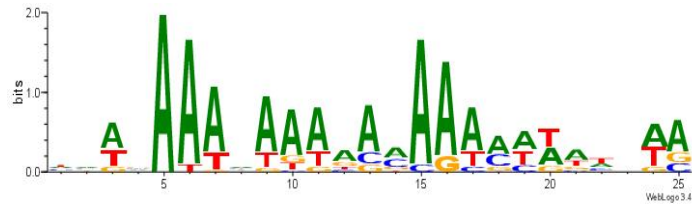
### Best Matches for Motif ID 3 (Highest to Lowest)

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

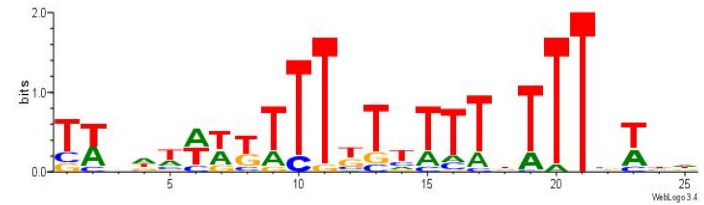
Alignment:

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

Original motif    Consensus sequence:  
 HDWVAAAHAAAAAMAAAMWWWHBWA



Reverse complement motif    Consensus sequence:  
 TWVHWWWYTTTTYTTTTTHTTTVWBH

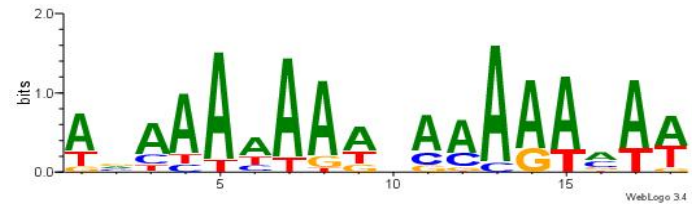
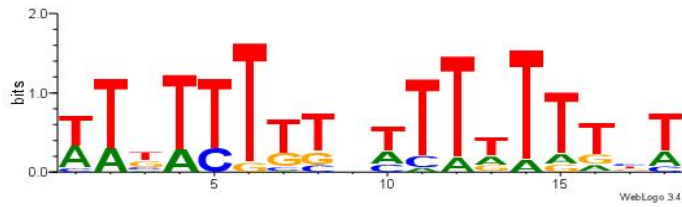


Dataset #: 5  
 Motif ID: 52  
 Motif name: TFM1  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 14  
 Similarity score: 0.0162962

Alignment:  
 ABAAAAAWhAAAAARAW  
 -----AWAAAWTWAAASWA

Original motif    Consensus sequence: WTKTTTTTHWTTTTTBT

Reverse complement motif    Consensus sequence:  
 ABAAAAAWhAAAAARAW



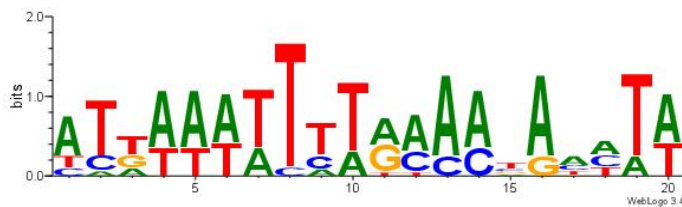
Dataset #: 5  
 Motif ID: 55  
 Motif name: TFM13  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 3  
 Number of overlap: 14  
 Similarity score: 0.037679

Alignment:

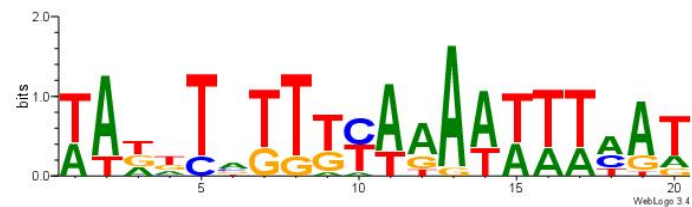
```

ATKAAWTTTTRMAABAHTW
--AWAAAWTWAAASWA----
  
```

Original motif      Consensus sequence: ATKAAWTTTTRMAABAHTW



Reverse complement motif      Consensus sequence: WAHHTVTTYKAAAATTRAT



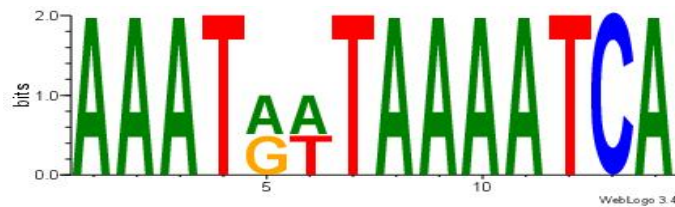
Dataset #: 2

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

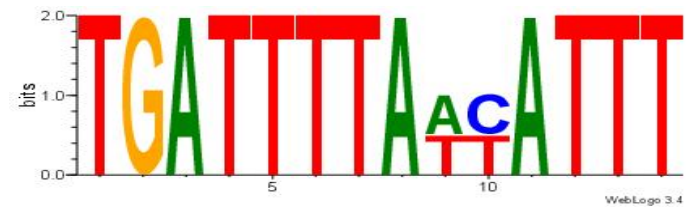
Alignment:

TGATTTTAWKATTT  
 TWSTTTWAWTTTWT

Original motif      Consensus sequence: AAATRWTAATCA



Reverse complement motif      Consensus sequence: TGATTTTAWKATTT

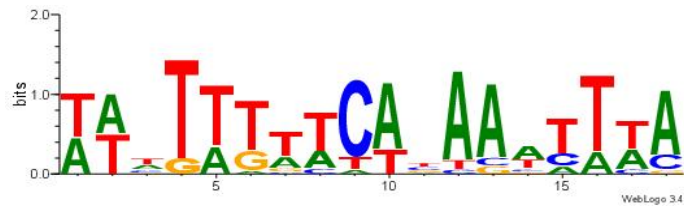


Dataset #: 5  
 Motif ID: 53  
 Motif name: TFM3  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 5  
 Number of overlap: 14  
 Similarity score: 0.0456419

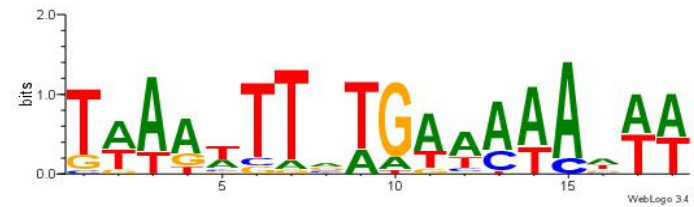
Alignment:

```
TWAAWTTVTGAAAAAHWW  
----AWAAAWTWAAASWA
```

Original motif      Consensus sequence: WWHTTTTTTCABAAWTTWA

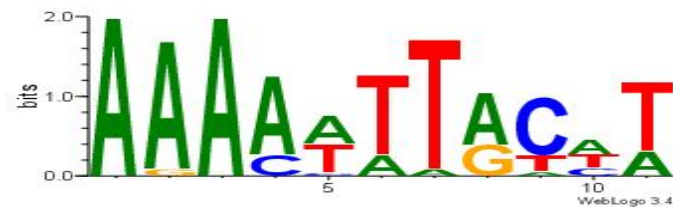


Reverse complement motif      Consensus sequence: TWAAWTTVTGAAAAAHWW



**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

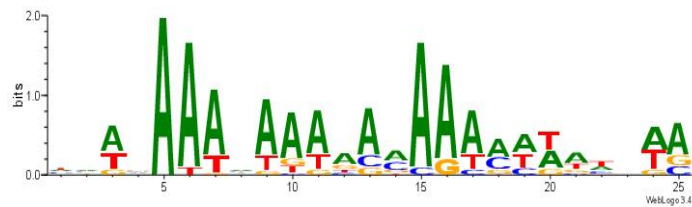


Position number: 14  
 Number of overlap: 11  
 Similarity score: 0.0718583

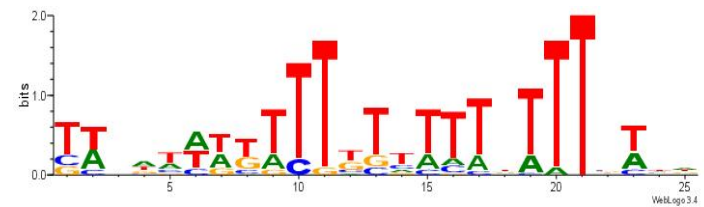
Alignment:

HDWVAAAHAAAAAMAAAMWWWHBWA  
 -----AAAAWTTRCWT-

Original motif Consensus sequence:  
 HDWVAAAHAAAAAMAAAMWWWHBWA



Reverse complement motif Consensus sequence:  
 TWVHWWYTTTTTTTTTTTHTTTVWBH

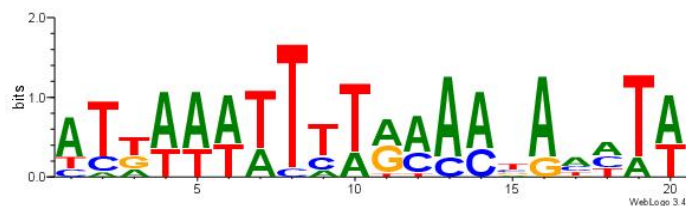


Dataset #: 5  
 Motif ID: 55  
 Motif name: TFM13  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 10  
 Number of overlap: 11  
 Similarity score: 0.0727073

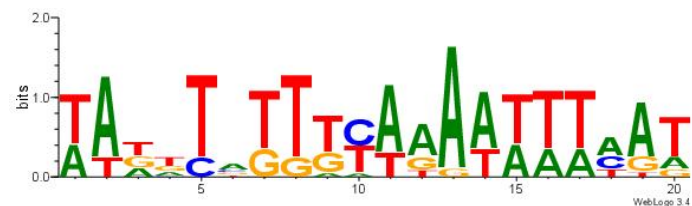
Alignment:

ATKAAWTTTTTRMAABAHHTW  
 AWGKAAWTTTT-----

Original motif      Consensus sequence: ATKAAWTTTTRMAABAHTW



Reverse complement motif      Consensus sequence: WAHHTVTTYKAAAATTRAT

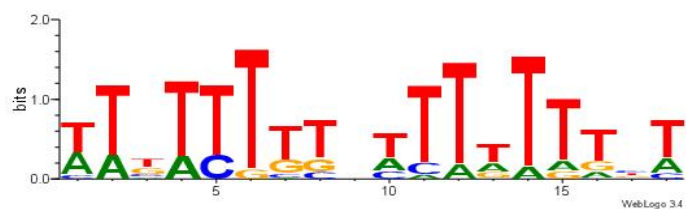


Dataset #: 5  
Motif ID: 52  
Motif name: TFM1  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Original Motif  
Direction: Backward  
Position number: 5  
Number of overlap: 11  
Similarity score: 0.0748297

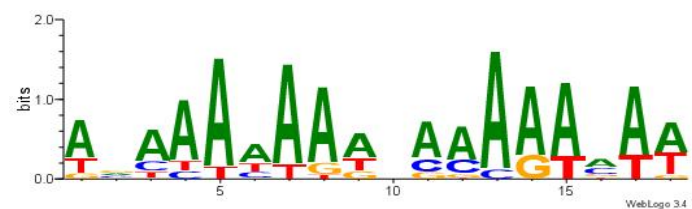
Alignment:

WTKTTTTTHWTTTTTTBT  
---AWGKAAWTTTT-----

Original motif      Consensus sequence: WTKTTTTTHWTTTTTTBT



Reverse complement motif      Consensus sequence: ABAAAAAWHAAAAARAW

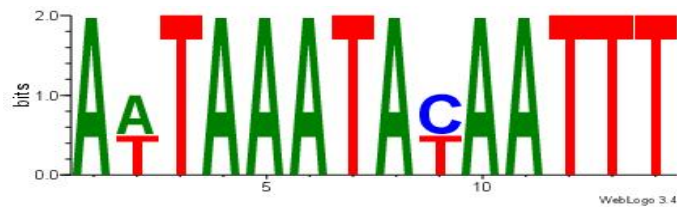


Dataset #: 2  
 Motif ID: 5  
 Motif name: Motif 5  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 4  
 Number of overlap: 11  
 Similarity score: 0.0786484

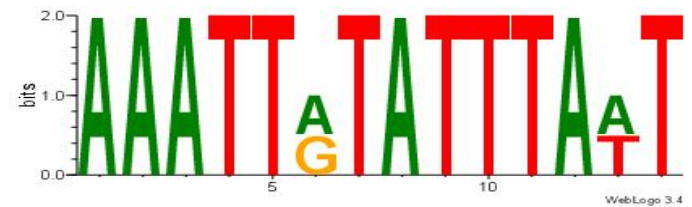
Alignment:

AAATTKTATTTAWT  
 AAAAWTTRCWT---

Original motif      Consensus sequence: AWTAAATAYAATTT



Reverse complement motif      Consensus sequence: AAATTKTATTTAWT



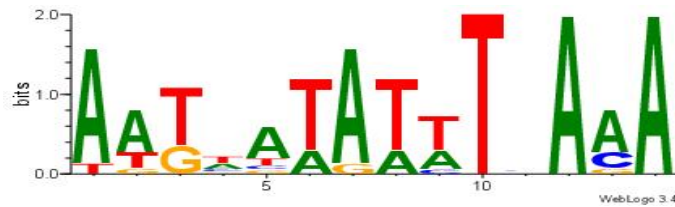
Dataset #: 2  
 Motif ID: 9  
 Motif name: Motif 9  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 4  
 Number of overlap: 11

Similarity score: 0.0820375

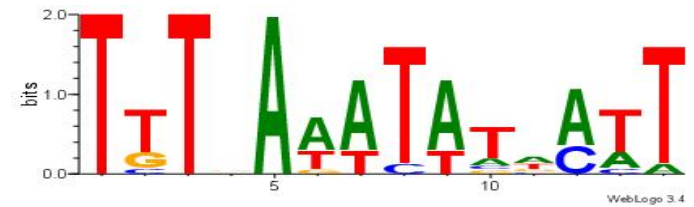
Alignment:

AATHATATWTHAAA  
AWGKAAWTTTT---

Original motif      Consensus sequence: AATHATATWTHAAA

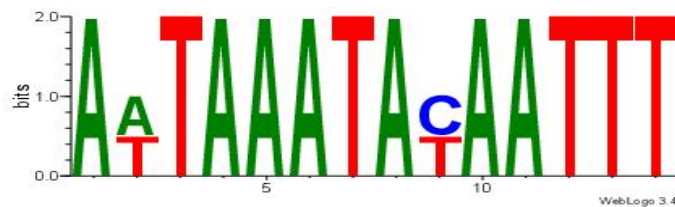


Reverse complement motif      Consensus sequence: TTTDAWATATHAT

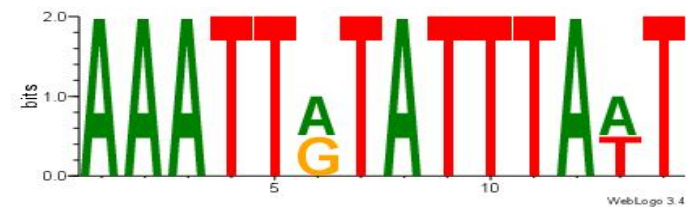


**Dataset #: 2      Motif ID: 5      Motif name: Motif 5**

Original motif      Consensus sequence: AWTAAATAYAATTT



Reverse complement motif      Consensus sequence: AAATTKTATTTAW



**Best Matches for Motif ID 5 (Highest to Lowest)**

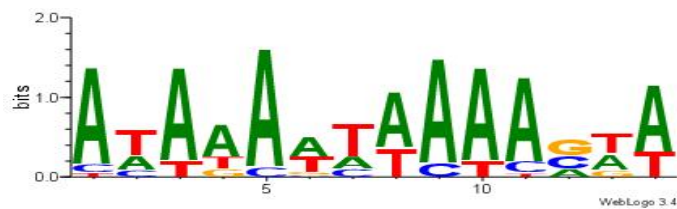
Dataset #:	2
Motif ID:	3
Motif name:	Motif 3
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward

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

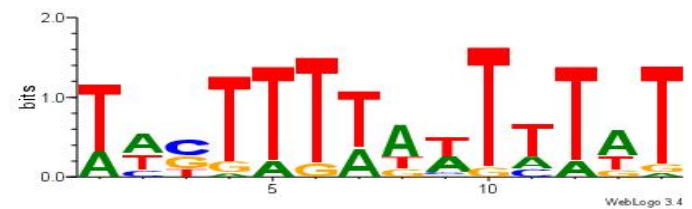
Alignment:

TWSTTTWAWTTTWT  
 AAATTKTATTTAWT

Original motif      Consensus sequence: AWAAAWTWAASWA



Reverse complement motif      Consensus sequence: TWSTTTWAWTTTWT



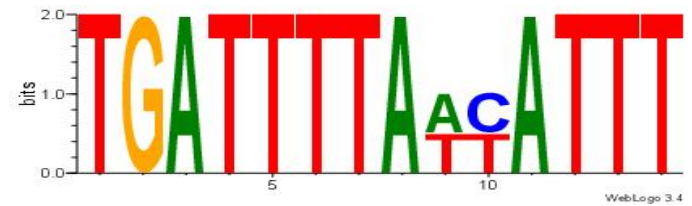
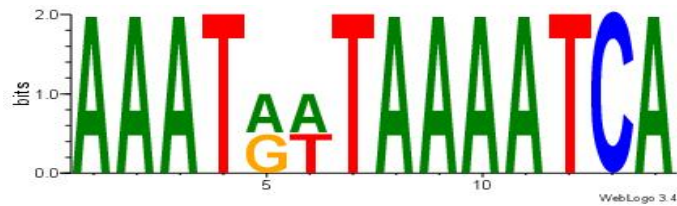
Dataset #: 2  
 Motif ID: 8  
 Motif name: Motif 8  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 14  
 Similarity score: 0.107143

Alignment:

TGATTTTAWKATTT  
 AAATTKTATTTAWT

Original motif      Consensus sequence: AAATRWAAAATCA

Reverse complement motif      Consensus sequence: TGATTTTAWKATTT



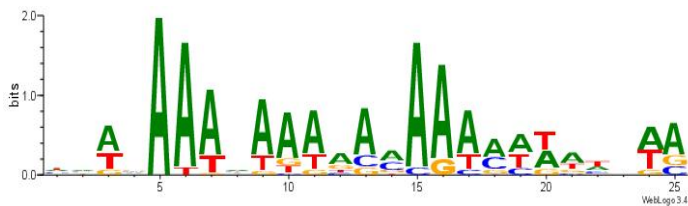
Dataset #: 5  
 Motif ID: 56  
 Motif name: TFM11  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 6  
 Number of overlap: 14  
 Similarity score: 0.109769

Alignment:

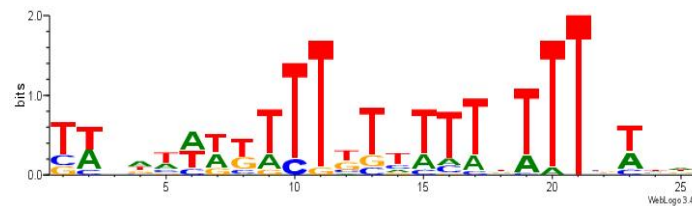
```

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

Original motif    Consensus sequence:  
 HDWVAAAHAAAAAMAAAMWWWHBWA



Reverse complement motif    Consensus sequence:  
 TWVHWWWYTTTYTTTTHTTTVWBH



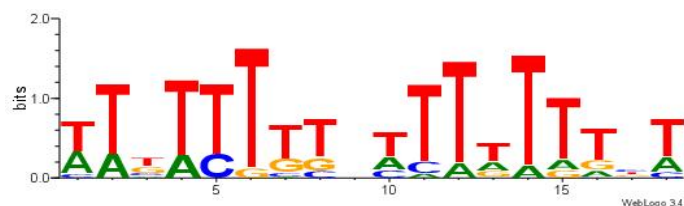
Dataset #: 5

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

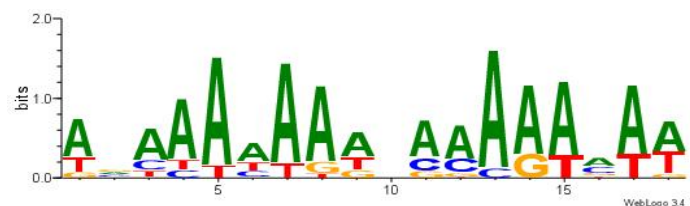
Alignment:

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:

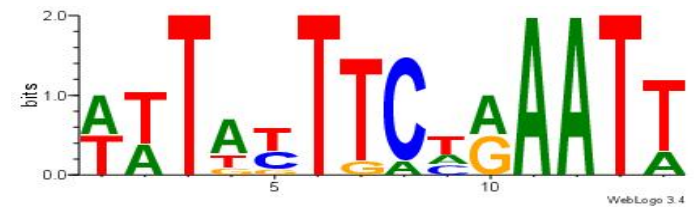
AATTYDGAARTAWW

AAATTKTATTTAWT

Original motif Consensus sequence: AATTYDGAARTAWW



Reverse complement motif Consensus sequence: WWTAKTTCDKAAAT

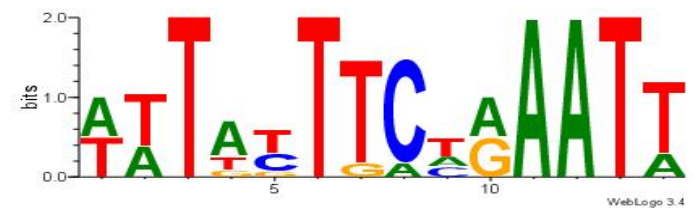


**Dataset #: 2 Motif ID: 6 Motif name: Motif 6**

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

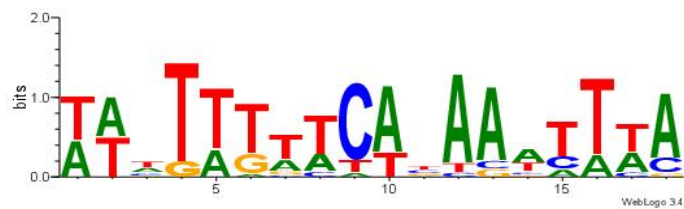


Position number: 4  
Number of overlap: 14  
Similarity score: 0.0325081

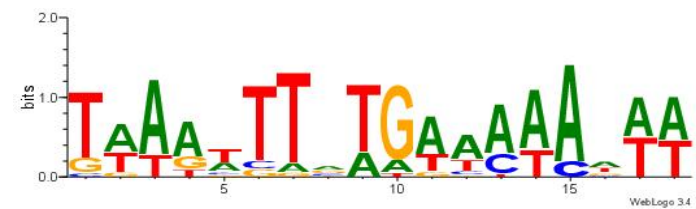
Alignment:

WWHTTTTTTCABAAWTTWA  
-WWTAKTTCDKAATT---

Original motif    Consensus sequence: WWHTTTTTTCABAAWTTWA



Reverse complement motif    Consensus sequence: TWAAWTTVTGAAAAHWW



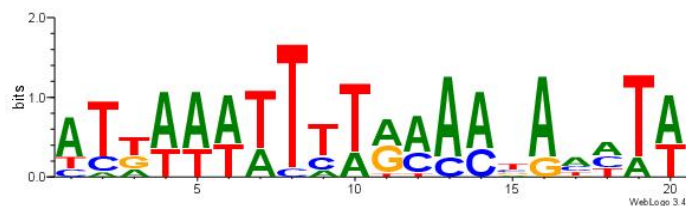
---

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

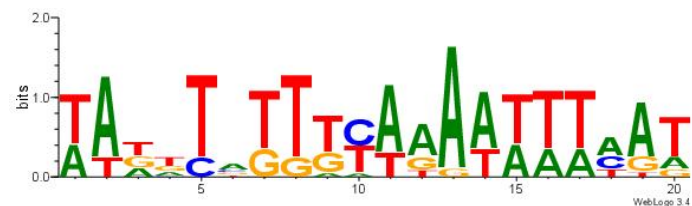
Alignment:

ATKAAWTTTTTRMAABAHHTW  
-----AATTYDGAARTAWW--

Original motif      Consensus sequence: ATKAAWTTTTRMAABAHTW



Reverse complement motif      Consensus sequence: WAHHTVTTYKAAAATTRAT

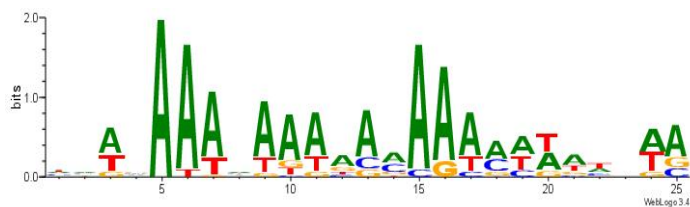


Dataset #: 5  
Motif ID: 56  
Motif name: TFM11  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Reverse Complement  
Direction: Backward  
Position number: 9  
Number of overlap: 14  
Similarity score: 0.0626838

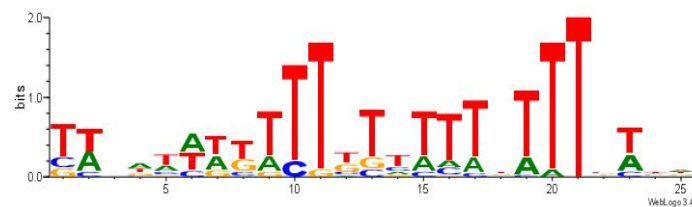
Alignment:

TWVHWWWYTTTTYTTTTTHTTTVWBH  
---WWTAKTTCDKAATT-----

Original motif      Consensus sequence: HDWVAAAHAAAAAMAAAMWWWHBWA



Reverse complement motif      Consensus sequence: TWVHWWWYTTTTYTTTTTHTTTVWBH

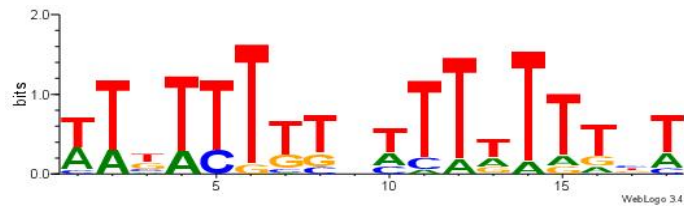


Dataset #: 5  
 Motif ID: 52  
 Motif name: TFM1  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 2  
 Number of overlap: 14  
 Similarity score: 0.0667239

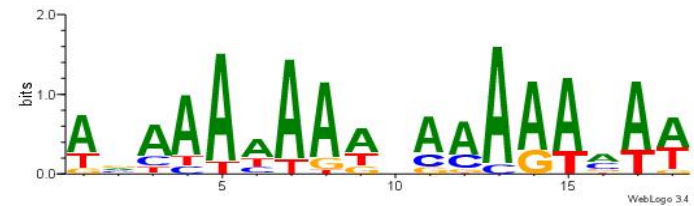
Alignment:

WKTTTTTHWTTTTTBT  
 -WWTAKTTCDKAATT---

Original motif      Consensus sequence: WKTTTTTHWTTTTTBT



Reverse complement motif      Consensus sequence: ABAAAAAWHAAAAARAW

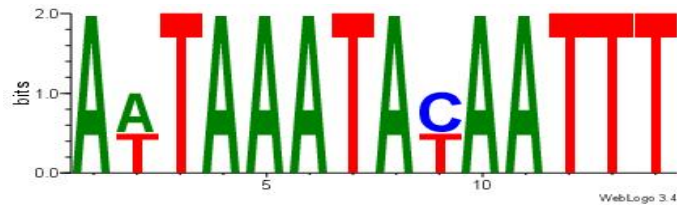


Dataset #: 2  
 Motif ID: 5  
 Motif name: Motif 5  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 1

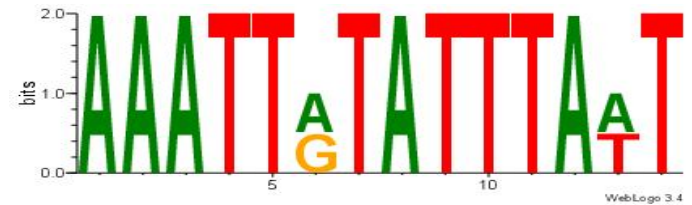
Number of overlap: 14  
 Similarity score: 0.0741071

Alignment:  
 AWTAAATAYAATTT  
 WWTAKTTCDKAATT

Original motif      Consensus sequence: AWTAAATAYAATTT

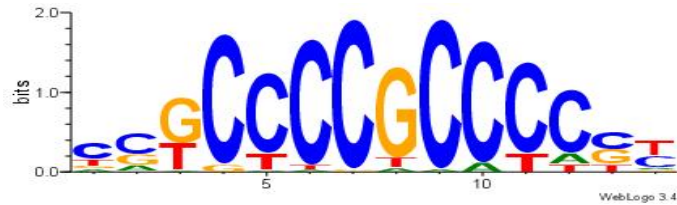


Reverse complement motif      Consensus sequence: AAATTKTATTTAW

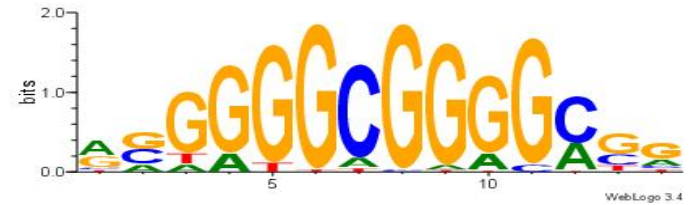


**Dataset #: 2      Motif ID: 7      Motif name: Motif 7**

Original motif      Consensus sequence: CSKCCCCGCCCSY



Reverse complement motif      Consensus sequence: MSGGGGCGGGY



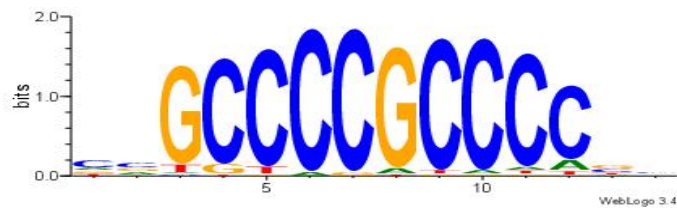
**Best Matches for Motif ID 7 (Highest to Lowest)**

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

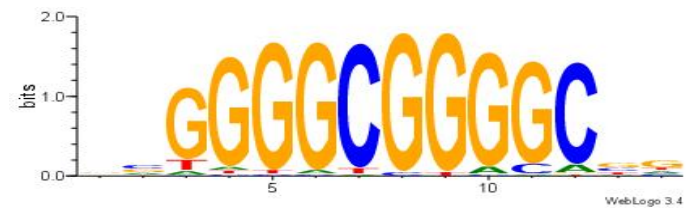
Direction: Forward  
Position number: 1  
Number of overlap: 14  
Similarity score: 0

Alignment:  
HVGCCCGCCCCBB  
CSKCCCGCCCCSY

Original motif    Consensus sequence: HVGCCCGCCCCBB



Reverse complement motif    Consensus sequence: BBGGGGCGGGGC

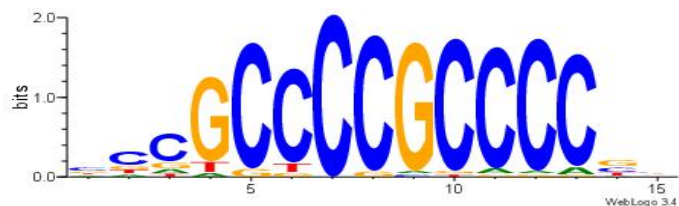


---

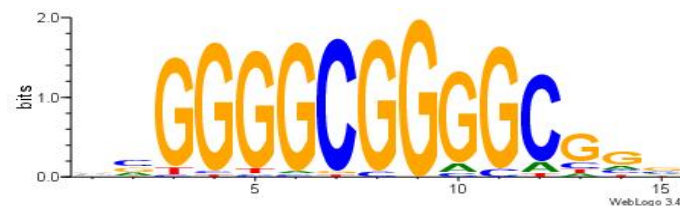
Dataset #: 4  
Motif ID: 38  
Motif name: cccGCCCCGCCCCsb  
Matching format of first motif: Original Motif  
Matching format of second motif: Original Motif  
Direction: Backward  
Position number: 1  
Number of overlap: 14  
Similarity score: 0.0012818

Alignment:  
BCCGCCCCGCCCCBB  
-CSKCCCGCCCCSY

Original motif      Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif      Consensus sequence: BBGGGGCGGGGCGGB

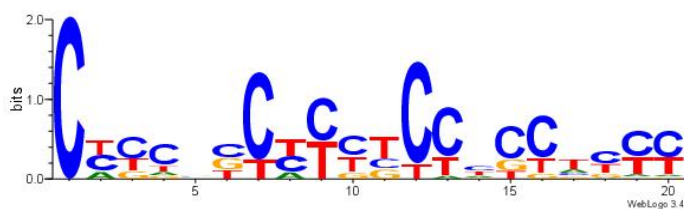


Dataset #: 5  
Motif ID: 54  
Motif name: TFM12  
Matching format of first motif: Original Motif  
Matching format of second motif: Original Motif  
Direction: Forward  
Position number: 4  
Number of overlap: 14  
Similarity score: 0.0537802

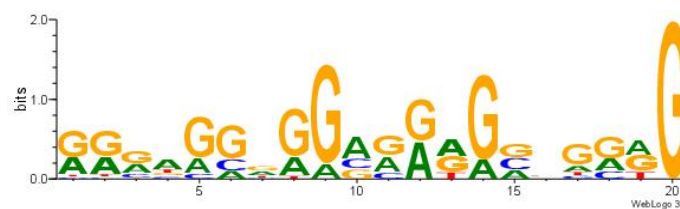
Alignment:

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

Original motif      Consensus sequence: CYYCBBBCYYYTCCHCCTYYY



Reverse complement motif      Consensus sequence: KKKAGGDGGAKKMGBBGKMG

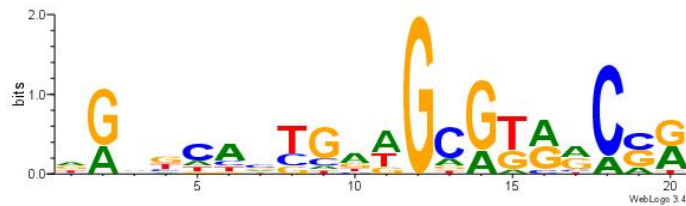


Dataset #: 3  
 Motif ID: 31  
 Motif name: Pax5  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 7  
 Number of overlap: 14  
 Similarity score: 0.0662825

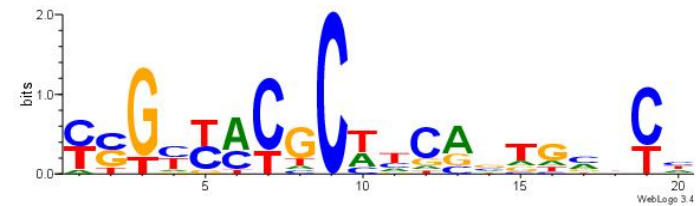
Alignment:

DGVBCABTGDWGCGRRCR  
 -----MSGGGGCGGGYSG

Original motif      Consensus sequence: DGVBCABTGDWGCGRRCR



Reverse complement motif      Consensus sequence: MSGKKRCGCWDCABTGBBCD

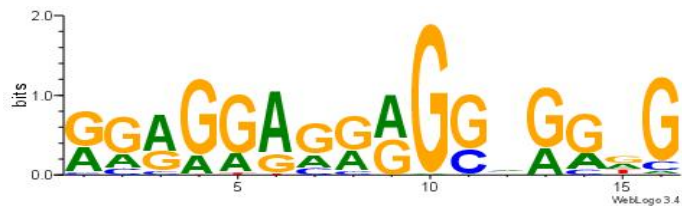


Dataset #: 5  
 Motif ID: 51  
 Motif name: TFM2  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 1

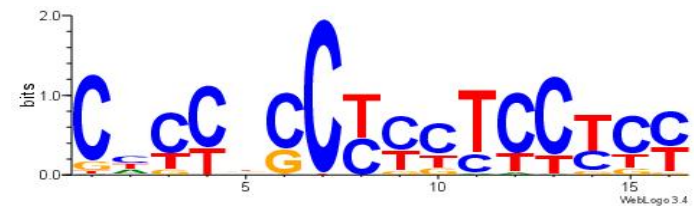
Number of overlap: 14  
 Similarity score: 0.0758609

Alignment:  
 CHCCBCKMCTCCKCM  
 CSKCCCCGCCCSY--

Original motif    Consensus sequence: RGRGGAGRRGGHGGDG

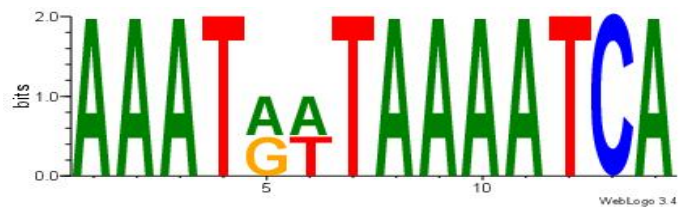


Reverse complement motif    Consensus sequence:  
 CHCCBCKMCTCCKCM

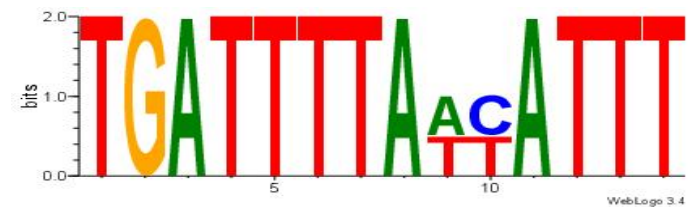


**Dataset #: 2      Motif ID: 8      Motif name: Motif 8**

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

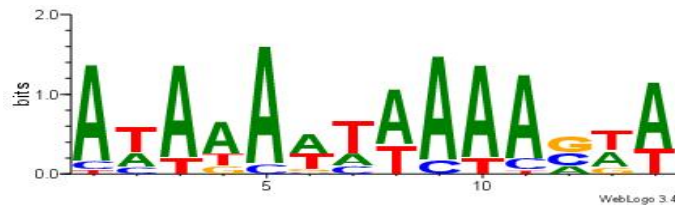


Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 14  
 Similarity score: 0.0961539

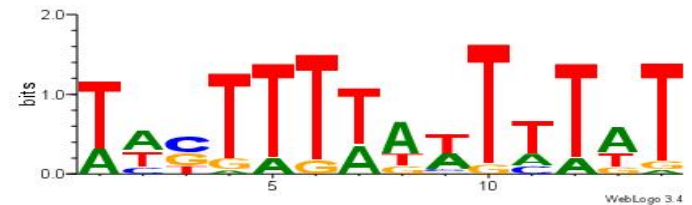
Alignment:

TWSTTTWAWTTTWT  
 TGATTTTAWKATTT

Original motif    Consensus sequence: AWAAAWTWAAASWA



Reverse complement motif    Consensus sequence: TWSTTTWAWTTTWT

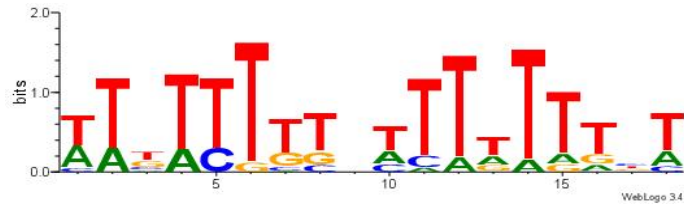


Dataset #: 5  
 Motif ID: 52  
 Motif name: TFM1  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 4  
 Number of overlap: 14  
 Similarity score: 0.10348

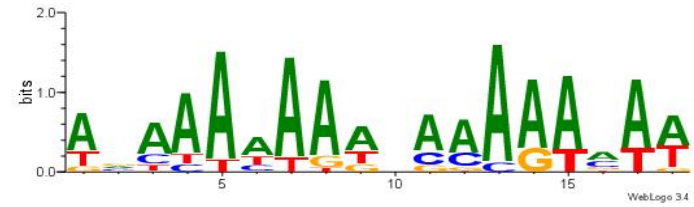
Alignment:

WKTTTTTHWTTTTTBT  
 -TGATTTTAWKATTT---

Original motif      Consensus sequence: WKTTTTTHWTTTTTBT



Reverse complement motif      Consensus sequence:  
 ABAAAAAWHAAAAARAW

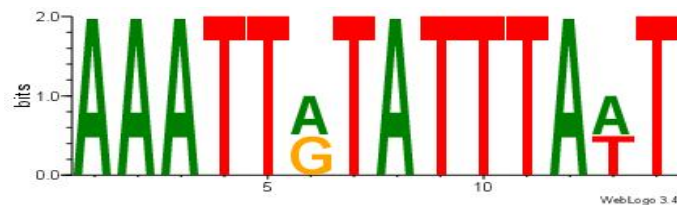
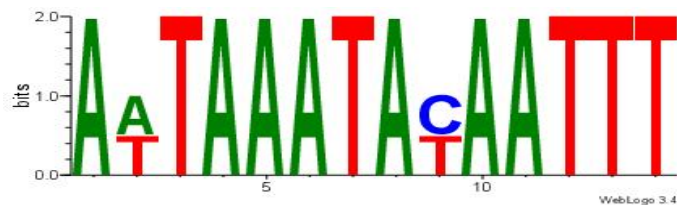


Dataset #: 2  
 Motif ID: 5  
 Motif name: Motif 5  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 14  
 Similarity score: 0.107143

Alignment:  
 AAATTKTATTTAWT  
 TGATTTTAWKATTT

Original motif      Consensus sequence: AWTAAATAYAATTT

Reverse complement motif      Consensus sequence: AAATTKTATTTAWT



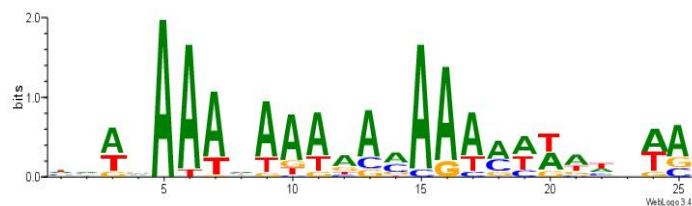
Dataset #: 5  
 Motif ID: 56  
 Motif name: TFM11  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 7  
 Number of overlap: 14  
 Similarity score: 0.111345

Alignment:

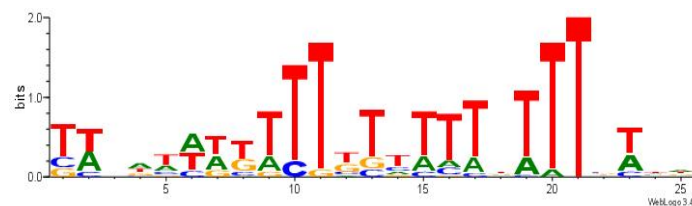
```

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

Original motif    Consensus sequence:  
 HDWVAAAHAAAAAMAAAMWWWHBWA



Reverse complement motif    Consensus sequence:  
 TWVHWWYTTTTTTTTTTTHTTTVWBH



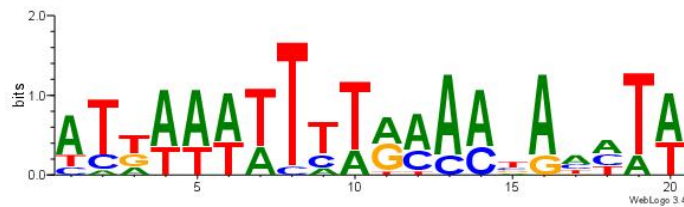
Dataset #: 5

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

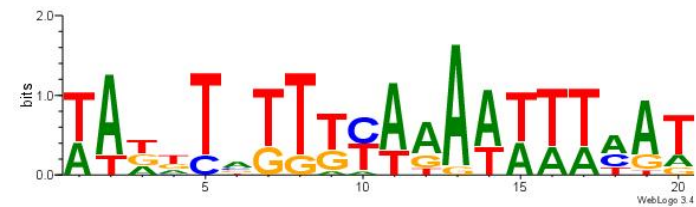
**Alignment:**

WAHHTVTTYKAAAATTRAT  
 ---TGATTTTAWKATTT---

Original motif      Consensus sequence: ATKAAWTTTTRMAABAHTW

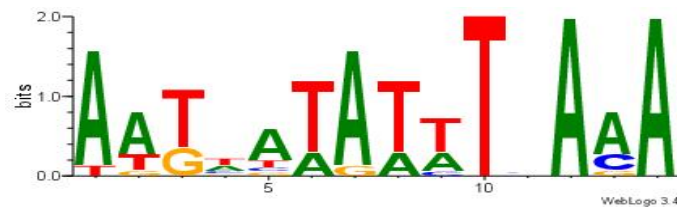


Reverse complement motif      Consensus sequence: WAHHTVTTYKAAAATTRAT

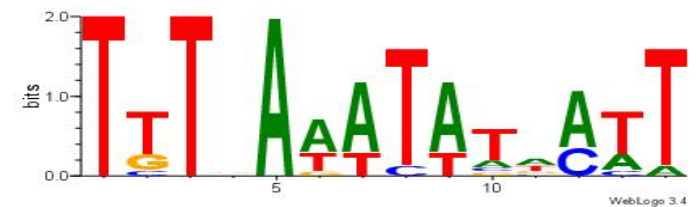


**Dataset #: 2      Motif ID: 9      Motif name: Motif 9**

Original motif      Consensus sequence: AATHATATWTHAAA



Reverse complement motif      Consensus sequence: TTTDAWATATHAT



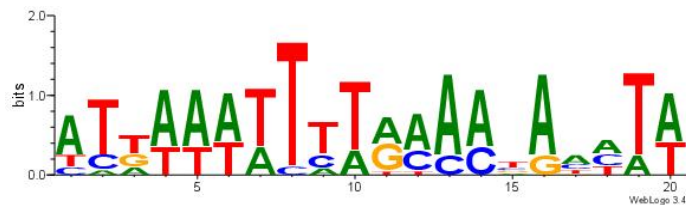
## Best Matches for Motif ID 9 (Highest to Lowest)

