MOTIFSIM - MOTIF SIMilarity Detection Tool

Version 2.0

INPUT

Input Parameters

Number of files:	5
Number of top significant motifs:	10
Number of best matches:	10
Similarity cutoff >=	0.75
Output file type:	All
Output file format:	All

Input files and motif counts

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

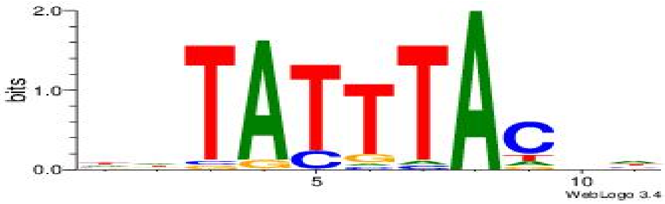
RESULTS

Top 10 Significant Motifs - Global Matching (Highest to Lowest)

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

Original motif   Consensus sequence: DBGTAAATAHD

Reverse complement motif   Consensus sequence: DHTATTTACBD



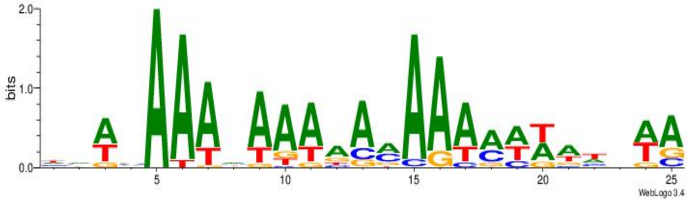
Best Matches for Top Significant Motif ID 45 (Highest to Lowest)

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

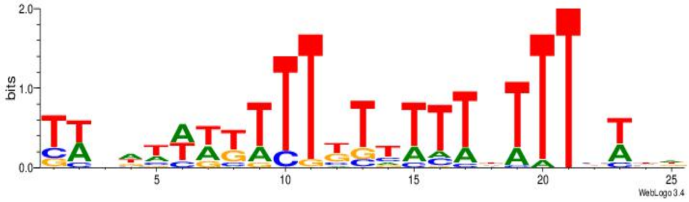
Alignment:

```
TWVHWWWYTTTYTTTTTHTTTVWBH
--------------DHTATTTACBD
```

Original motif   Consensus sequence:
HDWVAAAHAAAAAMAAAMWWWHBWA



Reverse complement motif   Consensus sequence:
TWVHWWWYTTTYTTTTTHTTTVWBH

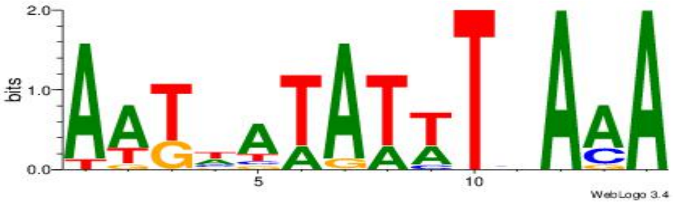


Dataset #:	2
Motif ID:	9
Motif name:	Motif 9
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	4
Number of overlap:	11
Similarity score:	0.0250541

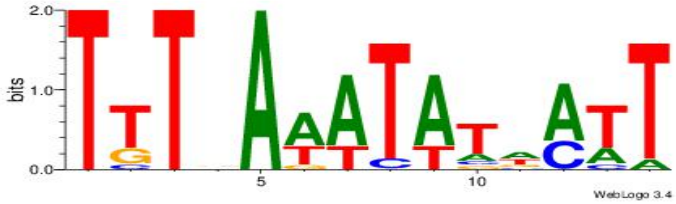
Alignment:

```
AATHATATWTHAAA
DHTATTTACBD---
```

Original motif Consensus sequence: AATHATATWTHAAA



Reverse complement motif Consensus sequence: TTTDAWATATHAT



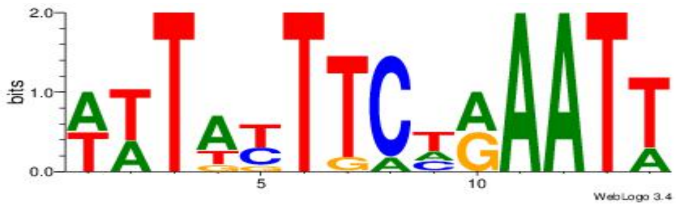
Dataset #:	2
Motif ID:	6
Motif name:	Motif 6
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1

Number of overlap: 11
Similarity score: 0.027895

Alignment:
```
AATTYDGAARTAWW
---DBGTAAATAHD
```

Original motif Consensus sequence: AATTYDGAARTAWW

Reverse complement motif Consensus sequence: WWTAKTTCDKAAT

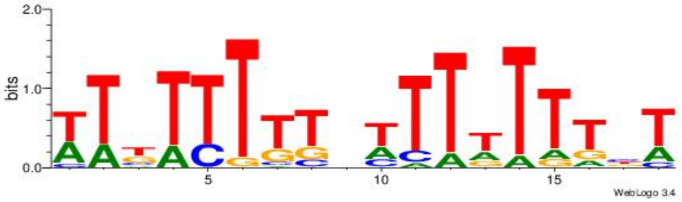


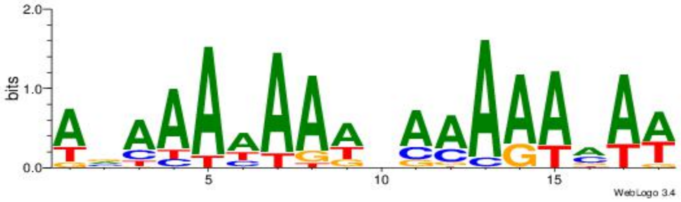
Dataset #: 5
Motif ID: 52
Motif name: TFM1
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 11
Similarity score: 0.0283217

Alignment:
```
ABAAAAAAWHAAAAARAW
DBGTAAATAHD-------
```

Original motif Consensus sequence: WTKTTTTTHWTTTTTTBT

Reverse complement motif Consensus sequence: ABAAAAAAWHAAAAARAW



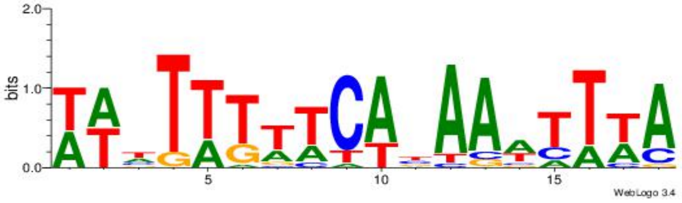


Dataset #:	5
Motif ID:	53
Motif name:	TFM3
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	2
Number of overlap:	11
Similarity score:	0.0308097

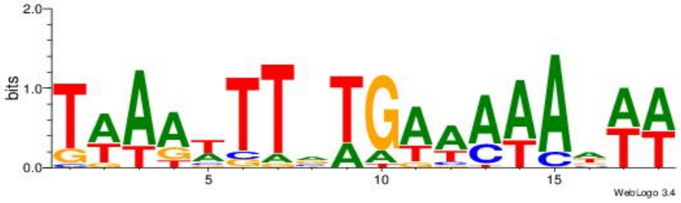
Alignment:

```
TWAAWTTVTGAAAAAHWW
------DBGTAAATAHD-
```

Original motif   Consensus sequence: WWHTTTTTCABAAWTTWA



Reverse complement motif   Consensus sequence: TWAAWTTVTGAAAAAHWW



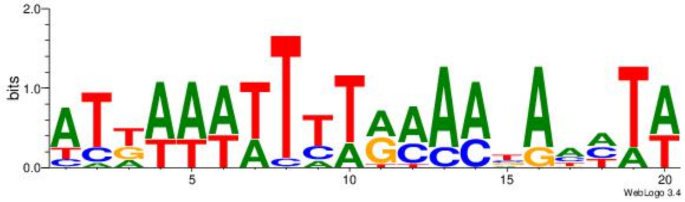
Dataset #:	5

Motif ID: 55
Motif name: TFM13
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 8
Number of overlap: 11
Similarity score: 0.0333874

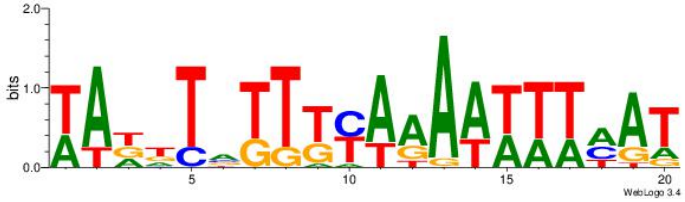
Alignment:

```
ATKAAWTTTTRMAABAHHTW
-------DBGTAAATAHD--
```

Original motif Consensus sequence: ATKAAWTTTTRMAABAHHTW



Reverse complement motif Consensus sequence: WAHHTVTTYKAAAAWTTRAT



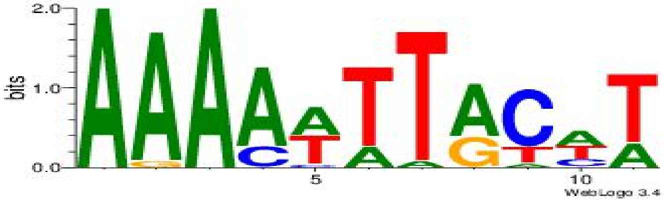
Dataset #: 2
Motif ID: 4
Motif name: Motif 4
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 11

Similarity score: 0.0361187

Alignment:

```
AWGKAAWTTTT
DBGTAAATAHD
```

Original motif Consensus sequence: AAAAWTTRCWT



Reverse complement motif Consensus sequence: AWGKAAWTTTT

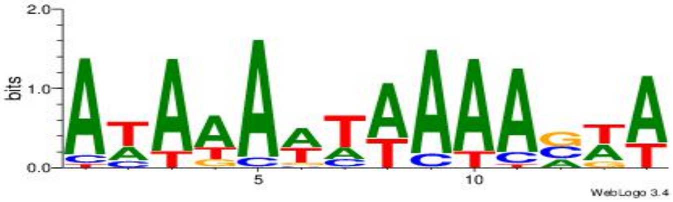
Dataset #:	2
Motif ID:	3
Motif name:	Motif 3
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2
Number of overlap:	11
Similarity score:	0.0410381

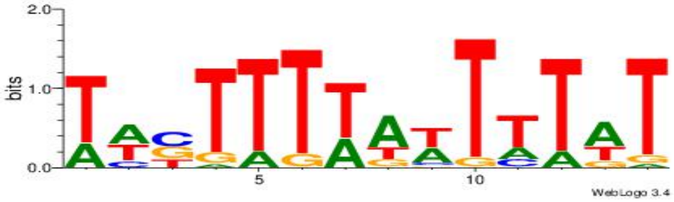
Alignment:

```
AWAAAWTWAAASWA
--DHTATTTACBD-
```

Original motif Consensus sequence: AWAAAWTWAAASWA

Reverse complement motif Consensus sequence: TWSTTTWAWTTTW



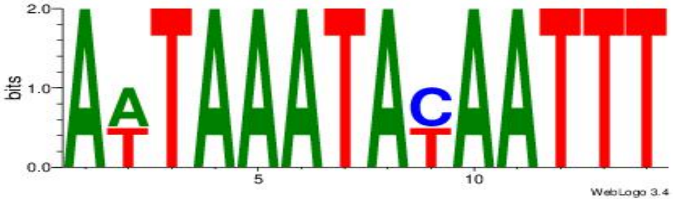


Dataset #:	2
Motif ID:	5
Motif name:	Motif 5
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	11
Similarity score:	0.0477814

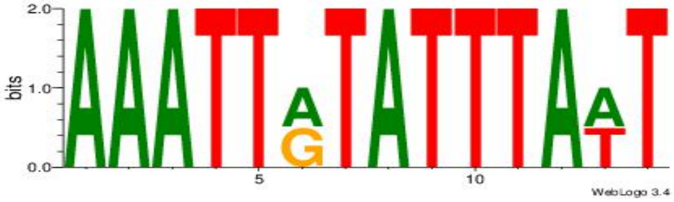
Alignment:

```
AWTAAATAYAATTT
---DHTATTTACBD
```

Original motif Consensus sequence: AWTAAATAYAATTT



Reverse complement motif Consensus sequence: AAATTKTATTTAW



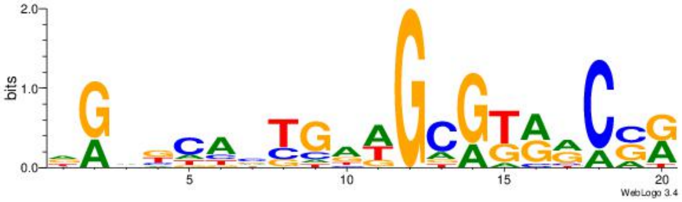
Dataset #:	3
Motif ID:	31

Motif name:	Pax5
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	10
Number of overlap:	11
Similarity score:	0.0512987

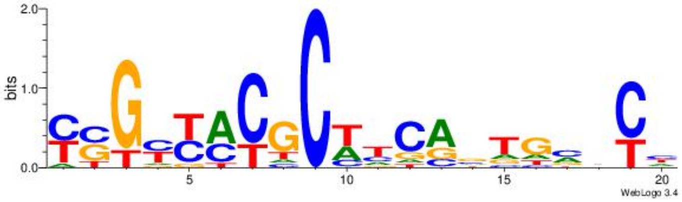
Alignment:

```
DGVBCABTGDWGCGKRRCSR
DBGTAAATAHD---------
```

Original motif Consensus sequence: DGVBCABTGDWGCGKRRCSR

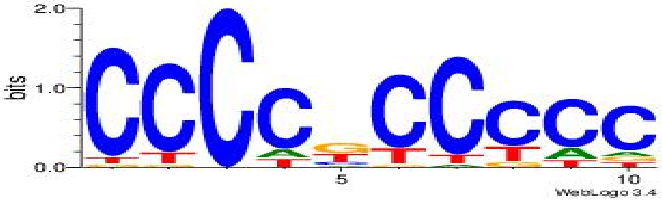


Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD

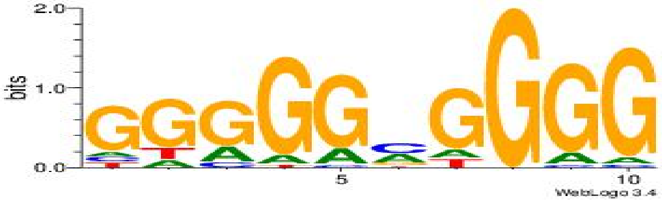


Dataset #: 3 Motif ID: 24 Motif name: SP1

Original motif Consensus sequence: CCCCKCCCCC



Reverse complement motif Consensus sequence: GGGGGYGGGG



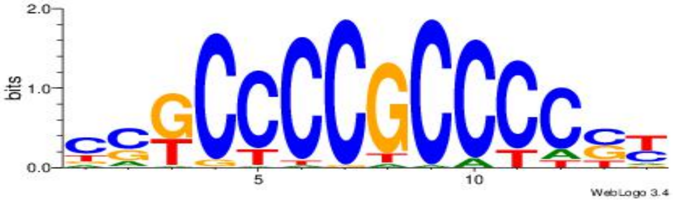
Best Matches for Top Significant Motif ID 24 (Highest to Lowest)

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

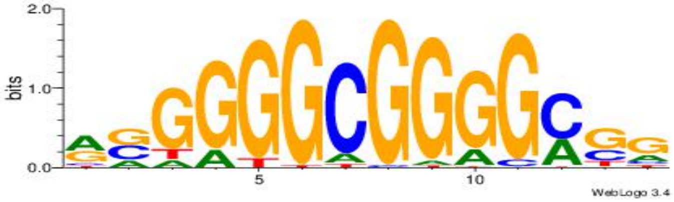
Alignment:

```
CSKCCCCGCCCCSY
---CCCCKCCCCC-
```

Original motif Consensus sequence: CSKCCCCGCCCCSY



Reverse complement motif Consensus sequence: MSGGGGCGGGGY



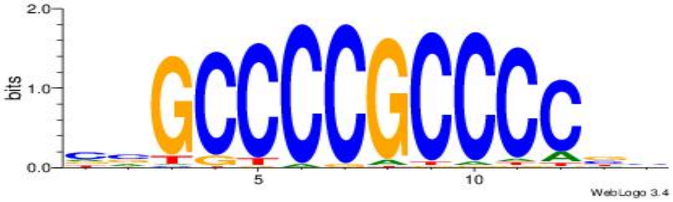
Dataset #:	4
Motif ID:	36
Motif name:	csGCCCCGCCCCsc
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif

Direction: Forward
Position number: 4
Number of overlap: 10
Similarity score: 0.00965796

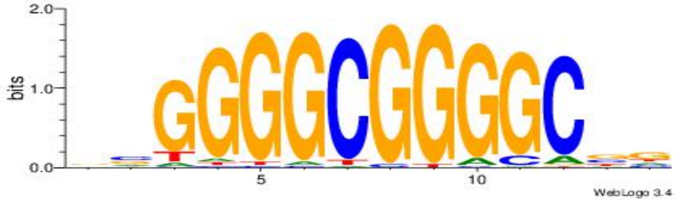
Alignment:

```
HVGCCCCGCCCCBB
---CCCCKCCCCC-
```

Original motif Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGC

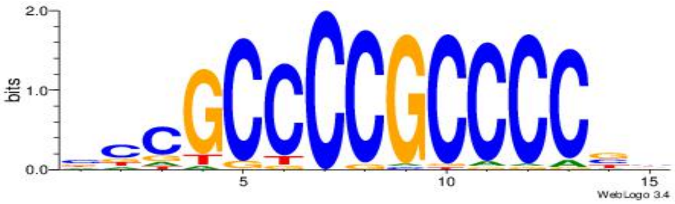


Dataset #: 4
Motif ID: 38
Motif name: cccGCCCCGCCCCsb
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2
Number of overlap: 10
Similarity score: 0.0127292

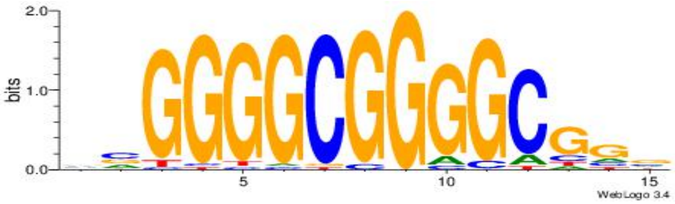
Alignment:

```
BCCGCCCCGCCCCBB
----CCCCKCCCCC-
```

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB



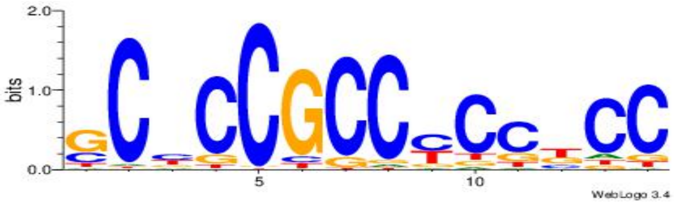
Dataset #: 5
Motif ID: 50
Motif name: TFF11
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 4
Number of overlap: 10
Similarity score: 0.0174405

Alignment:

```
GGMGGRGGCGGVGC
---GGGGGYGGGG-
```

Original motif Consensus sequence: GGMGGRGGCGGVGC

Reverse complement motif Consensus sequence: GCVCCGCCMCCY

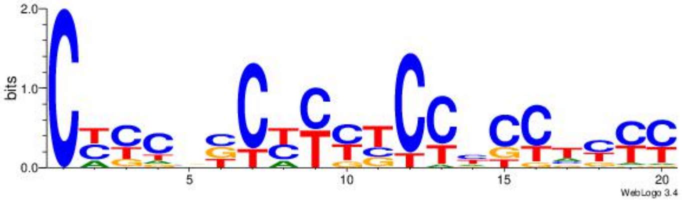


Dataset #:	5
Motif ID:	54
Motif name:	TFM12
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	5
Number of overlap:	10
Similarity score:	0.0301548

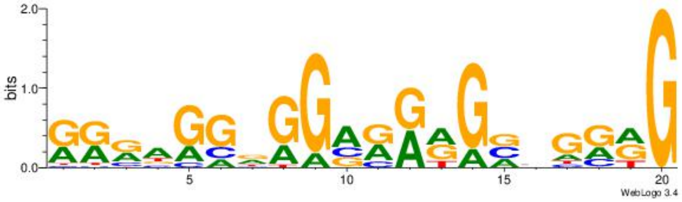
Alignment:

```
CYYCBBCYYYTCCHCCTYYY
------CCCCKCCCCC----
```

Original motif Consensus sequence: CYYCBBCYYYTCCHCCTYYY



Reverse complement motif Consensus sequence: KKKAGGDGGAKKMGBBGKMG

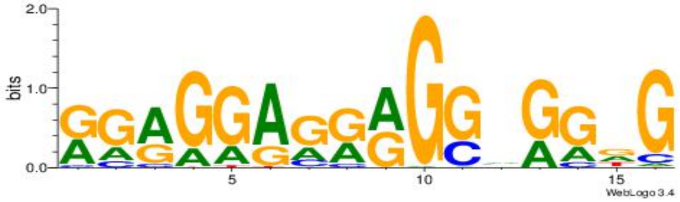


Dataset #:	5
Motif ID:	51
Motif name:	TFM2
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1

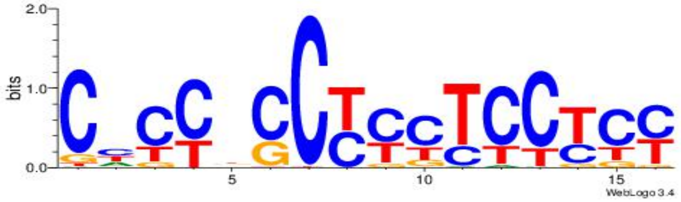
Number of overlap: 10
Similarity score: 0.0329167

Alignment:
```
RGRGGAGRRGGHGGDG
------GGGGGYGGGG
```

Original motif Consensus sequence: RGRGGAGRRGGHGGDG



Reverse complement motif Consensus sequence: CHCCBCCKMCTCCKCM



Dataset #: 5
Motif ID: 49
Motif name: TFF1
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 2
Number of overlap: 10
Similarity score: 0.0557738

Alignment:
```
GCVGCGGCBCCG
-CCCCKCCCCC-
```

Original motif Consensus sequence: CGGVGCCGCVGC

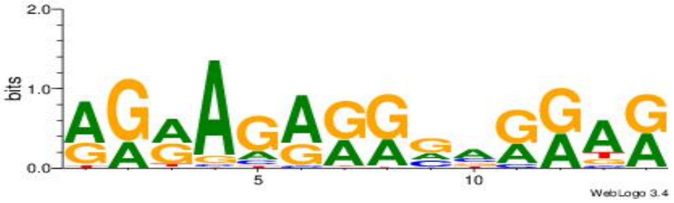
Reverse complement motif Consensus sequence: GCVGCGGCBCCG

Dataset #:	2
Motif ID:	2
Motif name:	Motif 2
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	10
Similarity score:	0.0648214

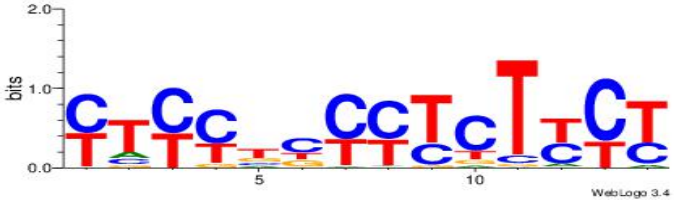
Alignment:

```
MTMMTCMMTCTKCK
----CCCCKCCCCC
```

Original motif Consensus sequence: RGRAGARRGARRAR



Reverse complement motif Consensus sequence: MTMMTCMMTCTK



Dataset #:	5
Motif ID:	48

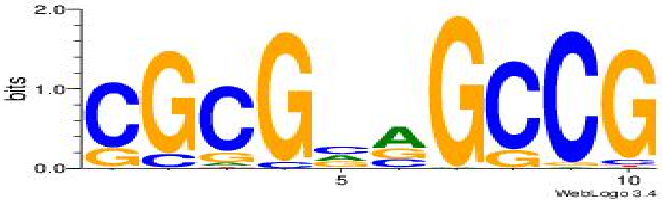
Motif name:	TFW3
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	10
Similarity score:	0.0762976

Alignment:

```
CGGCYBCGCG
CCCCKCCCCC
```

Original motif Consensus sequence: CGGCYBCGCG

Reverse complement motif Consensus sequence: CGCGBMGCCG

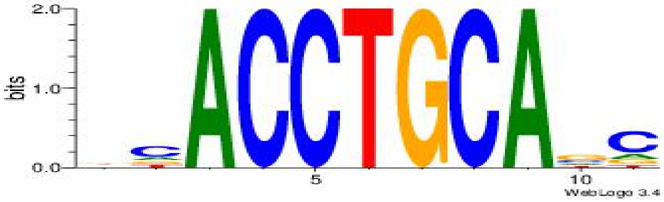


Dataset #:	4
Motif ID:	40
Motif name:	kcACCTGCAgc
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	10
Similarity score:	0.0841987

Alignment:

```
GBTGCAGGTGB
GGGGGYGGGG-
```

Original motif   Consensus sequence: BCACCTGCABC



Reverse complement motif   Consensus sequence: GBTGCAGGTGB

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

Original motif   Consensus sequence: YGCGTG

Reverse complement motif   Consensus sequence: CACGCM

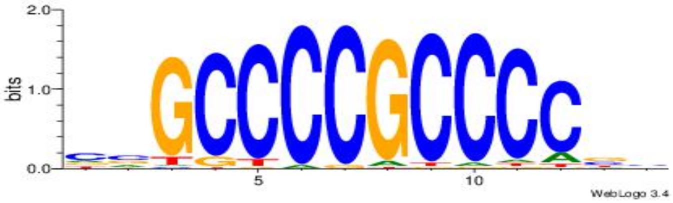
Best Matches for Top Significant Motif ID 32 (Highest to Lowest)

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

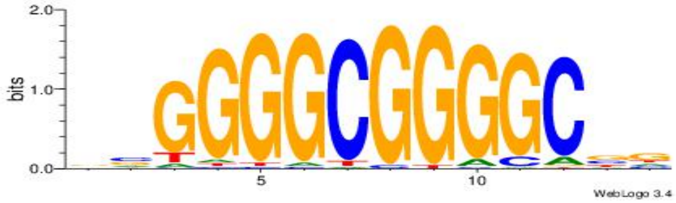
Number of overlap: 6
Similarity score: 0.0396403

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

Original motif Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGC



Dataset #: 1
Motif ID: 1
Motif name: Motif 1
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 3
Number of overlap: 6
Similarity score: 0.040625

Alignment:
GCCCCGCC
--CACGCM

Original motif Consensus sequence: GGCGGGGC

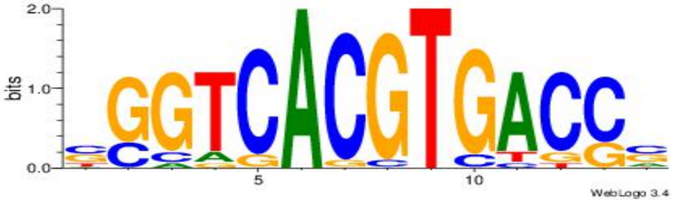
Reverse complement motif Consensus sequence: GCCCCGCC

Dataset #:	4
Motif ID:	42
Motif name:	sSGTCACGTGACSs
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	5
Number of overlap:	6
Similarity score:	0.0412037

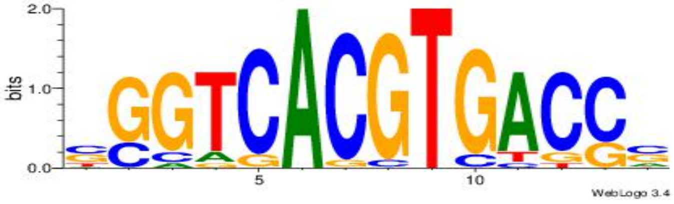
Alignment:

```
SGGTCACGTGACCS
----YGCGTG----
```

Original motif Consensus sequence: SGGTCACGTGACCS



Reverse complement motif Consensus sequence: SGGTCACGTGACC



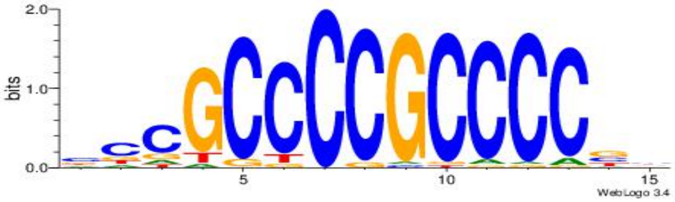
Dataset #:	4
Motif ID:	38

Motif name:	cccGCCCCGCCCCsb
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	6
Number of overlap:	6
Similarity score:	0.0425089

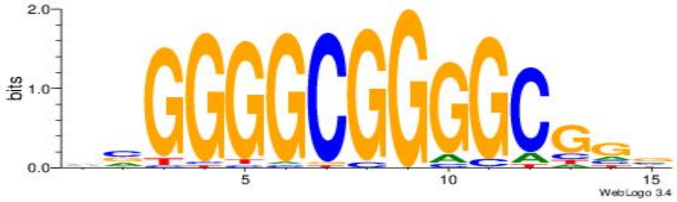
Alignment:

```
BCCGCCCCGCCCCBB
-----CACGCM----
```

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB

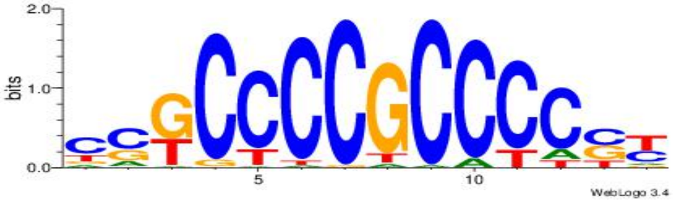


Dataset #:	2
Motif ID:	7
Motif name:	Motif 7
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	5
Number of overlap:	6
Similarity score:	0.0465867

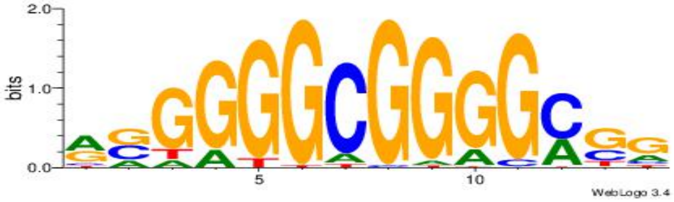
Alignment:

MSGGGGCGGGGYSG
----YGCGTG----

Original motif Consensus sequence: CSKCCCCGCCCCSY



Reverse complement motif Consensus sequence: MSGGGGCGGGGY



Dataset #:	5
Motif ID:	47
Motif name:	TFW2
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	6
Similarity score:	0.0469722

Alignment:

SCGCGCGG
-YGCGTG-

Original motif Consensus sequence: SCGCGCGG

Reverse complement motif Consensus sequence: CCGCGCGS

Dataset #:	5
Motif ID:	48
Motif name:	TFW3
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	6
Similarity score:	0.0586806

Alignment:

```
CGGCYBCGCG
----YGCGTG
```

Original motif Consensus sequence: CGGCYBCGCG

Reverse complement motif Consensus sequence: CGCGBMGCCG

Dataset #:	4
Motif ID:	40

Motif name: kcACCTGCAgc

Matching format of first motif: Original Motif

Matching format of second motif: Original Motif

Direction: Backward

Position number: 5

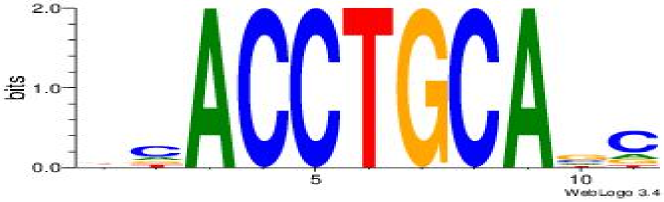
Number of overlap: 6

Similarity score: 0.0637286

Alignment:

```
BCACCTGCABC
-YGCGTG----
```

Original motif Consensus sequence: BCACCTGCABC



Reverse complement motif Consensus sequence: GBTGCAGGTGB

Dataset #: 5

Motif ID: 50

Motif name: TFF11

Matching format of first motif: Reverse Complement

Matching format of second motif: Reverse Complement

Direction: Forward

Position number: 3

Number of overlap: 6

Similarity score: 0.066121

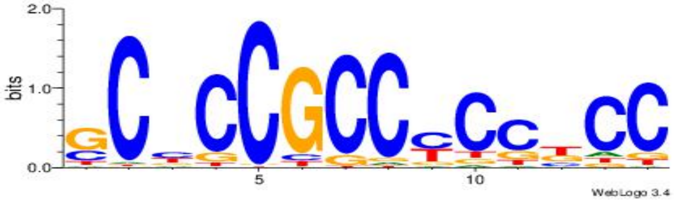
Alignment:

GCVCCGCCMCCYCC

--CACGCM------

Original motif   Consensus sequence: GGMGGRGGCGGVGC

Reverse complement motif   Consensus sequence: GCVCCGCCMCCYC



Dataset #:	5
Motif ID:	46
Motif name:	TFW1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	6
Similarity score:	0.0756826

Alignment:

CGCGAC

CACGCM

Original motif   Consensus sequence: GTCGCG   Reverse complement motif   Consensus sequence: CGCGAC

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

Original motif Consensus sequence: GGCGGGGC

Reverse complement motif Consensus sequence: GCCCCGCC

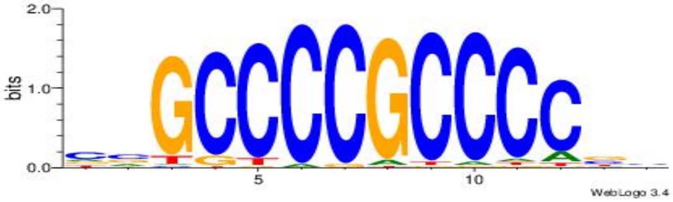
Best Matches for Top Significant Motif ID 1 (Highest to Lowest)

Dataset #:	4
Motif ID:	36
Motif name:	csGCCCCGCCCCsc
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	5
Number of overlap:	8
Similarity score:	0

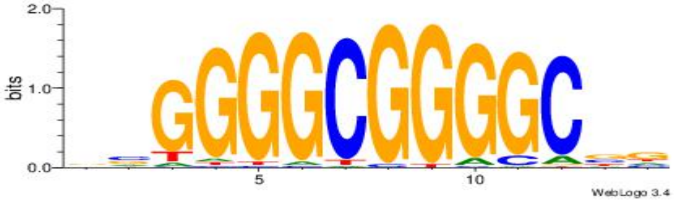
Alignment:

```
HVGCCCCGCCCCBB
--GCCCCGCC----
```

Original motif Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGC

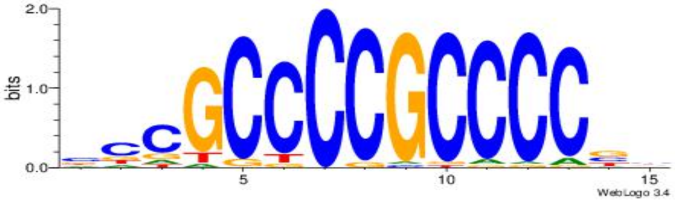


Dataset #:	4
Motif ID:	38
Motif name:	cccGCCCCGCCCCsb
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	5
Number of overlap:	8
Similarity score:	0.00250079

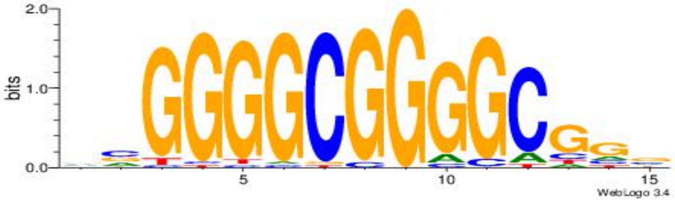
Alignment:

```
BCCGCCCCGCCCCBB
---GCCCCGCC----
```

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB

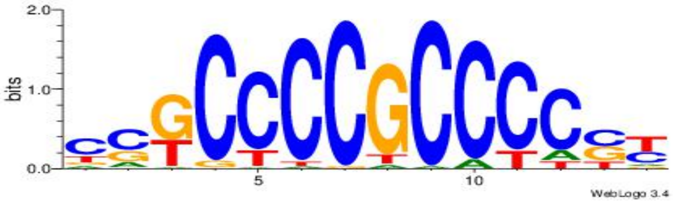


Dataset #: 2
Motif ID: 7
Motif name: Motif 7
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 5
Number of overlap: 8
Similarity score: 0.0149958

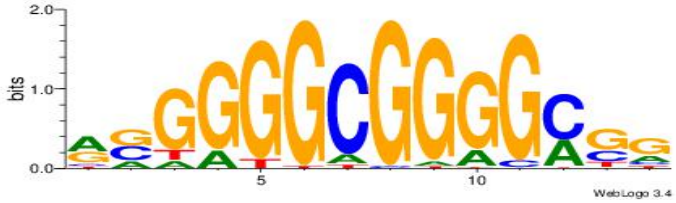
Alignment:

```
MSGGGGCGGGGYSG
----GGCGGGGC--
```

Original motif Consensus sequence: CSKCCCCGCCCCSY



Reverse complement motif Consensus sequence: MSGGGGCGGGGY



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

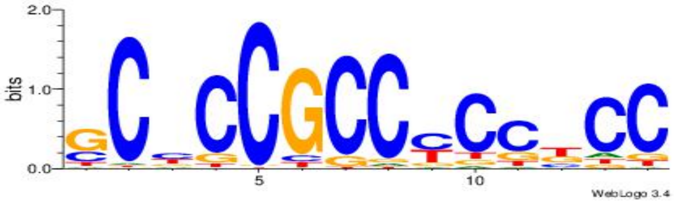
Similarity score: 0.0348969

Alignment:

```
GGMGGRGGCGGVGC
------GGCGGGGC
```

Original motif Consensus sequence: GGMGGRGGCGGVGC

Reverse complement motif Consensus sequence: GCVCCGCCMCCYC



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

Alignment:

```
DGGGYGKGGC
--GGCGGGGC
```

Original motif Consensus sequence: DGGGYGKGGC

Reverse complement motif Consensus sequence: GCCYCMCCCD

Dataset #: 3

Motif ID: 22

Motif name: Zfx

Matching format of first motif: Reverse Complement

Matching format of second motif: Reverse Complement

Direction: Forward

Position number: 4

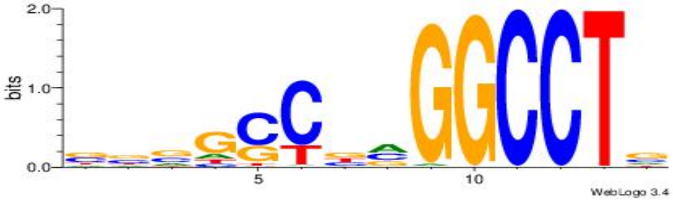
Number of overlap: 8

Similarity score: 0.0708224

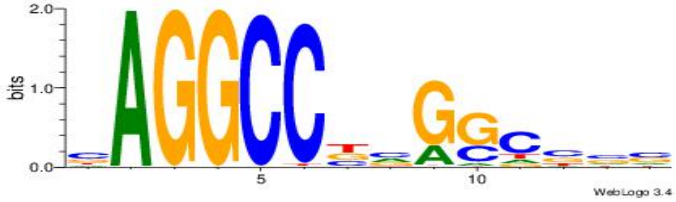
Alignment:

```
VAGGCCBBGGCVBB
---GCCCCGCC---
```

Original motif Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif Consensus sequence: VAGGCCBBGGCV



Dataset #: 5

Motif ID: 48

Motif name:	TFW3
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	2
Number of overlap:	8
Similarity score:	0.071681

Alignment:

```
CGCGBMGCCG
-GCCCCGCC-
```

Original motif Consensus sequence: CGGCYBCGCG

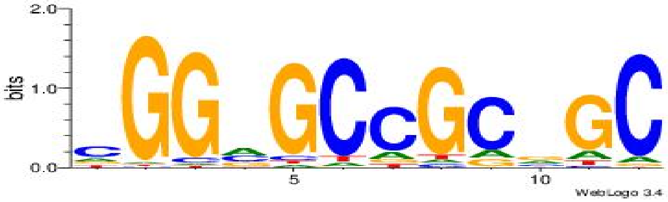
Reverse complement motif Consensus sequence: CGCGBMGCCG

Dataset #:	5
Motif ID:	49
Motif name:	TFF1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	3
Number of overlap:	8
Similarity score:	0.0803996

Alignment:

CGGVGCCGCVGC
--GCCCCGCC--

Original motif Consensus sequence: CGGVGCCGCVGC



Reverse complement motif Consensus sequence: GCVGCGGCBCCG

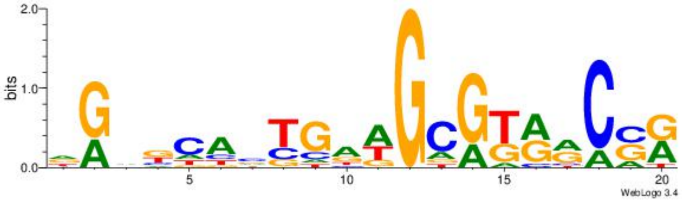
Dataset #:	3
Motif ID:	31
Motif name:	Pax5
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	3
Number of overlap:	8
Similarity score:	0.0853847

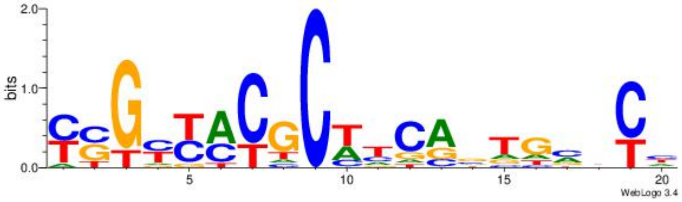
Alignment:

DGVBCABTGDWGCGKRRCSR
----------GGCGGGGC--

Original motif Consensus sequence: DGVBCABTGDWGCGKRRCSR

Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD





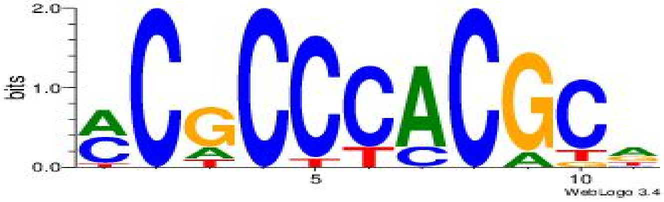
Dataset #: 3
Motif ID: 23
Motif name: Egr1
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 8
Similarity score: 0.0878731

Alignment:

```
YCGCCCACGCH
---GCCCCGCC
```

Original motif Consensus sequence: HGCGTGGGCGK

Reverse complement motif Consensus sequence: YCGCCCACGCH



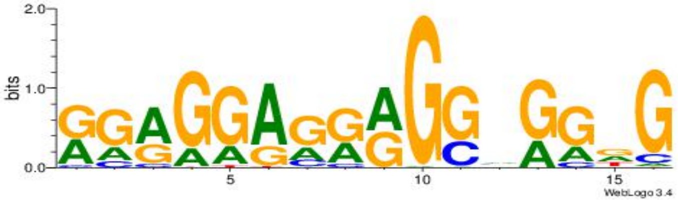
Dataset #: 5
Motif ID: 51

Motif name:	TFM2
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	3
Number of overlap:	8
Similarity score:	0.0928252

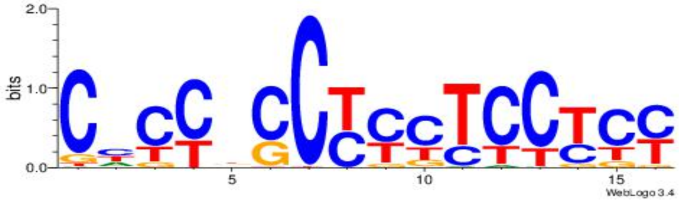
Alignment:

```
CHCCBCCKMCTCCKCM
--GCCCCGCC------
```

Original motif Consensus sequence: RGRGGAGRRGGHGGDG



Reverse complement motif Consensus sequence: CHCCBCCKMCTCCKCM



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

Original motif Consensus sequence: GTCGCG

Reverse complement motif Consensus sequence: CGCGAC

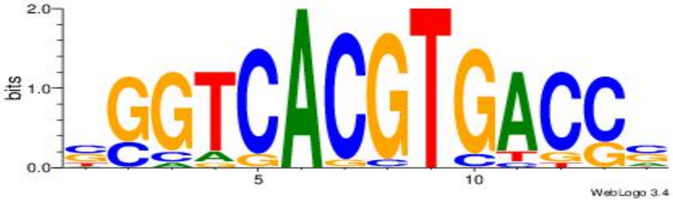
Best Matches for Top Significant Motif ID 46 (Highest to Lowest)

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

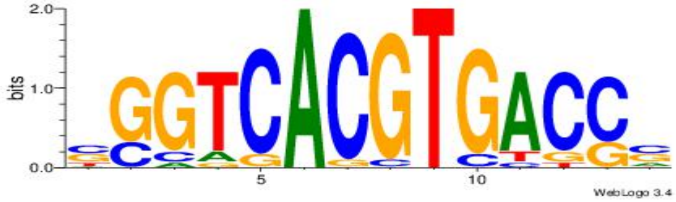
Alignment:

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

Original motif Consensus sequence: SGGTCACGTGACCS



Reverse complement motif Consensus sequence: SGGTCACGTGACC



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

Direction: Backward
Position number: 1
Number of overlap: 6
Similarity score: 0.0537993

Alignment:
```
GCCACGTGSD
----GTCGCG
```

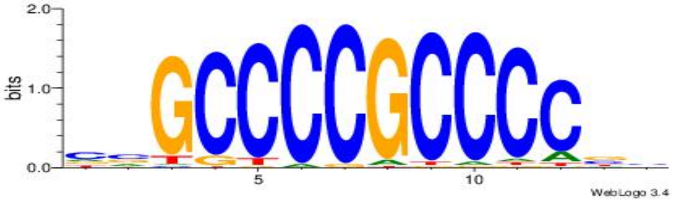
Original motif Consensus sequence: HSCACGTGGC

Reverse complement motif Consensus sequence: GCCACGTGSD

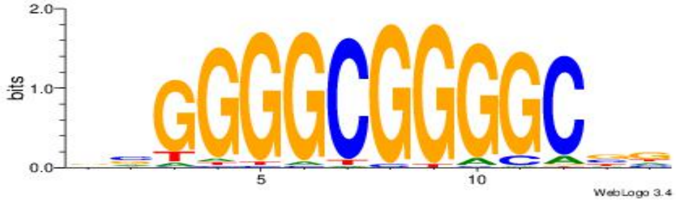
Dataset #: 4
Motif ID: 36
Motif name: csGCCCCGCCCCsc
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 7
Number of overlap: 6
Similarity score: 0.0539

Alignment:
```
HVGCCCCGCCCCBB
--GTCGCG------
```

Original motif Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGC



Dataset #:	1
Motif ID:	1
Motif name:	Motif 1
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	3
Number of overlap:	6
Similarity score:	0.0554263

Alignment:

```
GCCCCGCC
--GTCGCG
```

Original motif Consensus sequence: GGCGGGGC

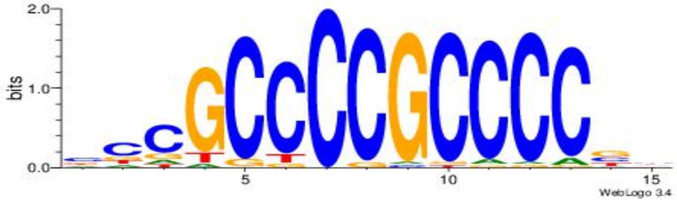
Reverse complement motif Consensus sequence: GCCCCGCC

Dataset #:	4
Motif ID:	38
Motif name:	cccGCCCCGCCCCsb
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	3
Number of overlap:	6
Similarity score:	0.0558733

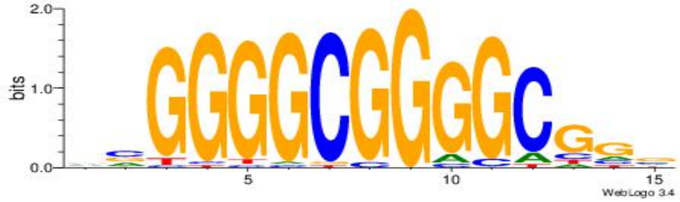
Alignment:

```
BBGGGGCGGGGCGGB
-------GTCGCG--
```

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB



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

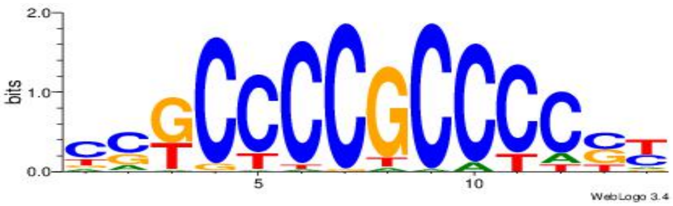
Number of overlap: 6

Similarity score: 0.0644512

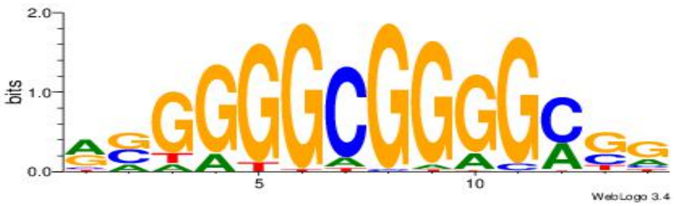
Alignment:

```
CSKCCCCGCCCCSY
--CGCGAC------
```

Original motif Consensus sequence: CSKCCCCGCCCCSY



Reverse complement motif Consensus sequence: MSGGGGCGGGGY



Dataset #: 3

Motif ID: 34

Motif name: Myc

Matching format of first motif: Original Motif

Matching format of second motif: Reverse Complement

Direction: Forward

Position number: 5

Number of overlap: 6

Similarity score: 0.0664905

Alignment:

```
DCCACGTGCV
----GTCGCG
```

Original motif Consensus sequence: VGCACGTGGH

Reverse complement motif Consensus sequence: DCCACGTGCV

Dataset #:	3
Motif ID:	28
Motif name:	E2F1
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2
Number of overlap:	6
Similarity score:	0.0698654

Alignment:

```
TTTSGCGC
-GTCGCG-
```

Original motif Consensus sequence: TTTSGCGC

Reverse complement motif Consensus sequence: GCGCSAAA

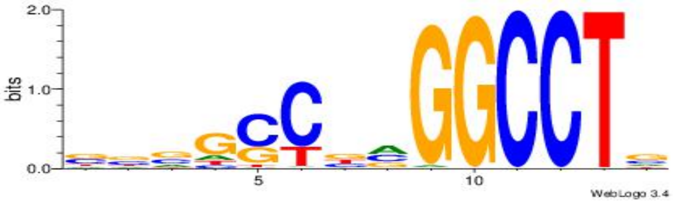
Dataset #:	3
Motif ID:	22

Motif name:	Zfx
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	6
Number of overlap:	6
Similarity score:	0.069909

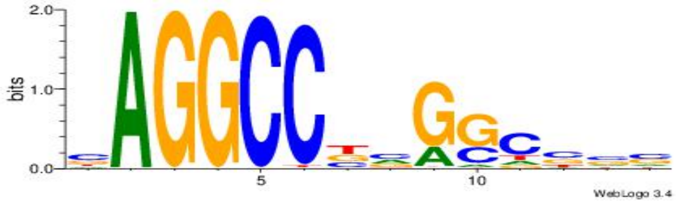
Alignment:

```
BBVGCCBVGGCCTV
---GTCGCG-----
```

Original motif Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif Consensus sequence: VAGGCCBBGGCV

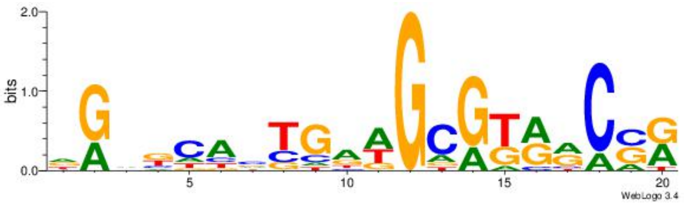


Dataset #:	3
Motif ID:	31
Motif name:	Pax5
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	7
Number of overlap:	6
Similarity score:	0.072456

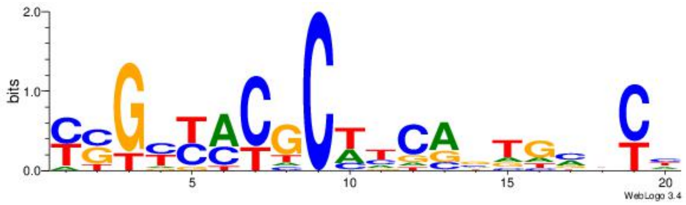
Alignment:

```
MSGKKRCGCWDCABTGBBCD
------CGCGAC--------
```

Original motif Consensus sequence: DGVBCABTGDWGCGKRRCSR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD



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

Original motif Consensus sequence: SCGCGCGG

Reverse complement motif Consensus sequence: CCGCGCGS

Best Matches for Top Significant Motif ID 47 (Highest to Lowest)

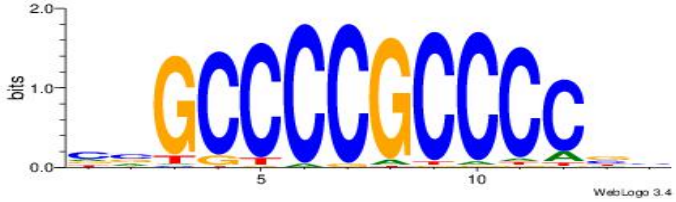
Dataset #:	4
Motif ID:	36
Motif name:	csGCCCCGCCCCsc
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward

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

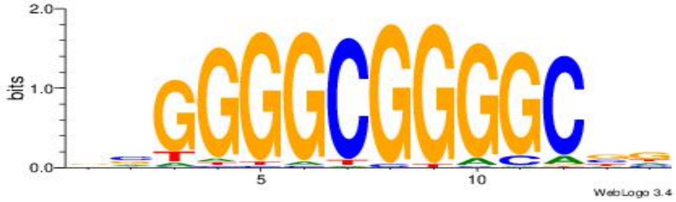
Alignment:

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

Original motif Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGC

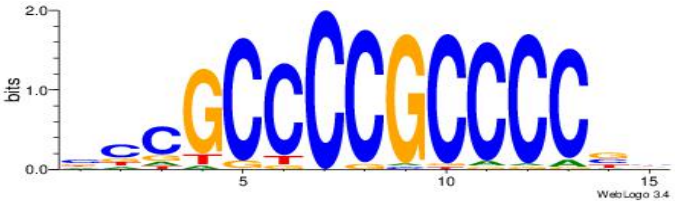


Dataset #:	4
Motif ID:	38
Motif name:	cccGCCCCGCCCCsb
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	7
Number of overlap:	8
Similarity score:	0.045686

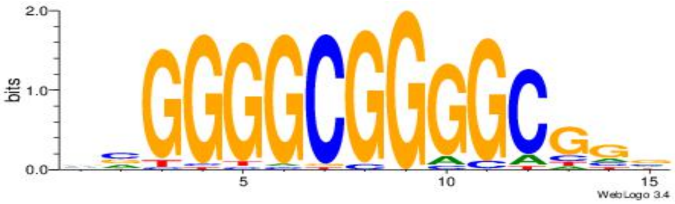
Alignment:

```
BBGGGGCGGGGCGGB
------SCGCGCGG-
```

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB

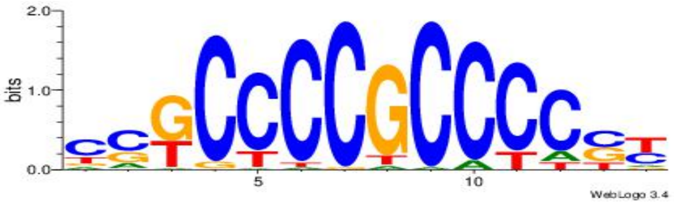


Dataset #:	2
Motif ID:	7
Motif name:	Motif 7
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	6
Number of overlap:	8
Similarity score:	0.0504058

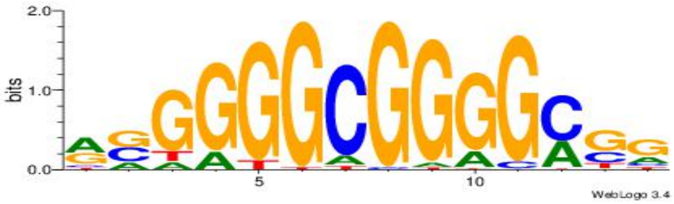
Alignment:

```
CSKCCCCGCCCCSY
-CCGCGCGS-----
```

Original motif Consensus sequence: CSKCCCCGCCCCSY



Reverse complement motif Consensus sequence: MSGGGGCGGGGY



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

Alignment:
HSCACGTGGC
-SCGCGCGG-

Original motif Consensus sequence: HSCACGTGGC

Reverse complement motif Consensus sequence: GCCACGTGSD

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

Similarity score: 0.0574543

Alignment:
```
VGCACGTGGH
-SCGCGCGG-
```

Original motif Consensus sequence: VGCACGTGGH

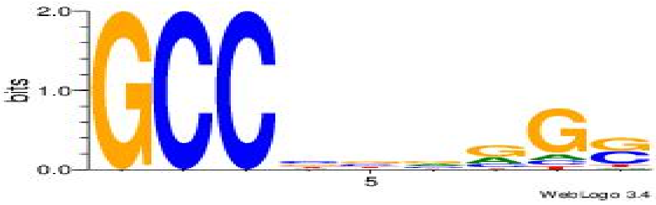
Reverse complement motif Consensus sequence: DCCACGTGCV

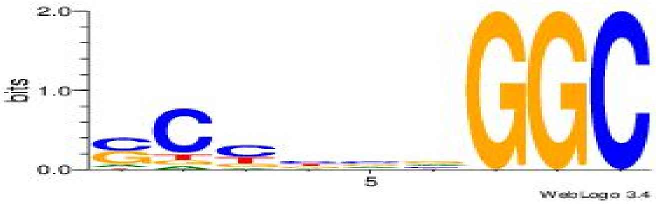
Dataset #: 3
Motif ID: 25
Motif name: TFAP2A
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 8
Similarity score: 0.0678925

Alignment:
```
SCMVBBGGC
-SCGCGCGG
```

Original motif Consensus sequence: GCCBBVRGS

Reverse complement motif Consensus sequence: SCMVBBGGC



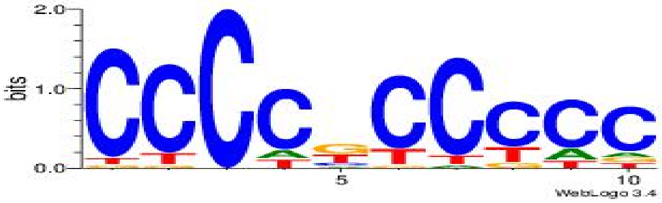


Dataset #:	3
Motif ID:	24
Motif name:	SP1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	3
Number of overlap:	8
Similarity score:	0.07018

Alignment:

```
CCCCKCCCCC
--CCGCGCGS
```

Original motif Consensus sequence: CCCCKCCCCC



Reverse complement motif Consensus sequence: GGGGGYGGGG

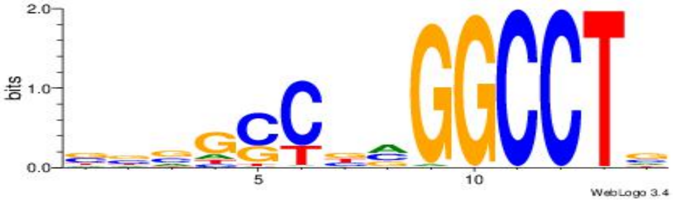
Dataset #:	3
Motif ID:	22

Motif name: Zfx
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 3
Number of overlap: 8
Similarity score: 0.0710499

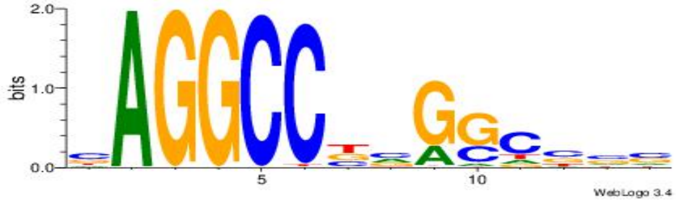
Alignment:

```
BBVGCCBVGGCCTV
--SCGCGCGG----
```

Original motif Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif Consensus sequence: VAGGCCBBGGCV



Dataset #: 3
Motif ID: 27
Motif name: Klf4
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 2
Number of overlap: 8
Similarity score: 0.0768965

Alignment:
DGGGYGKGGC
-SCGCGCGG-

Original motif Consensus sequence: DGGGYGKGGC

Reverse complement motif Consensus sequence: GCCYCMCCCD

Dataset #:	3
Motif ID:	26
Motif name:	MIZF
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	8
Similarity score:	0.0837414

Alignment:
GCGGACGTTV
--SCGCGCGG

Original motif Consensus sequence: BAACGTCCGC

Reverse complement motif Consensus sequence: GCGGACGTTV

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

Original motif Consensus sequence: VBACGTGV

Reverse complement motif Consensus sequence: VCACGTBV

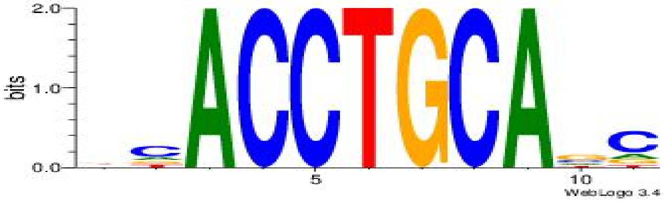
Best Matches for Top Significant Motif ID 29 (Highest to Lowest)

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

Alignment:

```
GBTGCAGGTGB
---VCACGTBV
```

Original motif Consensus sequence: BCACCTGCABC



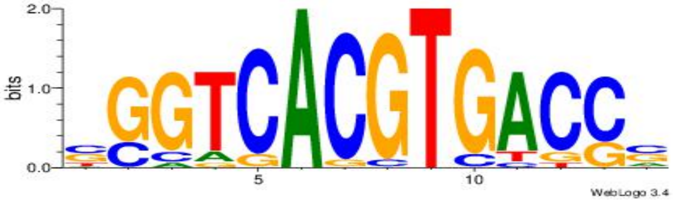
Reverse complement motif Consensus sequence: GBTGCAGGTGB

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

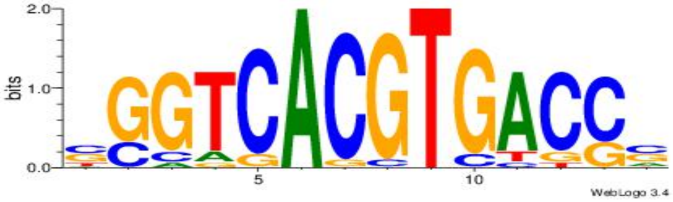
Alignment:

```
SGGTCACGTGACCS
---VCACGTBV---
```

Original motif Consensus sequence: SGGTCACGTGACCS



Reverse complement motif Consensus sequence: SGGTCACGTGACC

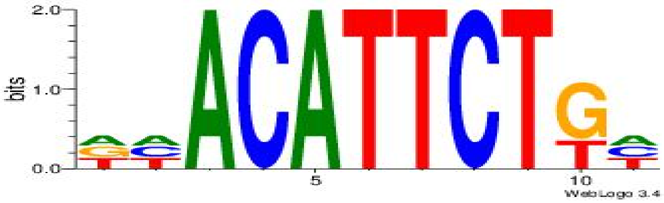


Dataset #:	4
Motif ID:	44
Motif name:	dhACATTCTkh
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	4
Number of overlap:	8
Similarity score:	0.0640024

Alignment:

```
DHACATTCTGH
VCACGTBV---
```

Original motif   Consensus sequence: DHACATTCTGH



Reverse complement motif   Consensus sequence: HCAGAATGTHD

Dataset #:	5
Motif ID:	47
Motif name:	TFW2
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	8

Similarity score:	0.0660185

Alignment:

```
CCGCGCGS
VBACGTGV
```

Original motif Consensus sequence: SCGCGCGG

Reverse complement motif Consensus sequence: CCGCGCGS

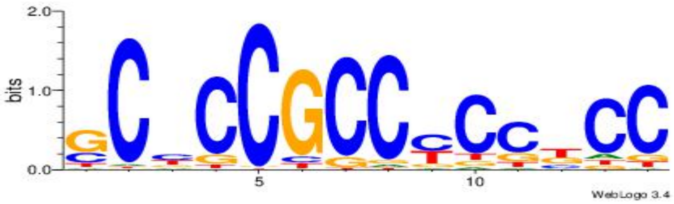
Dataset #:	5
Motif ID:	50
Motif name:	TFF11
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	8
Similarity score:	0.067219

Alignment:

```
GCVCCGCCMCCYCC
------VCACGTBV
```

Original motif Consensus sequence: GGMGGRGGCGGVGC

Reverse complement motif Consensus sequence: GCVCCGCCMCCYC

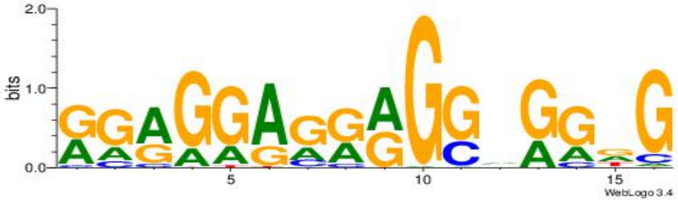


Dataset #:	5
Motif ID:	51
Motif name:	TFM2
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	6
Number of overlap:	8
Similarity score:	0.0698117

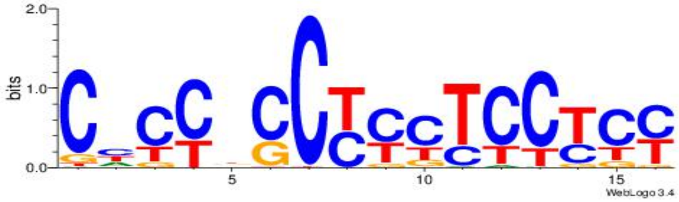
Alignment:

```
CHCCBCCKMCTCCKCM
-----VCACGTBV---
```

Original motif Consensus sequence: RGRGGAGRRGGHGGDG



Reverse complement motif Consensus sequence: CHCCBCCKMCTCCKCM



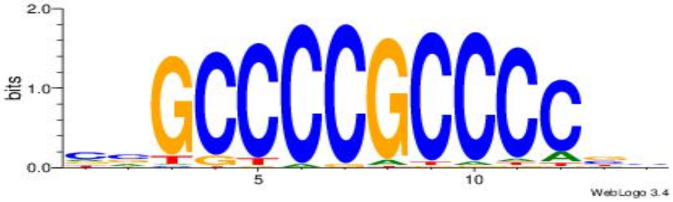
Dataset #:	4

Motif ID: 36
Motif name: csGCCCCGCCCCsc
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 4
Number of overlap: 8
Similarity score: 0.0711168

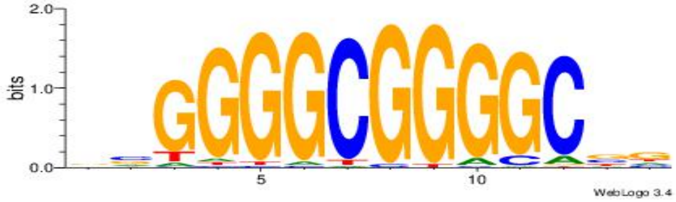
Alignment:

```
BBGGGGCGGGGCVD
---VBACGTGV---
```

Original motif Consensus sequence: HVGCCCCGCCCCBB



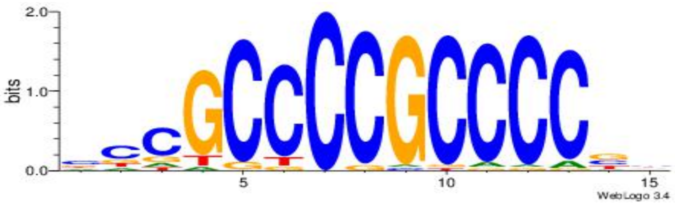
Reverse complement motif Consensus sequence: BBGGGGCGGGGC



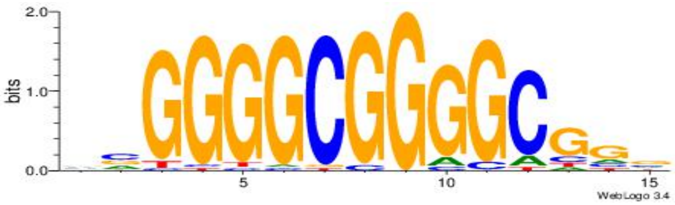
Dataset #: 4
Motif ID: 38
Motif name: cccGCCCCGCCCCsb
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 4
Number of overlap: 8
Similarity score: 0.0735453

Alignment:
BBGGGGCGGGGCGGB
---VBACGTGV----

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB

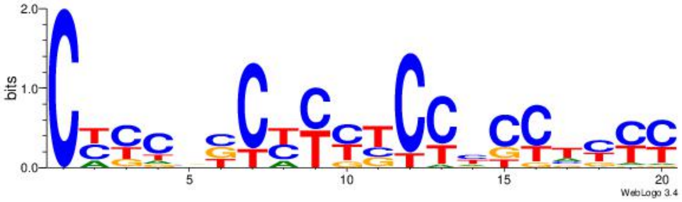


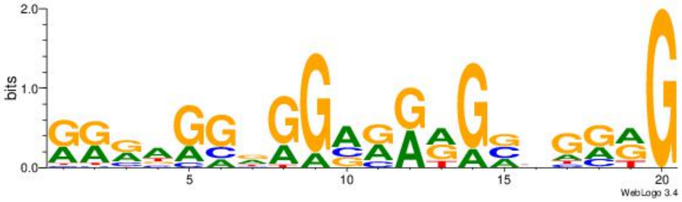
Dataset #:	5
Motif ID:	54
Motif name:	TFM12
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	12
Number of overlap:	8
Similarity score:	0.0757612

Alignment:
KKKAGGDGGAKKMGBBGKMG
-VBACGTGV-----------

Original motif Consensus sequence: CYYCBBCYYYTCCHCCTYYY

Reverse complement motif Consensus sequence: KKKAGGDGGAKKMGBBGKMG



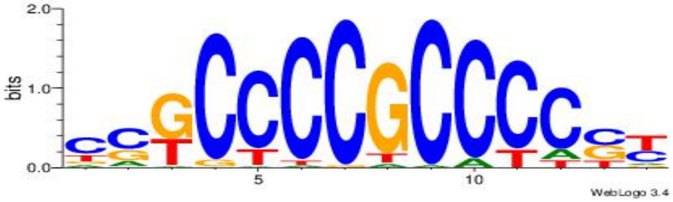


Dataset #:	2
Motif ID:	7
Motif name:	Motif 7
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	4
Number of overlap:	8
Similarity score:	0.0775335

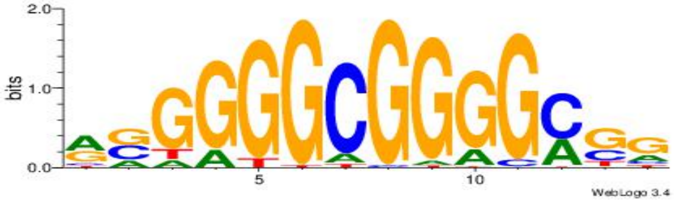
Alignment:

```
CSKCCCCGCCCCSY
---VCACGTBV---
```

Original motif   Consensus sequence: CSKCCCCGCCCCSY

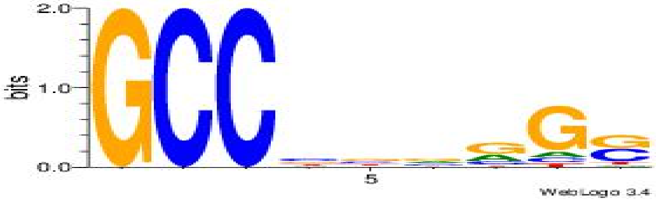


Reverse complement motif   Consensus sequence: MSGGGGCGGGGY

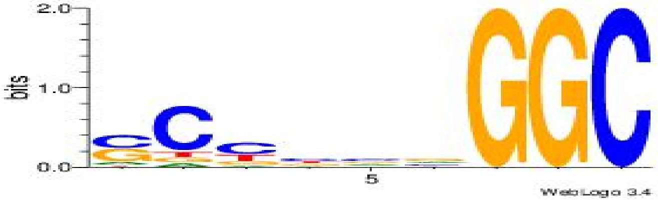


Dataset #: 3   Motif ID: 25   Motif name: TFAP2A

Original motif Consensus sequence: GCCBBVRGS



Reverse complement motif Consensus sequence: SCMVBBGGC



Best Matches for Top Significant Motif ID 25 (Highest to Lowest)

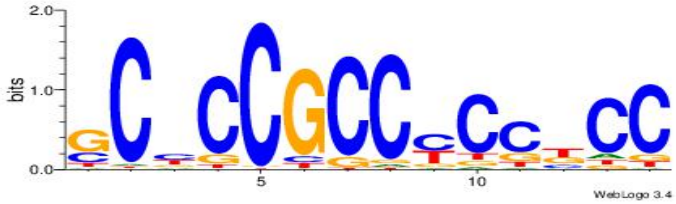
Dataset #:	5
Motif ID:	50
Motif name:	TFF11
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	9
Similarity score:	0.0415732

Alignment:

```
GGMGGRGGCGGVGC
SCMVBBGGC-----
```

Original motif Consensus sequence: GGMGGRGGCGGVGC

Reverse complement motif Consensus sequence: GCVCCGCCMCCY



Dataset #: 5
Motif ID: 48
Motif name: TFW3
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 2
Number of overlap: 9
Similarity score: 0.0552877

Alignment:

```
CGGCYBCGCG
-GCCBBVRGS
```

Original motif Consensus sequence: CGGCYBCGCG

Reverse complement motif Consensus sequence: CGCGBMGCCG

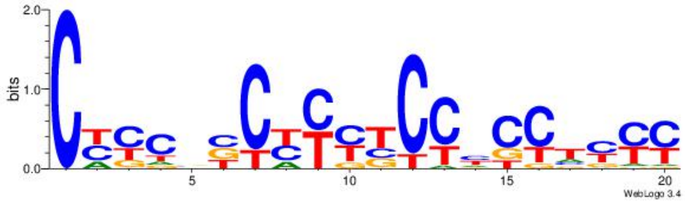
Dataset #: 5
Motif ID: 54
Motif name: TFM12
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 11
Number of overlap: 9

Similarity score: 0.0630429

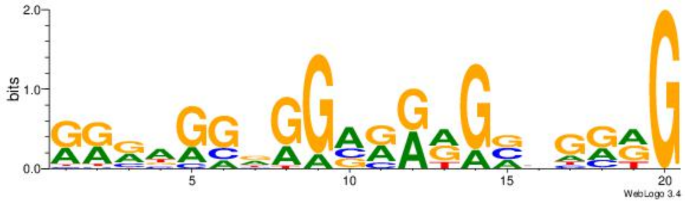
Alignment:

```
KKKAGGDGGAKKMGBBGKMG
-SCMVBBGGC----------
```

Original motif Consensus sequence: CYYCBBCYYYTCCHCCTYYY



Reverse complement motif Consensus sequence: KKKAGGDGGAKKMGBBGKMG



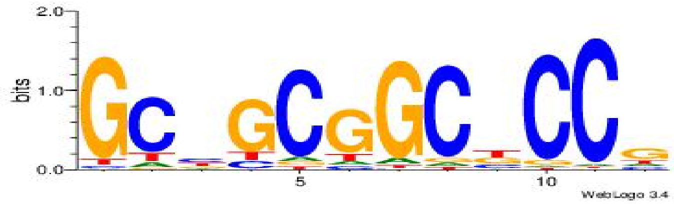
Dataset #:	5
Motif ID:	49
Motif name:	TFF1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	9
Similarity score:	0.0669772

Alignment:

```
GCVGCGGCBCCG
SCMVBBGGC---
```

Original motif Consensus sequence: CGGVGCCGCVGC

Reverse complement motif Consensus sequence: GCVGCGGCBCCG

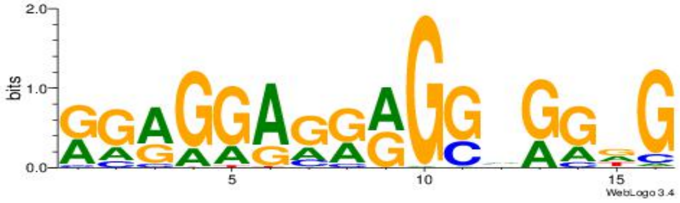


Dataset #:	5
Motif ID:	51
Motif name:	TFM2
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	9
Similarity score:	0.069755

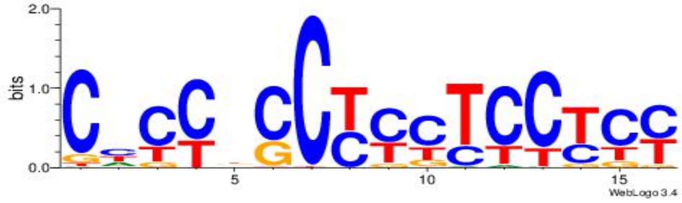
Alignment:

```
CHCCBCCKMCTCCKCM
SCMVBBGGC-------
```

Original motif   Consensus sequence: RGRGGAGRRGGHGGDG



Reverse complement motif   Consensus sequence: CHCCBCCKMCTCCKCM



Dataset #:	2

Motif ID: 2

Motif name: Motif 2

Matching format of first motif: Reverse Complement

Matching format of second motif: Reverse Complement

Direction: Backward

Position number: 2

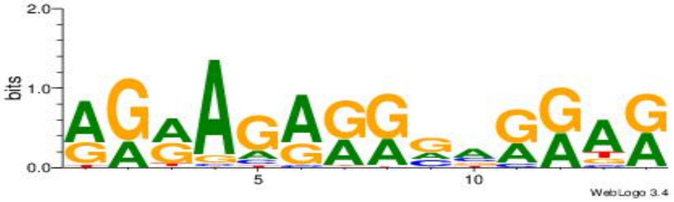
Number of overlap: 9

Similarity score: 0.0715961

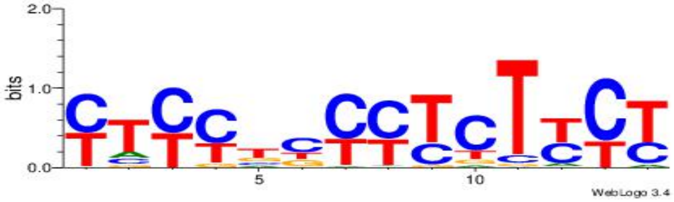
Alignment:

```
MTMMTCMMTCTKCK
----SCMVBBGGC-
```

Original motif Consensus sequence: RGRAGARRGARRAR



Reverse complement motif Consensus sequence: MTMMTCMMTCTK



Dataset #: 4

Motif ID: 38

Motif name: cccGCCCCGCCCCsb

Matching format of first motif: Original Motif

Matching format of second motif: Reverse Complement

Direction: Backward

Position number: 2

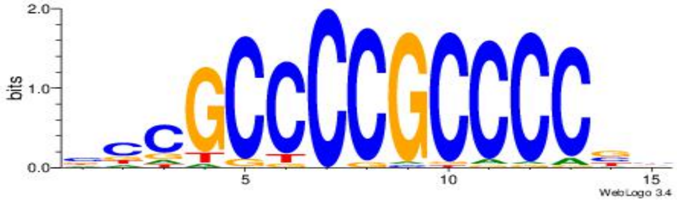
Number of overlap: 9

Similarity score: 0.0719489

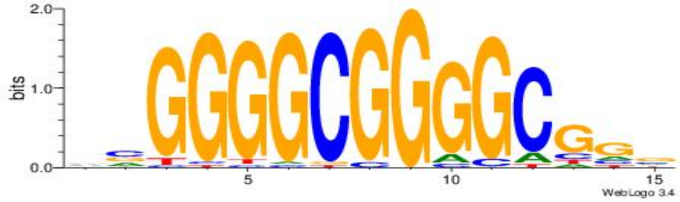
Alignment:

BBGGGGCGGGGCGGB
-----GCCBBVRGS-

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB



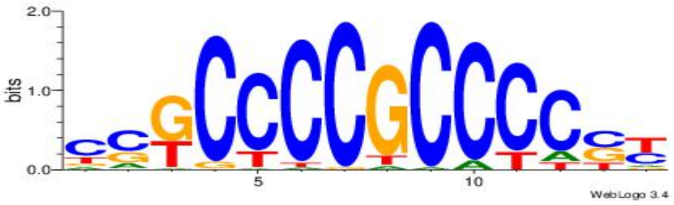
Dataset #:	2
Motif ID:	7
Motif name:	Motif 7
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	6
Number of overlap:	9
Similarity score:	0.0781606

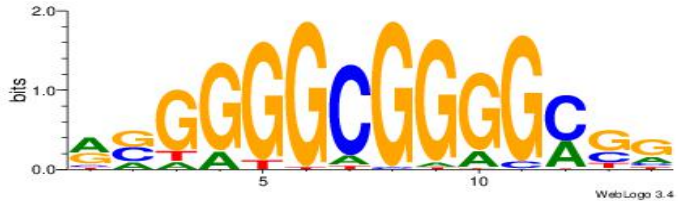
Alignment:

MSGGGGCGGGGYSG
GCCBBVRGS-----

Original motif Consensus sequence: CSKCCCCGCCCCSY

Reverse complement motif Consensus sequence: MSGGGGCGGGGY



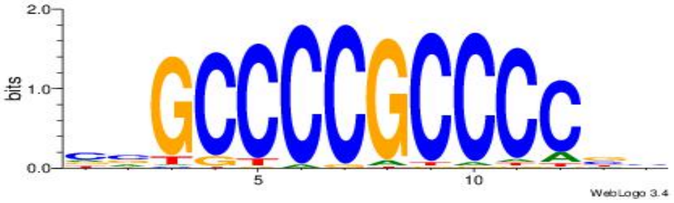


Dataset #:	4
Motif ID:	36
Motif name:	csGCCCCGCCCCsc
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	9
Similarity score:	0.0800026

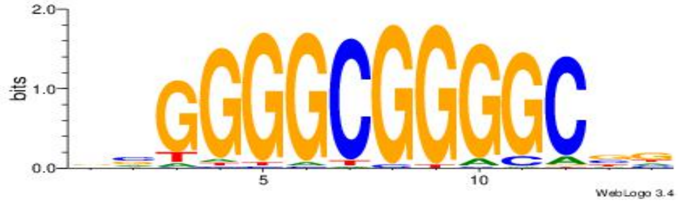
Alignment:

```
BBGGGGCGGGGCVD
-----GCCBBVRGS
```

Original motif Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGC



Dataset #:	4
Motif ID:	40

Motif name: kcACCTGCAgc

Matching format of first motif: Original Motif

Matching format of second motif: Original Motif

Direction: Backward

Position number: 1

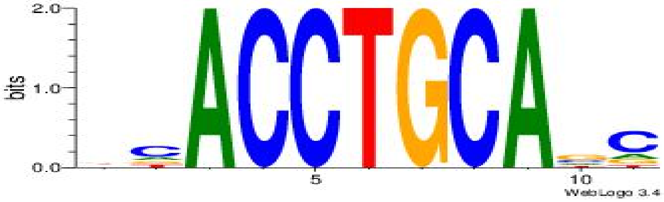
Number of overlap: 9

Similarity score: 0.0857416

Alignment:

```
BCACCTGCABC
--GCCBBVRGS
```

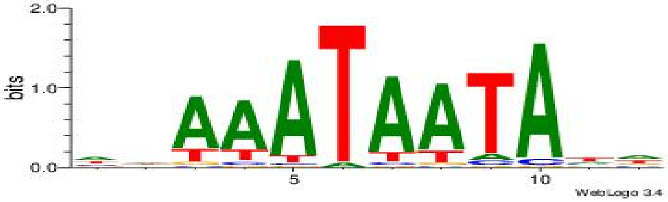
Original motif Consensus sequence: BCACCTGCABC



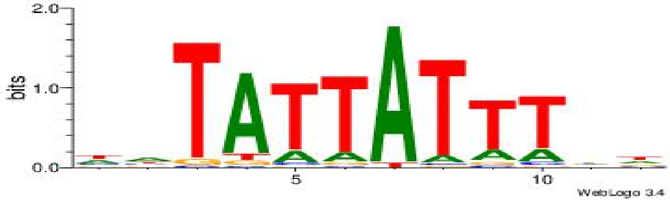
Reverse complement motif Consensus sequence: GBTGCAGGTGB

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

Original motif Consensus sequence: HDAAATAATADD



Reverse complement motif Consensus sequence: DDTATTATTTDH



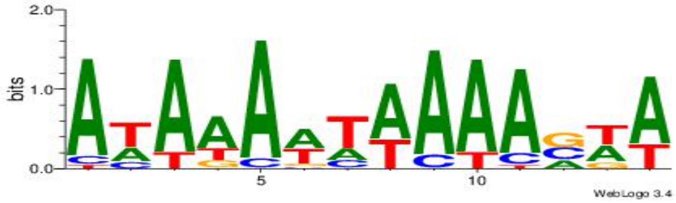
Best Matches for Top Significant Motif ID 41 (Highest to Lowest)

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

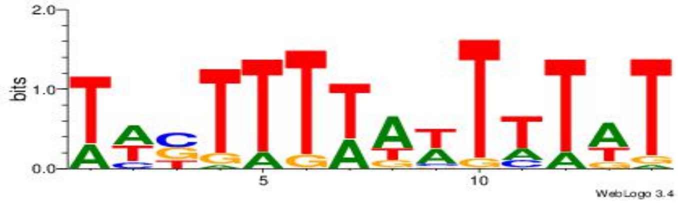
Alignment:

```
AWAAAWTWAAASWA
-HDAAATAATADD-
```

Original motif Consensus sequence: AWAAAWTWAAASWA



Reverse complement motif Consensus sequence: TWSTTTWAWTTTW



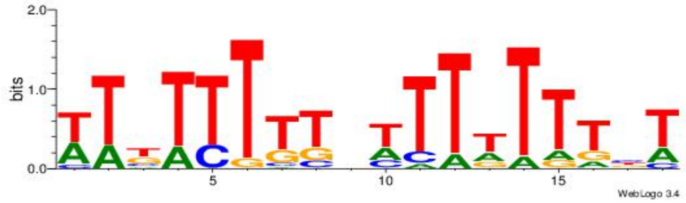
Dataset #: 5
Motif ID: 52
Motif name: TFM1
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 7
Number of overlap: 12

Similarity score: 0.0565705

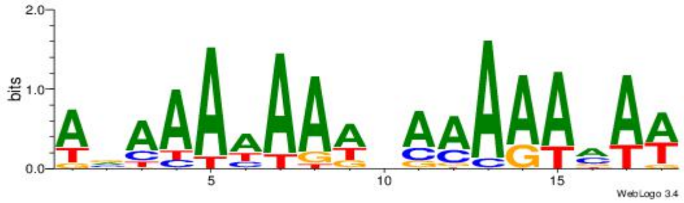
Alignment:

```
WTKTTTTTHWTTTTTTTBT
------DDTATTATTTDH
```

Original motif Consensus sequence: WTKTTTTTHWTTTTTTTBT



Reverse complement motif Consensus sequence: ABAAAAAAAWHAAAAARAW



Dataset #: 5

Motif ID: 56

Motif name: TFM11

Matching format of first motif: Original Motif

Matching format of second motif: Original Motif

Direction: Forward

Position number: 3

Number of overlap: 12

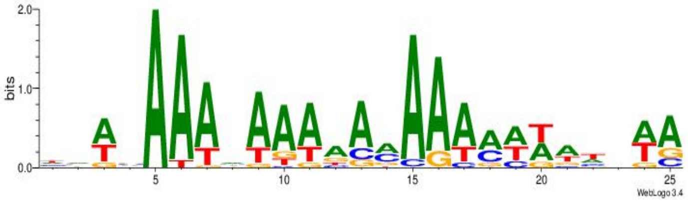
Similarity score: 0.0575935

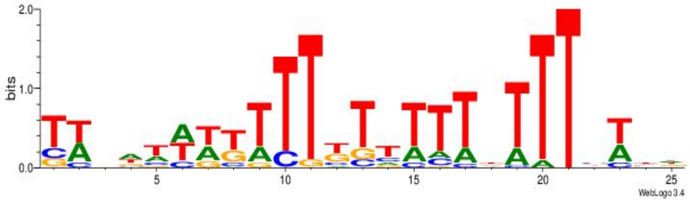
Alignment:

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

Original motif Consensus sequence: HDWVAAAHAAAAAMAAAMWWWHBWA

Reverse complement motif Consensus sequence: TWVHWWWYTTTYTTTTTHTTTVWBH



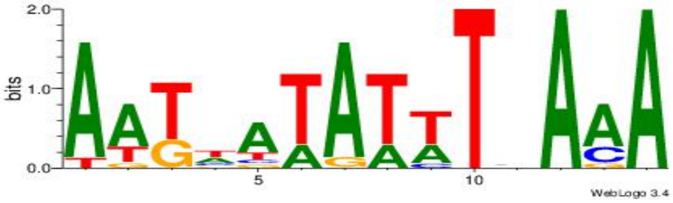


Dataset #:	2
Motif ID:	9
Motif name:	Motif 9
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	3
Number of overlap:	12
Similarity score:	0.0591821

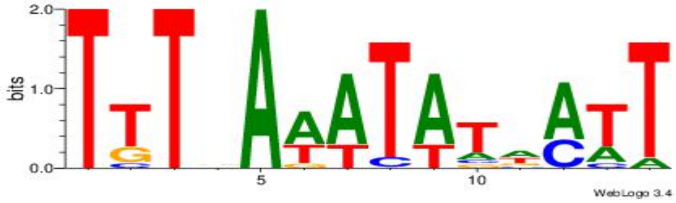
Alignment:

```
AATHATATWTHAAA
--DDTATTATTTDH
```

Original motif Consensus sequence: AATHATATWTHAAA



Reverse complement motif Consensus sequence: TTTDAWATATHAT



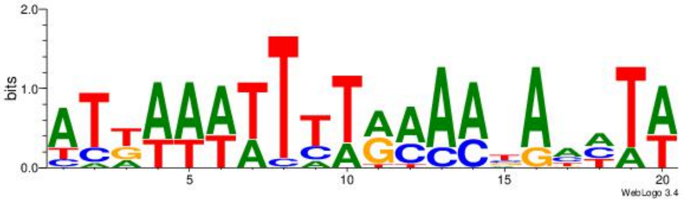
Dataset #:	5
Motif ID:	55

Motif name: TFM13
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: 0.0712963

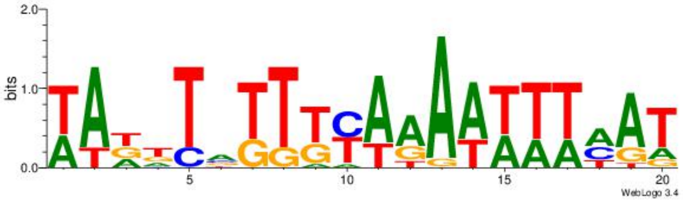
Alignment:

```
WAHHTVTTYKAAAAWTTRAT
--------HDAAATAATADD
```

Original motif Consensus sequence: ATKAAWTTTTRMAABAHHTW



Reverse complement motif Consensus sequence: WAHHTVTTYKAAAAWTTRAT

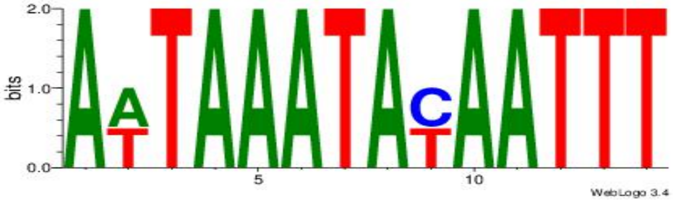


Dataset #: 2
Motif ID: 5
Motif name: Motif 5
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 2
Number of overlap: 12
Similarity score: 0.0715278

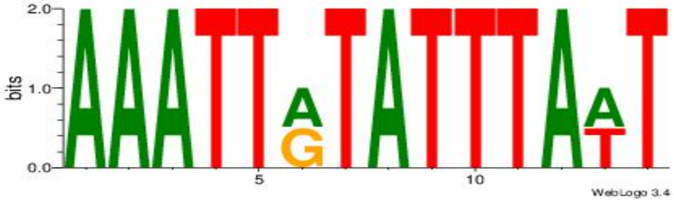
Alignment:

```
AAATTKTATTTAWT
-DDTATTATTTDH-
```

Original motif Consensus sequence: AWTAAATAYAATTT



Reverse complement motif Consensus sequence: AAATTKTATTTAW



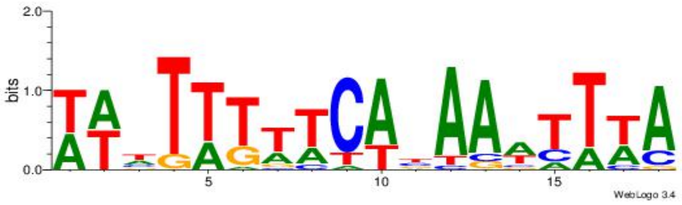
Dataset #:	5
Motif ID:	53
Motif name:	TFM3
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	12
Similarity score:	0.0733516

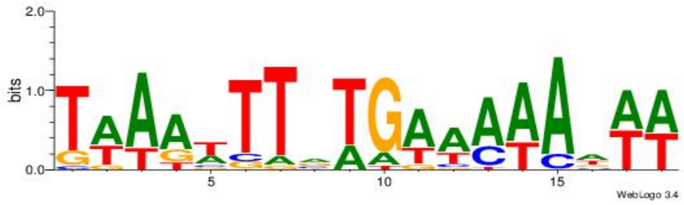
Alignment:

```
WWHTTTTTCABAAWTTWA
------DDTATTATTTDH
```

Original motif Consensus sequence: WWHTTTTTCABAAWTTWA

Reverse complement motif Consensus sequence: TWAAWTTVTGAAAAAHWW



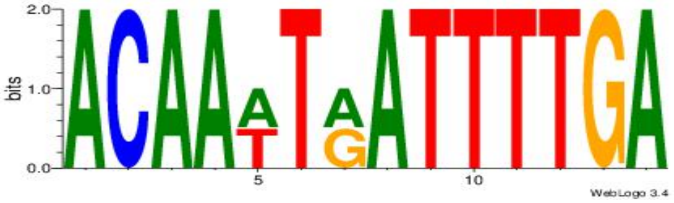


Dataset #:	2
Motif ID:	16
Motif name:	Motif 16
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	12
Similarity score:	0.0912037

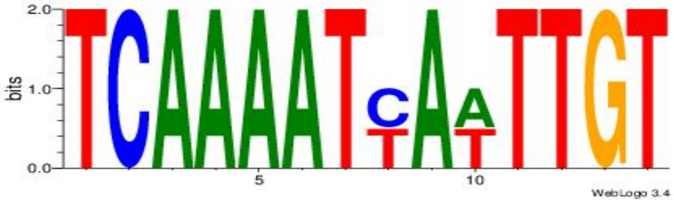
Alignment:

```
TCAAAATKAWTTGT
--DDTATTATTTDH
```

Original motif Consensus sequence: ACAAWTRATTTTGA



Reverse complement motif Consensus sequence: TCAAAATKAWTTG



Dataset #:	2
Motif ID:	6

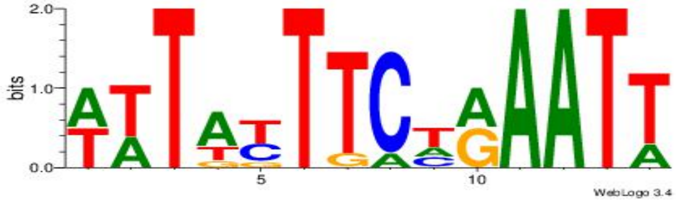
Motif name:	Motif 6
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	12
Similarity score:	0.0924576

Alignment:

```
WWTAKTTCDKAATT
DDTATTATTTDH--
```

Original motif Consensus sequence: AATTYDGAARTAWW

Reverse complement motif Consensus sequence: WWTAKTTCDKAAT

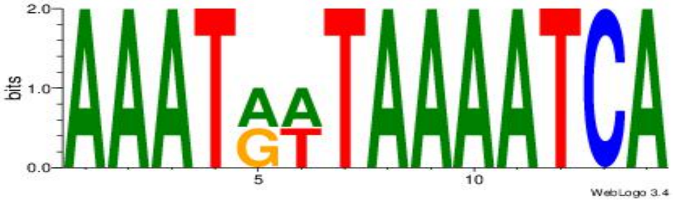


Dataset #:	2
Motif ID:	8
Motif name:	Motif 8
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	2
Number of overlap:	12
Similarity score:	0.0989198

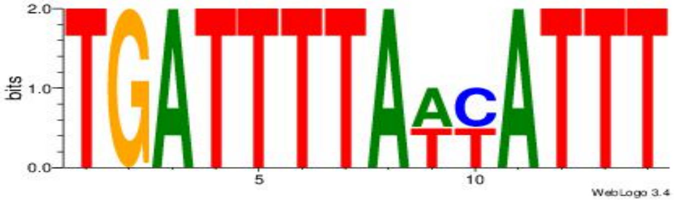
Alignment:

```
TGATTTTAWKATTT
-DDTATTATTTDH-
```

Original motif Consensus sequence: AAATRWTAAAATCA

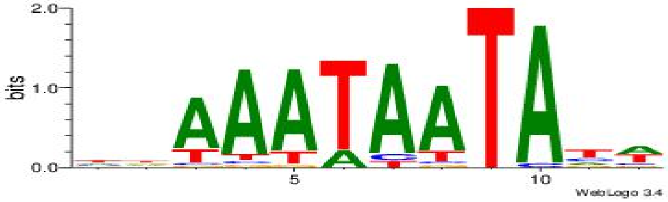


Reverse complement motif Consensus sequence: TGATTTTAWKATT

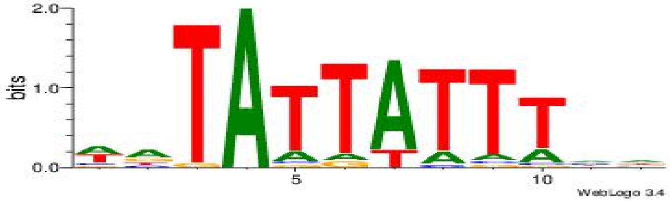


Dataset #: 4 Motif ID: 37 Motif name: tkAAATAATAtw

Original motif Consensus sequence: HDAAATAATAHW



Reverse complement motif Consensus sequence: WHTATTATTTDH



Best Matches for Top Significant Motif ID 37 (Highest to Lowest)

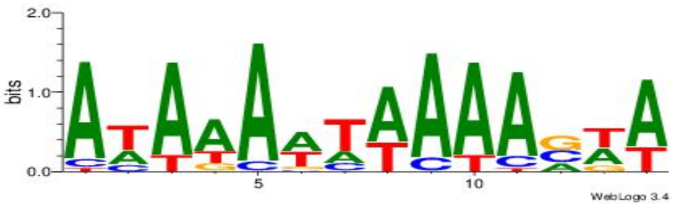
Dataset #:	2
Motif ID:	3
Motif name:	Motif 3
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	2

Number of overlap: 12
Similarity score: 0.0522317

Alignment:

```
TWSTTTWAWTTTWT
-WHTATTATTTDH-
```

Original motif Consensus sequence: AWAAAWTWAAASWA



Reverse complement motif Consensus sequence: TWSTTTWAWTTTW

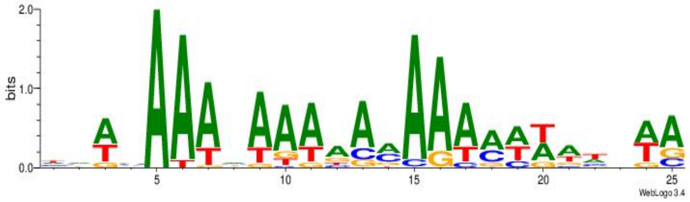
Dataset #: 5
Motif ID: 56
Motif name: TFM11
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 3
Number of overlap: 12
Similarity score: 0.0590505

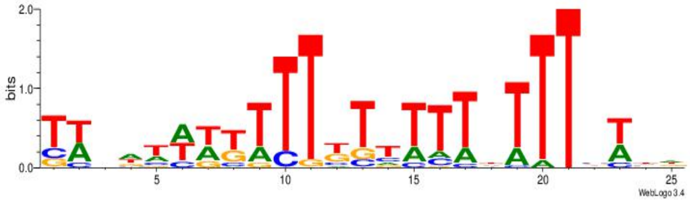
Alignment:

```
TWVHWWWYTTTYTTTTTHTTTVWBH
-----------WHTATTATTTDH--
```

Original motif Consensus sequence: HDWVAAAHAAAAAMAAAMWWWHBWA

Reverse complement motif Consensus sequence: TWVHWWWYTTTYTTTTTHTTTVWBH



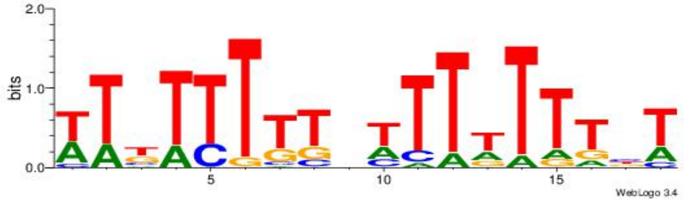


Dataset #: 5
Motif ID: 52
Motif name: TFM1
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 12
Similarity score: 0.0637702

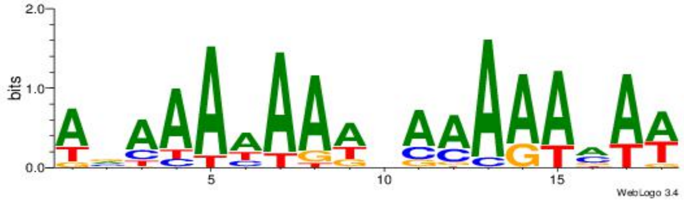
Alignment:

```
ABAAAAAAWHAAAAAARAW
HDAAATAATAHW------
```

Original motif Consensus sequence: WTKTTTTTHWTTTTTTBT



Reverse complement motif Consensus sequence: ABAAAAAAWHAAAAAARAW



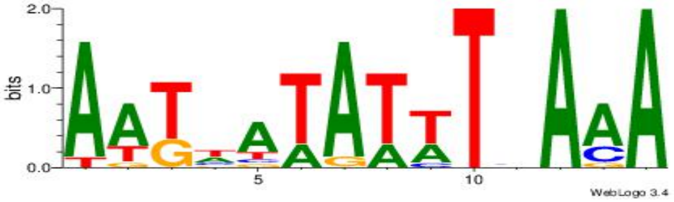
Dataset #: 2

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

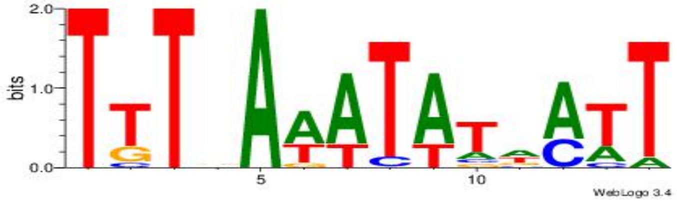
Alignment:

```
AATHATATWTHAAA
--WHTATTATTTDH
```

Original motif Consensus sequence: AATHATATWTHAAA



Reverse complement motif Consensus sequence: TTTDAWATATHAT

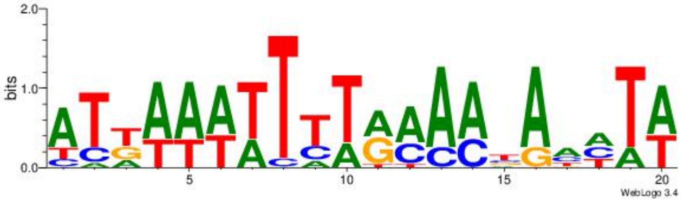


Dataset #: 5
Motif ID: 55
Motif name: TFM13
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 12
Similarity score: 0.0704475

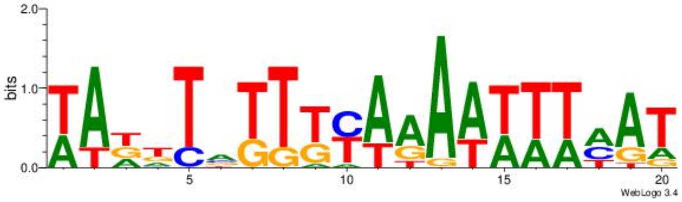
Alignment:

```
ATKAAWTTTTRMAABAHHTW
WHTATTATTTDH--------
```

Original motif   Consensus sequence: ATKAAWTTTTRMAABAHHTW



Reverse complement motif   Consensus sequence:
WAHHTVTTYKAAAAWTTRAT

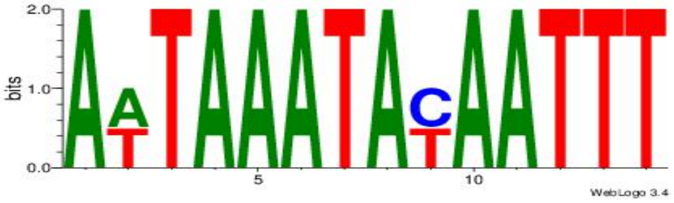


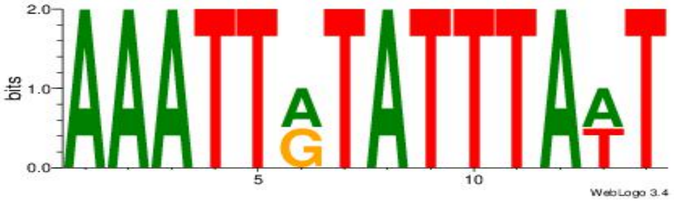
Dataset #:	2
Motif ID:	5
Motif name:	Motif 5
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	2
Number of overlap:	12
Similarity score:	0.0704475

Alignment:

```
AAATTKTATTTAWT
-WHTATTATTTDH-
```

Original motif   Consensus sequence: AWTAAATAYAATTT   Reverse complement motif   Consensus sequence: AAATTKTATTTAW



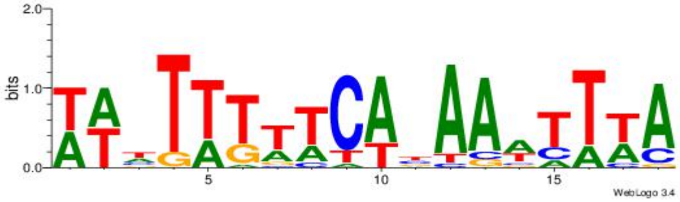


Dataset #:	5
Motif ID:	53
Motif name:	TFM3
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	12
Similarity score:	0.0763819

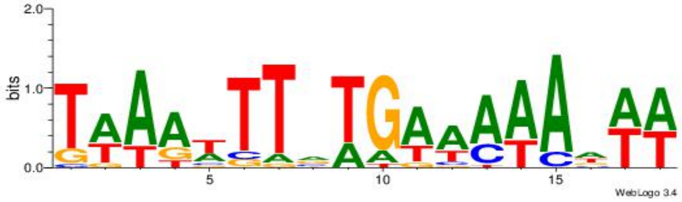
Alignment:

```
WWHTTTTTCABAAWTTWA
------WHTATTATTTDH
```

Original motif Consensus sequence: WWHTTTTTCABAAWTTWA



Reverse complement motif Consensus sequence: TWAAWTTVTGAAAAAHWW



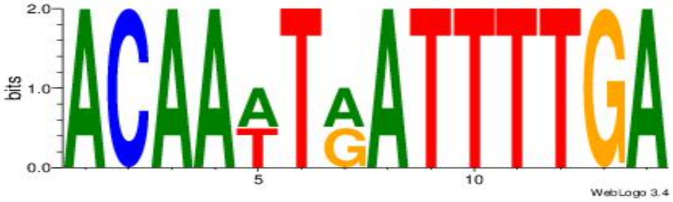
Dataset #:	2

Motif ID:	16
Motif name:	Motif 16
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	12
Similarity score:	0.0864198

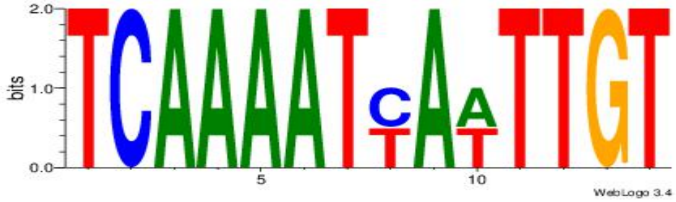
Alignment:

```
TCAAAATKAWTTGT
--WHTATTATTTDH
```

Original motif Consensus sequence: ACAAWTRATTTTGA



Reverse complement motif Consensus sequence: TCAAAATKAWTTG



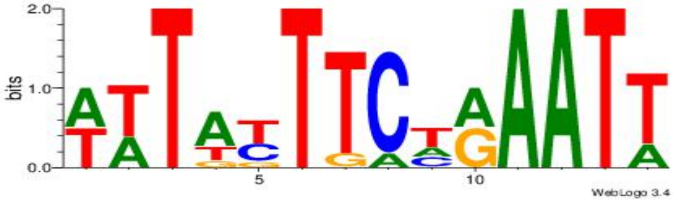
Dataset #:	2
Motif ID:	6
Motif name:	Motif 6
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	12
Similarity score:	0.09076

Alignment:

```
WWTAKTTCDKAATT
WHTATTATTTDH--
```

Original motif Consensus sequence: AATTYDGAARTAWW

Reverse complement motif Consensus sequence: WWTAKTTCDKAAT



Dataset #: 2

Motif ID: 19

Motif name: Motif 19

Matching format of first motif: Reverse Complement

Matching format of second motif: Reverse Complement

Direction: Backward

Position number: 2

Number of overlap: 12

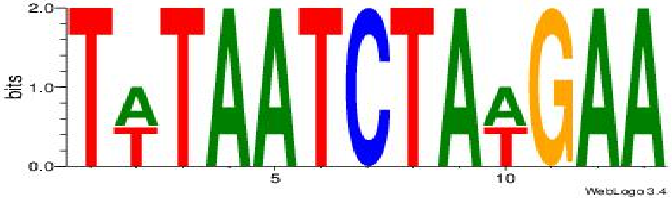
Similarity score: 0.096142

Alignment:

```
TWTAATCTAWGAA
WHTATTATTTDH-
```

Original motif Consensus sequence: TTCWTAGATTAWA

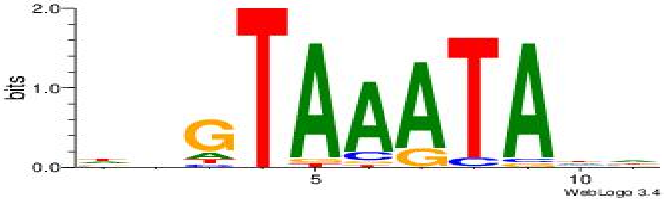
Reverse complement motif Consensus sequence: TWTAATCTAWGA



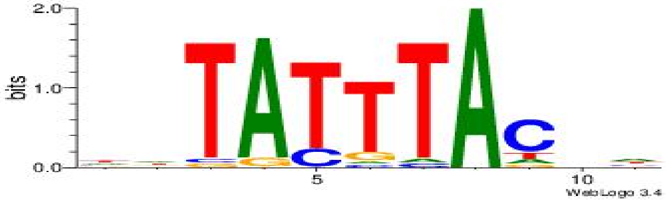
Significant Motifs - Global and Local Matching (Highest to Lowest)

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

Original motif Consensus sequence: DBGTAAATAHD



Reverse complement motif Consensus sequence: DHTATTTACBD



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

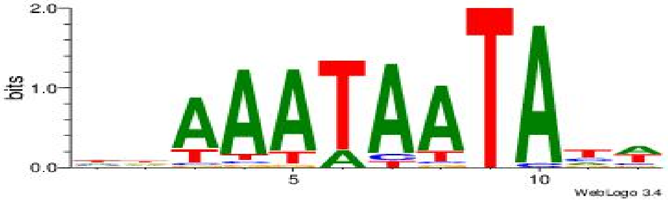
Dataset #:	4
Motif ID:	37
Motif name:	tkAAATAATAtw
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	11

Similarity score: 0.0162338

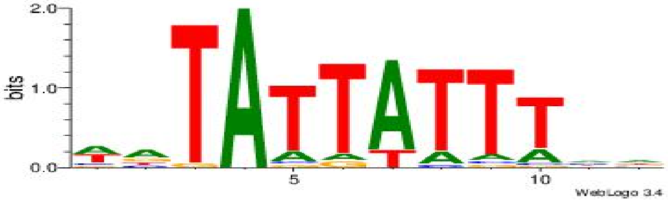
Alignment:

HDAAATAATAHW
-DBGTAAATAHD

Original motif Consensus sequence: HDAAATAATAHW



Reverse complement motif Consensus sequence: WHTATTATTTDH



Dataset #: 4

Motif ID: 41

Motif name: wwAAATAATAtw

Matching format of first motif: Reverse Complement

Matching format of second motif: Reverse Complement

Direction: Backward

Position number: 2

Number of overlap: 11

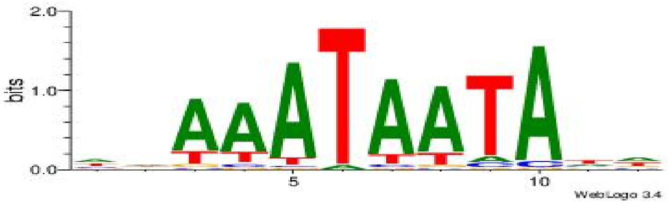
Similarity score: 0.0164863

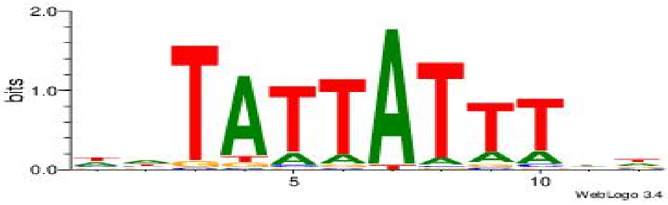
Alignment:

DDTATTATTTDH
DHTATTTACBD-

Original motif Consensus sequence: HDAAATAATADD

Reverse complement motif Consensus sequence: DDTATTATTTDH





Dataset #: 5

Motif ID: 56

Motif name: TFM11

Matching format of first motif: Reverse Complement

Matching format of second motif: Reverse Complement

Direction: Forward

Position number: 15

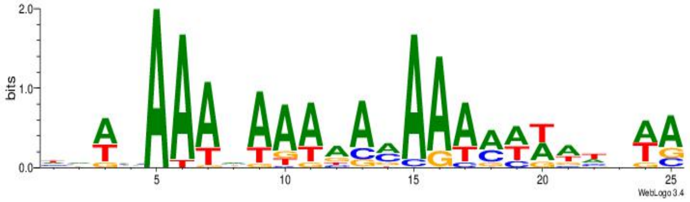
Number of overlap: 11

Similarity score: 0.0192768

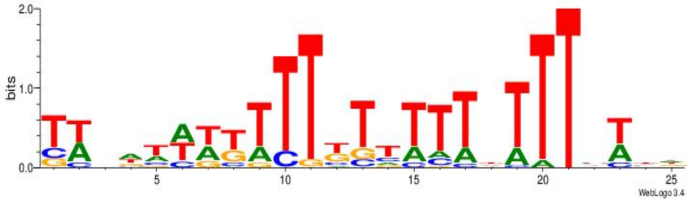
Alignment:

```
TWVHWWWYTTTYTTTTTHTTTVWBH
--------------DHTATTTACBD
```

Original motif Consensus sequence:
HDWVAAAHAAAAAMAAAMWWWHBWA



Reverse complement motif Consensus sequence:
TWVHWWWYTTTYTTTTTHTTTVWBH



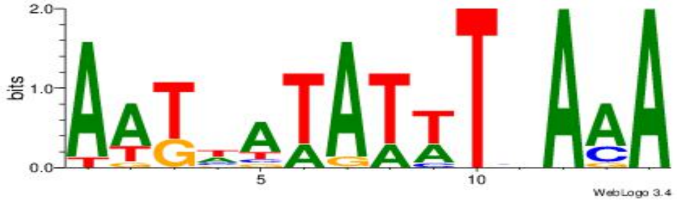
Dataset #: 2

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

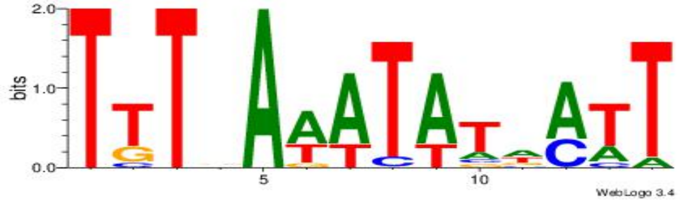
Alignment:

```
AATHATATWTHAAA
DHTATTTACBD---
```

Original motif   Consensus sequence: AATHATATWTHAAA



Reverse complement motif   Consensus sequence: TTTDAWATATHAT



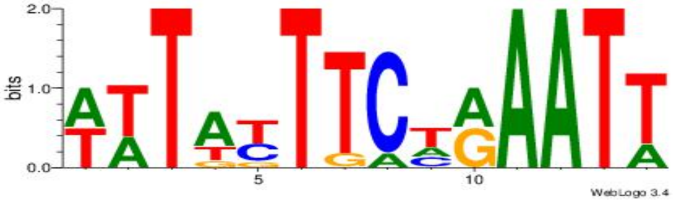
Dataset #:	2
Motif ID:	6
Motif name:	Motif 6
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	11
Similarity score:	0.027895

Alignment:

```
AATTYDGAARTAWW
---DBGTAAATAHD
```

Original motif Consensus sequence: AATTYDGAARTAWW

Reverse complement motif Consensus sequence: WWTAKTTCDKAAT



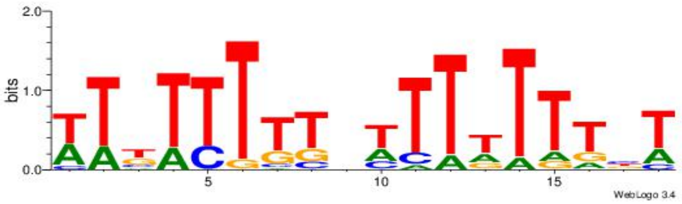
Dataset #:	5
Motif ID:	52
Motif name:	TFM1
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	11
Similarity score:	0.0283217

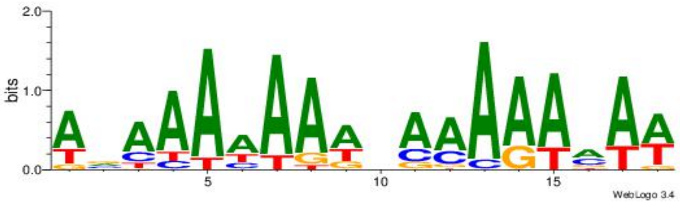
Alignment:

```
ABAAAAAAWHAAAAARAW
DBGTAAATAHD-------
```

Original motif Consensus sequence: WTKTTTTTHWTTTTTTBT

Reverse complement motif Consensus sequence: ABAAAAAAWHAAAAARAW



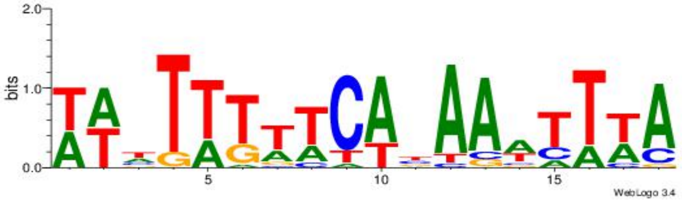


Dataset #: 5
Motif ID: 53
Motif name: TFM3
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 2
Number of overlap: 11
Similarity score: 0.0308097

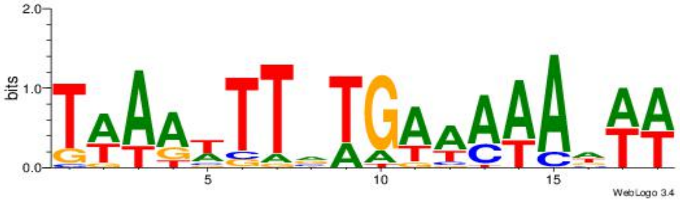
Alignment:

```
TWAAWTTVTGAAAAAHWW
------DBGTAAATAHD-
```

Original motif Consensus sequence: WWHTTTTTCABAAWTTWA



Reverse complement motif Consensus sequence: TWAAWTTVTGAAAAAHWW



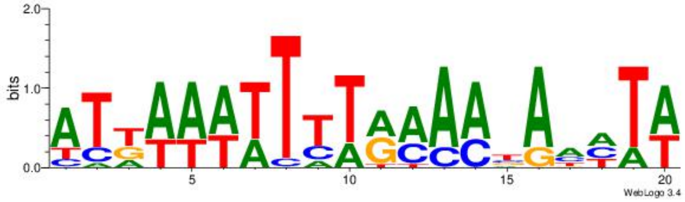
Dataset #: 5

Motif ID: 55
Motif name: TFM13
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 3
Number of overlap: 11
Similarity score: 0.0333874

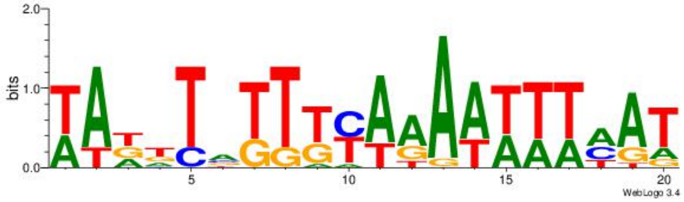
Alignment:

```
ATKAAWTTTTRMAABAHHTW
-------DBGTAAATAHD--
```

Original motif Consensus sequence: ATKAAWTTTTRMAABAHHTW



Reverse complement motif Consensus sequence: WAHHTVTTYKAAAAWTTRAT



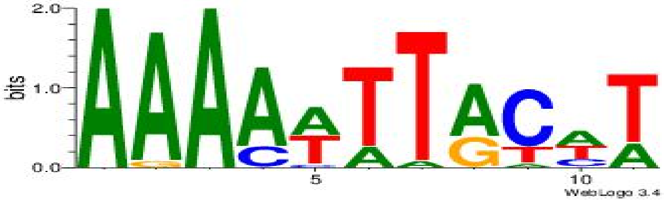
Dataset #: 2
Motif ID: 4
Motif name: Motif 4
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 11

Similarity score: 0.0361187

Alignment:

```
AWGKAAWTTTT
DBGTAAATAHD
```

Original motif Consensus sequence: AAAAWTTRCWT



Reverse complement motif Consensus sequence: AWGKAAWTTTT

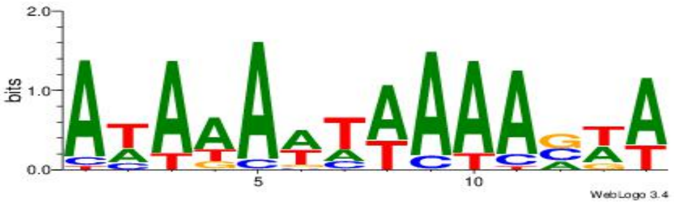
Dataset #:	2
Motif ID:	3
Motif name:	Motif 3
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2
Number of overlap:	11
Similarity score:	0.0410381

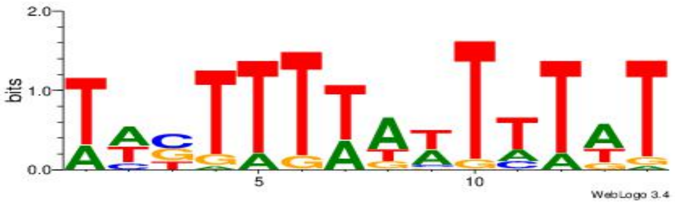
Alignment:

```
AWAAAWTWAAASWA
--DHTATTTACBD-
```

Original motif Consensus sequence: AWAAAWTWAAASWA

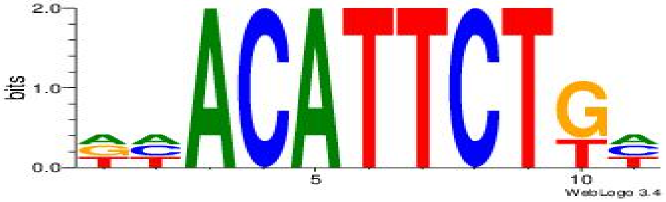
Reverse complement motif Consensus sequence: TWSTTTWAWTTT





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

Original motif Consensus sequence: DHACATTCTGH



Reverse complement motif Consensus sequence: HCAGAATGTHD

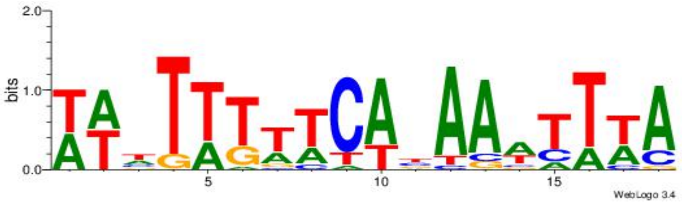
Best Matches for Significant Motif ID 44 (Highest to Lowest)

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

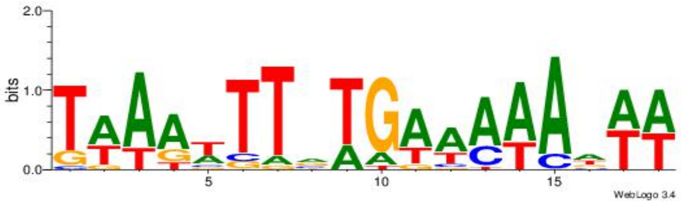
Alignment:

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

Original motif Consensus sequence: WWHTTTTTCABAAWTTWA



Reverse complement motif Consensus sequence: TWAAWTTVTGAAAAAHWW

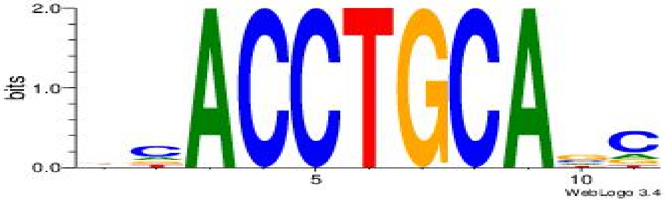


Dataset #:	4
Motif ID:	40
Motif name:	kcACCTGCAgc
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	11
Similarity score:	0.0238442

Alignment:

```
BCACCTGCABC
DHACATTCTGH
```

Original motif Consensus sequence: BCACCTGCABC

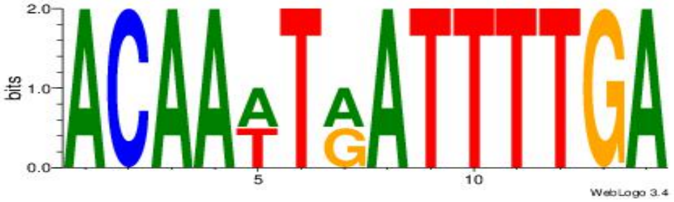


Reverse complement motif Consensus sequence: GBTGCAGGTGB

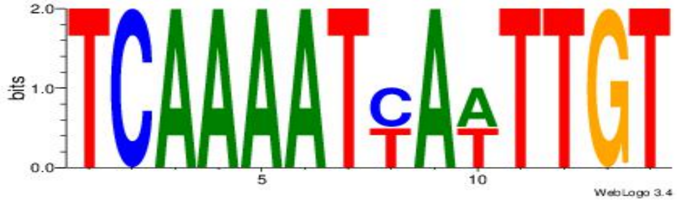
Dataset #: 2
Motif ID: 16
Motif name: Motif 16
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 4
Number of overlap: 11
Similarity score: 0.0258838

Alignment:
TCAAAATKAWTTGT
HCAGAATGTHD---

Original motif Consensus sequence: ACAAWTRATTTTGA



Reverse complement motif Consensus sequence: TCAAAATKAWTTG

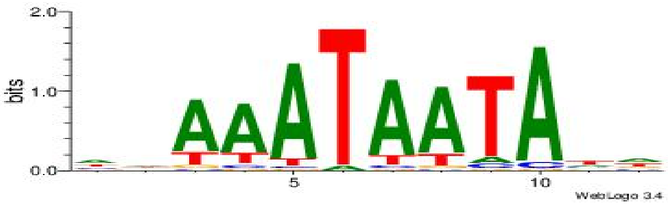


Dataset #: 4
Motif ID: 41
Motif name: wwAAATAATAtw
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 11

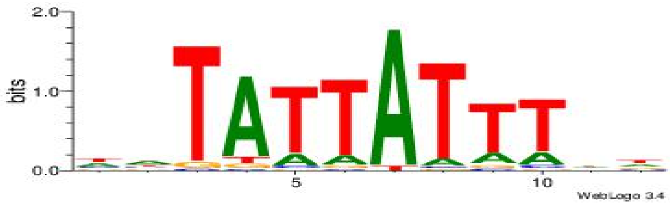
Similarity score: 0.0292508

Alignment:
```
DDTATTATTTDH
-HCAGAATGTHD
```

Original motif Consensus sequence: HDAAATAATADD



Reverse complement motif Consensus sequence: DDTATTATTTDH

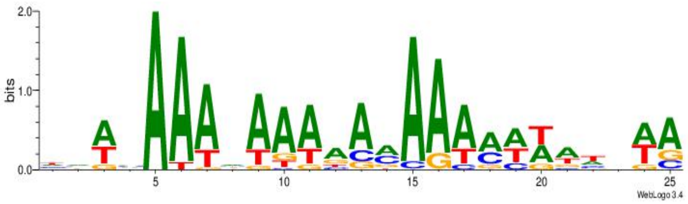


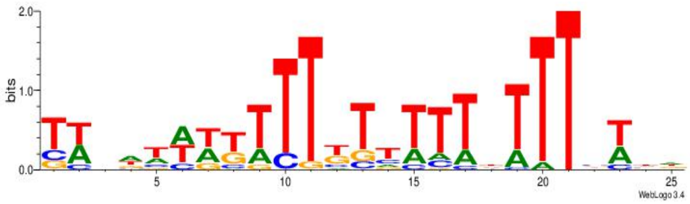
Dataset #: 5
Motif ID: 56
Motif name: TFM11
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 5
Number of overlap: 11
Similarity score: 0.0307858

Alignment:
```
TWVHWWWYTTTYTTTTTHTTTVWBH
----DHACATTCTGH----------
```

Original motif Consensus sequence:
HDWVAAAHAAAAAMAAAMWWWHBWA

Reverse complement motif Consensus sequence:
TWVHWWWYTTTYTTTTTHTTTVWBH



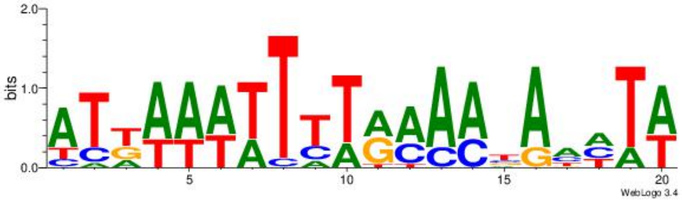


Dataset #:	5
Motif ID:	55
Motif name:	TFM13
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	9
Number of overlap:	11
Similarity score:	0.0357323

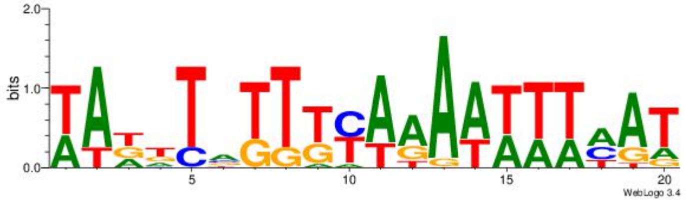
Alignment:

```
ATKAAWTTTTRMAABAHHTW
-DHACATTCTGH--------
```

Original motif Consensus sequence: ATKAAWTTTTRMAABAHHTW



Reverse complement motif Consensus sequence: WAHHTVTTYKAAAAWTTRAT



Dataset #:	4

Motif ID: 37

Motif name: tkAAATAATAtw

Matching format of first motif: Reverse Complement

Matching format of second motif: Reverse Complement

Direction: Forward

Position number: 2

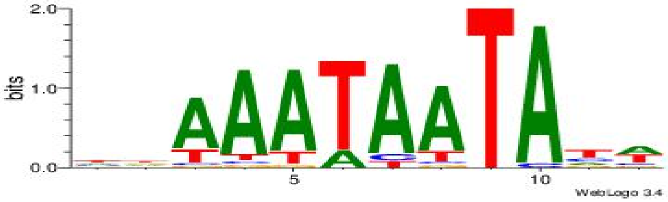
Number of overlap: 11

Similarity score: 0.0364899

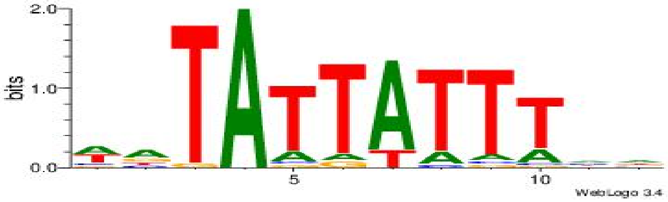
Alignment:

```
WHTATTATTTDH
-HCAGAATGTHD
```

Original motif Consensus sequence: HDAAATAATAHW



Reverse complement motif Consensus sequence: WHTATTATTTDH



Dataset #: 2

Motif ID: 6

Motif name: Motif 6

Matching format of first motif: Reverse Complement

Matching format of second motif: Original Motif

Direction: Backward

Position number: 4

Number of overlap: 11

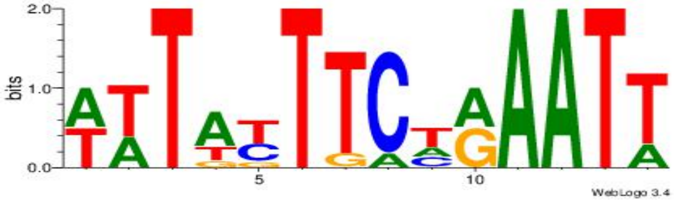
Similarity score: 0.0400884

Alignment:

```
AATTYDGAARTAWW
HCAGAATGTHD---
```

Original motif Consensus sequence: AATTYDGAARTAWW

Reverse complement motif Consensus sequence: WWTAKTTCDKAAT



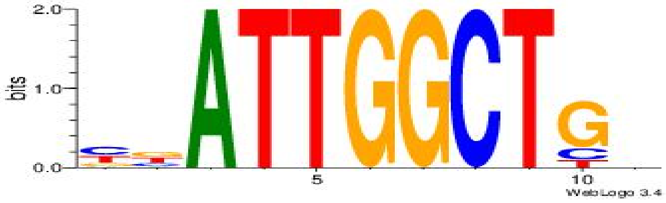
Dataset #:	4
Motif ID:	39
Motif name:	kCAGCCAATmr
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	11
Similarity score:	0.0412582

Alignment:

```
MBATTGGCTGH
DHACATTCTGH
```

Original motif Consensus sequence: DCAGCCAATVR

Reverse complement motif Consensus sequence: MBATTGGCTGH

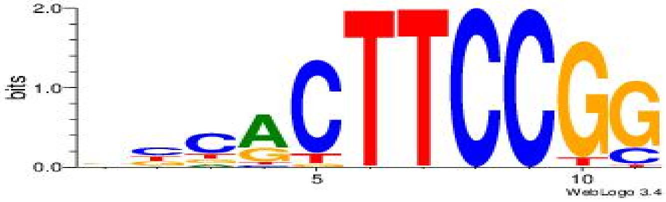


Dataset #: 3
Motif ID: 35
Motif name: GABPA
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 11
Similarity score: 0.0418896

Alignment:
CCGGAAGTGVV
HCAGAATGTHD

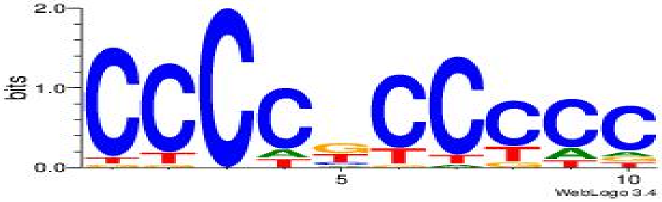
Original motif Consensus sequence: CCGGAAGTGVV

Reverse complement motif Consensus sequence: VVCACTTCCGG

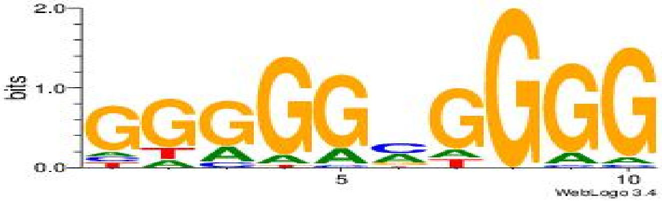


Dataset #: 3 Motif ID: 24 Motif name: SP1

Original motif Consensus sequence: CCCCKCCCCC



Reverse complement motif Consensus sequence: GGGGGYGGGG



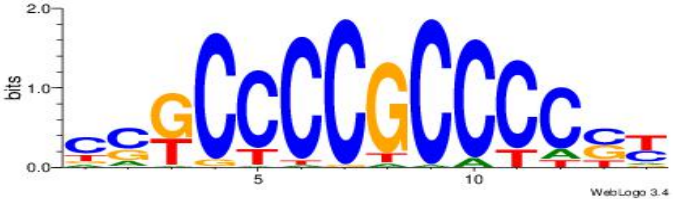
Best Matches for Significant Motif ID 24 (Highest to Lowest)

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

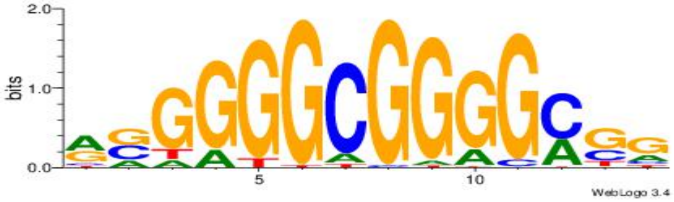
Alignment:

```
MSGGGGCGGGGYSG
-GGGGGYGGGG---
```

Original motif Consensus sequence: CSKCCCCGCCCCSY



Reverse complement motif Consensus sequence: MSGGGGCGGGGY

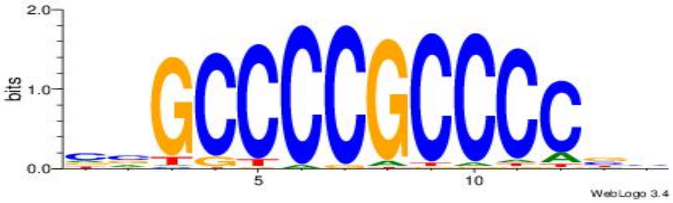


Dataset #:	4
Motif ID:	36
Motif name:	csGCCCCGCCCCsc
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	4
Number of overlap:	10
Similarity score:	0.00965796

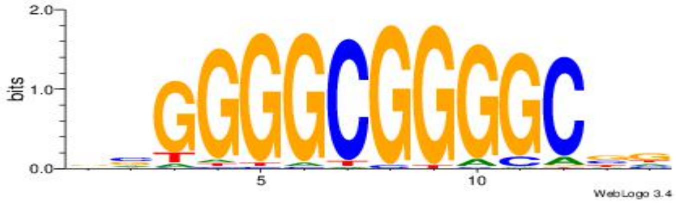
Alignment:

```
HVGCCCCGCCCCBB
---CCCCKCCCCC-
```

Original motif Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGC



Dataset #:	4
Motif ID:	38
Motif name:	cccGCCCCGCCCCsb
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2
Number of overlap:	10

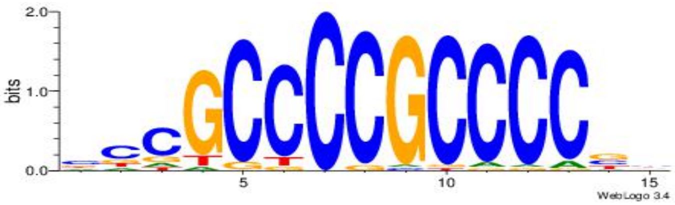
Similarity score: 0.0127292

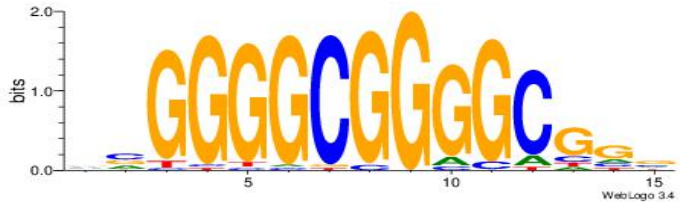
Alignment:

```
BCCGCCCCGCCCCBB
----CCCCKCCCCC-
```

Original motif Consensus sequence: BCCGCCCCGCCCCBB

Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB





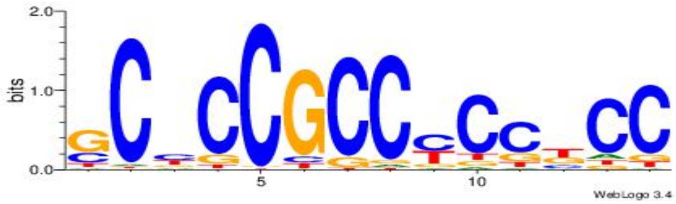
Dataset #:	5
Motif ID:	50
Motif name:	TFF11
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	4
Number of overlap:	10
Similarity score:	0.0174405

Alignment:

```
GGMGGRGGCGGVGC
---GGGGGYGGGG-
```

Original motif Consensus sequence: GGMGGRGGCGGVGC

Reverse complement motif Consensus sequence: GCVCCGCCMCCYC

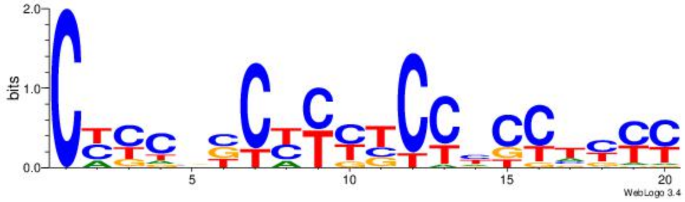


Dataset #:	5
Motif ID:	54
Motif name:	TFM12
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	7
Number of overlap:	10
Similarity score:	0.0301548

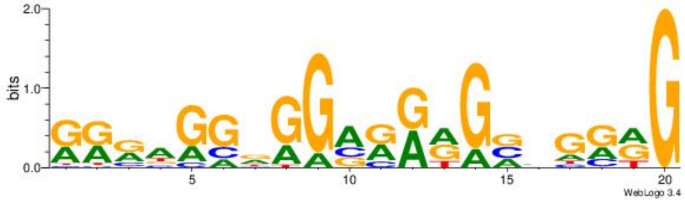
Alignment:

```
CYYCBBCYYYTCCHCCTYYY
------CCCCKCCCCC----
```

Original motif Consensus sequence: CYYCBBCYYYTCCHCCTYYY



Reverse complement motif Consensus sequence: KKKAGGDGGAKKMGBBGKMG



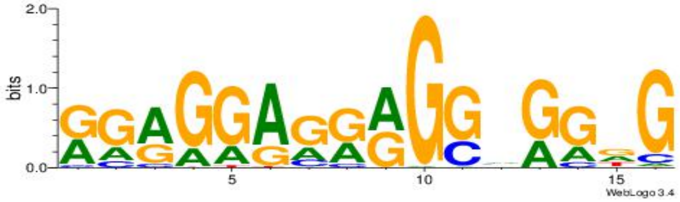
Dataset #:	5

Motif ID:	51
Motif name:	TFM2
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	10
Similarity score:	0.0329167

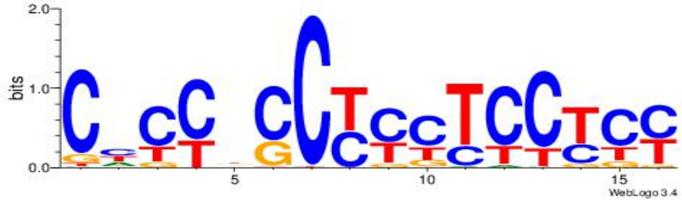
Alignment:

```
RGRGGAGRRGGHGGDG
------GGGGGYGGGG
```

Original motif   Consensus sequence: RGRGGAGRRGGHGGDG



Reverse complement motif   Consensus sequence: CHCCBCCKMCTCCKCM



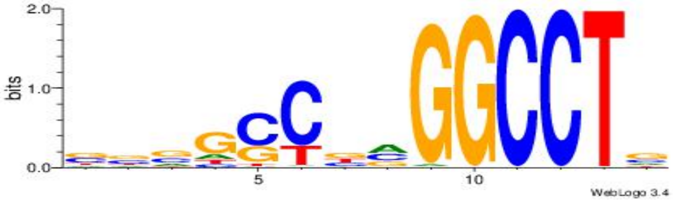
Dataset #:	3
Motif ID:	22
Motif name:	Zfx
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	5
Number of overlap:	10

Similarity score: 0.0540825

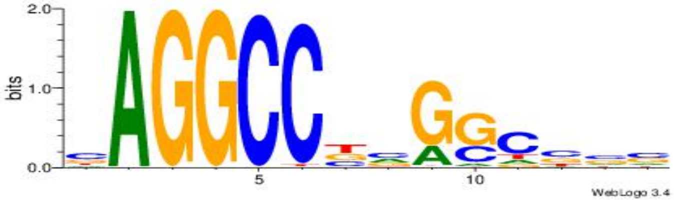
Alignment:

```
BBVGCCBVGGCCTV
----GGGGGYGGGG
```

Original motif Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif Consensus sequence: VAGGCCBBGGCV



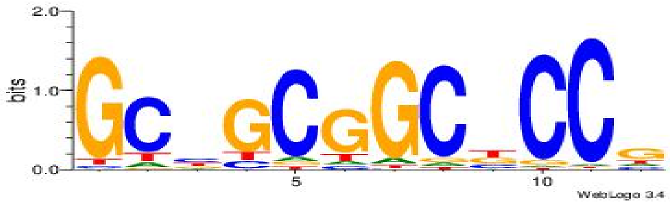
Dataset #:	5
Motif ID:	49
Motif name:	TFF1
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	2
Number of overlap:	10
Similarity score:	0.0557738

Alignment:

```
GCVGCGGCBCCG
-CCCCKCCCCC-
```

Original motif Consensus sequence: CGGVGCCGCVGC

Reverse complement motif Consensus sequence: GCVGCGGCBCCG

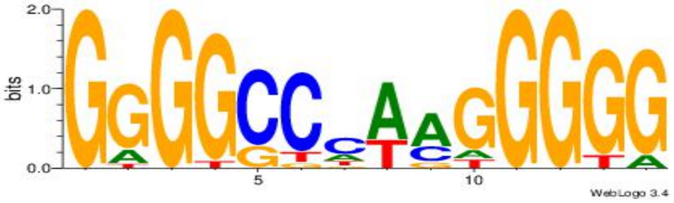


Dataset #: 3
Motif ID: 30
Motif name: PLAG1
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 4
Number of overlap: 10
Similarity score: 0.0600992

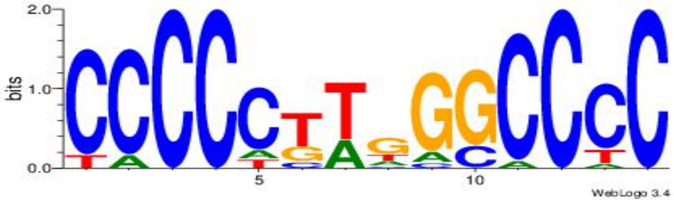
Alignment:

```
CCCCCTTGGGCCCC
-CCCCKCCCCCC---
```

Original motif Consensus sequence: GGGGCCCAAGGGGG



Reverse complement motif Consensus sequence: CCCCCTTGGGCCC



Dataset #: 3
Motif ID: 27

Motif name:	Klf4
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	10
Similarity score:	0.0637183

Alignment:

```
GCCYCMCCCD
CCCCKCCCCC
```

Original motif Consensus sequence: DGGGYGKGGC

Reverse complement motif Consensus sequence: GCCYCMCCCD

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

Original motif Consensus sequence: YGCGTG

Reverse complement motif Consensus sequence: CACGCM

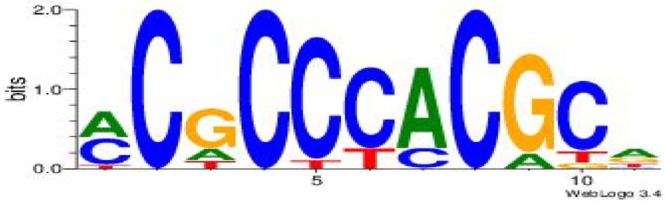
Best Matches for Significant Motif ID 32 (Highest to Lowest)

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

Alignment:
YCGCCCACGCH
-----CACGCM

Original motif Consensus sequence: HGCGTGGGCGK

Reverse complement motif Consensus sequence: YCGCCCACGCH



Dataset #: 3
Motif ID: 29
Motif name: HIF1AARNT
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 2
Number of overlap: 6

Similarity score: 0.0112447

Alignment:

VBACGTGV
-YGCGTG-

Original motif Consensus sequence: VBACGTGV

Reverse complement motif Consensus sequence: VCACGTBV

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

Alignment:

GCCACGTGSD
--YGCGTG--

Original motif Consensus sequence: HSCACGTGGC

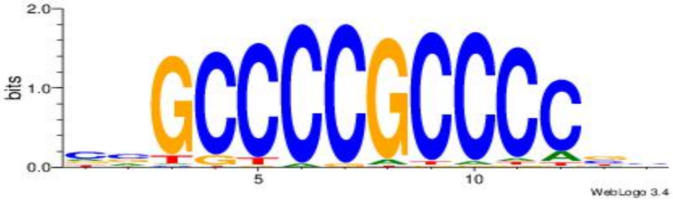
Reverse complement motif Consensus sequence: GCCACGTGSD

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

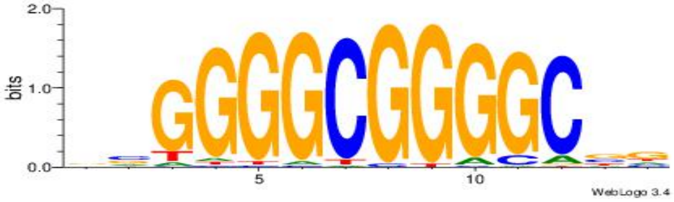
Alignment:

```
HVGCCCCGCCCCBB
----CACGCM----
```

Original motif Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGC



Dataset #:	3
Motif ID:	34

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

Alignment:

```
DCCACGTGCV
--YGCGTG--
```

Original motif Consensus sequence: VGCACGTGGH

Reverse complement motif Consensus sequence: DCCACGTGCV

Dataset #: 1
Motif ID: 1
Motif name: Motif 1
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 3
Number of overlap: 6
Similarity score: 0.040625

Alignment:

```
GCCCCGCC
--CACGCM
```

Original motif Consensus sequence: GGCGGGGC

Reverse complement motif Consensus sequence: GCCCCGCC

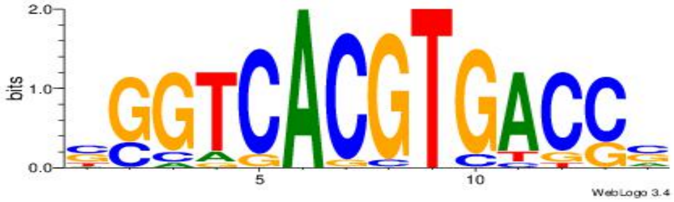
Dataset #:	4
Motif ID:	42
Motif name:	sSGTCACGTGACSs
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	5
Number of overlap:	6
Similarity score:	0.0412037

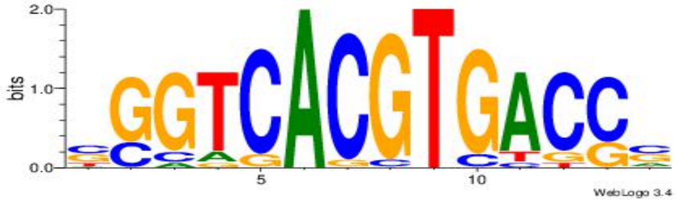
Alignment:

```
SGGTCACGTGACCS
----YGCGTG----
```

Original motif Consensus sequence: SGGTCACGTGACCS

Reverse complement motif Consensus sequence: SGGTCACGTGACC





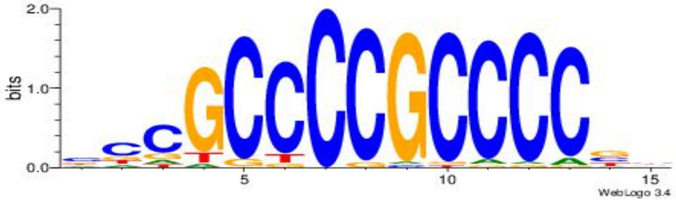
Dataset #:	4
Motif ID:	38
Motif name:	cccGCCCCGCCCCsb
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	6
Number of overlap:	6
Similarity score:	0.0425089

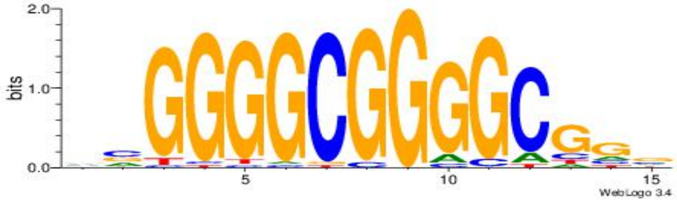
Alignment:

```
BCCGCCCCGCCCCBB
-----CACGCM----
```

Original motif Consensus sequence: BCCGCCCCGCCCCBB

Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB





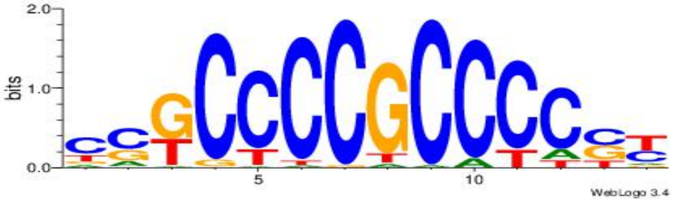
Dataset #:	2

Motif ID:	7
Motif name:	Motif 7
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	5
Number of overlap:	6
Similarity score:	0.0465867

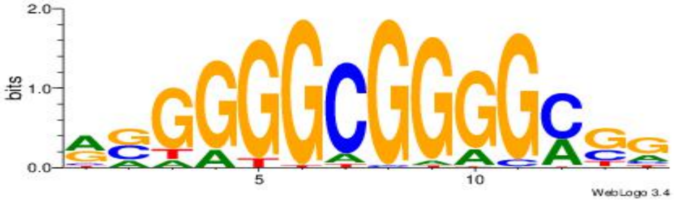
Alignment:

```
MSGGGGCGGGGYSG
----YGCGTG----
```

Original motif Consensus sequence: CSKCCCCGCCCCSY



Reverse complement motif Consensus sequence: MSGGGGCGGGGY



Dataset #:	5
Motif ID:	47
Motif name:	TFW2
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	6
Similarity score:	0.0469722

Alignment:

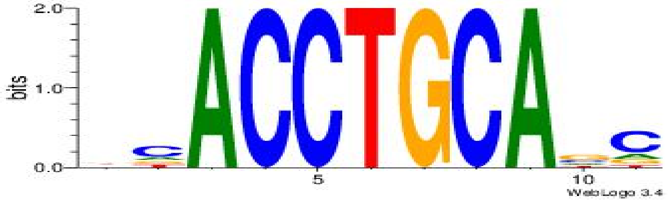
```
SCGCGCGG
-YGCGTG-
```

Original motif   Consensus sequence: SCGCGCGG

Reverse complement motif   Consensus sequence: CCGCGCGS

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

Original motif   Consensus sequence: BCACCTGCABC



Reverse complement motif   Consensus sequence: GBTGCAGGTGB

Best Matches for Significant Motif ID 40 (Highest to Lowest)

Dataset #:	4
Motif ID:	43
Motif name:	wsTACwGTAsw
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1

Number of overlap: 11
Similarity score: 0.0215284

Alignment:
DBTACWGTAVH
BCACCTGCABC

Original motif Consensus sequence: HVTACWGTABD

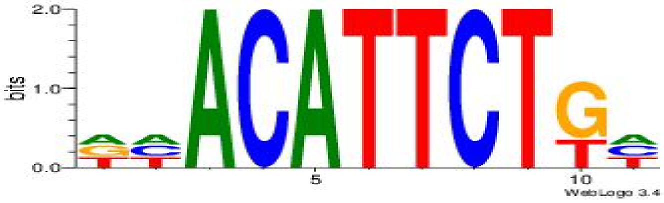
Reverse complement motif Consensus sequence: DBTACWGTAVH

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

Alignment:
DHACATTCTGH
BCACCTGCABC

Original motif Consensus sequence: DHACATTCTGH

Reverse complement motif Consensus sequence: HCAGAATGTHD

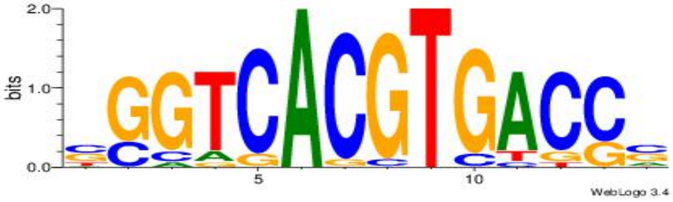


Dataset #:	4
Motif ID:	42
Motif name:	sSGTCACGTGACSs
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	4
Number of overlap:	11
Similarity score:	0.031338

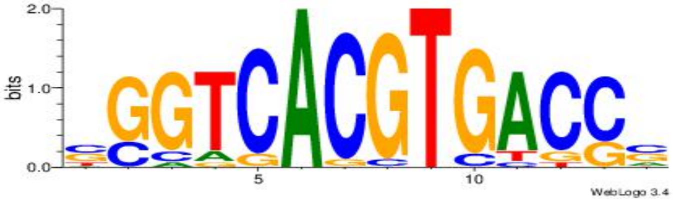
Alignment:

```
SGGTCACGTGACCS
---BCACCTGCABC
```

Original motif Consensus sequence: SGGTCACGTGACCS



Reverse complement motif Consensus sequence: SGGTCACGTGACC



Dataset #:	5
Motif ID:	50

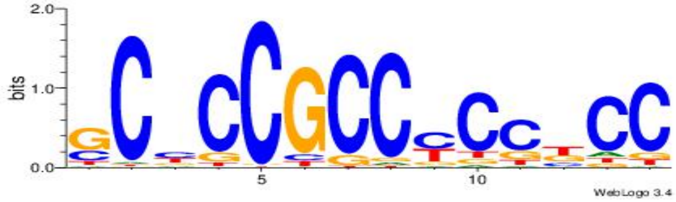
Motif name:	TFF11
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	4
Number of overlap:	11
Similarity score:	0.034471

Alignment:

```
GCVCCGCCMCCYCC
BCACCTGCABC---
```

Original motif   Consensus sequence: GGMGGRGGCGGVGC

Reverse complement motif   Consensus sequence: GCVCCGCCMCCYC

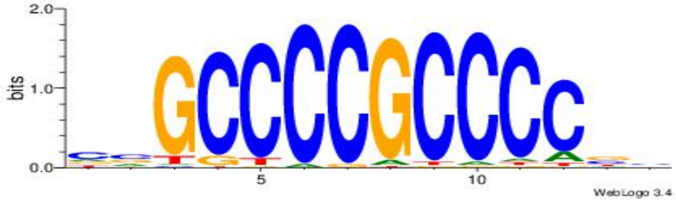


Dataset #:	4
Motif ID:	36
Motif name:	csGCCCCGCCCCsc
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	11
Similarity score:	0.0402518

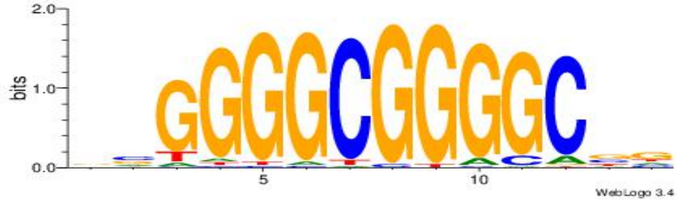
Alignment:

```
HVGCCCCGCCCCBB
-BCACCTGCABC--
```

Original motif   Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif   Consensus sequence: BBGGGGCGGGGC



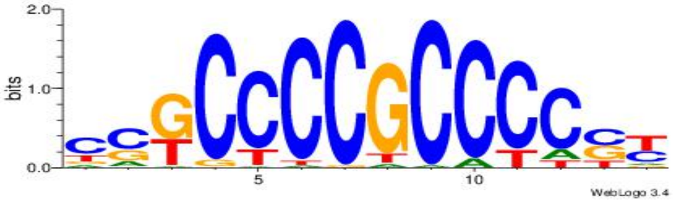
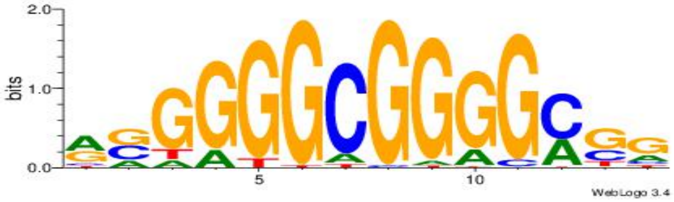
Dataset #:	2
Motif ID:	7
Motif name:	Motif 7
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	11
Similarity score:	0.0411257

Alignment:

```
CSKCCCCGCCCCSY
-BCACCTGCABC--
```

Original motif   Consensus sequence: CSKCCCCGCCCCSY

Reverse complement motif   Consensus sequence: MSGGGGCGGGGY

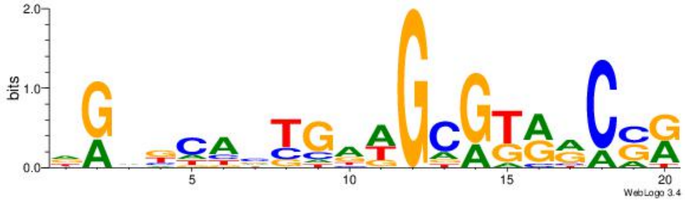



Dataset #:	3
Motif ID:	31
Motif name:	Pax5
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	5
Number of overlap:	11
Similarity score:	0.0420218

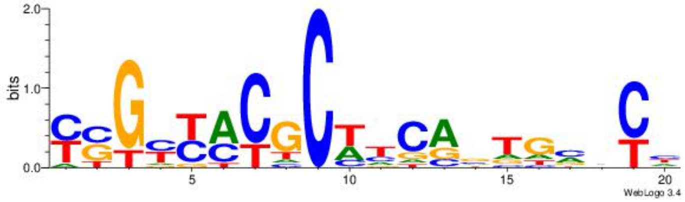
Alignment:

```
DGVBCABTGDWGCGKRRCSR
----GBTGCAGGTGB-----
```

Original motif Consensus sequence: DGVBCABTGDWGCGKRRCSR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD



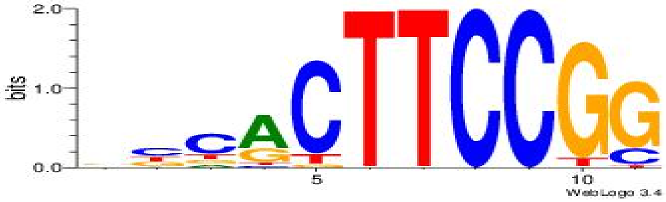
Dataset #: 3

Motif ID: 35
Motif name: GABPA
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 11
Similarity score: 0.0423275

Alignment:
```
CCGGAAGTGVV
GBTGCAGGTGB
```

Original motif Consensus sequence: CCGGAAGTGVV

Reverse complement motif Consensus sequence: VVCACTTCCGG

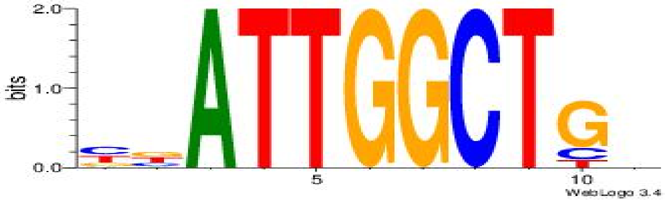


Dataset #: 4
Motif ID: 39
Motif name: kCAGCCAATmr
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 11
Similarity score: 0.0439586

Alignment:
DCAGCCAATVR
GBTGCAGGTGB

Original motif   Consensus sequence: DCAGCCAATVR

Reverse complement motif   Consensus sequence: MBATTGGCTGH

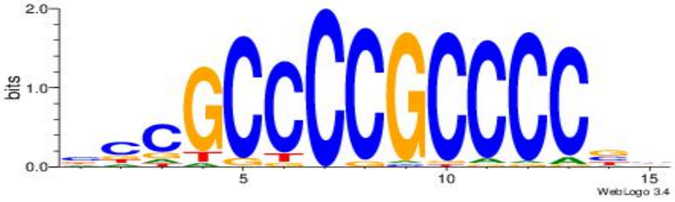


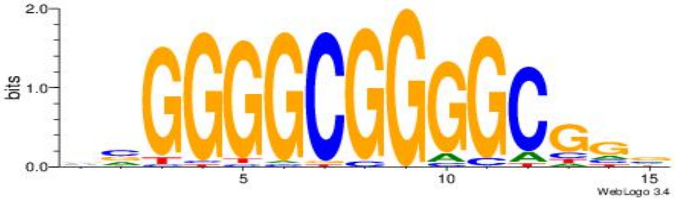
Dataset #:	4
Motif ID:	38
Motif name:	cccGCCCCGCCCCsb
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	3
Number of overlap:	11
Similarity score:	0.0461444

Alignment:
BCCGCCCCGCCCCBB
--BCACCTGCABC--

Original motif   Consensus sequence: BCCGCCCCGCCCCBB

Reverse complement motif   Consensus sequence: BBGGGGCGGGGCGGB





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

Original motif Consensus sequence: HVTACWGTABD

Reverse complement motif Consensus sequence: DBTACWGTAVH

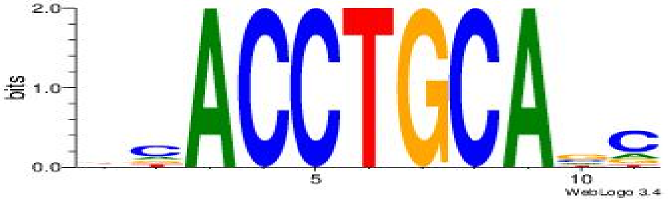
Best Matches for Significant Motif ID 43 (Highest to Lowest)

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

Alignment:

```
GBTGCAGGTGB
HVTACWGTABD
```

Original motif Consensus sequence: BCACCTGCABC



Reverse complement motif Consensus sequence: GBTGCAGGTGB

Dataset #: 4

Motif ID: 41

Motif name: wwAAATAATAtw

Matching format of first motif: Original Motif

Matching format of second motif: Reverse Complement

Direction: Backward

Position number: 1

Number of overlap: 11

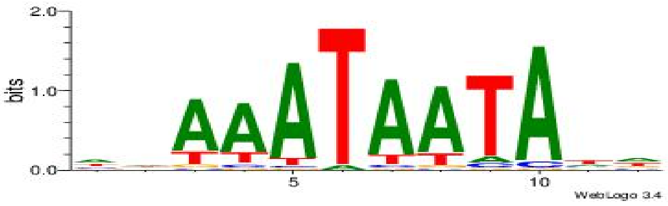
Similarity score: 0.0309343

Alignment:

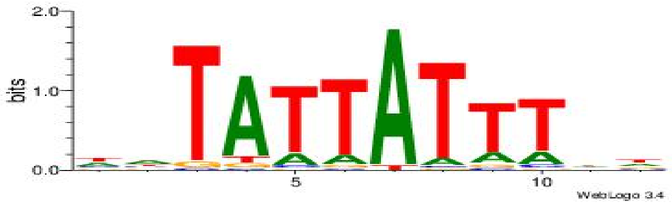
DDTATTATTTDH

-HVTACWGTABD

Original motif Consensus sequence: HDAAATAATADD



Reverse complement motif Consensus sequence: DDTATTATTTDH

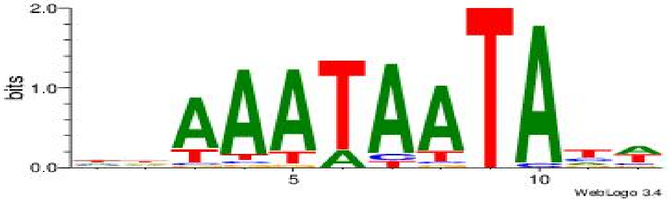


Dataset #: 4
Motif ID: 37
Motif name: tkAAATAATAtw
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 11
Similarity score: 0.0337121

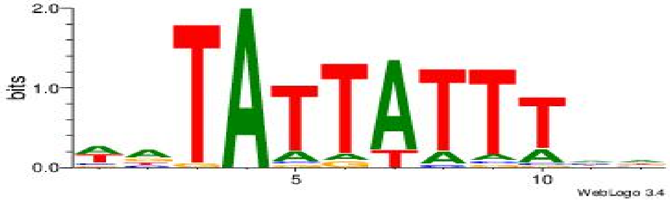
Alignment:

```
WHTATTATTTDH
-HVTACWGTABD
```

Original motif Consensus sequence: HDAAATAATAHW



Reverse complement motif Consensus sequence: WHTATTATTTDH



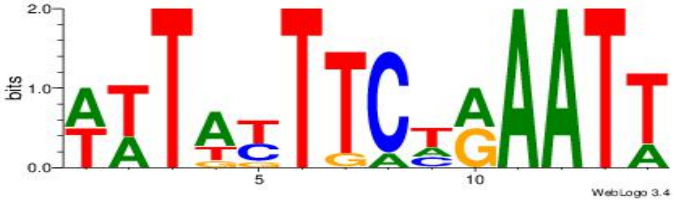
Dataset #: 2
Motif ID: 6
Motif name: Motif 6
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 4
Number of overlap: 11

Similarity score: 0.0353535

Alignment:
AATTYDGAARTAWW
HVTACWGTABD---

Original motif Consensus sequence: AATTYDGAARTAWW

Reverse complement motif Consensus sequence: WWTAKTTCDKAAT

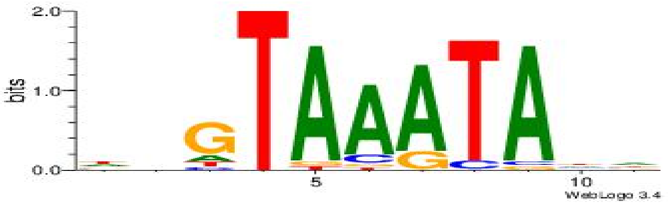


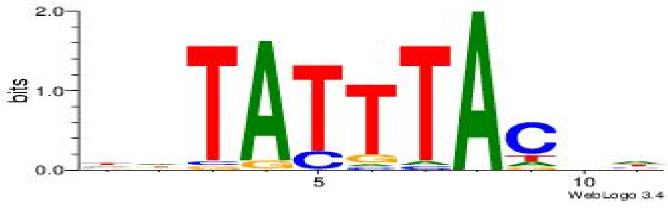
Dataset #: 4
Motif ID: 45
Motif name: wbgTAAATAww
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 11
Similarity score: 0.037518

Alignment:
DBGTAAATAHD
DBTACWGTAVH

Original motif Consensus sequence: DBGTAAATAHD

Reverse complement motif Consensus sequence: DHTATTTACBD



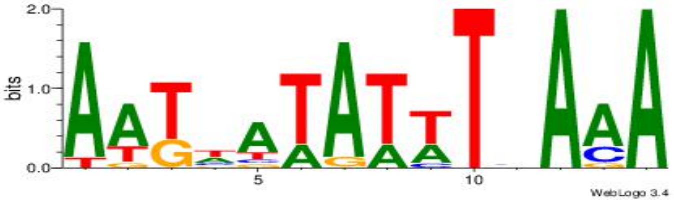


Dataset #:	2
Motif ID:	9
Motif name:	Motif 9
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	4
Number of overlap:	11
Similarity score:	0.0397727

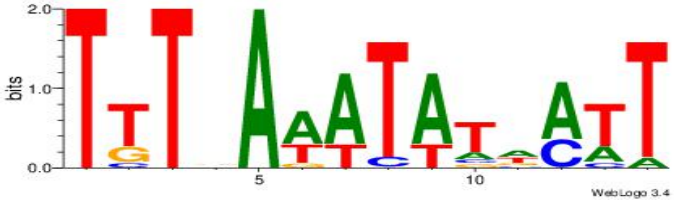
Alignment:

```
TTTDAWATATHATT
DBTACWGTAVH---
```

Original motif Consensus sequence: AATHATATWTHAAA



Reverse complement motif Consensus sequence: TTTDAWATATHAT



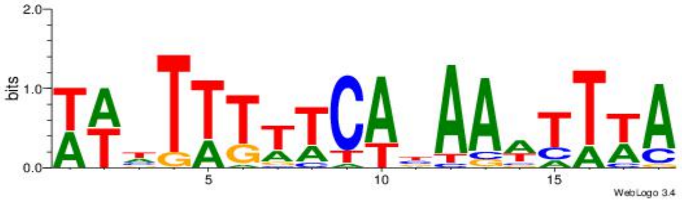
Dataset #:	5
Motif ID:	53

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

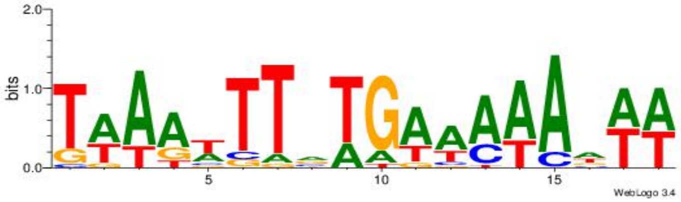
Alignment:

```
TWAAWTTVTGAAAAAHWW
---HVTACWGTABD----
```

Original motif Consensus sequence: WWHTTTTTCABAAWTTWA



Reverse complement motif Consensus sequence: TWAAWTTVTGAAAAAHWW

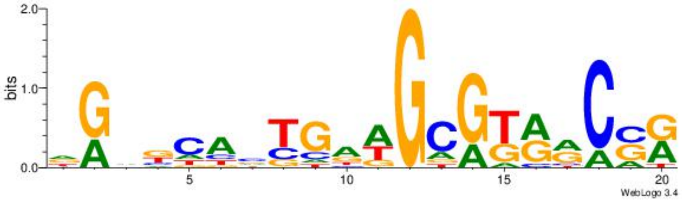


Dataset #: 3
Motif ID: 31
Motif name: Pax5
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 6
Number of overlap: 11
Similarity score: 0.042298

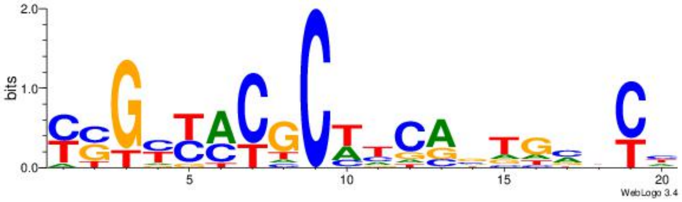
Alignment:

```
DGVBCABTGDWGCGKRRCSR
-----HVTACWGTABD----
```

Original motif Consensus sequence: DGVBCABTGDWGCGKRRCSR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD



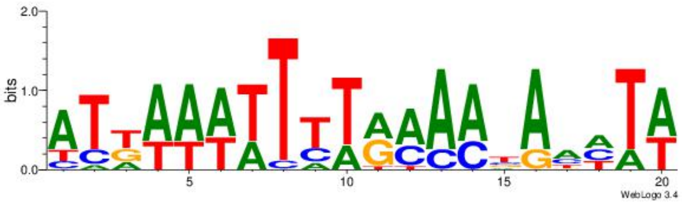
Dataset #:	5
Motif ID:	55
Motif name:	TFM13
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	3
Number of overlap:	11
Similarity score:	0.0445707

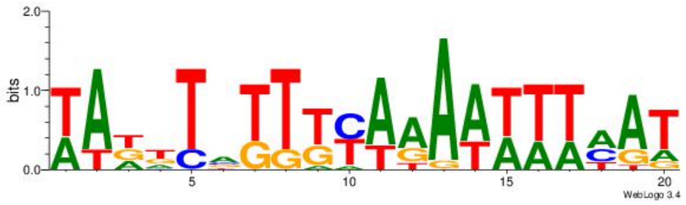
Alignment:

```
ATKAAWTTTTRMAABAHHTW
-------DBTACWGTAVH--
```

Original motif Consensus sequence: ATKAAWTTTTRMAABAHHTW

Reverse complement motif Consensus sequence: WAHHTVTTYKAAAAWTTRAT





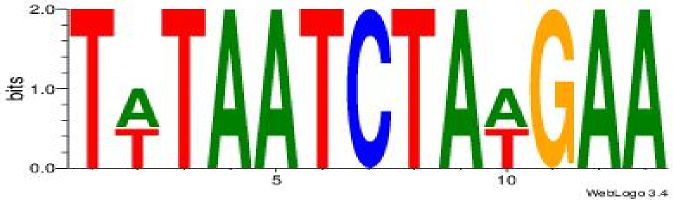
Dataset #:	2
Motif ID:	19
Motif name:	Motif 19
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	3
Number of overlap:	11
Similarity score:	0.0460859

Alignment:

```
TTCWTAGATTAWA
DBTACWGTAVH--
```

Original motif Consensus sequence: TTCWTAGATTAWA

Reverse complement motif Consensus sequence: TWTAATCTAWGAA



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

Original motif Consensus sequence: ATAAAA

Reverse complement motif Consensus sequence: TTTTAT

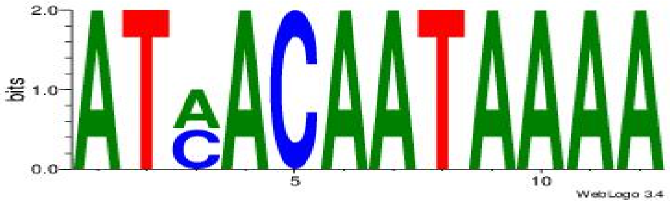
Best Matches for Significant Motif ID 21 (Highest to Lowest)

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

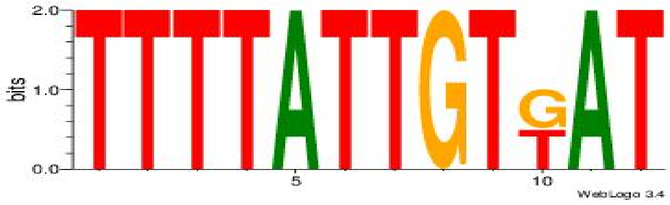
Alignment:

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

Original motif Consensus sequence: ATMACAATAAAA



Reverse complement motif Consensus sequence: TTTTATTGTYAT

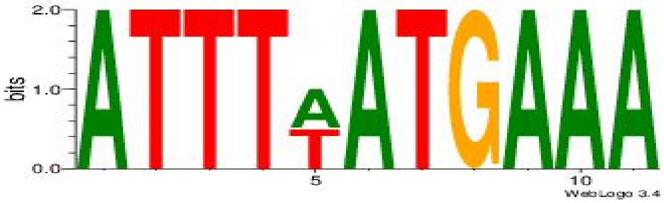


Dataset #: 2
Motif ID: 11
Motif name: Motif 11
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 5
Number of overlap: 6
Similarity score: 0.0208333

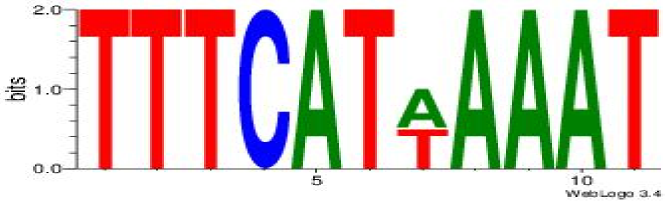
Alignment:

```
TTTCATWAAAT
-ATAAAA----
```

Original motif Consensus sequence: ATTTWATGAAA



Reverse complement motif Consensus sequence: TTTCATWAAAT

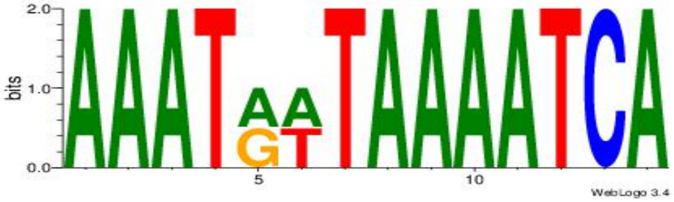


Dataset #: 2
Motif ID: 8
Motif name: Motif 8
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 6
Number of overlap: 6

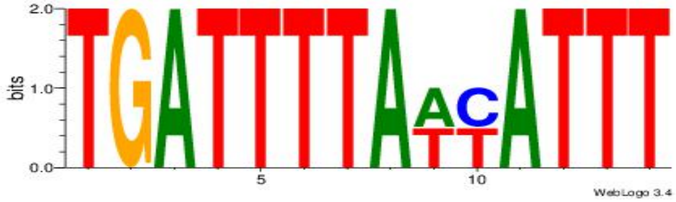
Similarity score: 0.0208333

Alignment:
AAATRWTAAAATCA
-----ATAAAA---

Original motif Consensus sequence: AAATRWTAAAATCA



Reverse complement motif Consensus sequence: TGATTTTAWKATT

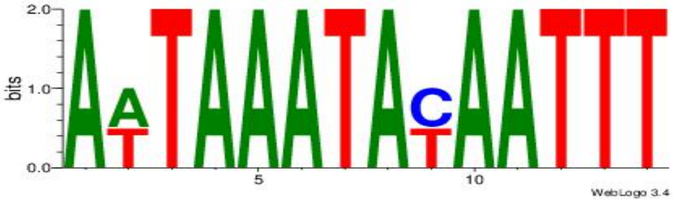


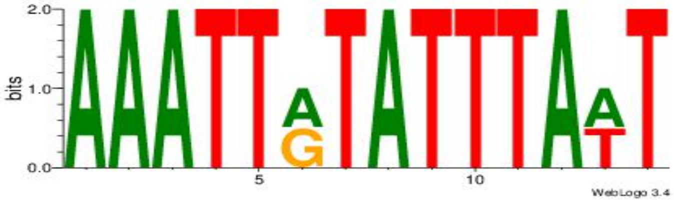
Dataset #:	2
Motif ID:	5
Motif name:	Motif 5
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	6
Number of overlap:	6
Similarity score:	0.0208333

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

Original motif Consensus sequence: AWTAAATAYAATTT

Reverse complement motif Consensus sequence: AAATTKTATTTAW



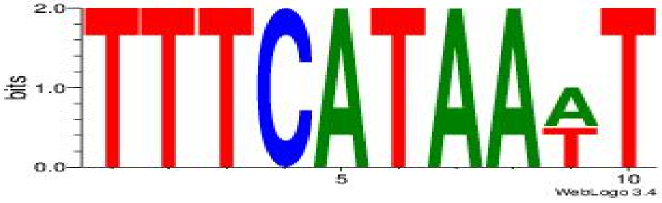


Dataset #:	2
Motif ID:	10
Motif name:	Motif 10
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	6
Similarity score:	0.0416667

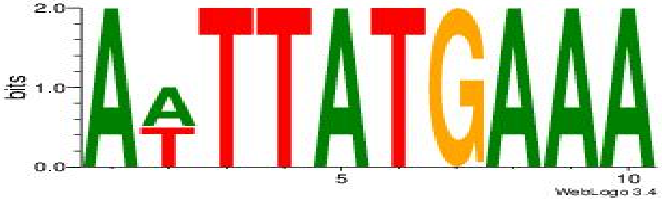
Alignment:

```
TTTCATAAWT
----TTTTAT
```

Original motif   Consensus sequence: TTTCATAAWT



Reverse complement motif   Consensus sequence: AWTTATGAAA



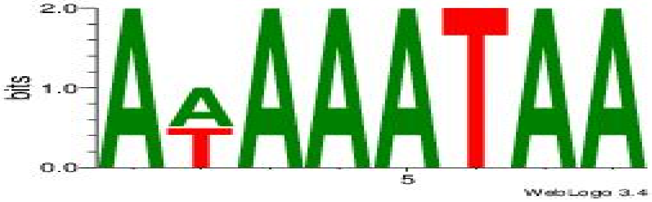
Dataset #:	2
Motif ID:	14

Motif name:	Motif 14
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	6
Similarity score:	0.0625

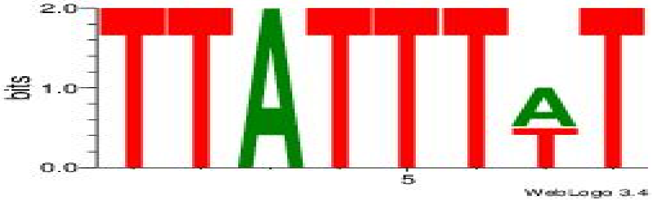
Alignment:

```
AWAAATAA
ATAAAA--
```

Original motif Consensus sequence: AWAAATAA



Reverse complement motif Consensus sequence: TTATTTWT

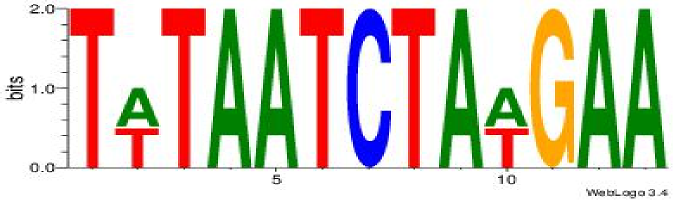


Dataset #:	2
Motif ID:	19
Motif name:	Motif 19
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	8
Number of overlap:	6
Similarity score:	0.0625

Alignment:
TWTAATCTAWGAA
TTTTAT-------

Original motif Consensus sequence: TTCWTAGATTAWA

Reverse complement motif Consensus sequence: TWTAATCTAWGA

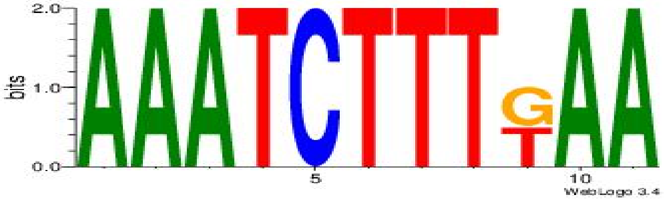


Dataset #:	2
Motif ID:	20
Motif name:	Motif 20
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	6
Number of overlap:	6
Similarity score:	0.0625

Alignment:
TTMAAAGATTT
ATAAAA-----

Original motif Consensus sequence: TTMAAAGATTT

Reverse complement motif Consensus sequence: AAATCTTTYAA



Dataset #: 4

Motif ID: 41

Motif name: wwAAATAATAtw

Matching format of first motif: Reverse Complement

Matching format of second motif: Reverse Complement

Direction: Forward

Position number: 3

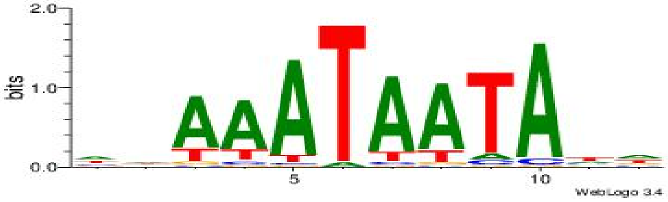
Number of overlap: 6

Similarity score: 0.0632716

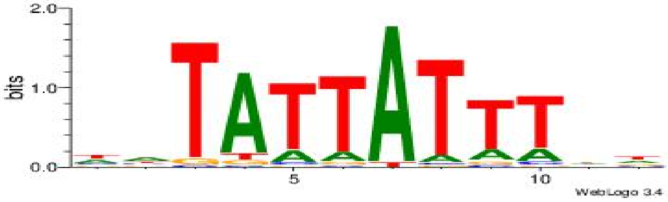
Alignment:

```
DDTATTATTTDH
--TTTTAT----
```

Original motif Consensus sequence: HDAAATAATADD



Reverse complement motif Consensus sequence: DDTATTATTTDH



Dataset #: 2

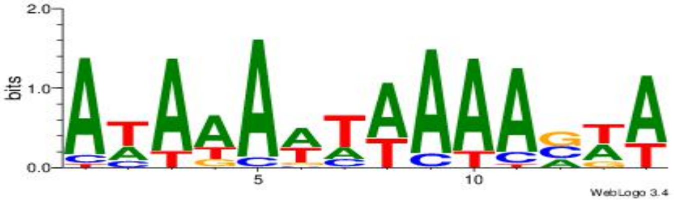
Motif ID: 3

Motif name:	Motif 3
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	4
Number of overlap:	6
Similarity score:	0.0689103

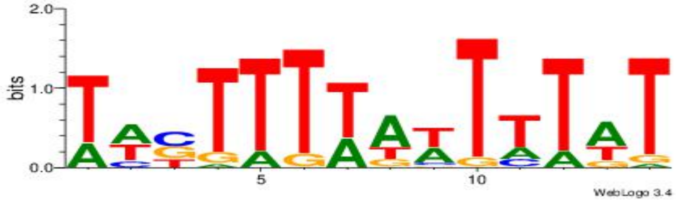
Alignment:

```
TWSTTTWAWTTTWT
---TTTTAT-----
```

Original motif   Consensus sequence: AWAAAWTWAAASWA



Reverse complement motif   Consensus sequence: TWSTTTWAWTTTW



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

Original motif   Consensus sequence: VBACGTGV

Reverse complement motif   Consensus sequence: VCACGTBV

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

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

Alignment:
GCCACGTGSD
-VBACGTGV-

Original motif   Consensus sequence: HSCACGTGGC

Reverse complement motif   Consensus sequence: GCCACGTGSD

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

Similarity score: 0.0144491

Alignment:
DCCACGTGCV
-VBACGTGV-

Original motif Consensus sequence: VGCACGTGGH

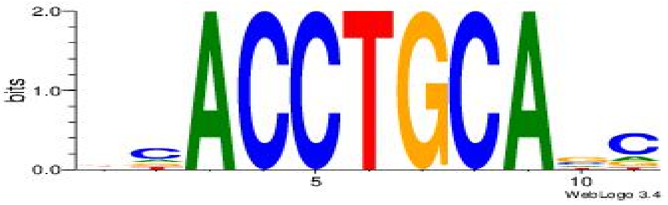
Reverse complement motif Consensus sequence: DCCACGTGCV

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

Alignment:
GBTGCAGGTGB
---VCACGTBV

Original motif Consensus sequence: BCACCTGCABC

Reverse complement motif Consensus sequence: GBTGCAGGTGB

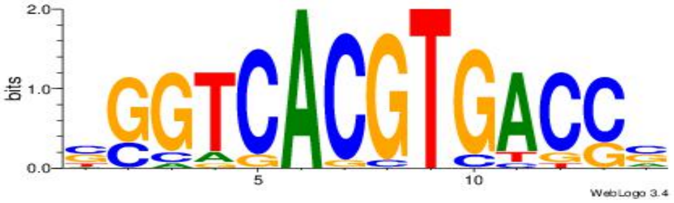


Dataset #:	4
Motif ID:	42
Motif name:	sSGTCACGTGACSs
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	4
Number of overlap:	8
Similarity score:	0.0314837

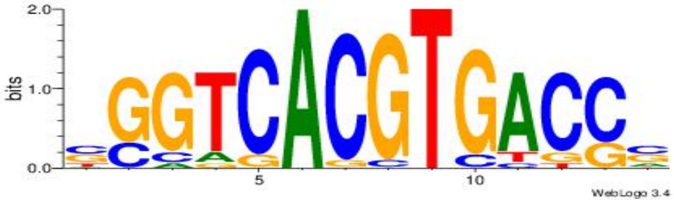
Alignment:

```
SGGTCACGTGACCS
---VCACGTBV---
```

Original motif Consensus sequence: SGGTCACGTGACCS



Reverse complement motif Consensus sequence: SGGTCACGTGACC



Dataset #:	3
Motif ID:	26

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

Alignment:

```
GCGGACGTTV
--VCACGTBV
```

Original motif Consensus sequence: BAACGTCCGC

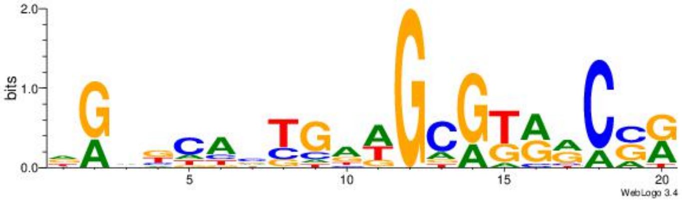
Reverse complement motif Consensus sequence: GCGGACGTTV

Dataset #: 3
Motif ID: 31
Motif name: Pax5
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 8
Number of overlap: 8
Similarity score: 0.0556891

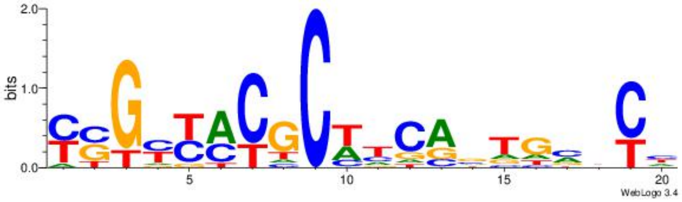
Alignment:

```
MSGKKRCGCWDCABTGBBCD
-----VCACGTBV-------
```

Original motif   Consensus sequence: DGVBCABTGDWGCGKRRCSR



Reverse complement motif   Consensus sequence: MSGKKRCGCWDCABTGBBCD



Dataset #: 4

Motif ID: 44

Motif name: dhACATTCTkh

Matching format of first motif: Reverse Complement

Matching format of second motif: Original Motif

Direction: Backward

Position number: 4

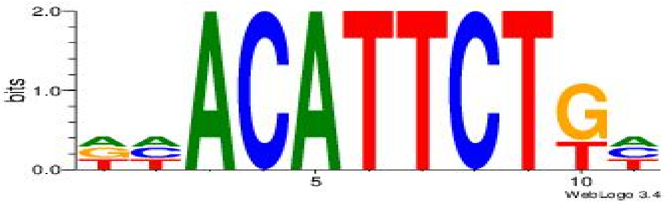
Number of overlap: 8

Similarity score: 0.0640024

Alignment:

```
DHACATTCTGH
VCACGTBV---
```

Original motif   Consensus sequence: DHACATTCTGH   Reverse complement motif   Consensus sequence: HCAGAATGTHD



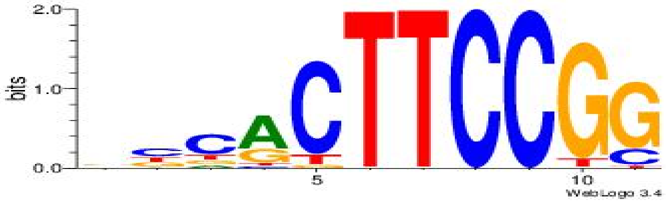
Dataset #:	3
Motif ID:	35
Motif name:	GABPA
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2
Number of overlap:	8
Similarity score:	0.0648153

Alignment:

```
CCGGAAGTGVV
--VCACGTBV-
```

Original motif Consensus sequence: CCGGAAGTGVV

Reverse complement motif Consensus sequence: VVCACTTCCGG



Dataset #:	5
Motif ID:	47

Motif name:	TFW2
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	8
Similarity score:	0.0660185

Alignment:

```
CCGCGCGS
VBACGTGV
```

Original motif   Consensus sequence: SCGCGCGG

Reverse complement motif   Consensus sequence: CCGCGCGS

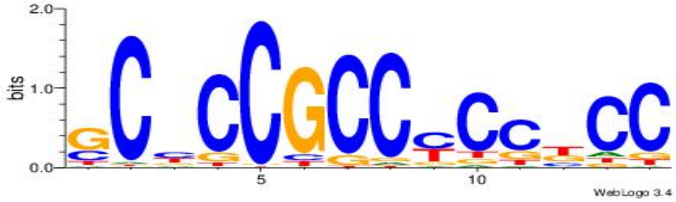
Dataset #:	5
Motif ID:	50
Motif name:	TFF11
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	8
Similarity score:	0.067219

Alignment:

```
GCVCCGCCMCCYCC
------VCACGTBV
```

Original motif Consensus sequence: GGMGGRGGCGGVGC

Reverse complement motif Consensus sequence: GCVCCGCCMCCYC



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

Original motif Consensus sequence: DGGGYGKGGC

Reverse complement motif Consensus sequence: GCCYCMCCCD

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

Dataset #:	2
Motif ID:	7
Motif name:	Motif 7
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	3

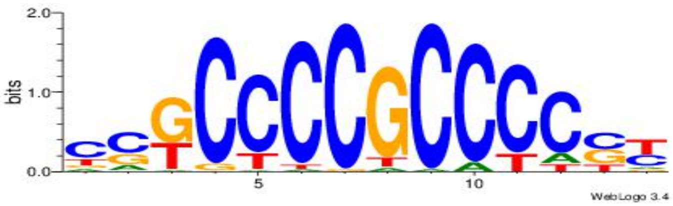
Number of overlap: 10

Similarity score: 0.0152457

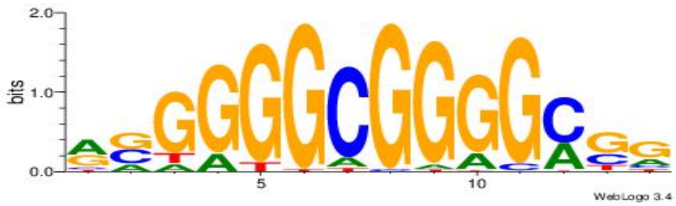
Alignment:

```
CSKCCCCGCCCCSY
--GCCYCMCCCD--
```

Original motif Consensus sequence: CSKCCCCGCCCCSY



Reverse complement motif Consensus sequence: MSGGGGCGGGGY



Dataset #: 4

Motif ID: 36

Motif name: csGCCCCGCCCCsc

Matching format of first motif: Original Motif

Matching format of second motif: Reverse Complement

Direction: Forward

Position number: 3

Number of overlap: 10

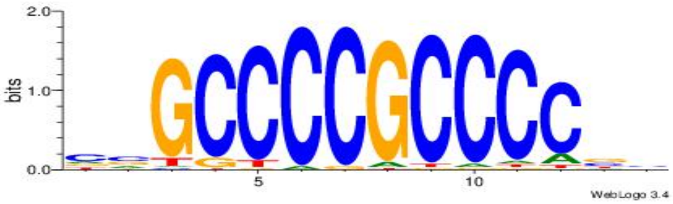
Similarity score: 0.0160185

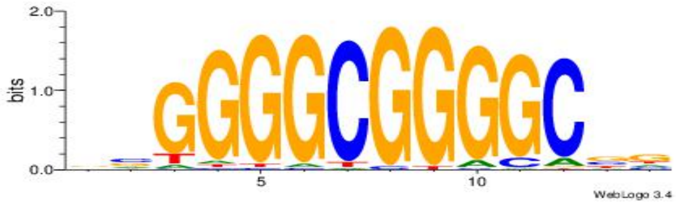
Alignment:

```
BBGGGGCGGGGCVD
--DGGGYGKGGC--
```

Original motif Consensus sequence: HVGCCCCGCCCCBB

Reverse complement motif Consensus sequence: BBGGGGCGGGGC



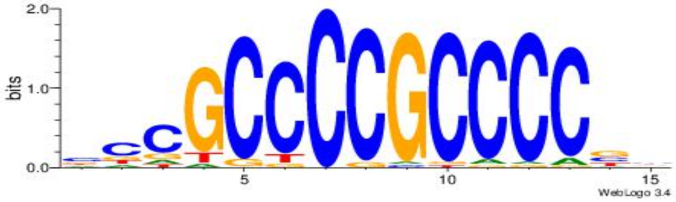


Dataset #:	4
Motif ID:	38
Motif name:	cccGCCCCGCCCCsb
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	3
Number of overlap:	10
Similarity score:	0.0194893

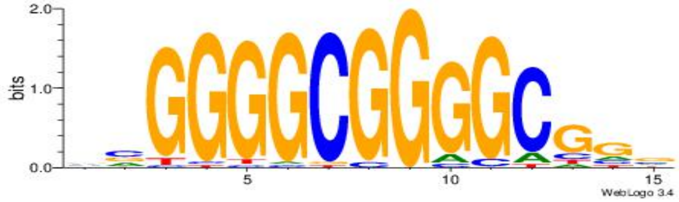
Alignment:

```
BBGGGGCGGGGCGGB
--DGGGYGKGGC---
```

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB



Dataset #:	5

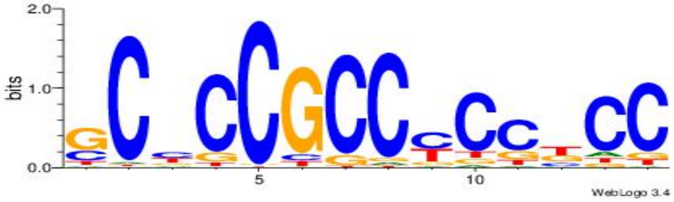
Motif ID:	50
Motif name:	TFF11
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	5
Number of overlap:	10
Similarity score:	0.0402906

Alignment:

```
GGMGGRGGCGGVGC
----DGGGYGKGGC
```

Original motif Consensus sequence: GGMGGRGGCGGVGC

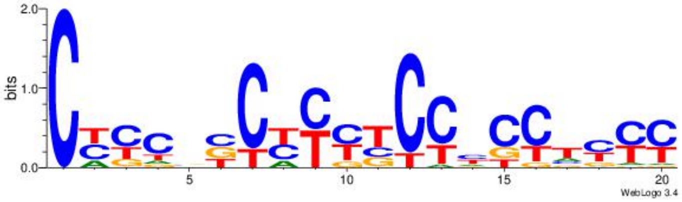
Reverse complement motif Consensus sequence: GCVCCGCCMCCYC



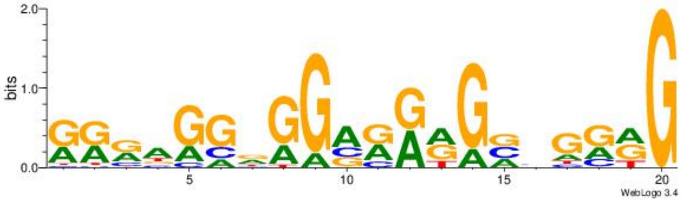
Dataset #:	5
Motif ID:	54
Motif name:	TFM12
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	7
Number of overlap:	10
Similarity score:	0.0556427

Alignment:
CYYCBBCYYYTCCHCCTYYY
----GCCYCMCCCD------

Original motif Consensus sequence: CYYCBBCYYYTCCHCCTYYY



Reverse complement motif Consensus sequence: KKKAGGDGGAKKMGBBGKMG

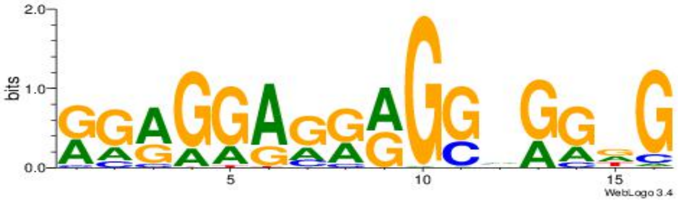


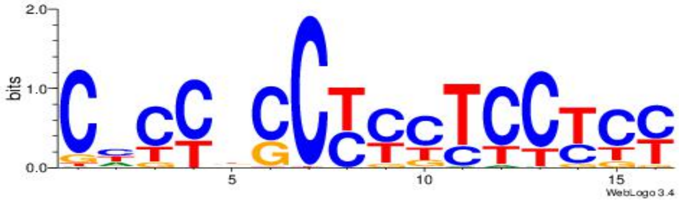
Dataset #:	5
Motif ID:	51
Motif name:	TFM2
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	5
Number of overlap:	10
Similarity score:	0.0606033

Alignment:
CHCCBCCKMCTCCKCM
----GCCYCMCCCD--

Original motif Consensus sequence: RGRGGAGRRGGHGGDG

Reverse complement motif Consensus sequence: CHCCBCCKMCTCCKCM



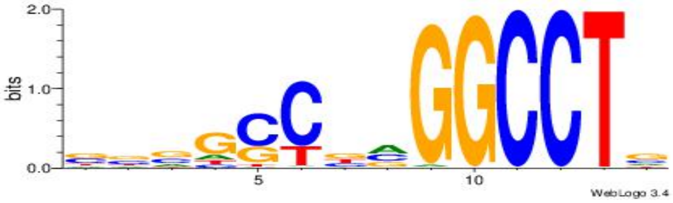


Dataset #:	3
Motif ID:	22
Motif name:	Zfx
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	4
Number of overlap:	10
Similarity score:	0.0623591

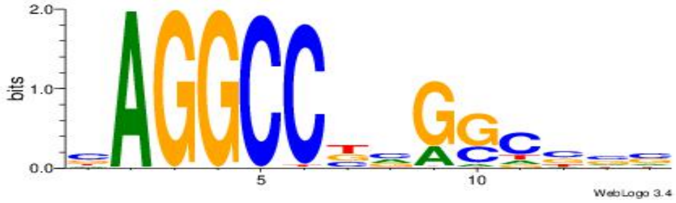
Alignment:

```
BBVGCCBVGGCCTV
-GCCYCMCCCD---
```

Original motif Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif Consensus sequence: VAGGCCBBGGCV

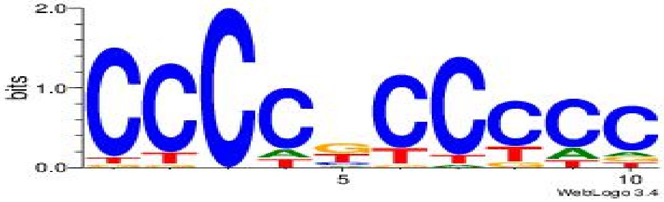


Dataset #:	3
Motif ID:	24

Motif name: SP1
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 10
Similarity score: 0.0663136

Alignment:
GGGGGYGGGG
DGGGYGKGGC

Original motif Consensus sequence: CCCCKCCCCC



Reverse complement motif Consensus sequence: GGGGGYGGGG

Dataset #: 3
Motif ID: 34
Motif name: Myc
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 10
Similarity score: 0.0686848

Alignment:

VGCACGTGGH
DGGGYGKGGC

Original motif Consensus sequence: VGCACGTGGH

Reverse complement motif Consensus sequence: DCCACGTGCV

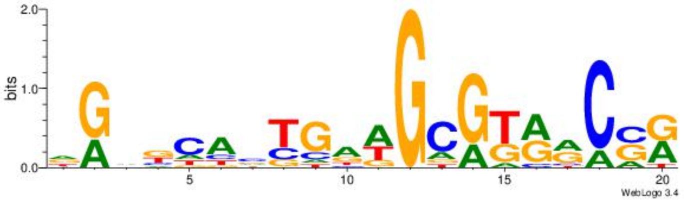
Dataset #:	3
Motif ID:	31
Motif name:	Pax5
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	9
Number of overlap:	10
Similarity score:	0.06956

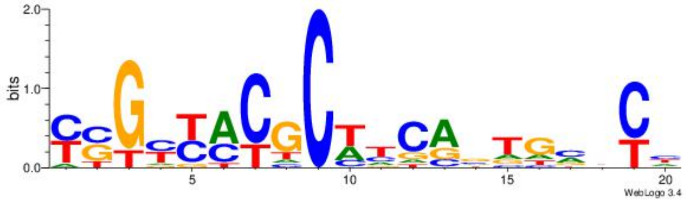
Alignment:

DGVBCABTGDWGCGKRRCSR
--------DGGGYGKGGC--

Original motif Consensus sequence: DGVBCABTGDWGCGKRRCSR

Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD

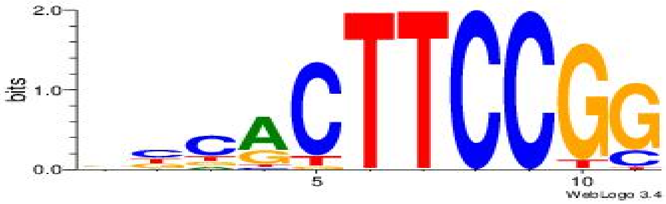




Dataset #: 3 Motif ID: 35 Motif name: GABPA

Original motif Consensus sequence: CCGGAAGTGVV

Reverse complement motif Consensus sequence: VVCACTTCCGG



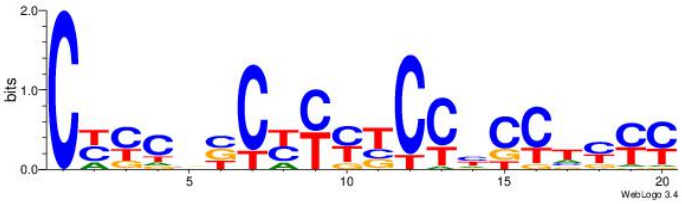
Best Matches for Significant Motif ID 35 (Highest to Lowest)

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

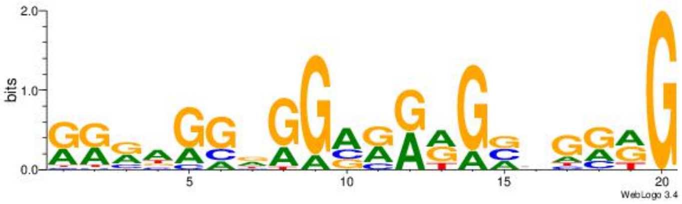
Alignment:

```
CYYCBBCYYYTCCHCCTYYY
----VVCACTTCCGG-----
```

Original motif Consensus sequence: CYYCBBCYYYTCCHCCTYYY



Reverse complement motif Consensus sequence: KKKAGGDGGAKKMGBBGKMG

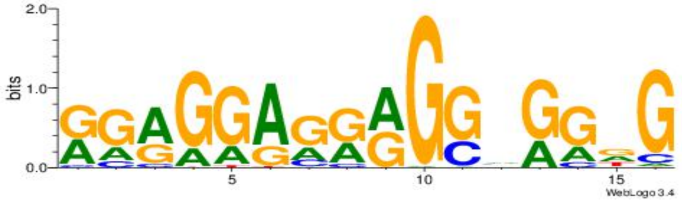


Dataset #:	5
Motif ID:	51
Motif name:	TFM2
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	5
Number of overlap:	11
Similarity score:	0.0445566

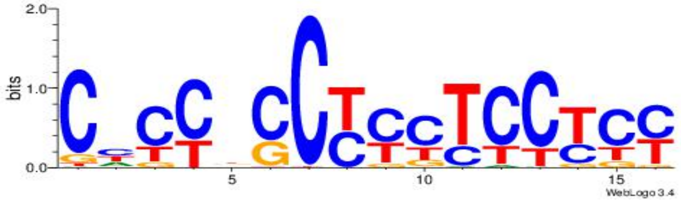
Alignment:

```
RGRGGAGRRGGHGGDG
-CCGGAAGTGVV----
```

Original motif Consensus sequence: RGRGGAGRRGGHGGDG



Reverse complement motif Consensus sequence: CHCCBCCKMCTCCKCM

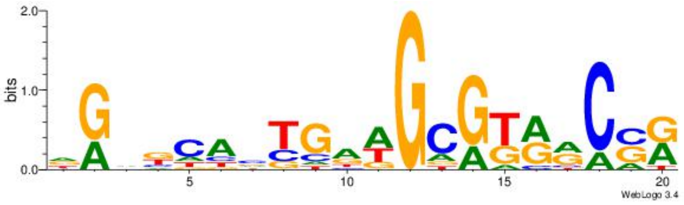


Dataset #: 3
Motif ID: 31
Motif name: Pax5
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 8
Number of overlap: 11
Similarity score: 0.0446257

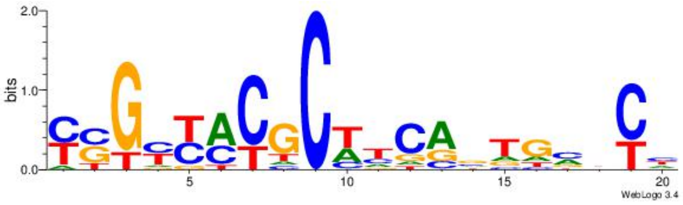
Alignment:

```
DGVBCABTGDWGCGKRRCSR
-------VVCACTTCCGG--
```

Original motif Consensus sequence: DGVBCABTGDWGCGKRRCSR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD

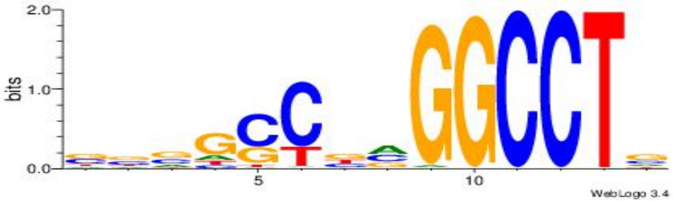


Dataset #: 3
Motif ID: 22
Motif name: Zfx
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1

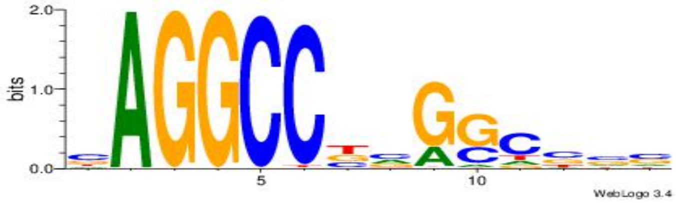
Number of overlap: 11
Similarity score: 0.0457327

Alignment:
BBVGCCBVGGCCTV
VVCACTTCCGG---

Original motif Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif Consensus sequence: VAGGCCBBGGCV

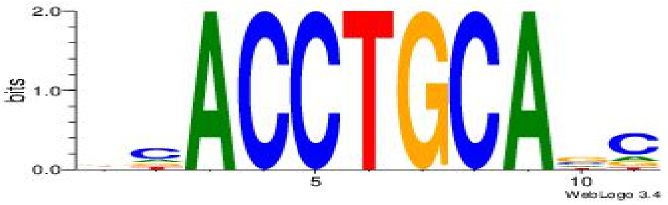


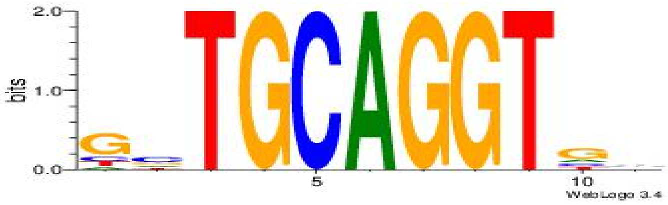
Dataset #: 4
Motif ID: 40
Motif name: kcACCTGCAgc
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 11
Similarity score: 0.0483841

Alignment:
BCACCTGCABC
VVCACTTCCGG

Original motif Consensus sequence: BCACCTGCABC

Reverse complement motif Consensus sequence: GBTGCAGGTGB



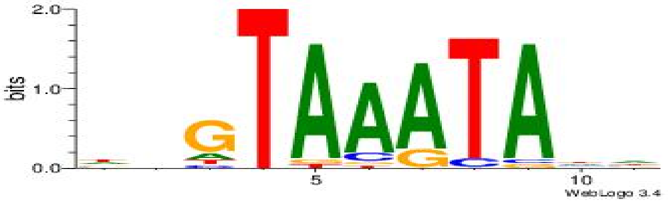


Dataset #:	4
Motif ID:	45
Motif name:	wbgTAAATAww
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	11
Similarity score:	0.0492127

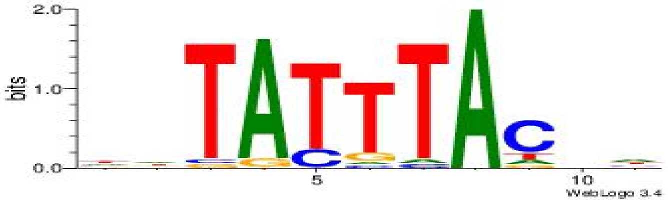
Alignment:

```
DBGTAAATAHD
CCGGAAGTGVV
```

Original motif Consensus sequence: DBGTAAATAHD



Reverse complement motif Consensus sequence: DHTATTTACBD



Dataset #:	4
Motif ID:	44

Motif name: dhACATTCTkh

Matching format of first motif: Reverse Complement

Matching format of second motif: Original Motif

Direction: Forward

Position number: 1

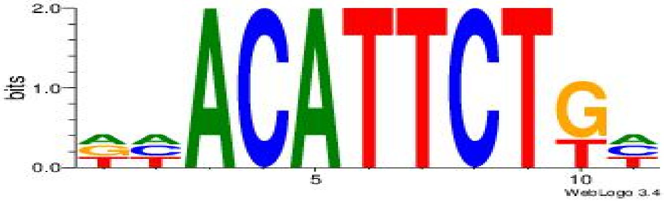
Number of overlap: 11

Similarity score: 0.0495154

Alignment:

```
DHACATTCTGH
VVCACTTCCGG
```

Original motif Consensus sequence: DHACATTCTGH



Reverse complement motif Consensus sequence: HCAGAATGTHD

Dataset #: 5

Motif ID: 50

Motif name: TFF11

Matching format of first motif: Original Motif

Matching format of second motif: Original Motif

Direction: Forward

Position number: 2

Number of overlap: 11

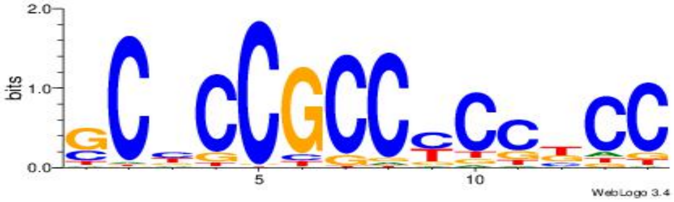
Similarity score: 0.0504656

Alignment:

```
GGMGGRGGCGGVGC
-CCGGAAGTGVV--
```

Original motif   Consensus sequence: GGMGGRGGCGGVGC

Reverse complement motif   Consensus sequence: GCVCCGCCMCCY



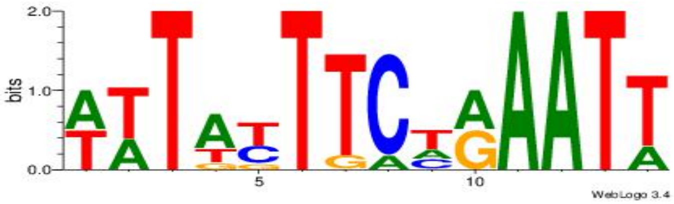
Dataset #:	2
Motif ID:	6
Motif name:	Motif 6
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	11
Similarity score:	0.0518418

Alignment:

```
AATTYDGAARTAWW
---CCGGAAGTGVV
```

Original motif   Consensus sequence: AATTYDGAARTAWW

Reverse complement motif   Consensus sequence: WWTAKTTCDKAA

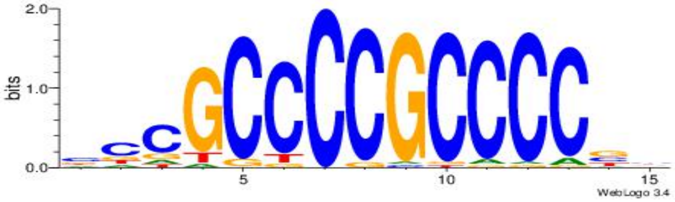


Dataset #:	4
Motif ID:	38
Motif name:	cccGCCCCGCCCCsb
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2
Number of overlap:	11
Similarity score:	0.0554249

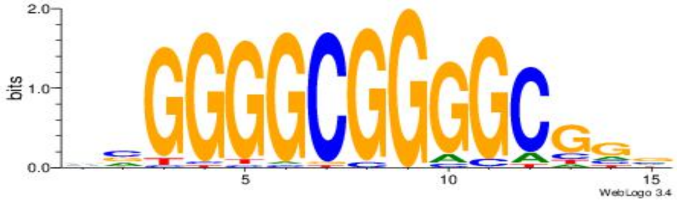
Alignment:

```
BCCGCCCCGCCCCBB
---VVCACTTCCGG-
```

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB



Best Matches for Each Motif (Highest to Lowest)

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

Original motif Consensus sequence: GGCGGGGC

Reverse complement motif Consensus sequence: GCCCCGCC

Best Matches for Motif ID 1 (Highest to Lowest)

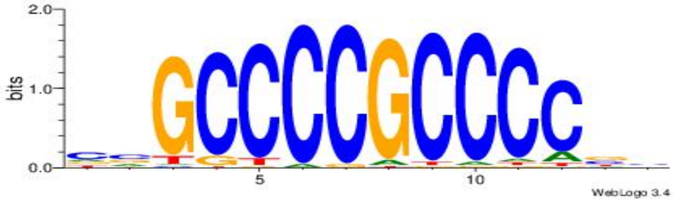
Dataset #:	4
Motif ID:	36
Motif name:	csGCCCCGCCCCsc
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	5
Number of overlap:	8
Similarity score:	0

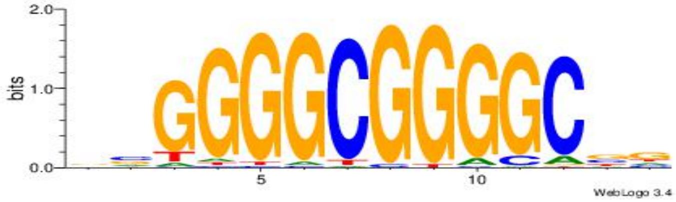
Alignment:

```
HVGCCCCGCCCCBB
--GCCCCGCC----
```

Original motif Consensus sequence: HVGCCCCGCCCCBB

Reverse complement motif Consensus sequence: BBGGGGCGGGGC



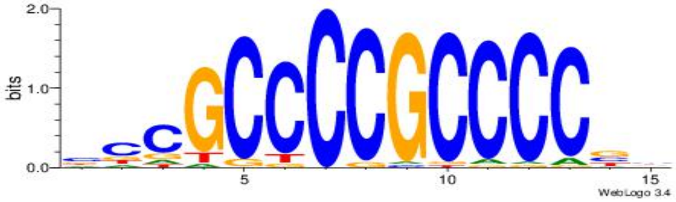


Dataset #: 4
Motif ID: 38
Motif name: cccGCCCCGCCCCsb
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 5
Number of overlap: 8
Similarity score: 0.00250079

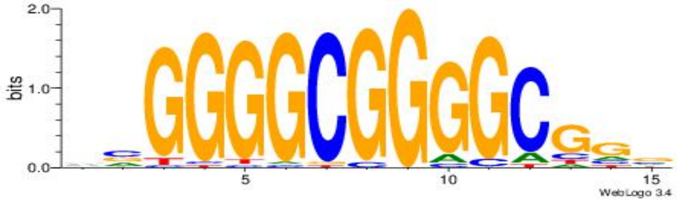
Alignment:

```
BCCGCCCCGCCCCBB
---GCCCCGCC----
```

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB



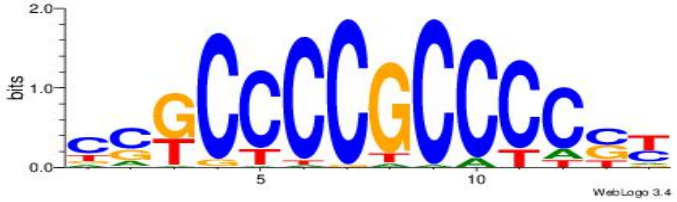
Dataset #: 2

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

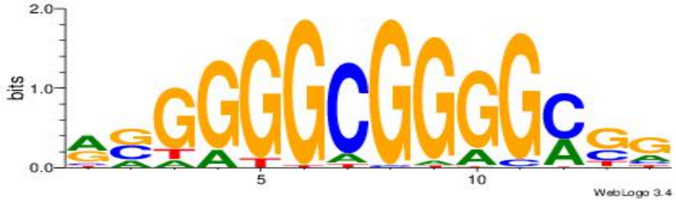
Alignment:

```
MSGGGGCGGGGYSG
----GGCGGGGC--
```

Original motif Consensus sequence: CSKCCCCGCCCCSY



Reverse complement motif Consensus sequence: MSGGGGCGGGGY



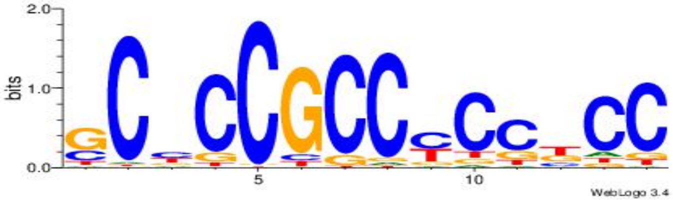
Dataset #: 5
Motif ID: 50
Motif name: TFF11
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 7
Number of overlap: 8
Similarity score: 0.0348969

Alignment:

```
GGMGGRGGCGGVGC
------GGCGGGGC
```

Original motif Consensus sequence: GGMGGRGGCGGVGC

Reverse complement motif Consensus sequence: GCVCCGCCMCCYC



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

Alignment:

```
DGGGYGKGGC
--GGCGGGGC
```

Original motif Consensus sequence: DGGGYGKGGC

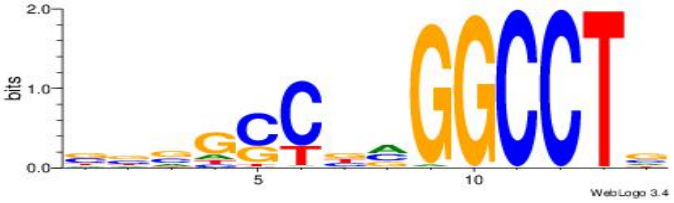
Reverse complement motif Consensus sequence: GCCYCMCCCD

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

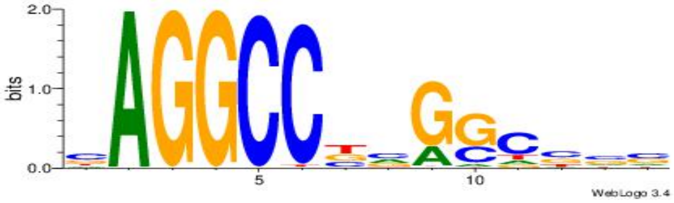
Alignment:

```
VAGGCCBBGGCVBB
---GCCCCGCC---
```

Original motif Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif Consensus sequence: VAGGCCBBGGCV



Dataset #:	5
Motif ID:	48

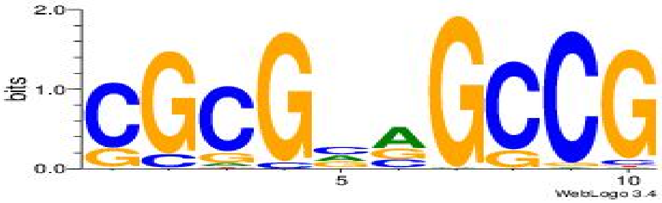
Motif name:	TFW3
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	2
Number of overlap:	8
Similarity score:	0.071681

Alignment:

```
CGCGBMGCCG
-GCCCCGCC-
```

Original motif Consensus sequence: CGGCYBCGCG

Reverse complement motif Consensus sequence: CGCGBMGCCG

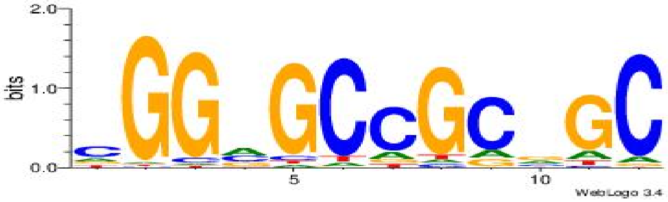


Dataset #:	5
Motif ID:	49
Motif name:	TFF1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	3
Number of overlap:	8
Similarity score:	0.0803996

