



MOTIFSIM - MOTIF SIMilarity Detection Tool

Version 2.2

INPUT

Input Parameters

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

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_DM05.txt	11	5

RESULTS

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

Dataset #: 5 **Motif ID: 46** **Motif name: TFW3**

Original motif Consensus sequence: GCACTG



Reverse complement motif Consensus sequence: CAGTGC



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

Dataset #: 4
Motif ID: 43
Motif name: wSTACwGTAsw
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: 0.00773193

Alignment:
DBTACWGTA VH
----CAGTGC--

Original motif Consensus sequence: HVTACWG TABD

Reverse complement motif Consensus sequence: DBTACWGTA VH

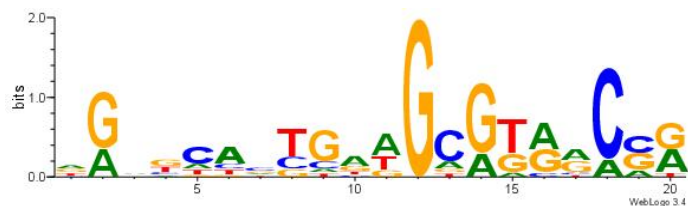


Dataset #: 3
 Motif ID: 31
 Motif name: Pax5
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 6
 Similarity score: 0.0111111

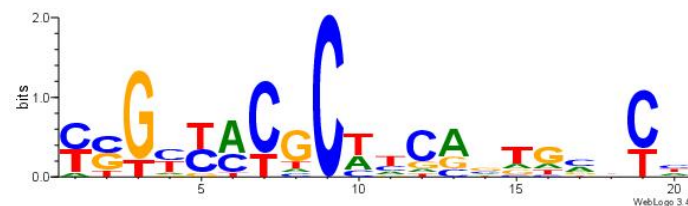
Alignment:

DGVCBABCATGDWCGKRRCSR
 ---GCACTG-----

Original motif Consensus sequence: DGVCBABCATGDWCGKRRCSR



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: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 6
 Similarity score: 0.0148473

Alignment:
 DCCACGTGCV
 ---CAGTGC-

Original motif Consensus sequence: VGCACGTGGH



Reverse complement motif Consensus sequence: DCCACGTGCV



Dataset #: 3
 Motif ID: 35
 Motif name: GABPA
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 6
 Similarity score: 0.0156785

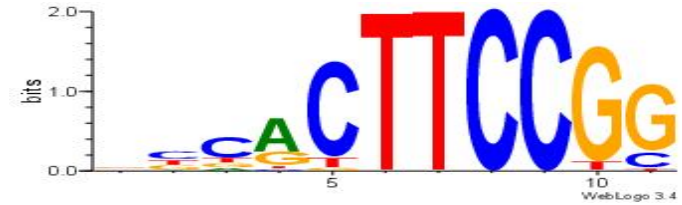
Alignment:

VVCACTTCCGG
----GCACTG--

Original motif Consensus sequence: CCGGAAGTGVV



Reverse complement motif Consensus sequence: VVCACTTCCGG



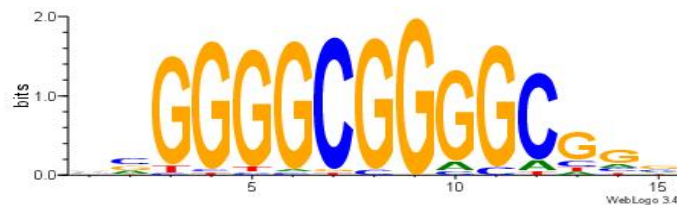
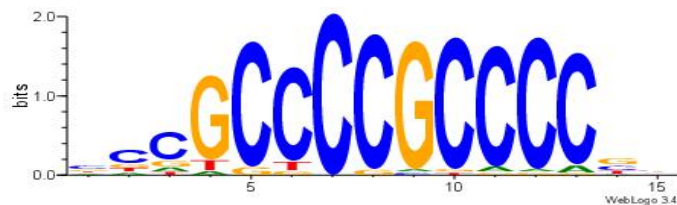
Dataset #: 4
Motif ID: 38
Motif name: cccGCCCCGCCCCsb
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 4
Number of overlap: 6
Similarity score: 0.0173006

Alignment:

BCCGCCCCGCCCCBB
---GCACTG-----

Original motif Consensus sequence: BCCGCCCCGCCCCBB

Reverse complement motif Consensus sequence:
BBGGGGCGGGGCGGB



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

Original motif Consensus sequence: DBGTAATAHD



Reverse complement motif Consensus sequence: DHTATTTACBD

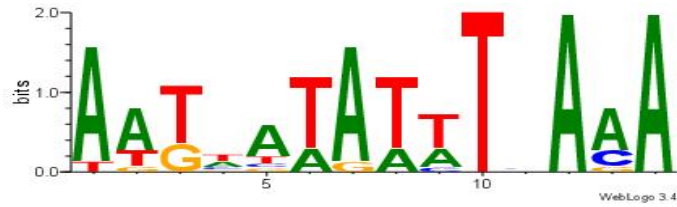


Best Matches for Top Significant Motif ID 45 (Highest to Lowest)

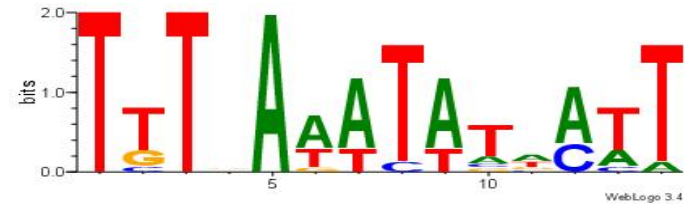
Dataset #:	2
Motif ID:	9
Motif name:	Motif 9
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	4
Number of overlap:	11
Similarity score:	0.0177412

Alignment:
AATHATATWTHAAA
DHTATTTACBD---

Original motif Consensus sequence: AATHATATWTHAAA



Reverse complement motif Consensus sequence: TTTDAWATATHAT

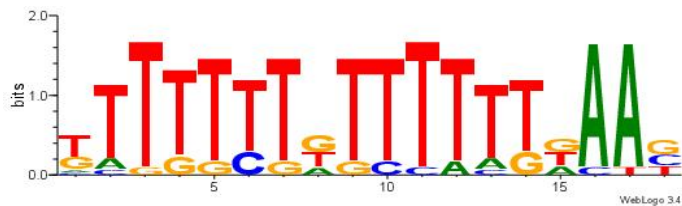


Dataset #: 5
 Motif ID: 53
 Motif name: TFM3
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 4
 Number of overlap: 11
 Similarity score: 0.0203792

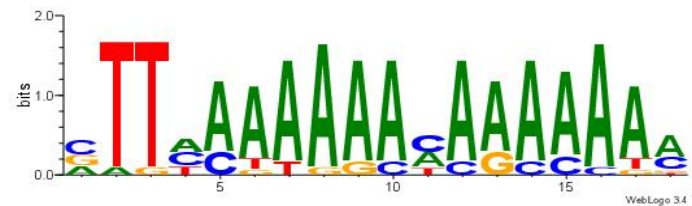
Alignment:

```
BTTHAAAAAYAAAAAR
---DBGTAATAHD----
```

Original motif Consensus sequence: KTTTTTKTTTTTTDAAB



Reverse complement motif Consensus sequence: BTTHAAAAAYAAAAAR



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: 0.0205821

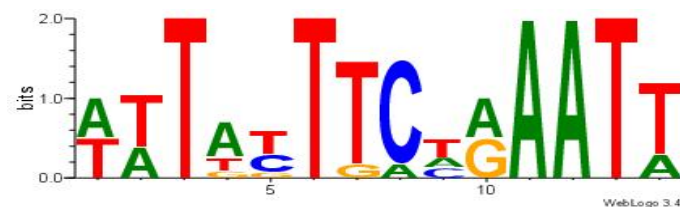
Alignment:

AATTYDGAARTAWW
 ---DBGTAAATAHD

Original motif Consensus sequence: AATTYDGAARTAWW



Reverse complement motif Consensus sequence: WWTAKTTCDKAAT



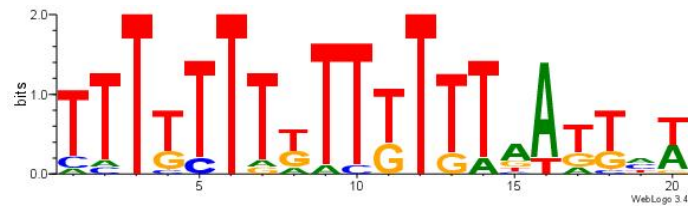
Dataset #: 5
 Motif ID: 56
 Motif name: TFM13
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 11

Similarity score: 0.0258581

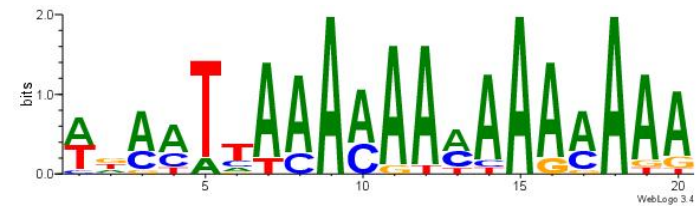
Alignment:

```
TTTTTTTKTTKTTTAATTHW  
-----DHTATTTACBD--
```

Original motif Consensus sequence: TTTTTTKTTKTTTAATTHW



Reverse complement motif Consensus sequence: WHAATTAARAARAAAAAA



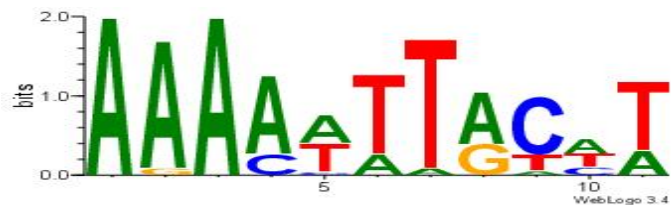
Dataset #:	2
Motif ID:	4
Motif name:	Motif 4
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	11
Similarity score:	0.0288058

Alignment:

```
AWGKAAWTTTT  
DBGTAATAHD
```

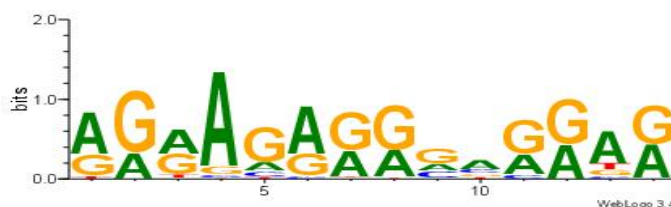
Original motif Consensus sequence: AAAAWTTRCWT

