



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
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Original motif Consensus sequence: GTCGCG



Reverse complement motif Consensus sequence: CGCGAC



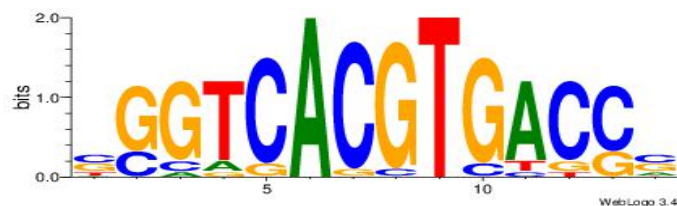
Best Matches for Top Significant Motif ID 1 (Highest to Lowest)

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

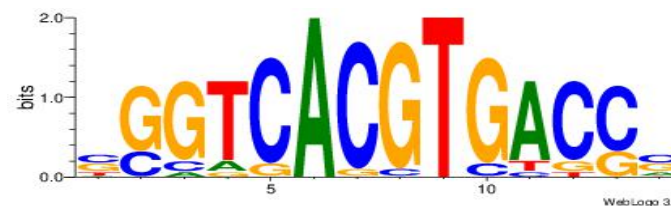
Alignment:

```
SGGTCACGTGACCS  
--GTCGCG-----
```

Original motif Consensus sequence: SGGTCACGTGACCS



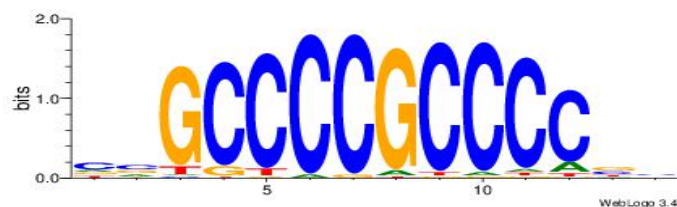
Reverse complement motif Consensus sequence: SGGTCACGTGACCS



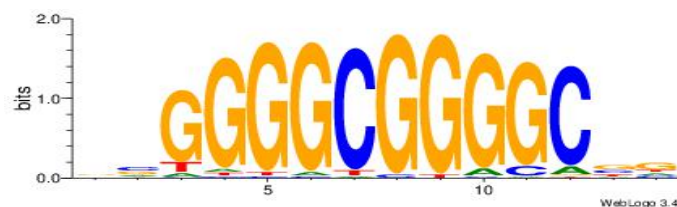
Dataset #: 2
 Motif ID: 12
 Motif name: csGCCCCGCCCCsc
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 7
 Number of overlap: 6
 Similarity score: 0.0539

Alignment:
 HVGCCCCGCCCCBB
 --GTCGCG-----

Original motif Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGC



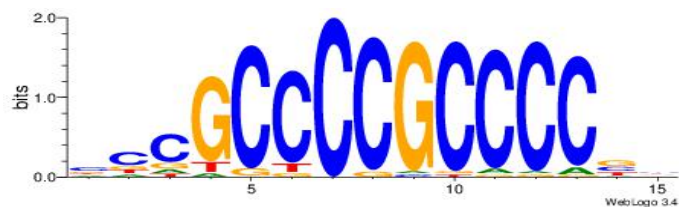
Dataset #: 2
 Motif ID: 14
 Motif name: cccGCCCCGCCCCsb
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 6

Similarity score: 0.0558733

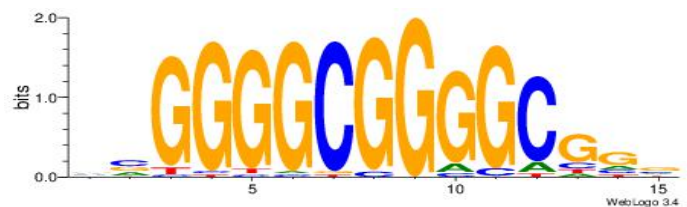
Alignment:

BCCGCCCCGCCCCBB
-----CGCGAC--

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB



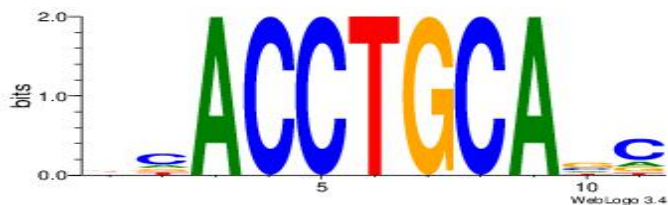
Dataset #: 2
Motif ID: 16
Motif name: kcACCTGCAGc
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 6
Number of overlap: 6
Similarity score: 0.0980422

Alignment:

BCACCTGCABC
-----CGCGAC

Original motif Consensus sequence: BCACCTGCABC

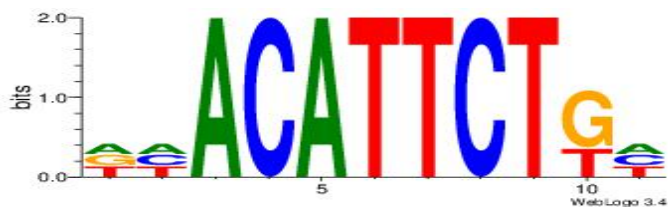
Reverse complement motif Consensus sequence: GBTGCAGGTGB



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



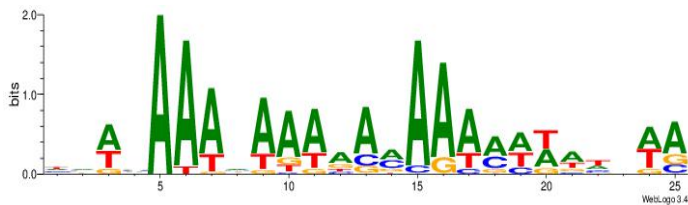
Best Matches for Top Significant Motif ID 21 (Highest to Lowest)

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

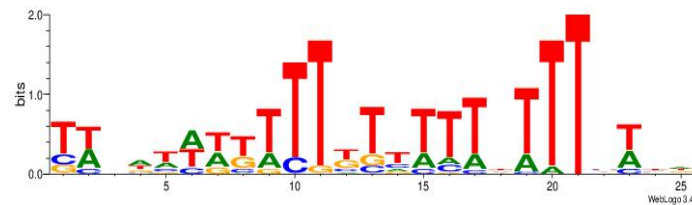
Alignment:

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

Original motif Consensus sequence:
HDWVAAAHAAAAAMAAAMWWWHBWA



Reverse complement motif Consensus sequence:
TWVHWWWYTTTYTTTTHTTTVWBH

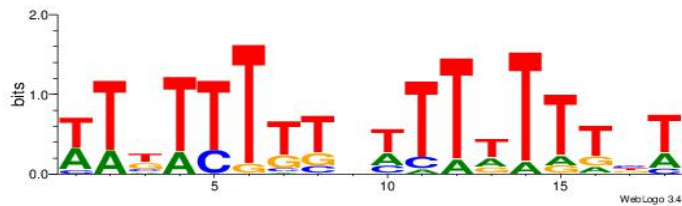


Dataset #: 1
 Motif ID: 7
 Motif name: TFM1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.0283217

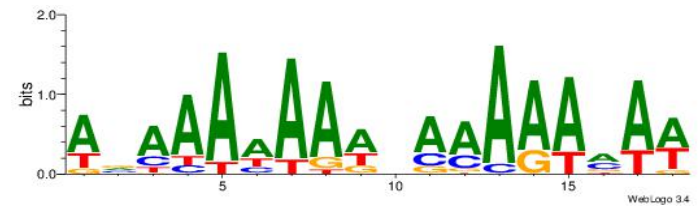
Alignment:

WKTTTTTHWTTTTTBT
 DHTATTTACBD-----

Original motif Consensus sequence: WKTTTTTHWTTTTTBT



Reverse complement motif Consensus sequence: ABAAAAAWHAAAAARAW



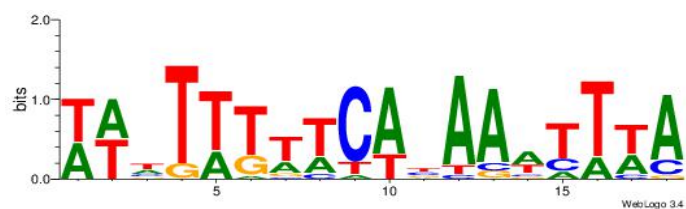
Dataset #: 1
 Motif ID: 8
 Motif name: TFM3
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2