Alignment:

```
CGGVGCCGCVGC
--GCCCCGCC--
```

Original motif   Consensus sequence: CGGVGCCGCVGC



Reverse complement motif   Consensus sequence: GCVGCGGCBCCG

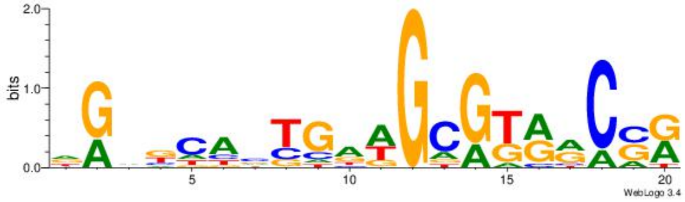
Dataset #:	3
Motif ID:	31
Motif name:	Pax5
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	3
Number of overlap:	8
Similarity score:	0.0853847

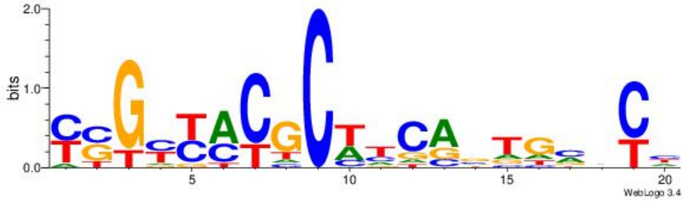
Alignment:

```
DGVBCABTGDWGCGKRRCSR
----------GGCGGGGC--
```

Original motif   Consensus sequence: DGVBCABTGDWGCGKRRCSR

Reverse complement motif   Consensus sequence: MSGKKRCGCWDCABTGBBCD





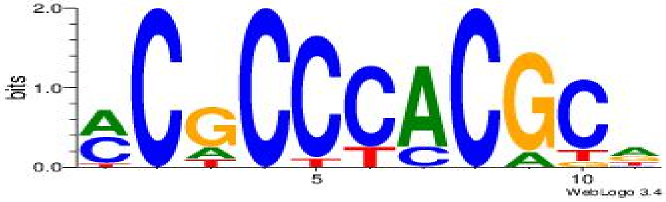
Dataset #:	3
Motif ID:	23
Motif name:	Egr1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	8
Similarity score:	0.0878731

Alignment:

```
YCGCCCACGCH
---GCCCCGCC
```

Original motif Consensus sequence: HGCGTGGGCGK

Reverse complement motif Consensus sequence: YCGCCCACGCH



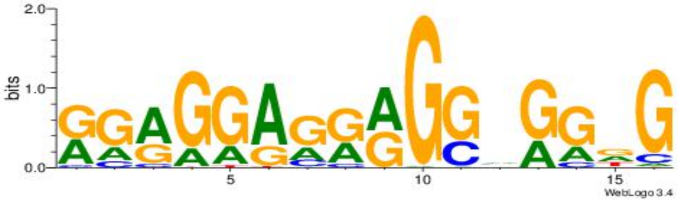
Dataset #:	5
Motif ID:	51

Motif name:	TFM2
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	3
Number of overlap:	8
Similarity score:	0.0928252

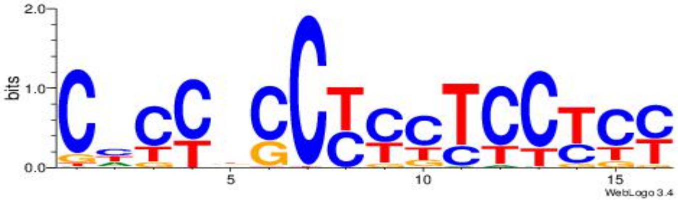
Alignment:

```
CHCCBCCKMCTCCKCM
--GCCCCGCC------
```

Original motif Consensus sequence: RGRGGAGRRGGHGGDG

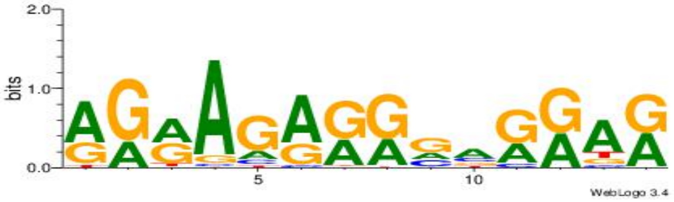


Reverse complement motif Consensus sequence: CHCCBCCKMCTCCKCM

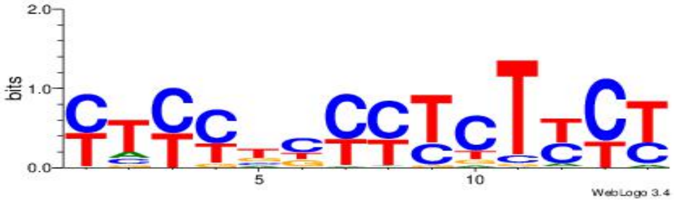


Dataset #: 2 **Motif ID: 2** **Motif name: Motif 2**

Original motif Consensus sequence: RGRAGARRGARRAR



Reverse complement motif Consensus sequence: MTMMTCMMTCTK



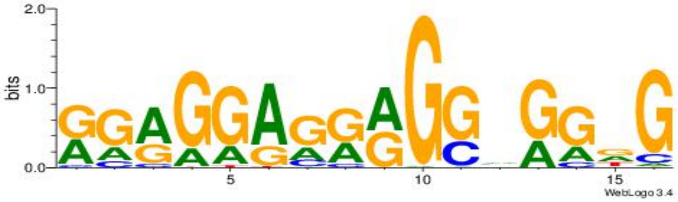
Best Matches for Motif ID 2 (Highest to Lowest)

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

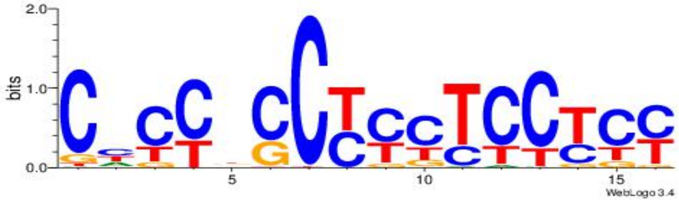
Alignment:

```
RGRGGAGRRGGHGGDG
--RGRAGARRGARRAR
```

Original motif Consensus sequence: RGRGGAGRRGGHGGDG



Reverse complement motif Consensus sequence: CHCCBCCKMCTCCKCM

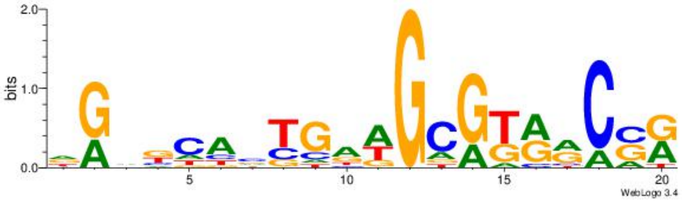


Dataset #:	3
Motif ID:	31
Motif name:	Pax5
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement

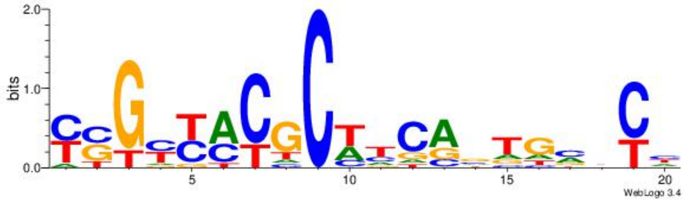
Direction: Forward
Position number: 7
Number of overlap: 14
Similarity score: 0.047364

Alignment:
MSGKKRCGCWDCABTGBBCD
------MTMMTCMMTCTKCK

Original motif Consensus sequence: DGVBCABTGDWGCGKRRCSR



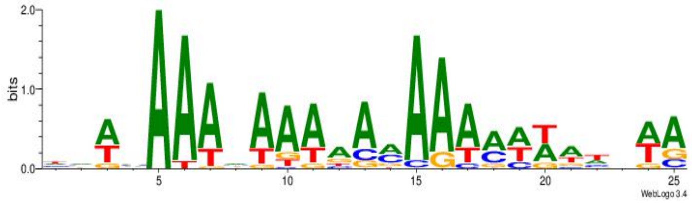
Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD



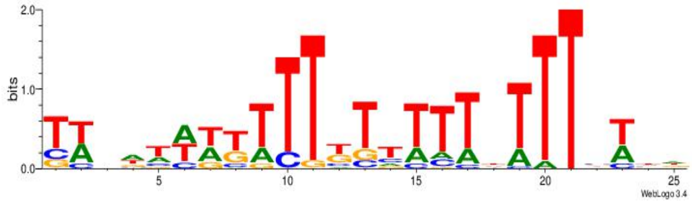
Dataset #: 5
Motif ID: 56
Motif name: TFM11
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 3
Number of overlap: 14
Similarity score: 0.0541717

Alignment:
HDWVAAAHAAAAAMAAAMWWWHBWA
---------RGRAGARRGARRAR--

Original motif Consensus sequence:
HDWVAAAHAAAAAMAAAMWWWHBWA



Reverse complement motif Consensus sequence:
TWVHWWWYTTTYTTTTTHTTTVWBH

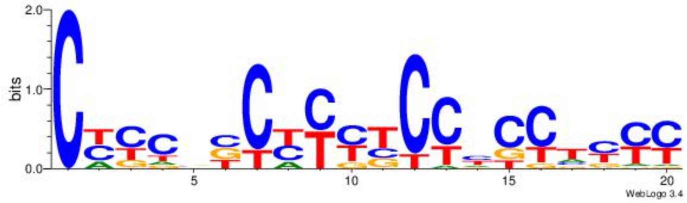


Dataset #:	5
Motif ID:	54
Motif name:	TFM12
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	7
Number of overlap:	14
Similarity score:	0.0545069

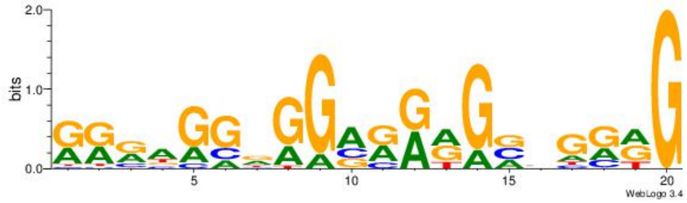
Alignment:

```
CYYCBBCYYYTCCHCCTYYY
------MTMMTCMMTCTKCK
```

Original motif Consensus sequence: CYYCBBCYYYTCCHCCTYYY



Reverse complement motif Consensus sequence:
KKKAGGDGGAKKMGBBGKMG

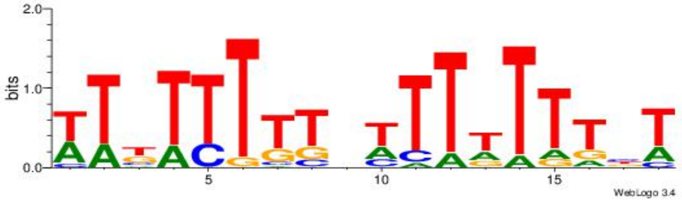


Dataset #: 5
Motif ID: 52
Motif name: TFM1
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 4
Number of overlap: 14
Similarity score: 0.0558935

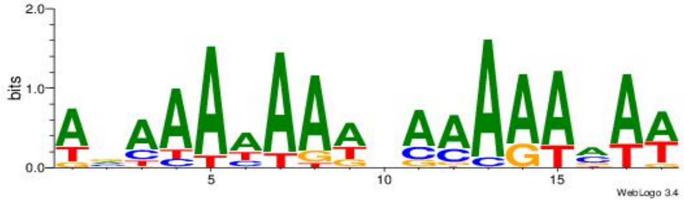
Alignment:

```
ABAAAAAAWHAAAAAARAW
-RGRAGARRGARRAR---
```

Original motif Consensus sequence: WTKTTTTTHWTTTTTTBT



Reverse complement motif Consensus sequence:
ABAAAAAAWHAAAAAARAW



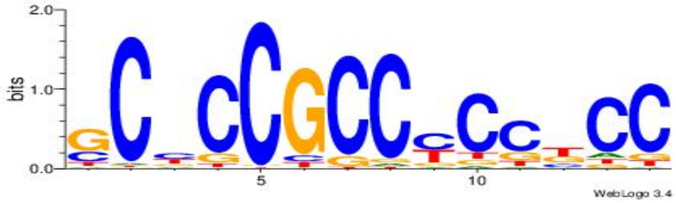
Dataset #: 5
Motif ID: 50
Motif name: TFF11
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1

Number of overlap: 14
Similarity score: 0.0689626

Alignment:
GGMGGRGGCGGVGC
RGRAGARRGARRAR

Original motif Consensus sequence: GGMGGRGGCGGVGC

Reverse complement motif Consensus sequence: GCVCCGCCMCCYC

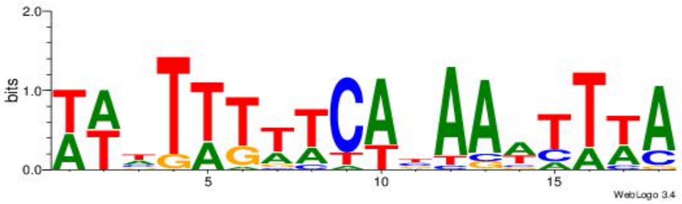


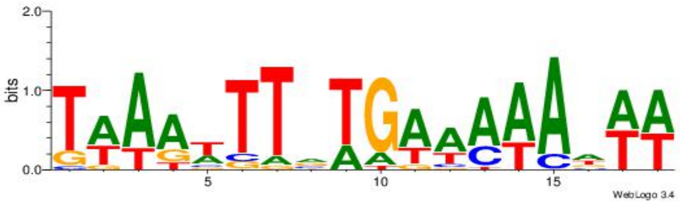
Dataset #: 5
Motif ID: 53
Motif name: TFM3
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 4
Number of overlap: 14
Similarity score: 0.0775356

Alignment:
TWAAWTTVTGAAAAAHWW
-RGRAGARRGARRAR---

Original motif Consensus sequence: WWHTTTTTCABAAWTTWA

Reverse complement motif Consensus sequence: TWAAWTTVTGAAAAAHWW



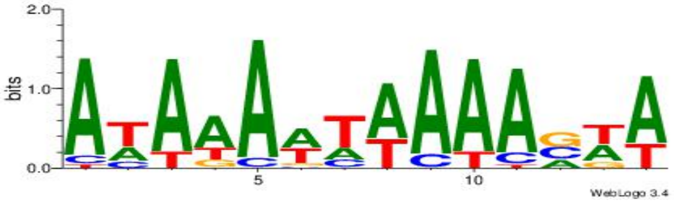


Dataset #:	2
Motif ID:	3
Motif name:	Motif 3
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	13
Similarity score:	0.57507

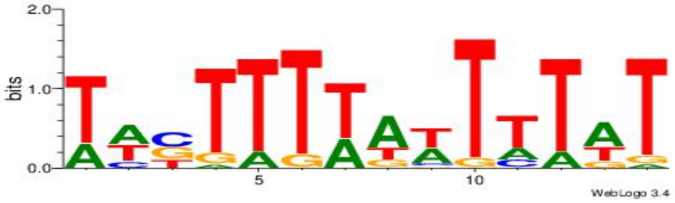
Alignment:

```
AWAAAWTWAAASWA-
-RGRAGARRGARRAR
```

Original motif Consensus sequence: AWAAAWTWAAASWA



Reverse complement motif Consensus sequence: TWSTTTWAWTTTW



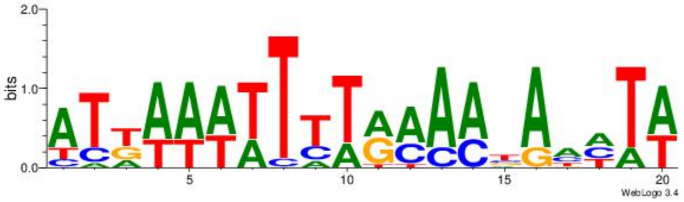
Dataset #:	5
Motif ID:	55

Motif name: TFM13
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 9
Number of overlap: 12
Similarity score: 1.0763

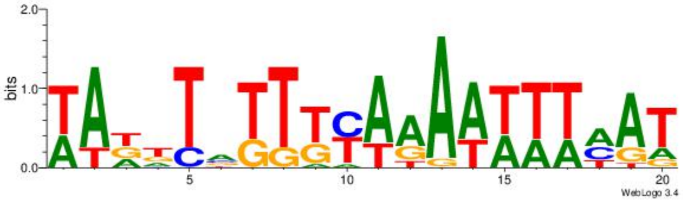
Alignment:

```
ATKAAWTTTTRMAABAHHTW--
--------MTMMTCMMTCTKCK
```

Original motif Consensus sequence: ATKAAWTTTTRMAABAHHTW



Reverse complement motif Consensus sequence: WAHHTVTTYKAAAAWTTRAT

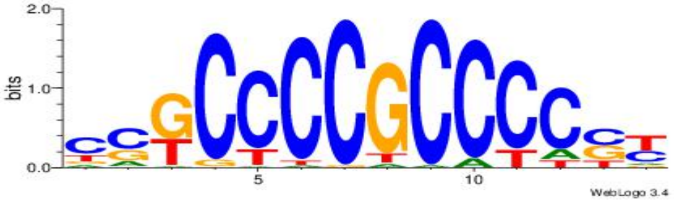


Dataset #: 2
Motif ID: 7
Motif name: Motif 7
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 4
Number of overlap: 11
Similarity score: 1.57133

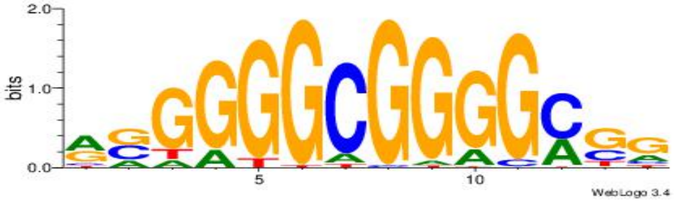
Alignment:

```
---MSGGGGCGGGGYSG
RGRAGARRGARRAR---
```

Original motif Consensus sequence: CSKCCCCGCCCCSY

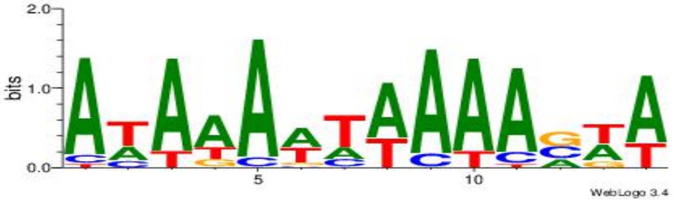


Reverse complement motif Consensus sequence: MSGGGGCGGGGY

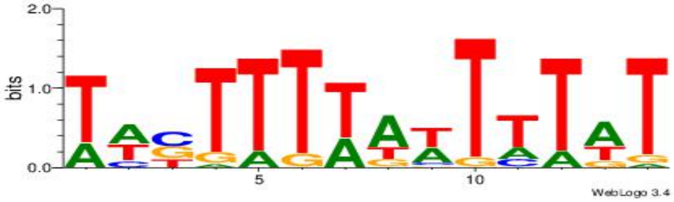


Dataset #: 2 Motif ID: 3 Motif name: Motif 3

Original motif Consensus sequence: AWAAAWTWAAASWA



Reverse complement motif Consensus sequence: TWSTTTWAWTTTW



Best Matches for Motif ID 3 (Highest to Lowest)

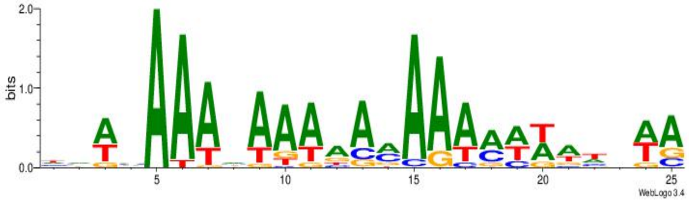
Dataset #:	5
Motif ID:	56
Motif name:	TFM11
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	7

Number of overlap:	14
Similarity score:	0.0137914

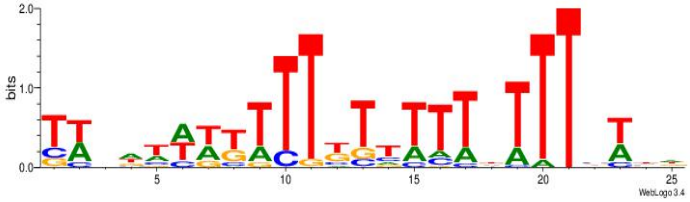
Alignment:

```
HDWVAAAHAAAAAMAAAMWWWHBWA
------AWAAAWTWAAASWA-----
```

Original motif Consensus sequence:
HDWVAAAHAAAAAMAAAMWWWHBWA



Reverse complement motif Consensus sequence:
TWVHWWWYTTTYTTTTTHTTTVWBH

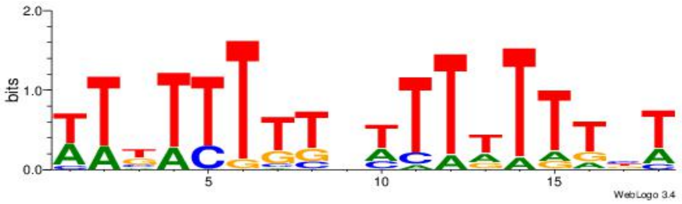


Dataset #:	5
Motif ID:	52
Motif name:	TFM1
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	5
Number of overlap:	14
Similarity score:	0.0162962

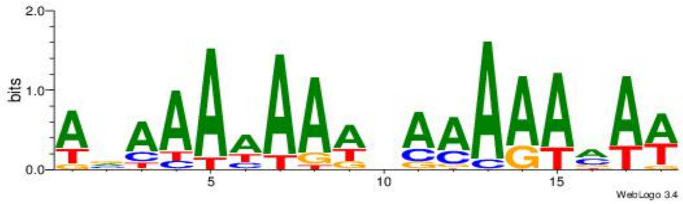
Alignment:

```
ABAAAAAAAWHAAAAAARAW
----AWAAAWTWAAASWA
```

Original motif Consensus sequence: WTKTTTTTHWTTTTTTBT



Reverse complement motif Consensus sequence: ABAAAAAAWHAAAAARAW

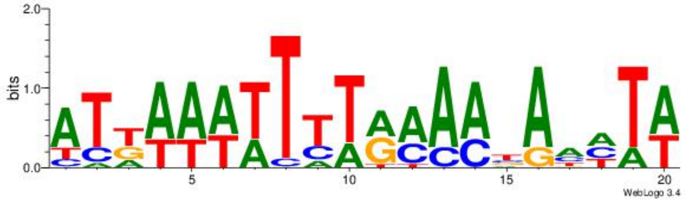


Dataset #:	5
Motif ID:	55
Motif name:	TFM13
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	3
Number of overlap:	14
Similarity score:	0.037679

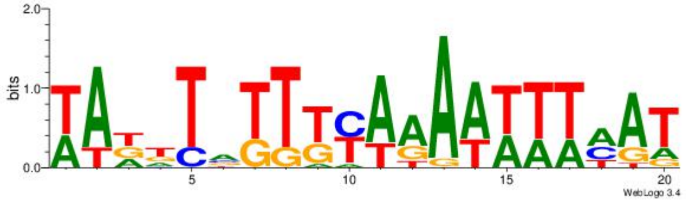
Alignment:

```
ATKAAWTTTTRMAABAHHTW
--AWAAAWTWAAASWA----
```

Original motif Consensus sequence: ATKAAWTTTTRMAABAHHTW



Reverse complement motif Consensus sequence: WAHHTVTTYKAAAAWTTRAT

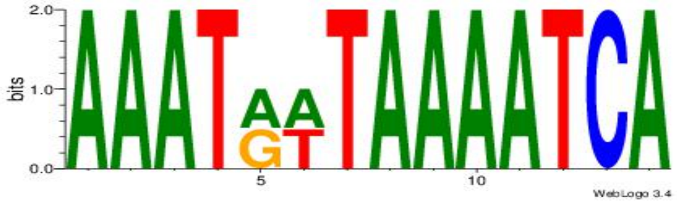


Dataset #:	2
Motif ID:	8
Motif name:	Motif 8
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	14
Similarity score:	0.0423952

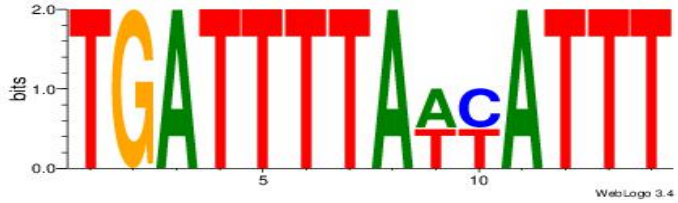
Alignment:

```
TGATTTTAWKATTT
TWSTTTWAWTTTWT
```

Original motif Consensus sequence: AAATRWTAAAATCA



Reverse complement motif Consensus sequence: TGATTTTAWKATT



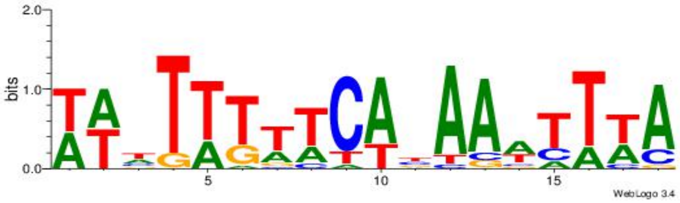
Dataset #:	5
Motif ID:	53
Motif name:	TFM3
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	5
Number of overlap:	14

Similarity score: 0.0456419

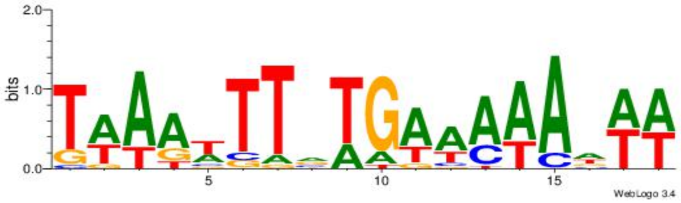
Alignment:

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

Original motif Consensus sequence: WWHTTTTTCABAAWTTWA



Reverse complement motif Consensus sequence: TWAAWTTVTGAAAAAHWW



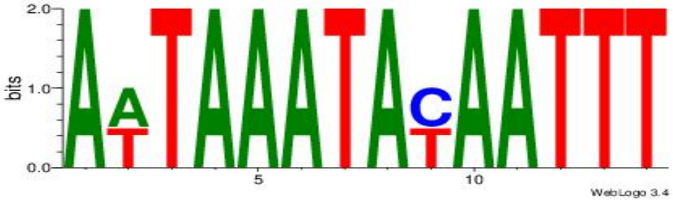
Dataset #: 2
Motif ID: 5
Motif name: Motif 5
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 14
Similarity score: 0.0478896

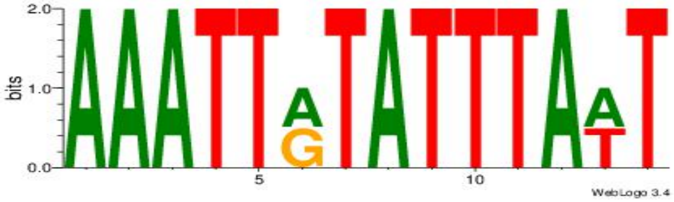
Alignment:

```
AAATTKTATTTAWT
TWSTTTWAWTTTWT
```

Original motif Consensus sequence: AWTAAATAYAATTT

Reverse complement motif Consensus sequence: AAATTKTATTTAW



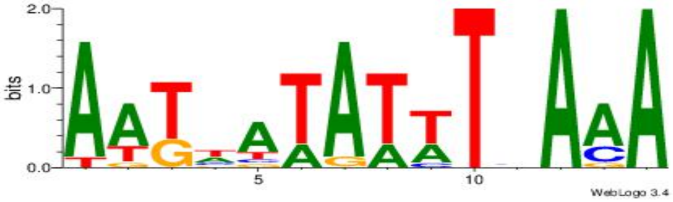


Dataset #:	2
Motif ID:	9
Motif name:	Motif 9
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	14
Similarity score:	0.0624272

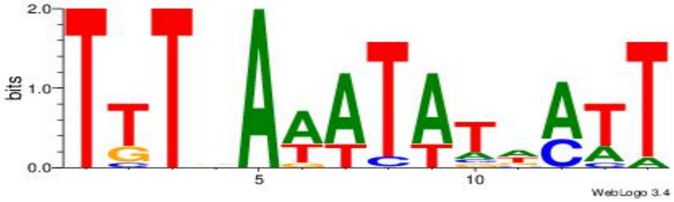
Alignment:

```
TTTDAWATATHATT
AWAAAWTWAAASWA
```

Original motif   Consensus sequence: AATHATATWTHAAA



Reverse complement motif   Consensus sequence: TTTDAWATATHAT



Dataset #:	2
Motif ID:	6

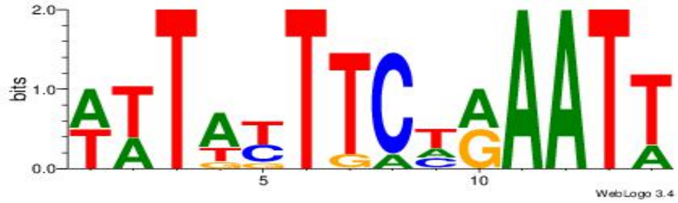
Motif name: Motif 6
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 14
Similarity score: 0.0702111

Alignment:

```
WWTAKTTCDKAATT
TWSTTTWAWTTTWT
```

Original motif Consensus sequence: AATTYDGAARTAWW

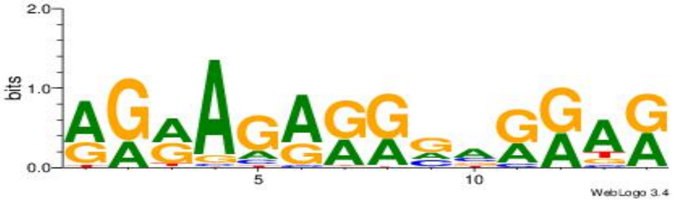
Reverse complement motif Consensus sequence: WWTAKTTCDKAAT



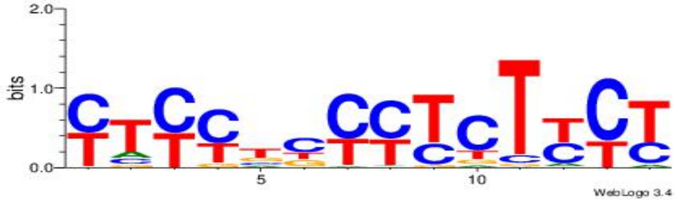
Dataset #: 2
Motif ID: 2
Motif name: Motif 2
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2
Number of overlap: 13
Similarity score: 0.567825

Alignment:
```
-RGRAGARRGARRAR
AWAAAWTWAAASWA-
```

Original motif Consensus sequence: RGRAGARRGARRAR



Reverse complement motif Consensus sequence: MTMMTCMMTCTK

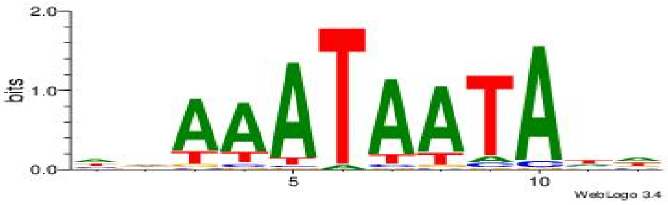


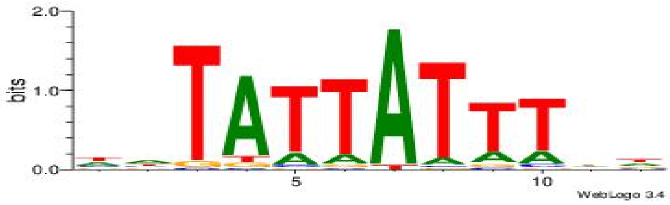
Dataset #:	4
Motif ID:	41
Motif name:	wwAAATAATAtw
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	12
Similarity score:	1.0432

Alignment:
```
HDAAATAATADD--
AWAAAWTWAAASWA
```

Original motif Consensus sequence: HDAAATAATADD

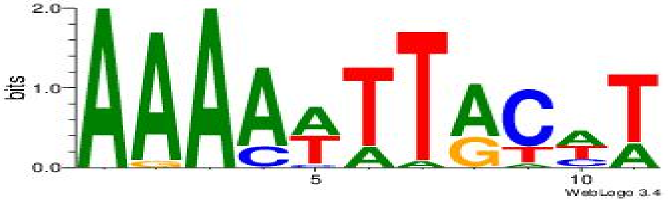
Reverse complement motif Consensus sequence: DDTATTATTTDH





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

Original motif Consensus sequence: AAAAWTTRCWT



Reverse complement motif Consensus sequence: AWGKAAWTTTT

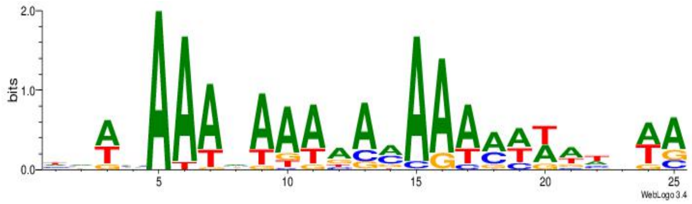
Best Matches for Motif ID 4 (Highest to Lowest)

Dataset #:	5
Motif ID:	56
Motif name:	TFM11
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	14
Number of overlap:	11
Similarity score:	0.0718583

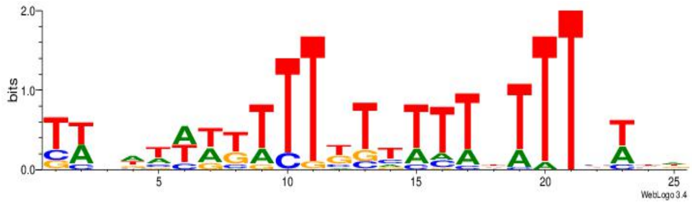
Alignment:

```
HDWVAAAHAAAAAMAAAMWWWHBWA
-------------AAAAWTTRCWT-
```

Original motif Consensus sequence: HDWVAAAHAAAAAMAAAMWWWHBWA



Reverse complement motif Consensus sequence: TWVHWWWYTTTYTTTTTHTTTVWBH

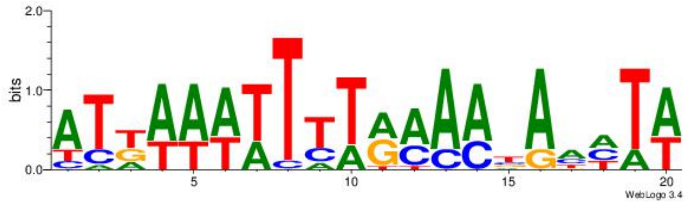


Dataset #:	5
Motif ID:	55
Motif name:	TFM13
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	11
Similarity score:	0.0727073

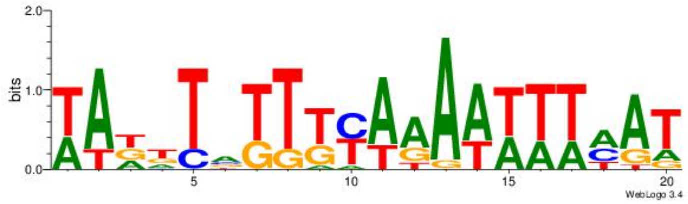
Alignment:

```
ATKAAWTTTTRMAABAHHTW
AWGKAAWTTTT---------
```

Original motif Consensus sequence: ATKAAWTTTTRMAABAHHTW



Reverse complement motif Consensus sequence: WAHHTVTTYKAAAAWTTRAT

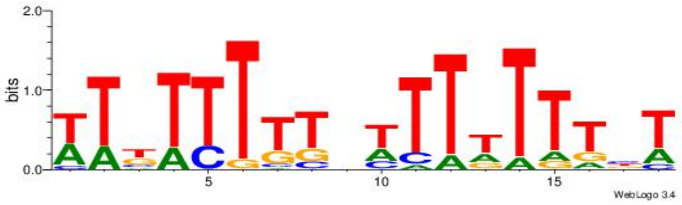


Dataset #: 5
Motif ID: 52
Motif name: TFM1
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 5
Number of overlap: 11
Similarity score: 0.0748297

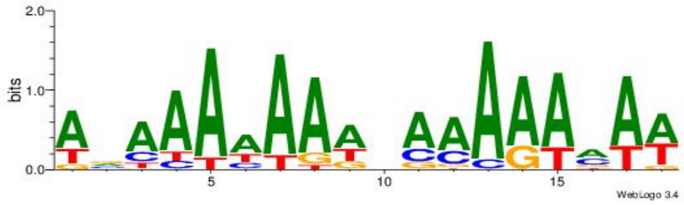
Alignment:

```
WTKTTTTTHWTTTTTTTBT
---AWGKAAWTTTT----
```

Original motif Consensus sequence: WTKTTTTTHWTTTTTTTBT



Reverse complement motif Consensus sequence: ABAAAAAAWHAAAAARAW



Dataset #: 2
Motif ID: 5
Motif name: Motif 5
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 4

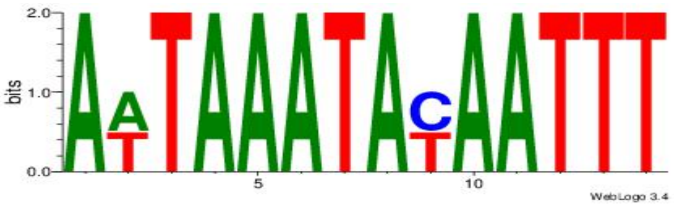
Number of overlap: 11

Similarity score: 0.0786484

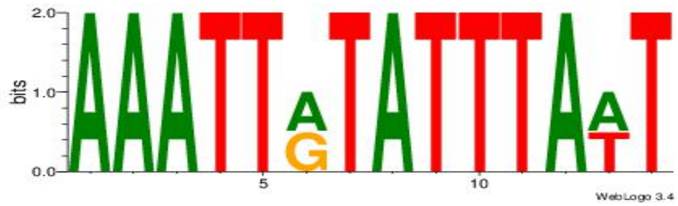
Alignment:

```
AAATTKTATTTAWT
AAAAWTTRCWT---
```

Original motif Consensus sequence: AWTAAATAYAATTT



Reverse complement motif Consensus sequence: AAATTKTATTTAW



Dataset #: 2

Motif ID: 9

Motif name: Motif 9

Matching format of first motif: Reverse Complement

Matching format of second motif: Original Motif

Direction: Backward

Position number: 4

Number of overlap: 11

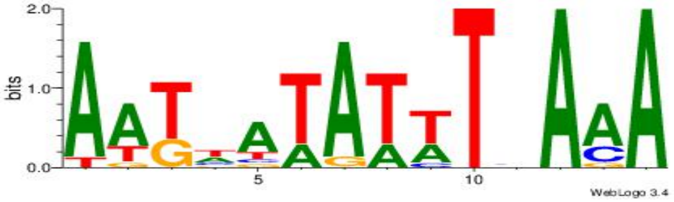
Similarity score: 0.0820375

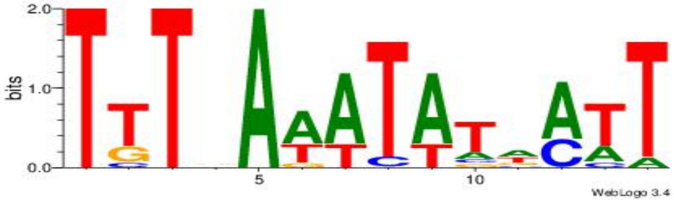
Alignment:

```
AATHATATWTHAAA
AWGKAAWTTTT---
```

Original motif Consensus sequence: AATHATATWTHAAA

Reverse complement motif Consensus sequence: TTTDAWATATHAT



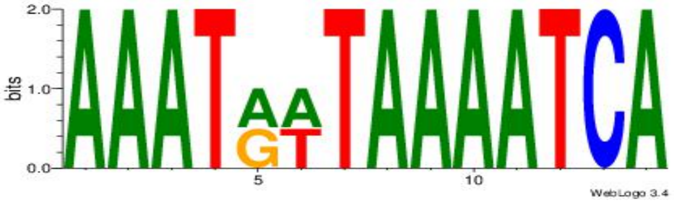


Dataset #:	2
Motif ID:	8
Motif name:	Motif 8
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	4
Number of overlap:	11
Similarity score:	0.083433

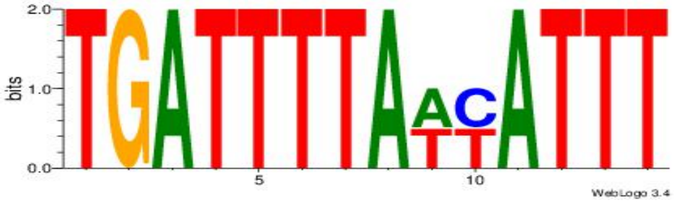
Alignment:

```
TGATTTTAWKATTT
---AWGKAAWTTTT
```

Original motif Consensus sequence: AAATRWTAAAATCA



Reverse complement motif Consensus sequence: TGATTTTAWKATT

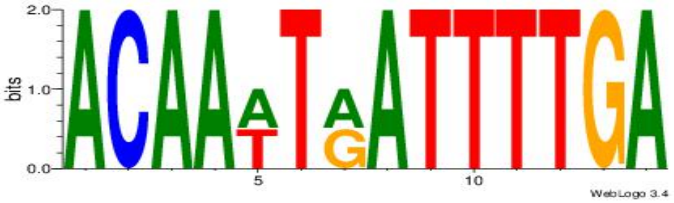


Dataset #:	2
Motif ID:	16

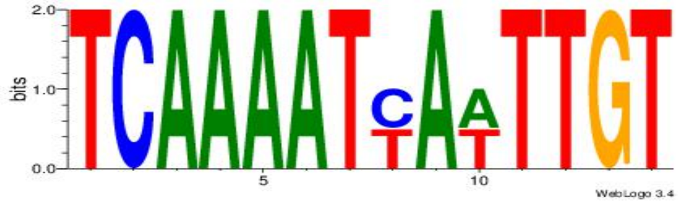
Motif name: Motif 16
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 11
Similarity score: 0.0852273

Alignment:
ACAAWTRATTTTGA
AAAAWTTRCWT---

Original motif Consensus sequence: ACAAWTRATTTTGA



Reverse complement motif Consensus sequence: TCAAAATKAWTTG

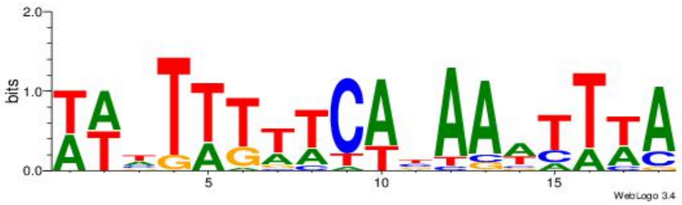


Dataset #: 5
Motif ID: 53
Motif name: TFM3
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 11
Similarity score: 0.0858797

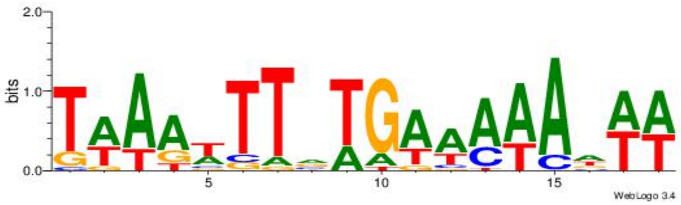
Alignment:

```
WWHTTTTTCABAAWTTWA
-------AWGKAAWTTTT
```

Original motif Consensus sequence: WWHTTTTTCABAAWTTWA



Reverse complement motif Consensus sequence: TWAAWTTVTGAAAAAHWW



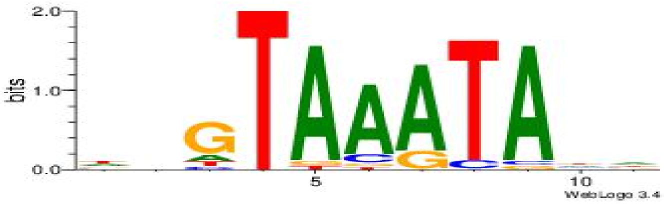
Dataset #:	4
Motif ID:	45
Motif name:	wbgTAAATAww
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	11
Similarity score:	0.086338

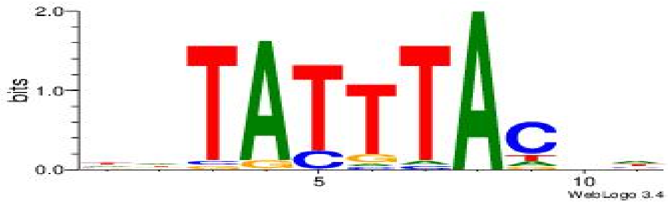
Alignment:

```
DHTATTTACBD
AAAAWTTRCWT
```

Original motif Consensus sequence: DBGTAAATAHD

Reverse complement motif Consensus sequence: DHTATTTACBD



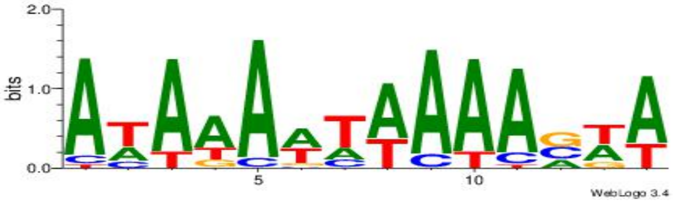


Dataset #:	2
Motif ID:	3
Motif name:	Motif 3
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	2
Number of overlap:	11
Similarity score:	0.0867914

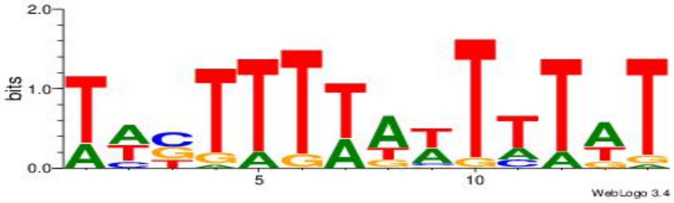
Alignment:

```
TWSTTTWAWTTTWT
--AWGKAAWTTTT-
```

Original motif Consensus sequence: AWAAAWTWAAASWA

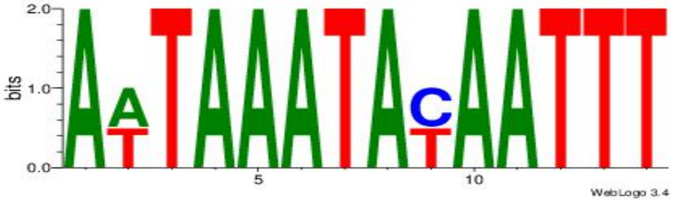


Reverse complement motif Consensus sequence: TWSTTTWAWTTTW

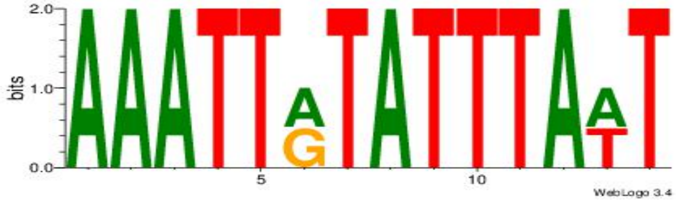


Dataset #: 2 Motif ID: 5 Motif name: Motif 5

Original motif Consensus sequence: AWTAAATAYAATTT



Reverse complement motif Consensus sequence: AAATTKTATTTAW



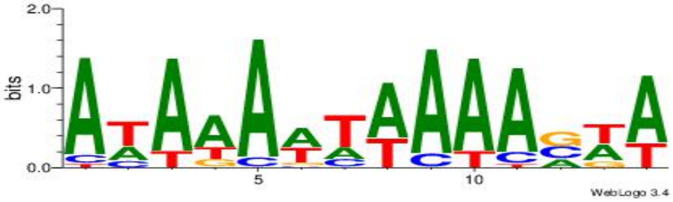
Best Matches for Motif ID 5 (Highest to Lowest)

Dataset #:	2
Motif ID:	3
Motif name:	Motif 3
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	14
Similarity score:	0.101648

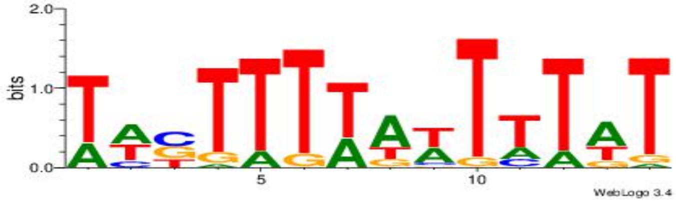
Alignment:

```
TWSTTTWAWTTTWT
AAATTKTATTTAWT
```

Original motif Consensus sequence: AWAAAWTWAAASWA



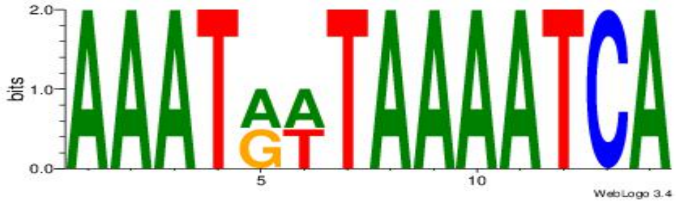
Reverse complement motif Consensus sequence: TWSTTTWAWTTT



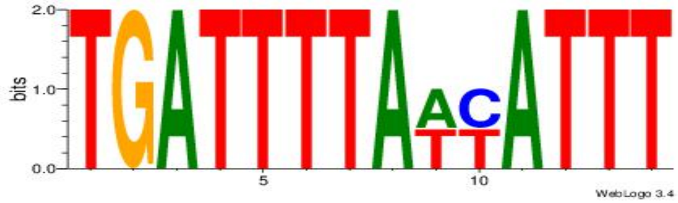
Dataset #: 2
Motif ID: 8
Motif name: Motif 8
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 14
Similarity score: 0.107143

Alignment:
```
TGATTTTAWKATTT
AAATTKTATTTAWT
```

Original motif Consensus sequence: AAATRWTAAAATCA



Reverse complement motif Consensus sequence: TGATTTTAWKATT



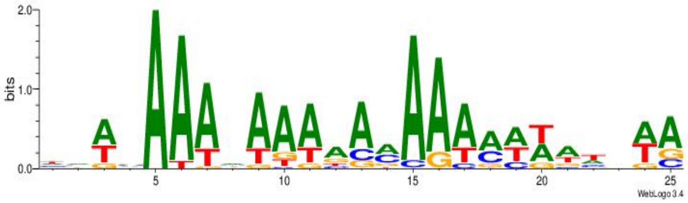
Dataset #: 5
Motif ID: 56
Motif name: TFM11
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 6
Number of overlap: 14

Similarity score: 0.109769

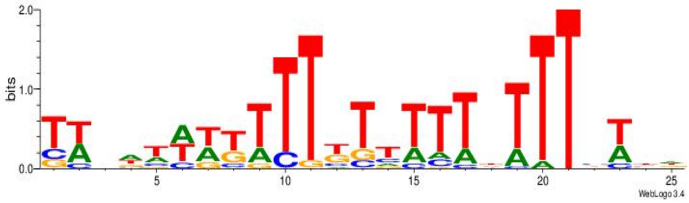
Alignment:

TWVHWWWYTTTYTTTTTHTTTVWBH
------AAATTKTATTTAWT-----

Original motif Consensus sequence:
HDWVAAAHAAAAAMAAAMWWWHBWA



Reverse complement motif Consensus sequence:
TWVHWWWYTTTYTTTTTHTTTVWBH



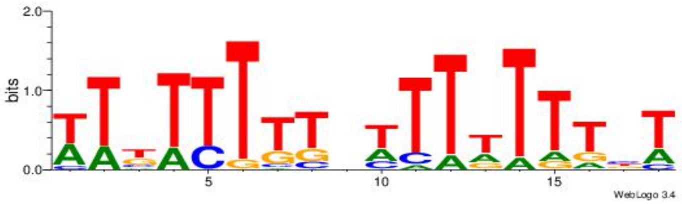
Dataset #:	5
Motif ID:	52
Motif name:	TFM1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	4
Number of overlap:	14
Similarity score:	0.110348

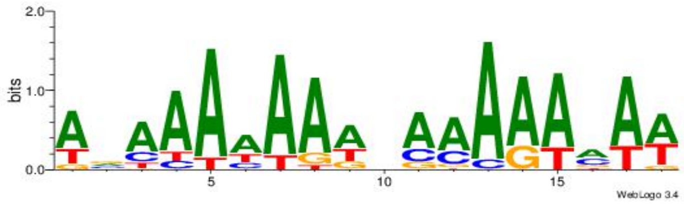
Alignment:

WTKTTTTTHWTTTTTTBT
-AAATTKTATTTAWT---

Original motif Consensus sequence: WTKTTTTTHWTTTTTTBT

Reverse complement motif Consensus sequence:
ABAAAAAAWHAAAAARAW





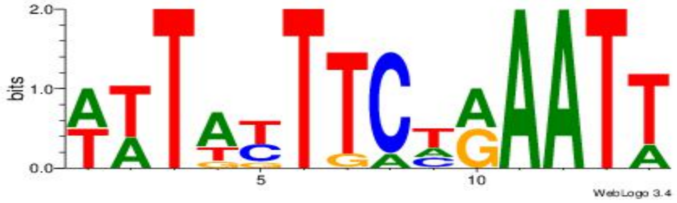
Dataset #:	2
Motif ID:	6
Motif name:	Motif 6
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	14
Similarity score:	0.111607

Alignment:

```
AATTYDGAARTAWW
AAATTKTATTTAWT
```

Original motif Consensus sequence: AATTYDGAARTAWW

Reverse complement motif Consensus sequence: WWTAKTTCDKAAT



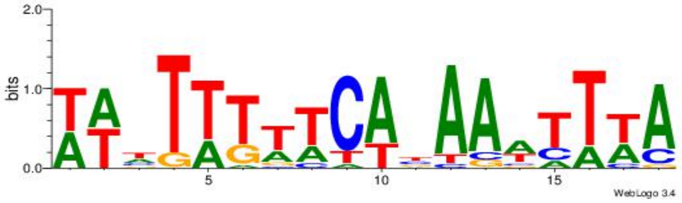
Dataset #:	5
Motif ID:	53

Motif name: TFM3
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 3
Number of overlap: 14
Similarity score: 0.124188

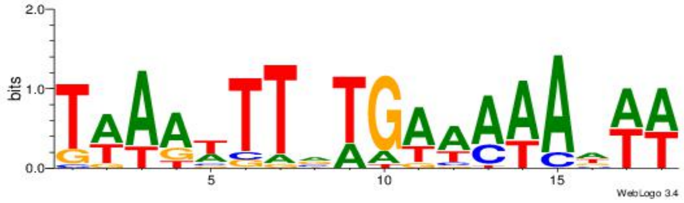
Alignment:

```
WWHTTTTTCABAAWTTWA
--AWTAAATAYAATTT--
```

Original motif Consensus sequence: WWHTTTTTCABAAWTTWA



Reverse complement motif Consensus sequence: TWAAWTTVTGAAAAAHWW

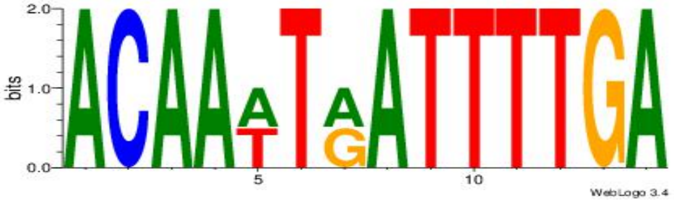


Dataset #: 2
Motif ID: 16
Motif name: Motif 16
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 14
Similarity score: 0.125

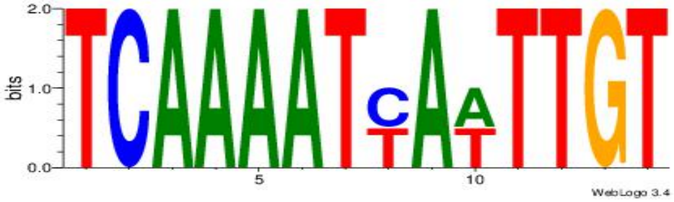
Alignment:

```
ACAAWTRATTTTGA
AAATTKTATTTAWT
```

Original motif Consensus sequence: ACAAWTRATTTTGA



Reverse complement motif Consensus sequence: TCAAAATKAWTTG



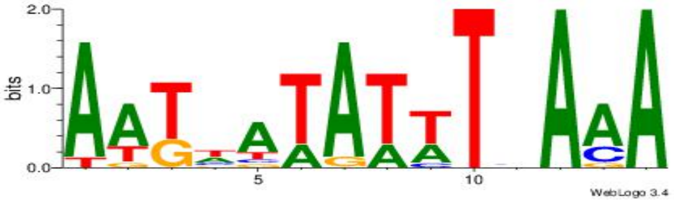
Dataset #:	2
Motif ID:	9
Motif name:	Motif 9
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	2
Number of overlap:	13
Similarity score:	0.596154

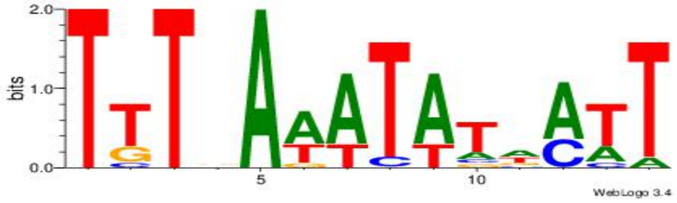
Alignment:

```
TTTDAWATATHATT-
-AWTAAATAYAATTT
```

Original motif Consensus sequence: AATHATATWTHAAA

Reverse complement motif Consensus sequence: TTTDAWATATHAT





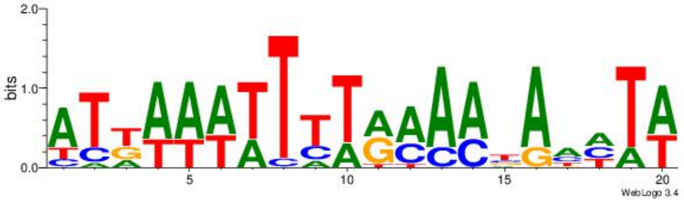
Dataset #:	5
Motif ID:	55
Motif name:	TFM13
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	9
Number of overlap:	12
Similarity score:	1.11736

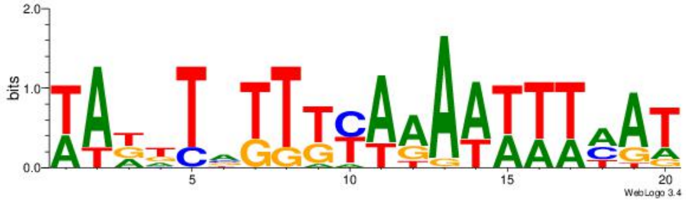
Alignment:

```
WAHHTVTTYKAAAAWTTRAT--
--------AWTAAATAYAATTT
```

Original motif Consensus sequence: ATKAAWTTTTRMAABAHHTW

Reverse complement motif Consensus sequence: WAHHTVTTYKAAAAWTTRAT





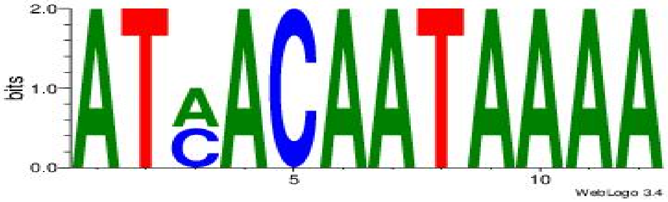
Dataset #:	2

Motif ID:	15
Motif name:	Motif 15
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	12
Similarity score:	1.125

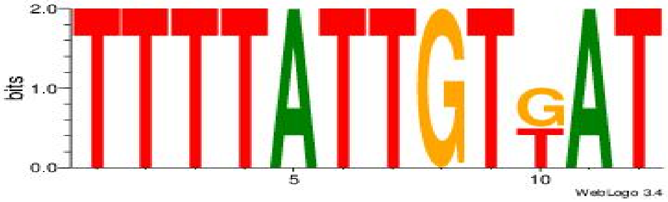
Alignment:

```
--TTTTATTGTYAT
AAATTKTATTTAWT
```

Original motif Consensus sequence: ATMACAATAAAA



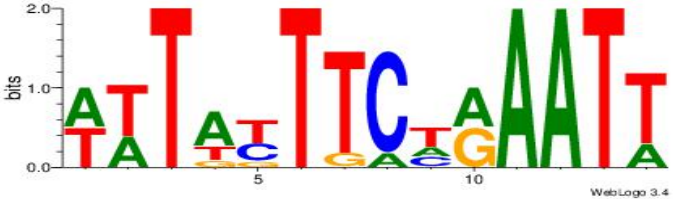
Reverse complement motif Consensus sequence: TTTTATTGTYAT



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

Original motif Consensus sequence: AATTYDGAARTAWW

Reverse complement motif Consensus sequence: WWTAKTTCDKAAT



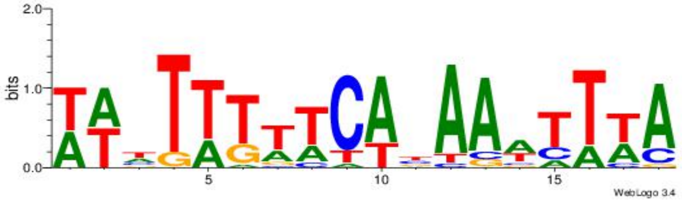
Best Matches for Motif ID 6 (Highest to Lowest)

Dataset #:	5
Motif ID:	53
Motif name:	TFM3
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	4
Number of overlap:	14
Similarity score:	0.0325081

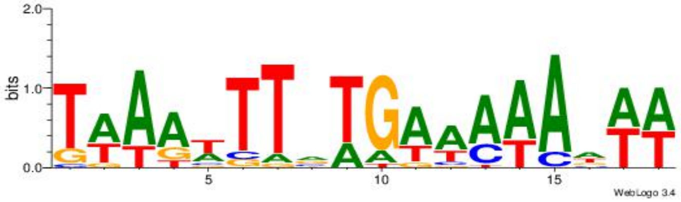
Alignment:

```
WWHTTTTTCABAAWTTWA
-WWTAKTTCDKAATT---
```

Original motif Consensus sequence: WWHTTTTTCABAAWTTWA



Reverse complement motif Consensus sequence: TWAAWTTVTGAAAAAHWW



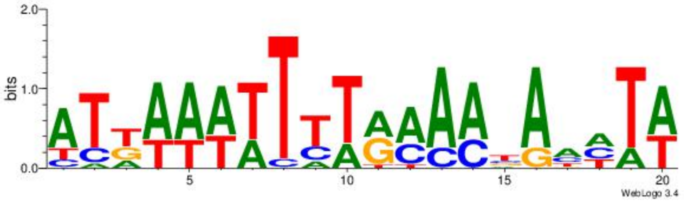
Dataset #:	5
Motif ID:	55
Motif name:	TFM13
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif

Direction:	Forward
Position number:	5
Number of overlap:	14
Similarity score:	0.0349702

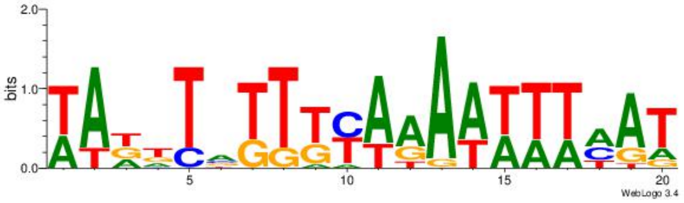
Alignment:

```
ATKAAWTTTTRMAABAHHTW
----AATTYDGAARTAWW--
```

Original motif Consensus sequence: ATKAAWTTTTRMAABAHHTW



Reverse complement motif Consensus sequence: WAHHTVTTYKAAAAWTTRAT

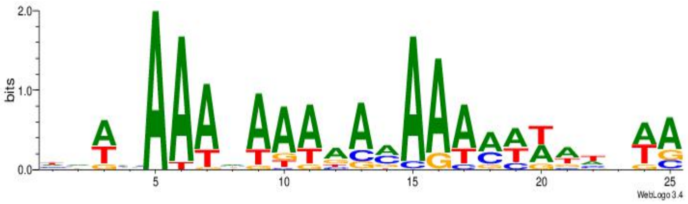


Dataset #:	5
Motif ID:	56
Motif name:	TFM11
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	9
Number of overlap:	14
Similarity score:	0.0626838

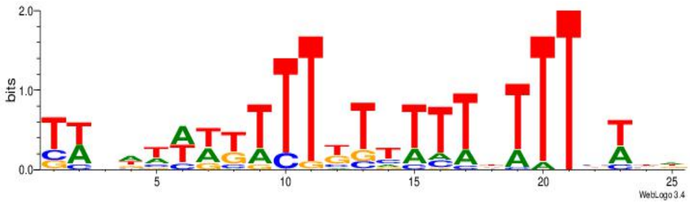
Alignment:

```
TWVHWWWYTTTYTTTTTHTTTVWBH
---WWTAKTTCDKAATT--------
```

Original motif Consensus sequence: HDWVAAAHAAAAAMAAAMWWWHBWA



Reverse complement motif Consensus sequence: TWVHWWWYTTTYTTTTTHTTTVWBH

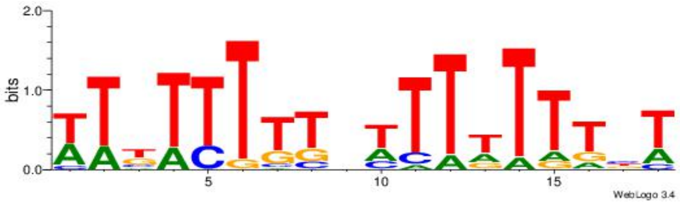


Dataset #:	5
Motif ID:	52
Motif name:	TFM1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	14
Similarity score:	0.0667239

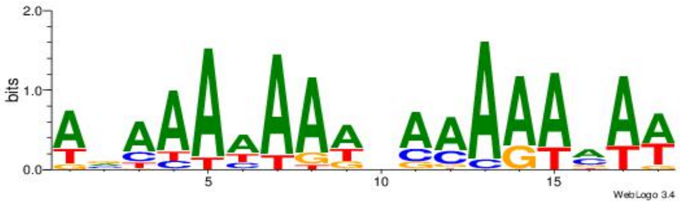
Alignment:

```
WTKTTTTTHWTTTTTTTBT
-WWTAKTTCDKAATT---
```

Original motif Consensus sequence: WTKTTTTTHWTTTTTTTBT



Reverse complement motif Consensus sequence: ABAAAAAAWHAAAAAARAW

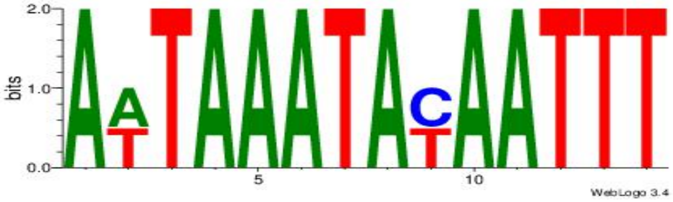


Dataset #: 2
Motif ID: 5
Motif name: Motif 5
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 14
Similarity score: 0.0741071

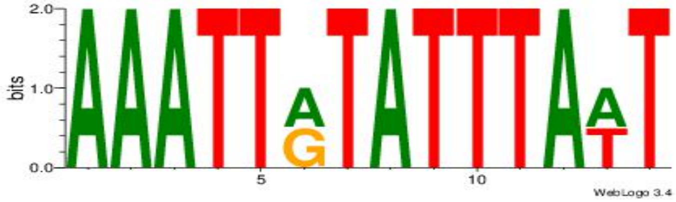
Alignment:

```
AWTAAATAYAATTT
WWTAKTTCDKAATT
```

Original motif Consensus sequence: AWTAAATAYAATTT



Reverse complement motif Consensus sequence: AAATTKTATTTAW

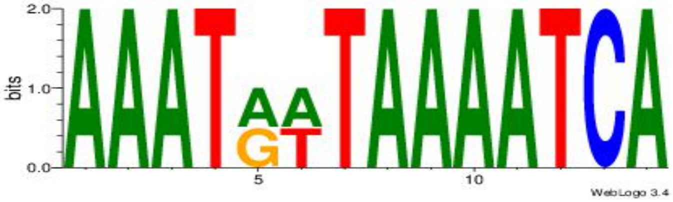


Dataset #: 2
Motif ID: 8
Motif name: Motif 8
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 14

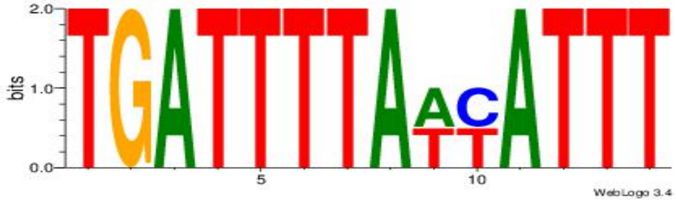
Similarity score:	0.0763393

Alignment:
TGATTTTAWKATTT
WWTAKTTCDKAATT

Original motif Consensus sequence: AAATRWTAAAATCA



Reverse complement motif Consensus sequence: TGATTTTAWKATT

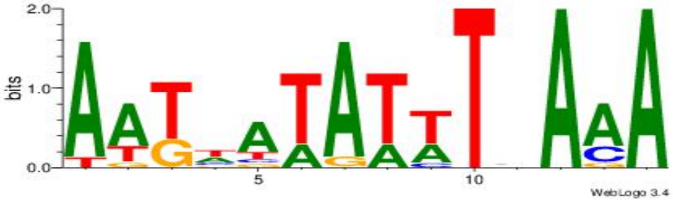


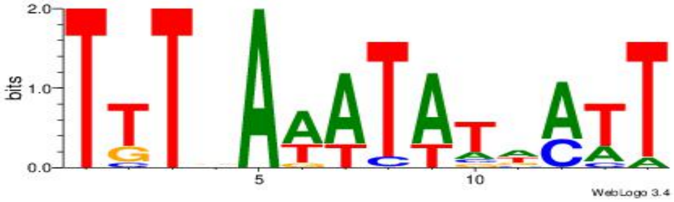
Dataset #:	2
Motif ID:	9
Motif name:	Motif 9
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	14
Similarity score:	0.0852679

Alignment:
TTTDAWATATHATT
WWTAKTTCDKAATT

Original motif Consensus sequence: AATHATATWTHAAA

Reverse complement motif Consensus sequence: TTTDAWATATHAT



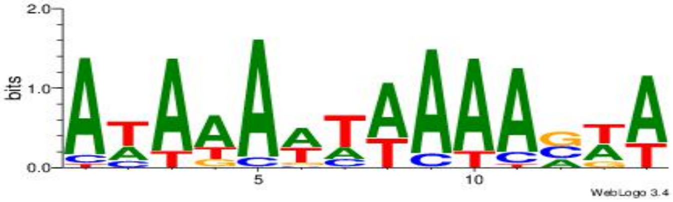


Dataset #:	2
Motif ID:	3
Motif name:	Motif 3
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	14
Similarity score:	0.0864698

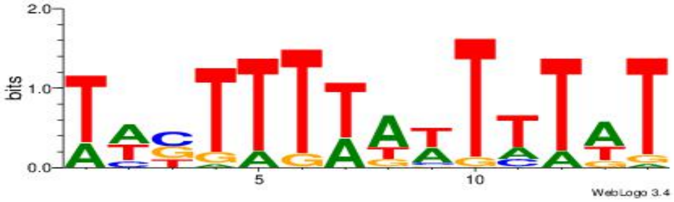
Alignment:

```
TWSTTTWAWTTTWT
WWTAKTTCDKAATT
```

Original motif Consensus sequence: AWAAAWTWAAASWA



Reverse complement motif Consensus sequence: TWSTTTWAWTTTW



Dataset #:	2
Motif ID:	19

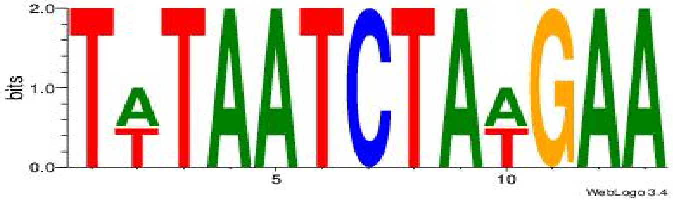
Motif name:	Motif 19
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2
Number of overlap:	12
Similarity score:	1.06667

Alignment:

```
--TTCWTAGATTAWA
AATTYDGAARTAWW-
```

Original motif Consensus sequence: TTCWTAGATTAWA

Reverse complement motif Consensus sequence: TWTAATCTAWGAA

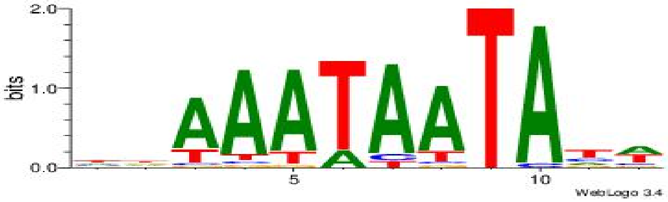


Dataset #:	4
Motif ID:	37
Motif name:	tkAAATAATAtw
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	12
Similarity score:	1.07587

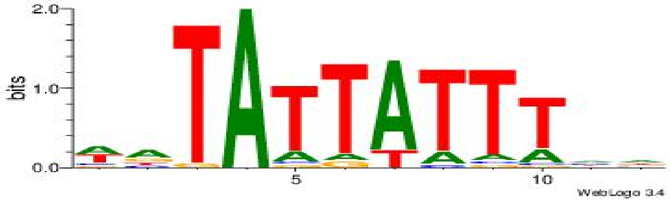
Alignment:

```
WHTATTATTTDH--
WWTAKTTCDKAATT
```

Original motif Consensus sequence: HDAAATAATAHW

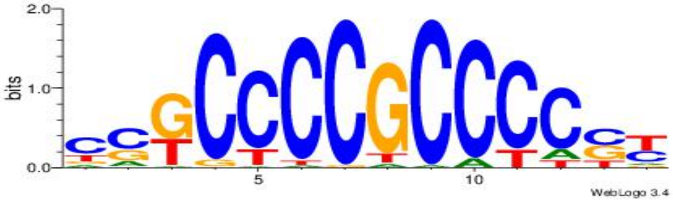


Reverse complement motif Consensus sequence: WHTATTATTTDH

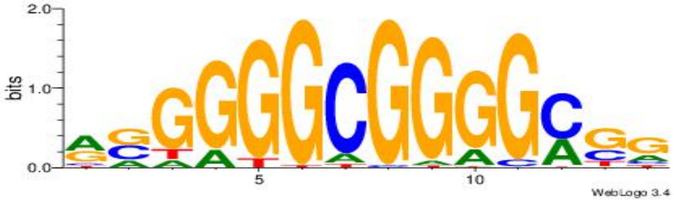


Dataset #: 2 Motif ID: 7 Motif name: Motif 7

Original motif Consensus sequence: CSKCCCCGCCCCSY



Reverse complement motif Consensus sequence: MSGGGGCGGGGY



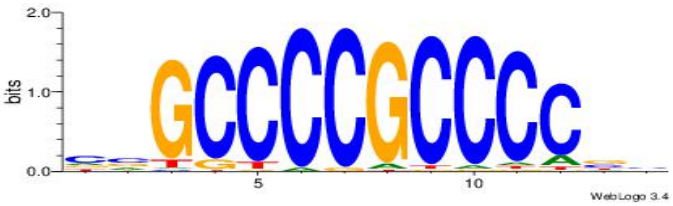
Best Matches for Motif ID 7 (Highest to Lowest)

Dataset #:	4
Motif ID:	36
Motif name:	csGCCCCGCCCCsc
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1

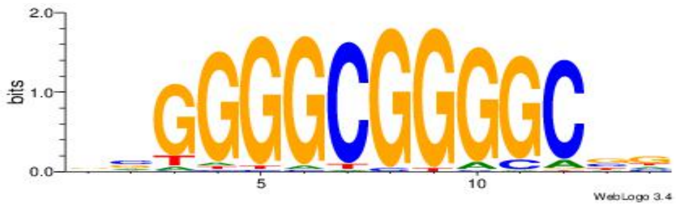
Number of overlap: 14
Similarity score: 0

Alignment:
```
HVGCCCCGCCCCBB
CSKCCCCGCCCCSY
```

Original motif Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGC

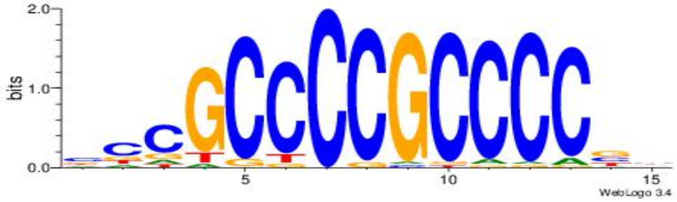


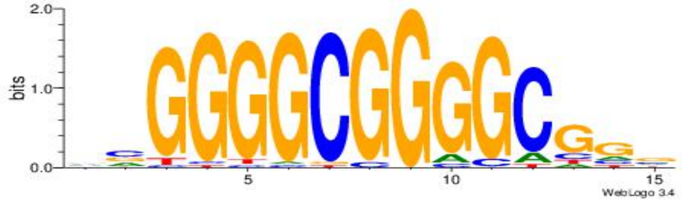
Dataset #: 4
Motif ID: 38
Motif name: cccGCCCCGCCCCsb
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 14
Similarity score: 0.0012818

Alignment:
```
BCCGCCCCGCCCCBB
-CSKCCCCGCCCCSY
```

Original motif Consensus sequence: BCCGCCCCGCCCCBB

Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB



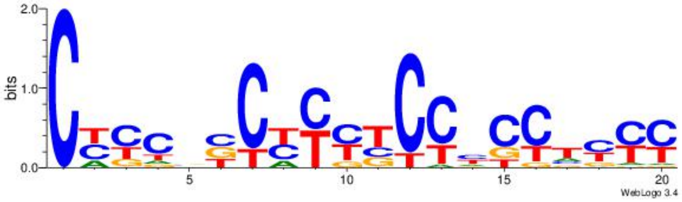


Dataset #:	5
Motif ID:	54
Motif name:	TFM12
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	4
Number of overlap:	14
Similarity score:	0.0537802

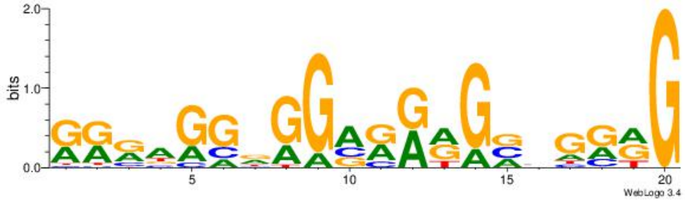
Alignment:

```
CYYCBBCYYYTCCHCCTYYY
---CSKCCCCGCCCCSY---
```

Original motif Consensus sequence: CYYCBBCYYYTCCHCCTYYY



Reverse complement motif Consensus sequence: KKKAGGDGGAKKMGBBGKMG



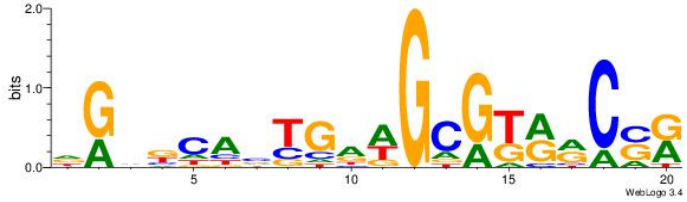
Dataset #:	3

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

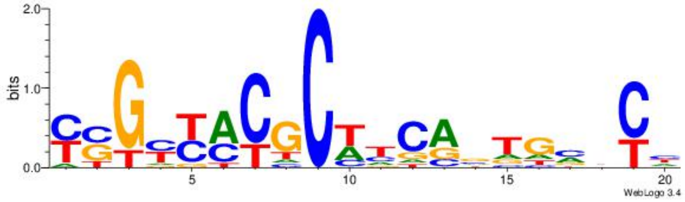
Alignment:

```
DGVBCABTGDWGCGKRRCSR
------MSGGGGCGGGGYSG
```

Original motif Consensus sequence: DGVBCABTGDWGCGKRRCSR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD



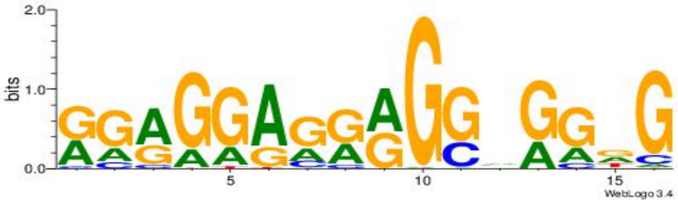
Dataset #: 5
Motif ID: 51
Motif name: TFM2
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 14

Similarity score: 0.0758609

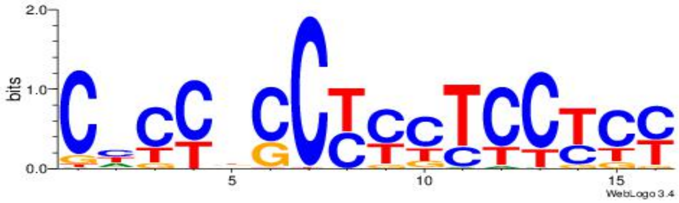
Alignment:

CHCCBCCKMCTCCKCM
CSKCCCCGCCCCSY--

Original motif Consensus sequence: RGRGGAGRRGGHGGDG



Reverse complement motif Consensus sequence: CHCCBCCKMCTCCKCM



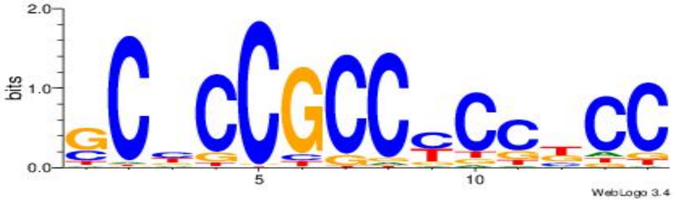
Dataset #:	5
Motif ID:	50
Motif name:	TFF11
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	14
Similarity score:	0.0829042

Alignment:

GCVCCGCCMCCYCC
CSKCCCCGCCCCSY

Original motif Consensus sequence: GGMGGRGGCGGVGC

Reverse complement motif Consensus sequence: GCVCCGCCMCCY



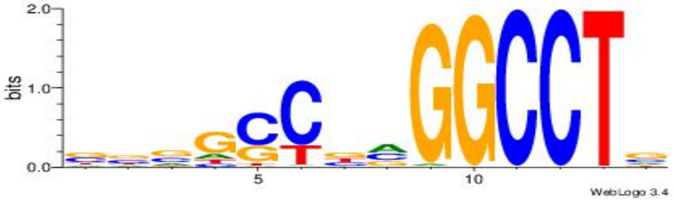
Dataset #:	3
Motif ID:	22
Motif name:	Zfx
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	14
Similarity score:	0.0912118

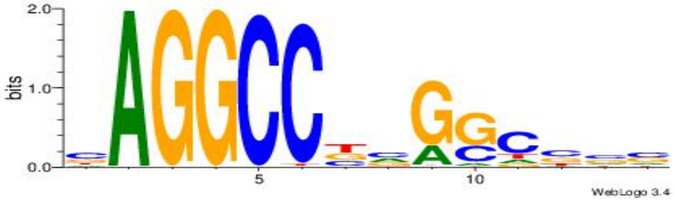
Alignment:

```
VAGGCCBBGGCVBB
CSKCCCCGCCCCSY
```

Original motif Consensus sequence: BBVGCCBVGGCCTV

Reverse complement motif Consensus sequence: VAGGCCBBGGCV





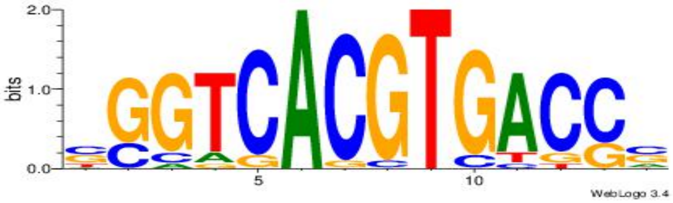
Dataset #:	4
Motif ID:	42

Motif name:	sSGTCACGTGACSs
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	14
Similarity score:	0.0948838

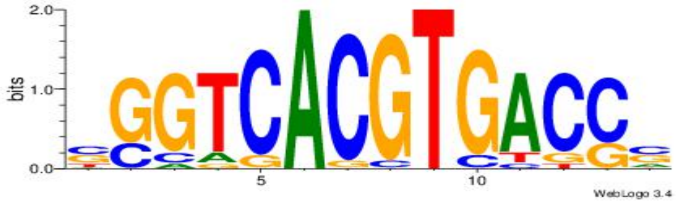
Alignment:

```
SGGTCACGTGACCS
MSGGGGCGGGGYSG
```

Original motif Consensus sequence: SGGTCACGTGACCS



Reverse complement motif Consensus sequence: SGGTCACGTGACC

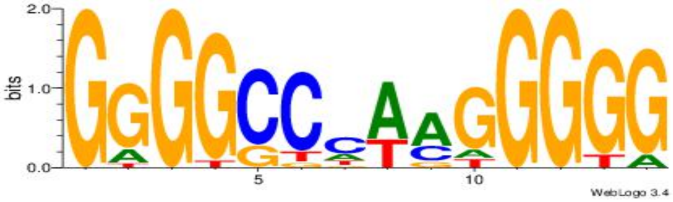


Dataset #:	3
Motif ID:	30
Motif name:	PLAG1
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	2
Number of overlap:	13
Similarity score:	0.590412

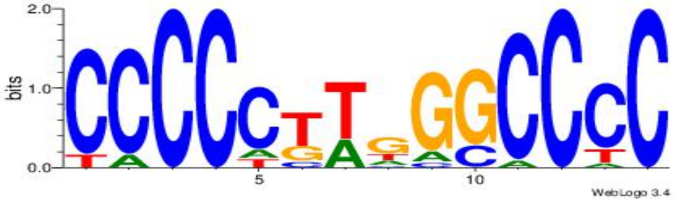
Alignment:

CCCCCTTGGGCCCC-
-CSKCCCCGCCCCSY

Original motif Consensus sequence: GGGGCCCAAGGGGG



Reverse complement motif Consensus sequence: CCCCCTTGGGCCC



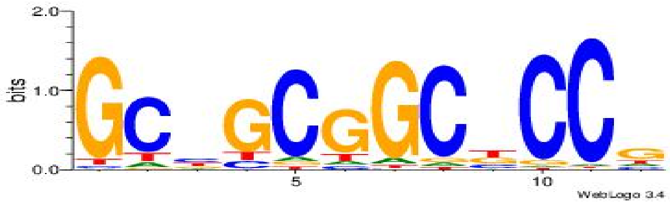
Dataset #:	5
Motif ID:	49
Motif name:	TFF1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	12
Similarity score:	1.07659

Alignment:

CGGVGCCGCVGC--
MSGGGGCGGGGYSG

Original motif Consensus sequence: CGGVGCCGCVGC

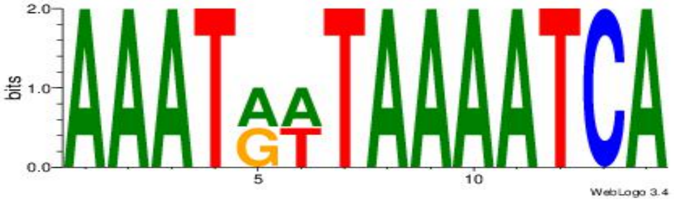
Reverse complement motif Consensus sequence: GCVGCGGCBCCG

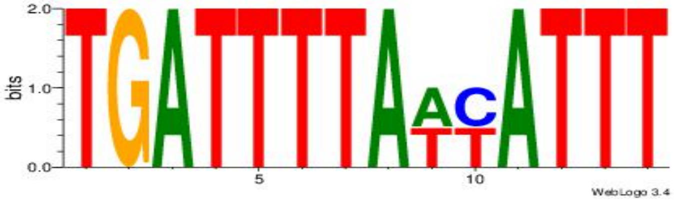


Dataset #: 2 **Motif ID: 8** **Motif name: Motif 8**

Original motif Consensus sequence: AAATRWTAAAATCA

Reverse complement motif Consensus sequence: TGATTTTAWKATT





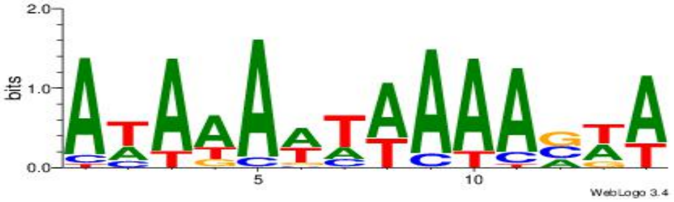
Best Matches for Motif ID 8 (Highest to Lowest)

Dataset #:	2
Motif ID:	3
Motif name:	Motif 3
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	14
Similarity score:	0.0961539

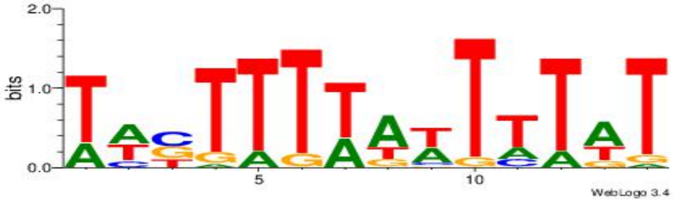
Alignment:

```
TWSTTTWAWTTTWT
TGATTTTAWKATTT
```

Original motif Consensus sequence: AWAAAWTWAAASWA



Reverse complement motif Consensus sequence: TWSTTTWAWTTTW

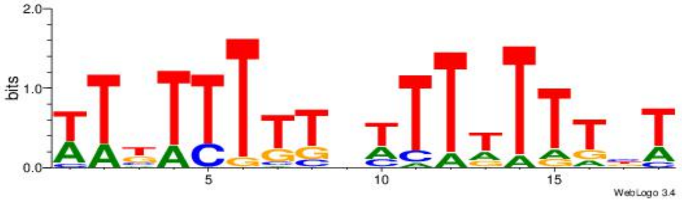


Dataset #:	5
Motif ID:	52
Motif name:	TFM1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	4
Number of overlap:	14
Similarity score:	0.10348

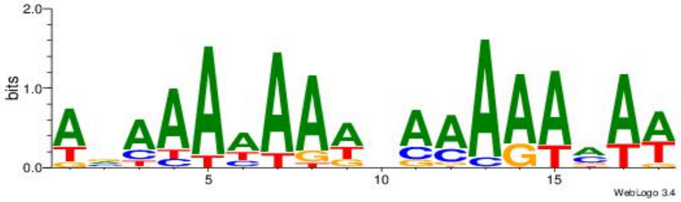
Alignment:

```
WTKTTTTTHWTTTTTTTBT
-TGATTTTAWKATTT---
```

Original motif Consensus sequence: WTKTTTTTHWTTTTTTTBT



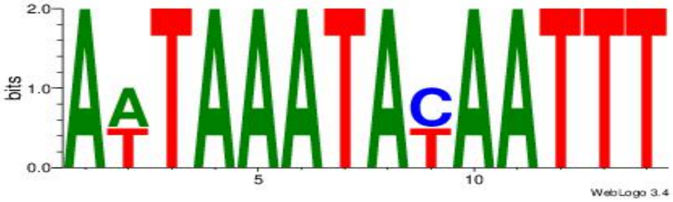
Reverse complement motif Consensus sequence:
ABAAAAAAAWHAAAAAARAW



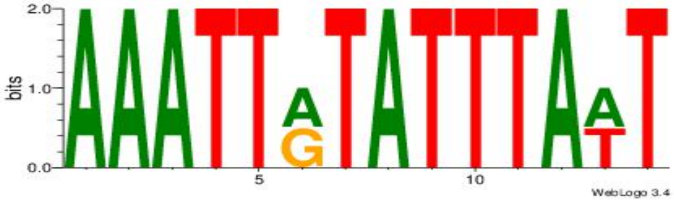
Dataset #:	2
Motif ID:	5
Motif name:	Motif 5
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	14
Similarity score:	0.107143

Alignment:
AAATTKTATTTAWT
TGATTTTAWKATTT

Original motif Consensus sequence: AWTAAATAYAATTT



Reverse complement motif Consensus sequence: AAATTKTATTTAW

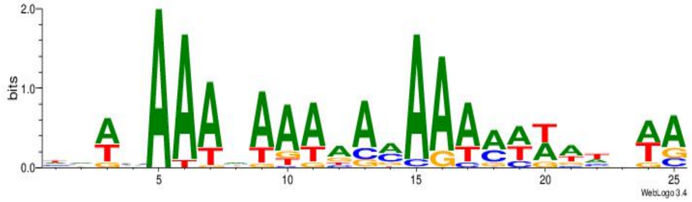


Dataset #:	5
Motif ID:	56
Motif name:	TFM11
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	7
Number of overlap:	14

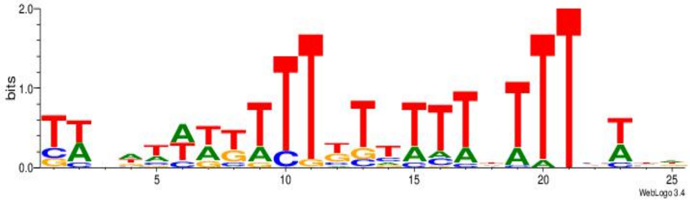
Similarity score: 0.111345

Alignment:
HDWVAAAHAAAAAMAAAMWWWHBWA
-----AAATRWTAAAATCA------

Original motif Consensus sequence:
HDWVAAAHAAAAAMAAAMWWWHBWA



Reverse complement motif Consensus sequence:
TWVHWWWYTTTYTTTTTHTTTVWBH

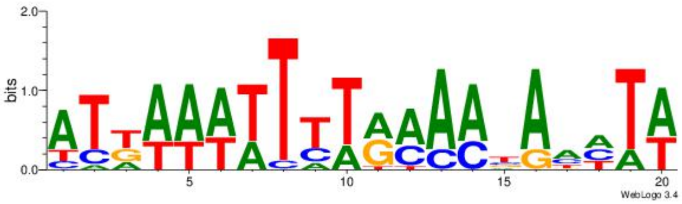


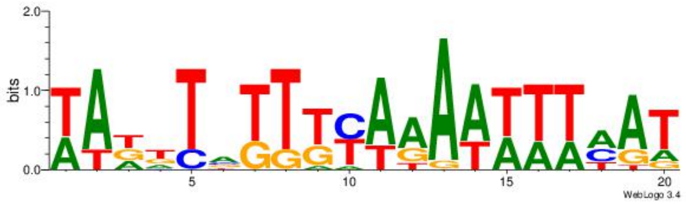
Dataset #:	5
Motif ID:	55
Motif name:	TFM13
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	4
Number of overlap:	14
Similarity score:	0.11369

Alignment:
WAHHTVTTYKAAAAWTTRAT
---TGATTTTAWKATTT---

Original motif Consensus sequence: ATKAAWTTTTRMAABAHHTW

Reverse complement motif Consensus sequence:
WAHHTVTTYKAAAAWTTRAT





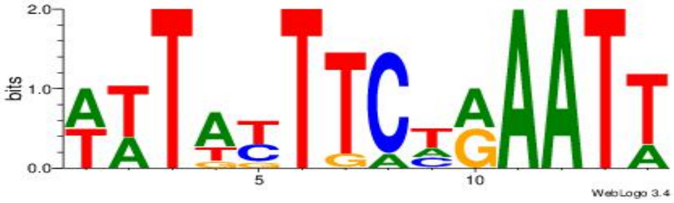
Dataset #:	2
Motif ID:	6
Motif name:	Motif 6
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	14
Similarity score:	0.113839

Alignment:

```
WWTAKTTCDKAATT
TGATTTTAWKATTT
```

Original motif Consensus sequence: AATTYDGAARTAWW

Reverse complement motif Consensus sequence: WWTAKTTCDKAAT



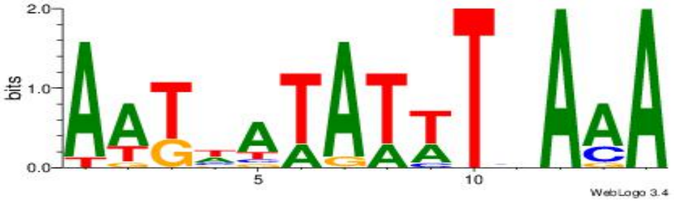
Dataset #:	2
Motif ID:	9

Motif name:	Motif 9
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2
Number of overlap:	13
Similarity score:	0.625

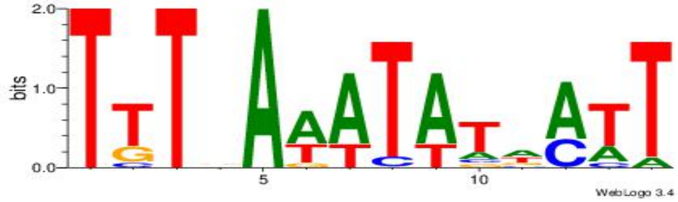
Alignment:

```
-AATHATATWTHAAA
AAATRWTAAAATCA-
```

Original motif   Consensus sequence: AATHATATWTHAAA



Reverse complement motif   Consensus sequence: TTTDAWATATHAT



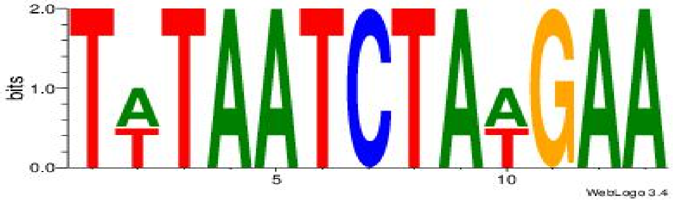
Dataset #:	2
Motif ID:	19
Motif name:	Motif 19
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	2
Number of overlap:	12
Similarity score:	1.10417

Alignment:

```
TWTAATCTAWGAA--
-TGATTTTAWKATTT
```

Original motif Consensus sequence: TTCWTAGATTAWA

Reverse complement motif Consensus sequence: TWTAATCTAWGAA



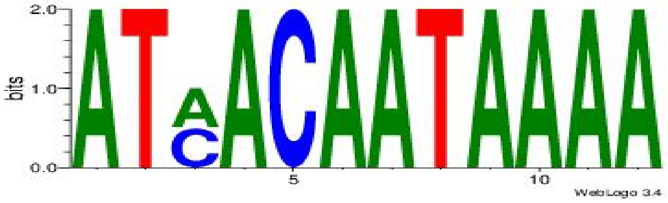
Dataset #:	2
Motif ID:	15
Motif name:	Motif 15
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	12
Similarity score:	1.10417

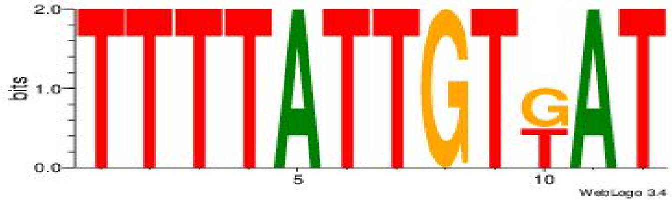
Alignment:

```
TTTTATTGTYAT--
TGATTTTAWKATTT
```

Original motif Consensus sequence: ATMACAATAAAA

Reverse complement motif Consensus sequence: TTTTATTGTYAT



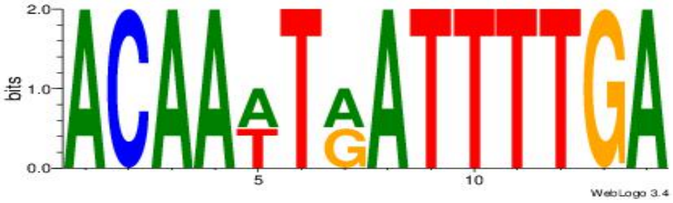


Dataset #:	2
Motif ID:	16
Motif name:	Motif 16
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	3
Number of overlap:	12
Similarity score:	1.125

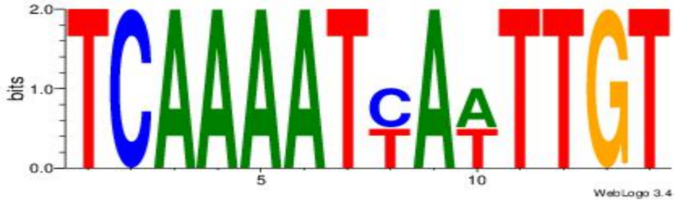
Alignment:

```
ACAAWTRATTTTGA--
--AAATRWTAAAATCA
```

Original motif Consensus sequence: ACAAWTRATTTTGA

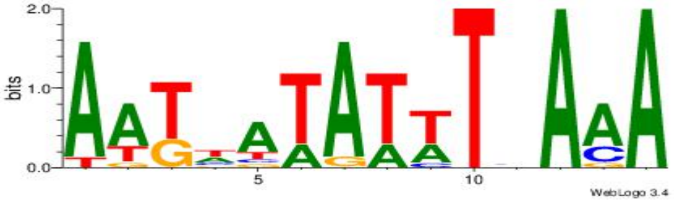


Reverse complement motif Consensus sequence: TCAAAATKAWTTG

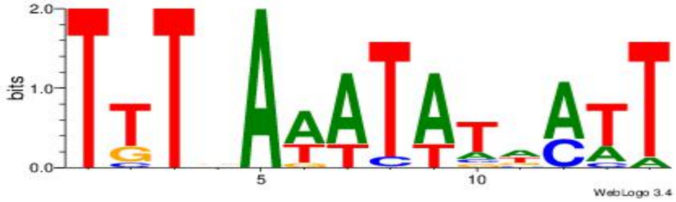


Dataset #: 2 Motif ID: 9 Motif name: Motif 9

Original motif   Consensus sequence: AATHATATWTHAAA



Reverse complement motif   Consensus sequence: TTTDAWATATHAT



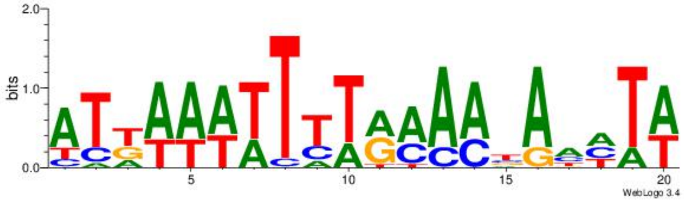
Best Matches for Motif ID 9 (Highest to Lowest)

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

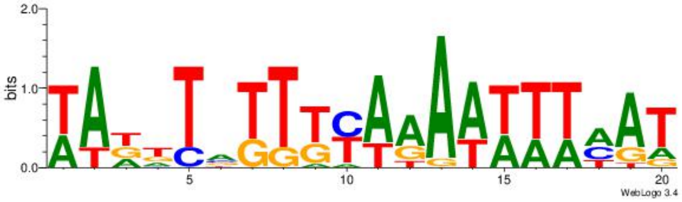
Alignment:

```
WAHHTVTTYKAAAAWTTRAT
------TTTDAWATATHATT
```

Original motif   Consensus sequence: ATKAAWTTTTRMAABAHHTW



Reverse complement motif   Consensus sequence: WAHHTVTTYKAAAAWTTRAT

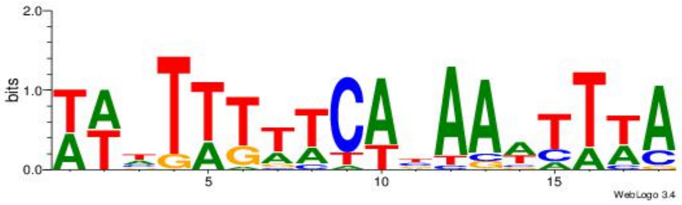


Dataset #:	5
Motif ID:	53
Motif name:	TFM3
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2
Number of overlap:	14
Similarity score:	0.0486562

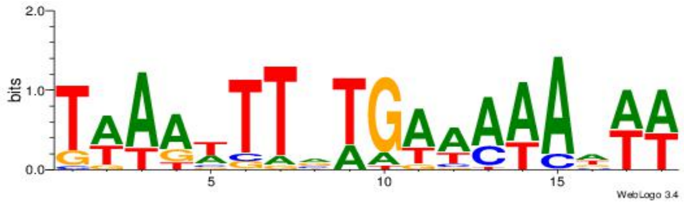
Alignment:

```
WWHTTTTTCABAAWTTWA
---TTTDAWATATHATT-
```

Original motif Consensus sequence: WWHTTTTTCABAAWTTWA



Reverse complement motif Consensus sequence: TWAAWTTVTGAAAAAHWW



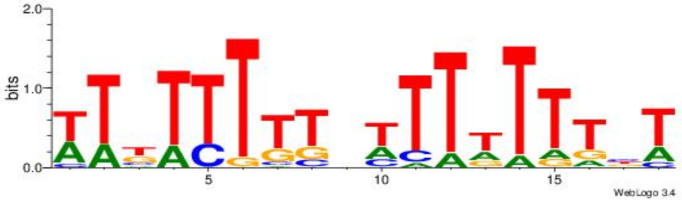
Dataset #:	5
Motif ID:	52
Motif name:	TFM1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	4

Number of overlap: 14
Similarity score: 0.0528083

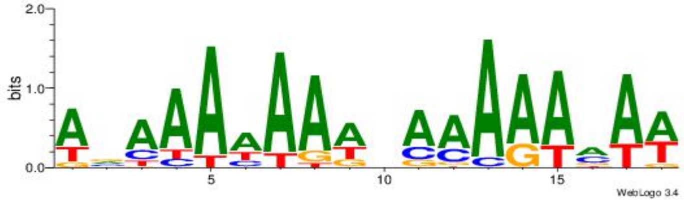
Alignment:

```
WTKTTTTTHWTTTTTTBT
---TTTDAWATATHATT-
```

Original motif   Consensus sequence: WTKTTTTTHWTTTTTTBT



Reverse complement motif   Consensus sequence: ABAAAAAAWHAAAAARAW

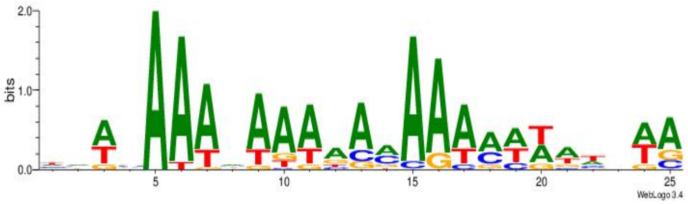


Dataset #: 5
Motif ID: 56
Motif name: TFM11
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 14
Similarity score: 0.054155

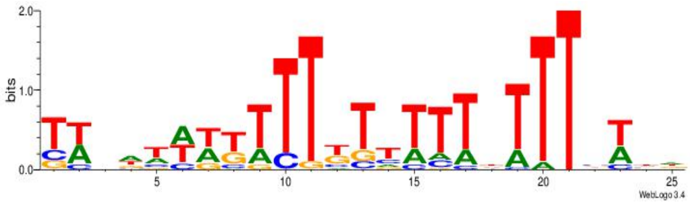
Alignment:

```
HDWVAAAHAAAAAMAAAMWWWHBWA
TTTDAWATATHATT-----------
```

Original motif Consensus sequence: HDWVAAAHAAAAAMAAAMWWWHBWA



Reverse complement motif Consensus sequence: TWVHWWWYTTTYTTTTTHTTTVWBH

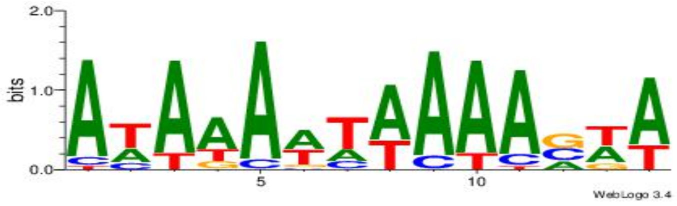


Dataset #:	2
Motif ID:	3
Motif name:	Motif 3
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	14
Similarity score:	0.0675748

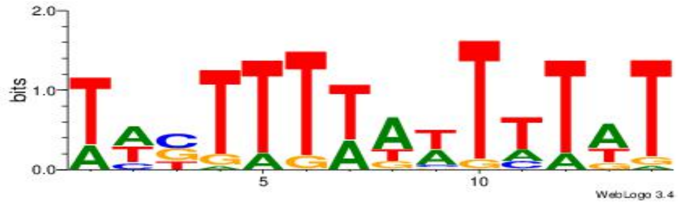
Alignment:

```
TWSTTTWAWTTTWT
AATHATATWTHAAA
```

Original motif Consensus sequence: AWAAAWTWAAASWA



Reverse complement motif Consensus sequence: TWSTTTWAWTTT



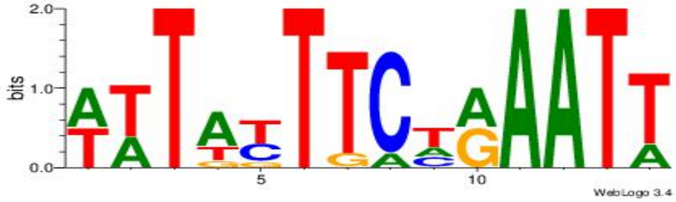
Dataset #:	2
Motif ID:	6
Motif name:	Motif 6
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	14
Similarity score:	0.0741568

Alignment:

```
WWTAKTTCDKAATT
TTTDAWATATHATT
```

Original motif   Consensus sequence: AATTYDGAARTAWW

Reverse complement motif   Consensus sequence: WWTAKTTCDKAAT

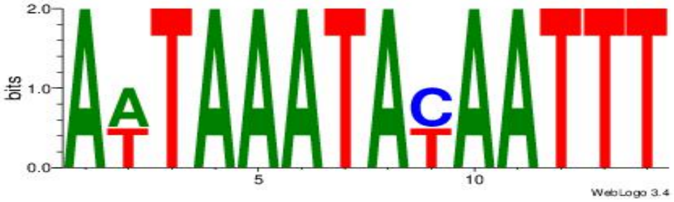


Dataset #:	2
Motif ID:	5
Motif name:	Motif 5
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	2
Number of overlap:	13

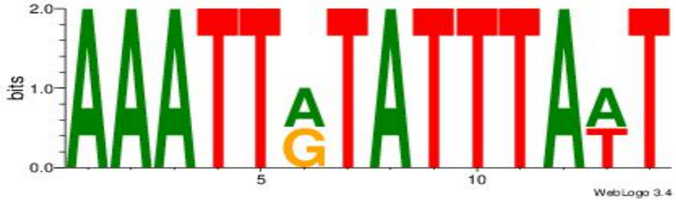
Similarity score: 0.547543

Alignment:
-AAATTKTATTTAWT
AATHATATWTHAAA-

Original motif Consensus sequence: AWTAAATAYAATTT



Reverse complement motif Consensus sequence: AAATTKTATTTAWT

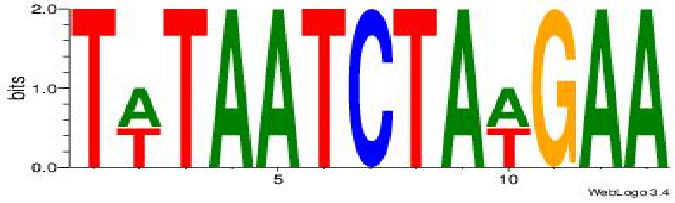


Dataset #:	2
Motif ID:	19
Motif name:	Motif 19
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	13
Similarity score:	0.557158

Alignment:
-TTCWTAGATTAWA
AATHATATWTHAAA

Original motif Consensus sequence: TTCWTAGATTAWA

Reverse complement motif Consensus sequence: TWTAATCTAWGAA



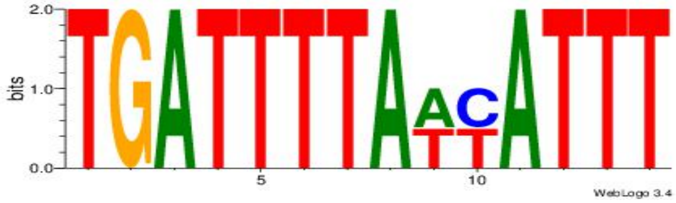
Dataset #:	2
Motif ID:	8
Motif name:	Motif 8
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	2
Number of overlap:	13
Similarity score:	0.576389

Alignment:

```
-TGATTTTAWKATTT
TTTDAWATATHATT-
```

Original motif Consensus sequence: AAATRWTAAAATCA

Reverse complement motif Consensus sequence: TGATTTTAWKATT



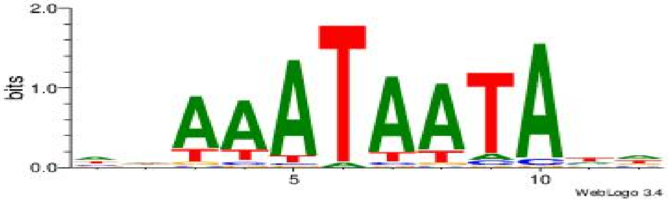
Dataset #:	4
Motif ID:	41

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:	1.03318

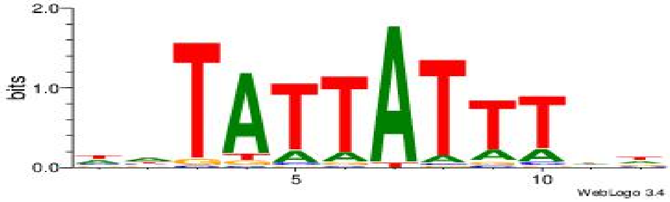
Alignment:

```
--HDAAATAATADD
TTTDAWATATHATT
```