Reverse complement motif Consensus sequence: AWGKAAWTTTT

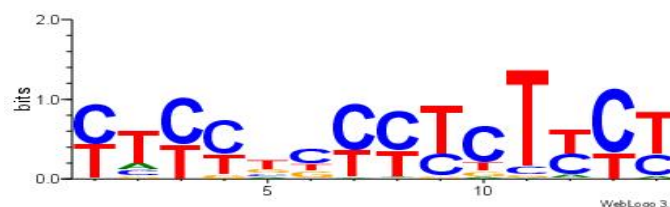


Dataset #: 2 Motif ID: 2 Motif name: Motif 2

Original motif Consensus sequence: RGRAGARRGARRAR



Reverse complement motif Consensus sequence: MTMMTCMMTCTK

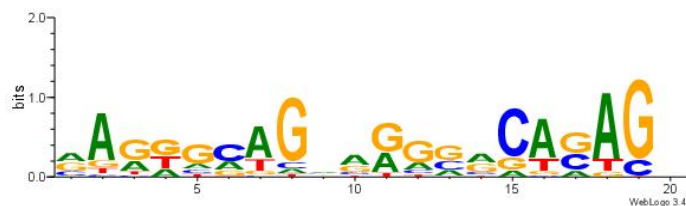


Best Matches for Top Significant Motif ID 2 (Highest to Lowest)

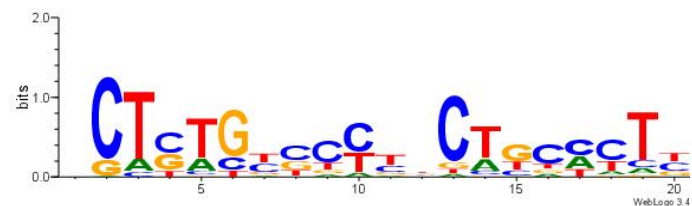
Dataset #:	5
Motif ID:	55
Motif name:	TFM12
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	4
Number of overlap:	14
Similarity score:	0.00215466

Alignment:
RAGKGMAGVRRGSRCASAGV
---RGRAGARRGARRAR---

Original motif Consensus sequence: RAGKGMAGVRRGSRCASAGV



Reverse complement motif Consensus sequence: VCTSTGKSCMKBCTRCYCTK

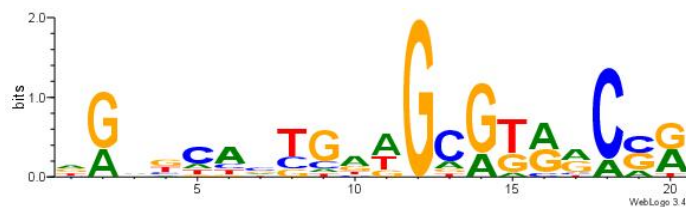


Dataset #: 3
Motif ID: 31
Motif name: Pax5
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 7
Number of overlap: 14
Similarity score: 0.0213256

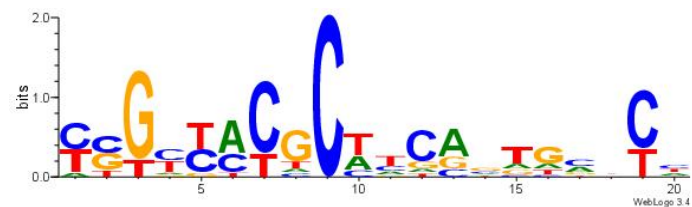
Alignment:

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

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTG B B C D

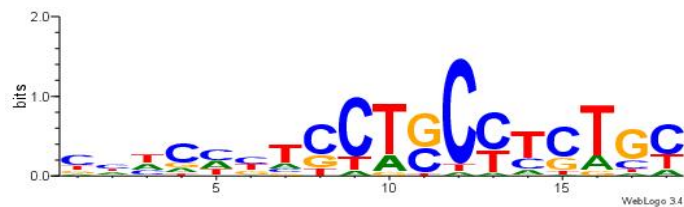


Dataset #: 5
 Motif ID: 52
 Motif name: TFM2
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 14
 Similarity score: 0.0283463

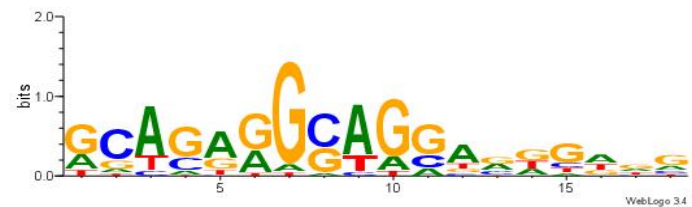
Alignment:

CHHCHBTCCTSCYTCTGC
 --MTMMTCMMTCTKCK--

Original motif Consensus sequence: CHHCHBTCCTSCYTCTGC



Reverse complement motif Consensus sequence: GCAGAKGSAGGABDGHDG

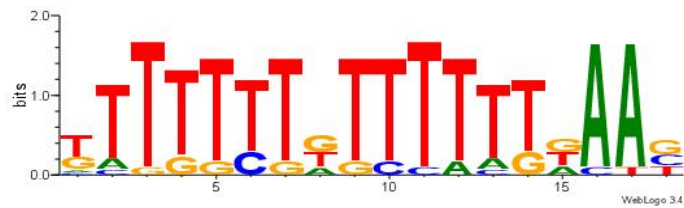


Dataset #: 5
 Motif ID: 53
 Motif name: TFM3
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 5

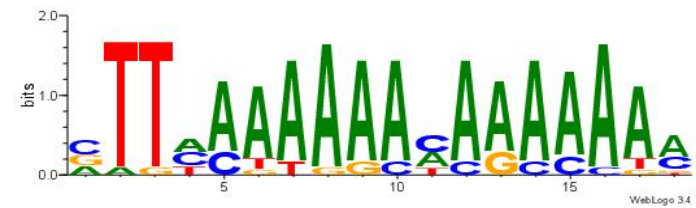
Number of overlap: 14
 Similarity score: 0.0316147

Alignment:
 BTTHAAAAAYAAAAAR
 ----RGRAGARRGARRAR

Original motif Consensus sequence: KTTTTTKTTTTTDAAB



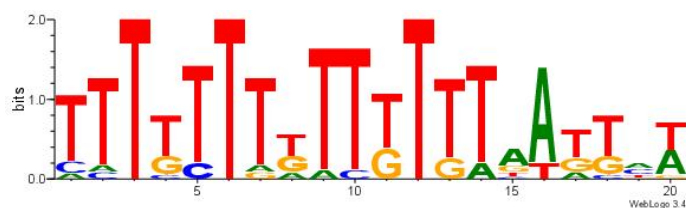
Reverse complement motif Consensus sequence: BTTHAAAAAYAAAAAR



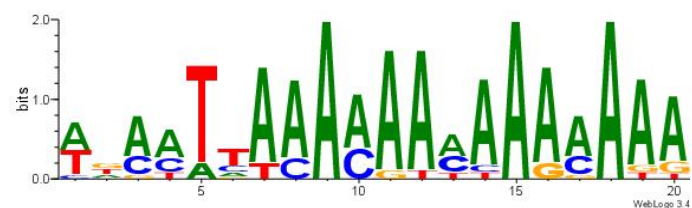
Dataset #: 5
 Motif ID: 56
 Motif name: TFM13
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 4
 Number of overlap: 14
 Similarity score: 0.0368869

Alignment:
 WHAATTAAARAARAAAAA
 ----RGRAGARRGARRAR----

Original motif Consensus sequence: TTTTTTKTTKTTTAATTHW

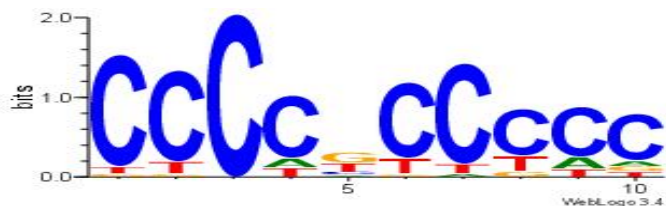


Reverse complement motif Consensus sequence: WHAATTAARAARAAAAA

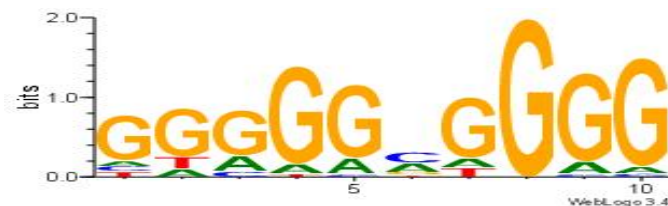


Dataset #: 3 Motif ID: 24 Motif name: SP1

Original motif Consensus sequence: CCCCKCCCC



Reverse complement motif Consensus sequence: GGGGGYGGGG



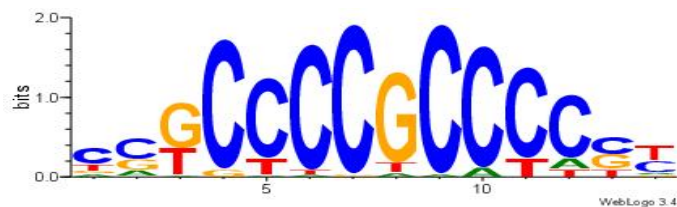
Best Matches for Top Significant Motif ID 24 (Highest to Lowest)

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

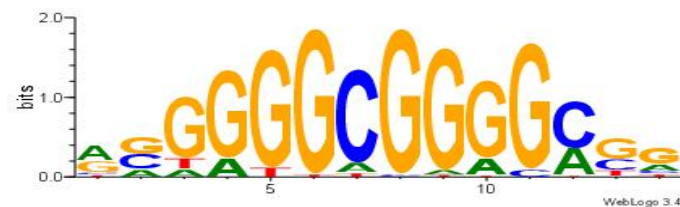
Alignment:

MSGGGGCGGGYSG
-GGGGYGGGG---

Original motif Consensus sequence: CSKCCCCGCCCSY



Reverse complement motif Consensus sequence: MSGGGGCGGGGY

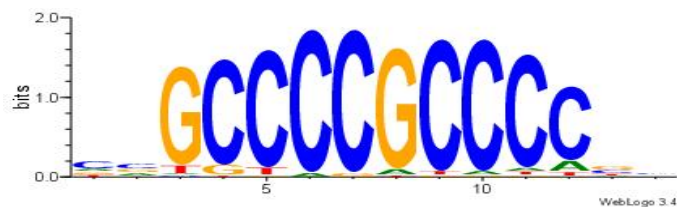


Dataset #: 4
Motif ID: 36
Motif name: csGCCCCGCCCS
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 4
Number of overlap: 10
Similarity score: 0.00965796

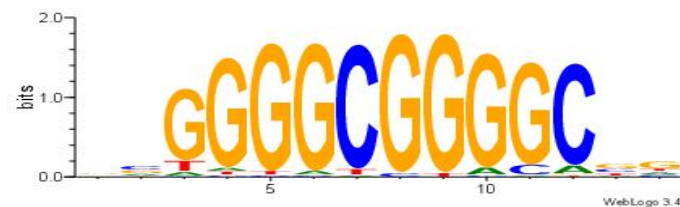
Alignment:

BBGGGGCGGGCVD
-GGGGYGGGG---

Original motif Consensus sequence: HVGCCCCGCCCB



Reverse complement motif Consensus sequence: BBGGGGCGGGGC

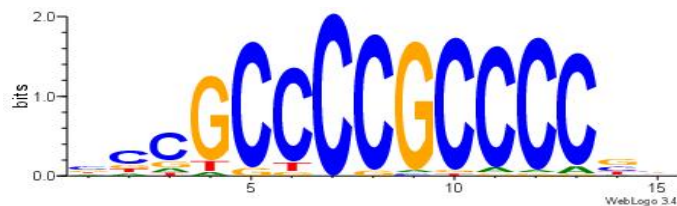


Dataset #: 4
 Motif ID: 38
 Motif name: cccGCCCCGCCCCsb
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 10
 Similarity score: 0.0127292

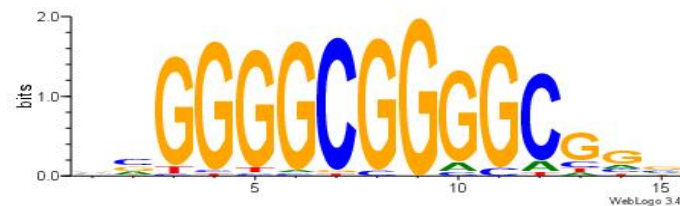
Alignment:

BCCGCCCCGCCCCBB
 ----CCCCKCCCC-

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB



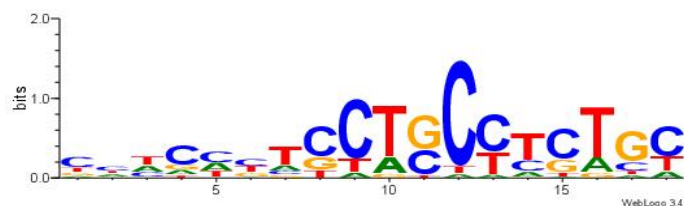
Dataset #: 5
 Motif ID: 52
 Motif name: TFM2
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward

Position number: 6
Number of overlap: 10
Similarity score: 0.0523047

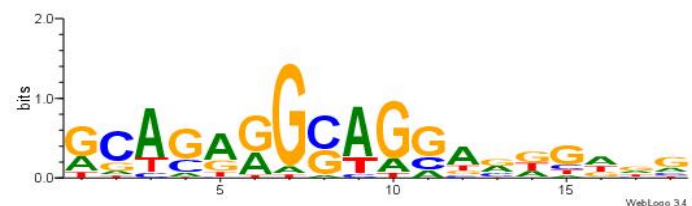
Alignment:

CHHCHBTCCTSCYTCTGC
-----CCCCKCCCC-----

Original motif Consensus sequence: CHHCHBTCCTSCYTCTGC



Reverse complement motif Consensus sequence:
GCAGAKGSAGGABDGHG

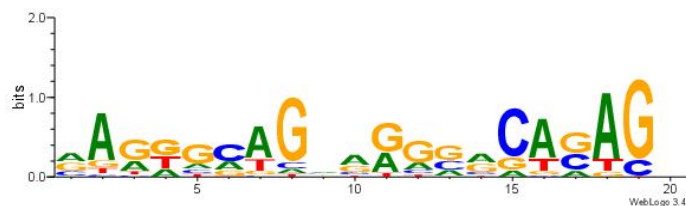


Dataset #: 5
Motif ID: 55
Motif name: TFM12
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 5
Number of overlap: 10
Similarity score: 0.0639596

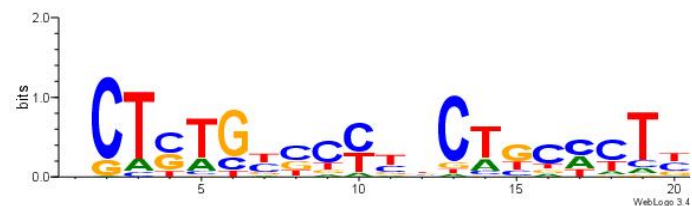
Alignment:

VCTSTGKSCMKBCTRCYCTK
-----CCCCKCCCC-----

Original motif Consensus sequence: RAGKGMAGVRRGSRCASAGV



Reverse complement motif Consensus sequence: VCTSTGKSCMKBCTRCYCTK

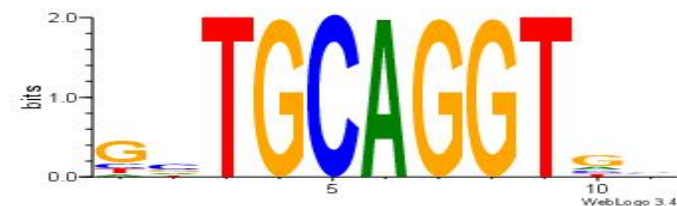


Dataset #: 4 Motif ID: 40 Motif name: kcACCTGCAGc

Original motif Consensus sequence: BCACCTGCABC



Reverse complement motif Consensus sequence: GBTGCAGGTGB



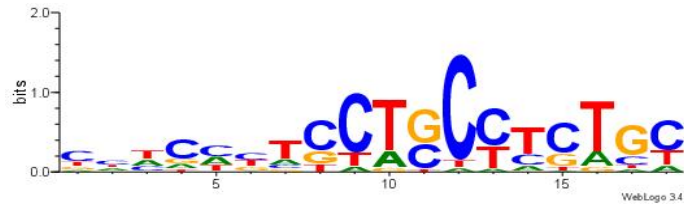
Best Matches for Top Significant Motif ID 40 (Highest to Lowest)

Dataset #:	5
Motif ID:	52
Motif name:	TFM2
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	5
Number of overlap:	11
Similarity score:	0.0194012

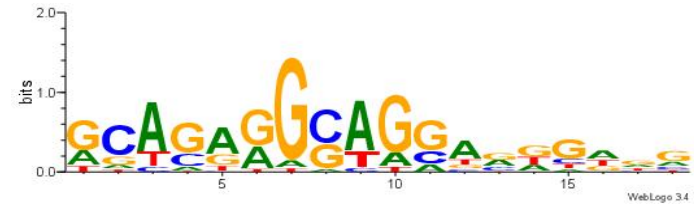
Alignment:

GCAGAKGSAGGABDGHDG
 ---GBTGCAGGTGB----

Original motif Consensus sequence: CHHCHBTCCTSCYTCTGC



Reverse complement motif Consensus sequence:
 GCAGAKGSAGGABDGHDG

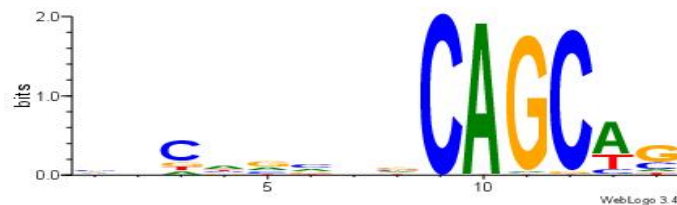
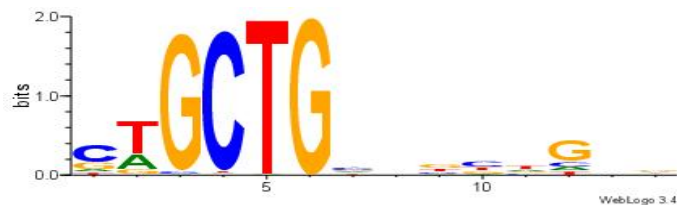


Dataset #:	5
Motif ID:	50
Motif name:	TFF11
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2
Number of overlap:	11
Similarity score:	0.0222944

Alignment:
 CTGCTGBDBBDGBD
 --GBTGCAGGTGB-

Original motif Consensus sequence: CTGCTGBDBBDGBD

Reverse complement motif Consensus sequence: HVCDBBDBCAGCA

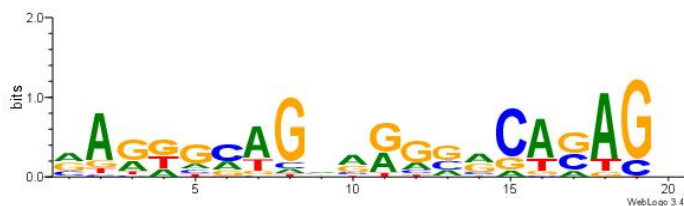


Dataset #: 5
 Motif ID: 55
 Motif name: TFM12
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 6
 Number of overlap: 11
 Similarity score: 0.0374254

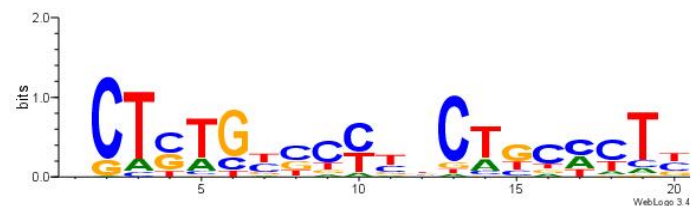
Alignment:

RAGKGMAGVRRGSRCASAGV
 ----GBTGCAGGTGB-----

Original motif Consensus sequence: RAGKGMAGVRRGSRCASAGV



Reverse complement motif Consensus sequence: VCTSTGKSCMKBCTRCYCTK



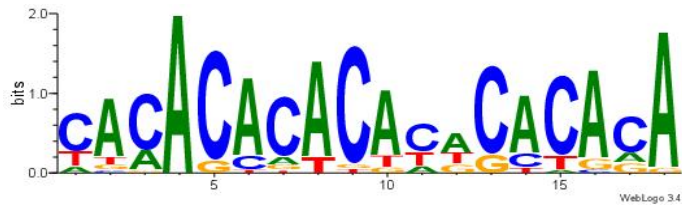
Dataset #: 5

Motif ID: 51
 Motif name: TFM1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 7
 Number of overlap: 11
 Similarity score: 0.0402527

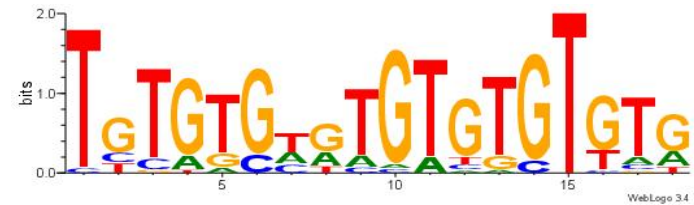
Alignment:

TGTGTGWGTGTGTGTGTG
 -----GBTGCAGGTGB-

Original motif Consensus sequence: CACACACACWCACACA



Reverse complement motif Consensus sequence: TGTGTGWGTGTGTGTGTG



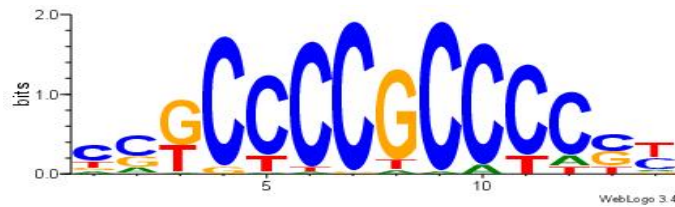
Dataset #: 2
 Motif ID: 7
 Motif name: Motif 7
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 11

