



MOTIFSIM - MOTIF SIMilarity Detection Tool

Version 2.2

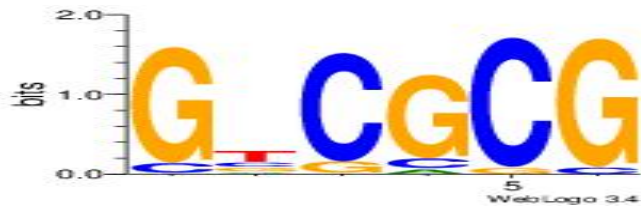
INPUT

Input Parameters		
Number of files:	2	
Number of top significant motifs:	10	
Number of best matches:	5	
Similarity cutoff >=	0.75	
Matching motif database:	UniProbe Mus Musculus	
Motif tree:	Yes	
Combined similar motifs:	Yes	
Output file type:	All	
Output file format:	All	
Input files and motif counts		
File name	Count of motifs	Dataset number
W-ChIPMotifs_DM230.txt	11	1
RSAT_peak-motifs_DM230.txt	10	2

RESULTS

Top 10 Significant Motifs - Global Matching (Highest to Lowest)		
Dataset #: 1	Motif ID: 1	Motif name: TFW1

Original motif Consensus sequence: GTCGCG



Reverse complement motif Consensus sequence: CGCGAC

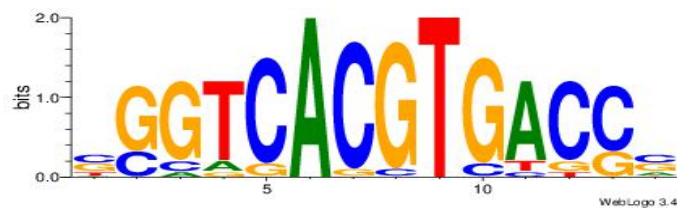


Best Matches for Top Significant Motif ID 1 (Highest to Lowest)

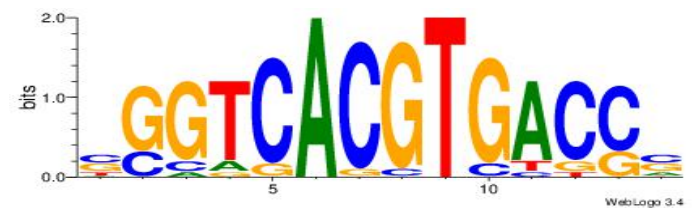
Dataset #: 2
Motif ID: 18
Motif name: sSGTCACGTGACCS
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 3
Number of overlap: 6
Similarity score: 0.0375102

Alignment:
SGGTCACGTGACCS
--GTCGCG-----

Original motif Consensus sequence: SGGTCACGTGACCS



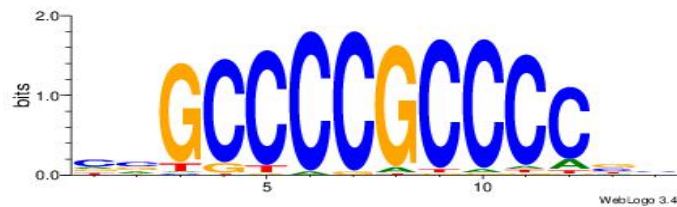
Reverse complement motif Consensus sequence: SGGTCACGTGACCS



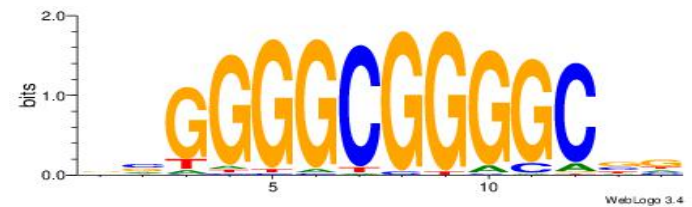
Dataset #: 2
 Motif ID: 12
 Motif name: csGCCCCGCCCCsc
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 7
 Number of overlap: 6
 Similarity score: 0.0539

Alignment:
 HVGCCCCGCCCCBB
 --GTCGCG-----

Original motif Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGC



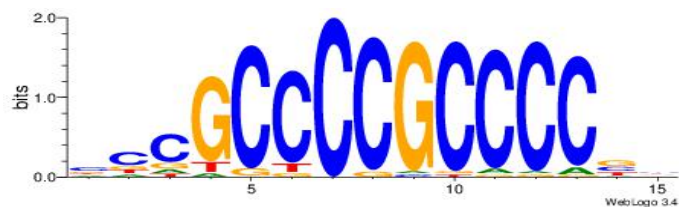
Dataset #: 2
 Motif ID: 14
 Motif name: cccGCCCCGCCCCsb
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 6

Similarity score: 0.0558733

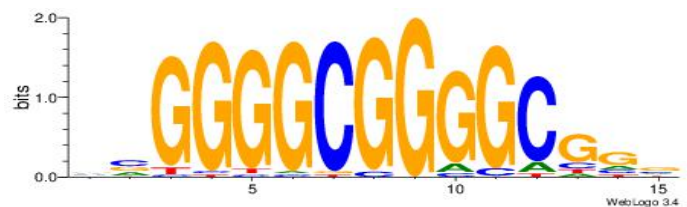
Alignment:

BCCGCCCCGCCCCBB
-----CGCGAC--

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB



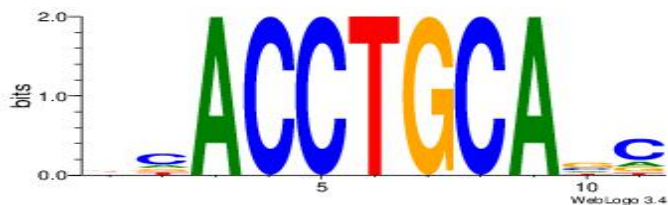
Dataset #: 2
Motif ID: 16
Motif name: kcACCTGCAGc
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 6
Number of overlap: 6
Similarity score: 0.0980422

Alignment:

BCACCTGCABC
-----CGCGAC

Original motif Consensus sequence: BCACCTGCABC

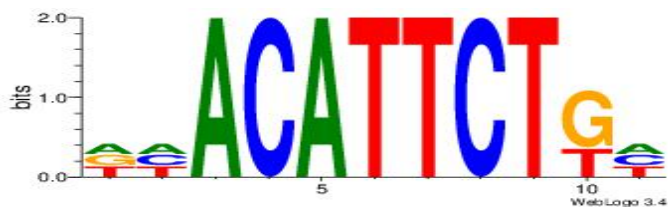
Reverse complement motif Consensus sequence: GBTGCAGGTGB



Dataset #: 2
 Motif ID: 20
 Motif name: dhACATTCTkh
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 8
 Number of overlap: 4
 Similarity score: 1.09467

Alignment:
 HCAGAATGTHD--
 -----GTCGCG

Original motif Consensus sequence: DHACATTCTGH



Reverse complement motif Consensus sequence: HCAGAATGTHD

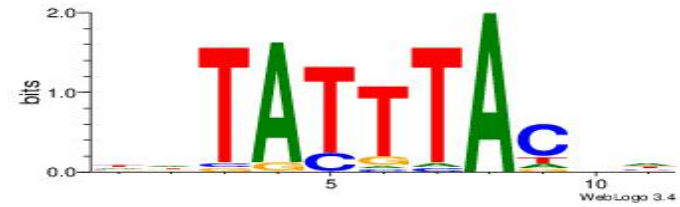


Dataset #: 2 Motif ID: 21 Motif name: wbgTAAATAww

Original motif Consensus sequence: DBGTAATAHD



Reverse complement motif Consensus sequence: DHTATTTACBD



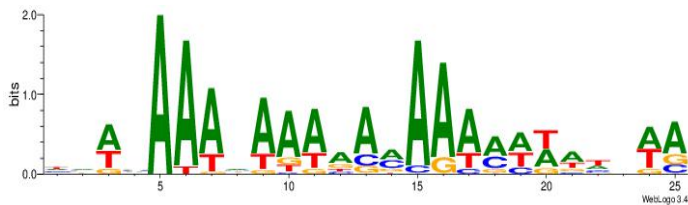
Best Matches for Top Significant Motif ID 21 (Highest to Lowest)

Dataset #: 1
 Motif ID: 11
 Motif name: TFM11
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 15
 Number of overlap: 11
 Similarity score: 0.0192768

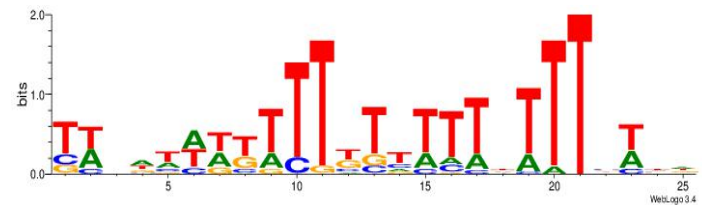
Alignment:

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

Original motif Consensus sequence: HDWVAAAHAAAAAMAAAMWWWHBWA



Reverse complement motif Consensus sequence: TWVHWWWYTTTYTTTTHTTTVWBH

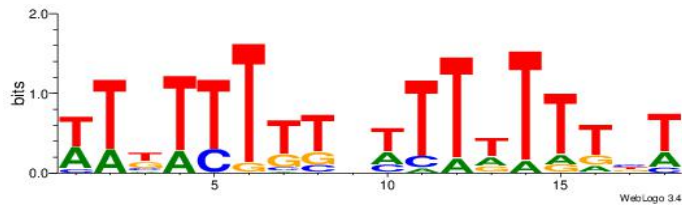


Dataset #: 1
 Motif ID: 7
 Motif name: TFM1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.0283217

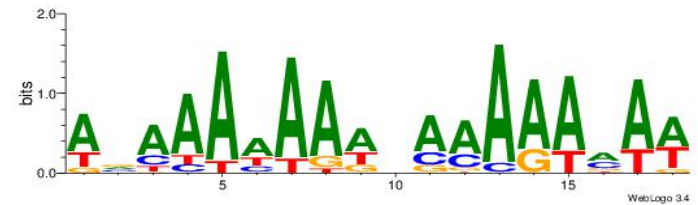
Alignment:

WKTTTTTHWTTTTTBT
 DHTATTTACBD-----

Original motif Consensus sequence: WKTTTTTHWTTTTTBT



Reverse complement motif Consensus sequence: ABAAAAAWHAAAAARAW

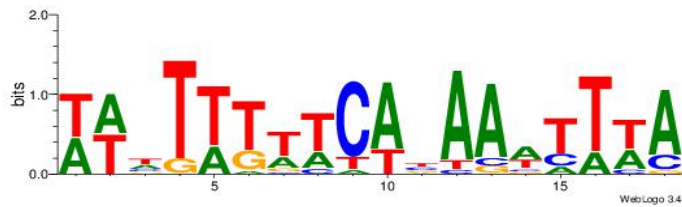


Dataset #: 1
 Motif ID: 8
 Motif name: TFM3
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2

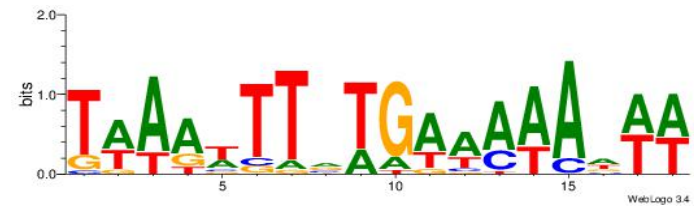
Number of overlap: 11
 Similarity score: 0.0308097

Alignment:
 WWHTTTTTTCABAAWTTWA
 -----DHTATTTACBD-

Original motif Consensus sequence: WWHTTTTTTCABAAWTTWA



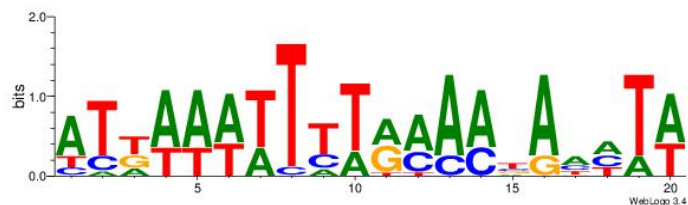
Reverse complement motif Consensus sequence: TAAWTTVTGAAAAHWW



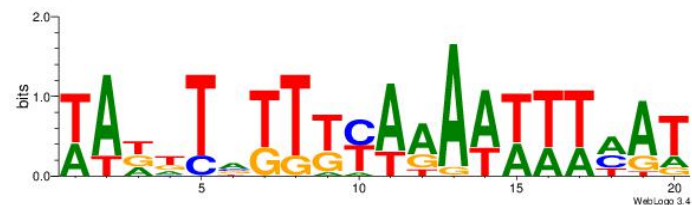
Dataset #: 1
 Motif ID: 10
 Motif name: TFM13
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 11
 Similarity score: 0.0333874

Alignment:
 ATKAAWTTTTTRMAABAHHTW
 -----DBGTAAATAHD--

Original motif Consensus sequence: ATKAAWTTTTRMAABAHTW



Reverse complement motif Consensus sequence: WAHHTVTTYKAAAATTRAT

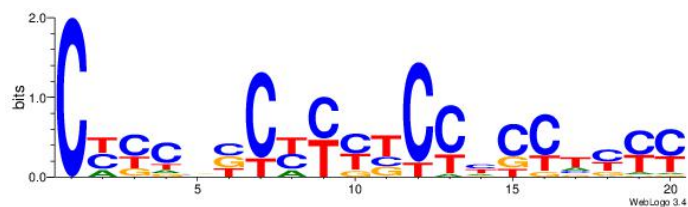


Dataset #: 1
Motif ID: 9
Motif name: TFM12
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 14
Number of overlap: 7
Similarity score: 2.0544

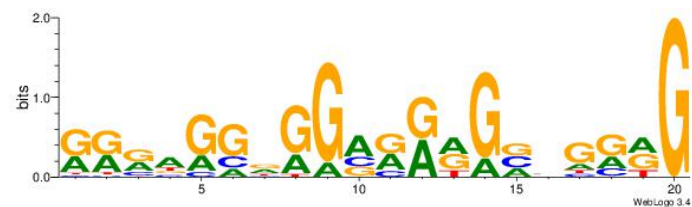
Alignment:

----KKKAGGDGGAKKMGBBGKMG
DHTATTTACBD-----

Original motif Consensus sequence: CYYCBCYYYTCCHCCTYYY



Reverse complement motif Consensus sequence: KKKAGGDGGAKKMGBBGKMG

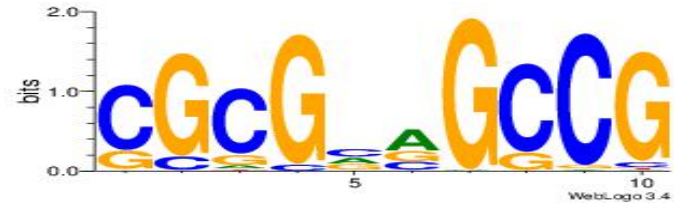


Dataset #: 1 Motif ID: 3 Motif name: TFW3

Original motif Consensus sequence: CGGCYBCGCG



Reverse complement motif Consensus sequence: CGCGBMGCCG

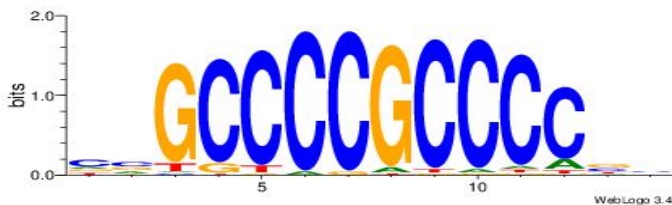


Best Matches for Top Significant Motif ID 3 (Highest to Lowest)

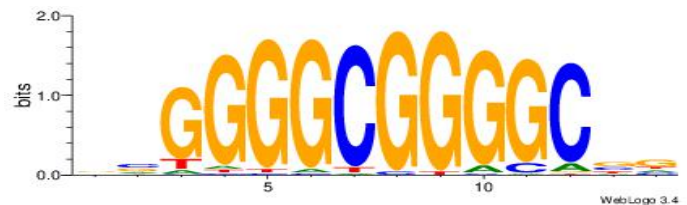
Dataset #: 2
 Motif ID: 12
 Motif name: csGCCCCGCCCCsc
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 5
 Number of overlap: 10
 Similarity score: 0.0718771

Alignment:
 HVGCCCCGCCCCBB
 CGGCYBCGCG-----

Original motif Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGCGGGGC

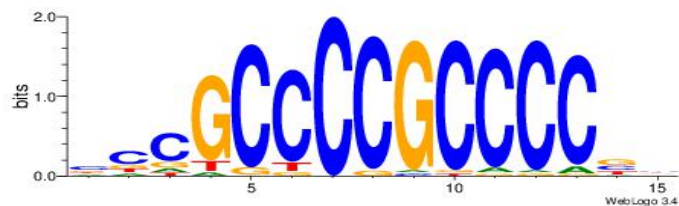


Dataset #: 2
 Motif ID: 14
 Motif name: cccGCCCCGCCCCsb
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 5
 Number of overlap: 10
 Similarity score: 0.0719604

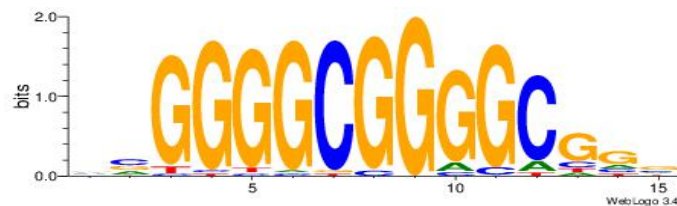
Alignment:

BCCGCCCCGCCCCBB
 -CGGCYBCGCG-----

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB



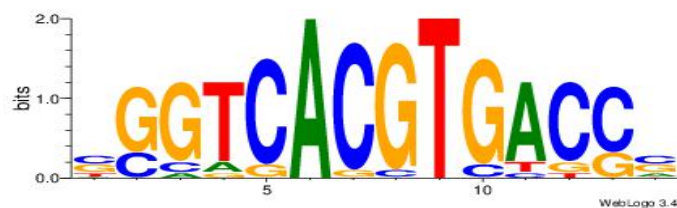
Dataset #: 2
 Motif ID: 18
 Motif name: sSGTCACGTGACSS
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward

Position number: 5
Number of overlap: 10
Similarity score: 0.0895189

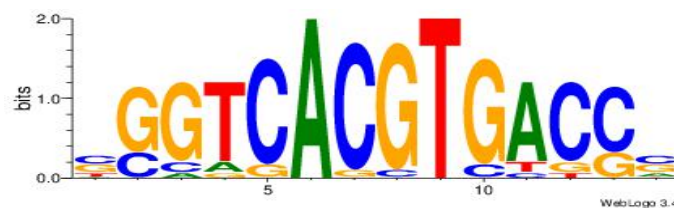
Alignment:

SGGTCACGTGACCS
----CGCGBMGCCG

Original motif Consensus sequence: SGGTCACGTGACCS



Reverse complement motif Consensus sequence: SGGTCACGTGACCS



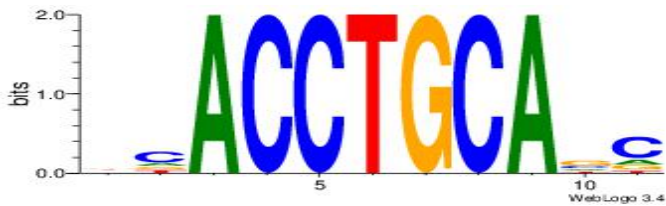
Dataset #: 2
Motif ID: 16
Motif name: kcACCTGCAGc
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 4
Number of overlap: 8
Similarity score: 1.10343

Alignment:

BCACCTGCABC--
---CGCGBMGCCG

Original motif Consensus sequence: BCACCTGCABC

Reverse complement motif Consensus sequence: GBTGCAGGTGB



Dataset #: 2
 Motif ID: 15
 Motif name: kCAGCCAATmr
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 5
 Number of overlap: 7
 Similarity score: 1.57732

Alignment:
 ---DCAGCCAATVR
 CGCGBMGCCG----

Original motif Consensus sequence: DCAGCCAATVR

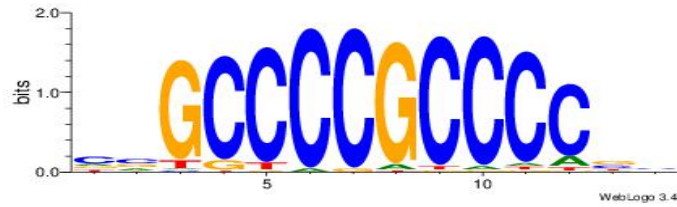


Reverse complement motif Consensus sequence: MBATTGGCTGH

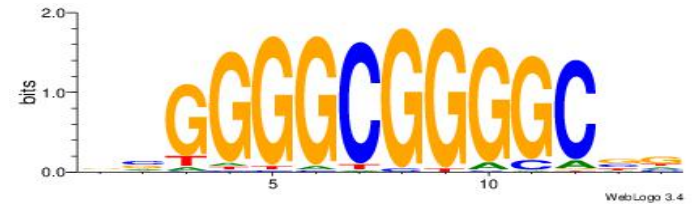


Dataset #: 2 Motif ID: 12 Motif name: csGCCCCGCCCCsc

Original motif Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGC



Best Matches for Top Significant Motif ID 12 (Highest to Lowest)

Dataset #:	1
Motif ID:	9
Motif name:	TFM12
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	4
Number of overlap:	14
Similarity score:	0.0777991

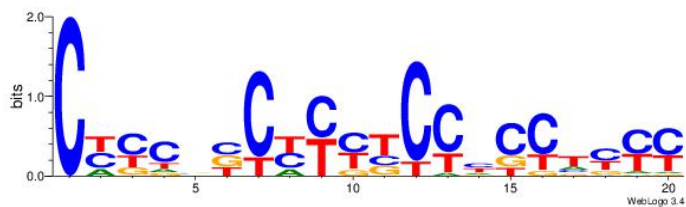
Alignment:

```

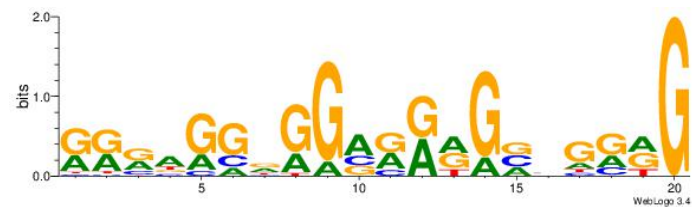
CYYCBBCYYYYTCCHCCTYYY
---HVGCCCCGCCCCBB---

```

Original motif Consensus sequence: CYYCBBCYYYYTCCHCCTYYY



Reverse complement motif Consensus sequence: KKKAGGDGGAKKMGBBGKMG

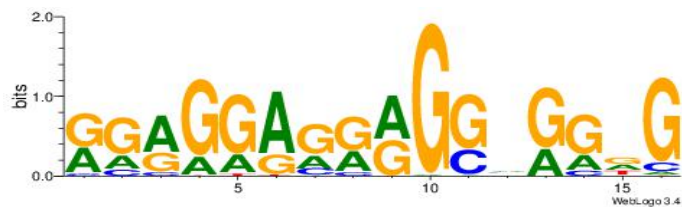


Dataset #: 1
 Motif ID: 6
 Motif name: TFM2
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 14
 Similarity score: 0.0880609

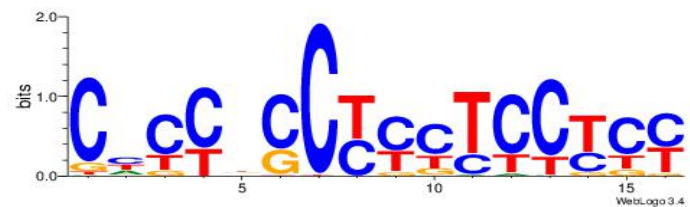
Alignment:

CHCCBCKMCTCCKCM
 HVGCCCGCCCCBB--

Original motif Consensus sequence: RGRGGAGRRGGHGGDG



Reverse complement motif Consensus sequence: CHCCBCKMCTCCKCM



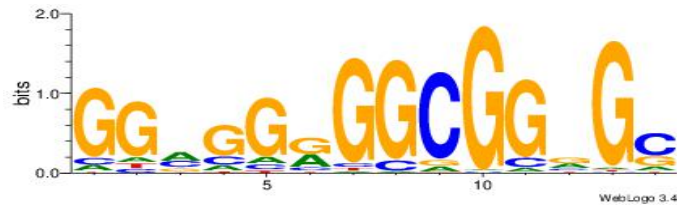
Dataset #: 1
 Motif ID: 5
 Motif name: TFF11
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1

Number of overlap: 14
Similarity score: 0.0937271

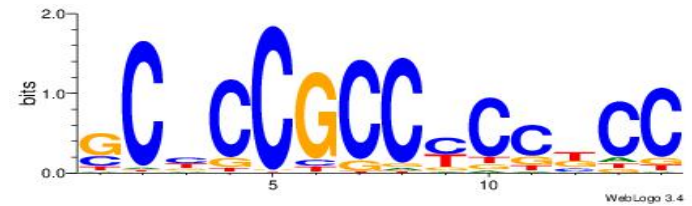
Alignment:

GGMGGRGGCGGVGC
BBGGGGCGGGGCVD

Original motif Consensus sequence: GGMGGRGGCGGVGC



Reverse complement motif Consensus sequence: GCVCCGCCMCCYC



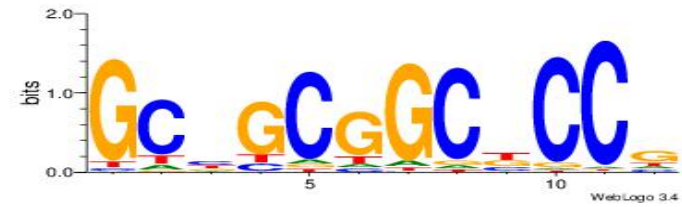
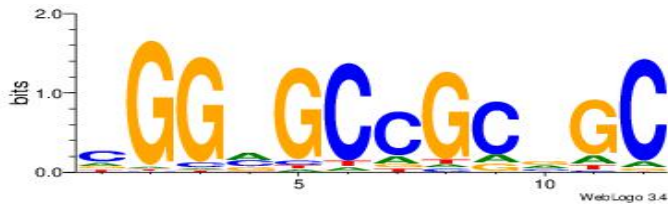
Dataset #: 1
Motif ID: 4
Motif name: TFF1
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 12
Similarity score: 1.08016

Alignment:

CGGVGCCGCVGC--
HVGCCCGCCCB

Original motif Consensus sequence: CGGVGCCGCVGC

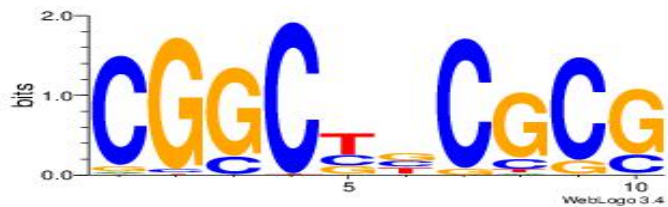
Reverse complement motif Consensus sequence: GCVCCGCCBCCG



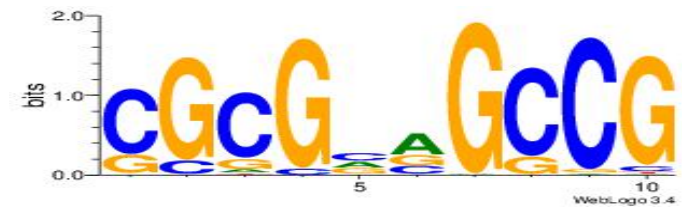
Dataset #: 1
 Motif ID: 3
 Motif name: TFW3
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 10
 Similarity score: 2.07757

Alignment:
 CGGCYBCGCG----
 HVGCCCCGCCCCBB

Original motif Consensus sequence: CGGCYBCGCG

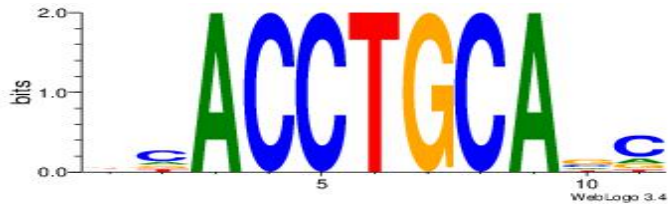


Reverse complement motif Consensus sequence: CGCGBMGCCG



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

Original motif Consensus sequence: BCACCTGCABC



Reverse complement motif Consensus sequence: GBTGCAGGTGB



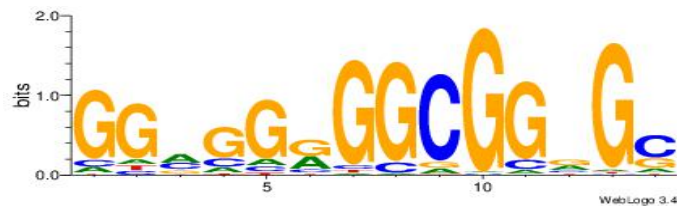
Best Matches for Top Significant Motif ID 16 (Highest to Lowest)

Dataset #:	1
Motif ID:	5
Motif name:	TFF11
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:	0.0312321

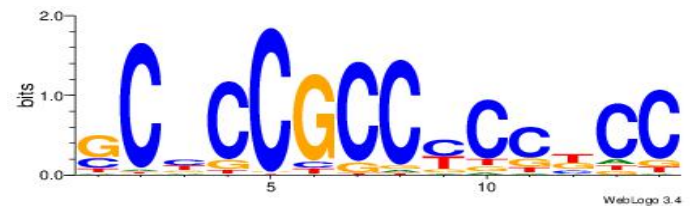
Alignment:

```
GGMGGRGGCGGVGC  
GBTGCAGGTGB---
```

Original motif Consensus sequence: GGMGGRGGCGGVGC



Reverse complement motif Consensus sequence: GCVCCGCCMCCYC

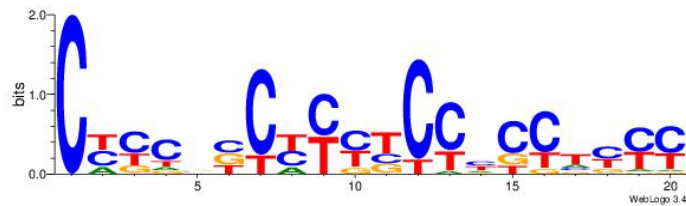


Dataset #: 1
 Motif ID: 9
 Motif name: TFM12
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 6
 Number of overlap: 11
 Similarity score: 0.0444938

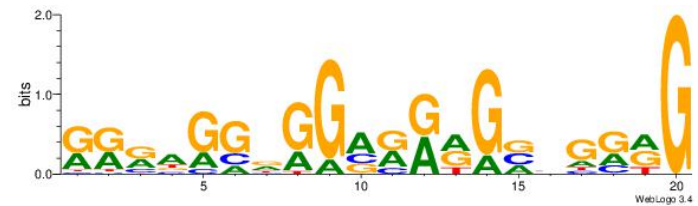
Alignment:

KKKAGGDGGAKKMGBBGKMG
 ----GBTGCAGGTGB-----

Original motif Consensus sequence: CYCBBCYYYTCCHCCTYYY



Reverse complement motif Consensus sequence: KKKAGGDGGAKKMGBBGKMG

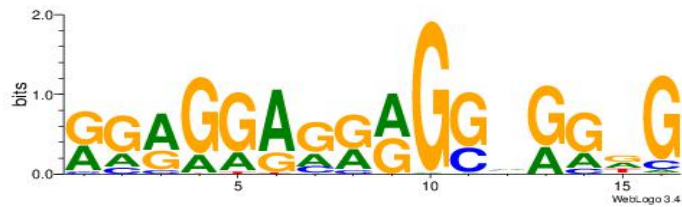


Dataset #: 1
 Motif ID: 6
 Motif name: TFM2
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 7

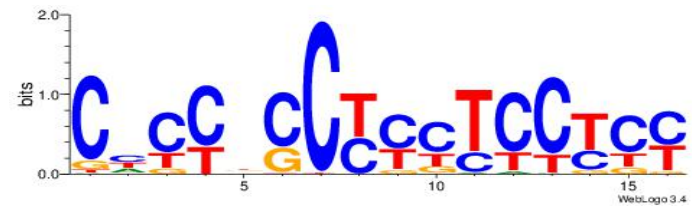
Number of overlap: 10
 Similarity score: 0.538471

Alignment:
 -RGRGGAGRRGGHGGDG
 GTGCAGGTGB-----

Original motif Consensus sequence: RGRGGAGRRGGHGGDG



Reverse complement motif Consensus sequence:
 CHCCBCKMCTCKCM

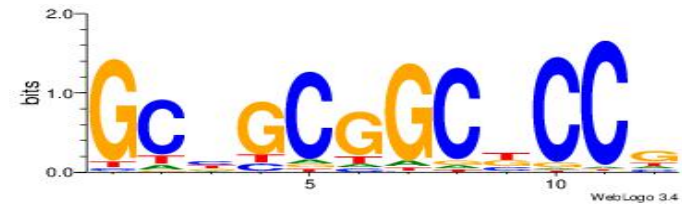
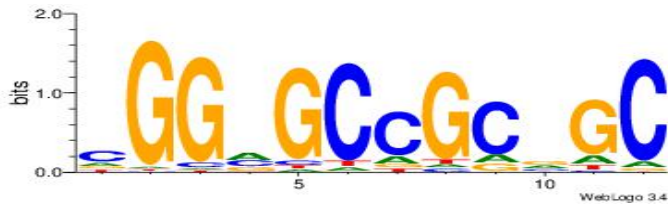


Dataset #: 1
 Motif ID: 4
 Motif name: TFF1
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 5
 Number of overlap: 8
 Similarity score: 1.54364

Alignment:
 GCVGCGGCBCCG---
 ----BCACCTGCABC

Original motif Consensus sequence: CGVGCCGCVGC

Reverse complement motif Consensus sequence: GCVGCGGCBCCG

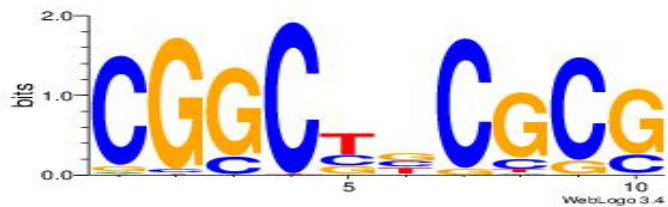


Dataset #: 1
 Motif ID: 3
 Motif name: TFW3
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 8
 Similarity score: 1.5466

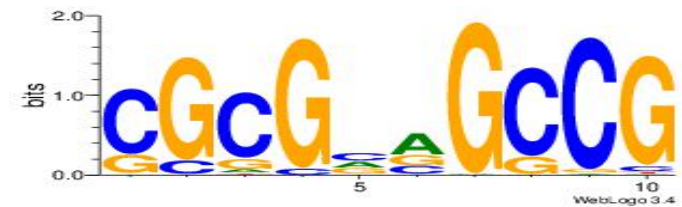
Alignment:

---CGGCYBCGCG
 GBTGCAGGTGB--

Original motif Consensus sequence: CGGCYBCGCG



Reverse complement motif Consensus sequence: CGCGBMGCCG



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

Original motif Consensus sequence: HVTACWGTABD



Reverse complement motif Consensus sequence: DBTACWGTAVH



Best Matches for Top Significant Motif ID 19 (Highest to Lowest)