Original motif Consensus sequence: HDAAATAATADD

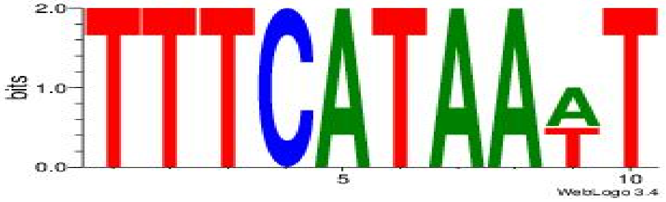


Reverse complement motif Consensus sequence: DDTATTATTTDH

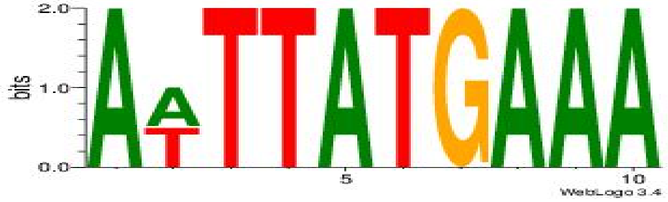


Dataset #: 2 **Motif ID: 10** **Motif name: Motif 10**

Original motif Consensus sequence: TTTCATAAWT



Reverse complement motif Consensus sequence: AWTTATGAAA

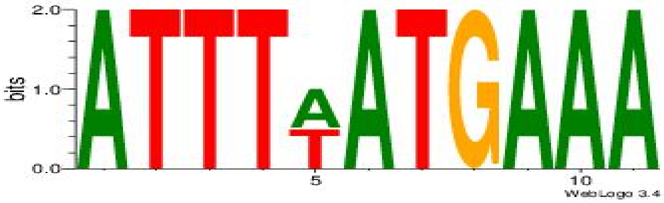


Best Matches for Motif ID 10 (Highest to Lowest)

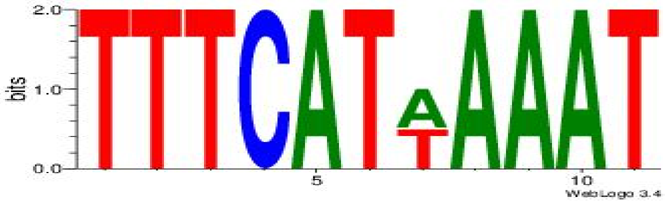
Dataset #: 2
Motif ID: 11
Motif name: Motif 11
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 2
Number of overlap: 10
Similarity score: 0.01875

Alignment:
ATTTWATGAAA
-AWTTATGAAA

Original motif Consensus sequence: ATTTWATGAAA



Reverse complement motif Consensus sequence: TTTCATWAAAT



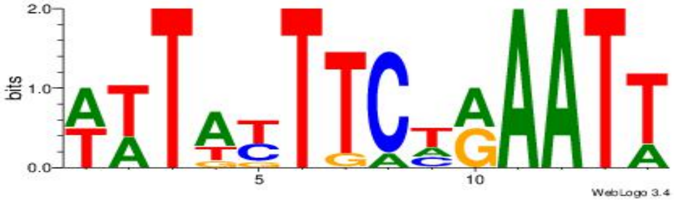
Dataset #: 2
Motif ID: 6
Motif name: Motif 6
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 5
Number of overlap: 10

Similarity score: 0.0375

Alignment:
AATTYDGAARTAWW
----AWTTATGAAA

Original motif Consensus sequence: AATTYDGAARTAWW

Reverse complement motif Consensus sequence: WWTAKTTCDKAAT

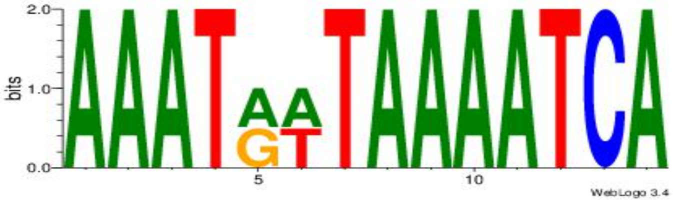


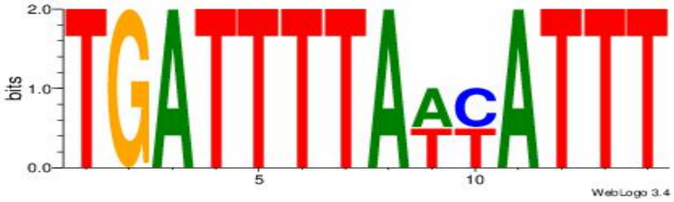
Dataset #:	2
Motif ID:	8
Motif name:	Motif 8
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	4
Number of overlap:	10
Similarity score:	0.04375

Alignment:
TGATTTTAWKATTT
-TTTCATAAWT---

Original motif Consensus sequence: AAATRWTAAAATCA

Reverse complement motif Consensus sequence: TGATTTTAWKATT



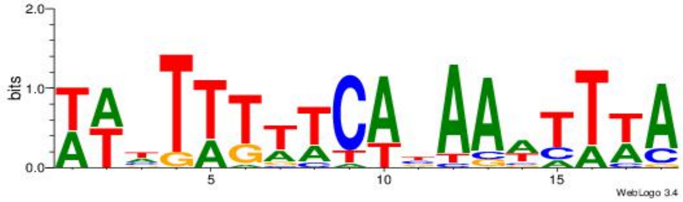


Dataset #:	5
Motif ID:	53
Motif name:	TFM3
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	6
Number of overlap:	10
Similarity score:	0.0448864

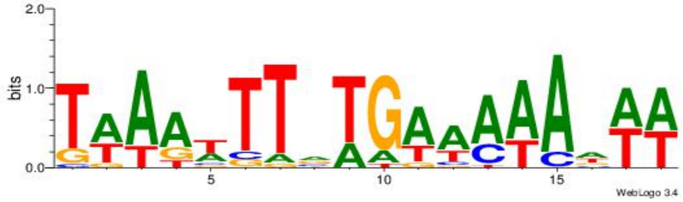
Alignment:

```
TWAAWTTVTGAAAAAHWW
---AWTTATGAAA-----
```

Original motif Consensus sequence: WWHTTTTTCABAAWTTWA



Reverse complement motif Consensus sequence: TWAAWTTVTGAAAAAHWW



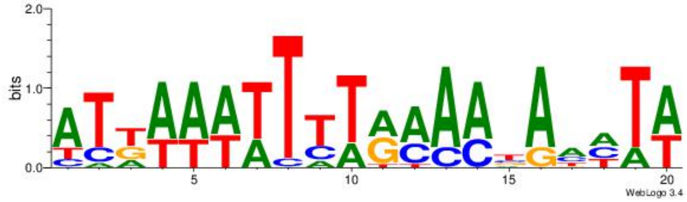
Dataset #:	5

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

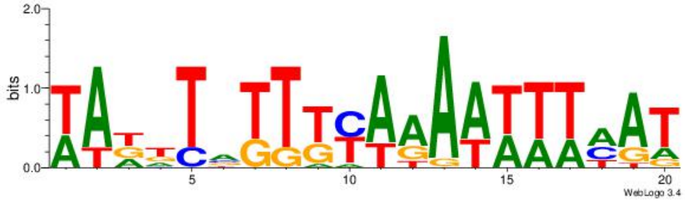
Alignment:

```
ATKAAWTTTTRMAABAHHTW
----AWTTATGAAA------
```

Original motif Consensus sequence: ATKAAWTTTTRMAABAHHTW



Reverse complement motif Consensus sequence: WAHHTVTTYKAAAAWTTRAT



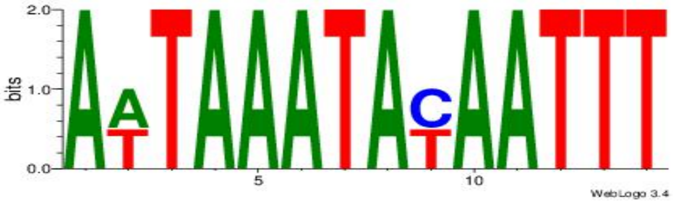
Dataset #: 2
Motif ID: 5
Motif name: Motif 5
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 10

Similarity score: 0.05625

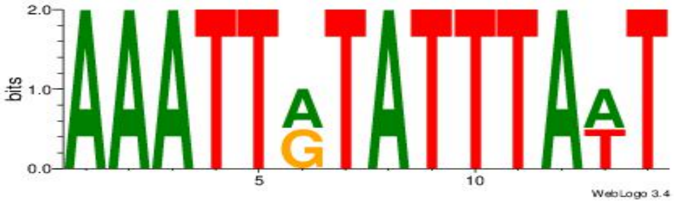
Alignment:

AWTAAATAYAATTT
----AWTTATGAAA

Original motif Consensus sequence: AWTAAATAYAATTT



Reverse complement motif Consensus sequence: AAATTKTATTTAW



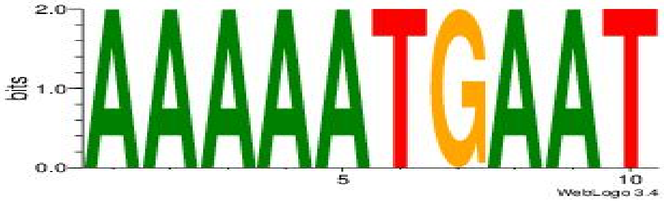
Dataset #:	2
Motif ID:	17
Motif name:	Motif 17
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	10
Similarity score:	0.05625

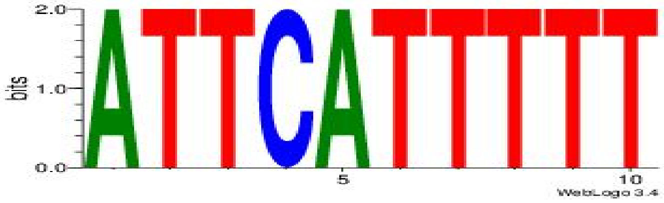
Alignment:

ATTCATTTTT
TTTCATAAWT

Original motif Consensus sequence: AAAAATGAAT

Reverse complement motif Consensus sequence: ATTCATTTTT



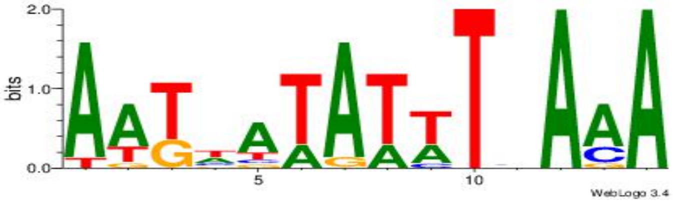


Dataset #:	2
Motif ID:	9
Motif name:	Motif 9
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	10
Similarity score:	0.0604166

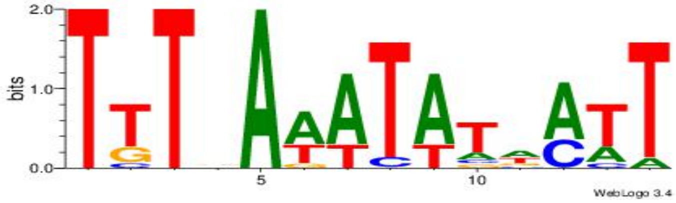
Alignment:

```
TTTDAWATATHATT
----TTTCATAAWT
```

Original motif Consensus sequence: AATHATATWTHAAA



Reverse complement motif Consensus sequence: TTTDAWATATHAT



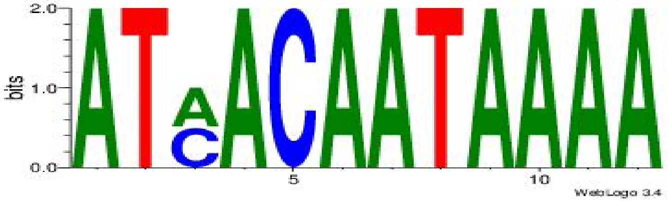
Dataset #:	2
Motif ID:	15

Motif name: Motif 15
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 10
Similarity score: 0.06875

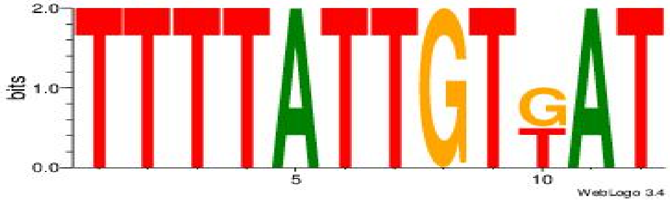
Alignment:

```
ATMACAATAAAA
--AWTTATGAAA
```

Original motif Consensus sequence: ATMACAATAAAA



Reverse complement motif Consensus sequence: TTTTATTGTYAT

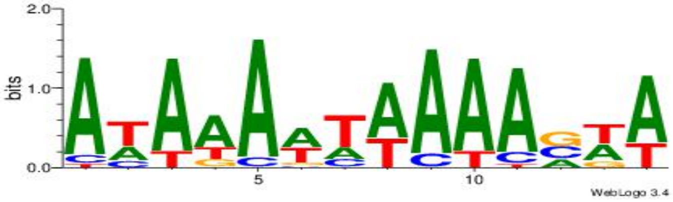


Dataset #: 2
Motif ID: 3
Motif name: Motif 3
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 5
Number of overlap: 10
Similarity score: 0.0706731

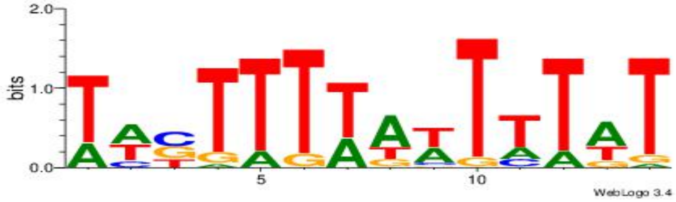
Alignment:

```
AWAAAWTWAAASWA
----AWTTATGAAA
```

Original motif Consensus sequence: AWAAAWTWAAASWA

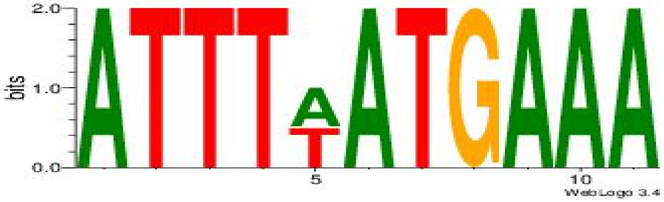


Reverse complement motif Consensus sequence: TWSTTTWAWTTTW

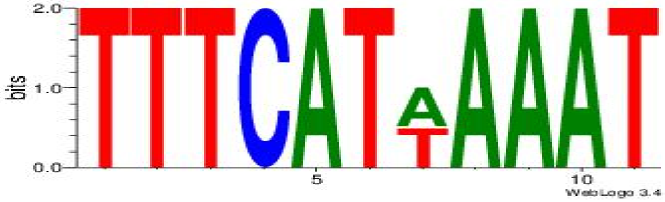


Dataset #: 2 **Motif ID: 11** **Motif name: Motif 11**

Original motif Consensus sequence: ATTTWATGAAA



Reverse complement motif Consensus sequence: TTTCATWAAAT



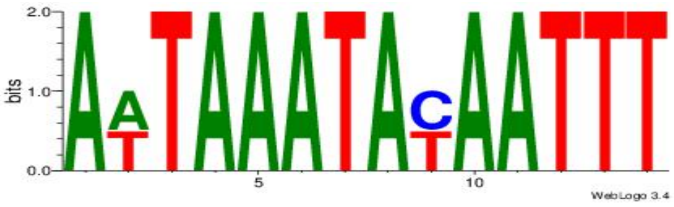
Best Matches for Motif ID 11 (Highest to Lowest)

Dataset #:	2
Motif ID:	5
Motif name:	Motif 5
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	3

Number of overlap: 11
Similarity score: 0.0795455

Alignment:
```
AWTAAATAYAATTT
--TTTCATWAAAT-
```

Original motif Consensus sequence: AWTAAATAYAATTT



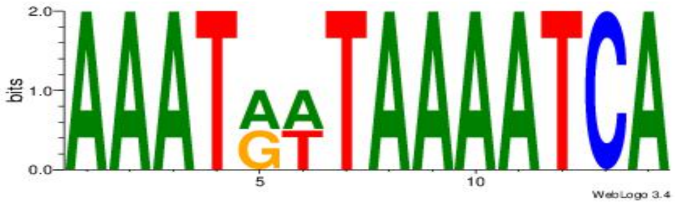
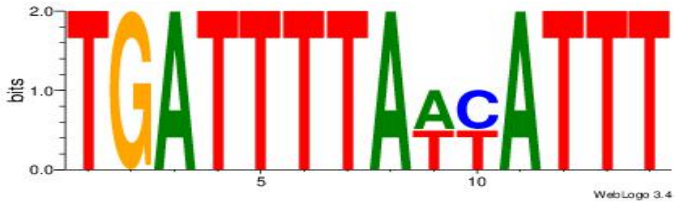
Reverse complement motif Consensus sequence: AAATTKTATTTAW

Dataset #: 2
Motif ID: 8
Motif name: Motif 8
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 3
Number of overlap: 11
Similarity score: 0.0795455

Alignment:
```
AAATRWTAAAATCA
--TTTCATWAAAT-
```

Original motif Consensus sequence: AAATRWTAAAATCA

Reverse complement motif Consensus sequence: TGATTTTAWKATT

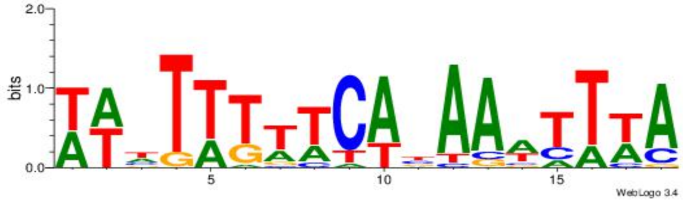



Dataset #:	5
Motif ID:	53
Motif name:	TFM3
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	6
Number of overlap:	11
Similarity score:	0.0991736

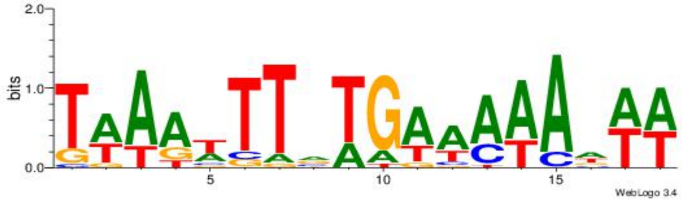
Alignment:

```
WWHTTTTTCABAAWTTWA
-----TTTCATWAAAT--
```

Original motif Consensus sequence: WWHTTTTTCABAAWTTWA



Reverse complement motif Consensus sequence: TWAAWTTVTGAAAAAHWW



Dataset #: 2

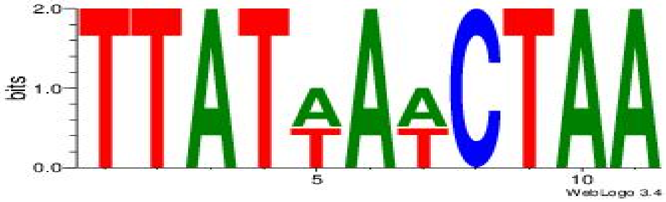
Motif ID: 18
Motif name: Motif 18
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 11
Similarity score: 0.102273

Alignment:

```
TTATWAWCTAA
ATTTWATGAAA
```

Original motif Consensus sequence: TTAGWTWATAA

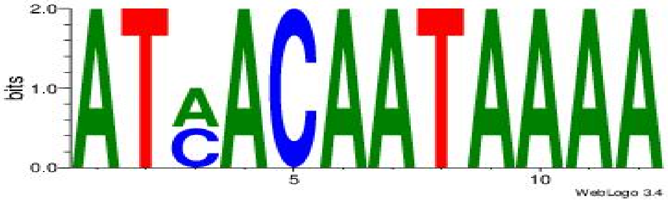
Reverse complement motif Consensus sequence: TTATWAWCTAA



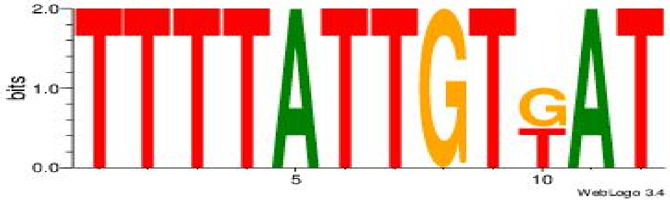
Dataset #: 2
Motif ID: 15
Motif name: Motif 15
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 11
Similarity score: 0.102273

Alignment:
TTTTATTGTYAT
ATTTWATGAAA-

Original motif Consensus sequence: ATMACAATAAAA



Reverse complement motif Consensus sequence: TTTTATTGTYAT

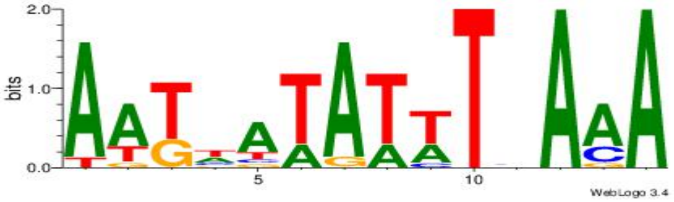


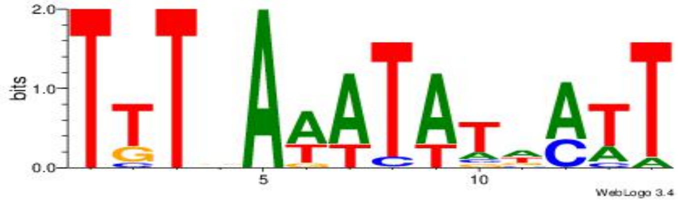
Dataset #:	2
Motif ID:	9
Motif name:	Motif 9
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	11
Similarity score:	0.109848

Alignment:
AATHATATWTHAAA
---ATTTWATGAAA

Original motif Consensus sequence: AATHATATWTHAAA

Reverse complement motif Consensus sequence: TTTDAWATATHAT





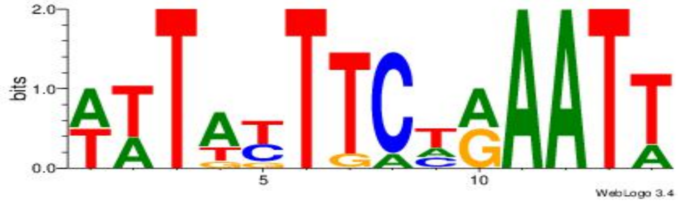
Dataset #:	2
Motif ID:	6
Motif name:	Motif 6
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	3
Number of overlap:	11
Similarity score:	0.113636

Alignment:

```
AATTYDGAARTAWW
-ATTTWATGAAA--
```

Original motif Consensus sequence: AATTYDGAARTAWW

Reverse complement motif Consensus sequence: WWTAKTTCDKAAT



Dataset #:	2
Motif ID:	19

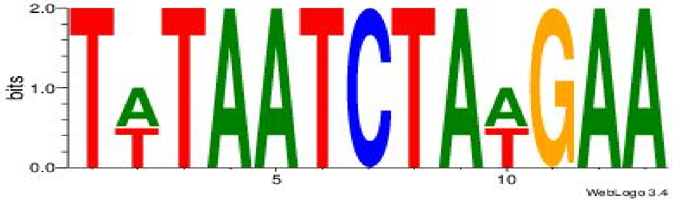
Motif name:	Motif 19
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	11
Similarity score:	0.113636

Alignment:

```
TWTAATCTAWGAA
TTTCATWAAAT--
```

Original motif Consensus sequence: TTCWTAGATTAWA

Reverse complement motif Consensus sequence: TWTAATCTAWGAA

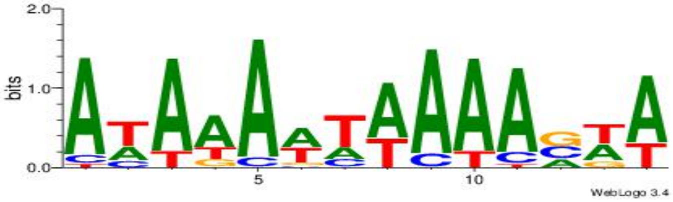


Dataset #:	2
Motif ID:	3
Motif name:	Motif 3
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	11
Similarity score:	0.113636

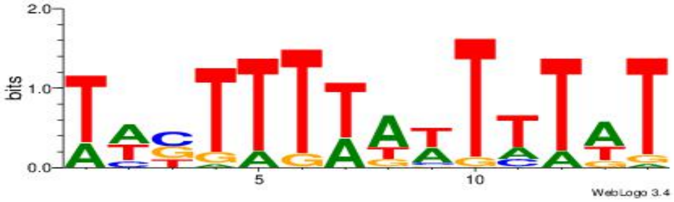
Alignment:

```
TWSTTTWAWTTTWT
---TTTCATWAAAT
```

Original motif Consensus sequence: AWAAAWTWAAASWA



Reverse complement motif Consensus sequence: TWSTTTWAWTTTW



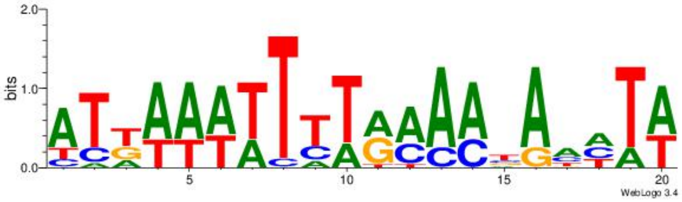
Dataset #:	5
Motif ID:	55
Motif name:	TFM13
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	4
Number of overlap:	11
Similarity score:	0.114394

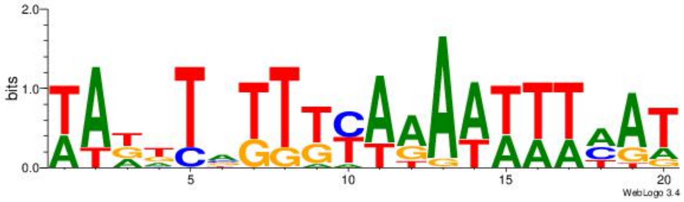
Alignment:

```
ATKAAWTTTTRMAABAHHTW
---ATTTWATGAAA------
```

Original motif Consensus sequence: ATKAAWTTTTRMAABAHHTW

Reverse complement motif Consensus sequence: WAHHTVTTYKAAAAWTTRAT





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

Original motif Consensus sequence: AAAACAAA

Reverse complement motif Consensus sequence: TTTGTTTT

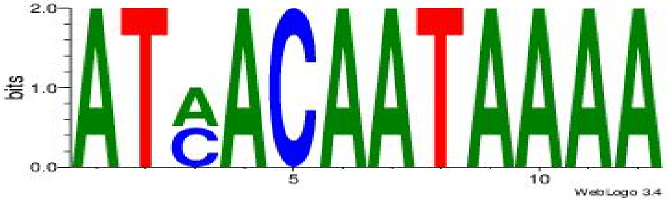
Best Matches for Motif ID 12 (Highest to Lowest)

Dataset #:	2
Motif ID:	15
Motif name:	Motif 15
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	2
Number of overlap:	8
Similarity score:	0.0625

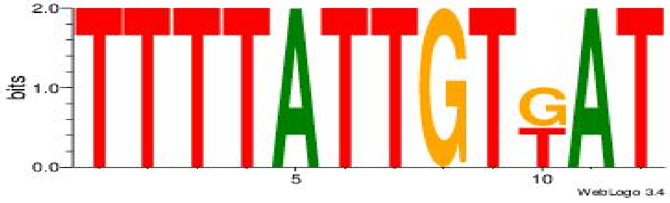
Alignment:

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

Original motif Consensus sequence: ATMACAATAAAA



Reverse complement motif Consensus sequence: TTTTATTGTYAT



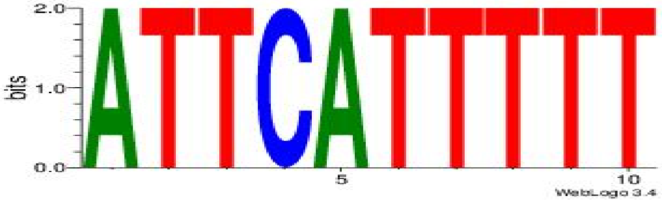
Dataset #:	2
Motif ID:	17
Motif name:	Motif 17
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	8
Similarity score:	0.0625

Alignment:

```
AAAAATGAAT
-AAAACAAA-
```

Original motif Consensus sequence: AAAAATGAAT

Reverse complement motif Consensus sequence: ATTCATTTTT

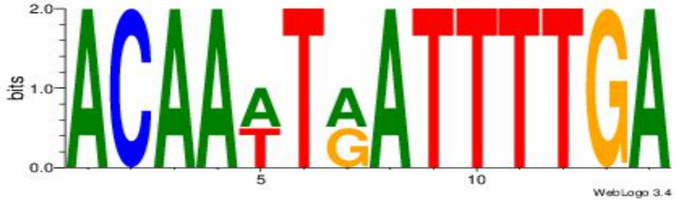


Dataset #: 2
Motif ID: 16
Motif name: Motif 16
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 5
Number of overlap: 8
Similarity score: 0.078125

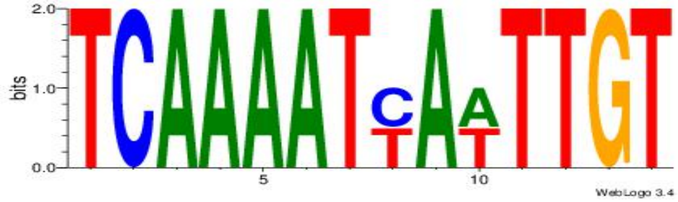
Alignment:

```
TCAAAATKAWTTGT
--AAAACAAA----
```

Original motif Consensus sequence: ACAAWTRATTTTGA



Reverse complement motif Consensus sequence: TCAAAATKAWTTG

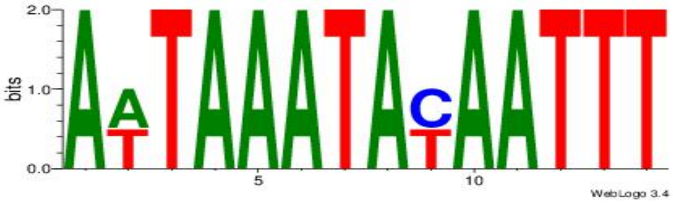


Dataset #: 2
Motif ID: 5
Motif name: Motif 5
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 3
Number of overlap: 8

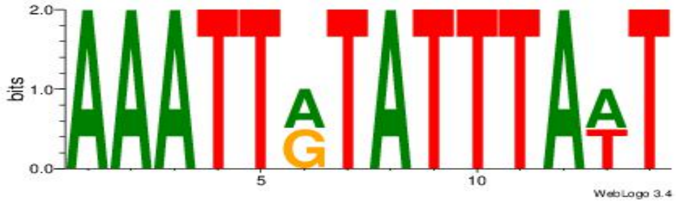
Similarity score: 0.078125

Alignment:
AAATTKTATTTAWT
--TTTGTTTT----

Original motif Consensus sequence: AWTAAATAYAATTT



Reverse complement motif Consensus sequence: AAATTKTATTTAW

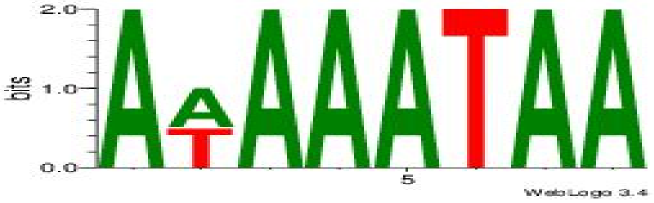


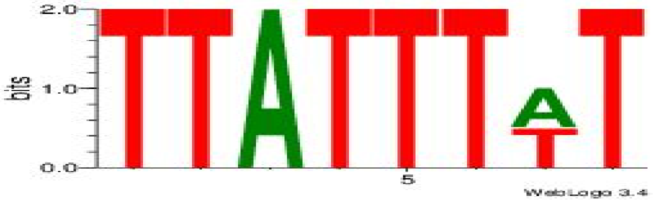
Dataset #:	2
Motif ID:	14
Motif name:	Motif 14
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	8
Similarity score:	0.078125

Alignment:
AWAAATAA
AAAACAAA

Original motif Consensus sequence: AWAAATAA

Reverse complement motif Consensus sequence: TTATTTWT



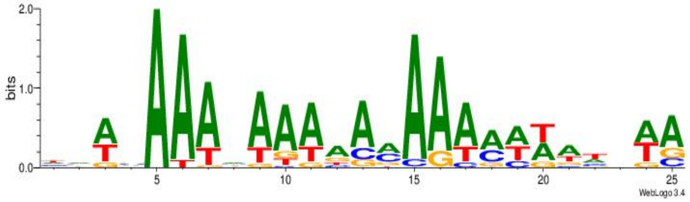


Dataset #:	5
Motif ID:	56
Motif name:	TFM11
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	10
Number of overlap:	8
Similarity score:	0.0790441

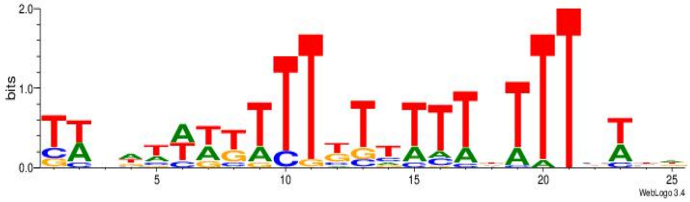
Alignment:

```
HDWVAAAHAAAAAMAAAMWWWHBWA
---------AAAACAAA--------
```

Original motif Consensus sequence:
HDWVAAAHAAAAAMAAAMWWWHBWA



Reverse complement motif Consensus sequence:
TWVHWWWYTTTYTTTTTHTTTVWBH



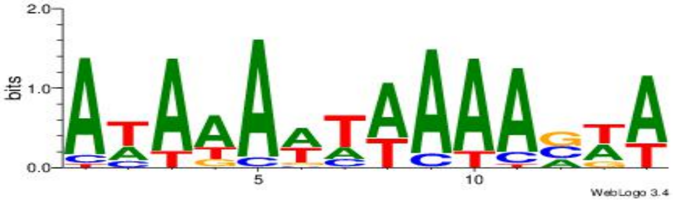
Dataset #:	2

Motif ID: 3
Motif name: Motif 3
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 3
Number of overlap: 8
Similarity score: 0.0805288

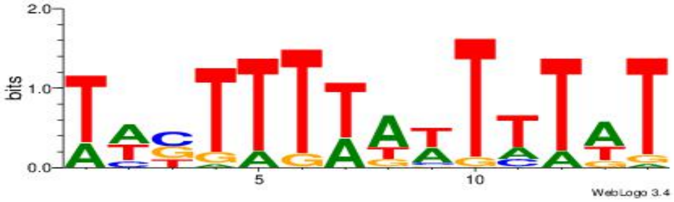
Alignment:

```
AWAAAWTWAAASWA
--AAAACAAA----
```

Original motif Consensus sequence: AWAAAWTWAAASWA



Reverse complement motif Consensus sequence: TWSTTTWAWTTT

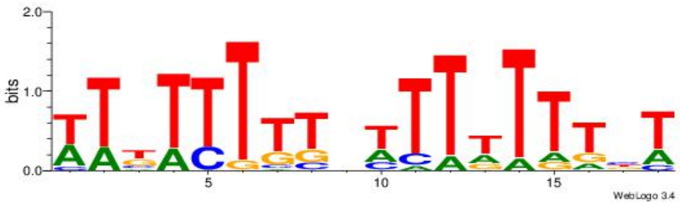


Dataset #: 5
Motif ID: 52
Motif name: TFM1
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 6
Number of overlap: 8
Similarity score: 0.0873397

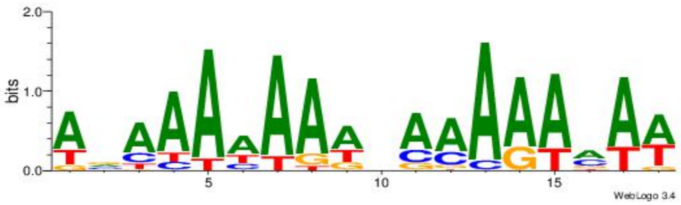
Alignment:

```
ABAAAAAAWHAAAAARAW
-----AAAACAAA-----
```

Original motif Consensus sequence: WTKTTTTTHWTTTTTTBT



Reverse complement motif Consensus sequence: ABAAAAAAWHAAAAARAW



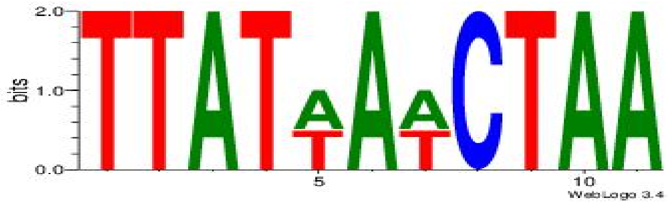
Dataset #:	2
Motif ID:	18
Motif name:	Motif 18
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	4
Number of overlap:	8
Similarity score:	0.09375

Alignment:

```
TTAGWTWATAA
TTTGTTTT---
```

Original motif Consensus sequence: TTAGWTWATAA

Reverse complement motif Consensus sequence: TTATWAWCTAA

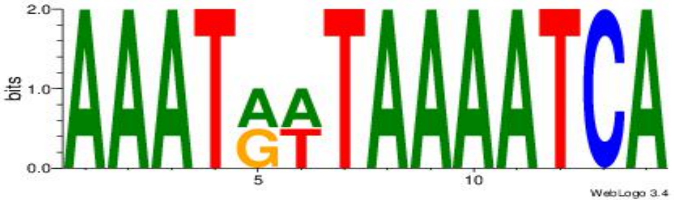


Dataset #: 2
Motif ID: 8
Motif name: Motif 8
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 3
Number of overlap: 8
Similarity score: 0.09375

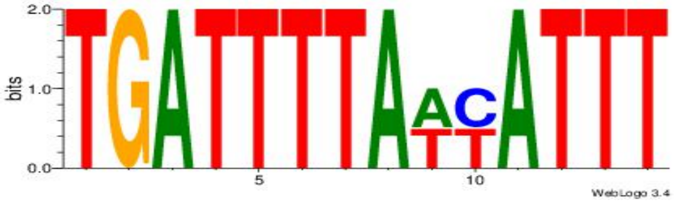
Alignment:

```
AAATRWTAAAATCA
--AAAACAAA----
```

Original motif Consensus sequence: AAATRWTAAAATCA



Reverse complement motif Consensus sequence: TGATTTTAWKATT



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

Original motif Consensus sequence: AAAGATTT

Reverse complement motif Consensus sequence: AAATCTTT

Best Matches for Motif ID 13 (Highest to Lowest)

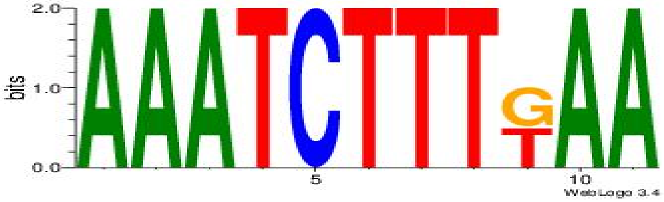
Dataset #:	2
Motif ID:	20
Motif name:	Motif 20
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	4
Number of overlap:	8
Similarity score:	0

Alignment:

```
AAATCTTTYAA
AAATCTTT---
```

Original motif Consensus sequence: TTMAAAGATTT

Reverse complement motif Consensus sequence: AAATCTTTYAA

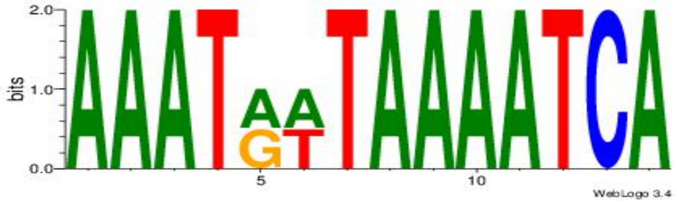


Dataset #: 2
Motif ID: 8
Motif name: Motif 8
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 8
Similarity score: 0.0625

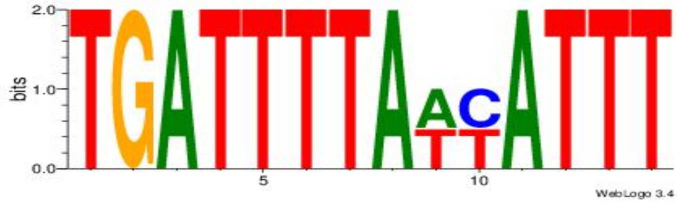
Alignment:

```
AAATRWTAAAATCA
------AAATCTTT
```

Original motif Consensus sequence: AAATRWTAAAATCA



Reverse complement motif Consensus sequence: TGATTTTAWKATT

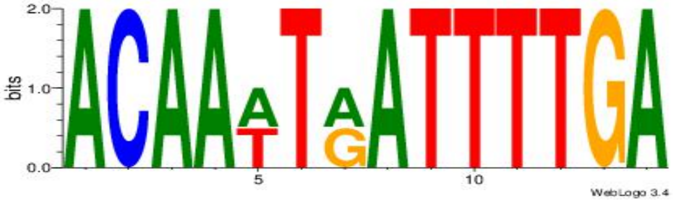


Dataset #: 2
Motif ID: 16
Motif name: Motif 16
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 4
Number of overlap: 8

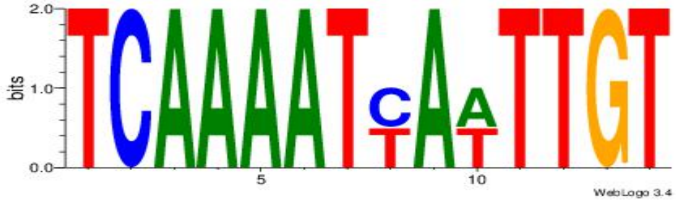
Similarity score: 0.0625

Alignment:
ACAAWTRATTTTGA
---AAAGATTT---

Original motif Consensus sequence: ACAAWTRATTTTGA



Reverse complement motif Consensus sequence: TCAAAATKAWTTG

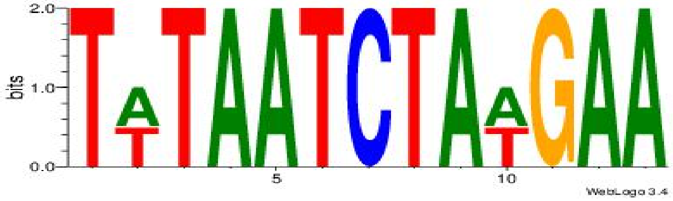


Dataset #:	2
Motif ID:	19
Motif name:	Motif 19
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	4
Number of overlap:	8
Similarity score:	0.078125

Alignment:
TTCWTAGATTAWA
---AAAGATTT--

Original motif Consensus sequence: TTCWTAGATTAWA

Reverse complement motif Consensus sequence: TWTAATCTAWGAA

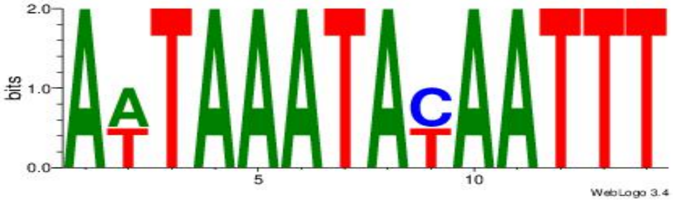


Dataset #:	2
Motif ID:	5
Motif name:	Motif 5
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	7
Number of overlap:	8
Similarity score:	0.078125

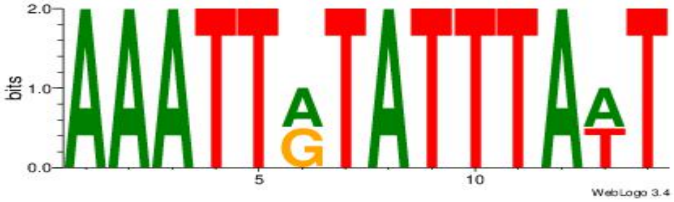
Alignment:

```
AAATTKTATTTAWT
AAATCTTT------
```

Original motif Consensus sequence: AWTAAATAYAATTT



Reverse complement motif Consensus sequence: AAATTKTATTTAW



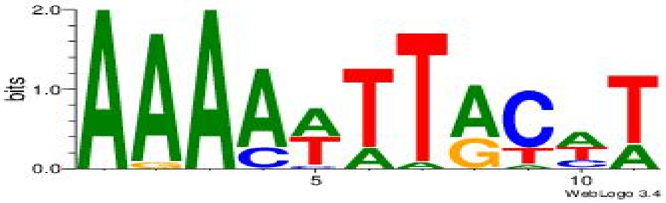
Dataset #:	2
Motif ID:	4

Motif name: Motif 4
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 4
Number of overlap: 8
Similarity score: 0.0822369

Alignment:

```
AWGKAAWTTTT
---AAATCTTT
```

Original motif Consensus sequence: AAAAWTTRCWT



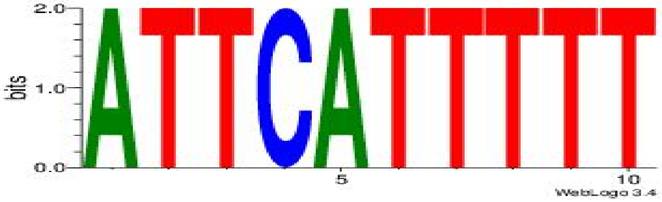
Reverse complement motif Consensus sequence: AWGKAAWTTTT

Dataset #: 2
Motif ID: 17
Motif name: Motif 17
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 8
Similarity score: 0.09375

Alignment:
AAAAATGAAT
--AAATCTTT

Original motif Consensus sequence: AAAAATGAAT

Reverse complement motif Consensus sequence: ATTCATTTTT

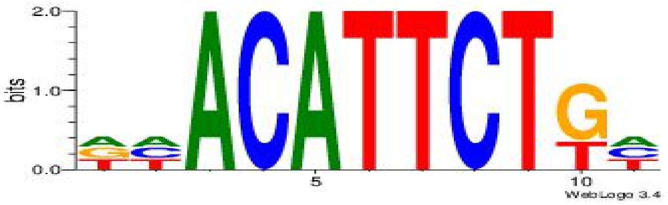


Dataset #:	4
Motif ID:	44
Motif name:	dhACATTCTkh
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	4
Number of overlap:	8
Similarity score:	0.104167

Alignment:
DHACATTCTGH
AAAGATTT---

Original motif Consensus sequence: DHACATTCTGH

Reverse complement motif Consensus sequence: HCAGAATGTHD

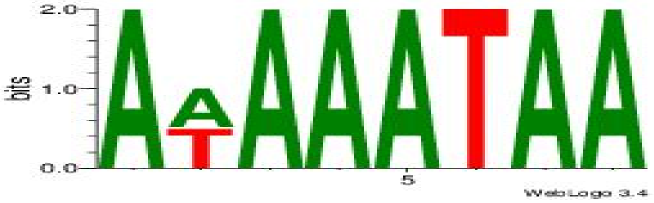


Dataset #:	2
Motif ID:	14
Motif name:	Motif 14
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	8
Similarity score:	0.109375

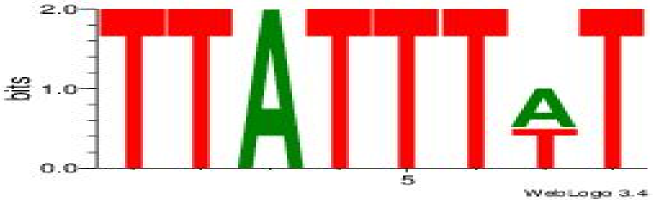
Alignment:

```
AWAAATAA
AAAGATTT
```

Original motif Consensus sequence: AWAAATAA



Reverse complement motif Consensus sequence: TTATTTWT



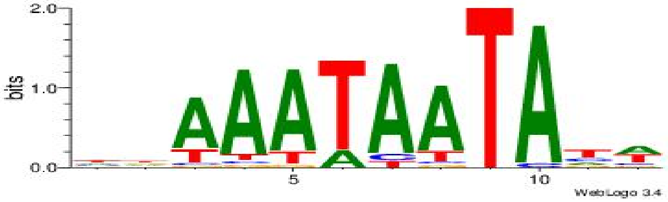
Dataset #:	4
Motif ID:	37

Motif name: tkAAATAATAtw
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 3
Number of overlap: 8
Similarity score: 0.110417

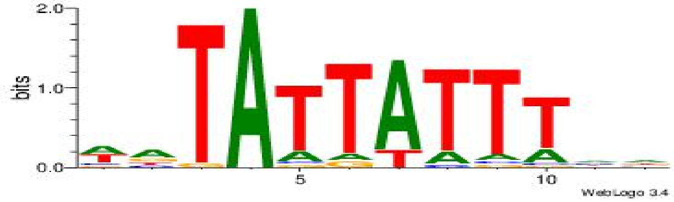
Alignment:

```
HDAAATAATAHW
--AAATCTTT--
```

Original motif Consensus sequence: HDAAATAATAHW

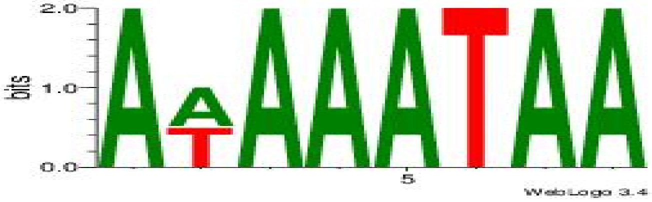


Reverse complement motif Consensus sequence: WHTATTATTTDH

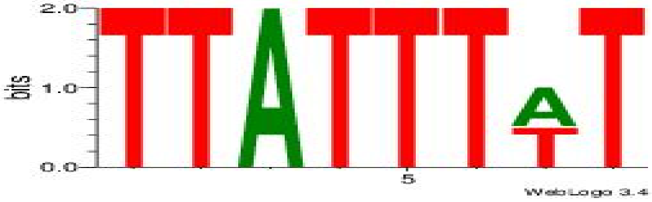


Dataset #: 2 Motif ID: 14 Motif name: Motif 14

Original motif Consensus sequence: AWAAATAA



Reverse complement motif Consensus sequence: TTATTTWT



Best Matches for Motif ID 14 (Highest to Lowest)

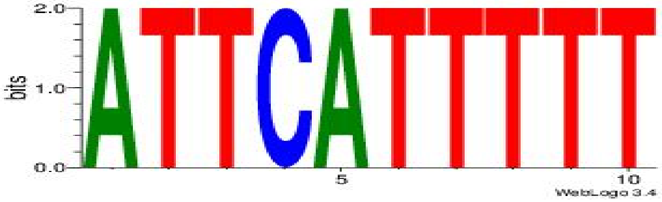
Dataset #: 2
Motif ID: 17
Motif name: Motif 17
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 3
Number of overlap: 8
Similarity score: 0.046875

Alignment:

```
ATTCATTTTT
--TTATTTWT
```

Original motif Consensus sequence: AAAAATGAAT

Reverse complement motif Consensus sequence: ATTCATTTTT

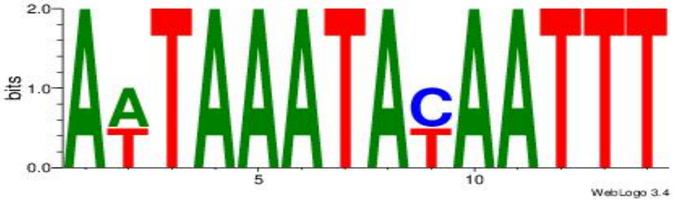


Dataset #: 2
Motif ID: 5
Motif name: Motif 5
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 2
Number of overlap: 8

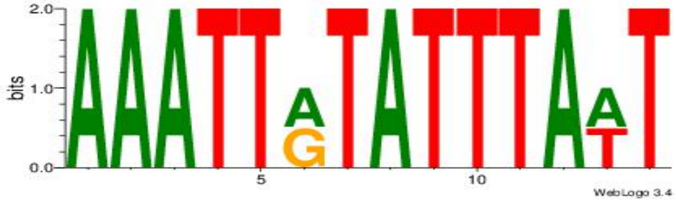
Similarity score:	0.046875

Alignment:
AAATTKTATTTAWT
-----TTATTTWT-

Original motif Consensus sequence: AWTAAATAYAATTT



Reverse complement motif Consensus sequence: AAATTKTATTTAW

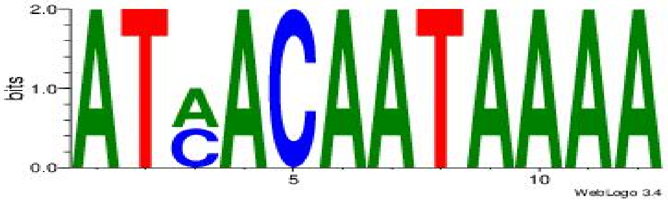


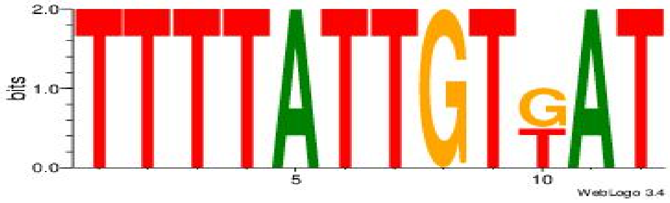
Dataset #:	2
Motif ID:	15
Motif name:	Motif 15
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	3
Number of overlap:	8
Similarity score:	0.0625

Alignment:
ATMACAATAAAA
--AWAAATAA--

Original motif Consensus sequence: ATMACAATAAAA

Reverse complement motif Consensus sequence: TTTTATTGTYAT



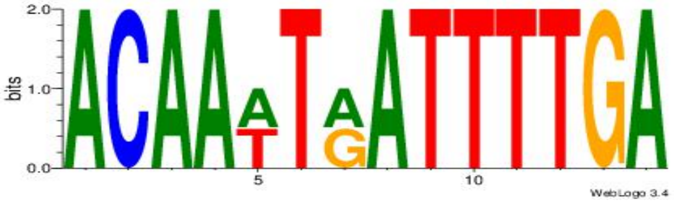


Dataset #:	2
Motif ID:	16
Motif name:	Motif 16
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	8
Similarity score:	0.0625

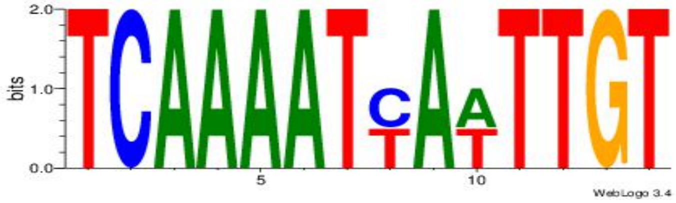
Alignment:

```
ACAAWTRATTTTGA
AWAAATAA------
```

Original motif   Consensus sequence: ACAAWTRATTTTGA



Reverse complement motif   Consensus sequence: TCAAAATKAWTTG



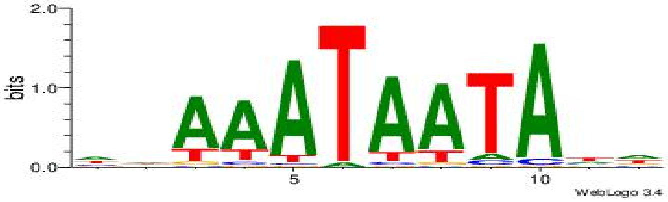
Dataset #:	4
Motif ID:	41

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

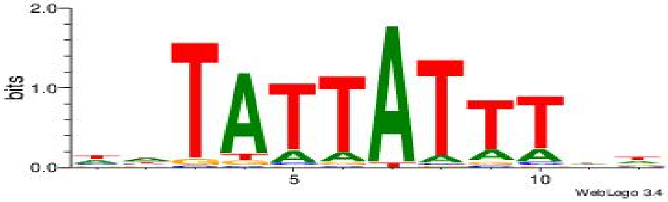
Alignment:

```
HDAAATAATADD
AWAAATAA----
```

Original motif Consensus sequence: HDAAATAATADD



Reverse complement motif Consensus sequence: DDTATTATTTDH

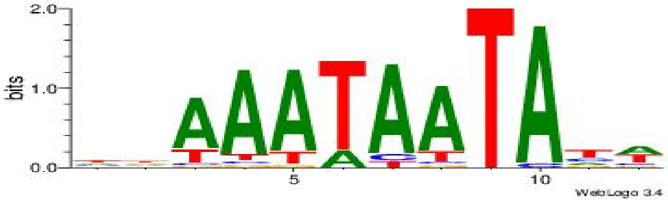


Dataset #:	4
Motif ID:	37
Motif name:	tkAAATAATAtw
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	5
Number of overlap:	8
Similarity score:	0.0697917

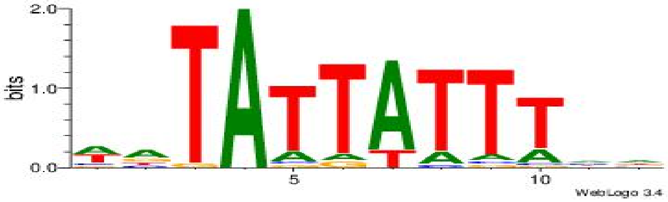
Alignment:

```
WHTATTATTTDH
----TTATTTWT
```

Original motif Consensus sequence: HDAAATAATAHW



Reverse complement motif Consensus sequence: WHTATTATTTDH



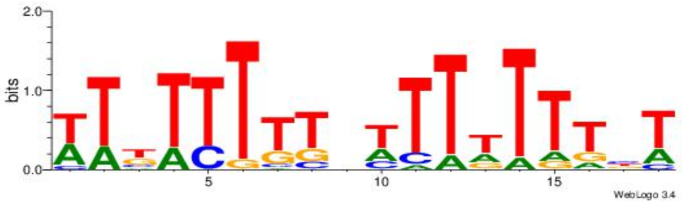
Dataset #:	5
Motif ID:	52
Motif name:	TFM1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	5
Number of overlap:	8
Similarity score:	0.078125

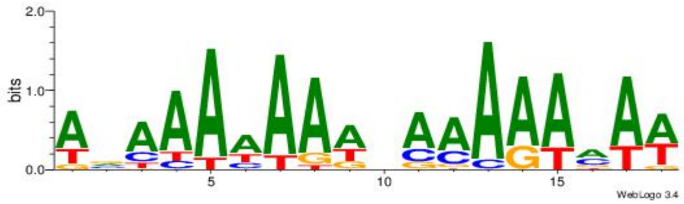
Alignment:

```
WTKTTTTTHWTTTTTTBT
------TTATTTWT----
```

Original motif Consensus sequence: WTKTTTTTHWTTTTTTBT

Reverse complement motif Consensus sequence: ABAAAAAAWHAAAAARAW



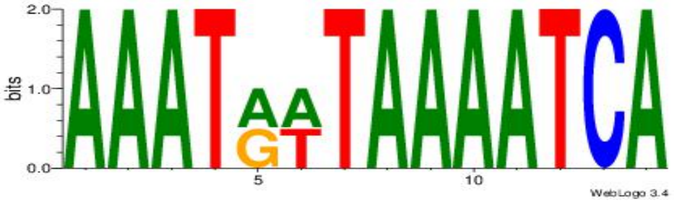


Dataset #:	2
Motif ID:	8
Motif name:	Motif 8
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	2
Number of overlap:	8
Similarity score:	0.078125

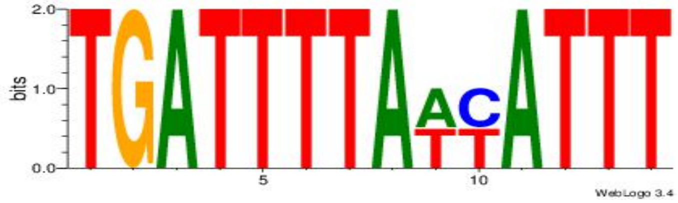
Alignment:

```
TGATTTTAWKATTT
-----TTATTTWT-
```

Original motif Consensus sequence: AAATRWTAAAATCA



Reverse complement motif Consensus sequence: TGATTTTAWKATT



Dataset #:	2
Motif ID:	12

Motif name:	Motif 12
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	8
Similarity score:	0.078125

Alignment:
AAAACAAA
AWAAATAA

Original motif Consensus sequence: AAAACAAA

Reverse complement motif Consensus sequence: TTTGTTTT

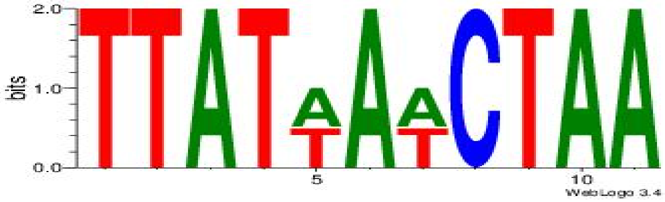
Dataset #:	2
Motif ID:	18
Motif name:	Motif 18
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	8
Similarity score:	0.078125

Alignment:

```
TTAGWTWATAA
---AWAAATAA
```

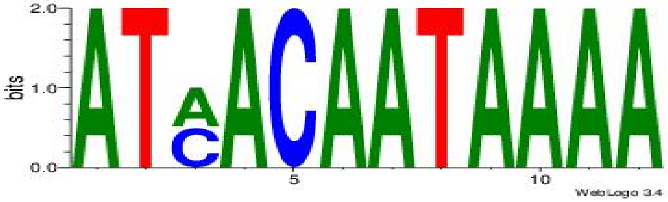
Original motif Consensus sequence: TTAGWTWATAA

Reverse complement motif Consensus sequence: TTATWAWCTAA

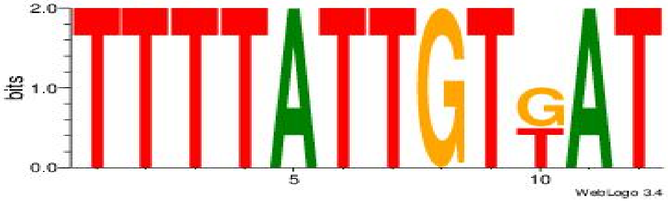


Dataset #: 2 **Motif ID: 15** **Motif name: Motif 15**

Original motif Consensus sequence: ATMACAATAAAA



Reverse complement motif Consensus sequence: TTTTATTGTYAT



Best Matches for Motif ID 15 (Highest to Lowest)

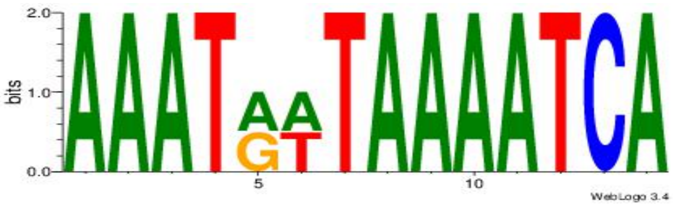
Dataset #:	2
Motif ID:	8
Motif name:	Motif 8
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	3

Number of overlap: 12
Similarity score: 0.104167

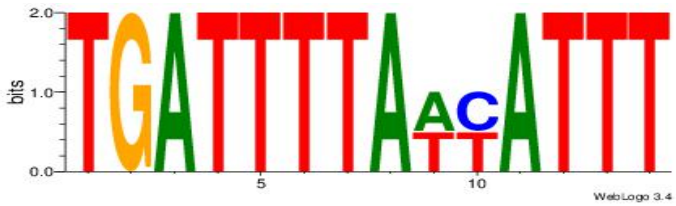
Alignment:

```
TGATTTTAWKATTT
TTTTATTGTYAT--
```

Original motif Consensus sequence: AAATRWTAAAATCA



Reverse complement motif Consensus sequence: TGATTTTAWKATT



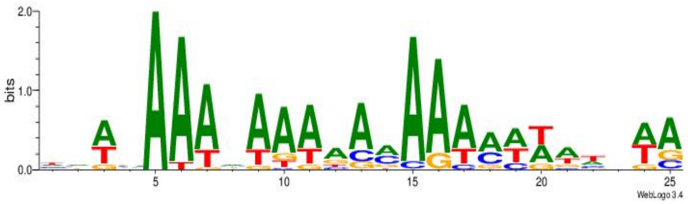
Dataset #: 5
Motif ID: 56
Motif name: TFM11
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 6
Number of overlap: 12
Similarity score: 0.109681

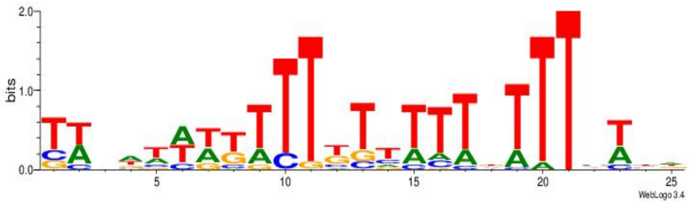
Alignment:

```
TWVHWWWYTTTYTTTTTHTTTVWBH
--------TTTTATTGTYAT-----
```

Original motif Consensus sequence:
HDWVAAAHAAAAAMAAAMWWWHBWA

Reverse complement motif Consensus sequence:
TWVHWWWYTTTYTTTTTHTTTVWBH





Dataset #: 2

Motif ID: 5

Motif name: Motif 5

Matching format of first motif: Original Motif

Matching format of second motif: Original Motif

Direction: Backward

Position number: 2

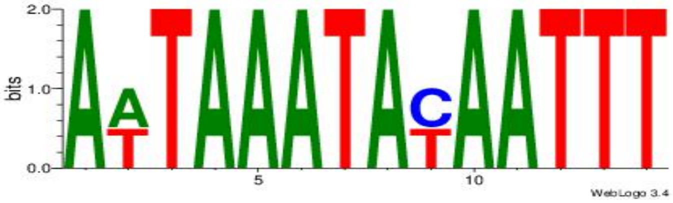
Number of overlap: 12

Similarity score: 0.114583

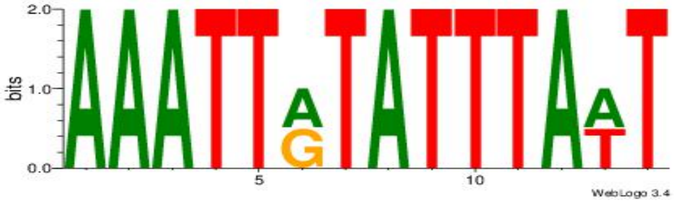
Alignment:

```
AWTAAATAYAATTT
-ATMACAATAAAA-
```

Original motif Consensus sequence: AWTAAATAYAATTT



Reverse complement motif Consensus sequence: AAATTKTATTTAWT



Dataset #: 2

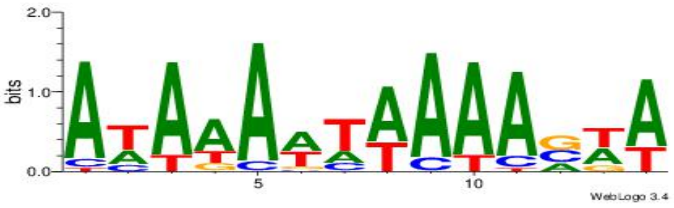
Motif ID: 3

Motif name:	Motif 3
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	3
Number of overlap:	12
Similarity score:	0.114583

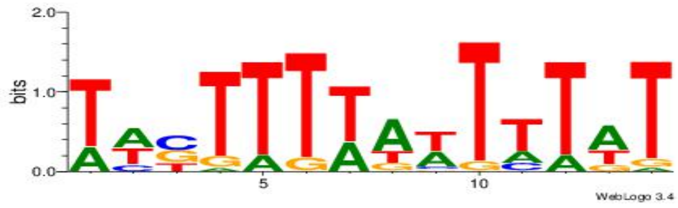
Alignment:

```
AWAAAWTWAAASWA
ATMACAATAAAA--
```

Original motif Consensus sequence: AWAAAWTWAAASWA



Reverse complement motif Consensus sequence: TWSTTTWAWTTTW

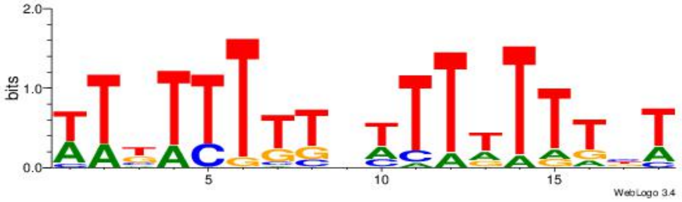


Dataset #:	5
Motif ID:	52
Motif name:	TFM1
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	3
Number of overlap:	12
Similarity score:	0.115652

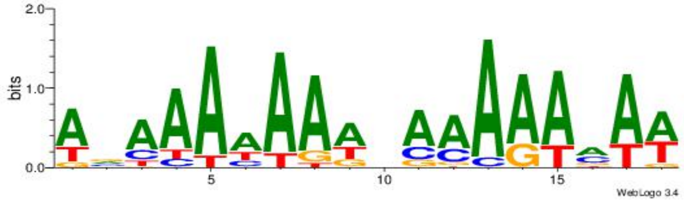
Alignment:

ABAAAAAAWHAAAAARAW
--ATMACAATAAAA----

Original motif Consensus sequence: WTKTTTTTHWTTTTTTBT



Reverse complement motif Consensus sequence: ABAAAAAAWHAAAAARAW



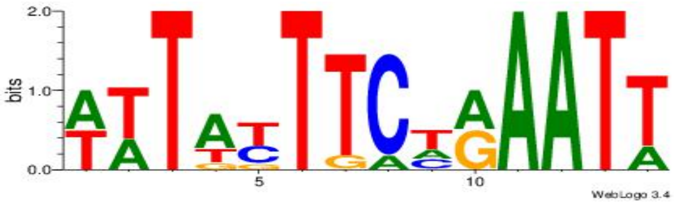
Dataset #:	2
Motif ID:	6
Motif name:	Motif 6
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	12
Similarity score:	0.119792

Alignment:

WWTAKTTCDKAATT
TTTTATTGTYAT--

Original motif Consensus sequence: AATTYDGAARTAWW

Reverse complement motif Consensus sequence: WWTAKTTCDKAAT

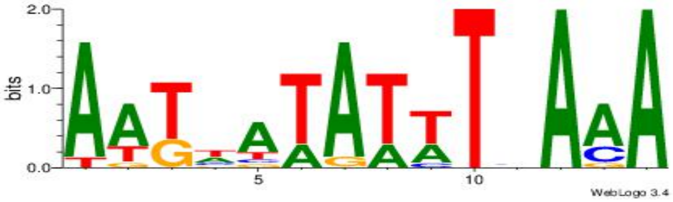


Dataset #:	2
Motif ID:	9
Motif name:	Motif 9
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	2
Number of overlap:	12
Similarity score:	0.121528

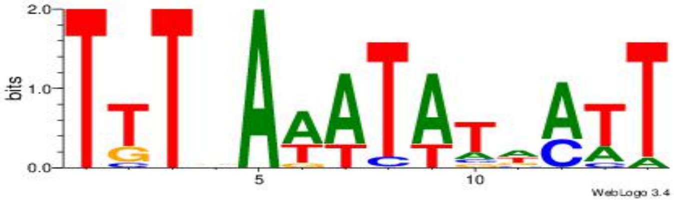
Alignment:

```
TTTDAWATATHATT
-TTTTATTGTYAT-
```

Original motif Consensus sequence: AATHATATWTHAAA



Reverse complement motif Consensus sequence: TTTDAWATATHAT



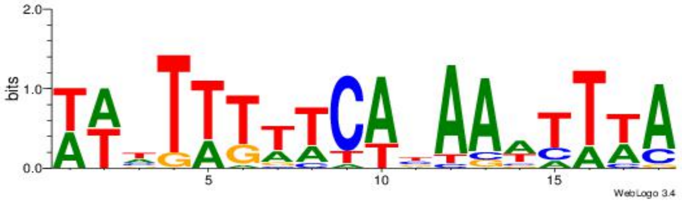
Dataset #:	5
Motif ID:	53

Motif name:	TFM3
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	7
Number of overlap:	12
Similarity score:	0.125

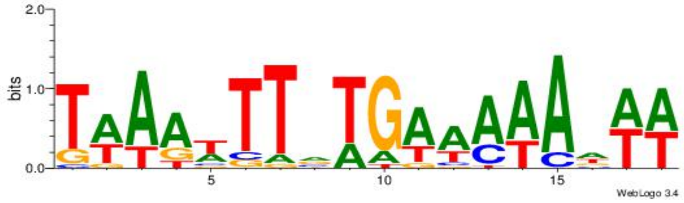
Alignment:

```
WWHTTTTTCABAAWTTWA
------ATMACAATAAAA
```

Original motif Consensus sequence: WWHTTTTTCABAAWTTWA



Reverse complement motif Consensus sequence: TWAAWTTVTGAAAAAHWW

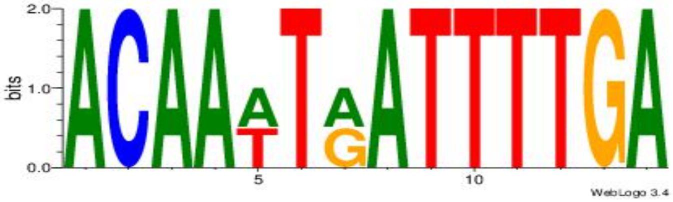


Dataset #:	2
Motif ID:	16
Motif name:	Motif 16
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	4
Number of overlap:	11
Similarity score:	0.590909

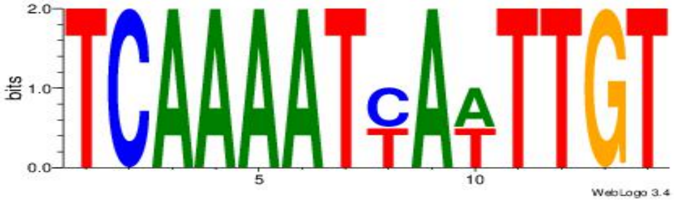
Alignment:

```
-TCAAAATKAWTTGT
ATMACAATAAAA---
```

Original motif Consensus sequence: ACAAWTRATTTTGA



Reverse complement motif Consensus sequence: TCAAAATKAWTTG



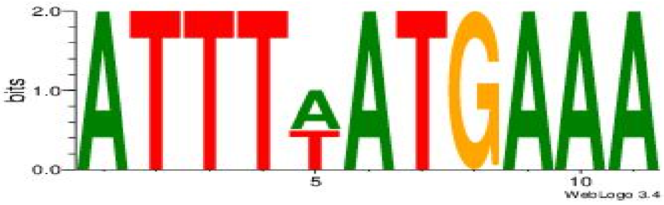
Dataset #:	2
Motif ID:	11
Motif name:	Motif 11
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	11
Similarity score:	0.602273

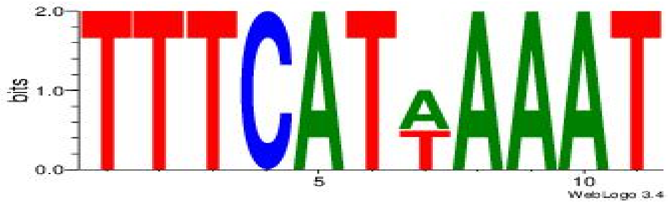
Alignment:

```
TTTCATWAAAT-
ATMACAATAAAA
```

Original motif Consensus sequence: ATTTWATGAAA

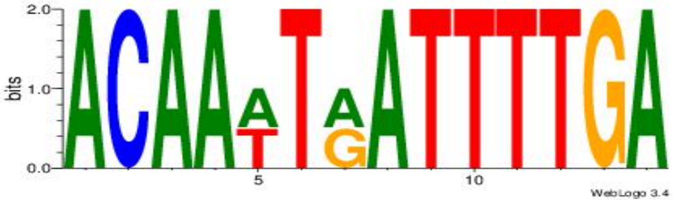
Reverse complement motif Consensus sequence: TTTCATWAAAT



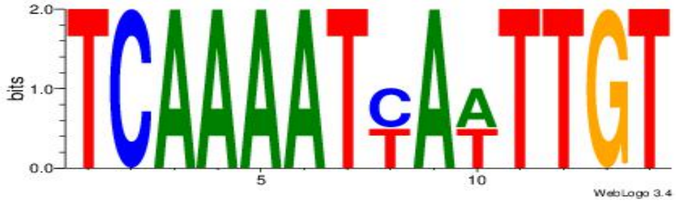


Dataset #: 2 Motif ID: 16 Motif name: Motif 16

Original motif Consensus sequence: ACAAWTRATTTTGA



Reverse complement motif Consensus sequence: TCAAAATKAWTTG



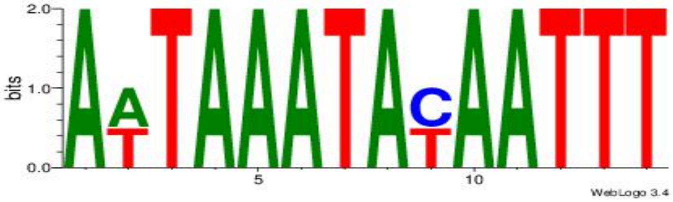
Best Matches for Motif ID 16 (Highest to Lowest)

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

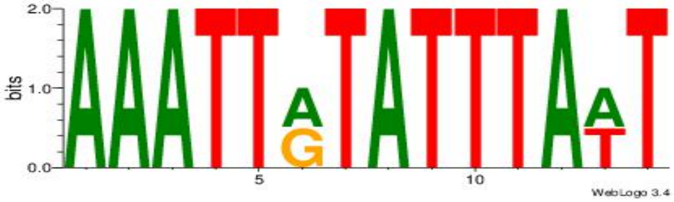
Alignment:

AWTAAATAYAATTT
TCAAAATKAWTTGT

Original motif Consensus sequence: AWTAAATAYAATTT



Reverse complement motif Consensus sequence: AAATTKTATTTAW

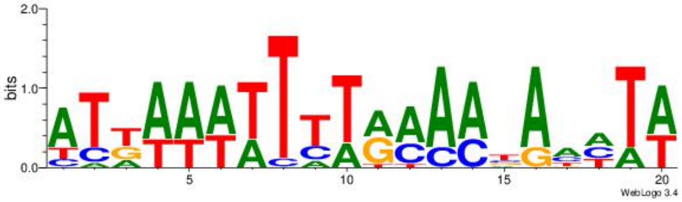


Dataset #:	5
Motif ID:	55
Motif name:	TFM13
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	8
Number of overlap:	13
Similarity score:	0.599359

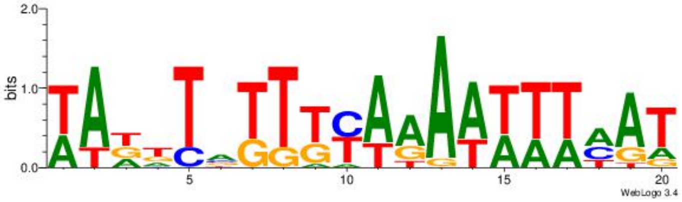
Alignment:

```
ATKAAWTTTTRMAABAHHTW-
-------TCAAAATKAWTTGT
```

Original motif Consensus sequence: ATKAAWTTTTRMAABAHHTW



Reverse complement motif Consensus sequence: WAHHTVTTYKAAAAWTTRAT

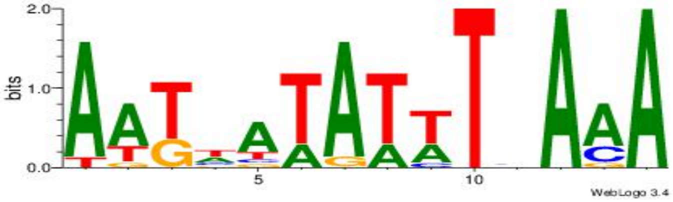


Dataset #:	2
Motif ID:	9
Motif name:	Motif 9
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	3
Number of overlap:	12
Similarity score:	1.08264

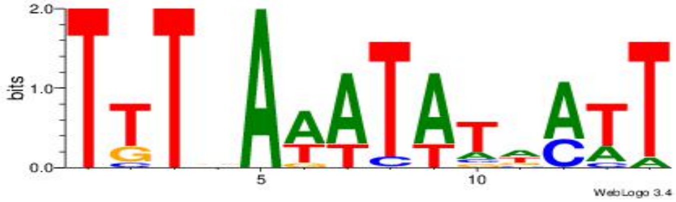
Alignment:

```
--AATHATATWTHAAA
ACAAWTRATTTTGA--
```

Original motif Consensus sequence: AATHATATWTHAAA



Reverse complement motif Consensus sequence: TTTDAWATATHAT

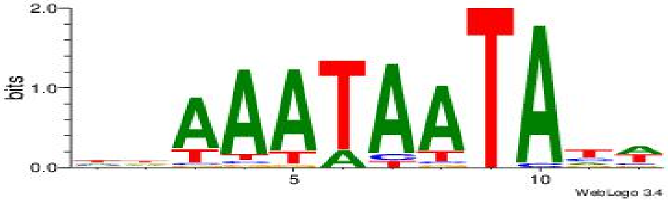


Dataset #:	4
Motif ID:	37
Motif name:	tkAAATAATAtw
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	12

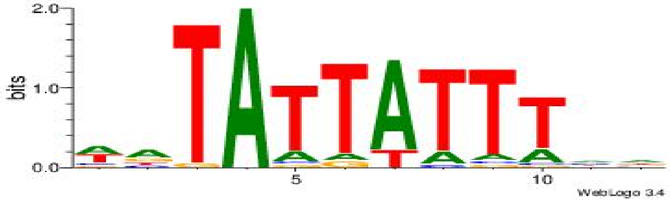
Similarity score:	1.08403

Alignment:
--WHTATTATTTDH
TCAAAATKAWTTGT

Original motif Consensus sequence: HDAAATAATAHW



Reverse complement motif Consensus sequence: WHTATTATTTDH

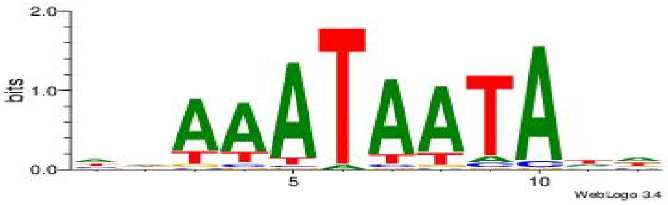


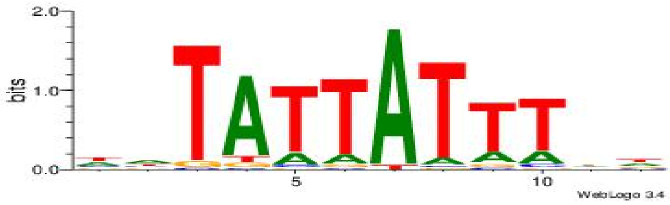
Dataset #:	4
Motif ID:	41
Motif name:	wwAAATAATAtw
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	12
Similarity score:	1.08881

Alignment:
--DDTATTATTTDH
TCAAAATKAWTTGT

Original motif Consensus sequence: HDAAATAATADD

Reverse complement motif Consensus sequence: DDTATTATTTDH





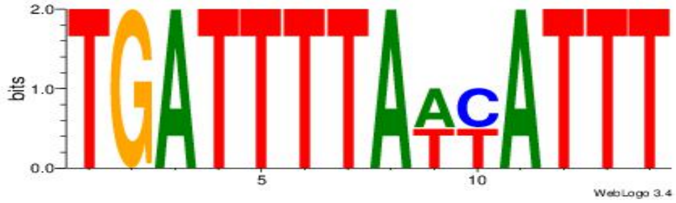
Dataset #: 2
Motif ID: 8
Motif name: Motif 8
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 3
Number of overlap: 12
Similarity score: 1.1

Alignment:

```
--AAATRWTAAAATCA
ACAAWTRATTTTGA--
```

Original motif Consensus sequence: AAATRWTAAAATCA

Reverse complement motif Consensus sequence: TGATTTTAWKATT



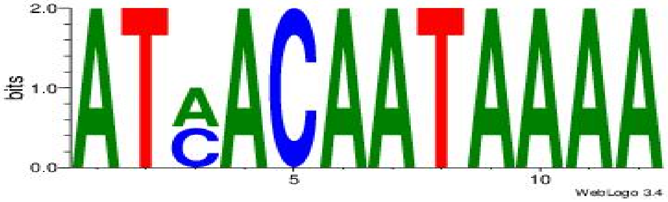
Dataset #: 2
Motif ID: 15

Motif name:	Motif 15
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	2
Number of overlap:	11
Similarity score:	1.56591

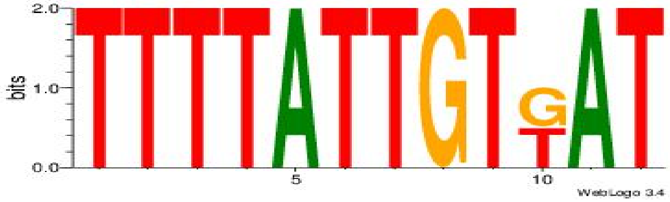
Alignment:

```
TTTTATTGTYAT---
-ACAAWTRATTTTGA
```

Original motif   Consensus sequence: ATMACAATAAAA



Reverse complement motif   Consensus sequence: TTTTATTGTYAT



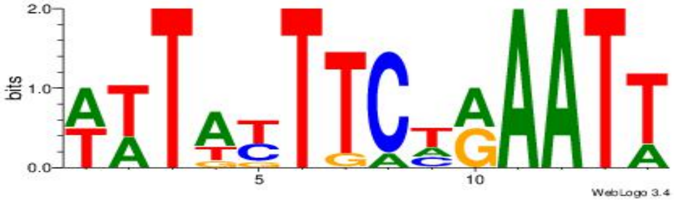
Dataset #:	2
Motif ID:	6
Motif name:	Motif 6
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	4
Number of overlap:	11
Similarity score:	1.56875

Alignment:

```
---AATTYDGAARTAWW
TCAAAATKAWTTGT---
```

Original motif Consensus sequence: AATTYDGAARTAWW

Reverse complement motif Consensus sequence: WWTAKTTCDKAAT



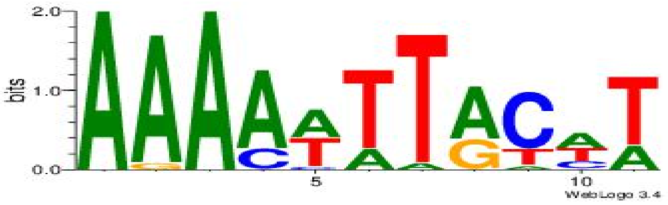
Dataset #:	2
Motif ID:	4
Motif name:	Motif 4
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	11
Similarity score:	1.57667

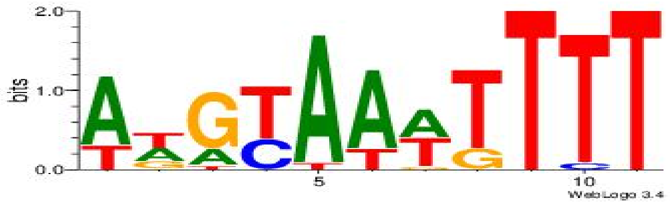
Alignment:

```
AAAAWTTRCWT---
ACAAWTRATTTTGA
```

Original motif Consensus sequence: AAAAWTTRCWT

Reverse complement motif Consensus sequence: AWGKAAWTTTT





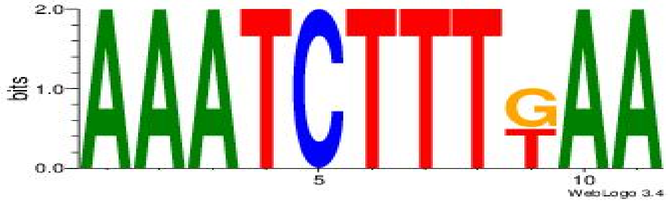
Dataset #:	2
Motif ID:	20
Motif name:	Motif 20
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	11
Similarity score:	1.57727

Alignment:

```
TTMAAAGATTT---
ACAAWTRATTTTGA
```

Original motif Consensus sequence: TTMAAAGATTT

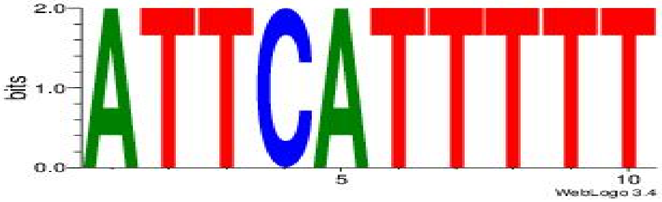
Reverse complement motif Consensus sequence: AAATCTTTYAA



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

Original motif Consensus sequence: AAAAATGAAT

Reverse complement motif Consensus sequence: ATTCATTTTT



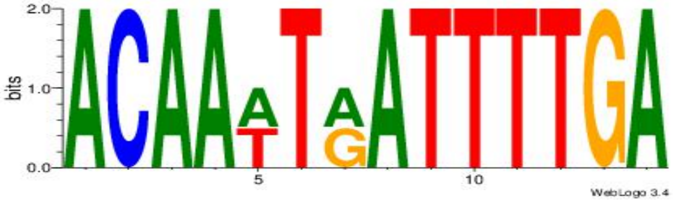
Best Matches for Motif ID 17 (Highest to Lowest)

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

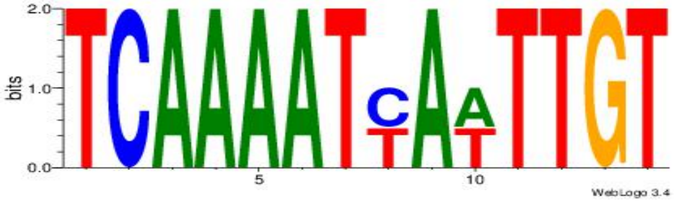
Alignment:

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

Original motif Consensus sequence: ACAAWTRATTTTGA



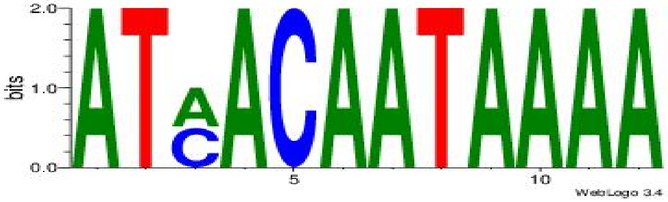
Reverse complement motif Consensus sequence: TCAAAATKAWTTG



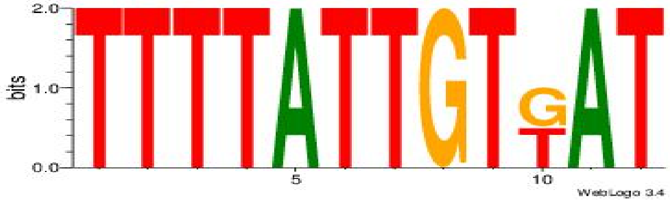
Dataset #: 2
Motif ID: 15
Motif name: Motif 15
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 3
Number of overlap: 10
Similarity score: 0.0875

Alignment:
TTTTATTGTYAT
ATTCATTTTT--

Original motif Consensus sequence: ATMACAATAAAA



Reverse complement motif Consensus sequence: TTTTATTGTYAT

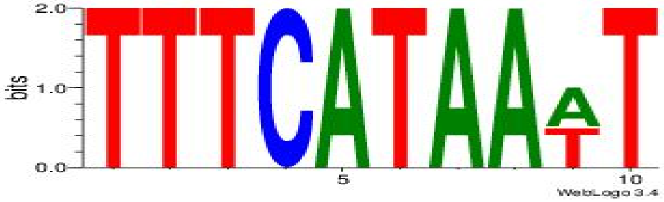


Dataset #: 2
Motif ID: 10
Motif name: Motif 10
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 10

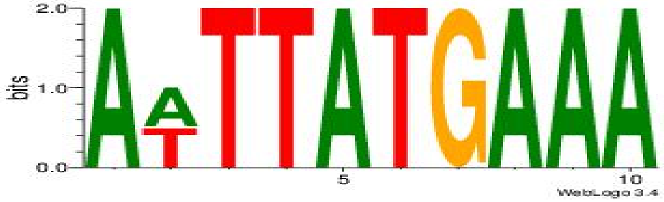
Similarity score: 0.0875

Alignment:
AWTTATGAAA
AAAAATGAAT

Original motif Consensus sequence: TTTCATAAWT



Reverse complement motif Consensus sequence: AWTTATGAAA

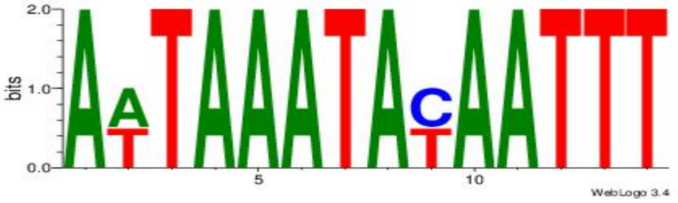


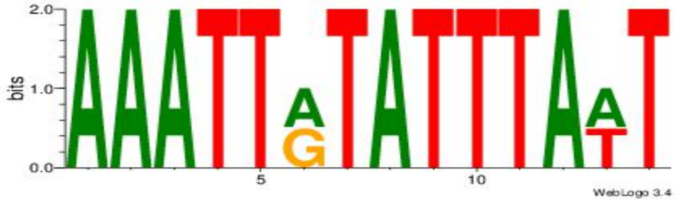
Dataset #: 2
Motif ID: 5
Motif name: Motif 5
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 4
Number of overlap: 10
Similarity score: 0.0875

Alignment:
AWTAAATAYAATTT
---AAAAATGAAT-

Original motif Consensus sequence: AWTAAATAYAATTT

Reverse complement motif Consensus sequence: AAATTKTATTTAW



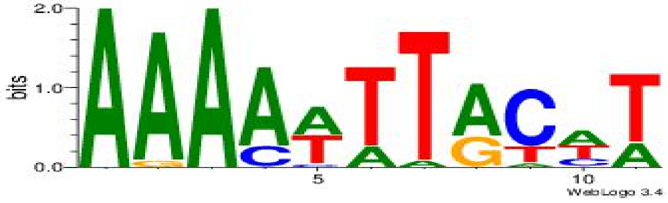


Dataset #:	2
Motif ID:	4
Motif name:	Motif 4
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	10
Similarity score:	0.0947369

Alignment:

```
AWGKAAWTTTT
-ATTCATTTTT
```

Original motif Consensus sequence: AAAAWTTRCWT



Reverse complement motif Consensus sequence: AWGKAAWTTTT

Dataset #:	2
Motif ID:	8

Motif name: Motif 8

Matching format of first motif: Original Motif

Matching format of second motif: Original Motif

Direction: Forward

Position number: 2

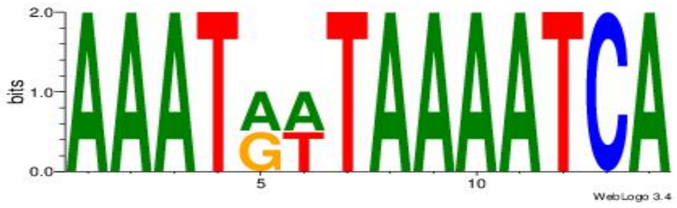
Number of overlap: 10

Similarity score: 0.1

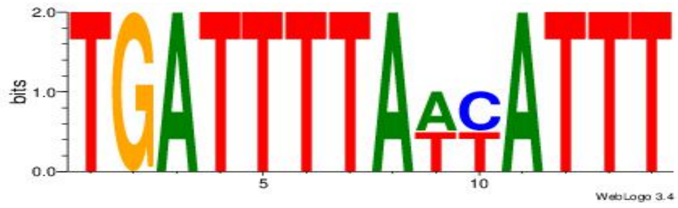
Alignment:

```
AAATRWTAAAATCA
-AAAAATGAAT---
```

Original motif Consensus sequence: AAATRWTAAAATCA



Reverse complement motif Consensus sequence: TGATTTTAWKATT



Dataset #: 4

Motif ID: 44

Motif name: dhACATTCTkh

Matching format of first motif: Reverse Complement

Matching format of second motif: Original Motif

Direction: Backward

Position number: 2

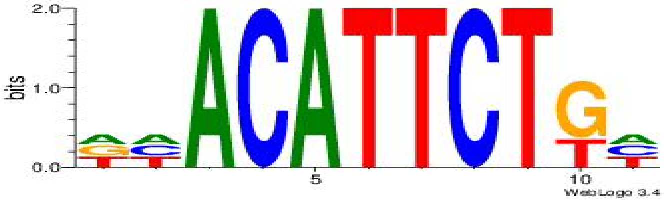
Number of overlap: 10

Similarity score: 0.1

Alignment:

```
DHACATTCTGH
ATTCATTTTT-
```

Original motif Consensus sequence: DHACATTCTGH



Reverse complement motif Consensus sequence: HCAGAATGTHD

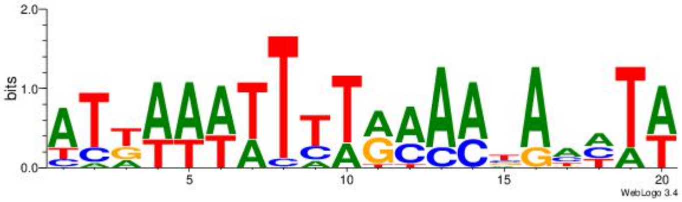
Dataset #:	5
Motif ID:	55
Motif name:	TFM13
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	11
Number of overlap:	10
Similarity score:	0.103333

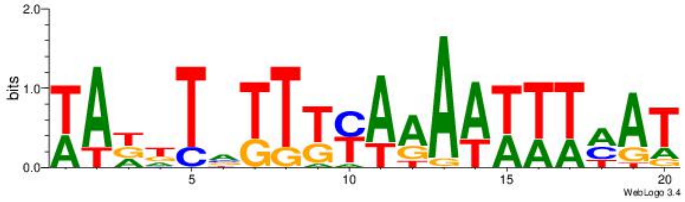
Alignment:

```
ATKAAWTTTTRMAABAHHTW
ATTCATTTTT----------
```

Original motif Consensus sequence: ATKAAWTTTTRMAABAHHTW

Reverse complement motif Consensus sequence: WAHHTVTTYKAAAAWTTRAT



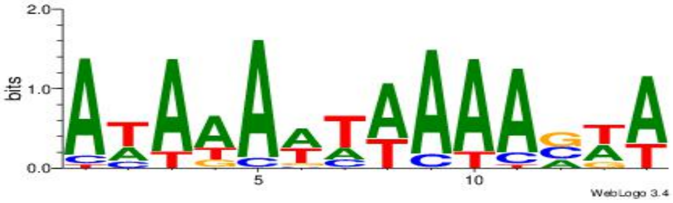


Dataset #:	2
Motif ID:	3
Motif name:	Motif 3
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	10
Similarity score:	0.104808

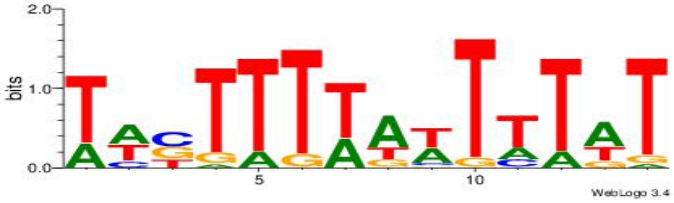
Alignment:

```
TWSTTTWAWTTTWT
----ATTCATTTTT
```

Original motif Consensus sequence: AWAAAWTWAAASWA



Reverse complement motif Consensus sequence: TWSTTTWAWTTTW



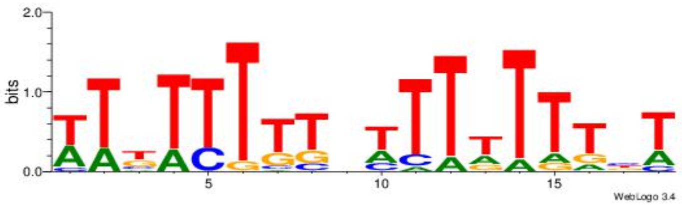
Dataset #:	5
Motif ID:	52

Motif name:	TFM1
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	5
Number of overlap:	10
Similarity score:	0.105128

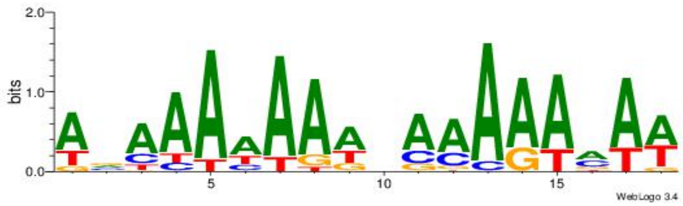
Alignment:

```
ABAAAAAAWHAAAAARAW
----AAAAATGAAT----
```

Original motif Consensus sequence: WTKTTTTTHWTTTTTTBT



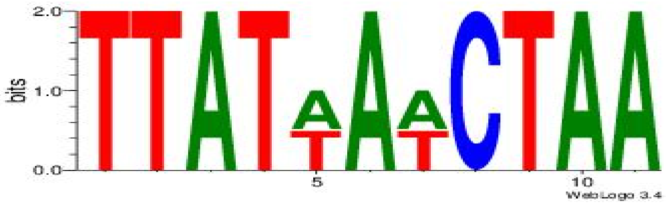
Reverse complement motif Consensus sequence: ABAAAAAAWHAAAAARAW



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

Original motif Consensus sequence: TTAGWTWATAA

Reverse complement motif Consensus sequence: TTATWAWCTAA



Best Matches for Motif ID 18 (Highest to Lowest)

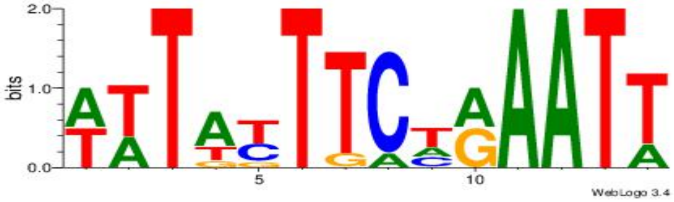
Dataset #: 2
Motif ID: 6
Motif name: Motif 6
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 3
Number of overlap: 11
Similarity score: 0.09375

Alignment:

```
AATTYDGAARTAWW
-TTATWAWCTAA--
```

Original motif Consensus sequence: AATTYDGAARTAWW

Reverse complement motif Consensus sequence: WWTAKTTCDKAAT



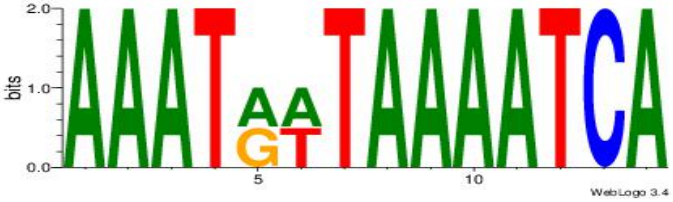
Dataset #: 2
Motif ID: 8
Motif name: Motif 8
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement

Direction:	Forward
Position number:	4
Number of overlap:	11
Similarity score:	0.102273

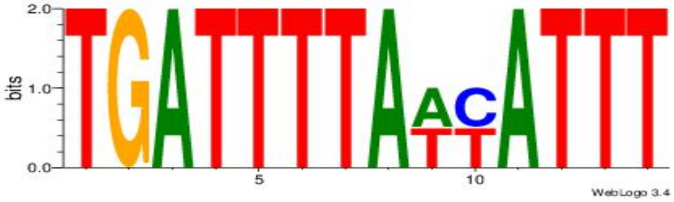
Alignment:

```
TGATTTTAWKATTT
---TTAGWTWATAA
```

Original motif Consensus sequence: AAATRWTAAAATCA



Reverse complement motif Consensus sequence: TGATTTTAWKATT

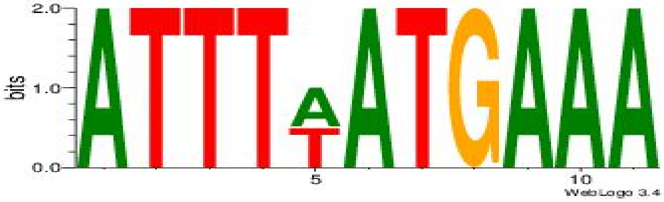


Dataset #:	2
Motif ID:	11
Motif name:	Motif 11
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	11
Similarity score:	0.102273

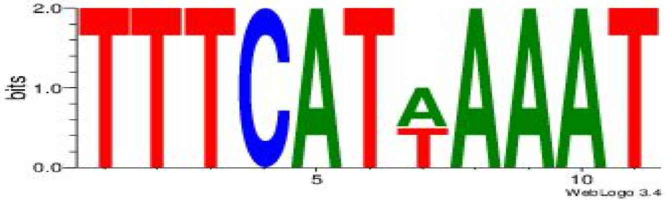
Alignment:

```
TTTCATWAAAT
TTAGWTWATAA
```

Original motif Consensus sequence: ATTTWATGAAA



Reverse complement motif Consensus sequence: TTTCATWAAAT

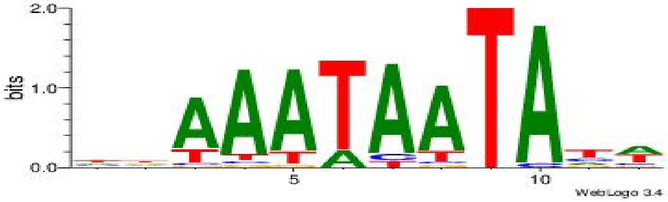


Dataset #:	4
Motif ID:	37
Motif name:	tkAAATAATAtw
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	2
Number of overlap:	11
Similarity score:	0.102273

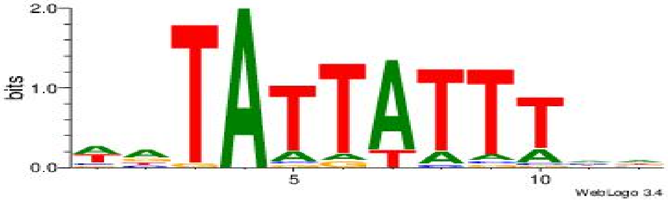
Alignment:

```
WHTATTATTTDH
-TTATWAWCTAA
```

Original motif Consensus sequence: HDAAATAATAHW



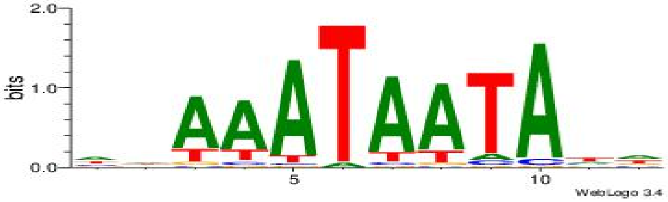
Reverse complement motif Consensus sequence: WHTATTATTTDH



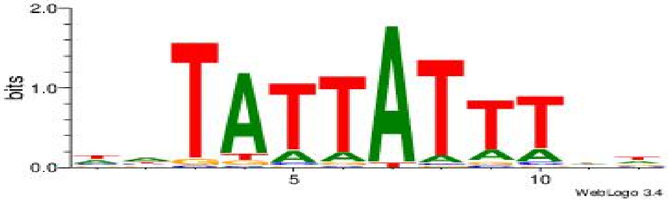
Dataset #: 4
Motif ID: 41
Motif name: wwAAATAATAtw
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 2
Number of overlap: 11
Similarity score: 0.104798

Alignment:
```
DDTATTATTTDH
-TTATWAWCTAA
```

Original motif Consensus sequence: HDAAATAATADD



Reverse complement motif Consensus sequence: DDTATTATTTDH



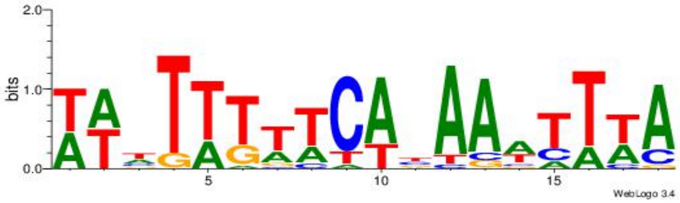
Dataset #: 5
Motif ID: 53
Motif name: TFM3
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 8
Number of overlap: 11

Similarity score:	0.108471

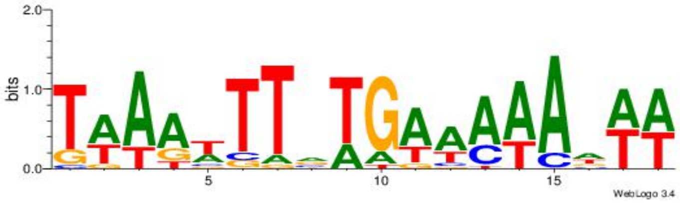
Alignment:

```
WWHTTTTTCABAAWTTWA
-------TTATWAWCTAA
```

Original motif Consensus sequence: WWHTTTTTCABAAWTTWA



Reverse complement motif Consensus sequence: TWAAWTTVTGAAAAAHWW



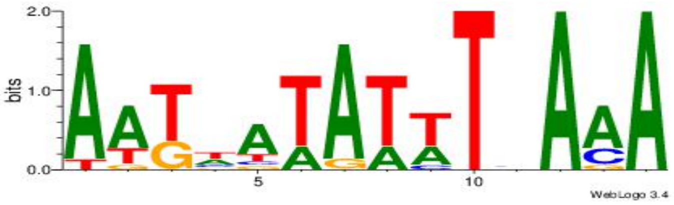
Dataset #:	2
Motif ID:	9
Motif name:	Motif 9
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	3
Number of overlap:	11
Similarity score:	0.109848

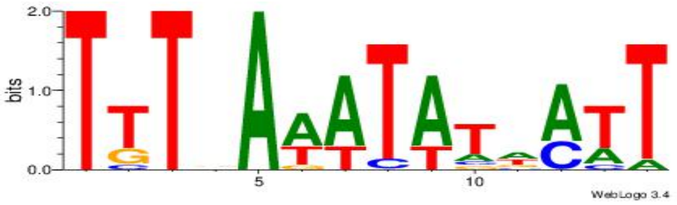
Alignment:

```
TTTDAWATATHATT
-TTAGWTWATAA--
```

Original motif Consensus sequence: AATHATATWTHAAA

Reverse complement motif Consensus sequence: TTTDAWATATHAT



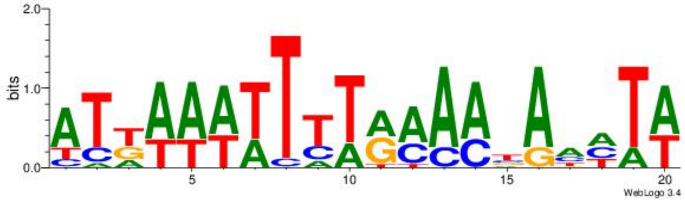


Dataset #:	5
Motif ID:	55
Motif name:	TFM13
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	4
Number of overlap:	11
Similarity score:	0.109848

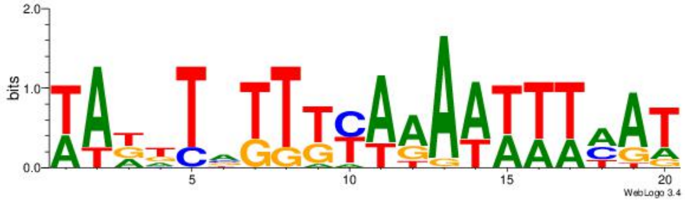
Alignment:

```
ATKAAWTTTTRMAABAHHTW
------TTATWAWCTAA---
```

Original motif Consensus sequence: ATKAAWTTTTRMAABAHHTW



Reverse complement motif Consensus sequence: WAHHTVTTYKAAAAWTTRAT



Dataset #:	2

Motif ID: 15

Motif name: Motif 15

Matching format of first motif: Original Motif

Matching format of second motif: Original Motif

Direction: Backward

Position number: 1

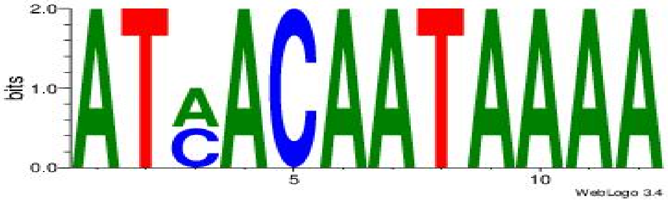
Number of overlap: 11

Similarity score: 0.113636

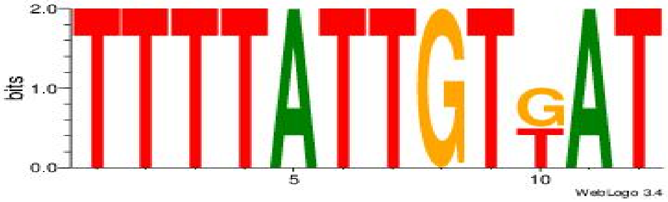
Alignment:

```
ATMACAATAAAA
-TTAGWTWATAA
```

Original motif   Consensus sequence: ATMACAATAAAA



Reverse complement motif   Consensus sequence: TTTTATTGTYAT



Dataset #: 2

Motif ID: 19

Motif name: Motif 19

Matching format of first motif: Reverse Complement

Matching format of second motif: Original Motif

Direction: Backward

Position number: 3

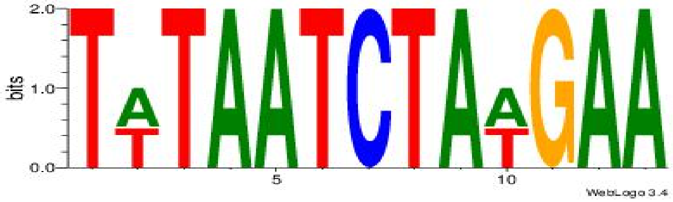
Number of overlap: 11

Similarity score: 0.113636

Alignment:
TTCWTAGATTAWA
TTATWAWCTAA--

Original motif Consensus sequence: TTCWTAGATTAWA

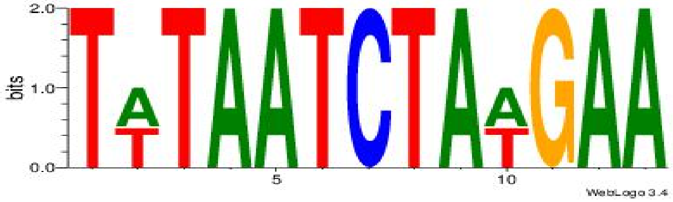
Reverse complement motif Consensus sequence: TWTAATCTAWGAA