Number of overlap: 11
Similarity score: 0.0308097

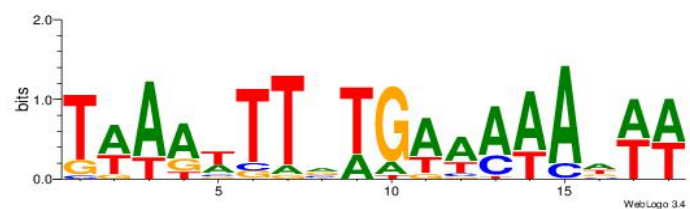
Alignment:

WWHTTTTTTCABAAWTTWA
-----DHTATTTACBD-

Original motif Consensus sequence: WWHTTTTTTCABAAWTTWA



Reverse complement motif Consensus sequence: TWAAWTTVTGAAAAHWW

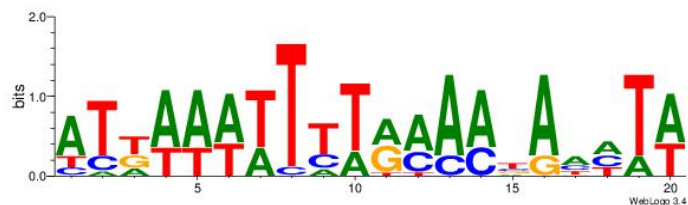


Dataset #: 1
Motif ID: 10
Motif name: TFM13
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 3
Number of overlap: 11
Similarity score: 0.0333874

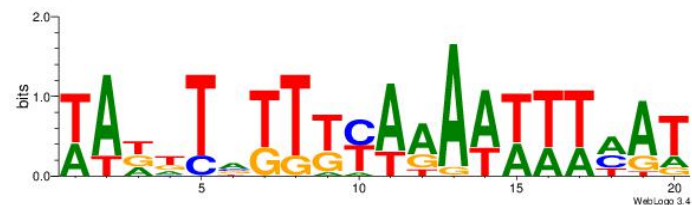
Alignment:

ATKAAWTTTTTRMAABAHHTW
-----DBGTAAATAHD--

Original motif Consensus sequence: ATKAAWTTTTRMAABAHTW



Reverse complement motif Consensus sequence: WAHHTVTTYKAAAATTRAT

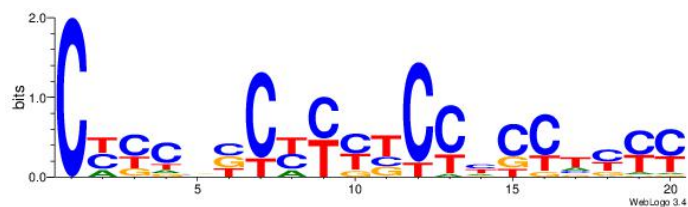


Dataset #: 1
Motif ID: 9
Motif name: TFM12
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 14
Number of overlap: 7
Similarity score: 2.0544

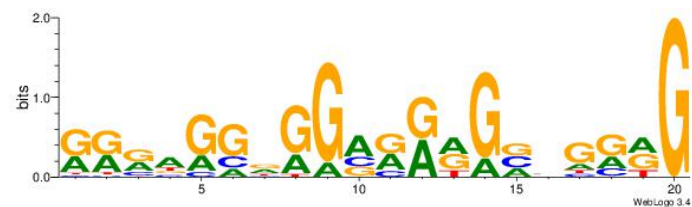
Alignment:

----KKKAGGDGGAKKMGBBGKMG
DHTATTTACBD-----

Original motif Consensus sequence: CYYCBCYYYTCCHCCTYYY



Reverse complement motif Consensus sequence: KKKAGGDGGAKKMGBBGKMG

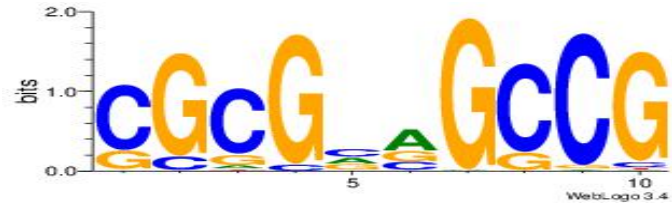


Dataset #: 1 Motif ID: 3 Motif name: TFW3

Original motif Consensus sequence: CGGCYBCGCG



Reverse complement motif Consensus sequence: CGCGBMGCCG

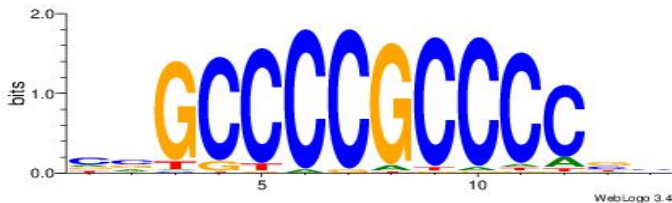


Best Matches for Top Significant Motif ID 3 (Highest to Lowest)

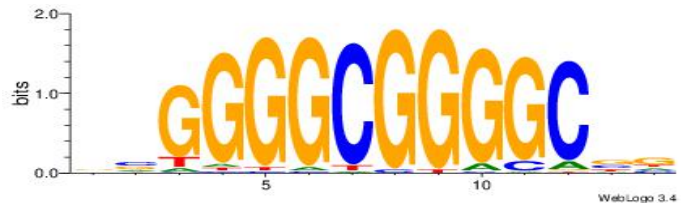
Dataset #: 2
 Motif ID: 12
 Motif name: csGCCCCGCCCCsc
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 5
 Number of overlap: 10
 Similarity score: 0.0718771

Alignment:
 HVGCCCCGCCCCBB
 CGGCYBCGCG-----

Original motif Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGC

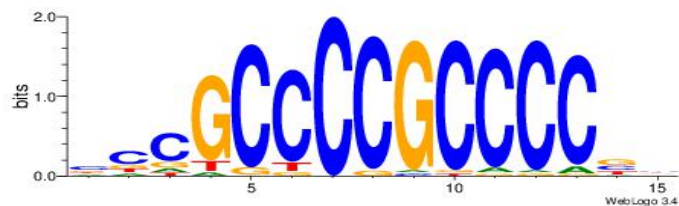


Dataset #: 2
 Motif ID: 14
 Motif name: cccGCCCCGCCCCsb
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 5
 Number of overlap: 10
 Similarity score: 0.0719604

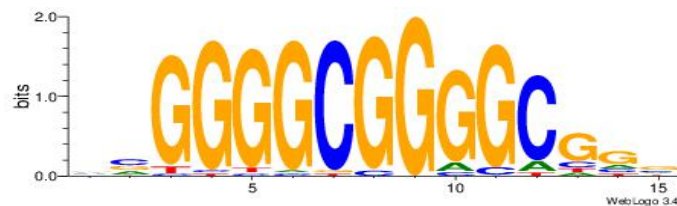
Alignment:

BCCGCCCCGCCCCBB
 -CGGCYBCGCG-----

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB

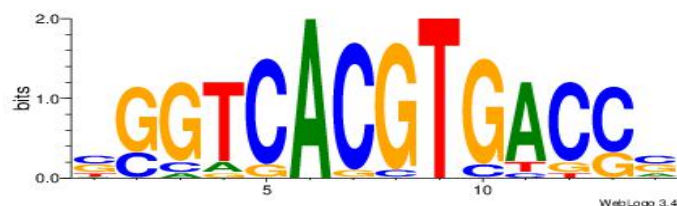


Dataset #: 2
 Motif ID: 18
 Motif name: sSGTCACGTGACSS
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward

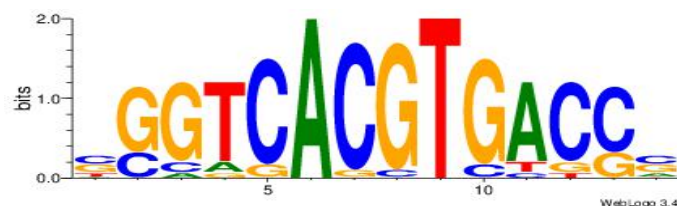
Position number: 5
 Number of overlap: 10
 Similarity score: 0.0895189