Similarity score: 0.0411257

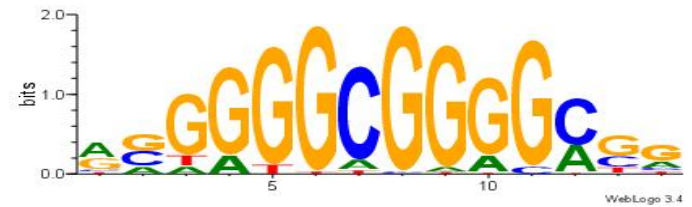
Alignment:

CSKCCCCGCCCSY
-BCACCTGCABC--

Original motif Consensus sequence: CSKCCCCGCCCSY



Reverse complement motif Consensus sequence: MSGGGGCGGGGY



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

Dataset #: 5 Motif ID: 46 Motif name: TFW3

Original motif Consensus sequence: GCACTG



Reverse complement motif Consensus sequence: CAGTGC



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

Dataset #: 4

Motif ID: 43
 Motif name: wsTACwGTAsw
 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: 0.00773193

Alignment:
 DBTACWGTAVH
 ----CAGTGC-

Original motif Consensus sequence: HVTACWG TABD



Reverse complement motif Consensus sequence: DBTACWGTAVH

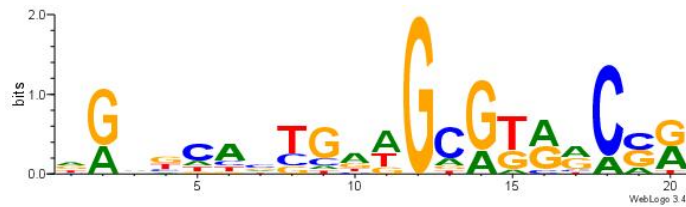


Dataset #: 3
 Motif ID: 31
 Motif name: Pax5
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 6
 Similarity score: 0.0111111

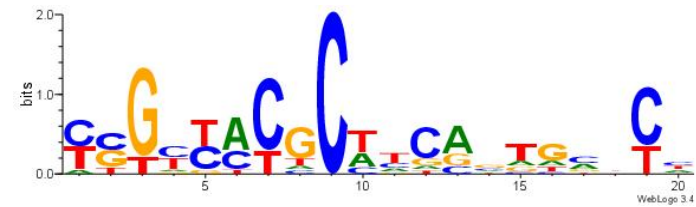
Alignment:

DGVBCABTGDWGCGRRCR
---GCACTG-----

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR



Reverse complement motif Consensus sequence:
MSGKKRCGCWDCABTGBBCD



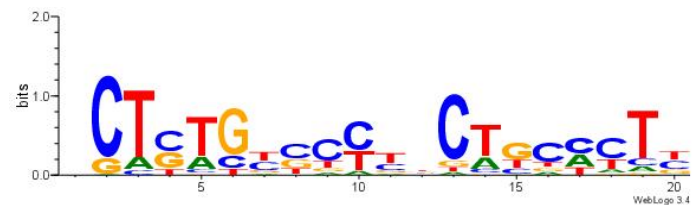
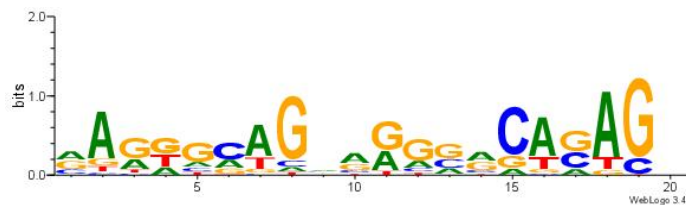
Dataset #: 5
Motif ID: 55
Motif name: TFM12
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 14
Number of overlap: 6
Similarity score: 0.0147489

Alignment:

RAGKGMAGVRRGSRASAGV
-----GCACTG--

Original motif Consensus sequence: RAGKGMAGVRRGSRASAGV

Reverse complement motif Consensus sequence:
VCTSTGKSCMKBCTRCYCTK



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: 4
 Number of overlap: 6
 Similarity score: 0.0148473

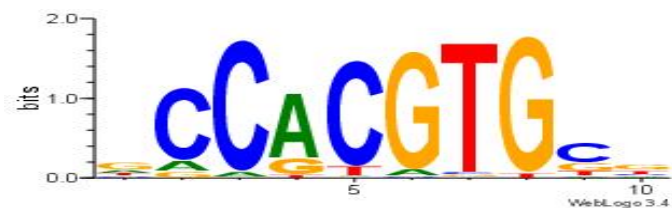
Alignment:

DCCACGTGCV
 ---CAGTGC-

Original motif Consensus sequence: VGCACGTGGH



Reverse complement motif Consensus sequence: DCCACGTGCV



Dataset #: 3
 Motif ID: 35

Motif name: GABPA
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 6
 Similarity score: 0.0156785

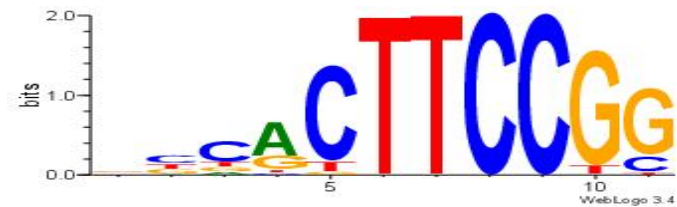
Alignment:

VVCACTTCCGG
 ----GCACTG-

Original motif Consensus sequence: CCGGAAGTG



Reverse complement motif Consensus sequence: VVCACTTCCGG

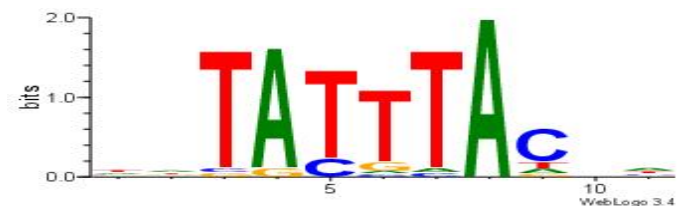


Dataset #: 4 Motif ID: 45 Motif name: wbgTAAATAww

Original motif Consensus sequence: DBGTAATAHD



Reverse complement motif Consensus sequence: DHTATTTACBD



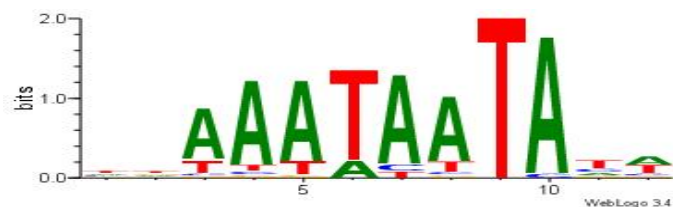
Best Matches for Significant Motif ID 45 (Highest to Lowest)

Dataset #: 4
 Motif ID: 37
 Motif name: tkAAATAATAtw
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.00892084

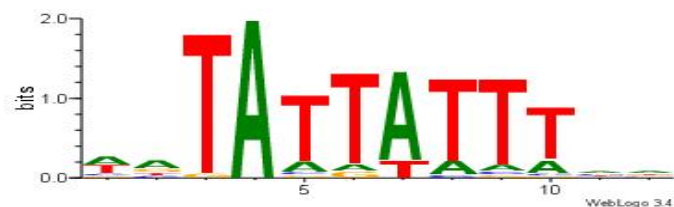
Alignment:

HDAAATAATAHW
 -DBGTAAATAHD

Original motif Consensus sequence: HDAAATAATAHW



Reverse complement motif Consensus sequence: WHTATTATTTDH



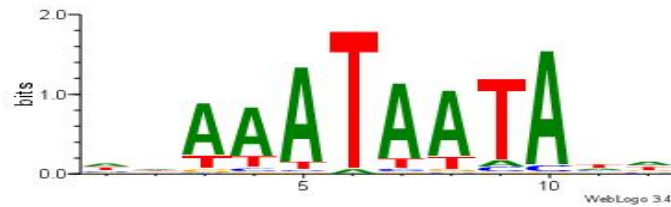
Dataset #: 4
 Motif ID: 41
 Motif name: wwAAATAATAtw
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 11

Similarity score: 0.00917337

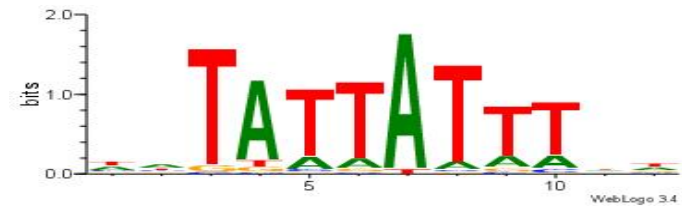
Alignment:

DDTATTATTTDH
DHTATTTACBD-

Original motif Consensus sequence: HDAAATAATADD



Reverse complement motif Consensus sequence: DDTATTATTTDH



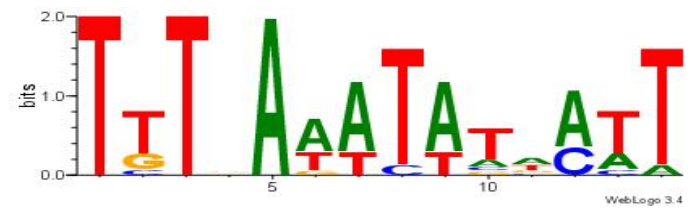
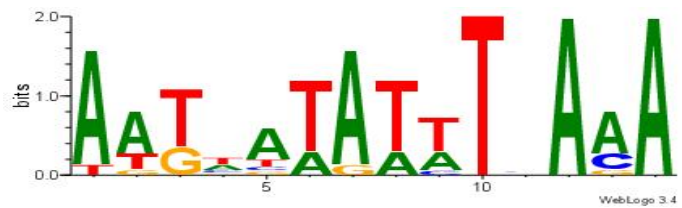
Dataset #: 2
Motif ID: 9
Motif name: Motif 9
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 4
Number of overlap: 11
Similarity score: 0.0177412

Alignment:

AATHATATWTHAAA
DHTATTTACBD---

Original motif Consensus sequence: AATHATATWTHAAA

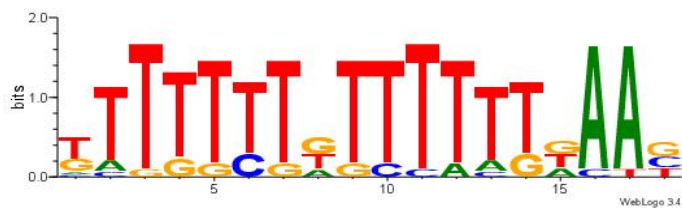
Reverse complement motif Consensus sequence: TTTDAWATATHAT