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

Original motif Consensus sequence: TTCWTAGATTAWA

Reverse complement motif Consensus sequence: TWTAATCTAWGAA



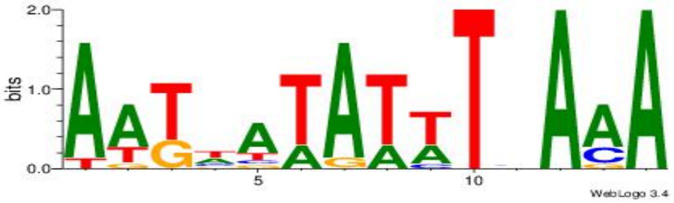
Best Matches for Motif ID 19 (Highest to Lowest)

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

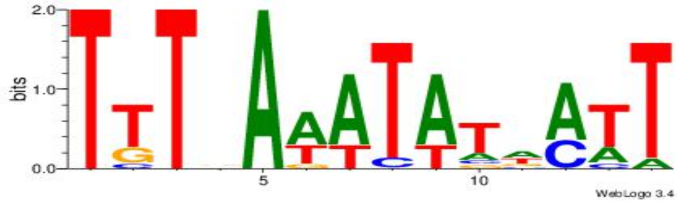
Number of overlap: 13
Similarity score: 0.0641025

Alignment:
AATHATATWTHAAA
-TTCWTAGATTAWA

Original motif Consensus sequence: AATHATATWTHAAA



Reverse complement motif Consensus sequence: TTTDAWATATHAT

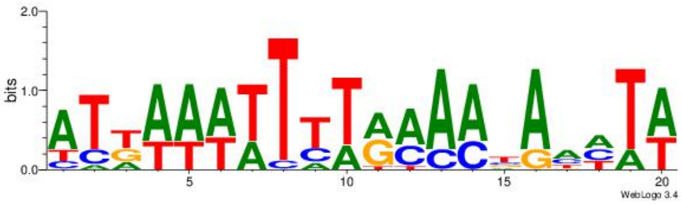


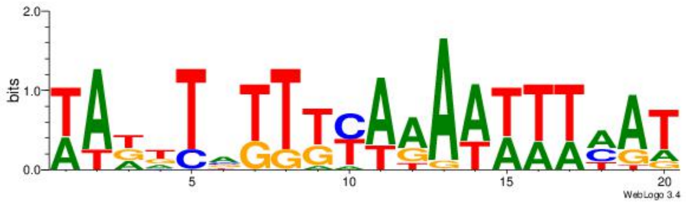
Dataset #: 5
Motif ID: 55
Motif name: TFM13
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 7
Number of overlap: 13
Similarity score: 0.0762821

Alignment:
WAHHTVTTYKAAAAWTTRAT
------TTCWTAGATTAWA-

Original motif Consensus sequence: ATKAAWTTTTRMAABAHHTW

Reverse complement motif Consensus sequence: WAHHTVTTYKAAAAWTTRAT



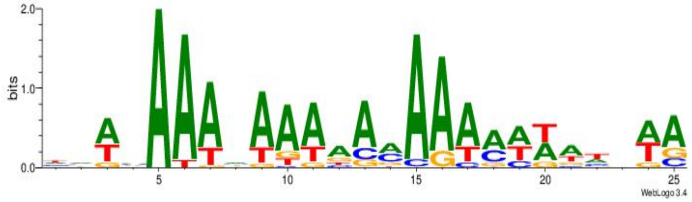


Dataset #:	5
Motif ID:	56
Motif name:	TFM11
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	12
Number of overlap:	13
Similarity score:	0.0810709

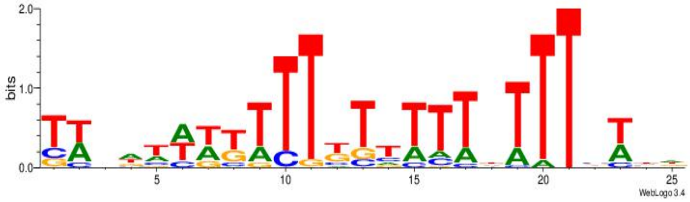
Alignment:

```
HDWVAAAHAAAAAMAAAMWWWHBWA
-TWTAATCTAWGAA-----------
```

Original motif Consensus sequence:
HDWVAAAHAAAAAMAAAMWWWHBWA



Reverse complement motif Consensus sequence:
TWVHWWWYTTTYTTTTTHTTTVWBH



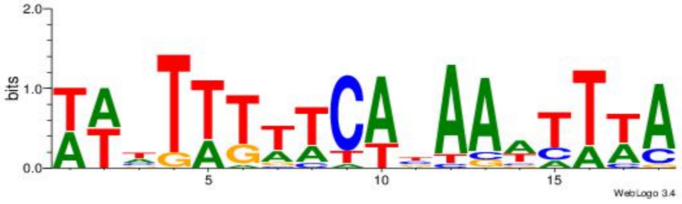
Dataset #:	5

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

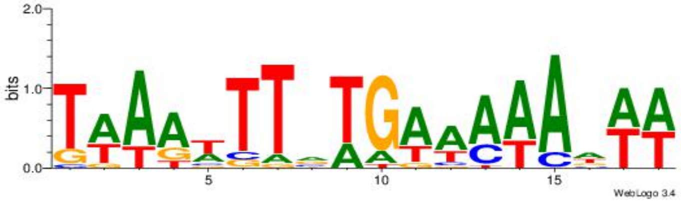
Alignment:

```
TWAAWTTVTGAAAAAHWW
-----TTCWTAGATTAWA
```

Original motif Consensus sequence: WWHTTTTTCABAAWTTWA



Reverse complement motif Consensus sequence: TWAAWTTVTGAAAAAHWW



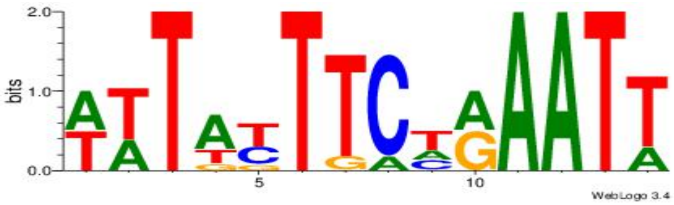
Dataset #: 2
Motif ID: 6
Motif name: Motif 6
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 3
Number of overlap: 12

Similarity score: 0.5625

Alignment:
AATTYDGAARTAWW-
--TTCWTAGATTAWA

Original motif Consensus sequence: AATTYDGAARTAWW

Reverse complement motif Consensus sequence: WWTAKTTCDKAAT

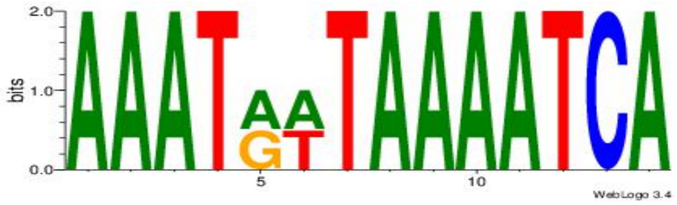


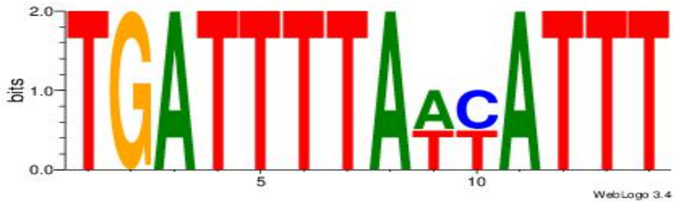
Dataset #: 2
Motif ID: 8
Motif name: Motif 8
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 3
Number of overlap: 12
Similarity score: 0.5625

Alignment:
-TGATTTTAWKATTT
TWTAATCTAWGAA--

Original motif Consensus sequence: AAATRWTAAAATCA

Reverse complement motif Consensus sequence: TGATTTTAWKATT



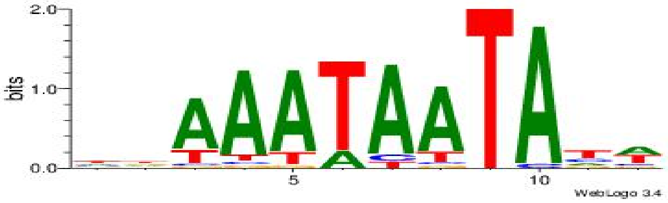


Dataset #:	4
Motif ID:	37
Motif name:	tkAAATAATAtw
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	12
Similarity score:	0.577083

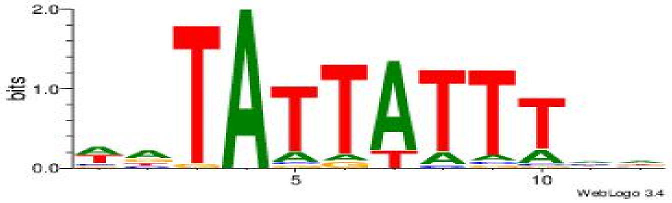
Alignment:

WHTATTATTTDH-
TWTAATCTAWGAA

Original motif Consensus sequence: HDAAATAATAHW



Reverse complement motif Consensus sequence: WHTATTATTTDH



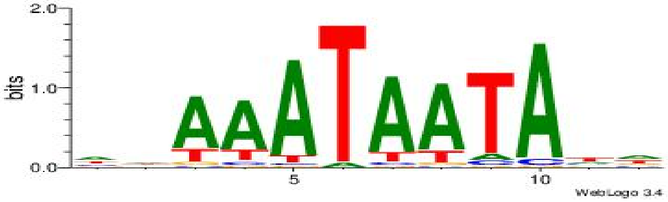
Dataset #:	4
Motif ID:	41

Motif name:	wwAAATAATAtw
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	12
Similarity score:	0.58179

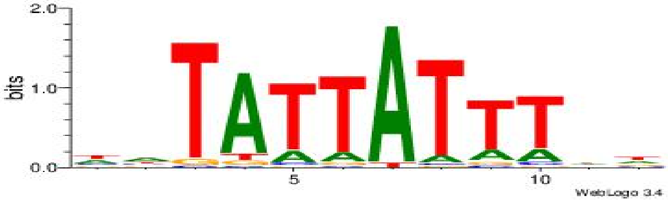
Alignment:

```
DDTATTATTTDH-
TWTAATCTAWGAA
```

Original motif Consensus sequence: HDAAATAATADD



Reverse complement motif Consensus sequence: DDTATTATTTDH

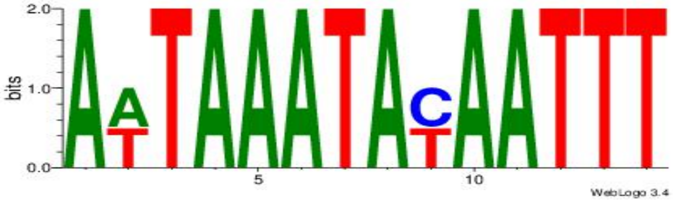


Dataset #:	2
Motif ID:	5
Motif name:	Motif 5
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	3
Number of overlap:	12
Similarity score:	0.583333

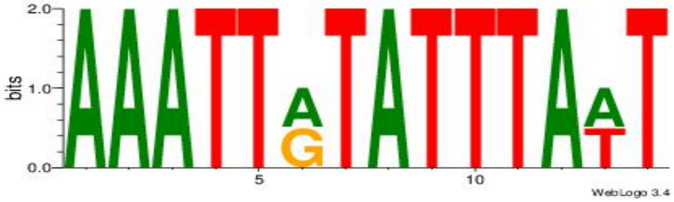
Alignment:

```
AWTAAATAYAATTT-
--TTCWTAGATTAWA
```

Original motif Consensus sequence: AWTAAATAYAATTT



Reverse complement motif Consensus sequence: AAATTKTATTTAW



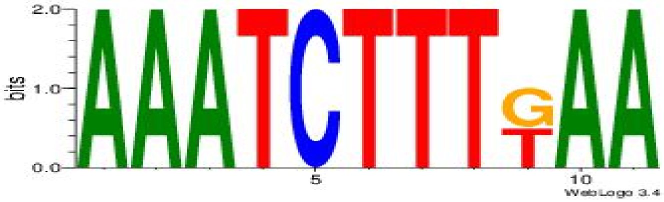
Dataset #:	2
Motif ID:	20
Motif name:	Motif 20
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	11
Similarity score:	1.02652

Alignment:

```
TTMAAAGATTT--
TTCWTAGATTAWA
```

Original motif Consensus sequence: TTMAAAGATTT

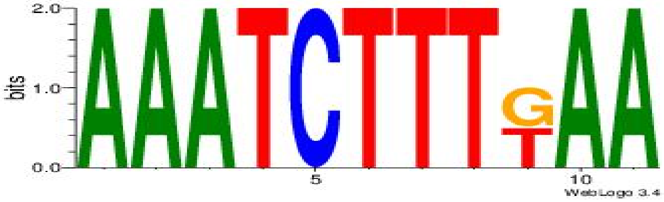
Reverse complement motif Consensus sequence: AAATCTTTYAA



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

Original motif Consensus sequence: TTMAAAGATTT

Reverse complement motif Consensus sequence: AAATCTTTYAA



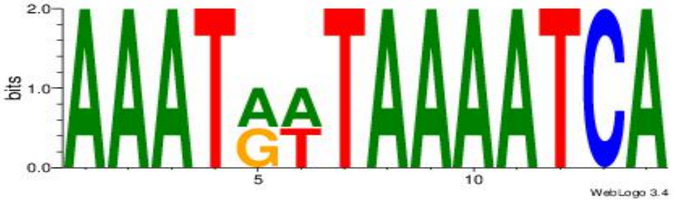
Best Matches for Motif ID 20 (Highest to Lowest)

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

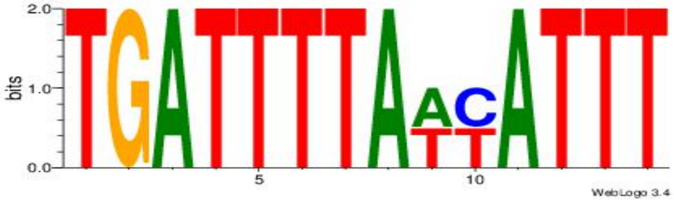
Alignment:

```
AAATRWTAAAATCA
---AAATCTTTYAA
```

Original motif Consensus sequence: AAATRWTAAAATCA



Reverse complement motif Consensus sequence: TGATTTTAWKATT



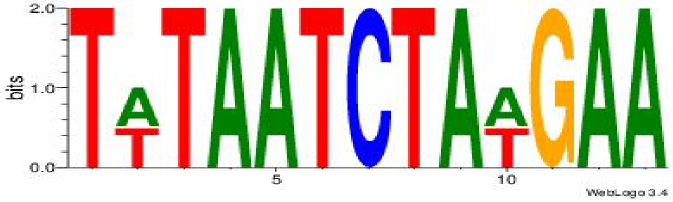
Dataset #: 2
Motif ID: 19
Motif name: Motif 19
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 11
Similarity score: 0.0681818

Alignment:

```
TTCWTAGATTAWA
TTMAAAGATTT--
```

Original motif Consensus sequence: TTCWTAGATTAWA

Reverse complement motif Consensus sequence: TWTAATCTAWGAA

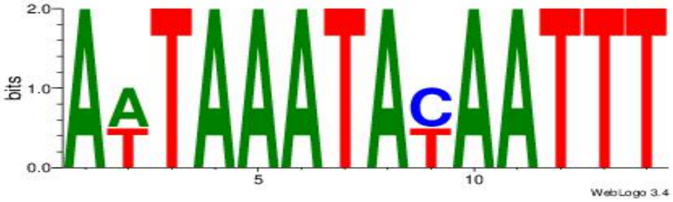


Dataset #: 2
Motif ID: 5
Motif name: Motif 5
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 3
Number of overlap: 11
Similarity score: 0.102273

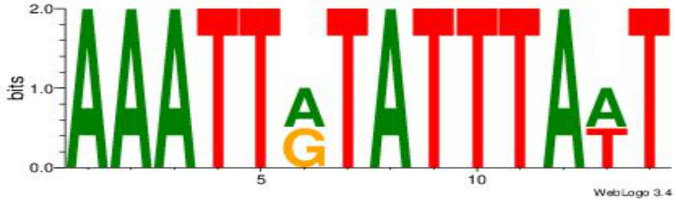
Alignment:

```
AAATTKTATTTAWT
-AAATCTTTYAA--
```

Original motif Consensus sequence: AWTAAATAYAATTT



Reverse complement motif Consensus sequence: AAATTKTATTTAWT

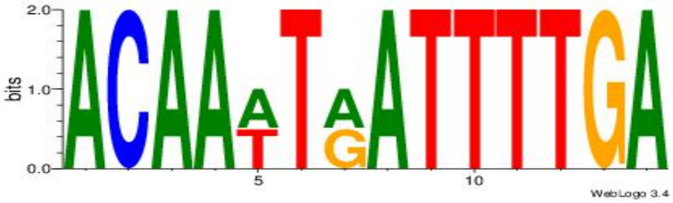


Dataset #: 2
Motif ID: 16
Motif name: Motif 16
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 11

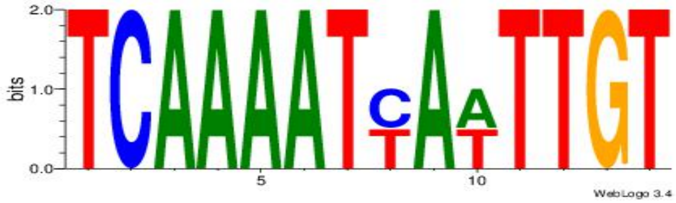
Similarity score:	0.102273

Alignment:
ACAAWTRATTTTGA
TTMAAAGATTT---

Original motif Consensus sequence: ACAAWTRATTTTGA



Reverse complement motif Consensus sequence: TCAAAATKAWTTG

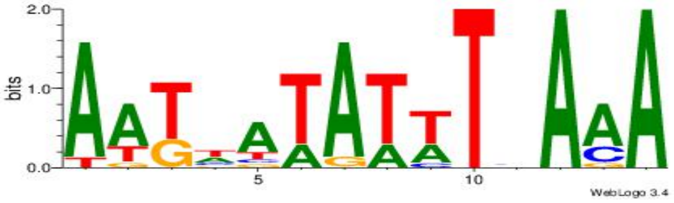


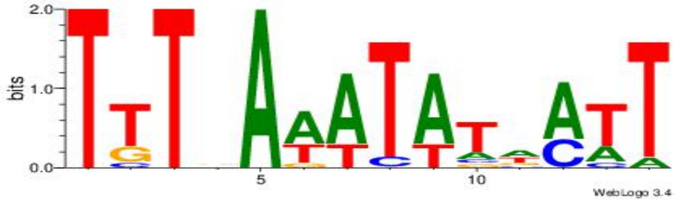
Dataset #:	2
Motif ID:	9
Motif name:	Motif 9
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	2
Number of overlap:	11
Similarity score:	0.106061

Alignment:
TTTDAWATATHATT
--TTMAAAGATTT-

Original motif Consensus sequence: AATHATATWTHAAA

Reverse complement motif Consensus sequence: TTTDAWATATHAT





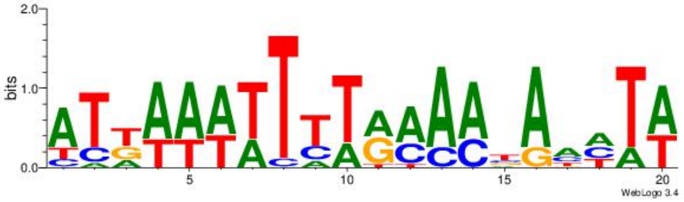
Dataset #:	5
Motif ID:	55
Motif name:	TFM13
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	2
Number of overlap:	11
Similarity score:	0.110606

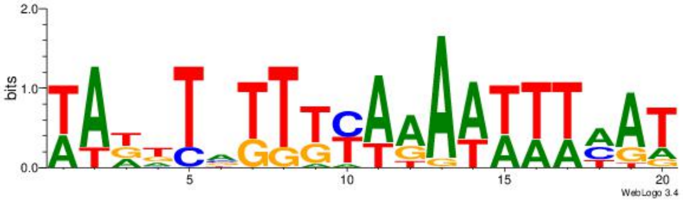
Alignment:

```
WAHHTVTTYKAAAAWTTRAT
-AAATCTTTYAA--------
```

Original motif Consensus sequence: ATKAAWTTTTRMAABAHHTW

Reverse complement motif Consensus sequence: WAHHTVTTYKAAAAWTTRAT





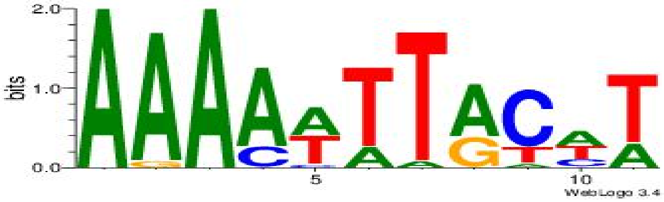
Dataset #:	2

Motif ID: 4
Motif name: Motif 4
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: 0.110646

Alignment:

```
AWGKAAWTTTT
TTMAAAGATTT
```

Original motif Consensus sequence: AAAAWTTRCWT



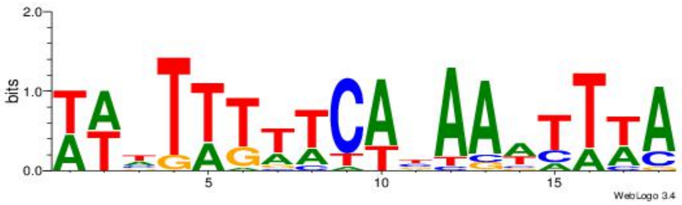
Reverse complement motif Consensus sequence: AWGKAAWTTTT

Dataset #: 5
Motif ID: 53
Motif name: TFM3
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 7
Number of overlap: 11
Similarity score: 0.113636

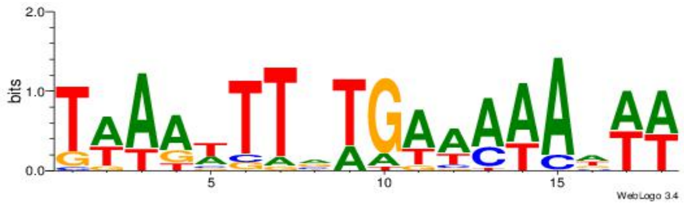
Alignment:

```
WWHTTTTTCABAAWTTWA
------TTMAAAGATTT-
```

Original motif   Consensus sequence: WWHTTTTTCABAAWTTWA



Reverse complement motif   Consensus sequence: TWAAWTTVTGAAAAAHWW

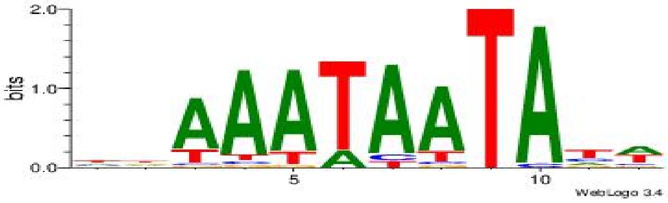


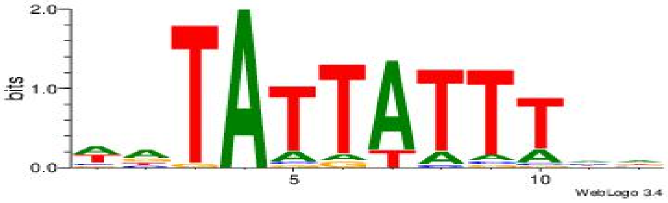
Dataset #:	4
Motif ID:	37
Motif name:	tkAAATAATAtw
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	11
Similarity score:	0.124242

Alignment:

```
WHTATTATTTDH
-AAATCTTTYAA
```

Original motif   Consensus sequence: HDAAATAATAHW   Reverse complement motif   Consensus sequence: WHTATTATTTDH



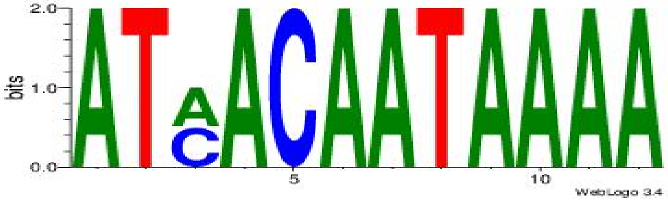


Dataset #:	2
Motif ID:	15
Motif name:	Motif 15
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	11
Similarity score:	0.125

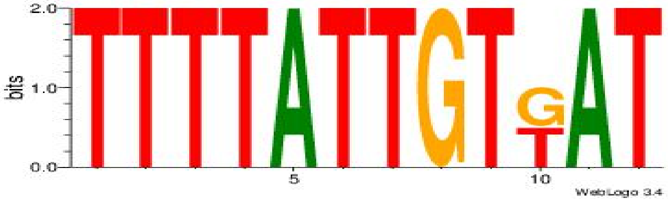
Alignment:

```
ATMACAATAAAA
-AAATCTTTYAA
```

Original motif Consensus sequence: ATMACAATAAAA



Reverse complement motif Consensus sequence: TTTTATTGTYAT



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

Original motif Consensus sequence: ATAAAA

Reverse complement motif Consensus sequence: TTTTAT

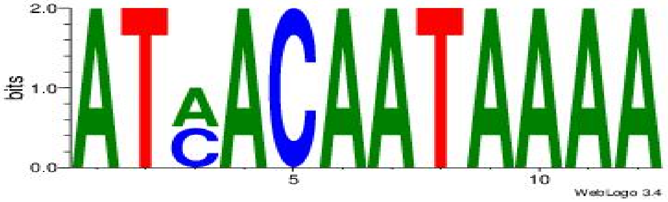
Best Matches for Motif ID 21 (Highest to Lowest)

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

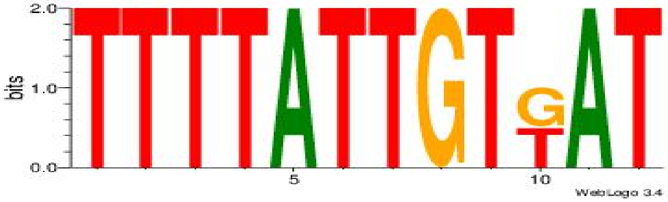
Alignment:

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

Original motif Consensus sequence: ATMACAATAAAA



Reverse complement motif Consensus sequence: TTTTATTGTYAT

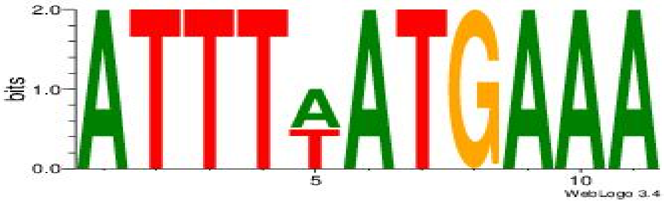


Dataset #:	2
Motif ID:	11
Motif name:	Motif 11
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	5
Number of overlap:	6
Similarity score:	0.0208333

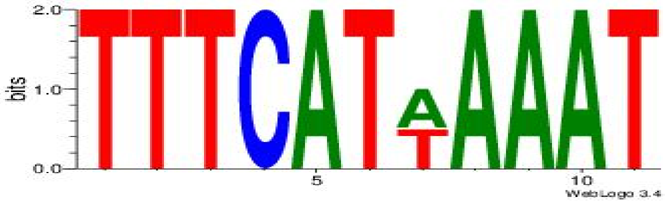
Alignment:

TTTCATWAAAT
-ATAAAA----

Original motif Consensus sequence: ATTTWATGAAA



Reverse complement motif Consensus sequence: TTTCATWAAAT

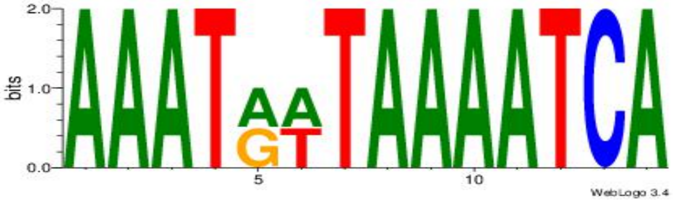


Dataset #:	2
Motif ID:	8
Motif name:	Motif 8
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	6
Number of overlap:	6

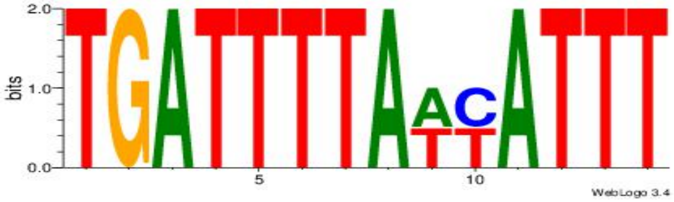
Similarity score: 0.0208333

Alignment:
```
AAATRWTAAAATCA
-----ATAAAA---
```

Original motif Consensus sequence: AAATRWTAAAATCA



Reverse complement motif Consensus sequence: TGATTTTAWKATT

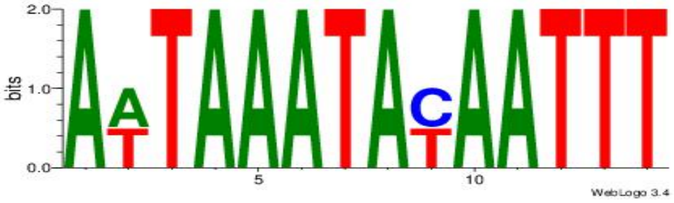


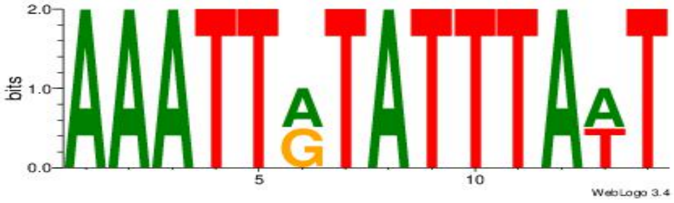
Dataset #:	2
Motif ID:	5
Motif name:	Motif 5
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	6
Number of overlap:	6
Similarity score:	0.0208333

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

Original motif Consensus sequence: AWTAAATAYAATTT

Reverse complement motif Consensus sequence: AAATTKTATTTAW



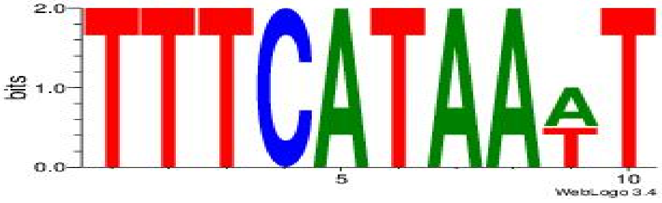


Dataset #:	2
Motif ID:	10
Motif name:	Motif 10
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	6
Similarity score:	0.0416667

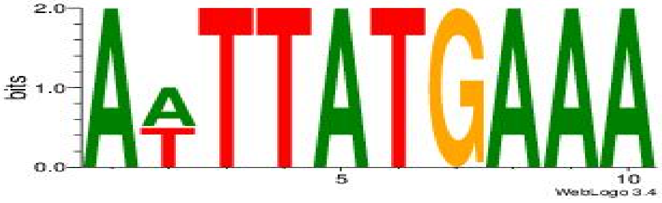
Alignment:

```
TTTCATAAWT
----TTTTAT
```

Original motif Consensus sequence: TTTCATAAWT



Reverse complement motif Consensus sequence: AWTTATGAAA

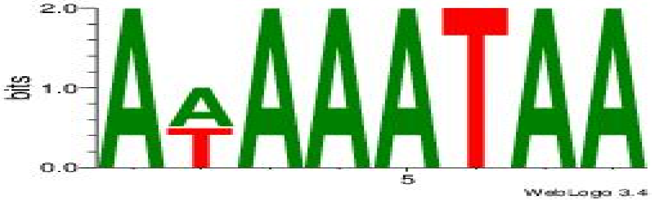


Dataset #:	2
Motif ID:	14

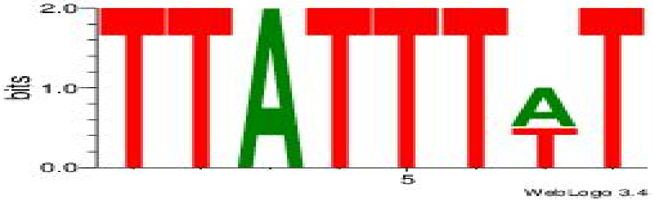
Motif name: Motif 14
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 6
Similarity score: 0.0625

Alignment:
AWAAATAA
ATAAAA--

Original motif Consensus sequence: AWAAATAA



Reverse complement motif Consensus sequence: TTATTTWT



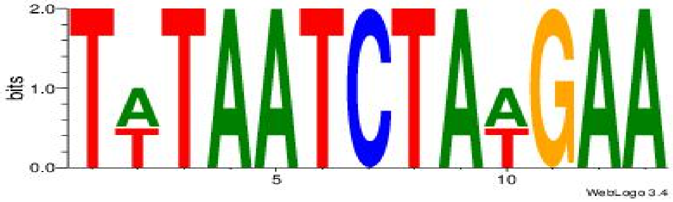
Dataset #: 2
Motif ID: 19
Motif name: Motif 19
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 8
Number of overlap: 6
Similarity score: 0.0625

Alignment:

```
TWTAATCTAWGAA
TTTTAT-------
```

Original motif Consensus sequence: TTCWTAGATTAWA

Reverse complement motif Consensus sequence: TWTAATCTAWGAA



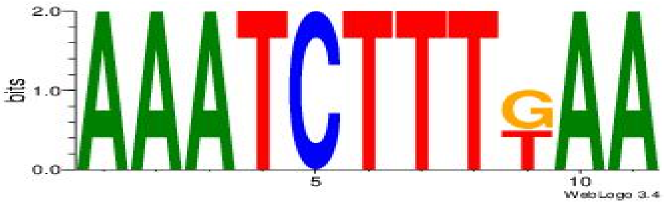
Dataset #:	2
Motif ID:	20
Motif name:	Motif 20
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	6
Number of overlap:	6
Similarity score:	0.0625

Alignment:

```
TTMAAAGATTT
ATAAAA-----
```

Original motif Consensus sequence: TTMAAAGATTT

Reverse complement motif Consensus sequence: AAATCTTTYAA

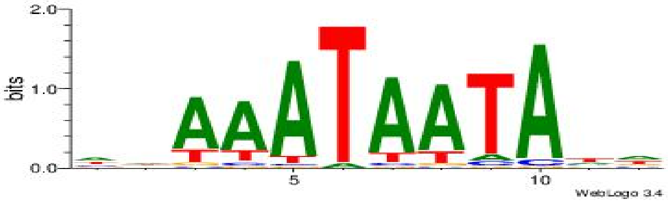


Dataset #: 4
Motif ID: 41
Motif name: wwAAATAATAtw
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 3
Number of overlap: 6
Similarity score: 0.0632716

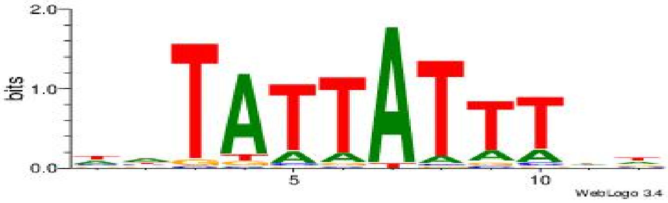
Alignment:

```
DDTATTATTTDH
--TTTTAT----
```

Original motif Consensus sequence: HDAAATAATADD



Reverse complement motif Consensus sequence: DDTATTATTTDH



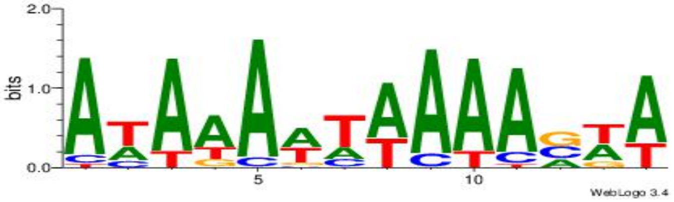
Dataset #: 2
Motif ID: 3

Motif name: Motif 3
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 4
Number of overlap: 6
Similarity score: 0.0689103

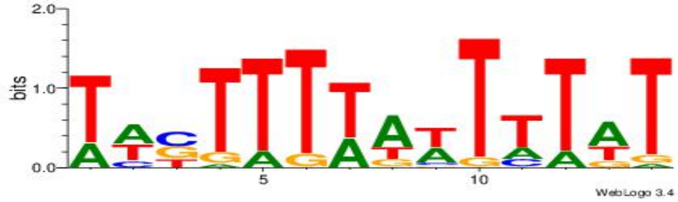
Alignment:

```
TWSTTTWAWTTTWT
---TTTTAT-----
```

Original motif Consensus sequence: AWAAAWTWAAASWA

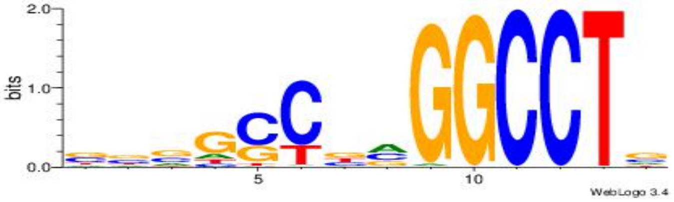


Reverse complement motif Consensus sequence: TWSTTTWAWTTTW

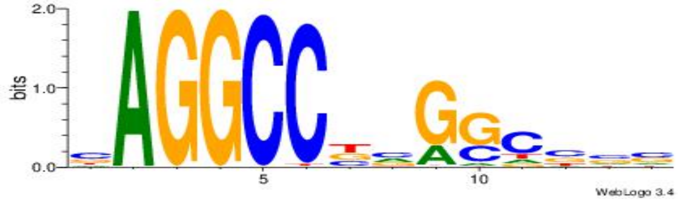


Dataset #: 3 Motif ID: 22 Motif name: Zfx

Original motif Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif Consensus sequence: VAGGCCBBGGCVB

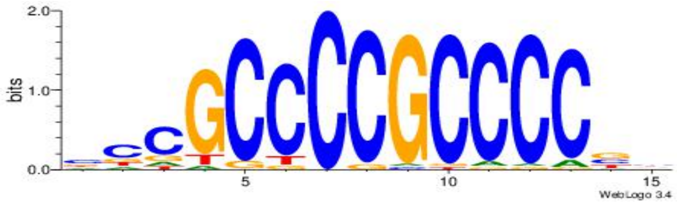


Best Matches for Motif ID 22 (Highest to Lowest)

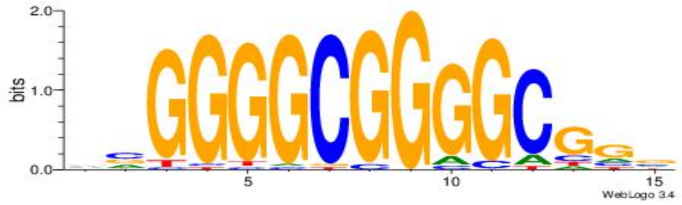
Dataset #: 4
Motif ID: 38
Motif name: cccGCCCCGCCCCsb
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2
Number of overlap: 14
Similarity score: 0.0514008

Alignment:
BCCGCCCCGCCCCBB
BBVGCCBVGGCCTV-

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB

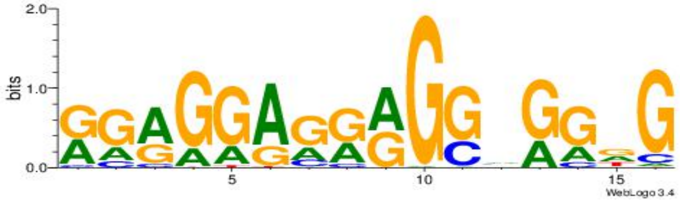


Dataset #: 5
Motif ID: 51
Motif name: TFM2
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 2

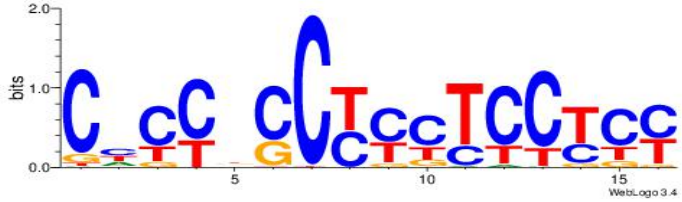
Number of overlap: 14
Similarity score: 0.0590031

Alignment:
```
CHCCBCCKMCTCCKCM
-BBVGCCBVGGCCTV-
```

Original motif Consensus sequence: RGRGGAGRRGGHGGDG



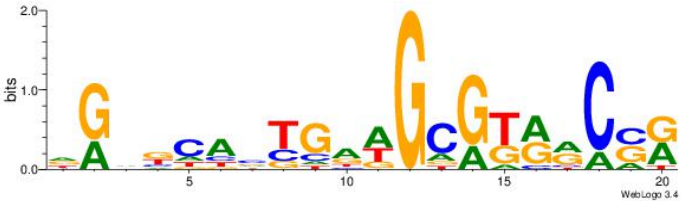
Reverse complement motif Consensus sequence: CHCCBCCKMCTCCKCM



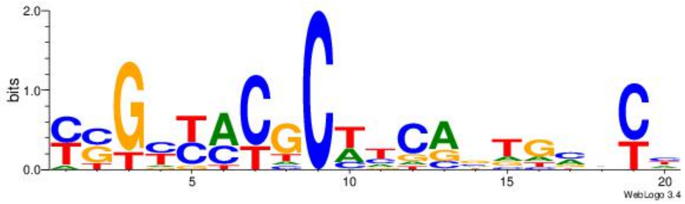
Dataset #: 3
Motif ID: 31
Motif name: Pax5
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 5
Number of overlap: 14
Similarity score: 0.0611182

Alignment:
```
DGVBCABTGDWGCGKRRCSR
--BBVGCCBVGGCCTV----
```

Original motif Consensus sequence: DGVBCABTGDWGCGKRRCSR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD

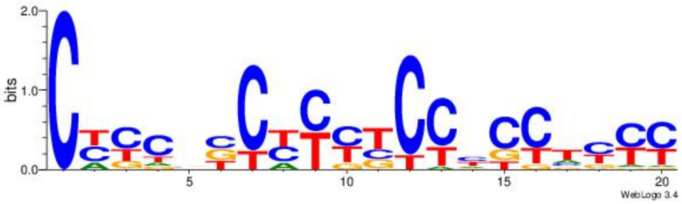


Dataset #:	5
Motif ID:	54
Motif name:	TFM12
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	6
Number of overlap:	14
Similarity score:	0.0629383

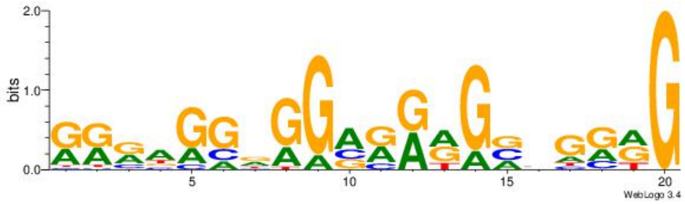
Alignment:

```
KKKAGGDGGAKKMGBBGKMG
-----VAGGCCBBGGCVBB-
```

Original motif Consensus sequence: CYYCBBCYYYTCCHCCTYYY



Reverse complement motif Consensus sequence: KKKAGGDGGAKKMGBBGKMG

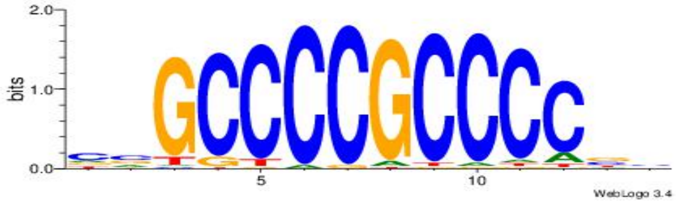


Dataset #: 4
Motif ID: 36
Motif name: csGCCCCGCCCCsc
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 14
Similarity score: 0.0654514

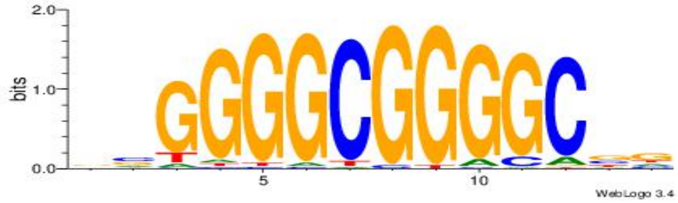
Alignment:

```
HVGCCCCGCCCCBB
VAGGCCBBGGCVBB
```

Original motif Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGC



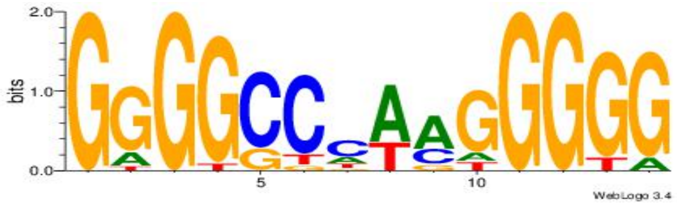
Dataset #: 3
Motif ID: 30
Motif name: PLAG1
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 14

Similarity score: 0.0796879

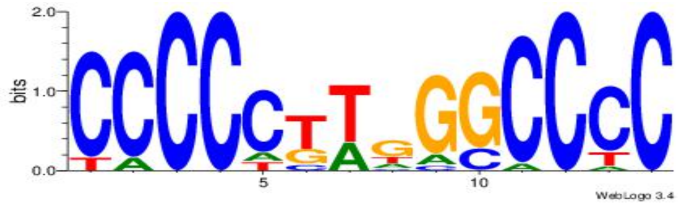
Alignment:

CCCCCTTGGGCCCC
BBVGCCBVGGCCTV

Original motif Consensus sequence: GGGGCCCAAGGGGG



Reverse complement motif Consensus sequence: CCCCCTTGGGCCC



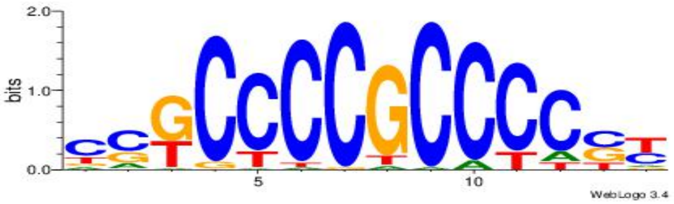
Dataset #: 2
Motif ID: 7
Motif name: Motif 7
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 14
Similarity score: 0.0799116

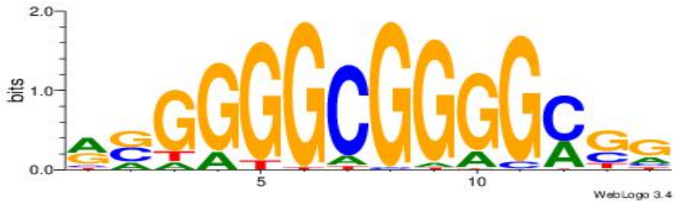
Alignment:

MSGGGGCGGGGYSG
BBVGCCBVGGCCTV

Original motif Consensus sequence: CSKCCCCGCCCCSY

Reverse complement motif Consensus sequence: MSGGGGCGGGGY





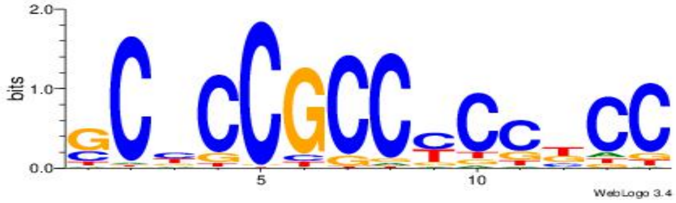
Dataset #:	5
Motif ID:	50
Motif name:	TFF11
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	2
Number of overlap:	13
Similarity score:	0.583338

Alignment:

```
-GCVCCGCCMCCYCC
BBVGCCBVGGCCTV-
```

Original motif Consensus sequence: GGMGGRGGCGGVGC

Reverse complement motif Consensus sequence: GCVCCGCCMCCYC



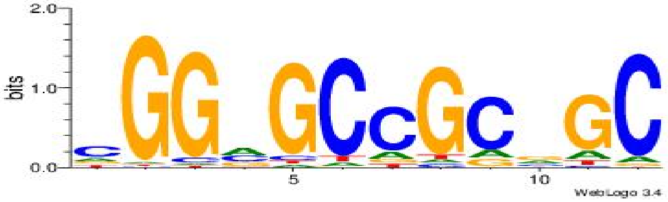
Dataset #:	5
Motif ID:	49

Motif name: TFF1
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: 1.55068

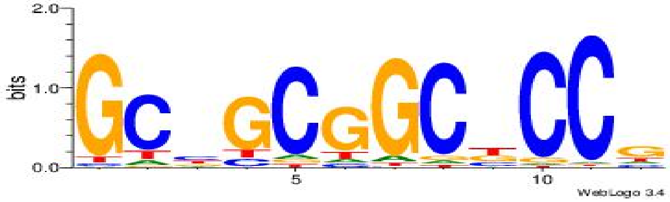
Alignment:

```
CGGVGCCGCVGC---
-BBVGCCBVGGCCTV
```

Original motif Consensus sequence: CGGVGCCGCVGC



Reverse complement motif Consensus sequence: GCVGCGGCBCCG



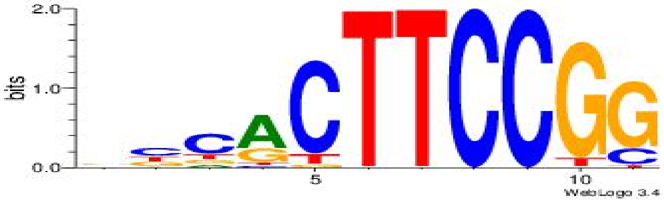
Dataset #: 3
Motif ID: 35
Motif name: GABPA
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 11
Similarity score: 1.57592

Alignment:

CCGGAAGTGVV---
VAGGCCBBGGCVBB

Original motif   Consensus sequence: CCGGAAGTGVV

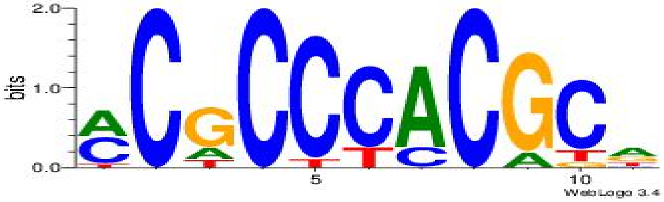
Reverse complement motif   Consensus sequence: VVCACTTCCGG



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

Original motif   Consensus sequence: HGCGTGGGCGK

Reverse complement motif   Consensus sequence: YCGCCCACGCH



Best Matches for Motif ID 23 (Highest to Lowest)

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

Number of overlap: 11

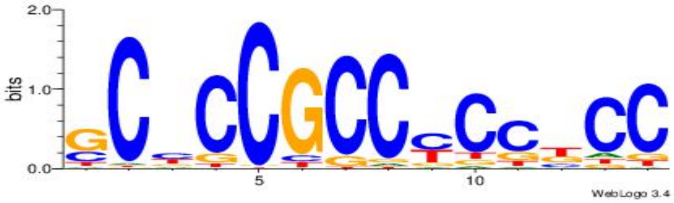
Similarity score: 0.0514701

Alignment:

```
GCVCCGCCMCCYCC
---YCGCCCACGCH
```

Original motif Consensus sequence: GGMGGRGGCGGVGC

Reverse complement motif Consensus sequence: GCVCCGCCMCCYC



Dataset #: 5

Motif ID: 51

Motif name: TFM2

Matching format of first motif: Reverse Complement

Matching format of second motif: Reverse Complement

Direction: Forward

Position number: 6

Number of overlap: 11

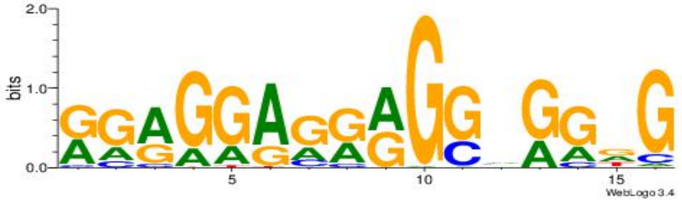
Similarity score: 0.0698683

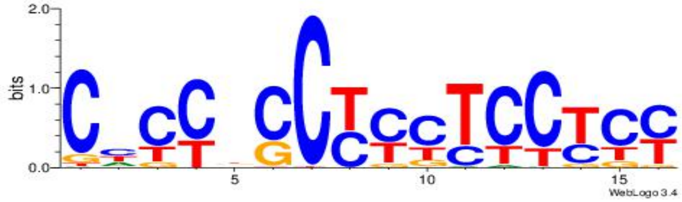
Alignment:

```
CHCCBCCKMCTCCKCM
-----YCGCCCACGCH
```

Original motif Consensus sequence: RGRGGAGRRGGHGGDG

Reverse complement motif Consensus sequence: CHCCBCCKMCTCCKCM





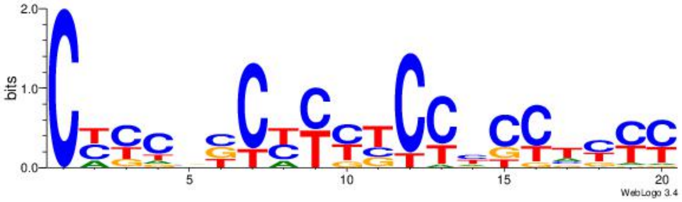
Dataset #:	5
Motif ID:	54
Motif name:	TFM12
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	9
Number of overlap:	11
Similarity score:	0.0718056

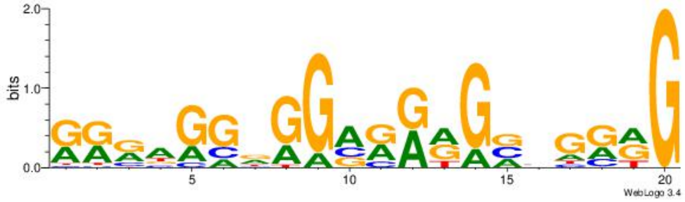
Alignment:

```
KKKAGGDGGAKKMGBBGKMG
-HGCGTGGGCGK--------
```

Original motif Consensus sequence: CYYCBBCYYYTCCHCCTYYY

Reverse complement motif Consensus sequence: KKKAGGDGGAKKMGBBGKMG





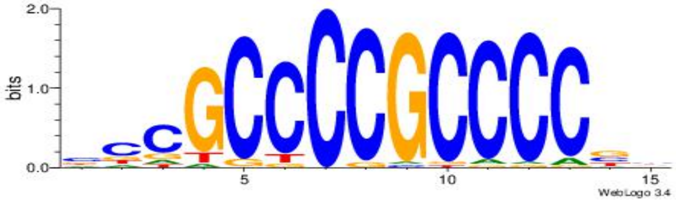
Dataset #:	4

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

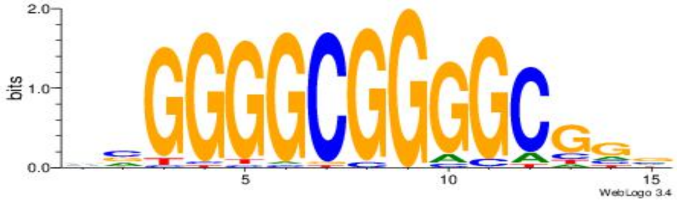
Alignment:

```
BBGGGGCGGGGCGGB
----HGCGTGGGCGK
```

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB

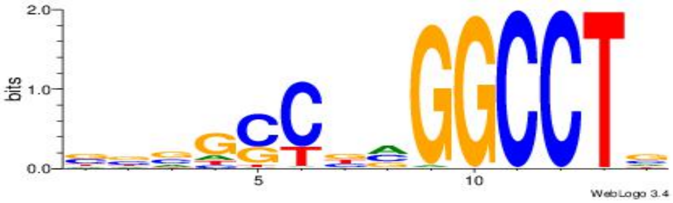


Dataset #:	3
Motif ID:	22
Motif name:	Zfx
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2
Number of overlap:	11

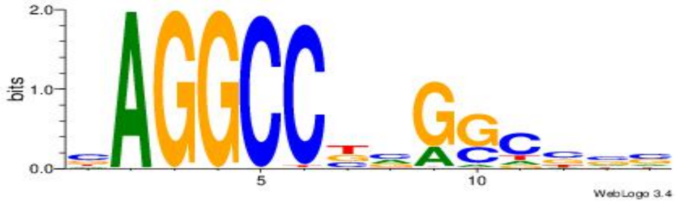
Similarity score: 0.0764878

Alignment:
BBVGCCBVGGCCTV
--HGCGTGGGCGK-

Original motif Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif Consensus sequence: VAGGCCBBGGCVE

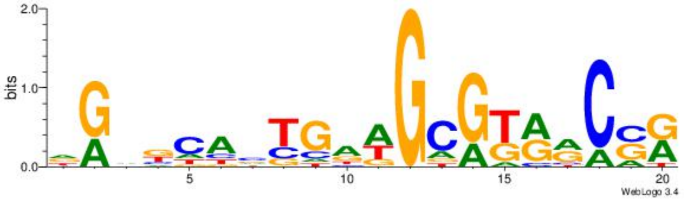


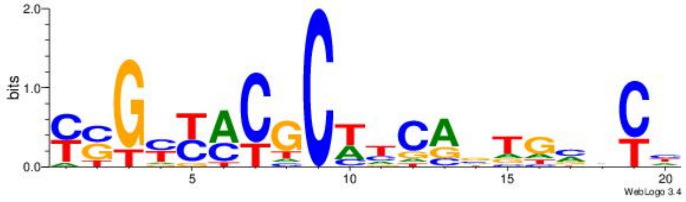
Dataset #: 3
Motif ID: 31
Motif name: Pax5
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 6
Number of overlap: 11
Similarity score: 0.0765783

Alignment:
DGVBCABTGDWGCGKRRCSR
----HGCGTGGGCGK-----

Original motif Consensus sequence: DGVBCABTGDWGCGKRRCSR

Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD



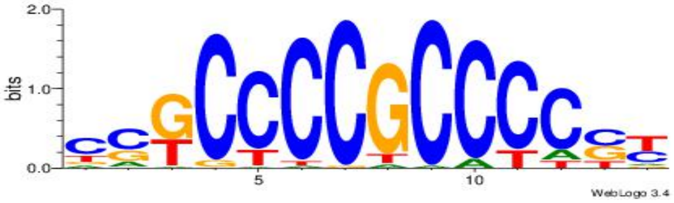


Dataset #: 2
Motif ID: 7
Motif name: Motif 7
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 3
Number of overlap: 11
Similarity score: 0.0771215

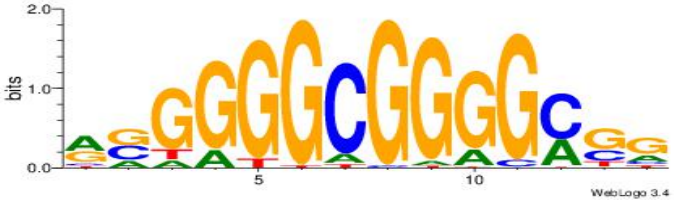
Alignment:

```
CSKCCCCGCCCCSY
-YCGCCCACGCH--
```

Original motif Consensus sequence: CSKCCCCGCCCCSY



Reverse complement motif Consensus sequence: MSGGGGCGGGGY



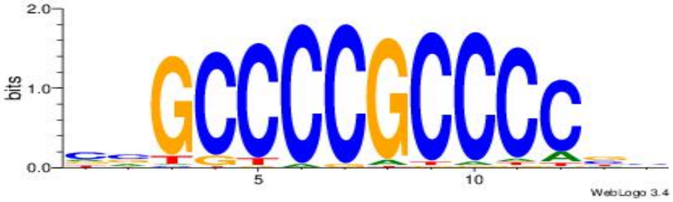
Dataset #: 4
Motif ID: 36

Motif name:	csGCCCCGCCCCsc
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	11
Similarity score:	0.0825032

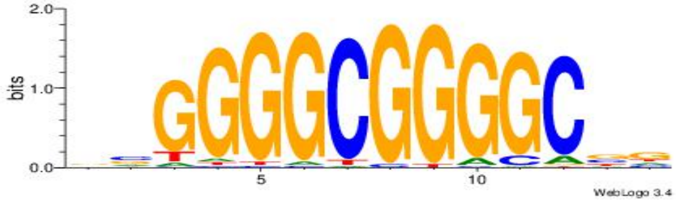
Alignment:

```
HVGCCCCGCCCCBB
-YCGCCCACGCH--
```

Original motif Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGC



Dataset #:	5
Motif ID:	48
Motif name:	TFW3
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	10
Similarity score:	0.550222

Alignment:
CGCGBMGCCG-
HGCGTGGGCGK

Original motif Consensus sequence: CGGCYBCGCG

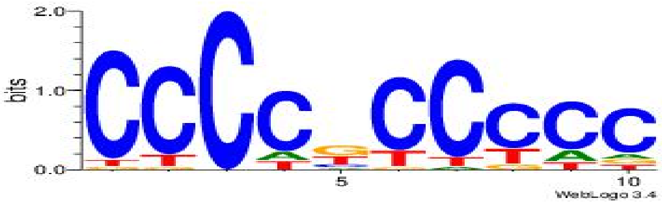
Reverse complement motif Consensus sequence: CGCGBMGCCG

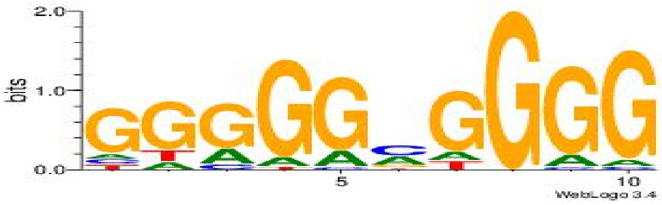
Dataset #:	3
Motif ID:	24
Motif name:	SP1
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	10
Similarity score:	0.572401

Alignment:
GGGGGYGGGG-
HGCGTGGGCGK

Original motif Consensus sequence: CCCCKCCCCC

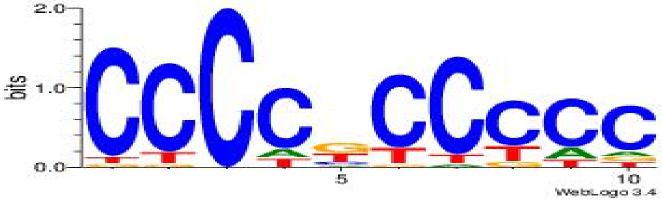
Reverse complement motif Consensus sequence: GGGGGYGGGG





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

Original motif Consensus sequence: CCCCKCCCCC



Reverse complement motif Consensus sequence: GGGGGYGGGG

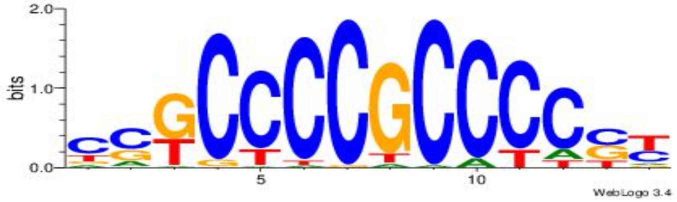
Best Matches for Motif ID 24 (Highest to Lowest)

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

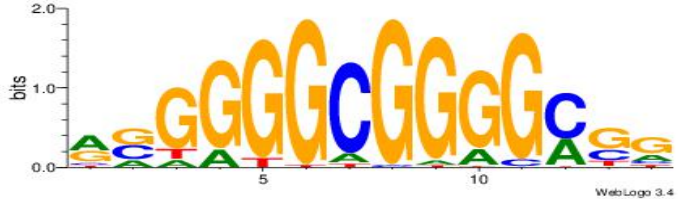
Alignment:

```
MSGGGGCGGGGYSG
-GGGGGYGGGG---
```

Original motif Consensus sequence: CSKCCCCGCCCCSY



Reverse complement motif Consensus sequence: MSGGGGCGGGGY

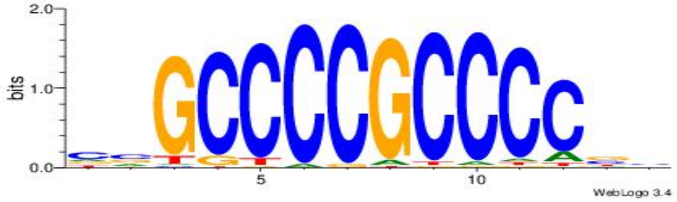


Dataset #:	4
Motif ID:	36
Motif name:	csGCCCCGCCCCsc
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	4
Number of overlap:	10
Similarity score:	0.00965796

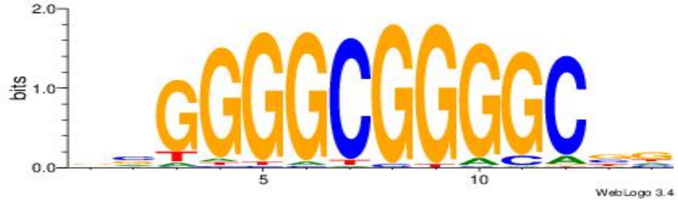
Alignment:

```
HVGCCCCGCCCCBB
---CCCCKCCCCC-
```

Original motif Consensus sequence: HVGCCCCGCCCCBB



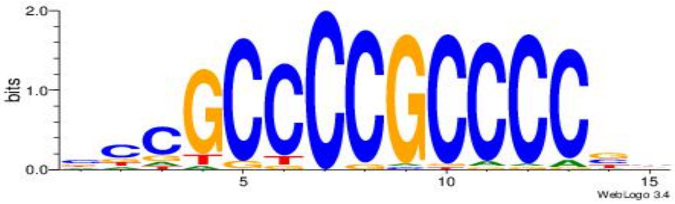
Reverse complement motif Consensus sequence: BBGGGGCGGGGC



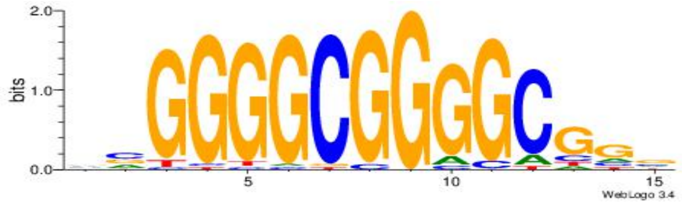
Dataset #: 4
Motif ID: 38
Motif name: cccGCCCCGCCCCsb
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2
Number of overlap: 10
Similarity score: 0.0127292

Alignment:
BCCGCCCCGCCCCBB
----CCCCKCCCCC-

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB



Dataset #: 5
Motif ID: 50
Motif name: TFF11
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 4

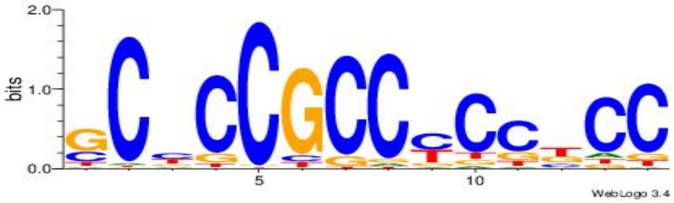
Number of overlap:	10
Similarity score:	0.0174405

Alignment:

```
GGMGGRGGCGGVGC
---GGGGGYGGGG-
```

Original motif Consensus sequence: GGMGGRGGCGGVGC

Reverse complement motif Consensus sequence: GCVCCGCCMCCYC



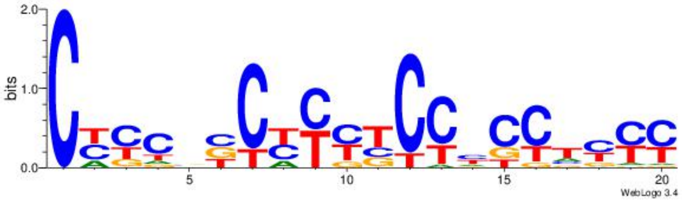
Dataset #:	5
Motif ID:	54
Motif name:	TFM12
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	7
Number of overlap:	10
Similarity score:	0.0301548

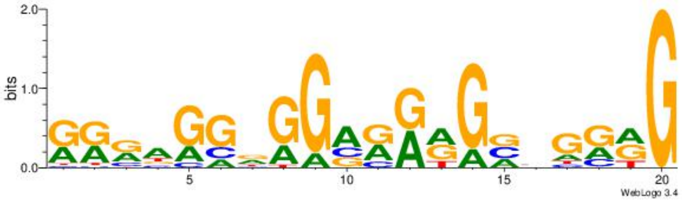
Alignment:

```
CYYCBBCYYYTCCHCCTYYY
------CCCCKCCCCC----
```

Original motif Consensus sequence: CYYCBBCYYYTCCHCCTYYY

Reverse complement motif Consensus sequence: KKKAGGDGGAKKMGBBGKMG



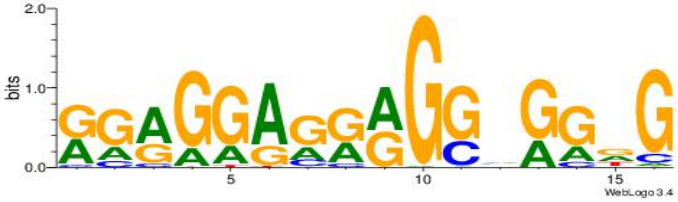


Dataset #:	5
Motif ID:	51
Motif name:	TFM2
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	10
Similarity score:	0.0329167

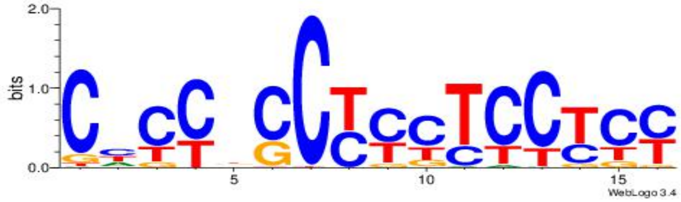
Alignment:

```
RGRGGAGRRGGHGGDG
------GGGGGYGGGG
```

Original motif Consensus sequence: RGRGGAGRRGGHGGDG



Reverse complement motif Consensus sequence: CHCCBCCKMCTCCKCM

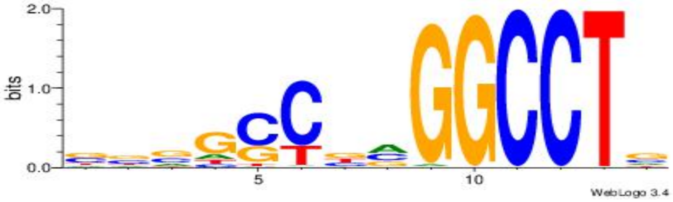


Dataset #:	3

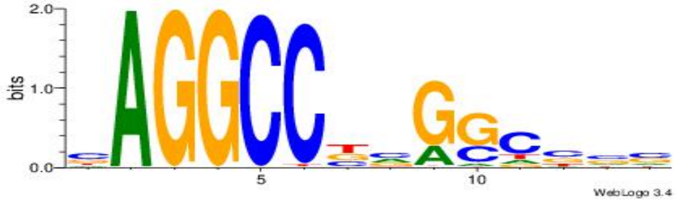
Motif ID: 22
Motif name: Zfx
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 5
Number of overlap: 10
Similarity score: 0.0540825

Alignment:
```
BBVGCCBVGGCCTV
----GGGGGYGGGG
```

Original motif   Consensus sequence: BBVGCCBVGGCCTV



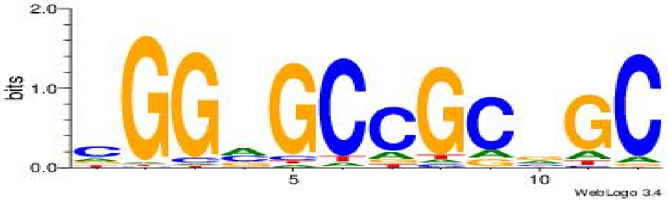
Reverse complement motif   Consensus sequence: VAGGCCBBGGCV



Dataset #: 5
Motif ID: 49
Motif name: TFF1
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 2
Number of overlap: 10
Similarity score: 0.0557738

Alignment:
GCVGCGGCBCCG
-CCCCKCCCCC-

Original motif   Consensus sequence: CGGVGCCGCVGC



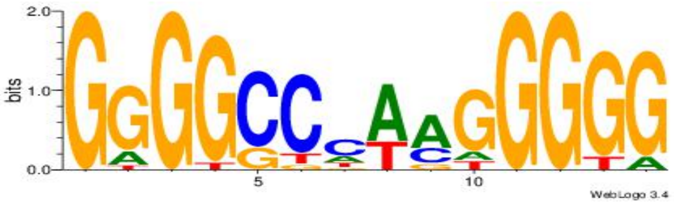
Reverse complement motif   Consensus sequence: GCVGCGGCBCCG

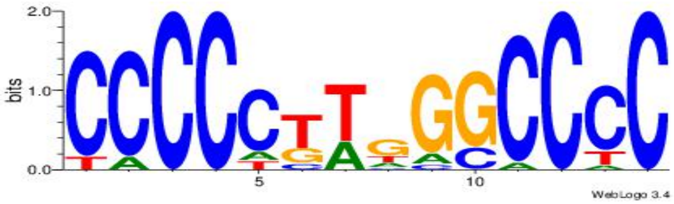
Dataset #:	3
Motif ID:	30
Motif name:	PLAG1
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	4
Number of overlap:	10
Similarity score:	0.0600992

Alignment:
CCCCCTTGGGCCCC
-CCCCKCCCCC---

Original motif   Consensus sequence: GGGGCCCAAGGGGG

Reverse complement motif   Consensus sequence: CCCCCTTGGGCCC





Dataset #:	3
Motif ID:	27
Motif name:	Klf4
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	10
Similarity score:	0.0637183

Alignment:

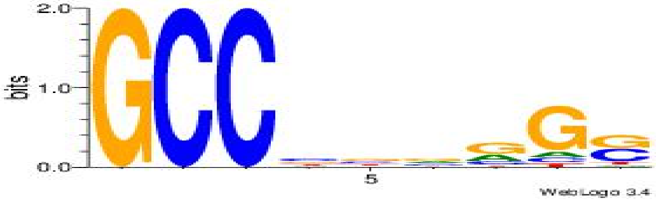
```
GCCYCMCCCD
CCCCKCCCCC
```

Original motif Consensus sequence: DGGGYGKGGC

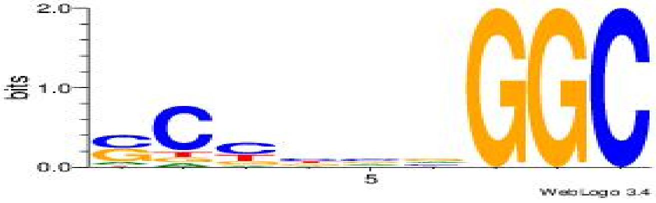
Reverse complement motif Consensus sequence: GCCYCMCCCD

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

Original motif Consensus sequence: GCCBBVRGS



Reverse complement motif Consensus sequence: SCMVBBGGC



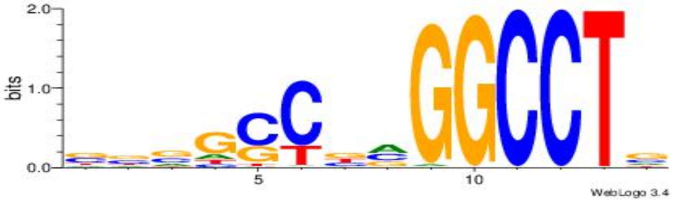
Best Matches for Motif ID 25 (Highest to Lowest)

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

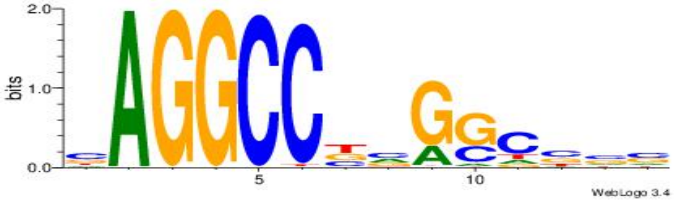
Alignment:

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

Original motif Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif Consensus sequence: VAGGCCBBGGCV

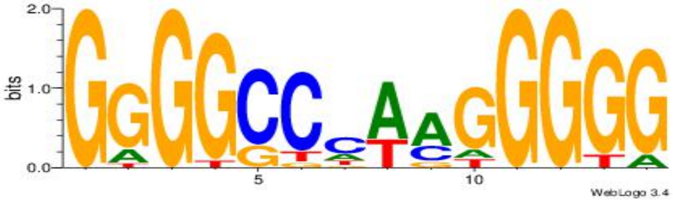


Dataset #:	3
Motif ID:	30
Motif name:	PLAG1
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	4
Number of overlap:	9
Similarity score:	0.0414588

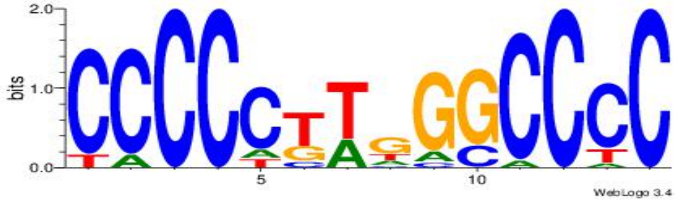
Alignment:

```
GGGGCCCAAGGGGG
---GCCBBVRGS--
```

Original motif   Consensus sequence: GGGGCCCAAGGGGG



Reverse complement motif   Consensus sequence: CCCCCTTGGGCCC



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

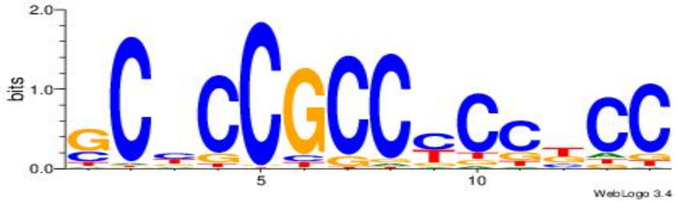
Similarity score: 0.0415732

Alignment:

```
GGMGGRGGCGGVGC
SCMVBBGGC-----
```

Original motif Consensus sequence: GGMGGRGGCGGVGC

Reverse complement motif Consensus sequence: GCVCCGCCMCCYC



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

Alignment:

```
HSCACGTGGC
-SCMVBBGGC
```

Original motif Consensus sequence: HSCACGTGGC

Reverse complement motif Consensus sequence: GCCACGTGSD


Dataset #:	5
Motif ID:	48
Motif name:	TFW3
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	9
Similarity score:	0.0552877

Alignment:

```
CGGCYBCGCG
-GCCBBVRGS
```

Original motif Consensus sequence: CGGCYBCGCG

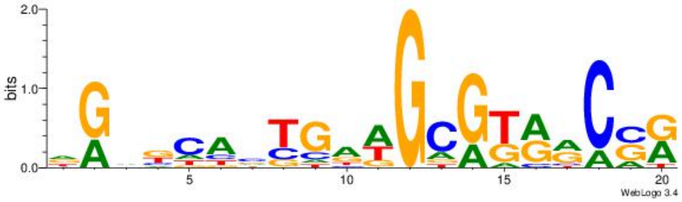
Reverse complement motif Consensus sequence: CGCGBMGCCG

Dataset #:	3
Motif ID:	31

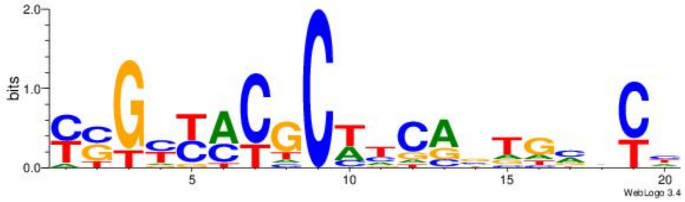
Motif name:	Pax5
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	8
Number of overlap:	9
Similarity score:	0.0581255

Alignment:
MSGKKRCGCWDCABTGBBCD
-------GCCBBVRGS----

Original motif   Consensus sequence: DGVBCABTGDWGCGKRRCSR



Reverse complement motif   Consensus sequence: MSGKKRCGCWDCABTGBBCD



Dataset #:	3
Motif ID:	34
Motif name:	Myc
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	9
Similarity score:	0.0613455

Alignment:
VGCACGTGGH
-SCMVBBGGC

Original motif Consensus sequence: VGCACGTGGH

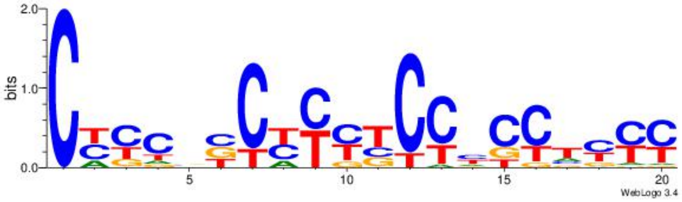
Reverse complement motif Consensus sequence: DCCACGTGCV

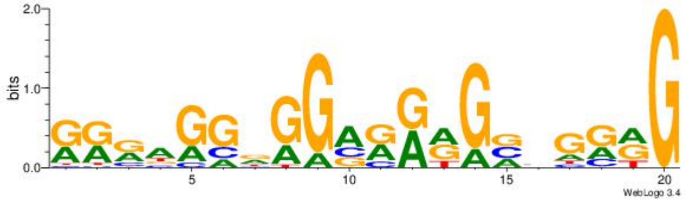
Dataset #:	5
Motif ID:	54
Motif name:	TFM12
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	11
Number of overlap:	9
Similarity score:	0.0630429

Alignment:
KKKAGGDGGAKKMGBBGKMG
-SCMVBBGGC----------

Original motif Consensus sequence: CYYCBBCYYYTCCHCCTYYY

Reverse complement motif Consensus sequence: KKKAGGDGGAKKMGBBGKMG

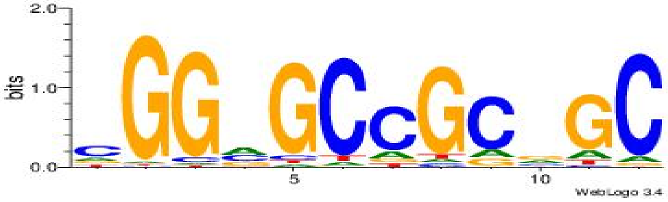




Dataset #: 5
Motif ID: 49
Motif name: TFF1
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 9
Similarity score: 0.0669772

Alignment:
GCVGCGGCBCCG
SCMVBBGGC---

Original motif Consensus sequence: CGGVGCCGCVGC



Reverse complement motif Consensus sequence: GCVGCGGCBCCG

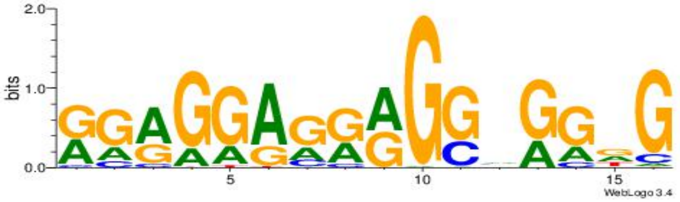
Dataset #: 5
Motif ID: 51

Motif name:	TFM2
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	9
Similarity score:	0.069755

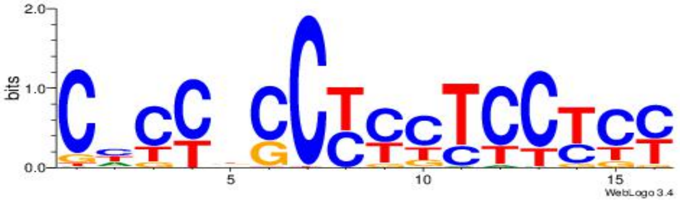
Alignment:

```
CHCCBCCKMCTCCKCM
SCMVBBGGC-------
```

Original motif Consensus sequence: RGRGGAGRRGGHGGDG



Reverse complement motif Consensus sequence: CHCCBCCKMCTCCKCM



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

Original motif Consensus sequence: BAACGTCCGC

Reverse complement motif Consensus sequence: GCGGACGTTV

Best Matches for Motif ID 26 (Highest to Lowest)

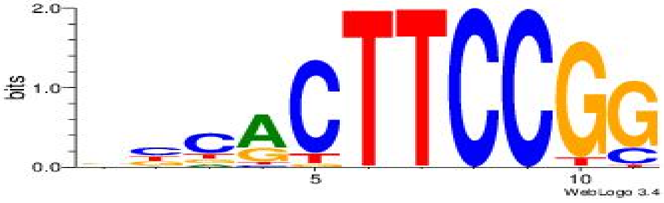
Dataset #:	3
Motif ID:	35
Motif name:	GABPA
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2
Number of overlap:	10
Similarity score:	0.0459305

Alignment:

```
CCGGAAGTGVV
GCGGACGTTV-
```

Original motif Consensus sequence: CCGGAAGTGVV

Reverse complement motif Consensus sequence: VVCACTTCCGG

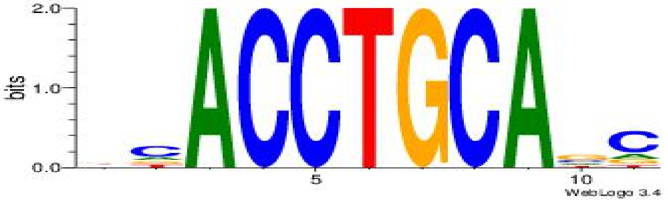


Dataset #:	4
Motif ID:	40
Motif name:	kcACCTGCAgc
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif

Direction: Forward
Position number: 1
Number of overlap: 10
Similarity score: 0.0778314

Alignment:
BCACCTGCABC
BAACGTCCGC-

Original motif Consensus sequence: BCACCTGCABC

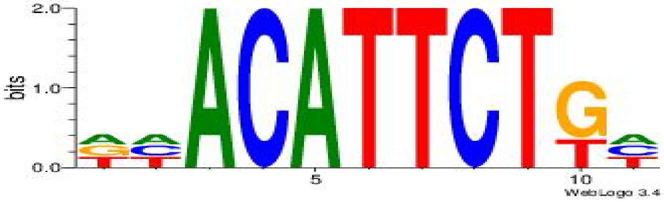


Reverse complement motif Consensus sequence: GBTGCAGGTGB

Dataset #: 4
Motif ID: 44
Motif name: dhACATTCTkh
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 10
Similarity score: 0.0794339

Alignment:
DHACATTCTGH
BAACGTCCGC-

Original motif Consensus sequence: DHACATTCTGH



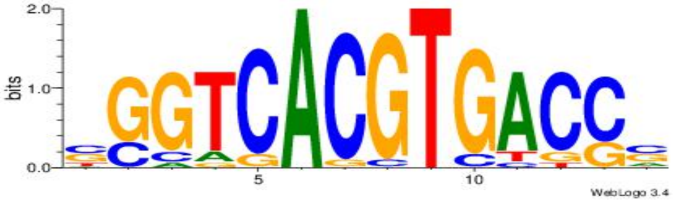
Reverse complement motif Consensus sequence: HCAGAATGTHD

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

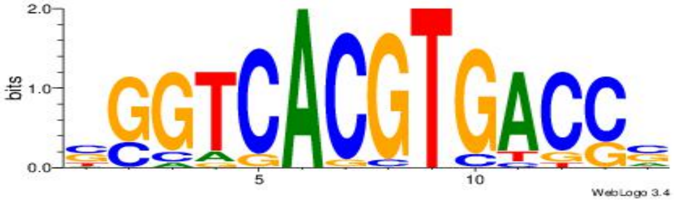
Alignment:

```
SGGTCACGTGACCS
---BAACGTCCGC-
```

Original motif Consensus sequence: SGGTCACGTGACCS



Reverse complement motif Consensus sequence: SGGTCACGTGACC



Dataset #: 5

Motif ID: 50

Motif name: TFF11

Matching format of first motif: Original Motif

Matching format of second motif: Reverse Complement

Direction: Backward

Position number: 4

Number of overlap: 10

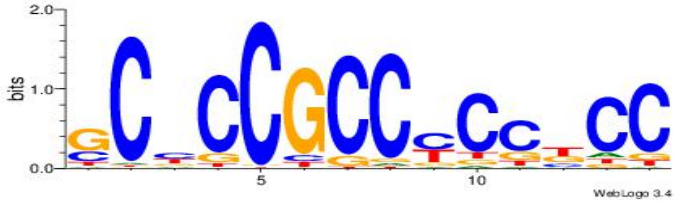
Similarity score: 0.0861006

Alignment:

```
GCVCCGCCMCCYCC
-BAACGTCCGC---
```

Original motif Consensus sequence: GGMGGRGGCGGVGC

Reverse complement motif Consensus sequence: GCVCCGCCMCCYC



Dataset #: 5

Motif ID: 54

Motif name: TFM12

Matching format of first motif: Original Motif

Matching format of second motif: Original Motif

Direction: Backward

Position number: 6

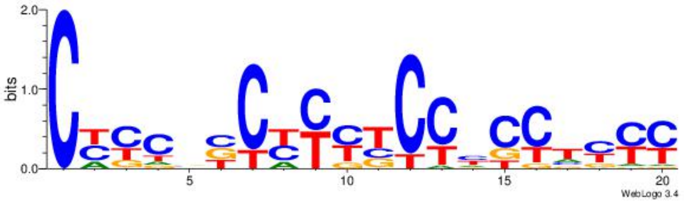
Number of overlap: 10

Similarity score:	0.0871006

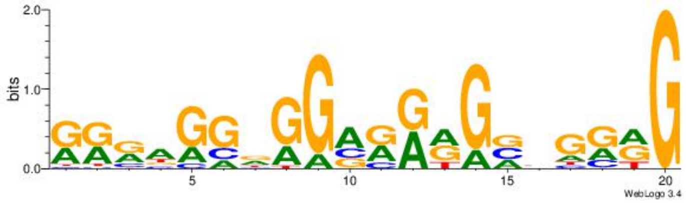
Alignment:

```
CYYCBBCYYYTCCHCCTYYY
-----BAACGTCCGC-----
```

Original motif Consensus sequence: CYYCBBCYYYTCCHCCTYYY



Reverse complement motif Consensus sequence: KKKAGGDGGAKKMGBBGKMG



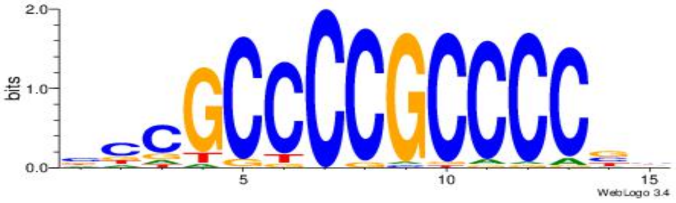
Dataset #:	4
Motif ID:	38
Motif name:	cccGCCCCGCCCCsb
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	10
Similarity score:	0.0877229

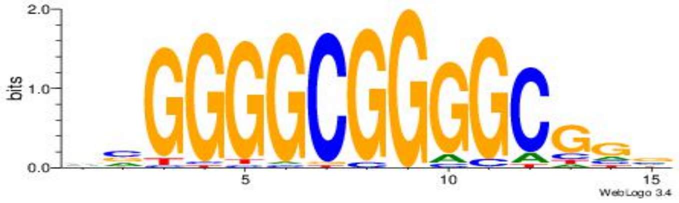
Alignment:

```
BCCGCCCCGCCCCBB
BAACGTCCGC-----
```

Original motif Consensus sequence: BCCGCCCCGCCCCBB

Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB



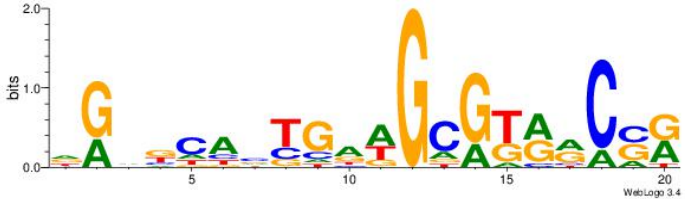


Dataset #:	3
Motif ID:	31
Motif name:	Pax5
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	10
Number of overlap:	10
Similarity score:	0.0877672

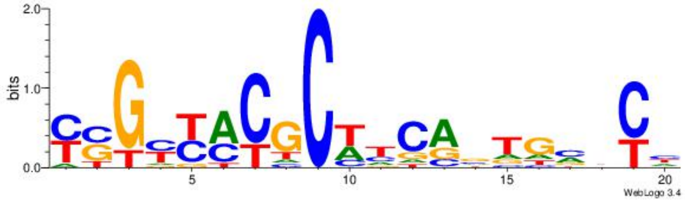
Alignment:

```
MSGKKRCGCWDCABTGBBCD
-GCGGACGTTV---------
```

Original motif Consensus sequence: DGVBCABTGDWGCGKRRCSR



Reverse complement motif Consensus sequence:
MSGKKRCGCWDCABTGBBCD



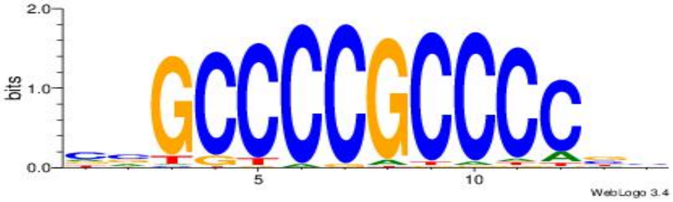
Dataset #:	4

Motif ID:	36
Motif name:	csGCCCCGCCCCsc
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	4
Number of overlap:	10
Similarity score:	0.0884513

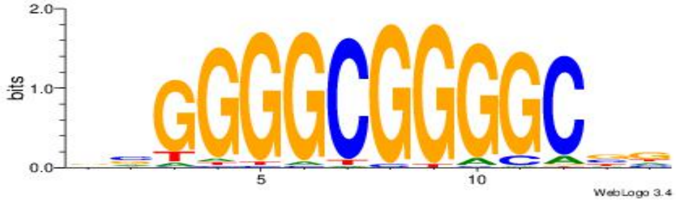
Alignment:

```
HVGCCCCGCCCCBB
---BAACGTCCGC-
```

Original motif Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGC

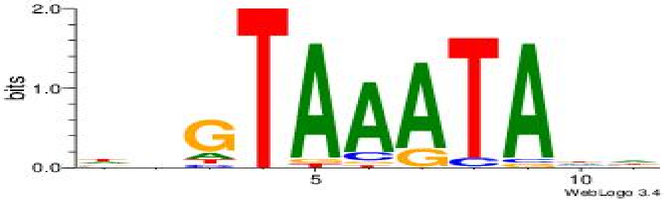


Dataset #:	4
Motif ID:	45
Motif name:	wbgTAAATAww
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2
Number of overlap:	10
Similarity score:	0.0893149

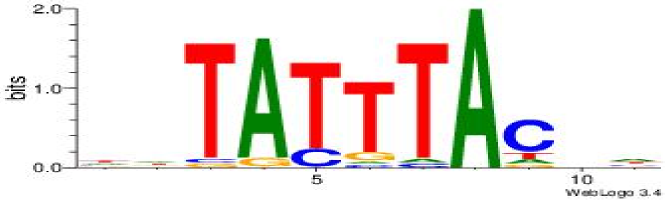
Alignment:

```
DBGTAAATAHD
GCGGACGTTV-
```

Original motif Consensus sequence: DBGTAAATAHD



Reverse complement motif Consensus sequence: DHTATTTACBD



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

Original motif Consensus sequence: DGGGYGKGGC

Reverse complement motif Consensus sequence: GCCYCMCCCD

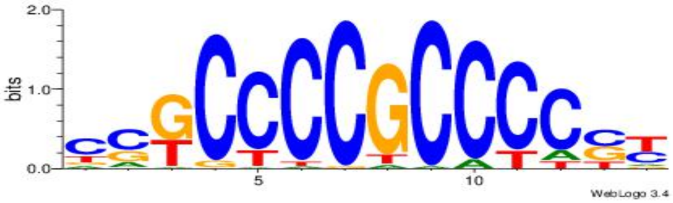
Best Matches for Motif ID 27 (Highest to Lowest)

Dataset #:	2
Motif ID:	7
Motif name:	Motif 7
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	3

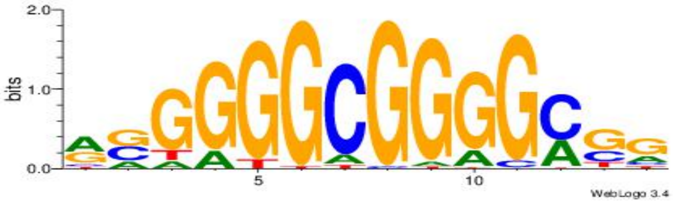
Number of overlap: 10
Similarity score: 0.0152457

Alignment:
CSKCCCCGCCCCSY
--GCCYCMCCCD--

Original motif Consensus sequence: CSKCCCCGCCCCSY



Reverse complement motif Consensus sequence: MSGGGGCGGGGY

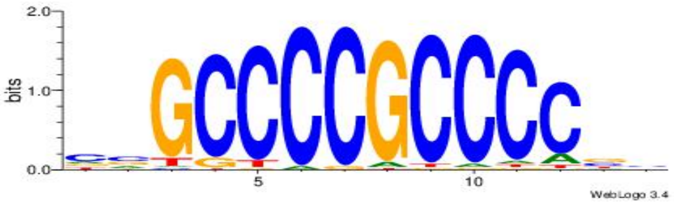


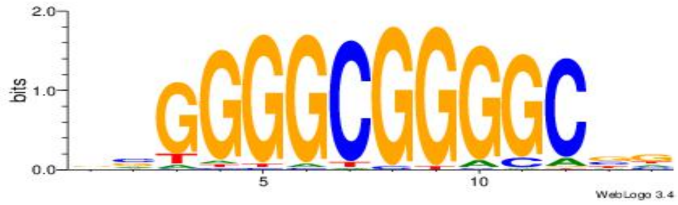
Dataset #: 4
Motif ID: 36
Motif name: csGCCCCGCCCCsc
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 3
Number of overlap: 10
Similarity score: 0.0160185

Alignment:
BBGGGGCGGGGCVD
--DGGGYGKGGC--

Original motif Consensus sequence: HVGCCCCGCCCCBB

Reverse complement motif Consensus sequence: BBGGGGCGGGGC



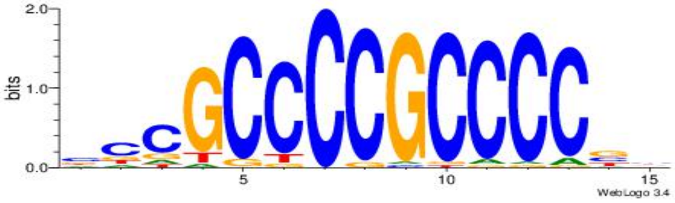


Dataset #:	4
Motif ID:	38
Motif name:	cccGCCCCGCCCCsb
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	3
Number of overlap:	10
Similarity score:	0.0194893

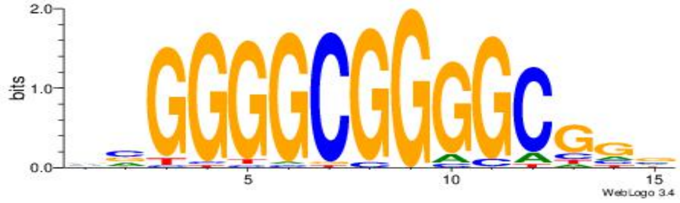
Alignment:

```
BBGGGGCGGGGCGGB
--DGGGYGKGGC---
```

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB



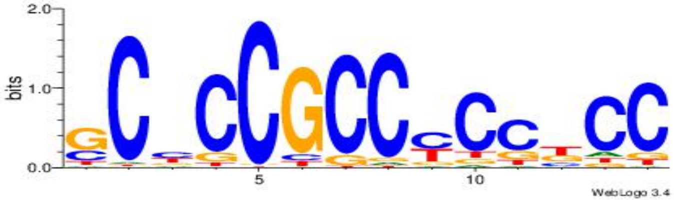
Dataset #:	5

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

Alignment:
```
GGMGGRGGCGGVGC
----DGGGYGKGGC
```

Original motif Consensus sequence: GGMGGRGGCGGVGC

Reverse complement motif Consensus sequence: GCVCCGCCMCCY

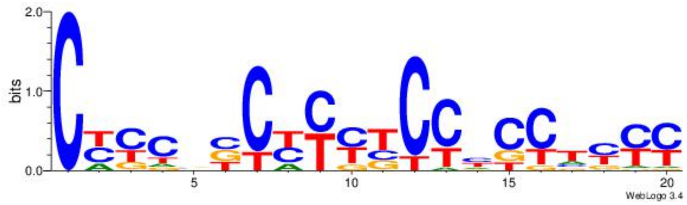


Dataset #: 5
Motif ID: 54
Motif name: TFM12
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 7
Number of overlap: 10
Similarity score: 0.0556427

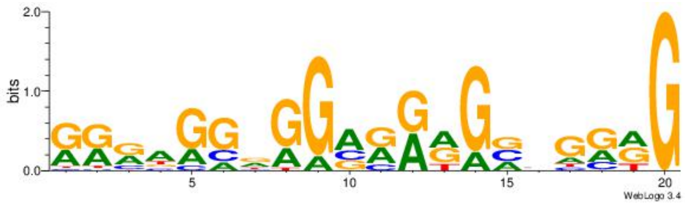
Alignment:

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

Original motif Consensus sequence: CYYCBBCYYYTCCHCCTYYY



Reverse complement motif Consensus sequence: KKKAGGDGGAKKMGBBGKMG



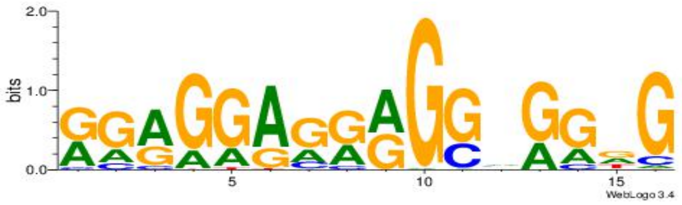
Dataset #:	5
Motif ID:	51
Motif name:	TFM2
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	5
Number of overlap:	10
Similarity score:	0.0606033

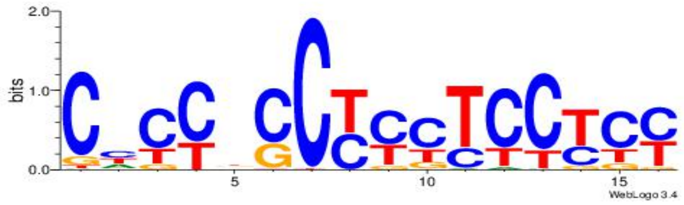
Alignment:

```
CHCCBCCKMCTCCKCM
----GCCYCMCCCD--
```

Original motif Consensus sequence: RGRGGAGRRGGHGGDG

Reverse complement motif Consensus sequence: CHCCBCCKMCTCCKCM



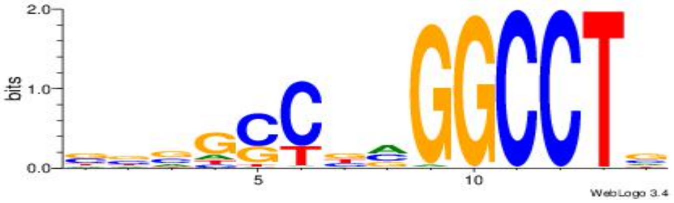


Dataset #:	3
Motif ID:	22
Motif name:	Zfx
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	4
Number of overlap:	10
Similarity score:	0.0623591

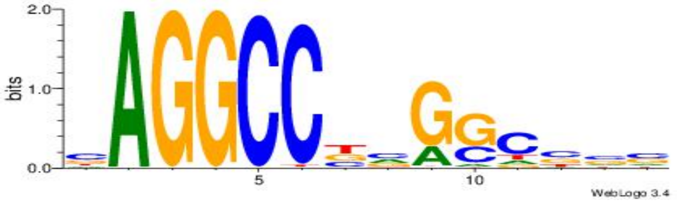
Alignment:

```
BBVGCCBVGGCCTV
-GCCYCMCCCD---
```

Original motif Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif Consensus sequence: VAGGCCBBGGCV

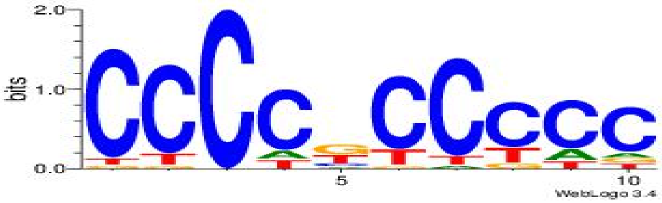


Dataset #:	3
Motif ID:	24

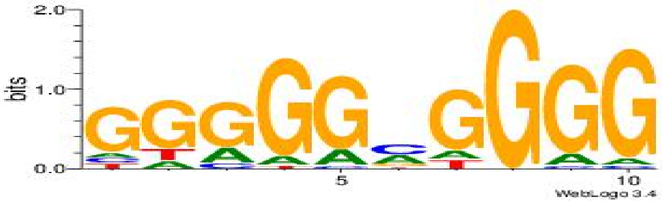
Motif name: SP1
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 10
Similarity score: 0.0663136

Alignment:
GGGGGYGGGG
DGGGYGKGGC

Original motif Consensus sequence: CCCCKCCCCC



Reverse complement motif Consensus sequence: GGGGGYGGGG



Dataset #: 3
Motif ID: 34
Motif name: Myc
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 10
Similarity score: 0.0686848

Alignment:
VGCACGTGGH
DGGGYGKGGC

Original motif Consensus sequence: VGCACGTGGH

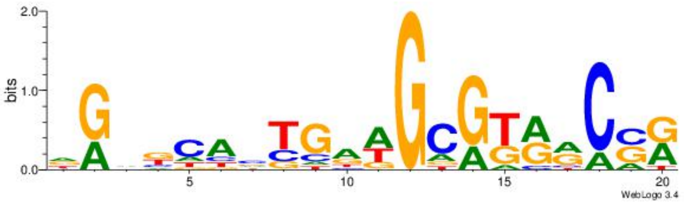
Reverse complement motif Consensus sequence: DCCACGTGCV

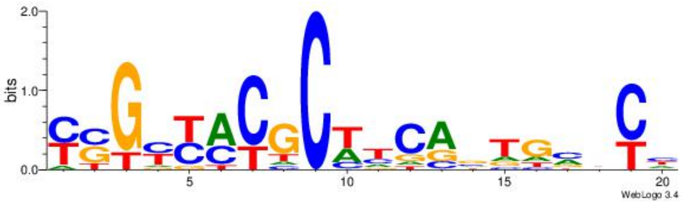
Dataset #:	3
Motif ID:	31
Motif name:	Pax5
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	9
Number of overlap:	10
Similarity score:	0.06956

Alignment:
DGVBCABTGDWGCGKRRCSR
--------DGGGYGKGGC--

Original motif Consensus sequence: DGVBCABTGDWGCGKRRCSR

Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD





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

Original motif Consensus sequence: TTTSGCGC

Reverse complement motif Consensus sequence: GCGCSAAA

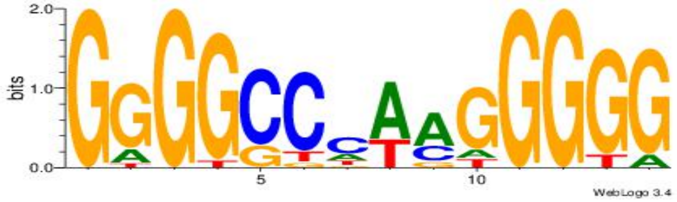
Best Matches for Motif ID 28 (Highest to Lowest)

Dataset #:	3
Motif ID:	30
Motif name:	PLAG1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	8
Similarity score:	0.0568827

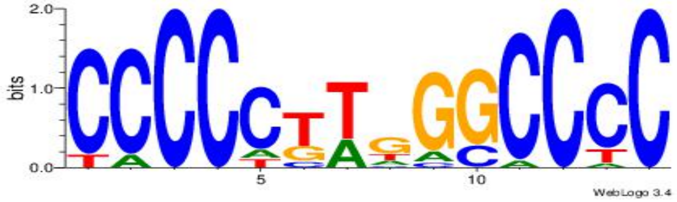
Alignment:

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

Original motif   Consensus sequence: GGGGCCCAAGGGGG



Reverse complement motif   Consensus sequence: CCCCCTTGGGCCC



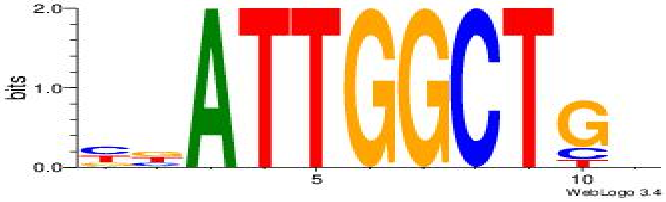
Dataset #:	4
Motif ID:	39
Motif name:	kCAGCCAATmr
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	3
Number of overlap:	8
Similarity score:	0.0624791

Alignment:

```
DCAGCCAATVR
-GCGCSAAA--
```

Original motif   Consensus sequence: DCAGCCAATVR

Reverse complement motif   Consensus sequence: MBATTGGCTGH



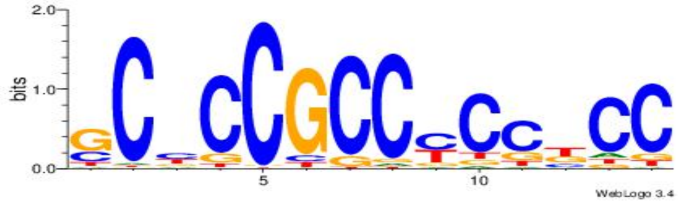
Dataset #: 5
Motif ID: 50
Motif name: TFF11
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 4
Number of overlap: 8
Similarity score: 0.0781129

Alignment:

```
GCVCCGCCMCCYCC
---GCGCSAAA---
```

Original motif Consensus sequence: GGMGGRGGCGGVGC

Reverse complement motif Consensus sequence: GCVCCGCCMCCYC



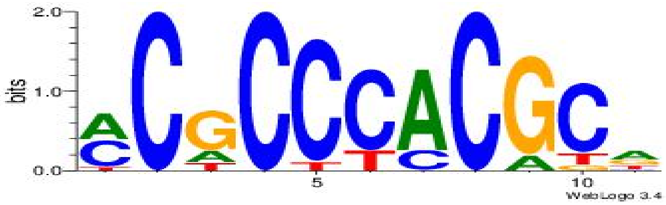
Dataset #: 3
Motif ID: 23
Motif name: Egr1
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 4
Number of overlap: 8

Similarity score: 0.0784105

Alignment:
YCGCCCACGCH
GCGCSAAA---

Original motif Consensus sequence: HGCGTGGGCGK

Reverse complement motif Consensus sequence: YCGCCCACGCH



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

Alignment:
CGGVGCCGCVGC
--GCGCSAAA--

Original motif Consensus sequence: CGGVGCCGCVGC

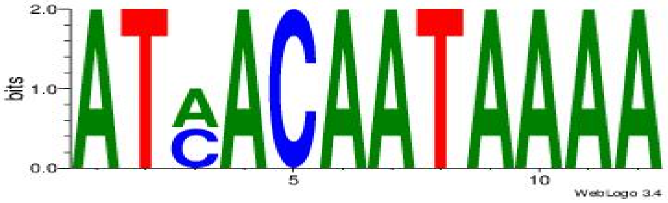
Reverse complement motif Consensus sequence: GCVGCGGCBCCG

Dataset #:	2
Motif ID:	15
Motif name:	Motif 15
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	2
Number of overlap:	8
Similarity score:	0.0836188

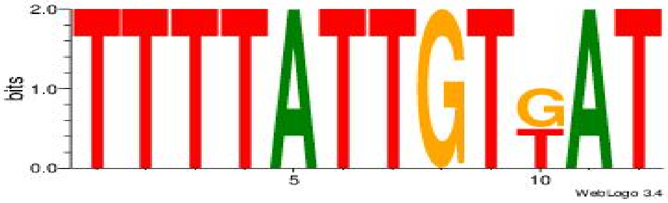
Alignment:

```
TTTTATTGTYAT
---TTTSGCGC-
```

Original motif Consensus sequence: ATMACAATAAAA



Reverse complement motif Consensus sequence: TTTTATTGTYAT



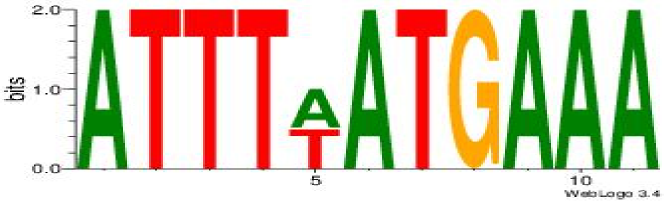
Dataset #:	2
Motif ID:	11

Motif name:	Motif 11
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	2
Number of overlap:	8
Similarity score:	0.0836188

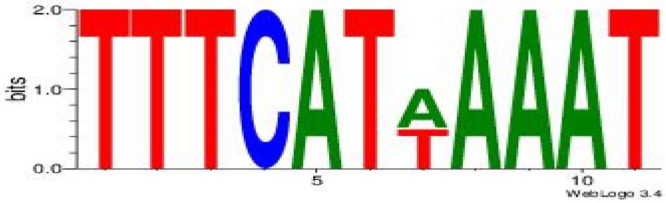
Alignment:

```
TTTCATWAAAT
--GCGCSAAA-
```

Original motif Consensus sequence: ATTTWATGAAA



Reverse complement motif Consensus sequence: TTTCATWAAAT

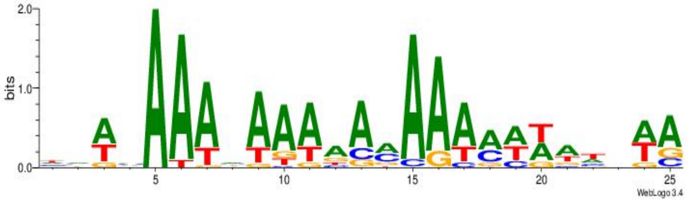


Dataset #:	5
Motif ID:	56
Motif name:	TFM11
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	19
Number of overlap:	7
Similarity score:	0.569963