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

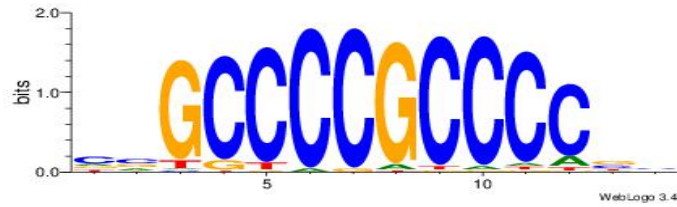


Reverse complement motif Consensus sequence: MBATTGGCTGH

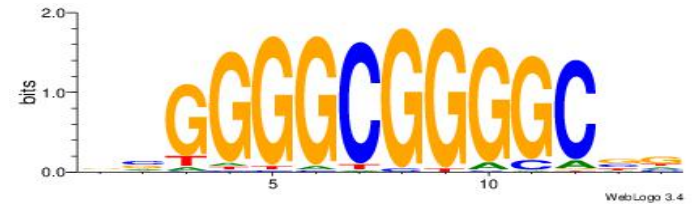


Dataset #: 2 Motif ID: 12 Motif name: csGCCCCGCCCCsc

Original motif Consensus sequence: HVGCCCCGCCCB



Reverse complement motif Consensus sequence: BBGGGGCGGGGC



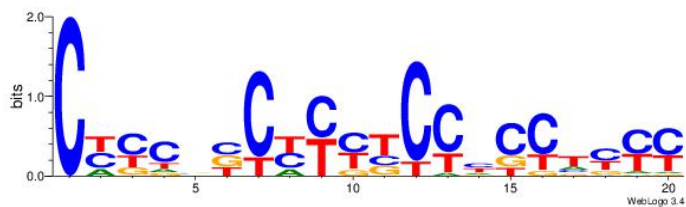
Best Matches for Top Significant Motif ID 12 (Highest to Lowest)

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

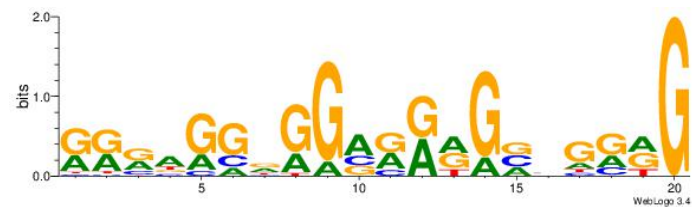
Alignment:

```
CYVCBBCYYYTCCHCCTYYY
---HVGCCCCGCCCB---
```

Original motif Consensus sequence: CYVCBBCYYYTCCHCCTYYY



Reverse complement motif Consensus sequence: KKKAGGDGGAKKMGBBGKMG

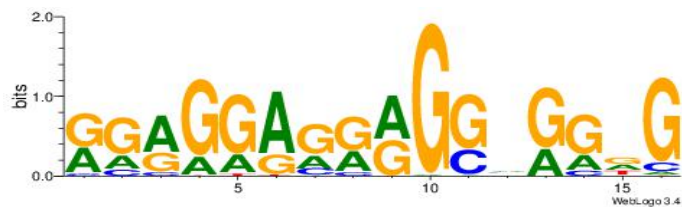


Dataset #: 1
 Motif ID: 6
 Motif name: TFM2
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 14
 Similarity score: 0.0880609

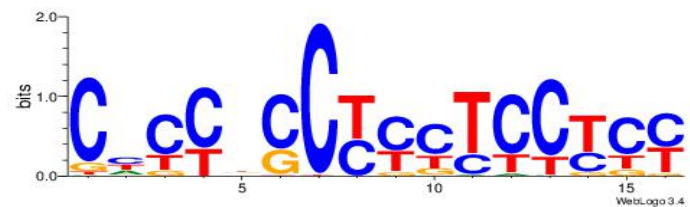
Alignment:

CHCCBCKMCTCCKCM
 HVGCCCGCCCCBB--

Original motif Consensus sequence: RGRGGAGRRGGHGGDG



Reverse complement motif Consensus sequence: CHCCBCKMCTCCKCM

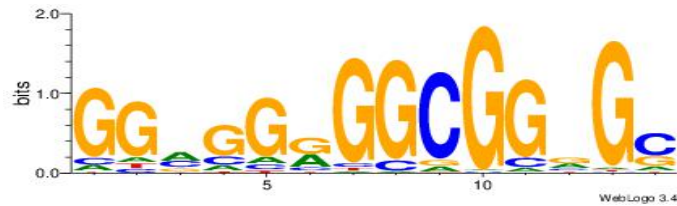


Dataset #: 1
 Motif ID: 5
 Motif name: TFF11
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1

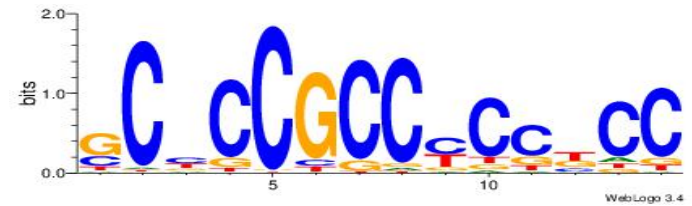
Number of overlap: 14
 Similarity score: 0.0937271

Alignment:
 GGMGGRGGCGGVGC
 BBGGGGCGGGGCVD

Original motif Consensus sequence: GGMGGRGGCGGVGC



Reverse complement motif Consensus sequence: GCVCCGCCMCCYC

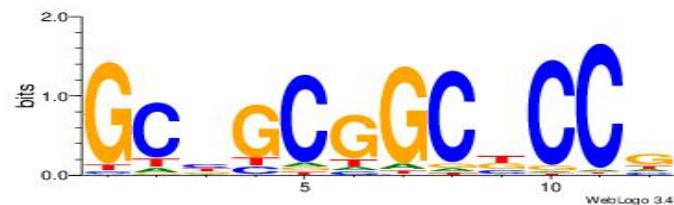
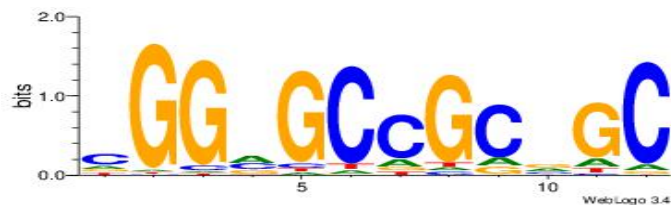


Dataset #: 1
 Motif ID: 4
 Motif name: TFF1
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 12
 Similarity score: 1.08016

Alignment:
 CGGVGCCGCVGC--
 HVGCCCGCCCB

Original motif Consensus sequence: CGGVGCCGCVGC

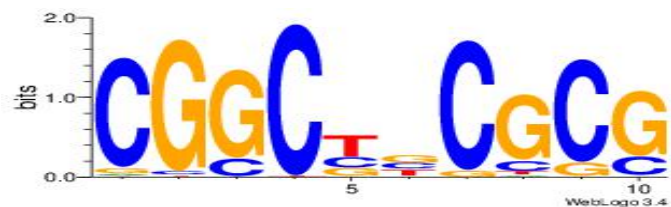
Reverse complement motif Consensus sequence: GCVCCGCCMCCYC



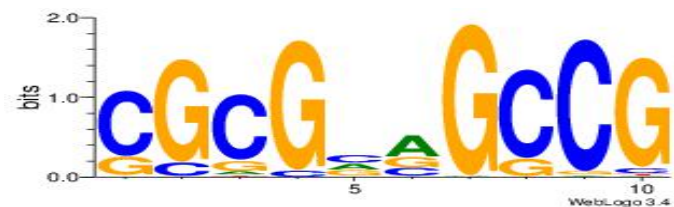
Dataset #: 1
 Motif ID: 3
 Motif name: TFW3
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 10
 Similarity score: 2.07757