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

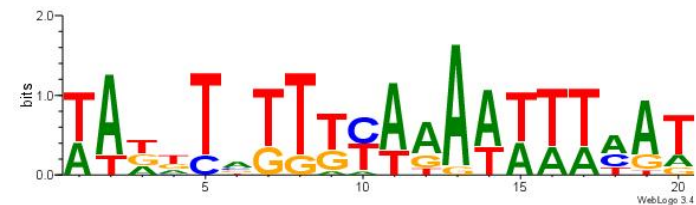
### Alignment:

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

Original motif      Consensus sequence: ATKAAWTTTTRMAABAHTW



Reverse complement motif      Consensus sequence:  
WAHHTVTTYKAAAATTRAT



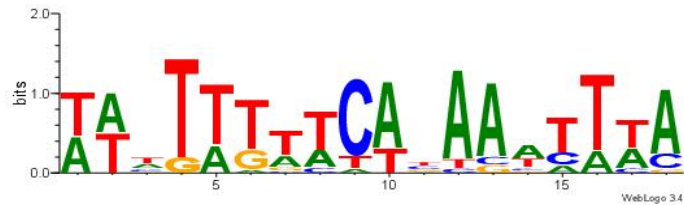
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Dataset #: 5  
Motif ID: 53  
Motif name: TFM3  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Original Motif

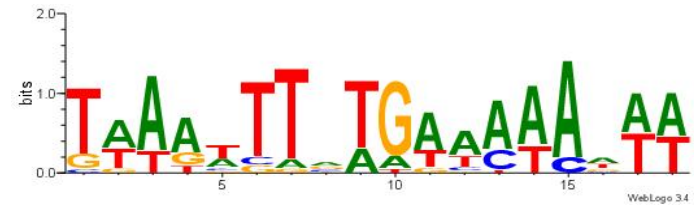
Direction: Backward  
 Position number: 2  
 Number of overlap: 14  
 Similarity score: 0.0486562

Alignment:  
 WWHTTTTTTCABAAWTTWA  
 ---TTTDAWATATHATT-

Original motif    Consensus sequence: WWHTTTTTTCABAAWTTWA



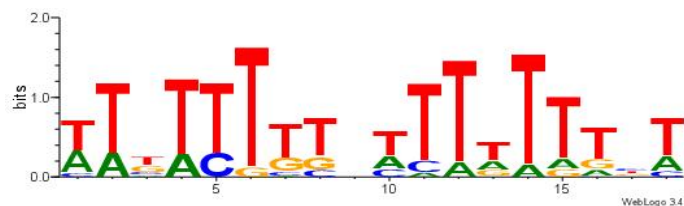
Reverse complement motif    Consensus sequence: TWAAWTTVTGAAAAHWW



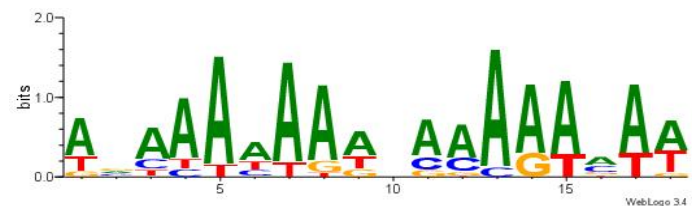
Dataset #: 5  
 Motif ID: 52  
 Motif name: TFM1  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 4  
 Number of overlap: 14  
 Similarity score: 0.0528083

Alignment:  
 WKTTTTTTHWTTTTTTBT  
 ---TTTDAWATATHATT-

Original motif      Consensus sequence: WTKTTTTTHWTTTTTBT



Reverse complement motif      Consensus sequence: ABAAAAAWHAAAAARAW

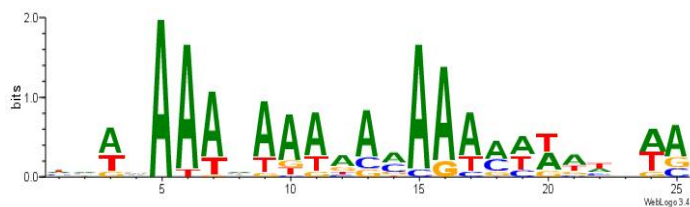


Dataset #: 5  
Motif ID: 56  
Motif name: TFM11  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Original Motif  
Direction: Forward  
Position number: 1  
Number of overlap: 14  
Similarity score: 0.054155

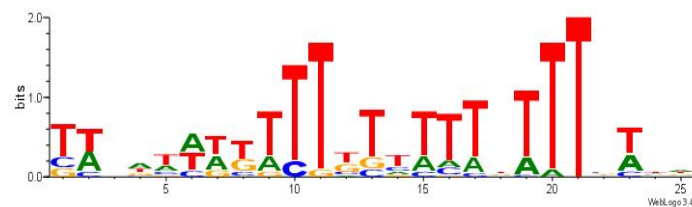
Alignment:

HDWVAAAHAAAAAMAAAMWWWHBWA  
TTTDAWATATHATT-----

Original motif      Consensus sequence: HDWVAAAHAAAAAMAAAMWWWHBWA



Reverse complement motif      Consensus sequence: TWVHWWWYTTTTYTTTTTHTTTTVWBH

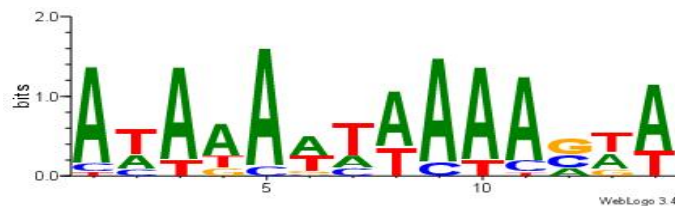


Dataset #: 2  
 Motif ID: 3  
 Motif name: Motif 3  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 14  
 Similarity score: 0.0675748

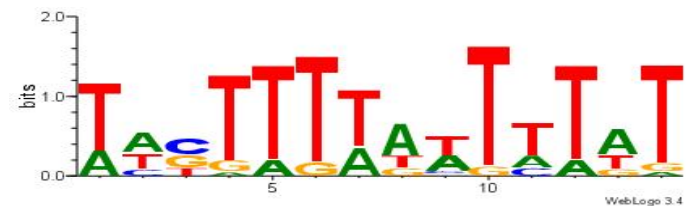
Alignment:

TWSTTTWAWTTTWT  
 AATHATATWTHAAA

Original motif      Consensus sequence: AWAAAWTWAASWA

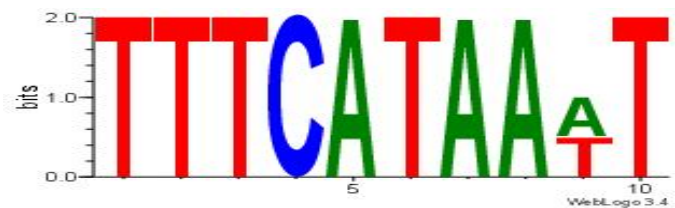


Reverse complement motif      Consensus sequence: TWSTTTWAWTTTWT

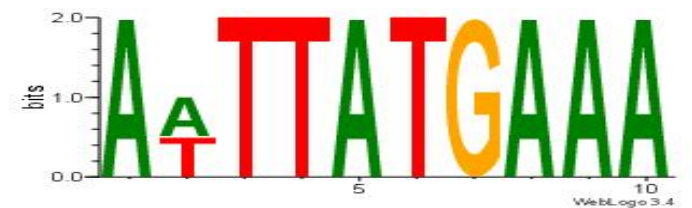


**Dataset #: 2      Motif ID: 10      Motif name: Motif 10**

Original motif      Consensus sequence: TTCATAAWT



Reverse complement motif      Consensus sequence: AWTTATGAAA





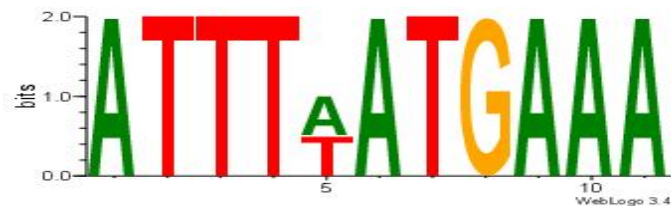
## Best Matches for Motif ID 10 (Highest to Lowest)

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

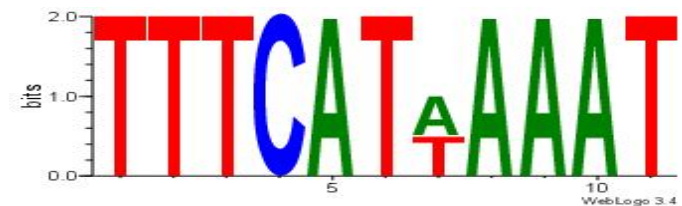
### Alignment:

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

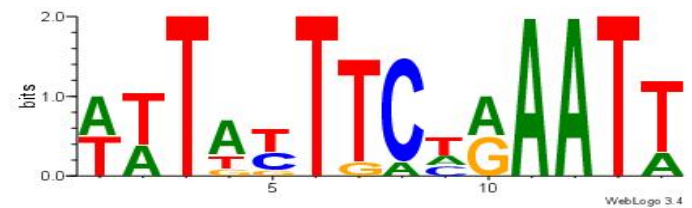
**Alignment:**

AATTYDGAARTAWW  
 ----AWTTATGAAA

Original motif      Consensus sequence: AATTYDGAARTAWW



Reverse complement motif      Consensus sequence: WWTAKTTCDKAAT

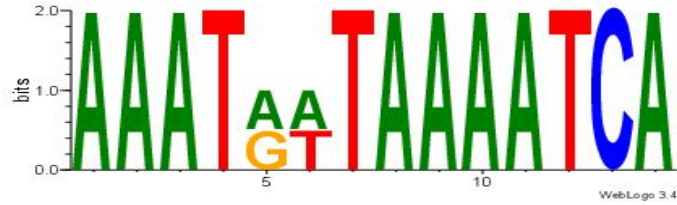


Dataset #: 2  
 Motif ID: 8  
 Motif name: Motif 8  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 4  
 Number of overlap: 10  
 Similarity score: 0.04375

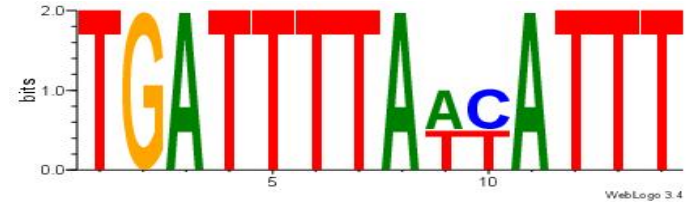
**Alignment:**

TGATTTTAWKATTT  
 -TTTCATAAWT---

Original motif      Consensus sequence: AAATRWTAATCA



Reverse complement motif      Consensus sequence: TGATTTAWKATT

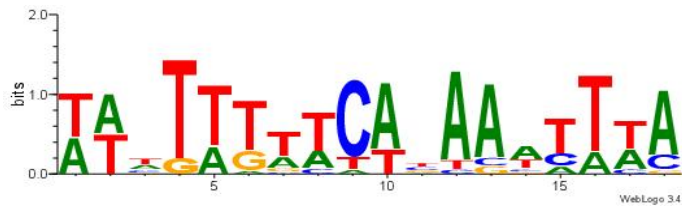


Dataset #: 5  
 Motif ID: 53  
 Motif name: TFM3  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 6  
 Number of overlap: 10  
 Similarity score: 0.0448864

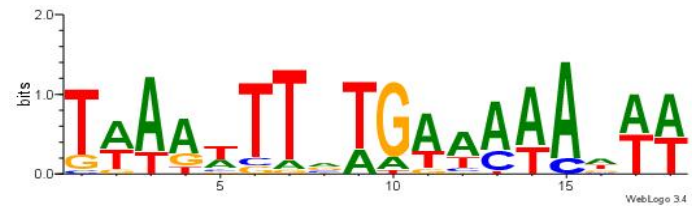
Alignment:

TWAAWTTVTGAAAAHWW  
 ---AWTTATGAAA-----

Original motif      Consensus sequence: WWHTTTTTCABAATTWA



Reverse complement motif      Consensus sequence: TWAAWTTVTGAAAAHWW

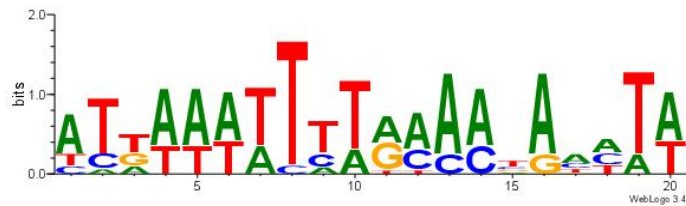


Dataset #: 5  
 Motif ID: 55  
 Motif name: TFM13  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 5  
 Number of overlap: 10  
 Similarity score: 0.0545833

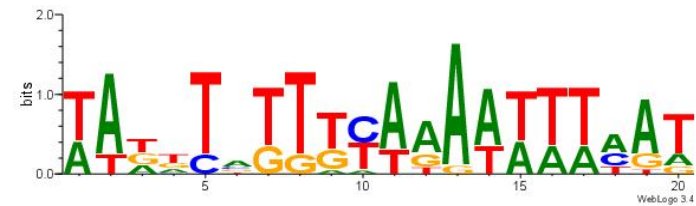
Alignment:

ATKAAWTTTTRMAABAHTW  
 ----AWTTATGAAA-----

Original motif      Consensus sequence: ATKAAWTTTTRMAABAHTW



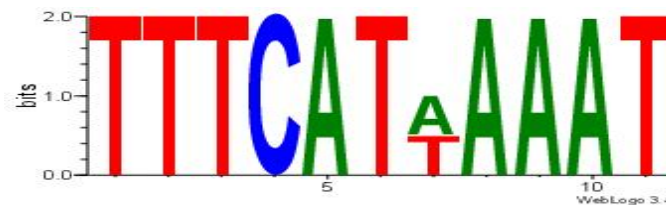
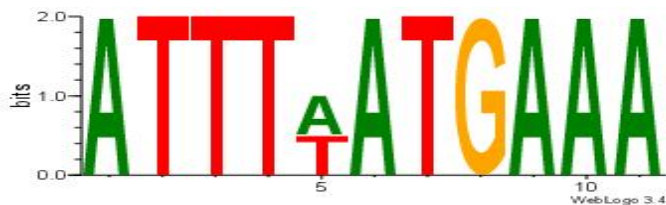
Reverse complement motif      Consensus sequence: WAHHTVTTYKAAAATTRAT



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

Original motif      Consensus sequence: ATTTWATGAAA

Reverse complement motif      Consensus sequence: TTTCATWAAAT

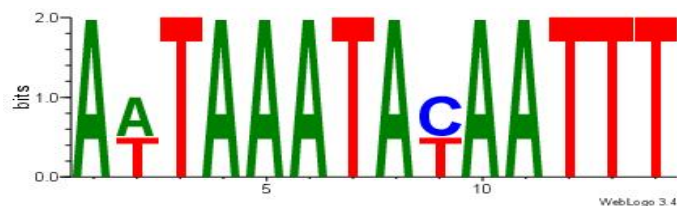


**Best Matches for Motif ID 11 (Highest to Lowest)**

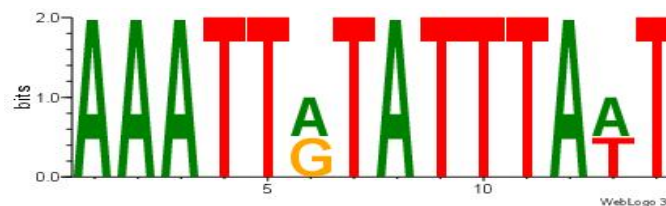
Dataset #: 2  
 Motif ID: 5  
 Motif name: Motif 5  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 4  
 Number of overlap: 11  
 Similarity score: 0.0795455

Alignment:  
 AAATTKTATTTAWT  
 ---TTTCATWAAAT

Original motif      Consensus sequence: AWTAAATAYAATTT



Reverse complement motif      Consensus sequence: AAATTKTATTTAWT



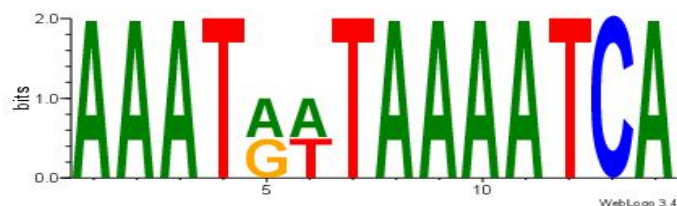
Dataset #: 2

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

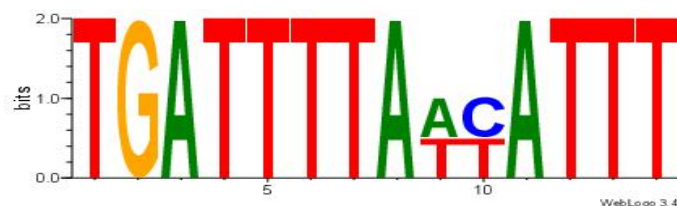
Alignment:

AAATRWTA~~AA~~ATCA  
 --TTTCATWAAAT--

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



Reverse complement motif      Consensus sequence: TGATTTTAWKATT

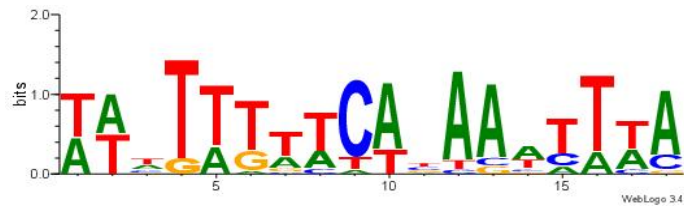


Dataset #: 5  
 Motif ID: 53  
 Motif name: TFM3  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 6  
 Number of overlap: 11  
 Similarity score: 0.0991736

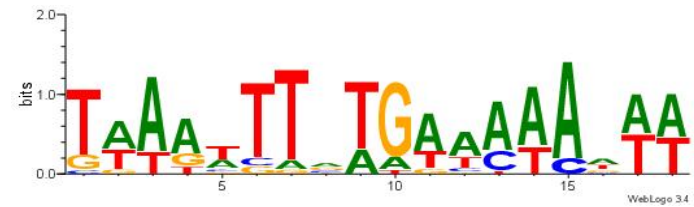
Alignment:

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

Original motif      Consensus sequence: WWHTTTTTTCABAAWTTWA



Reverse complement motif      Consensus sequence:  
TAAWTTTGTGAAAAHWW



---

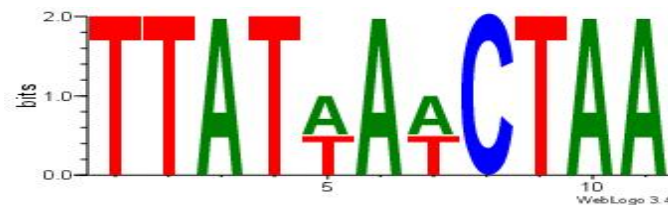
Dataset #:	2
Motif ID:	18
Motif name:	Motif 18
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	11
Similarity score:	0.102273

Alignment:

```
TTATWAWCTAA  
ATTTWATGAAA
```

Original motif      Consensus sequence: TTAGWTWATAA

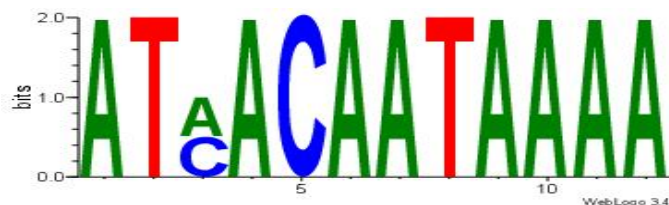
Reverse complement motif      Consensus sequence: TTATWAWCTAA



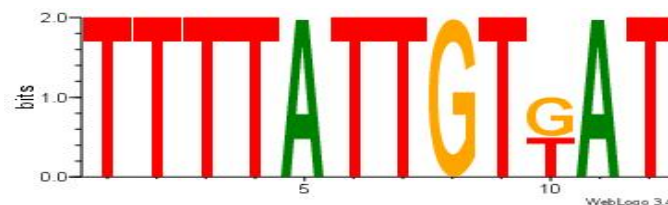
Dataset #: 2  
 Motif ID: 15  
 Motif name: Motif 15  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 11  
 Similarity score: 0.102273

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



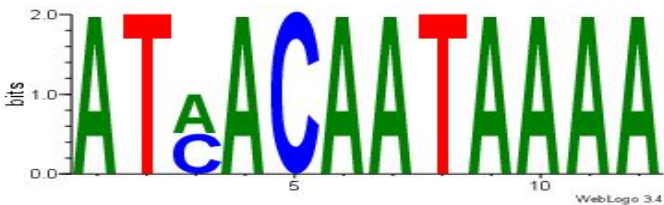
### Best Matches for Motif ID 12 (Highest to Lowest)

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

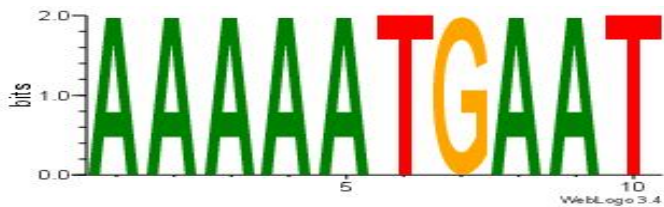


Dataset #: 2  
 Motif ID: 17  
 Motif name: Motif 17  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 2  
 Number of overlap: 8  
 Similarity score: 0.0625

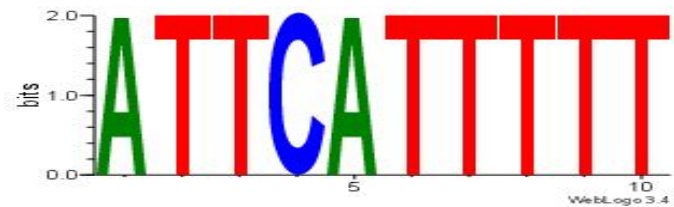
Alignment:

AAAAATGAAT  
 -AAAACAAA-

Original motif      Consensus sequence: AAAAATGAAT



Reverse complement motif      Consensus sequence: ATTCA TTTT



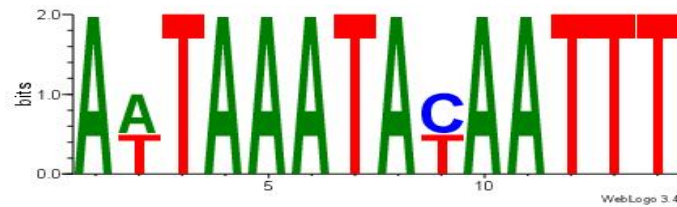
Dataset #: 2  
 Motif ID: 5  
 Motif name: Motif 5  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 3  
 Number of overlap: 8

Similarity score: 0.078125

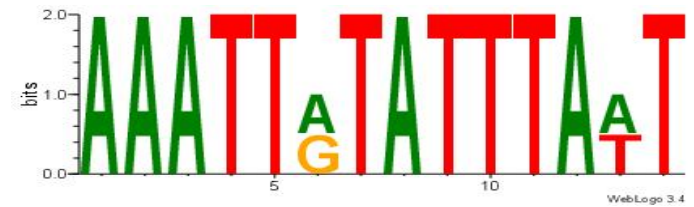
Alignment:

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

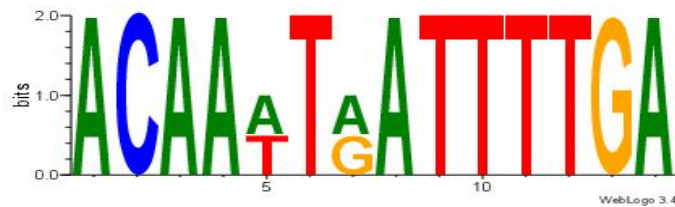
Reverse complement motif      Consensus sequence: TTATTTWT



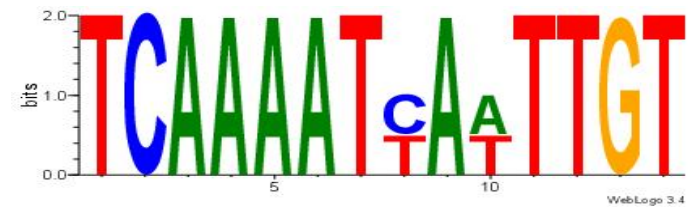
Dataset #: 2  
 Motif ID: 16  
 Motif name: Motif 16  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 5  
 Number of overlap: 8  
 Similarity score: 0.078125

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

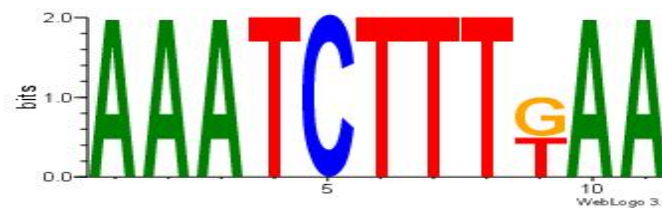
Alignment:

AAATCTTTYAA  
AAATCTTT---

Original motif    Consensus sequence: TTMAAGATTT



Reverse complement motif    Consensus sequence: AAATCTTTYAA

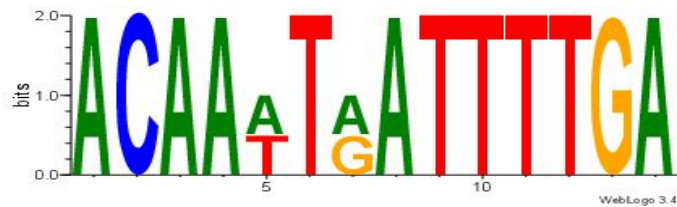


Dataset #: 2  
 Motif ID: 16  
 Motif name: Motif 16  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 5  
 Number of overlap: 8  
 Similarity score: 0.0625

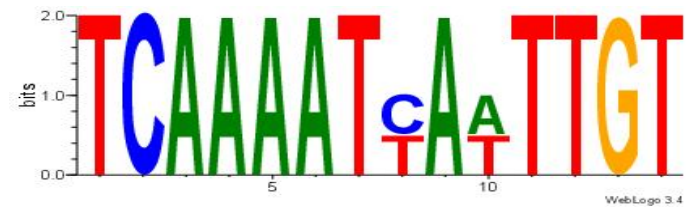
Alignment:

TCAAAATKAWTTGT  
 ----AAAGATTT--

Original motif      Consensus sequence: ACAAWTRATTTTGA



Reverse complement motif      Consensus sequence: TCAAAATKAWTTG



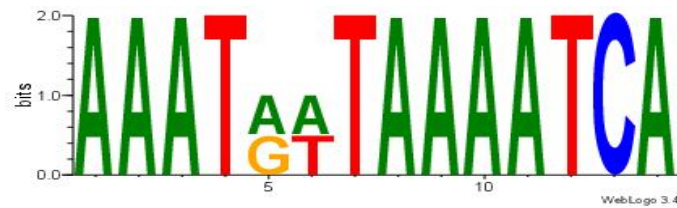
Dataset #: 2  
 Motif ID: 8  
 Motif name: Motif 8  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 8

Similarity score: 0.0625

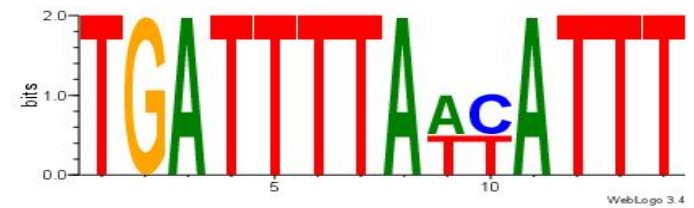
Alignment:

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

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



Reverse complement motif      Consensus sequence: TGATTTAWKATT



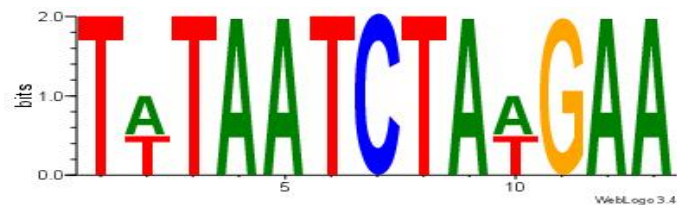
Dataset #: 2  
Motif ID: 19  
Motif name: Motif 19  
Matching format of first motif: Original Motif  
Matching format of second motif: Original Motif  
Direction: Backward  
Position number: 3  
Number of overlap: 8  
Similarity score: 0.078125

Alignment:

TTCWTAGATTAWA  
---AAAGATTT--

Original motif      Consensus sequence: TTCWTAGATTAWA

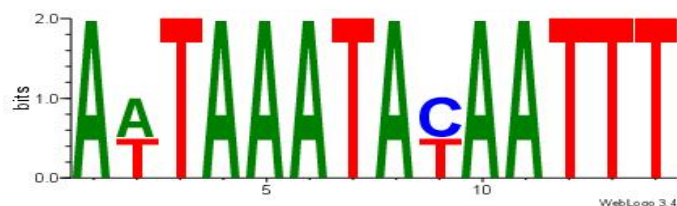
Reverse complement motif      Consensus sequence: TWTAATCTAWGAA



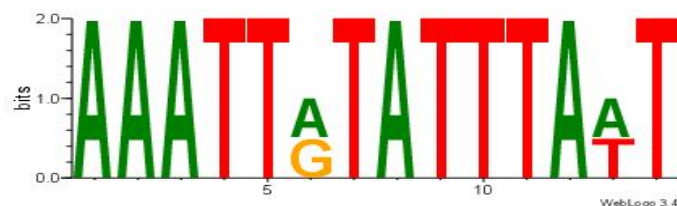
Dataset #: 2  
 Motif ID: 5  
 Motif name: Motif 5  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 8  
 Similarity score: 0.078125

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

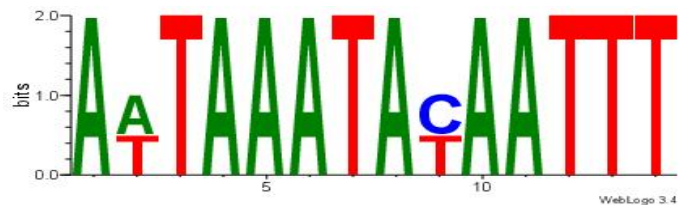


**Best Matches for Motif ID 14 (Highest to Lowest)**

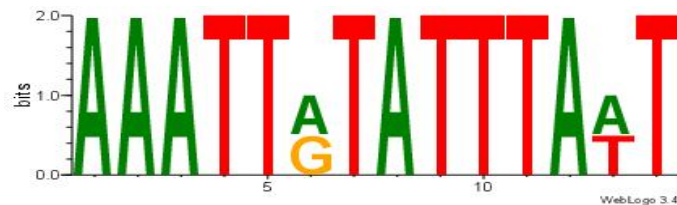
Dataset #: 2  
 Motif ID: 5  
 Motif name: Motif 5  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 6  
 Number of overlap: 8  
 Similarity score: 0.046875

Alignment:  
 AAATTKTATTTAWT  
 -----TTATTTWT-

Original motif      Consensus sequence: AWTAAATAYAATTT



Reverse complement motif      Consensus sequence: AAATTKTATTTAW

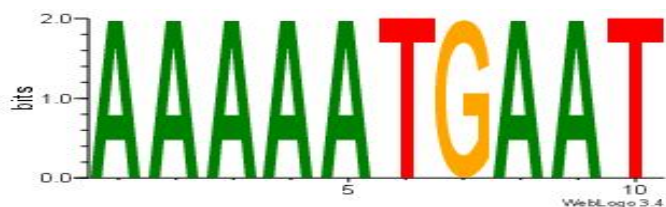


Dataset #: 2  
 Motif ID: 17  
 Motif name: Motif 17  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 8  
 Similarity score: 0.046875

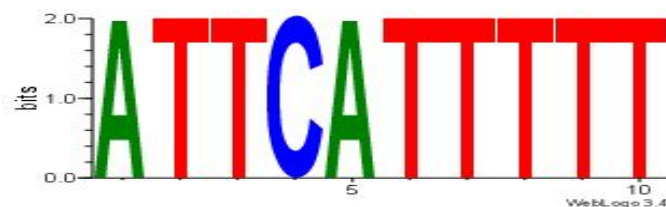
Alignment:

AAAAATGAAT  
 AWAAATAA--

Original motif      Consensus sequence: AAAAATGAAT



Reverse complement motif      Consensus sequence: ATTCA TTTT



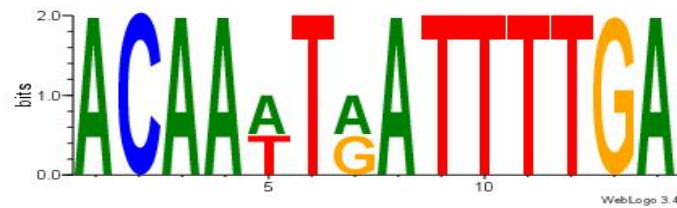
Dataset #: 2  
 Motif ID: 16  
 Motif name: Motif 16  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 8

Similarity score: 0.0625

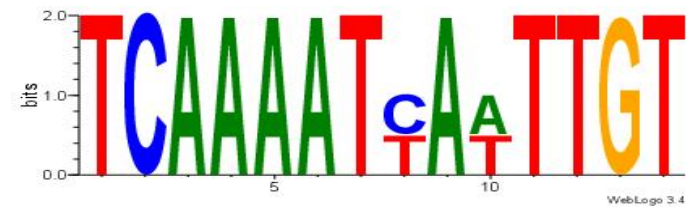
Alignment:

TCAAAATKAWTTGT  
-----TTATTTWT

Original motif      Consensus sequence: ACAAWTRATTTTGA



Reverse complement motif      Consensus sequence: TCAAAATKAWTTG



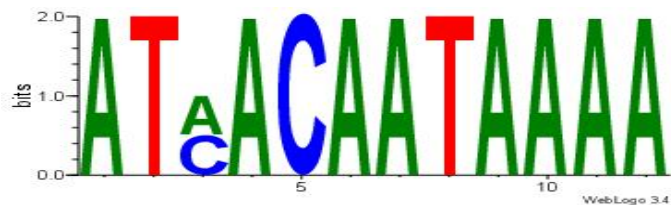
Dataset #: 2  
Motif ID: 15  
Motif name: Motif 15  
Matching format of first motif: Original Motif  
Matching format of second motif: Original Motif  
Direction: Backward  
Position number: 3  
Number of overlap: 8  
Similarity score: 0.0625

Alignment:

ATMACAATAAAA  
--AWAAATAA--

Original motif      Consensus sequence: ATMACAATAAAA

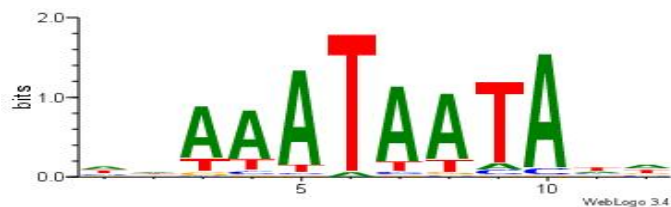
Reverse complement motif      Consensus sequence: TTTTATTGTYAT



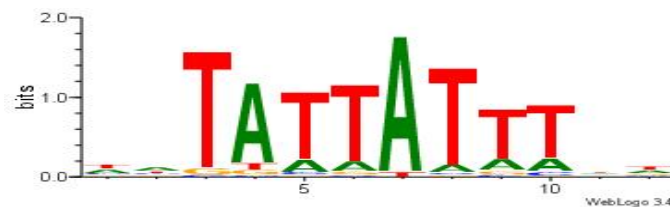
Dataset #: 4  
 Motif ID: 41  
 Motif name: wwAAATAATAtw  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 5  
 Number of overlap: 8  
 Similarity score: 0.0636574

Alignment:  
 HDAAATAATADD  
 AWAAATAA----

Original motif    Consensus sequence: HDAAATAATADD

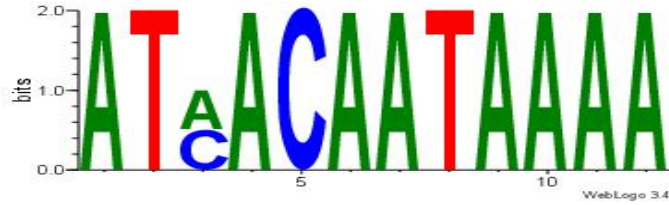


Reverse complement motif    Consensus sequence: DDTATTATTTDH

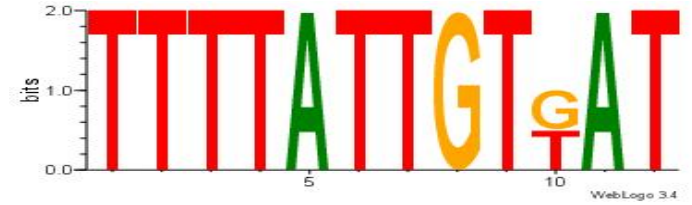


**Dataset #: 2      Motif ID: 15      Motif name: Motif 15**

Original motif      Consensus sequence: ATMACAATAAAA



Reverse complement motif      Consensus sequence: TTTTATTGTYAT



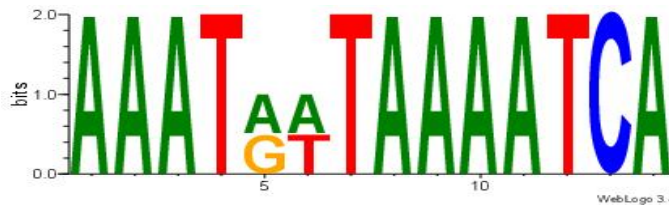
### Best Matches for Motif ID 15 (Highest to Lowest)

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

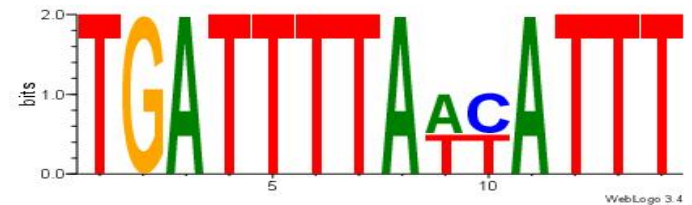
Alignment:

```
AAATRWTAATAATCA
--ATMACAATAAAA
```

Original motif      Consensus sequence: AAATRWTAATAATCA



Reverse complement motif      Consensus sequence: TGATTTAWKATT

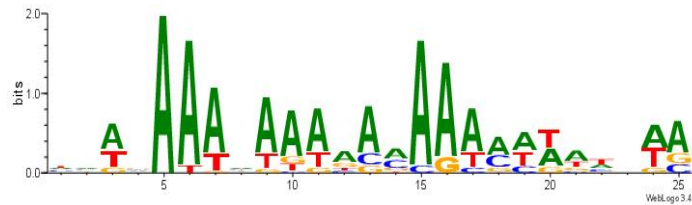


Dataset #: 5  
 Motif ID: 56  
 Motif name: TFM11  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 6  
 Number of overlap: 12  
 Similarity score: 0.109681

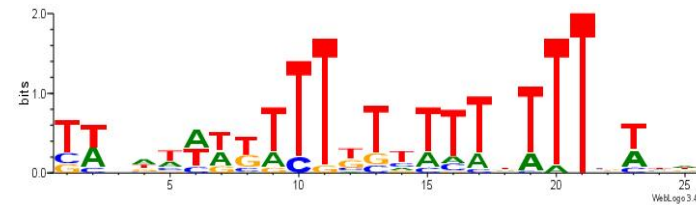
Alignment:

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

Original motif    Consensus sequence:  
 HDWVAAAHAAAAAMAAAMWWWHBWA



Reverse complement motif    Consensus sequence:  
 TWVHWWWYTTTYTTTTHTTTVWBH

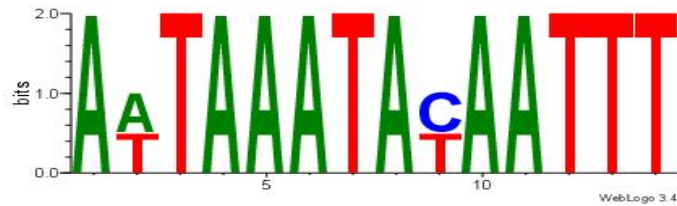


Dataset #: 2  
 Motif ID: 5  
 Motif name: Motif 5  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 2

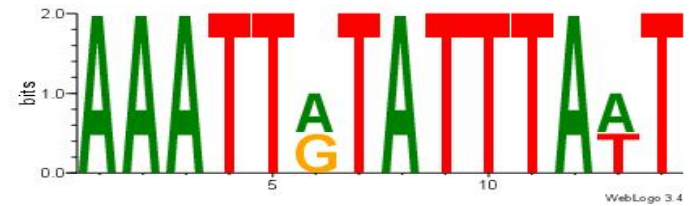
Number of overlap: 12  
 Similarity score: 0.114583

Alignment:  
 AWTAAATAYAATTT  
 -ATMACAATAAAA-

Original motif      Consensus sequence: AWTAAATAYAATTT



Reverse complement motif      Consensus sequence: AAATTKTATTTAW

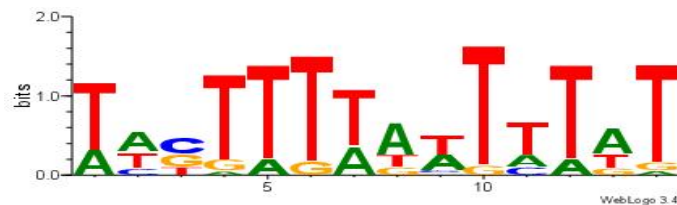
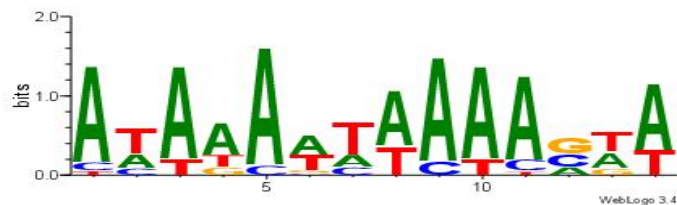


Dataset #: 2  
 Motif ID: 3  
 Motif name: Motif 3  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 12  
 Similarity score: 0.114583

Alignment:  
 AWAAAWTWAAASWA  
 ATMACAATAAAA--

Original motif      Consensus sequence: AWAAAWTWAAASWA

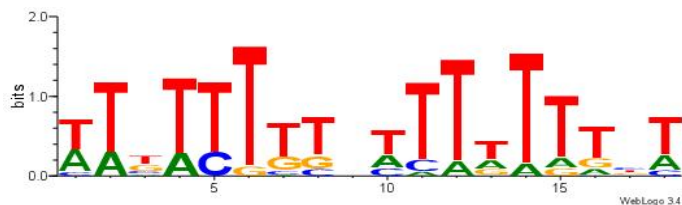
Reverse complement motif      Consensus sequence: TWSTTTWAWTTT



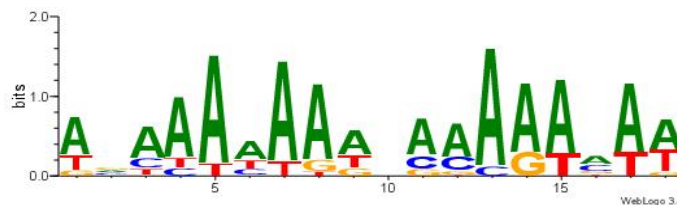
Dataset #: 5  
 Motif ID: 52  
 Motif name: TFM1  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 3  
 Number of overlap: 12  
 Similarity score: 0.115652

Alignment:  
 ABAAAAA WHAAAAARAW  
 --ATMACAATAAAA----

Original motif      Consensus sequence: WTKTTTTTHWTTTTTTBT



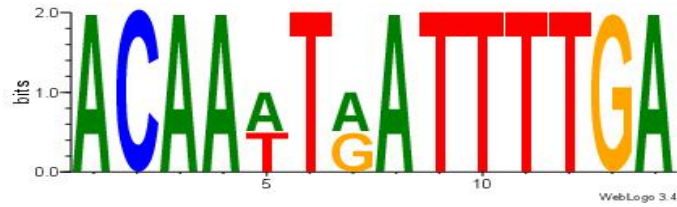
Reverse complement motif      Consensus sequence: ABAAAAA WHAAAAARAW



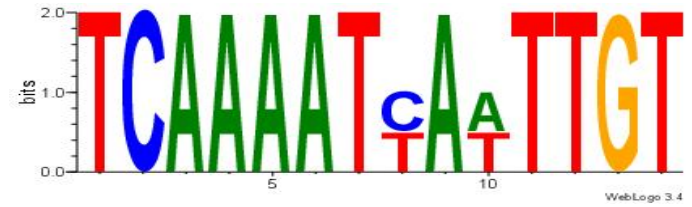
**Dataset #: 2      Motif ID: 16      Motif name: Motif 16**



Original motif      Consensus sequence: ACAAWTRATTTTGA



Reverse complement motif      Consensus sequence: TCAAAAATKAWTTG

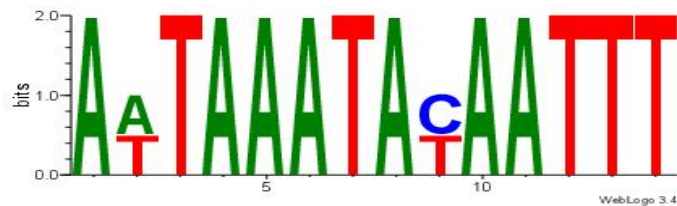


**Best Matches for Motif ID 16 (Highest to Lowest)**

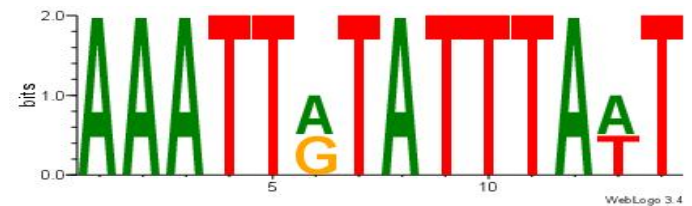
Dataset #: 2  
 Motif ID: 5  
 Motif name: Motif 5  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 14  
 Similarity score: 0.1