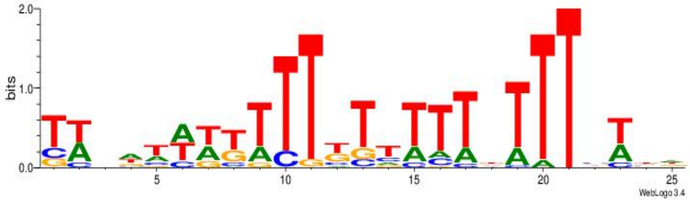
Alignment:

```
-HDWVAAAHAAAAAMAAAMWWWHBWA
GCGCSAAA------------------
```

Original motif Consensus sequence:
HDWVAAAHAAAAAMAAAMWWWHBWA



Reverse complement motif Consensus sequence:
TWVHWWWYTTTYTTTTTHTTTVWBH



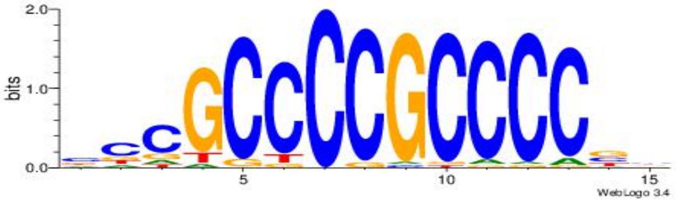
Dataset #: 4
Motif ID: 38
Motif name: cccGCCCCGCCCCsb
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 9
Number of overlap: 7
Similarity score: 0.571005

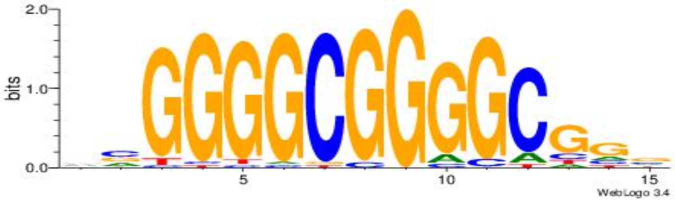
Alignment:

```
-BBGGGGCGGGGCGGB
TTTSGCGC--------
```

Original motif Consensus sequence: BCCGCCCCGCCCCBB

Reverse complement motif Consensus sequence:
BBGGGGCGGGGCGGB





Dataset #:	5
Motif ID:	48
Motif name:	TFW3
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	4
Number of overlap:	7
Similarity score:	0.571119

Alignment:

```
CGGCYBCGCG-
---TTTSGCGC
```

Original motif Consensus sequence: CGGCYBCGCG

Reverse complement motif Consensus sequence: CGCGBMGCCG

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

Original motif Consensus sequence: VBACGTGV

Reverse complement motif Consensus sequence: VCACGTBV

Best Matches for Motif ID 29 (Highest to Lowest)

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

Alignment:

```
GCCACGTGSD
-VBACGTGV-
```

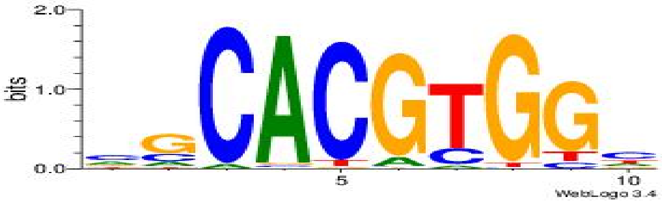
Original motif Consensus sequence: HSCACGTGGC

Reverse complement motif Consensus sequence: GCCACGTGSD

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

Alignment:
```
DCCACGTGCV
-VBACGTGV-
```

Original motif Consensus sequence: VGCACGTGGH



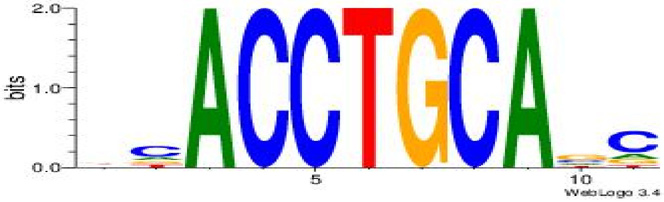
Reverse complement motif Consensus sequence: DCCACGTGCV

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

Similarity score: 0.0295473

Alignment:
GBTGCAGGTGB
---VCACGTBV

Original motif Consensus sequence: BCACCTGCABC



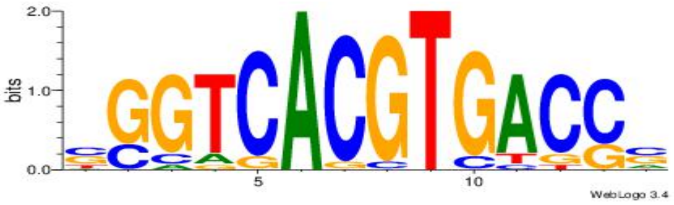
Reverse complement motif Consensus sequence: GBTGCAGGTGB

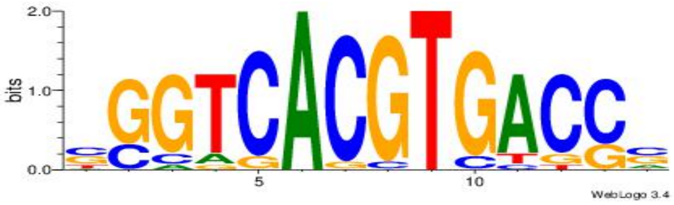
Dataset #: 4
Motif ID: 42
Motif name: sSGTCACGTGACSs
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 4
Number of overlap: 8
Similarity score: 0.0314837

Alignment:
SGGTCACGTGACCS
---VCACGTBV---

Original motif Consensus sequence: SGGTCACGTGACCS

Reverse complement motif Consensus sequence: SGGTCACGTGACC





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

Alignment:

```
GCGGACGTTV
--VCACGTBV
```

Original motif Consensus sequence: BAACGTCCGC

Reverse complement motif Consensus sequence: GCGGACGTTV

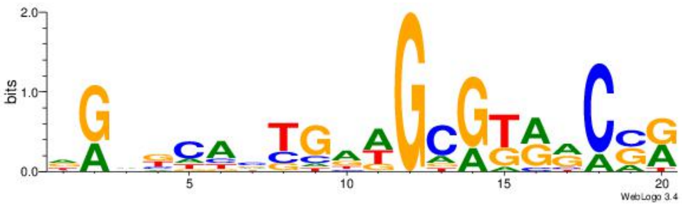
Dataset #:	3
Motif ID:	31

Motif name: Pax5
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 8
Number of overlap: 8
Similarity score: 0.0556891

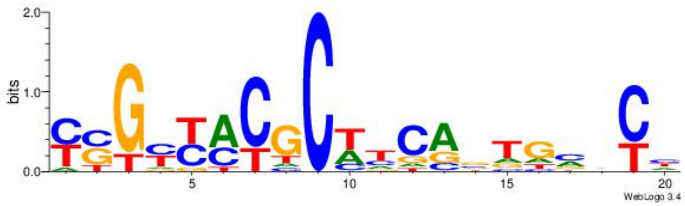
Alignment:

```
MSGKKRCGCWDCABTGBBCD
-----VCACGTBV-------
```

Original motif Consensus sequence: DGVBCABTGDWGCGKRRCSR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD

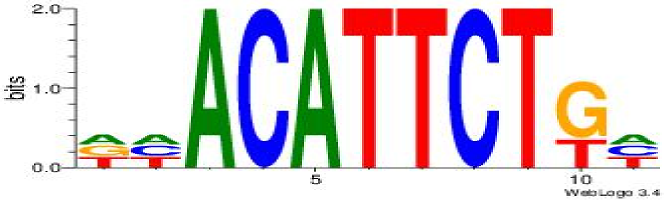


Dataset #: 4
Motif ID: 44
Motif name: dhACATTCTkh
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 4
Number of overlap: 8
Similarity score: 0.0640024

Alignment:

```
DHACATTCTGH
VCACGTBV---
```

Original motif   Consensus sequence: DHACATTCTGH



Reverse complement motif   Consensus sequence: HCAGAATGTHD

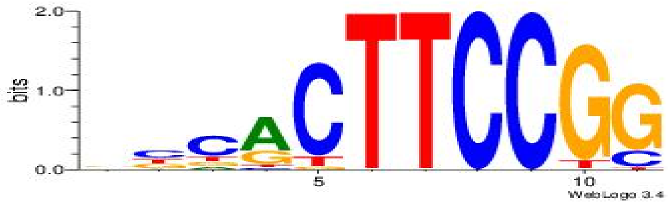
Dataset #:	3
Motif ID:	35
Motif name:	GABPA
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2
Number of overlap:	8
Similarity score:	0.0648153

Alignment:

```
CCGGAAGTGVV
--VCACGTBV-
```

Original motif   Consensus sequence: CCGGAAGTGVV

Reverse complement motif   Consensus sequence: VVCACTTCCGG



Dataset #:	5
Motif ID:	47
Motif name:	TFW2
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	8
Similarity score:	0.0660185

Alignment:

```
CCGCGCGS
VBACGTGV
```

Original motif   Consensus sequence: SCGCGCGG

Reverse complement motif   Consensus sequence: CCGCGCGS

Dataset #:	5
Motif ID:	50

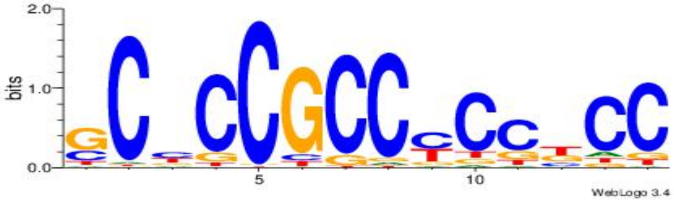
Motif name:	TFF11
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	8
Similarity score:	0.067219

Alignment:

```
GCVCCGCCMCCYCC
------VCACGTBV
```

Original motif Consensus sequence: GGMGGRGGCGGVGC

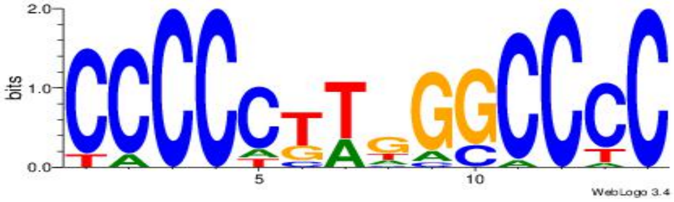
Reverse complement motif Consensus sequence: GCVCCGCCMCCYC



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

Original motif Consensus sequence: GGGGCCCAAGGGGG

Reverse complement motif Consensus sequence: CCCCCTTGGGCCC



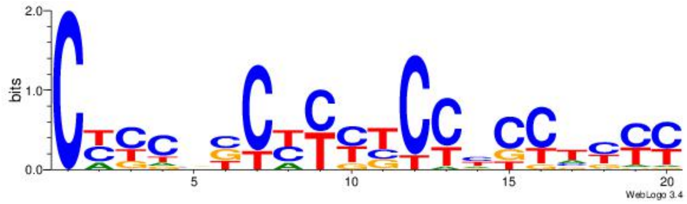
Best Matches for Motif ID 30 (Highest to Lowest)

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

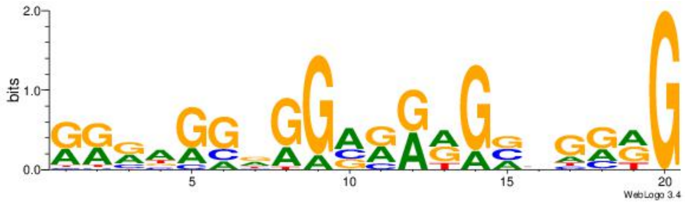
Alignment:

CYYCBBCYYYTCCHCCTYYY
-CCCCCTTGGGCCCC-----

Original motif Consensus sequence: CYYCBBCYYYTCCHCCTYYY



Reverse complement motif Consensus sequence: KKKAGGDGGAKKMGBBGKMG



Dataset #:	5
Motif ID:	51
Motif name:	TFM2
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	3

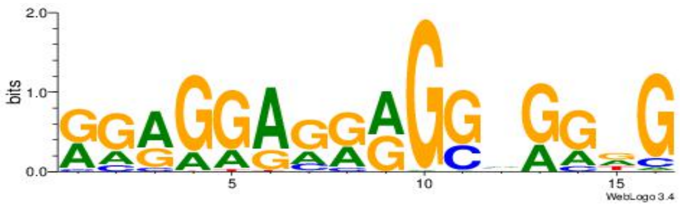
Number of overlap: 14

Similarity score: 0.0880716

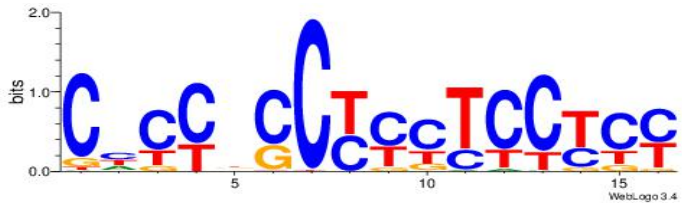
Alignment:

```
CHCCBCCKMCTCCKCM
--CCCCCTTGGGCCCC
```

Original motif Consensus sequence: RGRGGAGRRGGHGGDG



Reverse complement motif Consensus sequence: CHCCBCCKMCTCCKCM



Dataset #: 3

Motif ID: 22

Motif name: Zfx

Matching format of first motif: Original Motif

Matching format of second motif: Reverse Complement

Direction: Forward

Position number: 1

Number of overlap: 14

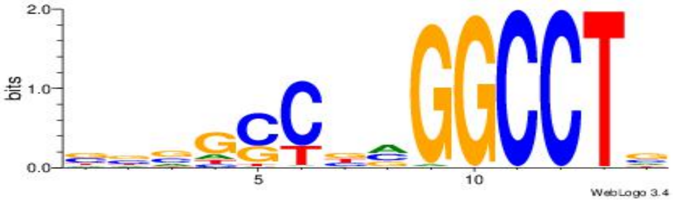
Similarity score: 0.0886295

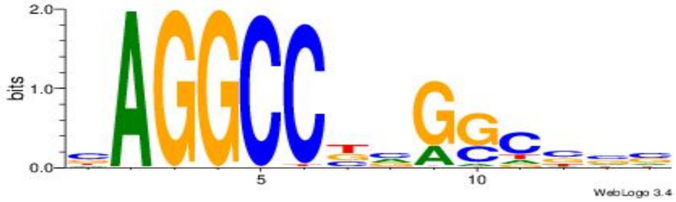
Alignment:

```
VAGGCCBBGGCVBB
GGGGCCCAAGGGGG
```

Original motif Consensus sequence: BBVGCCBVGGCCTV

Reverse complement motif Consensus sequence: VAGGCCBBGGCVB



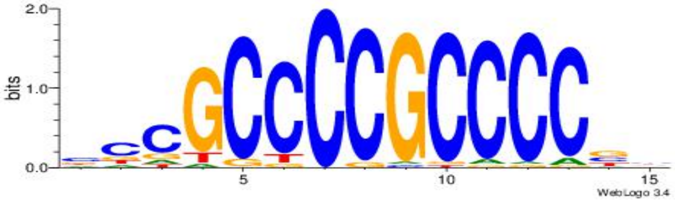


Dataset #:	4
Motif ID:	38
Motif name:	cccGCCCCGCCCCsb
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2
Number of overlap:	14
Similarity score:	0.0904945

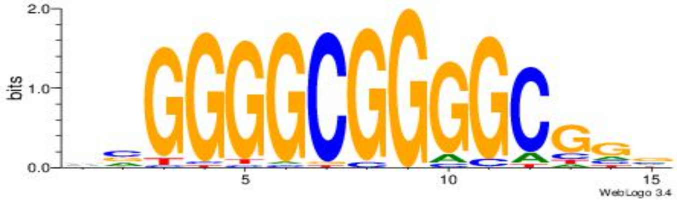
Alignment:

```
BCCGCCCCGCCCCBB
CCCCCTTGGGCCCC-
```

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB



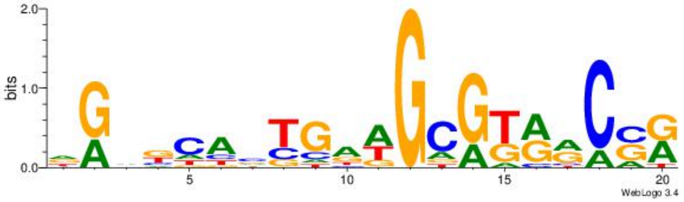
Dataset #: 3

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

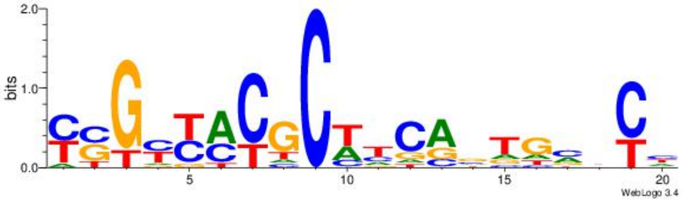
Alignment:

```
DGVBCABTGDWGCGKRRCSR
GGGGCCCAAGGGGG------
```

Original motif   Consensus sequence: DGVBCABTGDWGCGKRRCSR



Reverse complement motif   Consensus sequence: MSGKKRCGCWDCABTGBBCD



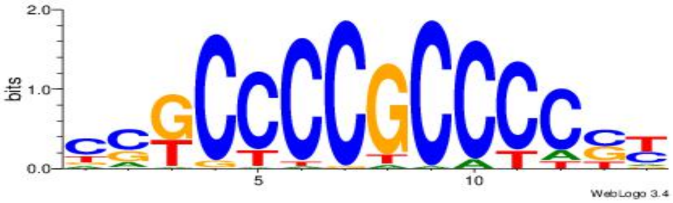
Dataset #: 2
Motif ID: 7
Motif name: Motif 7
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 2
Number of overlap: 13

Similarity score:	0.588053

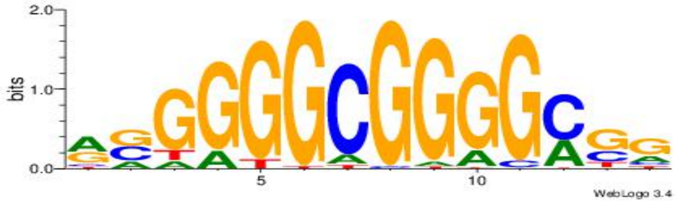
Alignment:

```
-MSGGGGCGGGGYSG
GGGGCCCAAGGGGG-
```

Original motif Consensus sequence: CSKCCCCGCCCCSY



Reverse complement motif Consensus sequence: MSGGGGCGGGGY



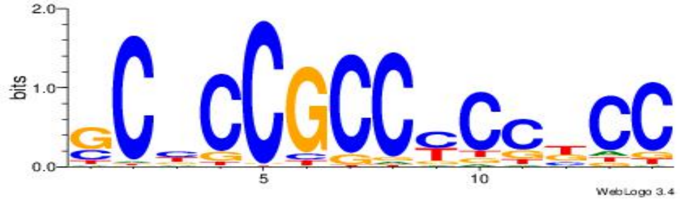
Dataset #:	5
Motif ID:	50
Motif name:	TFF11
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	2
Number of overlap:	13
Similarity score:	0.589357

Alignment:

```
GCVCCGCCMCCYCC-
-CCCCCTTGGGCCCC
```

Original motif Consensus sequence: GGMGGRGGCGGVGC

Reverse complement motif Consensus sequence: GCVCCGCCMCCYC

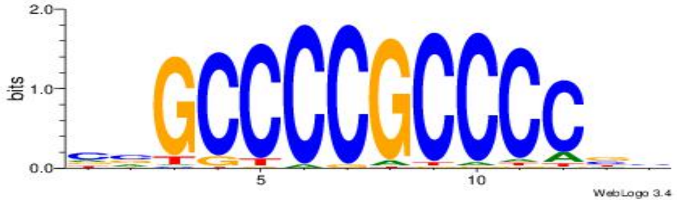


Dataset #:	4
Motif ID:	36
Motif name:	csGCCCCGCCCCsc
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2
Number of overlap:	13
Similarity score:	0.595227

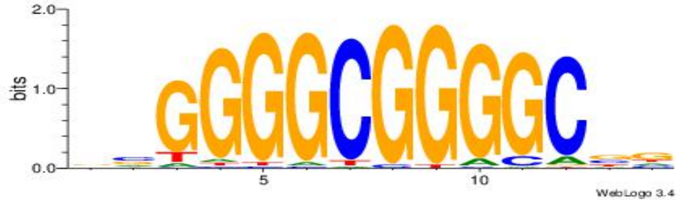
Alignment:

```
-HVGCCCCGCCCCBB
CCCCCTTGGGCCCC-
```

Original motif Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGC



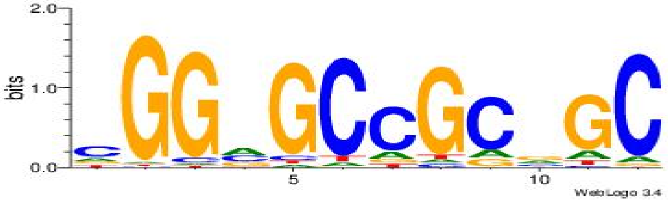
Dataset #:	5
Motif ID:	49

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: 1.09276

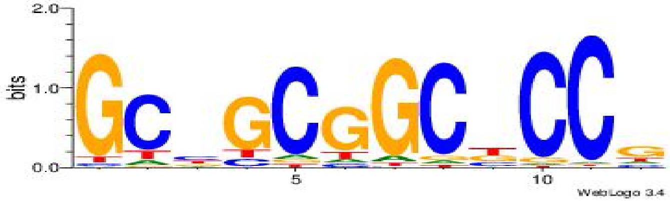
Alignment:

```
CGGVGCCGCVGC--
GGGGCCCAAGGGGG
```

Original motif Consensus sequence: CGGVGCCGCVGC



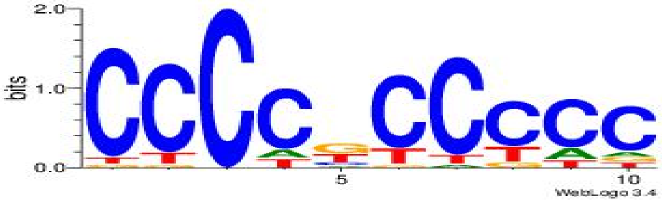
Reverse complement motif Consensus sequence: GCVGCGGCBCCG



Dataset #: 3
Motif ID: 24
Motif name: SP1
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 10
Similarity score: 2.07807

Alignment:
```
----GGGGGYGGGG
GGGGCCCAAGGGGG
```

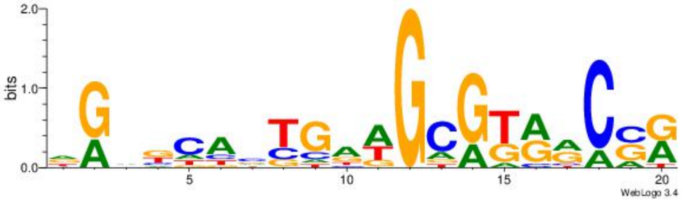
Original motif Consensus sequence: CCCCKCCCCC



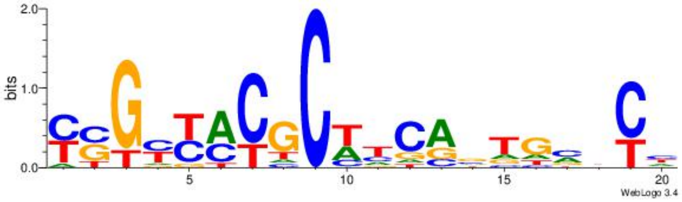
Reverse complement motif Consensus sequence: GGGGGYGGGG

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

Original motif Consensus sequence: DGVBCABTGDWGCGKRRCSR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD



Best Matches for Motif ID 31 (Highest to Lowest)

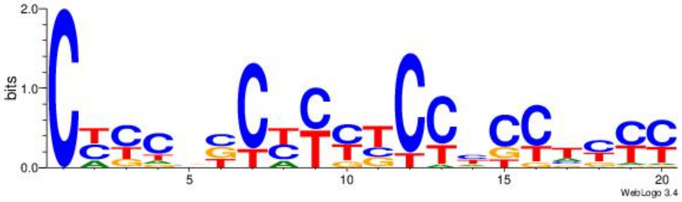
Dataset #:	5
Motif ID:	54
Motif name:	TFM12
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward

Position number: 1
Number of overlap: 20
Similarity score: 0.0373929

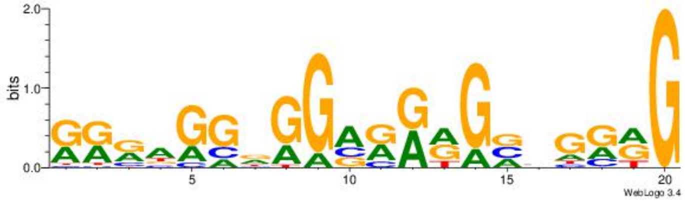
Alignment:

```
KKKAGGDGGAKKMGBBGKMG
DGVBCABTGDWGCGKRRCSR
```

Original motif   Consensus sequence: CYYCBBCYYYTCCHCCTYYY



Reverse complement motif   Consensus sequence: KKKAGGDGGAKKMGBBGKMG

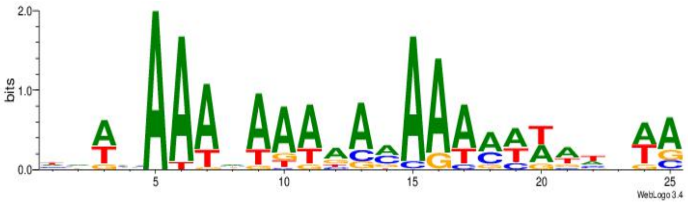


Dataset #: 5
Motif ID: 56
Motif name: TFM11
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 6
Number of overlap: 20
Similarity score: 0.0546306

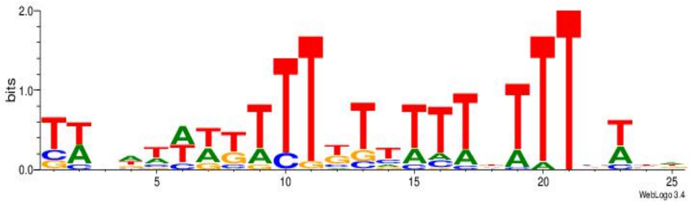
Alignment:

```
HDWVAAAHAAAAAMAAAMWWWHBWA
DGVBCABTGDWGCGKRRCSR-----
```

Original motif   Consensus sequence: HDWVAAAHAAAAAMAAAMWWWHBWA



Reverse complement motif   Consensus sequence: TWVHWWWYTTTYTTTTTHTTTVWBH

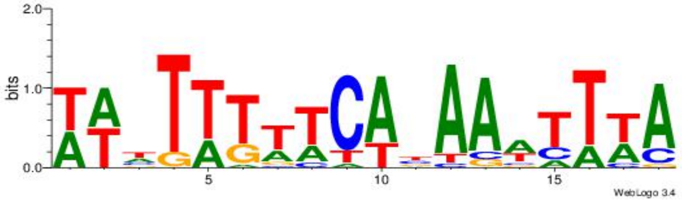


Dataset #:	5
Motif ID:	53
Motif name:	TFM3
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	2
Number of overlap:	17
Similarity score:	1.5457

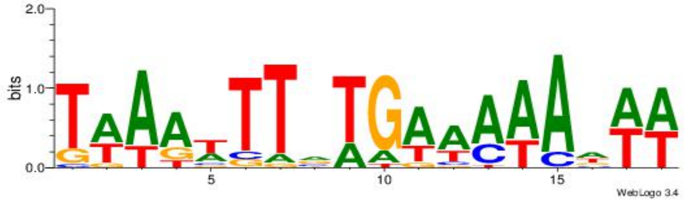
Alignment:

```
TWAAWTTVTGAAAAAHWW---
-DGVBCABTGDWGCGKRRCSR
```

Original motif   Consensus sequence: WWHTTTTTCABAAWTTWA



Reverse complement motif   Consensus sequence: TWAAWTTVTGAAAAAHWW

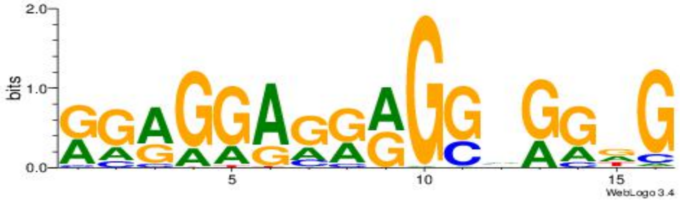


Dataset #:	5
Motif ID:	51
Motif name:	TFM2
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	16
Similarity score:	2.0519

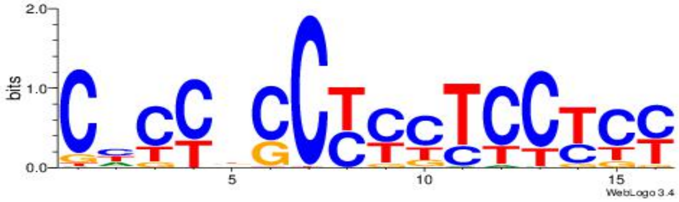
Alignment:

```
RGRGGAGRRGGHGGDG----
MSGKKRCGCWDCABTGBBCD
```

Original motif Consensus sequence: RGRGGAGRRGGHGGDG



Reverse complement motif Consensus sequence: CHCCBCCKMCTCCKCM



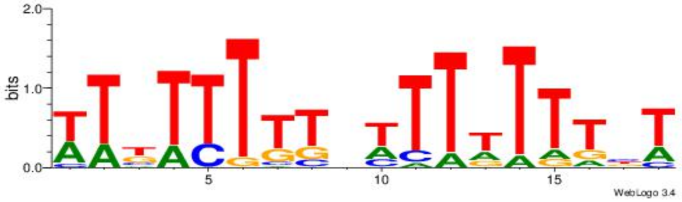
Dataset #:	5
Motif ID:	52
Motif name:	TFM1
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	3

Number of overlap:	16
Similarity score:	2.05456

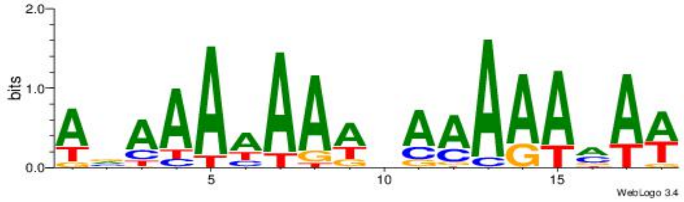
Alignment:

```
ABAAAAAAWHAAAAARAW----
--DGVBCABTGDWGCGKRRCSR
```

Original motif Consensus sequence: WTKTTTTTHWTTTTTTBT



Reverse complement motif Consensus sequence: ABAAAAAAWHAAAAARAW

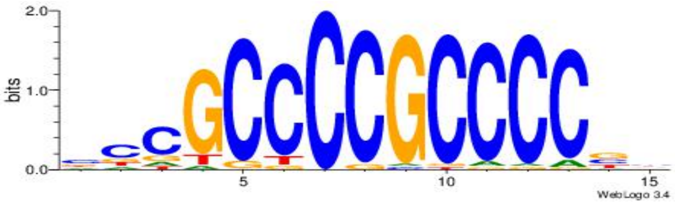


Dataset #:	4
Motif ID:	38
Motif name:	cccGCCCCGCCCCsb
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	15
Similarity score:	2.54483

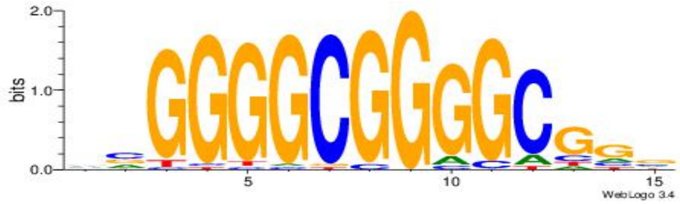
Alignment:

```
BBGGGGCGGGGCGGB-----
MSGKKRCGCWDCABTGBBCD
```

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB

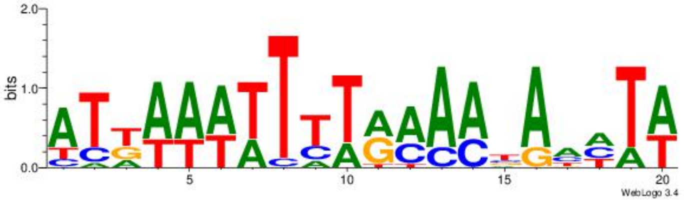


Dataset #: 5
Motif ID: 55
Motif name: TFM13
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 6
Number of overlap: 15
Similarity score: 2.55478

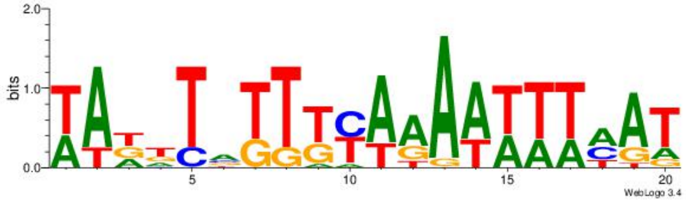
Alignment:

```
WAHHTVTTYKAAAAWTTRAT-----
-----MSGKKRCGCWDCABTGBBCD
```

Original motif Consensus sequence: ATKAAWTTTTRMAABAHHTW



Reverse complement motif Consensus sequence: WAHHTVTTYKAAAAWTTRAT

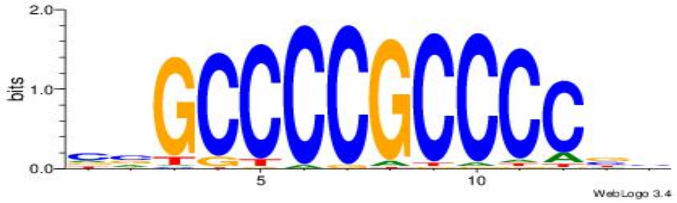


Dataset #:	4
Motif ID:	36
Motif name:	csGCCCCGCCCCsc
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	14
Similarity score:	3.0203

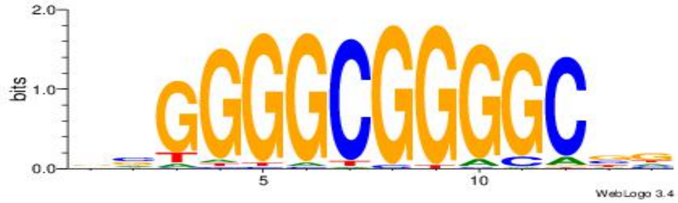
Alignment:

```
------BBGGGGCGGGGCVD
DGVBCABTGDWGCGKRRCSR
```

Original motif   Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif   Consensus sequence: BBGGGGCGGGGC

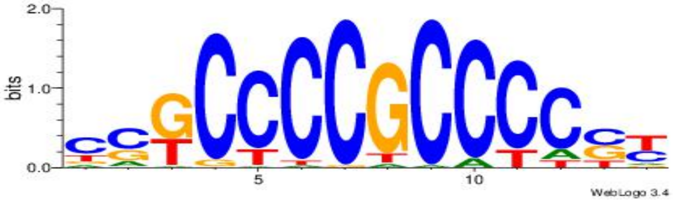


Dataset #:	2
Motif ID:	7
Motif name:	Motif 7
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	14

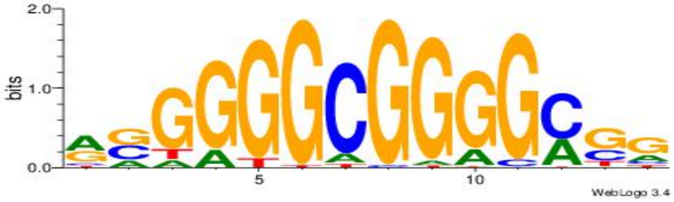
Similarity score: 3.02361

Alignment:
------CSKCCCCGCCCCSY
MSGKKRCGCWDCABTGBBCD

Original motif Consensus sequence: CSKCCCCGCCCCSY



Reverse complement motif Consensus sequence: MSGGGGCGGGGY

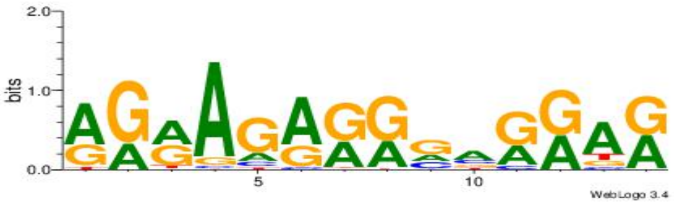


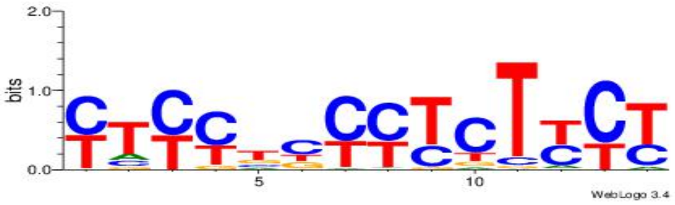
Dataset #: 2
Motif ID: 2
Motif name: Motif 2
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 14
Similarity score: 3.02394

Alignment:
------MTMMTCMMTCTKCK
MSGKKRCGCWDCABTGBBCD

Original motif Consensus sequence: RGRAGARRGARRAR

Reverse complement motif Consensus sequence: MTMMTCMMTCTK





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

Original motif Consensus sequence: YGCGTG

Reverse complement motif Consensus sequence: CACGCM

Best Matches for Motif ID 32 (Highest to Lowest)

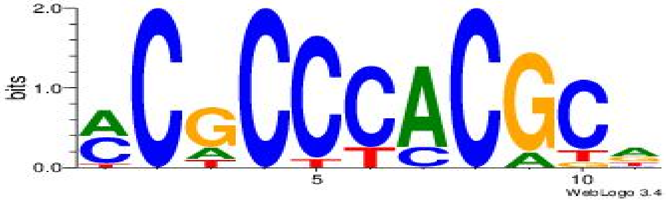
Dataset #:	3
Motif ID:	23
Motif name:	Egr1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	6
Similarity score:	0

Alignment:

```
YCGCCCACGCH
-----CACGCM
```

Original motif Consensus sequence: HGCGTGGGCGK

Reverse complement motif Consensus sequence: YCGCCCACGCH



Dataset #:	3
Motif ID:	29
Motif name:	HIF1AARNT
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	6
Similarity score:	0.0112447

Alignment:

```
VBACGTGV
-YGCGTG-
```

Original motif Consensus sequence: VBACGTGV

Reverse complement motif Consensus sequence: VCACGTBV

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

Alignment:

```
GCCACGTGSD
--YGCGTG--
```

Original motif Consensus sequence: HSCACGTGGC

Reverse complement motif Consensus sequence: GCCACGTGSD

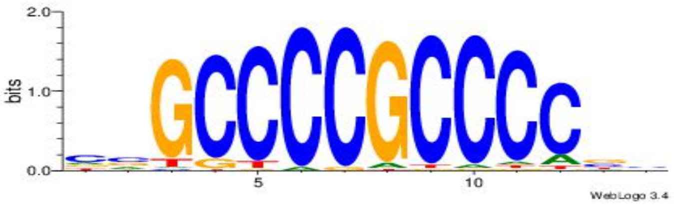
Dataset #: 4
Motif ID: 36
Motif name: csGCCCCGCCCCsc
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 5
Number of overlap: 6

Similarity score: 0.0396403

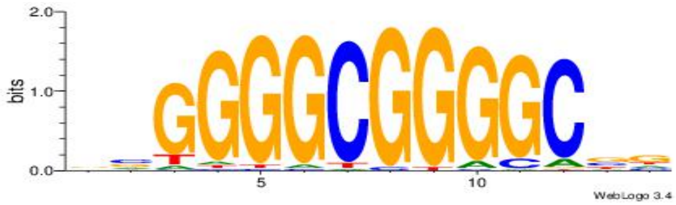
Alignment:

```
HVGCCCCGCCCCBB
----CACGCM----
```

Original motif Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGC



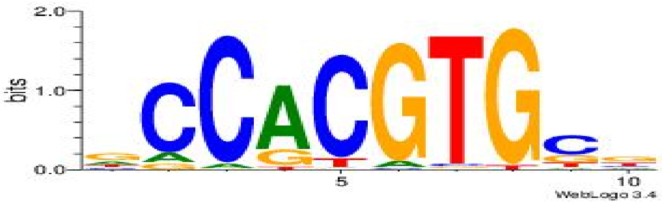
Dataset #:	3
Motif ID:	34
Motif name:	Myc
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	3
Number of overlap:	6
Similarity score:	0.0399214

Alignment:

```
DCCACGTGCV
--YGCGTG--
```

Original motif Consensus sequence: VGCACGTGGH

Reverse complement motif Consensus sequence: DCCACGTGCV



Dataset #:	1
Motif ID:	1
Motif name:	Motif 1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	3
Number of overlap:	6
Similarity score:	0.040625

Alignment:

```
GCCCCGCC
--CACGCM
```

Original motif Consensus sequence: GGCGGGGC

Reverse complement motif Consensus sequence: GCCCCGCC

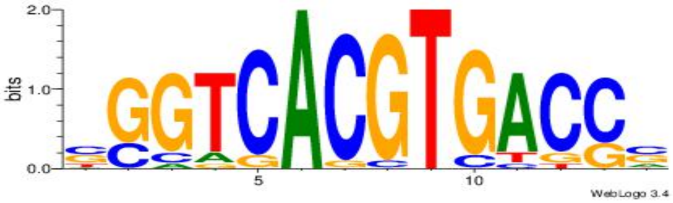
Dataset #:	4
Motif ID:	42

Motif name:	sSGTCACGTGACSs
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	5
Number of overlap:	6
Similarity score:	0.0412037

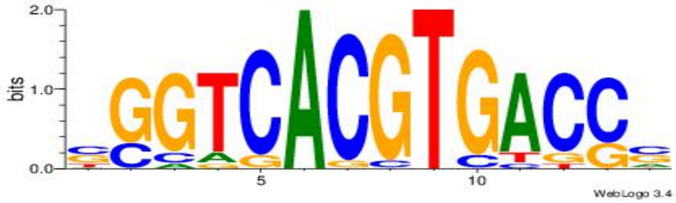
Alignment:

```
SGGTCACGTGACCS
----YGCGTG----
```

Original motif Consensus sequence: SGGTCACGTGACCS



Reverse complement motif Consensus sequence: SGGTCACGTGACC

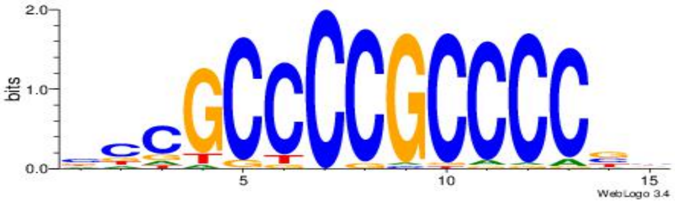


Dataset #:	4
Motif ID:	38
Motif name:	cccGCCCCGCCCCsb
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	6
Number of overlap:	6
Similarity score:	0.0425089

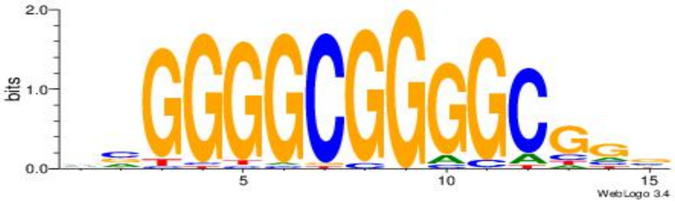
Alignment:

```
BCCGCCCCGCCCCBB
-----CACGCM----
```

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB



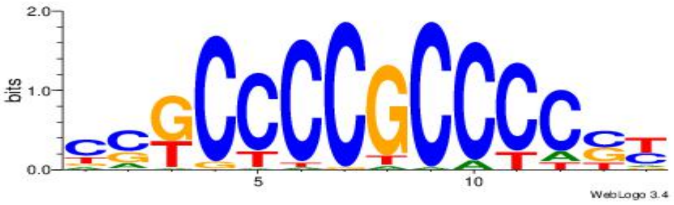
Dataset #:	2
Motif ID:	7
Motif name:	Motif 7
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	5
Number of overlap:	6
Similarity score:	0.0465867

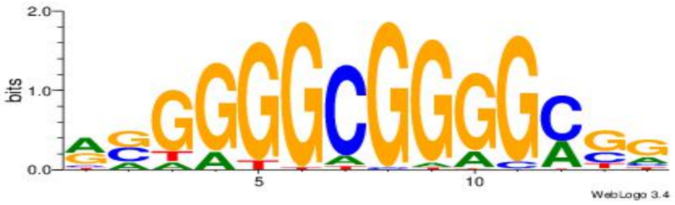
Alignment:

```
MSGGGGCGGGGYSG
----YGCGTG----
```

Original motif Consensus sequence: CSKCCCCGCCCCSY

Reverse complement motif Consensus sequence: MSGGGGCGGGGY





Dataset #: 5
Motif ID: 47
Motif name: TFW2
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 2
Number of overlap: 6
Similarity score: 0.0469722

Alignment:

```
SCGCGCGG
-YGCCGTG-
```

Original motif Consensus sequence: SCGCGCGG

Reverse complement motif Consensus sequence: CCGCGCGS

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

Original motif Consensus sequence: HSCACGTGGC

Reverse complement motif Consensus sequence: GCCACGTGSD

Best Matches for Motif ID 33 (Highest to Lowest)

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

Alignment:

```
DCCACGTGCV
GCCACGTGSD
```

Original motif Consensus sequence: VGCACGTGGH

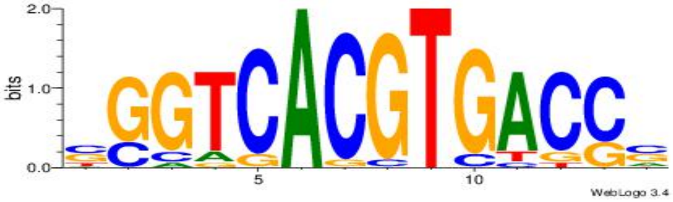
Reverse complement motif Consensus sequence: DCCACGTGCV

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

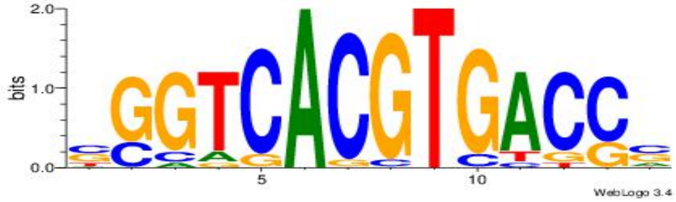
Alignment:

```
SGGTCACGTGACCS
--HSCACGTGGC--
```

Original motif Consensus sequence: SGGTCACGTGACCS



Reverse complement motif Consensus sequence: SGGTCACGTGACC



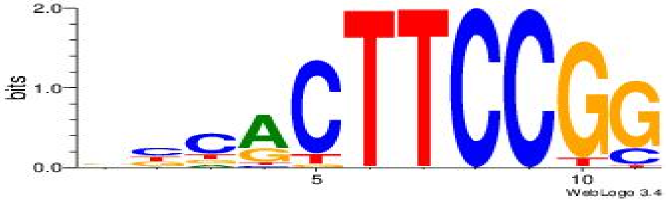
Dataset #:	3
Motif ID:	35
Motif name:	GABPA
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	10

Similarity score: 0.0884396

Alignment:
VVCACTTCCGG
GCCACGTGSD-

Original motif Consensus sequence: CCGGAAGTGVV

Reverse complement motif Consensus sequence: VVCACTTCCGG



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

Alignment:
DGGGYGKGGC
HSCACGTGGC

Original motif Consensus sequence: DGGGYGKGGC

Reverse complement motif Consensus sequence: GCCYCMCCCD

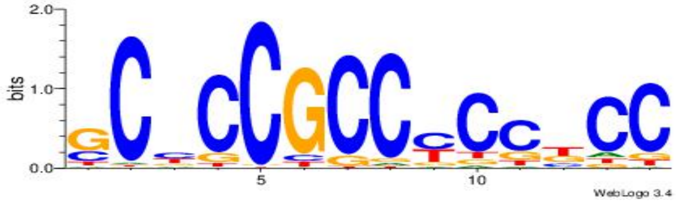
Dataset #:	5
Motif ID:	50
Motif name:	TFF11
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	3
Number of overlap:	10
Similarity score:	0.0895444

Alignment:

```
GGMGGRGGCGGVGC
--HSCACGTGGC--
```

Original motif Consensus sequence: GGMGGRGGCGGVGC

Reverse complement motif Consensus sequence: GCVCCGCCMCCYC



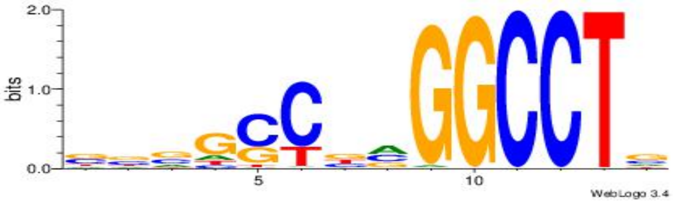
Dataset #:	3
Motif ID:	22

Motif name: Zfx
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 4
Number of overlap: 10
Similarity score: 0.0899944

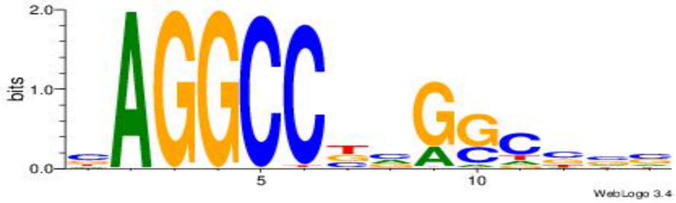
Alignment:

```
VAGGCCBBGGCVBB
---GCCACGTGSD-
```

Original motif Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif Consensus sequence: VAGGCCBBGGCV



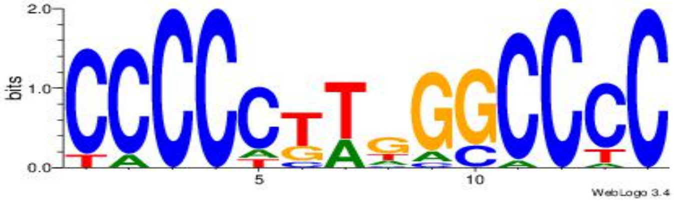
Dataset #: 3
Motif ID: 30
Motif name: PLAG1
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 5
Number of overlap: 10
Similarity score: 0.0921439

Alignment:

```
CCCCCTTGGGCCCC
----HSCACGTGGC
```

Original motif Consensus sequence: GGGGCCCAAGGGGG

Reverse complement motif Consensus sequence: CCCCCTTGGGCCC



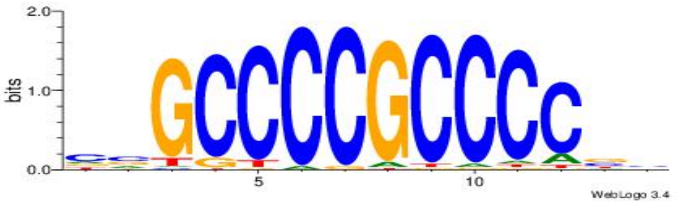
Dataset #:	4
Motif ID:	36
Motif name:	csGCCCCGCCCCsc
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	3
Number of overlap:	10
Similarity score:	0.093472

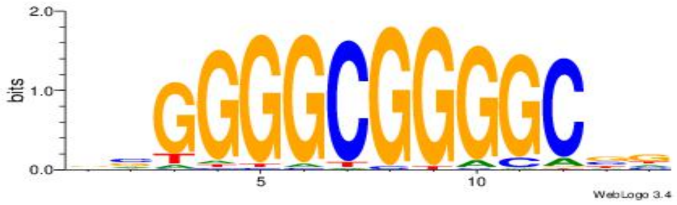
Alignment:

```
HVGCCCCGCCCCBB
--GCCACGTGSD--
```

Original motif Consensus sequence: HVGCCCCGCCCCBB

Reverse complement motif Consensus sequence: BBGGGGCGGGGC



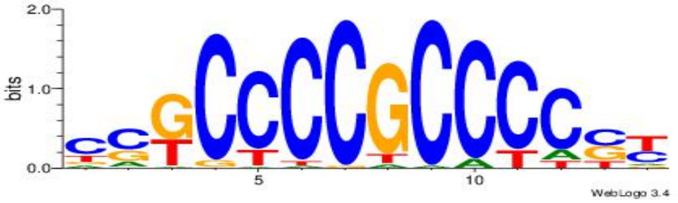


Dataset #:	2
Motif ID:	7
Motif name:	Motif 7
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	3
Number of overlap:	10
Similarity score:	0.0964516

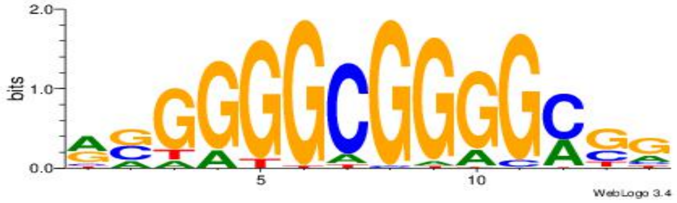
Alignment:

```
MSGGGGCGGGGYSG
--HSCACGTGGC--
```

Original motif Consensus sequence: CSKCCCCGCCCCSY



Reverse complement motif Consensus sequence: MSGGGGCGGGGY



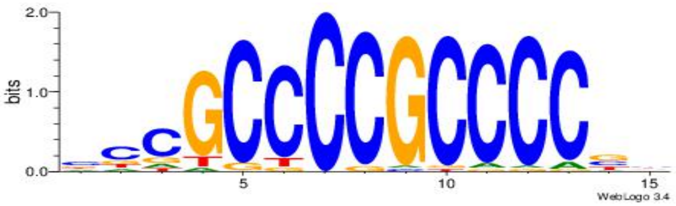
Dataset #:	4
Motif ID:	38

Motif name:	cccGCCCCGCCCCsb
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	3
Number of overlap:	10
Similarity score:	0.0979367

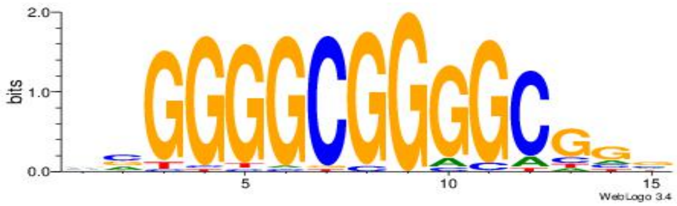
Alignment:

```
BCCGCCCCGCCCCBB
---GCCACGTGSD--
```

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB



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

Original motif Consensus sequence: VGCACGTGGH

Reverse complement motif Consensus sequence: DCCACGTGCV

Best Matches for Motif ID 34 (Highest to Lowest)

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

Alignment:

```
HSCACGTGGC
VGCACGTGGH
```

Original motif Consensus sequence: HSCACGTGGC

Reverse complement motif Consensus sequence: GCCACGTGSD

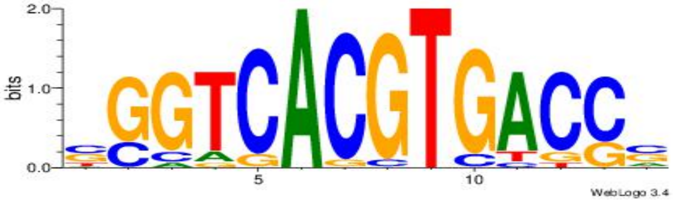
Dataset #:	4
Motif ID:	42
Motif name:	sSGTCACGTGACSs
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif

Direction: Backward
Position number: 3
Number of overlap: 10
Similarity score: 0.0646601

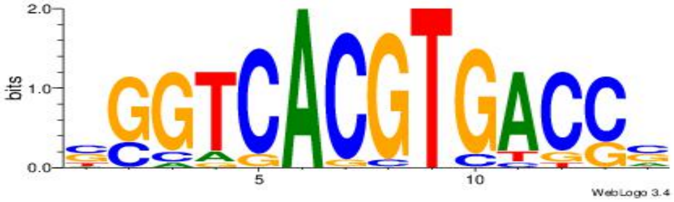
Alignment:

```
SGGTCACGTGACCS
--DCCACGTGCV--
```

Original motif   Consensus sequence: SGGTCACGTGACCS



Reverse complement motif   Consensus sequence: SGGTCACGTGACC



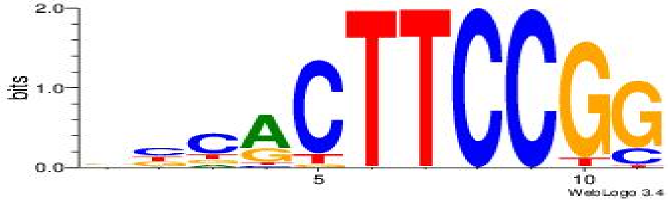
Dataset #: 3
Motif ID: 35
Motif name: GABPA
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 2
Number of overlap: 10
Similarity score: 0.0840341

Alignment:

```
VVCACTTCCGG
DCCACGTGCV-
```

Original motif Consensus sequence: CCGGAAGTGVV

Reverse complement motif Consensus sequence: VVCACTTCCGG



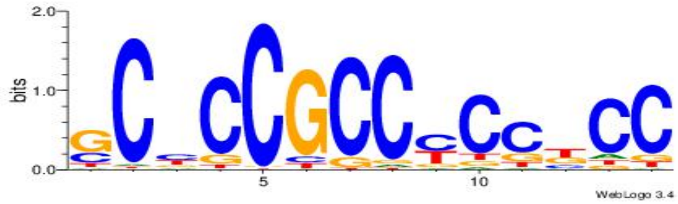
Dataset #:	5
Motif ID:	50
Motif name:	TFF11
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	3
Number of overlap:	10
Similarity score:	0.0851555

Alignment:

```
GGMGGRGGCGGVGC
--VGCACGTGGH--
```

Original motif Consensus sequence: GGMGGRGGCGGVGC

Reverse complement motif Consensus sequence: GCVCCGCCMCCY



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

Alignment:
```
DGGGYGKGGC
VGCACGTGGH
```

Original motif Consensus sequence: DGGGYGKGGC

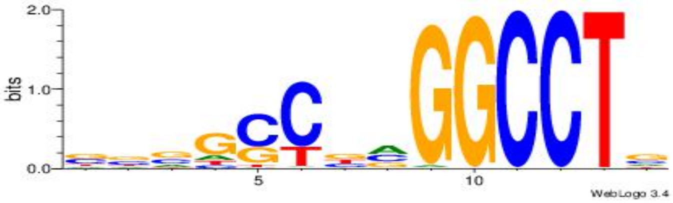
Reverse complement motif Consensus sequence: GCCYCMCCCD

Dataset #: 3
Motif ID: 22
Motif name: Zfx
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 2
Number of overlap: 10

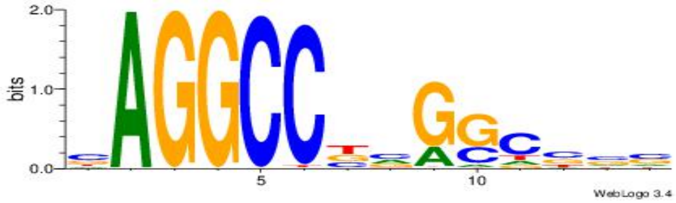
Similarity score: 0.0925451

Alignment:
VAGGCCBBGGCVBB
---DCCACGTGCV-

Original motif Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif Consensus sequence: VAGGCCBBGGCV

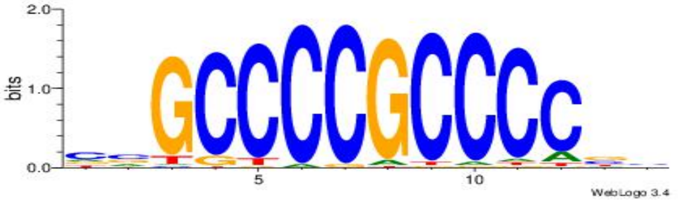


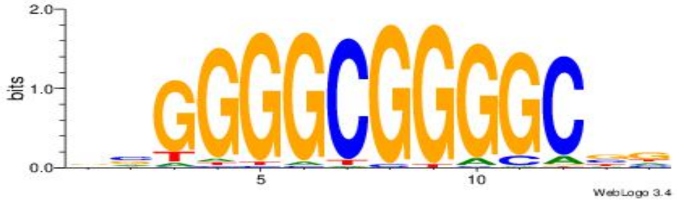
Dataset #: 4
Motif ID: 36
Motif name: csGCCCCGCCCCsc
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 3
Number of overlap: 10
Similarity score: 0.0928504

Alignment:
HVGCCCCGCCCCBB
--DCCACGTGCV--

Original motif Consensus sequence: HVGCCCCGCCCCBB

Reverse complement motif Consensus sequence: BBGGGGCGGGGC



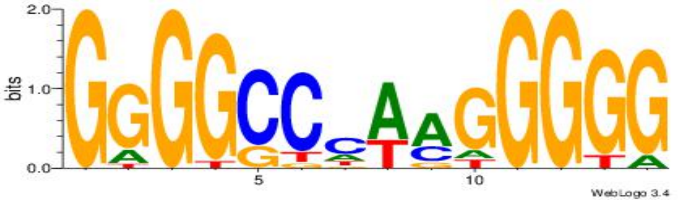


Dataset #:	3
Motif ID:	30
Motif name:	PLAG1
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	5
Number of overlap:	10
Similarity score:	0.0930375

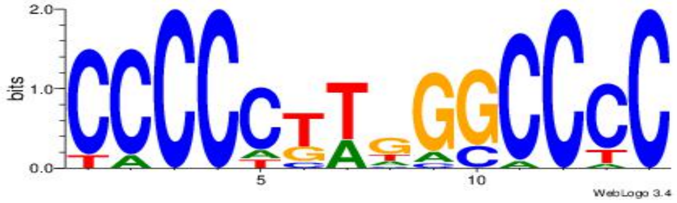
Alignment:

```
CCCCCTTGGGCCCC
----VGCACGTGGH
```

Original motif Consensus sequence: GGGGCCCAAGGGGG



Reverse complement motif Consensus sequence: CCCCCTTGGGCCC



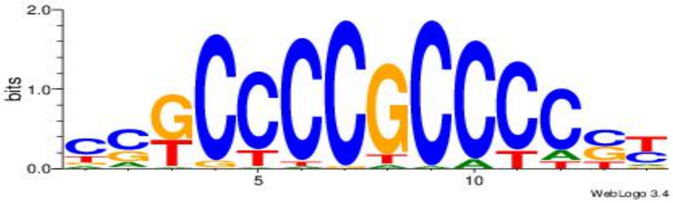
Dataset #:	2
Motif ID:	7

Motif name: Motif 7
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 3
Number of overlap: 10
Similarity score: 0.0941376

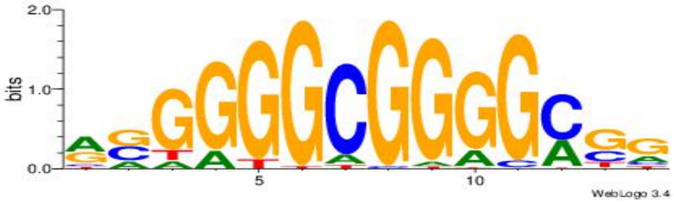
Alignment:

```
MSGGGGCGGGGYSG
--VGCACGTGGH--
```

Original motif Consensus sequence: CSKCCCCGCCCCSY



Reverse complement motif Consensus sequence: MSGGGGCGGGGY

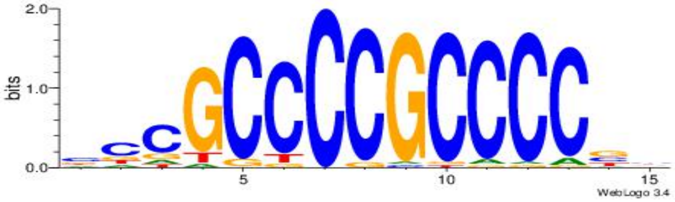


Dataset #: 4
Motif ID: 38
Motif name: cccGCCCCGCCCCsb
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 3
Number of overlap: 10
Similarity score: 0.0974172

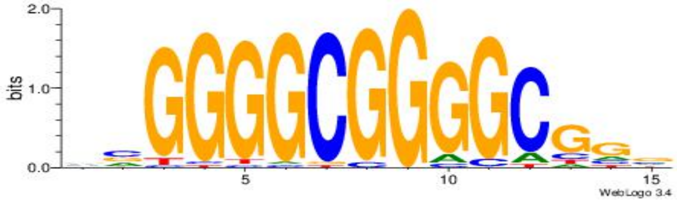
Alignment:

```
BCCGCCCCGCCCCBB
---DCCACGTGCV--
```

Original motif Consensus sequence: BCCGCCCCGCCCCBB



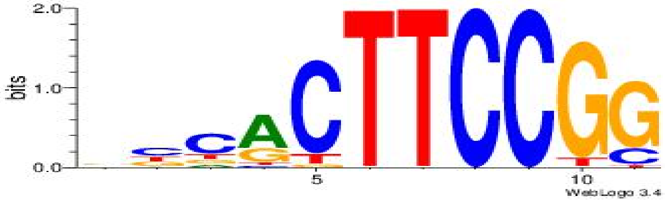
Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB



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

Original motif Consensus sequence: CCGGAAGTGVV

Reverse complement motif Consensus sequence: VVCACTTCCGG



Best Matches for Motif ID 35 (Highest to Lowest)

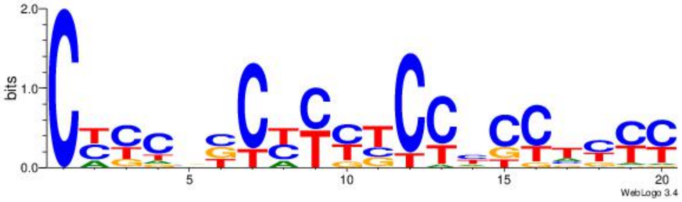
Dataset #:	5
Motif ID:	54
Motif name:	TFM12
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward

Position number:	5
Number of overlap:	11
Similarity score:	0.0360984

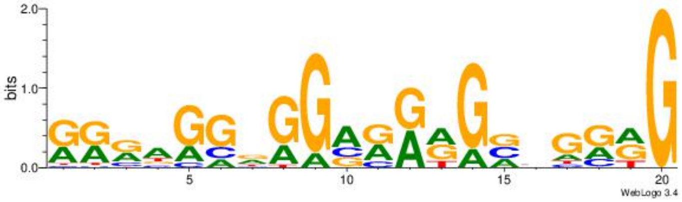
Alignment:

```
CYYCBBCYYYTCCHCCTYYY
----VVCACTTCCGG-----
```

Original motif Consensus sequence: CYYCBBCYYYTCCHCCTYYY



Reverse complement motif Consensus sequence: KKKAGGDGGAKKMGBBGKMG

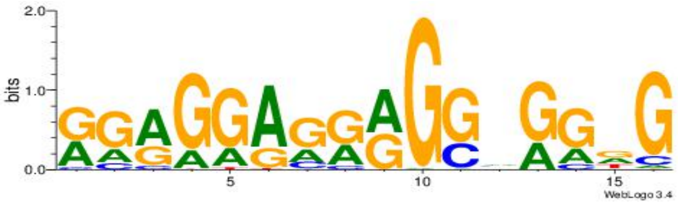


Dataset #:	5
Motif ID:	51
Motif name:	TFM2
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	5
Number of overlap:	11
Similarity score:	0.0445566

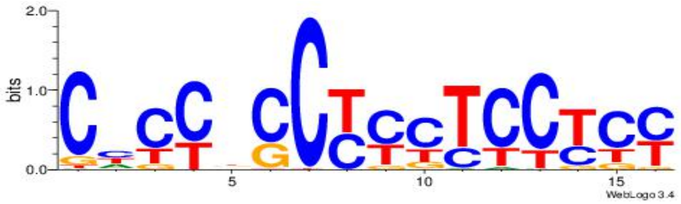
Alignment:

```
RGRGGAGRRGGHGGDG
-CCGGAAGTGVV----
```

Original motif Consensus sequence: RGRGGAGRRGGHGGDG



Reverse complement motif Consensus sequence: CHCCBCCKMCTCCKCM

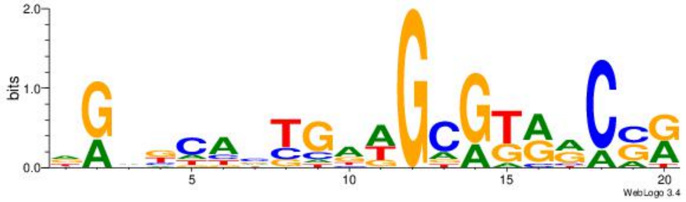


Dataset #:	3
Motif ID:	31
Motif name:	Pax5
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	8
Number of overlap:	11
Similarity score:	0.0446257

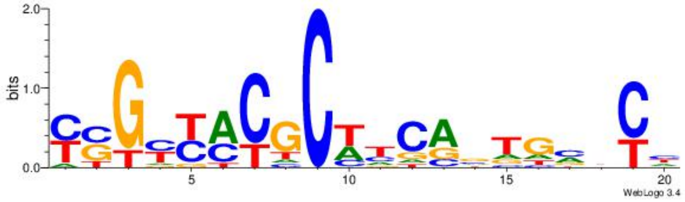
Alignment:

```
DGVBCABTGDWGCGKRRCSR
-------VVCACTTCCGG--
```

Original motif Consensus sequence: DGVBCABTGDWGCGKRRCSR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD

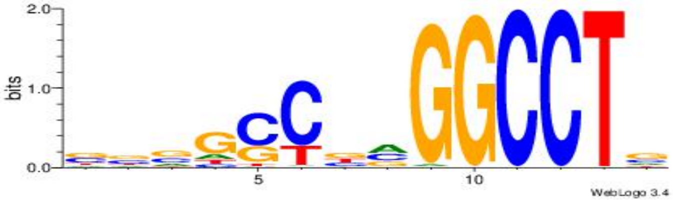


Dataset #:	3
Motif ID:	22
Motif name:	Zfx
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	11
Similarity score:	0.0457327

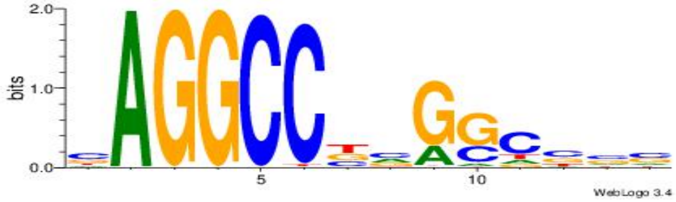
Alignment:

```
BBVGCCBVGGCCTV
VVCACTTCCGG---
```

Original motif Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif Consensus sequence: VAGGCCBBGGCV

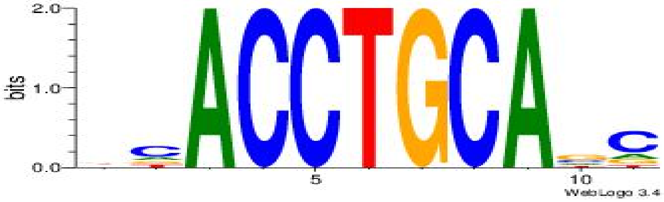


Dataset #:	4
Motif ID:	40
Motif name:	kcACCTGCAgc
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	11

Similarity score: 0.0483841

Alignment:
BCACCTGCABC
VVCACTTCCGG

Original motif Consensus sequence: BCACCTGCABC



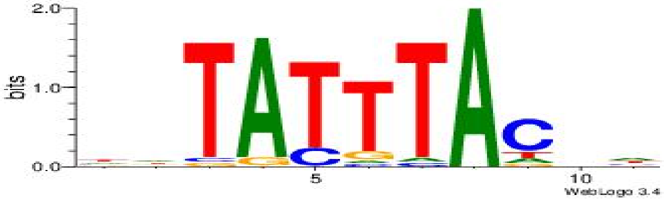
Reverse complement motif Consensus sequence: GBTGCAGGTGB

Dataset #: 4
Motif ID: 45
Motif name: wbgTAAATAww
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: 0.0492127

Alignment:
DBGTAAATAHD
CCGGAAGTGVV

Original motif Consensus sequence: DBGTAAATAHD

Reverse complement motif Consensus sequence: DHTATTTACBD

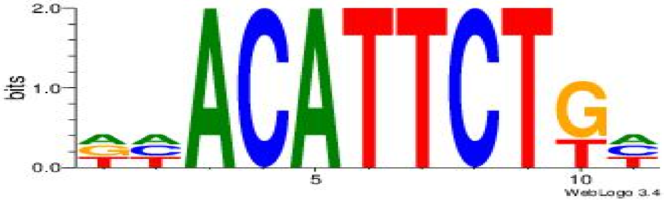


Dataset #:	4
Motif ID:	44
Motif name:	dhACATTCTkh
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	11
Similarity score:	0.0495154

Alignment:

```
DHACATTCTGH
VVCACTTCCGG
```

Original motif Consensus sequence: DHACATTCTGH



Reverse complement motif Consensus sequence: HCAGAATGTHD

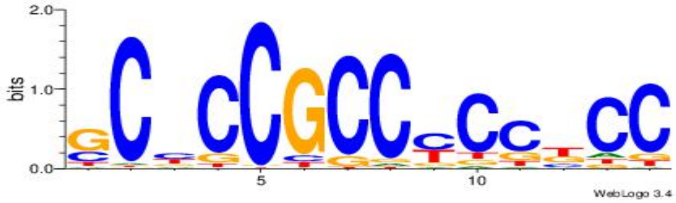
Dataset #:	5
Motif ID:	50

Motif name: TFF11
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 2
Number of overlap: 11
Similarity score: 0.0504656

Alignment:
GGMGGRGGCGGVGC
-CCGGAAGTGVV--

Original motif Consensus sequence: GGMGGRGGCGGVGC

Reverse complement motif Consensus sequence: GCVCCGCCMCCYC



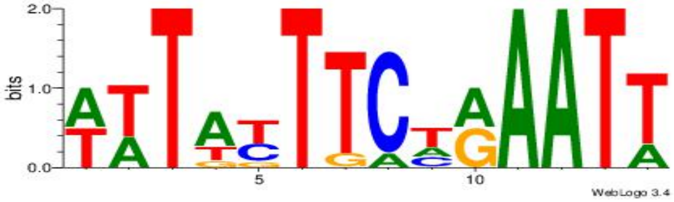
Dataset #: 2
Motif ID: 6
Motif name: Motif 6
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 11
Similarity score: 0.0518418

Alignment:

AATTYDGAARTAWW
---CCGGAAGTGVV

Original motif Consensus sequence: AATTYDGAARTAWW

Reverse complement motif Consensus sequence: WWTAKTTCDKAAT



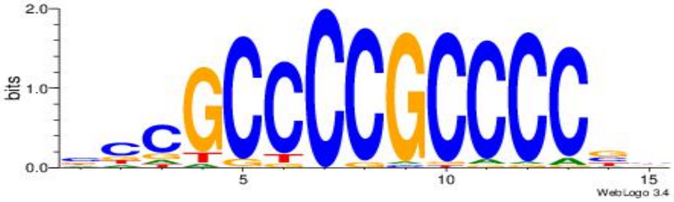
Dataset #:	4
Motif ID:	38
Motif name:	cccGCCCCGCCCCsb
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2
Number of overlap:	11
Similarity score:	0.0554249

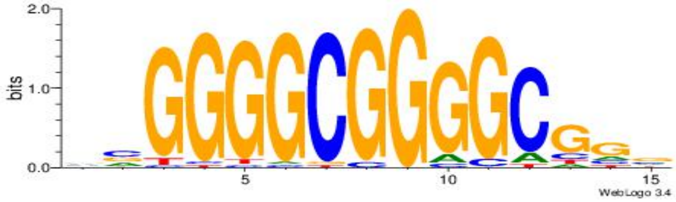
Alignment:

BCCGCCCCGCCCCBB
---VVCACTTCCGG-

Original motif Consensus sequence: BCCGCCCCGCCCCBB

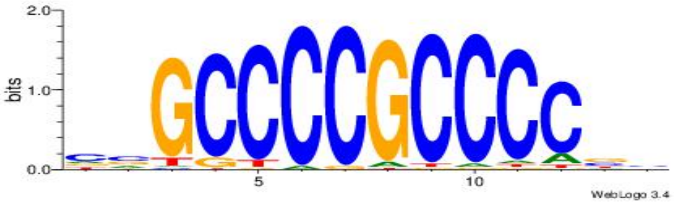
Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB



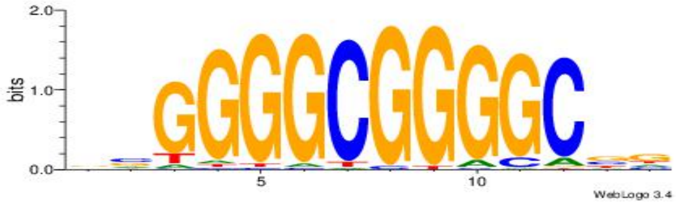


Dataset #: 4 Motif ID: 36 Motif name: csGCCCCGCCCCsc

Original motif Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGC



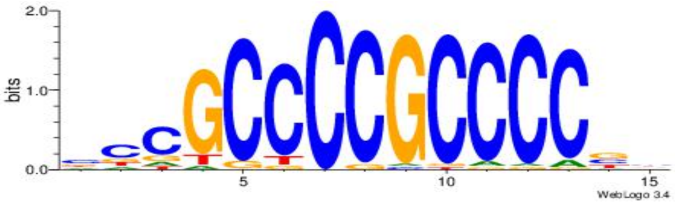
Best Matches for Motif ID 36 (Highest to Lowest)

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

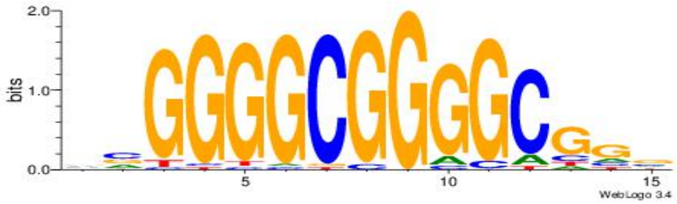
Alignment:

```
BBGGGGCGGGGCGGB
BBGGGGCGGGGCVD-
```

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB

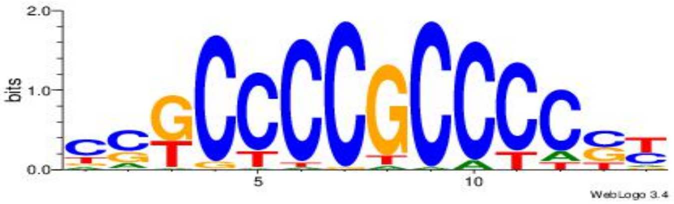


Dataset #:	2
Motif ID:	7
Motif name:	Motif 7
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	14
Similarity score:	0.0117332

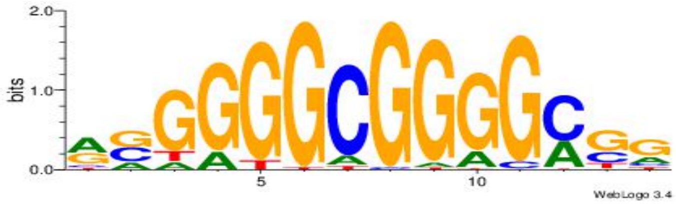
Alignment:

```
CSKCCCCGCCCCSY
HVGCCCCGCCCCBB
```

Original motif Consensus sequence: CSKCCCCGCCCCSY



Reverse complement motif Consensus sequence: MSGGGGCGGGGY

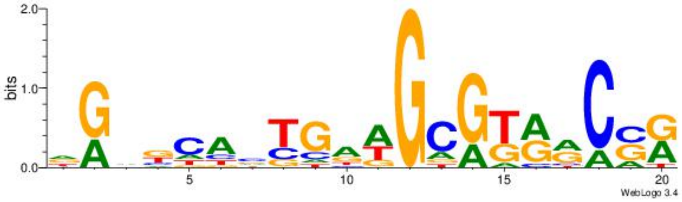


Dataset #:	3
Motif ID:	31
Motif name:	Pax5
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	14
Similarity score:	0.0747029

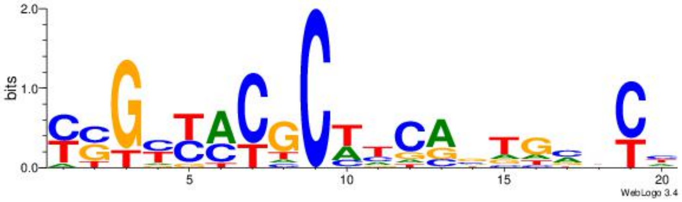
Alignment:

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

Original motif Consensus sequence: DGVBCABTGDWGCGKRRCSR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD



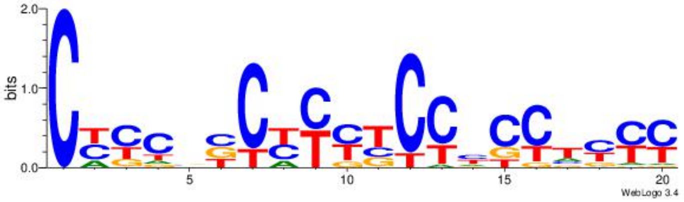
Dataset #:	5
Motif ID:	54
Motif name:	TFM12
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	4

Number of overlap: 14
Similarity score: 0.0777991

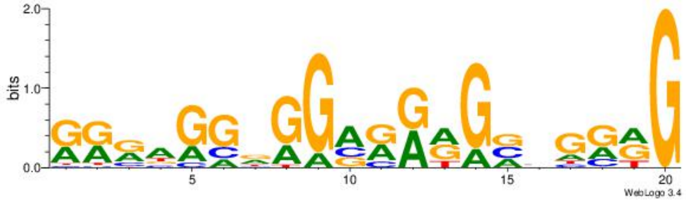
Alignment:

```
CYYCBBCYYYTCCHCCTYYY
---HVGCCCCGCCCCBB---
```

Original motif Consensus sequence: CYYCBBCYYYTCCHCCTYYY



Reverse complement motif Consensus sequence: KKKAGGDGGAKKMGBBGKMG

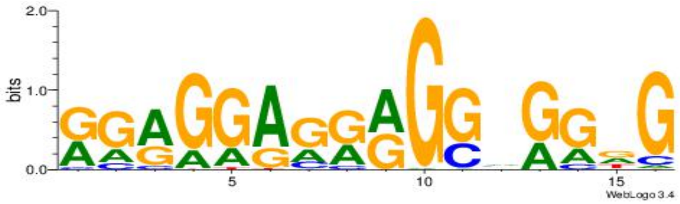


Dataset #: 5
Motif ID: 51
Motif name: TFM2
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 3
Number of overlap: 14
Similarity score: 0.0880609

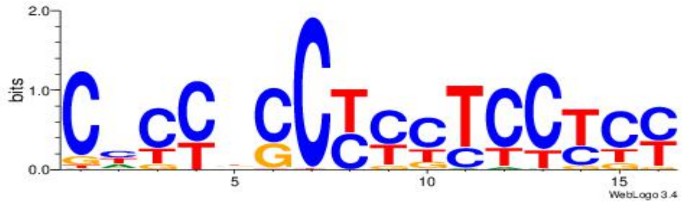
Alignment:

```
RGRGGAGRRGGHGGDG
BBGGGGCGGGGCVD--
```

Original motif Consensus sequence: RGRGGAGRRGGHGGDG



Reverse complement motif Consensus sequence: CHCCBCCKMCTCCKCM

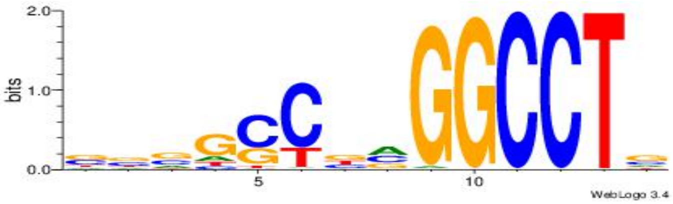


Dataset #:	3
Motif ID:	22
Motif name:	Zfx
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	14
Similarity score:	0.0884848

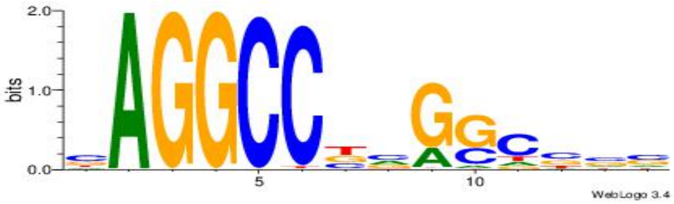
Alignment:

```
BBVGCCBVGGCCTV
BBGGGGCGGGGCVD
```

Original motif Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif Consensus sequence: VAGGCCBBGGCV

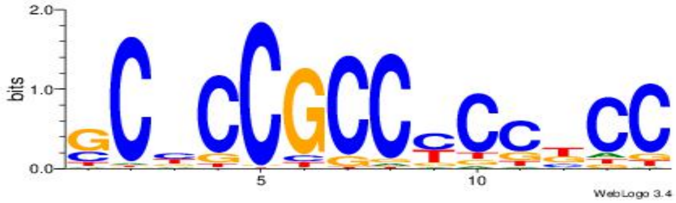


Dataset #: 5
Motif ID: 50
Motif name: TFF11
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 14
Similarity score: 0.0937271

Alignment:
GCVCCGCCMCCYCC
HVGCCCCGCCCCBB

Original motif Consensus sequence: GGMGGRGGCGGVGC

Reverse complement motif Consensus sequence: GCVCCGCCMCCYC

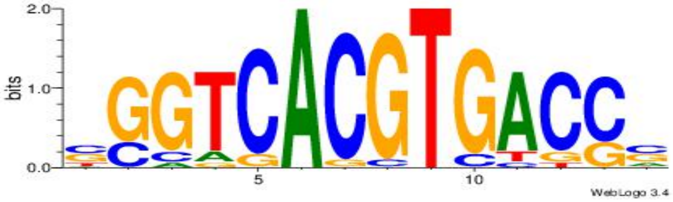


Dataset #: 4
Motif ID: 42
Motif name: sSGTCACGTGACSs
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 14

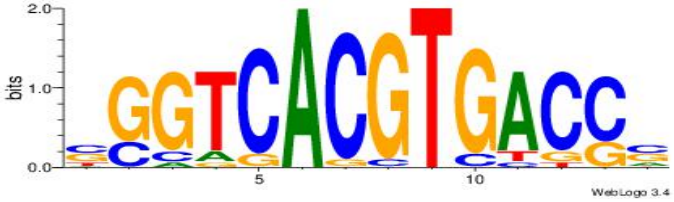
Similarity score: 0.0971132

Alignment:
SGGTCACGTGACCS
HVGCCCCGCCCCBB

Original motif Consensus sequence: SGGTCACGTGACCS



Reverse complement motif Consensus sequence: SGGTCACGTGACC

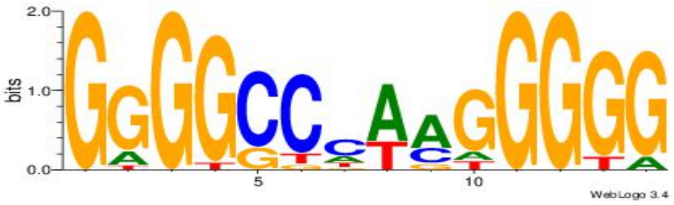


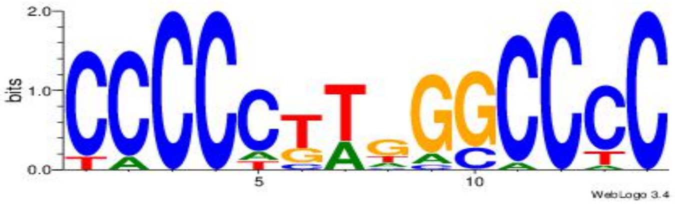
Dataset #:	3
Motif ID:	30
Motif name:	PLAG1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	13
Similarity score:	0.609319

Alignment:
GGGGCCCAAGGGGG-
-BBGGGGCGGGGCVD

Original motif Consensus sequence: GGGGCCCAAGGGGG

Reverse complement motif Consensus sequence: CCCCCTTGGGCCC



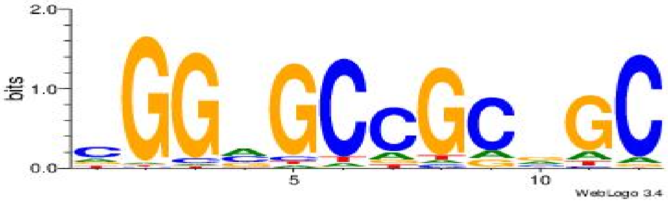


Dataset #:	5
Motif ID:	49
Motif name:	TFF1
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	12
Similarity score:	1.08016

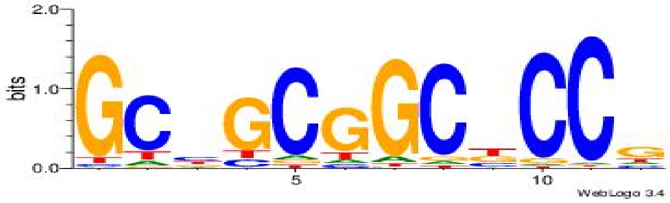
Alignment:

```
CGGVGCCGCVGC--
HVGCCCCGCCCCBB
```

Original motif Consensus sequence: CGGVGCCGCVGC

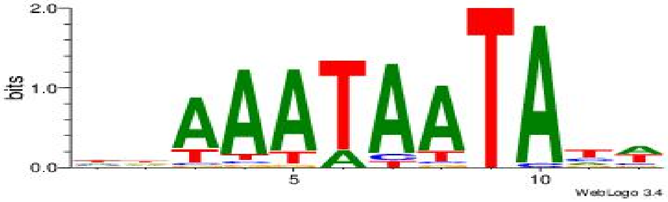


Reverse complement motif Consensus sequence: GCVGCGGCBCCG

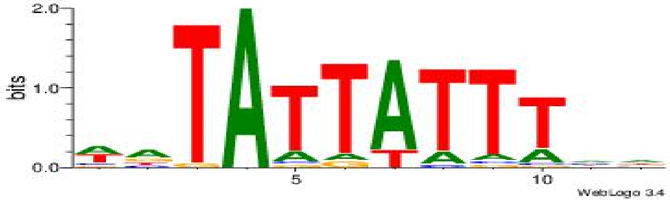


Dataset #: 4 Motif ID: 37 Motif name: tkAAATAATAtw

Original motif   Consensus sequence: HDAAATAATAHW



Reverse complement motif   Consensus sequence: WHTATTATTTDH



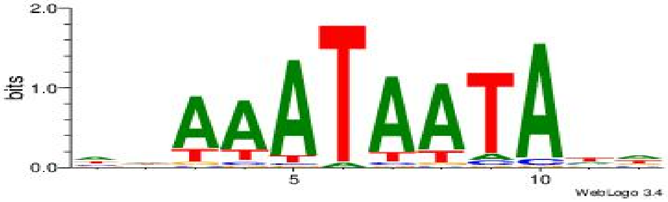
Best Matches for Motif ID 37 (Highest to Lowest)

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

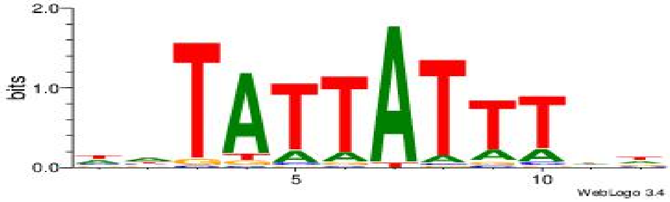
Alignment:

```
HDAAATAATADD
HDAAATAATAHW
```

Original motif   Consensus sequence: HDAAATAATADD



Reverse complement motif   Consensus sequence: DDTATTATTTDH

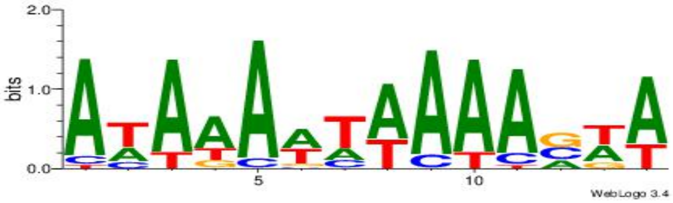


Dataset #:	2
Motif ID:	3
Motif name:	Motif 3
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	2
Number of overlap:	12
Similarity score:	0.0522317

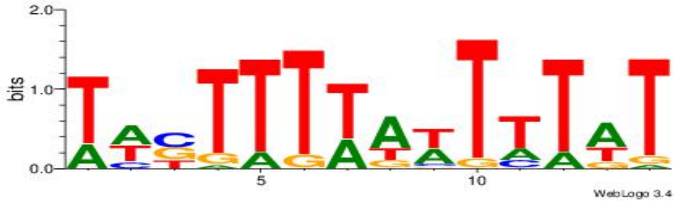
Alignment:

```
TWSTTTWAWTTTWT
-WHTATTATTTDH-
```

Original motif   Consensus sequence: AWAAAWTWAAASWA



Reverse complement motif   Consensus sequence: TWSTTTWAWTTT



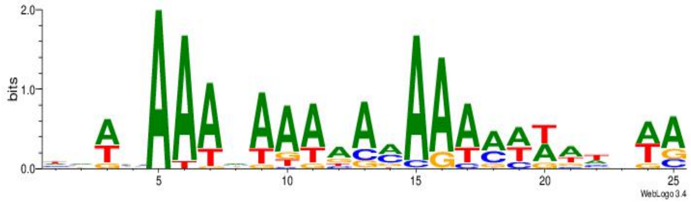
Dataset #:	5
Motif ID:	56
Motif name:	TFM11
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	12
Number of overlap:	12

Similarity score: 0.0590505

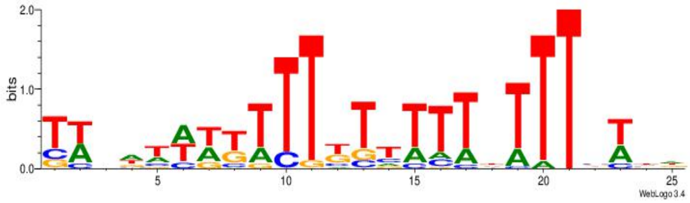
Alignment:

```
TWVHWWWYTTTYTTTTTHTTTVWBH
-----------WHTATTATTTDH--
```

Original motif Consensus sequence:
HDWVAAAHAAAAAMAAAMWWWHBWA



Reverse complement motif Consensus sequence:
TWVHWWWYTTTYTTTTTHTTTVWBH



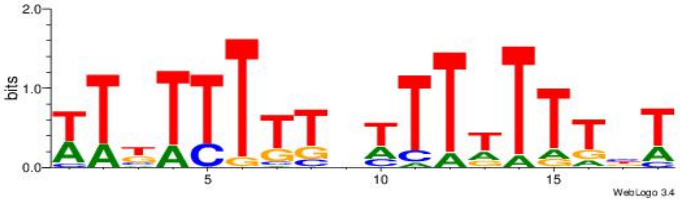
Dataset #:	5
Motif ID:	52
Motif name:	TFM1
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	12
Similarity score:	0.0637702

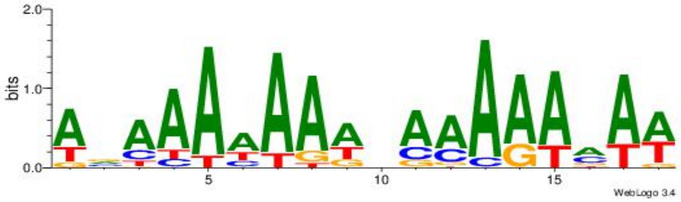
Alignment:

```
ABAAAAAAWHAAAAARAW
HDAAATAATAHW------
```

Original motif Consensus sequence: WTKTTTTTHWTTTTTTBT

Reverse complement motif Consensus sequence:
ABAAAAAAWHAAAAARAW



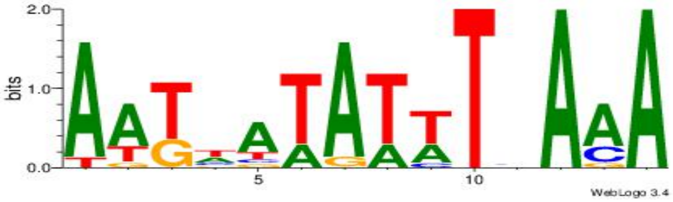


Dataset #:	2
Motif ID:	9
Motif name:	Motif 9
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	12
Similarity score:	0.0641975

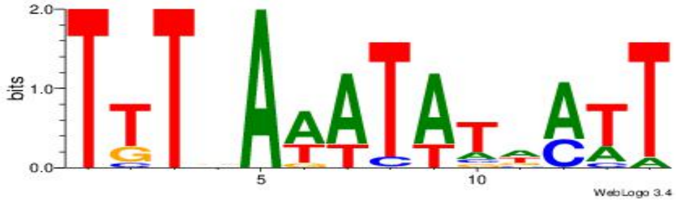
Alignment:

```
AATHATATWTHAAA
--WHTATTATTTDH
```

Original motif Consensus sequence: AATHATATWTHAAA



Reverse complement motif Consensus sequence: TTTDAWATATHAT

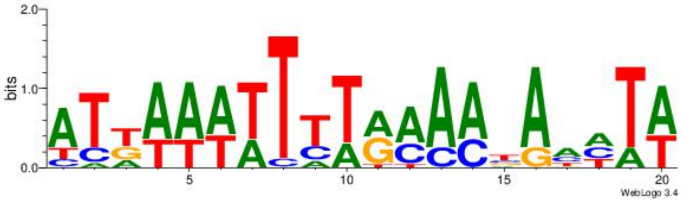


Dataset #:	5
Motif ID:	55

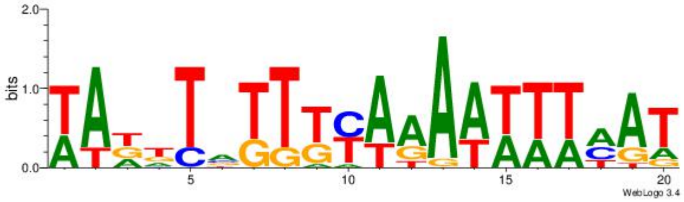
Motif name: TFM13
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 12
Similarity score: 0.0704475

Alignment:
```
ATKAAWTTTTRMAABAHHTW
WHTATTATTTDH--------
```

Original motif Consensus sequence: ATKAAWTTTTRMAABAHHTW



Reverse complement motif Consensus sequence: WAHHTVTTYKAAAAWTTRAT

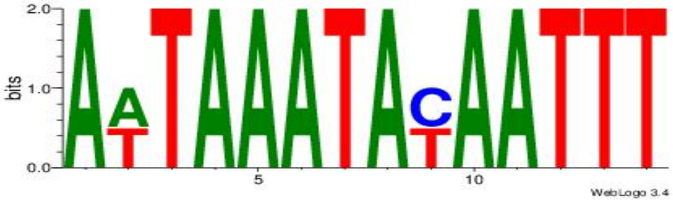


Dataset #: 2
Motif ID: 5
Motif name: Motif 5
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 2
Number of overlap: 12
Similarity score: 0.0704475

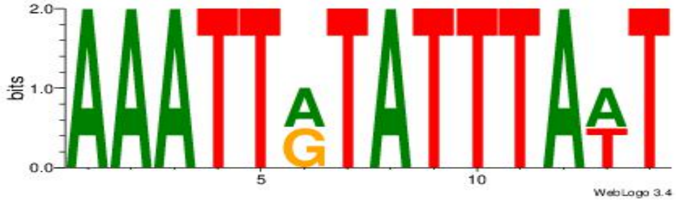
Alignment:

```
AAATTKTATTTAWT
-WHTATTATTTDH-
```

Original motif   Consensus sequence: AWTAAATAYAATTT



Reverse complement motif   Consensus sequence: AAATTKTATTTAW



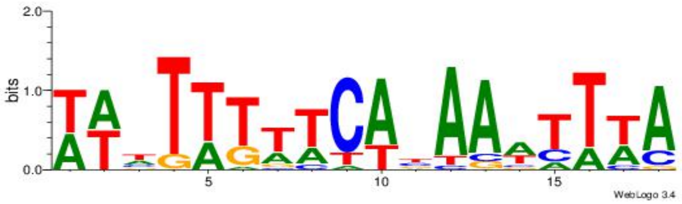
Dataset #:	5
Motif ID:	53
Motif name:	TFM3
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	12
Similarity score:	0.0763819

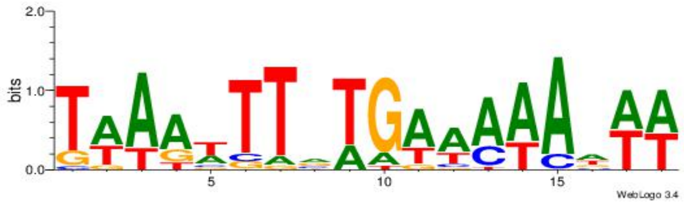
Alignment:

```
WWHTTTTTCABAAWTTWA
------WHTATTATTTDH
```

Original motif   Consensus sequence: WWHTTTTTCABAAWTTWA

Reverse complement motif   Consensus sequence: TWAAWTTVTGAAAAAHWW



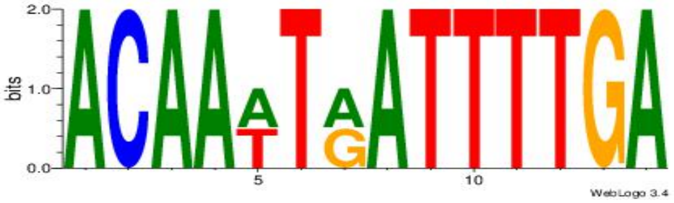


Dataset #:	2
Motif ID:	16
Motif name:	Motif 16
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	12
Similarity score:	0.0864198

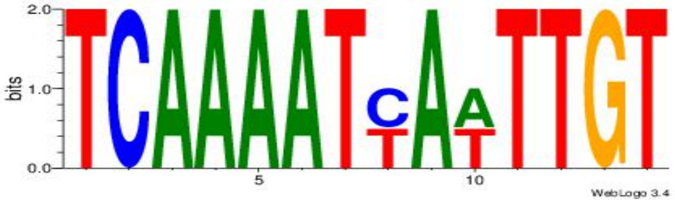
Alignment:

```
TCAAAATKAWTTGT
--WHTATTATTTDH
```

Original motif Consensus sequence: ACAAWTRATTTTGA



Reverse complement motif Consensus sequence: TCAAAATKAWTTG



Dataset #:	2
Motif ID:	6

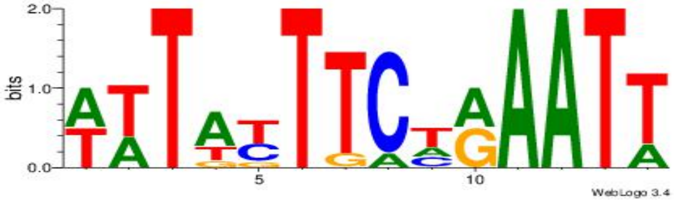
Motif name:	Motif 6
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	12
Similarity score:	0.09076

Alignment:

```
WWTAKTTCDKAATT
WHTATTATTTDH--
```

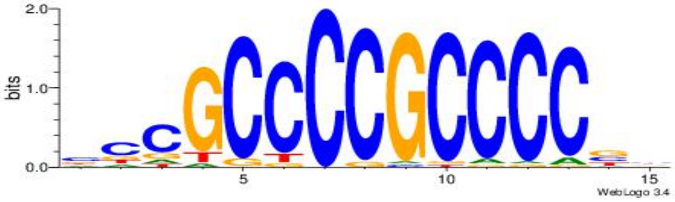
Original motif Consensus sequence: AATTYDGAARTAWW

Reverse complement motif Consensus sequence: WWTAKTTCDKAAT

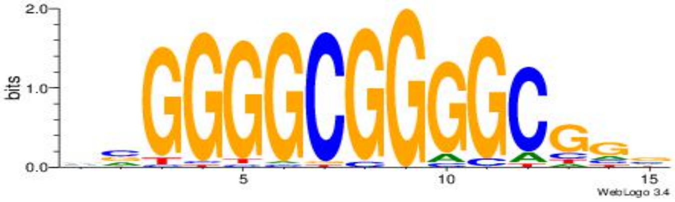


Dataset #: 4 Motif ID: 38 Motif name: cccGCCCCGCCCCsb

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB



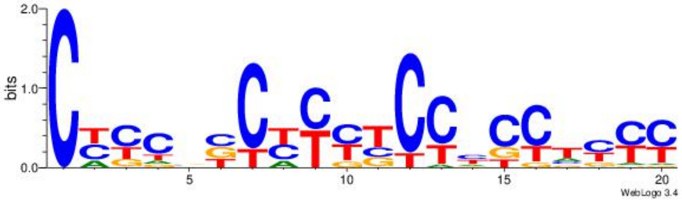
Best Matches for Motif ID 38 (Highest to Lowest)

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

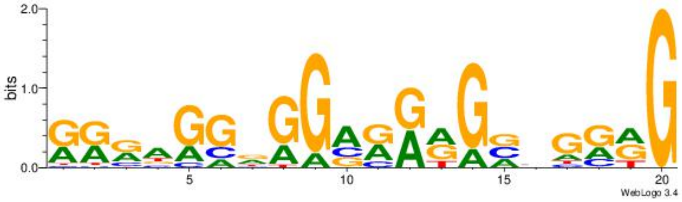
Alignment:

```
CYYCBBCYYYTCCHCCTYYY
--BCCGCCCCGCCCCBB---
```

Original motif   Consensus sequence: CYYCBBCYYYTCCHCCTYYY



Reverse complement motif   Consensus sequence: KKKAGGDGGAKKMGBBGKMG



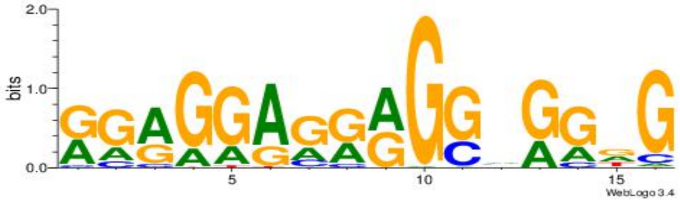
Dataset #:	5
Motif ID:	51
Motif name:	TFM2
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif

Direction:	Forward
Position number:	1
Number of overlap:	15
Similarity score:	0.0869149

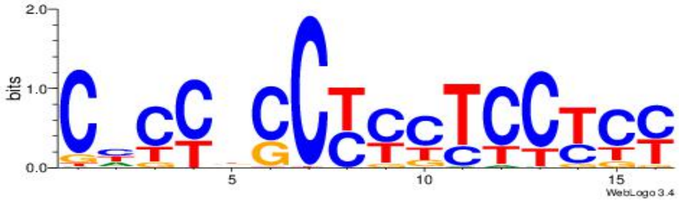
Alignment:

```
RGRGGAGRRGGHGGDG
BBGGGGCGGGGCGGB-
```

Original motif Consensus sequence: RGRGGAGRRGGHGGDG



Reverse complement motif Consensus sequence: CHCCBCCKMCTCCKCM

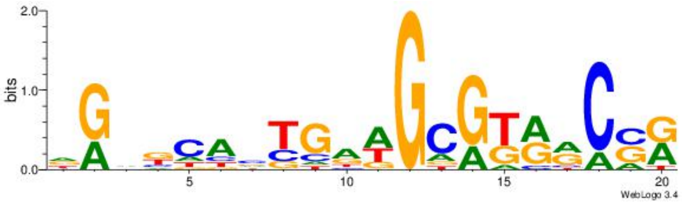


Dataset #:	3
Motif ID:	31
Motif name:	Pax5
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	15
Similarity score:	0.0992376

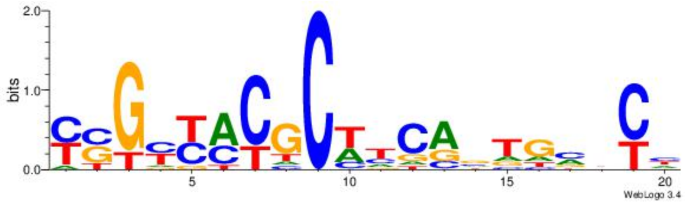
Alignment:

```
MSGKKRCGCWDCABTGBBCD
BBGGGGCGGGGCGGB-----
```

Original motif Consensus sequence: DGVBCABTGDWGCGKRRCSR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD

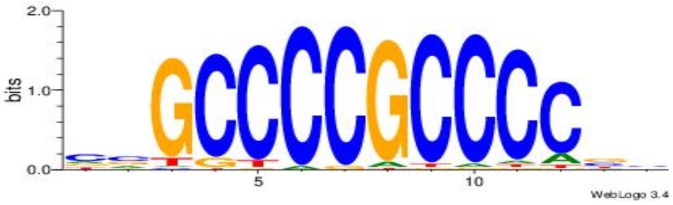


Dataset #:	4
Motif ID:	36
Motif name:	csGCCCCGCCCCsc
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	14
Similarity score:	0.5

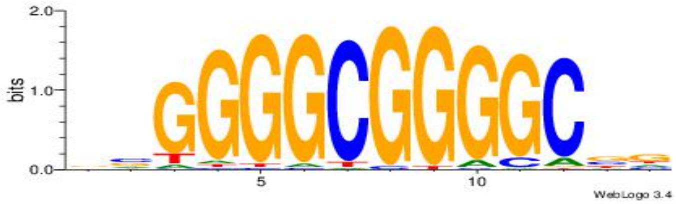
Alignment:

```
-HVGCCCCGCCCCBB
BCCGCCCCGCCCCBB
```

Original motif Consensus sequence: HVGCCCCGCCCCBB



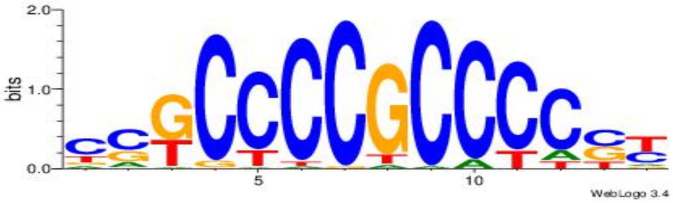
Reverse complement motif Consensus sequence: BBGGGGCGGGGC



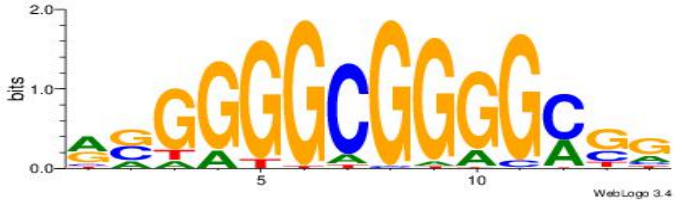
Dataset #: 2
Motif ID: 7
Motif name: Motif 7
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 14
Similarity score: 0.513015

Alignment:
-CSKCCCCGCCCCSY
BCCGCCCCGCCCCBB

Original motif Consensus sequence: CSKCCCCGCCCCSY



Reverse complement motif Consensus sequence: MSGGGGCGGGGY

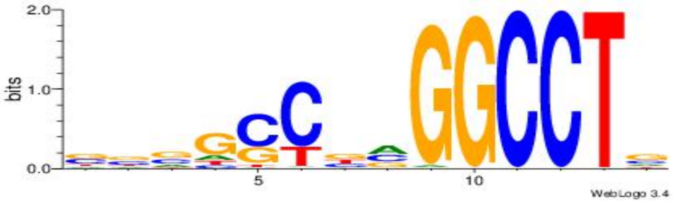


Dataset #: 3
Motif ID: 22
Motif name: Zfx
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 14

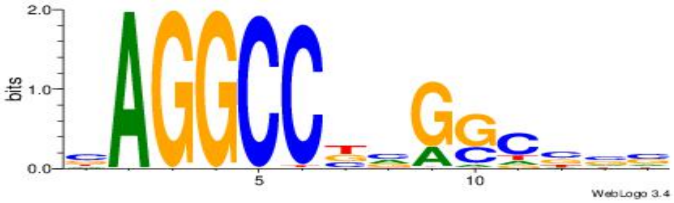
Similarity score: 0.574434

Alignment:
BBVGCCBVGGCCTV-
BCCGCCCCGCCCCBB

Original motif Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif Consensus sequence: VAGGCCBBGGCV

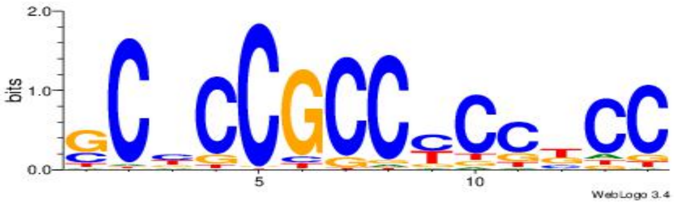


Dataset #:	5
Motif ID:	50
Motif name:	TFF11
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	14
Similarity score:	0.58333

Alignment:
GCVCCGCCMCCYCC-
BCCGCCCCGCCCCBB

Original motif Consensus sequence: GGMGGRGGCGGVGC

Reverse complement motif Consensus sequence: GCVCCGCCMCCY

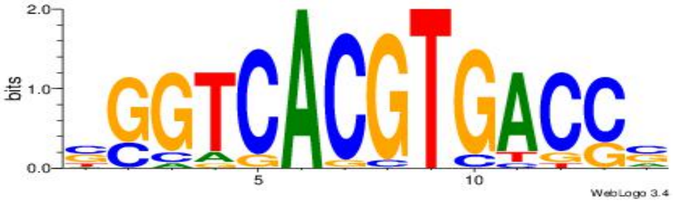


Dataset #:	4
Motif ID:	42
Motif name:	sSGTCACGTGACSs
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	14
Similarity score:	0.601399