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



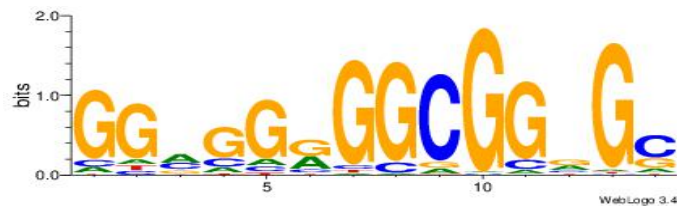
Best Matches for Top Significant Motif ID 16 (Highest to Lowest)

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

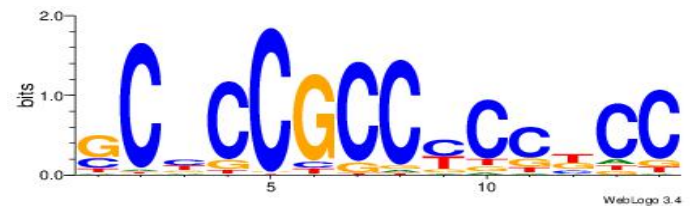
Alignment:

```
GGMGGRGGCGGVGC  
GBTGCAGGTGB---
```

Original motif Consensus sequence: GGMGGRGGCGGVGC



Reverse complement motif Consensus sequence: GCVCCGCCMCCYC

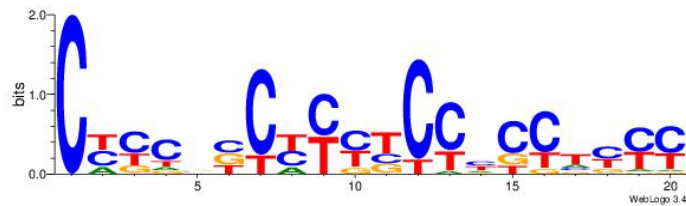


Dataset #: 1
 Motif ID: 9
 Motif name: TFM12
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 6
 Number of overlap: 11
 Similarity score: 0.0444938

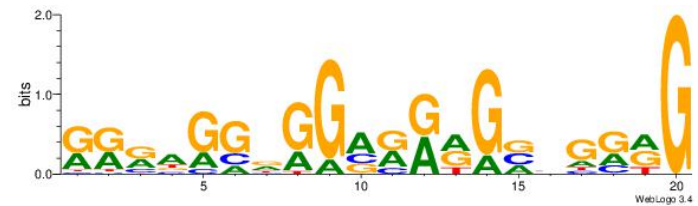
Alignment:

KKKAGGDGGAKKMGBBGKMG
 ----GBTGCAGGTGB-----

Original motif Consensus sequence: CYCBBYYYTCCHCCTYYY



Reverse complement motif Consensus sequence: KKKAGGDGGAKKMGBBGKMG

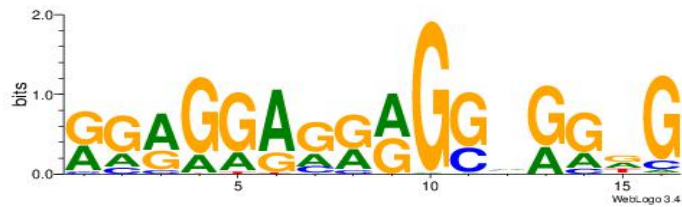


Dataset #: 1
 Motif ID: 6
 Motif name: TFM2
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 7

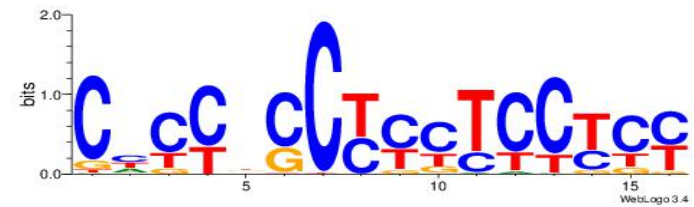
Number of overlap: 10
Similarity score: 0.538471

Alignment:
-RGRGGAGRRGGHGGDG
GBTGCAGGTGB-----

Original motif Consensus sequence: RGRGGAGRRGGHGGDG



Reverse complement motif Consensus sequence:
CHCCBCKMCTCKCM

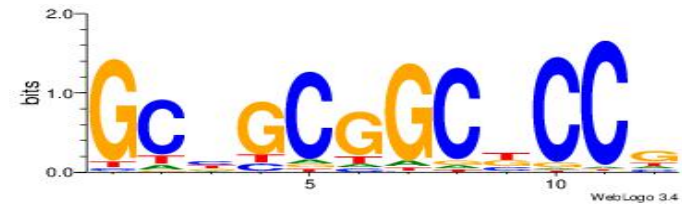
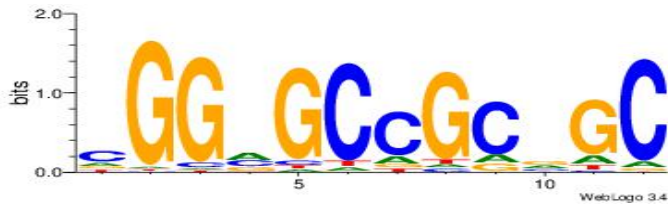


Dataset #: 1
Motif ID: 4
Motif name: TFF1
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 5
Number of overlap: 8
Similarity score: 1.54364

Alignment:
GCVGCGGCBCCG---
----BCACCTGCABC

Original motif Consensus sequence: CGVGCCGCVGC

Reverse complement motif Consensus sequence: GCVGCGGCBCCG

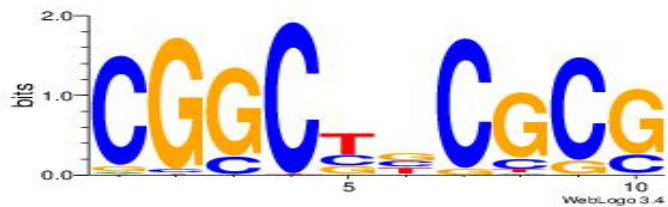


Dataset #: 1
 Motif ID: 3
 Motif name: TFW3
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 8
 Similarity score: 1.5466

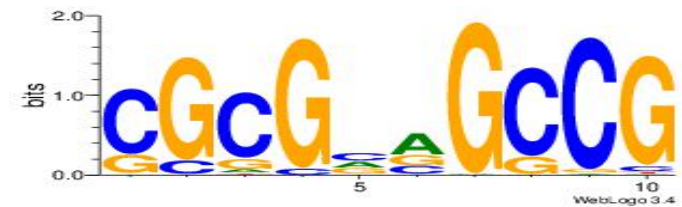
Alignment:

---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: HVTACWG TABD



Reverse complement motif Consensus sequence: DBTACWG TAVH



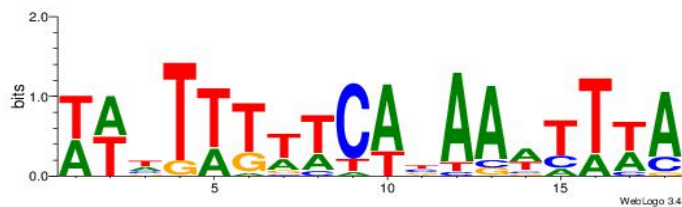
Best Matches for Top Significant Motif ID 19 (Highest to Lowest)

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

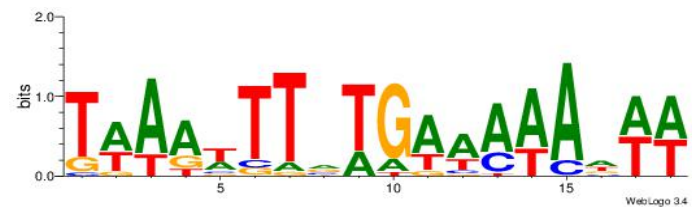
Alignment:

WWHTTTTTTCABAAWTTWA
 ---DBTACWG TAVH----

Original motif Consensus sequence: WWHTTTTTTCABAAWTTWA



Reverse complement motif Consensus sequence: TAAWTTVTGAAAAHWW

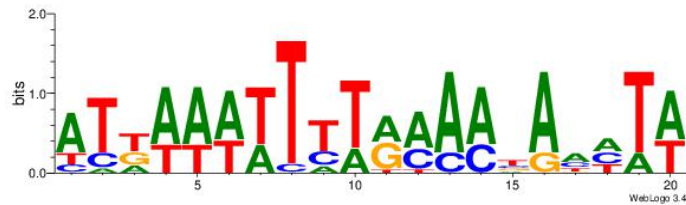


Dataset #: 1
 Motif ID: 10
 Motif name: TFM13
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 11
 Similarity score: 0.0445707