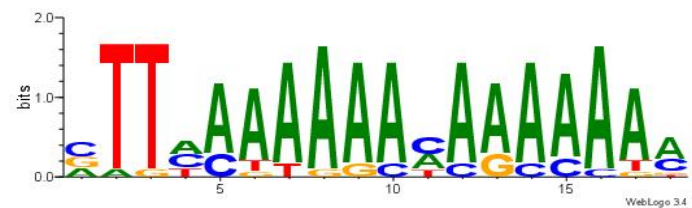
Dataset #: 5
 Motif ID: 53
 Motif name: TFM3
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 4
 Number of overlap: 11
 Similarity score: 0.0203792

Alignment:
 BTTHAAAAAYAAAAAR
 ---DBGTAAATAHD----

Original motif Consensus sequence: KTTTTTKTTTTTDAAB



Reverse complement motif Consensus sequence: BTTHAAAAAYAAAAAR



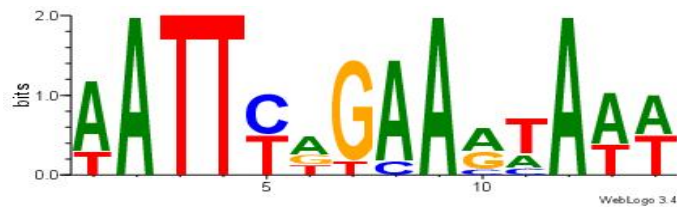
Dataset #: 2

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: 0.0205821

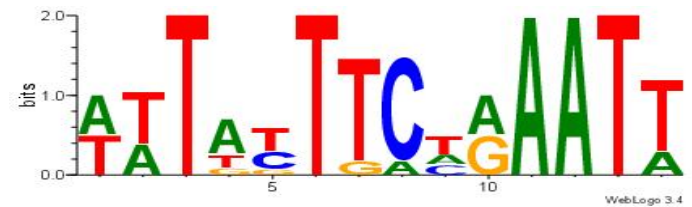
Alignment:

AATTYDGAARTAWW
 ---DBGTAATAHD

Original motif Consensus sequence: AATTYDGAARTAWW



Reverse complement motif Consensus sequence: WWTAKTTCDKAAAT



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

Original motif Consensus sequence: ATAAAA



Reverse complement motif Consensus sequence: TTTTAT



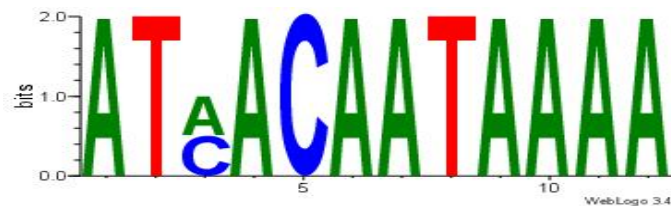
Best Matches for Significant Motif ID 21 (Highest to Lowest)

Dataset #: 2
Motif ID: 15
Motif name: Motif 15
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 7
Number of overlap: 6
Similarity score: 0

Alignment:

```
ATMACAATAAAA  
-----ATAAAA
```

Original motif Consensus sequence: ATMACAATAAAA



Reverse complement motif Consensus sequence: TTTTATTGTYAT

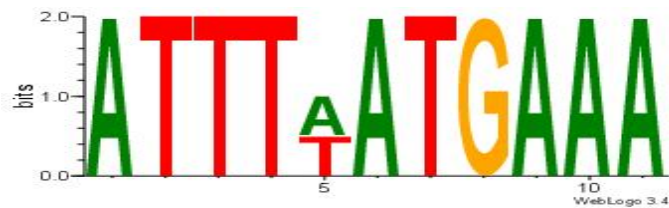


Dataset #: 2
Motif ID: 11
Motif name: Motif 11
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif

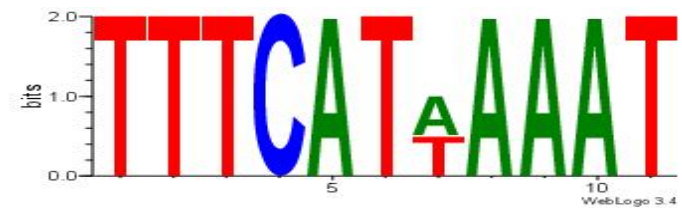
Direction: Forward
 Position number: 5
 Number of overlap: 6
 Similarity score: 0.0208333

Alignment:
 ATTTWATGAAA
 ----TTTTAT-

Original motif Consensus sequence: ATTTWATGAAA



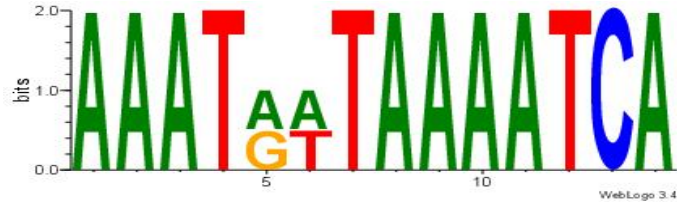
Reverse complement motif Consensus sequence: TTTCAWAAAT



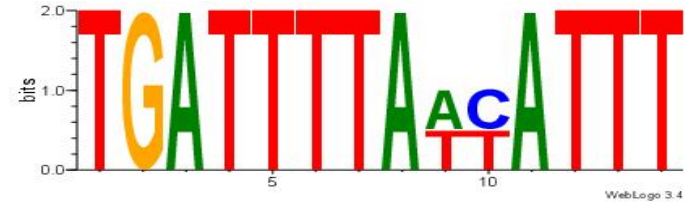
Dataset #: 2
 Motif ID: 8
 Motif name: Motif 8
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 6
 Number of overlap: 6
 Similarity score: 0.0208333

Alignment:
 AAATRWTAATAATCA
 -----ATAAAA----

Original motif Consensus sequence: AAATRWTAATCA



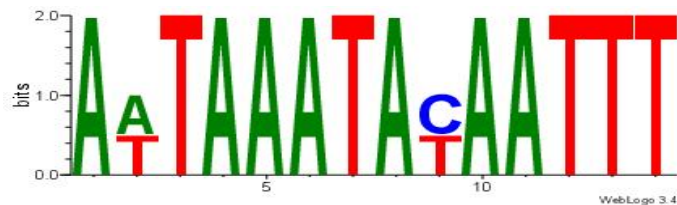
Reverse complement motif Consensus sequence: TGATTTAWKATT



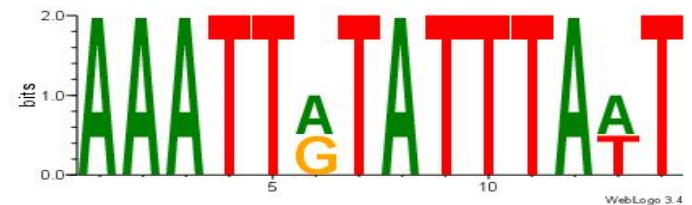
Dataset #: 2
Motif ID: 5
Motif name: Motif 5
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 4
Number of overlap: 6
Similarity score: 0.0208333

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

Original motif Consensus sequence: AWTAAATAYAATTT



Reverse complement motif Consensus sequence: AAATTKTATTTAW



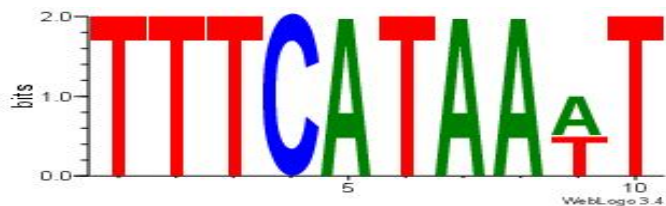
Dataset #: 2
 Motif ID: 10
 Motif name: Motif 10
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 5
 Number of overlap: 6
 Similarity score: 0.0416667

Alignment:

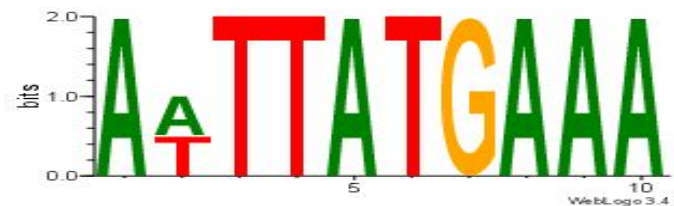
AWTTATGAAA

ATAAAA-----

Original motif Consensus sequence: TTTCATAAWT

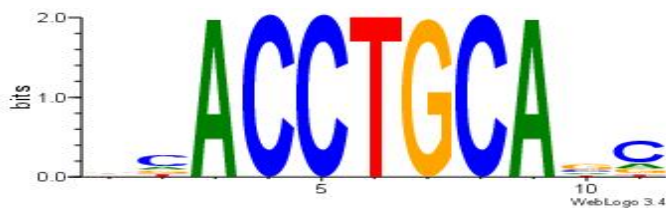


Reverse complement motif Consensus sequence: AWTTATGAAA



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)

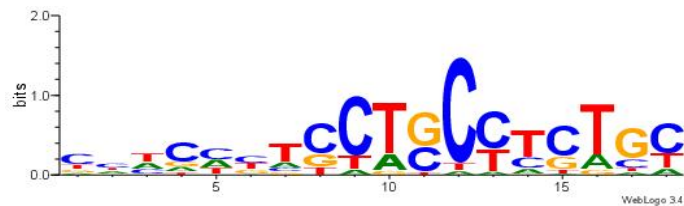
Dataset #: 5
 Motif ID: 52
 Motif name: TFM2
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 4
 Number of overlap: 11
 Similarity score: 0.0194012

Alignment:

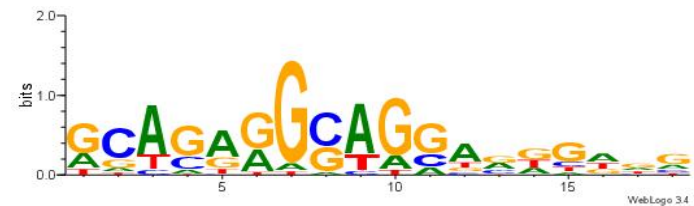
```

GCAGAKGSAGGABDGH DG
---GBTGCAGGTGB-----
  
```

Original motif Consensus sequence: CHHCHBTCCTSCYTCTGC



Reverse complement motif Consensus sequence:
GCAGAKGSAGGABDGH DG



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



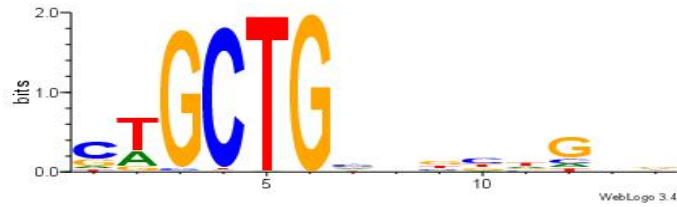
Reverse complement motif Consensus sequence: DBTACWGTAVH