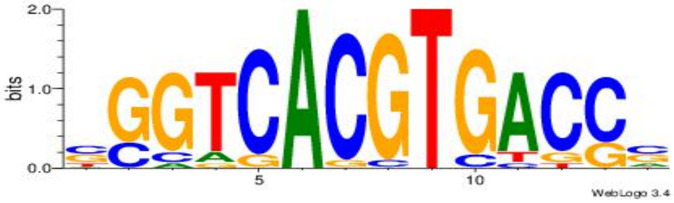
Alignment:

```
SGGTCACGTGACCS-
BBGGGGCGGGGCGGB
```

Original motif Consensus sequence: SGGTCACGTGACCS



Reverse complement motif Consensus sequence: SGGTCACGTGACC



Dataset #:	3
Motif ID:	30

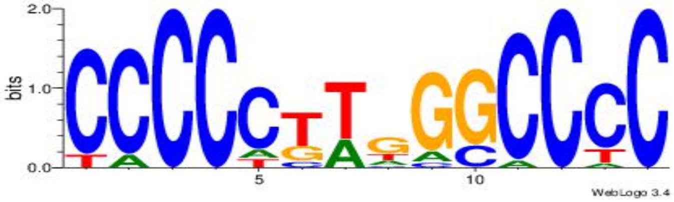
Motif name: PLAG1
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 14
Similarity score: 0.604586

Alignment:

```
GGGGCCCAAGGGGG-
BBGGGGCGGGGCGGB
```

Original motif Consensus sequence: GGGGCCCAAGGGGG

Reverse complement motif Consensus sequence: CCCCCCTTGGGCCC

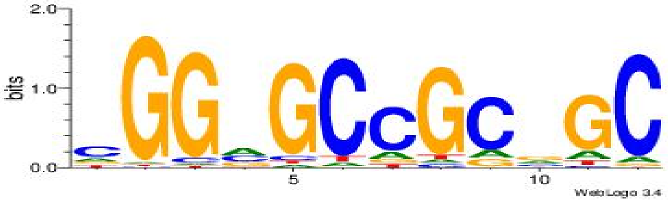


Dataset #: 5
Motif ID: 49
Motif name: TFF1
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 12
Similarity score: 1.58073

Alignment:

```
---GCVGCGGCBCCG
BCCGCCCCGCCCCBB
```

Original motif Consensus sequence: CGGVGCCGCVGC

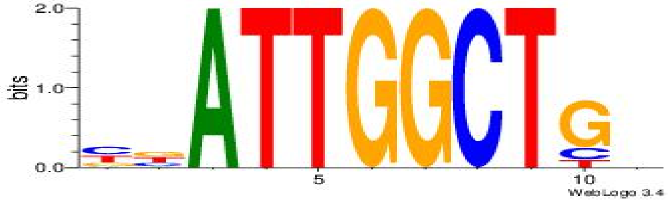


Reverse complement motif Consensus sequence: GCVGCGGCBCCG

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

Original motif Consensus sequence: DCAGCCAATVR

Reverse complement motif Consensus sequence: MBATTGGCTGH



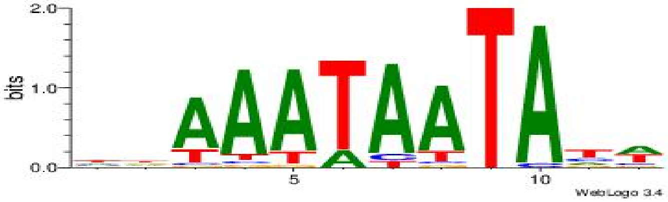
Best Matches for Motif ID 39 (Highest to Lowest)

Dataset #:	4
Motif ID:	37
Motif name:	tkAAATAATAtw
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	2

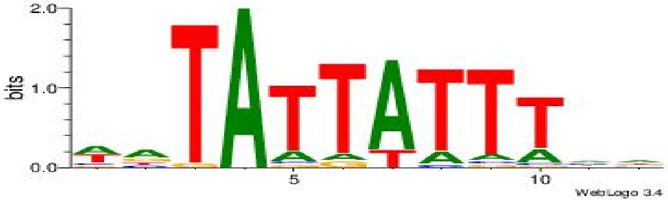
Number of overlap: 11
Similarity score: 0.0559269

Alignment:
`WHTATTATTTDH`
`-MBATTGGCTGH`

Original motif Consensus sequence: HDAAATAATAHW



Reverse complement motif Consensus sequence: WHTATTATTTDH

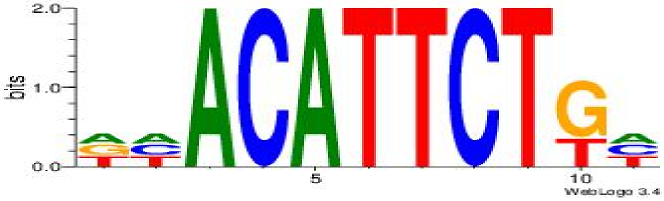


Dataset #: 4
Motif ID: 44
Motif name: dhACATTCTkh
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 11
Similarity score: 0.0588235

Alignment:
`HCAGAATGTHD`
`DCAGCCAATVR`

Original motif Consensus sequence: DHACATTCTGH

Reverse complement motif Consensus sequence: HCAGAATGTHD



Dataset #: 4

Motif ID: 41

Motif name: wwAAATAATAtw

Matching format of first motif: Reverse Complement

Matching format of second motif: Reverse Complement

Direction: Backward

Position number: 1

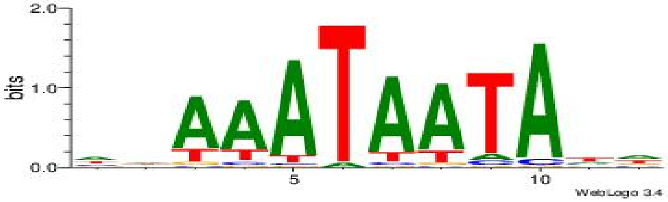
Number of overlap: 11

Similarity score: 0.0597643

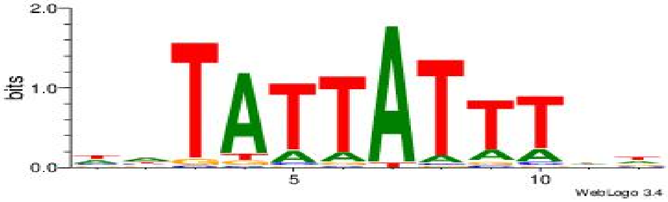
Alignment:

```
DDTATTATTTDH
-MBATTGGCTGH
```

Original motif Consensus sequence: HDAAATAATADD



Reverse complement motif Consensus sequence: DDTATTATTTDH



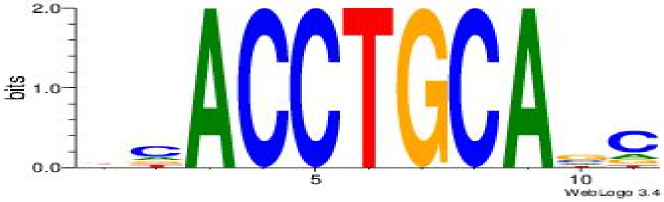
Dataset #: 4

Motif ID: 40

Motif name: kcACCTGCAgc
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 11
Similarity score: 0.0599548

Alignment:
```
BCACCTGCABC
MBATTGGCTGH
```

Original motif Consensus sequence: BCACCTGCABC



Reverse complement motif Consensus sequence: GBTGCAGGTGB

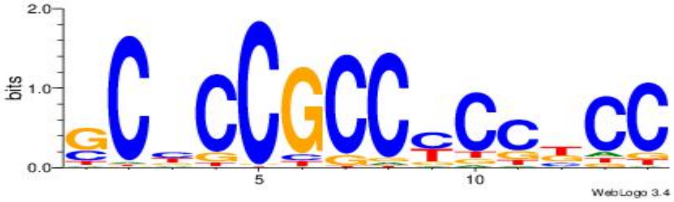
Dataset #: 5
Motif ID: 50
Motif name: TFF11
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 2
Number of overlap: 11
Similarity score: 0.0614719

Alignment:

```
GCVCCGCCMCCYCC
--DCAGCCAATVR-
```

Original motif Consensus sequence: GGMGGRGGCGGVGC

Reverse complement motif Consensus sequence: GCVCCGCCMCCYC



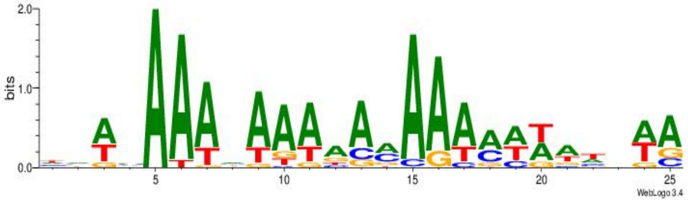
Dataset #:	5
Motif ID:	56
Motif name:	TFM11
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	7
Number of overlap:	11
Similarity score:	0.0635027

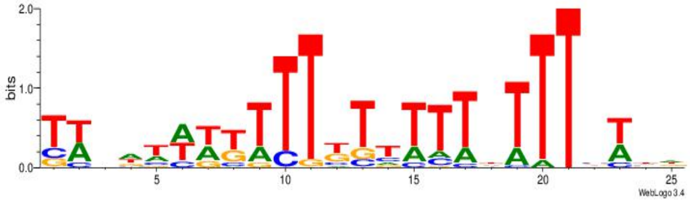
Alignment:

```
HDWVAAAHAAAAAMAAAMWWWHBWA
--------DCAGCCAATVR------
```

Original motif Consensus sequence: HDWVAAAHAAAAAMAAAMWWWHBWA

Reverse complement motif Consensus sequence: TWVHWWWYTTTYTTTTTHTTTVWBH





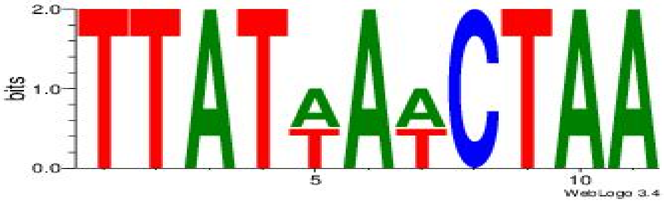
Dataset #:	2
Motif ID:	18
Motif name:	Motif 18
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	11
Similarity score:	0.0661765

Alignment:

```
TTAGWTWATAA
DCAGCCAATVR
```

Original motif Consensus sequence: TTAGWTWATAA

Reverse complement motif Consensus sequence: TTATWAWCTAA



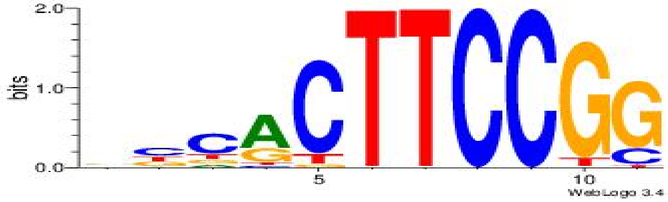
Dataset #:	3
Motif ID:	35

Motif name: GABPA
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2
Number of overlap: 10
Similarity score: 0.56089

Alignment:
-CCGGAAGTGVV
DCAGCCAATVR-

Original motif Consensus sequence: CCGGAAGTGVV

Reverse complement motif Consensus sequence: VVCACTTCCGG

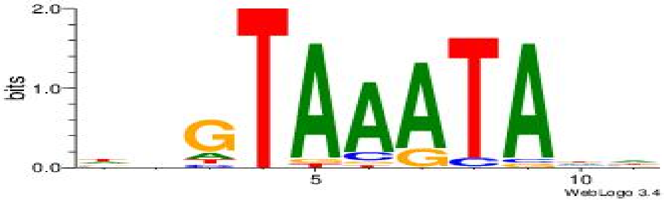


Dataset #: 4
Motif ID: 45
Motif name: wbgTAAATAww
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 2
Number of overlap: 10
Similarity score: 0.561975

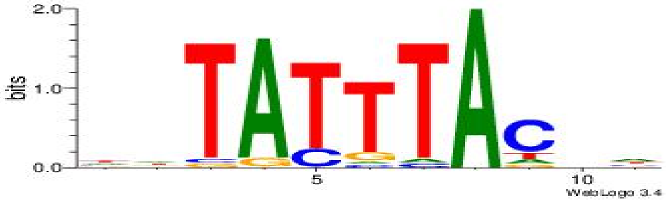
Alignment:

```
DHTATTTACBD-
-MBATTGGCTGH
```

Original motif Consensus sequence: DBGTAAATAHD



Reverse complement motif Consensus sequence: DHTATTTACBD



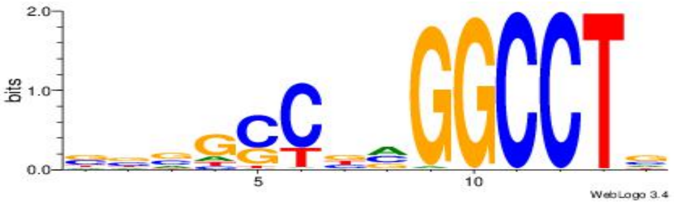
Dataset #:	3
Motif ID:	22
Motif name:	Zfx
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	5
Number of overlap:	10
Similarity score:	0.563709

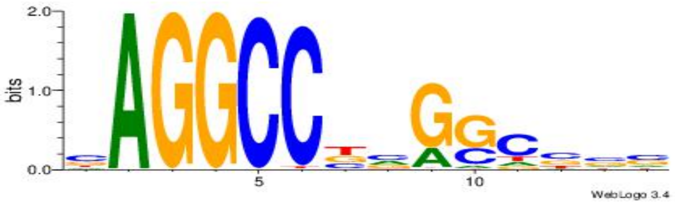
Alignment:

```
VAGGCCBBGGCVBB-
----DCAGCCAATVR
```

Original motif Consensus sequence: BBVGCCBVGGCCTV

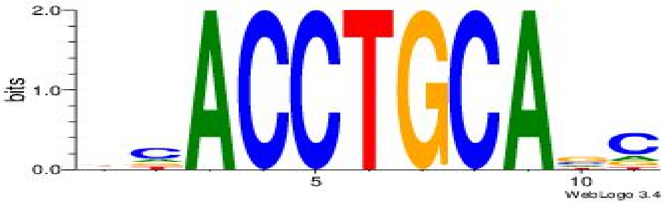
Reverse complement motif Consensus sequence: VAGGCCBBGGCVE





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

Original motif Consensus sequence: BCACCTGCABC



Reverse complement motif Consensus sequence: GBTGCAGGTGB

Best Matches for Motif ID 40 (Highest to Lowest)

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

Alignment:

```
DBTACWGTAVH
BCACCTGCABC
```

Original motif Consensus sequence: HVTACWGTABD

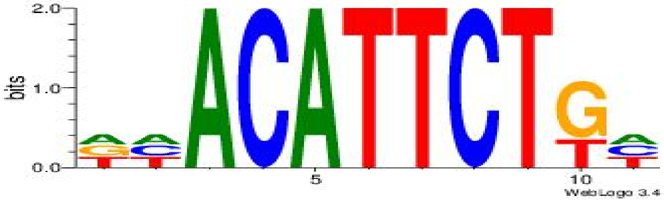
Reverse complement motif Consensus sequence: DBTACWGTAVH

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

Alignment:

```
DHACATTCTGH
BCACCTGCABC
```

Original motif Consensus sequence: DHACATTCTGH



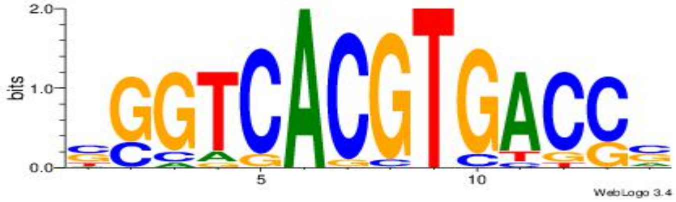
Reverse complement motif Consensus sequence: HCAGAATGTHD

Dataset #: 4
Motif ID: 42
Motif name: sSGTCACGTGACSs
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 4
Number of overlap: 11
Similarity score: 0.031338

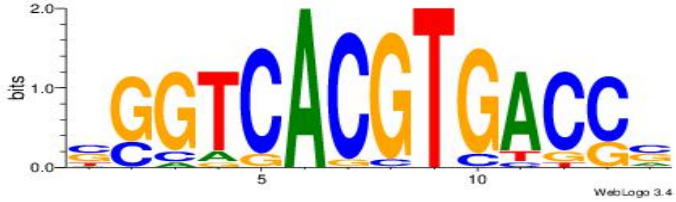
Alignment:

```
SGGTCACGTGACCS
---BCACCTGCABC
```

Original motif Consensus sequence: SGGTCACGTGACCS



Reverse complement motif Consensus sequence: SGGTCACGTGACC



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

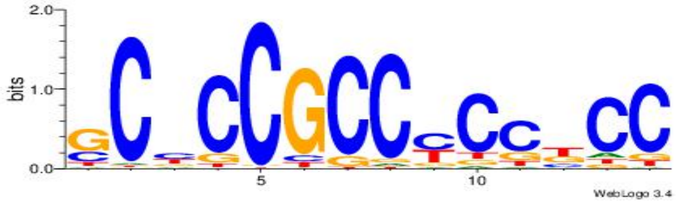
Similarity score: 0.034471

Alignment:

```
GCVCCGCCMCCYCC
BCACCTGCABC---
```

Original motif Consensus sequence: GGMGGRGGCGGVGC

Reverse complement motif Consensus sequence: GCVCCGCCMCCYC



Dataset #: 4

Motif ID: 36

Motif name: csGCCCCGCCCCsc

Matching format of first motif: Original Motif

Matching format of second motif: Original Motif

Direction: Forward

Position number: 2

Number of overlap: 11

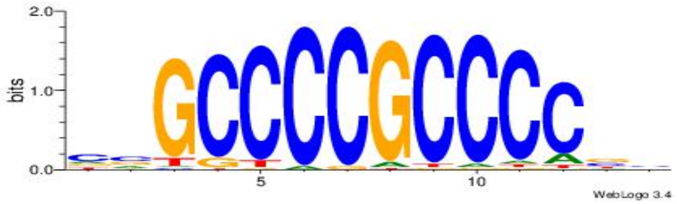
Similarity score: 0.0402518

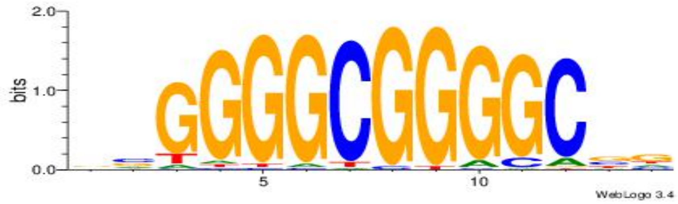
Alignment:

```
HVGCCCCGCCCCBB
-BCACCTGCABC--
```

Original motif Consensus sequence: HVGCCCCGCCCCBB

Reverse complement motif Consensus sequence: BBGGGGCGGGGC



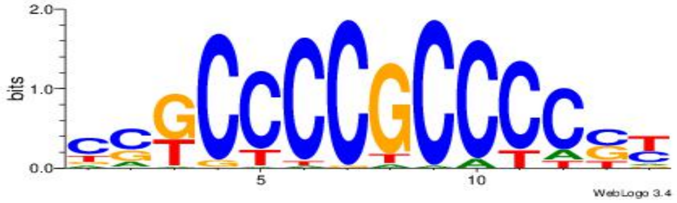


Dataset #:	2
Motif ID:	7
Motif name:	Motif 7
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	11
Similarity score:	0.0411257

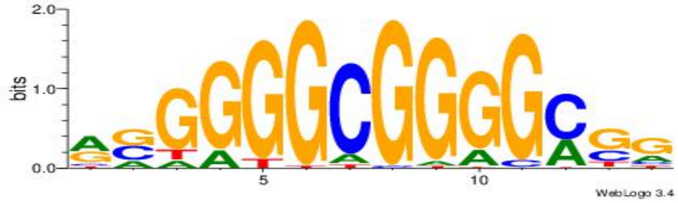
Alignment:

```
CSKCCCCGCCCCSY
-BCACCTGCABC--
```

Original motif Consensus sequence: CSKCCCCGCCCCSY



Reverse complement motif Consensus sequence: MSGGGGCGGGGY



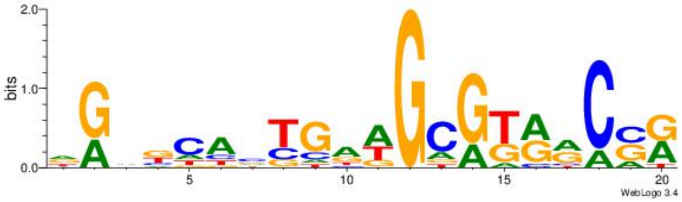
Dataset #:	3
Motif ID:	31

Motif name: Pax5
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 5
Number of overlap: 11
Similarity score: 0.0420218

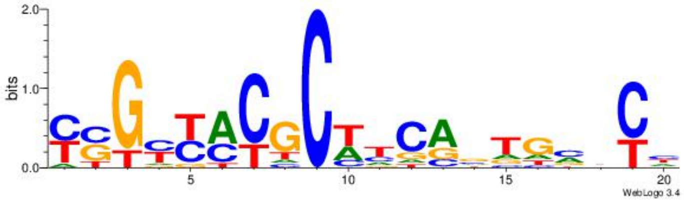
Alignment:

```
DGVBCABTGDWGCGKRRCSR
----GBTGCAGGTGB-----
```

Original motif Consensus sequence: DGVBCABTGDWGCGKRRCSR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD



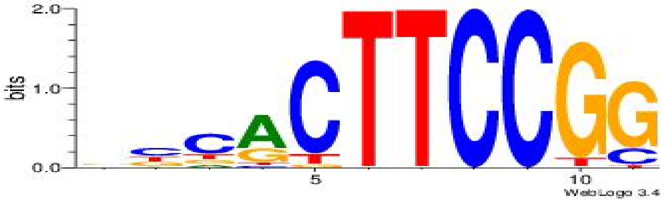
Dataset #: 3
Motif ID: 35
Motif name: GABPA
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 11
Similarity score: 0.0423275

Alignment:

```
CCGGAAGTGVV
GBTGCAGGTGB
```

Original motif Consensus sequence: CCGGAAGTGVV

Reverse complement motif Consensus sequence: VVCACTTCCGG



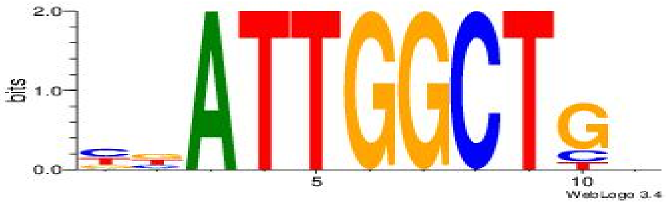
Dataset #:	4
Motif ID:	39
Motif name:	kCAGCCAATmr
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	11
Similarity score:	0.0439586

Alignment:

```
DCAGCCAATVR
GBTGCAGGTGB
```

Original motif Consensus sequence: DCAGCCAATVR

Reverse complement motif Consensus sequence: MBATTGGCTGH

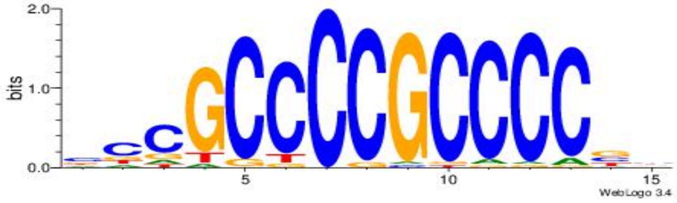


Dataset #:	4
Motif ID:	38
Motif name:	cccGCCCCGCCCCsb
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	3
Number of overlap:	11
Similarity score:	0.0461444

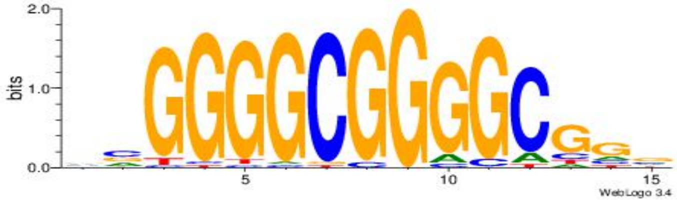
Alignment:

```
BCCGCCCCGCCCCBB
--BCACCTGCABC--
```

Original motif   Consensus sequence: BCCGCCCCGCCCCBB

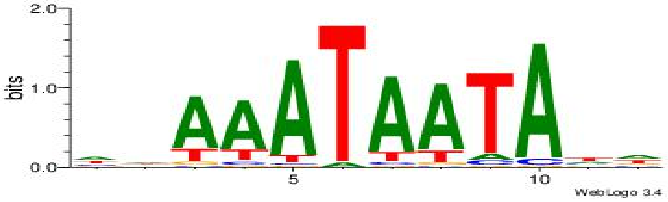


Reverse complement motif   Consensus sequence: BBGGGGCGGGGCGGB

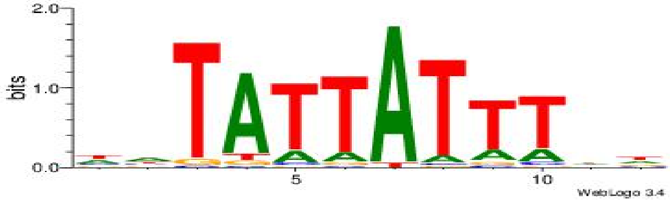


Dataset #: 4   Motif ID: 41   Motif name: wwAAATAATAtw

Original motif Consensus sequence: HDAAATAATADD



Reverse complement motif Consensus sequence: DDTATTATTTDH



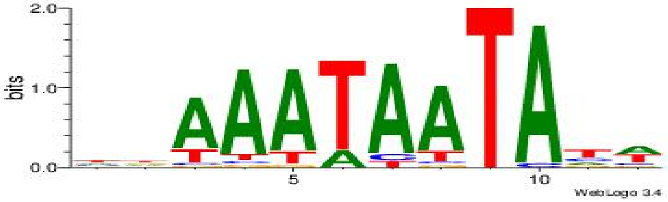
Best Matches for Motif ID 41 (Highest to Lowest)

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

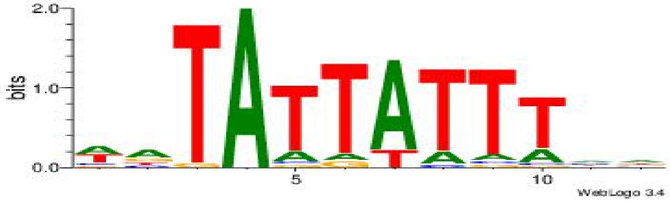
Alignment:

```
HDAAATAATAHW
HDAAATAATADD
```

Original motif Consensus sequence: HDAAATAATAHW



Reverse complement motif Consensus sequence: WHTATTATTTDH

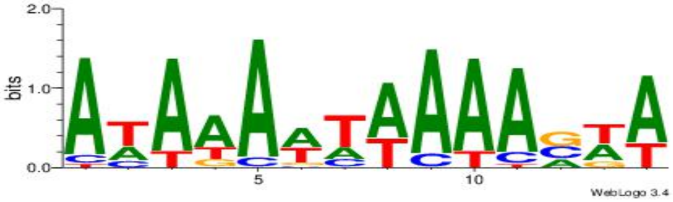


Dataset #:	2
Motif ID:	3
Motif name:	Motif 3
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	12
Similarity score:	0.0536028

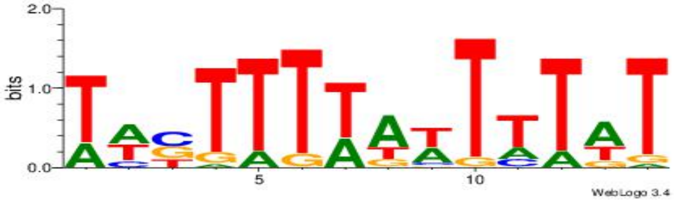
Alignment:

```
AWAAAWTWAAASWA
-HDAAATAATADD-
```

Original motif Consensus sequence: AWAAAWTWAAASWA



Reverse complement motif Consensus sequence: TWSTTTWAWTTTW



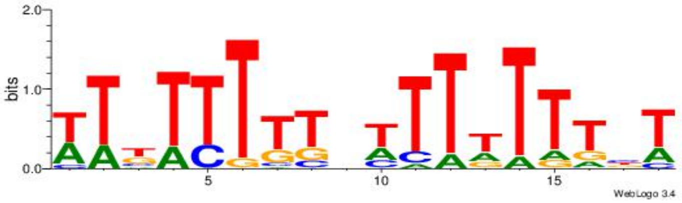
Dataset #:	5
Motif ID:	52
Motif name:	TFM1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	7
Number of overlap:	12

Similarity score:	0.0565705

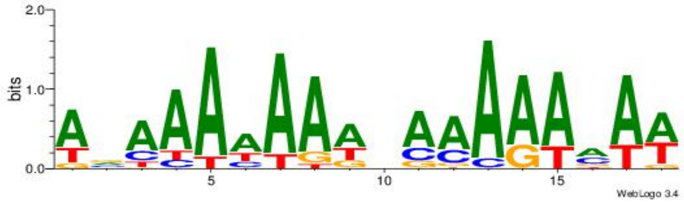
Alignment:

WTKTTTTTHWTTTTTTTBT
------DDTATTATTTDH

Original motif Consensus sequence: WTKTTTTTHWTTTTTTTBT



Reverse complement motif Consensus sequence: ABAAAAAAWHAAAAAARAW



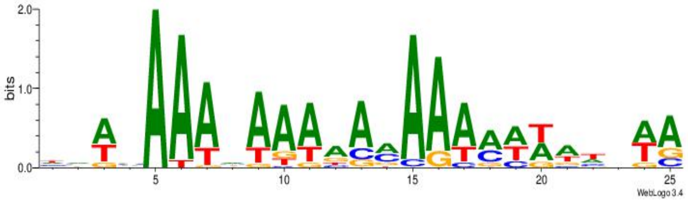
Dataset #:	5
Motif ID:	56
Motif name:	TFM11
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	3
Number of overlap:	12
Similarity score:	0.0575935

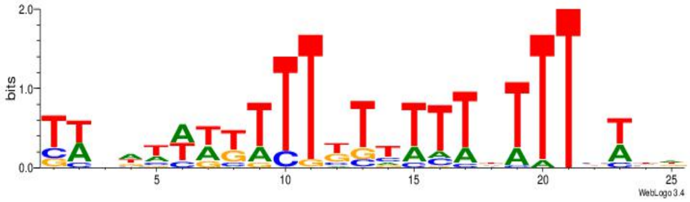
Alignment:

HDWVAAAHAAAAAMAAAMWWWHBWA
--HDAAATAATADD-----------

Original motif Consensus sequence: HDWVAAAHAAAAAMAAAMWWWHBWA

Reverse complement motif Consensus sequence: TWVHWWWYTTTYTTTTTHTTTVWBH



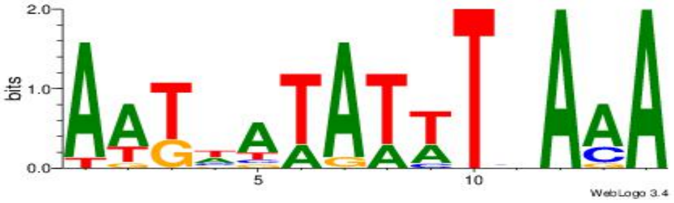


Dataset #: 2
Motif ID: 9
Motif name: Motif 9
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 3
Number of overlap: 12
Similarity score: 0.0591821

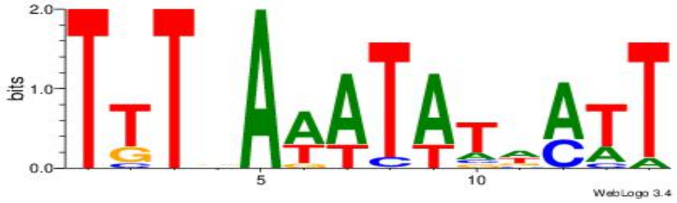
Alignment:

```
AATHATATWTHAAA
--DDTATTATTTDH
```

Original motif Consensus sequence: AATHATATWTHAAA



Reverse complement motif Consensus sequence: TTTDAWATATHAT



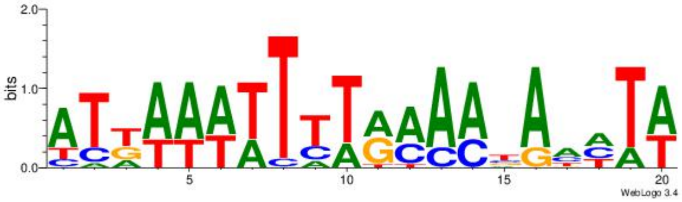
Dataset #: 5
Motif ID: 55

Motif name: TFM13
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: 0.0712963

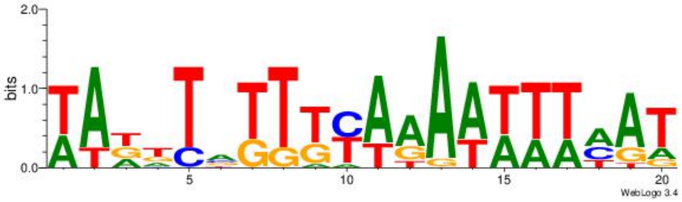
Alignment:

```
WAHHTVTTYKAAAAWTTRAT
--------HDAAATAATADD
```

Original motif Consensus sequence: ATKAAWTTTTRMAABAHHTW



Reverse complement motif Consensus sequence: WAHHTVTTYKAAAAWTTRAT

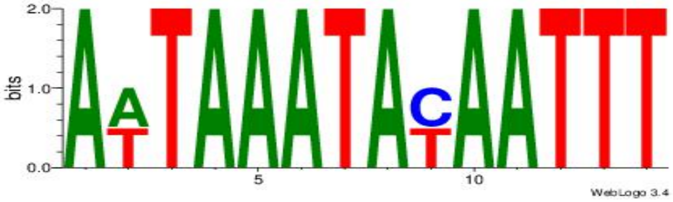


Dataset #: 2
Motif ID: 5
Motif name: Motif 5
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 2
Number of overlap: 12
Similarity score: 0.0715278

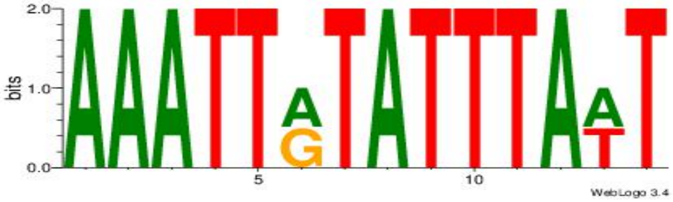
Alignment:

```
AAATTKTATTTAWT
-DDTATTATTTDH-
```

Original motif Consensus sequence: AWTAAATAYAATTT



Reverse complement motif Consensus sequence: AAATTKTATTTAW



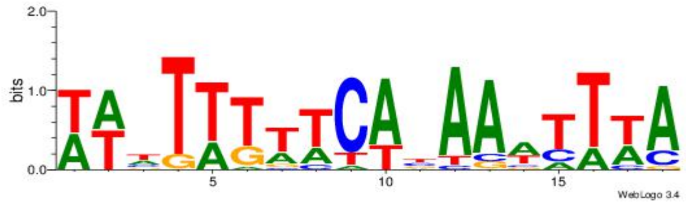
Dataset #:	5
Motif ID:	53
Motif name:	TFM3
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	12
Similarity score:	0.0733516

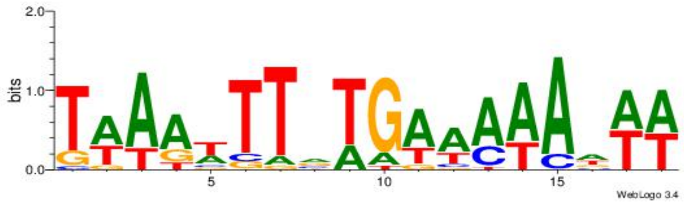
Alignment:

```
WWHTTTTTCABAAWTTWA
------DDTATTATTTDH
```

Original motif Consensus sequence: WWHTTTTTCABAAWTTWA

Reverse complement motif Consensus sequence: TWAAWTTVTGAAAAAHWW



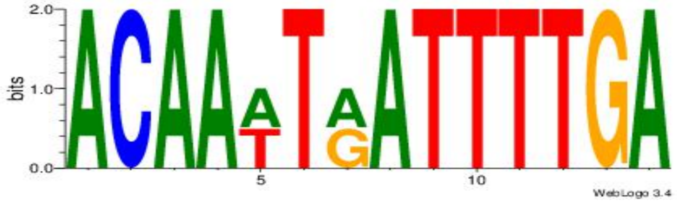


Dataset #: 2
Motif ID: 16
Motif name: Motif 16
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 12
Similarity score: 0.0912037

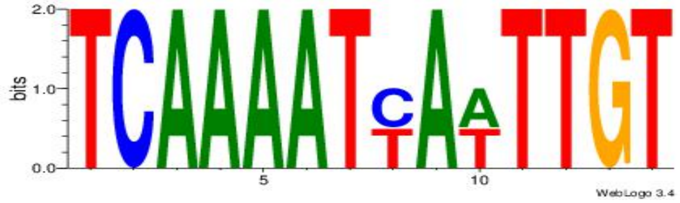
Alignment:

```
TCAAAATKAWTTGT
--DDTATTATTTDH
```

Original motif Consensus sequence: ACAAWTRATTTTGA



Reverse complement motif Consensus sequence: TCAAAATKAWTTG



Dataset #: 2
Motif ID: 6

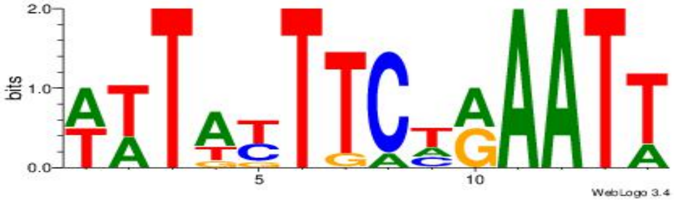
Motif name:	Motif 6
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	3
Number of overlap:	12
Similarity score:	0.0924576

Alignment:

```
WWTAKTTCDKAATT
DDTATTATTTDH--
```

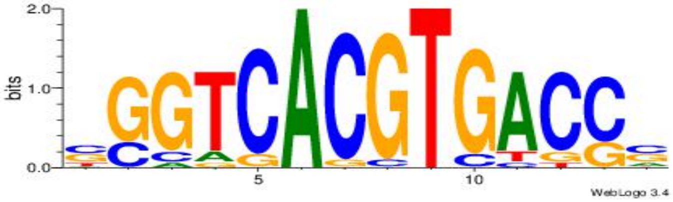
Original motif   Consensus sequence: AATTYDGAARTAWW

Reverse complement motif   Consensus sequence: WWTAKTTCDKAAT

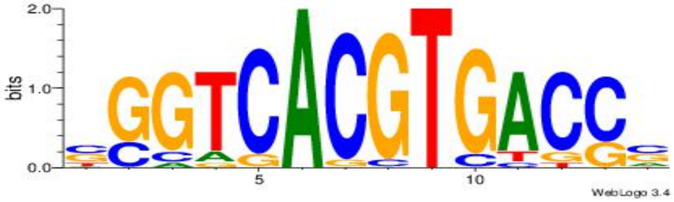


Dataset #: 4   Motif ID: 42   Motif name: sSGTCACGTGACSs

Original motif   Consensus sequence: SGGTCACGTGACCS



Reverse complement motif   Consensus sequence: SGGTCACGTGACC



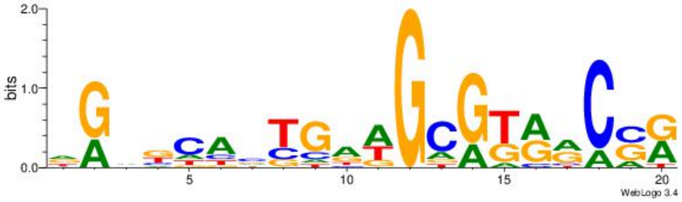
Best Matches for Motif ID 42 (Highest to Lowest)

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

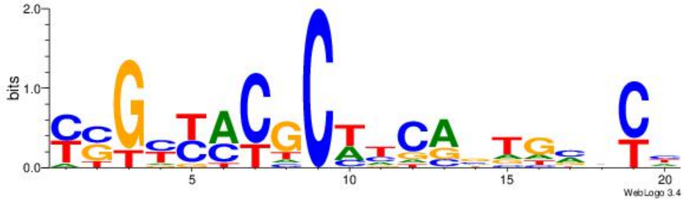
Alignment:

```
DGVBCABTGDWGCGKRRCSR
------SGGTCACGTGACCS
```

Original motif   Consensus sequence: DGVBCABTGDWGCGKRRCSR



Reverse complement motif   Consensus sequence: MSGKKRCGCWDCABTGBBCD

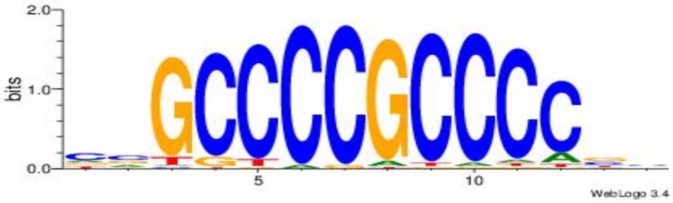


Dataset #: 4
Motif ID: 36
Motif name: csGCCCCGCCCCsc
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1

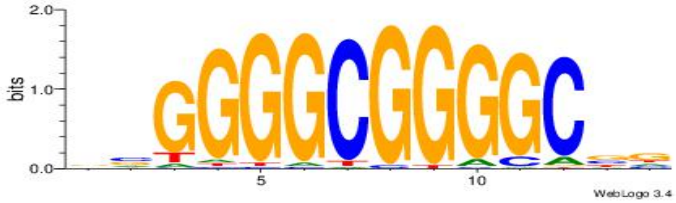
Number of overlap: 14
Similarity score: 0.0539097

Alignment:
BBGGGGCGGGGCVD
SGGTCACGTGACCS

Original motif Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGC

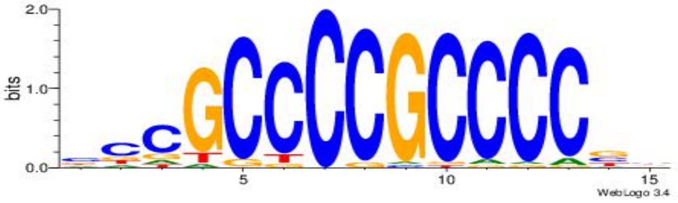


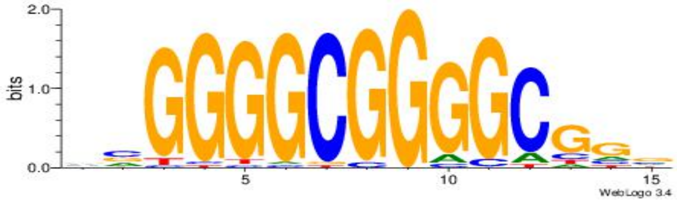
Dataset #: 4
Motif ID: 38
Motif name: cccGCCCCGCCCCsb
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 14
Similarity score: 0.0581955

Alignment:
BCCGCCCCGCCCCBB
SGGTCACGTGACCS-

Original motif Consensus sequence: BCCGCCCCGCCCCBB

Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB



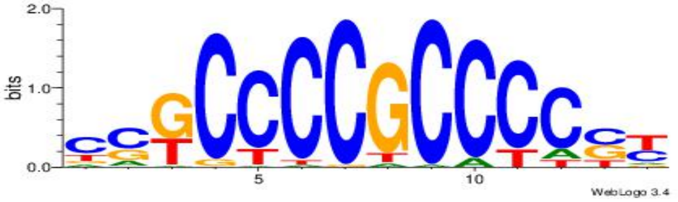


Dataset #: 2
Motif ID: 7
Motif name: Motif 7
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 14
Similarity score: 0.0634135

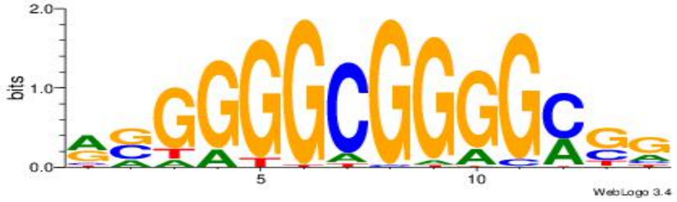
Alignment:

```
MSGGGGCGGGGYSG
SGGTCACGTGACCS
```

Original motif Consensus sequence: CSKCCCCGCCCCSY



Reverse complement motif Consensus sequence: MSGGGGCGGGGY



Dataset #: 5
Motif ID: 50

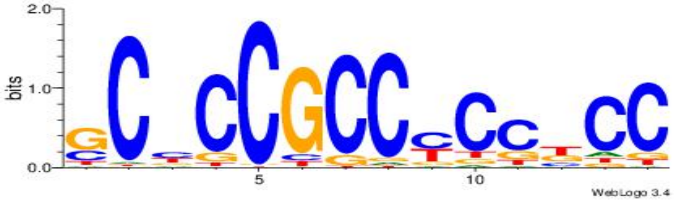
Motif name:	TFF11
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	3
Number of overlap:	12
Similarity score:	1.05855

Alignment:

```
--GCVCCGCCMCCYCC
SGGTCACGTGACCS--
```

Original motif Consensus sequence: GGMGGRGGCGGVGC

Reverse complement motif Consensus sequence: GCVCCGCCMCCYC

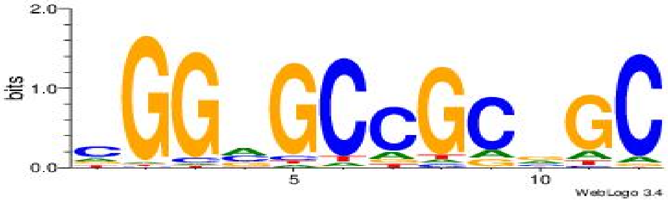


Dataset #:	5
Motif ID:	49
Motif name:	TFF1
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	12
Similarity score:	1.06047

Alignment:

```
--GCVGCGGCBCCG
SGGTCACGTGACCS
```

Original motif   Consensus sequence: CGGVGCCGCVGC



Reverse complement motif   Consensus sequence: GCVGCGGCBCCG

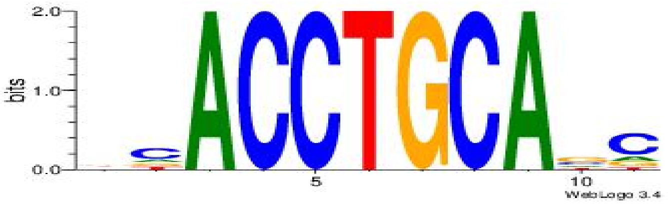
Dataset #:	4
Motif ID:	40
Motif name:	kcACCTGCAgc
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	11
Similarity score:	1.54742

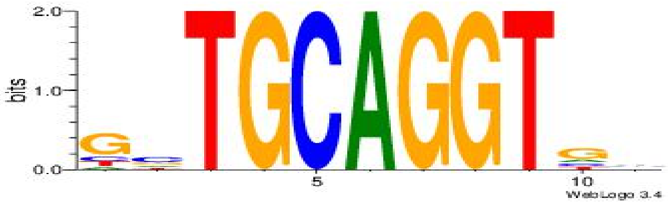
Alignment:

```
---BCACCTGCABC
SGGTCACGTGACCS
```

Original motif   Consensus sequence: BCACCTGCABC

Reverse complement motif   Consensus sequence: GBTGCAGGTGB





Dataset #:	5
Motif ID:	48
Motif name:	TFW3
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	10
Similarity score:	2.05201

Alignment:

```
----CGCGBMGCCG
SGGTCACGTGACCS
```

Original motif Consensus sequence: CGGCYBCGCG

Reverse complement motif Consensus sequence: CGCGBMGCCG

Dataset #:	3
Motif ID:	23

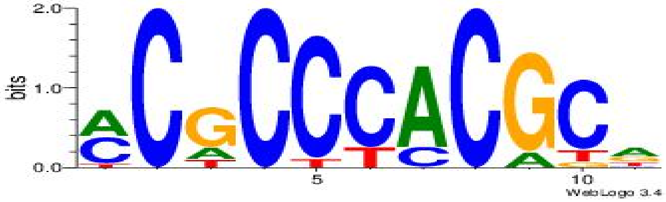
Motif name:	Egr1
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	2
Number of overlap:	10
Similarity score:	2.06209

Alignment:

```
----YCGCCCACGCH
SGGTCACGTGACCS-
```

Original motif   Consensus sequence: HGCGTGGGCGK

Reverse complement motif   Consensus sequence: YCGCCCACGCH

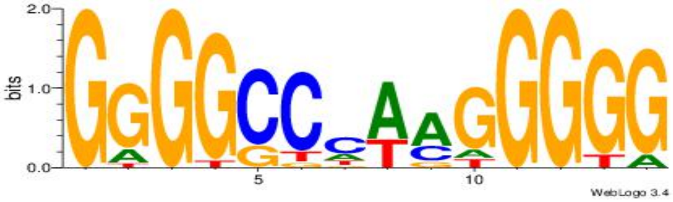


Dataset #:	3
Motif ID:	30
Motif name:	PLAG1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	8
Number of overlap:	7
Similarity score:	3.53253

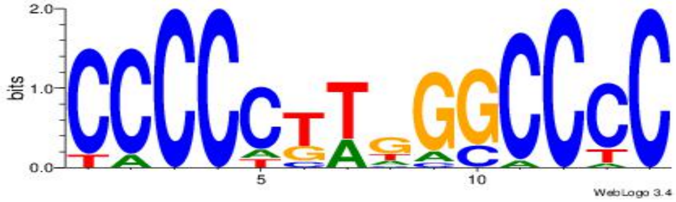
Alignment:

```
CCCCCTTGGGCCCC-------
-------SGGTCACGTGACCS
```

Original motif Consensus sequence: GGGGCCCAAGGGGG



Reverse complement motif Consensus sequence: CCCCCTTGGGCCC



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

Original motif Consensus sequence: HVTACWGTABD

Reverse complement motif Consensus sequence: DBTACWGTAVH

Best Matches for Motif ID 43 (Highest to Lowest)

Dataset #:	4
Motif ID:	40
Motif name:	kcACCTGCAgc
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1

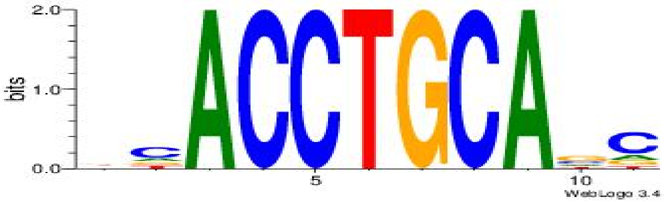
Number of overlap: 11

Similarity score: 0.0199592

Alignment:

```
GBTGCAGGTGB
HVTACWGTABD
```

Original motif Consensus sequence: BCACCTGCABC



Reverse complement motif Consensus sequence: GBTGCAGGTGB

Dataset #: 4

Motif ID: 41

Motif name: wwAAATAATAtw

Matching format of first motif: Original Motif

Matching format of second motif: Reverse Complement

Direction: Backward

Position number: 1

Number of overlap: 11

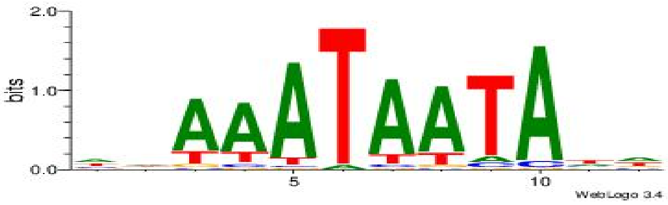
Similarity score: 0.0309343

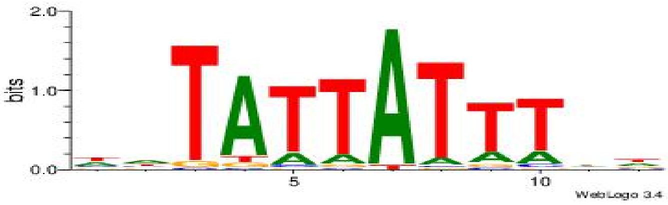
Alignment:

```
DDTATTATTTDH
-HVTACWGTABD
```

Original motif Consensus sequence: HDAAATAATADD

Reverse complement motif Consensus sequence: DDTATTATTTDH



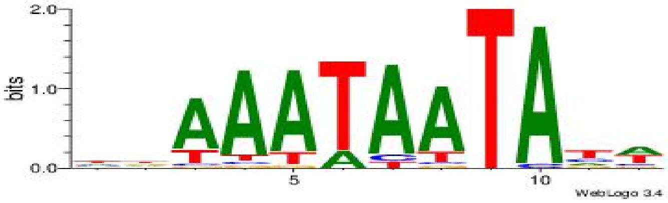


Dataset #:	4
Motif ID:	37
Motif name:	tkAAATAATAtw
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	11
Similarity score:	0.0337121

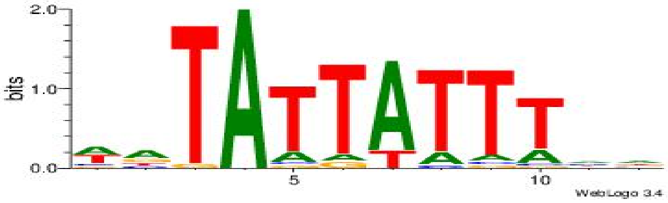
Alignment:

```
WHTATTATTTDH
-HVTACWGTABD
```

Original motif Consensus sequence: HDAAATAATAHW



Reverse complement motif Consensus sequence: WHTATTATTTDH



Dataset #:	2
Motif ID:	6

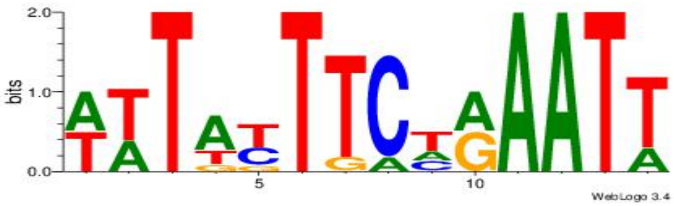
Motif name:	Motif 6
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	4
Number of overlap:	11
Similarity score:	0.0353535

Alignment:

```
AATTYDGAARTAWW
HVTACWGTABD---
```

Original motif Consensus sequence: AATTYDGAARTAWW

Reverse complement motif Consensus sequence: WWTAKTTCDKAAT

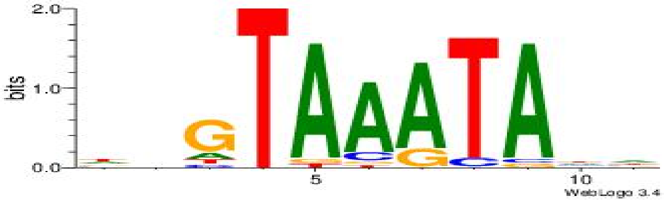


Dataset #:	4
Motif ID:	45
Motif name:	wbgTAAATAww
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	11
Similarity score:	0.037518

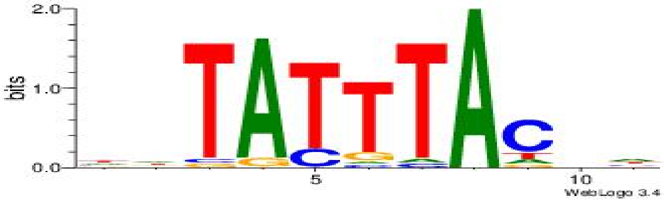
Alignment:

```
DBGTAAATAHD
DBTACWGTAVH
```

Original motif Consensus sequence: DBGTAAATAHD



Reverse complement motif Consensus sequence: DHTATTTACBD



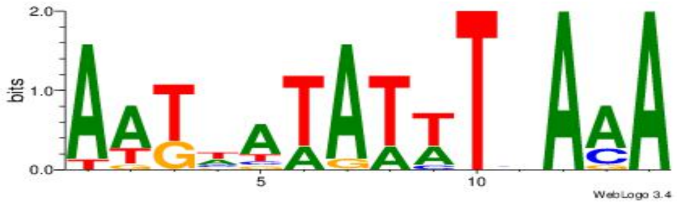
Dataset #:	2
Motif ID:	9
Motif name:	Motif 9
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	4
Number of overlap:	11
Similarity score:	0.0397727

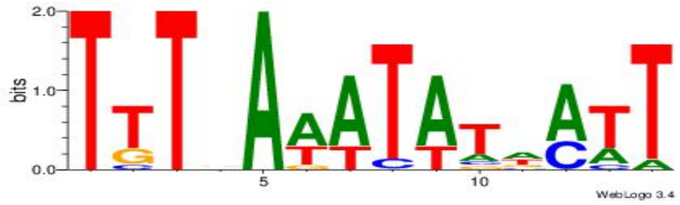
Alignment:

```
TTTDAWATATHATT
DBTACWGTAVH---
```

Original motif Consensus sequence: AATHATATWTHAAA

Reverse complement motif Consensus sequence: TTTDAWATATHAT



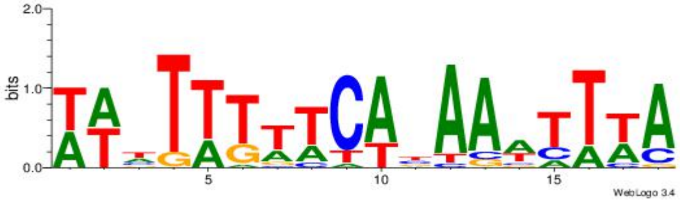


Dataset #:	5
Motif ID:	53
Motif name:	TFM3
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	5
Number of overlap:	11
Similarity score:	0.0413797

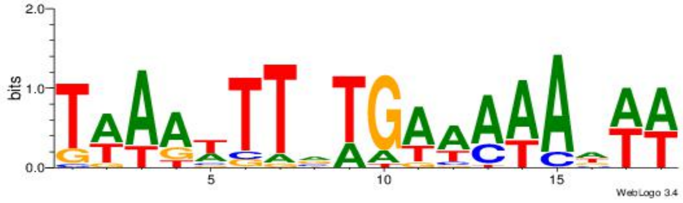
Alignment:

```
TWAAWTTVTGAAAAAHWW
---HVTACWGTABD----
```

Original motif Consensus sequence: WWHTTTTTCABAAWTTWA



Reverse complement motif Consensus sequence: TWAAWTTVTGAAAAAHWW



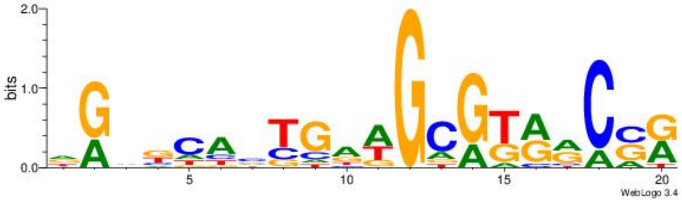
Dataset #:	3

Motif ID:	31
Motif name:	Pax5
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	6
Number of overlap:	11
Similarity score:	0.042298

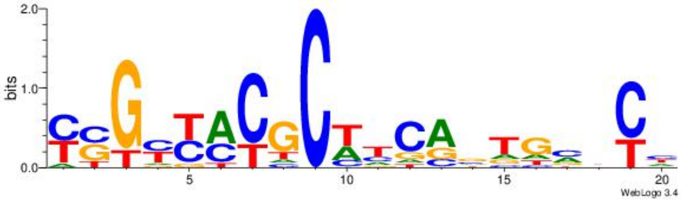
Alignment:

```
DGVBCABTGDWGCGKRRCSR
-----HVTACWGTABD----
```

Original motif Consensus sequence: DGVBCABTGDWGCGKRRCSR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD



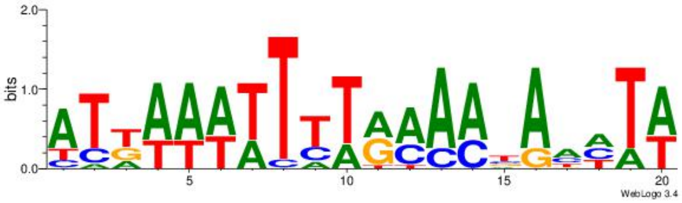
Dataset #:	5
Motif ID:	55
Motif name:	TFM13
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	3
Number of overlap:	11

Similarity score: 0.0445707

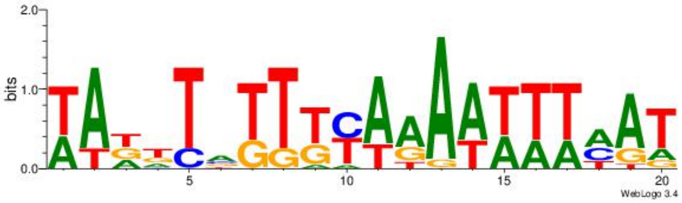
Alignment:

```
ATKAAWTTTTRMAABAHHTW
-------DBTACWGTAVH--
```

Original motif Consensus sequence: ATKAAWTTTTRMAABAHHTW



Reverse complement motif Consensus sequence: WAHHTVTTYKAAAAWTTRAT



Dataset #: 2

Motif ID: 19

Motif name: Motif 19

Matching format of first motif: Reverse Complement

Matching format of second motif: Original Motif

Direction: Backward

Position number: 3

Number of overlap: 11

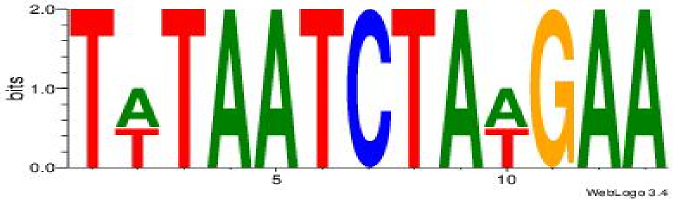
Similarity score: 0.0460859

Alignment:

```
TTCWTAGATTAWA
DBTACWGTAVH--
```

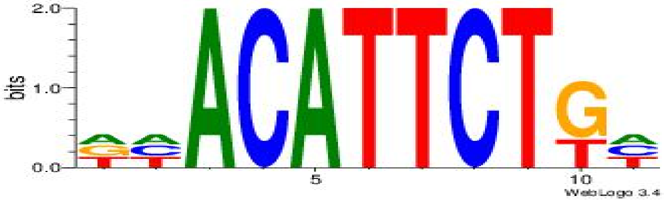
Original motif Consensus sequence: TTCWTAGATTAWA

Reverse complement motif Consensus sequence: TWTAATCTAWGAA



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

Original motif Consensus sequence: DHACATTCTGH



Reverse complement motif Consensus sequence: HCAGAATGTHD

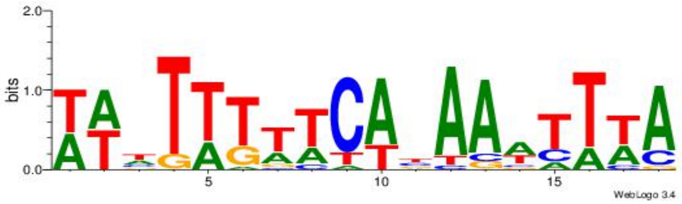
Best Matches for Motif ID 44 (Highest to Lowest)

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

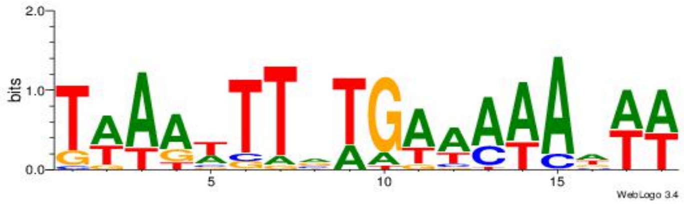
Alignment:

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

Original motif Consensus sequence: WWHTTTTTCABAAWTTWA



Reverse complement motif Consensus sequence: TWAAWTTVTGAAAAAHWW

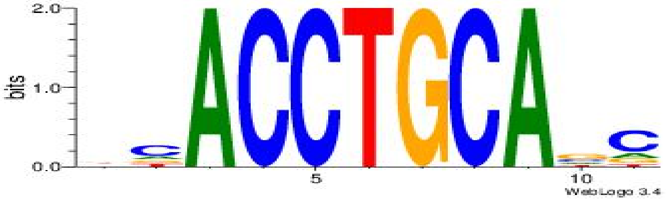


Dataset #:	4
Motif ID:	40
Motif name:	kcACCTGCAgc
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	11
Similarity score:	0.0238442

Alignment:

```
BCACCTGCABC
DHACATTCTGH
```

Original motif Consensus sequence: BCACCTGCABC



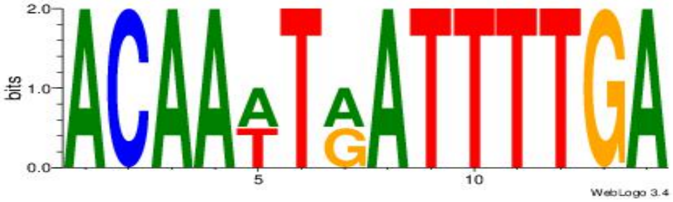
Reverse complement motif Consensus sequence: GBTGCAGGTGB

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

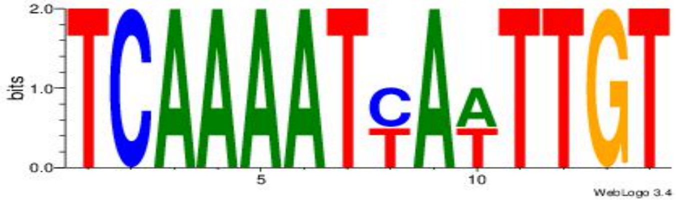
Alignment:

```
TCAAAATKAWTTGT
HCAGAATGTHD---
```

Original motif Consensus sequence: ACAAWTRATTTTGA



Reverse complement motif Consensus sequence: TCAAAATKAWTTG



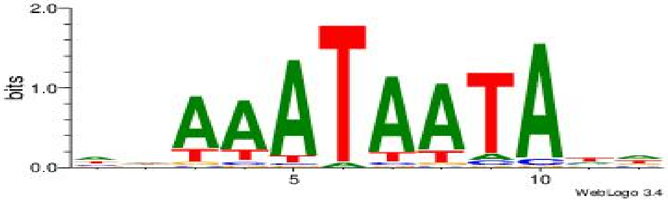
Dataset #: 4
Motif ID: 41
Motif name: wwAAATAATAtw
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 11

Similarity score: 0.0292508

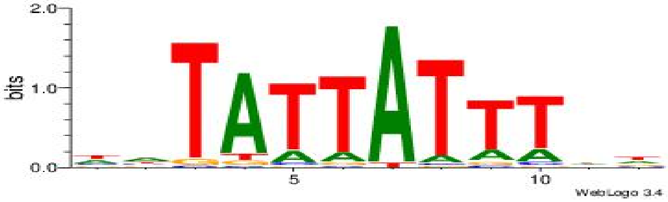
Alignment:

```
DDTATTATTTDH
-HCAGAATGTHD
```

Original motif Consensus sequence: HDAAATAATADD



Reverse complement motif Consensus sequence: DDTATTATTTDH



Dataset #: 5

Motif ID: 56

Motif name: TFM11

Matching format of first motif: Original Motif

Matching format of second motif: Reverse Complement

Direction: Forward

Position number: 5

Number of overlap: 11

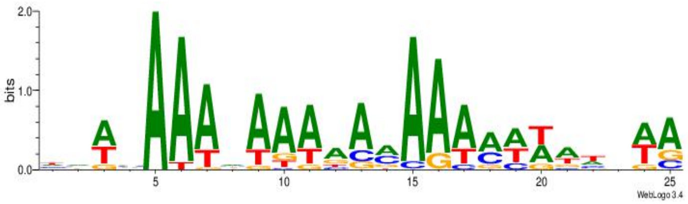
Similarity score: 0.0307858

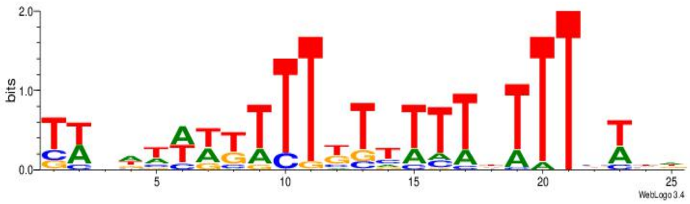
Alignment:

```
TWVHWWWYTTTYTTTTTHTTTVWBH
----DHACATTCTGH----------
```

Original motif Consensus sequence: HDWVAAAHAAAAAMAAAMWWWHBWA

Reverse complement motif Consensus sequence: TWVHWWWYTTTYTTTTTHTTTVWBH



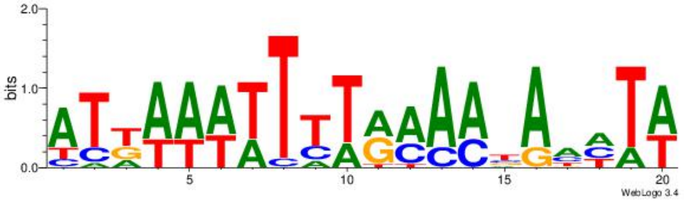


Dataset #:	5
Motif ID:	55
Motif name:	TFM13
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	9
Number of overlap:	11
Similarity score:	0.0357323

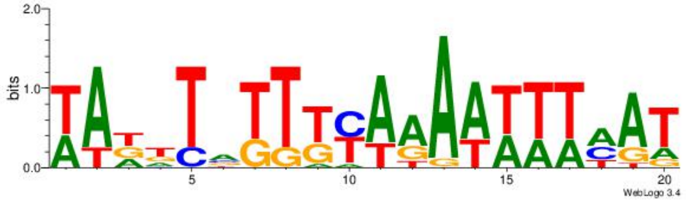
Alignment:

```
ATKAAWTTTTRMAABAHHTW
-DHACATTCTGH--------
```

Original motif Consensus sequence: ATKAAWTTTTRMAABAHHTW



Reverse complement motif Consensus sequence: WAHHTVTTYKAAAAWTTRAT



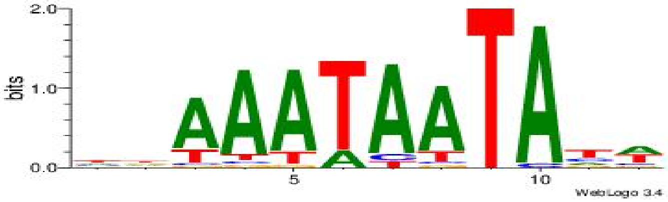
Dataset #: 4

Motif ID: 37
Motif name: tkAAATAATAtw
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 2
Number of overlap: 11
Similarity score: 0.0364899

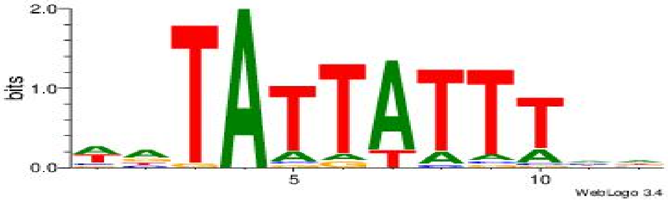
Alignment:

```
WHTATTATTTDH
-HCAGAATGTHD
```

Original motif Consensus sequence: HDAAATAATAHW



Reverse complement motif Consensus sequence: WHTATTATTTDH



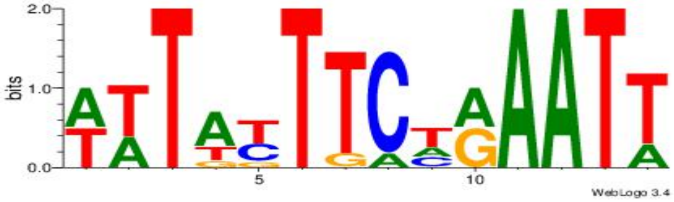
Dataset #: 2
Motif ID: 6
Motif name: Motif 6
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 4
Number of overlap: 11
Similarity score: 0.0400884

Alignment:

```
AATTYDGAARTAWW
HCAGAATGTHD---
```

Original motif Consensus sequence: AATTYDGAARTAWW

Reverse complement motif Consensus sequence: WWTAKTTCDKAAT



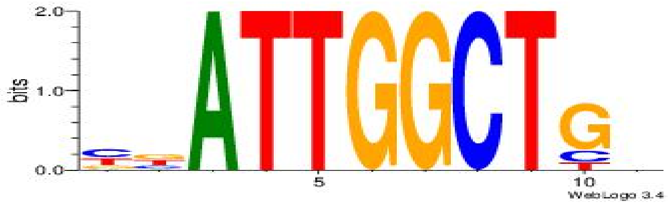
Dataset #:	4
Motif ID:	39
Motif name:	kCAGCCAATmr
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	11
Similarity score:	0.0412582

Alignment:

```
MBATTGGCTGH
DHACATTCTGH
```

Original motif Consensus sequence: DCAGCCAATVR

Reverse complement motif Consensus sequence: MBATTGGCTGH



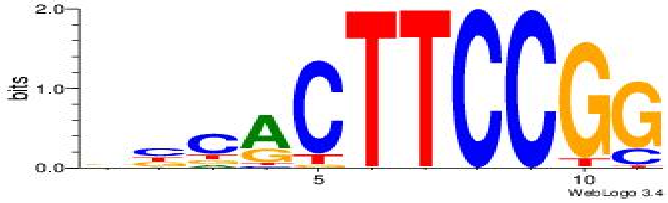
Dataset #:	3
Motif ID:	35
Motif name:	GABPA
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	11
Similarity score:	0.0418896

Alignment:

```
CCGGAAGTGVV
HCAGAATGTHD
```

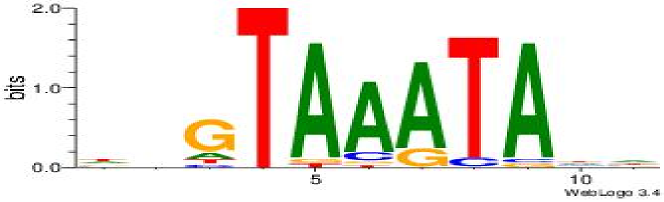
Original motif Consensus sequence: CCGGAAGTGVV

Reverse complement motif Consensus sequence: VVCACTTCCGG

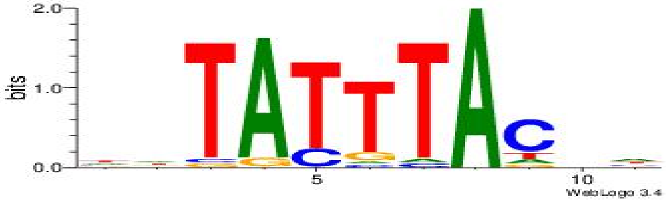


Dataset #: 4 Motif ID: 45 Motif name: wbgTAAATAww

Original motif Consensus sequence: DBGTAAATAHD



Reverse complement motif Consensus sequence: DHTATTTACBD



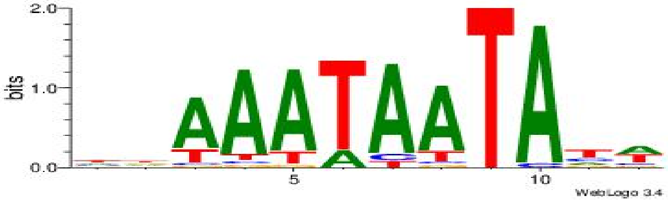
Best Matches for Motif ID 45 (Highest to Lowest)

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

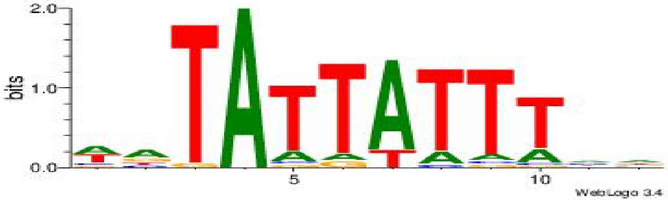
Alignment:

```
HDAAATAATAHW
-DBGTAAATAHD
```

Original motif Consensus sequence: HDAAATAATAHW



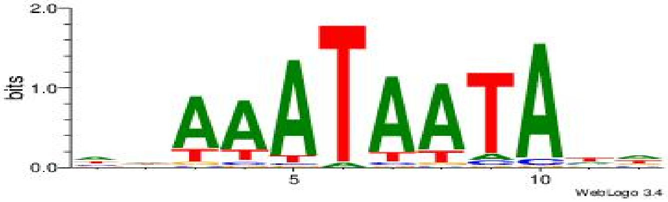
Reverse complement motif Consensus sequence: WHTATTATTTDH



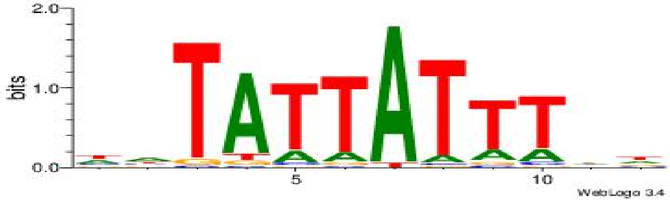
Dataset #: 4
Motif ID: 41
Motif name: wwAAATAATAtw
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 2
Number of overlap: 11
Similarity score: 0.0164863

Alignment:
DDTATTATTTDH
DHTATTTACBD-

Original motif Consensus sequence: HDAAATAATADD



Reverse complement motif Consensus sequence: DDTATTATTTDH



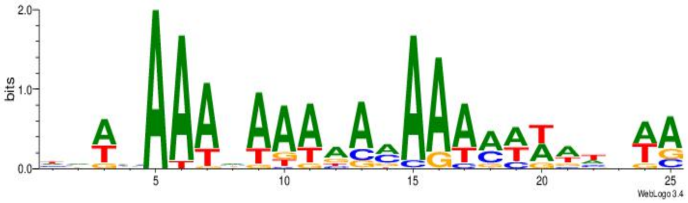
Dataset #: 5
Motif ID: 56
Motif name: TFM11
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 15
Number of overlap: 11

Similarity score: 0.0192768

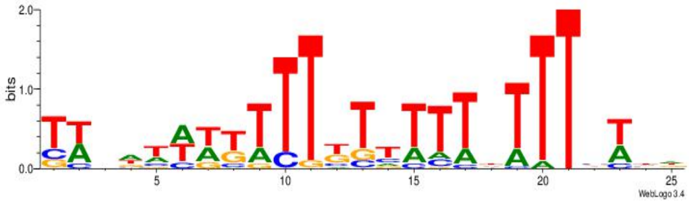
Alignment:

TWVHWWWYTTTYTTTTTHTTTVWBH
--------------DHTATTTACBD

Original motif Consensus sequence: HDWVAAAHAAAAAMAAAMWWWHBWA



Reverse complement motif Consensus sequence: TWVHWWWYTTTYTTTTTHTTTVWBH



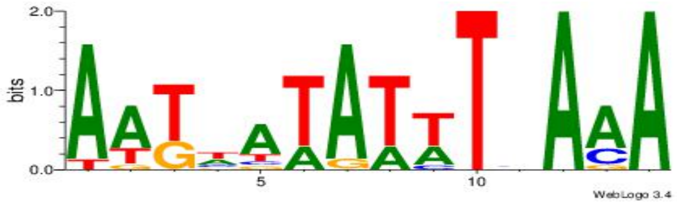
Dataset #:	2
Motif ID:	9
Motif name:	Motif 9
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	4
Number of overlap:	11
Similarity score:	0.0250541

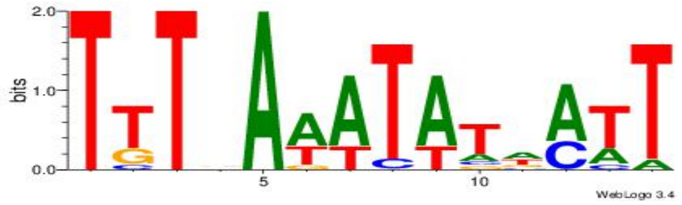
Alignment:

AATHATATWTHAAA
DHTATTTACBD---

Original motif Consensus sequence: AATHATATWTHAAA

Reverse complement motif Consensus sequence: TTTDAWATATHAT





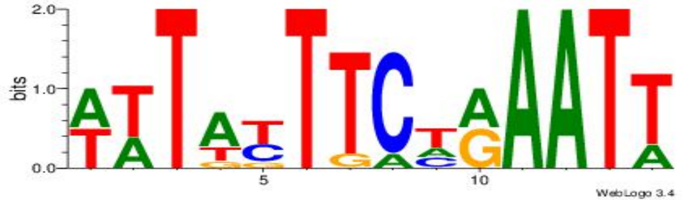
Dataset #:	2
Motif ID:	6
Motif name:	Motif 6
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	11
Similarity score:	0.027895

Alignment:

```
AATTYDGAARTAWW
---DBGTAAATAHD
```

Original motif Consensus sequence: AATTYDGAARTAWW

Reverse complement motif Consensus sequence: WWTAKTTCDKAAT



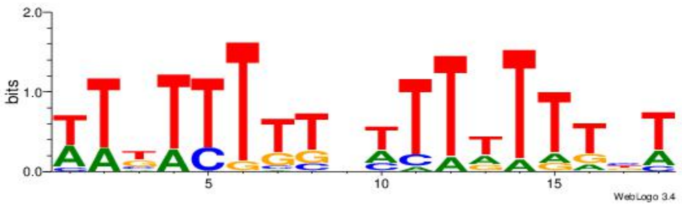
Dataset #:	5
Motif ID:	52

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

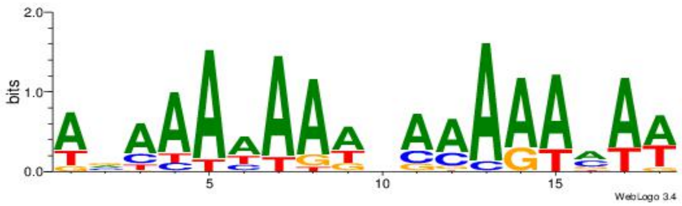
Alignment:

```
ABAAAAAAWHAAAAARAW
DBGTAAATAHD-------
```

Original motif Consensus sequence: WTKTTTTTHWTTTTTTBT



Reverse complement motif Consensus sequence: ABAAAAAAWHAAAAARAW

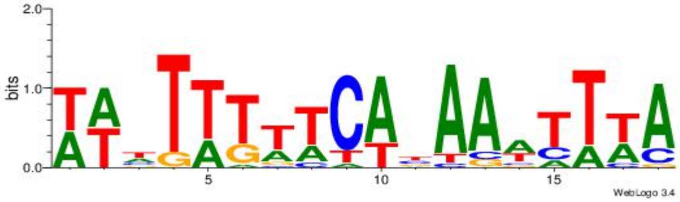


Dataset #: 5
Motif ID: 53
Motif name: TFM3
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 2
Number of overlap: 11
Similarity score: 0.0308097

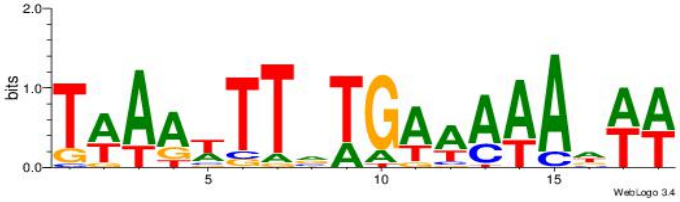
Alignment:

TWAAWTTVTGAAAAAHWW
------DBGTAAATAHD-

Original motif Consensus sequence: WWHTTTTTCABAAWTTWA



Reverse complement motif Consensus sequence: TWAAWTTVTGAAAAAHWW



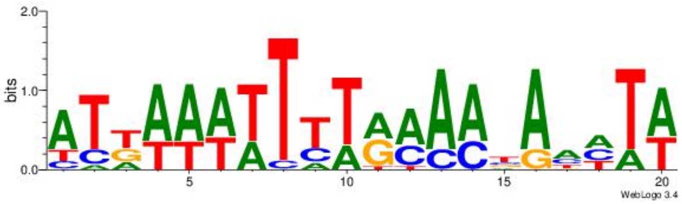
Dataset #:	5
Motif ID:	55
Motif name:	TFM13
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	3
Number of overlap:	11
Similarity score:	0.0333874

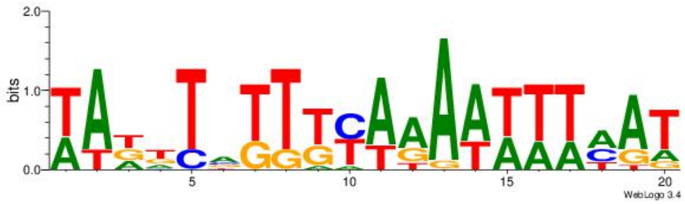
Alignment:

ATKAAWTTTTRMAABAHHTW
-------DBGTAAATAHD--

Original motif Consensus sequence: ATKAAWTTTTRMAABAHHTW

Reverse complement motif Consensus sequence: WAHHTVTTYKAAAAWTTRAT



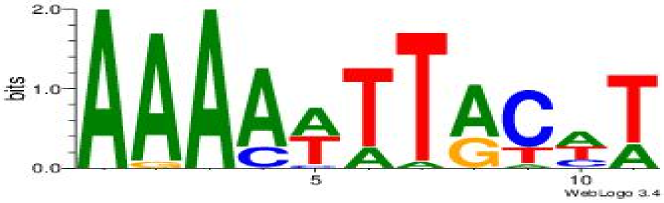


Dataset #:	2
Motif ID:	4
Motif name:	Motif 4
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	11
Similarity score:	0.0361187

Alignment:

```
AWGKAAWTTTT
DBGTAAATAHD
```

Original motif   Consensus sequence: AAAAWTTRCWT



Reverse complement motif   Consensus sequence: AWGKAAWTTTT

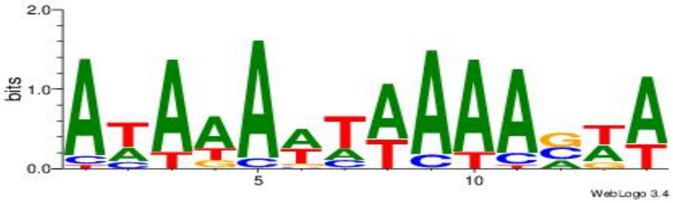
Dataset #:	2
Motif ID:	3

Motif name:	Motif 3
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:	0.0410381

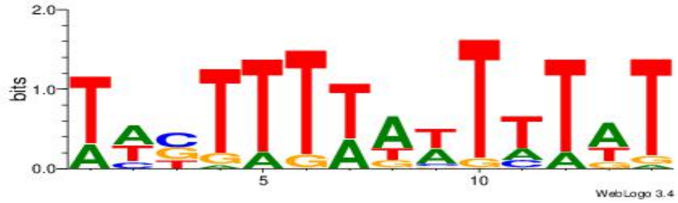
Alignment:

```
AWAAAWTWAAASWA
--DHTATTTACBD-
```

Original motif Consensus sequence: AWAAAWTWAAASWA



Reverse complement motif Consensus sequence: TWSTTTWAWTTT



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

Original motif Consensus sequence: GTCGCG

Reverse complement motif Consensus sequence: CGCGAC

Best Matches for Motif ID 46 (Highest to Lowest)

Dataset #:	5
Motif ID:	48
Motif name:	TFW3
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	6
Similarity score:	0.0350356

Alignment:

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

Original motif Consensus sequence: CGGCYBCGCG

Reverse complement motif Consensus sequence: CGCGBMGCCG

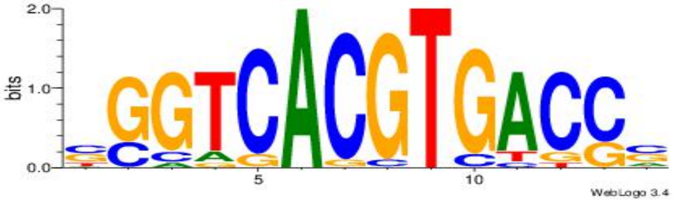
Dataset #:	4
Motif ID:	42
Motif name:	sSGTCACGTGACSs
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	7
Number of overlap:	6

Similarity score: 0.0375102

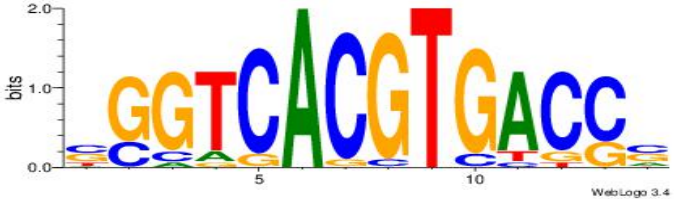
Alignment:

SGGTCACGTGACCS
--GTCGCG------

Original motif Consensus sequence: SGGTCACGTGACCS



Reverse complement motif Consensus sequence: SGGTCACGTGACC



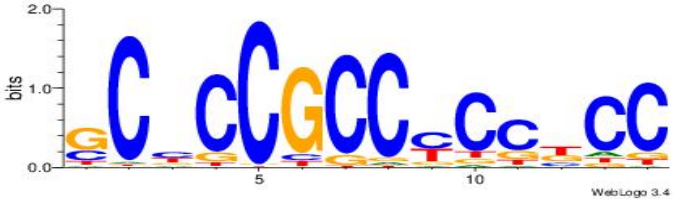
Dataset #:	5
Motif ID:	50
Motif name:	TFF11
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	5
Number of overlap:	6
Similarity score:	0.0381641

Alignment:

GCVCCGCCMCCYCC
----CGCGAC----

Original motif Consensus sequence: GGMGGRGGCGGVGC

Reverse complement motif Consensus sequence: GCVCCGCCMCCY

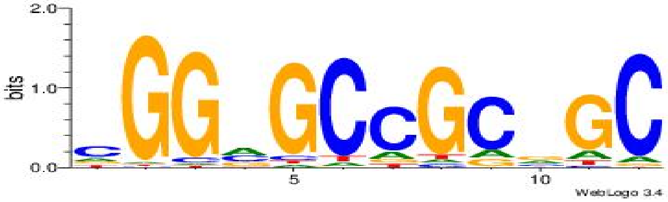


Dataset #:	5
Motif ID:	49
Motif name:	TFF1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	7
Number of overlap:	6
Similarity score:	0.0431161

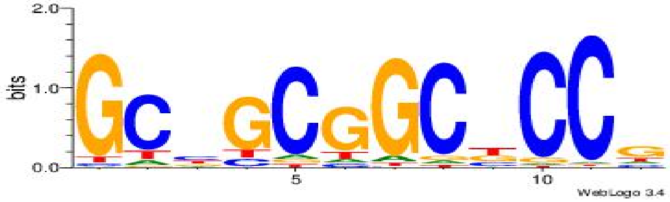
Alignment:

```
CGGVGCCGCVGC
------CGCGAC
```

Original motif Consensus sequence: CGGVGCCGCVGC



Reverse complement motif Consensus sequence: GCVGCGGCBCCG



Dataset #:	5
Motif ID:	47

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

Alignment:

```
CCGCGCGS
-CGCGAC-
```

Original motif Consensus sequence: SCGCGCGG

Reverse complement motif Consensus sequence: CCGCGCGS

Dataset #: 3
Motif ID: 33
Motif name: Mycn
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 6
Similarity score: 0.0537993

Alignment:

```
GCCACGTGSD
----GTCGCG
```

Original motif Consensus sequence: HSCACGTGGC

Reverse complement motif Consensus sequence: GCCACGTGSD

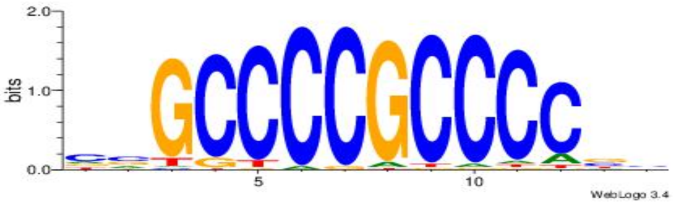
Dataset #:	4
Motif ID:	36
Motif name:	csGCCCCGCCCCsc
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	7
Number of overlap:	6
Similarity score:	0.0539

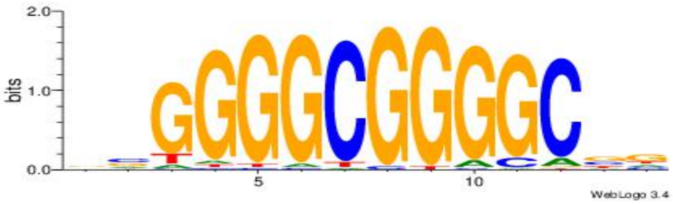
Alignment:

```
HVGCCCCGCCCCBB
--GTCGCG------
```

Original motif Consensus sequence: HVGCCCCGCCCCBB

Reverse complement motif Consensus sequence: BBGGGGCGGGGC





Dataset #:	1
Motif ID:	1
Motif name:	Motif 1
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	3
Number of overlap:	6
Similarity score:	0.0554263

Alignment:

```
GCCCCGCC
--GTCGCG
```

Original motif Consensus sequence: GGCGGGGC

Reverse complement motif Consensus sequence: GCCCCGCC

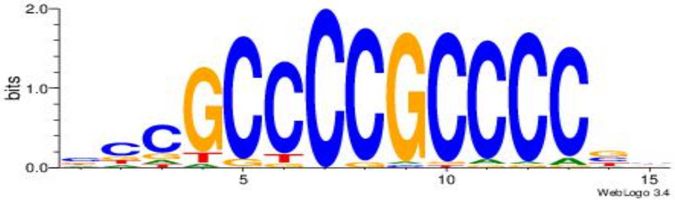
Dataset #:	4
Motif ID:	38

Motif name: cccGCCCCGCCCCsb
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 3
Number of overlap: 6
Similarity score: 0.0558733

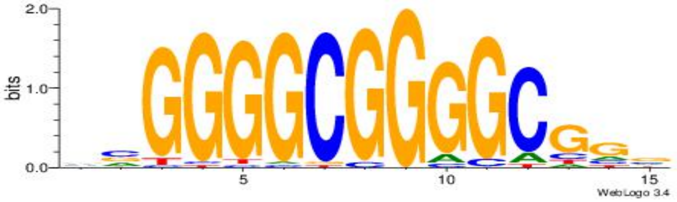
Alignment:

```
BBGGGGCGGGGCGGB
-------GTCGCG--
```

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB

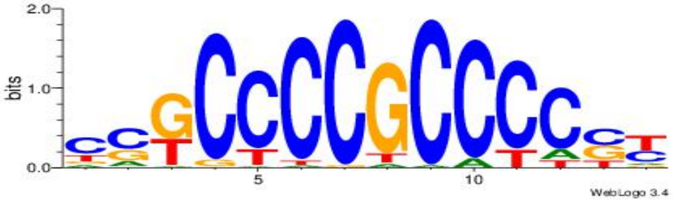


Dataset #: 2
Motif ID: 7
Motif name: Motif 7
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 7
Number of overlap: 6
Similarity score: 0.0644512

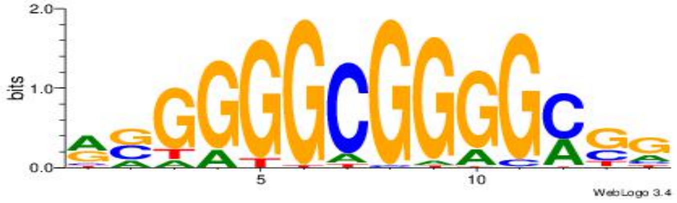
Alignment:

```
CSKCCCCGCCCCSY
--CGCGAC------
```

Original motif   Consensus sequence: CSKCCCCGCCCCSY



Reverse complement motif   Consensus sequence: MSGGGGCGGGGY



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

Original motif   Consensus sequence: SCGCGCGG

Reverse complement motif   Consensus sequence: CCGCGCGS

Best Matches for Motif ID 47 (Highest to Lowest)

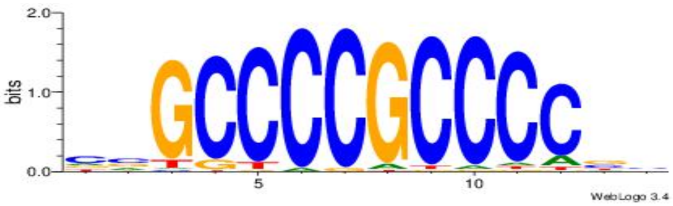
Dataset #:	4
Motif ID:	36
Motif name:	csGCCCCGCCCCsc
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	6

Number of overlap:	8
Similarity score:	0.0456233

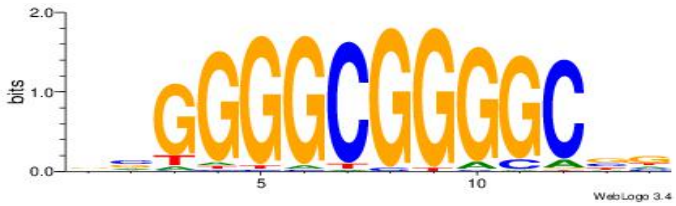
Alignment:

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

Original motif   Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif   Consensus sequence: BBGGGGCGGGGC



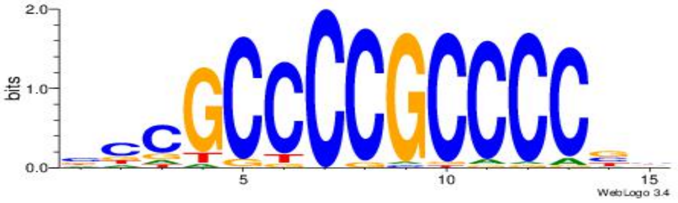
Dataset #:	4
Motif ID:	38
Motif name:	cccGCCCCGCCCCsb
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	7
Number of overlap:	8
Similarity score:	0.045686

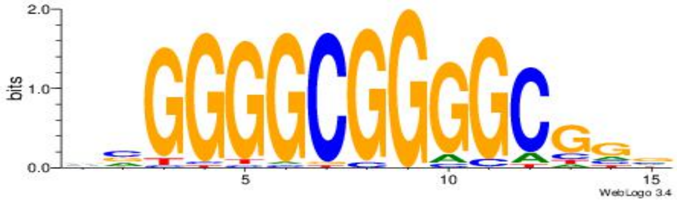
Alignment:

```
BBGGGGCGGGGCGGB
------SCGCGCGG-
```

Original motif   Consensus sequence: BCCGCCCCGCCCCBB

Reverse complement motif   Consensus sequence: BBGGGGCGGGGCGGB



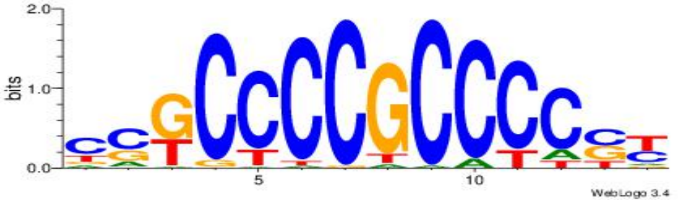


Dataset #: 2
Motif ID: 7
Motif name: Motif 7
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 6
Number of overlap: 8
Similarity score: 0.0504058

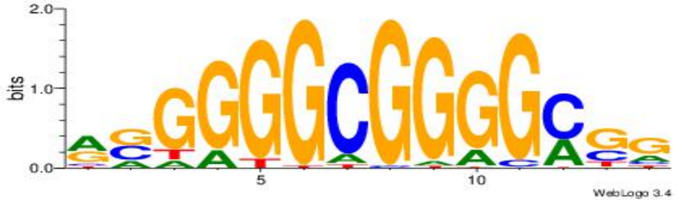
Alignment:

```
CSKCCCCGCCCCSY
-CCGCGCGS-----
```

Original motif Consensus sequence: CSKCCCCGCCCCSY



Reverse complement motif Consensus sequence: MSGGGGCGGGGY



Dataset #: 3
Motif ID: 33

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

Alignment:

```
HSCACGTGGC
-SCGCGCGG-
```

Original motif Consensus sequence: HSCACGTGGC

Reverse complement motif Consensus sequence: GCCACGTGSD

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

Alignment:

```
VGCACGTGGH
-SCGCGCGG-
```

Original motif Consensus sequence: VGCACGTGGH

Reverse complement motif Consensus sequence: DCCACGTGCV

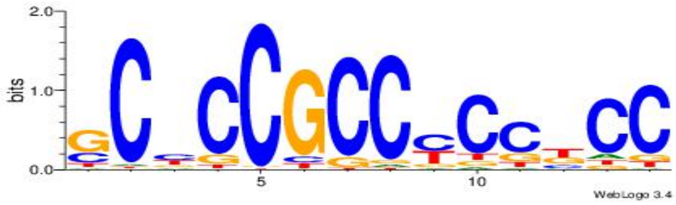
Dataset #:	5
Motif ID:	50
Motif name:	TFF11
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	4
Number of overlap:	8
Similarity score:	0.0583967

Alignment:

```
GCVCCGCCMCCYCC
---CCGCGCGS---
```

Original motif Consensus sequence: GGMGGRGGCGGVGC

Reverse complement motif Consensus sequence: GCVCCGCCMCCYC

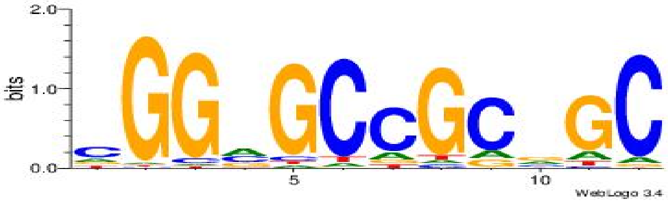


Dataset #:	5
Motif ID:	49
Motif name:	TFF1
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	5
Number of overlap:	8
Similarity score:	0.060966

Alignment:

```
CGGVGCCGCVGC
SCGCGCGG----
```

Original motif Consensus sequence: CGGVGCCGCVGC



Reverse complement motif Consensus sequence: GCVGCGGCBCCG

Dataset #:	3
Motif ID:	25

Motif name: TFAP2A

Matching format of first motif: Original Motif

Matching format of second motif: Reverse Complement

Direction: Backward

Position number: 1

Number of overlap: 8

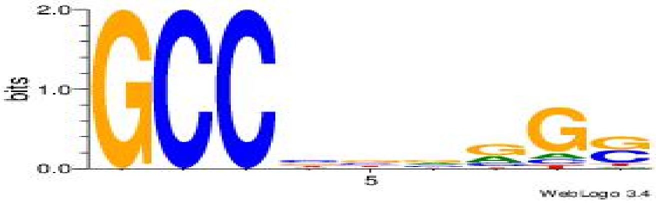
Similarity score: 0.0678925

Alignment:

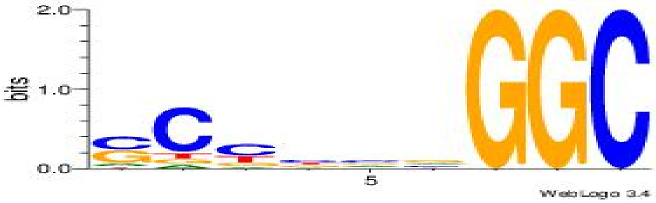
SCMVBBGGC

-SCGCGCGG

Original motif Consensus sequence: GCCBBVRGS



Reverse complement motif Consensus sequence: SCMVBBGGC



Dataset #: 3

Motif ID: 24

Motif name: SP1

Matching format of first motif: Original Motif

Matching format of second motif: Reverse Complement

Direction: Backward

Position number: 3

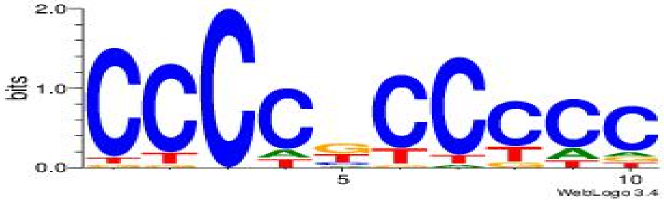
Number of overlap: 8

Similarity score: 0.07018

Alignment:

```
GGGGGYGGGG
SCGCGCGG--
```

Original motif Consensus sequence: CCCCKCCCCC



Reverse complement motif Consensus sequence: GGGGGYGGGG

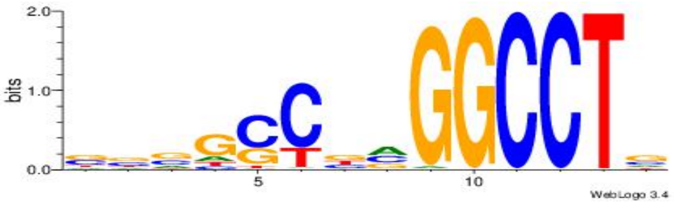
Dataset #:	3
Motif ID:	22
Motif name:	Zfx
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	3
Number of overlap:	8
Similarity score:	0.0710499

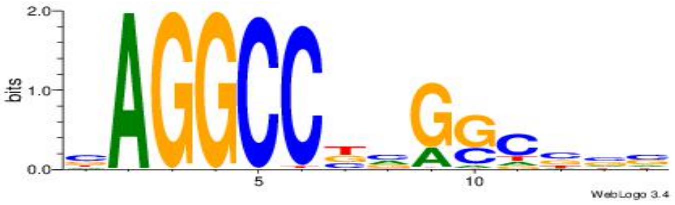
Alignment:

```
BBVGCCBVGGCCTV
--SCGCGCGG----
```

Original motif Consensus sequence: BBVGCCBVGGCCTV

Reverse complement motif Consensus sequence: VAGGCCBBGGCV





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

Original motif Consensus sequence: CGGCYBCGCG

Reverse complement motif Consensus sequence: CGCGBMGCCG

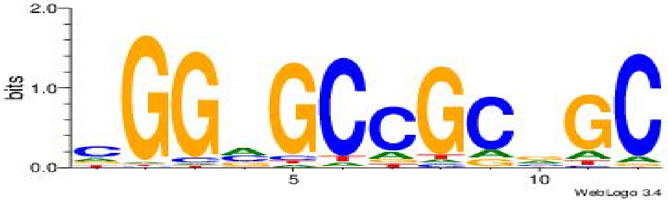
Best Matches for Motif ID 48 (Highest to Lowest)

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

Alignment:

```
CGGVGCCGCVGC
CGGCYBCGCG--
```

Original motif Consensus sequence: CGGVGCCGCVGC



Reverse complement motif Consensus sequence: GCVGCGGCBCCG

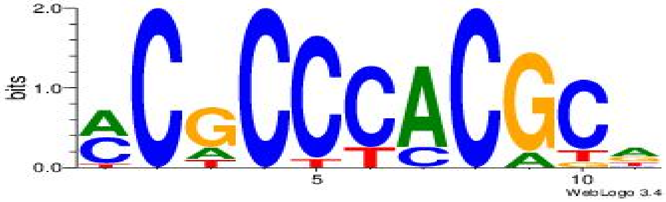
Dataset #:	3
Motif ID:	23
Motif name:	Egr1
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	2
Number of overlap:	10
Similarity score:	0.0630189

Alignment:

```
YCGCCCACGCH
CGGCYBCGCG-
```

Original motif Consensus sequence: HGCGTGGGCGK

Reverse complement motif Consensus sequence: YCGCCCACGCH

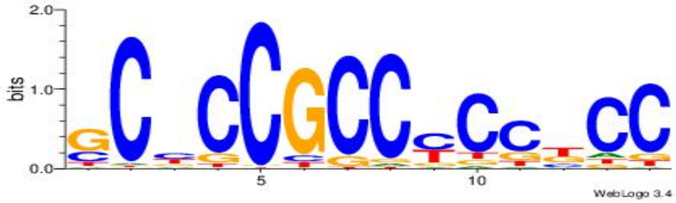


Dataset #: 5
Motif ID: 50
Motif name: TFF11
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 10
Similarity score: 0.0645308

Alignment:
GGMGGRGGCGGVGC
CGCGBMGCCG----

Original motif Consensus sequence: GGMGGRGGCGGVGC

Reverse complement motif Consensus sequence: GCVCCGCCMCCYC



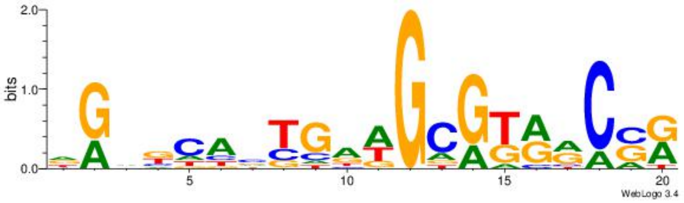
Dataset #: 3
Motif ID: 31
Motif name: Pax5
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 11
Number of overlap: 10

Similarity score: 0.0714355

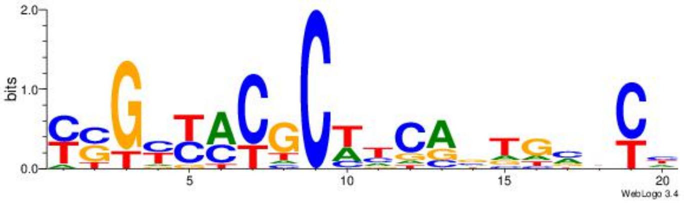
Alignment:

```
MSGKKRCGCWDCABTGBBCD
----------CGGCYBCGCG
```

Original motif Consensus sequence: DGVBCABTGDWGCGKRRCSR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD



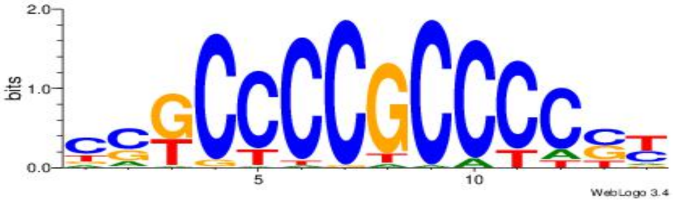
Dataset #: 2
Motif ID: 7
Motif name: Motif 7
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 10
Similarity score: 0.0717594

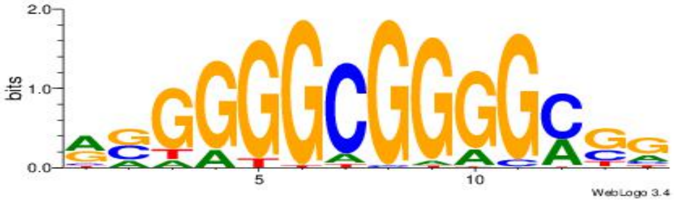
Alignment:

```
CSKCCCCGCCCCSY
CGGCYBCGCG----
```

Original motif Consensus sequence: CSKCCCCGCCCCSY

Reverse complement motif Consensus sequence: MSGGGGCGGGGY



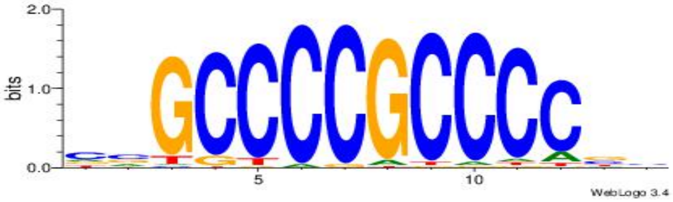


Dataset #: 4
Motif ID: 36
Motif name: csGCCCCGCCCCsc
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 5
Number of overlap: 10
Similarity score: 0.0718771

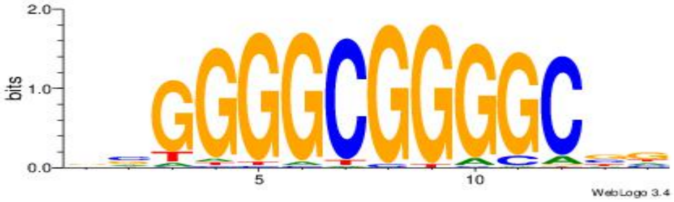
Alignment:

```
HVGCCCCGCCCCBB
CGGCYBCGCG----
```

Original motif Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGC



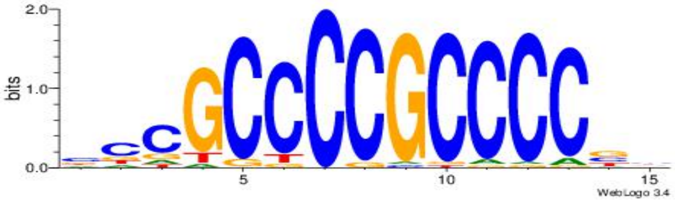
Dataset #: 4
Motif ID: 38

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

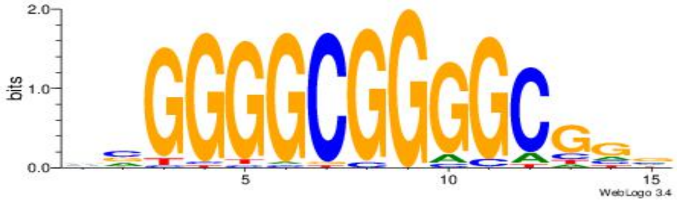
Alignment:

```
BCCGCCCCGCCCCBB
-CGGCYBCGCG----
```

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB

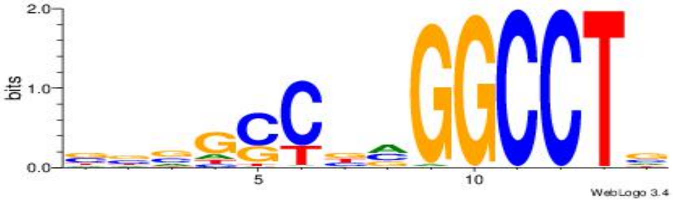


Dataset #: 3
Motif ID: 22
Motif name: Zfx
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 3
Number of overlap: 10
Similarity score: 0.0766755

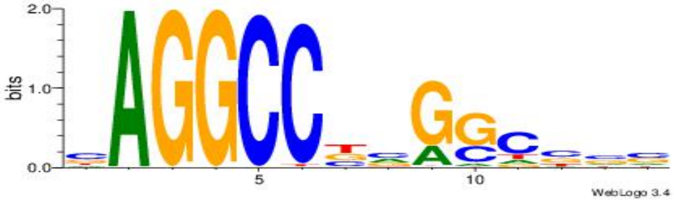
Alignment:

```
VAGGCCBBGGCVBB
--CGGCYBCGCG--
```

Original motif Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif Consensus sequence: VAGGCCBBGGCV