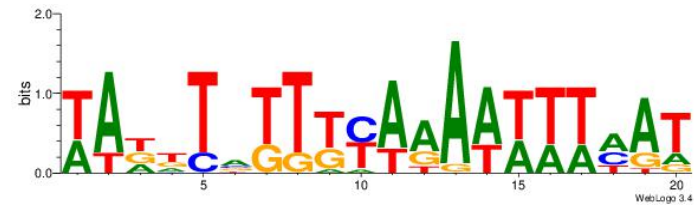
Alignment:

WAHHTVTTYKAAAATTRAT
 -----HVTACWG TABD--

Original motif Consensus sequence: ATKAAWTTTTRMAABAHTW



Reverse complement motif Consensus sequence: WAHHTVTTYKAAAATTRAT



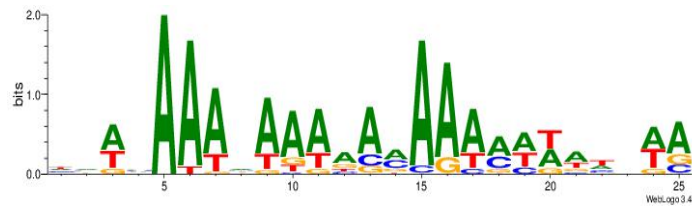
Dataset #: 1
 Motif ID: 11
 Motif name: TFM11
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4

Number of overlap: 11
Similarity score: 0.0472742

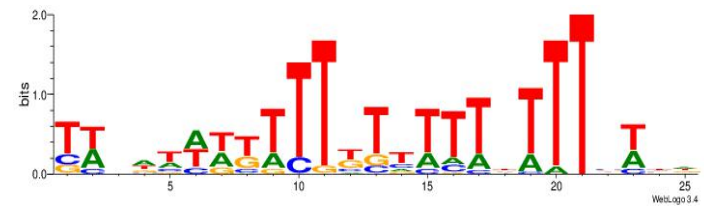
Alignment:

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

Original motif Consensus sequence:
HDWVAAAHA AAAA MAAA MWWW HBWA



Reverse complement motif Consensus sequence:
TWVHWWWYTTTTTTTTTHTTTVWBH

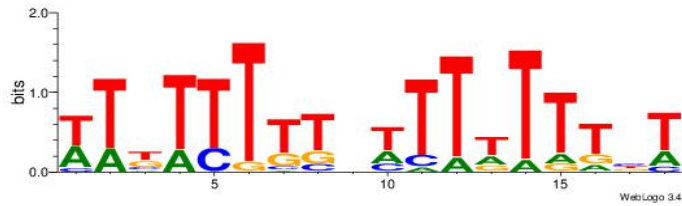


Dataset #: 1
Motif ID: 7
Motif name: TFM1
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 10
Number of overlap: 9
Similarity score: 1.04742

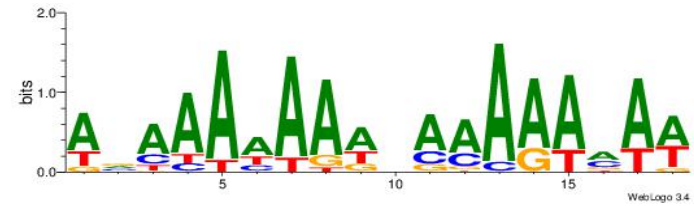
Alignment:

WKTTTTTTHWTTTTTTBT--
-----DBTACWGTAVH

Original motif Consensus sequence: WTKTTTTTHWTTTTTTBT



Reverse complement motif Consensus sequence: ABAAAAAWHAAAAARAW

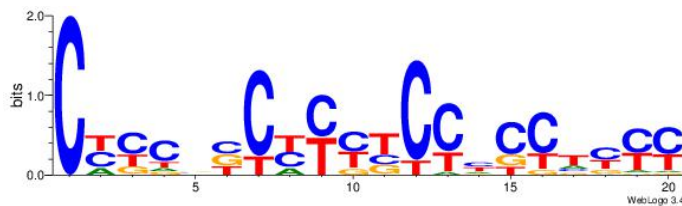


Dataset #: 1
Motif ID: 9
Motif name: TFM12
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 15
Number of overlap: 6
Similarity score: 2.54736

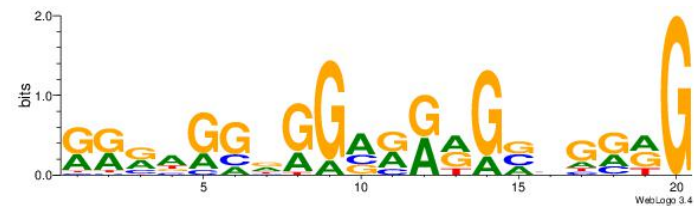
Alignment:

```
-----CYYCBBCYYYTCCHCCTYYY  
DBTACWGTAHV-----
```

Original motif Consensus sequence: CYYCBBCYYYTCCHCCTYYY

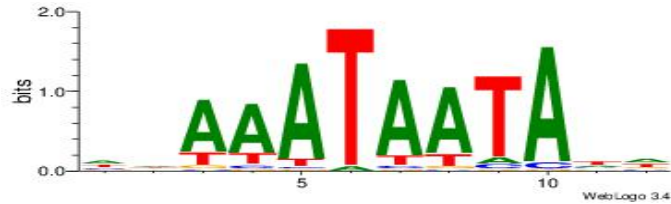


Reverse complement motif Consensus sequence: KKKAGGDGGAKKMGBBGKMG

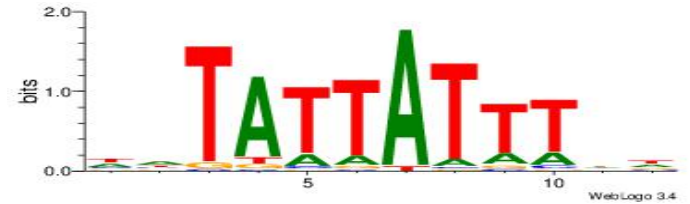


Dataset #: 2 Motif ID: 17 Motif name: wwAAATAATAtw

Original motif Consensus sequence: HDAAATAATADD



Reverse complement motif Consensus sequence: DDTATTATTTDH



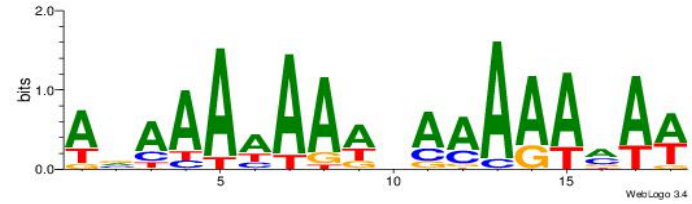
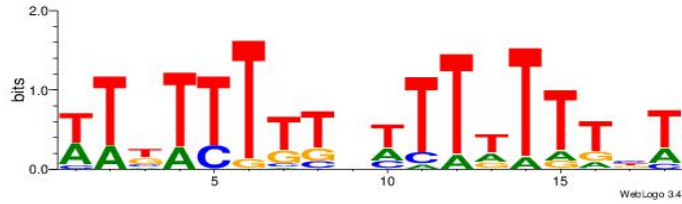
Best Matches for Top Significant Motif ID 17 (Highest to Lowest)

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:
 ABAAAAAWhAAAAARAW
 -----HDAAATAATADD

Original motif Consensus sequence: WTKTTTTTHWTTTTTTBT

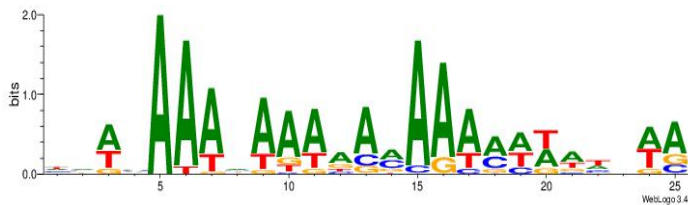
Reverse complement motif Consensus sequence:
 ABAAAAAWhAAAAARAW