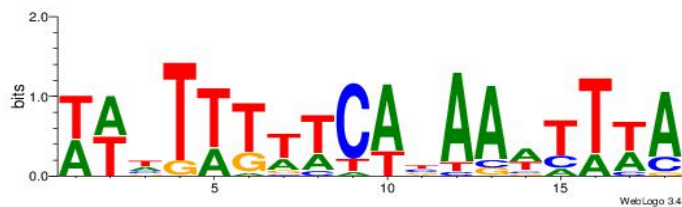
Dataset #: 1
 Motif ID: 8
 Motif name: TFM3
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 5
 Number of overlap: 11
 Similarity score: 0.0413797

Alignment:

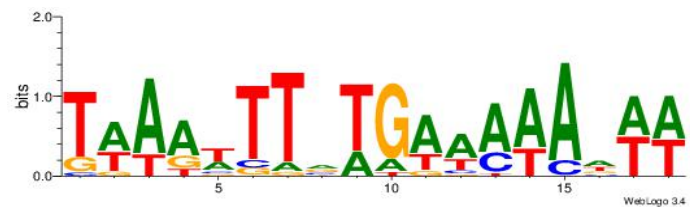
```

WWHTTTTTTCABAAWTTWA
---DBTACWGTAVH-----
    
```

Original motif Consensus sequence: WWHTTTTTTCABAAWTTWA



Reverse complement motif Consensus sequence: TAAWTTVTGAAAAHWW

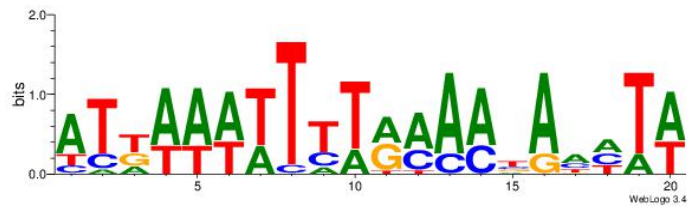


Dataset #: 1
 Motif ID: 10
 Motif name: TFM13
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 11
 Similarity score: 0.0445707

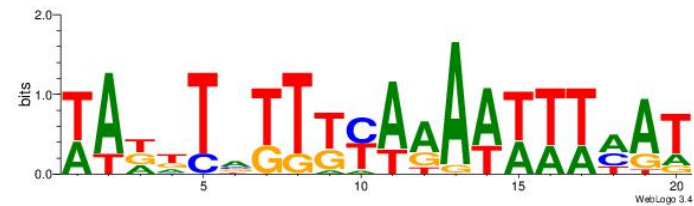
Alignment:

WAHHTVTTYKAAAATTRAT
 -----HVTACWG TABD--

Original motif Consensus sequence: ATKAAWTTTTRMAABAHTW



Reverse complement motif Consensus sequence: WAHHTVTTYKAAAATTRAT



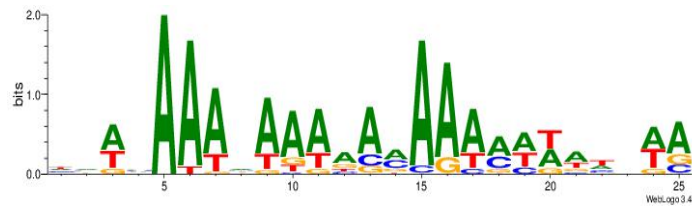
Dataset #: 1
 Motif ID: 11
 Motif name: TFM11
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4

Number of overlap: 11
 Similarity score: 0.0472742

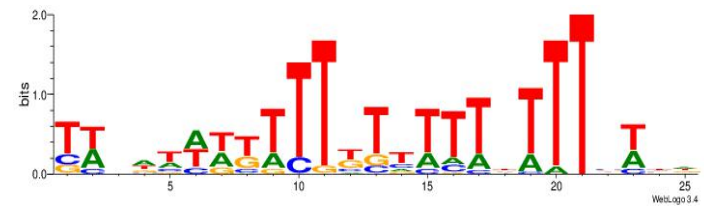
Alignment:

HDWVAAAHA AAAA MAAA MWWW HBWA
 ---DBTACWGTAVH-----

Original motif Consensus sequence:
 HDWVAAAHA AAAA MAAA MWWW HBWA



Reverse complement motif Consensus sequence:
 TWVHWWWYTTTTTTTTTHTTTVWBH

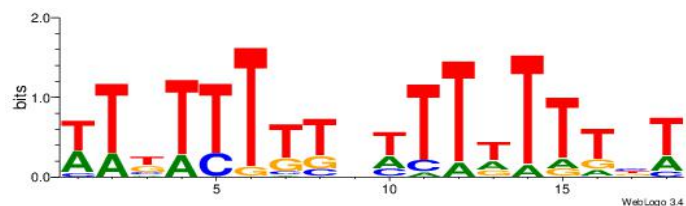


Dataset #: 1
 Motif ID: 7
 Motif name: TFM1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 10
 Number of overlap: 9
 Similarity score: 1.04742

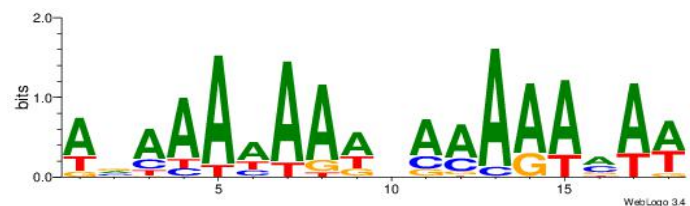
Alignment:

WKTTTTTTHWTTTTTTBT--
 -----DBTACWGTAVH

Original motif Consensus sequence: WTKTTTTTHWTTTTTBT



Reverse complement motif Consensus sequence: ABAAAAAWHAAAAARAW

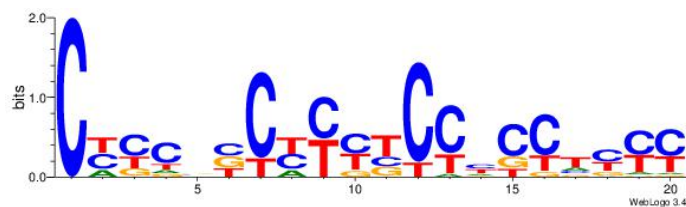


Dataset #: 1
 Motif ID: 9
 Motif name: TFM12
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 15
 Number of overlap: 6
 Similarity score: 2.54736

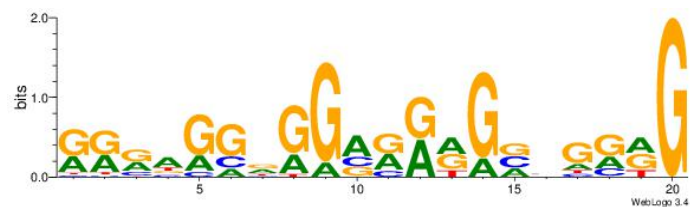
Alignment:

-----CYYCBBCYYYTCCHCCTYYY
 DBTACWGTAHV-----

Original motif Consensus sequence: CYYCBBCYYYTCCHCCTYYY

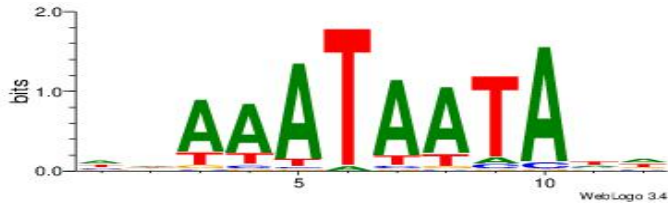


Reverse complement motif Consensus sequence: KKKAGGDGGAKKMGBBGKMG

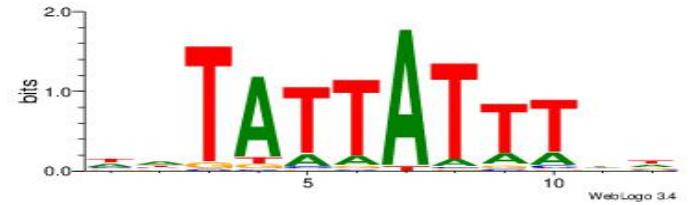


Dataset #: 2 Motif ID: 17 Motif name: wwAAATAATAtw

Original motif Consensus sequence: HDAAATAATADD



Reverse complement motif Consensus sequence: DDTATTATTTDH



Best Matches for Top Significant Motif ID 17 (Highest to Lowest)

Dataset #:	1
Motif ID:	7
Motif name:	TFM1
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	7
Number of overlap:	12
Similarity score:	0.0565705

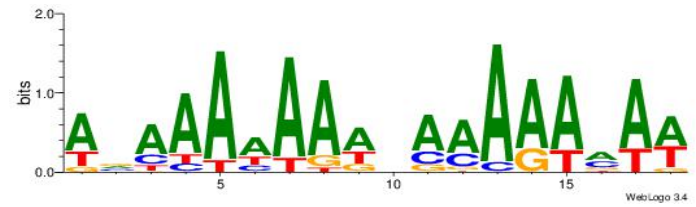
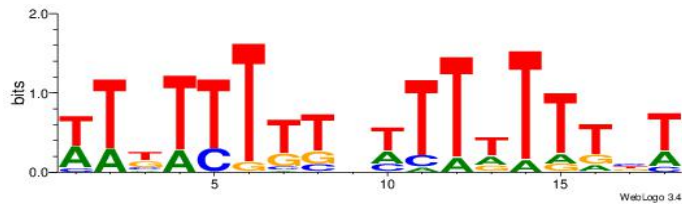
Alignment:

```

ABAAAAAAWHAAAAARAW
-----HDAAATAATADD
  
```

Original motif Consensus sequence: WTKTTTTTHWTTTTTTBT

Reverse complement motif Consensus sequence:
ABAAAAAAWHAAAAARAW



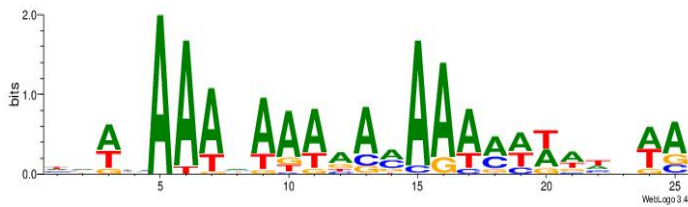
Dataset #: 1
 Motif ID: 11
 Motif name: TFM11
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 12
 Similarity score: 0.0575935

Alignment:

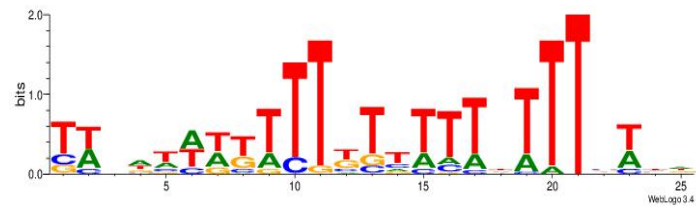
```

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

Original motif Consensus sequence:
 HDWVAAAHAAAAAMAAAMWWWHBWA



Reverse complement motif Consensus sequence:
 TWVHWWWYTTTTTTTTTHTTTVWBH



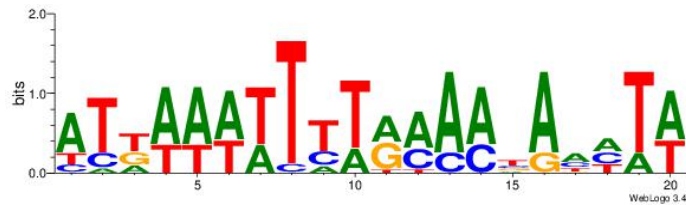
Dataset #: 1

Motif ID: 10
 Motif name: TFM13
 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: 0.0712963

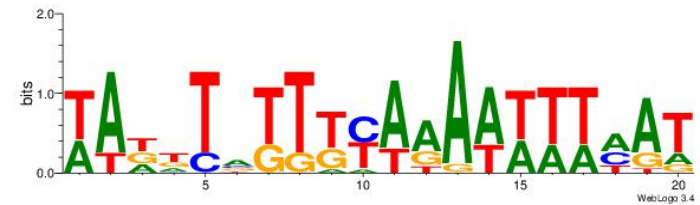
Alignment:

ATKAAWTTTTTRMAABAHTW
 -----DDTATTATTTDH

Original motif Consensus sequence: ATKAAWTTTTTRMAABAHTW



Reverse complement motif Consensus sequence: WAHHTVTTYKAAAATTRAT



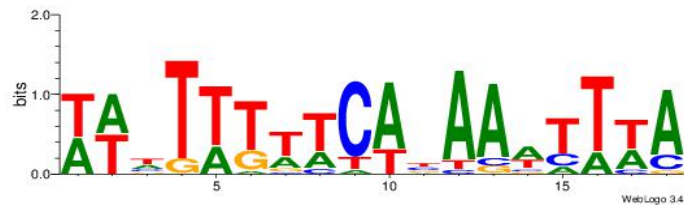
Dataset #: 1
 Motif ID: 8
 Motif name: TFM3
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 12

Similarity score: 0.0733516

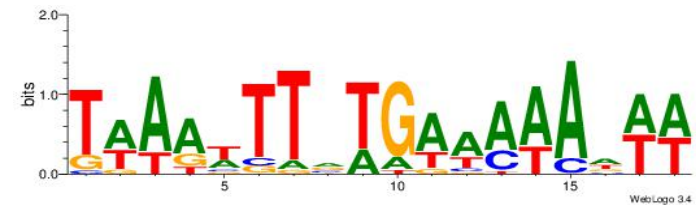
Alignment:

TWAAWTTVTGAAAAHWW
-----HDAAATAATADD

Original motif Consensus sequence: WWHTTTTTTCABAAWTTWA



Reverse complement motif Consensus sequence:
TAAWTTTVTGAAAAHWW



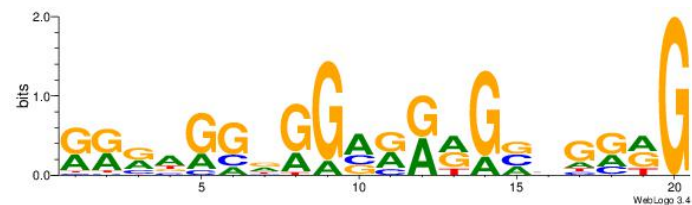
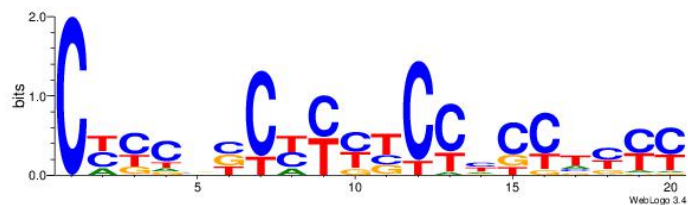
Dataset #: 1
Motif ID: 9
Motif name: TFM12
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 16
Number of overlap: 5
Similarity score: 3.59569

Alignment:

-----KKKAGGDGGAKKMGBBGKMG
DDTATTATTDDH-----

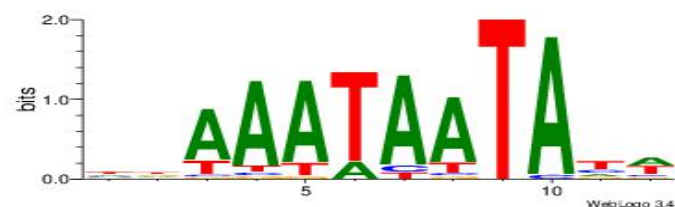
Original motif Consensus sequence: CYCBBYYYTCCHCCTYYY

Reverse complement motif Consensus sequence:
KKKAGGDGGAKKMGBBGKMG

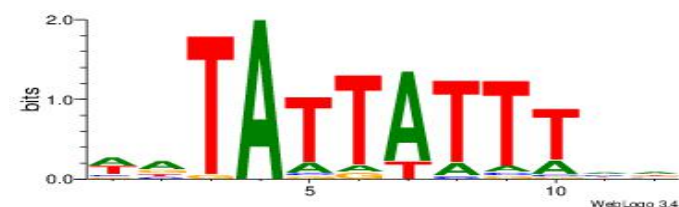


Dataset #: 2 Motif ID: 13 Motif name: tkAAATAATAtw

Original motif Consensus sequence: HDAAATAATAHW



Reverse complement motif Consensus sequence: WHTATTATTTDH



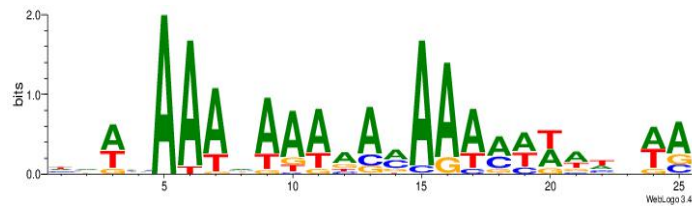
Best Matches for Top Significant Motif ID 13 (Highest to Lowest)

Dataset #:	1
Motif ID:	11
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

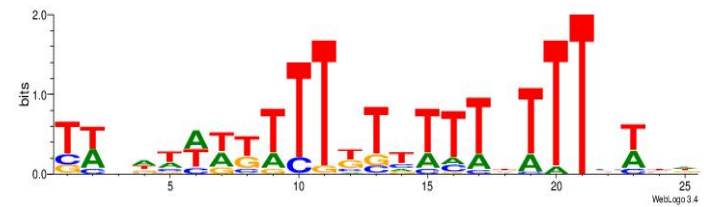
Alignment:

```
TWVHWWWYTTTYTTTTHTTTVWBH
-----WHTATTATTTDH--
```

Original motif Consensus sequence:
 HDWVAAAHAAAAAMAAAMWWWHBWA



Reverse complement motif Consensus sequence:
 TWVHWWWYTTTTTTTTTHTTTVWBH

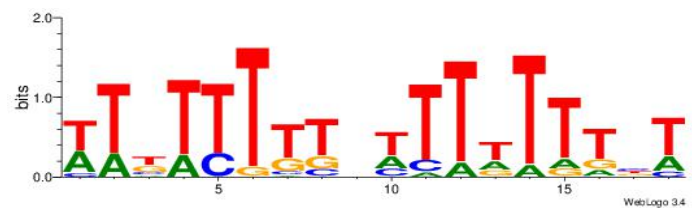


Dataset #: 1
 Motif ID: 7
 Motif name: TFM1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 12
 Similarity score: 0.0637702

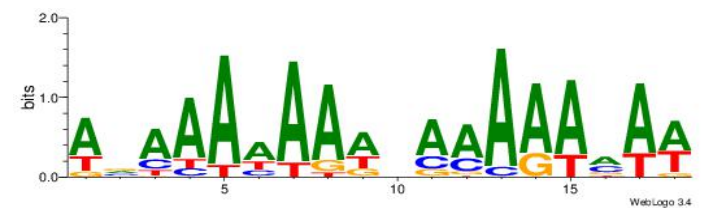
Alignment:

WTKTTTTTHWTTTTTTBT
 WHTATTATTTDH-----

Original motif Consensus sequence: WTKTTTTTHWTTTTTTBT



Reverse complement motif Consensus sequence:
 ABAAAAAWHAAAAARAW

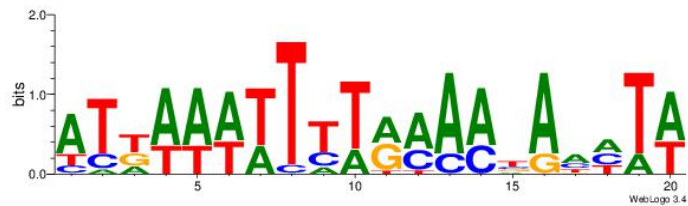


Dataset #: 1
 Motif ID: 10
 Motif name: TFM13
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 9
 Number of overlap: 12
 Similarity score: 0.0704475

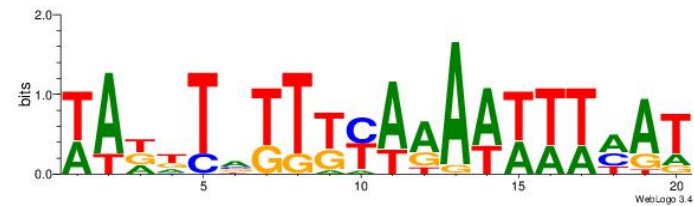
Alignment:

ATKAAWTTTTRMAABAHTW
 -----WHTATTATTTDH

Original motif Consensus sequence: ATKAAWTTTTRMAABAHTW



Reverse complement motif Consensus sequence: WAHHTVTTYKAAAATTRAT



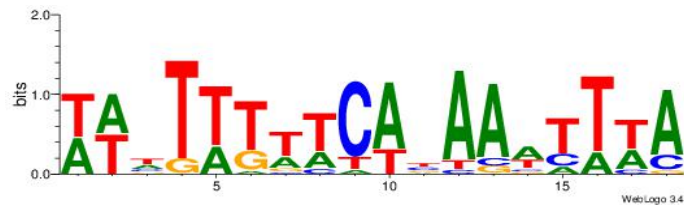
Dataset #: 1
 Motif ID: 8
 Motif name: TFM3
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1

Number of overlap: 12
 Similarity score: 0.0763819

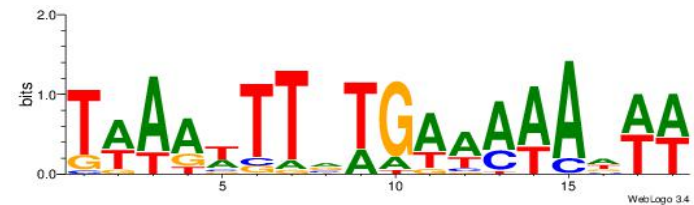
Alignment:

TWAAWTTVTGAAAAHWW
 -----HDAAATAATAHW

Original motif Consensus sequence: WWHTTTTTTCABAAWTTWA



Reverse complement motif Consensus sequence: TWAAWTTVTGAAAAHWW

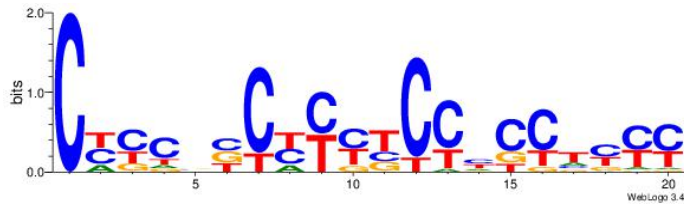


Dataset #: 1
 Motif ID: 9
 Motif name: TFM12
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 16
 Number of overlap: 5
 Similarity score: 3.59273

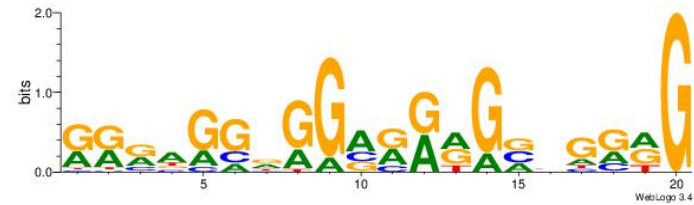
Alignment:

-----KKKAGGDGGAKKMGBBGKMG
 WHTATTATTTDH-----

Original motif Consensus sequence: CYCBBYYYTCCHCCTYYY



Reverse complement motif Consensus sequence: KKKAGGDGGAKKMGBBGKMG



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

Original motif Consensus sequence: DHACATTCTGH



Reverse complement motif Consensus sequence: HCAGAATGTHD



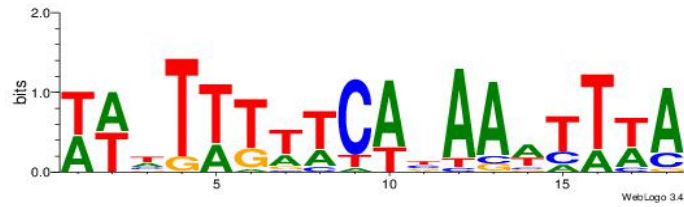
Best Matches for Top Significant Motif ID 20 (Highest to Lowest)

Dataset #:	1
Motif ID:	8
Motif name:	TFM3
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	8
Number of overlap:	11
Similarity score:	0.00522383

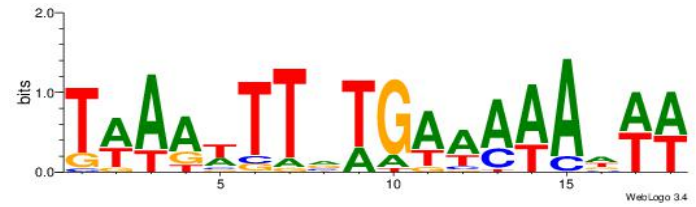
Alignment:

WWHTTTTTTCABAAWTTWA
 HCAGAATGTHD-----

Original motif Consensus sequence: WWHTTTTTTCABAAWTTWA



Reverse complement motif Consensus sequence: TWAAWTTVTGAAAAHWW



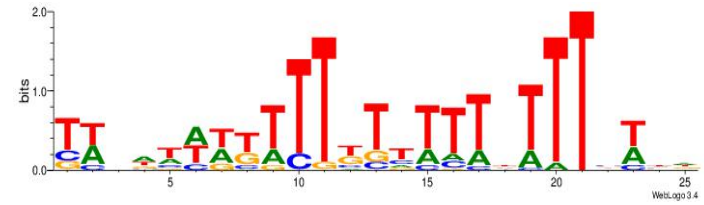
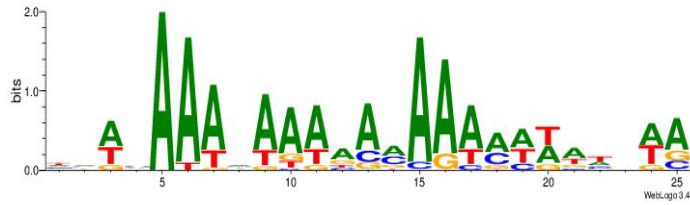
Dataset #: 1
 Motif ID: 11
 Motif name: TFM11
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 11
 Number of overlap: 11
 Similarity score: 0.014258

Alignment:

HDWVAAAHA AAAAAMAAAMWWWHBWA
 ----HCAGAATGTHD-----

Original motif Consensus sequence:
 HDWVAAAHA AAAAAMAAAMWWWHBWA

Reverse complement motif Consensus sequence:
 TWVHWWWYTTTTTTTTTTTTHTTTVWBH

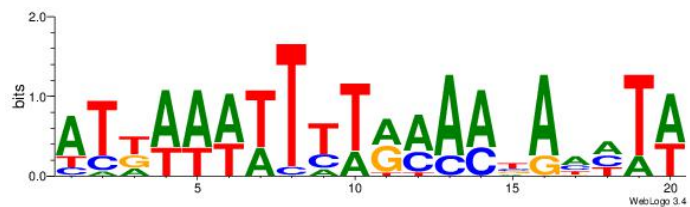


Dataset #: 1
 Motif ID: 10
 Motif name: TFM13
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 9
 Number of overlap: 11
 Similarity score: 0.0192045

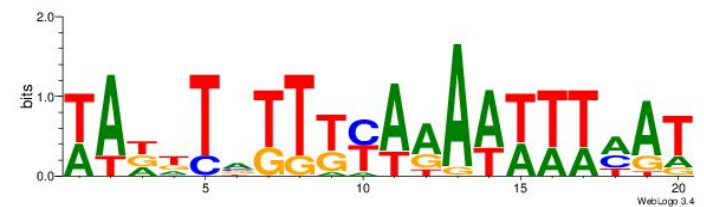
Alignment:

ATKAAWTTTTRMAABAHTW
 -DHACATTCTGH-----

Original motif Consensus sequence: ATKAAWTTTTRMAABAHTW



Reverse complement motif Consensus sequence: WAHHTVTTYKAAAATTRAT



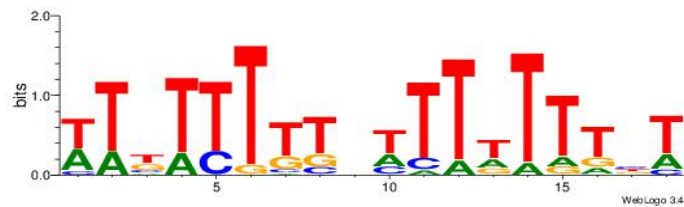
Dataset #: 1

Motif ID: 7
 Motif name: TFM1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 9
 Number of overlap: 10
 Similarity score: 0.519904

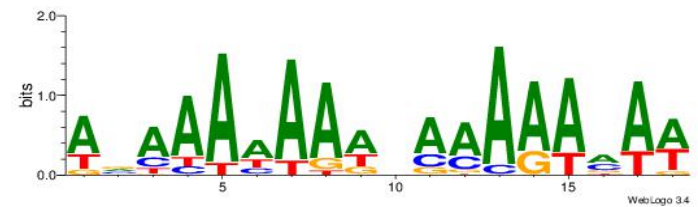
Alignment:

ABAAAAA WHAAAAARAW-
 -----HCAGAATGTHD

Original motif Consensus sequence: WTKTTTTTHWTTTTTTBT



Reverse complement motif Consensus sequence: ABAAAAA WHAAAAARAW



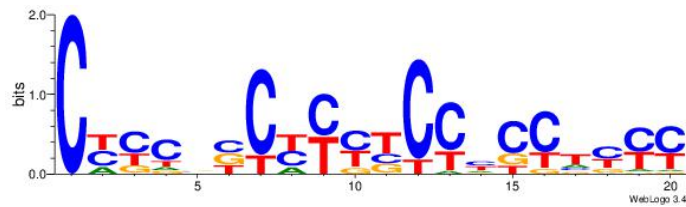
Dataset #: 1
 Motif ID: 9
 Motif name: TFM12
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 17
 Number of overlap: 4

Similarity score: 3.5

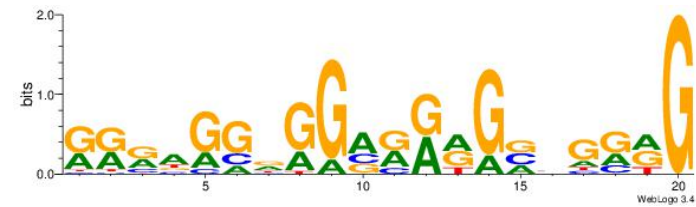
Alignment:

-----CYYCBBCYYYTCCHCCTYYY
DHACATTCTGH-----

Original motif Consensus sequence: CYYCBBCYYYTCCHCCTYYY



Reverse complement motif Consensus sequence: KKKAGGDGGAKKMGBBGKMG



Dataset #: 1 Motif ID: 2 Motif name: TFW2

Original motif Consensus sequence: SCGCGCGG



Reverse complement motif Consensus sequence: CCGCGCGS



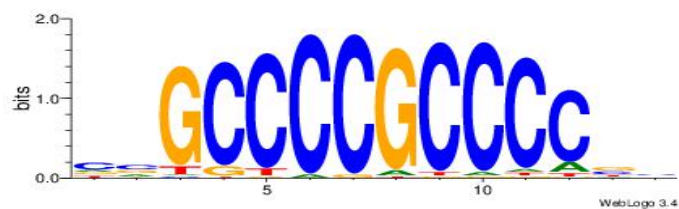
Best Matches for Top Significant Motif ID 2 (Highest to Lowest)

Dataset #:	2
Motif ID:	12
Motif name:	csGCCCCGCCCCsc
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement

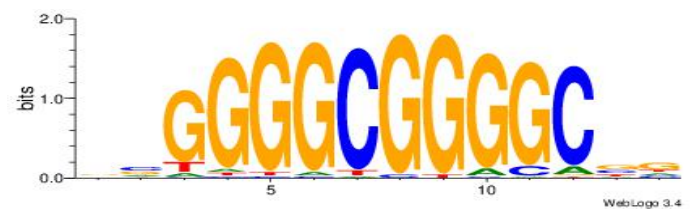
Direction: Forward
 Position number: 2
 Number of overlap: 8
 Similarity score: 0.0456233

Alignment:
 BBGGGGCGGGGCVD
 -SCGCGCGG-----

Original motif Consensus sequence: HVGCCCCGCCCCBB



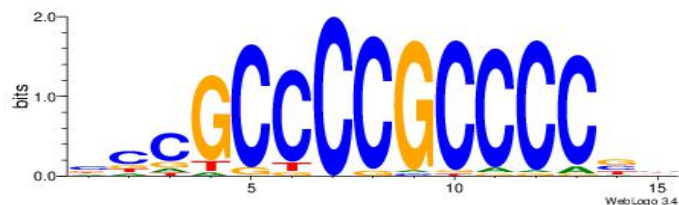
Reverse complement motif Consensus sequence: BBGGGGCGGGGC



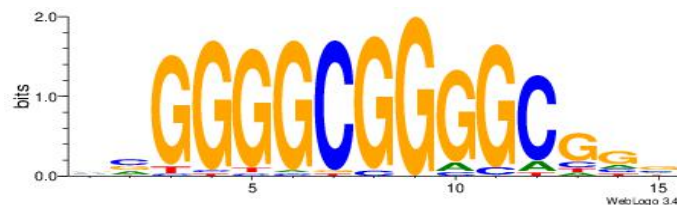
Dataset #: 2
 Motif ID: 14
 Motif name: cccGCCCCGCCCCsb
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 7
 Number of overlap: 8
 Similarity score: 0.045686

Alignment:
 BCCGCCCCGCCCCBB
 -----CCGCGCGS-

Original motif Consensus sequence: BCGCCCCGCCCB



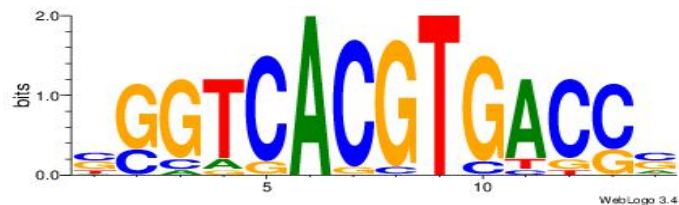
Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB



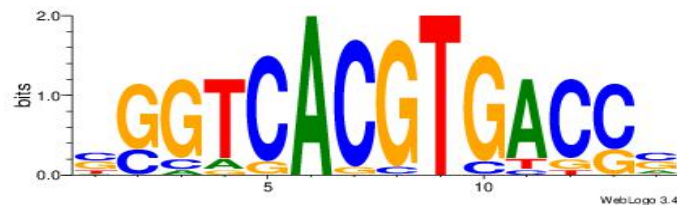
Dataset #: 2
Motif ID: 18
Motif name: sSGTCACGTGACCS
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 4
Number of overlap: 8
Similarity score: 0.0988223

Alignment:
SGGTCACGTGACCS
---SCGCGCGG---

Original motif Consensus sequence: SGGTCACGTGACCS



Reverse complement motif Consensus sequence: SGGTCACGTGACCS

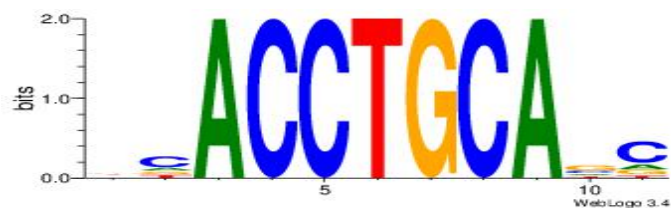


Dataset #: 2
 Motif ID: 16
 Motif name: kcACCTGCAGc
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 8
 Number of overlap: 4
 Similarity score: 2.08456

Alignment:

----GBTGCAGGTGB
 SCGCGCGG-----

Original motif Consensus sequence: BCACCTGCABC



Reverse complement motif Consensus sequence: GBTGCAGGTGB



Dataset #: 2
 Motif ID: 15
 Motif name: kCAGCCAATmr
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 8
 Number of overlap: 4

Similarity score: 2.0901

Alignment:

MBATTGGCTGH-----
-----CCGCGCGS

Original motif Consensus sequence: DCAGCCAATVR



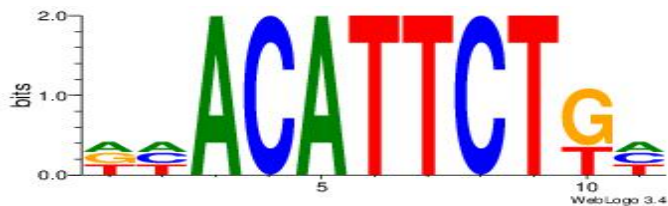
Reverse complement motif Consensus sequence: MBATTGGCTGH



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

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

Original motif Consensus sequence: DHACATTCTGH



Reverse complement motif Consensus sequence: HCAGAATGTHD



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

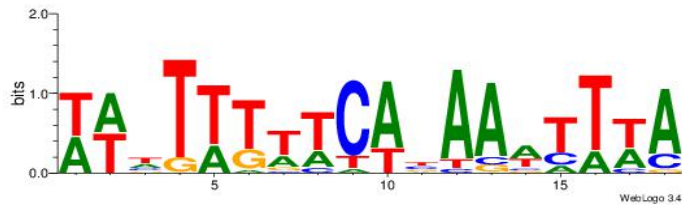
Dataset #: 1

Motif ID: 8
 Motif name: TFM3
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 8
 Number of overlap: 11
 Similarity score: 0.00522383

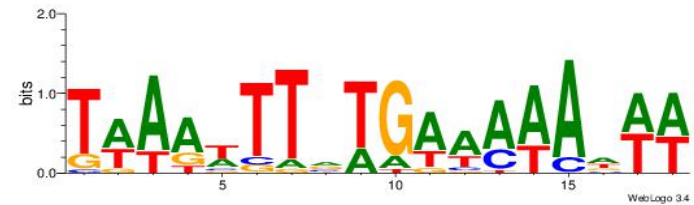
Alignment:

WWHTTTTTTCABAAWTTWA
 HCAGAATGTHD-----

Original motif Consensus sequence: WWHTTTTTTCABAAWTTWA



Reverse complement motif Consensus sequence: TAAWTTVTGAAAAHWW



Dataset #: 2
 Motif ID: 16
 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: 0.00731643

Alignment:

BCACCTGCABC

DHACATTCTGH

Original motif Consensus sequence: BCACCTGCABC



Reverse complement motif Consensus sequence: GBTGCAGGTGB



Dataset #: 2
Motif ID: 17
Motif name: wwAAATAATAtw
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: 0.0127231

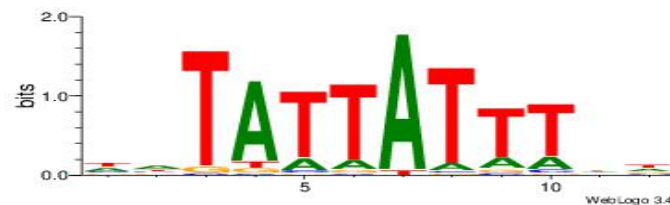
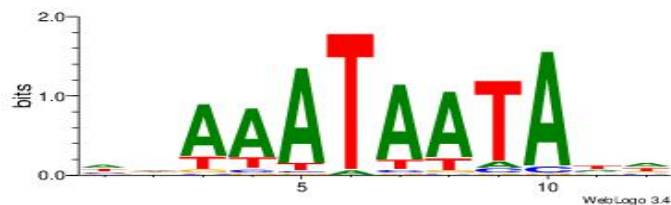
Alignment:

DDTATTATTTDH

-HCAGAATGTHD

Original motif Consensus sequence: HDAAATAATADD

Reverse complement motif Consensus sequence: DDTATTATTTDH

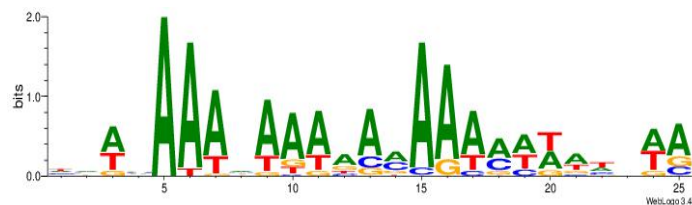


Dataset #: 1
 Motif ID: 11
 Motif name: TFM11
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 5
 Number of overlap: 11
 Similarity score: 0.014258

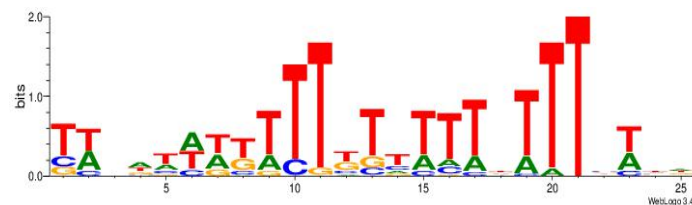
Alignment:

```
HDWVAAAHAAAAAMAAAMWWWHBWA
----HCAGAATGTHD-----
```

Original motif Consensus sequence:
 HDWVAAAHAAAAAMAAAMWWWHBWA



Reverse complement motif Consensus sequence:
 TWVHWWWYTTTTTTTTTHTTTVWBH



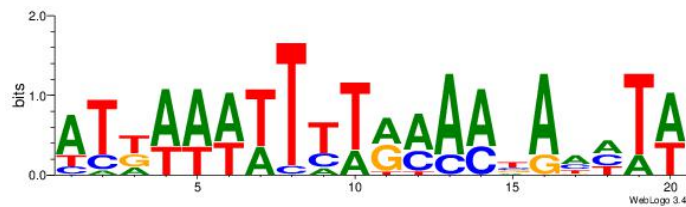
Dataset #: 1

Motif ID: 10
 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: 0.0192045

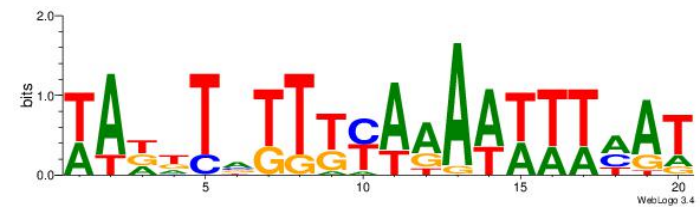
Alignment:

ATKAAWTTTTRMAABAHTW
 -DHACATTCTGH-----

Original motif Consensus sequence: ATKAAWTTTTRMAABAHTW



Reverse complement motif Consensus sequence: WAHHTVTTYKAAAATTRAT



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

Original motif Consensus sequence: DBGTAATAHD



Reverse complement motif Consensus sequence: DHTATTTACBD



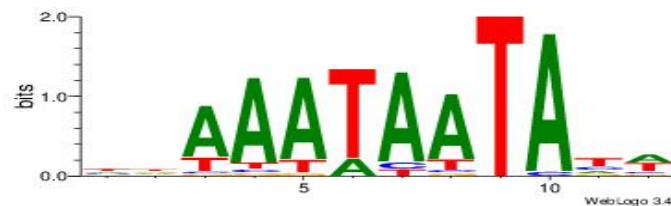
Best Matches for Significant Motif ID 21 (Highest to Lowest)

Dataset #: 2
Motif ID: 13
Motif name: tkAAATAATAtw
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 11
Similarity score: 0.0162338

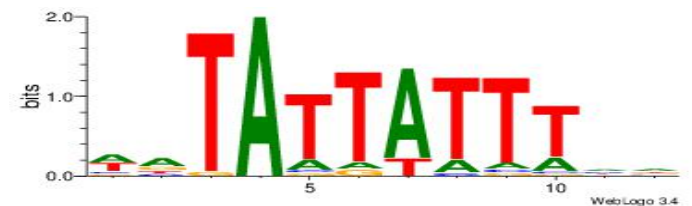
Alignment:

HDAAATAATAHW
-DBGTAATAAHD

Original motif Consensus sequence: HDAAATAATAHW



Reverse complement motif Consensus sequence: WHTATTATTTDH

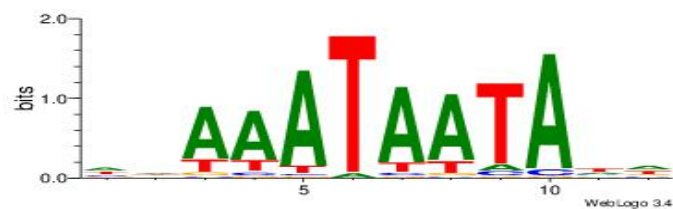


Dataset #: 2
Motif ID: 17
Motif name: wwAAATAATAtw
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement

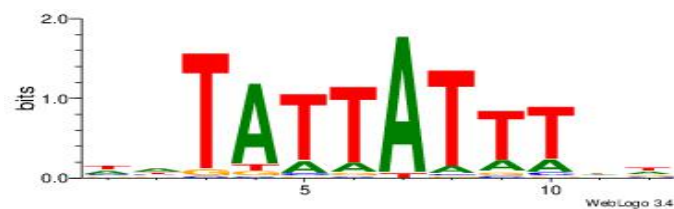
Direction: Backward
 Position number: 2
 Number of overlap: 11
 Similarity score: 0.0164863

Alignment:
 DDTATTATTTDH
 DHTATTTACBD-

Original motif Consensus sequence: HDAAATAATADD



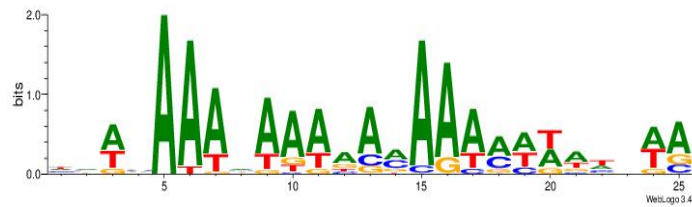
Reverse complement motif Consensus sequence: DDTATTATTTDH



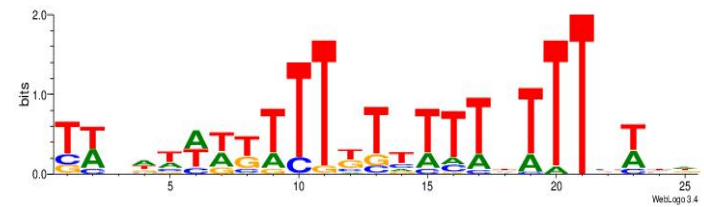
Dataset #: 1
 Motif ID: 11
 Motif name: TFM11
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 15
 Number of overlap: 11
 Similarity score: 0.0192768

Alignment:
 TWVHWWYTTTTYTTTTTHTTTVWBH
 -----DHTATTTACBD

Original motif Consensus sequence:
 HDWVAAAHAAAAAMAAAMWWWHBWA



Reverse complement motif Consensus sequence:
 TWVHWWWYTTTTTTTTTHTTTVWBH

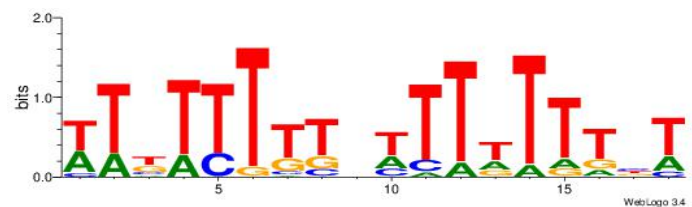


Dataset #: 1
 Motif ID: 7
 Motif name: TFM1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.0283217

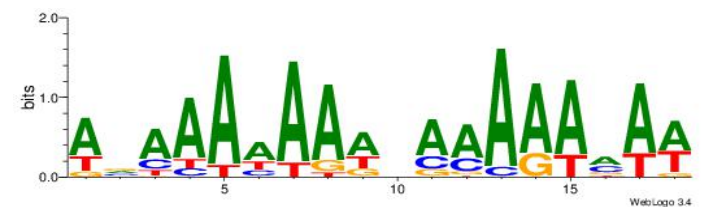
Alignment:

WTKTTTTTHWTTTTTTBT
 DHTATTTACBD-----

Original motif Consensus sequence: WTKTTTTTHWTTTTTTBT



Reverse complement motif Consensus sequence:
 ABAAAAAWHAAAAARAW

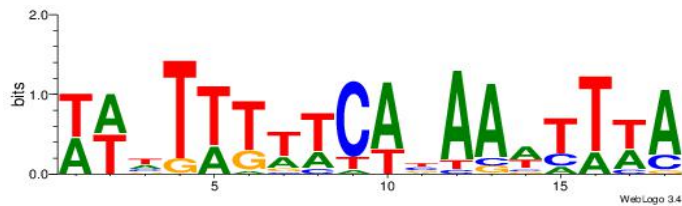


Dataset #: 1
 Motif ID: 8
 Motif name: TFM3
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 11
 Similarity score: 0.0308097

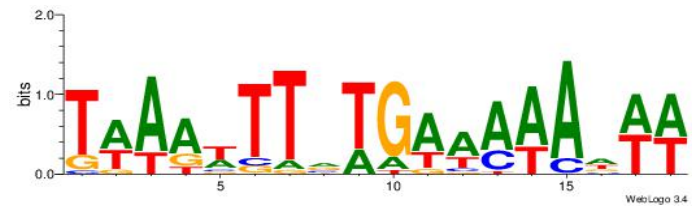
Alignment:

WWHTTTTTTCABAAWTTWA
 -----DHTATTTACBD-

Original motif Consensus sequence: WWHTTTTTTCABAAWTTWA



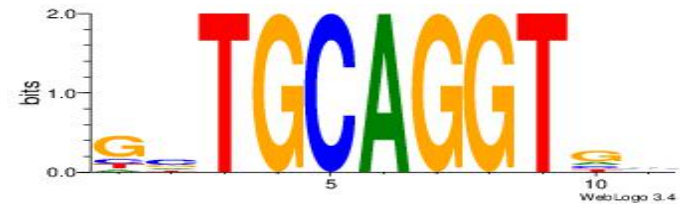
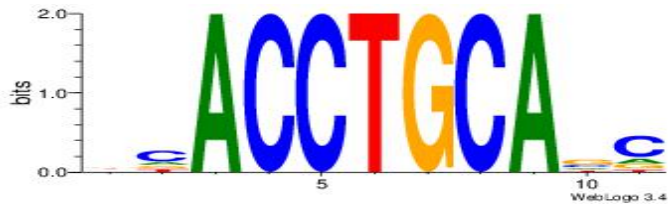
Reverse complement motif Consensus sequence: TAAWTTVTGAAAAHWW



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

Original motif Consensus sequence: BCACCTGCABC

Reverse complement motif Consensus sequence: GBTGCAGGTGB



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

Dataset #: 2
 Motif ID: 19
 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: 0.0182895

Alignment:
 DBTACWGTA VH
 BCACCTGC ABC

Original motif Consensus sequence: HVTACWG TABD



Reverse complement motif Consensus sequence: DBTACWGTA VH

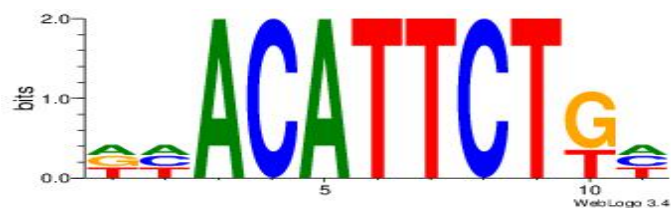


Dataset #: 2

Motif ID: 20
 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: 0.0221745

Alignment:
 DHACATTCTGH
 BCACCTGCABC

Original motif Consensus sequence: DHACATTCTGH



Reverse complement motif Consensus sequence: HCAGAATGTHD

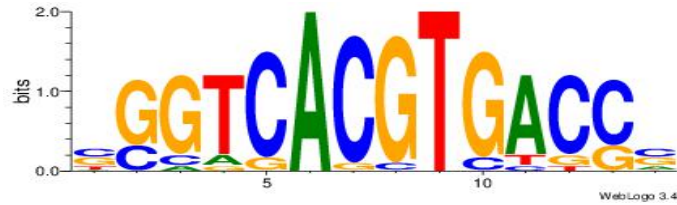


Dataset #: 2
 Motif ID: 18
 Motif name: sSGTCACGTGACSS
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 11
 Similarity score: 0.0280991

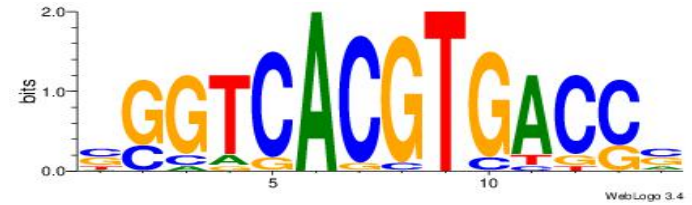
Alignment:

SGGTCACGTGACCS
---BCACCTGCABC

Original motif Consensus sequence: SGGTCACGTGACCS



Reverse complement motif Consensus sequence: SGGTCACGTGACCS



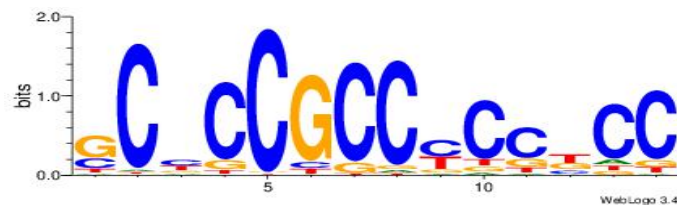
Dataset #: 1
Motif ID: 5
Motif name: TFF11
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 4
Number of overlap: 11
Similarity score: 0.0312321

Alignment:

GGMGGRGGCGGVGC
GBTGCAGGTGB---

Original motif Consensus sequence: GGMGGRGGCGGVGC

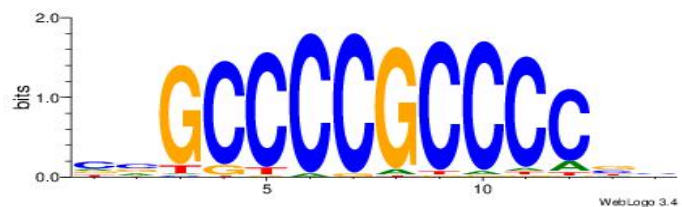
Reverse complement motif Consensus sequence: GCVCCGCCMCCYCC



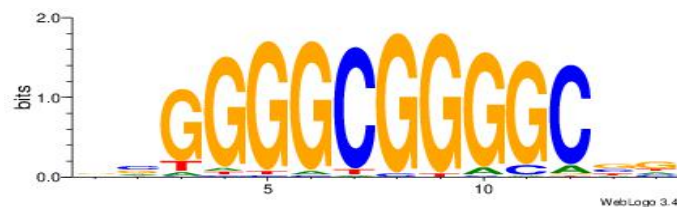
Dataset #: 2
 Motif ID: 12
 Motif name: csGCCCCGCCCCsc
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 11
 Similarity score: 0.0370129

Alignment:
 HVGCCCCGCCCCBB
 -BCACCTGCABC--

Original motif Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGC



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

Original motif Consensus sequence: HVTACWG TABD



Reverse complement motif Consensus sequence: DBTACWG TAVH



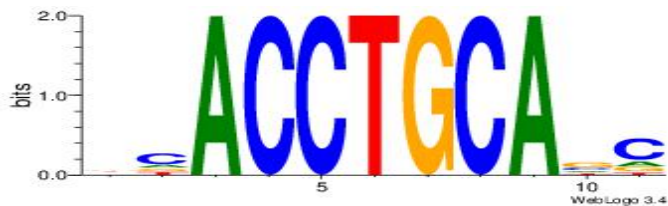
Best Matches for Significant Motif ID 19 (Highest to Lowest)

Dataset #:	2
Motif ID:	16
Motif name:	kcACCTGC Agc
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:	0.0199592

Alignment:

GBTGCAGGTGB
HVTACWG TABD

Original motif Consensus sequence: BCACCTGC ABC



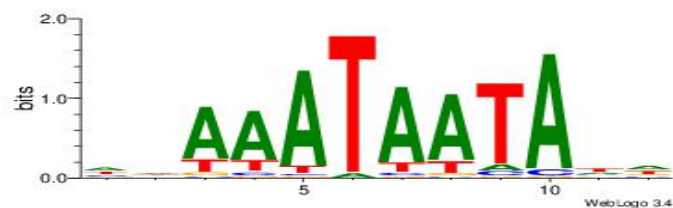
Reverse complement motif Consensus sequence: GBTGCAGGTGB



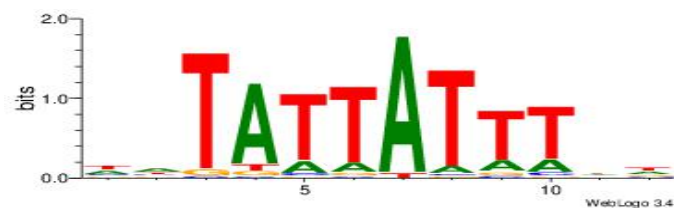
Dataset #: 2
 Motif ID: 17
 Motif name: wwAAATAATAtw
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.0309343

Alignment:
 DDTATTATTTDH
 -HVTACWGTABD

Original motif Consensus sequence: HDAAATAATADD



Reverse complement motif Consensus sequence: DDTATTATTTDH

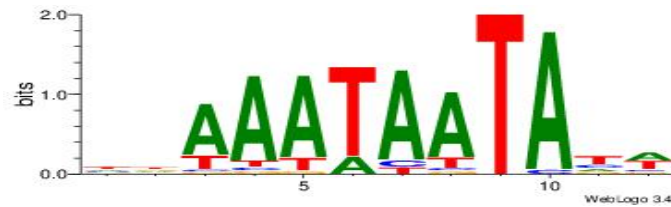


Dataset #: 2
 Motif ID: 13
 Motif name: tkAAATAATAtw
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 11

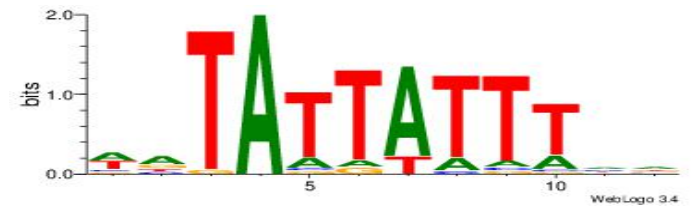
Similarity score: 0.0337121

Alignment:
HDAAATAATAHW
DBTACWGTAVH-

Original motif Consensus sequence: HDAAATAATAHW



Reverse complement motif Consensus sequence: WHTATTATTTDH

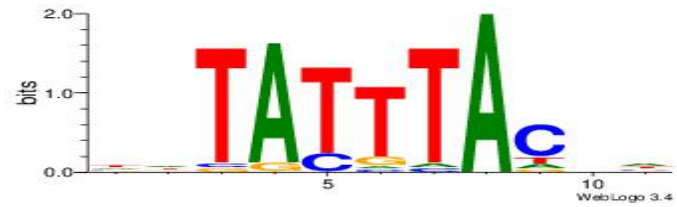


Dataset #: 2
Motif ID: 21
Motif name: wbgTAAATAww
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 11
Similarity score: 0.037518

Alignment:
DBGTAAATAHD
DBTACWGTAVH

Original motif Consensus sequence: DBGTAAATAHD

Reverse complement motif Consensus sequence: DHTATTTACBD

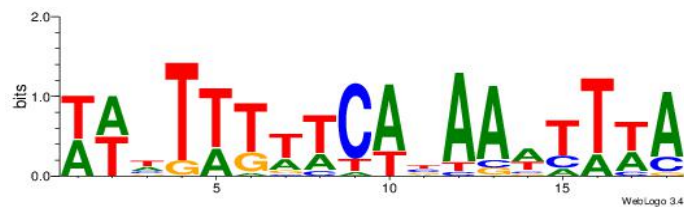


Dataset #: 1
 Motif ID: 8
 Motif name: TFM3
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 5
 Number of overlap: 11
 Similarity score: 0.0413797

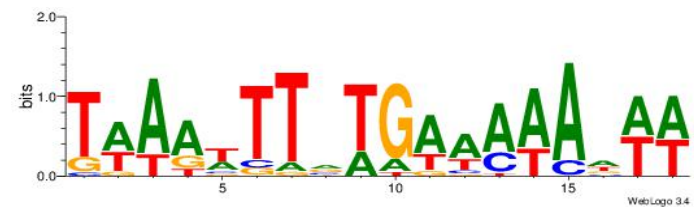
Alignment:

WWHTTTTTTCABAAWTTWA
 ---DBTACWGTAHV----

Original motif Consensus sequence: WWHTTTTTTCABAAWTTWA



Reverse complement motif Consensus sequence: TAAWTTVTGAAAAHWW



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

Original motif Consensus sequence: DCAGCCAATVR



Reverse complement motif Consensus sequence: MBATTGGCTGH



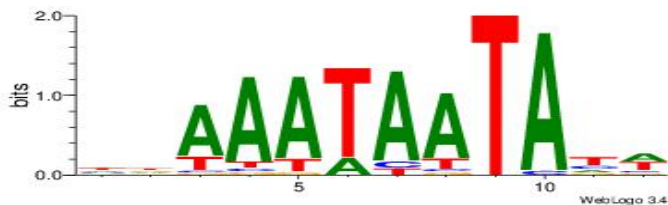
Best Matches for Significant Motif ID 15 (Highest to Lowest)

Dataset #:	2
Motif ID:	13
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:	0.0320614

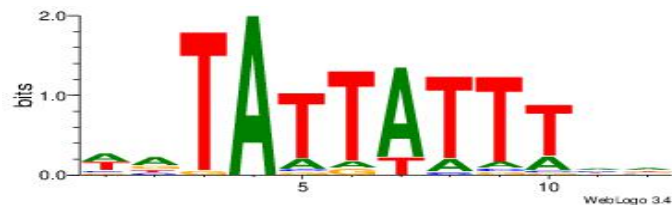
Alignment:

WHTATTATTTDH
-MBATTGGCTGH

Original motif Consensus sequence: HDAATAATAHW



Reverse complement motif Consensus sequence: WHTATTATTTDH

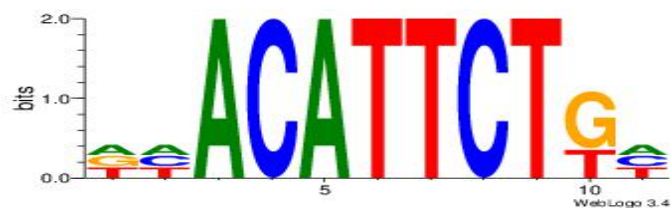


Dataset #: 2
 Motif ID: 20
 Motif name: dhACATTCTkh
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.034958

Alignment:

HCAGAATGTHD
 DCAGCCAATVR

Original motif Consensus sequence: DHACATTCTGH



Reverse complement motif Consensus sequence: HCAGAATGTHD



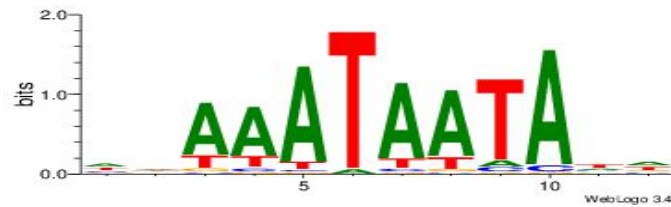
Dataset #: 2
 Motif ID: 17
 Motif name: wwAAATAATAtw
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 11

Similarity score: 0.0358988

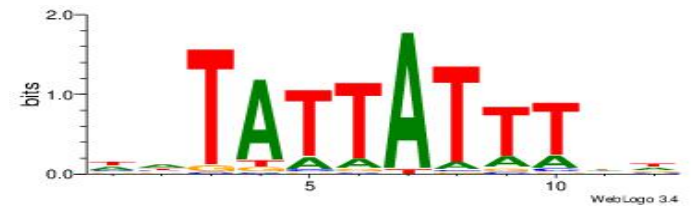
Alignment:

DDTATTATTTDH
-MBATTGGCTGH

Original motif Consensus sequence: HDAAATAATADD



Reverse complement motif Consensus sequence: DDTATTATTTDH



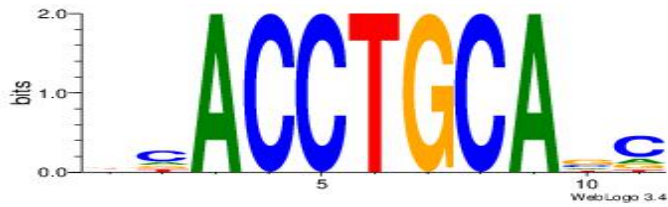
Dataset #: 2
Motif ID: 16
Motif name: kcACCTGCAGc
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 11
Similarity score: 0.0360892

Alignment:

BCACCTGCABC
MBATTGGCTGH

Original motif Consensus sequence: BCACCTGCABC

Reverse complement motif Consensus sequence: GBTGCAGGTGB



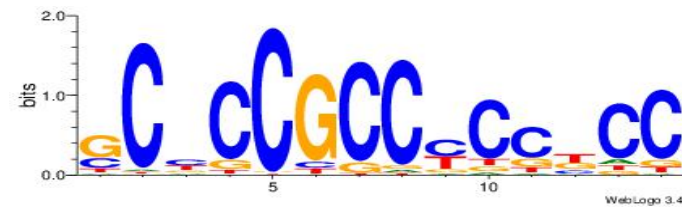
Dataset #: 1
 Motif ID: 5
 Motif name: TFF11
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 11
 Similarity score: 0.0376063

Alignment:
 GGMGRRGGCGGVGC
 --MBATTGGCTGH-

Original motif Consensus sequence: GGMGRRGGCGGVGC

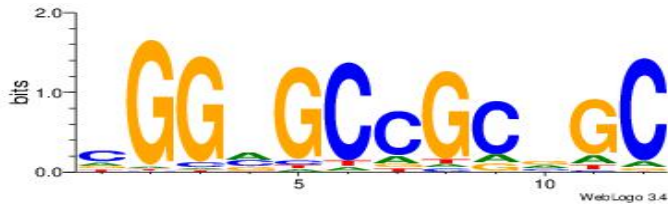


Reverse complement motif Consensus sequence: GCVCCGCCMCCYCC

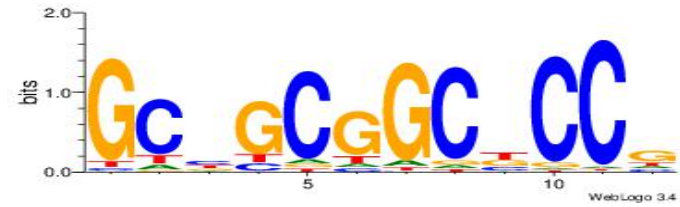


Dataset #: 1 Motif ID: 4 Motif name: TFF1

Original motif Consensus sequence: CGGVGCCGCVGC



Reverse complement motif Consensus sequence: GCVGCCGCBCCG



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

Dataset #:	1
Motif ID:	5
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

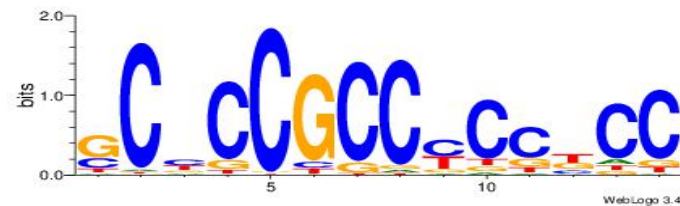
Alignment:

```
GGMGGRGGCGGVGC
--CGGVGCCGCVGC
```

Original motif Consensus sequence: GGMGGRGGCGGVGC



Reverse complement motif Consensus sequence: GCVCCGCCMCCYC

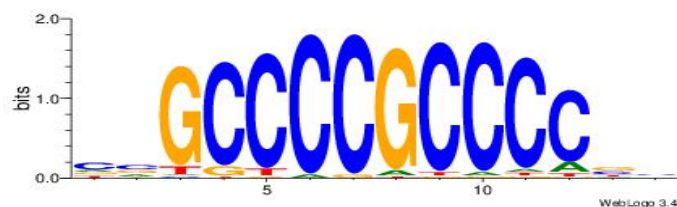


Dataset #: 2
 Motif ID: 12
 Motif name: csGCCCCGCCCCsc
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 12
 Similarity score: 0.0542674

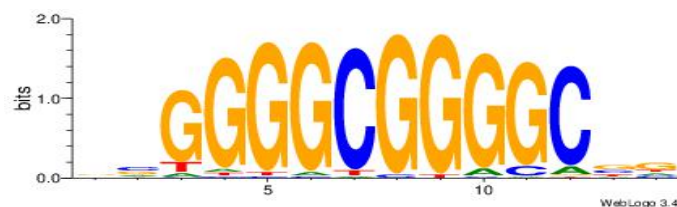
Alignment:

HVGCCCCGCCCCBB
 CGGVGCCGCVGC--

Original motif Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGC



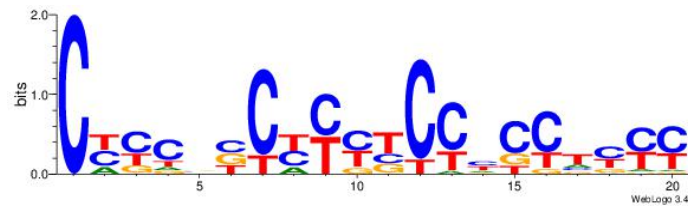
Dataset #: 1
 Motif ID: 9
 Motif name: TFM12
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 7
 Number of overlap: 12

Similarity score: 0.0543272

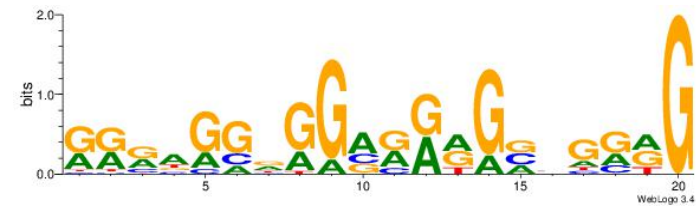
Alignment:

KKKAGGDGGAKKMGBBGKMG
-----CGGVGCCGCVGC--

Original motif Consensus sequence: CYCBBCYYYTCCHCCTYYY



Reverse complement motif Consensus sequence: KKKAGGDGGAKKMGBBGKMG



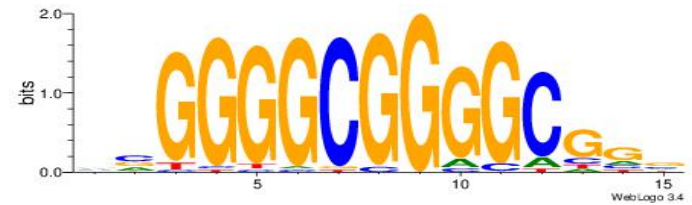
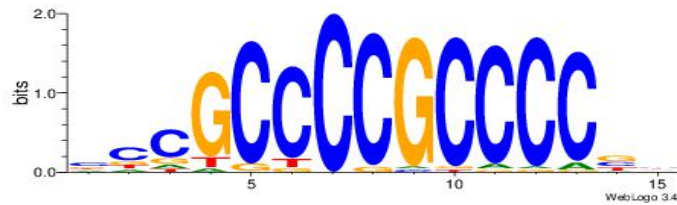
Dataset #: 2
Motif ID: 14
Motif name: cccGCCCCGCCCCsb
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 4
Number of overlap: 12
Similarity score: 0.0548371

Alignment:

BCCGCCCCGCCCCBB
---GCVGCGGCBCCG

Original motif Consensus sequence: BCCGCCCCGCCCCBB

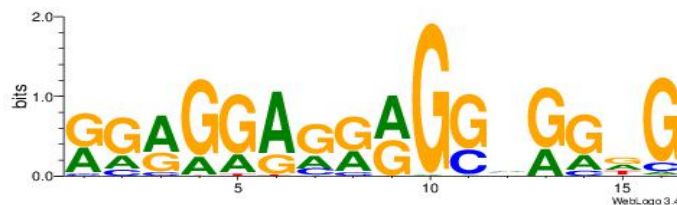
Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB



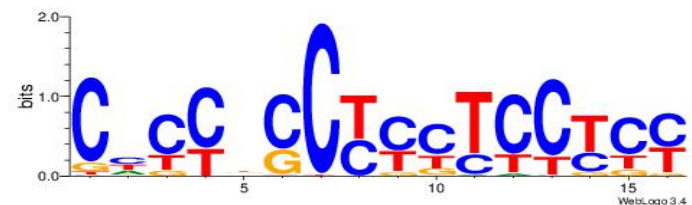
Dataset #: 1
 Motif ID: 6
 Motif name: TFM2
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 12
 Similarity score: 0.0594165

Alignment:
 CHCCBCKMCTCCKCM
 --GCVGCGGCBCCG--

Original motif Consensus sequence: RGRGGAGRRGGHGGDG

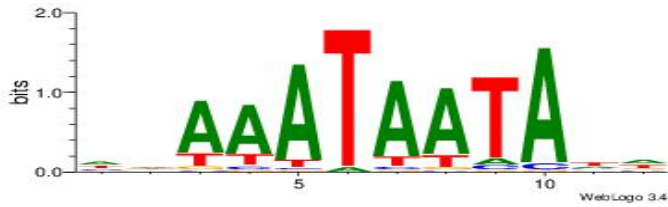


Reverse complement motif Consensus sequence: CHCCBCKMCTCCKCM

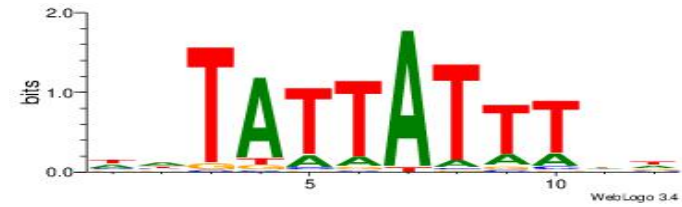


Dataset #: 2 Motif ID: 17 Motif name: wwAAATAATAtw

Original motif Consensus sequence: HDAAATAATADD



Reverse complement motif Consensus sequence: DDTATTATTTDH

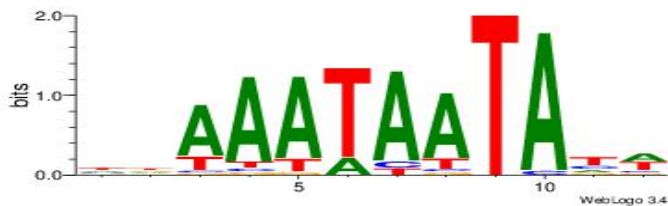


Best Matches for Significant Motif ID 17 (Highest to Lowest)

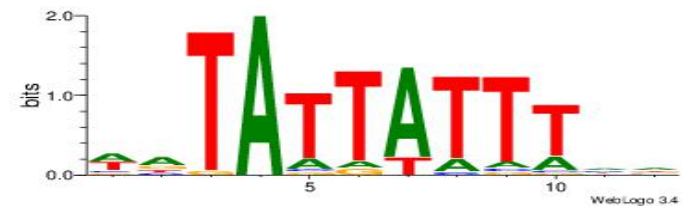
Dataset #: 2
Motif ID: 13
Motif name: tkAAATAATAtw
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 12
Similarity score: 0

Alignment:
HDAAATAATAHW
HDAAATAATADD

Original motif Consensus sequence: HDAAATAATAHW



Reverse complement motif Consensus sequence: WHTATTATTTDH

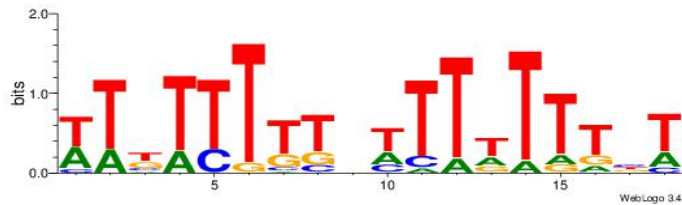


Dataset #: 1
 Motif ID: 7
 Motif name: TFM1
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 7
 Number of overlap: 12
 Similarity score: 0.0565705

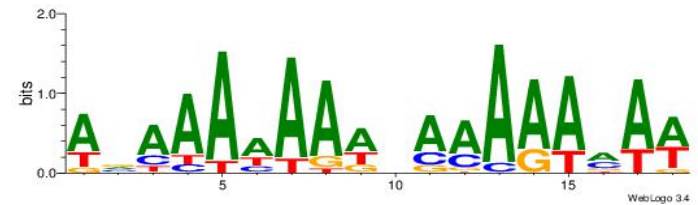
Alignment:

ABAAAAAWhAAAAARAW
 -----HDAATAATADD

Original motif Consensus sequence: WTKTTTTTHWTTTTTTBT



Reverse complement motif Consensus sequence: ABAAAAAWhAAAAARAW



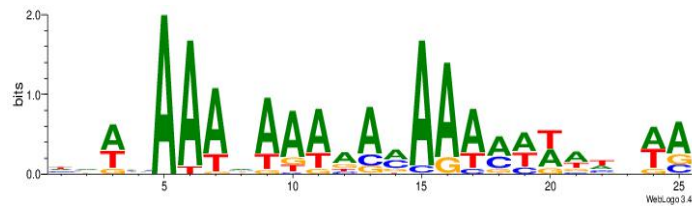
Dataset #: 1
 Motif ID: 11
 Motif name: TFM11
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3

Number of overlap: 12
 Similarity score: 0.0575935

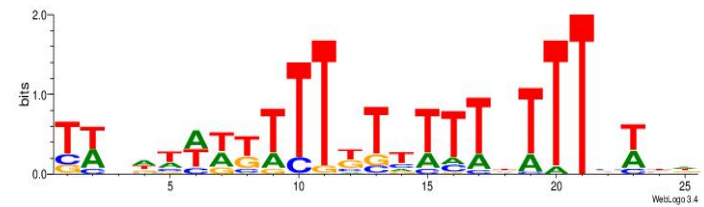
Alignment:

HDWVAAAHAAAAAAMAAAMWWWHBWA
 --HDAAATAATADD-----

Original motif Consensus sequence:
 HDWVAAAHAAAAAAMAAAMWWWHBWA



Reverse complement motif Consensus sequence:
 TWVHWWWYTTTTTTTTTHTTTVWBH

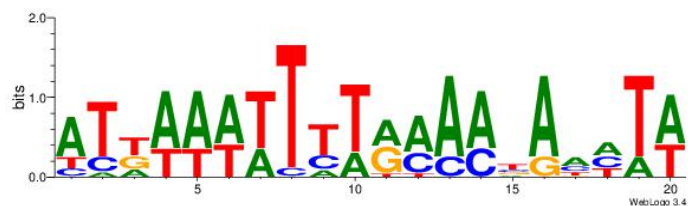


Dataset #: 1
 Motif ID: 10
 Motif name: TFM13
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 12
 Similarity score: 0.0712963

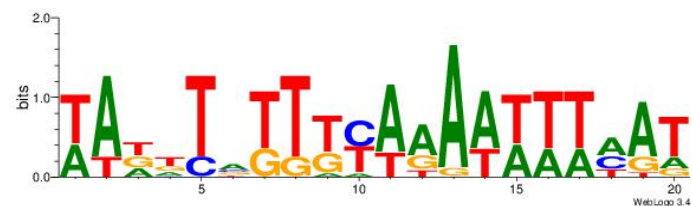
Alignment:

ATKAAWTTTTTRMAABAHHTW
 -----DDTATTATTTDH

Original motif Consensus sequence: ATKAAWTTTTRMAABAHTW



Reverse complement motif Consensus sequence: WAHHTVTTYKAAAATTRAT

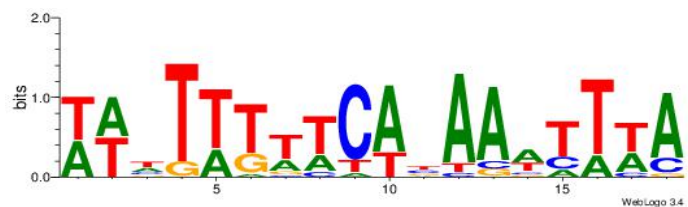


Dataset #: 1
Motif ID: 8
Motif name: TFM3
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 12
Similarity score: 0.0733516

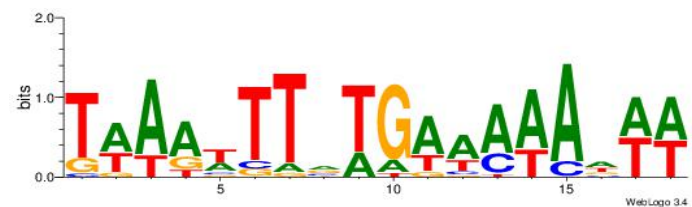
Alignment:

```
TWAAWTTVTGAAAAHWW  
-----HDAAATAATADD
```

Original motif Consensus sequence: WWHTTTTTTCABAAWTTWA



Reverse complement motif Consensus sequence: TWAAWTTVTGAAAAHWW



Dataset #: 1 **Motif ID: 1** **Motif name: TFW1**

Original motif Consensus sequence: GTCGCG



Reverse complement motif Consensus sequence: CGCGAC



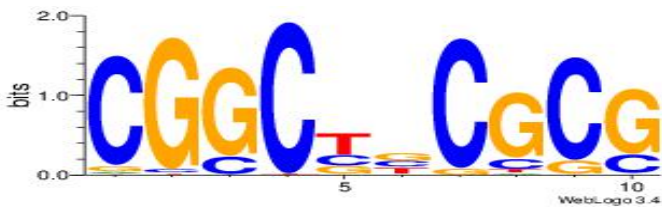
Best Matches for Significant Motif ID 1 (Highest to Lowest)

Dataset #: 1
Motif ID: 3
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

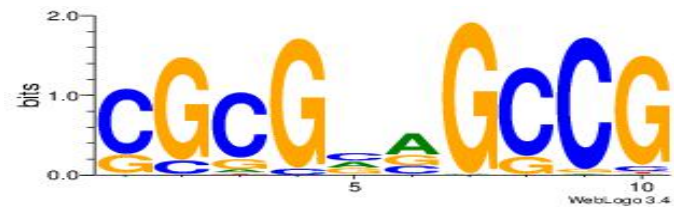
Alignment:

CGGCYBCGCG
----GTCGCG

Original motif Consensus sequence: CGGCYBCGCG



Reverse complement motif Consensus sequence: CGCGBMGCCG

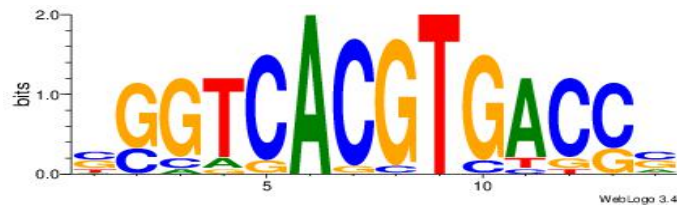


Dataset #: 2
 Motif ID: 18
 Motif name: sSGTCACGTGACSS
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 6
 Similarity score: 0.0375102

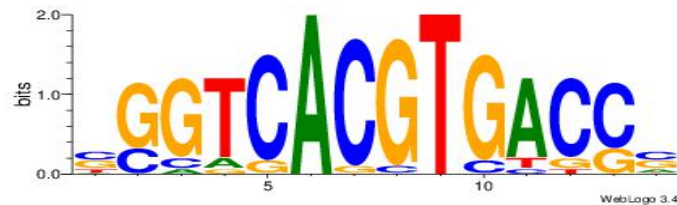
Alignment:

SGGTCACGTGACCS
 --GTCGCG-----

Original motif Consensus sequence: SGGTCACGTGACCS



Reverse complement motif Consensus sequence: SGGTCACGTGACCS

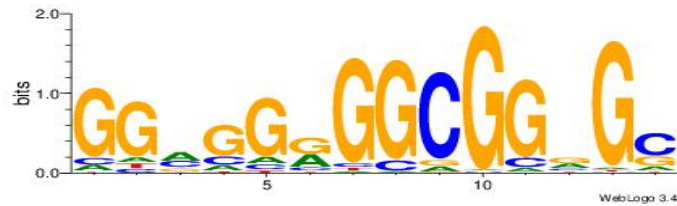


Dataset #: 1
 Motif ID: 5
 Motif name: TFF11
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 5

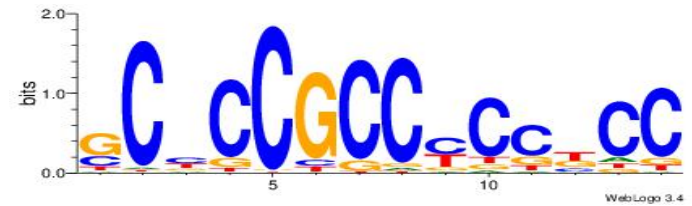
Number of overlap: 6
Similarity score: 0.0381641

Alignment:
GCVCCGCCMCCYCC
-----CGCGAC-----

Original motif Consensus sequence: GGMGRRGGCGGVGC



Reverse complement motif Consensus sequence: GCVCCGCCMCCYCC

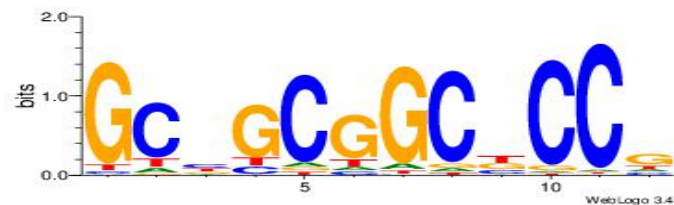
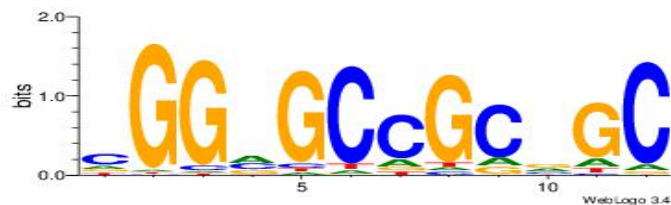


Dataset #: 1
Motif ID: 4
Motif name: TFF1
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 6
Similarity score: 0.0431161

Alignment:
CGGVGCCGCVGC
-----CGCGAC

Original motif Consensus sequence: CGGVGCCGCVGC

Reverse complement motif Consensus sequence: GCVCCGCCMCCYCC



Dataset #: 1
 Motif ID: 2
 Motif name: TFW2
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 6
 Similarity score: 0.052047

Alignment:
 CCGCGCGS
 -CGCGAC-

Original motif Consensus sequence: SCGCGCGG



Reverse complement motif Consensus sequence: CCGCGCGS



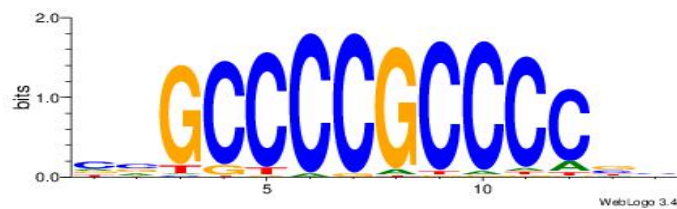
Dataset #: 2
 Motif ID: 12

Motif name: csGCCCCGCCCCsc
 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: 0.0539

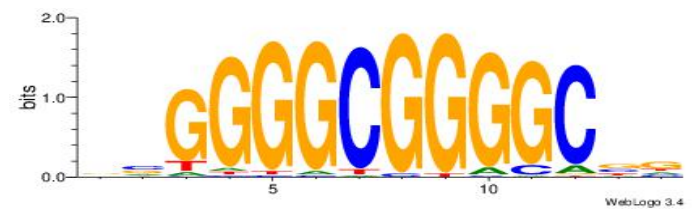
Alignment:

HVGCCCCGCCCCBB
 --GTCGCG-----

Original motif Consensus sequence: HVGCCCCGCCCCBB

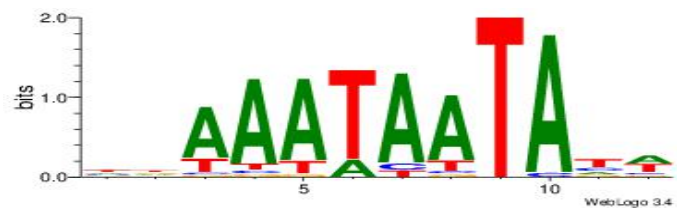


Reverse complement motif Consensus sequence: BBGGGGCGGGGC

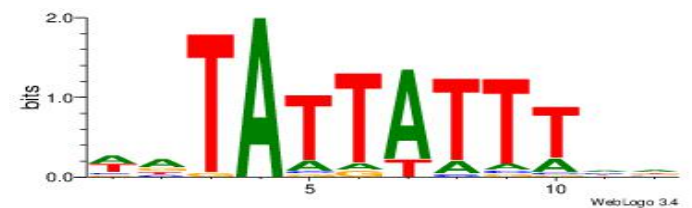


Dataset #: 2 Motif ID: 13 Motif name: tkAAATAATatw

Original motif Consensus sequence: HDAAATAATAHW



Reverse complement motif Consensus sequence: WHTATTATTTDH

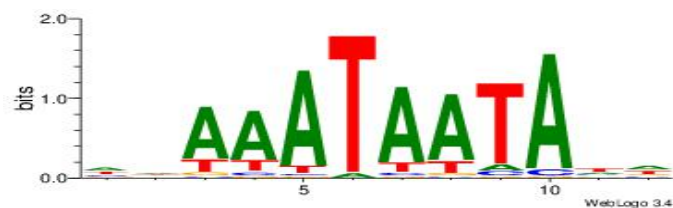


Best Matches for Significant Motif ID 13 (Highest to Lowest)

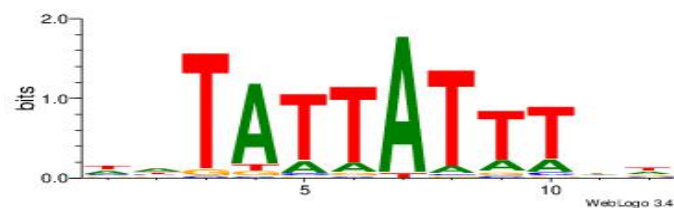
Dataset #: 2
 Motif ID: 17
 Motif name: wwAAATAATAtw
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 12
 Similarity score: 0

Alignment:
 HDAAATAATADD
 HDAAATAATAHW

Original motif Consensus sequence: HDAAATAATADD



Reverse complement motif Consensus sequence: DDTATTATTTDH



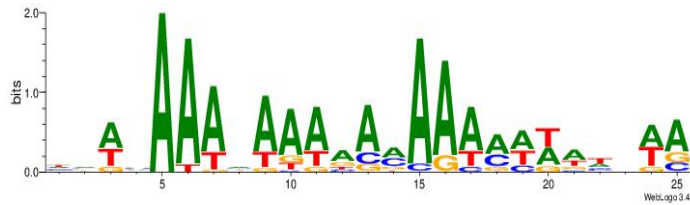
Dataset #: 1
 Motif ID: 11
 Motif name: TFM11
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 12
 Number of overlap: 12

Similarity score: 0.0590505

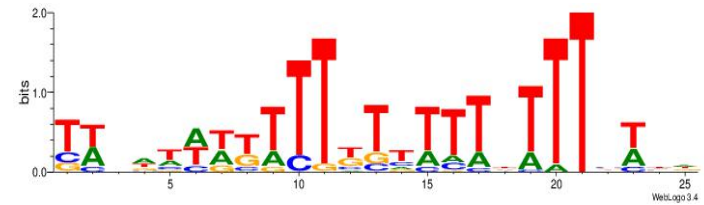
Alignment:

TWVHWWYTTTYTTTTHTTTVWBH
-----WHTATTATTTDH--

Original motif Consensus sequence:
HDWVAAAHAAAAAMAAAMWWWHBWA



Reverse complement motif Consensus sequence:
TWVHWWYTTTYTTTTHTTTVWBH



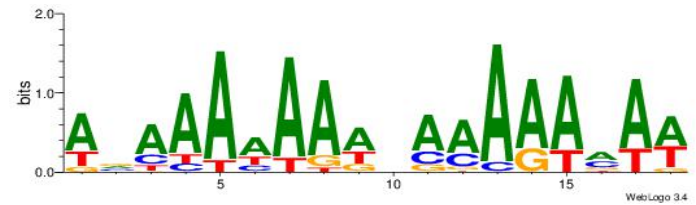
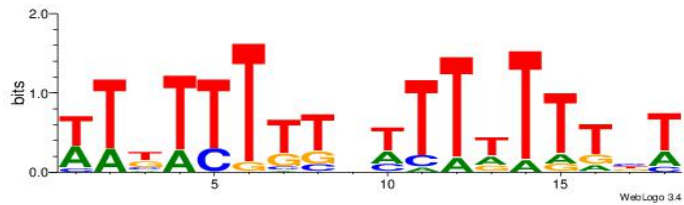
Dataset #: 1
Motif ID: 7
Motif name: TFM1
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 12
Similarity score: 0.0637702

Alignment:

WTKTTTTTHWTTTTTTBT
WHTATTATTTDH-----

Original motif Consensus sequence: WTKTTTTTHWTTTTTTBT

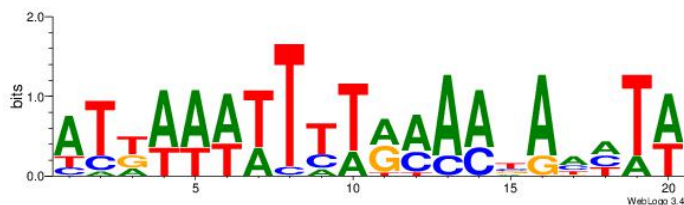
Reverse complement motif Consensus sequence:
ABAAAAAWHAAAAARAW



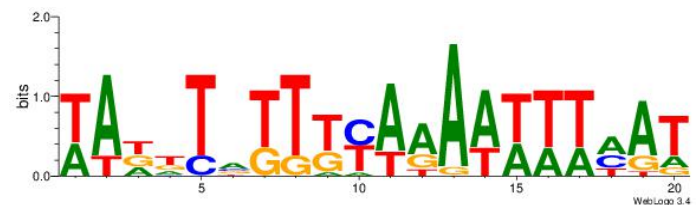
Dataset #: 1
 Motif ID: 10
 Motif name: TFM13
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 9
 Number of overlap: 12
 Similarity score: 0.0704475

Alignment:
 ATKAAWTTTTRMAABAHTW
 -----WHTATTATTTDH

Original motif Consensus sequence: ATKAAWTTTTRMAABAHTW



Reverse complement motif Consensus sequence: WAHHTVTTYKAAAATTRAT



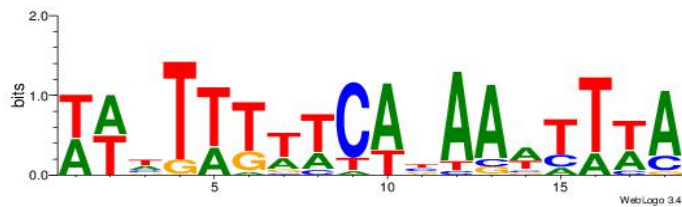
Dataset #: 1

Motif ID: 8
 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: 12
 Similarity score: 0.0763819

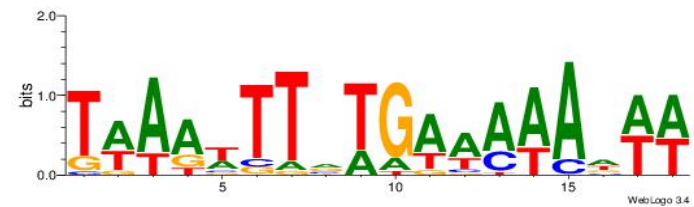
Alignment:

TWAAWTTVTGAAAAHWW
 -----HDAAATAATAHW

Original motif Consensus sequence: WWHTTTTTTCABAAWTTWA



Reverse complement motif Consensus sequence: TWAAWTTVTGAAAAHWW



Dataset #: 1 Motif ID: 2 Motif name: TFW2

Original motif Consensus sequence: SCGCGCGG



Reverse complement motif Consensus sequence: CCGCGCGS



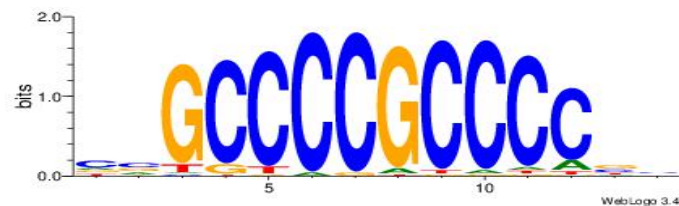
Best Matches for Significant Motif ID 2 (Highest to Lowest)

Dataset #: 2
Motif ID: 12
Motif name: csGCCCCGCCCCsc
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 2
Number of overlap: 8
Similarity score: 0.0456233

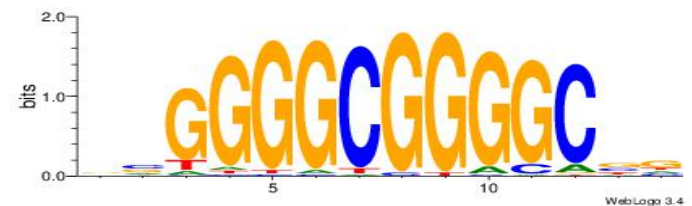
Alignment:

```
BBGGGGCGGGGCVD  
-SCGCGCGG-----
```

Original motif Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGC

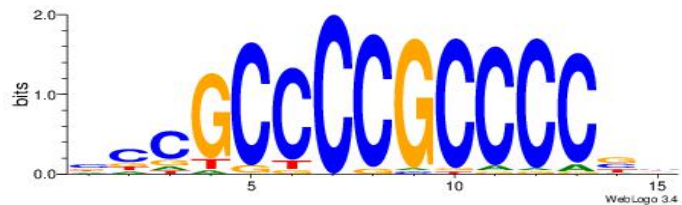


Dataset #: 2
Motif ID: 14
Motif name: cccGCCCCGCCCCsb
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif

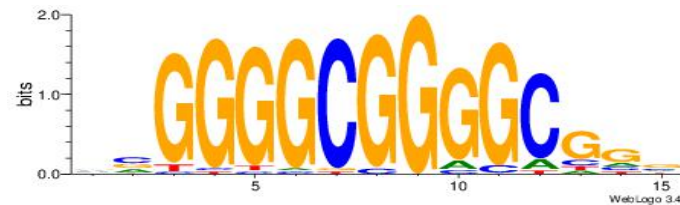
Direction: Forward
 Position number: 7
 Number of overlap: 8
 Similarity score: 0.045686

Alignment:
 BCCGCCCCGCCCCBB
 -----CCGCGCGS--

Original motif Consensus sequence: BCCGCCCCGCCCCBB



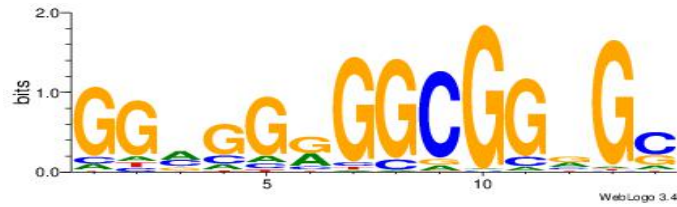
Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB



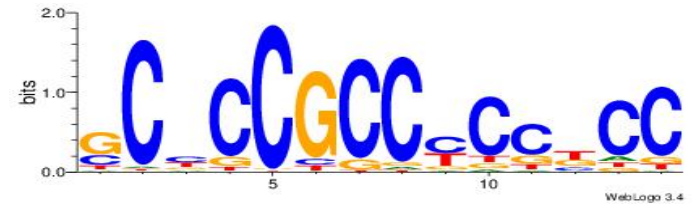
Dataset #: 1
 Motif ID: 5
 Motif name: TFF11
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 8
 Similarity score: 0.0583967

Alignment:
 GGMGGRGGCGGVGC
 ---SCGCGCGG---

Original motif Consensus sequence: GGMGRRGGCGGVGC



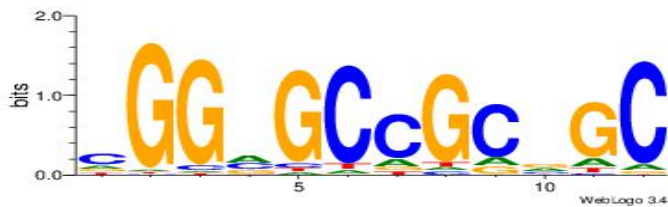
Reverse complement motif Consensus sequence: GCVCCGCCMCCYC



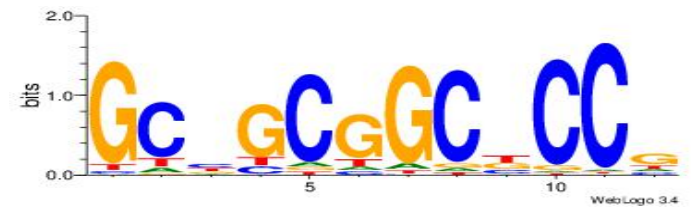
Dataset #: 1
Motif ID: 4
Motif name: TFF1
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 5
Number of overlap: 8
Similarity score: 0.060966

Alignment:
CGGVGCCGCVGC
SCGCGCGG----

Original motif Consensus sequence: CGGVGCCGCVGC



Reverse complement motif Consensus sequence: GCVGCGGCBCCG

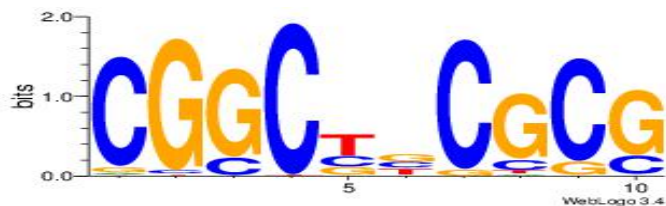


Dataset #: 1
 Motif ID: 3
 Motif name: TFW3
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3
 Number of overlap: 8
 Similarity score: 0.0906073

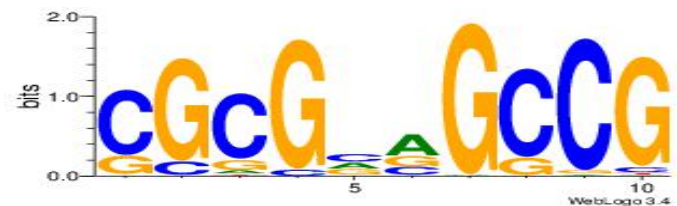
Alignment:

CGCGBMGCCG
 --SCGCGCGG

Original motif Consensus sequence: CGGCYBCGCG



Reverse complement motif Consensus sequence: CGCGBMGCCG



Best Matches for Each Motif (Highest to Lowest)

Dataset #: 1 Motif ID: 1 Motif name: TFW1

Original motif Consensus sequence: GTCGCG

Reverse complement motif Consensus sequence: CGCGAC



Best Matches for Motif ID 1 (Highest to Lowest)

Dataset #: 1
 Motif ID: 3
 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

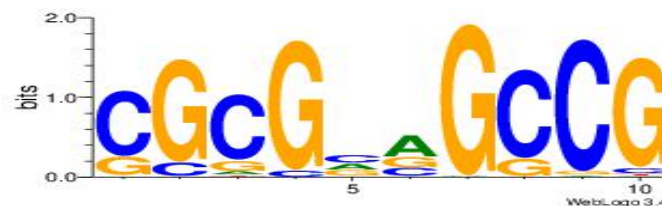
Alignment:

CGGCYBCGCG
 ----GTCGCG

Original motif Consensus sequence: CGGCYBCGCG



Reverse complement motif Consensus sequence: CGCGBMGCCG

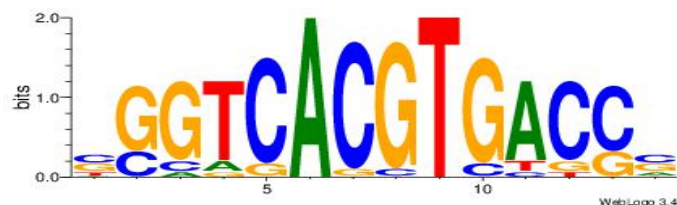


Dataset #: 2

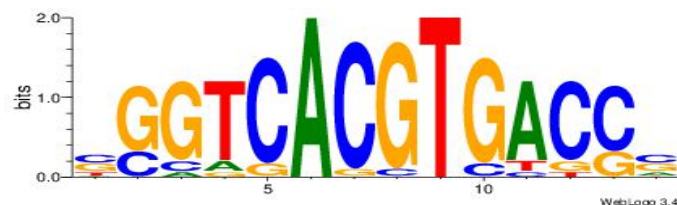
Motif ID: 18
 Motif name: sSGTCACGTGACSS
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 6
 Similarity score: 0.0375102

Alignment:
 SGGTCACGTGACCS
 --GTCGCG-----

Original motif Consensus sequence: SGGTCACGTGACCS



Reverse complement motif Consensus sequence: SGGTCACGTGACCS

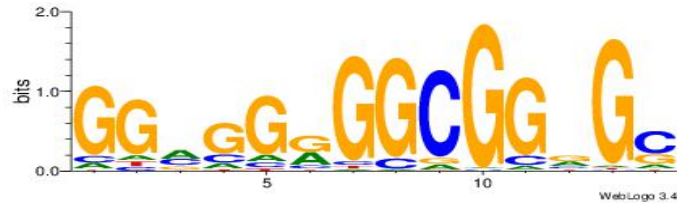


Dataset #: 1
 Motif ID: 5
 Motif name: TFF11
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 5
 Number of overlap: 6
 Similarity score: 0.0381641

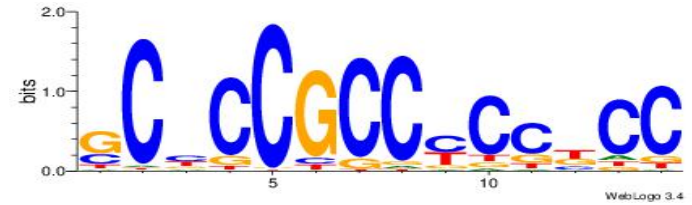
Alignment:

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

Original motif Consensus sequence: GGMGRRGGCGGVGC



Reverse complement motif Consensus sequence: GCVCCGCCMCCYCC



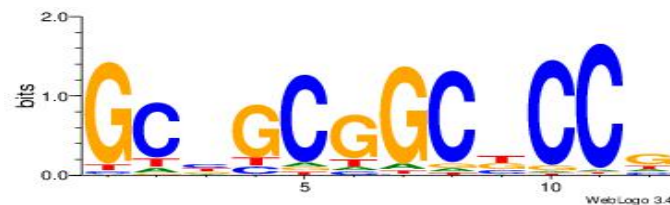
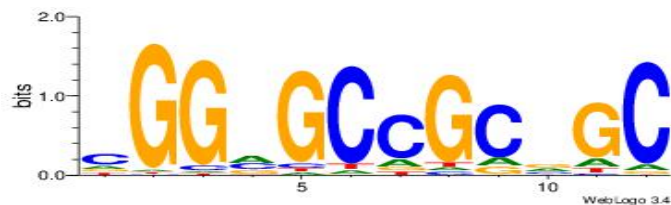
Dataset #: 1
Motif ID: 4
Motif name: TFF1
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 6
Similarity score: 0.0431161

Alignment:

CGGVGCCGCVGC
-----CGCGAC

Original motif Consensus sequence: CGGVGCCGCVGC

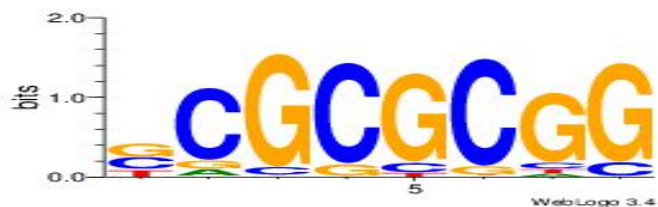
Reverse complement motif Consensus sequence: GCVCCGCCMCCYCC



Dataset #: 1
 Motif ID: 2
 Motif name: TFW2
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 6
 Similarity score: 0.052047

Alignment:
 CCGCGCGS
 -CGCGAC-

Original motif Consensus sequence: SCGCGCGG



Reverse complement motif Consensus sequence: CCGCGCGS

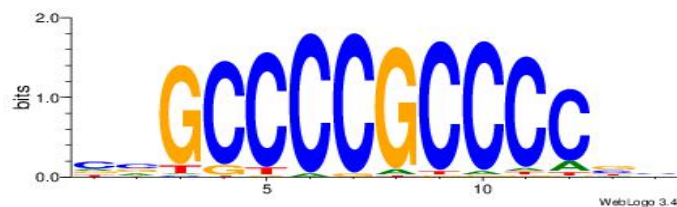


Dataset #: 2
 Motif ID: 12

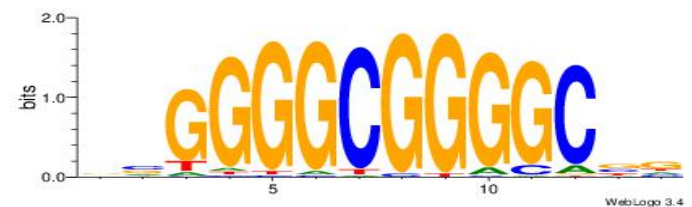
Motif name: csGCCCCGCCCCsc
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 7
 Number of overlap: 6
 Similarity score: 0.0539

Alignment:
 HVGCCCCGCCCCBB
 --GTCGCG-----

Original motif Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGCGGGGC



Dataset #: 1 Motif ID: 2 Motif name: TFW2

Original motif Consensus sequence: SCGCGCGG



Reverse complement motif Consensus sequence: CCGCGCGS

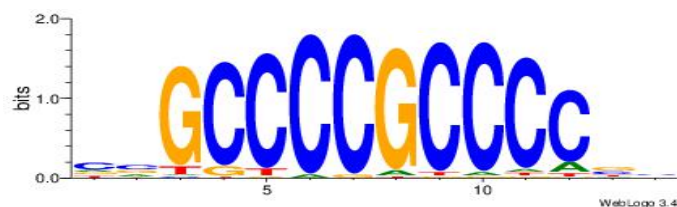


Best Matches for Motif ID 2 (Highest to Lowest)

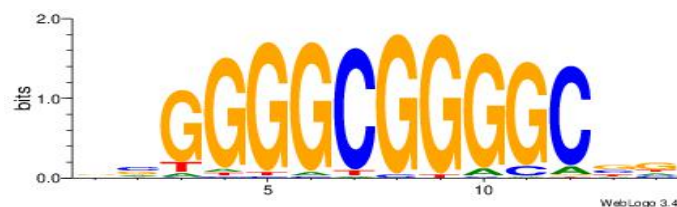
Dataset #: 2
 Motif ID: 12
 Motif name: csGCCCCGCCCCsc
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 8
 Similarity score: 0.0456233

Alignment:
 BBGGGGCGGGGCVD
 -SCGCGCGG-----

Original motif Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGC



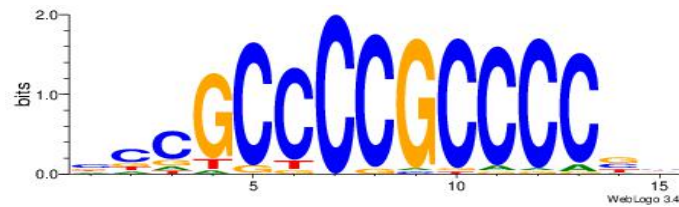
Dataset #: 2
 Motif ID: 14
 Motif name: cccGCCCCGCCCCsb
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 7
 Number of overlap: 8

Similarity score: 0.045686

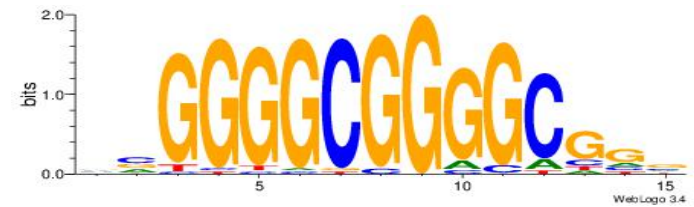
Alignment:

BCCGCCCCGCCCCBB
-----CCGCGCGS-

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB



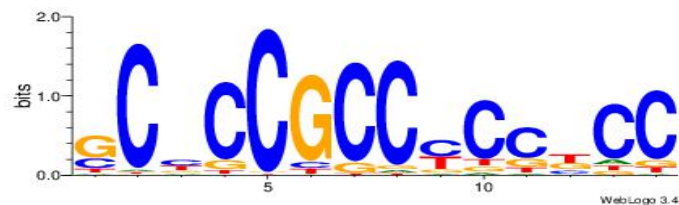
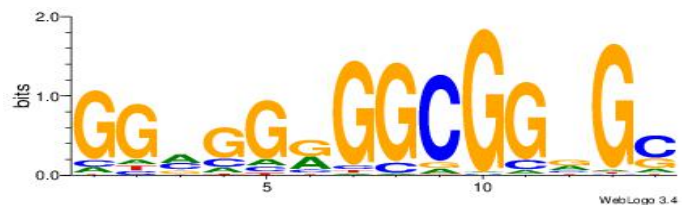
Dataset #: 1
Motif ID: 5
Motif name: TFF11
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 4
Number of overlap: 8
Similarity score: 0.0583967

Alignment:

GGMGGRGGCGGVGC
---SCGCGCGG---

Original motif Consensus sequence: GGMGGRGGCGGVGC

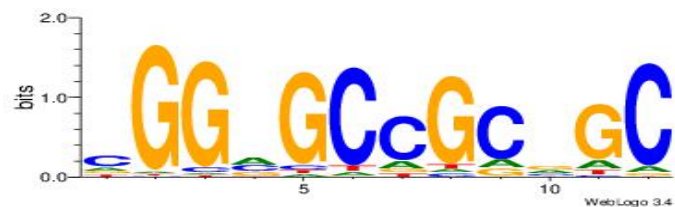
Reverse complement motif Consensus sequence: GCVCCGCCMCCY



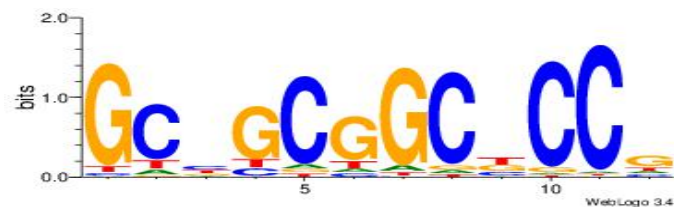
Dataset #: 1
 Motif ID: 4
 Motif name: TFF1
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 5
 Number of overlap: 8
 Similarity score: 0.060966

Alignment:
 CGGVGCCGCVGC
 SCGCGCGG----

Original motif Consensus sequence: CGGVGCCGCVGC



Reverse complement motif Consensus sequence: GCVGCCGCBCCG



Dataset #: 1
 Motif ID: 3

Motif name: TFW3
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3
 Number of overlap: 8
 Similarity score: 0.0906073

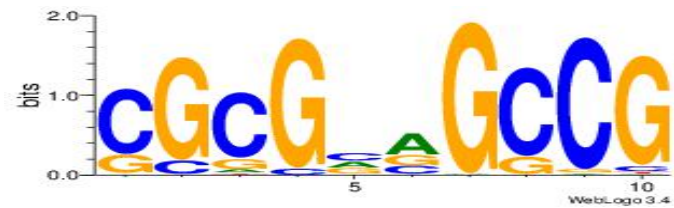
Alignment:

CGCGBMGCCG
 --SCGCGCGG

Original motif Consensus sequence: CGGCYBCGCG

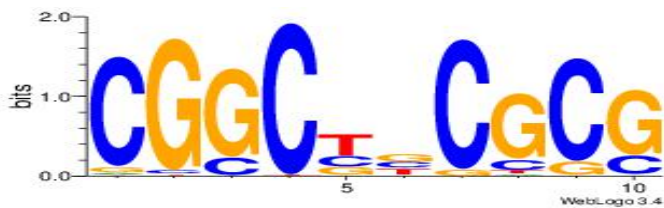


Reverse complement motif Consensus sequence: CGCGBMGCCG

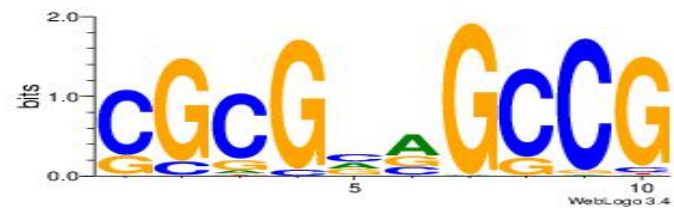


Dataset #: 1 Motif ID: 3 Motif name: TFW3

Original motif Consensus sequence: CGGCYBCGCG



Reverse complement motif Consensus sequence: CGCGBMGCCG



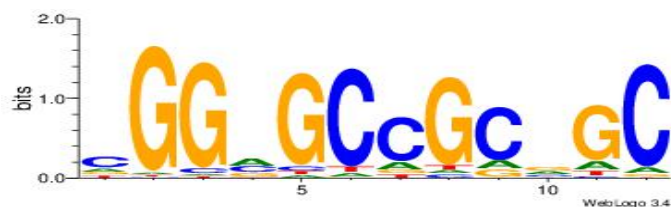
Best Matches for Motif ID 3 (Highest to Lowest)

Dataset #: 1
 Motif ID: 4
 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

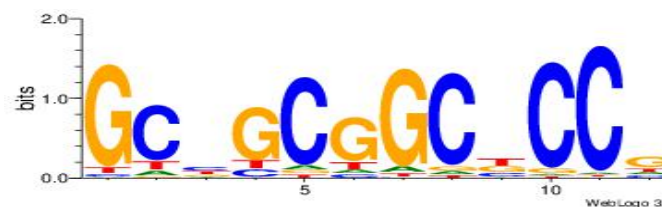
Alignment:

CGGVGCCGCVGC
 CGGCYBCGCG--

Original motif Consensus sequence: CGGVGCCGCVGC



Reverse complement motif Consensus sequence: GCVGCGGCBCCG



Dataset #: 1
 Motif ID: 5
 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

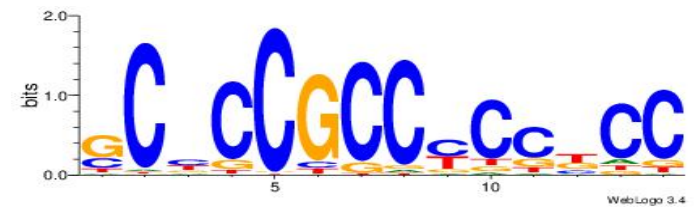
Alignment:

GGMGGRGGCGGVGC
CGCGBMGCCG-----

Original motif Consensus sequence: GGMGGRGGCGGVGC



Reverse complement motif Consensus sequence: GCVCCGCCMCCYC



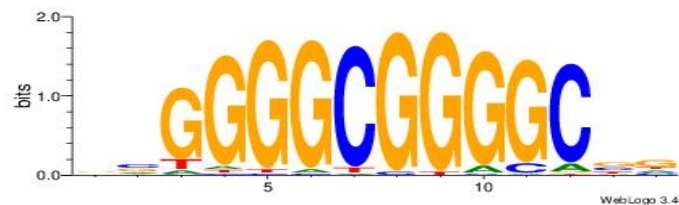
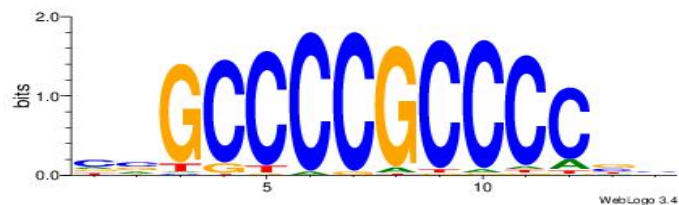
Dataset #: 2
Motif ID: 12
Motif name: csGCCCCGCCCCsc
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 5
Number of overlap: 10
Similarity score: 0.0718771

Alignment:

HVCCCCGCCCCBB
CGGCYBCGCG-----

Original motif Consensus sequence: HVCCCCGCCCCBB

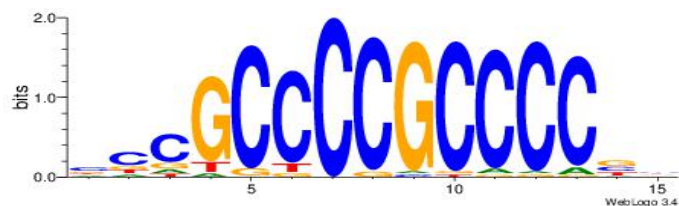
Reverse complement motif Consensus sequence: BBGGGCGGGGC



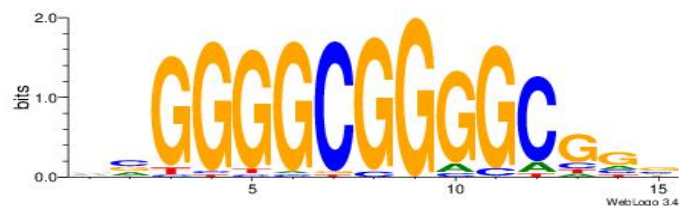
Dataset #: 2
 Motif ID: 14
 Motif name: cccGCCCCGCCCCsb
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 5
 Number of overlap: 10
 Similarity score: 0.0719604

Alignment:
 BCCGCCCCGCCCCBB
 -CGGCYBCGCG----

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB



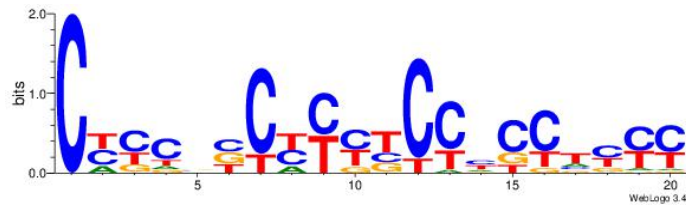
Dataset #: 1

Motif ID: 9
 Motif name: TFM12
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 11
 Number of overlap: 10
 Similarity score: 0.0767689

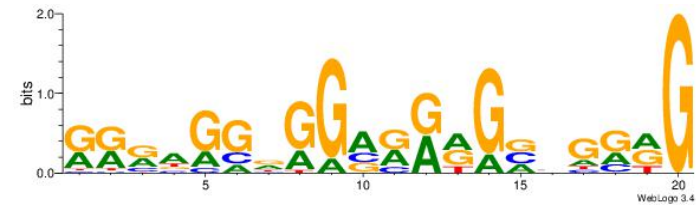
Alignment:

KKKAGGDGGAKKMGBBGKMG
 -----CGCGBMGCCG

Original motif Consensus sequence: CYCBBCYYYTCCHCCTYYY

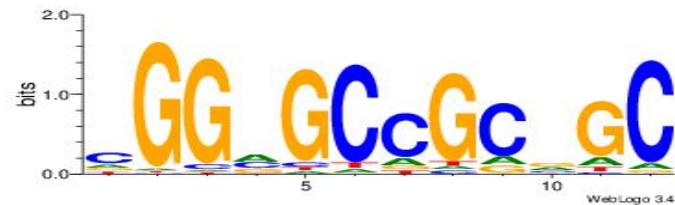


Reverse complement motif Consensus sequence: KKKAGGDGGAKKMGBBGKMG

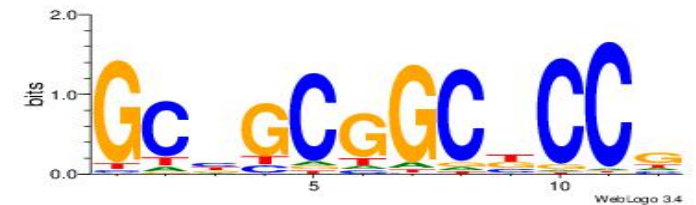


Dataset #: 1 Motif ID: 4 Motif name: TFF1

Original motif Consensus sequence: CGGVGCCGCVGC



Reverse complement motif Consensus sequence: GCVGCCGCBCCG



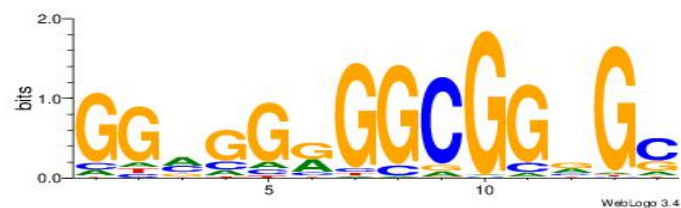
Best Matches for Motif ID 4 (Highest to Lowest)

Dataset #: 1
Motif ID: 5
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

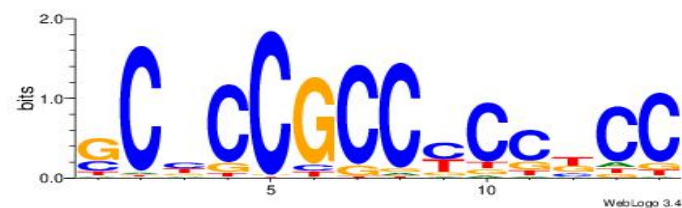
Alignment:

```
GGMGGRGGCGGVGC  
--CGGVGCCGCVGC
```

Original motif Consensus sequence: GGMGGRGGCGGVGC



Reverse complement motif Consensus sequence: GCVCCGCCMCCYC

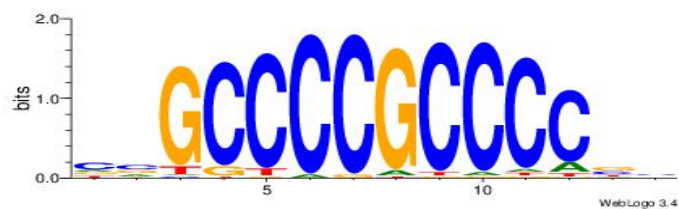


Dataset #: 2
Motif ID: 12
Motif name: csGCCCCGCCCCsc
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif

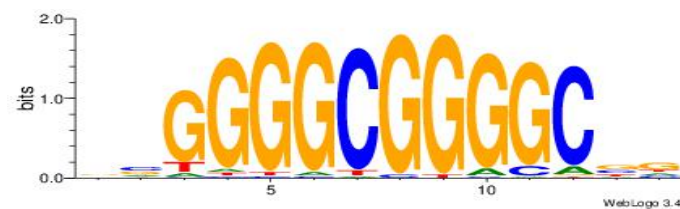
Direction: Forward
 Position number: 1
 Number of overlap: 12
 Similarity score: 0.0542674

Alignment:
 HVGCCCGCCCCBB
 CGGVGCCGCVGC--

Original motif Consensus sequence: HVGCCCGCCCCBB



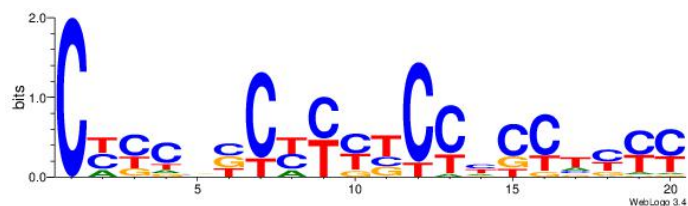
Reverse complement motif Consensus sequence: BBGGGGCGGGGC



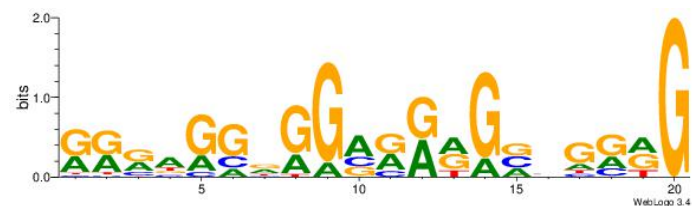
Dataset #: 1
 Motif ID: 9
 Motif name: TFM12
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 7
 Number of overlap: 12
 Similarity score: 0.0543272

Alignment:
 KKKAGGDGGAKKMGBBGKMG
 -----CGGVGCCGCVGC--

Original motif Consensus sequence: CYCBBYYYTCCHCCTYYY



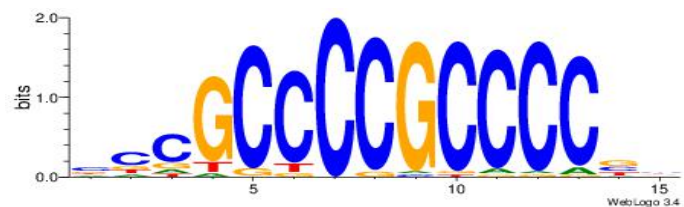
Reverse complement motif Consensus sequence: KKKAGGDGGAKKMGBBGKMG



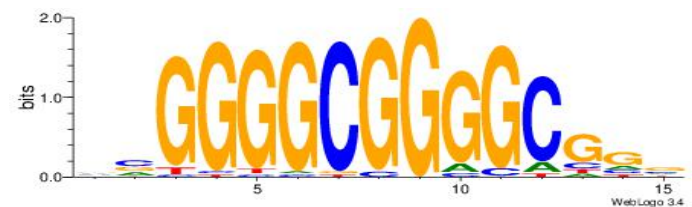
Dataset #: 2
Motif ID: 14
Motif name: cccGCCCCGCCCCsb
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 4
Number of overlap: 12
Similarity score: 0.0548371

Alignment:
BCCGCCCCGCCCCBB
---GCVGCGGCBCCG

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB

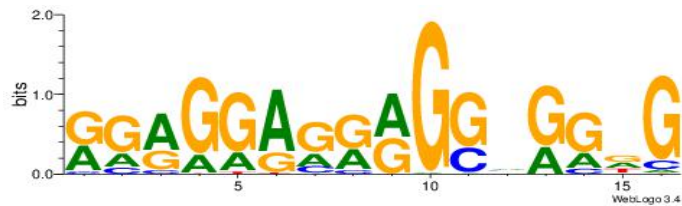


Dataset #: 1
 Motif ID: 6
 Motif name: TFM2
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 12
 Similarity score: 0.0594165

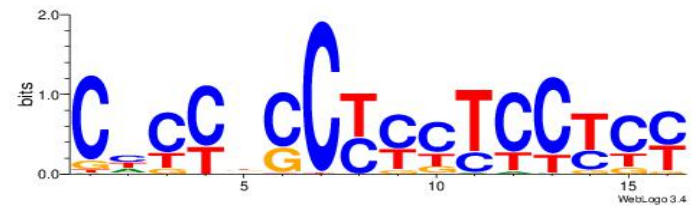
Alignment:

CHCCBCKMCTCCKCM
 --GCVGCGGCBCCG--

Original motif Consensus sequence: RGRGGAGRRGGHGGDG



Reverse complement motif Consensus sequence: CHCCBCKMCTCCKCM



Dataset #: 1 Motif ID: 5 Motif name: TFF11

Original motif Consensus sequence: GGMGRRGGCGVGC

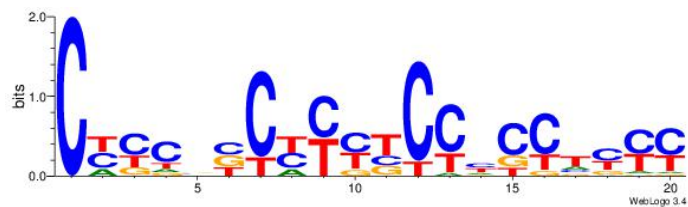
Reverse complement motif Consensus sequence: GCVCCGCCMCCYC

Dataset #: 1
 Motif ID: 9
 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

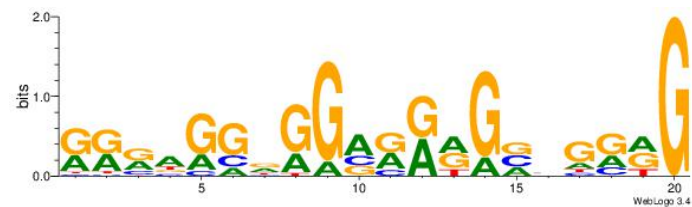
Alignment:

CYYCBBCYYYTCCHCCTYYY
 -----GCVCCGCCMCCYCC-

Original motif Consensus sequence: CYYCBBCYYYTCCHCCTYYY



Reverse complement motif Consensus sequence: KKKAGGDGGAKKMGBBGKMG

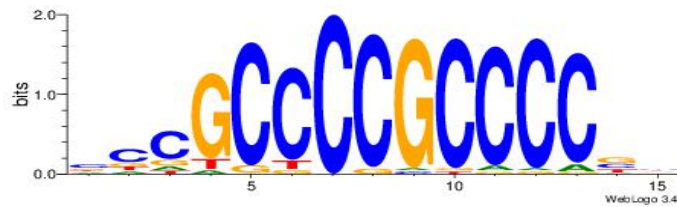


Dataset #: 2
 Motif ID: 14
 Motif name: cccGCCCCGCCCCsb
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2

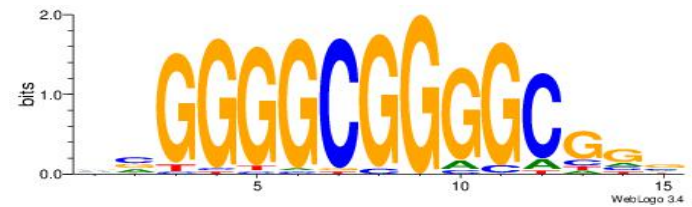
Number of overlap: 14
Similarity score: 0.0548198

Alignment:
BCCGCCCCGCCCCBB
GCVCCGCCMCCYCC-

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence:
BBGGGGCGGGGCGGB

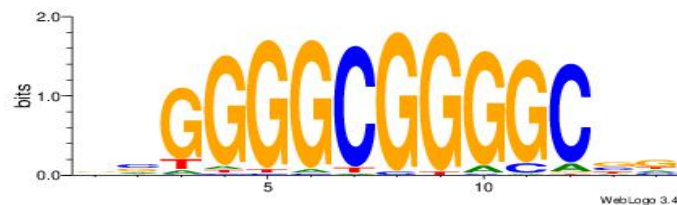
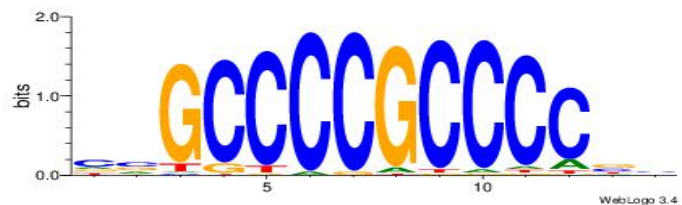


Dataset #: 2
Motif ID: 12
Motif name: csGCCCCGCCCCsc
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 14
Similarity score: 0.0652173

Alignment:
HVGCCCCGCCCCBB
GCVCCGCCMCCYCC

Original motif Consensus sequence: HVGCCCCGCCCCBB

Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB

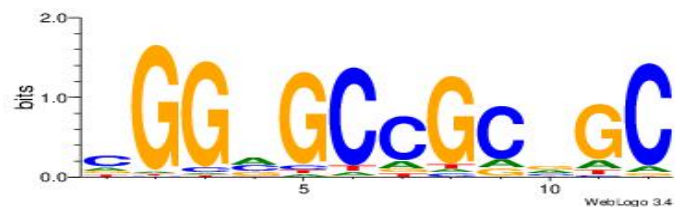


Dataset #: 1
 Motif ID: 4
 Motif name: TFF1
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 12
 Similarity score: 1.02659

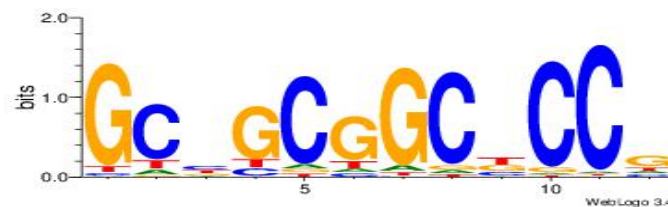
Alignment:

--CGGVGCCGCVGC
 GGMGRRGGCGGVGC

Original motif Consensus sequence: CGGVGCCGCVGC

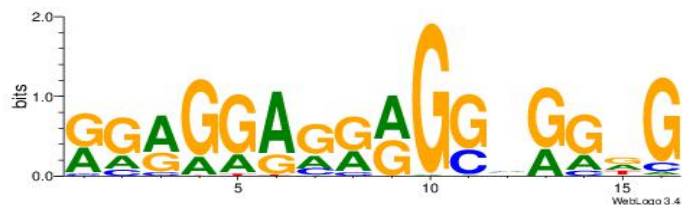


Reverse complement motif Consensus sequence: GCVGCCGCBCCG

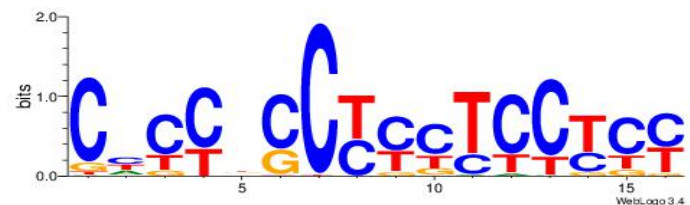


Dataset #: 1 Motif ID: 6 Motif name: TFM2

Original motif Consensus sequence: RGRGGAGRRGGHGGDG



Reverse complement motif Consensus sequence: CHCCBCKMCTCCKCM



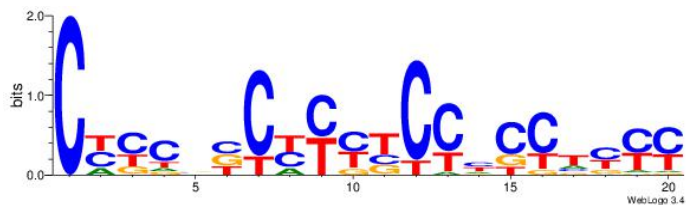
Best Matches for Motif ID 6 (Highest to Lowest)

Dataset #:	1
Motif ID:	9
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

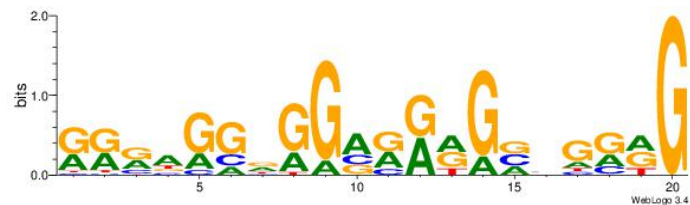
Alignment:

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

Original motif Consensus sequence: CYYCBBCYYYYTCCHCCTYYY



Reverse complement motif Consensus sequence: KKKAGGDGGAKKMGBBGKMG

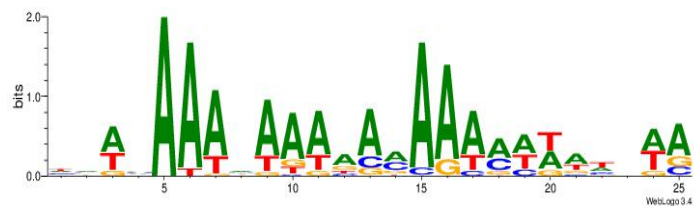


Dataset #: 1
 Motif ID: 11
 Motif name: TFM11
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 8
 Number of overlap: 16
 Similarity score: 0.0794752

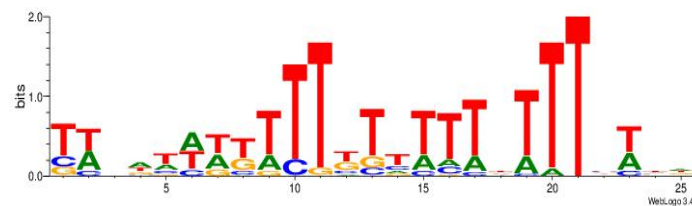
Alignment:

HDWVAAAHA AAAA MAAA MWWW HBWA
 -----RGRGGAGRRGGHGGDG--

Original motif Consensus sequence:
 HDWVAAAHA AAAA MAAA MWWW HBWA



Reverse complement motif Consensus sequence:
 TWVHWWWYTTTTTTTTTHTTTVWBH



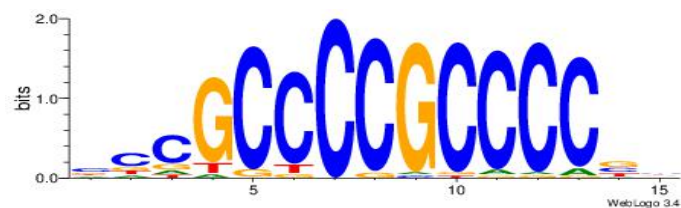
Dataset #: 2
 Motif ID: 14
 Motif name: cccGCCCCGCCCCsb
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward

Position number: 1
Number of overlap: 15
Similarity score: 0.558405

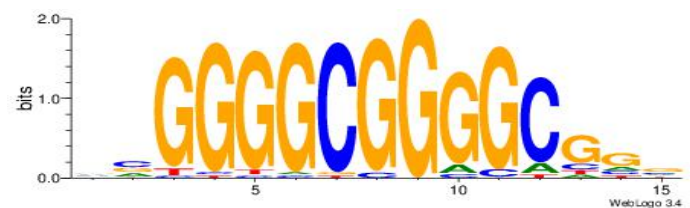
Alignment:

BBGGGGCGGGGCGGB-
RGRGGAGRRGGHGGDG

Original motif Consensus sequence: BCCGCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB

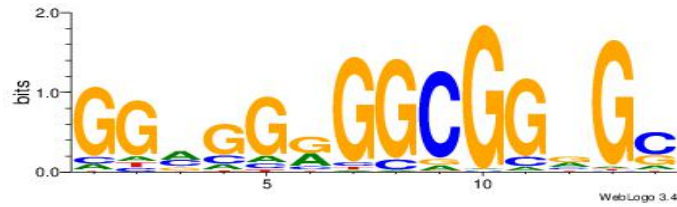


Dataset #: 1
Motif ID: 5
Motif name: TFF11
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 14
Similarity score: 1.03372

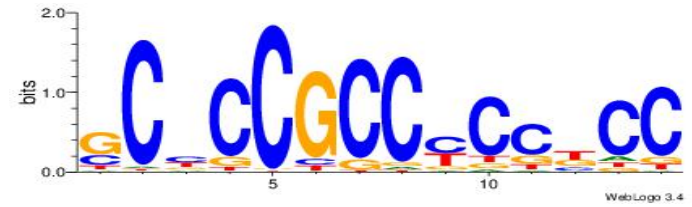
Alignment:

GGMGGRGGCGGVGC--
RGRGGAGRRGGHGGDG

Original motif Consensus sequence: GGMGRRGGCGGVGC



Reverse complement motif Consensus sequence: GCVCCGCCMCCYC

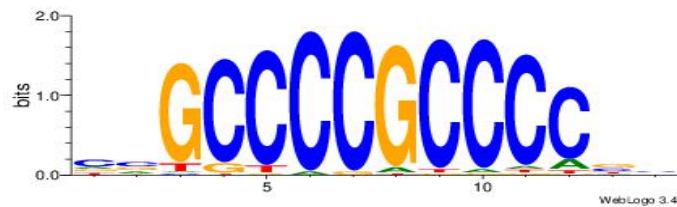


Dataset #: 2
Motif ID: 12
Motif name: csGCCCCGCCCCsc
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 14
Similarity score: 1.05955

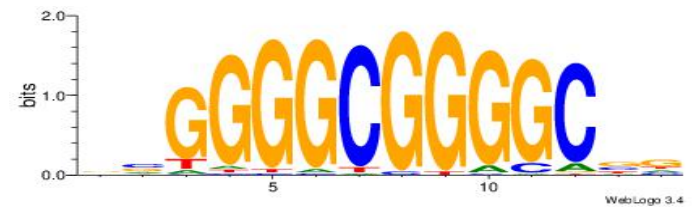
Alignment:

BBGGGGCGGGGCVD--
RGRGGAGRRGGHGGDG

Original motif Consensus sequence: HVGCCCCGCCCCBB

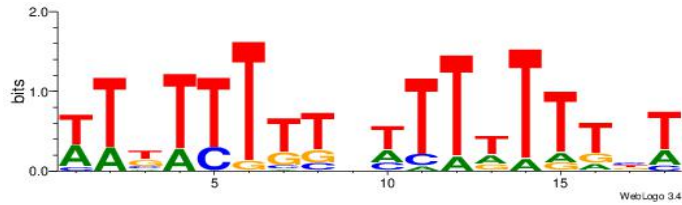


Reverse complement motif Consensus sequence: BBGGGGCGGGGC

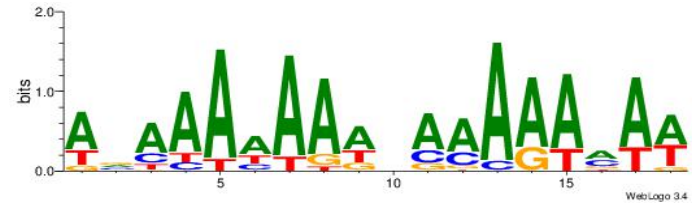


Dataset #: 1 Motif ID: 7 Motif name: TFM1

Original motif Consensus sequence: WTKTTTTTHWTTTTTBT



Reverse complement motif Consensus sequence: ABAAAAAWHAAAAARAW



Best Matches for Motif ID 7 (Highest to Lowest)

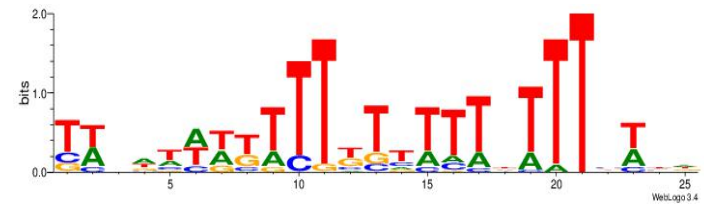
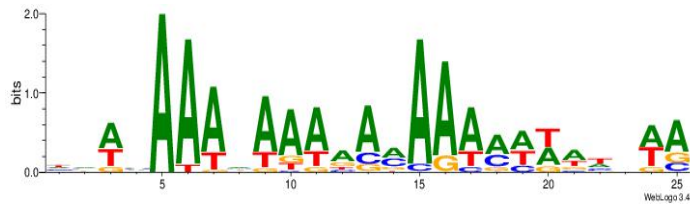
Dataset #: 1
 Motif ID: 11
 Motif name: TFM11
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 6
 Number of overlap: 18
 Similarity score: 0

Alignment:

```
TWVHWWWYTTTTYTTTTTHTTTVWBH
-----WTKTTTTTHWTTTTTBT--
```

Original motif Consensus sequence:
 HDWVAAAHAAAAAAMAAAMWWWHBWA

Reverse complement motif Consensus sequence:
 TWVHWWWYTTTTYTTTTTHTTTVWBH

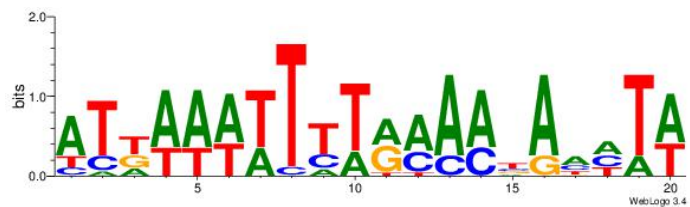


Dataset #: 1
 Motif ID: 10
 Motif name: TFM13
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 18
 Similarity score: 0.0364672

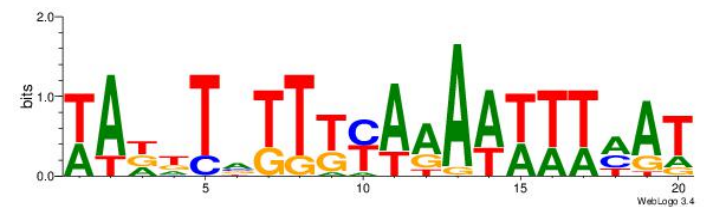
Alignment:

ATKAAWTTTTRMAABAHTW
 ABAAAAA WHAAAAARAW--

Original motif Consensus sequence: ATKAAWTTTTRMAABAHTW



Reverse complement motif Consensus sequence: WAHHTVTTYKAAAATTRAT



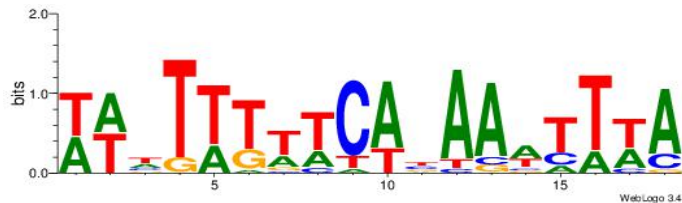
Dataset #: 1

Motif ID: 8
 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

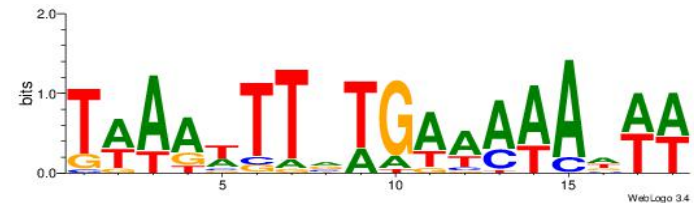
Alignment:

WWHTTTTTTCABAAWTTWA
 WKTTTTTTHWTTTTTTBT

Original motif Consensus sequence: WWHTTTTTTCABAAWTTWA



Reverse complement motif Consensus sequence: TAAWTTVTGAAAAHWW



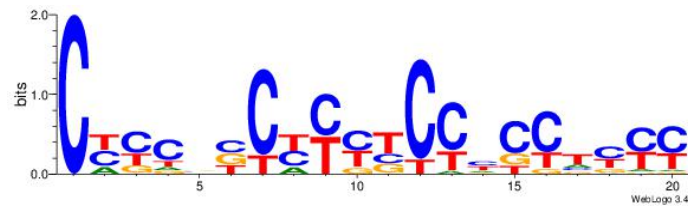
Dataset #: 1
 Motif ID: 9
 Motif name: TFM12
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 17

Similarity score: 0.572783

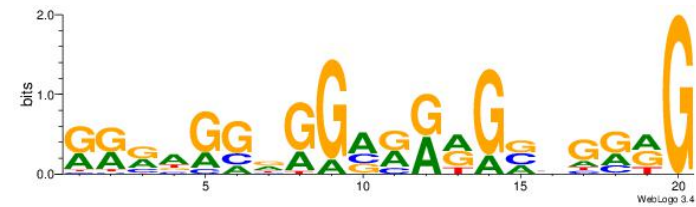
Alignment:

```
CYYCBBCYYYYTCCHCCTYYY-  
---WTKTTTTTHWTTTTTTBT
```

Original motif Consensus sequence: CYYCBBCYYYYTCCHCCTYYY



Reverse complement motif Consensus sequence: KKKAGGDGGAKKMGBBGKMG



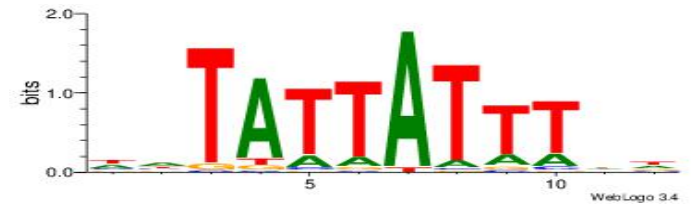
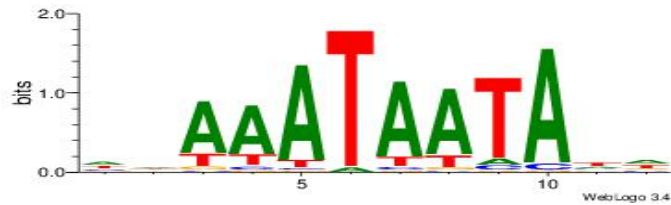
Dataset #: 2
Motif ID: 17
Motif name: wwAAATAATAtw
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 12
Similarity score: 3.0279

Alignment:

```
-----DDTATTATTTDH  
WTKTTTTTHWTTTTTTBT
```

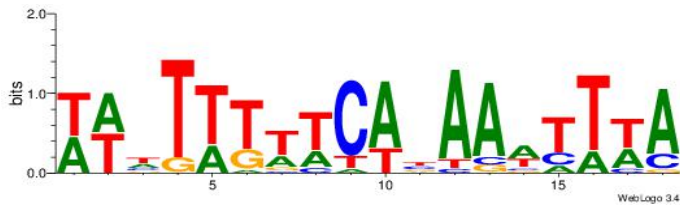
Original motif Consensus sequence: HDAAATAATADD

Reverse complement motif Consensus sequence: DDTATTATTTDH

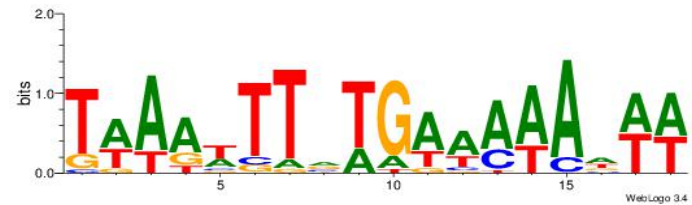


Dataset #: 1 Motif ID: 8 Motif name: TFM3

Original motif Consensus sequence: WWHTTTTTCABAAWTTWA



Reverse complement motif Consensus sequence: TWAAWTTVTGAAAAHWW



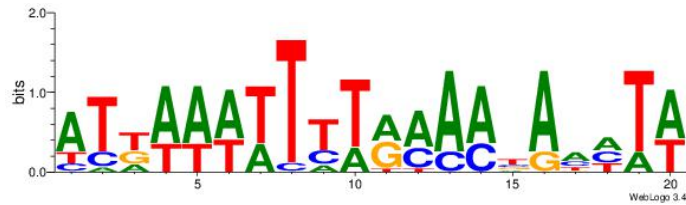
Best Matches for Motif ID 8 (Highest to Lowest)

Dataset #:	1
Motif ID:	10
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:	0.00833981

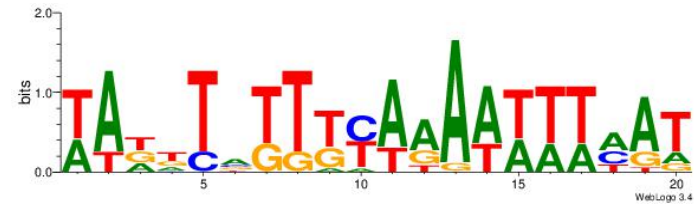
Alignment:

ATKAAWTTTTRMAABAHTW
 -TAAWTTVTGAAAAHWW-

Original motif Consensus sequence: ATKAAWTTTTRMAABAHTW



Reverse complement motif Consensus sequence: WAHHTVTTYKAAAATTRAT



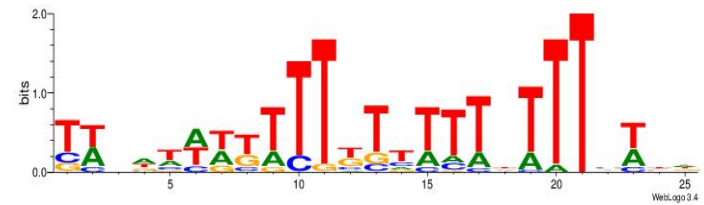
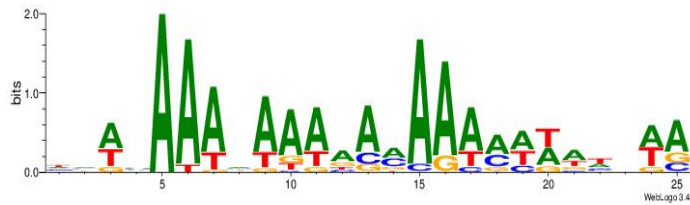
Dataset #:	1
Motif ID:	11
Motif name:	TFM11
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	5
Number of overlap:	18
Similarity score:	0.0346965

Alignment:

TWVHWWWYTTTTYTTTTTHTTTVWBH
 ---WWHTTTTTCABAAWTTWA---

Original motif Consensus sequence:
 HDWVAAAHAAAAAMAAAMWWWHBWA

Reverse complement motif Consensus sequence:
 TWVHWWWYTTTTYTTTTTHTTTVWBH

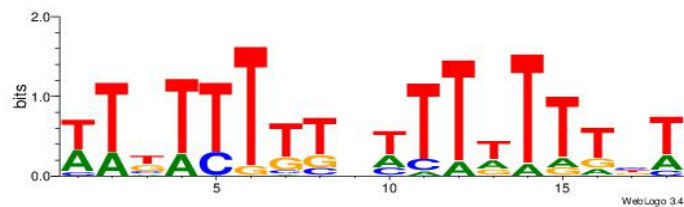


Dataset #: 1
 Motif ID: 7
 Motif name: TFM1
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 18
 Similarity score: 0.0376845

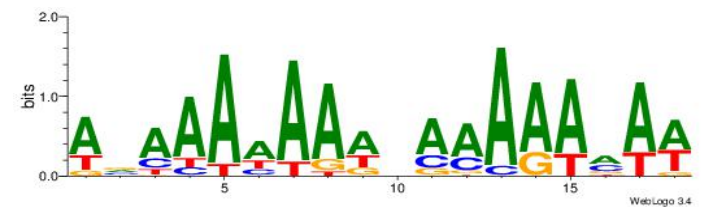
Alignment:

WKTTTTTHWTTTTTBT
 WWHTTTTTCABAAWTTWA

Original motif Consensus sequence: WKTTTTTHWTTTTTBT



Reverse complement motif Consensus sequence: ABAAAAAWHAAAAARAW

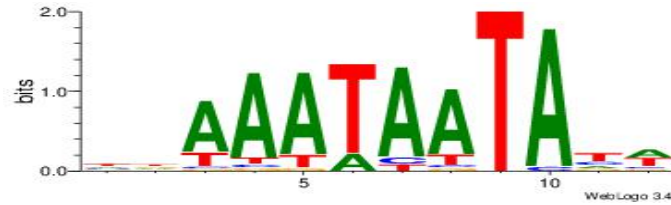


Dataset #: 2

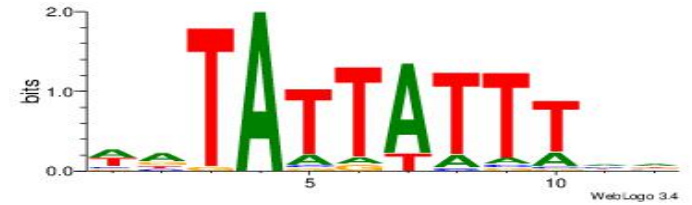
Alignment:

-----WHTATTATTTDH
WWHTTTTTTCABAAWTTWA

Original motif Consensus sequence: HDAAATAATAHW

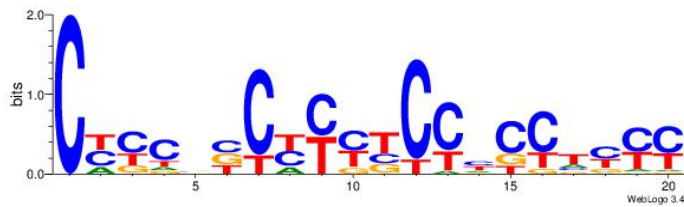


Reverse complement motif Consensus sequence: WHTATTATTTDH

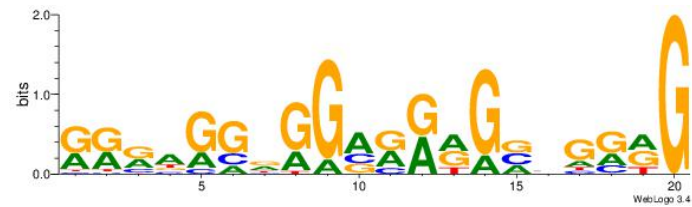


Dataset #: 1 Motif ID: 9 Motif name: TFM12

Original motif Consensus sequence: CYCBBYYYTCCHCCTYYY



Reverse complement motif Consensus sequence: KKKAGGDGGAKKMGBBGKMG



Best Matches for Motif ID 9 (Highest to Lowest)

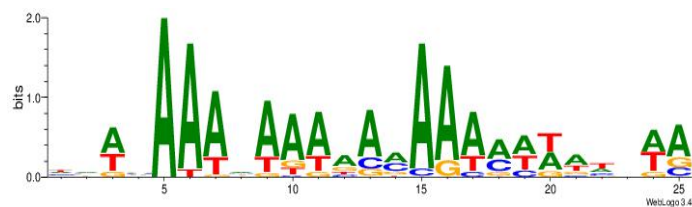
Dataset #:	1
Motif ID:	11
Motif name:	TFM11
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward

Position number: 6
 Number of overlap: 20
 Similarity score: 0.0550447

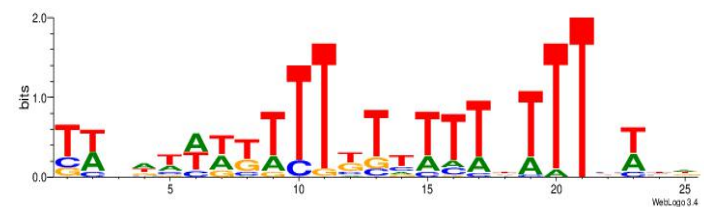
Alignment:

TWVHWWWYTTTYTTTTTHTTTVWBH
 CYYCBBCYYYTCCHCCTYYY-----

Original motif Consensus sequence:
 HDWVAAAHAAAAAMAAAMWWWHBWA



Reverse complement motif Consensus sequence:
 TWVHWWWYTTTYTTTTTHTTTVWBH

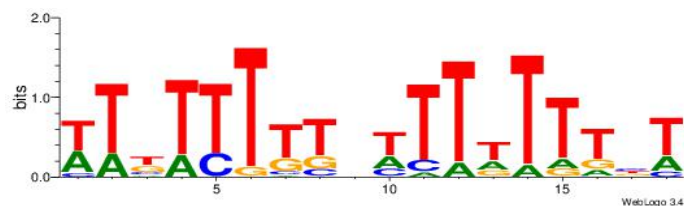


Dataset #: 1
 Motif ID: 7
 Motif name: TFM1
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 17
 Similarity score: 1.56027

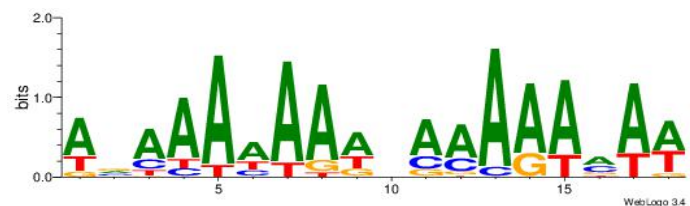
Alignment:

---WTKTTTTTHWTTTTTBT
 CYYCBBCYYYTCCHCCTYYY-

Original motif Consensus sequence: WTKTTTTTHWTTTTTBT



Reverse complement motif Consensus sequence: ABAAAAAWHAAAAARAW

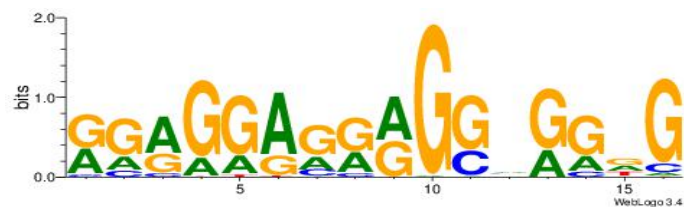


Dataset #: 1
Motif ID: 6
Motif name: TFM2
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 16
Similarity score: 2.0134

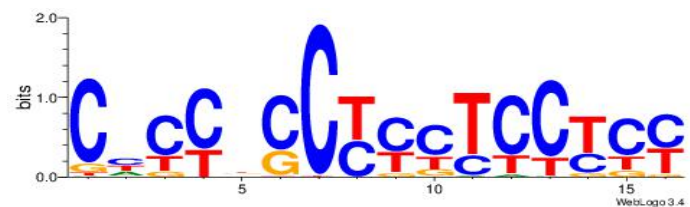
Alignment:

RGRGGAGRRGGHGGDG-----
KKKAGGDGGAKKMGBBGKMG

Original motif Consensus sequence: RGRGGAGRRGGHGGDG



Reverse complement motif Consensus sequence: CHCCBCKMCTCCKCM



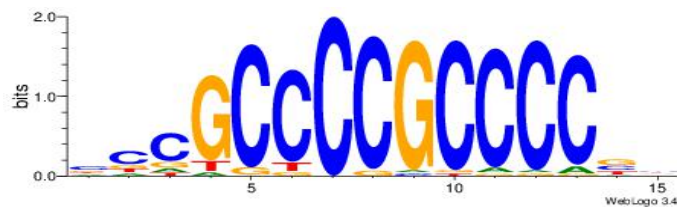
Dataset #: 2
 Motif ID: 14
 Motif name: cccGCCCCGCCCCsb
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 15
 Similarity score: 2.54994

Alignment:

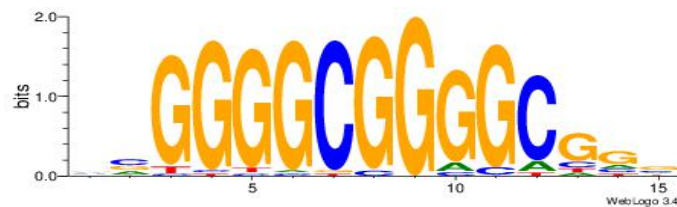
```

-----BCCGCCCCGCCCCBB
CYYCBBCYYYTCCHCCTYYY
  
```

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB



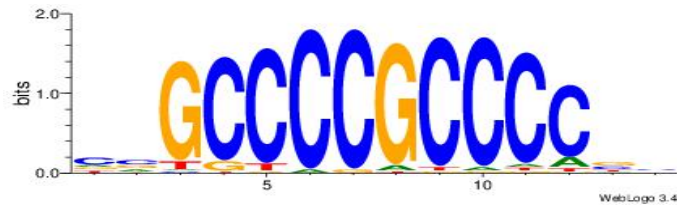
Dataset #: 2
 Motif ID: 12
 Motif name: csGCCCCGCCCCsc
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1

Number of overlap: 14
 Similarity score: 3.04796

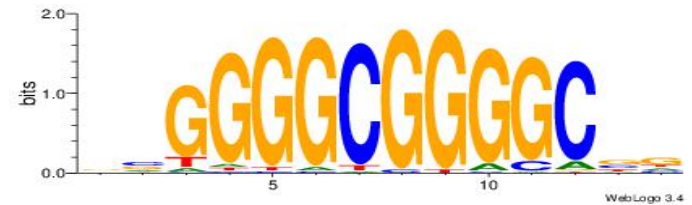
Alignment:

-----BBGGGGCGGGGCVD
 KKKAGGDGGAKKMGBBGKMG

Original motif Consensus sequence: HVGCCCCGCCCCBB

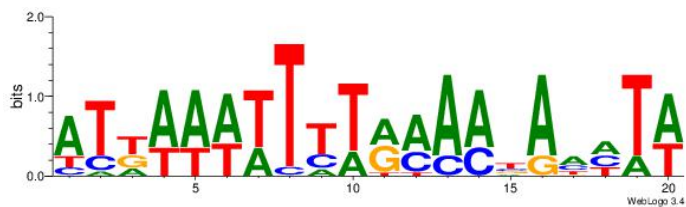


Reverse complement motif Consensus sequence: BBGGGGCGGGGC

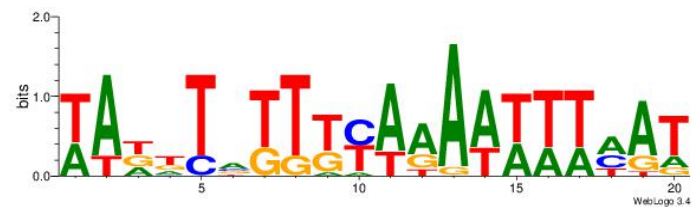


Dataset #: 1 Motif ID: 10 Motif name: TFM13

Original motif Consensus sequence: ATKAAWTTTTTRMAABAHTW



Reverse complement motif Consensus sequence: WAHHTVTTYKAAAATTRAT



Best Matches for Motif ID 10 (Highest to Lowest)

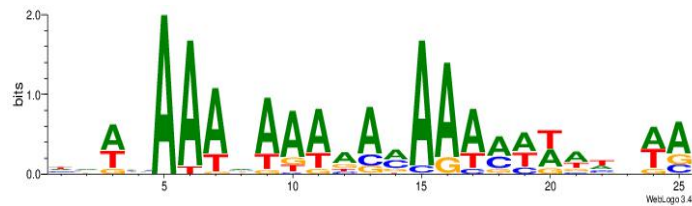
Dataset #: 1
 Motif ID: 11
 Motif name: TFM11
 Matching format of first motif: Reverse Complement

Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 5
 Number of overlap: 20
 Similarity score: 0.0352451

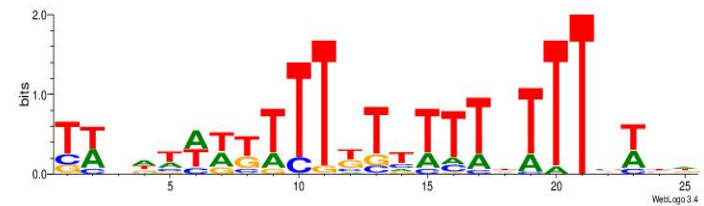
Alignment:

TWVHWWWYTTTTYTTTTTHTTTVWBH
 ---WAHHTVTTYKAAAATTRAT-

Original motif Consensus sequence:
 HDWVAAAHAAAAAMAAAMWWWHBWA



Reverse complement motif Consensus sequence:
 TWVHWWWYTTTTYTTTTTHTTTVWBH

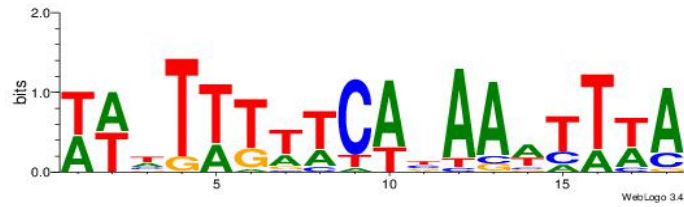


Dataset #: 1
 Motif ID: 8
 Motif name: TFM3
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 18
 Similarity score: 1.02254

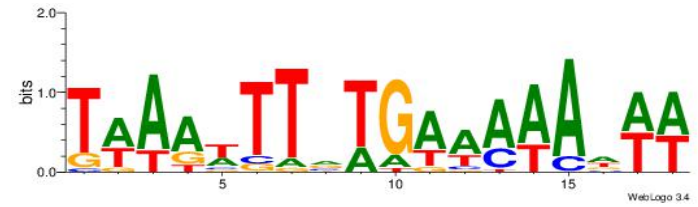
Alignment:

TWAAWTTVTGAAAAHWW--
 ATKAAWTTTTTRMAABAHHTW

Original motif Consensus sequence: WWHTTTTTTCABAAWTTWA



Reverse complement motif Consensus sequence: TWAAWTTVTGAAAAHWW

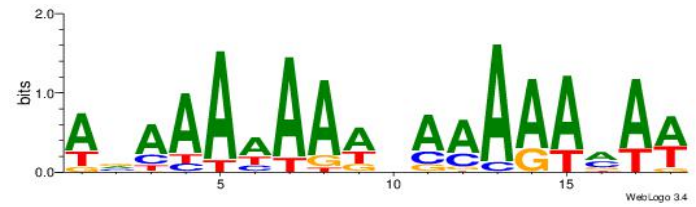
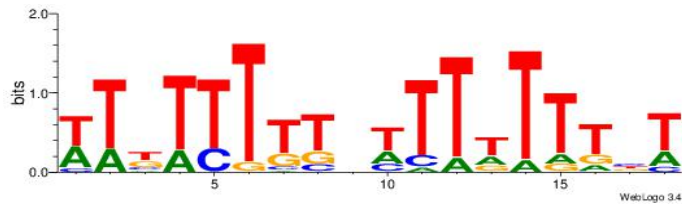


Dataset #: 1
 Motif ID: 7
 Motif name: TFM1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 18
 Similarity score: 1.02868

Alignment:
 WKTTTTTTHWTTTTTTBT--
 WAHHTVTTYKAAAATTRAT

Original motif Consensus sequence: WTKTTTTTHWTTTTTTBT

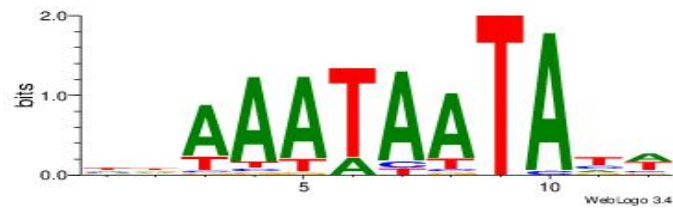
Reverse complement motif Consensus sequence: ABAAAAAWHAAAAARAW



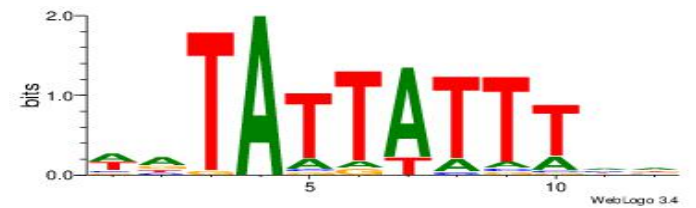
Dataset #: 2
 Motif ID: 13
 Motif name: tkAAATAATAtw
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 12
 Similarity score: 4.03399

Alignment:
 -----HDAAATAATAHW
 WAHHTVTTYKAAAATTRAT

Original motif Consensus sequence: HDAAATAATAHW



Reverse complement motif Consensus sequence: WHTATTATTTDH



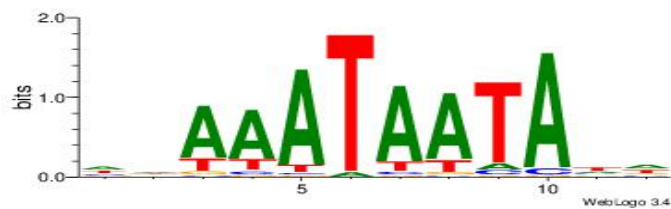
Dataset #: 2
 Motif ID: 17

Motif name: wwAAATAATAtw
 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: 4.03484

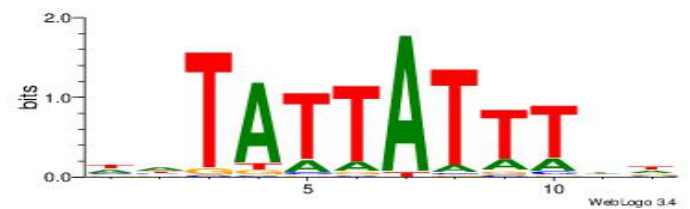
Alignment:

-----HDAAATAATADD
 WAHHTVTTYKAAAATTRAT

Original motif Consensus sequence: HDAAATAATADD

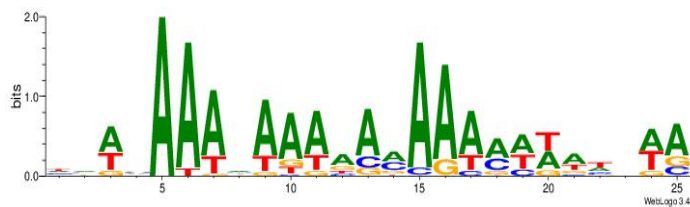


Reverse complement motif Consensus sequence: DDTATTATTDDH

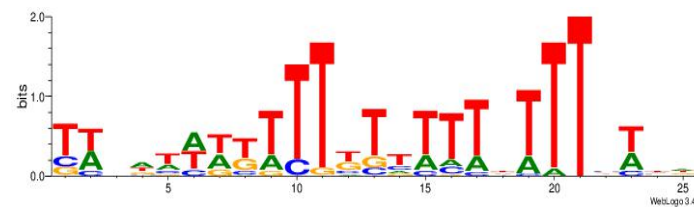


Dataset #: 1 Motif ID: 11 Motif name: TFM11

Original motif Consensus sequence:
 HDWVAAAHAAAAAAMAAAMWWWHBWA



Reverse complement motif Consensus sequence:
 TWVHWWWYTTTTTTTTTHTTTVWBH



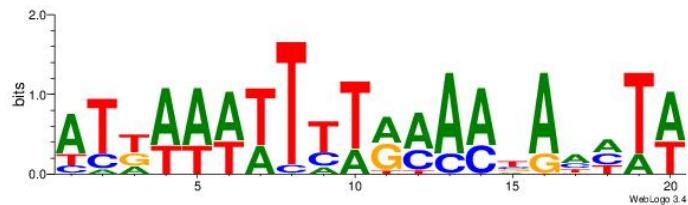
Best Matches for Motif ID 11 (Highest to Lowest)

Dataset #: 1
 Motif ID: 10
 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

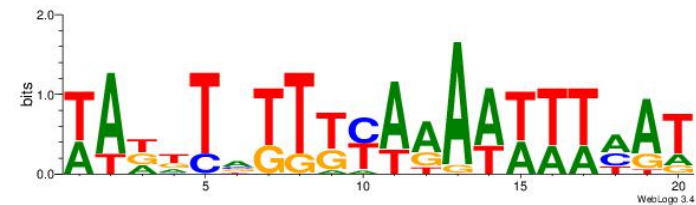
Alignment:

WAHHTVTTYKAAAATTRAT-----
 TWVHWWYTTTTYTTTTTHTTTVWBH

Original motif Consensus sequence: ATKAAWTTTTRMAABAHTW



Reverse complement motif Consensus sequence: WAHHTVTTYKAAAATTRAT



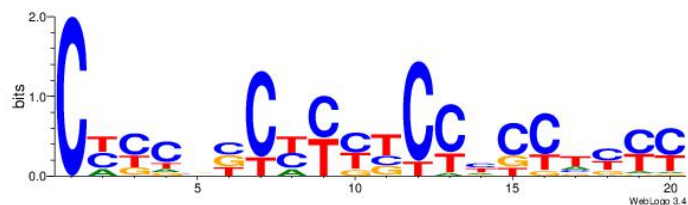
Dataset #: 1
 Motif ID: 9
 Motif name: TFM12
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement

Direction: Forward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.0693284

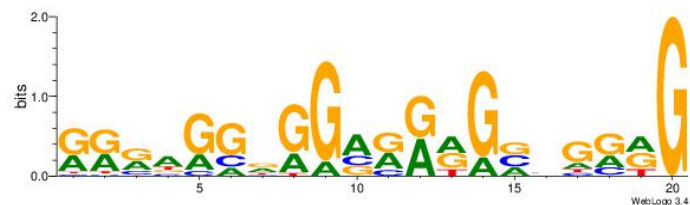
Alignment:

KKKAGGDGGAKKMGBBGKMG-----
 HDWVAAAHA AAAA MAAA MWWW HBWA

Original motif Consensus sequence: CYCBBY YYTCCHCCTYYY



Reverse complement motif Consensus sequence: KKKAGGDGGAKKMGBBGKMG

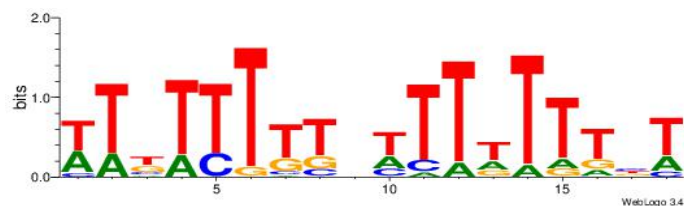


Dataset #: 1
 Motif ID: 7
 Motif name: TFM1
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 18
 Similarity score: 1.0232

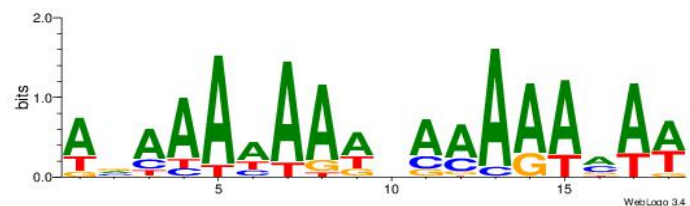
Alignment:

-----ABAAAAA WHAAAA RAW
 HDWVAAAHA AAAA MAAA MWWW HBWA

Original motif Consensus sequence: WTKTTTTTHWTTTTTBT



Reverse complement motif Consensus sequence: ABAAAAAWHAAAAARAW

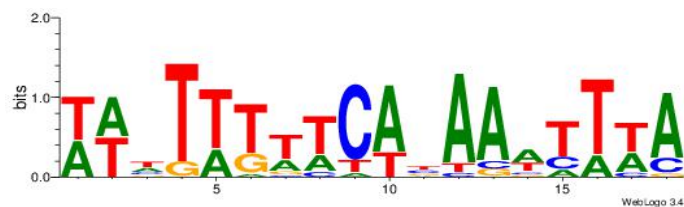


Dataset #: 1
Motif ID: 8
Motif name: TFM3
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 18
Similarity score: 1.05388

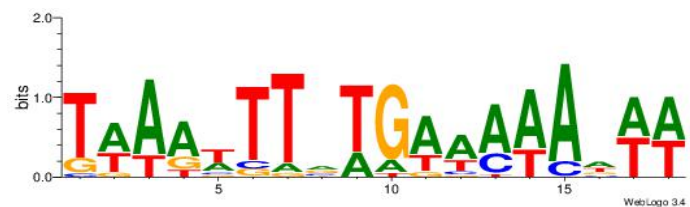
Alignment:

WWHTTTTTTCABAAWTTWA-----
TWVHWWWYTTTTYTTTTTHTTTVWBH

Original motif Consensus sequence: WWHTTTTTTCABAAWTTWA



Reverse complement motif Consensus sequence: TWAAWTTVTGAAAAAHWW

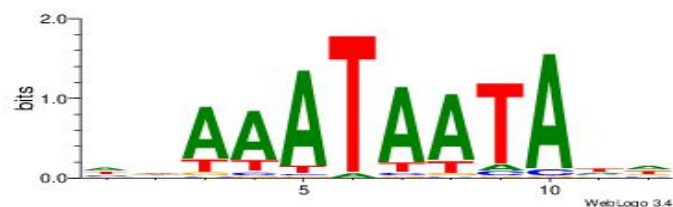


Dataset #: 2
 Motif ID: 17
 Motif name: wwAAATAATAtw
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 12
 Similarity score: 4.03464

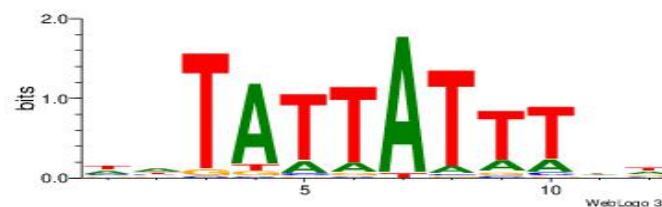
Alignment:

HDAAATAATADD-----
 HDWVAAAHA AAAA MAAAMWWWHBWA

Original motif Consensus sequence: HDAAATAATADD

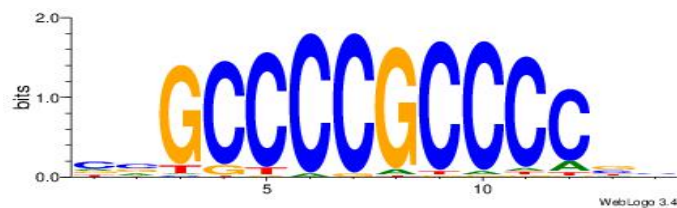


Reverse complement motif Consensus sequence: DDTATTATTTDH

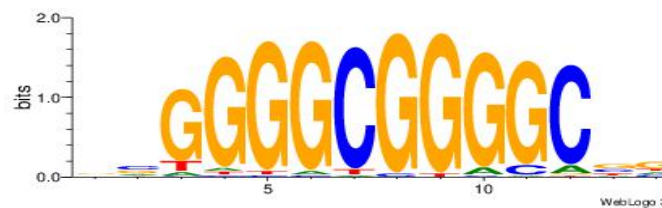


Dataset #: 2 Motif ID: 12 Motif name: csGCCCCGCCCCsc

Original motif Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGC



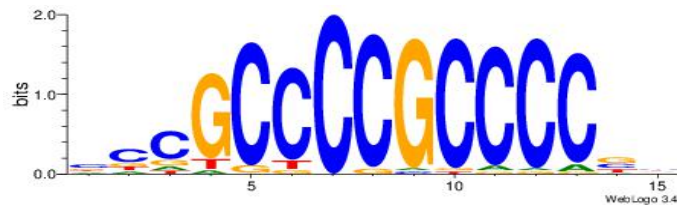
Best Matches for Motif ID 12 (Highest to Lowest)

Dataset #: 2
Motif ID: 14
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

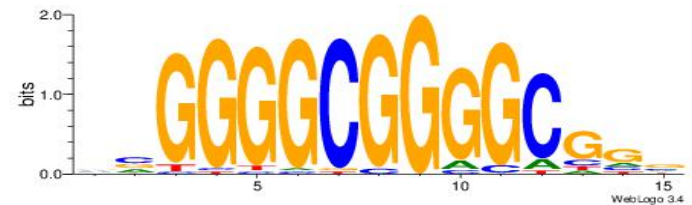
Alignment:

```
BCCGCCCCGCCCCBB  
-HVGCCCCGCCCCBB
```

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB



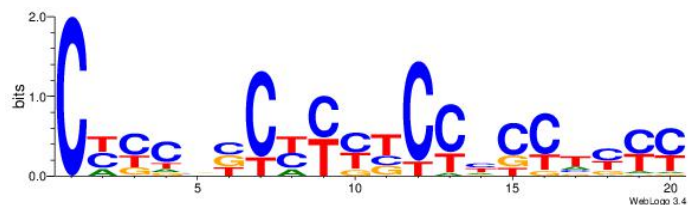
Dataset #: 1
Motif ID: 9
Motif name: TFM12
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif

Direction: Backward
 Position number: 4
 Number of overlap: 14
 Similarity score: 0.0777991

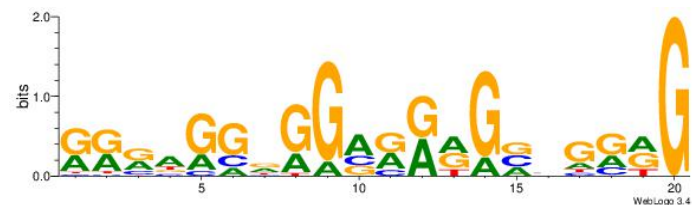
Alignment:

CYYCBBCYYYTCCHCCTYYY
 ---HVGCCCGCCCB---

Original motif Consensus sequence: CYYCBBCYYYTCCHCCTYYY



Reverse complement motif Consensus sequence: KKKAGGDGGAKKMGBBGKMG

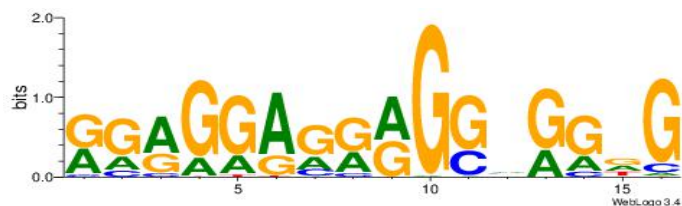


Dataset #: 1
 Motif ID: 6
 Motif name: TFM2
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 14
 Similarity score: 0.0880609

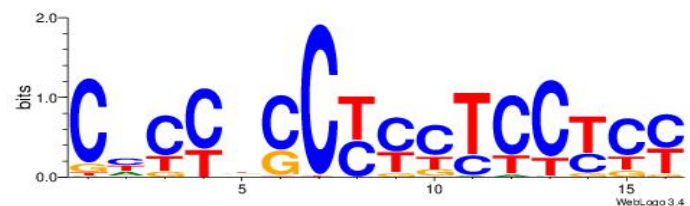
Alignment:

CHCCBCKMCTCCKCM
 HVGCCCGCCCB---

Original motif Consensus sequence: RGRGGAGRRGGHGGDG



Reverse complement motif Consensus sequence: CHCCBCKMCTCKCM

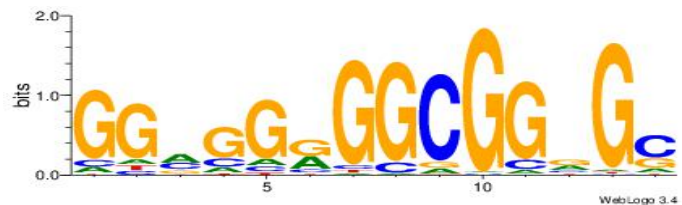


Dataset #: 1
Motif ID: 5
Motif name: TFF11
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 14
Similarity score: 0.0937271

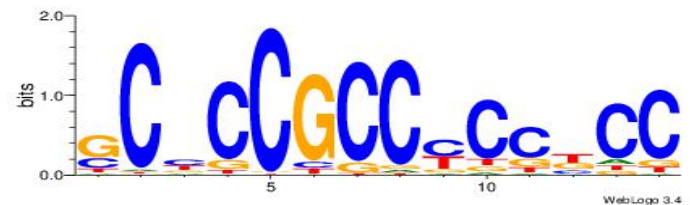
Alignment:

GGMGRRGGCGGVGC
BBGGGGCGGGGCVD

Original motif Consensus sequence: GGMGRRGGCGGVGC



Reverse complement motif Consensus sequence: GCVCCGCCMCCY

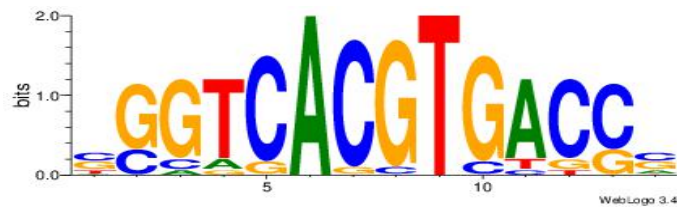


Dataset #: 2
 Motif ID: 18
 Motif name: sSGTCACGTGACsS
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0.0971132

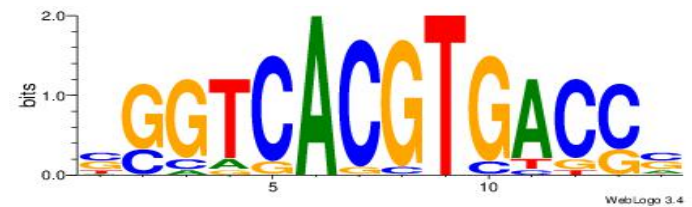
Alignment:

SGGTCACGTGACCS
 HVGCCCGCCCB

Original motif Consensus sequence: SGGTCACGTGACCS

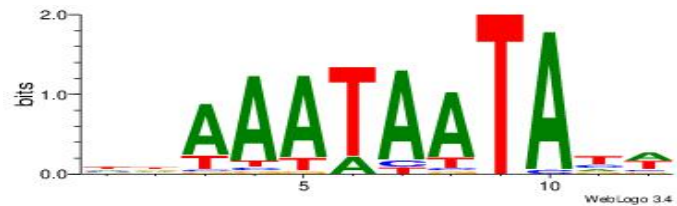


Reverse complement motif Consensus sequence: SGGTCACGTGACCS

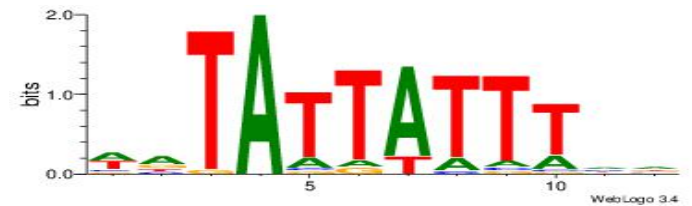


Dataset #: 2 Motif ID: 13 Motif name: tkAAATAATatw

Original motif Consensus sequence: HDAAATAATAHW



Reverse complement motif Consensus sequence: WHTATTATTTDH



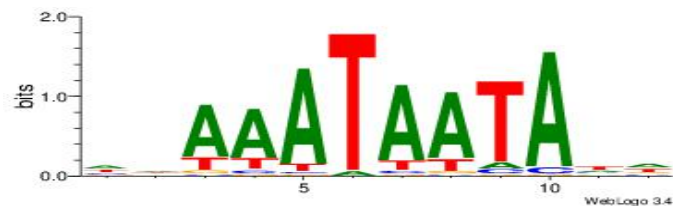
Best Matches for Motif ID 13 (Highest to Lowest)

Dataset #: 2
Motif ID: 17
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

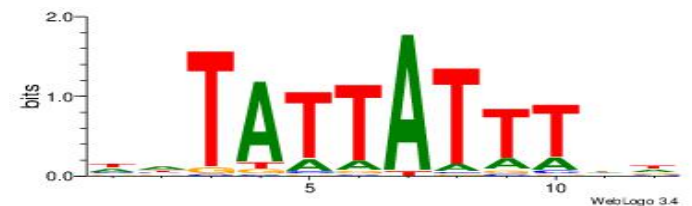
Alignment:

HDAAATAATADD
HDAAATAATAHW

Original motif Consensus sequence: HDAAATAATADD



Reverse complement motif Consensus sequence: DDTATTATTTDH



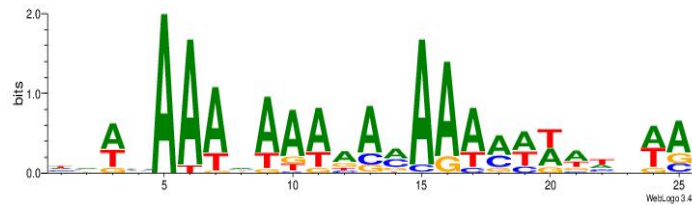
Dataset #: 1
Motif ID: 11
Motif name: TFM11
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement

Direction: Forward
 Position number: 12
 Number of overlap: 12
 Similarity score: 0.0590505

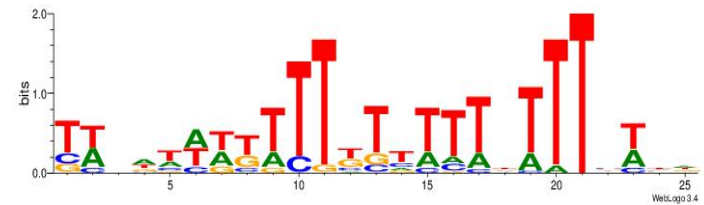
Alignment:

TWVHWWYTTTYTTTTHTTTVWBH
 -----WHTATTATTTDH--

Original motif Consensus sequence:
 HDWVAAAHAAAAAMAAAMWWWHBWA



Reverse complement motif Consensus sequence:
 TWVHWWYTTTYTTTTHTTTVWBH

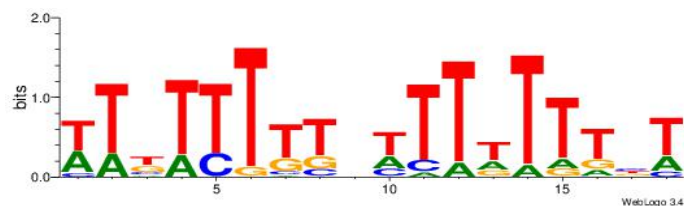


Dataset #: 1
 Motif ID: 7
 Motif name: TFM1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 12
 Similarity score: 0.0637702

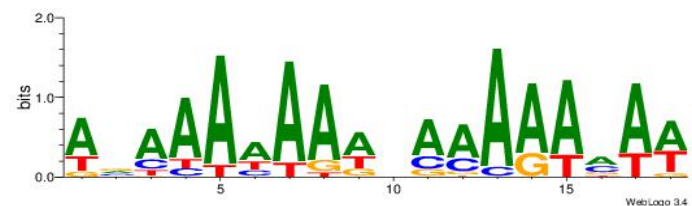
Alignment:

WKTTTTTHWTTTTTTBT
 WHTATTATTTDH-----

Original motif Consensus sequence: WTKTTTTTHWTTTTTBT



Reverse complement motif Consensus sequence: ABAAAAAWHAAAAARAW

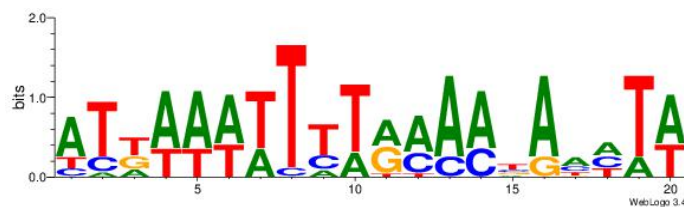


Dataset #: 1
Motif ID: 10
Motif name: TFM13
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 9
Number of overlap: 12
Similarity score: 0.0704475

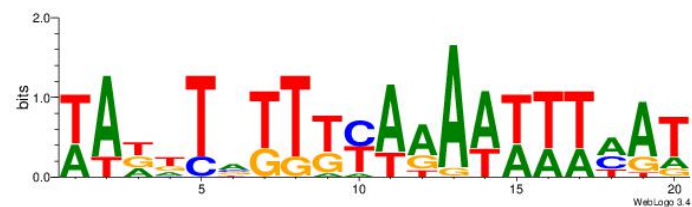
Alignment:

ATKAAWTTTTRMAABAHHTW
-----WHTATTATTTDH

Original motif Consensus sequence: ATKAAWTTTTRMAABAHHTW



Reverse complement motif Consensus sequence: WAHHTVTTYKAAAATTRAT

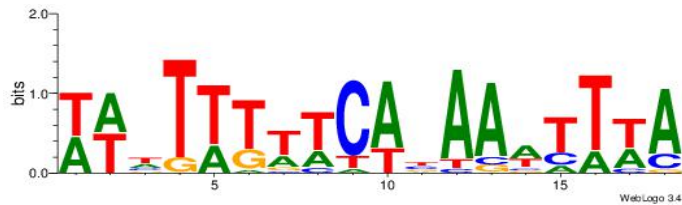


Dataset #: 1
 Motif ID: 8
 Motif name: TFM3
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 12
 Similarity score: 0.0763819

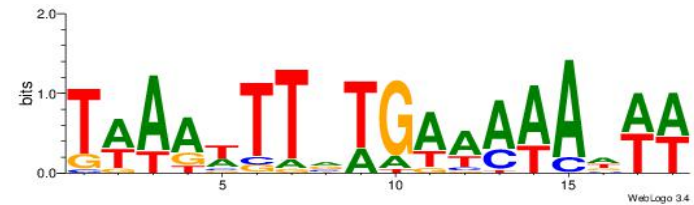
Alignment:

TWAAWTTVTGAAAAHWW
 -----HDAAATAATAHW

Original motif Consensus sequence: WWHTTTTTCABAAWTTWA



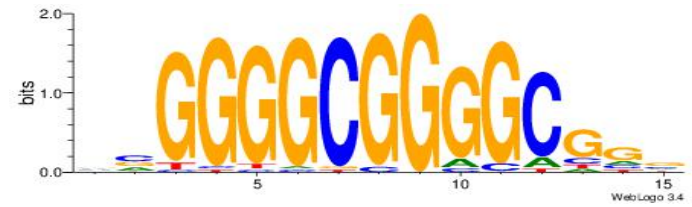
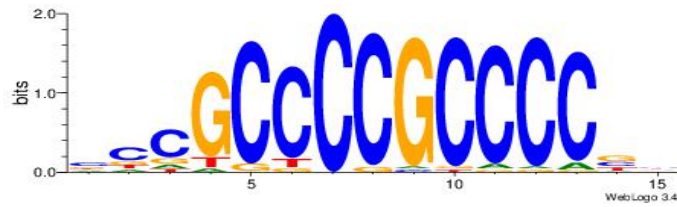
Reverse complement motif Consensus sequence: TWAAWTTVTGAAAAHWW



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

Original motif Consensus sequence: BCCGCCCGCCCCBB

Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB

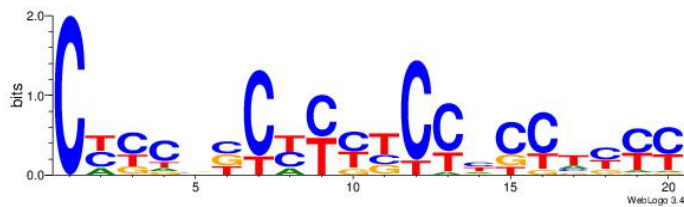


Best Matches for Motif ID 14 (Highest to Lowest)

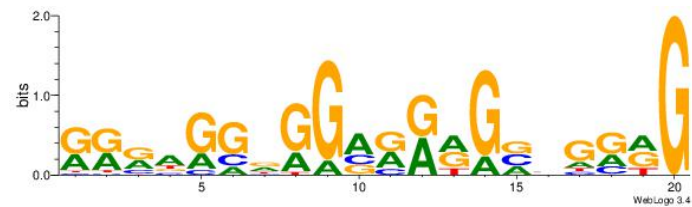
Dataset #: 1
 Motif ID: 9
 Motif name: TFM12
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 15
 Similarity score: 0.0773345

Alignment:
 CYYCBBCYYYYTCCHCCTYYY
 --BCCGCCCCGCCCCBB---

Original motif Consensus sequence: CYYCBBCYYYYTCCHCCTYYY



Reverse complement motif Consensus sequence: KKKAGGDGGAKKMGBBGKMG

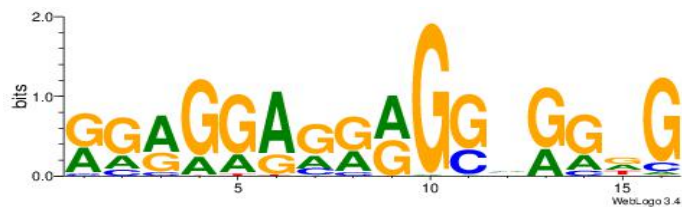


Dataset #: 1
 Motif ID: 6
 Motif name: TFM2
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 15
 Similarity score: 0.0869149

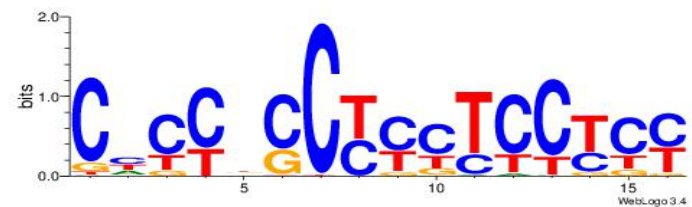
Alignment:

CHCCBCKMCTCCKCM
 BCCGCCCCGCCCCBB-

Original motif Consensus sequence: RGRGGAGRRGGHGGDG



Reverse complement motif Consensus sequence: CHCCBCKMCTCCKCM



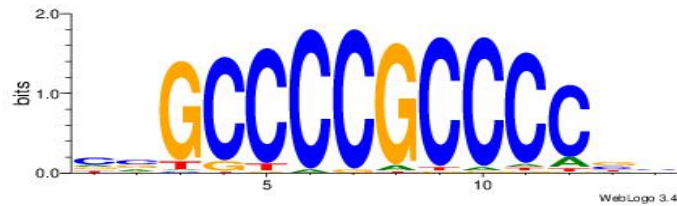
Dataset #: 2
 Motif ID: 12
 Motif name: csGCCCCGCCCCsc
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1

Number of overlap: 14
Similarity score: 0.5

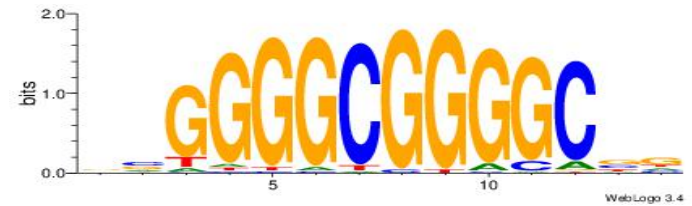
Alignment:

BBGGGGCGGGGCVD-
BBGGGGCGGGGCGB

Original motif Consensus sequence: HVGCCCCGCCCB



Reverse complement motif Consensus sequence: BBGGGGCGGGGC



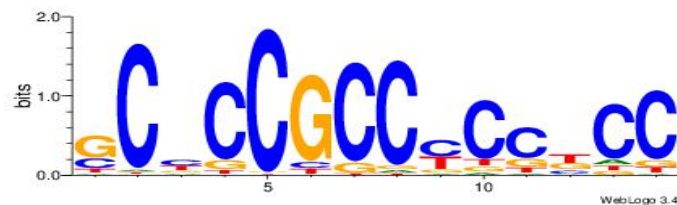
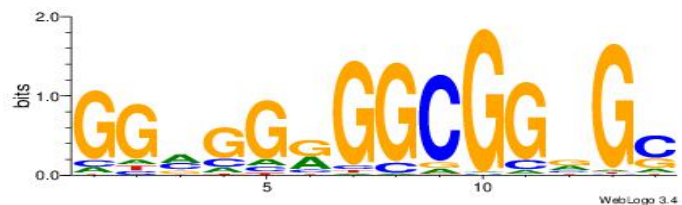
Dataset #: 1
Motif ID: 5
Motif name: TFF11
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 14
Similarity score: 0.58333

Alignment:

GGMGGRGGCGGVGC-
BBGGGGCGGGGCGB

Original motif Consensus sequence: GGMGGRGGCGGVGC

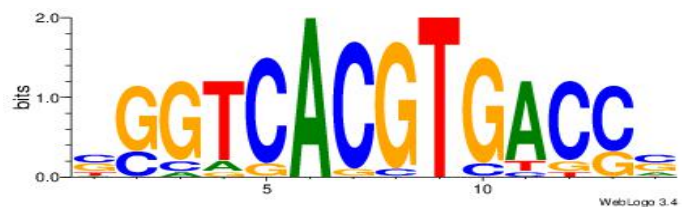
Reverse complement motif Consensus sequence: GCVCCGCCMCCYC



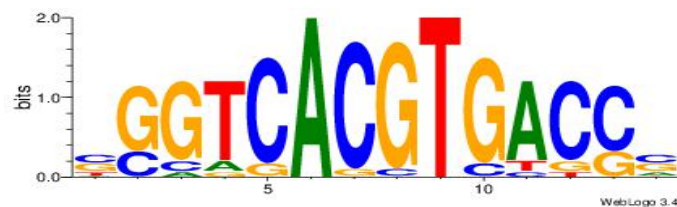
Dataset #: 2
 Motif ID: 18
 Motif name: sSGTCACGTGACCSs
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0.601399

Alignment:
 SGGTCACGTGACCS-
 BBGGGGCGGGGCGGB

Original motif Consensus sequence: SGGTCACGTGACCS



Reverse complement motif Consensus sequence: SGGTCACGTGACCS



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

Original motif Consensus sequence: DCAGCCAATVR



Reverse complement motif Consensus sequence: MBATTGGCTGH



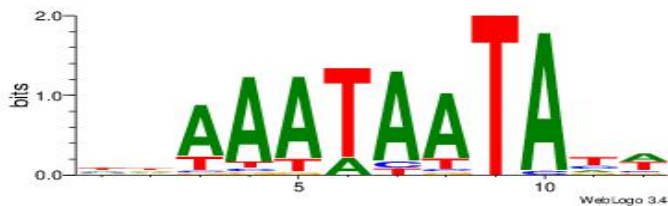
Best Matches for Motif ID 15 (Highest to Lowest)

Dataset #:	2
Motif ID:	13
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:	0.0320614

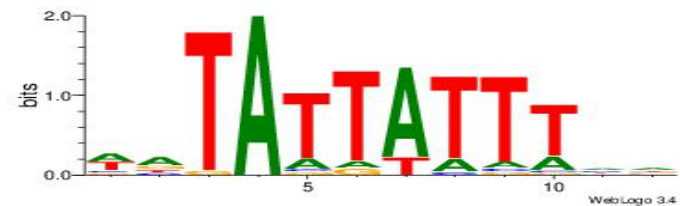
Alignment:

WHTATTATTTDH
-MBATTGGCTGH

Original motif Consensus sequence: HDAATAATAHW



Reverse complement motif Consensus sequence: WHTATTATTTDH

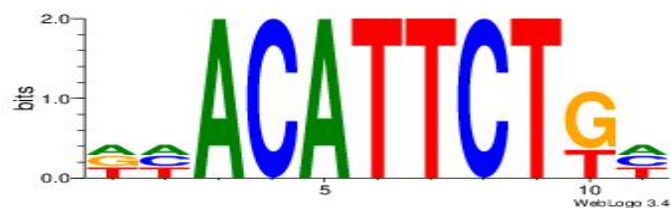


Dataset #: 2
 Motif ID: 20
 Motif name: dhACATTCTkh
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.034958

Alignment:

HCAGAATGTHD
 DCAGCCAATVR

Original motif Consensus sequence: DHACATTCTGH



Reverse complement motif Consensus sequence: HCAGAATGTHD



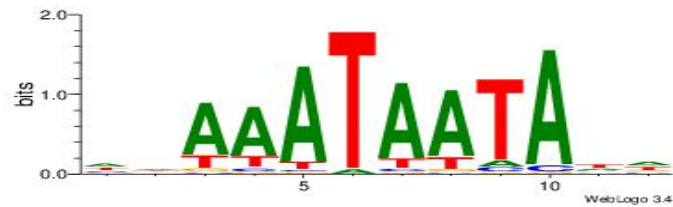
Dataset #: 2
 Motif ID: 17
 Motif name: wwAAATAATAtw
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 11

Similarity score: 0.0358988

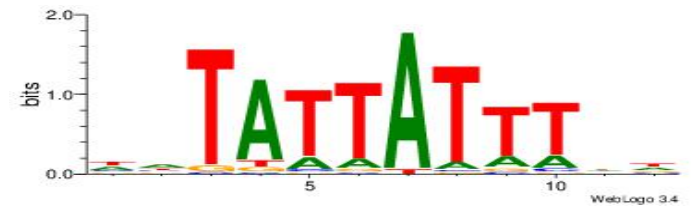
Alignment:

DDTATTATTTDH
-MBATTGGCTGH

Original motif Consensus sequence: HDAAATAATADD



Reverse complement motif Consensus sequence: DDTATTATTTDH



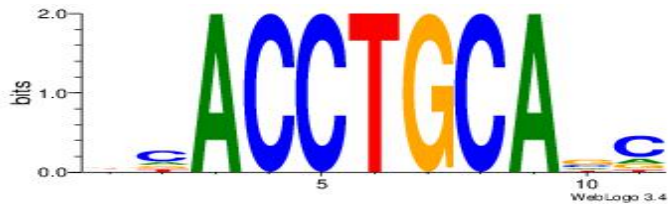
Dataset #: 2
Motif ID: 16
Motif name: kcACCTGCAGc
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 11
Similarity score: 0.0360892

Alignment:

BCACCTGCABC
MBATTGGCTGH

Original motif Consensus sequence: BCACCTGCABC

Reverse complement motif Consensus sequence: GBTGCAGGTGB



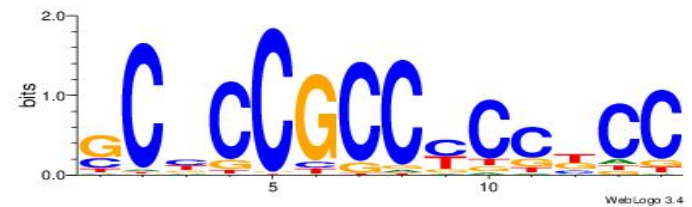
Dataset #: 1
 Motif ID: 5
 Motif name: TFF11
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 11
 Similarity score: 0.0376063

Alignment:
 GGMGRRGGCGGVGC
 --MBATTGGCTGH-

Original motif Consensus sequence: GGMGRRGGCGGVGC



Reverse complement motif Consensus sequence: GCVCCGCCMCCYCC



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

Original motif Consensus sequence: BCACCTGCABC



Reverse complement motif Consensus sequence: GBTGCAGGTGB



Best Matches for Motif ID 16 (Highest to Lowest)

Dataset #:	2
Motif ID:	19
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:	0.0182895

Alignment:

DBTACWGTA VH
BCACCTGCABC

Original motif Consensus sequence: HVTACWGTA BD



Reverse complement motif Consensus sequence: DBTACWGTA VH

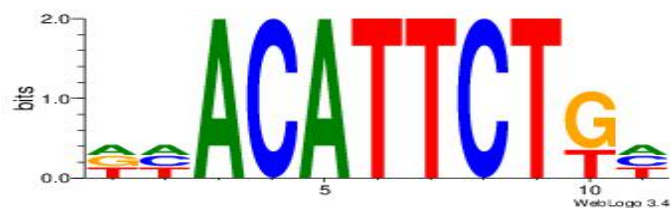


Dataset #: 2
 Motif ID: 20
 Motif name: dhACATTCTkh
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.0221745

Alignment:

DHACATTCTGH
 BCACCTGCABC

Original motif Consensus sequence: DHACATTCTGH



Reverse complement motif Consensus sequence: HCAGAATGTHD



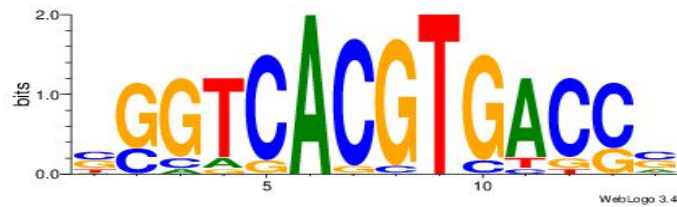
Dataset #: 2
 Motif ID: 18
 Motif name: sSGTCACGTGACSS
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 11

Similarity score: 0.0280991

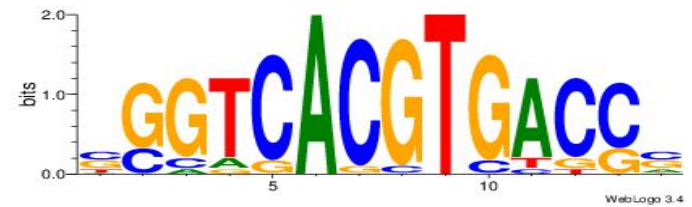
Alignment:

SGGTCACGTGACCS
---BCACCTGCABC

Original motif Consensus sequence: SGGTCACGTGACCS



Reverse complement motif Consensus sequence: SGGTCACGTGACCS



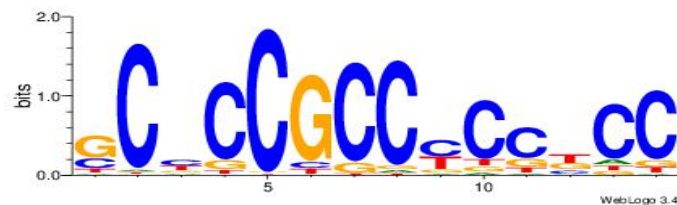
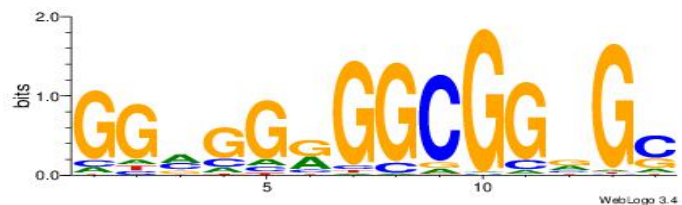
Dataset #: 1
Motif ID: 5
Motif name: TFF11
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 4
Number of overlap: 11
Similarity score: 0.0312321

Alignment:

GGMGRRGGCGGVGC
GBTGCAGGTGB---

Original motif Consensus sequence: GGMGRRGGCGGVGC

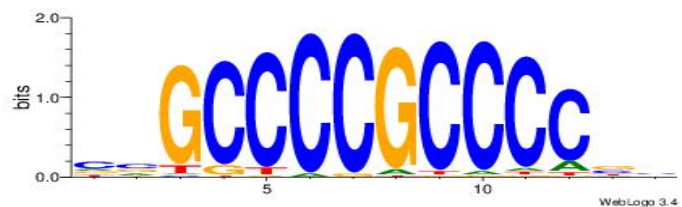
Reverse complement motif Consensus sequence: GCVCCGCCMCCYCC



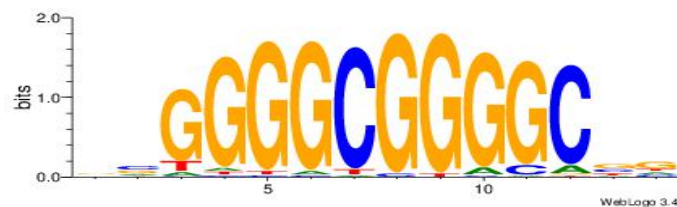
Dataset #: 2
 Motif ID: 12
 Motif name: csGCCCCGCCCCsc
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 11
 Similarity score: 0.0370129

Alignment:
 HVGCCCCGCCCCBB
 -BCACCTGCABC--

Original motif Consensus sequence: HVGCCCCGCCCCBB

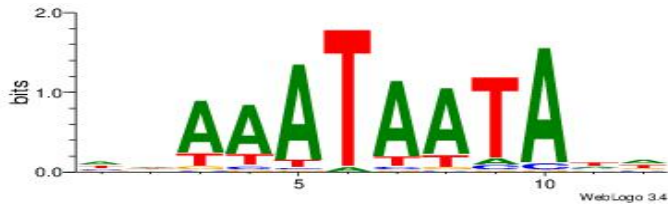


Reverse complement motif Consensus sequence: BBGGGGCGGGGC

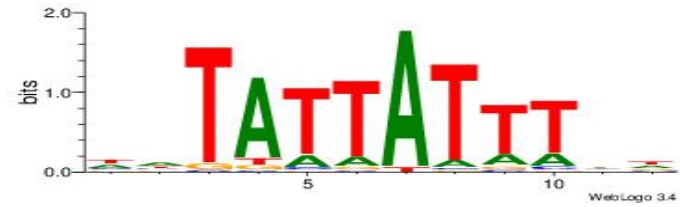


Dataset #: 2 Motif ID: 17 Motif name: wwAAATAATAtw

Original motif Consensus sequence: HDAAATAATADD



Reverse complement motif Consensus sequence: DDTATTATTTDH



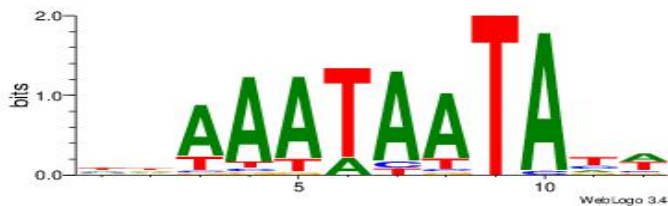
Best Matches for Motif ID 17 (Highest to Lowest)

Dataset #:	2
Motif ID:	13
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

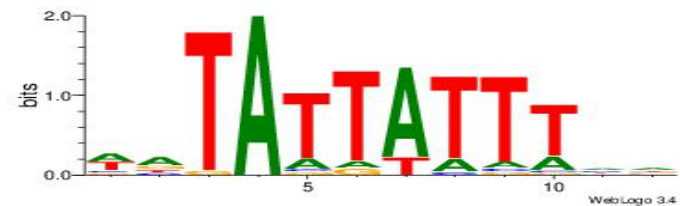
Alignment:

HDAAATAATAHW
HDAAATAATADD

Original motif Consensus sequence: HDAAATAATAHW



Reverse complement motif Consensus sequence: WHTATTATTTDH

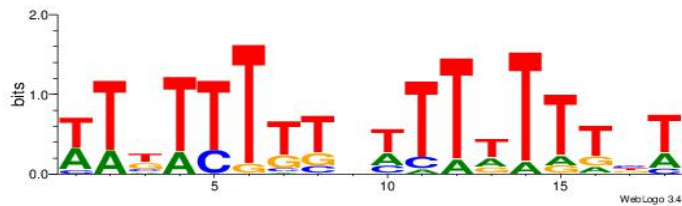


Dataset #: 1
 Motif ID: 7
 Motif name: TFM1
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 7
 Number of overlap: 12
 Similarity score: 0.0565705

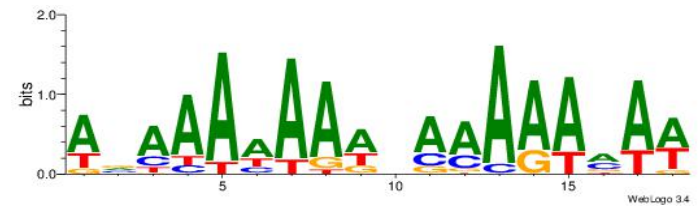
Alignment:

ABAAAAAWhAAAAARAW
 -----HDAATAATADD

Original motif Consensus sequence: WTKTTTTTHWTTTTTTBT



Reverse complement motif Consensus sequence: ABAAAAAWhAAAAARAW



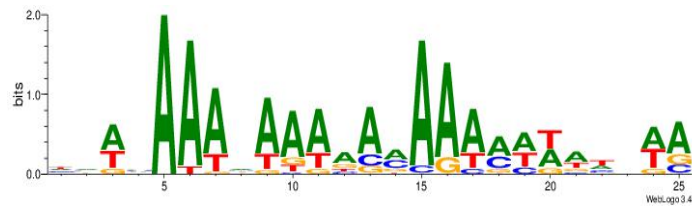
Dataset #: 1
 Motif ID: 11
 Motif name: TFM11
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3

Number of overlap: 12
Similarity score: 0.0575935

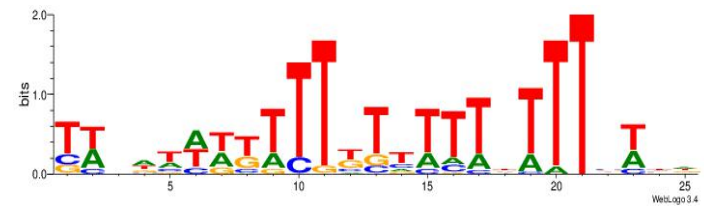
Alignment:

HDWVAAAHAAAAAAMAAAMWWWHBWA
--HDAAATAATADD-----

Original motif Consensus sequence:
HDWVAAAHAAAAAAMAAAMWWWHBWA



Reverse complement motif Consensus sequence:
TWVHWWWYTTTTTTTTTHTTTVWBH

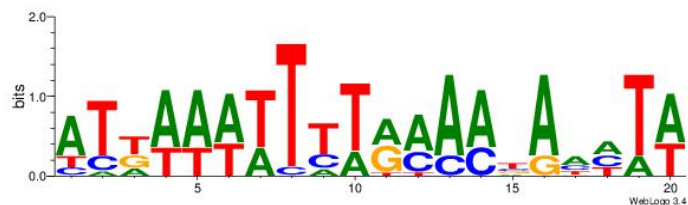


Dataset #: 1
Motif ID: 10
Motif name: TFM13
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 12
Similarity score: 0.0712963

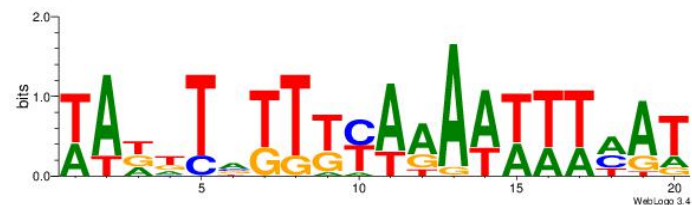
Alignment:

ATKAAWTTTTTRMAABAHHTW
-----DDTATTATTTDH

Original motif Consensus sequence: ATKAAWTTTTRMAABAHTW



Reverse complement motif Consensus sequence: WAHHTVTTYKAAAATTRAT

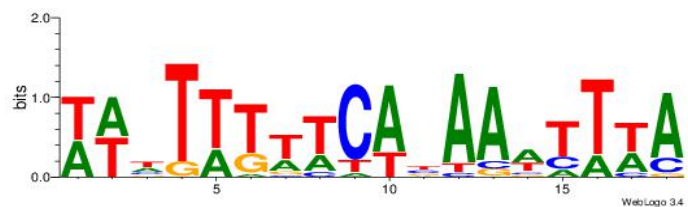


Dataset #: 1
Motif ID: 8
Motif name: TFM3
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 12
Similarity score: 0.0733516

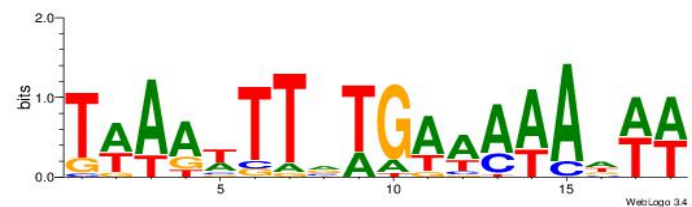
Alignment:

```
TWAAWTTVTGAAAAHWW  
-----HDAAATAATADD
```

Original motif Consensus sequence: WWHTTTTTTCABAAWTTWA

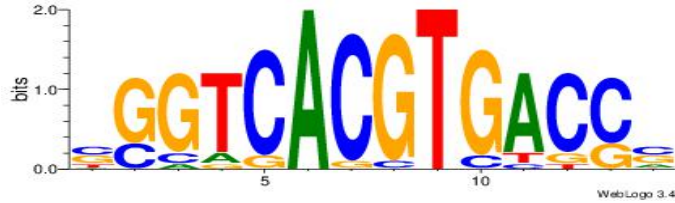


Reverse complement motif Consensus sequence: TWAAWTTVTGAAAAHWW

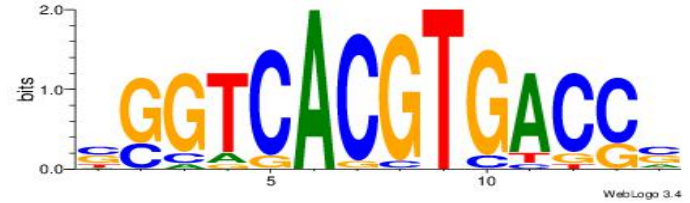


Dataset #: 2 Motif ID: 18 Motif name: sSGTCACGTGACCS

Original motif Consensus sequence: SGGTCACGTGACCS



Reverse complement motif Consensus sequence: SGGTCACGTGACCS



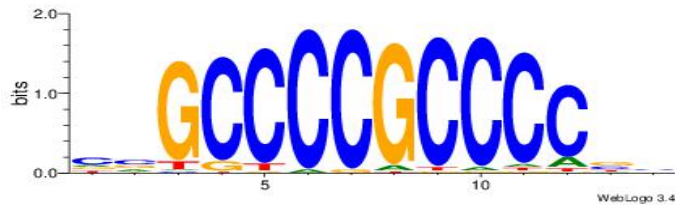
Best Matches for Motif ID 18 (Highest to Lowest)

Dataset #:	2
Motif ID:	12
Motif name:	csGCCCCGCCCCsc
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	14
Similarity score:	0.0539097

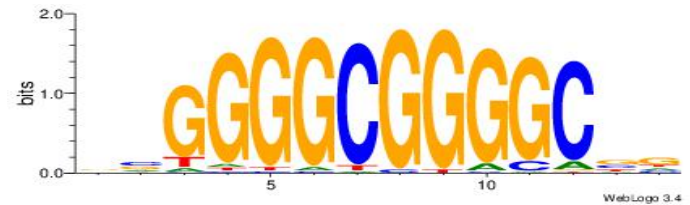
Alignment:

BBGGGGCGGGGCVD
SGGTCACGTGACCS

Original motif Consensus sequence: HVGCCCCGCCCB



Reverse complement motif Consensus sequence: BBGGGGCGGGGC

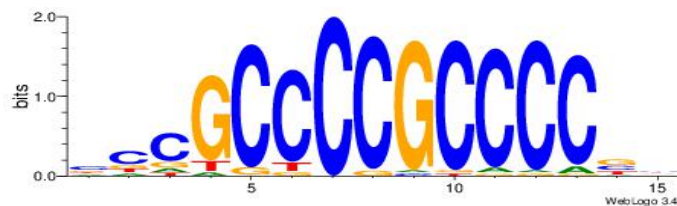


Dataset #: 2
 Motif ID: 14
 Motif name: cccGCCCCGCCCCsb
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0.0581955

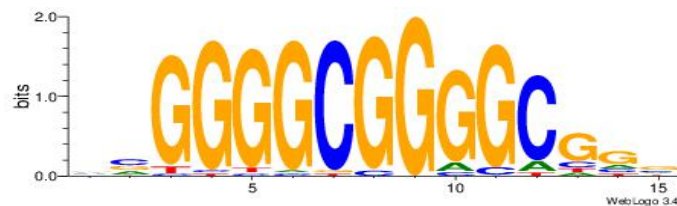
Alignment:

BCCGCCCCGCCCCBB
 SGGTCACGTGACCS-

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB



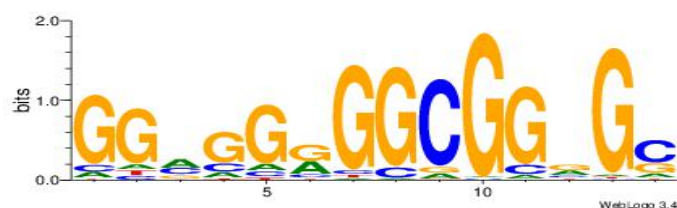
Dataset #: 1
 Motif ID: 5
 Motif name: TFF11
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward

Position number: 3
Number of overlap: 12
Similarity score: 1.05855

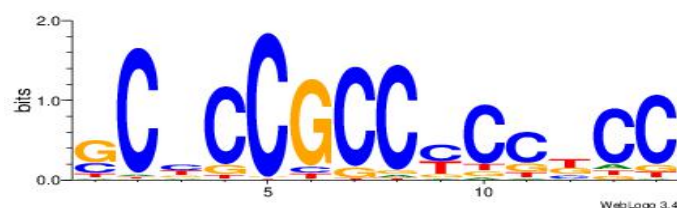
Alignment:

--GCVCCGCCMCCYCC
SGGTCACGTGACCS--

Original motif Consensus sequence: GGMGRRGGCGGVGC



Reverse complement motif Consensus sequence: GCVCCGCCMCCYCC



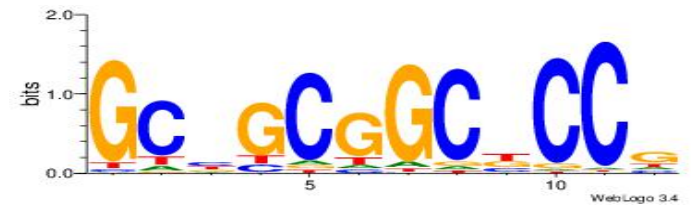
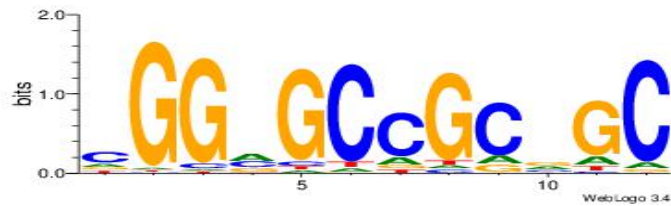
Dataset #: 1
Motif ID: 4
Motif name: TFF1
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 12
Similarity score: 1.06047

Alignment:

--CGGVGCCGCVGC
SGGTCACGTGACCS

Original motif Consensus sequence: CGGVGCCGCVGC

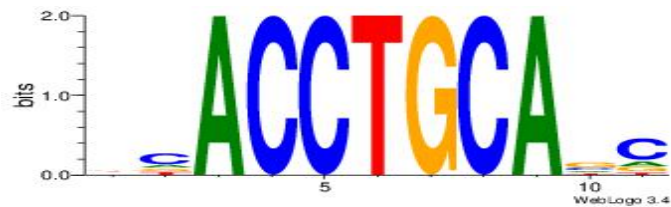
Reverse complement motif Consensus sequence: GCVCCGCCMCCYCC



Dataset #: 2
 Motif ID: 16
 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: 1.54742

Alignment:
 ---BCACCTGCABC
 SGGTCACGTGACCS

Original motif Consensus sequence: BCACCTGCABC



Reverse complement motif Consensus sequence: GBTGCAGGTGB



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

Original motif Consensus sequence: HVTACWG TABD



Reverse complement motif Consensus sequence: DBTACWG TAVH



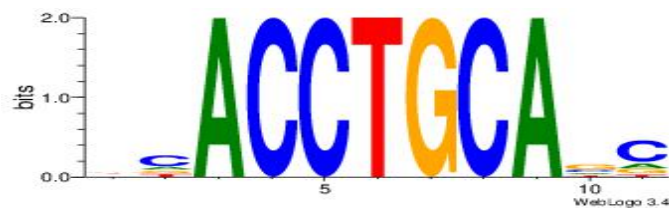
Best Matches for Motif ID 19 (Highest to Lowest)

Dataset #: 2
Motif ID: 16
Motif name: kcACCTGCAGc
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: 0.0199592

Alignment:

GBTGCAGGTGB
HVTACWG TABD

Original motif Consensus sequence: BCACCTGCABC



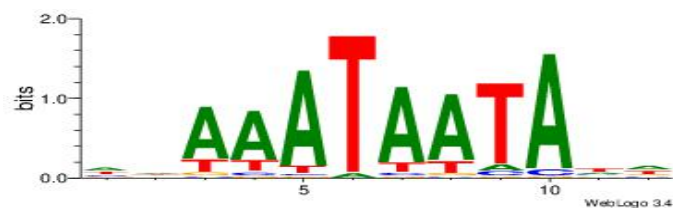
Reverse complement motif Consensus sequence: GBTGCAGGTGB



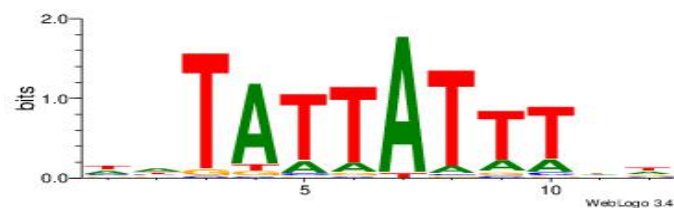
Dataset #: 2
 Motif ID: 17
 Motif name: wwAAATAATAtw
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.0309343

Alignment:
 DDTATTATTTDH
 -HVTACWGTABD

Original motif Consensus sequence: HDAAATAATADD



Reverse complement motif Consensus sequence: DDTATTATTTDH



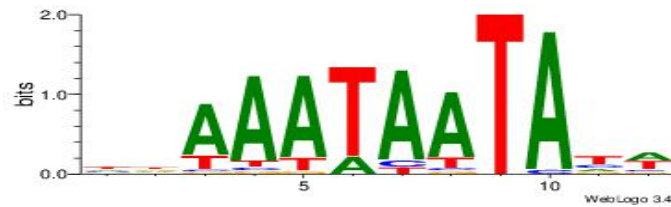
Dataset #: 2
 Motif ID: 13
 Motif name: tkAAATAATAtw
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 11

Similarity score: 0.0337121

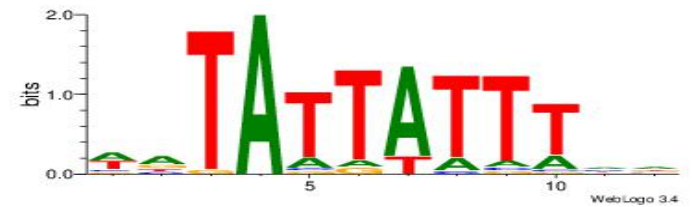
Alignment:

HDAAATAATAHW
DBTACWGTAVH-

Original motif Consensus sequence: HDAAATAATAHW



Reverse complement motif Consensus sequence: WHTATTATTTDH



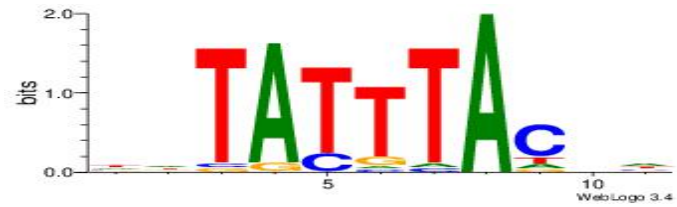
Dataset #: 2
Motif ID: 21
Motif name: wbgTAAATAww
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 11
Similarity score: 0.037518

Alignment:

DBGTAAATAHD
DBTACWGTAVH

Original motif Consensus sequence: DBGTAAATAHD

Reverse complement motif Consensus sequence: DHTATTTACBD

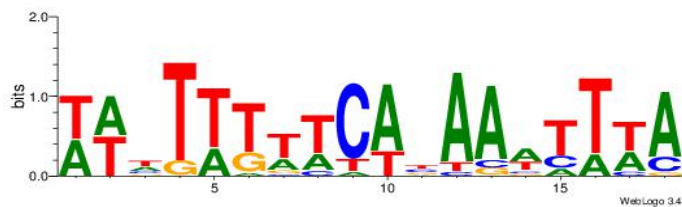


Dataset #: 1
 Motif ID: 8
 Motif name: TFM3
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 5
 Number of overlap: 11
 Similarity score: 0.0413797

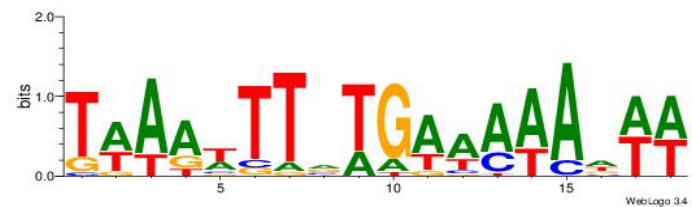
Alignment:

WWHTTTTTTCABAAWTTWA
 ---DBTACWGTAVH----

Original motif Consensus sequence: WWHTTTTTTCABAAWTTWA

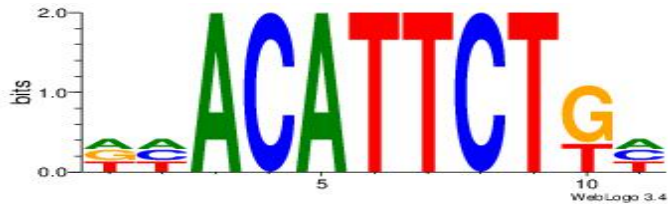


Reverse complement motif Consensus sequence: TAAWTTVTGAAAAHWW



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

Original motif Consensus sequence: DHACATTCTGH



Reverse complement motif Consensus sequence: HCAGAATGTHD



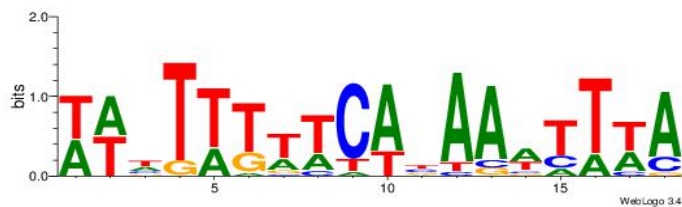
Best Matches for Motif ID 20 (Highest to Lowest)

Dataset #: 1
 Motif ID: 8
 Motif name: TFM3
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 8
 Number of overlap: 11
 Similarity score: 0.00522383

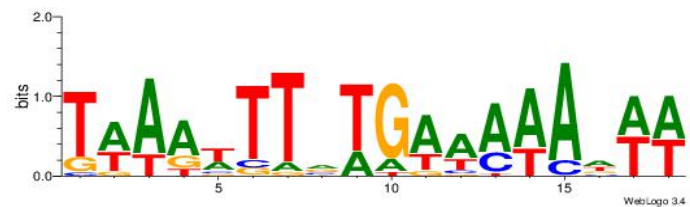
Alignment:

WWHTTTTTTCABAAWTTWA
 HCAGAATGTHD-----

Original motif Consensus sequence: WWHTTTTTTCABAAWTTWA



Reverse complement motif Consensus sequence: TAAWTTVTGAAAAHWW



Dataset #: 2
 Motif ID: 16
 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: 0.00731643

Alignment:

BCACCTGCABC
 DHACATTCTGH

Original motif Consensus sequence: BCACCTGCABC



Reverse complement motif Consensus sequence: GBTGCAGGTGB



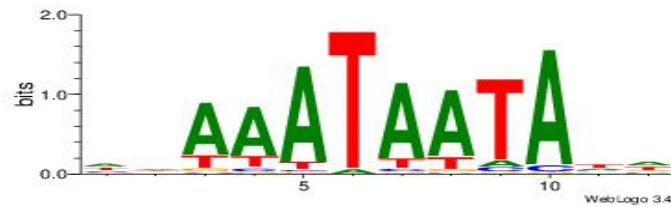
Dataset #: 2
 Motif ID: 17
 Motif name: wwAAATAATAtw
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 11

Similarity score: 0.0127231

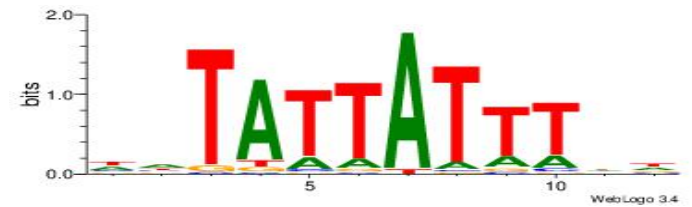
Alignment:

DDTATTATTTDH
-HCAGAATGTHD

Original motif Consensus sequence: HDAAATAATADD



Reverse complement motif Consensus sequence: DDTATTATTTDH



Dataset #: 1
Motif ID: 11
Motif name: TFM11
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: 0.014258

Alignment:

HDWVAAAHAAAAAMAAAMWWWHBWA
-----HCAGAATGTHD-----

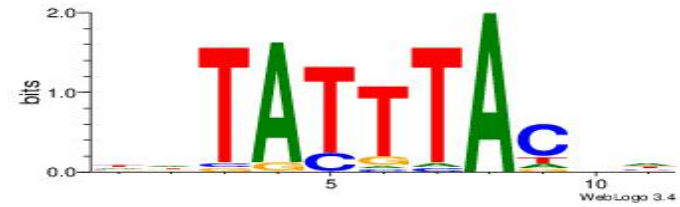
Original motif Consensus sequence:
HDWVAAAHAAAAAMAAAMWWWHBWA

Reverse complement motif Consensus sequence:
TWVHWWWYTTTTYTTTTTHTTTVWBH

Original motif Consensus sequence: DBGTAATAHD



Reverse complement motif Consensus sequence: DHTATTTACBD



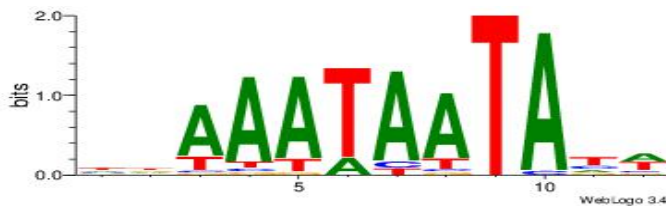
Best Matches for Motif ID 21 (Highest to Lowest)

Dataset #:	2
Motif ID:	13
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

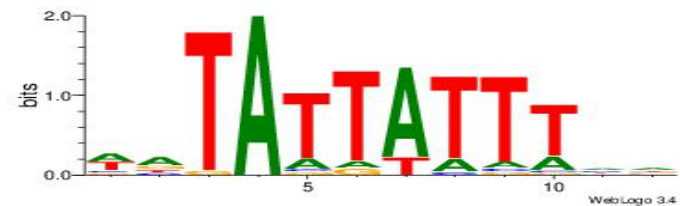
Alignment:

HDAAATAATAHW
-DBGTAATAHD

Original motif Consensus sequence: HDAAATAATAHW



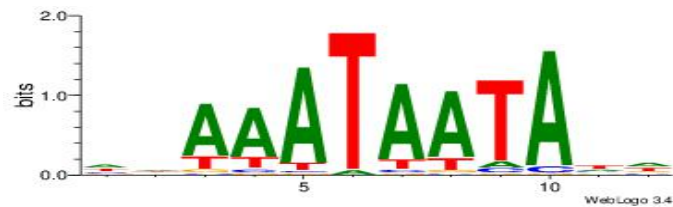
Reverse complement motif Consensus sequence: WHTATTATTTDH



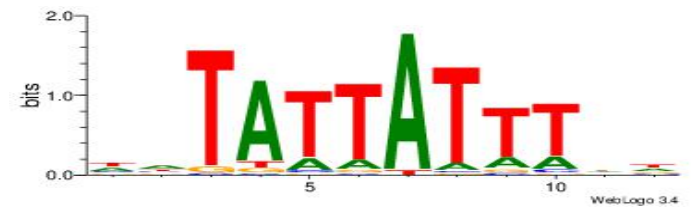
Dataset #: 2
 Motif ID: 17
 Motif name: wwAAATAATAtw
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 11
 Similarity score: 0.0164863

Alignment:
 DDTATTATTTDH
 DHTATTTACBD-

Original motif Consensus sequence: HDAAATAATADD



Reverse complement motif Consensus sequence: DDTATTATTTDH



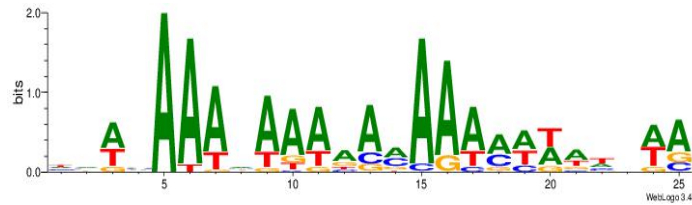
Dataset #: 1
 Motif ID: 11
 Motif name: TFM11
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 15
 Number of overlap: 11

Similarity score: 0.0192768

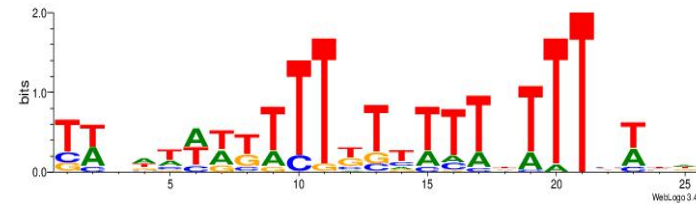
Alignment:

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

Original motif Consensus sequence:
HDWVAAAHAAAAAMAAAMWWWHBWA



Reverse complement motif Consensus sequence:
TWVHWWYTTTYTTTTHTTTVWBH



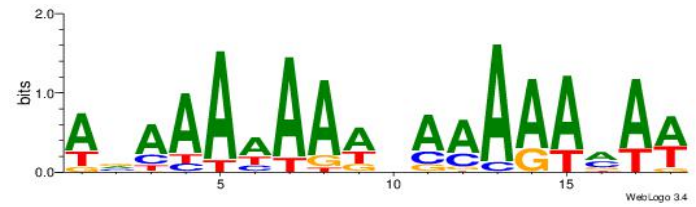
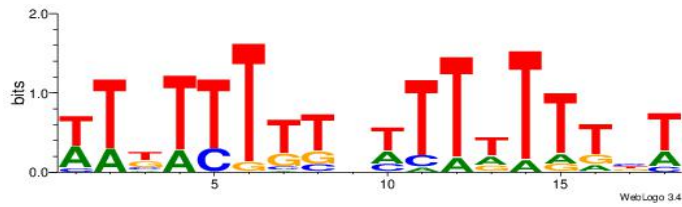
Dataset #: 1
Motif ID: 7
Motif name: TFM1
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 11
Similarity score: 0.0283217

Alignment:

```
WTKTTTTTHWTTTTTTBT  
DHTATTTACBD-----
```

Original motif Consensus sequence: WTKTTTTTHWTTTTTTBT

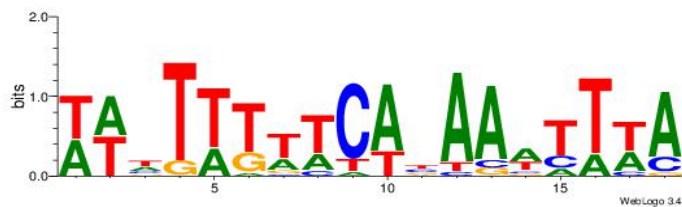
Reverse complement motif Consensus sequence:
ABAAAAAWHAAAAARAW



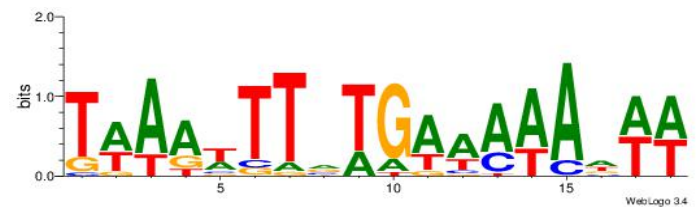
Dataset #: 1
 Motif ID: 8
 Motif name: TFM3
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 11
 Similarity score: 0.0308097

Alignment:
 WWHTTTTTCABAAWTTWA
 -----DHTATTTACBD-

Original motif Consensus sequence: WWHTTTTTCABAAWTTWA



Reverse complement motif Consensus sequence: TAAWTTVTGAAAAHWW



Results created by MOTIFSIM on 06-18-2018 21:47:01
Runtime: 633.592 seconds

MOTIFSIM is written by Ngoc Tam L. Tran
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