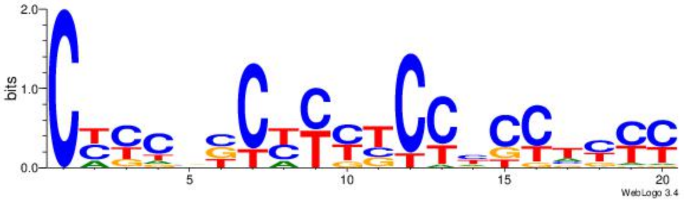
Dataset #:	5
Motif ID:	54
Motif name:	TFM12
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	10
Similarity score:	0.0767689

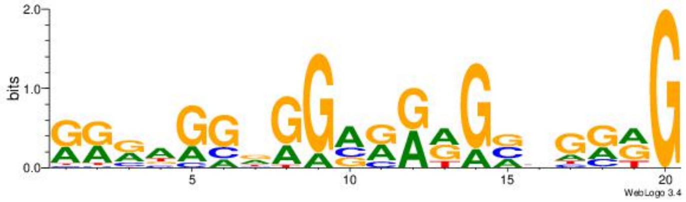
Alignment:

```
KKKAGGDGGAKKMGBBGKMG
----------CGCGBMGCCG
```

Original motif Consensus sequence: CYYCBBCYYYTCCHCCTYYY

Reverse complement motif Consensus sequence: KKKAGGDGGAKKMGBBGKMG



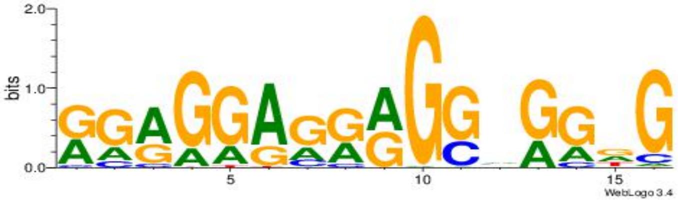


Dataset #: 5
Motif ID: 51
Motif name: TFM2
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 7
Number of overlap: 10
Similarity score: 0.0814831

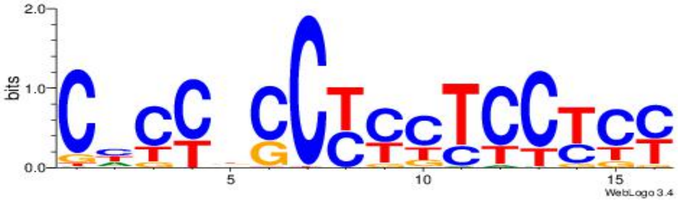
Alignment:

```
CHCCBCCKMCTCCKCM
CGGCYBCGCG------
```

Original motif Consensus sequence: RGRGGAGRRGGHGGDG

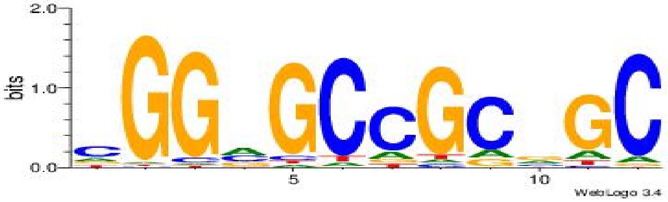


Reverse complement motif Consensus sequence: CHCCBCCKMCTCCKCM

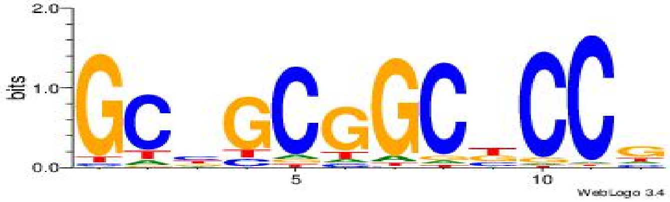


Dataset #: 5 Motif ID: 49 Motif name: TFF1

Original motif Consensus sequence: CGGVGCCGCVGC



Reverse complement motif Consensus sequence: GCVGCGGCBCCG



Best Matches for Motif ID 49 (Highest to Lowest)

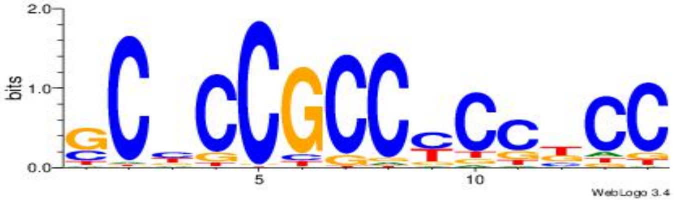
Dataset #:	5
Motif ID:	50
Motif name:	TFF11
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	12
Similarity score:	0.0292081

Alignment:

```
GGMGGRGGCGGVGC
--CGGVGCCGCVGC
```

Original motif Consensus sequence: GGMGGRGGCGGVGC

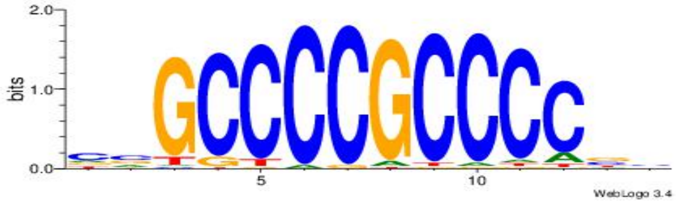
Reverse complement motif Consensus sequence: GCVCCGCCMCCYC



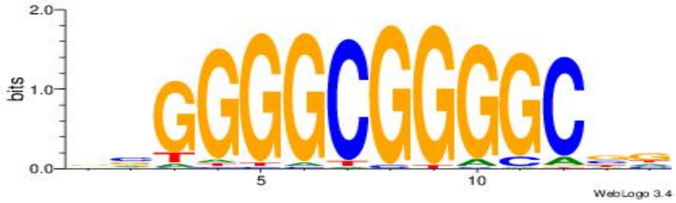
Dataset #: 4
Motif ID: 36
Motif name: csGCCCCGCCCCsc
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 12
Similarity score: 0.0542674

Alignment:
HVGCCCCGCCCCBB
CGGVGCCGCVGC--

Original motif Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGC



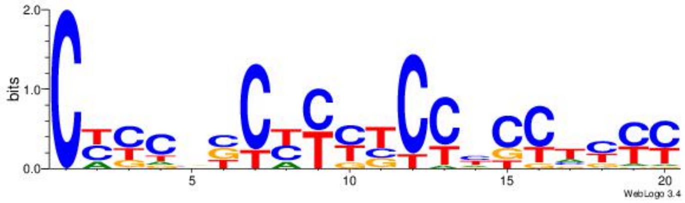
Dataset #: 5
Motif ID: 54
Motif name: TFM12
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 7
Number of overlap: 12

Similarity score:	0.0543272

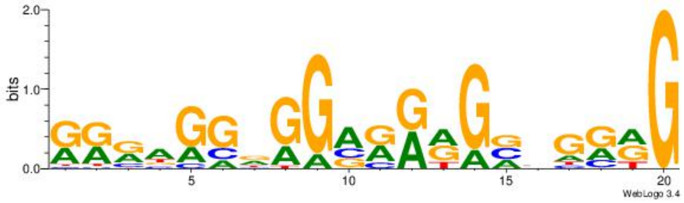
Alignment:

```
KKKAGGDGGAKKMGBBGKMG
------CGGVGCCGCVGC--
```

Original motif Consensus sequence: CYYCBBCYYYTCCHCCTYYY



Reverse complement motif Consensus sequence: KKKAGGDGGAKKMGBBGKMG



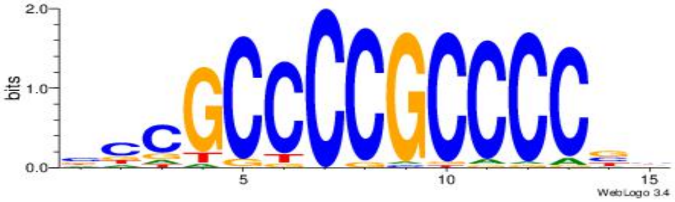
Dataset #:	4
Motif ID:	38
Motif name:	cccGCCCCGCCCCsb
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	4
Number of overlap:	12
Similarity score:	0.0548371

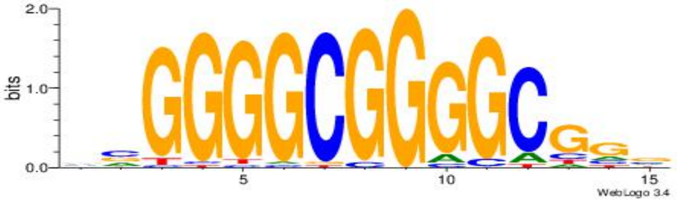
Alignment:

```
BBGGGGCGGGGCGGB
---CGGVGCCGCVGC
```

Original motif Consensus sequence: BCCGCCCCGCCCCBB

Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB



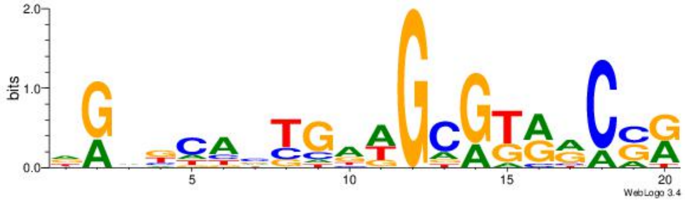


Dataset #:	3
Motif ID:	31
Motif name:	Pax5
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	12
Similarity score:	0.0556962

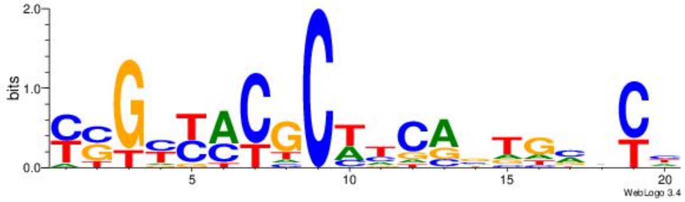
Alignment:

```
DGVBCABTGDWGCGKRRCSR
GCVGCGGCBCCG--------
```

Original motif Consensus sequence: DGVBCABTGDWGCGKRRCSR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD



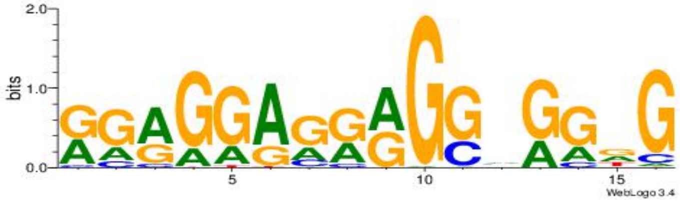
Dataset #:	5

Motif ID: 51
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

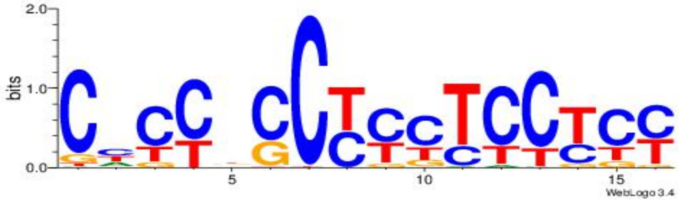
Alignment:

```
CHCCBCCKMCTCCKCM
--GCVGCGGCBCCG--
```

Original motif Consensus sequence: RGRGGAGRRGGHGGDG



Reverse complement motif Consensus sequence: CHCCBCCKMCTCCKCM



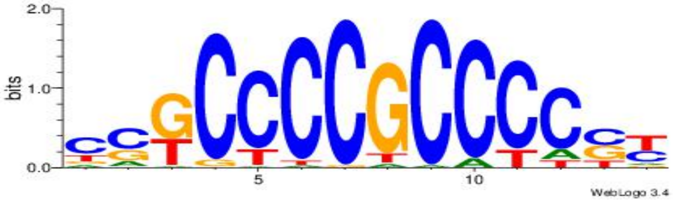
Dataset #: 2
Motif ID: 7
Motif name: Motif 7
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 12

Similarity score: 0.0624366

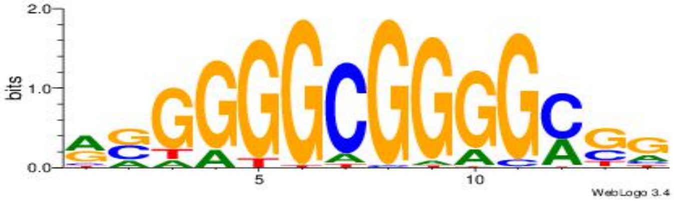
Alignment:

```
CSKCCCCGCCCCSY
GCVGCGGCBCCG--
```

Original motif Consensus sequence: CSKCCCCGCCCCSY



Reverse complement motif Consensus sequence: MSGGGGCGGGGY



Dataset #: 4

Motif ID: 42

Motif name: sSGTCACGTGACSs

Matching format of first motif: Original Motif

Matching format of second motif: Reverse Complement

Direction: Backward

Position number: 1

Number of overlap: 12

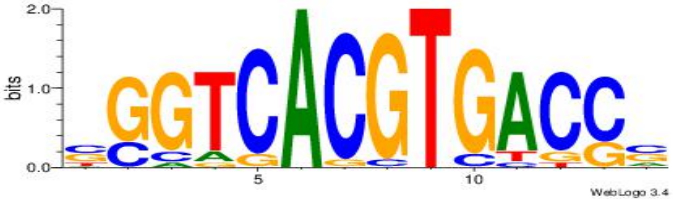
Similarity score: 0.0777862

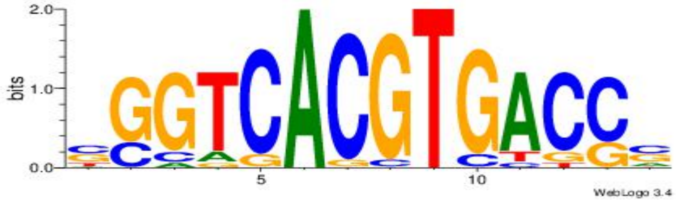
Alignment:

```
SGGTCACGTGACCS
--CGGVGCCGCVGC
```

Original motif Consensus sequence: SGGTCACGTGACCS

Reverse complement motif Consensus sequence: SGGTCACGTGACC



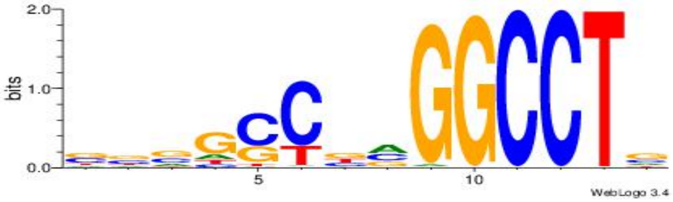


Dataset #:	3
Motif ID:	22
Motif name:	Zfx
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	12
Similarity score:	0.0779228

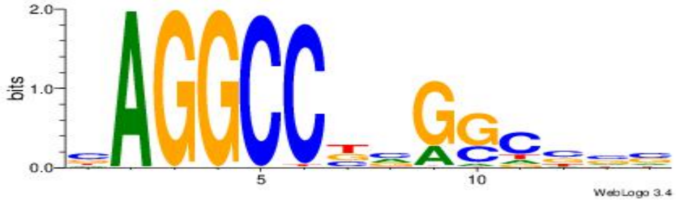
Alignment:

```
BBVGCCBVGGCCTV
-GCVGCGGCBCCG-
```

Original motif Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif Consensus sequence: VAGGCCBBGGCV



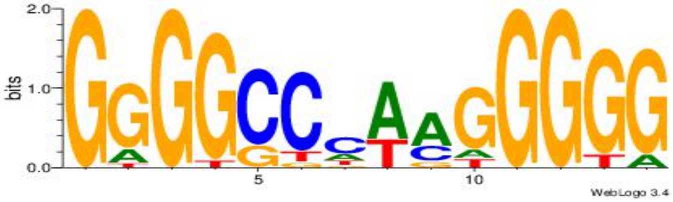
Dataset #:	3
Motif ID:	30

Motif name:	PLAG1
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	12
Similarity score:	0.0809608

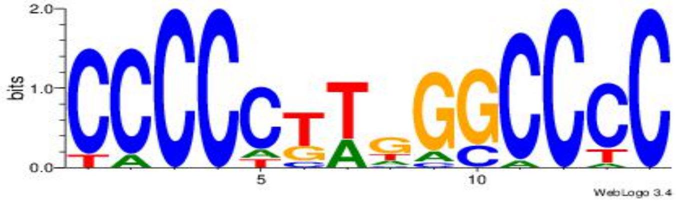
Alignment:

```
GGGGCCCAAGGGGG
CGGVGCCGCVGC--
```

Original motif Consensus sequence: GGGGCCCAAGGGGG



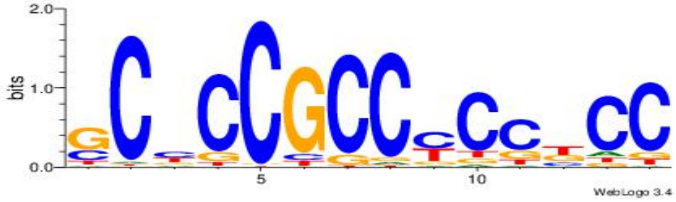
Reverse complement motif Consensus sequence: CCCCCTTGGGCCC



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

Original motif Consensus sequence: GGMGGRGGCGGVGC

Reverse complement motif Consensus sequence: GCVCCGCCMCCYC



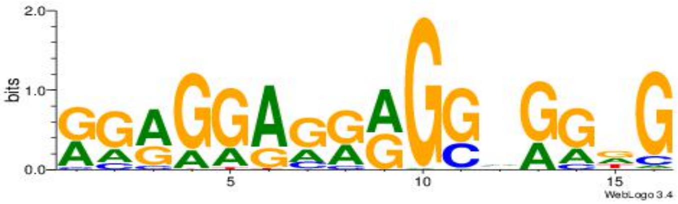
Best Matches for Motif ID 50 (Highest to Lowest)

Dataset #: 5
Motif ID: 51
Motif name: TFM2
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 3
Number of overlap: 14
Similarity score: 0.033716

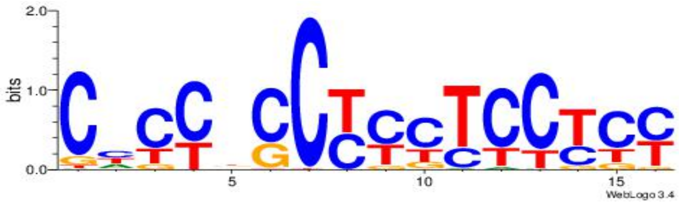
Alignment:

```
RGRGGAGRRGGHGGDG
GGMGGRGGCGGVGC--
```

Original motif Consensus sequence: RGRGGAGRRGGHGGDG



Reverse complement motif Consensus sequence: CHCCBCCKMCTCCKCM

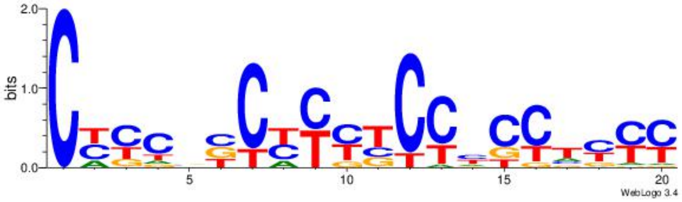


Dataset #: 5
Motif ID: 54
Motif name: TFM12
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 6

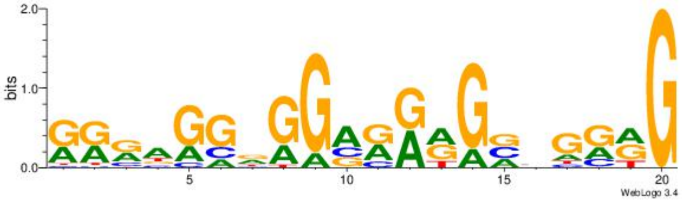
Number of overlap: 14
Similarity score: 0.0386905

Alignment:
```
CYYCBBCYYYTCCHCCTYYY
-----GCVCCGCCMCCYCC-
```

Original motif Consensus sequence: CYYCBBCYYYTCCHCCTYYY



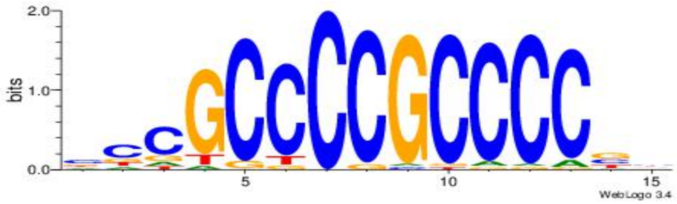
Reverse complement motif Consensus sequence: KKKAGGDGGAKKMGBBGKMG



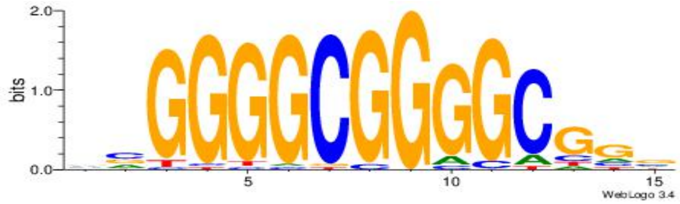
Dataset #: 4
Motif ID: 38
Motif name: cccGCCCCGCCCCsb
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 2
Number of overlap: 14
Similarity score: 0.0548198

Alignment:
```
BBGGGGCGGGGCGGB
GGMGGRGGCGGVGC-
```

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB

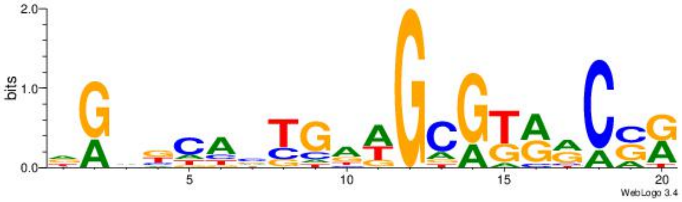


Dataset #:	3
Motif ID:	31
Motif name:	Pax5
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	3
Number of overlap:	14
Similarity score:	0.0573129

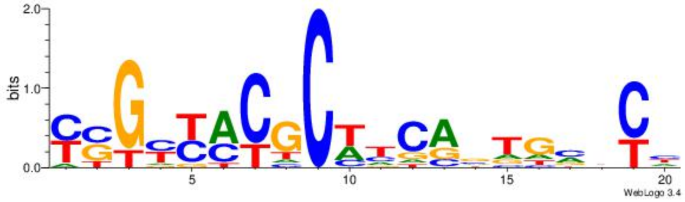
Alignment:

```
DGVBCABTGDWGCGKRRCSR
----GGMGGRGGCGGVGC--
```

Original motif Consensus sequence: DGVBCABTGDWGCGKRRCSR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD

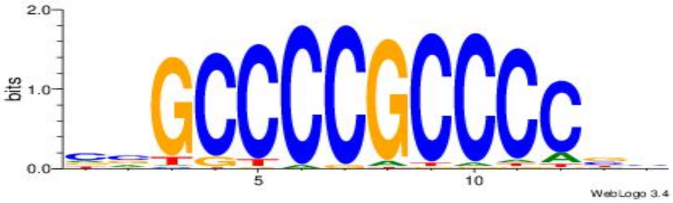


Dataset #:	4
Motif ID:	36
Motif name:	csGCCCCGCCCCsc
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	14
Similarity score:	0.0652173

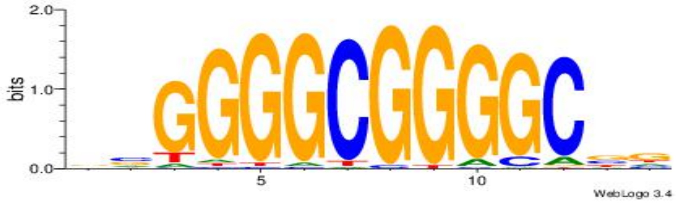
Alignment:

```
BBGGGGCGGGGCVD
GGMGGRGGCGGVGC
```

Original motif Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGC

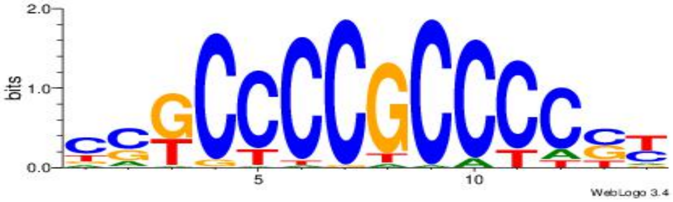


Dataset #:	2
Motif ID:	7
Motif name:	Motif 7
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	14

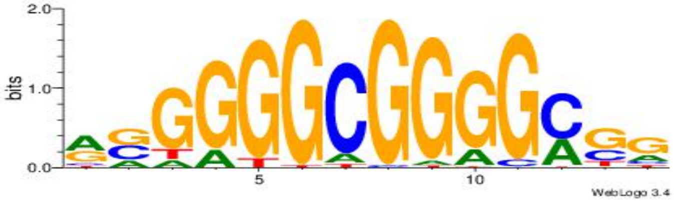
Similarity score: 0.0661275

Alignment:
MSGGGGCGGGGYSG
GGMGGRGGCGGVGC

Original motif Consensus sequence: CSKCCCCGCCCCSY



Reverse complement motif Consensus sequence: MSGGGGCGGGGY

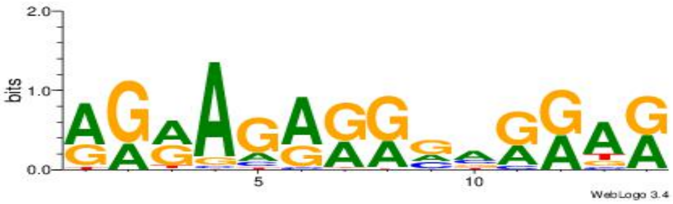


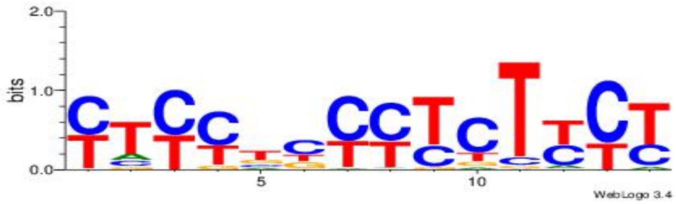
Dataset #: 2
Motif ID: 2
Motif name: Motif 2
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 14
Similarity score: 0.0714286

Alignment:
RGRAGARRGARRAR
GGMGGRGGCGGVGC

Original motif Consensus sequence: RGRAGARRGARRAR

Reverse complement motif Consensus sequence: MTMMTCMMTCTK





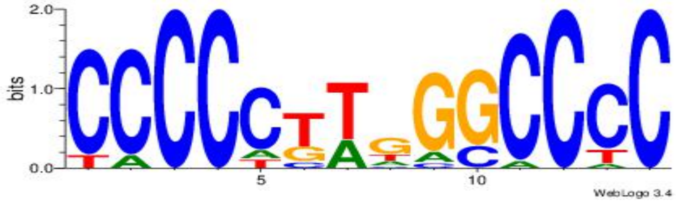
Dataset #:	3
Motif ID:	30
Motif name:	PLAG1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	2
Number of overlap:	13
Similarity score:	0.574939

Alignment:

```
-CCCCCTTGGGCCCC
GCVCCGCCMCCYCC-
```

Original motif Consensus sequence: GGGGCCCAAGGGGG

Reverse complement motif Consensus sequence: CCCCCTTGGGCCC

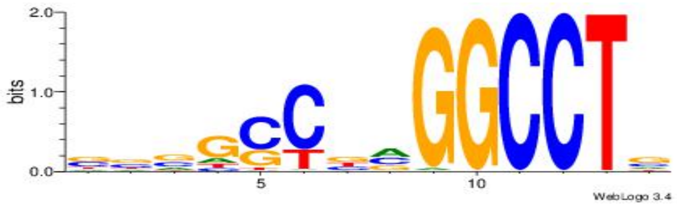


Dataset #:	3
Motif ID:	22

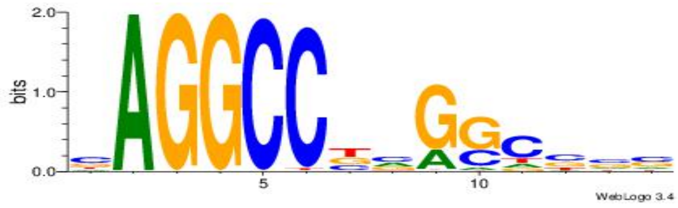
Motif name: Zfx
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 2
Number of overlap: 13
Similarity score: 0.577861

Alignment:
```
VAGGCCBBGGCVBB-
-GGMGGRGGCGGVGC
```

Original motif Consensus sequence: BBVGCCBVGGCCTV



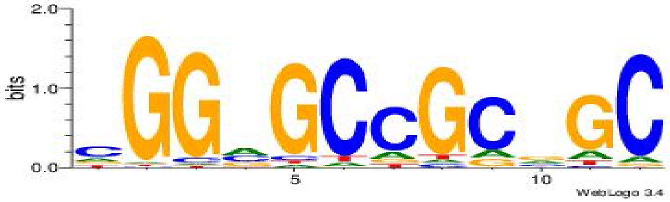
Reverse complement motif Consensus sequence: VAGGCCBBGGCV



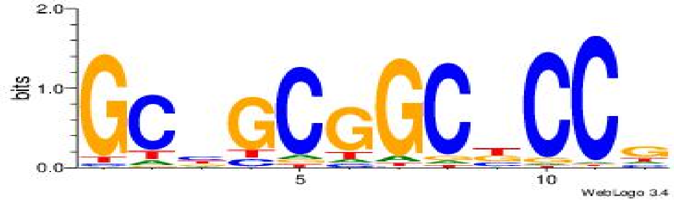
Dataset #: 5
Motif ID: 49
Motif name: TFF1
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 12
Similarity score: 1.02659

Alignment:
`--CGGVGCCGCVGC`
`GGMGGRGGCGGVGC`

Original motif   Consensus sequence: CGGVGCCGCVGC

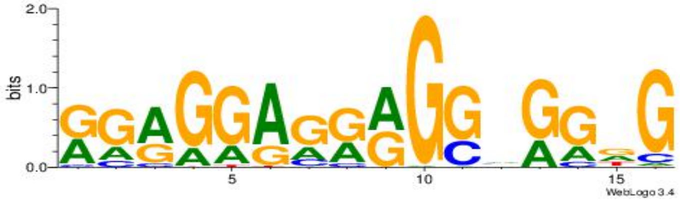


Reverse complement motif   Consensus sequence: GCVGCGGCBCCG

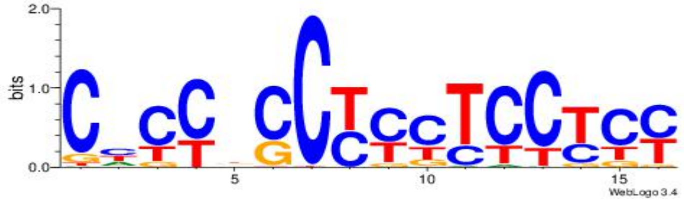


Dataset #: 5   **Motif ID: 51**   **Motif name: TFM2**

Original motif   Consensus sequence: RGRGGAGRRGGHGGDG



Reverse complement motif   Consensus sequence:
CHCCBCCKMCTCCKCM



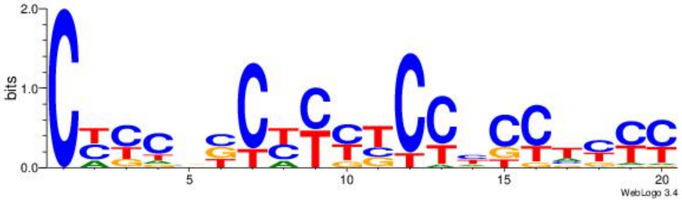
Best Matches for Motif ID 51 (Highest to Lowest)

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

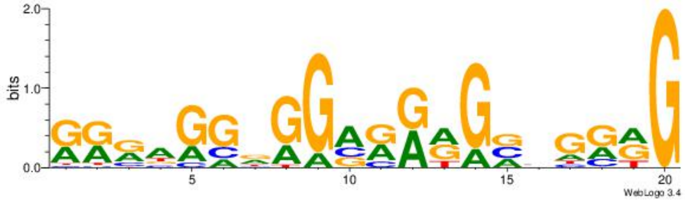
Position number: 1
Number of overlap: 16
Similarity score: 0.0331473

Alignment:
CYYCBBCYYYTCCHCCTYYY
CHCCBCCKMCTCCKCM----

Original motif Consensus sequence: CYYCBBCYYYTCCHCCTYYY



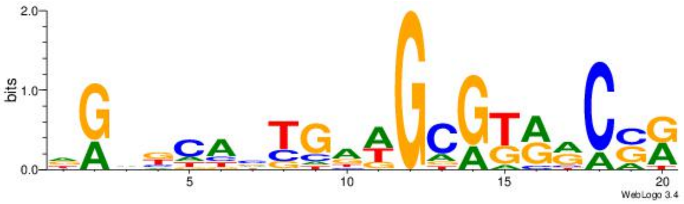
Reverse complement motif Consensus sequence:
KKKAGGDGGAKKMGBBGKMG



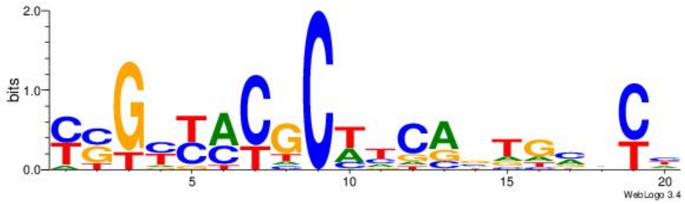
Dataset #: 3
Motif ID: 31
Motif name: Pax5
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 2
Number of overlap: 16
Similarity score: 0.0668155

Alignment:
DGVBCABTGDWGCGKRRCSR
-RGRGGAGRRGGHGGDG---

Original motif Consensus sequence: DGVBCABTGDWGCGKRRCSR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD

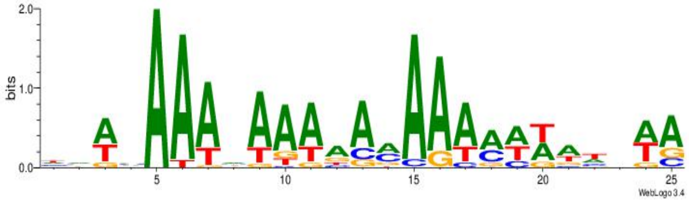


Dataset #:	5
Motif ID:	56
Motif name:	TFM11
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	8
Number of overlap:	16
Similarity score:	0.0794752

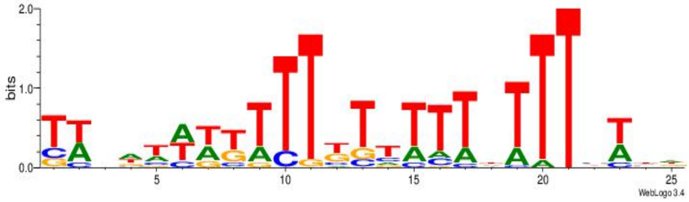
Alignment:

```
HDWVAAAHAAAAAMAAAMWWWHBWA
-------RGRGGAGRRGGHGGDG--
```

Original motif Consensus sequence: HDWVAAAHAAAAAMAAAMWWWHBWA



Reverse complement motif Consensus sequence: TWVHWWWYTTTYTTTTTHTTTVWBH

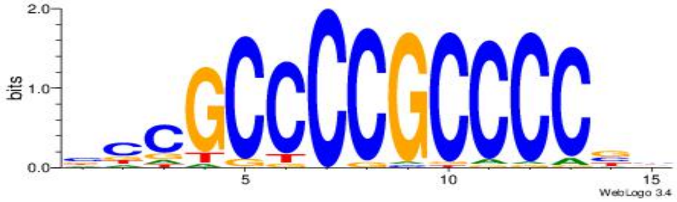


Dataset #: 4
Motif ID: 38
Motif name: cccGCCCCGCCCCsb
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 15
Similarity score: 0.558405

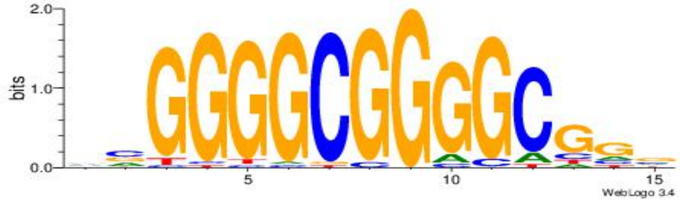
Alignment:

```
BCCGCCCCGCCCCBB-
CHCCBCCKMCTCCKCM
```

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB

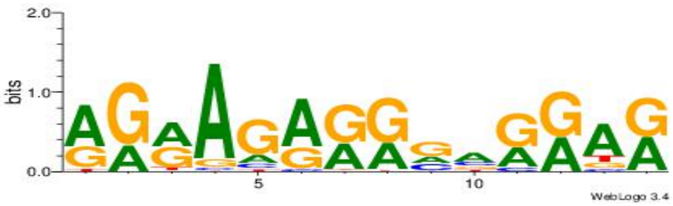


Dataset #: 2
Motif ID: 2
Motif name: Motif 2
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1

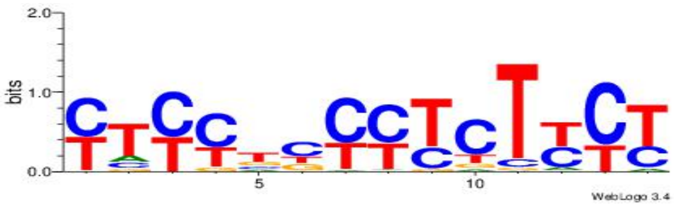
Number of overlap: 14
Similarity score: 1.01195

Alignment:
```
--RGRAGARRGARRAR
RGRGGAGRRGGHGGDG
```

Original motif Consensus sequence: RGRAGARRGARRAR



Reverse complement motif Consensus sequence: MTMMTCMMTCTK

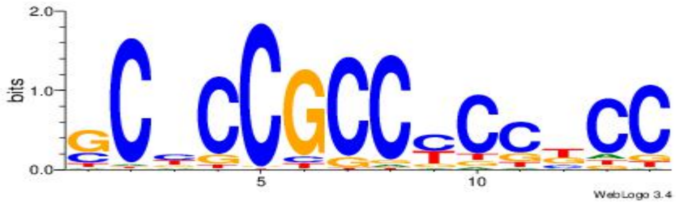


Dataset #: 5
Motif ID: 50
Motif name: TFF11
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 14
Similarity score: 1.03372

Alignment:
```
GGMGGRGGCGGVGC--
RGRGGAGRRGGHGGDG
```

Original motif Consensus sequence: GGMGGRGGCGGVGC

Reverse complement motif Consensus sequence: GCVCCGCCMCCY

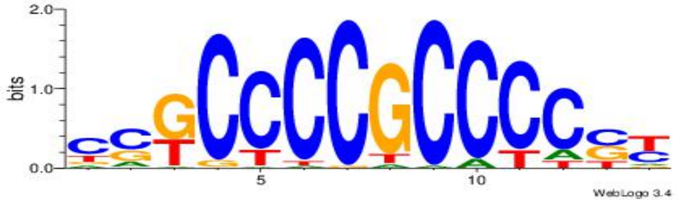


Dataset #:	2
Motif ID:	7
Motif name:	Motif 7
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	14
Similarity score:	1.05908

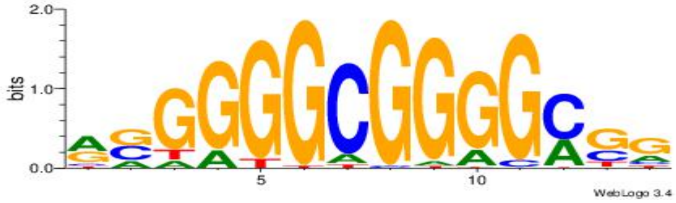
Alignment:

```
MSGGGGCGGGGYSG--
RGRGGAGRRGGHGGDG
```

Original motif Consensus sequence: CSKCCCCGCCCCSY



Reverse complement motif Consensus sequence: MSGGGGCGGGGY

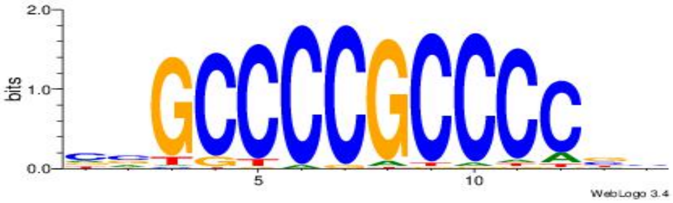


Dataset #:	4
Motif ID:	36

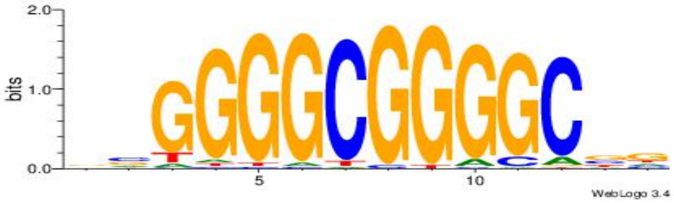
Motif name:	csGCCCCGCCCCsc
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	14
Similarity score:	1.05955

Alignment:
HVGCCCCGCCCCBB--
CHCCBCCKMCTCCKCM

Original motif Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGC

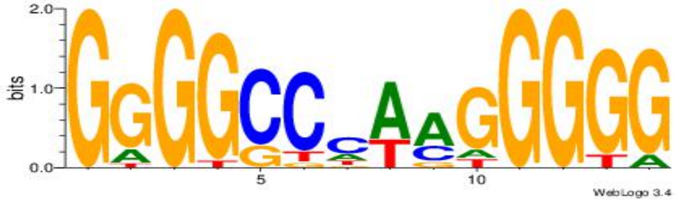


Dataset #:	3
Motif ID:	30
Motif name:	PLAG1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	14
Similarity score:	1.07365

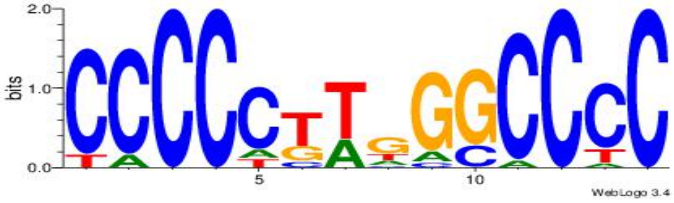
Alignment:

```
--CCCCCTTGGGCCCC
CHCCBCCKMCTCCKCM
```

Original motif Consensus sequence: GGGGCCCAAGGGGG



Reverse complement motif Consensus sequence: CCCCCTTGGGCCC



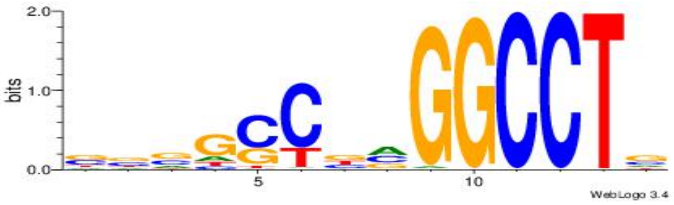
Dataset #:	3
Motif ID:	22
Motif name:	Zfx
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	3
Number of overlap:	12
Similarity score:	2.06908

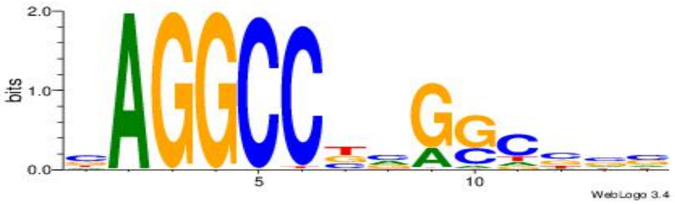
Alignment:

```
VAGGCCBBGGCVBB----
--RGRGGAGRRGGHGGDG
```

Original motif Consensus sequence: BBVGCCBVGGCCTV

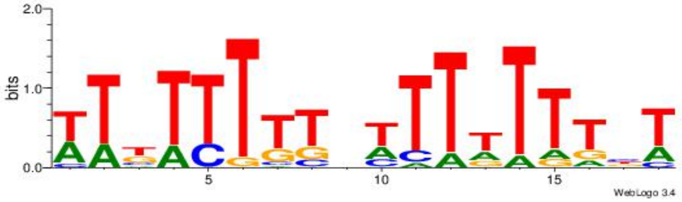
Reverse complement motif Consensus sequence: VAGGCCBBGGCV



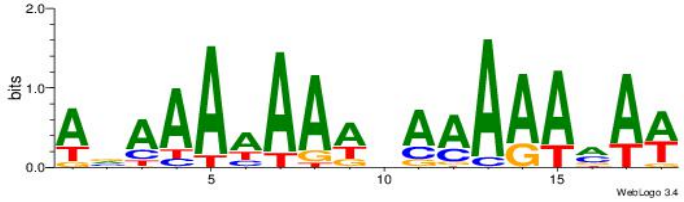


Dataset #: 5 Motif ID: 52 Motif name: TFM1

Original motif Consensus sequence: WTKTTTTTHWTTTTTTBT



Reverse complement motif Consensus sequence: ABAAAAAAWHAAAAARAW



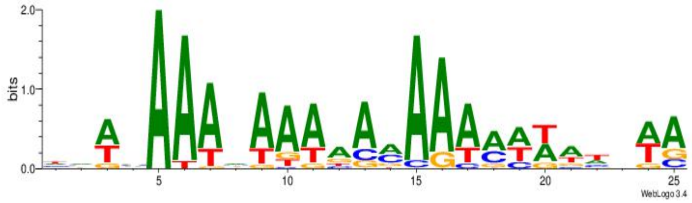
Best Matches for Motif ID 52 (Highest to Lowest)

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

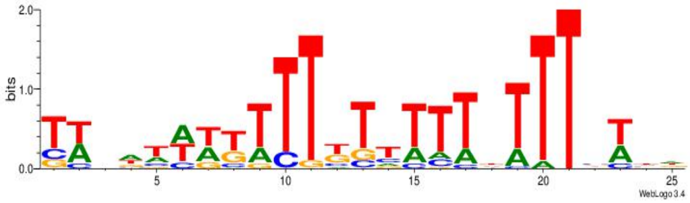
Alignment:

TWVHWWWYTTTYTTTTTHTTTVWBH
-----WTKTTTTTHWTTTTTTTBT--

Original motif Consensus sequence:
HDWVAAAHAAAAAMAAAMWWWHBWA



Reverse complement motif Consensus sequence:
TWVHWWWYTTTYTTTTTHTTTVWBH

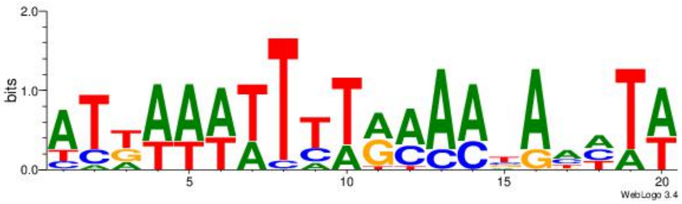


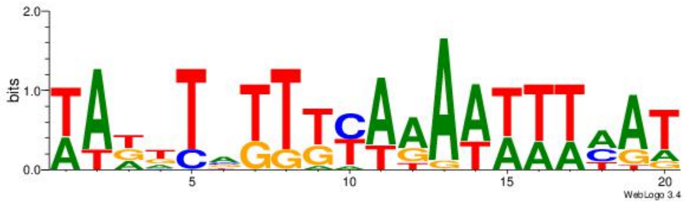
Dataset #:	5
Motif ID:	55
Motif name:	TFM13
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	3
Number of overlap:	18
Similarity score:	0.0364672

Alignment:
ATKAAWTTTTRMAABAHHTW
ABAAAAAAWHAAAAAARAW--

Original motif Consensus sequence: ATKAAWTTTTRMAABAHHTW

Reverse complement motif Consensus sequence:
WAHHTVTTYKAAAAWTTRAT





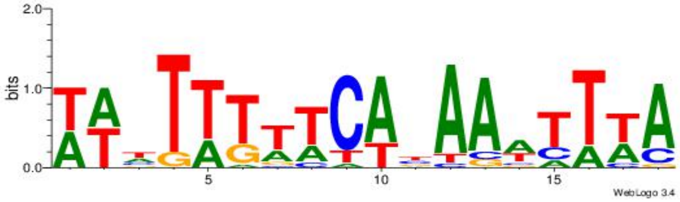
Dataset #:	5
Motif ID:	53
Motif name:	TFM3
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	18
Similarity score:	0.0456974

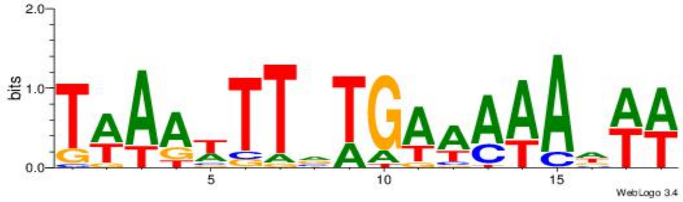
Alignment:

```
WWHTTTTTCABAAWTTWA
WTKTTTTTHWTTTTTTBT
```

Original motif Consensus sequence: WWHTTTTTCABAAWTTWA

Reverse complement motif Consensus sequence: TWAAWTTVTGAAAAAHWW





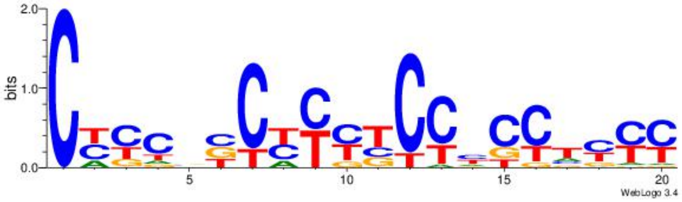
Dataset #:	5

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

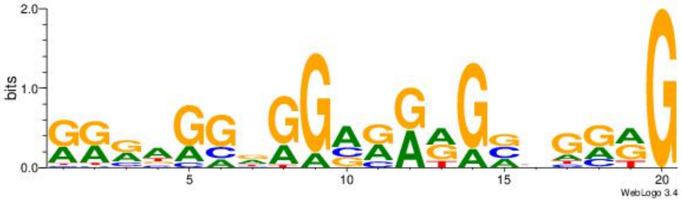
Alignment:

```
CYYCBBCYYYTCCHCCTYYY-
---WTKTTTTTHWTTTTTTBT
```

Original motif Consensus sequence: CYYCBBCYYYTCCHCCTYYY



Reverse complement motif Consensus sequence: KKKAGGDGGAKKMGBBGKMG



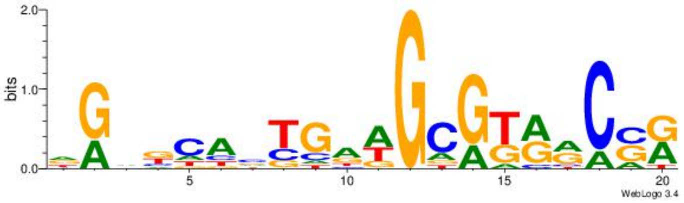
Dataset #:	3
Motif ID:	31
Motif name:	Pax5
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	5
Number of overlap:	16

Similarity score: 1.07322

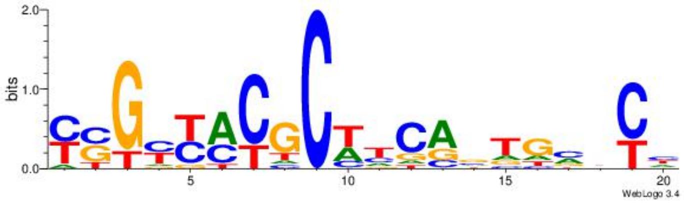
Alignment:

```
--MSGKKRCGCWDCABTGBBCD
WTKTTTTTHWTTTTTTBT----
```

Original motif Consensus sequence: DGVBCABTGDWGCGKRRCSR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD



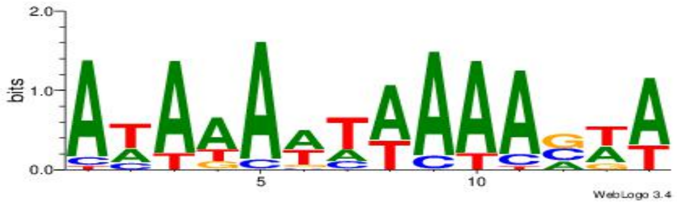
Dataset #: 2
Motif ID: 3
Motif name: Motif 3
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 14
Similarity score: 2.01877

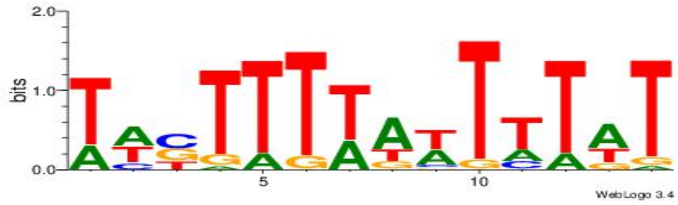
Alignment:

```
----TWSTTTWAWTTTWT
WTKTTTTTHWTTTTTTBT
```

Original motif Consensus sequence: AWAAAWTWAAASWA

Reverse complement motif Consensus sequence: TWSTTTWAWTTTW





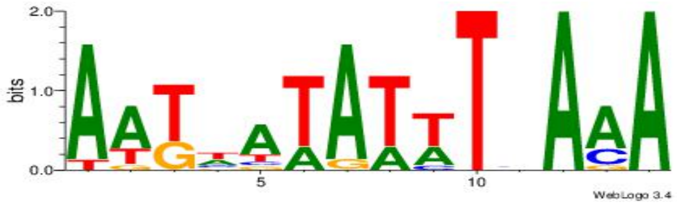
Dataset #:	2
Motif ID:	9
Motif name:	Motif 9
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	14
Similarity score:	2.05025

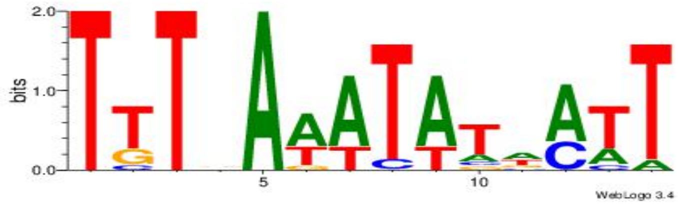
Alignment:

```
----AATHATATWTHAAA
ABAAAAAAWHAAAAAARAW
```

Original motif Consensus sequence: AATHATATWTHAAA

Reverse complement motif Consensus sequence: TTTDAWATATHAT





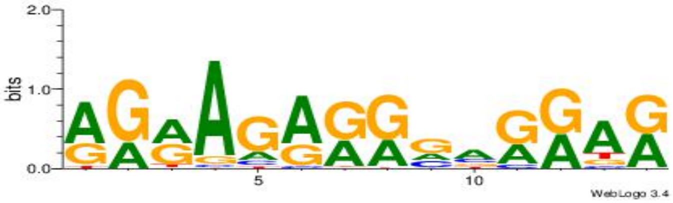
Dataset #:	2
Motif ID:	2

Motif name:	Motif 2
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:	2.05187

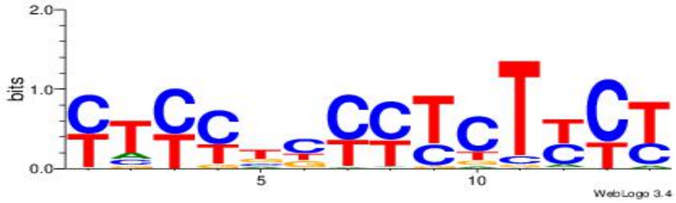
Alignment:

```
MTMMTCMMTCTKCK----
WTKTTTTTHWTTTTTTBT
```

Original motif   Consensus sequence: RGRAGARRGARRAR



Reverse complement motif   Consensus sequence: MTMMTCMMTCTKC

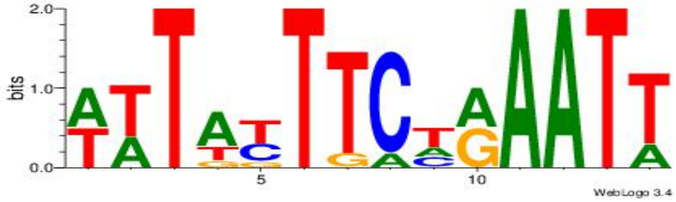


Dataset #:	2
Motif ID:	6
Motif name:	Motif 6
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	14
Similarity score:	2.0566

Alignment:
AATTYDGAARTAWW----
ABAAAAAAWHAAAAARAW

Original motif Consensus sequence: AATTYDGAARTAWW

Reverse complement motif Consensus sequence: WWTAKTTCDKAAT

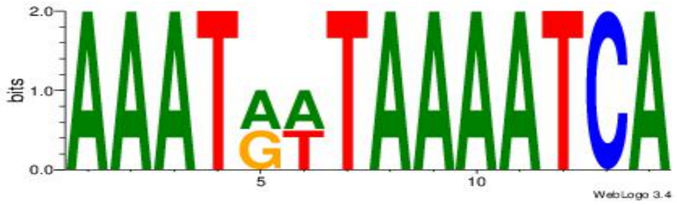


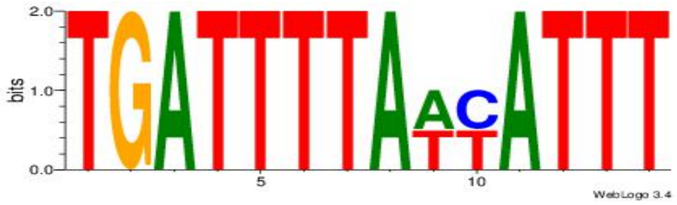
Dataset #:	2
Motif ID:	8
Motif name:	Motif 8
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	14
Similarity score:	2.07166

Alignment:
AAATRWTAAAATCA----
ABAAAAAAWHAAAAARAW

Original motif Consensus sequence: AAATRWTAAAATCA

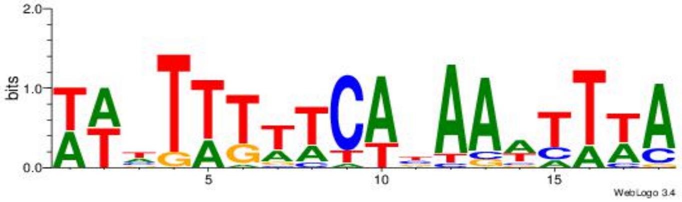
Reverse complement motif Consensus sequence: TGATTTTAWKATT



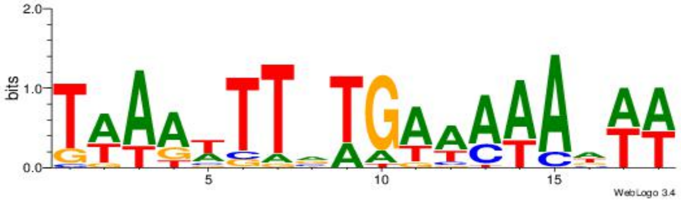


Dataset #: 5 **Motif ID: 53** **Motif name: TFM3**

Original motif Consensus sequence: WWHTTTTTCABAAWTTWA



Reverse complement motif Consensus sequence: TWAAWTTVTGAAAAAHWW



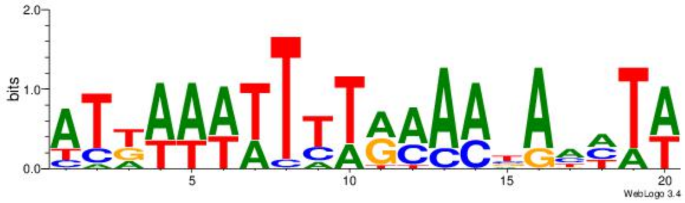
Best Matches for Motif ID 53 (Highest to Lowest)

Dataset #:	5
Motif ID:	55
Motif name:	TFM13
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	18
Similarity score:	0.013876

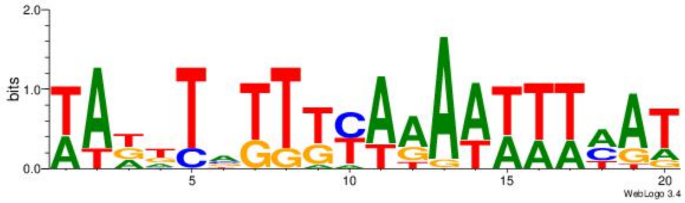
Alignment:

```
ATKAAWTTTTRMAABAHHTW
-TWAAWTTVTGAAAAAHWW-
```

Original motif Consensus sequence: ATKAAWTTTTRMAABAHHTW



Reverse complement motif Consensus sequence: WAHHTVTTYKAAAAWTTRAT



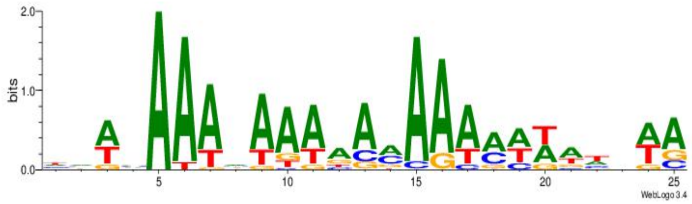
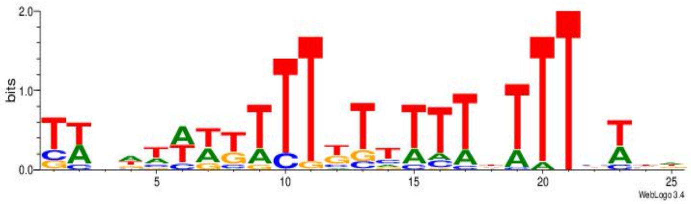
Dataset #:	5
Motif ID:	56
Motif name:	TFM11
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	5
Number of overlap:	18
Similarity score:	0.0402327

Alignment:

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

Original motif Consensus sequence: HDWVAAAHAAAAAMAAAMWWWHBWA

Reverse complement motif Consensus sequence: TWVHWWWYTTTYTTTTTHTTTVWBH

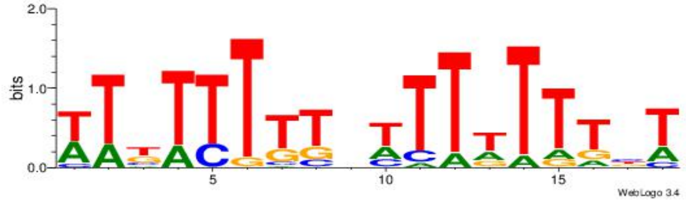



Dataset #:	5
Motif ID:	52
Motif name:	TFM1
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	18
Similarity score:	0.0432207

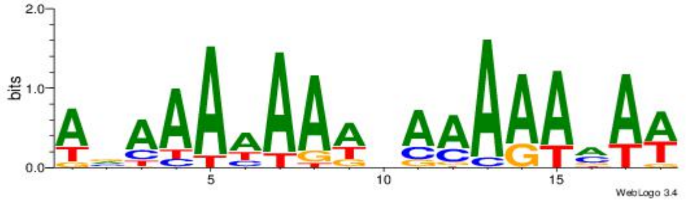
Alignment:

```
WTKTTTTTHWTTTTTTTBT
WWHTTTTTCABAAWTTWA
```

Original motif Consensus sequence: WTKTTTTTHWTTTTTTTBT



Reverse complement motif Consensus sequence: ABAAAAAAAWHAAAAARAW



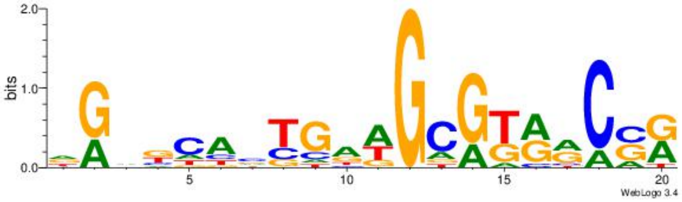
Dataset #:	3

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

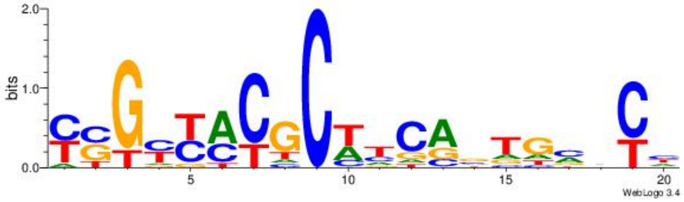
Alignment:

```
-MSGKKRCGCWDCABTGBBCD
WWHTTTTTCABAAWTTWA---
```

Original motif Consensus sequence: DGVBCABTGDWGCGKRRCSR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD



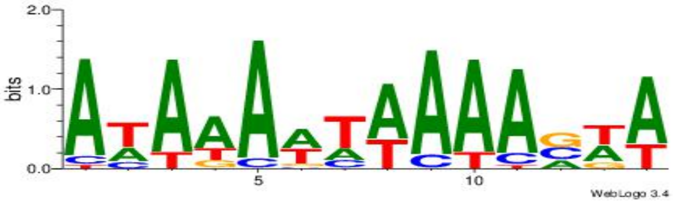
Dataset #:	2
Motif ID:	3
Motif name:	Motif 3
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	14

Similarity score: 2.04564

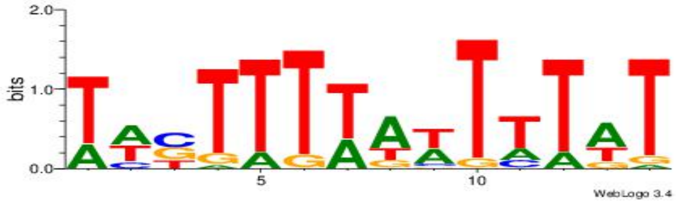
Alignment:

```
----TWSTTTWAWTTTWT
WWHTTTTTCABAAWTTWA
```

Original motif Consensus sequence: AWAAAWTWAAASWA



Reverse complement motif Consensus sequence: TWSTTTWAWTTTW



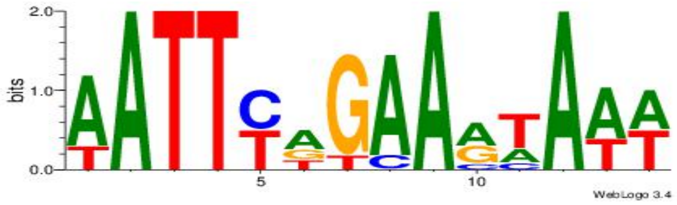
Dataset #:	2
Motif ID:	6
Motif name:	Motif 6
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	14
Similarity score:	2.04628

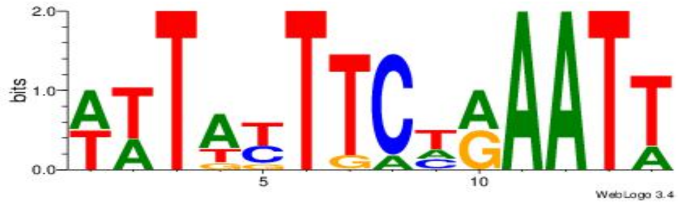
Alignment:

```
WWTAKTTCDKAATT----
TWAAWTTVTGAAAAAHWW
```

Original motif Consensus sequence: AATTYDGAARTAWW

Reverse complement motif Consensus sequence: WWTAKTTCDKAAT





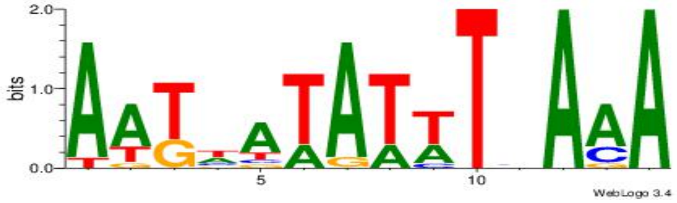
Dataset #:	2
Motif ID:	9
Motif name:	Motif 9
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	14
Similarity score:	2.04784

Alignment:

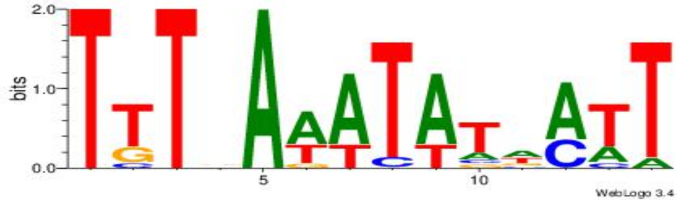
AATHATATWTHAAA----

WWHTTTTTCABAAWTTWA

Original motif Consensus sequence: AATHATATWTHAAA



Reverse complement motif Consensus sequence: TTTDAWATATHAT



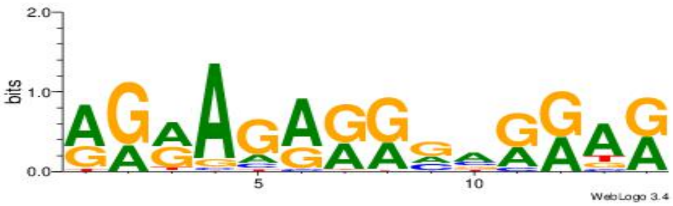
Dataset #:	2
Motif ID:	2

Motif name:	Motif 2
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2
Number of overlap:	13
Similarity score:	2.56928

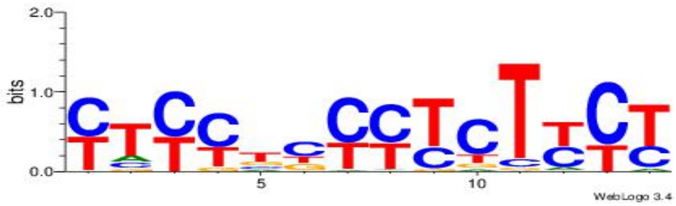
Alignment:

```
-----RGRAGARRGARRAR
TWAAWTTVTGAAAAAHWW-
```

Original motif Consensus sequence: RGRAGARRGARRAR



Reverse complement motif Consensus sequence: MTMMTCMMTCTK



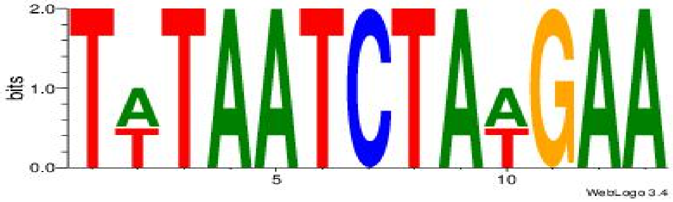
Dataset #:	2
Motif ID:	19
Motif name:	Motif 19
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	13
Similarity score:	2.56949

Alignment:

```
-----TWTAATCTAWGAA
WWHTTTTTCABAAWTTWA
```

Original motif   Consensus sequence: TTCWTAGATTAWA

Reverse complement motif   Consensus sequence: TWTAATCTAWGAA



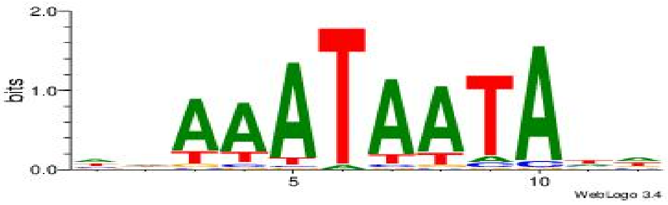
Dataset #:	4
Motif ID:	41
Motif name:	wwAAATAATAtw
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	12
Similarity score:	3.0422

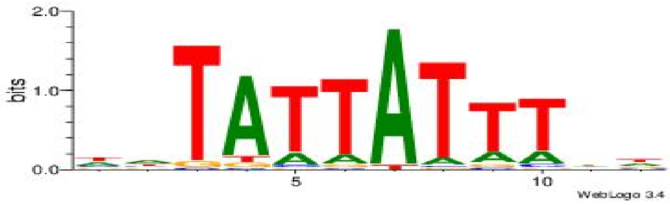
Alignment:

```
------HDAAATAATADD
TWAAWTTVTGAAAAAHWW
```

Original motif   Consensus sequence: HDAAATAATADD

Reverse complement motif   Consensus sequence: DDTATTATTTDH

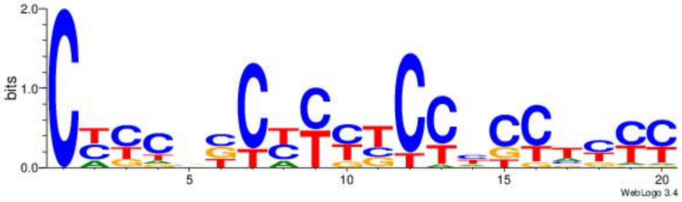


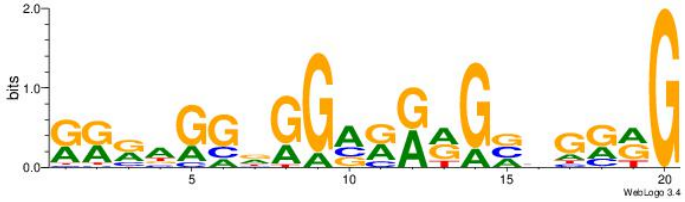


Dataset #: 5 **Motif ID: 54** **Motif name: TFM12**

Original motif Consensus sequence: CYYCBBCYYYTCCHCCTYYY

Reverse complement motif Consensus sequence: KKKAGGDGGAKKMGBBGKMG





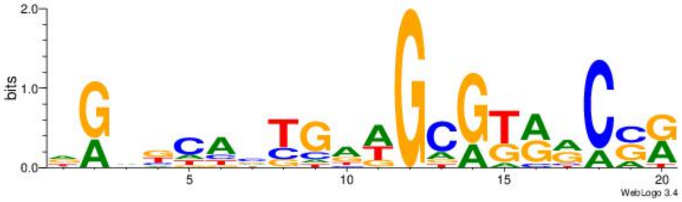
Best Matches for Motif ID 54 (Highest to Lowest)

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

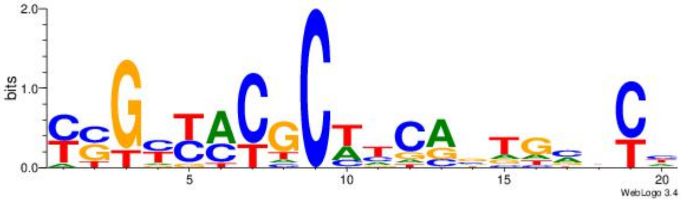
Alignment:

```
MSGKKRCGCWDCABTGBBCD
CYYCBBCYYYTCCHCCTYYY
```

Original motif Consensus sequence: DGVBCABTGDWGCGKRRCSR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD



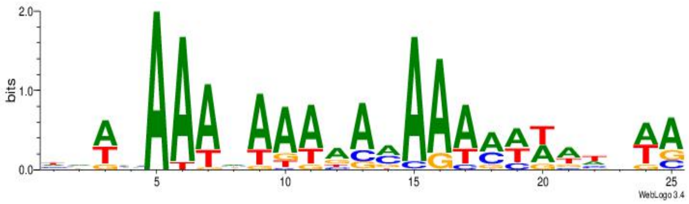
Dataset #:	5
Motif ID:	56
Motif name:	TFM11
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	6
Number of overlap:	20
Similarity score:	0.0573204

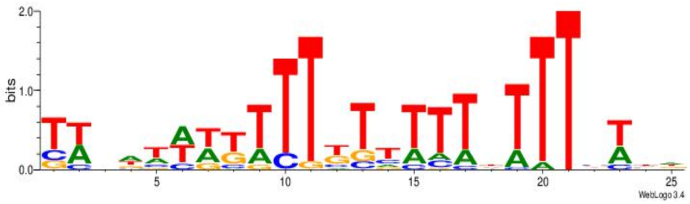
Alignment:

```
TWVHWWWYTTTYTTTTTHTTTVWBH
CYYCBBCYYYTCCHCCTYYY-----
```

Original motif Consensus sequence: HDWVAAAHAAAAAMAAAMWWWHBWA

Reverse complement motif Consensus sequence: TWVHWWWYTTTYTTTTTHTTTVWBH



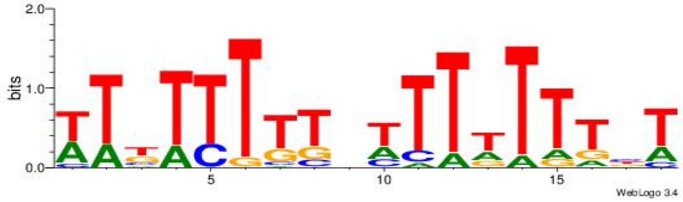


Dataset #:	5
Motif ID:	52
Motif name:	TFM1
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2
Number of overlap:	17
Similarity score:	1.56255

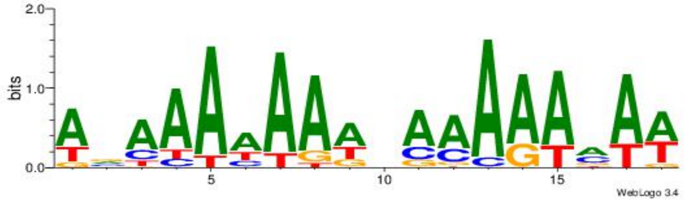
Alignment:

```
---WTKTTTTTHWTTTTTTBT
CYYCBBCYYYTCCHCCTYYY-
```

Original motif   Consensus sequence: WTKTTTTTHWTTTTTTBT



Reverse complement motif   Consensus sequence: ABAAAAAAWHAAAAARAW



Dataset #:	5

Motif ID: 51

Motif name: TFM2

Matching format of first motif: Reverse Complement

Matching format of second motif: Original Motif

Direction: Forward

Position number: 1

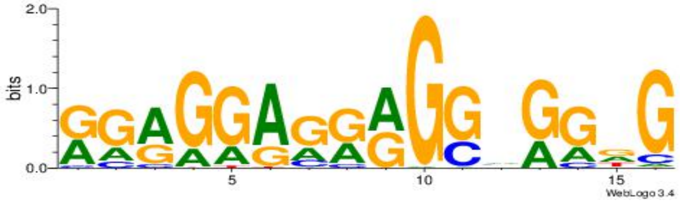
Number of overlap: 16

Similarity score: 2.01568

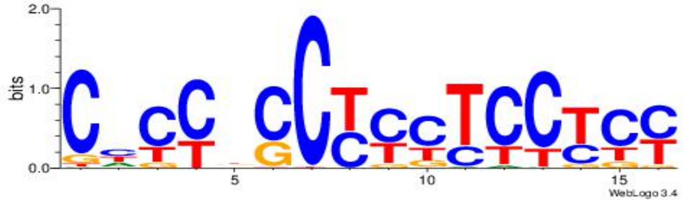
Alignment:

```
RGRGGAGRRGGHGGDG----
KKKAGGDGGAKKMGBBGKMG
```

Original motif Consensus sequence: RGRGGAGRRGGHGGDG



Reverse complement motif Consensus sequence: CHCCBCCKMCTCCKCM



Dataset #: 4

Motif ID: 38

Motif name: cccGCCCCGCCCCsb

Matching format of first motif: Original Motif

Matching format of second motif: Original Motif

Direction: Backward

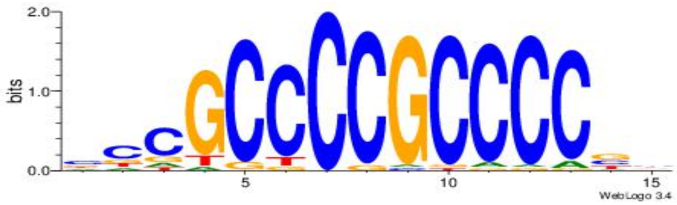
Position number: 1

Number of overlap: 15

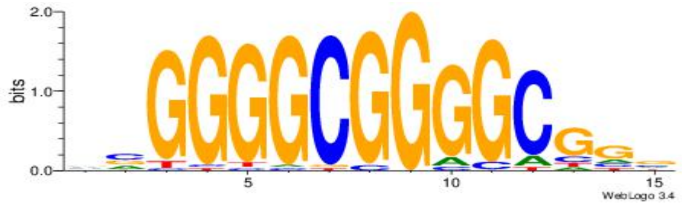
Similarity score: 2.55221

Alignment:
-----BCCGCCCCGCCCCBB
CYYCBBCYYYTCCHCCTYYY

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB

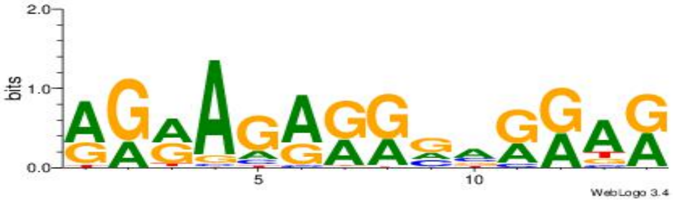


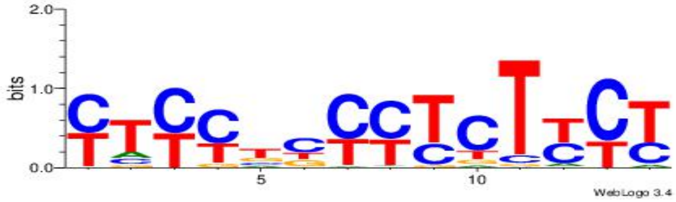
Dataset #: 2
Motif ID: 2
Motif name: Motif 2
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 14
Similarity score: 3.0395

Alignment:
------RGRAGARRGARRAR
KKKAGGDGGAKKMGBBGKMG

Original motif Consensus sequence: RGRAGARRGARRAR

Reverse complement motif Consensus sequence: MTMMTCMMTCTK

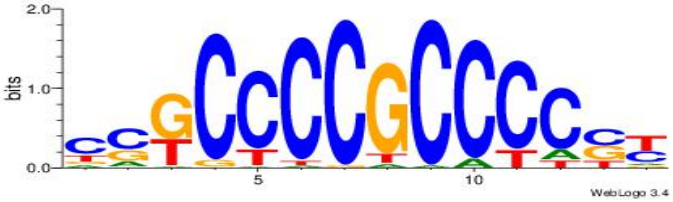




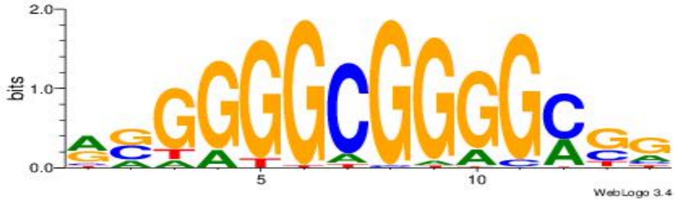
Dataset #: 2
Motif ID: 7
Motif name: Motif 7
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 14
Similarity score: 3.04463

Alignment:
```
------CSKCCCCGCCCCSY
CYYCBBCYYYTCCHCCTYYY
```

Original motif Consensus sequence: CSKCCCCGCCCCSY



Reverse complement motif Consensus sequence: MSGGGGCGGGGY



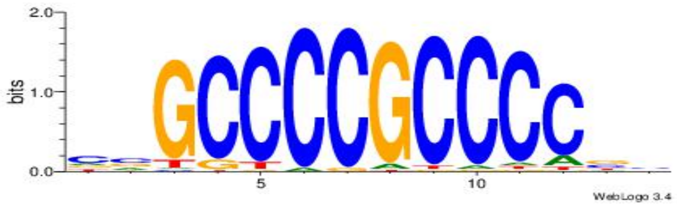
Dataset #: 4
Motif ID: 36

Motif name: csGCCCCGCCCCsc
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 14
Similarity score: 3.05024

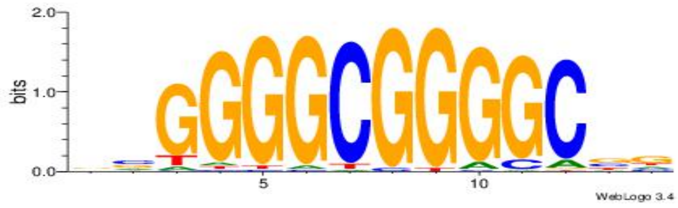
Alignment:

```
------BBGGGGCGGGGCVD
KKKAGGDGGAKKMGBBGKMG
```

Original motif Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGC



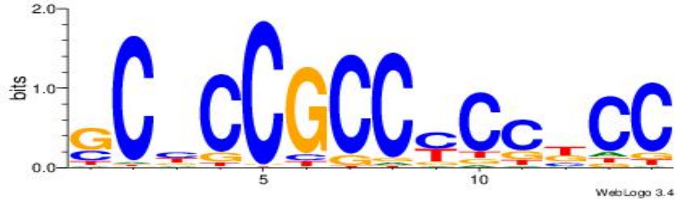
Dataset #: 5
Motif ID: 50
Motif name: TFF11
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 14
Similarity score: 3.0542

Alignment:

```
GGMGGRGGCGGVGC------
KKKAGGDGGAKKMGBBGKMG
```

Original motif Consensus sequence: GGMGGRGGCGGVGC

Reverse complement motif Consensus sequence: GCVCCGCCMCCY



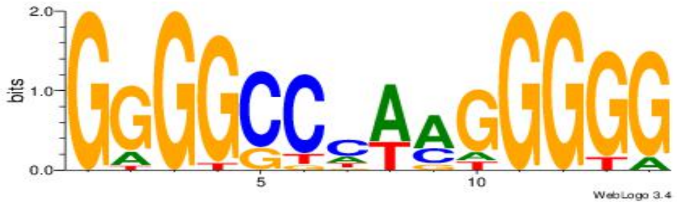
Dataset #:	3
Motif ID:	30
Motif name:	PLAG1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	14
Similarity score:	3.06074

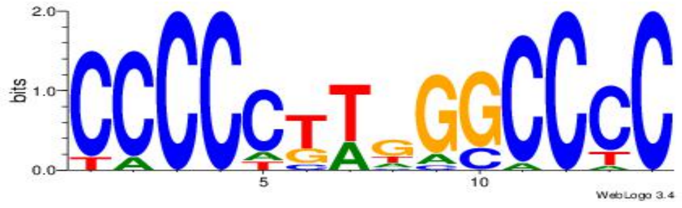
Alignment:

```
GGGGCCCAAGGGGG------
KKKAGGDGGAKKMGBBGKMG
```

Original motif Consensus sequence: GGGGCCCAAGGGGG

Reverse complement motif Consensus sequence: CCCCCTTGGGCC

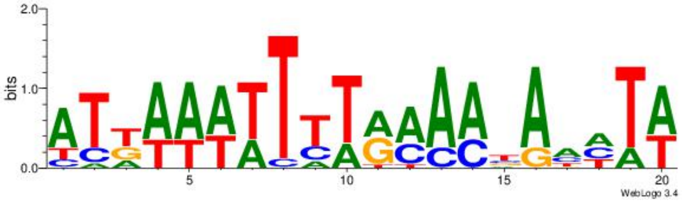


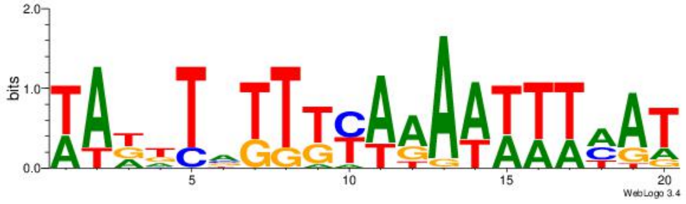


Dataset #: 5 **Motif ID: 55** **Motif name: TFM13**

Original motif Consensus sequence: ATKAAWTTTTRMAABAHHTW

Reverse complement motif Consensus sequence: WAHHTVTTYKAAAAWTTRAT





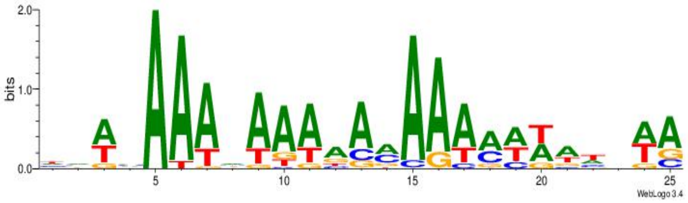
Best Matches for Motif ID 55 (Highest to Lowest)

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

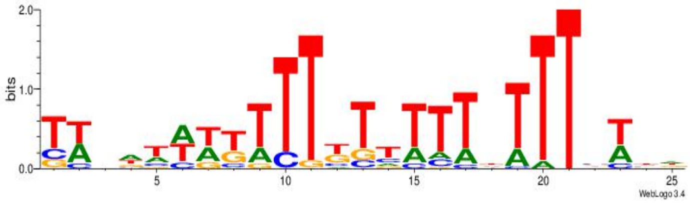
Alignment:

TWVHWWWYTTTYTTTTTHTTTVWBH
----WAHHTVTTYKAAAAWTTRAT-

Original motif Consensus sequence:
HDWVAAAHAAAAAMAAAMWWWHBWA



Reverse complement motif Consensus sequence:
TWVHWWWYTTTYTTTTTHTTTVWBH

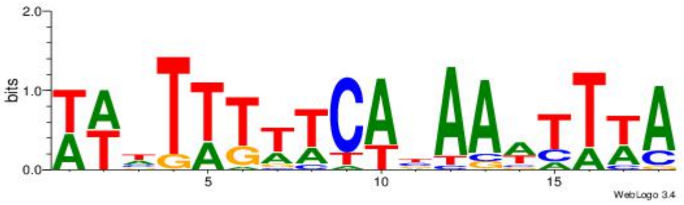


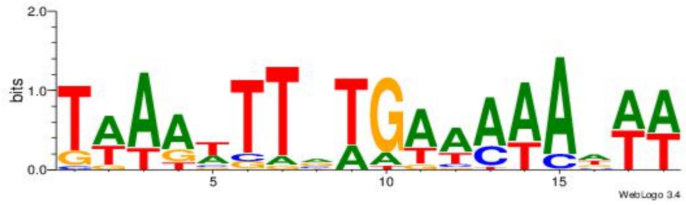
Dataset #:	5
Motif ID:	53
Motif name:	TFM3
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	18
Similarity score:	1.02254

Alignment:
TWAAWTTVTGAAAAAHWW--
ATKAAWTTTTRMAABAHHTW

Original motif Consensus sequence: WWHTTTTTCABAAWTTWA

Reverse complement motif Consensus sequence:
TWAAWTTVTGAAAAAHWW

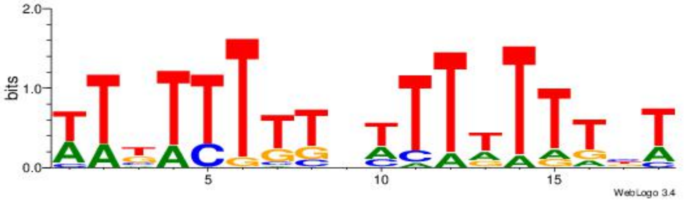




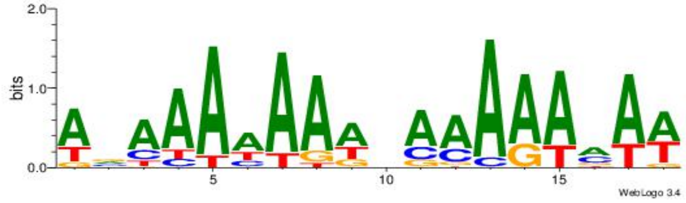
Dataset #:	5
Motif ID:	52
Motif name:	TFM1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	18
Similarity score:	1.02868

Alignment:
```
WTKTTTTTHWTTTTTTTBT--
WAHHTVTTYKAAAAWTTRAT
```

Original motif Consensus sequence: WTKTTTTTHWTTTTTTTBT



Reverse complement motif Consensus sequence: ABAAAAAAAWHAAAAARAW



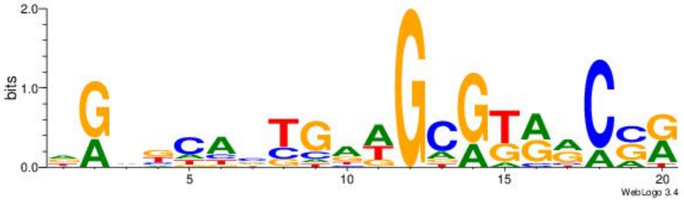
Dataset #:	3

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

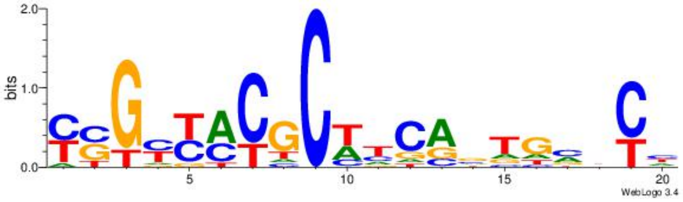
Alignment:

```
-----MSGKKRCGCWDCABTGBBCD
WAHHTVTTYKAAAAWTTRAT-----
```

Original motif Consensus sequence: DGVBCABTGDWGCGKRRCSR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD



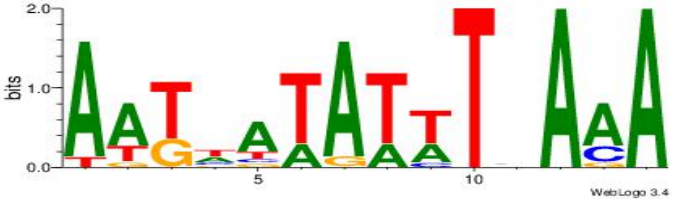
Dataset #: 2
Motif ID: 9
Motif name: Motif 9
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 14

Similarity score: 3.02278

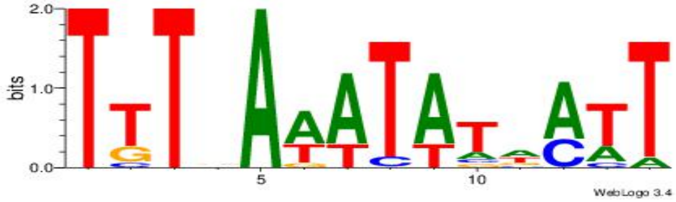
Alignment:

```
------TTTDAWATATHATT
WAHHTVTTYKAAAAWTTRAT
```

Original motif Consensus sequence: AATHATATWTHAAA



Reverse complement motif Consensus sequence: TTTDAWATATHAT



Dataset #: 2

Motif ID: 3

Motif name: Motif 3

Matching format of first motif: Original Motif

Matching format of second motif: Original Motif

Direction: Forward

Position number: 1

Number of overlap: 14

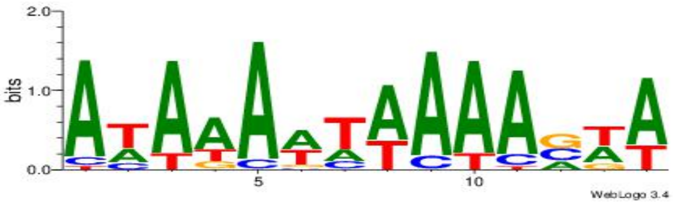
Similarity score: 3.04317

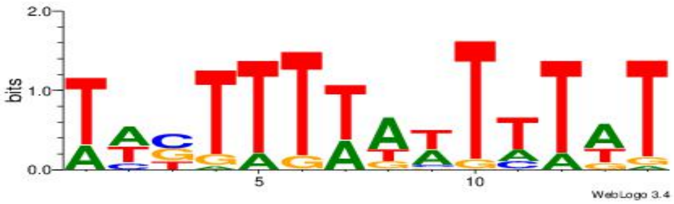
Alignment:

```
AWAAAWTWAAASWA------
ATKAAWTTTTRMAABAHHTW
```

Original motif Consensus sequence: AWAAAWTWAAASWA

Reverse complement motif Consensus sequence: TWSTTTWAWTTTW





Dataset #: 2

Motif ID: 6

Motif name: Motif 6

Matching format of first motif: Reverse Complement

Matching format of second motif: Reverse Complement

Direction: Forward

Position number: 1

Number of overlap: 14

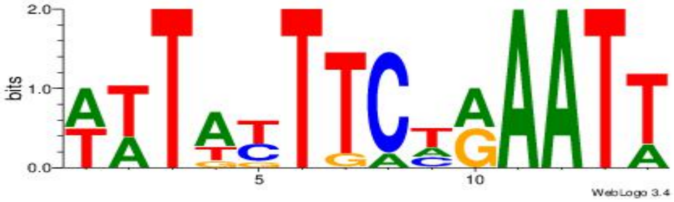
Similarity score: 3.05135

Alignment:

```
WWTAKTTCDKAATT------
WAHHTVTTYKAAAAWTTRAT
```

Original motif Consensus sequence: AATTYDGAARTAWW

Reverse complement motif Consensus sequence: WWTAKTTCDKAAT



Dataset #: 2

Motif ID: 19

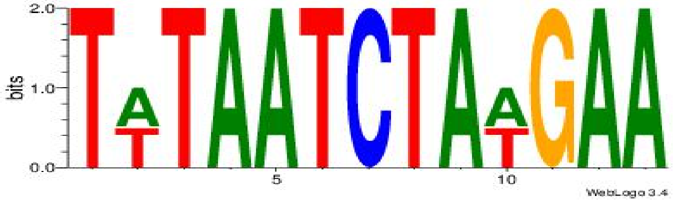
Motif name: Motif 19
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 13
Similarity score: 3.56273

Alignment:

```
TTCWTAGATTAWA-------
WAHHTVTTYKAAAAWTTRAT
```

Original motif Consensus sequence: TTCWTAGATTAWA

Reverse complement motif Consensus sequence: TWTAATCTAWGA

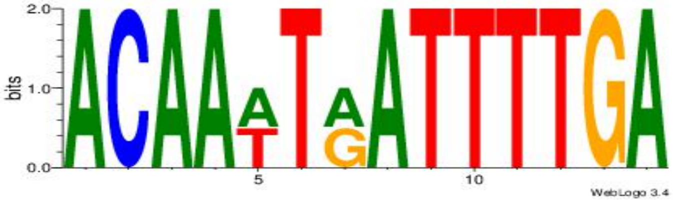


Dataset #: 2
Motif ID: 16
Motif name: Motif 16
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2
Number of overlap: 13
Similarity score: 3.56529

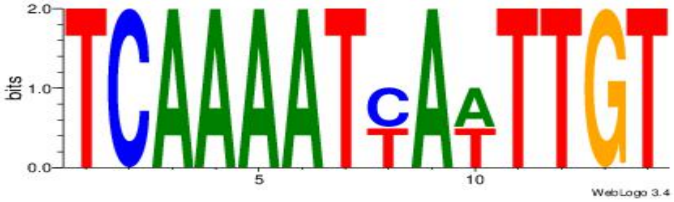
Alignment:

```
-------ACAAWTRATTTTGA
WAHHTVTTYKAAAAWTTRAT-
```

Original motif Consensus sequence: ACAAWTRATTTTGA



Reverse complement motif Consensus sequence: TCAAAATKAWTTG



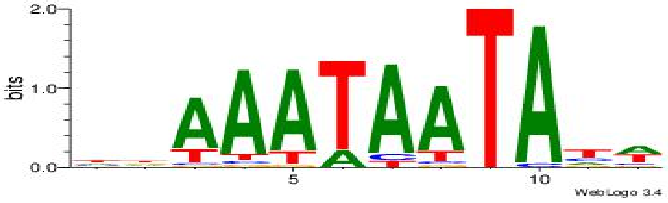
Dataset #:	4
Motif ID:	37
Motif name:	tkAAATAATAtw
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	12
Similarity score:	4.03399

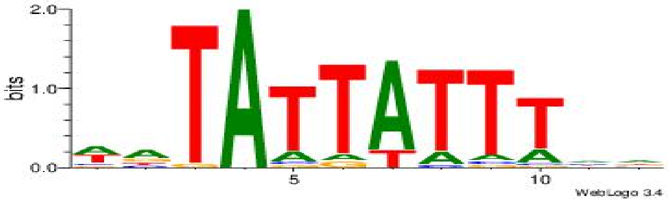
Alignment:

```
HDAAATAATAHW--------
WAHHTVTTYKAAAAWTTRAT
```

Original motif Consensus sequence: HDAAATAATAHW

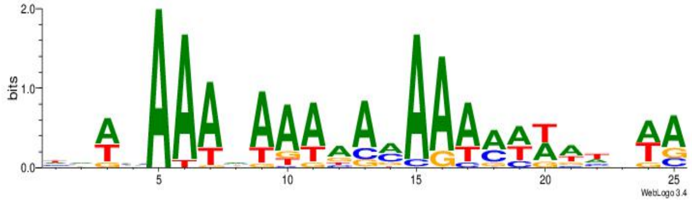
Reverse complement motif Consensus sequence: WHTATTATTTDH



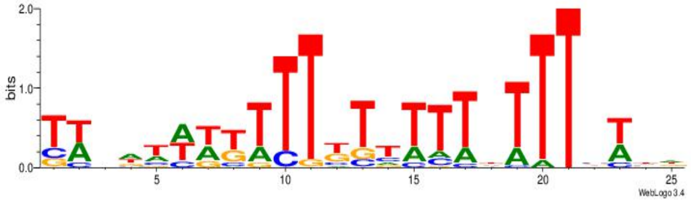


Dataset #: 5 Motif ID: 56 Motif name: TFM11

Original motif Consensus sequence:
HDWVAAAHAAAAAMAAAMWWWHBWA



Reverse complement motif Consensus sequence:
TWVHWWWYTTTYTTTTTHTTTVWBH



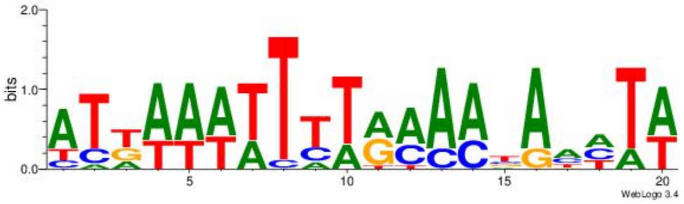
Best Matches for Motif ID 56 (Highest to Lowest)

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

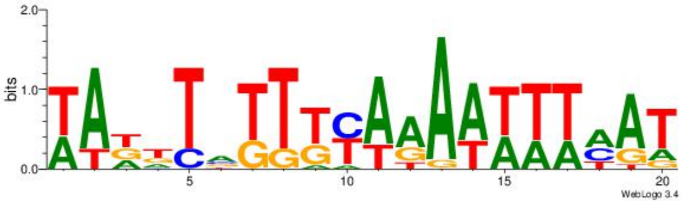
Alignment:

WAHHTVTTYKAAAAWTTRAT-----
TWVHWWWYTTTYTTTTTHTTTVWBH

Original motif Consensus sequence: ATKAAWTTTTRMAABAHHTW



Reverse complement motif Consensus sequence: WAHHTVTTYKAAAAWTTRAT

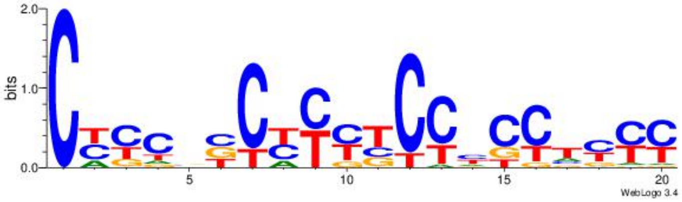


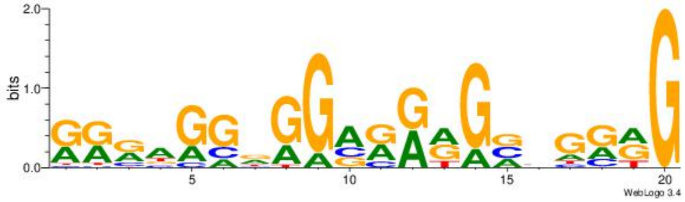
Dataset #:	5
Motif ID:	54
Motif name:	TFM12
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	20
Similarity score:	0.0693284

Alignment:
KKKAGGDGGAKKMGBBGKMG-----
HDWVAAAHAAAAAMAAAMWWWHBWA

Original motif Consensus sequence: CYYCBBCYYYTCCHCCTYYY

Reverse complement motif Consensus sequence: KKKAGGDGGAKKMGBBGKMG



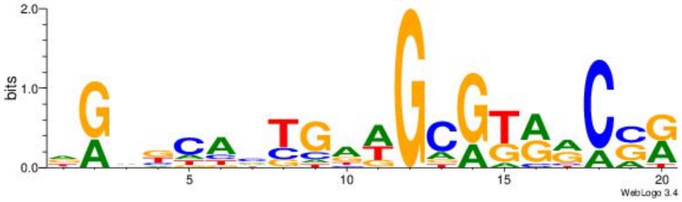


Dataset #:	3
Motif ID:	31
Motif name:	Pax5
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	20
Similarity score:	0.0750613

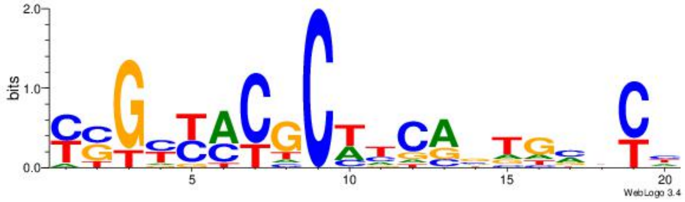
Alignment:

```
DGVBCABTGDWGCGKRRCSR-----
HDWVAAAHAAAAAMAAAMWWWHBWA
```

Original motif   Consensus sequence: DGVBCABTGDWGCGKRRCSR



Reverse complement motif   Consensus sequence: MSGKKRCGCWDCABTGBBCD



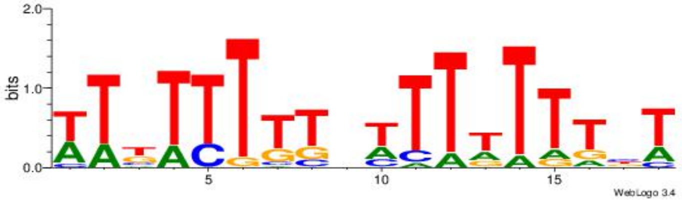
Dataset #:	5

Motif ID: 52
Motif name: TFM1
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 18
Similarity score: 1.0232

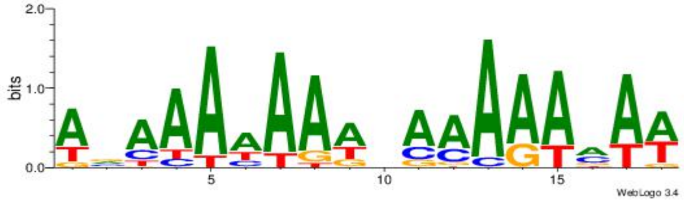
Alignment:

```
-------ABAAAAAAWHAAAAARAW
HDWVAAAHAAAAAMAAAMWWWHBWA
```

Original motif Consensus sequence: WTKTTTTTHWTTTTTTBT



Reverse complement motif Consensus sequence: ABAAAAAAWHAAAAARAW



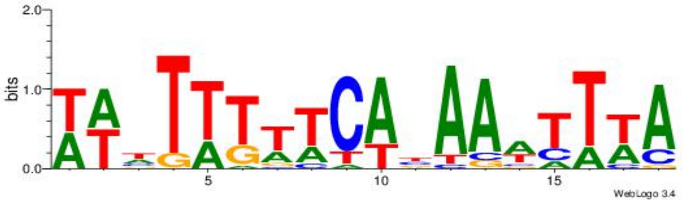
Dataset #: 5
Motif ID: 53
Motif name: TFM3
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 18

Similarity score: 1.05388

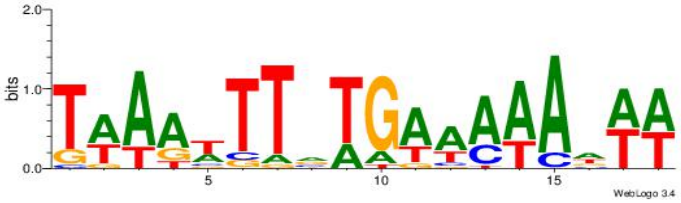
Alignment:

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

Original motif Consensus sequence: WWHTTTTTCABAAWTTWA



Reverse complement motif Consensus sequence: TWAAWTTVTGAAAAAHWW



Dataset #: 2

Motif ID: 3

Motif name: Motif 3

Matching format of first motif: Reverse Complement

Matching format of second motif: Reverse Complement

Direction: Forward

Position number: 1

Number of overlap: 14

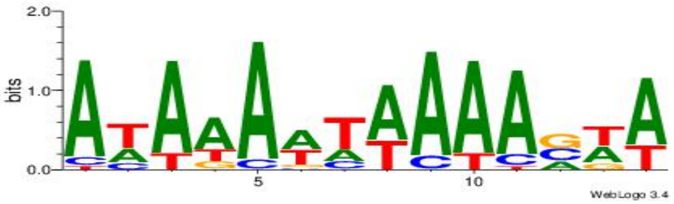
Similarity score: 3.04236

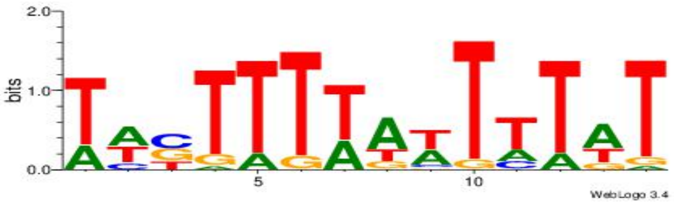
Alignment:

```
TWSTTTWAWTTTWT-----------
TWVHWWWYTTTYTTTTTHTTTVWBH
```

Original motif Consensus sequence: AWAAAWTWAAASWA

Reverse complement motif Consensus sequence: TWSTTTWAWTTT





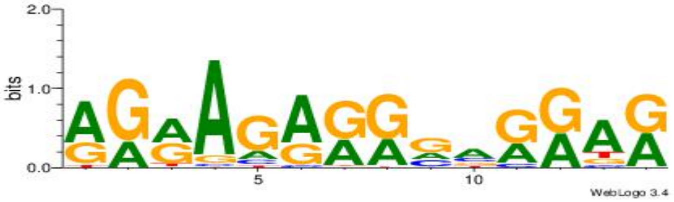
Dataset #:	2
Motif ID:	2
Motif name:	Motif 2
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	14
Similarity score:	3.05212

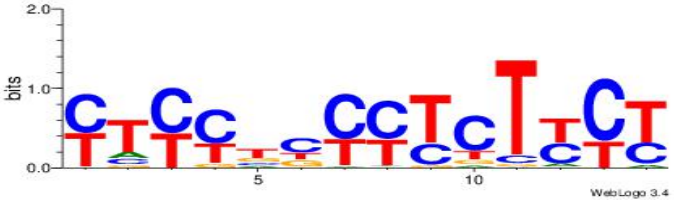
Alignment:

```
-----------RGRAGARRGARRAR
HDWVAAAHAAAAAMAAAMWWWHBWA
```

Original motif Consensus sequence: RGRAGARRGARRAR

Reverse complement motif Consensus sequence: MTMMTCMMTCTK



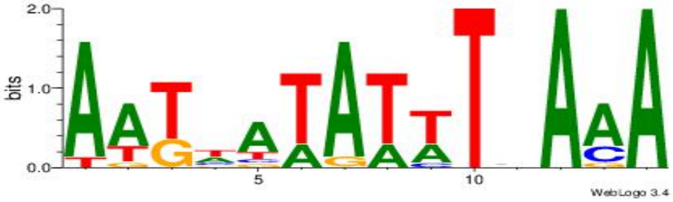


Dataset #:	2
Motif ID:	9

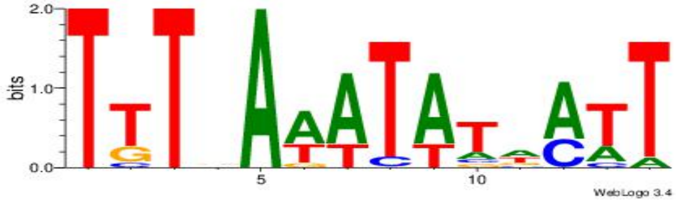
Motif name: Motif 9
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 14
Similarity score: 3.05326

Alignment:
AATHATATWTHAAA-----------
TWVHWWWYTTTYTTTTTHTTTVWBH

Original motif Consensus sequence: AATHATATWTHAAA



Reverse complement motif Consensus sequence: TTTDAWATATHAT



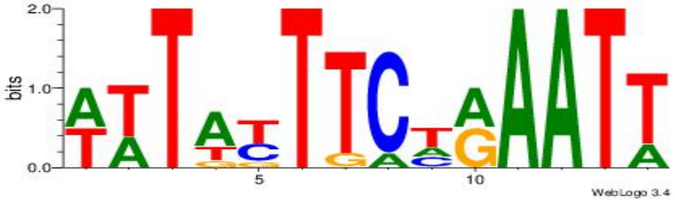
Dataset #: 2
Motif ID: 6
Motif name: Motif 6
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 14
Similarity score: 3.06919

Alignment:

WWTAKTTCDKAATT-----------
TWVHWWWYTTTYTTTTTHTTTVWBH

Original motif Consensus sequence: AATTYDGAARTAWW

Reverse complement motif Consensus sequence: WWTAKTTCDKAAT



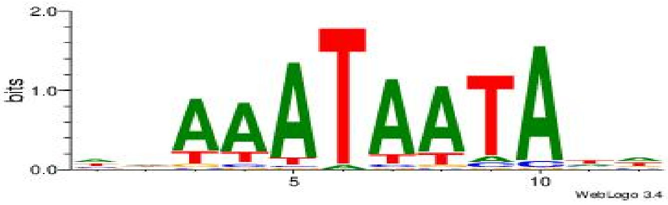
Dataset #:	4
Motif ID:	41
Motif name:	wwAAATAATAtw
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	12
Similarity score:	4.03464

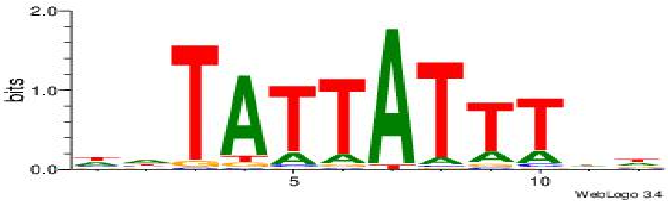
Alignment:

HDAAATAATADD-------------
HDWVAAAHAAAAAMAAAMWWWHBWA

Original motif Consensus sequence: HDAAATAATADD

Reverse complement motif Consensus sequence: DDTATTATTTDH





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Runtime: 75.0307 seconds.

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