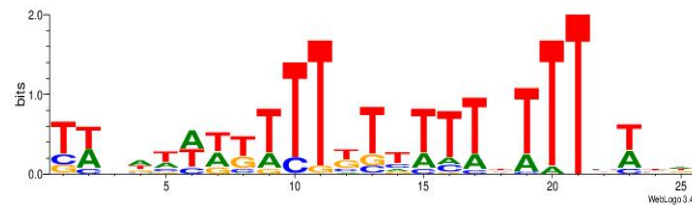
Dataset #: 1
 Motif ID: 11
 Motif name: TFM11
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 12
 Similarity score: 0.0575935

Alignment:
 HDWVAAAHA AAAAAMAAAMWWWHBWA
 --HDAATAATADD-----

Original motif Consensus sequence:
 HDWVAAAHA AAAAAMAAAMWWWHBWA



Reverse complement motif Consensus sequence:
 TWVHWWWYTTTTTTTTTHTTTVWBH



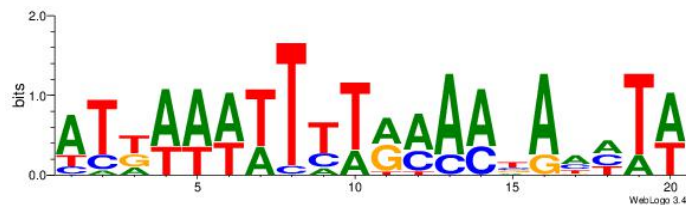
Dataset #: 1

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

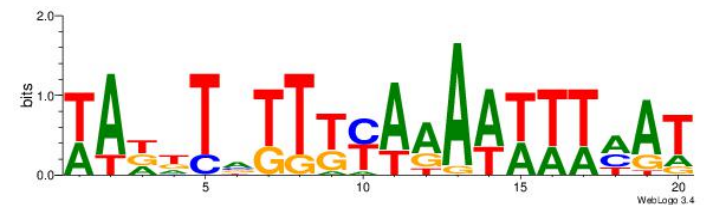
Alignment:

ATKAAWTTTTTRMAABAHTW
 -----DDTATTATTTDH

Original motif Consensus sequence: ATKAAWTTTTTRMAABAHTW



Reverse complement motif Consensus sequence: WAHHTVTTYKAAAATTRAT



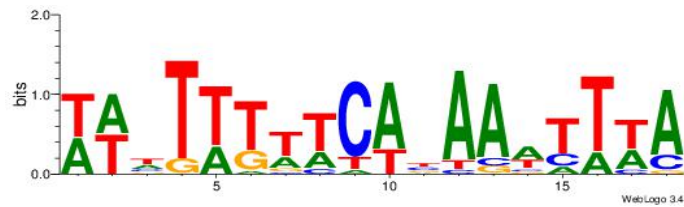
Dataset #: 1
 Motif ID: 8
 Motif name: TFM3
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 12

Similarity score: 0.0733516

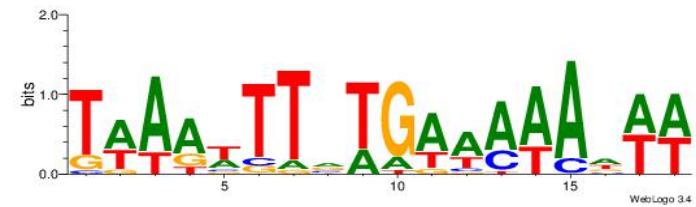
Alignment:

TWAAWTTVTGAAAAHWW
-----HDAAATAATADD

Original motif Consensus sequence: WWHTTTTTTCABAAWTTWA



Reverse complement motif Consensus sequence:
TAAWTTTVTGAAAAHWW



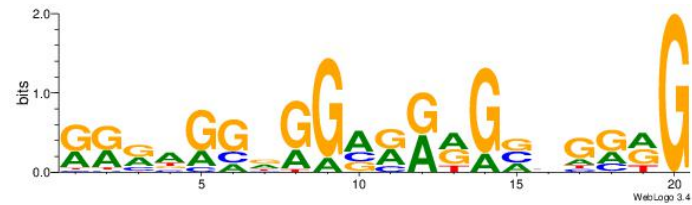
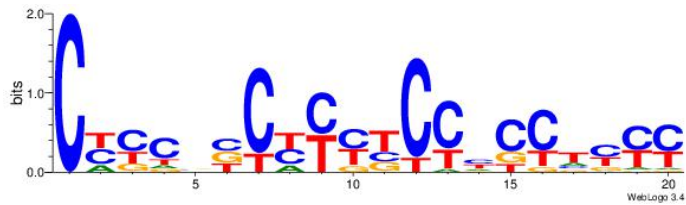
Dataset #: 1
Motif ID: 9
Motif name: TFM12
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 16
Number of overlap: 5
Similarity score: 3.59569

Alignment:

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

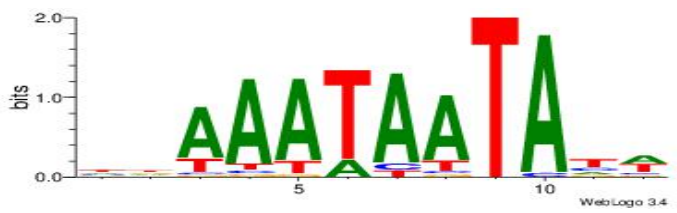
Original motif Consensus sequence: CYYCBCYYYTCCHCCTYYY

Reverse complement motif Consensus sequence:
KKKAGGDGGAKKMGBBGKMG

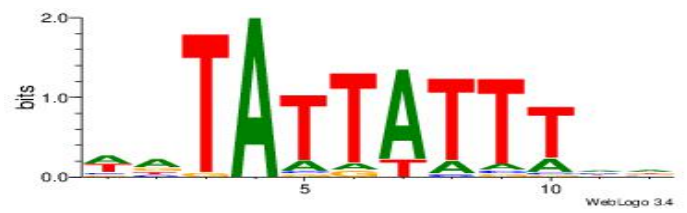


Dataset #: 2 Motif ID: 13 Motif name: tkAAATAATAtw

Original motif Consensus sequence: HDAAATAATAHW



Reverse complement motif Consensus sequence: WHTATTATTTDH

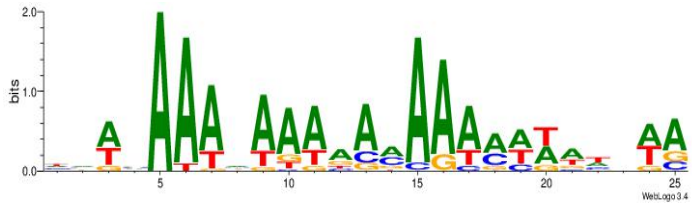


Best Matches for Top Significant Motif ID 13 (Highest to Lowest)

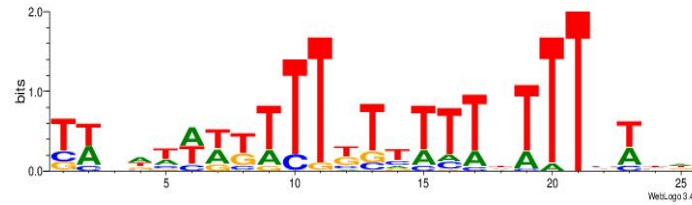
Dataset #:	1
Motif ID:	11
Motif name:	TFM11
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	3
Number of overlap:	12
Similarity score:	0.0590505

Alignment:
 TWVHWWWYTTTYTTTTTHTTTVWBH
 -----WHTATTATTTDH--

Original motif Consensus sequence:
 HDWVAAAHAAAAAMAAAMWWWHBWA



Reverse complement motif Consensus sequence:
 TWVHWWWYTTTTTTTTTHTTTVWBH

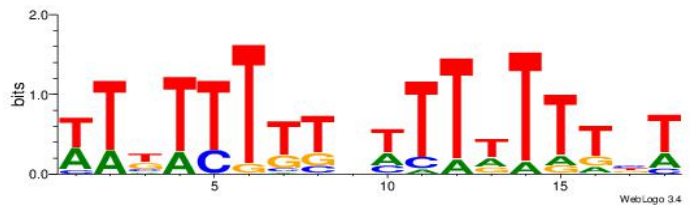


Dataset #: 1
 Motif ID: 7
 Motif name: TFM1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 12
 Similarity score: 0.0637702