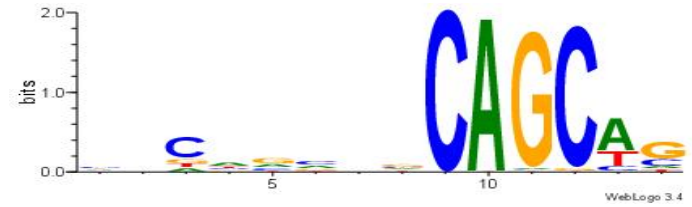
Dataset #: 5
 Motif ID: 50
 Motif name: TFF11
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 11
 Similarity score: 0.0222944

Alignment:
 CTGCTGBDBBDGDB
 --GBTGCAGGTGB--

Original motif Consensus sequence: CTGCTGBDBBDGBD



Reverse complement motif Consensus sequence: HVCDBBDBCAGCA

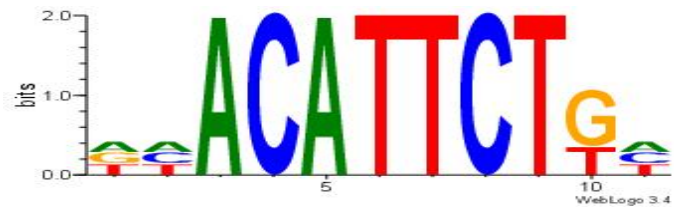


Dataset #: 4
Motif ID: 44
Motif name: dhACATTCTkh
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 11
Similarity score: 0.0254134

Alignment:

DHACATTCTGH
BCACCTGCABC

Original motif Consensus sequence: DHACATTCTGH



Reverse complement motif Consensus sequence: HCAGAATGTHD

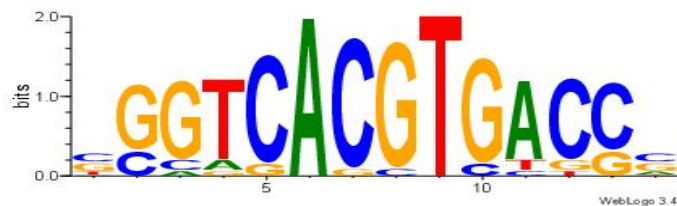


Dataset #: 4
 Motif ID: 42
 Motif name: sSGTCACGTGACSS
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 11
 Similarity score: 0.031338

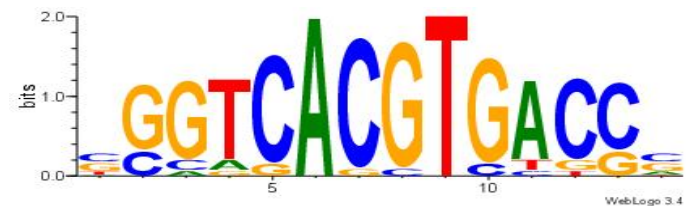
Alignment:

SGGTCACGTGACCS
 ---BCACCTGCABC

Original motif Consensus sequence: SGGTCACGTGACCS

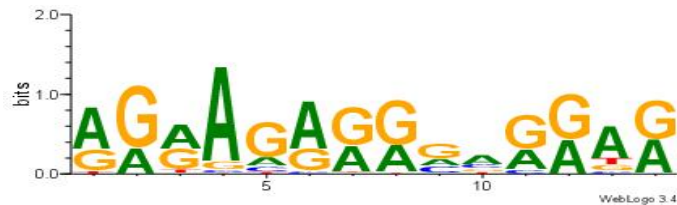


Reverse complement motif Consensus sequence: SGGTCACGTGACCS

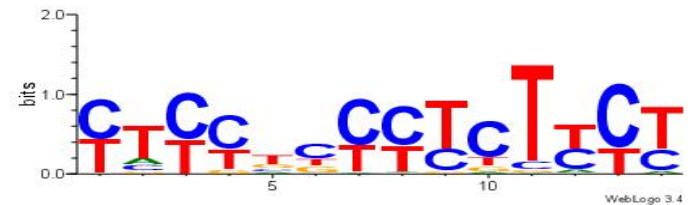


Dataset #: 2 Motif ID: 2 Motif name: Motif 2

Original motif Consensus sequence: RGRAGARRGARRAR



Reverse complement motif Consensus sequence: MTMMTCMMTCTK



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

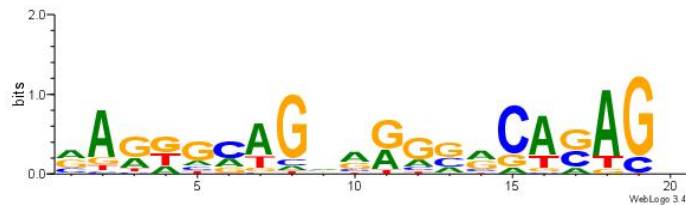
Dataset #: 5
 Motif ID: 55
 Motif name: TFM12
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 14
 Similarity score: 0.00215466

Alignment:

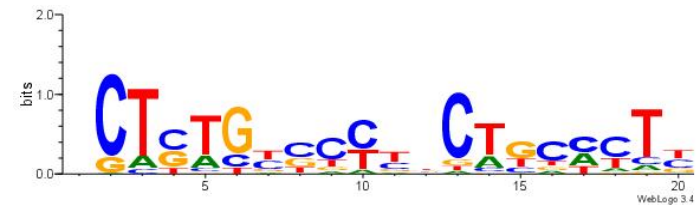
```

RAGKGMAGVRRGSRCASAGV
---RGRAGARRGARRAR---
  
```

Original motif Consensus sequence: RAGKGMAGVRRGSRCASAGV



Reverse complement motif Consensus sequence: VCTSTGKSCMKBCTRCYCTK



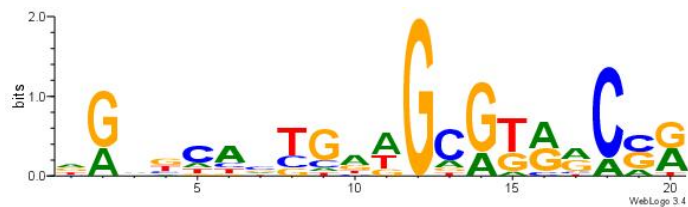
Dataset #: 3
 Motif ID: 31
 Motif name: Pax5
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement

Direction: Forward
 Position number: 7
 Number of overlap: 14
 Similarity score: 0.0213256

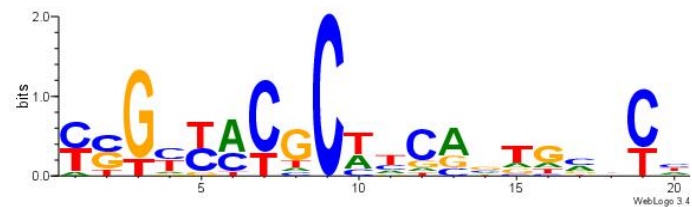
Alignment:

MSGKKRCGCWDCABTGBBCD
 -----MTMMTCMMTCTKCK

Original motif Consensus sequence: DGVCABTGDWGCGRRCR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD

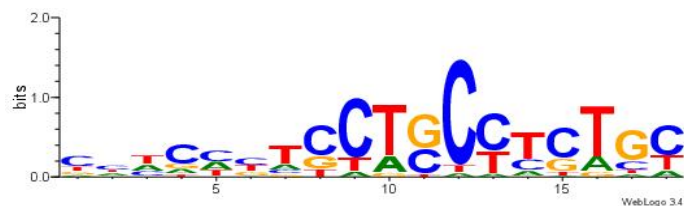


Dataset #: 5
 Motif ID: 52
 Motif name: TFM2
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 14
 Similarity score: 0.0283463

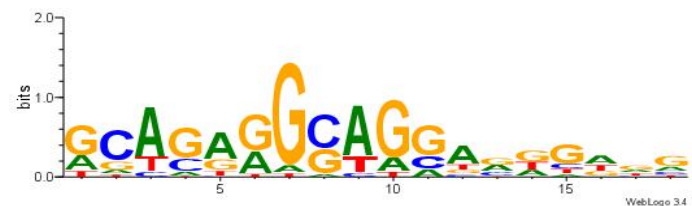
Alignment:

CHHCHBTCCTSCYTCTGC
 --MTMMTCMMTCTKCK--

Original motif Consensus sequence: CHHCHBTCCTSCYTCTGC



Reverse complement motif Consensus sequence: GCAGAKGSAGGABDGHDG

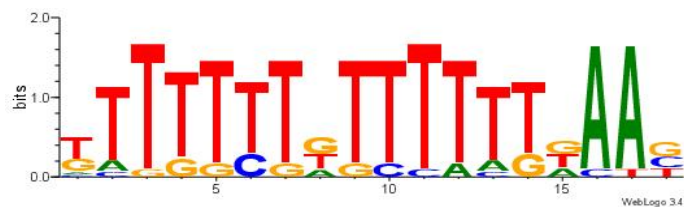


Dataset #: 5
Motif ID: 53
Motif name: TFM3
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 5
Number of overlap: 14
Similarity score: 0.0316147

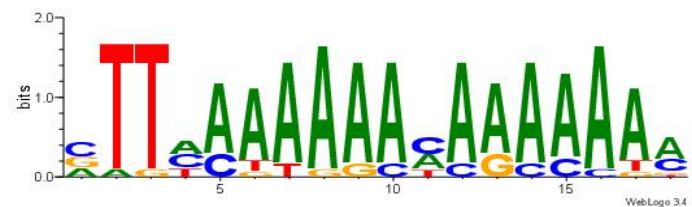
Alignment:

```
BTTHAAAAAYAAAAAR  
----RGRAGARRRAR
```

Original motif Consensus sequence: KTTTTTKTTTTTDAAB



Reverse complement motif Consensus sequence: BTTHAAAAAYAAAAAR

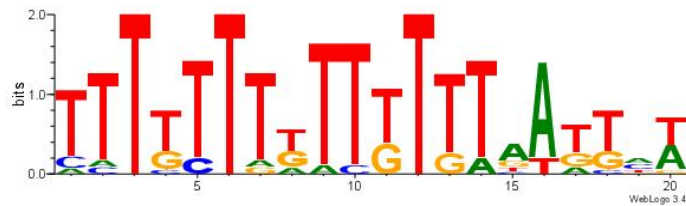


Dataset #: 5
 Motif ID: 56
 Motif name: TFM13
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 4
 Number of overlap: 14
 Similarity score: 0.0368869

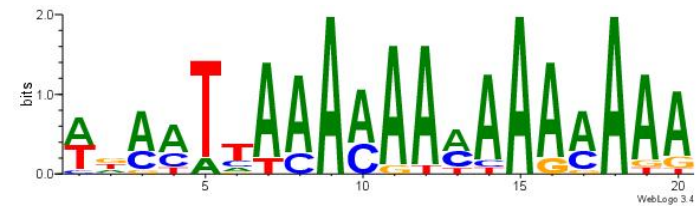
Alignment:

WHAATTAAARAARAAAAAAA
 ---RGRAGARRGARRAR---

Original motif Consensus sequence: TTTTTTKTKTTTAATTHW



Reverse complement motif Consensus sequence: WHAATTAAARAARAAAAAAA



Best Matches for Each Motif (Highest to Lowest)