Alignment:  
 AWTAAATAYAATTT  
 TCAAAAATKAWTTGT

Original motif      Consensus sequence: AWTAAATAYAATTT



Reverse complement motif      Consensus sequence: AAATTKATTAW

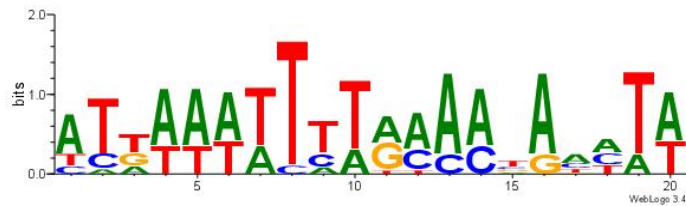


Dataset #: 5  
 Motif ID: 55  
 Motif name: TFM13  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 8  
 Number of overlap: 13  
 Similarity score: 0.599359

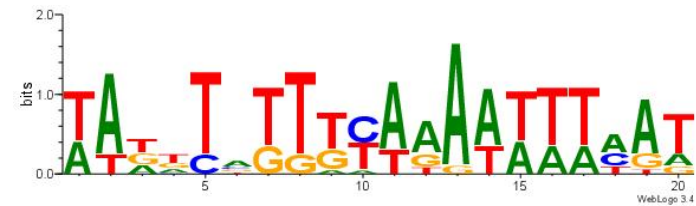
Alignment:

ATKAAWTTTTRMAABAHTW-  
 -----TCAAATKAWTTGT

Original motif      Consensus sequence: ATKAAWTTTTRMAABAHTW



Reverse complement motif      Consensus sequence: WAHHTVTTYKAAAATTRAT



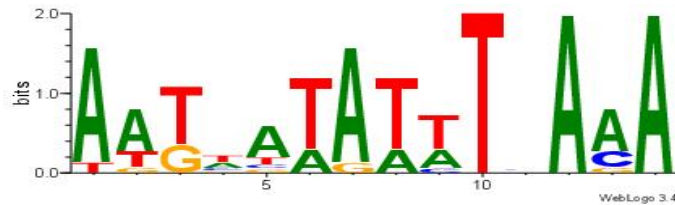
Dataset #: 2  
 Motif ID: 9  
 Motif name: Motif 9  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 3

Number of overlap: 12  
Similarity score: 1.08264

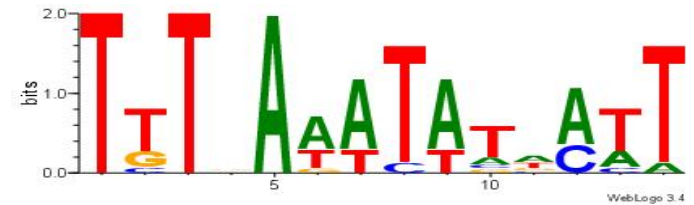
Alignment:

--AATHATATWTHAAA  
ACAAWTRATTTTGA--

Original motif    Consensus sequence: AATHATATWTHAAA



Reverse complement motif    Consensus sequence: TTTDAWATATHAT



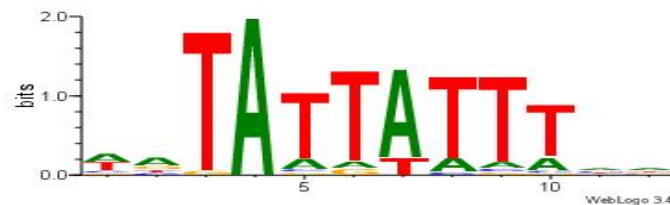
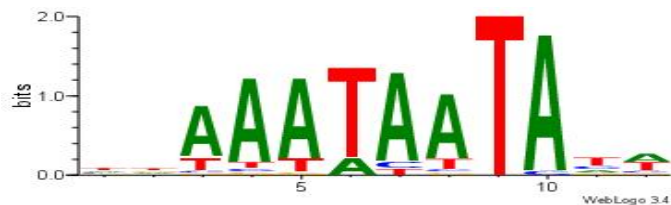
Dataset #: 4  
Motif ID: 37  
Motif name: tkAAATAATAtw  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Reverse Complement  
Direction: Backward  
Position number: 1  
Number of overlap: 12  
Similarity score: 1.08403

Alignment:

--WHTATTATTTDH  
TCAAATKAWTTGT

Original motif    Consensus sequence: HDAAATAATAHW

Reverse complement motif    Consensus sequence: WHTATTATTTDH



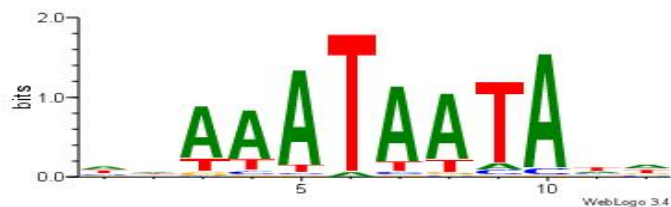
Dataset #: 4  
 Motif ID: 41  
 Motif name: wwAAATAATw  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 12  
 Similarity score: 1.08881

Alignment:

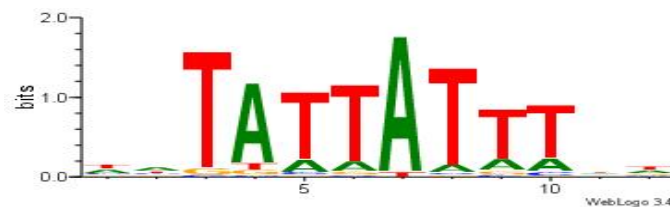
```

--DDTATTATTTDH
TCAAATKAWTTGT
  
```

Original motif    Consensus sequence: HDAAATAATADD



Reverse complement motif    Consensus sequence: DDTATTATTTDH

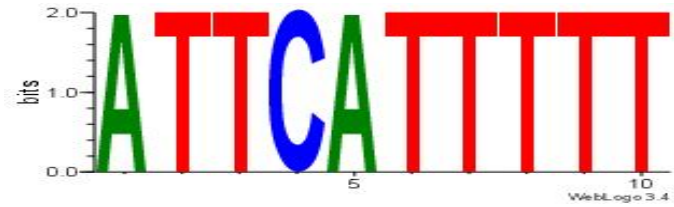


**Dataset #: 2      Motif ID: 17      Motif name: Motif 17**

Original motif      Consensus sequence: AAAAATGAAT



Reverse complement motif      Consensus sequence: ATTCATTTTT



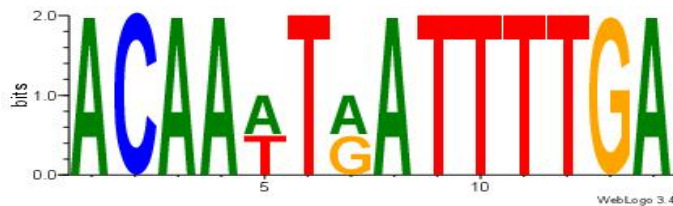
### Best Matches for Motif ID 17 (Highest to Lowest)

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

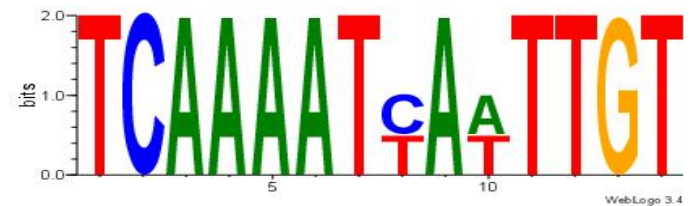
Alignment:

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

Original motif      Consensus sequence: ACAAWTRATTTTGA



Reverse complement motif      Consensus sequence: TCAAATKAWTTG

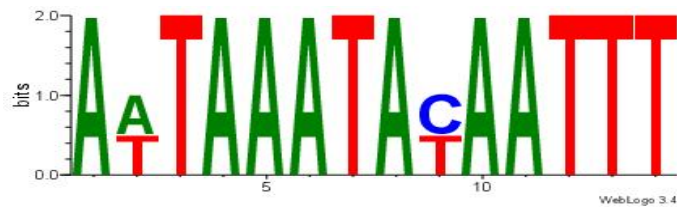


Dataset #: 2  
 Motif ID: 5  
 Motif name: Motif 5  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 4  
 Number of overlap: 10  
 Similarity score: 0.0875

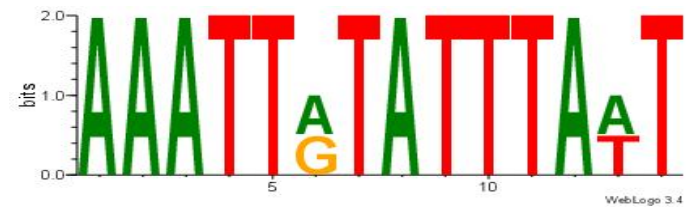
Alignment:

AWTAAATAYAATTT  
 ---AAAAATGAAT-

Original motif      Consensus sequence: AWTAAATAYAATTT



Reverse complement motif      Consensus sequence: AAATTKTATTTAW



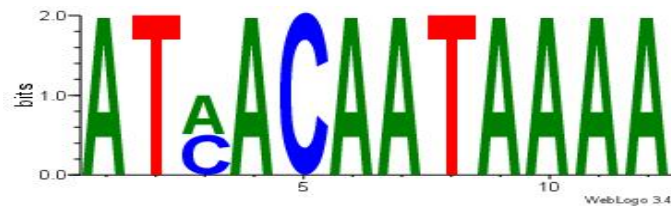
Dataset #: 2  
 Motif ID: 15  
 Motif name: Motif 15  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 3  
 Number of overlap: 10

Similarity score: 0.0875

Alignment:

ATMACAATAAAA  
--AAAAATGAAT

Original motif      Consensus sequence: ATMACAATAAAA



Reverse complement motif      Consensus sequence: TTTTATTGTYAT



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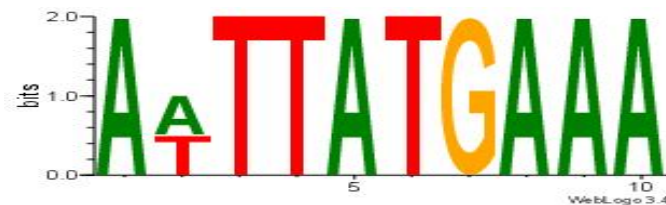
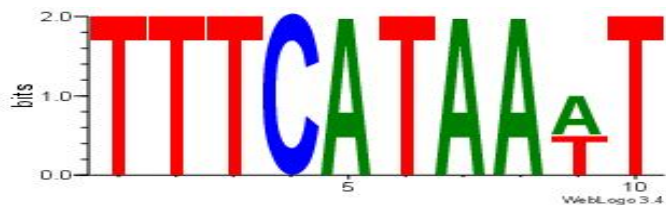
Dataset #: 2  
Motif ID: 10  
Motif name: Motif 10  
Matching format of first motif: Original Motif  
Matching format of second motif: Reverse Complement  
Direction: Backward  
Position number: 1  
Number of overlap: 10  
Similarity score: 0.0875

Alignment:

AWTTATGAAA  
AAAAATGAAT

Original motif      Consensus sequence: TTTCATAAWT

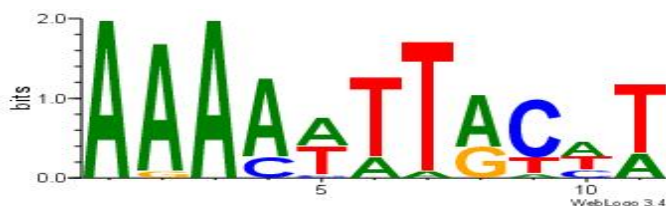
Reverse complement motif      Consensus sequence: AWTTATGAAA



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



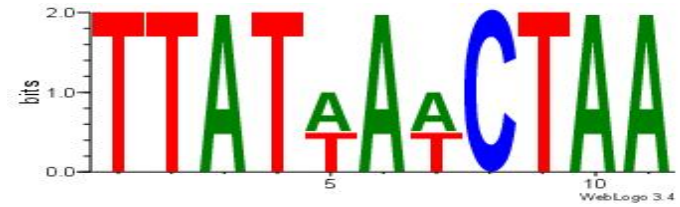
**Dataset #: 2      Motif ID: 18      Motif name: Motif 18**



Original motif      Consensus sequence: TTAGWTWATAA



Reverse complement motif      Consensus sequence: TTATWAWCTAA



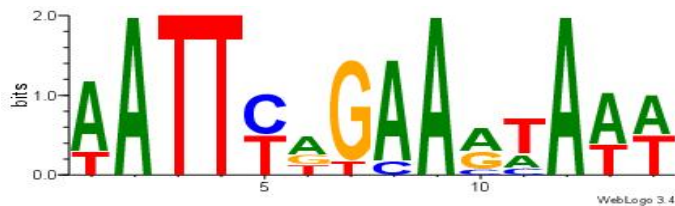
### Best Matches for Motif ID 18 (Highest to Lowest)

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

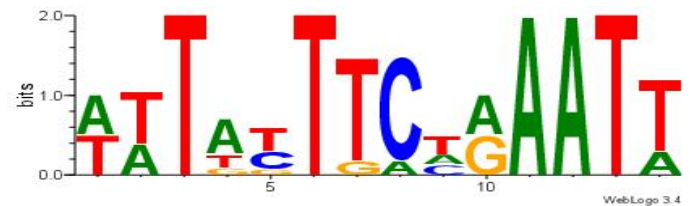
Alignment:

```
AATTYDGAARTAWW
-TTATWAWCTAA--
```

Original motif      Consensus sequence: AATTYDGAARTAWW



Reverse complement motif      Consensus sequence: WWTAKTTCDKAAT

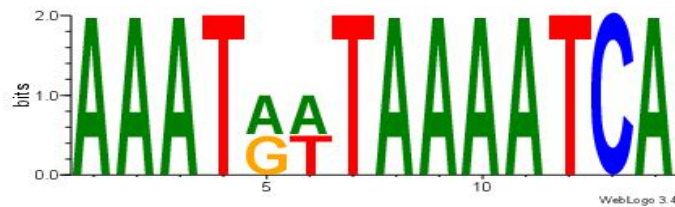


Dataset #: 2  
 Motif ID: 8  
 Motif name: Motif 8  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 4  
 Number of overlap: 11  
 Similarity score: 0.102273

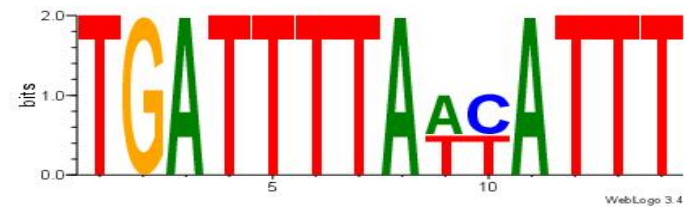
Alignment:

AAATRWTA~~AA~~ATCA  
 TTATWAWCTAA---

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



Reverse complement motif      Consensus sequence: TGATTTAWKATT



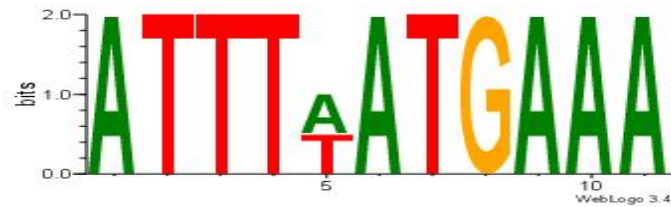
Dataset #: 2  
 Motif ID: 11  
 Motif name: Motif 11  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 11

Similarity score: 0.102273

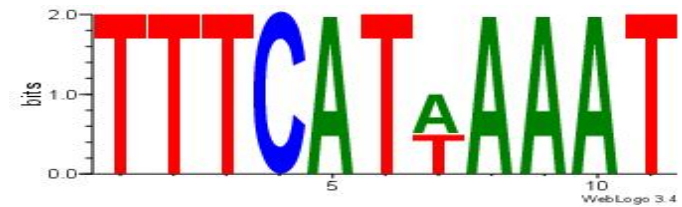
Alignment:

TTTCATWAAAT  
TTAGWTWATAA

Original motif      Consensus sequence: ATTTWATGAAA



Reverse complement motif      Consensus sequence: TTTCATWAAAT



---

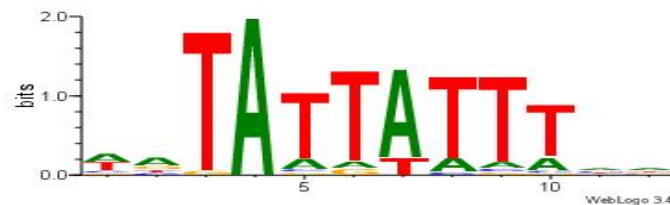
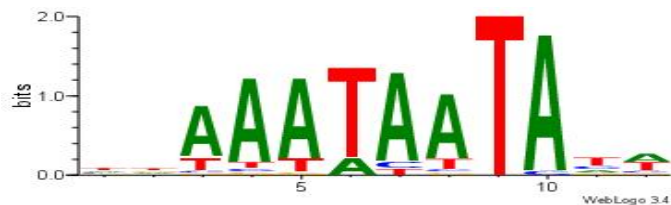
Dataset #: 4  
Motif ID: 37  
Motif name: tkAAATAATAtw  
Matching format of first motif: Original Motif  
Matching format of second motif: Original Motif  
Direction: Backward  
Position number: 2  
Number of overlap: 11  
Similarity score: 0.102273

Alignment:

HDAAATAATAHW  
TTAGWTWATAA-

Original motif      Consensus sequence: HDAAATAATAHW

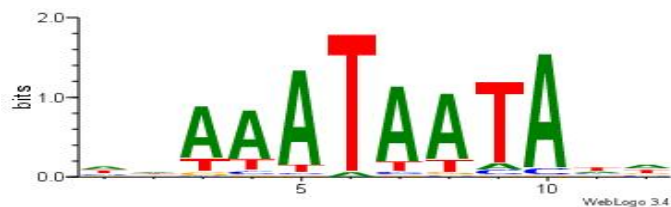
Reverse complement motif      Consensus sequence: WHTATTATTTDH



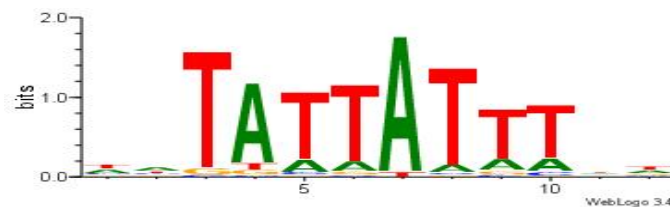
Dataset #: 4  
 Motif ID: 41  
 Motif name: wwAAATAATAtw  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 11  
 Similarity score: 0.104798

Alignment:  
 DDTATTATTTDH  
 -TTATWAWCTAA

Original motif    Consensus sequence: HDAAATAATADD



Reverse complement motif    Consensus sequence: DDTATTATTTDH

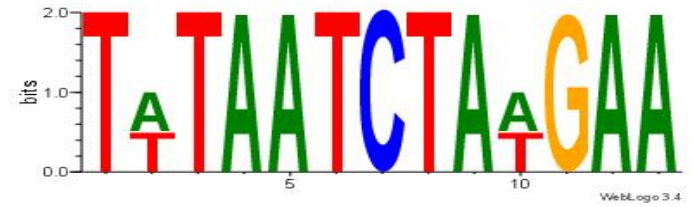


**Dataset #: 2      Motif ID: 19      Motif name: Motif 19**

Original motif    Consensus sequence: TTCWTAGATTAWA



Reverse complement motif    Consensus sequence: TWTAACTAWGAA



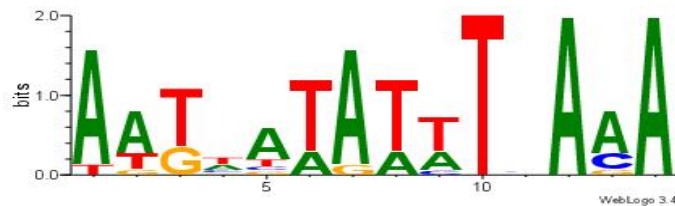
**Best Matches for Motif ID 19 (Highest to Lowest)**

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

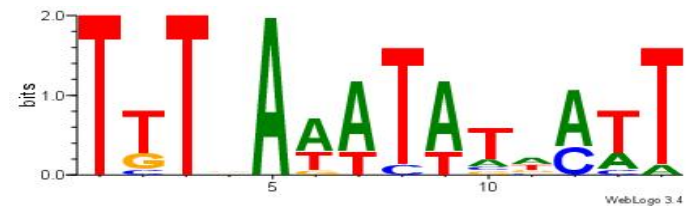
Alignment:

AATHATATWTHAAA  
 -TTCWTAGATTAWA

Original motif    Consensus sequence: AATHATATWTHAAA



Reverse complement motif    Consensus sequence: TTTDAWATATHAT

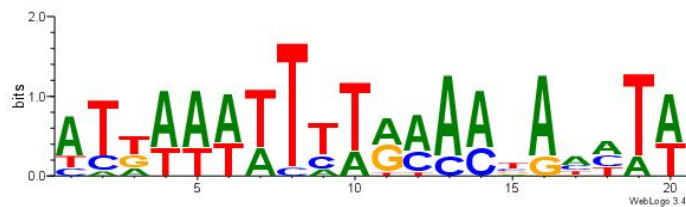


Dataset #: 5  
 Motif ID: 55  
 Motif name: TFM13  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 7  
 Number of overlap: 13  
 Similarity score: 0.0762821

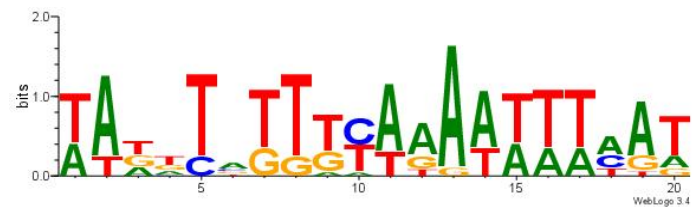
Alignment:

WAHHTVTTYKAAAATTRAT  
 -----TTCWTAGATTAWA-

Original motif      Consensus sequence: ATKAAWTTTTRMAABAHTW



Reverse complement motif      Consensus sequence: WAHHTVTTYKAAAATTRAT



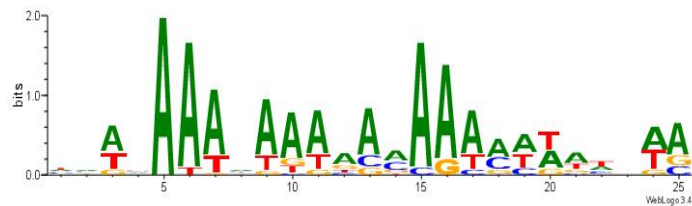
Dataset #: 5  
 Motif ID: 56  
 Motif name: TFM11  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 12

Number of overlap: 13  
 Similarity score: 0.0810709

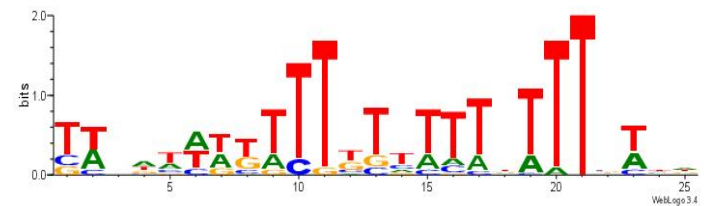
Alignment:

HDWVAAAHAAAAAAMAAAMWWWHBWA  
 -TWTAATCTAWGAA-----

Original motif    Consensus sequence:  
 HDWVAAAHAAAAAAMAAAMWWWHBWA



Reverse complement motif    Consensus sequence:  
 TWVHWWWYTTTTTTTTTHTTTVWBH

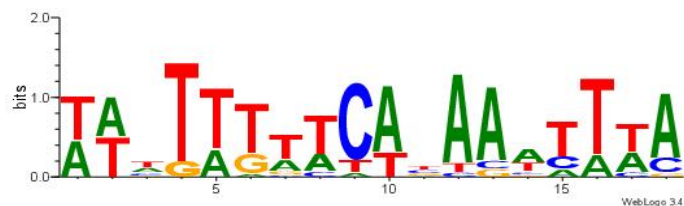


Dataset #: 5  
 Motif ID: 53  
 Motif name: TFM3  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 13  
 Similarity score: 0.0815851

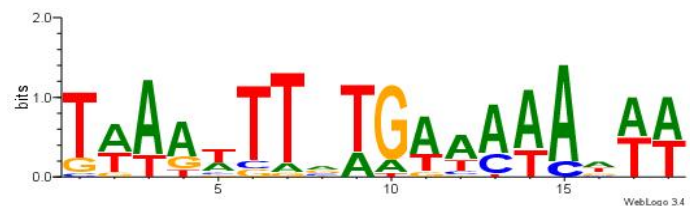
Alignment:

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

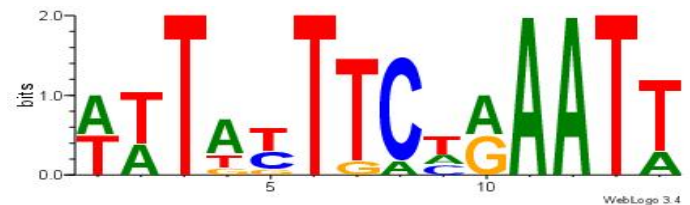
Alignment:

AATTYDGAARTAWW-  
 --TTCWTAGATTAWA

Original motif      Consensus sequence: AATTYDGAARTAWW



Reverse complement motif      Consensus sequence: WWTAKTTCDKAAAT



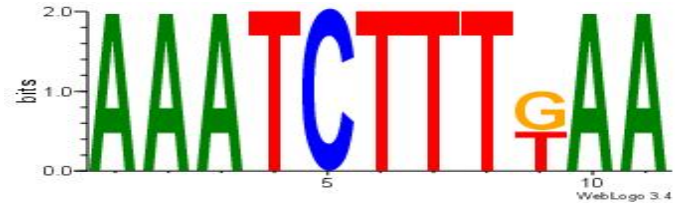


**Dataset #: 2      Motif ID: 20      Motif name: Motif 20**

Original motif      Consensus sequence: TTMAAAGATTT



Reverse complement motif      Consensus sequence: AAATCTTTYAA



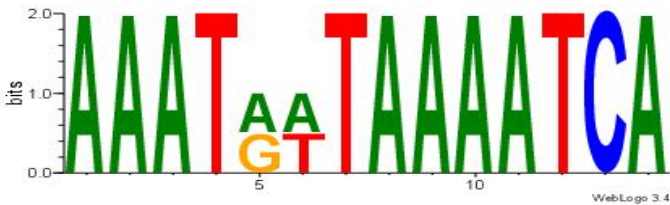
**Best Matches for Motif ID 20 (Highest to Lowest)**

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

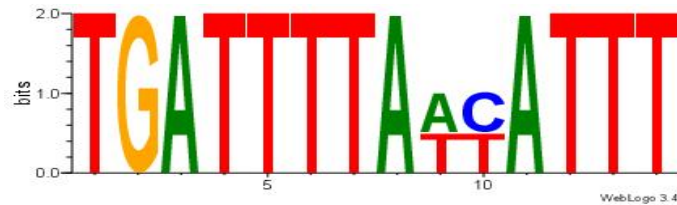
**Alignment:**

```
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

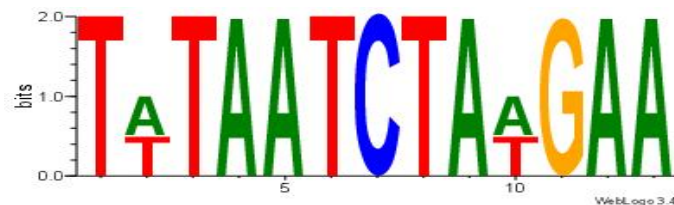
Alignment:

TTCWTAGATTAWA  
 TTMAAAGATTT--

Original motif    Consensus sequence: TTCWTAGATTAWA



Reverse complement motif    Consensus sequence: TWTAATCTAWGAA

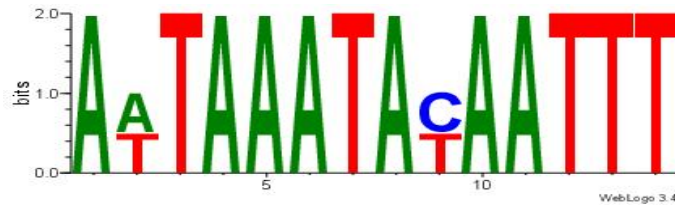


Dataset #: 2  
 Motif ID: 5  
 Motif name: Motif 5  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 2

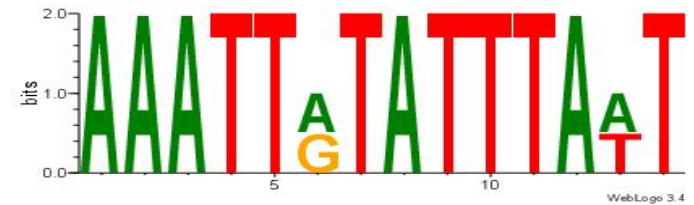
Number of overlap: 11  
Similarity score: 0.102273

Alignment:  
AAATTKTATTTAWT  
-AAATCTTTYAA--

Original motif      Consensus sequence: AWTAAATAYAATTT



Reverse complement motif      Consensus sequence: AAATTKTATTTAWT

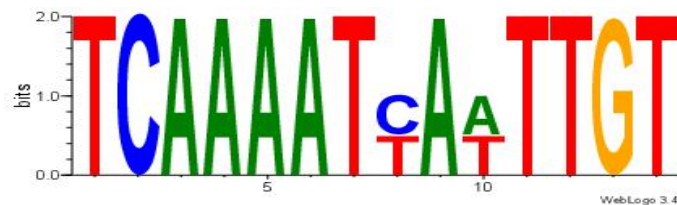
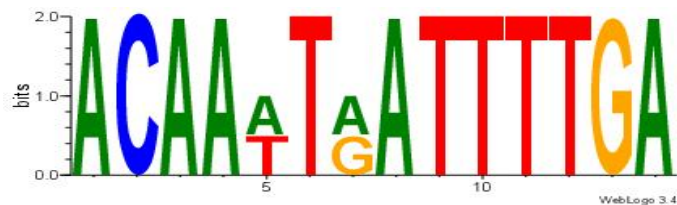


Dataset #: 2  
Motif ID: 16  
Motif name: Motif 16  
Matching format of first motif: Original Motif  
Matching format of second motif: Original Motif  
Direction: Forward  
Position number: 1  
Number of overlap: 11  
Similarity score: 0.102273

Alignment:  
ACAAWTRATTTTGA  
TTMAAAGATTT---

Original motif      Consensus sequence: ACAAWTRATTTTGA

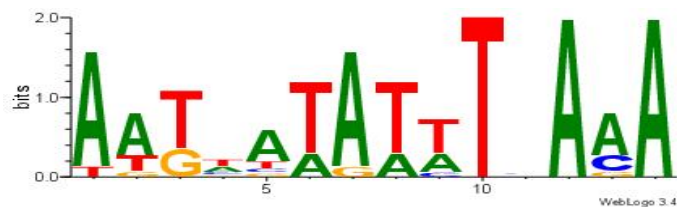
Reverse complement motif      Consensus sequence: TCAAAATKAWTTG



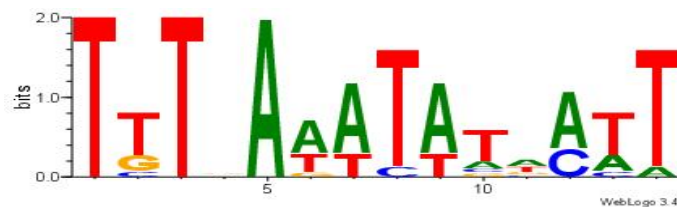
Dataset #: 2  
 Motif ID: 9  
 Motif name: Motif 9  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 2  
 Number of overlap: 11  
 Similarity score: 0.106061

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

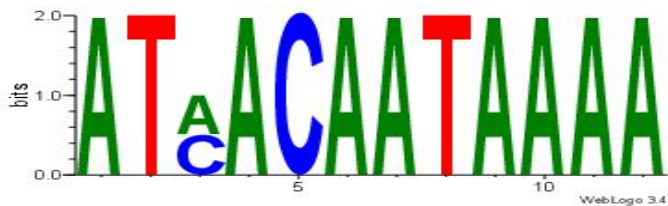


**Best Matches for Motif ID 21 (Highest to Lowest)**

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



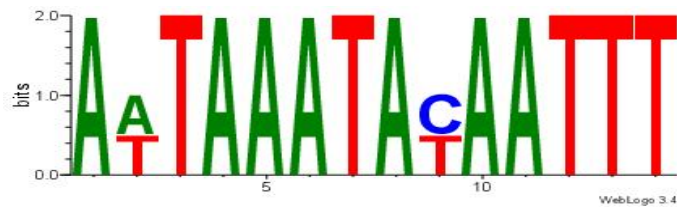
Reverse complement motif      Consensus sequence: TTTTATTGTYAT



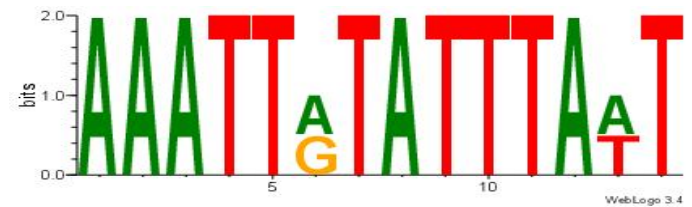
Dataset #: 2  
 Motif ID: 5  
 Motif name: Motif 5  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 6  
 Number of overlap: 6  
 Similarity score: 0.0208333

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

Original motif      Consensus sequence: AWTAAATAYAATTT



Reverse complement motif      Consensus sequence: AAATTKTATTTAWT



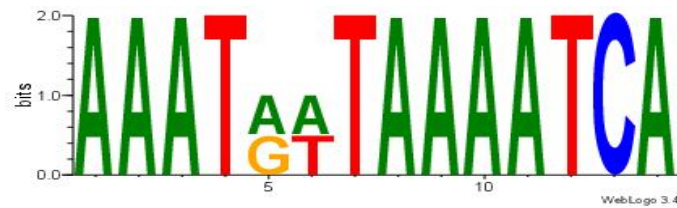
Dataset #: 2  
 Motif ID: 8  
 Motif name: Motif 8  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 4  
 Number of overlap: 6

Similarity score: 0.0208333

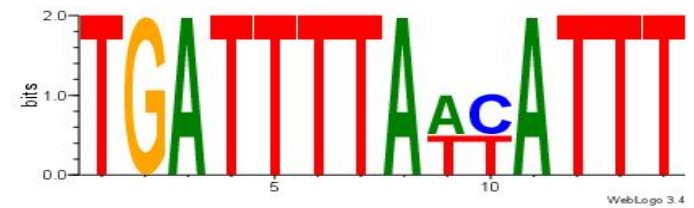
Alignment:

AAATRWATAAATCA  
-----ATAAAA---

Original motif      Consensus sequence: AAATRWATAAATCA



Reverse complement motif      Consensus sequence: TGATTTAWKATT



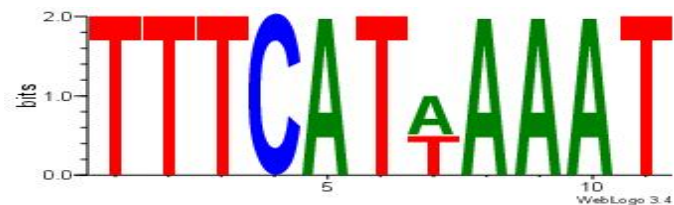
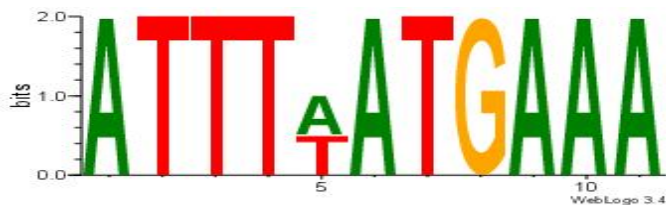
Dataset #: 2  
Motif ID: 11  
Motif name: Motif 11  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Original Motif  
Direction: Backward  
Position number: 2  
Number of overlap: 6  
Similarity score: 0.0208333

Alignment:

ATTTWATGAAA  
-----TTTAT-

Original motif      Consensus sequence: ATTTWATGAAA

Reverse complement motif      Consensus sequence: TTTATWAAAT

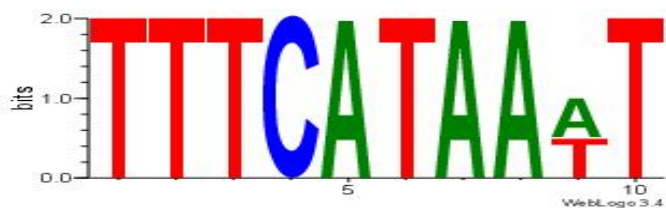


Dataset #: 2  
 Motif ID: 10  
 Motif name: Motif 10  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 6  
 Similarity score: 0.0416667

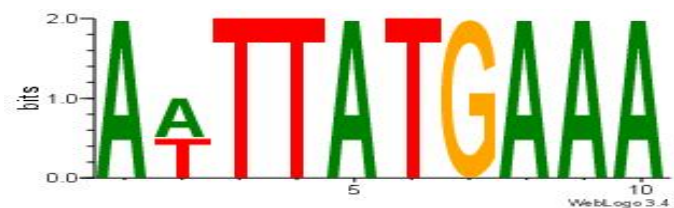
Alignment:

TTTCATAAWT  
 ----TTTTAT

Original motif      Consensus sequence: TTTCATAAWT



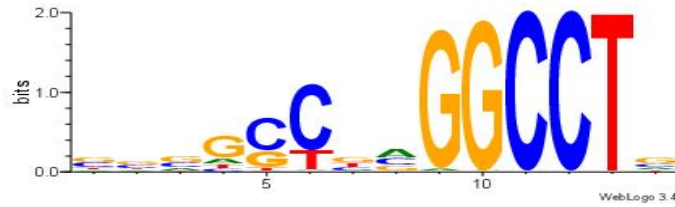
Reverse complement motif      Consensus sequence: AWTTATGAAA



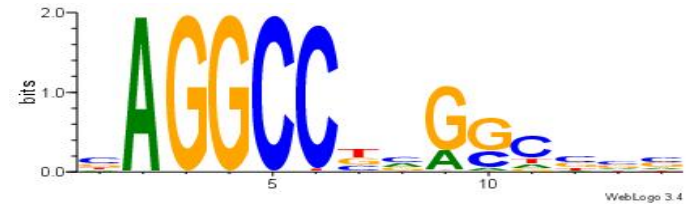
**Dataset #: 3      Motif ID: 22      Motif name: Zfx**



Original motif      Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif      Consensus sequence: VAGGCCBBGGCCTV



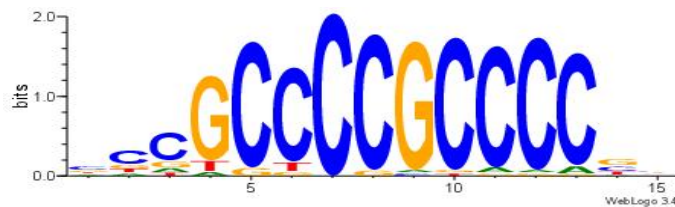
### Best Matches for Motif ID 22 (Highest to Lowest)

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

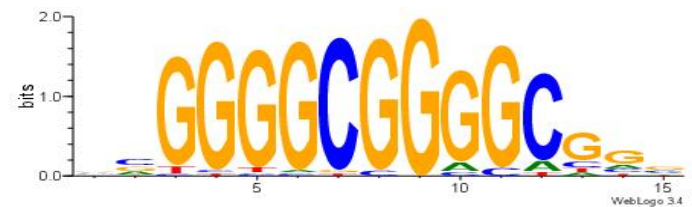
Alignment:

```
BCCGCCCCGCCCCBB  
BBVGCCBVGGCCTV-
```

Original motif      Consensus sequence: BCCGCCCCGCCCCBB



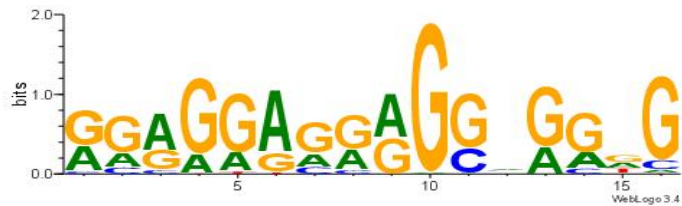
Reverse complement motif      Consensus sequence: BBGGGGCGGGGCGGB



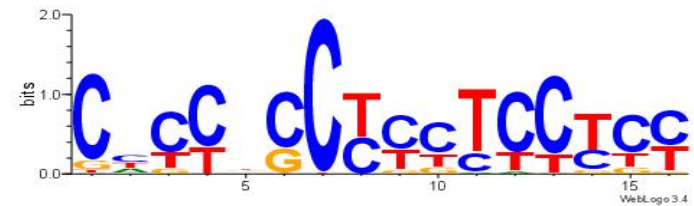
Dataset #: 5  
 Motif ID: 51  
 Motif name: TFM2  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 2  
 Number of overlap: 14  
 Similarity score: 0.0590031

Alignment:  
 CHCCBCKMCTCCKCM  
 -BBVGCCBVGGCCTV-

Original motif    Consensus sequence: RGRGGAGRRGGHGGDG



Reverse complement motif    Consensus sequence: CHCCBCKMCTCCKCM



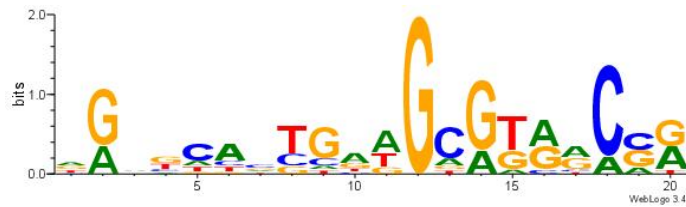
Dataset #: 3  
 Motif ID: 31  
 Motif name: Pax5  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 5

Number of overlap: 14  
Similarity score: 0.0611182

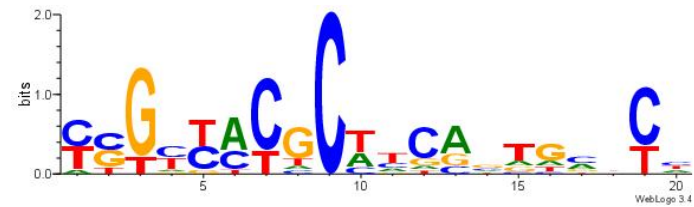
Alignment:

DGVBCABTGDWGCGRRCR  
--BBVGCCBVGGCCTV----

Original motif    Consensus sequence: DGVBCABTGDWGCGRRCR



Reverse complement motif    Consensus sequence:  
MSGKKRCGCWDCABTGBBCD

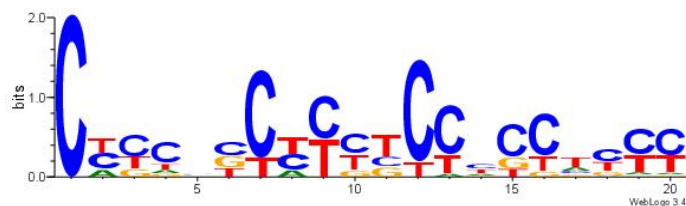


Dataset #: 5  
Motif ID: 54  
Motif name: TFM12  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Reverse Complement  
Direction: Forward  
Position number: 6  
Number of overlap: 14  
Similarity score: 0.0629383

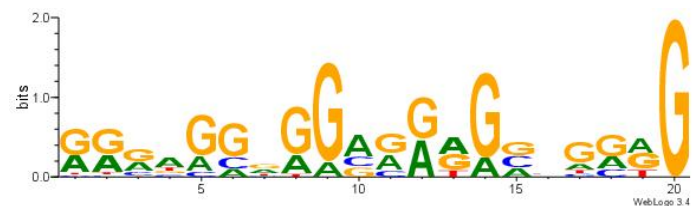
Alignment:

KKKAGGDGGAKKMGBBGKMG  
-----VAGGCCBBGGCVBB-

Original motif      Consensus sequence: CYCBBYYYTCCHCCTYYY



Reverse complement motif      Consensus sequence: KKKAGGDGGAKKMGBBGKMG

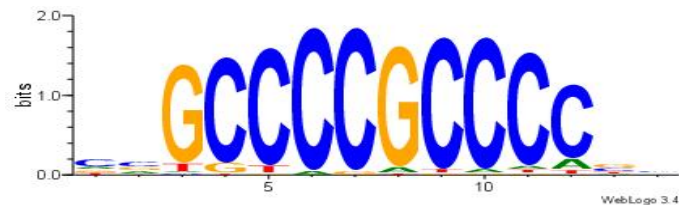


Dataset #: 4  
Motif ID: 36  
Motif name: csGCCCCGCCCCsc  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Original Motif  
Direction: Forward  
Position number: 1  
Number of overlap: 14  
Similarity score: 0.0654514

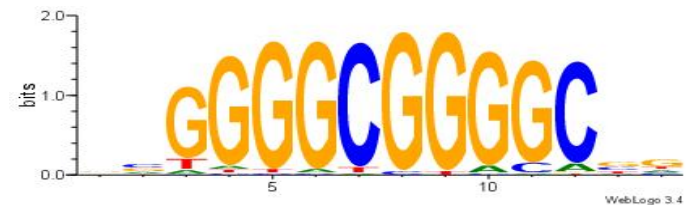
Alignment:

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)**

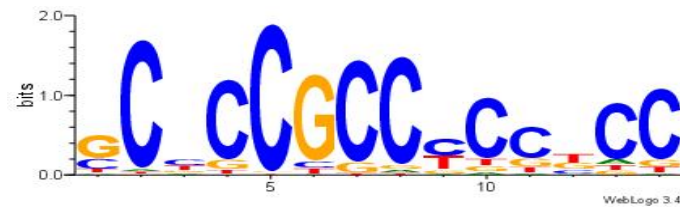
Dataset #:	5
Motif ID:	50
Motif name:	TFF11
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	4
Number of overlap:	11
Similarity score:	0.0514701

Alignment:  
GCVCCGCCMCCYCC  
---YCGCCACGCH

Original motif      Consensus sequence: GGMGRRGGCGGVGC



Reverse complement motif      Consensus sequence: GCVCCGCCMCCYCC

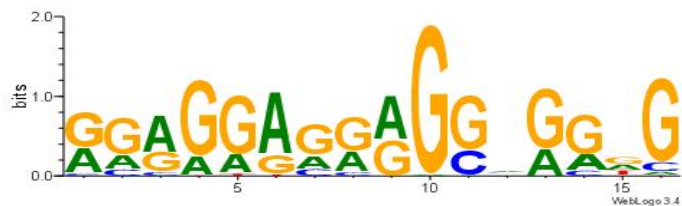


Dataset #: 5  
 Motif ID: 51  
 Motif name: TFM2  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 6  
 Number of overlap: 11  
 Similarity score: 0.0698683

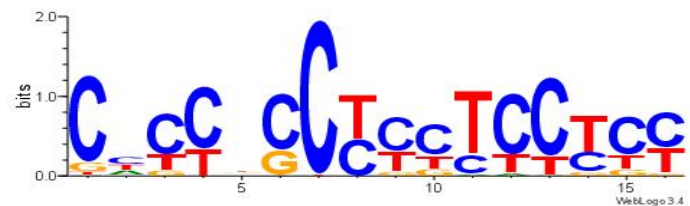
Alignment:

CHCCBCKMCTCCKCM  
 -----YCGCCACGCH

Original motif    Consensus sequence: RGRGGAGRRGGHGGDG



Reverse complement motif    Consensus sequence: CHCCBCKMCTCCKCM



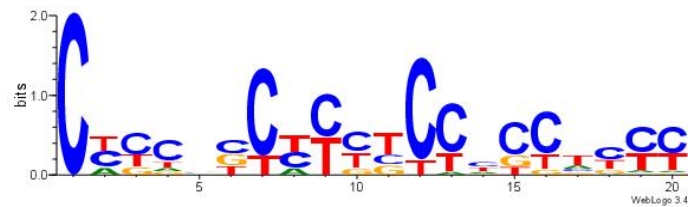
Dataset #: 5  
 Motif ID: 54  
 Motif name: TFM12  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Backward

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

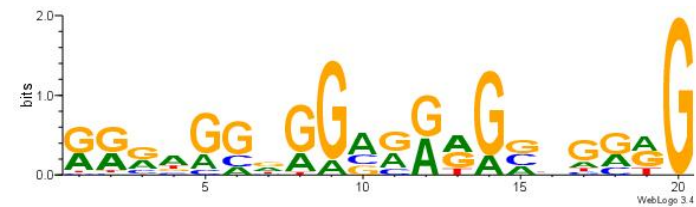
Alignment:

KKKAGGDGGAKKMGBBGKMG  
-HGCGTGGGCGK-----

Original motif    Consensus sequence: CYCBBYYYTCCHCCTYYY



Reverse complement motif    Consensus sequence: KKKAGGDGGAKKMGBBGKMG



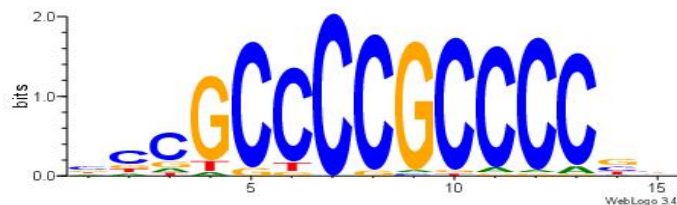
---

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

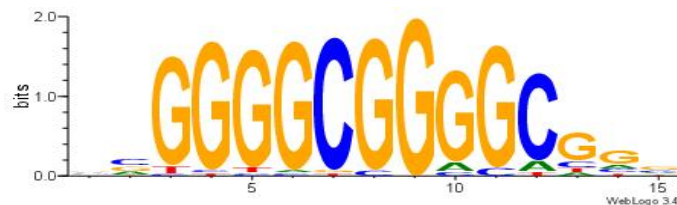
Alignment:

BBGGGGCGGGGCGGB  
----HGCGTGGGCGK

Original motif      Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif      Consensus sequence: BBGGGGCGGGGCGGB

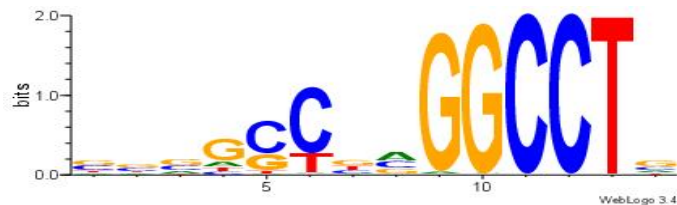


Dataset #: 3  
Motif ID: 22  
Motif name: Zfx  
Matching format of first motif: Original Motif  
Matching format of second motif: Original Motif  
Direction: Backward  
Position number: 2  
Number of overlap: 11  
Similarity score: 0.0764878

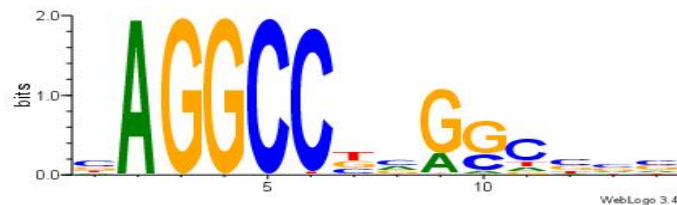
Alignment:

BBVGCCBVGGCCTV  
--HGCGTGGGCGK-

Original motif      Consensus sequence: BBVGCCBVGGCCTV



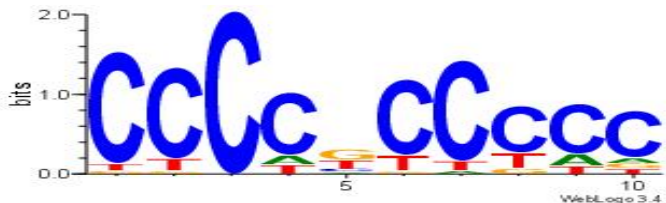
Reverse complement motif      Consensus sequence: VAGGCCBBGGCV



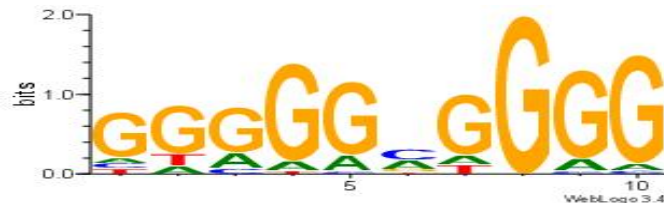


**Dataset #: 3      Motif ID: 24      Motif name: SP1**

Original motif      Consensus sequence: CCCCKCCCC



Reverse complement motif      Consensus sequence: GGGGYGGGG



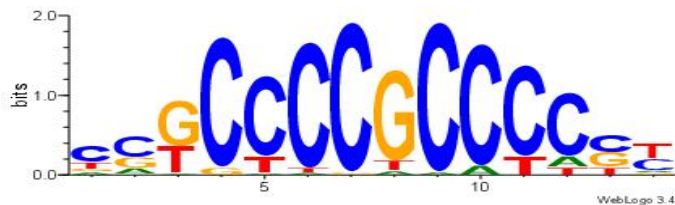
**Best Matches for Motif ID 24 (Highest to Lowest)**

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

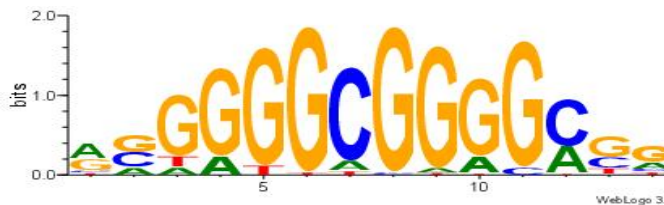
Alignment:

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

Original motif      Consensus sequence: CSKCCCCGCCCSY



Reverse complement motif      Consensus sequence: MSGGGCGGGGY

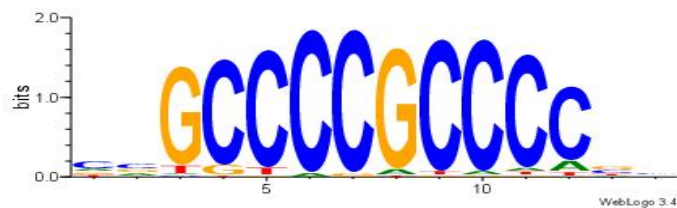


Dataset #: 4  
 Motif ID: 36  
 Motif name: csGCCCCGCCCCsc  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 4  
 Number of overlap: 10  
 Similarity score: 0.00965796

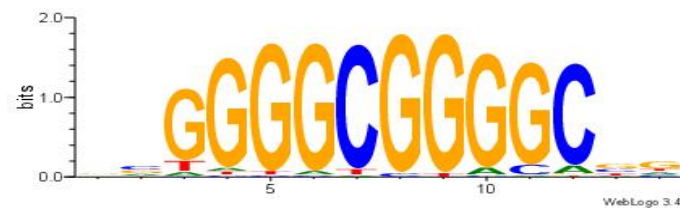
Alignment:

BBGGGGCGGGGCVD  
 -GGGGYGGGG---

Original motif    Consensus sequence: HVGCCCCGCCCB



Reverse complement motif    Consensus sequence: BBGGGGCGGGGC

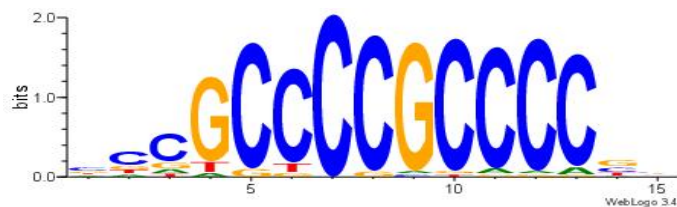


Dataset #: 4  
 Motif ID: 38  
 Motif name: cccGCCCCGCCCSb  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 5

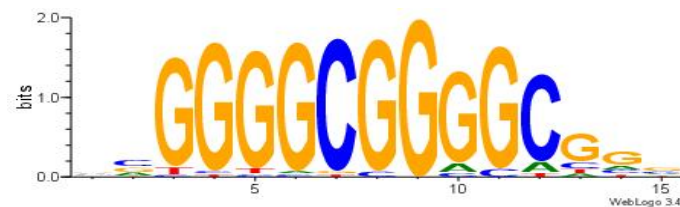
Number of overlap: 10  
Similarity score: 0.0127292

Alignment:  
BCCGCCCCGCCCCBB  
----CCCCKCCCC--

Original motif    Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif    Consensus sequence:  
BBGGGGCGGGGCGGB

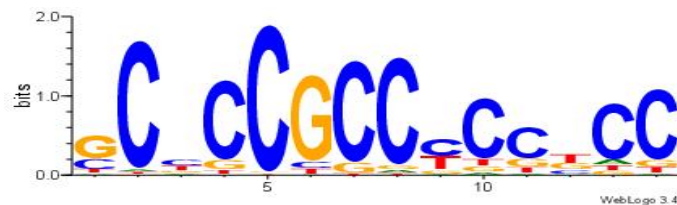


Dataset #: 5  
Motif ID: 50  
Motif name: TFF11  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Original Motif  
Direction: Forward  
Position number: 4  
Number of overlap: 10  
Similarity score: 0.0174405

Alignment:  
GGMGRRGGCGGVGC  
---GGGGYGGGG--

Original motif    Consensus sequence: GGMGRRGGCGGVGC

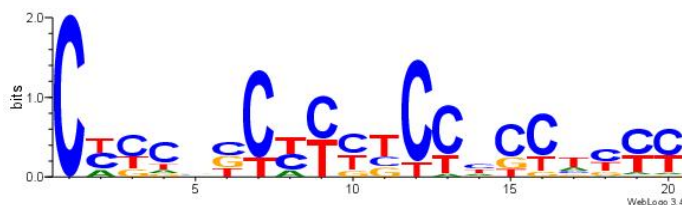
Reverse complement motif    Consensus sequence: GCVCCGCCMCCYCC



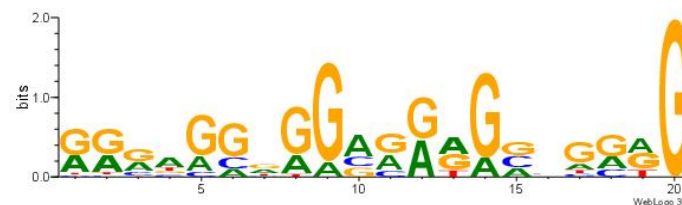
Dataset #: 5  
 Motif ID: 54  
 Motif name: TFM12  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 5  
 Number of overlap: 10  
 Similarity score: 0.0301548

Alignment:  
 CYCBBCYYYTCCHCCTYYY  
 -----CCCCKCCCC-----

Original motif      Consensus sequence: CYCBBCYYYTCCHCCTYYY

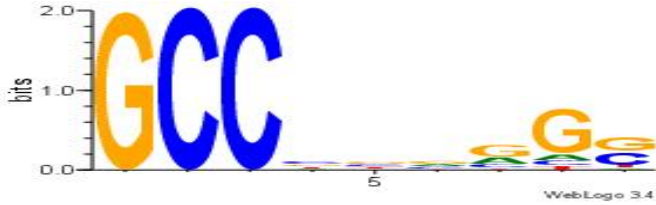


Reverse complement motif      Consensus sequence: KKKAGGDGGAKKMGBBGKMG

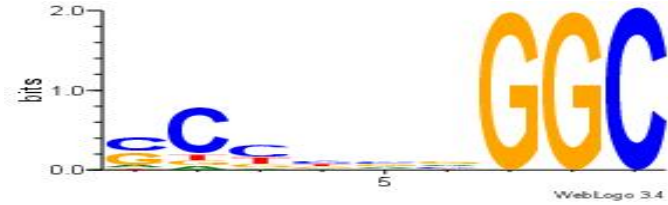


**Dataset #: 3      Motif ID: 25      Motif name: TFAP2A**

Original motif      Consensus sequence: GCCBBVRGS



Reverse complement motif      Consensus sequence: SCMVBGGC



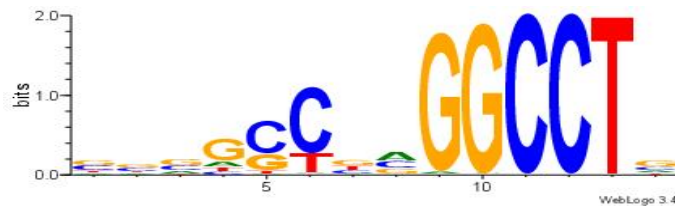
### Best Matches for Motif ID 25 (Highest to Lowest)

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

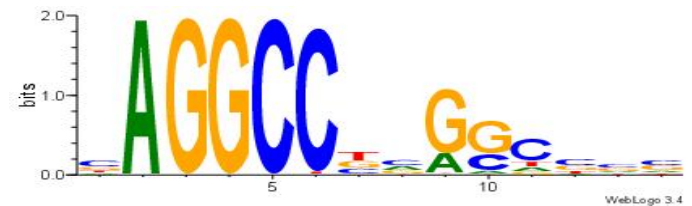
#### Alignment:

```
BBVGCCBVGCCCTV
---SCMVBBGGC---
```

Original motif      Consensus sequence: BBVGCCBVGCCCTV



Reverse complement motif      Consensus sequence: VAGGCCBBGGCV

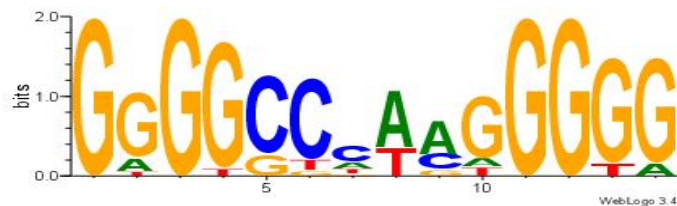


Dataset #: 3  
 Motif ID: 30  
 Motif name: PLAG1  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 4  
 Number of overlap: 9  
 Similarity score: 0.0414588

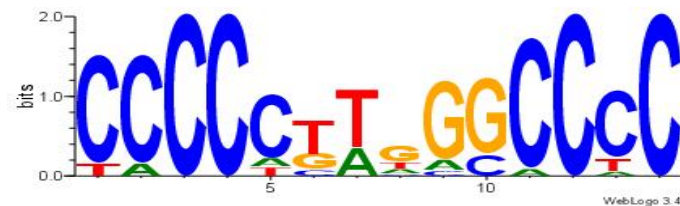
Alignment:

GGGGCCCAAGGGG  
 ---GCCBBVRGS--

Original motif    Consensus sequence: GGGGCCCAAGGGG



Reverse complement motif    Consensus sequence: CCCCTTGGGCC



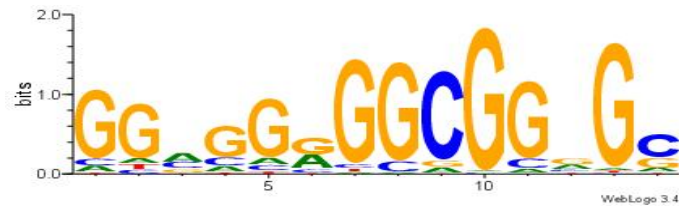
Dataset #: 5  
 Motif ID: 50  
 Motif name: TFF11  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 9

Similarity score: 0.0415732

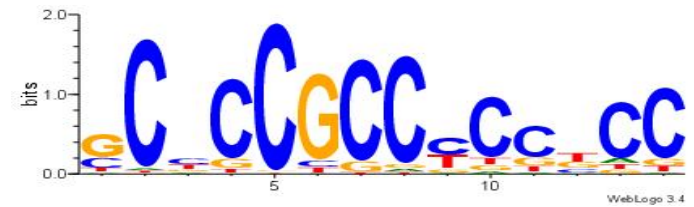
Alignment:

GGMGGRGGCGGVGC  
SCMVBBGGC-----

Original motif    Consensus sequence: GGMGGRGGCGGVGC



Reverse complement motif    Consensus sequence: GCVCCGCCMCCYC



---

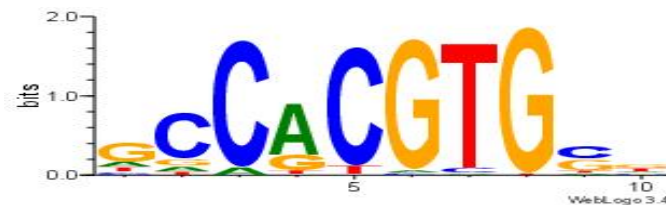
Dataset #: 3  
Motif ID: 33  
Motif name: Mycn  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Original Motif  
Direction: Forward  
Position number: 2  
Number of overlap: 9  
Similarity score: 0.0550803

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:

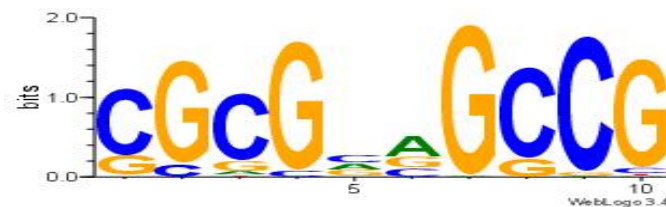
CGGCYBCGCG

-GCCBBVRGS

Original motif      Consensus sequence: CGGCYBCGCG



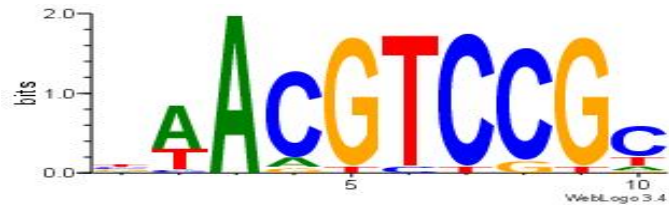
Reverse complement motif      Consensus sequence: CGCGBMGCCG



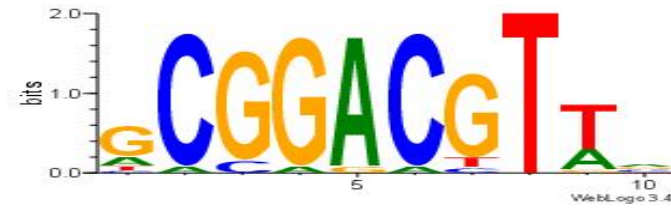
**Dataset #: 3      Motif ID: 26      Motif name: MIZF**



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

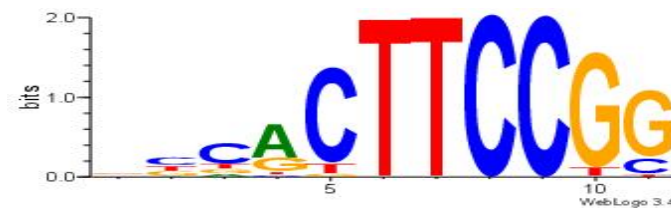
Alignment:

```
CCGGAAGTGVV  
GCGGACGTTV-
```

Original motif      Consensus sequence: CCGGAAGTG



Reverse complement motif      Consensus sequence: VVCACTCCGG

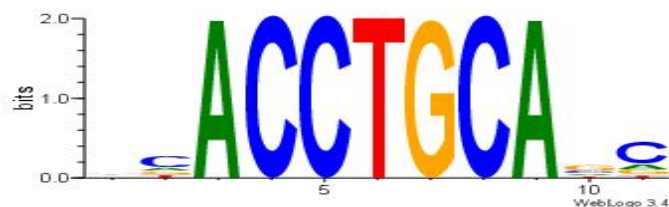


Dataset #: 4  
 Motif ID: 40  
 Motif name: kcACCTGCAGc  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 10  
 Similarity score: 0.0778314

Alignment:

BCACCTGCABC  
 BAACGTCCGC-

Original motif      Consensus sequence: BCACCTGCABC



Reverse complement motif      Consensus sequence: GBTGCAGGTGB



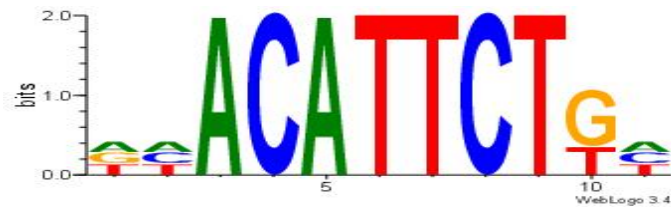
Dataset #: 4  
 Motif ID: 44  
 Motif name: dhACATTCTkh  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 10

Similarity score: 0.0794339

Alignment:

DHACATTCTGH  
BAACGTCCGC-

Original motif      Consensus sequence: DHACATTCTGH



Reverse complement motif      Consensus sequence: HCAGAATGTHD



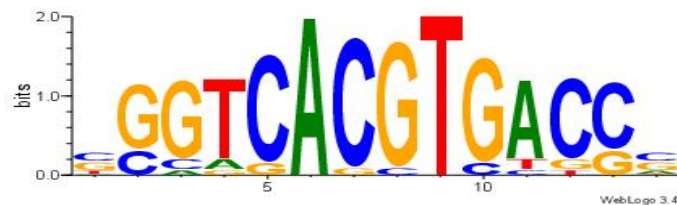
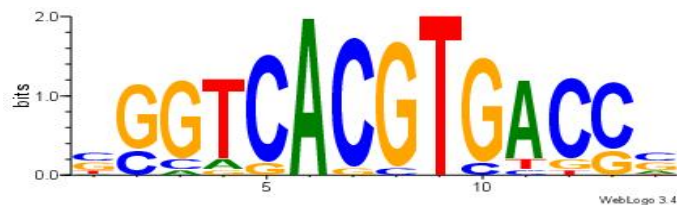
Dataset #: 4  
Motif ID: 42  
Motif name: sSGTCACGTGACCS  
Matching format of first motif: Original Motif  
Matching format of second motif: Original Motif  
Direction: Backward  
Position number: 2  
Number of overlap: 10  
Similarity score: 0.0804061

Alignment:

SGGTCACGTGACCS  
---BAACGTCCGC-

Original motif      Consensus sequence: SGGTCACGTGACCS

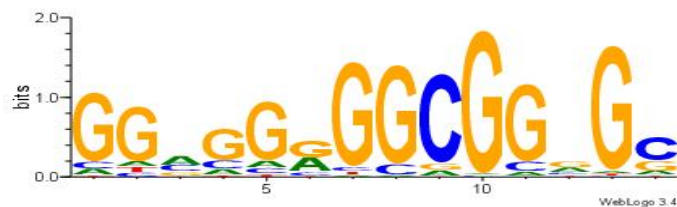
Reverse complement motif      Consensus sequence: SGGTCACGTGACCS



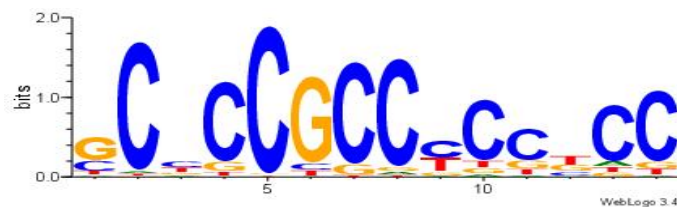
Dataset #: 5  
 Motif ID: 50  
 Motif name: TFF11  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 2  
 Number of overlap: 10  
 Similarity score: 0.0861006

Alignment:  
 GCVCCGCCMCCYCC  
 -BAACGTCCGC---

Original motif    Consensus sequence: GGMGRRGGCGGVGC



Reverse complement motif    Consensus sequence: GCVCCGCCMCCYCC

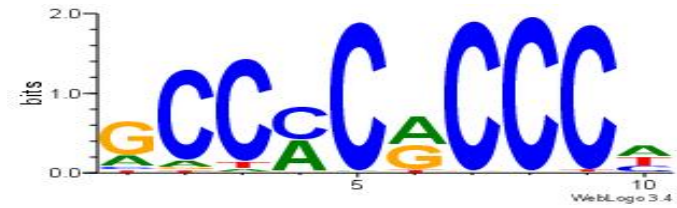


**Dataset #: 3      Motif ID: 27      Motif name: Klf4**

Original motif    Consensus sequence: DGGGYGKGGC



Reverse complement motif    Consensus sequence: GCCYCMCCCD



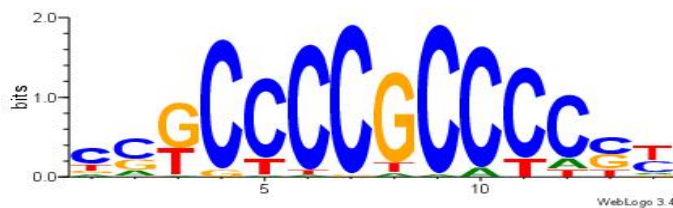
### Best Matches for Motif ID 27 (Highest to Lowest)

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

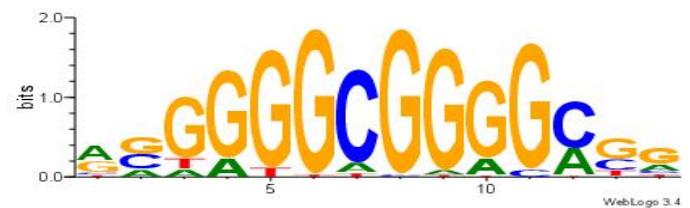
#### Alignment:

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

Original motif    Consensus sequence: CSKCCCCGCCCSY



Reverse complement motif    Consensus sequence: MSGGGCGGGGY

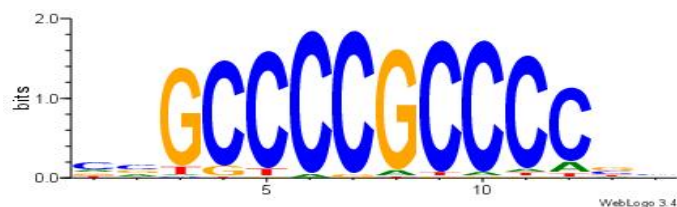


Dataset #: 4  
 Motif ID: 36  
 Motif name: csGCCCCGCCCCsc  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 3  
 Number of overlap: 10  
 Similarity score: 0.0160185

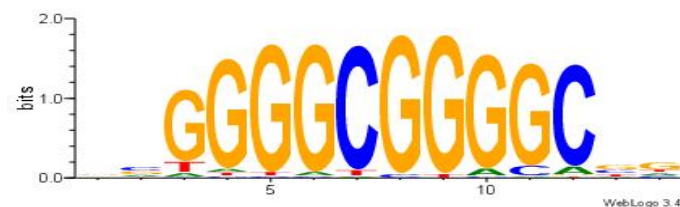
Alignment:

BBGGGGCGGGGCVD  
 --DGGGYGKGGC--

Original motif    Consensus sequence: HVGCCCCGCCCB



Reverse complement motif    Consensus sequence: BBGGGGCGGGGC



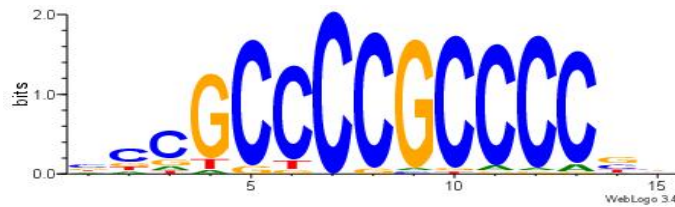
Dataset #: 4  
 Motif ID: 38  
 Motif name: cccGCCCCGCCCCsb  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 3  
 Number of overlap: 10

Similarity score: 0.0194893

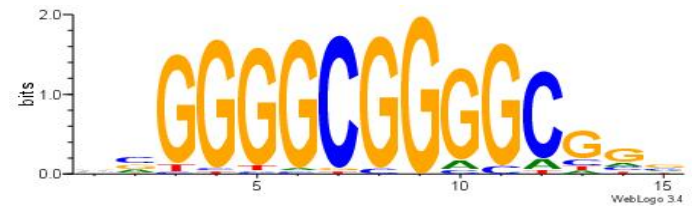
Alignment:

BBGGGGCGGGGCGGB  
--DGGGYGKGGC---

Original motif      Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif      Consensus sequence: BBGGGGCGGGGCGGB



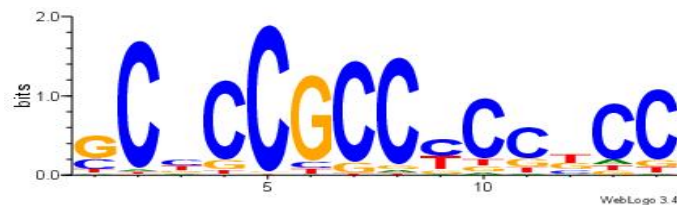
Dataset #: 5  
Motif ID: 50  
Motif name: TFF11  
Matching format of first motif: Original Motif  
Matching format of second motif: Original Motif  
Direction: Forward  
Position number: 5  
Number of overlap: 10  
Similarity score: 0.0402906

Alignment:

GGMGGRGGCGGVGC  
----DGGGYGKGGC

Original motif      Consensus sequence: GGMGGRGGCGGVGC

Reverse complement motif      Consensus sequence: GCVCCGCCMCCY



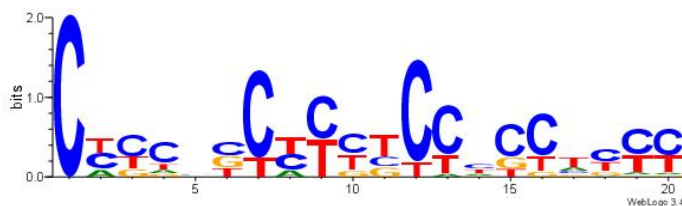
Dataset #: 5  
 Motif ID: 54  
 Motif name: TFM12  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 7  
 Number of overlap: 10  
 Similarity score: 0.0556427

Alignment:

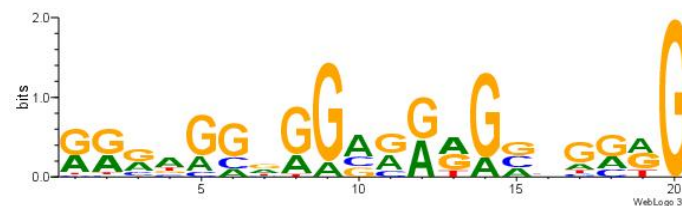
```

CYYCBBCYYYTCCHCCTYYY
----GCCYCMCCCD-----
  
```

Original motif      Consensus sequence: CYYCBBCYYYTCCHCCTYYY



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

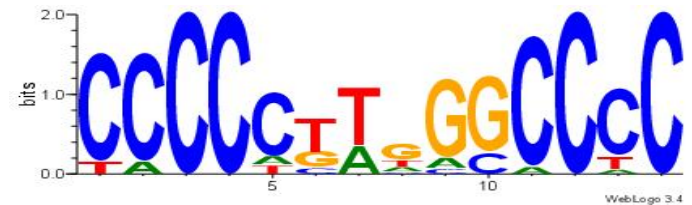
Alignment:

```
GGGGCCCAAGGGGG
-GCGCSAAA-----
```

Original motif      Consensus sequence: GGGGCCAAGGGGG



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

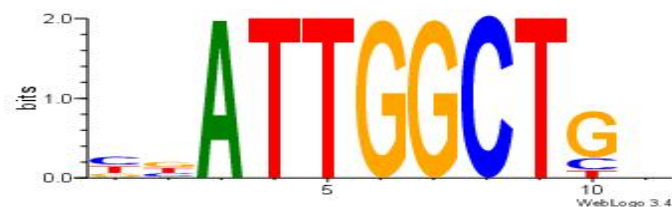
Alignment:

DCAGCCAATVR  
 -GCGCSAAA--

Original motif      Consensus sequence: DCAGCCAATVR



Reverse complement motif      Consensus sequence: MBATTGGCTGH



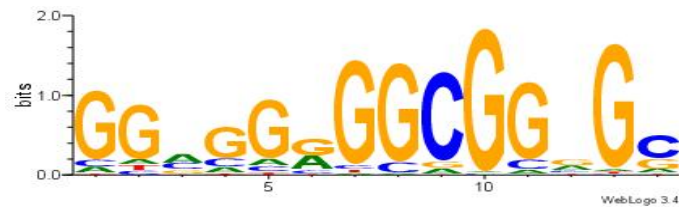
Dataset #: 5  
 Motif ID: 50  
 Motif name: TFF11  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 4  
 Number of overlap: 8

Similarity score: 0.0781129

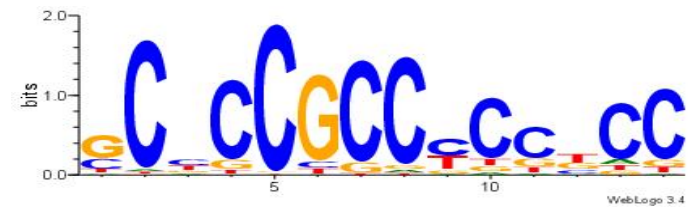
Alignment:

GCVCCGCCMCCYCC  
---GCGCSAAA---

Original motif    Consensus sequence: GGMGRRGGCGGVGC



Reverse complement motif    Consensus sequence: GCVCCGCCMCCYCC



---

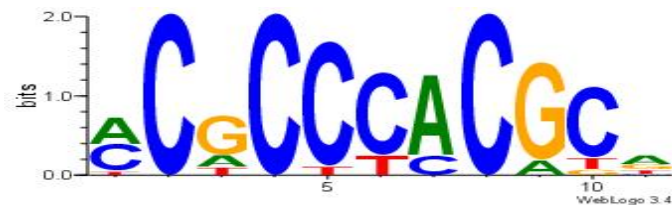
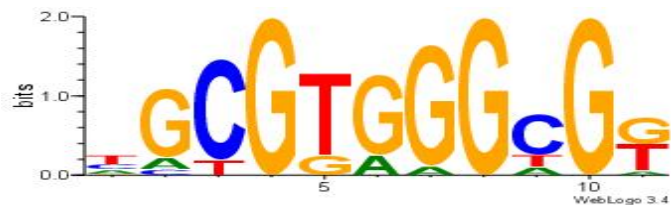
Dataset #: 3  
Motif ID: 23  
Motif name: Egr1  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Reverse Complement  
Direction: Backward  
Position number: 4  
Number of overlap: 8  
Similarity score: 0.0784105

Alignment:

YCGCCCACGCH  
GCGCSAAA---

Original motif    Consensus sequence: HGCGTGGGCGK

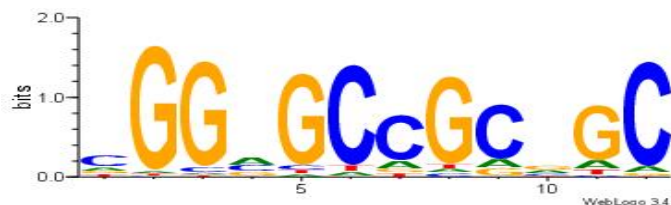
Reverse complement motif    Consensus sequence: YCGCCCACGCH



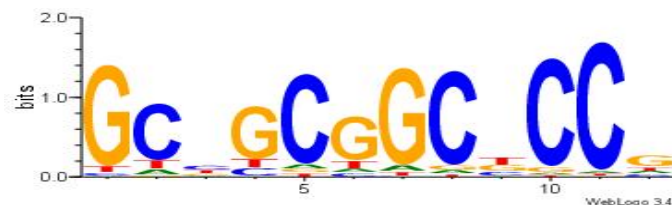
Dataset #: 5  
 Motif ID: 49  
 Motif name: TFF1  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 3  
 Number of overlap: 8  
 Similarity score: 0.0798986

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



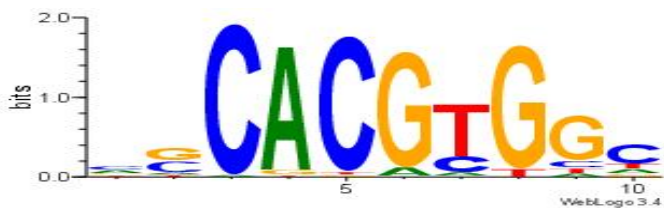
### Best Matches for Motif ID 29 (Highest to Lowest)

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

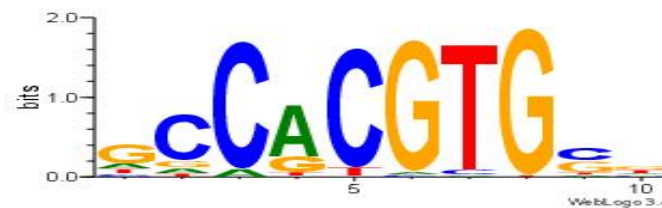
Alignment:

```
GCCACGTGSD  
-VBACGTGV-
```

Original motif      Consensus sequence: HSCACGTGGC



Reverse complement motif      Consensus sequence: GCCACGTGSD

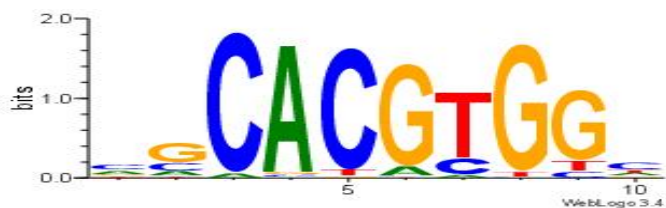


Dataset #: 3  
 Motif ID: 34  
 Motif name: Myc  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 2  
 Number of overlap: 8  
 Similarity score: 0.0144491

Alignment:

DCCACGTGCV  
 -VBACGTGV-

Original motif      Consensus sequence: VGCACGTGGH



Reverse complement motif      Consensus sequence: DCCACGTGCV



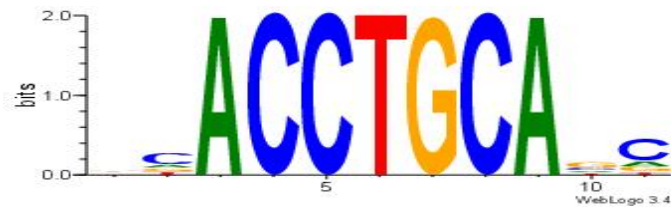
Dataset #: 4  
 Motif ID: 40  
 Motif name: kcACCTGCAGc  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 8

Similarity score: 0.0295473

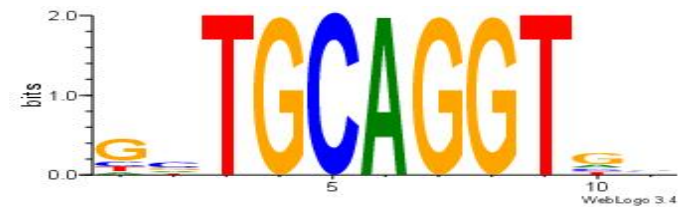
Alignment:

GBTGCAGGTGB  
---VCACGTBV

Original motif      Consensus sequence: BCACCTGCABC



Reverse complement motif      Consensus sequence: GBTGCAGGTGB



---

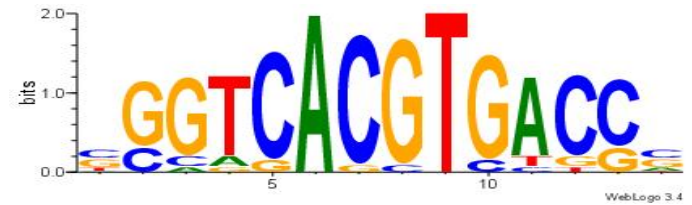
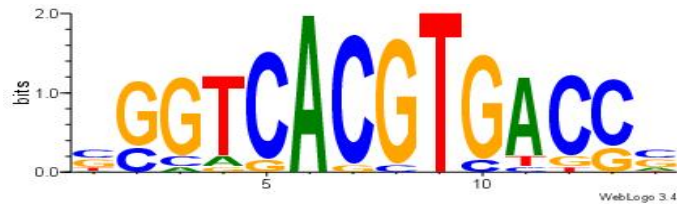
Dataset #: 4  
Motif ID: 42  
Motif name: sSGTCACGTGACSS  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Original Motif  
Direction: Forward  
Position number: 4  
Number of overlap: 8  
Similarity score: 0.0314837

Alignment:

SGGTCACGTGACCS  
---VCACGTBV---

Original motif      Consensus sequence: SGGTCACGTGACCS

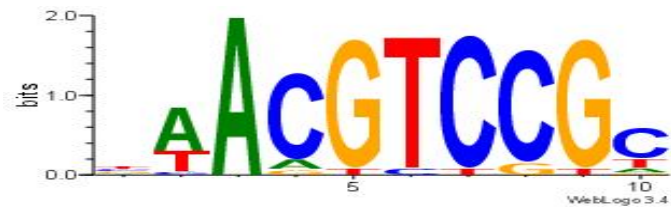
Reverse complement motif      Consensus sequence: SGGTCACGTGACCS



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



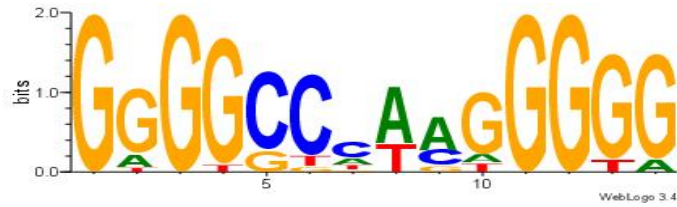
Reverse complement motif      Consensus sequence: GCGGACGTTV



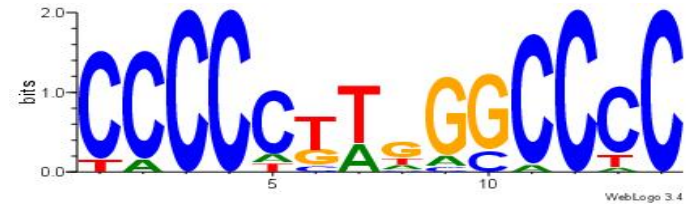
**Dataset #: 3      Motif ID: 30      Motif name: PLAG1**



Original motif    Consensus sequence: GGGCCCAAGGGG



Reverse complement motif    Consensus sequence: CCCCTTGGCC



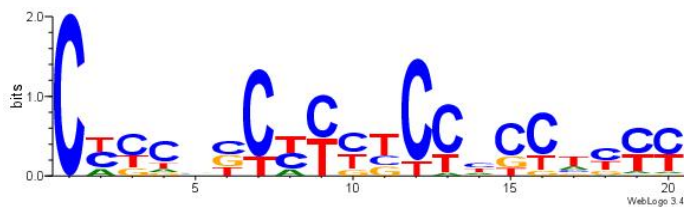
**Best Matches for Motif ID 30 (Highest to Lowest)**

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

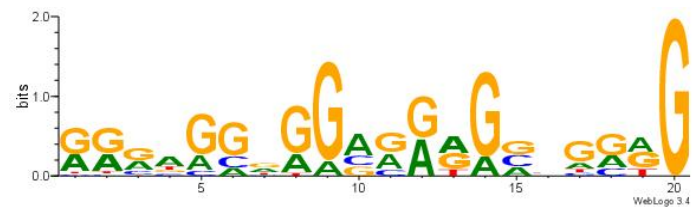
**Alignment:**

CYCBBCYYYTCCHCCTYYY  
 -CCCCCTGGGCC--

Original motif    Consensus sequence: CYCBBCYYYTCCHCCTYYY



Reverse complement motif    Consensus sequence: KKKAGGDGGAKKMGBBGKMG

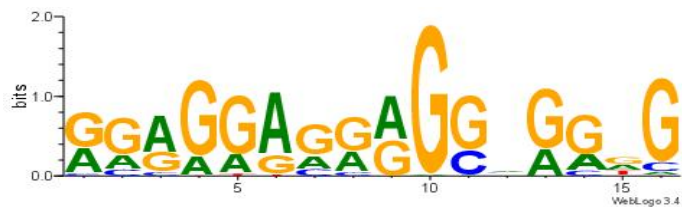


Dataset #: 5  
 Motif ID: 51  
 Motif name: TFM2  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 3  
 Number of overlap: 14  
 Similarity score: 0.0880716

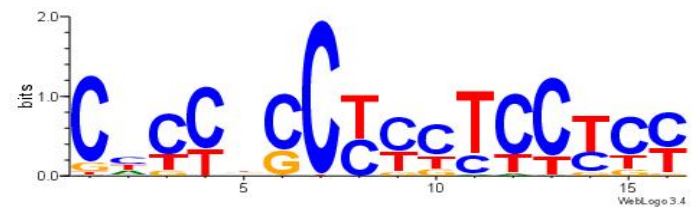
Alignment:

CHCCBCKMCTCCKCM  
 --CCCCCTGGGCCCC

Original motif      Consensus sequence: RGRGGAGRRGGHGGDG



Reverse complement motif      Consensus sequence: CHCCBCKMCTCCKCM



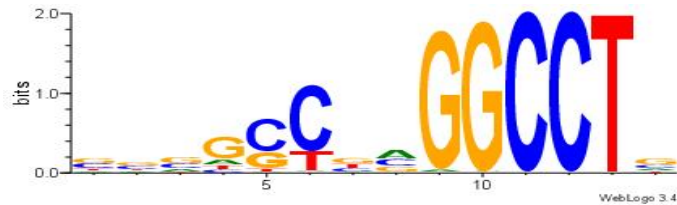
Dataset #: 3  
 Motif ID: 22  
 Motif name: Zfx  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 1

Number of overlap: 14  
Similarity score: 0.0886295

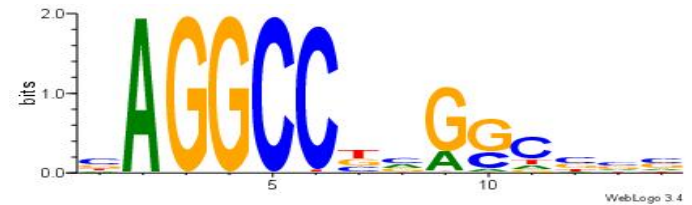
Alignment:

VAGGCCBBGGCVBB  
GGGGCCCAAGGGGG

Original motif      Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif      Consensus sequence: VAGGCCBBGGCVBB



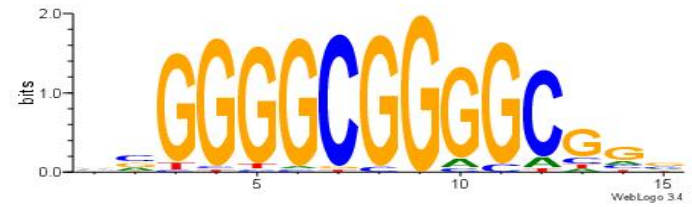
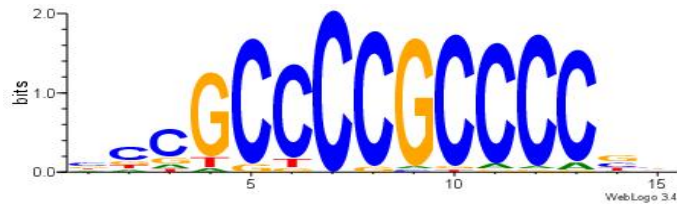
Dataset #: 4  
Motif ID: 38  
Motif name: cccGCCCCGCCCCsb  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Original Motif  
Direction: Backward  
Position number: 2  
Number of overlap: 14  
Similarity score: 0.0904945

Alignment:

BCCGCCCCGCCCCBB  
CCCCCTTGGGCCCC-

Original motif      Consensus sequence: BCCGCCCCGCCCCBB

Reverse complement motif      Consensus sequence:  
BBGGGGCGGGGCGGB

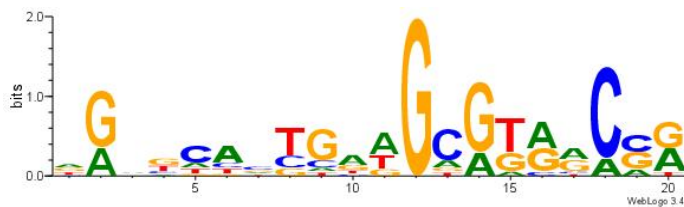


Dataset #: 3  
 Motif ID: 31  
 Motif name: Pax5  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 14  
 Similarity score: 0.0943783

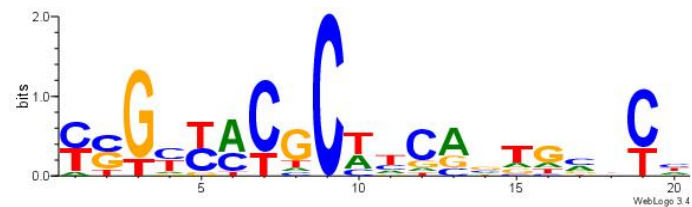
Alignment:

DGVCABTGDWCGKRRCSR  
 GGGGCCCAAGGGG-----

Original motif      Consensus sequence: DGVCABTGDWCGKRRCSR

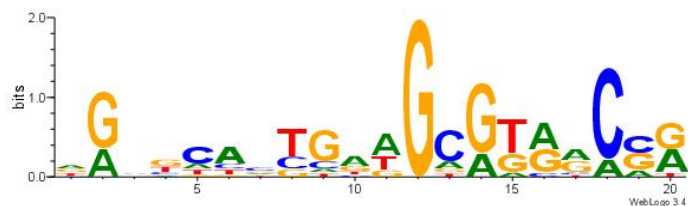


Reverse complement motif      Consensus sequence: MSGKKRCGCWDCABTGBCD

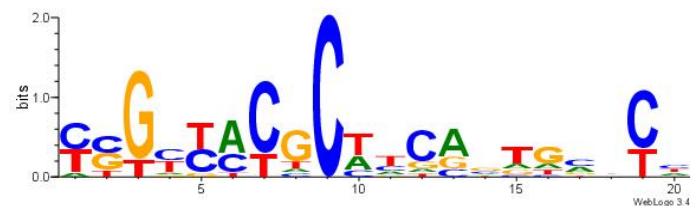


**Dataset #: 3      Motif ID: 31      Motif name: Pax5**

Original motif    Consensus sequence: DGVBCABTGDWGCGRRCR



Reverse complement motif    Consensus sequence: MSGKKRCGCWDCABTGBBCD



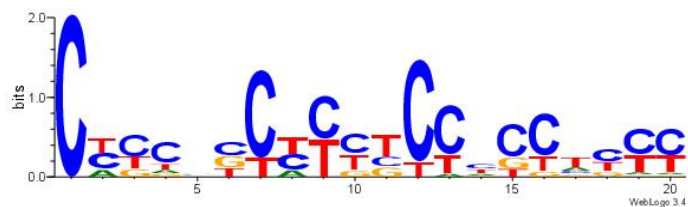
### Best Matches for Motif ID 31 (Highest to Lowest)

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

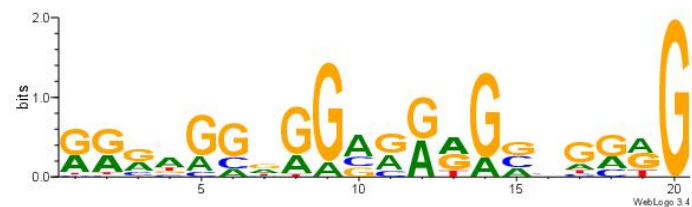
#### Alignment:

KKKAGGDGGAKKMGBBGKMG  
DGVBCABTGDWGCGRRCR

Original motif    Consensus sequence: CYYCBCYYYTCCHCCTYYY



Reverse complement motif    Consensus sequence: KKKAGGDGGAKKMGBBGKMG



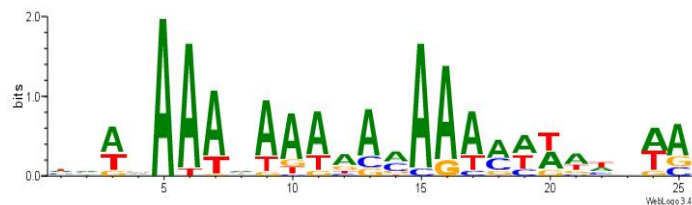
Dataset #: 5  
 Motif ID: 56  
 Motif name: TFM11  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 6  
 Number of overlap: 20  
 Similarity score: 0.0546306

Alignment:

HDWVAAAHAAAAAAMAAAMWWWHBWA  
 DGVBCABTGDWGCGRRCR-----

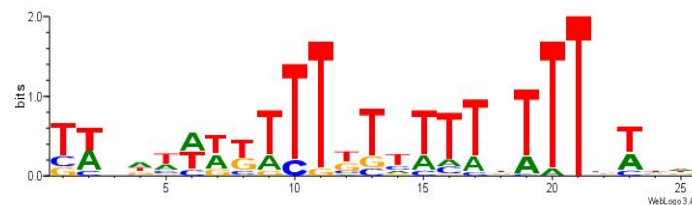
Original motif    Consensus sequence:

HDWVAAAHAAAAAAMAAAMWWWHBWA



Reverse complement motif    Consensus sequence:

TWVHWWWYTTTTTTTTTHTTTVWBH



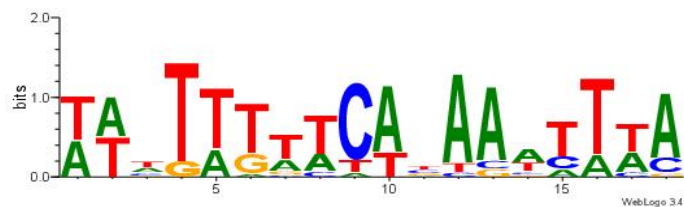
Dataset #: 5  
 Motif ID: 53  
 Motif name: TFM3  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward

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

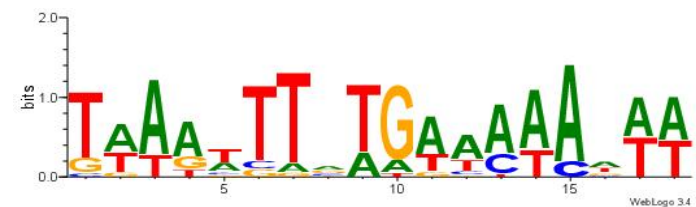
**Alignment:**

TWAAWTTVTGAAAAAHWW---  
 -DGVBCABTGDWGCGRRCR

Original motif    Consensus sequence: WWHTTTTTTCABAAWTTWA



Reverse complement motif    Consensus sequence: TWAAWTTVTGAAAAAHWW

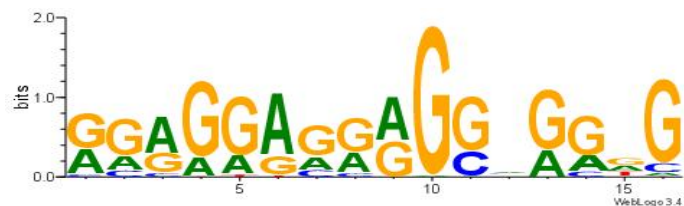


Dataset #: 5  
 Motif ID: 51  
 Motif name: TFM2  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 16  
 Similarity score: 2.0519

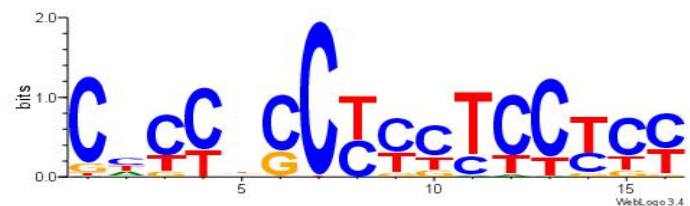
**Alignment:**

RGRGGAGRRGGHGGDG----  
 MSGKKRCGCWDCABTGBBCD

Original motif      Consensus sequence: RGRGGAGRRGGHGGDG



Reverse complement motif      Consensus sequence: CHCCBCCKMCTCCKCM

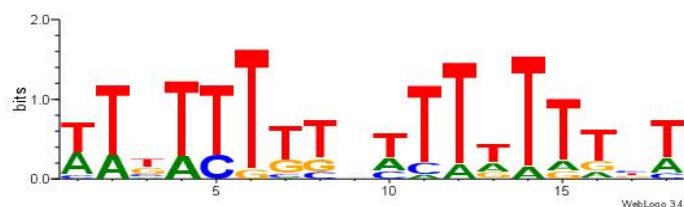


Dataset #: 5  
Motif ID: 52  
Motif name: TFM1  
Matching format of first motif: Original Motif  
Matching format of second motif: Reverse Complement  
Direction: Forward  
Position number: 3  
Number of overlap: 16  
Similarity score: 2.05456

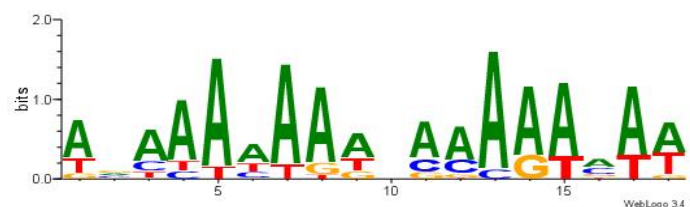
Alignment:

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: YGCCCCAGCH



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

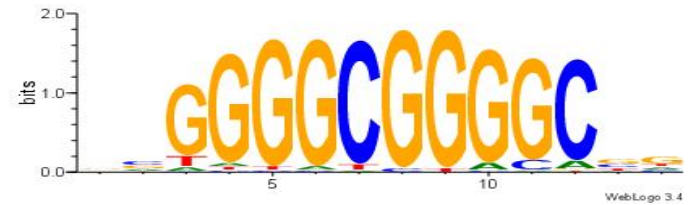
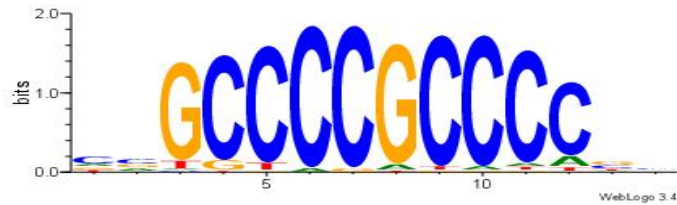


Dataset #: 4  
Motif ID: 36  
Motif name: csGCCCCGCCCCsc  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Original Motif  
Direction: Forward  
Position number: 5  
Number of overlap: 6  
Similarity score: 0.0396403

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

Original motif      Consensus sequence: HVGCCCCGCCCCBB

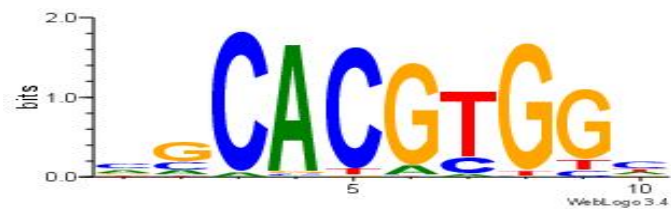
Reverse complement motif      Consensus sequence: BBGGGCGGGGC



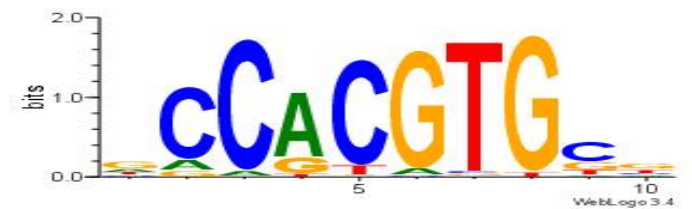
Dataset #: 3  
 Motif ID: 34  
 Motif name: Myc  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 3  
 Number of overlap: 6  
 Similarity score: 0.0399214

Alignment:  
 DCCACGTGCV  
 --YGCCGTG--

Original motif      Consensus sequence: VGCACGTGGH

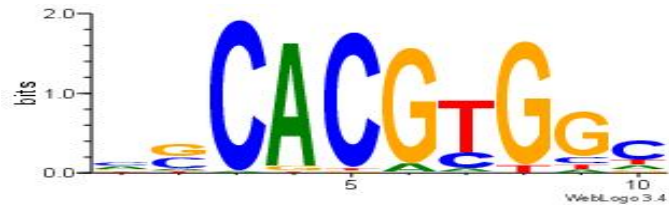


Reverse complement motif      Consensus sequence: DCCACGTGCV

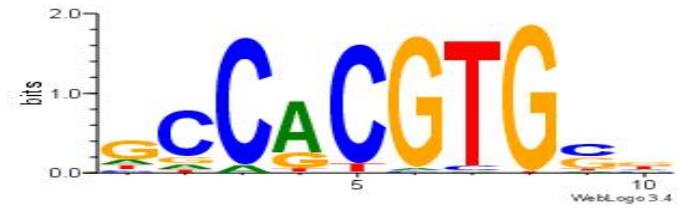


**Dataset #: 3      Motif ID: 33      Motif name: Mycn**

Original motif      Consensus sequence: HSCACGTGGC



Reverse complement motif      Consensus sequence: GCCACGTGSD



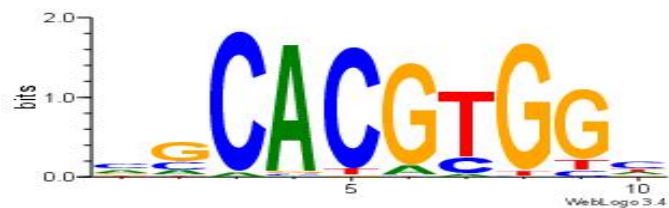
### Best Matches for Motif ID 33 (Highest to Lowest)

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

Alignment:

VGCACGTGGH  
HSCACGTGGC

Original motif      Consensus sequence: VGCACGTGGH



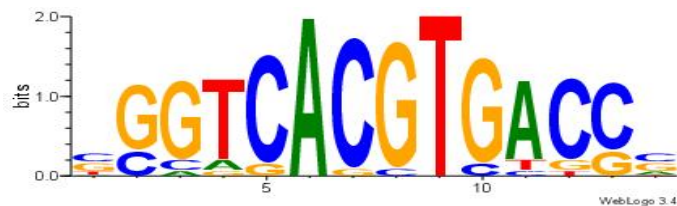
Reverse complement motif      Consensus sequence: DCCACGTGCV



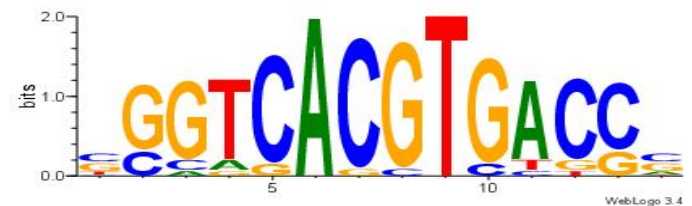
Dataset #: 4  
 Motif ID: 42  
 Motif name: sSGTCACGTGACSS  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 3  
 Number of overlap: 10  
 Similarity score: 0.0628441

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

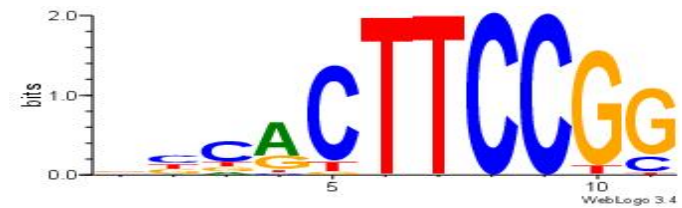
Alignment:

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

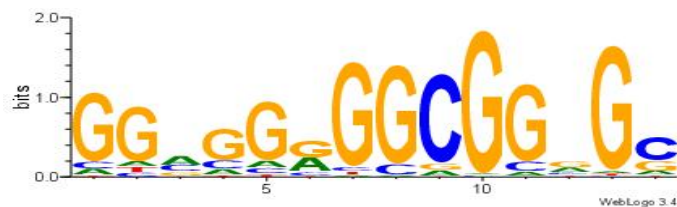
Reverse complement motif      Consensus sequence: GCCYCMCCCD



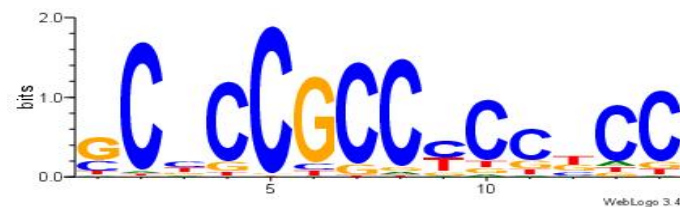
Dataset #: 5  
 Motif ID: 50  
 Motif name: TFF11  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 3  
 Number of overlap: 10  
 Similarity score: 0.0895444

Alignment:  
 GGMGGRGGCGGVGC  
 --HSCACGTGGC--

Original motif    Consensus sequence: GGMGGRGGCGGVGC



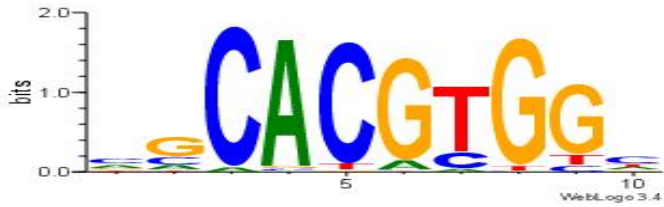
Reverse complement motif    Consensus sequence: GCVCCGCCMCCYC



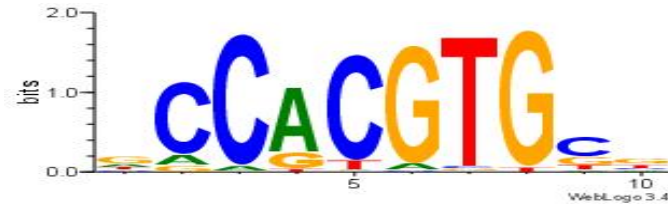
**Dataset #: 3      Motif ID: 34      Motif name: Myc**



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

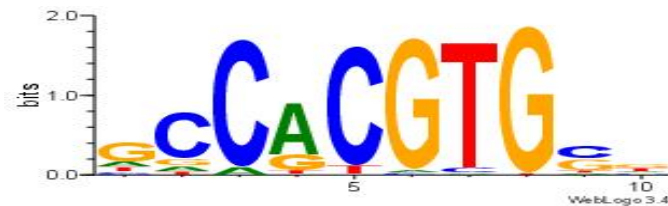
Alignment:

```
GCCACGTGSD  
DCCACGTGCV
```

Original motif      Consensus sequence: HSCACGTGGC



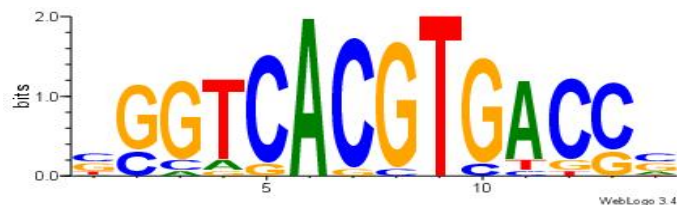
Reverse complement motif      Consensus sequence: GCCACGTGSD



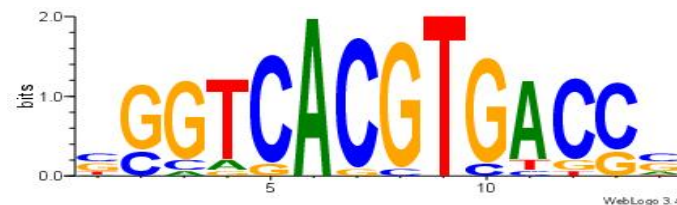
Dataset #: 4  
 Motif ID: 42  
 Motif name: sSGTCACGTGACsS  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 3  
 Number of overlap: 10  
 Similarity score: 0.0646601

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

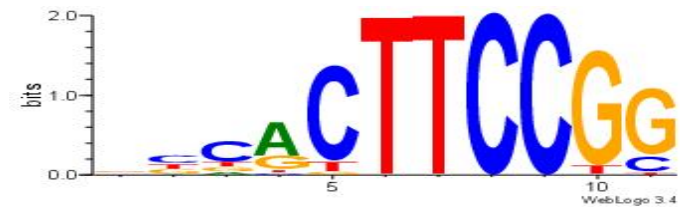
Alignment:

VVCACTTCCGG  
DCCACGTGCV-

Original motif    Consensus sequence: CCGGAAGTGVV



Reverse complement motif    Consensus sequence: VVCACTTCCGG



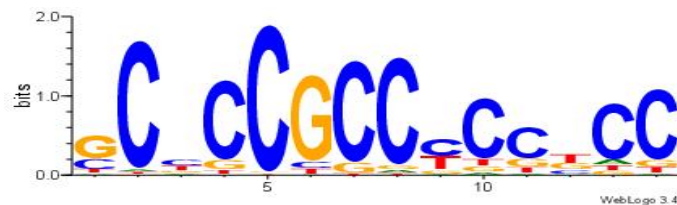
Dataset #: 5  
Motif ID: 50  
Motif name: TFF11  
Matching format of first motif: Original Motif  
Matching format of second motif: Original Motif  
Direction: Forward  
Position number: 3  
Number of overlap: 10  
Similarity score: 0.0851555

Alignment:

GGMGRRGGCGGVGC  
--VGCACGTGGH--

Original motif    Consensus sequence: GGMGRRGGCGGVGC

Reverse complement motif    Consensus sequence: GCVCCGCCMCCYGC

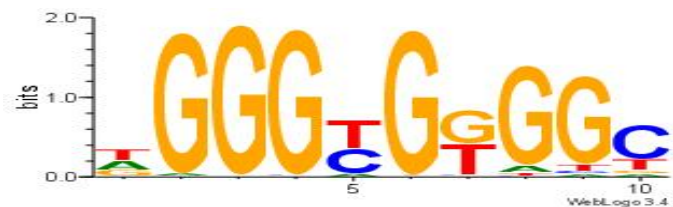


Dataset #: 3  
 Motif ID: 27  
 Motif name: Klf4  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 10  
 Similarity score: 0.0883745

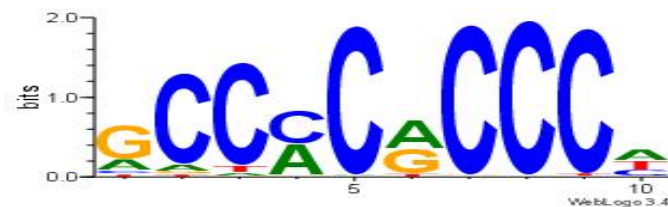
Alignment:

DGGYGKGGC  
 VGCACGTGGH

Original motif      Consensus sequence: DGGYGKGGC



Reverse complement motif      Consensus sequence: GCCYCMCCCD

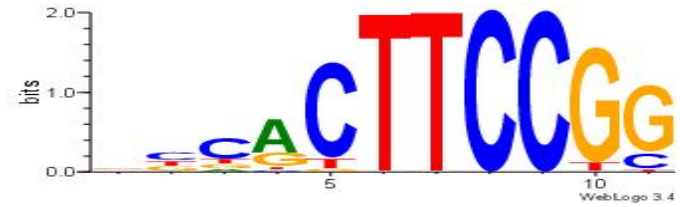


**Dataset #: 3      Motif ID: 35      Motif name: GABPA**

Original motif      Consensus sequence: CCGGAAGTGVV



Reverse complement motif      Consensus sequence: VVCACTTCCGG



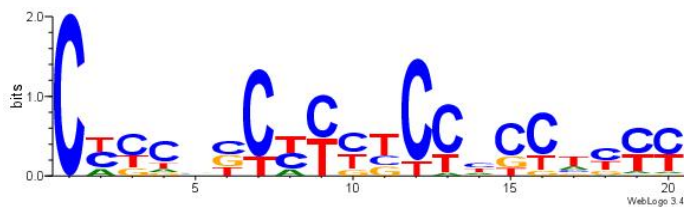
### Best Matches for Motif ID 35 (Highest to Lowest)

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

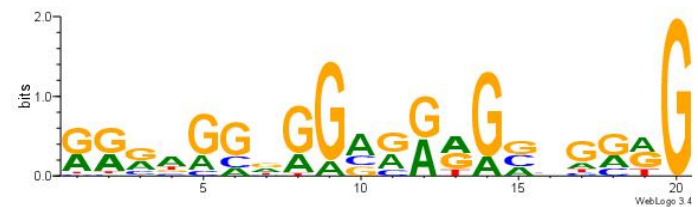
Alignment:

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

Original motif      Consensus sequence: CYVCBBCYYYTCCHCCTYYY



Reverse complement motif      Consensus sequence: KKKAGGDGGAKKMGBBGKMG

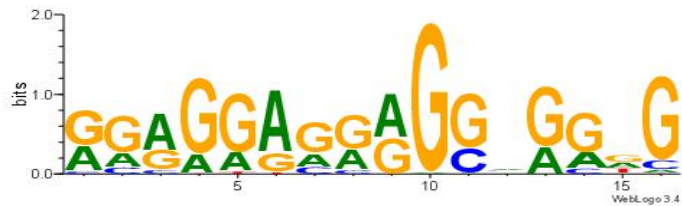


Dataset #: 5  
 Motif ID: 51  
 Motif name: TFM2  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 5  
 Number of overlap: 11  
 Similarity score: 0.0445566

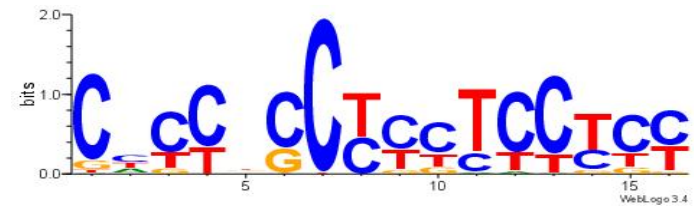
Alignment:

RGRGGAGRRGGHGGDG  
 -CCGGAAGTGVV-----

Original motif      Consensus sequence: RGRGGAGRRGGHGGDG



Reverse complement motif      Consensus sequence: CHCCBCKMCTCCKCM



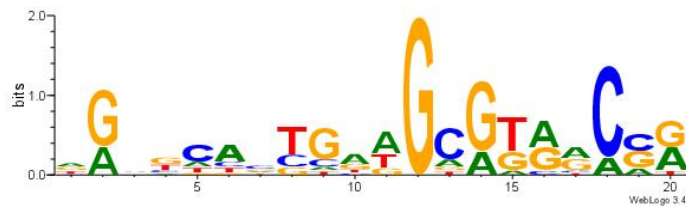
Dataset #: 3  
 Motif ID: 31  
 Motif name: Pax5  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 3

Number of overlap: 11  
Similarity score: 0.0446257

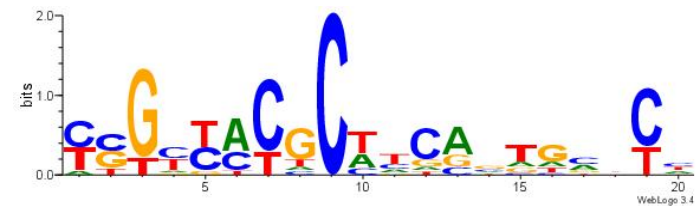
Alignment:

DGVBCABTGDWGCGRRCR  
-----VVCACTTCCGG--

Original motif      Consensus sequence: DGVBCABTGDWGCGRRCR



Reverse complement motif      Consensus sequence:  
MSGKKRCGCWDCABTGBBCD



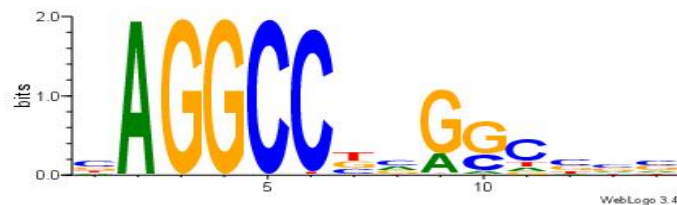
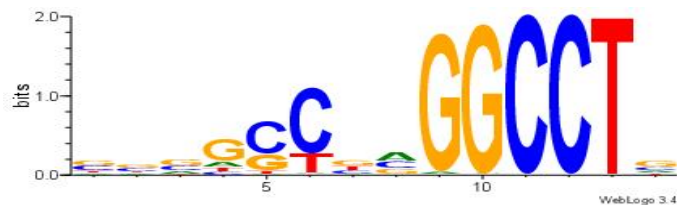
Dataset #: 3  
Motif ID: 22  
Motif name: Zfx  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Original Motif  
Direction: Backward  
Position number: 4  
Number of overlap: 11  
Similarity score: 0.0457327

Alignment:

BBVGCCBVGGCCTV  
VVCACTTCCGG---

Original motif      Consensus sequence: BBVGCCBVGGCCTV

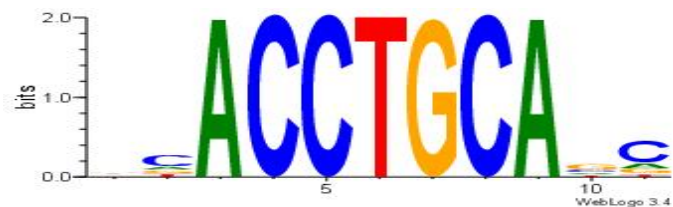
Reverse complement motif      Consensus sequence: VAGGCCBBGGCV



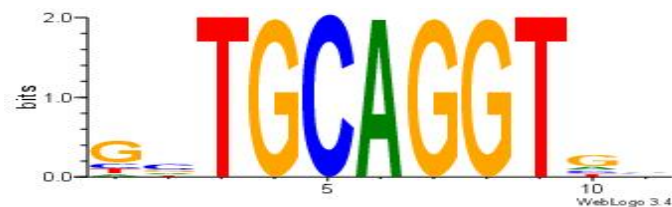
Dataset #: 4  
 Motif ID: 40  
 Motif name: kcACCTGCAGc  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 11  
 Similarity score: 0.0483841

Alignment:  
 BCACCTGCABC  
 VVCACTTCCGG

Original motif      Consensus sequence: BCACCTGCABC



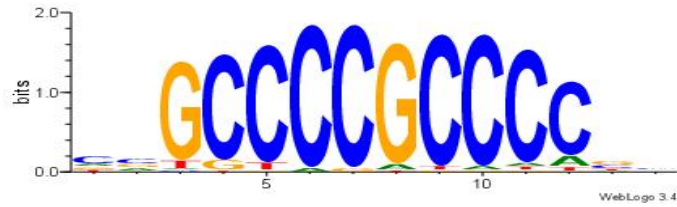
Reverse complement motif      Consensus sequence: GBTGCAGGTGB



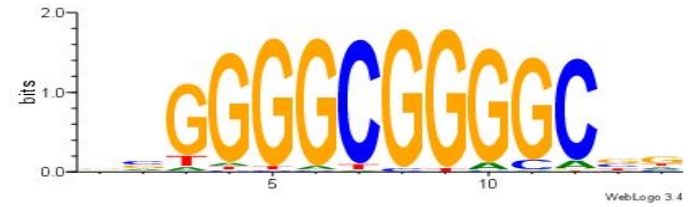
**Dataset #: 4      Motif ID: 36      Motif name: csGCCCCGCCCCsc**



Original motif    Consensus sequence: HVGCCCCGCCCB



Reverse complement motif    Consensus sequence: BBGGGCGGGGC



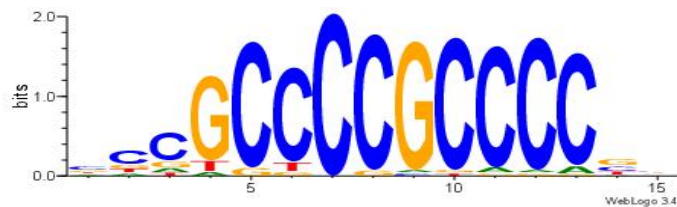
### Best Matches for Motif ID 36 (Highest to Lowest)

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

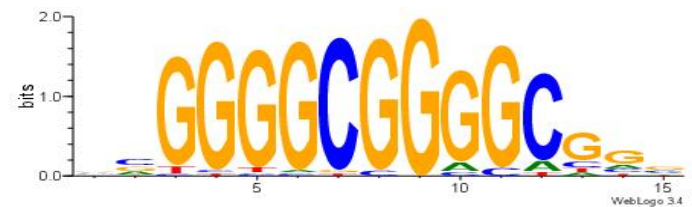
#### Alignment:

BBGGGCGGGGCGGB  
 BBGGGCGGGGCVD-

Original motif    Consensus sequence: BCCGCCCGCCCCB



Reverse complement motif    Consensus sequence: BBGGGCGGGGCGGB

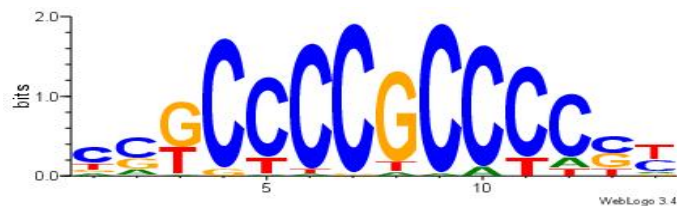


Dataset #: 2  
 Motif ID: 7  
 Motif name: Motif 7  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 14  
 Similarity score: 0.0117332

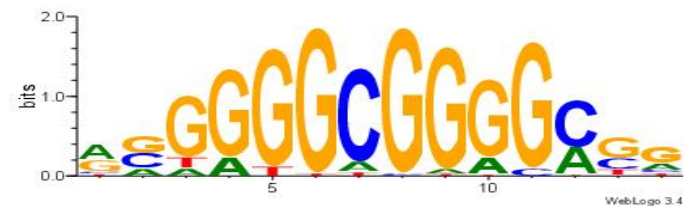
Alignment:

CSKCCCCGCCCSY  
 HVGCCCCGCCCB

Original motif      Consensus sequence: CSKCCCCGCCCSY



Reverse complement motif      Consensus sequence: MSGGGCGGGY



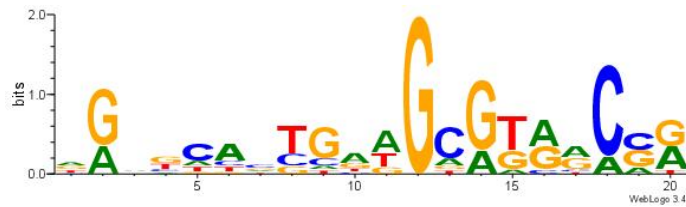
Dataset #: 3  
 Motif ID: 31  
 Motif name: Pax5  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 14

Similarity score: 0.0747029

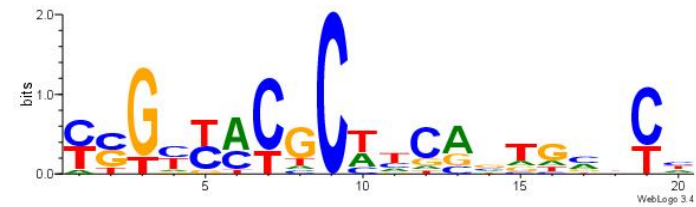
Alignment:

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:

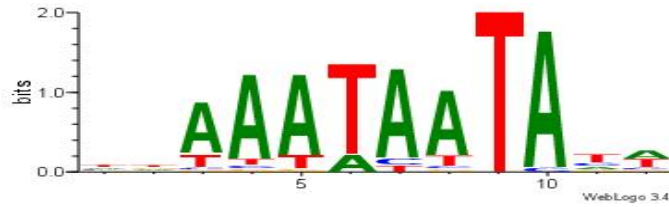
CYYCBBCYYYYTCCHCCTYYY  
---HVGCCCCGCCCCBB---

Original motif      Consensus sequence: CYYCBBCYYYYTCCHCCTYYY

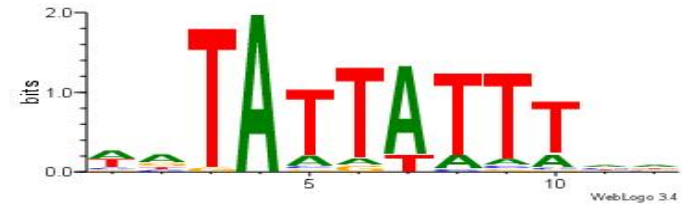
Reverse complement motif      Consensus sequence:  
KKKAGGDGGAKKMGBBGKMG



Original motif    Consensus sequence: HDAAATAATAHW



Reverse complement motif    Consensus sequence: WHTATTATTTDH



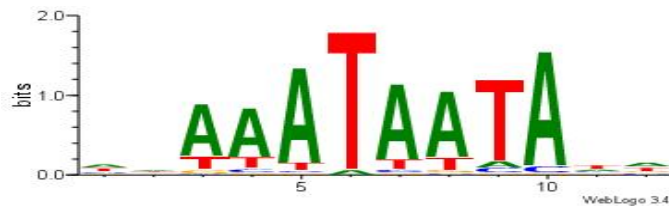
### Best Matches for Motif ID 37 (Highest to Lowest)

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

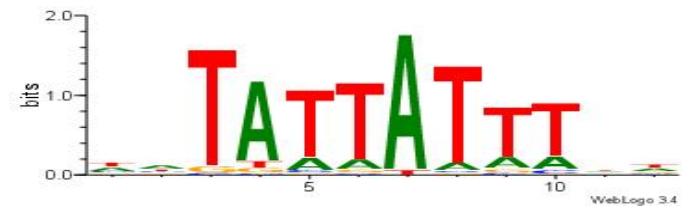
Alignment:

```
HDAAATAATADD
HDAAATAATAHW
```

Original motif    Consensus sequence: HDAAATAATADD



Reverse complement motif    Consensus sequence: DDTATTATTTDH

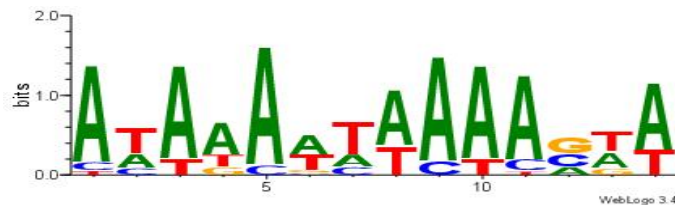


Dataset #: 2  
 Motif ID: 3  
 Motif name: Motif 3  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 2  
 Number of overlap: 12  
 Similarity score: 0.0522317

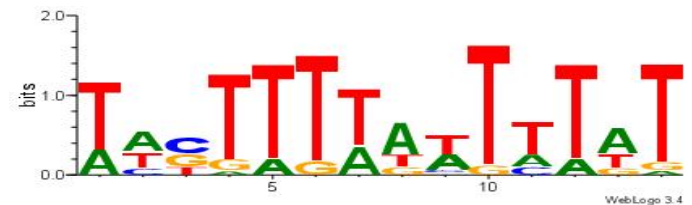
Alignment:

TWSTTTWAWTTTWT  
 -WHTATTATTTDH-

Original motif      Consensus sequence: AWAAAWTWAAASWA



Reverse complement motif      Consensus sequence: TWSTTTWAWTTTWT



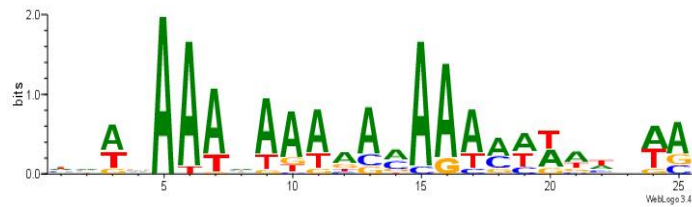
Dataset #: 5  
 Motif ID: 56  
 Motif name: TFM11  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 3  
 Number of overlap: 12

Similarity score: 0.0590505

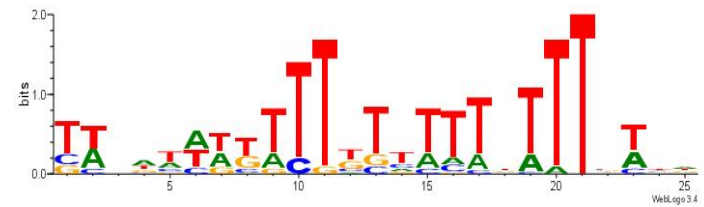
Alignment:

TWVHWWYTTTYTTTTHTTTVWBH  
-----WHTATTATTTDH--

Original motif    Consensus sequence:  
HDWVAAAHAAAAAMAAAMWWWHBWA



Reverse complement motif    Consensus sequence:  
TWVHWWYTTTYTTTTHTTTVWBH



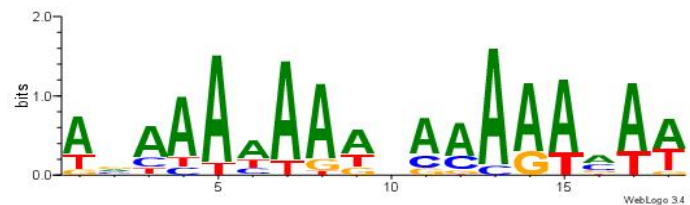
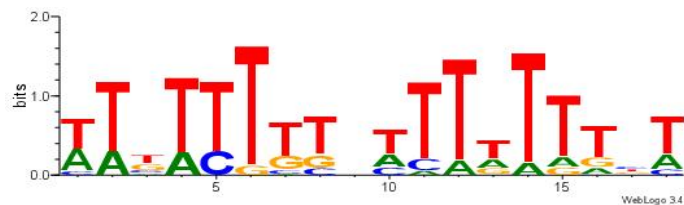
Dataset #: 5  
Motif ID: 52  
Motif name: TFM1  
Matching format of first motif: Original Motif  
Matching format of second motif: Reverse Complement  
Direction: Forward  
Position number: 1  
Number of overlap: 12  
Similarity score: 0.0637702

Alignment:

ABAAAAAWhAAAAARAW  
HDAAATAATAHW-----

Original motif    Consensus sequence: WTKTTTTTHWTTTTTTTBT

Reverse complement motif    Consensus sequence:  
ABAAAAAWhAAAAARAW

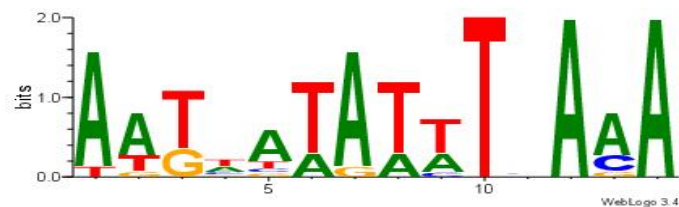


Dataset #: 2  
 Motif ID: 9  
 Motif name: Motif 9  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 12  
 Similarity score: 0.0641975

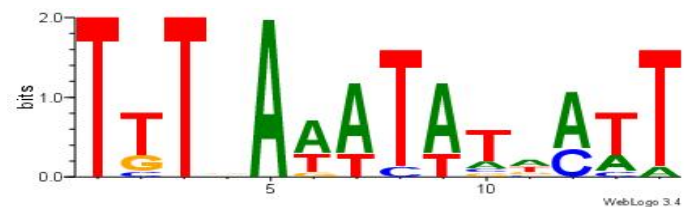
Alignment:

AATHATATWTHAAA  
 --WHTATTATTTDH

Original motif      Consensus sequence: AATHATATWTHAAA



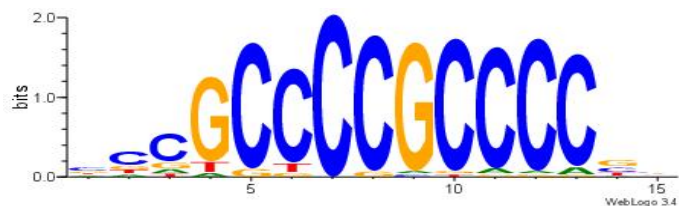
Reverse complement motif      Consensus sequence: TTTDAWATATHAT



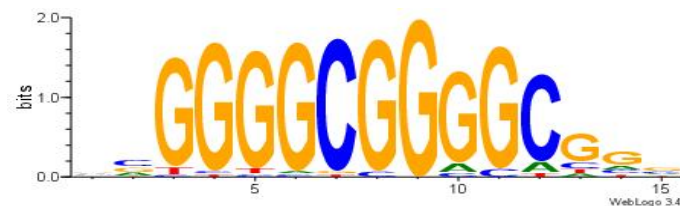
**Dataset #: 4      Motif ID: 38      Motif name: cccGCCCGCCCSb**



Original motif      Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif      Consensus sequence: BBGGGGCGGGGCGGB



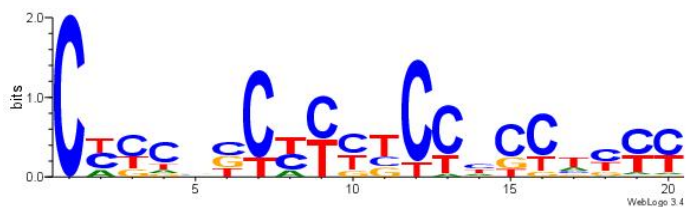
### Best Matches for Motif ID 38 (Highest to Lowest)

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

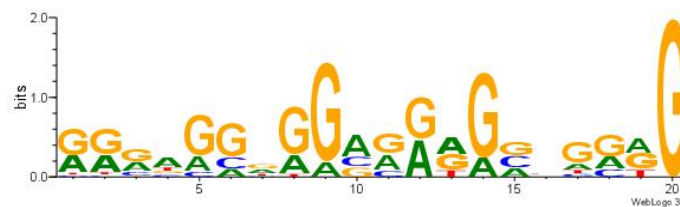
#### Alignment:

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

Original motif      Consensus sequence: CYYCBBBCYYYTCCHCCTYYY



Reverse complement motif      Consensus sequence: KKKAGGDGGAKKMGBBGKMG

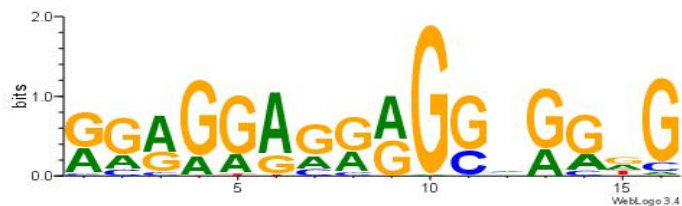


Dataset #: 5  
 Motif ID: 51  
 Motif name: TFM2  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 2  
 Number of overlap: 15  
 Similarity score: 0.0869149

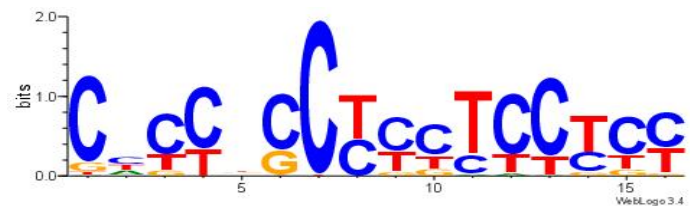
Alignment:

RGRGGAGRRGGHGGDG  
 BBGGGGCGGGGCGGB-

Original motif    Consensus sequence: RGRGGAGRRGGHGGDG



Reverse complement motif    Consensus sequence: CHCCBCKMCTCKCM



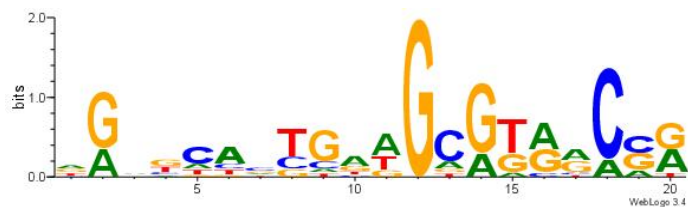
Dataset #: 3  
 Motif ID: 31  
 Motif name: Pax5  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward

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

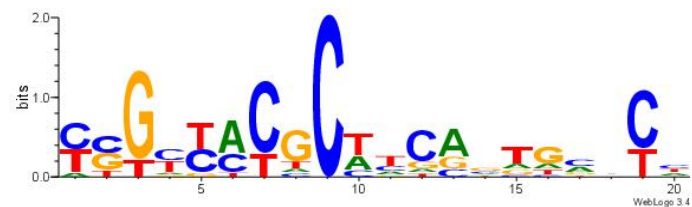
**Alignment:**

MSGKKRCGCWDCABTGBBCD  
 BBGGGGCGGGGCGGB-----

Original motif      Consensus sequence: DGVBCABTGDWGCGRRCR



Reverse complement motif      Consensus sequence: MSGKKRCGCWDCABTGBBCD

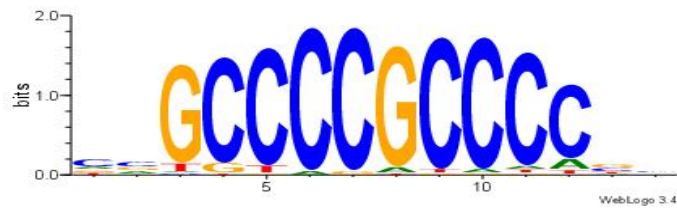


Dataset #: 4  
 Motif ID: 36  
 Motif name: csGCCCCGCCCCsc  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 14  
 Similarity score: 0.5

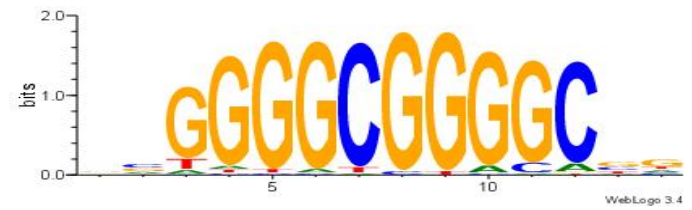
**Alignment:**

-HVGCCCCGCCCCBB  
 BCCGCCCCGCCCCBB

Original motif      Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif      Consensus sequence: BBGGGGCGGGGC

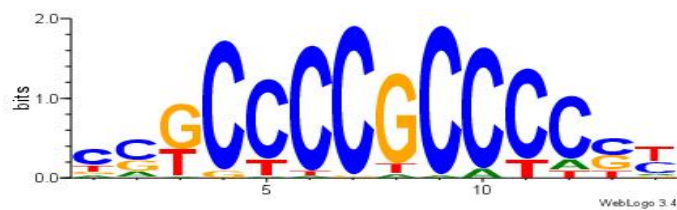


Dataset #: 2  
Motif ID: 7  
Motif name: Motif 7  
Matching format of first motif: Original Motif  
Matching format of second motif: Original Motif  
Direction: Backward  
Position number: 1  
Number of overlap: 14  
Similarity score: 0.513015

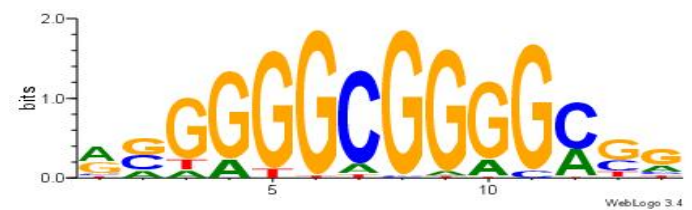
Alignment:

-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)

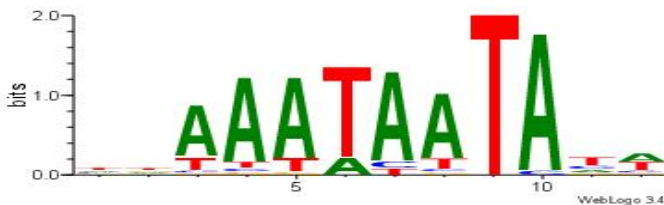
Dataset #:	4
Motif ID:	37
Motif name:	tkAAATAATAtw
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	2
Number of overlap:	11
Similarity score:	0.0559269

Alignment:

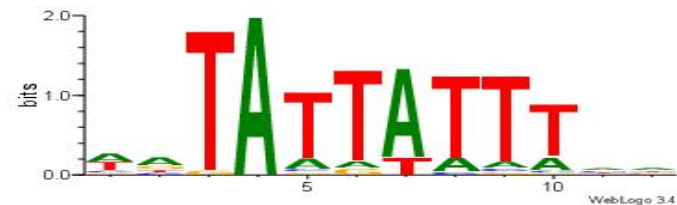
WHTATTATTTDH

-MBATTGGCTGH

Original motif      Consensus sequence: HDAAATAATAHW



Reverse complement motif      Consensus sequence: WHTATTATTTDH

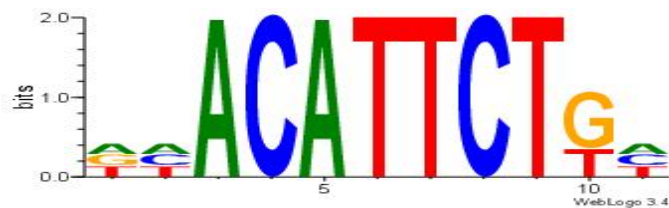


Dataset #: 4  
 Motif ID: 44  
 Motif name: dhACATTCTkh  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 11  
 Similarity score: 0.0588235

Alignment:

HCAGAATGTHD  
 DCAGCCAATVR

Original motif      Consensus sequence: DHACATTCTGH



Reverse complement motif      Consensus sequence: HCAGAATGTHD

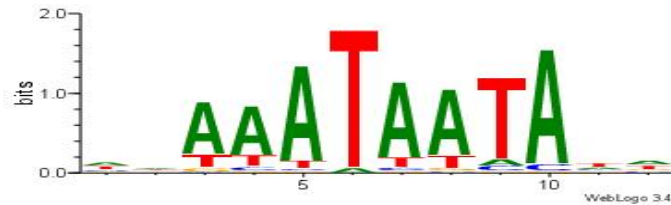


Dataset #: 4  
 Motif ID: 41  
 Motif name: wwAAATAATAtw  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 1

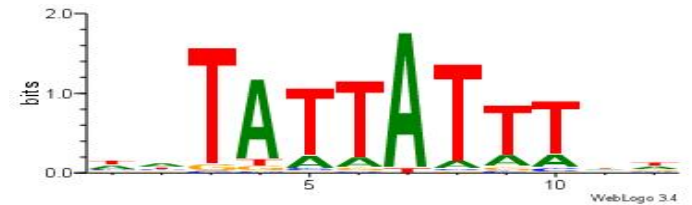
Number of overlap: 11  
Similarity score: 0.0597643

Alignment:  
DDTATTATTTDH  
-MBATTGGCTGH

Original motif    Consensus sequence: HDAAATAATADD



Reverse complement motif    Consensus sequence: DDTATTATTTDH

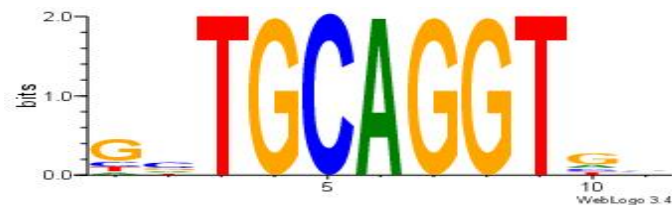
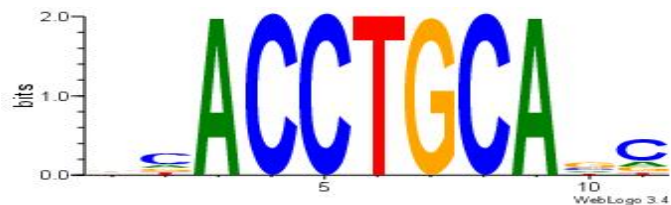


Dataset #: 4  
Motif ID: 40  
Motif name: kcACCTGCAGc  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Original Motif  
Direction: Backward  
Position number: 1  
Number of overlap: 11  
Similarity score: 0.0599548

Alignment:  
BCACCTGCABC  
MBATTGGCTGH

Original motif    Consensus sequence: BCACCTGCABC

Reverse complement motif    Consensus sequence: GBTGCAGGTGB



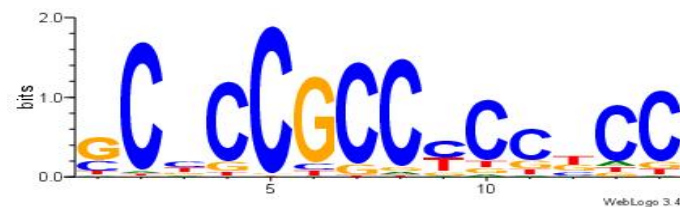
Dataset #: 5  
 Motif ID: 50  
 Motif name: TFF11  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 2  
 Number of overlap: 11  
 Similarity score: 0.0614719

Alignment:  
 GCVCCGCCMCCYCC  
 --DCAGCCAATVR--

Original motif    Consensus sequence: GGMGRRGGCGGVGC



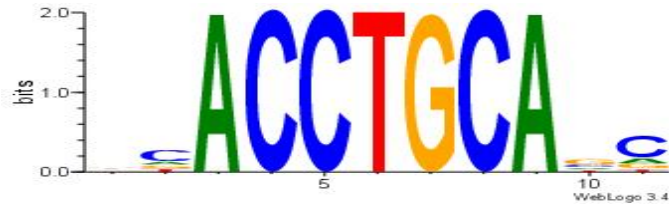
Reverse complement motif    Consensus sequence: GCVCCGCCMCCYCC



**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

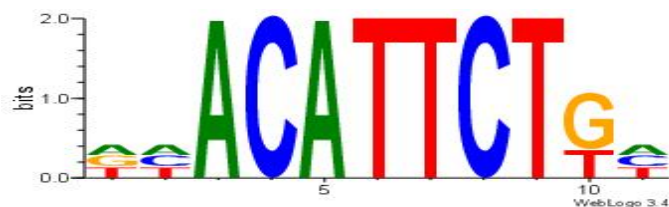


Dataset #: 4  
 Motif ID: 44  
 Motif name: dhACATTCTkh  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 11  
 Similarity score: 0.0254134

Alignment:

DHACATTCTGH  
 BCACCTGCABC

Original motif      Consensus sequence: DHACATTCTGH



Reverse complement motif      Consensus sequence: HCAGAATGTHD



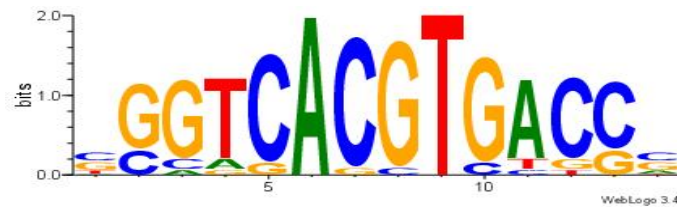
Dataset #: 4  
 Motif ID: 42  
 Motif name: sSGTCACGTGACSS  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 4  
 Number of overlap: 11

Similarity score: 0.031338

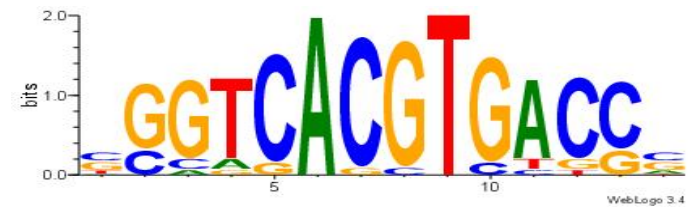
Alignment:

SGGTCACGTGACCS  
---BCACCTGCABC

Original motif    Consensus sequence: SGGTCACGTGACCS



Reverse complement motif    Consensus sequence: SGGTCACGTGACCS



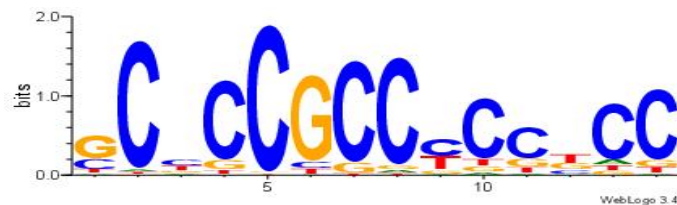
Dataset #: 5  
Motif ID: 50  
Motif name: TFF11  
Matching format of first motif: Original Motif  
Matching format of second motif: Reverse Complement  
Direction: Backward  
Position number: 4  
Number of overlap: 11  
Similarity score: 0.034471

Alignment:

GCVCCGCCMCCYCC  
BCACCTGCABC---

Original motif    Consensus sequence: GGMGRRGGCGGVGC

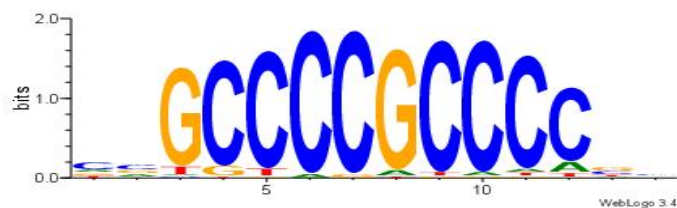
Reverse complement motif    Consensus sequence: GCVCCGCCMCCYCC



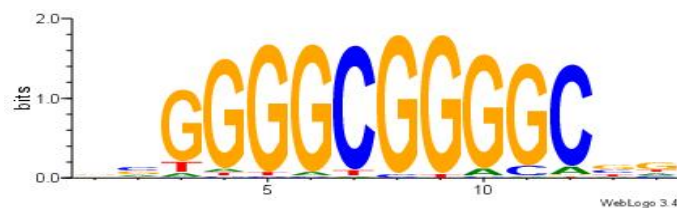
Dataset #: 4  
 Motif ID: 36  
 Motif name: csGCCCCGCCCCsc  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 3  
 Number of overlap: 11  
 Similarity score: 0.0402518

Alignment:  
 HVGCCCCGCCCCBB  
 -BCACCTGCABC--

Original motif    Consensus sequence: HVGCCCCGCCCCBB

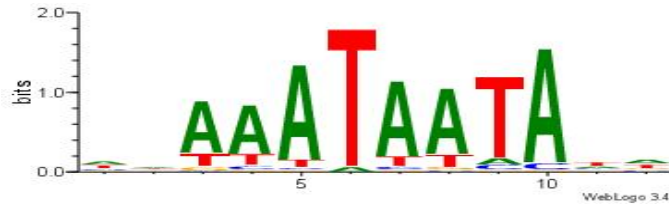


Reverse complement motif    Consensus sequence: BBGGGCGGGGC

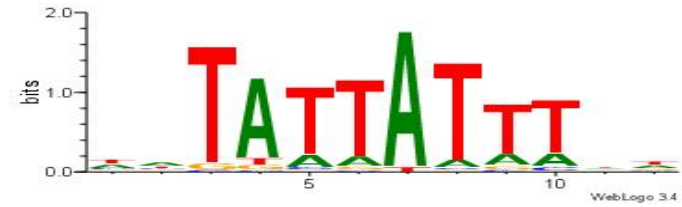


**Dataset #: 4      Motif ID: 41      Motif name: wwAAATAATAtw**

Original motif    Consensus sequence: HDAAATAATADD



Reverse complement motif    Consensus sequence: DDTATTATTTDH



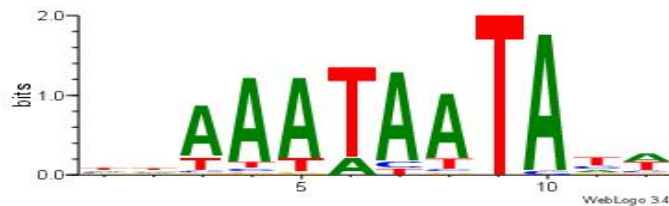
### Best Matches for Motif ID 41 (Highest to Lowest)

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

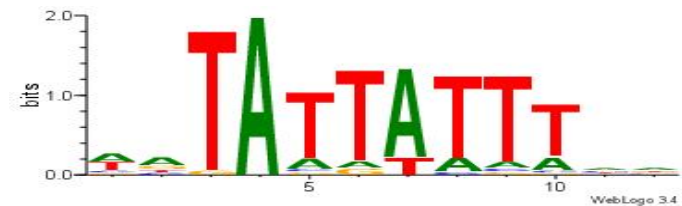
Alignment:

HDAAATAATAHW  
HDAAATAATADD

Original motif    Consensus sequence: HDAAATAATAHW



Reverse complement motif    Consensus sequence: WHTATTATTTDH

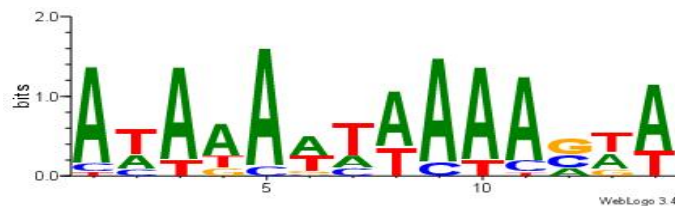


Dataset #: 2  
 Motif ID: 3  
 Motif name: Motif 3  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 2  
 Number of overlap: 12  
 Similarity score: 0.0536028

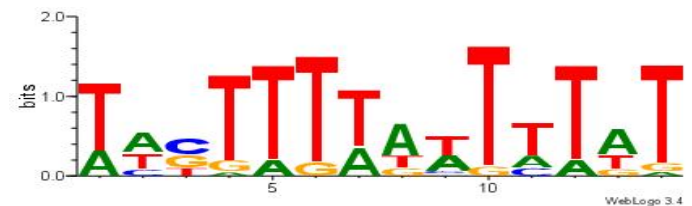
Alignment:

AWAAAWTWAAASWA  
 -HDAAATAATADD-

Original motif      Consensus sequence: AWAAAWTWAAASWA



Reverse complement motif      Consensus sequence: TWSTTTWAWTTT



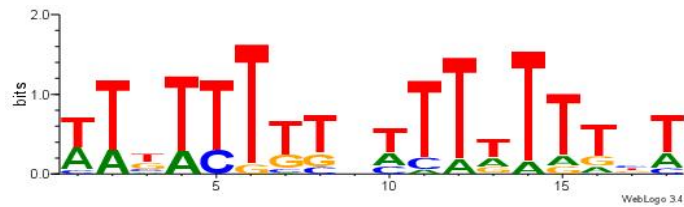
Dataset #: 5  
 Motif ID: 52  
 Motif name: TFM1  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 7  
 Number of overlap: 12

Similarity score: 0.0565705

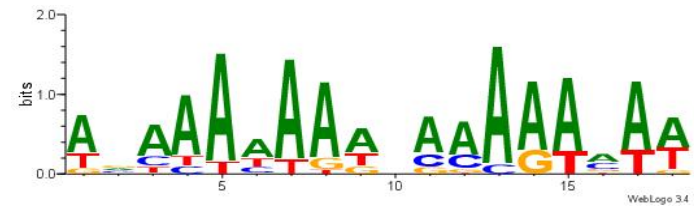
Alignment:

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

Original motif      Consensus sequence: WKTTTTTHWTTTTTBT



Reverse complement motif      Consensus sequence:  
ABAAAAAWHAAAAARAW



---

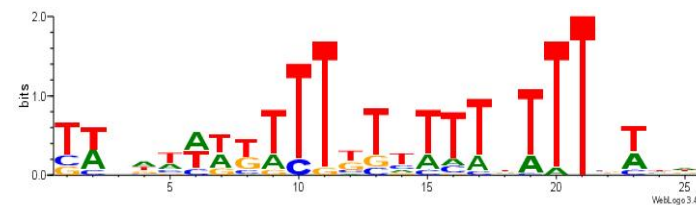
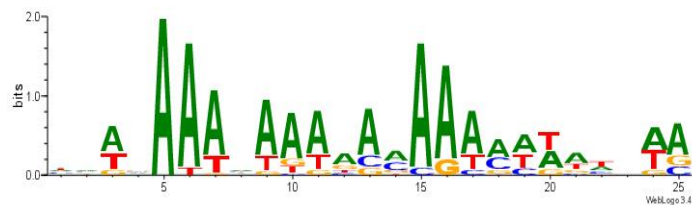
Dataset #: 5  
Motif ID: 56  
Motif name: TFM11  
Matching format of first motif: Original Motif  
Matching format of second motif: Original Motif  
Direction: Forward  
Position number: 3  
Number of overlap: 12  
Similarity score: 0.0575935

Alignment:

```
HDWVAAAHAAAAAMAAAMWWWHBWA  
--HDAATAATADD-----
```

Original motif      Consensus sequence:  
HDWVAAAHAAAAAMAAAMWWWHBWA

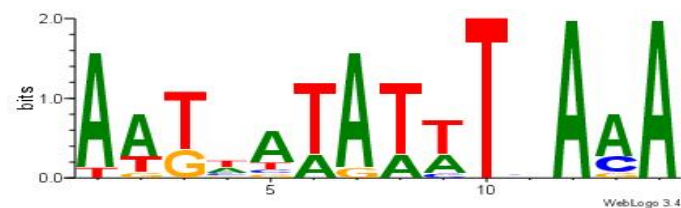
Reverse complement motif      Consensus sequence:  
TWVHWWWYTTTTTTTTTHTTTVWBH



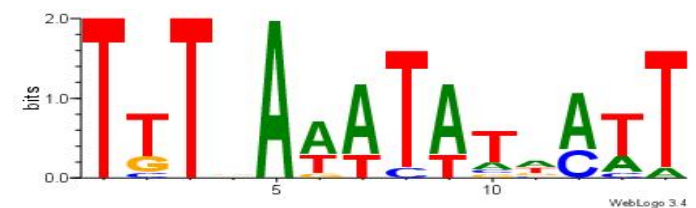
Dataset #: 2  
 Motif ID: 9  
 Motif name: Motif 9  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 3  
 Number of overlap: 12  
 Similarity score: 0.0591821

Alignment:  
 AATHATATWTHAAA  
 --DDTATTATTTDH

Original motif      Consensus sequence: AATHATATWTHAAA



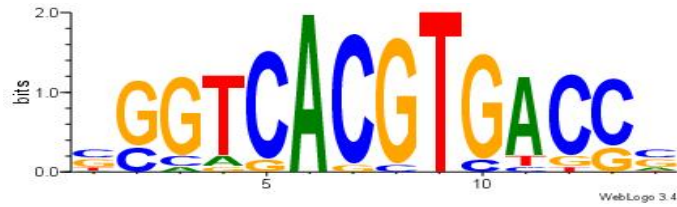
Reverse complement motif      Consensus sequence: TTTDAWATATHAT



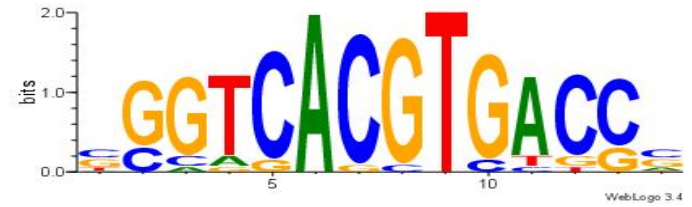
**Dataset #: 4      Motif ID: 42      Motif name: sSGTCACGTGACsS**



Original motif    Consensus sequence: SGGTCACGTGACCS



Reverse complement motif    Consensus sequence: SGGTCACGTGACCS



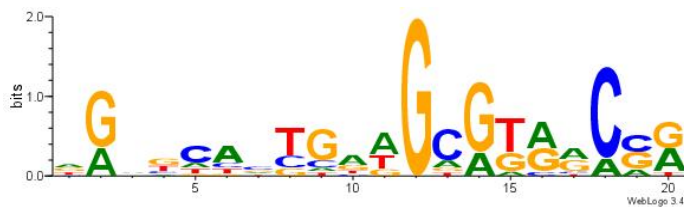
### Best Matches for Motif ID 42 (Highest to Lowest)

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

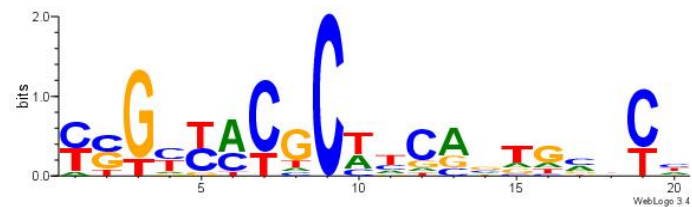
#### Alignment:

```
DGVBCABTGDWGCGRRCR
-----SSGGTCACGTGACCS
```

Original motif    Consensus sequence: DGVBCABTGDWGCGRRCR



Reverse complement motif    Consensus sequence: MSGKKRCGCWDCABTGBCD

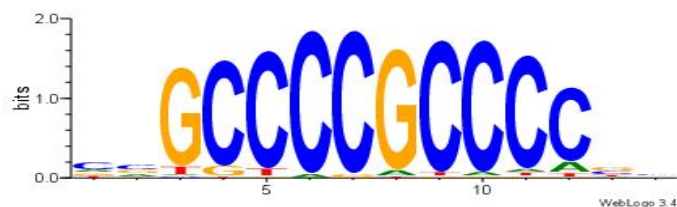


Dataset #: 4  
 Motif ID: 36  
 Motif name: csGCCCCGCCCCsc  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 14  
 Similarity score: 0.0539097

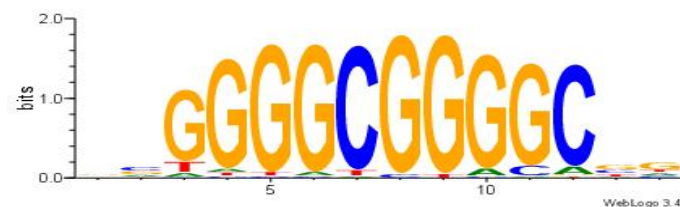
Alignment:

BBGGGGCGGGCVD  
 SGGTCACGTGACCS

Original motif    Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif    Consensus sequence: BBGGGGCGGGGC



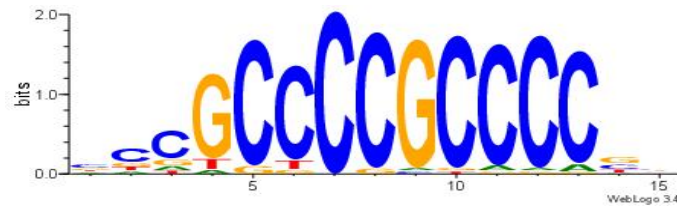
Dataset #: 4  
 Motif ID: 38  
 Motif name: cccGCCCCGCCCCsb  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 14

Similarity score: 0.0581955

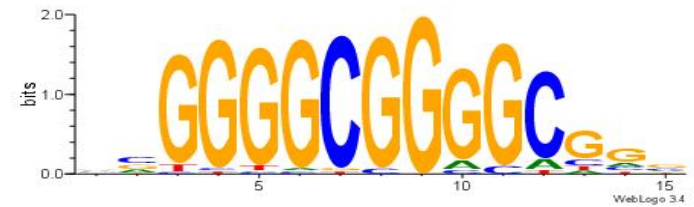
Alignment:

BCCGCCCCGCCCCBB  
SGGTCACGTGACCS-

Original motif      Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif      Consensus sequence: BBGGGGCGGGGCGGB



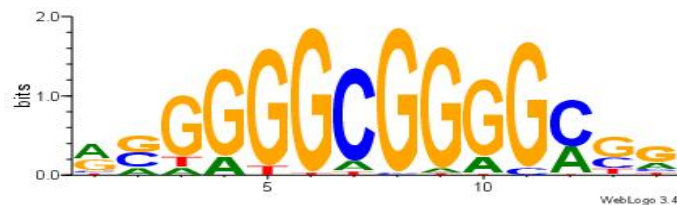
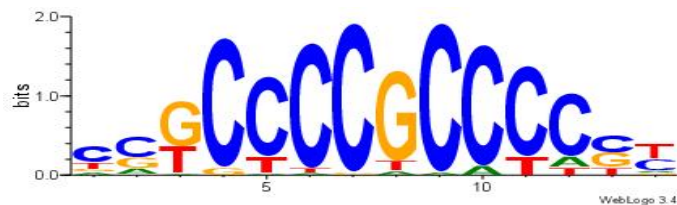
Dataset #: 2  
Motif ID: 7  
Motif name: Motif 7  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Reverse Complement  
Direction: Backward  
Position number: 1  
Number of overlap: 14  
Similarity score: 0.0634135

Alignment:

MSGGGGCGGGGYSG  
SGGTCACGTGACCS

Original motif      Consensus sequence: CSKCCCCGCCCCSY

Reverse complement motif      Consensus sequence: MSGGGGCGGGGY



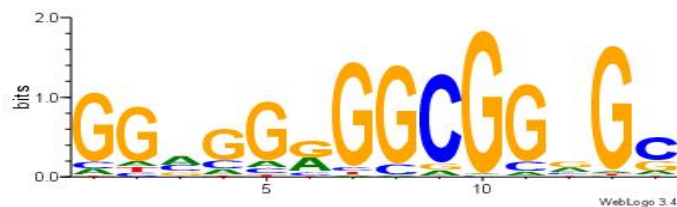
Dataset #: 5  
 Motif ID: 50  
 Motif name: TFF11  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 3  
 Number of overlap: 12  
 Similarity score: 1.05855

Alignment:

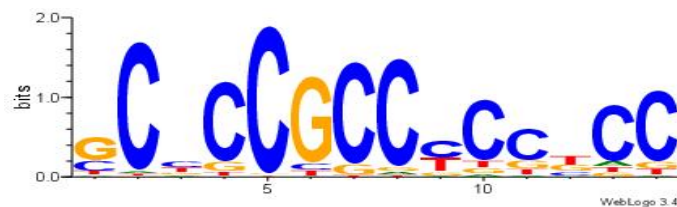
```

--GCVCCGCCMCCYCC
SGGTCACGTGACCS--
  
```

Original motif      Consensus sequence: GGMGRRGGCGGVGC



Reverse complement motif      Consensus sequence: GCVCCGCCMCCYCC

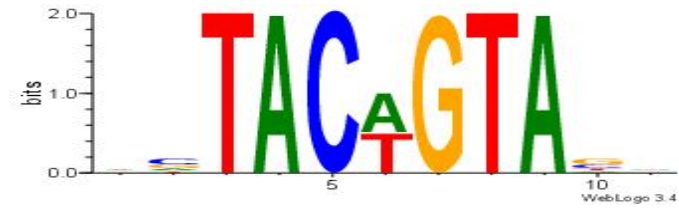


**Dataset #: 4      Motif ID: 43      Motif name: wsTACwGTAsw**

Original motif      Consensus sequence: HVTACWG TABD



Reverse complement motif      Consensus sequence: DBTACWG TAVH



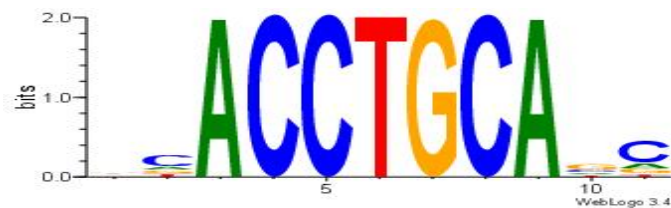
### Best Matches for Motif ID 43 (Highest to Lowest)

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

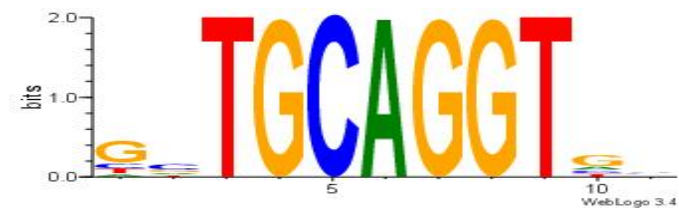
Alignment:

GBTGCAGGTGB  
HVTACWG TABD

Original motif      Consensus sequence: BCACCTGC ABC



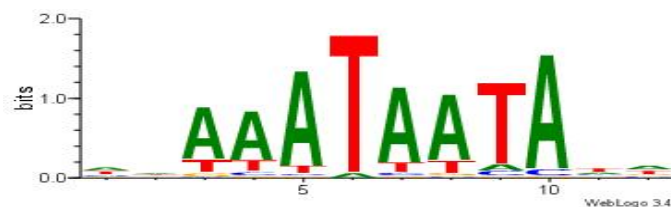
Reverse complement motif      Consensus sequence: GBTGCAGGTGB



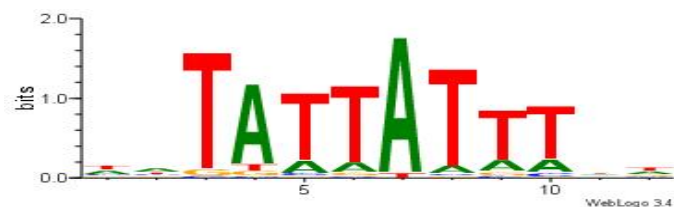
Dataset #: 4  
 Motif ID: 41  
 Motif name: wwAAATAATAtw  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 2  
 Number of overlap: 11  
 Similarity score: 0.0309343

Alignment:  
 DDTATTATTTDH  
 -HVTACWGTABD

Original motif      Consensus sequence: HDAAATAATADD



Reverse complement motif      Consensus sequence: DDTATTATTTDH

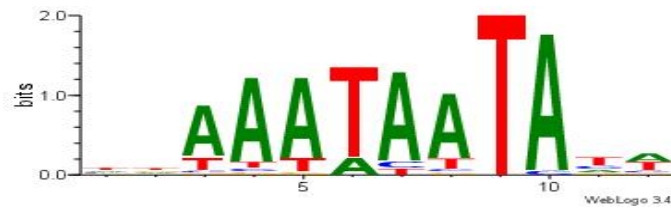


Dataset #: 4  
 Motif ID: 37  
 Motif name: tkAAATAATAtw  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 11

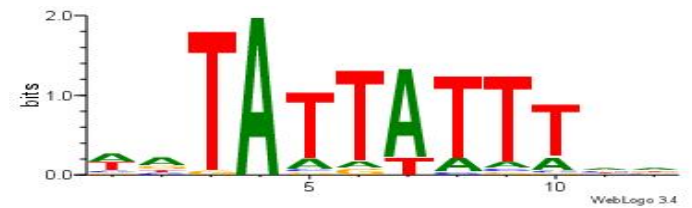
Similarity score: 0.0337121

Alignment:  
HDAAATAATAHW  
DBTACWGTAVH-

Original motif      Consensus sequence: HDAAATAATAHW



Reverse complement motif      Consensus sequence: WHTATTATTTDH

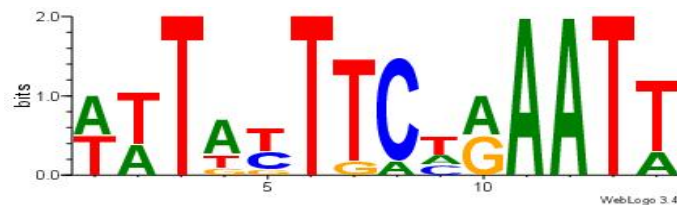


Dataset #: 2  
Motif ID: 6  
Motif name: Motif 6  
Matching format of first motif: Original Motif  
Matching format of second motif: Original Motif  
Direction: Backward  
Position number: 4  
Number of overlap: 11  
Similarity score: 0.0353535

Alignment:  
AATTYDGAARTAWW  
HVTACWGTABD---

Original motif      Consensus sequence: AATTYDGAARTAWW

Reverse complement motif      Consensus sequence: WWTAKTTCDKAAAT



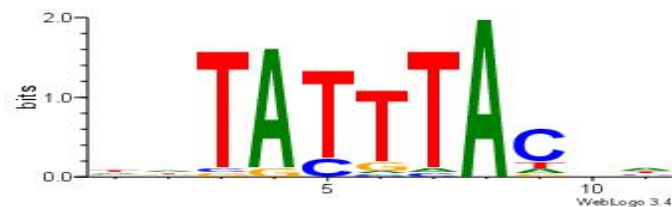
Dataset #: 4  
 Motif ID: 45  
 Motif name: wbgTAAATAww  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 11  
 Similarity score: 0.037518

Alignment:  
 DBGTAATAHD  
 DBTACWGTAVH

Original motif      Consensus sequence: DBGTAATAHD



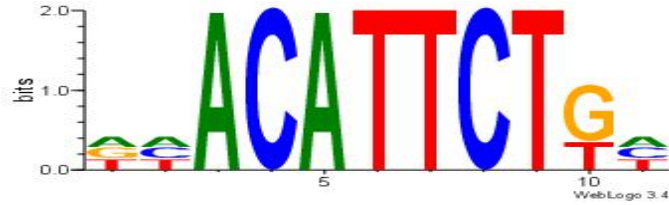
Reverse complement motif      Consensus sequence: DHTATTTACBD



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



Original motif      Consensus sequence: DHACATTCTGH



Reverse complement motif      Consensus sequence: HCAGAATGTHD



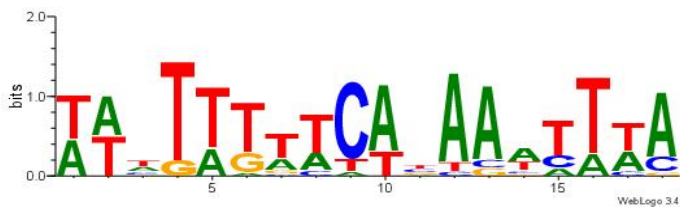
### Best Matches for Motif ID 44 (Highest to Lowest)

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

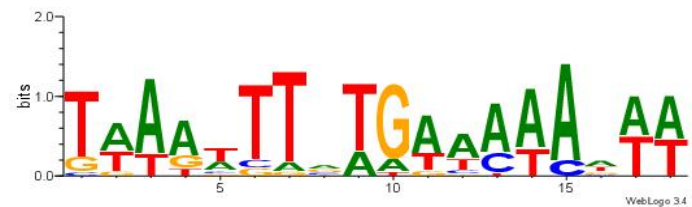
Alignment:

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

Original motif      Consensus sequence: WWHTTTTTCABAATTWA



Reverse complement motif      Consensus sequence: TWAAWTTVTGAAAAHWW

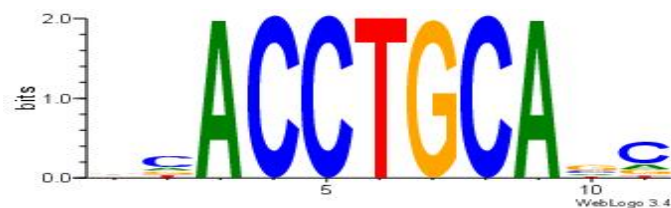


Dataset #: 4  
 Motif ID: 40  
 Motif name: kcACCTGCAGc  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 11  
 Similarity score: 0.0238442

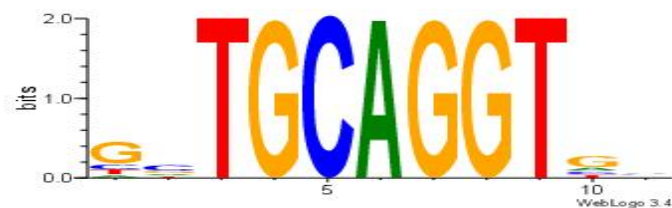
Alignment:

BCACCTGCABC  
 DHACATTCTGH

Original motif      Consensus sequence: BCACCTGCABC



Reverse complement motif      Consensus sequence: GBTGCAGGTGB



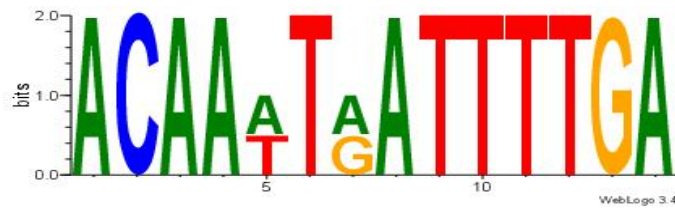
Dataset #: 2  
 Motif ID: 16  
 Motif name: Motif 16  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 11

Similarity score: 0.0258838

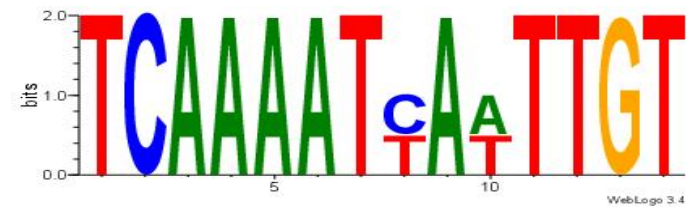
Alignment:

TCAAAATKAWTTGT  
HCAGAATGTHD---

Original motif    Consensus sequence: ACAAWTRATTTTGA



Reverse complement motif    Consensus sequence: TCAAAATKAWTTG



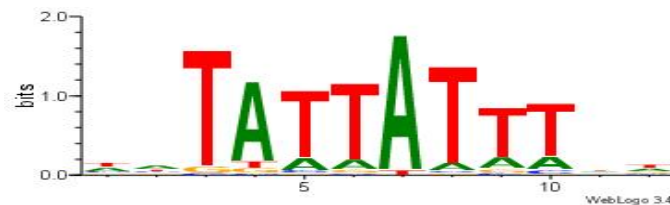
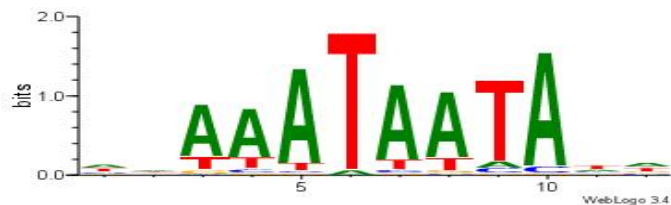
Dataset #: 4  
Motif ID: 41  
Motif name: wwAAATAATAtw  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Reverse Complement  
Direction: Backward  
Position number: 1  
Number of overlap: 11  
Similarity score: 0.0292508

Alignment:

DDTATTATTTDH  
-HCAGAATGTHD

Original motif    Consensus sequence: HDAAATAATADD

Reverse complement motif    Consensus sequence: DDTATTATTTDH



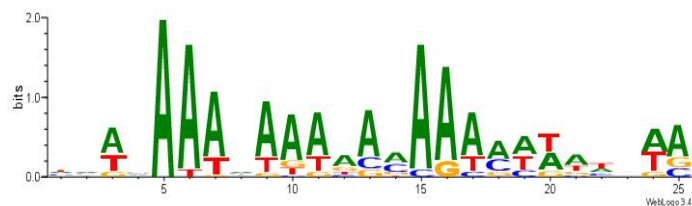
Dataset #: 5  
 Motif ID: 56  
 Motif name: TFM11  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 11  
 Number of overlap: 11  
 Similarity score: 0.0307858

Alignment:

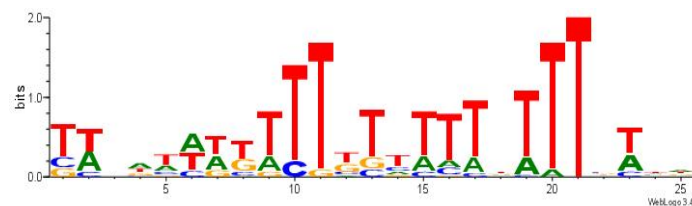
```