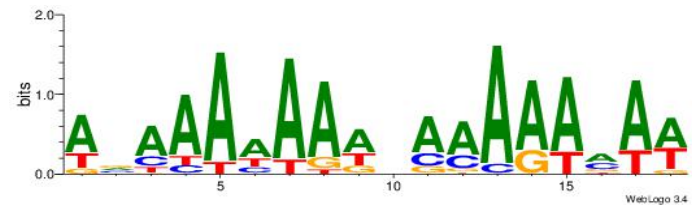
Alignment:

WTKTTTTTHWTTTTTTBT
 WHTATTATTTDH-----

Original motif Consensus sequence: WTKTTTTTHWTTTTTTBT



Reverse complement motif Consensus sequence:
 ABAAAAAWHAAAAARAW

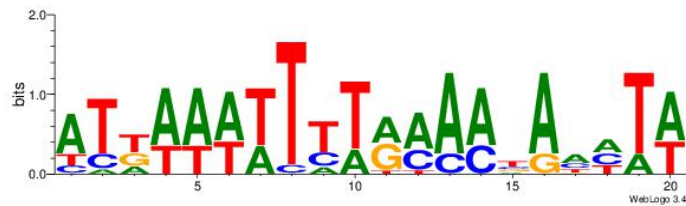


Dataset #: 1
 Motif ID: 10
 Motif name: TFM13
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 9
 Number of overlap: 12
 Similarity score: 0.0704475

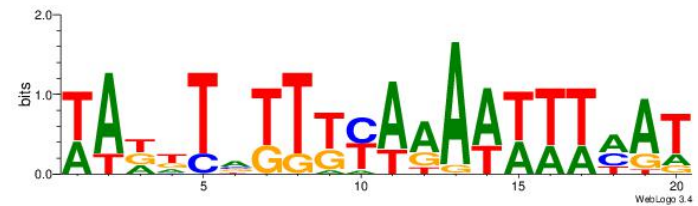
Alignment:

ATKAAWTTTTRMAABAHTW
 -----WHTATTATTTDH

Original motif Consensus sequence: ATKAAWTTTTRMAABAHTW



Reverse complement motif Consensus sequence: WAHHTVTTYKAAAATTRAT



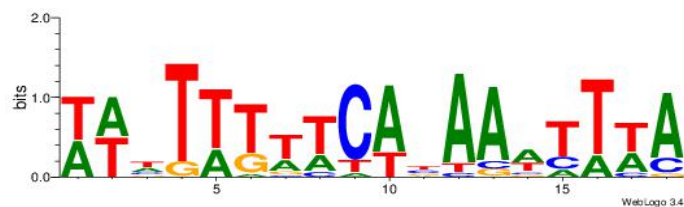
Dataset #: 1
 Motif ID: 8
 Motif name: TFM3
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1

Number of overlap: 12
 Similarity score: 0.0763819

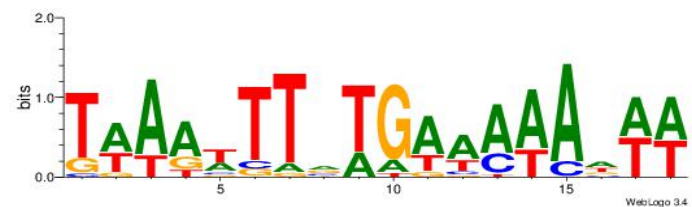
Alignment:

TWAAWTTVTGAAAAAHWW
 -----HDAAATAATAHW

Original motif Consensus sequence: WWHTTTTTTCABAAWTTWA



Reverse complement motif Consensus sequence: TWAAWTTVTGAAAAAHWW

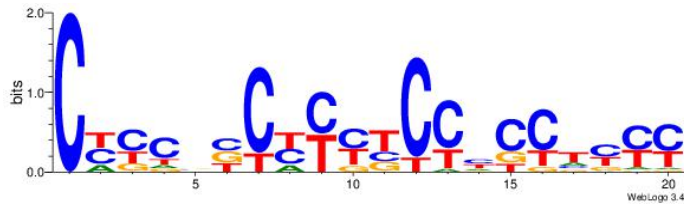


Dataset #: 1
 Motif ID: 9
 Motif name: TFM12
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 16
 Number of overlap: 5
 Similarity score: 3.59273

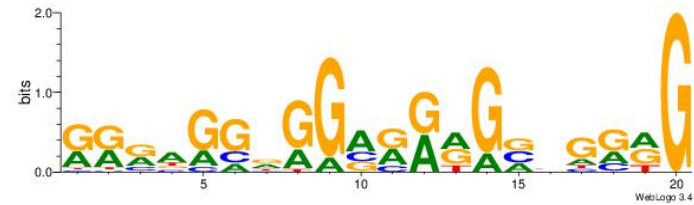
Alignment:

-----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



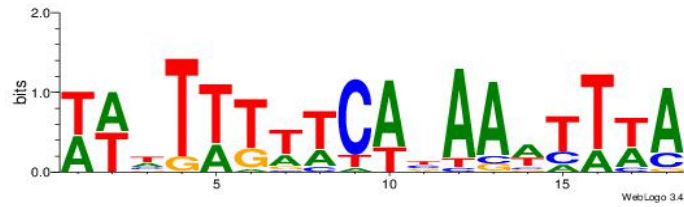
Best Matches for Top Significant Motif ID 20 (Highest to Lowest)

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

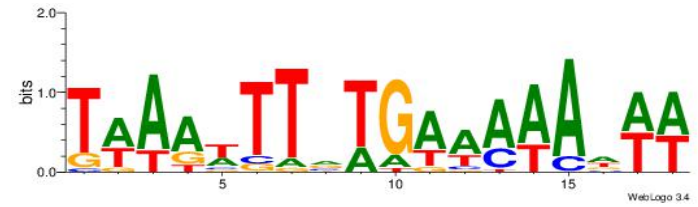
Alignment:

WWHTTTTTTCABAAWTTWA
 HCAGAATGTHD-----

Original motif Consensus sequence: WWHTTTTTTCABAAWTTWA



Reverse complement motif Consensus sequence:
 TWAAWTTVTGAAAAHWW



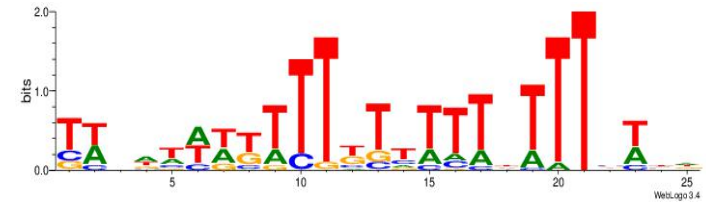
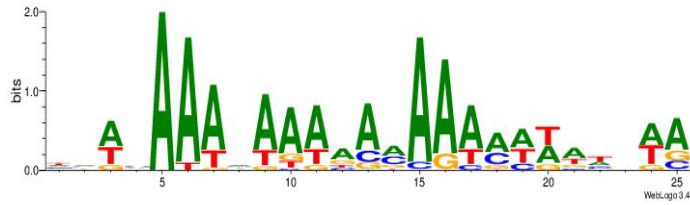
Dataset #: 1
 Motif ID: 11
 Motif name: TFM11
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 11
 Number of overlap: 11
 Similarity score: 0.014258

Alignment:

HDWVAAAHAAAAAMAAAMWWWHBWA
 ----HCAGAATGTHD-----

Original motif Consensus sequence:
 HDWVAAAHAAAAAMAAAMWWWHBWA

Reverse complement motif Consensus sequence:
 TWVHWWWYTTTTTTTTTTTTHVWBH

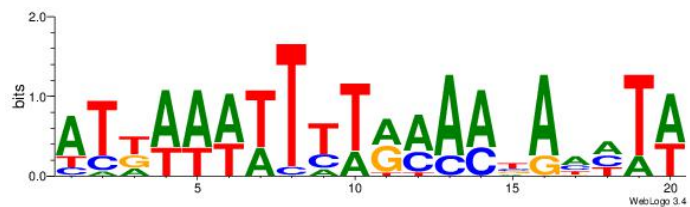


Dataset #: 1
 Motif ID: 10
 Motif name: TFM13
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 9
 Number of overlap: 11
 Similarity score: 0.0192045