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

Original motif Consensus sequence: GGCGGGGC

Reverse complement motif Consensus sequence: GCCCGGCC

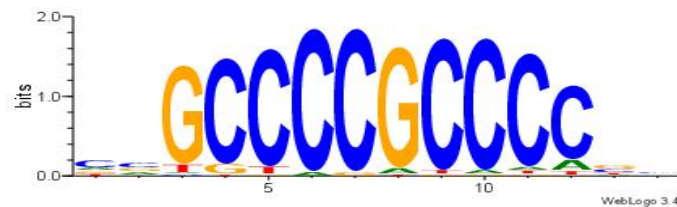


Best Matches for Motif ID 1 (Highest to Lowest)

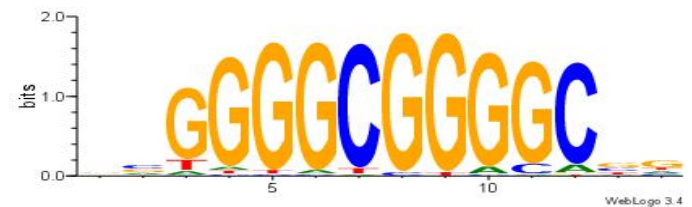
Dataset #: 4
 Motif ID: 36
 Motif name: csGCCCCGCCCCsc
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 5
 Number of overlap: 8
 Similarity score: 0

Alignment:
 BBGGGGCGGGGCVD
 ----GGCGGGGC--

Original motif Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGC

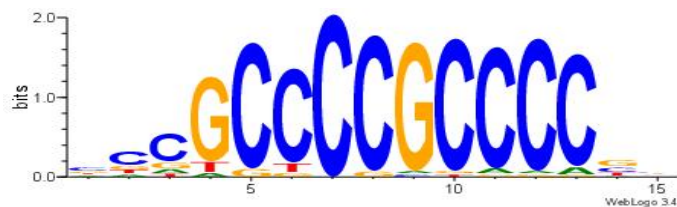


Dataset #: 4

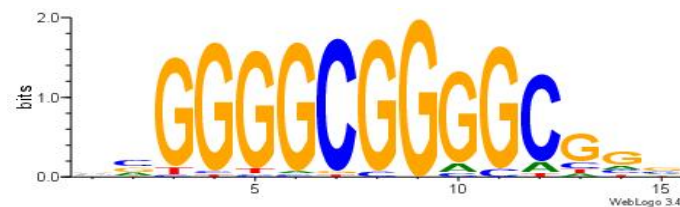
Motif ID: 38
 Motif name: cccGCCCCGCCCCsb
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 4
 Number of overlap: 8
 Similarity score: 0.00250079

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

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB



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

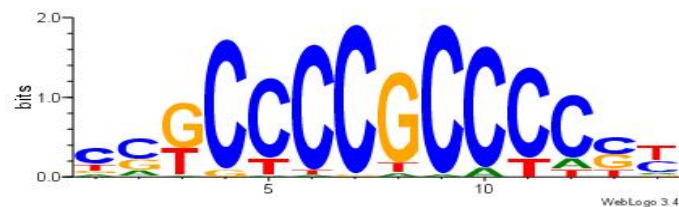
Similarity score: 0.0149958

Alignment:

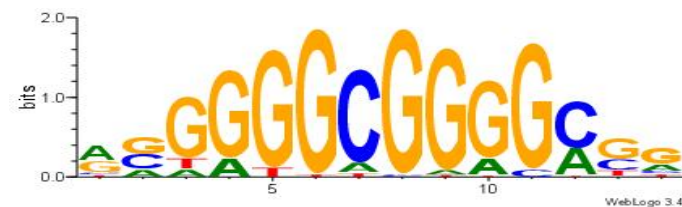
MSGGGGCGGGYSG

----GGCGGGGC--

Original motif Consensus sequence: CSKCCCCGCCCSY



Reverse complement motif Consensus sequence: MSGGGGCGGGY



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

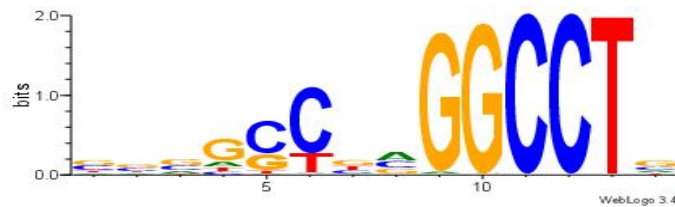


Dataset #: 3
 Motif ID: 22
 Motif name: Zfx
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 4
 Number of overlap: 8
 Similarity score: 0.0708224

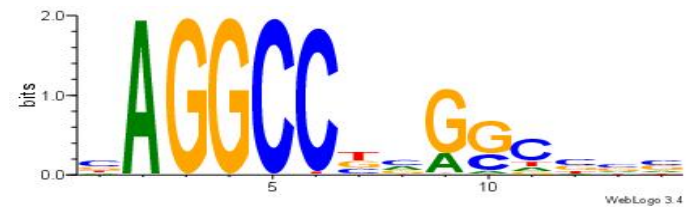
Alignment:

VAGGCCBBGGCVBB
 ---GCCCCGCC---

Original motif Consensus sequence: BBVGCCBVGCCCTV



Reverse complement motif Consensus sequence: VAGGCCBBGGCVBB



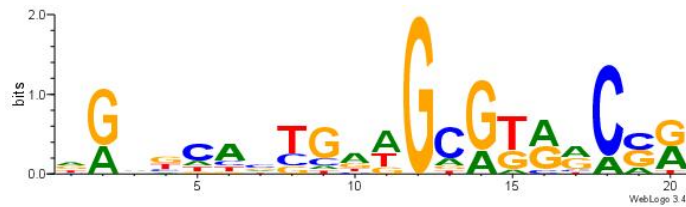
Dataset #: 3
 Motif ID: 31

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

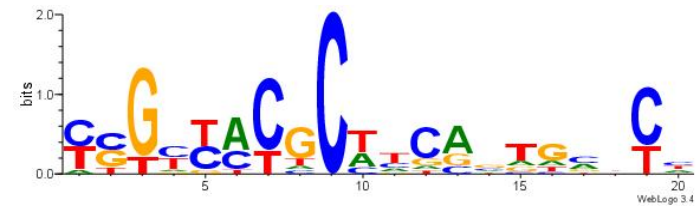
Alignment:

DGVBCABTGDWGCGRRCR
 -----GGCGGGGC--

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR

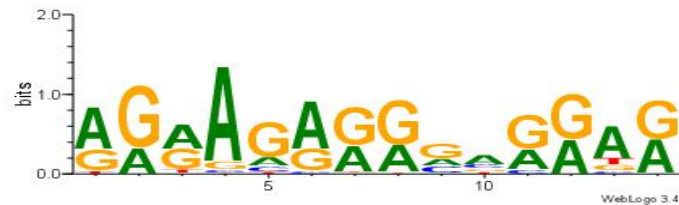


Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD

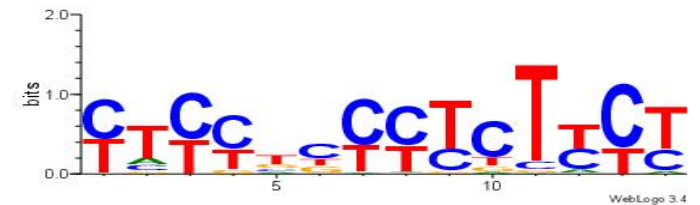


Dataset #: 2 Motif ID: 2 Motif name: Motif 2

Original motif Consensus sequence: RGRAGARRGARRAR



Reverse complement motif Consensus sequence: MTMMTCMMTCTK



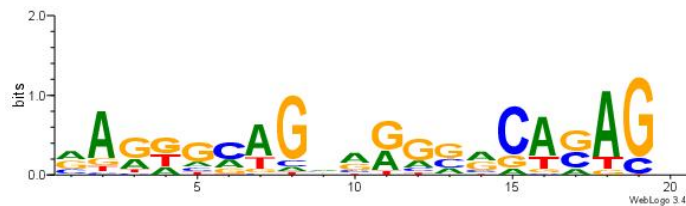
Best Matches for Motif ID 2 (Highest to Lowest)

Dataset #: 5
Motif ID: 55
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: 0.00215466

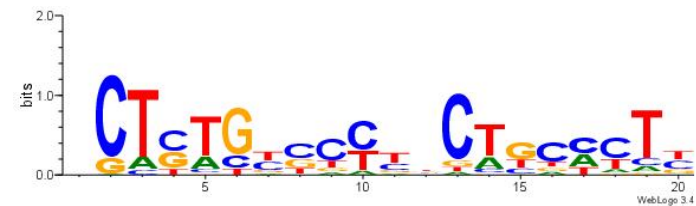
Alignment:

```
RAGKGMAGVRRGSRCASAGV  
---RGRAGARRGARRAR---
```

Original motif Consensus sequence: RAGKGMAGVRRGSRCASAGV



Reverse complement motif Consensus sequence: VCTSTGKSCMKBCTRCYCTK



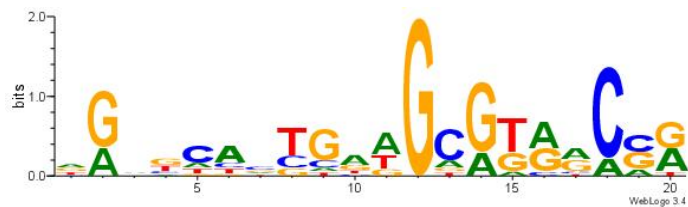
Dataset #: 3
Motif ID: 31
Motif name: Pax5
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement

Direction: Forward
 Position number: 7
 Number of overlap: 14
 Similarity score: 0.0213256

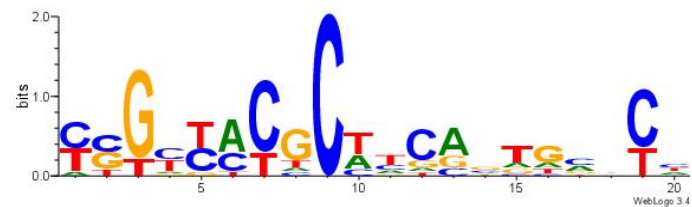
Alignment:

MSGKKRCGCWDCABTGBBCD
 -----MTMMTCMMTCTKCK

Original motif Consensus sequence: DGVCABTGDWGCGRRCR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD

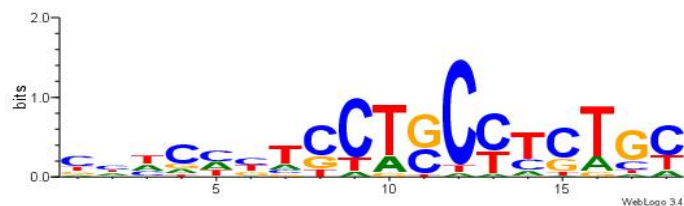


Dataset #: 5
 Motif ID: 52
 Motif name: TFM2
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 14
 Similarity score: 0.0283463