TWVHWWYTTTTYTTTTHTTTVWBH
----DHACATTCTGH-----
  
```

Original motif Consensus sequence:  
 HDWVAAAHAAAAAMAAAMWWWHBWA

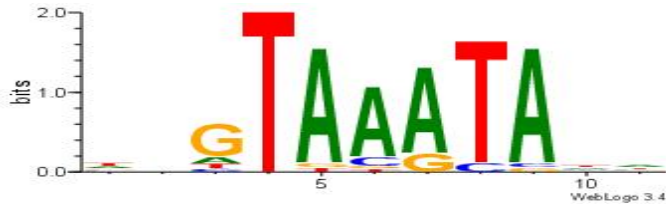


Reverse complement motif Consensus sequence:  
 TWVHWWYTTTTYTTTTHTTTVWBH



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

Original motif      Consensus sequence: DBGTAATAHD



Reverse complement motif      Consensus sequence: DHTATTTACBD



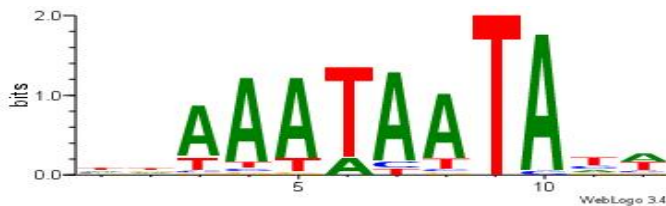
### Best Matches for Motif ID 45 (Highest to Lowest)

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

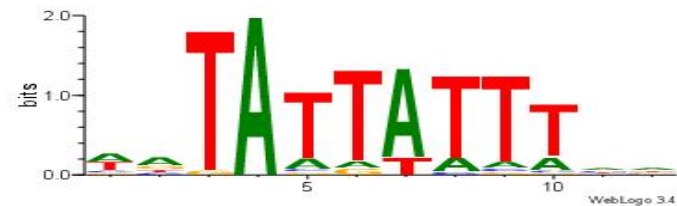
#### Alignment:

HDAAATAATAHW  
-DBGTAATAHD

Original motif      Consensus sequence: HDAAATAATAHW



Reverse complement motif      Consensus sequence: WHTATTATTTDH

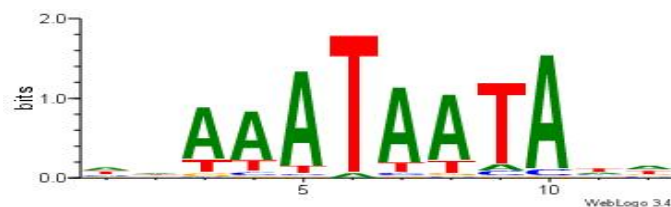


Dataset #: 4  
 Motif ID: 41  
 Motif name: wwAAATAATAtw  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 2  
 Number of overlap: 11  
 Similarity score: 0.0164863

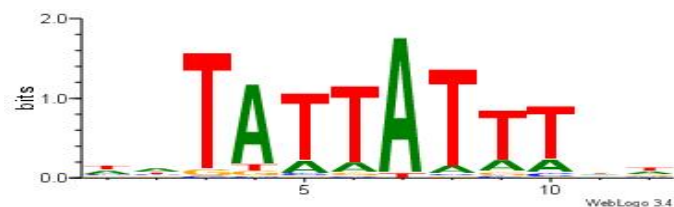
Alignment:

DDTATTATTTDH  
 DHTATTTACBD-

Original motif      Consensus sequence: HDAAATAATADD



Reverse complement motif      Consensus sequence: DDTATTATTTDH



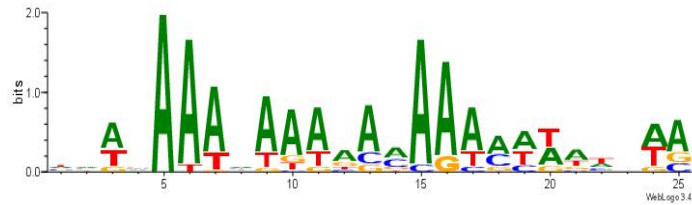
Dataset #: 5  
 Motif ID: 56  
 Motif name: TFM11  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 15  
 Number of overlap: 11

Similarity score: 0.0192768

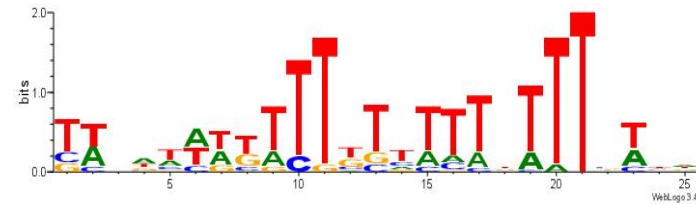
Alignment:

```
TWVHWWYTTTYTTTTHTTTVWBH  
-----DHTATTTACBD
```

Original motif    Consensus sequence:  
HDWVAAAHAAAAAMAAAMWWWHBWA



Reverse complement motif    Consensus sequence:  
TWVHWWYTTTYTTTTHTTTVWBH



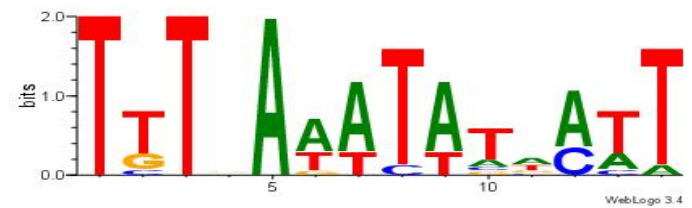
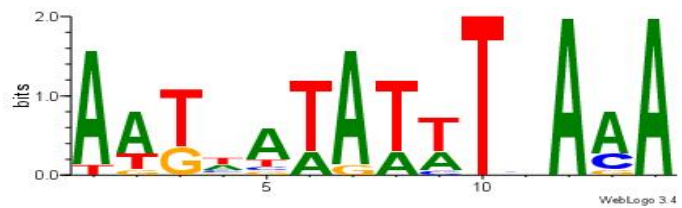
Dataset #: 2  
Motif ID: 9  
Motif name: Motif 9  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Original Motif  
Direction: Backward  
Position number: 4  
Number of overlap: 11  
Similarity score: 0.0250541

Alignment:

```
AATHATATWTHAAA  
DHTATTTACBD---
```

Original motif    Consensus sequence: AATHATATWTHAAA

Reverse complement motif    Consensus sequence: TTTDAWATATHAT



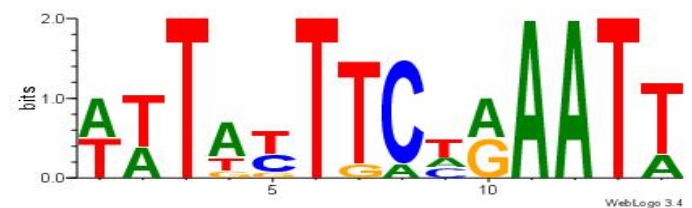
Dataset #: 2  
 Motif ID: 6  
 Motif name: Motif 6  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 11  
 Similarity score: 0.027895

Alignment:  
 AATTYDGAARTAWW  
 ---DBGTAAATAHD

Original motif      Consensus sequence: AATTYDGAARTAWW



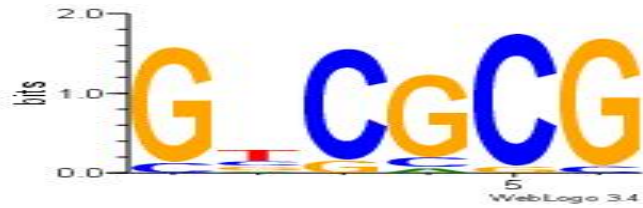
Reverse complement motif      Consensus sequence: WWTAKTTCDKAAAT



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



Original motif      Consensus sequence: GTCGCG



Reverse complement motif      Consensus sequence: CGCGAC



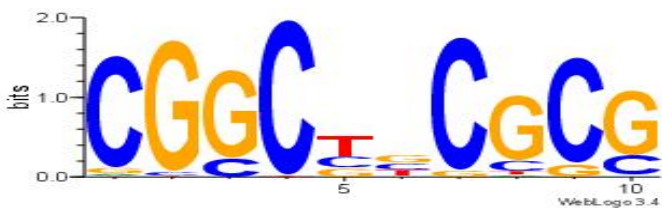
### Best Matches for Motif ID 46 (Highest to Lowest)

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

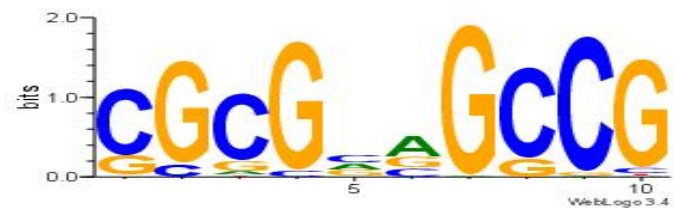
Alignment:

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

Original motif      Consensus sequence: CGGCYBCGCG



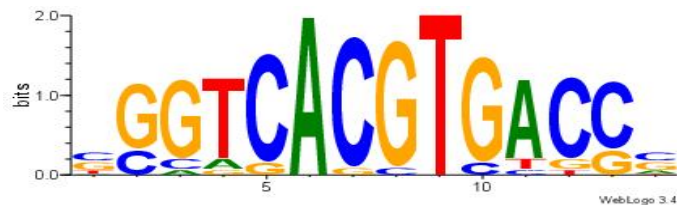
Reverse complement motif      Consensus sequence: CGCGBMGCCG



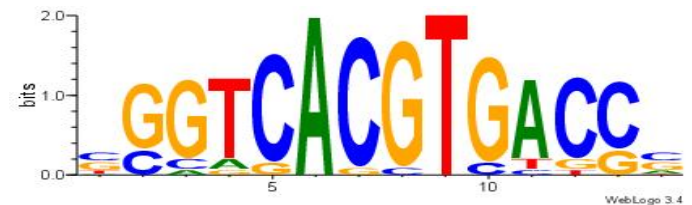
Dataset #: 4  
 Motif ID: 42  
 Motif name: sSGTCACGTGACSS  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 7  
 Number of overlap: 6  
 Similarity score: 0.0375102

Alignment:  
 SGGTCACGTGACCS  
 --GTCGCG-----

Original motif      Consensus sequence: SGGTCACGTGACCS



Reverse complement motif      Consensus sequence: SGGTCACGTGACCS



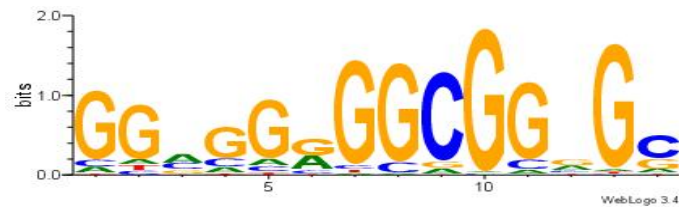
Dataset #: 5  
 Motif ID: 50  
 Motif name: TFF11  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 5  
 Number of overlap: 6

Similarity score: 0.0381641

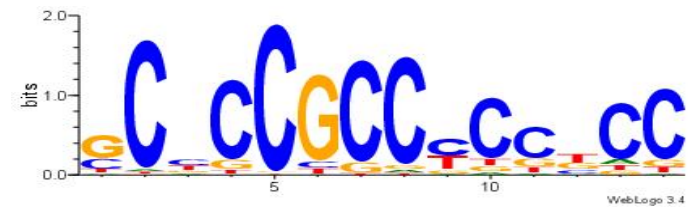
Alignment:

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

Original motif      Consensus sequence: GGMGGRGGCGGVGC



Reverse complement motif      Consensus sequence: GCVCCGCCMCCYCC



---

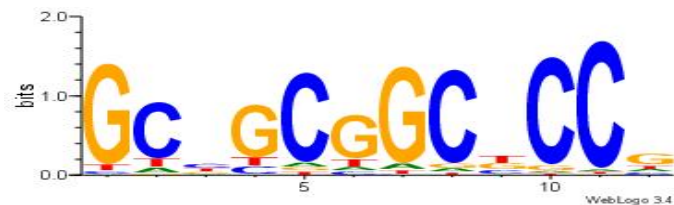
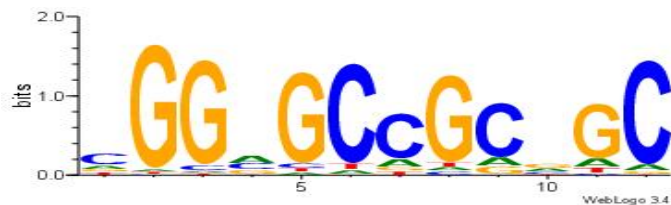
Dataset #: 5  
Motif ID: 49  
Motif name: TFF1  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Original Motif  
Direction: Backward  
Position number: 1  
Number of overlap: 6  
Similarity score: 0.0431161

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



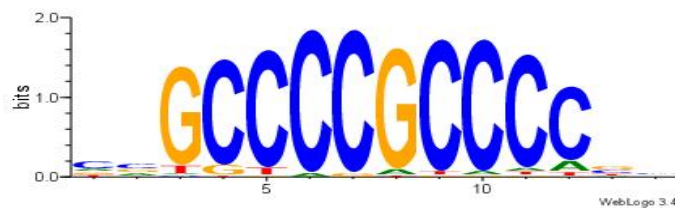
### Best Matches for Motif ID 47 (Highest to Lowest)

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

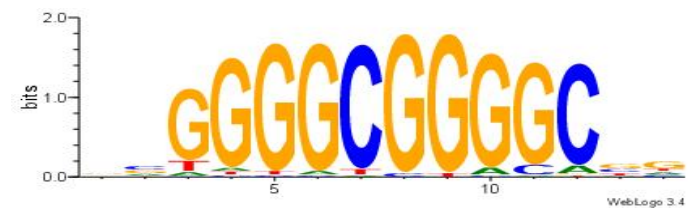
#### Alignment:

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

Original motif    Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif    Consensus sequence: BBGGGGCGGGGC

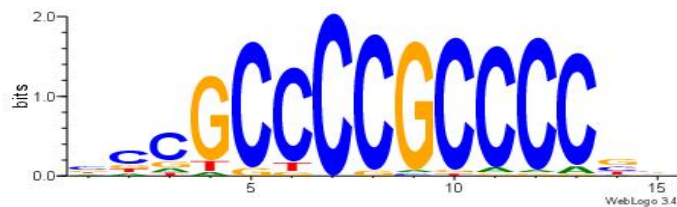


Dataset #: 4  
 Motif ID: 38  
 Motif name: cccGCCCCGCCCCsb  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 7  
 Number of overlap: 8  
 Similarity score: 0.045686

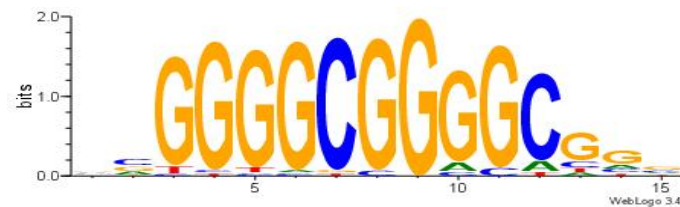
Alignment:

BBGGGGCGGGGCGGB  
 -----SCGCGCGG-

Original motif      Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif      Consensus sequence: BBGGGGCGGGGCGGB



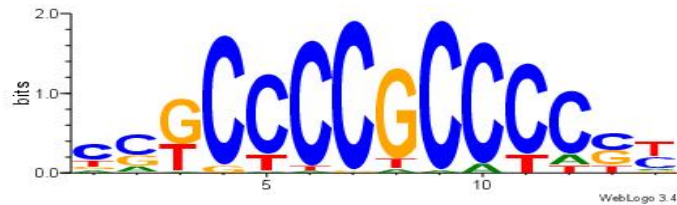
Dataset #: 2  
 Motif ID: 7  
 Motif name: Motif 7  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 6

Number of overlap: 8  
Similarity score: 0.0504058

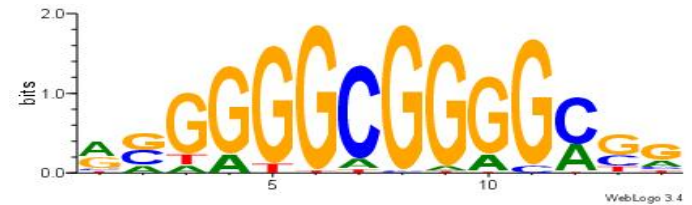
Alignment:

CSKCCCCGCCCCSY  
-CCGCGCGS-----

Original motif    Consensus sequence: CSKCCCCGCCCCSY



Reverse complement motif    Consensus sequence: MSGGGGCGGGY



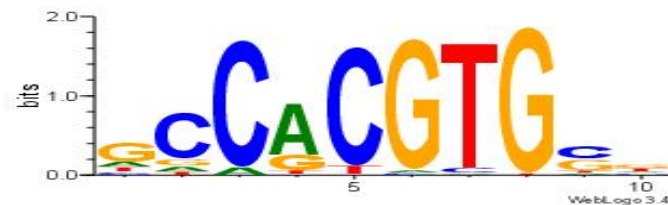
Dataset #: 3  
Motif ID: 33  
Motif name: Mycn  
Matching format of first motif: Original Motif  
Matching format of second motif: Original Motif  
Direction: Forward  
Position number: 2  
Number of overlap: 8  
Similarity score: 0.0527532

Alignment:

HSCACGTGGC  
-SCGCGCGG-

Original motif    Consensus sequence: HSCACGTGGC

Reverse complement motif    Consensus sequence: GCCACGTGSD

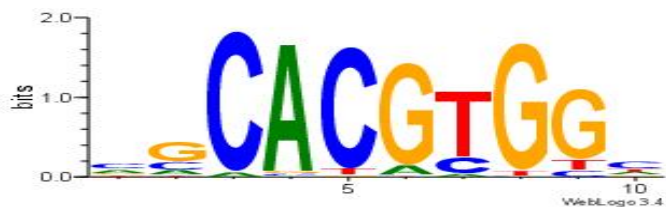


Dataset #: 3  
 Motif ID: 34  
 Motif name: Myc  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 2  
 Number of overlap: 8  
 Similarity score: 0.0574543

Alignment:

VGCACGTGGH  
 -SCGCGCGG-

Original motif      Consensus sequence: VGCACGTGGH



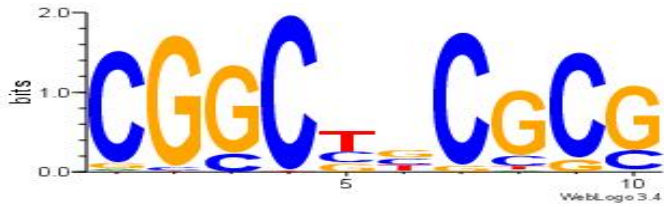
Reverse complement motif      Consensus sequence: DCCACGTGCV



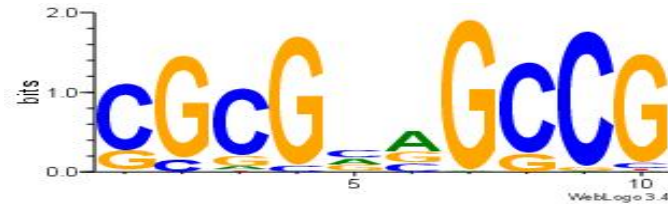
**Dataset #: 5      Motif ID: 48      Motif name: TFW3**



Original motif      Consensus sequence: CGGCYBCGCG



Reverse complement motif      Consensus sequence: CGCGBMGCCG



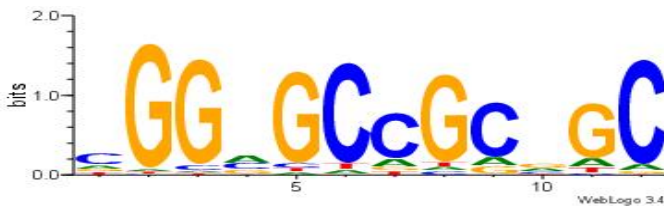
### Best Matches for Motif ID 48 (Highest to Lowest)

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

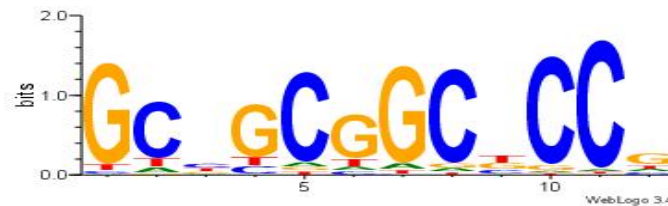
Alignment:

```
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



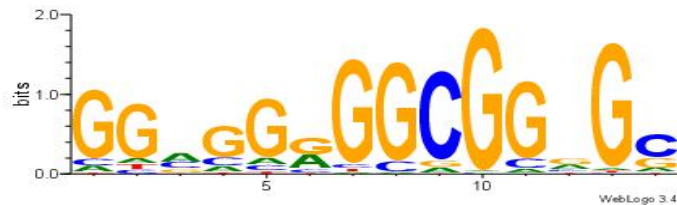
Dataset #: 5  
 Motif ID: 50  
 Motif name: TFF11  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 10

Similarity score: 0.0645308

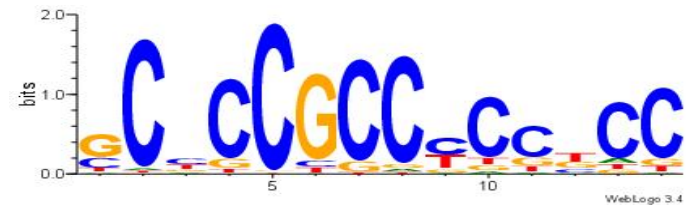
Alignment:

GGMGGRGGCGGVGC  
CGCGBMGCCG-----

Original motif    Consensus sequence: GGMGGRGGCGGVGC



Reverse complement motif    Consensus sequence: GCVCCGCCMCCYC



---

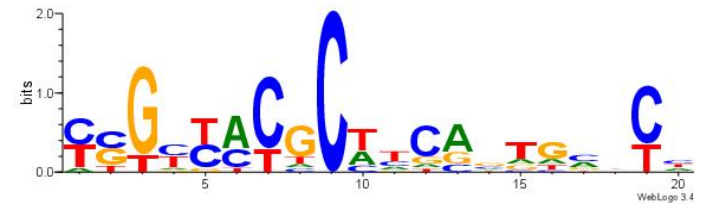
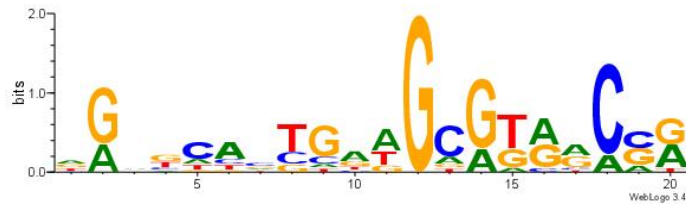
Dataset #: 3  
Motif ID: 31  
Motif name: Pax5  
Matching format of first motif: Original Motif  
Matching format of second motif: Reverse Complement  
Direction: Forward  
Position number: 11  
Number of overlap: 10  
Similarity score: 0.0714355

Alignment:

MSGKKRCGCWDCABTGBCD  
-----CGGCYBCGCG

Original motif    Consensus sequence: DGVBCABTDWGCGKRRCSR

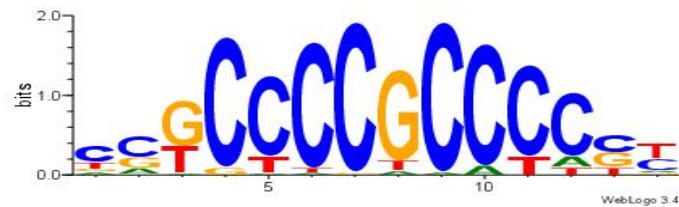
Reverse complement motif    Consensus sequence:  
MSGKKRCGCWDCABTGBCD



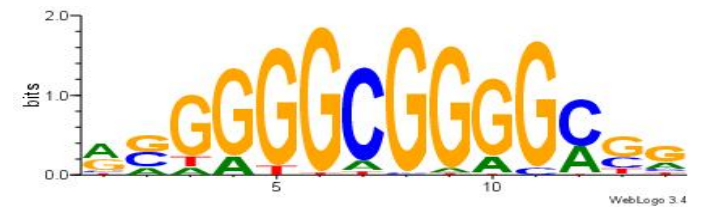
Dataset #: 2  
 Motif ID: 7  
 Motif name: Motif 7  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 10  
 Similarity score: 0.0717594

Alignment:  
 CSKCCCCGCCCSY  
 CGGCYBCGCG----

Original motif    Consensus sequence: CSKCCCCGCCCSY

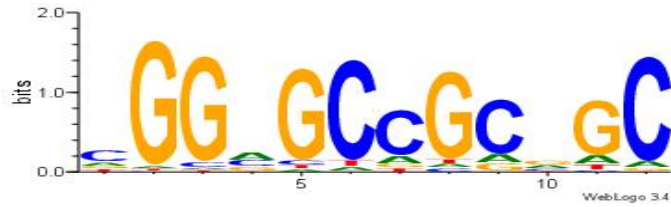


Reverse complement motif    Consensus sequence: MSGGGGCGGGY

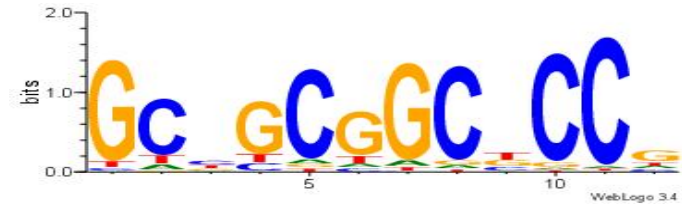


**Dataset #: 5      Motif ID: 49      Motif name: TFF1**

Original motif    Consensus sequence: CGGVGCCGCVGC



Reverse complement motif    Consensus sequence: GCVGCCGCBCCG



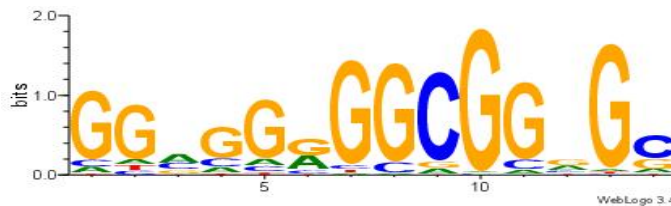
### Best Matches for Motif ID 49 (Highest to Lowest)

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

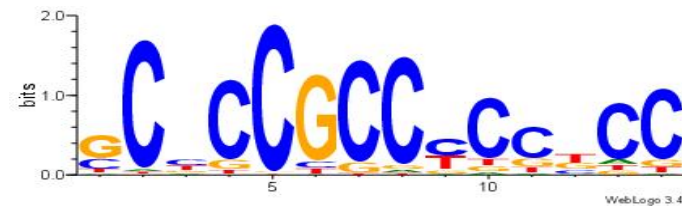
#### Alignment:

```
GGMGGRGGCGGVGC
--CGGVGCCGCVGC
```

Original motif    Consensus sequence: GGMGGRGGCGGVGC



Reverse complement motif    Consensus sequence: GCVCCGCCMCCYC

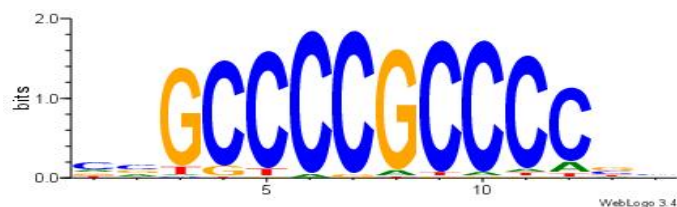


Dataset #: 4  
 Motif ID: 36  
 Motif name: csGCCCCGCCCCsc  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 12  
 Similarity score: 0.0542674

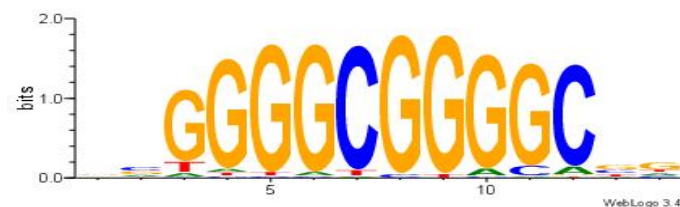
**Alignment:**

HVGCCCCGCCCCBB  
 CGGVGCCGCVGC--

Original motif    Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif    Consensus sequence: BBGGGGCGGGGC



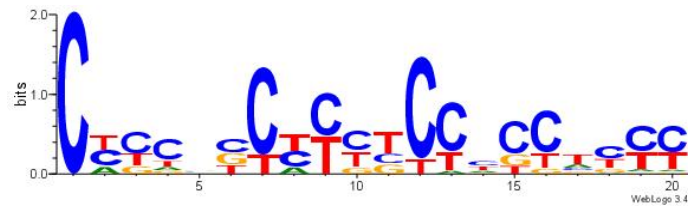
Dataset #: 5  
 Motif ID: 54  
 Motif name: TFM12  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 3  
 Number of overlap: 12

Similarity score: 0.0543272

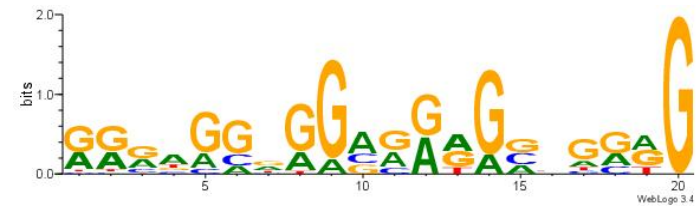
Alignment:

KKKAGGDGGAKKMGBBGKMG  
-----CGGVGCCGCVGC--

Original motif      Consensus sequence: CYCBBYYYTCCHCCTYYY



Reverse complement motif      Consensus sequence:  
KKKAGGDGGAKKMGBBGKMG



---

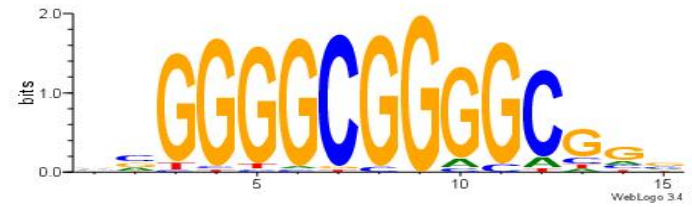
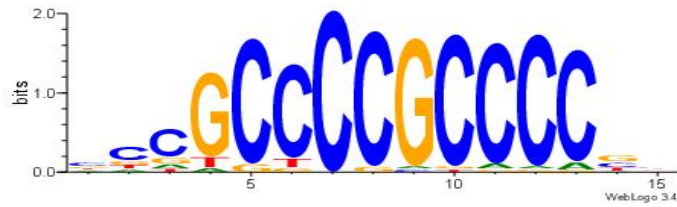
Dataset #: 4  
Motif ID: 38  
Motif name: cccGCCCCGCCCCsb  
Matching format of first motif: Original Motif  
Matching format of second motif: Reverse Complement  
Direction: Forward  
Position number: 4  
Number of overlap: 12  
Similarity score: 0.0548371

Alignment:

BBGGGGCGGGGCGGB  
---CGGVGCCGCVGC

Original motif      Consensus sequence: BCCGCCCCGCCCCBB

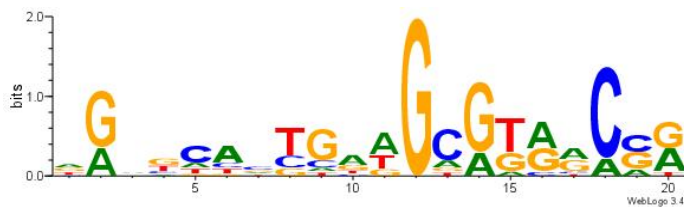
Reverse complement motif      Consensus sequence:  
BBGGGGCGGGGCGGB



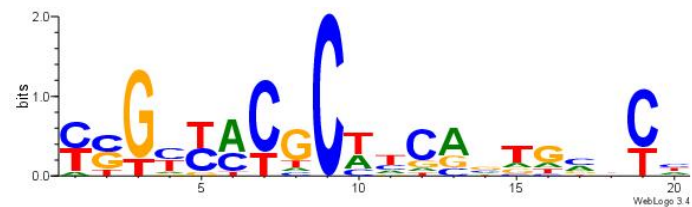
Dataset #: 3  
 Motif ID: 31  
 Motif name: Pax5  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 12  
 Similarity score: 0.0556962

Alignment:  
 DGVCABTGDWGCGRRCR  
 GCVGCGCBCCG-----

Original motif      Consensus sequence: DGVCABTGDWGCGRRCR



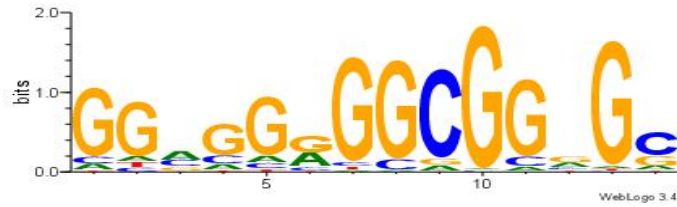
Reverse complement motif      Consensus sequence: MSGKKRCGCWDCABTGBCD



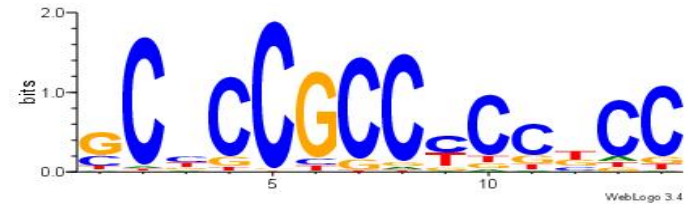
**Dataset #: 5      Motif ID: 50      Motif name: TFF11**



Original motif    Consensus sequence: GGMGRRGGCGGVGC



Reverse complement motif    Consensus sequence: GCVCCGCCMCCYCC



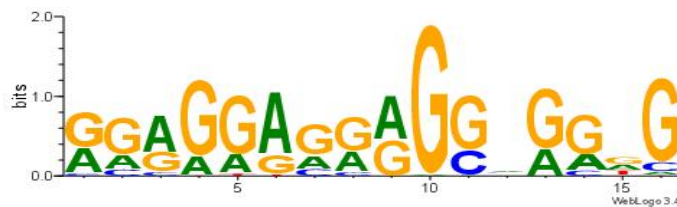
**Best Matches for Motif ID 50 (Highest to Lowest)**

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

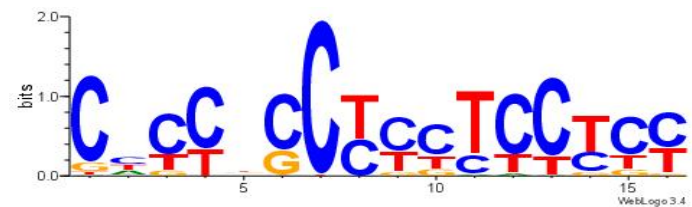
**Alignment:**

RGRGGAGRRGGHGGDG  
 GGMGRRGGCGGVGC--

Original motif    Consensus sequence: RGRGGAGRRGGHGGDG



Reverse complement motif    Consensus sequence: CHCCBCKMCTCCKCM

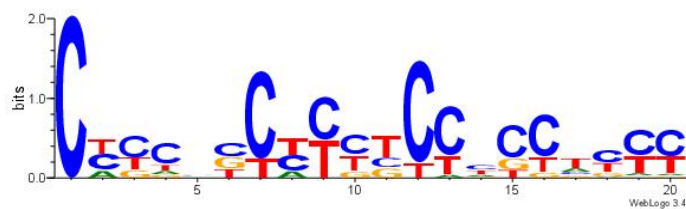


Dataset #: 5  
 Motif ID: 54  
 Motif name: TFM12  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 6  
 Number of overlap: 14  
 Similarity score: 0.0386905

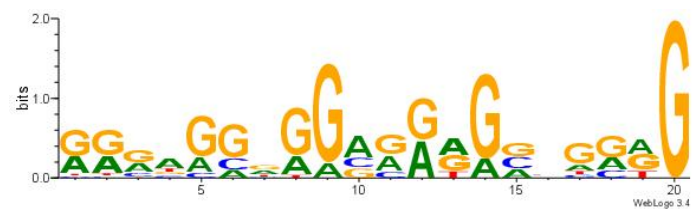
Alignment:

CYYCBBCYYYTCCHCCTYYY  
 -----GCVCCGCCMCCYCC-

Original motif      Consensus sequence: CYYCBBCYYYTCCHCCTYYY



Reverse complement motif      Consensus sequence: KKKAGGDGGAKKMGBBGKMG

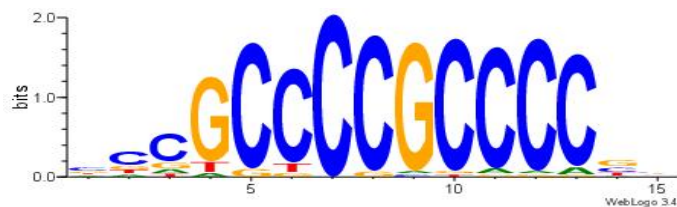


Dataset #: 4  
 Motif ID: 38  
 Motif name: cccGCCCCGCCCCsb  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 2

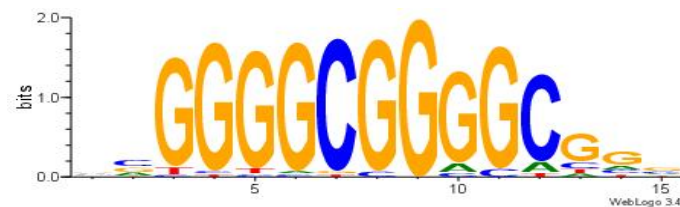
Number of overlap: 14  
Similarity score: 0.0548198

Alignment:  
BBGGGGCGGGGCGGB  
GGMGRRGGCGGVGC-

Original motif    Consensus sequence: BCCGCCCGCCCCBB



Reverse complement motif    Consensus sequence: BBGGGGCGGGGCGGB

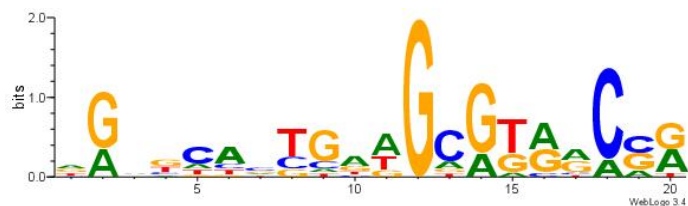


---

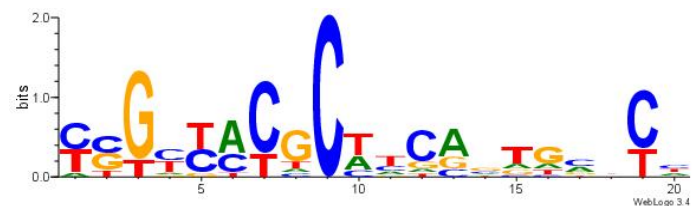
Dataset #: 3  
Motif ID: 31  
Motif name: Pax5  
Matching format of first motif: Original Motif  
Matching format of second motif: Original Motif  
Direction: Backward  
Position number: 3  
Number of overlap: 14  
Similarity score: 0.0573129

Alignment:  
DGVBCABTGDWCGKRRCSR  
----GGMGRRGGCGGVGC--

Original motif      Consensus sequence: DGVBCABTGDWGCGRRCR



Reverse complement motif      Consensus sequence: MSGKKRCGCWDCABTGBBCD

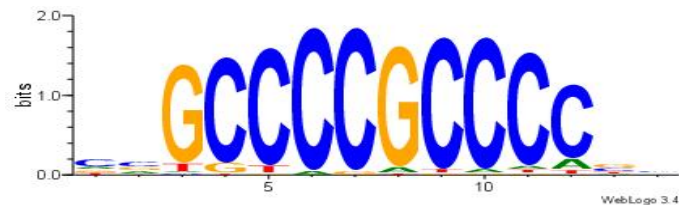


Dataset #: 4  
Motif ID: 36  
Motif name: csGCCCCGCCCCsc  
Matching format of first motif: Original Motif  
Matching format of second motif: Reverse Complement  
Direction: Forward  
Position number: 1  
Number of overlap: 14  
Similarity score: 0.0652173

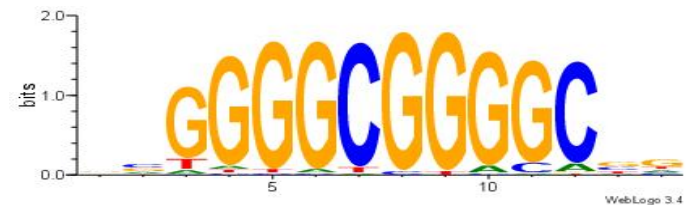
Alignment:

BBGGGGCGGGGCVD  
GGMGGRGGCGGVGC

Original motif      Consensus sequence: HVGCCCCGCCCCBB

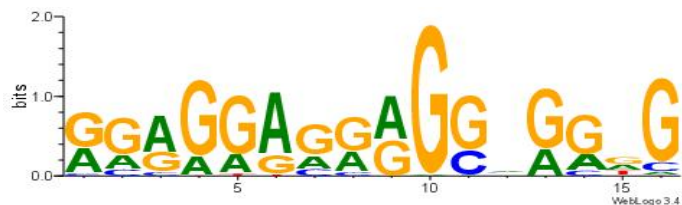


Reverse complement motif      Consensus sequence: BBGGGGCGGGGC

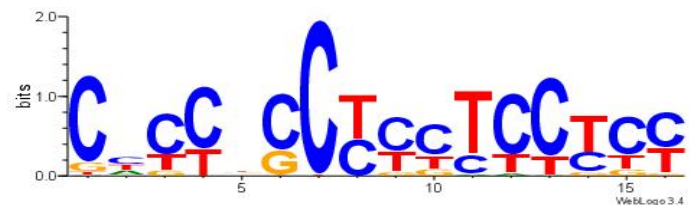


**Dataset #: 5**      **Motif ID: 51**      **Motif name: TFM2**

Original motif      Consensus sequence: RGRGGAGRRGGHGGDG



Reverse complement motif      Consensus sequence: CHCCBCKMCTCCKCM



### Best Matches for Motif ID 51 (Highest to Lowest)

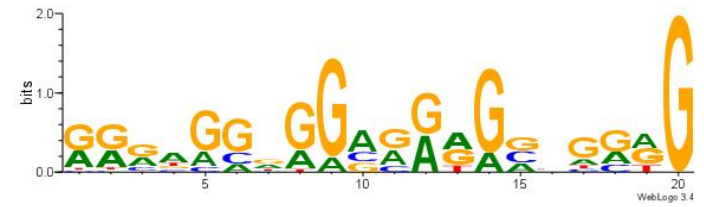
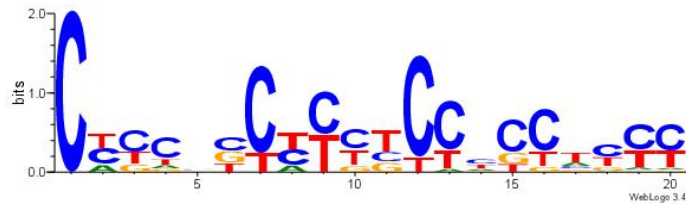
Dataset #:	5
Motif ID:	54
Motif name:	TFM12
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	16
Similarity score:	0.0331473

#### Alignment:

```
CYYCBBCYYYYTCCHCCTYYY  
CHCCBCKMCTCCKCM-----
```

Original motif      Consensus sequence: CYYCBBCYYYYTCCHCCTYYY

Reverse complement motif      Consensus sequence: KKKAGGDGGAKKMGBBGKMG

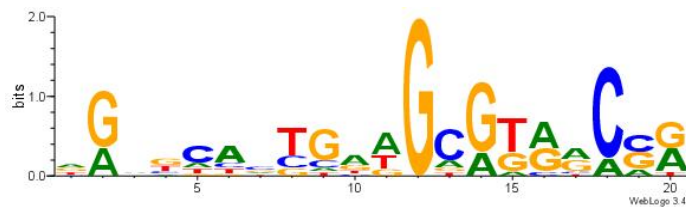


Dataset #: 3  
 Motif ID: 31  
 Motif name: Pax5  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 2  
 Number of overlap: 16  
 Similarity score: 0.0668155