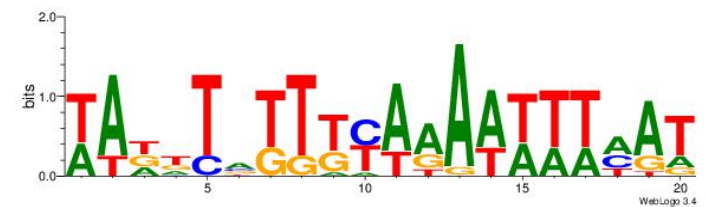
Alignment:

ATKAAWTTTTRMAABAHTW
 -DHACATTCTGH-----

Original motif Consensus sequence: ATKAAWTTTTRMAABAHTW



Reverse complement motif Consensus sequence: WAHHTVTTYKAAAATTRAT



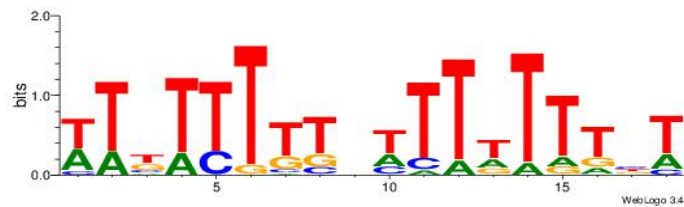
Dataset #: 1

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

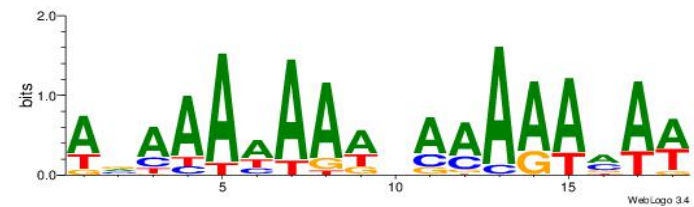
Alignment:

ABAAAAA WHAAAAARAW-
 -----HCAGAATGTHD

Original motif Consensus sequence: WTKTTTTTHWTTTTTTBT



Reverse complement motif Consensus sequence: ABAAAAA WHAAAAARAW



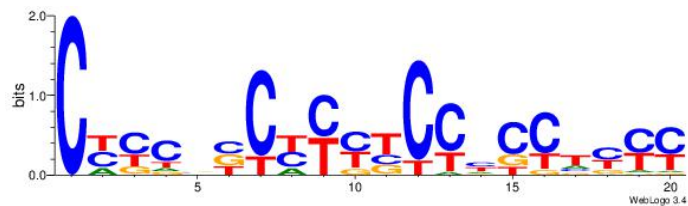
Dataset #: 1
 Motif ID: 9
 Motif name: TFM12
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 17
 Number of overlap: 4

Similarity score: 3.5

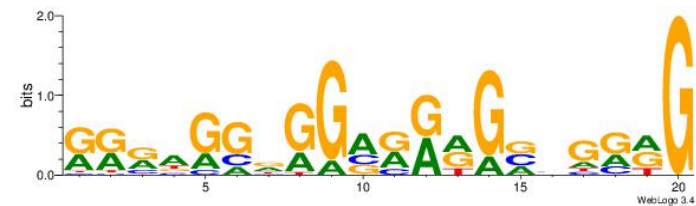
Alignment:

-----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



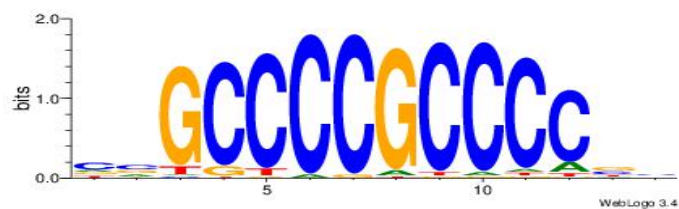
Best Matches for Top Significant Motif ID 2 (Highest to Lowest)

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

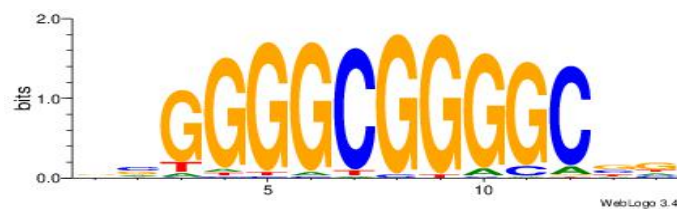
Direction: Forward
 Position number: 2
 Number of overlap: 8
 Similarity score: 0.0456233

Alignment:
 BBGGGGCGGGGCVD
 -SCGCGCGG-----

Original motif Consensus sequence: HVGCCCCGCCCCBB



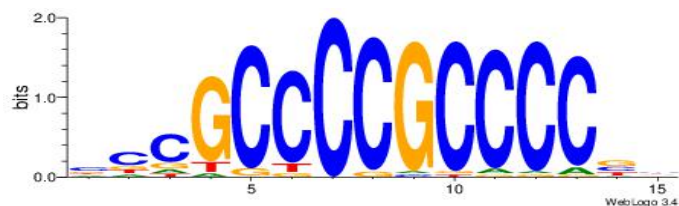
Reverse complement motif Consensus sequence: BBGGGGCGGGGC



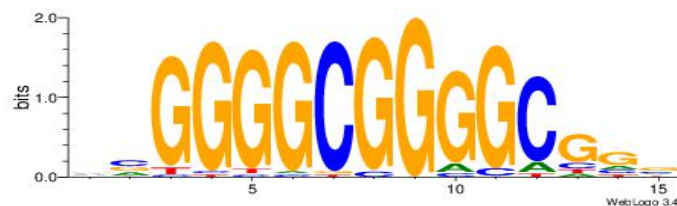
Dataset #: 2
 Motif ID: 14
 Motif name: cccGCCCCGCCCCsb
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 7
 Number of overlap: 8
 Similarity score: 0.045686

Alignment:
 BCCGCCCCGCCCCBB
 -----CCGCGCGS-

Original motif Consensus sequence: BCCGCCCCGCCCCBB



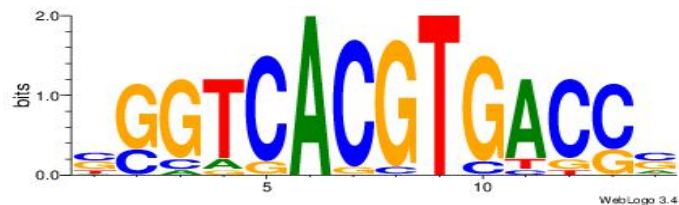
Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB



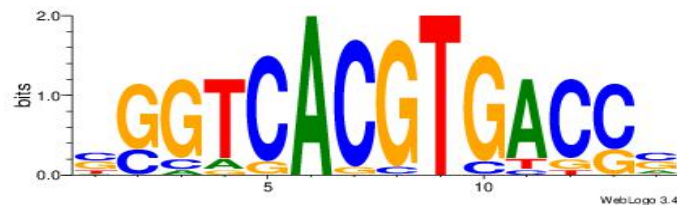
Dataset #: 2
Motif ID: 18
Motif name: sSGTCACGTGACCS
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 4
Number of overlap: 8
Similarity score: 0.0988223

Alignment:
SGGTCACGTGACCS
---SCGCGCGG---

Original motif Consensus sequence: SGGTCACGTGACCS



Reverse complement motif Consensus sequence: SGGTCACGTGACCS

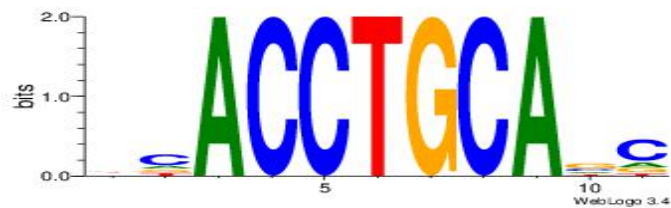


Dataset #: 2
 Motif ID: 16
 Motif name: kcACCTGCAGc
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 8
 Number of overlap: 4
 Similarity score: 2.08456

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



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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