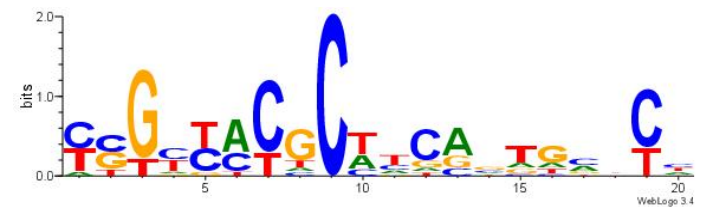
**Alignment:**

DGVCABTGDWGCGRRCR  
 -RGRGGAGRRGGHGGD---

Original motif      Consensus sequence: DGVCABTGDWGCGRRCR



Reverse complement motif      Consensus sequence: MSGKKRCGCWDCABTGBCD



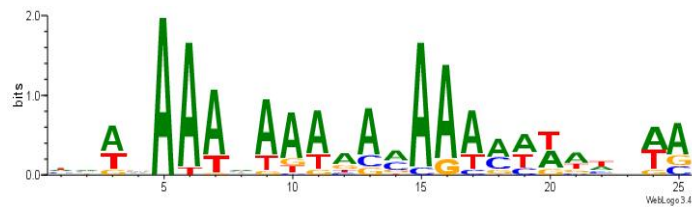
Dataset #: 5

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

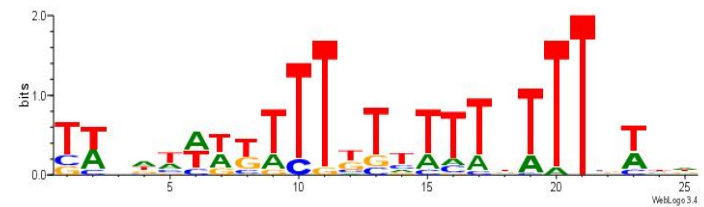
**Alignment:**

HDWVAAAHAAAAAMAAAMWWWHBWA  
 -----RGRGGAGRRGGHGGDG--

Original motif    Consensus sequence:  
 HDWVAAAHAAAAAMAAAMWWWHBWA



Reverse complement motif    Consensus sequence:  
 TWVHWWWYTTTTTTTTTHTTTVWBH



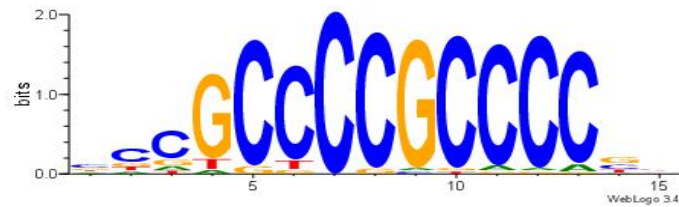
Dataset #: 4  
 Motif ID: 38  
 Motif name: cccGCCCGCCCCsb  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 15

Similarity score: 0.558405

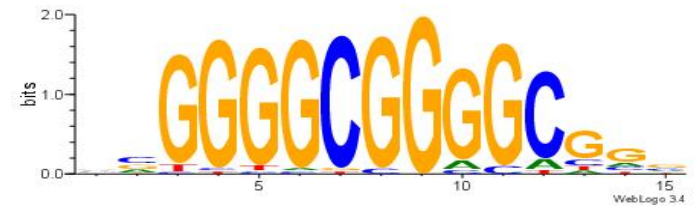
Alignment:

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

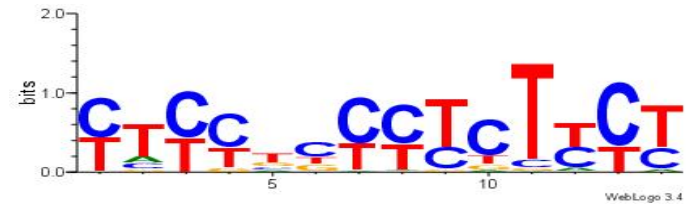
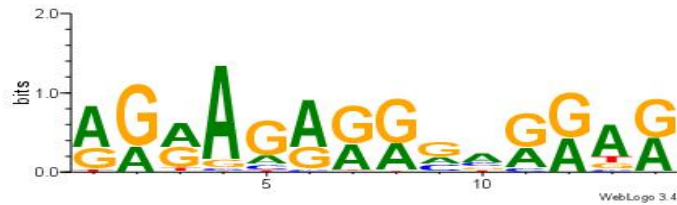
Alignment:

--RGRAGARRGARRAR  
RGRGGAGRRGGHGGDG

Original motif      Consensus sequence: RGRAGARRGARRAR

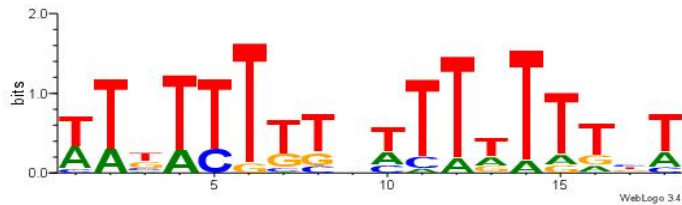
Reverse complement motif      Consensus sequence: MTMMTCMMTCTK



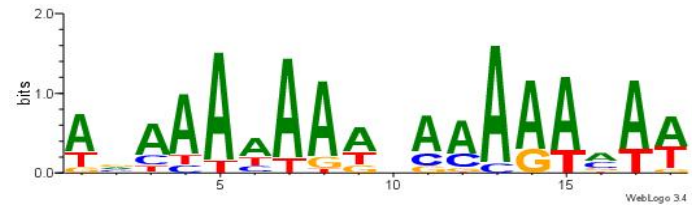


**Dataset #: 5      Motif ID: 52      Motif name: TFM1**

Original motif      Consensus sequence: WTKTTTTTHWTTTTTTBT



Reverse complement motif      Consensus sequence: ABAAAAA WHAAAAARAW



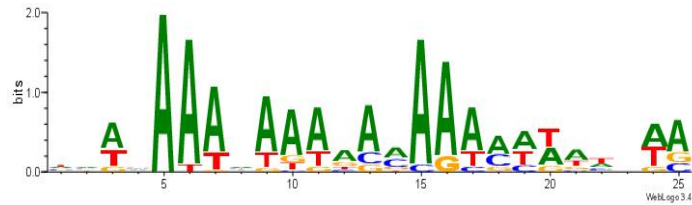
**Best Matches for Motif ID 52 (Highest to Lowest)**

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

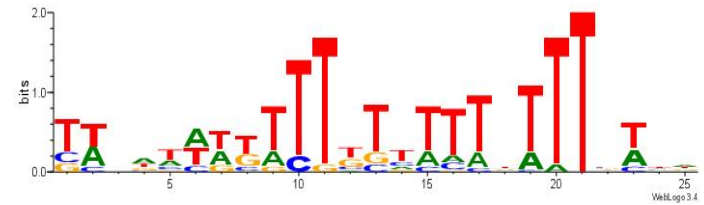
Alignment:

TWVHWWYTTTYTTTTHTTTVWBH  
 -----WTKTTTTTHWTTTTTTBT--

Original motif    Consensus sequence:  
 HDWVAAAHAAAAAMAAAMWWWHBWA



Reverse complement motif    Consensus sequence:  
 TWVHWWYTTTYTTTTHTTTVWBH

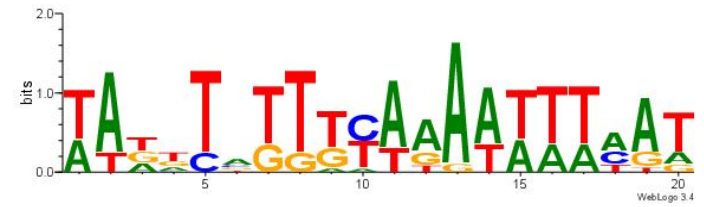
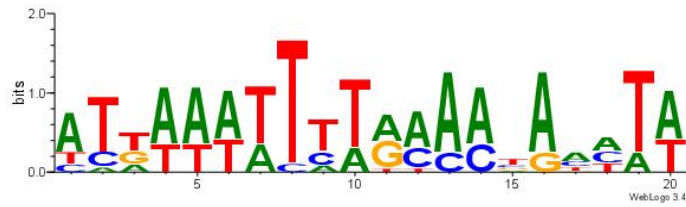


Dataset #: 5  
 Motif ID: 55  
 Motif name: TFM13  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 3  
 Number of overlap: 18  
 Similarity score: 0.0364672

Alignment:  
 ATKAAWTTTTRMAABAHTW  
 ABAAAAAWhAAAAARAW--

Original motif    Consensus sequence: ATKAAWTTTTRMAABAHTW

Reverse complement motif    Consensus sequence:  
 WAHHTVTTYKAAAATTRAT

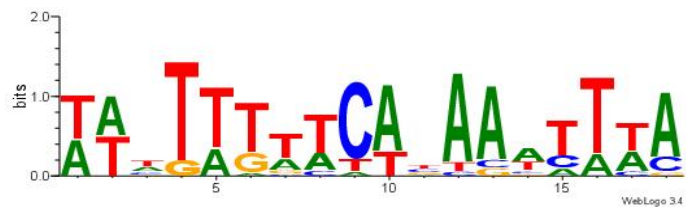


Dataset #: 5  
 Motif ID: 53  
 Motif name: TFM3  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 18  
 Similarity score: 0.0456974

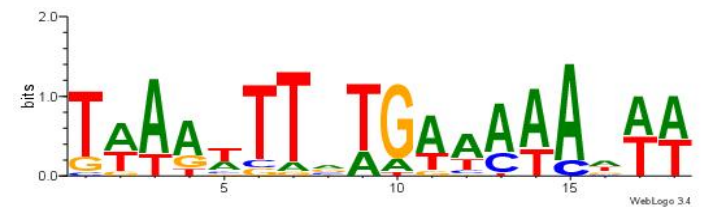
Alignment:

WWHTTTTTTCABAAWTTWA  
 WKTTTTTTHWTTTTTTBT

Original motif      Consensus sequence: WWHTTTTTTCABAAWTTWA



Reverse complement motif      Consensus sequence: TAAWTTVTGAAAAHWW



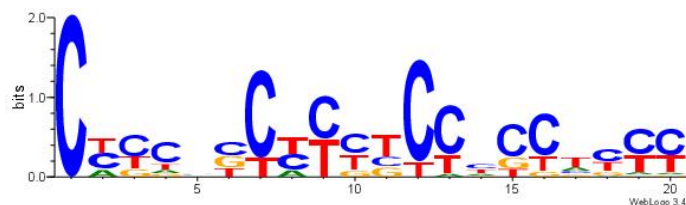
Dataset #: 5

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

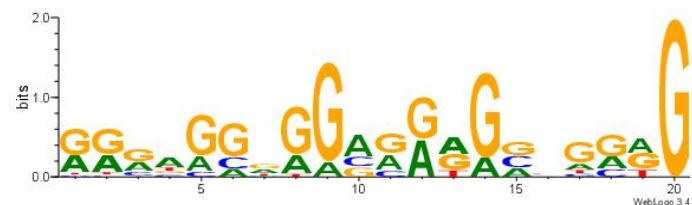
**Alignment:**

CYYCBBCYYYTCCHCCTYYY-  
 ---WTKTTTTTHWTTTTTBT

Original motif      Consensus sequence: CYYCBBCYYYTCCHCCTYYY



Reverse complement motif      Consensus sequence: KKKAGGDGGAKKMGBBGKMG



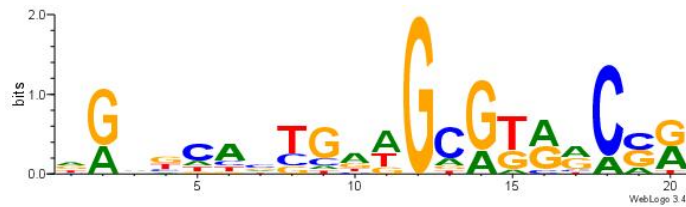
Dataset #: 3  
 Motif ID: 31  
 Motif name: Pax5  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 5  
 Number of overlap: 16

Similarity score: 1.07322

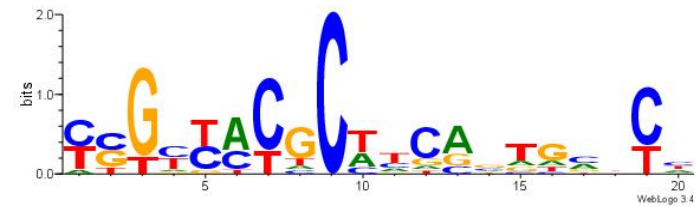
Alignment:

```
--MSGKKRCGCWDCABTGBBCD  
WKTTTTTTHWTTTTTTBT----
```

Original motif      Consensus sequence: DGVBCABTGDWGCGRRCR

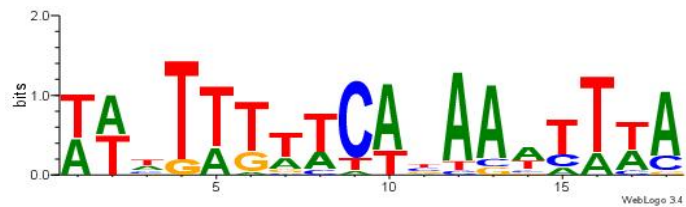


Reverse complement motif      Consensus sequence:  
MSGKKRCGCWDCABTGBBCD

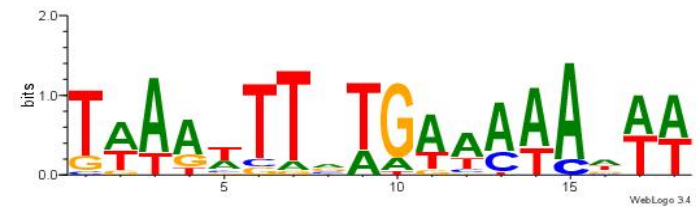


**Dataset #: 5      Motif ID: 53      Motif name: TFM3**

Original motif      Consensus sequence: WWHTTTTTCABAATTWA



Reverse complement motif      Consensus sequence:  
TWAAWTTVTGAAAAHWW



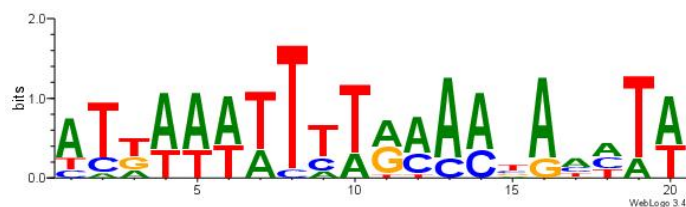
**Best Matches for Motif ID 53 (Highest to Lowest)**

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

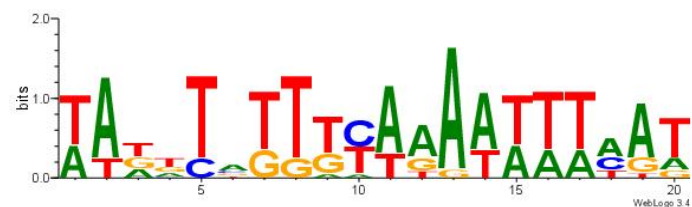
Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 2  
 Number of overlap: 18  
 Similarity score: 0.013876

Alignment:  
 ATKAAWTTTTRMAABAHTW  
 -TWAAWTTVTGAAAAHWW-

Original motif      Consensus sequence: ATKAAWTTTTRMAABAHTW



Reverse complement motif      Consensus sequence: WAHHTVTTYKAAAATTRAT

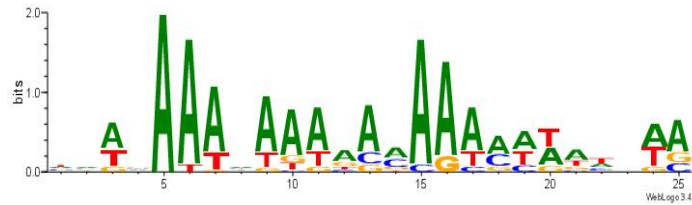


Dataset #: 5  
 Motif ID: 56  
 Motif name: TFM11  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 5  
 Number of overlap: 18  
 Similarity score: 0.0402327

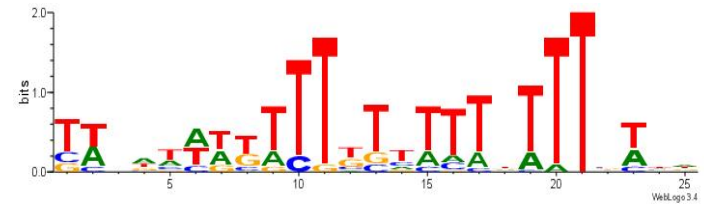
Alignment:

TWVHWWYTTTYTTTTHTTTVWBH  
 ---WWHTTTTTCABAAWTTWA---

Original motif    Consensus sequence:  
 HDWVAAAHAAAAAMAAAMWWWHBWA



Reverse complement motif    Consensus sequence:  
 TWVHWWYTTTYTTTTHTTTVWBH



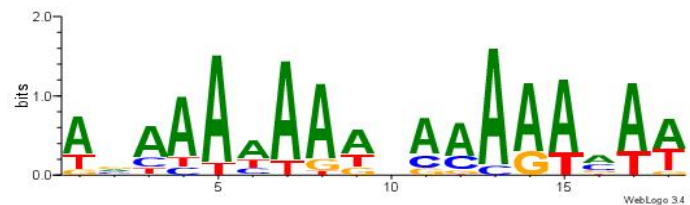
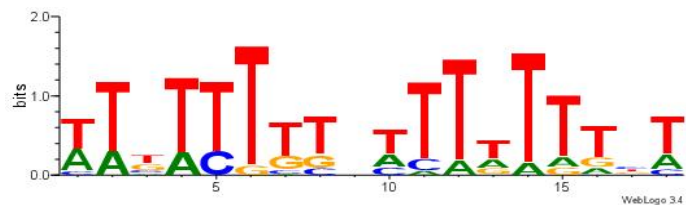
Dataset #: 5  
 Motif ID: 52  
 Motif name: TFM1  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 18  
 Similarity score: 0.0432207

Alignment:

WKTTTTTHWTTTTTBT  
 WWHTTTTTCABAAWTTWA

Original motif    Consensus sequence: WKTTTTTHWTTTTTBT

Reverse complement motif    Consensus sequence:  
 ABAAAAAWhAAAAARAW



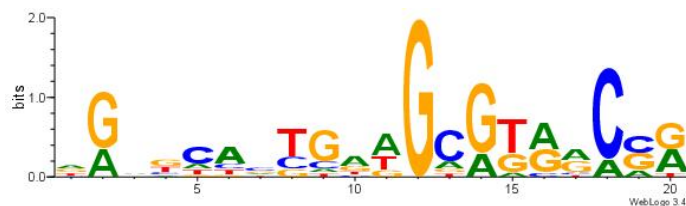
Dataset #: 3  
 Motif ID: 31  
 Motif name: Pax5  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 4  
 Number of overlap: 17  
 Similarity score: 0.561883

Alignment:

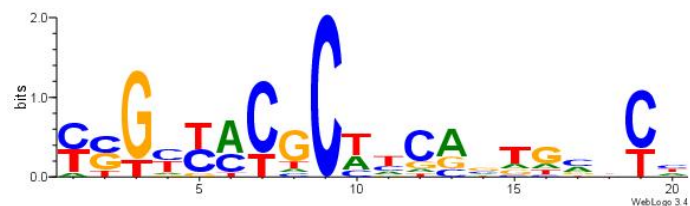
```

-MSGKKRCGCWDCABTGBBCD
WWHTTTTTTCABAAWTTWA---
  
```

Original motif      Consensus sequence: DGVBCABTGDWGCGRRCR



Reverse complement motif      Consensus sequence: MSGKKRCGCWDCABTGBBCD



Dataset #: 2

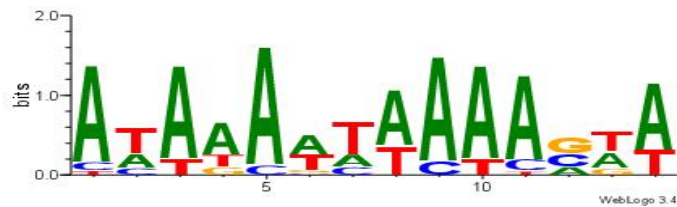


Motif ID: 3  
 Motif name: Motif 3  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 14  
 Similarity score: 2.04564

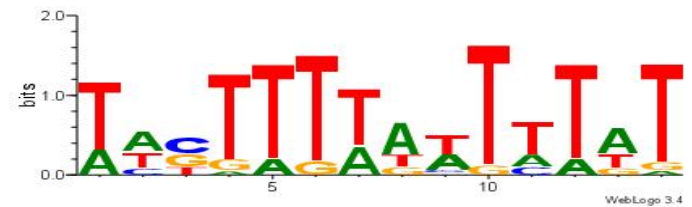
Alignment:

----TWSTTTWAWTTTWT  
 WWHTTTTTTCABAAWTTWA

Original motif      Consensus sequence: AWAAAWTWAAASWA

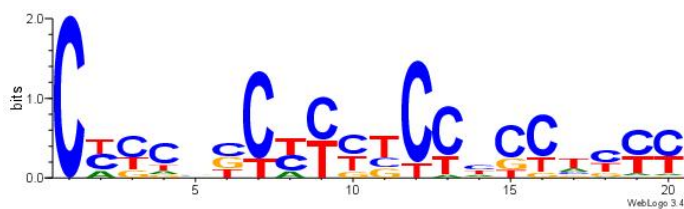


Reverse complement motif      Consensus sequence: TWSTTTWAWTTTWT

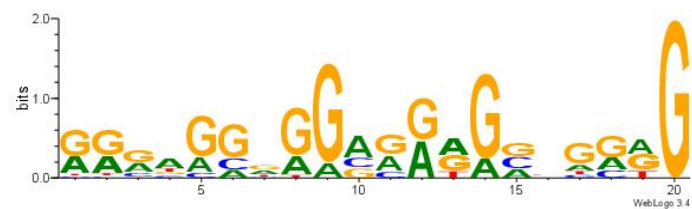


**Dataset #: 5      Motif ID: 54      Motif name: TFM12**

Original motif      Consensus sequence: CYCBBCYYYTCCHCCTYYY



Reverse complement motif      Consensus sequence: KKKAGGDGGAKKMGBBGKMG



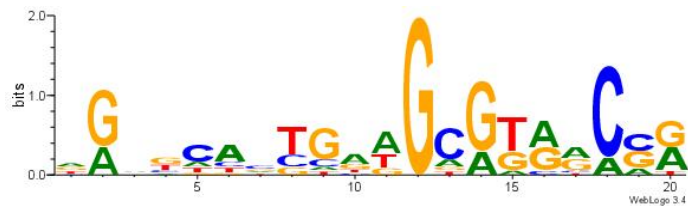
## Best Matches for Motif ID 54 (Highest to Lowest)

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

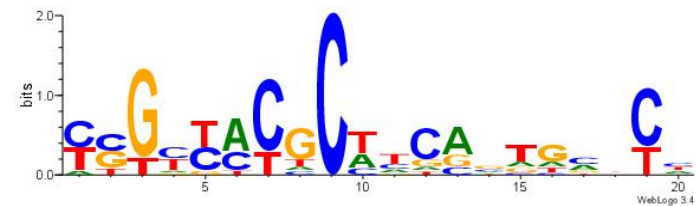
### Alignment:

```
MSGKKRCGCWDCABTGBBCD  
CYVCBBCYYYTCCHCCTYYY
```

Original motif      Consensus sequence: DGVBCABTGDWGCGRRCR



Reverse complement motif      Consensus sequence:  
MSGKKRCGCWDCABTGBBCD



---

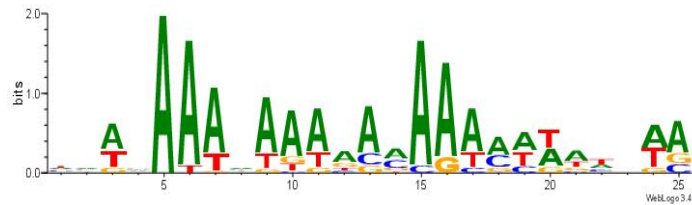
Dataset #: 5  
Motif ID: 56  
Motif name: TFM11  
Matching format of first motif: Original Motif  
Matching format of second motif: Reverse Complement

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

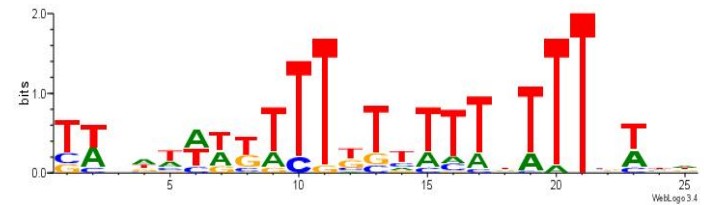
**Alignment:**

TWVHWWWYTTTYTTTTTHTTTVWBH  
 CYVCBBCYYYTCCHCCTYYY-----

Original motif    Consensus sequence:  
 HDWVAAAHAAAAAMAAAMWWWHBWA



Reverse complement motif    Consensus sequence:  
 TWVHWWWYTTTYTTTTTHTTTVWBH

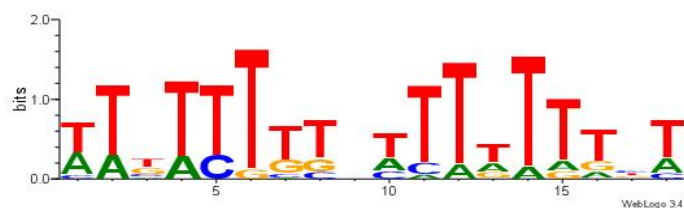


Dataset #: 5  
 Motif ID: 52  
 Motif name: TFM1  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 2  
 Number of overlap: 17  
 Similarity score: 1.56255

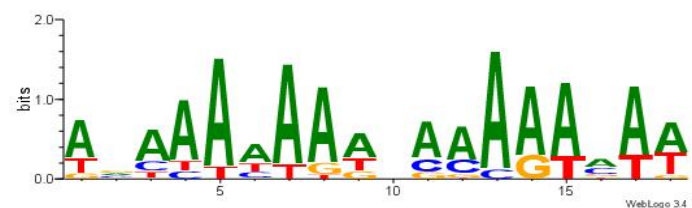
**Alignment:**

---WTKTTTTTHWTTTTTTBT  
 CYVCBBCYYYTCCHCCTYYY-

Original motif      Consensus sequence: WTKTTTTTHWTTTTTTBT



Reverse complement motif      Consensus sequence: ABAAAAAWhAAAAARAW

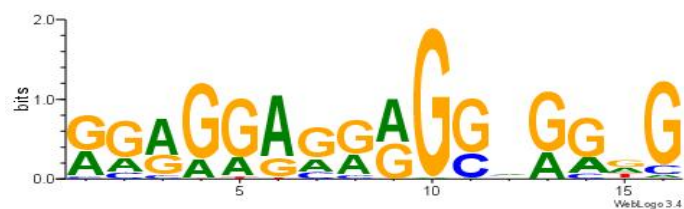


Dataset #: 5  
Motif ID: 51  
Motif name: TFM2  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Original Motif  
Direction: Forward  
Position number: 1  
Number of overlap: 16  
Similarity score: 2.01568

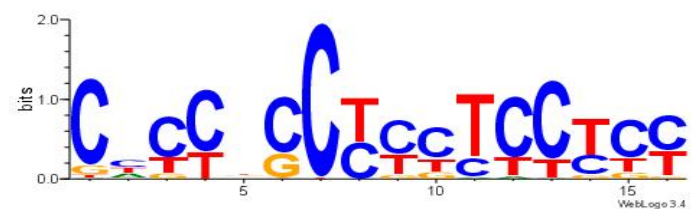
Alignment:

RGRGGAGRRGGHGGDG-----  
KKKAGGDGGAKKMGBBGKMG

Original motif      Consensus sequence: RGRGGAGRRGGHGGDG



Reverse complement motif      Consensus sequence: CHCCBCKMCTCCKCM

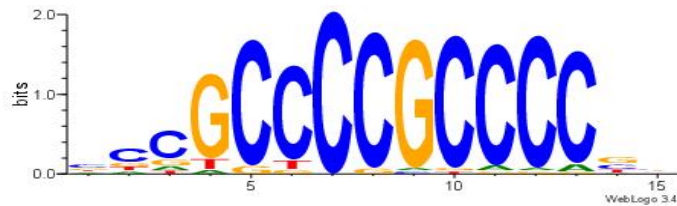


Dataset #: 4  
 Motif ID: 38  
 Motif name: cccGCCCCGCCCCsb  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 15  
 Similarity score: 2.55221

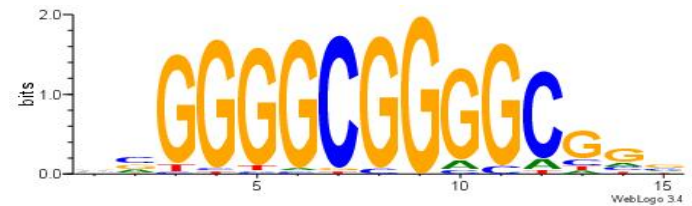
Alignment:

-----BCCGCCCCGCCCCBB  
 CYYCBBCYYYTCCHCCTYYY

Original motif      Consensus sequence: BCCGCCCCGCCCCBB



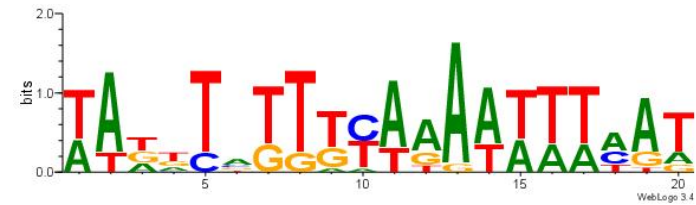
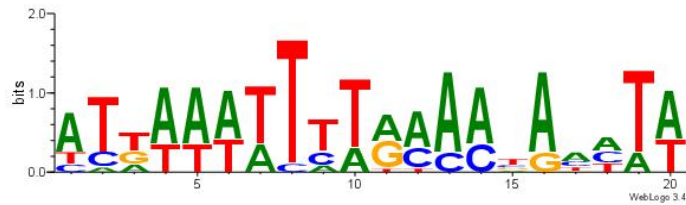
Reverse complement motif      Consensus sequence: BBGGGGCGGGGCGGB



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

Original motif      Consensus sequence: ATKAAWTTTTTRMAABAHTW

Reverse complement motif      Consensus sequence: WAHHTVTTYKAAAATTRAT



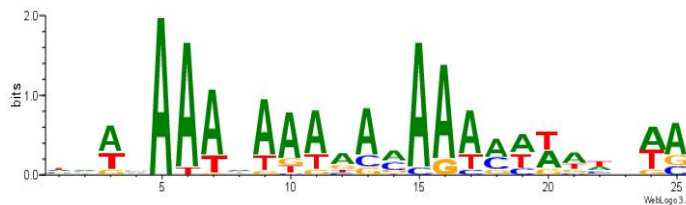
**Best Matches for Motif ID 55 (Highest to Lowest)**

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

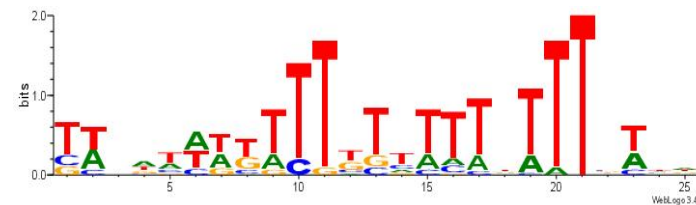
**Alignment:**

```
TWVHWWWYTTTYTTTTTHTTTVWBH
----WAHHTVTTYKAAAATTRAT-
```

Original motif    Consensus sequence:  
 HDWVAAAHAAAAAMAAAMWWWHBWA



Reverse complement motif    Consensus sequence:  
 TWVHWWWYTTTYTTTTTHTTTVWBH

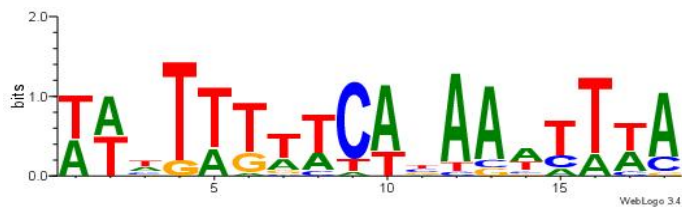


Dataset #: 5  
 Motif ID: 53  
 Motif name: TFM3  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 18  
 Similarity score: 1.02254

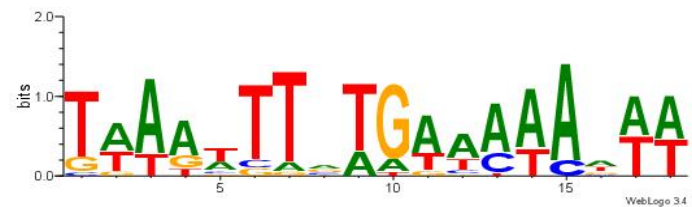
Alignment:

TWAAWTTVTGAAAAHWW--  
 ATKAAWTTTTRMAABAHHTW

Original motif    Consensus sequence: WWHTTTTTTCABAAWTTWA



Reverse complement motif    Consensus sequence: TWAAWTTVTGAAAAHWW



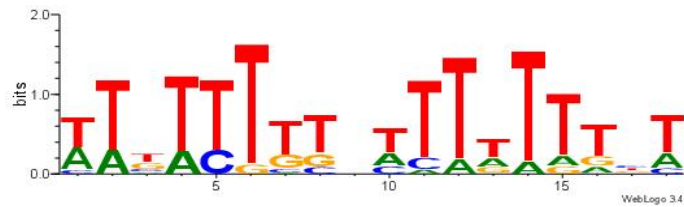
Dataset #: 5  
 Motif ID: 52  
 Motif name: TFM1  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 1

Number of overlap: 18  
Similarity score: 1.02868

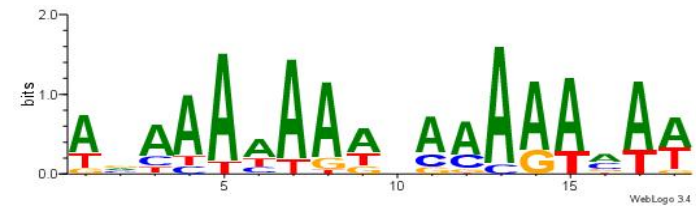
Alignment:

WKTTTTTTHWTTTTTTBT--  
WAHHTVTTYKAAAATTRAT

Original motif    Consensus sequence: WTKTTTTTHWTTTTTTBT



Reverse complement motif    Consensus sequence:  
ABAAAAAWHAAAAARAW



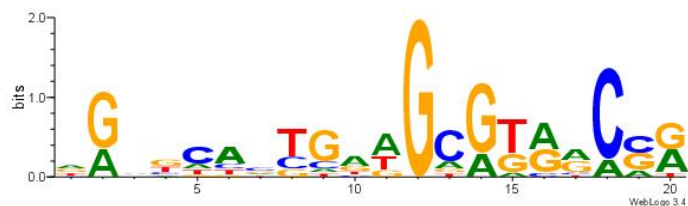
Dataset #: 3  
Motif ID: 31  
Motif name: Pax5  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Reverse Complement  
Direction: Backward  
Position number: 6  
Number of overlap: 15  
Similarity score: 2.56565

Alignment:

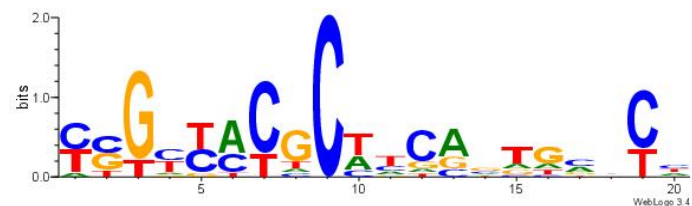
-----MSGKKRCGCWDCABTGBBCD  
WAHHTVTTYKAAAATTRAT-----



Original motif      Consensus sequence: DGVBCABTGDWGCGRCSR



Reverse complement motif      Consensus sequence: MSGKKRCGCWDCABTGBBCD

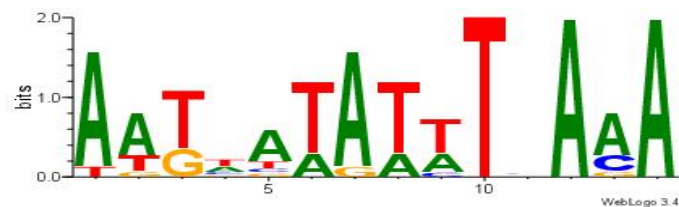


Dataset #: 2  
Motif ID: 9  
Motif name: Motif 9  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Reverse Complement  
Direction: Backward  
Position number: 1  
Number of overlap: 14  
Similarity score: 3.02278

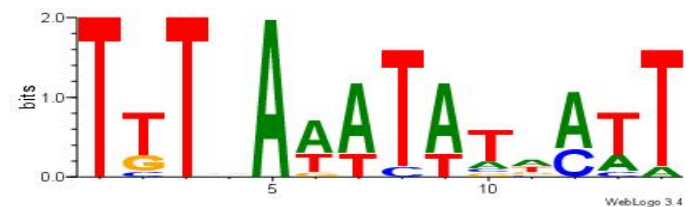
Alignment:

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

Original motif      Consensus sequence: AATHATATWTHAAA

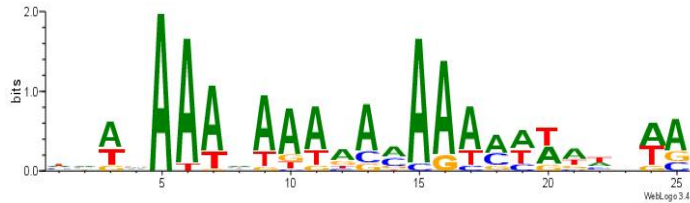


Reverse complement motif      Consensus sequence: TTTDAWATATHATT

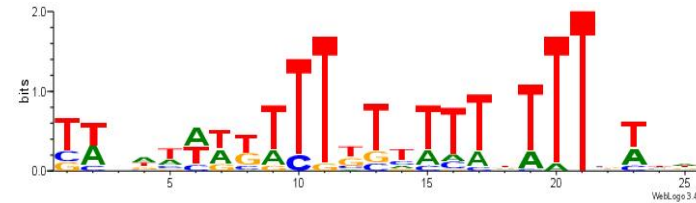


**Dataset #: 5      Motif ID: 56      Motif name: TFM11**

Original motif      Consensus sequence:  
HDWVAAAHAAAAAMAAAMWWWHBWA



Reverse complement motif      Consensus sequence:  
TWVHWWWYTTTTYTTTTTHTTTVWBH



### Best Matches for Motif ID 56 (Highest to Lowest)

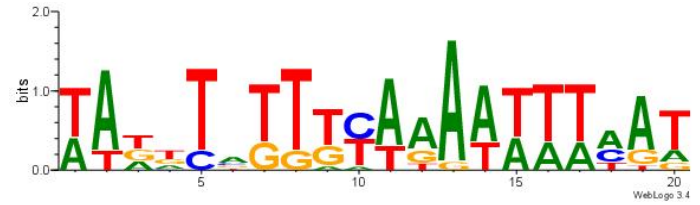
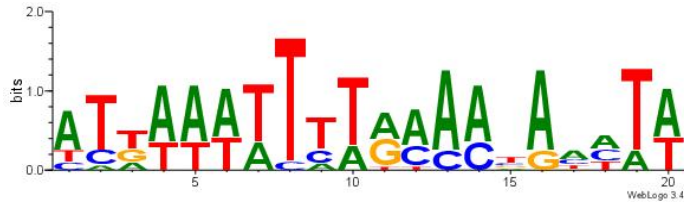
Dataset #:	5
Motif ID:	55
Motif name:	TFM13
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	20
Similarity score:	0.0486765

#### Alignment:

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

Original motif      Consensus sequence: ATKAAWTTTTRMAABAHTW

Reverse complement motif      Consensus sequence:  
WAHHTVTTYKAAAATTRAT

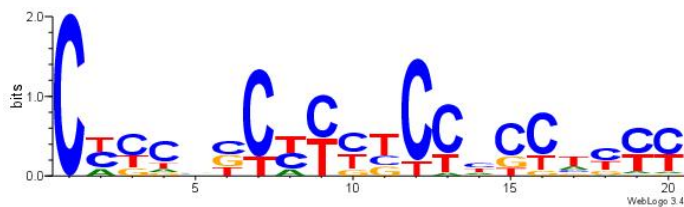


Dataset #: 5  
 Motif ID: 54  
 Motif name: TFM12  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 20  
 Similarity score: 0.0693284

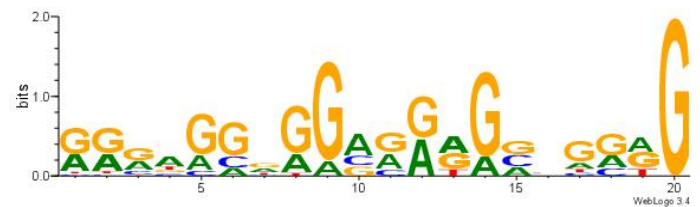
Alignment:

KKKAGGDGGAKKMGBBGKMG-----  
 HDWVAAAHAAAAAMAAAMWWWHBWA

Original motif      Consensus sequence: CYCBCYYYTCCHCCTYYY



Reverse complement motif      Consensus sequence: KKKAGGDGGAKKMGBBGKMG



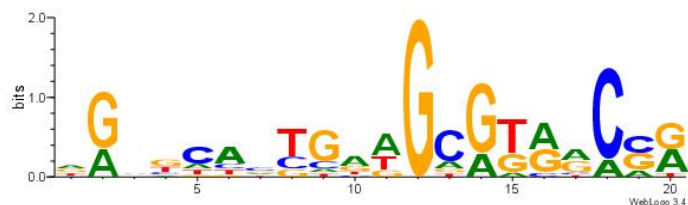
Dataset #: 3

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

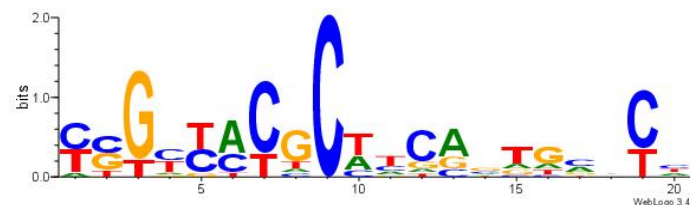
**Alignment:**

DGVBCABTGDWGCGRRCR-----  
 HDWVAAAHA AAAAAMAAAMWWWHBWA

Original motif      Consensus sequence: DGVBCABTGDWGCGRRCR



Reverse complement motif      Consensus sequence: MSGKKRCGCWDCABTGBBCD



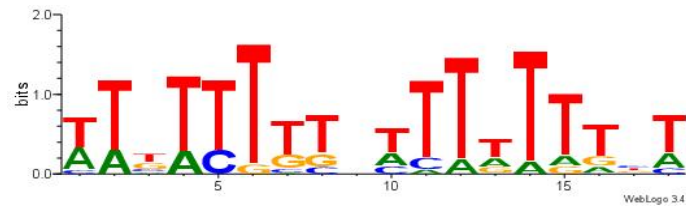
Dataset #: 5  
 Motif ID: 52  
 Motif name: TFM1  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 18

Similarity score: 1.0232

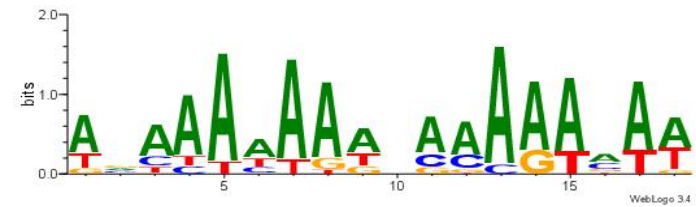
Alignment:

```
-----ABAAAAAWHAAAAARAW  
HDWVAAAHAAAAAMAAAMWWWHBWA
```

Original motif      Consensus sequence: WTKTTTTTHWTTTTTTBT



Reverse complement motif      Consensus sequence:  
ABAAAAAWHAAAAARAW



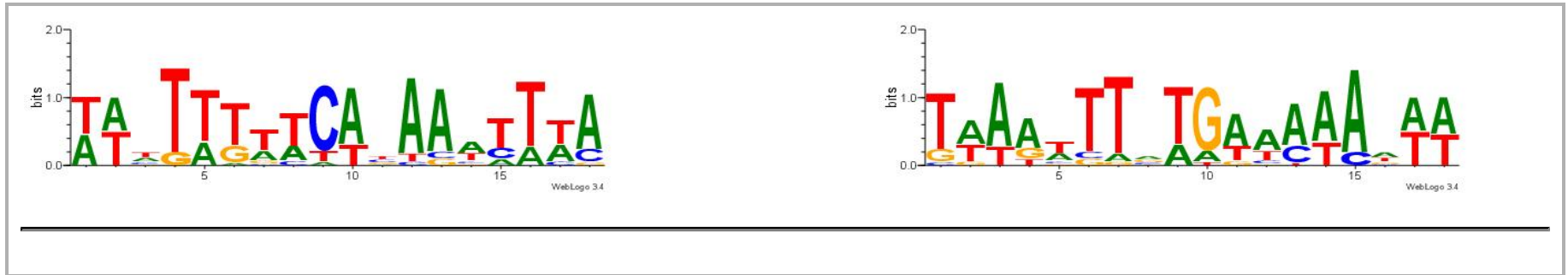
Dataset #: 5  
Motif ID: 53  
Motif name: TFM3  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Original Motif  
Direction: Forward  
Position number: 1  
Number of overlap: 18  
Similarity score: 1.05388

Alignment:

```
WWHTTTTTCABAAWTTWA-----  
TWVHWWWYTTTYTTTTTHTTTVWBH
```

Original motif      Consensus sequence: WWHTTTTTCABAAWTTWA

Reverse complement motif      Consensus sequence:  
TAAWTTVTGAAAAAHWW



Results created by MOTIFSIM on 11-14-2022 18:30:07  
 Runtime: 350.348 seconds

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