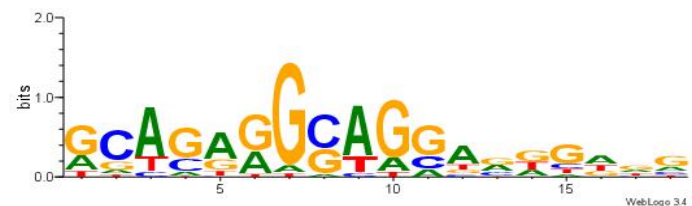
Alignment:

CHHCHBTCCTSCYTCTGC
 --MTMMTCMMTCTKCK--

Original motif Consensus sequence: CHHCHBTCCTSCYTCTGC



Reverse complement motif Consensus sequence: GCAGAKGSAGGABDGHDG

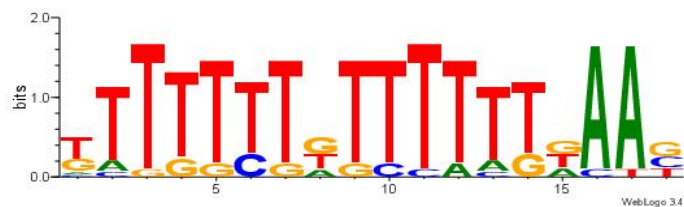


Dataset #: 5
Motif ID: 53
Motif name: TFM3
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 5
Number of overlap: 14
Similarity score: 0.0316147

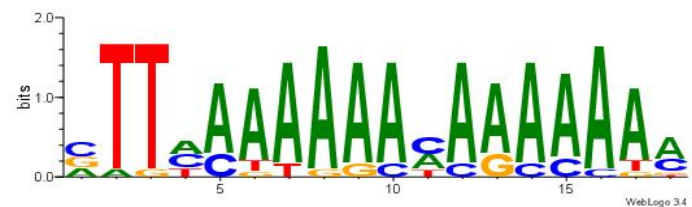
Alignment:

```
BTTHAAAAAYAAAAAR  
----RGRAGARRRARR
```

Original motif Consensus sequence: KTTTTTKTTTTTDAAB



Reverse complement motif Consensus sequence: BTTHAAAAAYAAAAAR

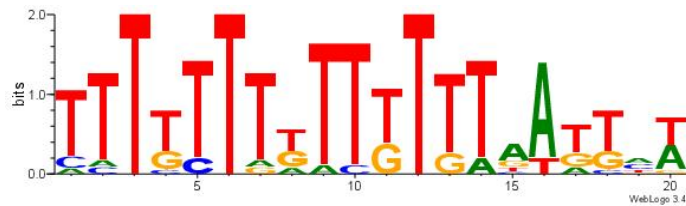


Dataset #: 5
 Motif ID: 56
 Motif name: TFM13
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 4
 Number of overlap: 14
 Similarity score: 0.0368869

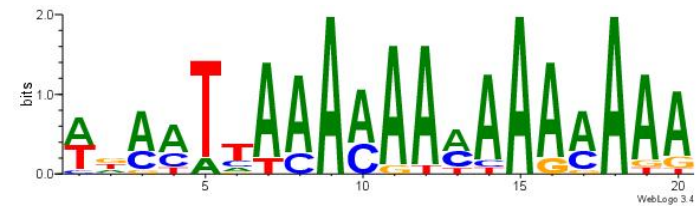
Alignment:

WHAATTAAARAARAAAAAAA
 ---RGRAGARRGARRAR---

Original motif Consensus sequence: TTTTTTKTTKTTTAATTHW



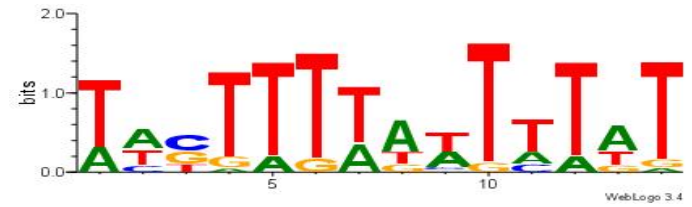
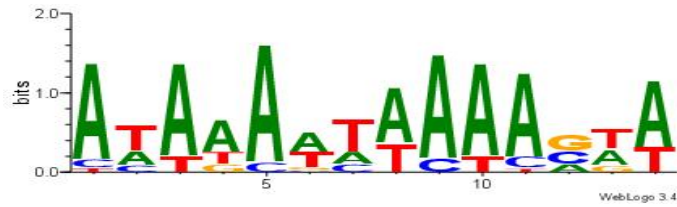
Reverse complement motif Consensus sequence: WHAATTAAARAARAAAAAAA



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

Original motif Consensus sequence: AWAAWTWAAASWA

Reverse complement motif Consensus sequence: TWSTTTWAWTTT

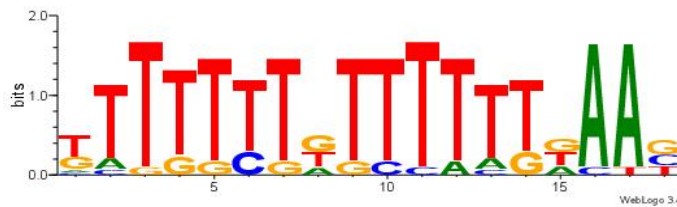


Best Matches for Motif ID 3 (Highest to Lowest)

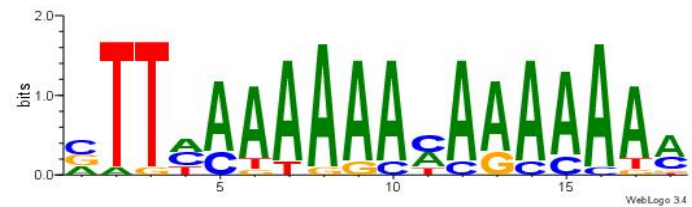
Dataset #: 5
 Motif ID: 53
 Motif name: TFM3
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 5
 Number of overlap: 14
 Similarity score: 0.020364

Alignment:
 BTTHAAAAAYAAAAAR
 ----AWAAAWTWAAASWA

Original motif Consensus sequence: KTTTTTKTTTTTDAAB



Reverse complement motif Consensus sequence: BTTHAAAAAYAAAAAR

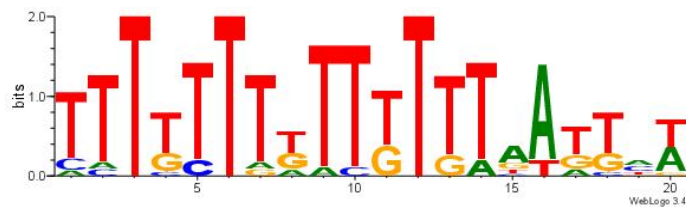


Dataset #: 5
 Motif ID: 56
 Motif name: TFM13
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 7
 Number of overlap: 14
 Similarity score: 0.0250981

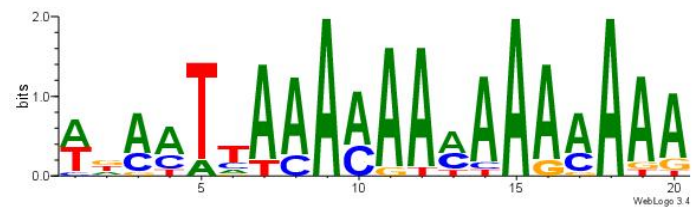
Alignment:

WHAATTAAARAARAAAAAAA
 -----AWAAAWTWAAASWA

Original motif Consensus sequence: TTTTTTKTKTTTAATTHW



Reverse complement motif Consensus sequence: WHAATTAAARAARAAAAAAA



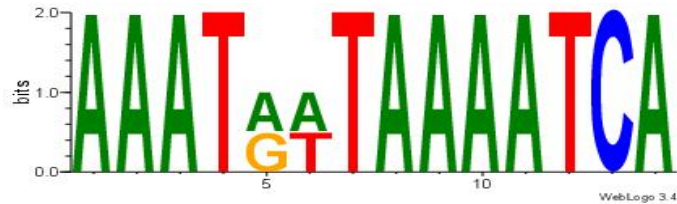
Dataset #: 2
 Motif ID: 8
 Motif name: Motif 8
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1

Number of overlap: 14
Similarity score: 0.0394231

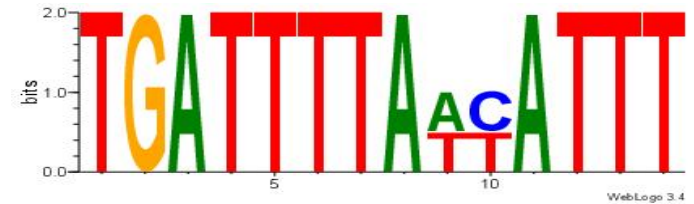
Alignment:

TGATTTTAWKATTT
TWSTTTWAWTTTWT

Original motif Consensus sequence: AAATRWATAAATCA



Reverse complement motif Consensus sequence: TGATTTTAWKATTT



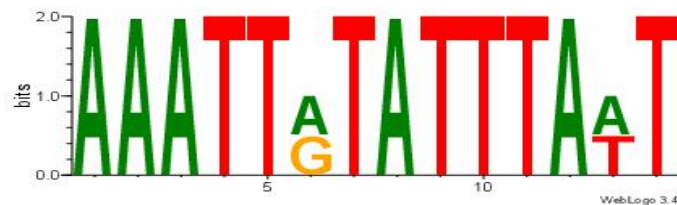
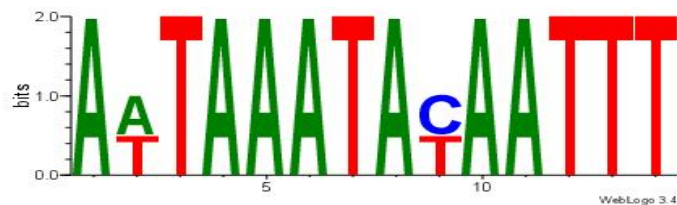
Dataset #: 2
Motif ID: 5
Motif name: Motif 5
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 14
Similarity score: 0.0449176

Alignment:

AAATTKTATTTAWT
TWSTTTWAWTTTWT

Original motif Consensus sequence: AWTAAATAYAATTT

Reverse complement motif Consensus sequence: AAATTKTATTTAWT

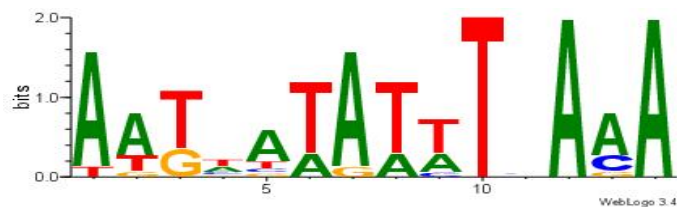


Dataset #: 2
 Motif ID: 9
 Motif name: Motif 9
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0.0594551

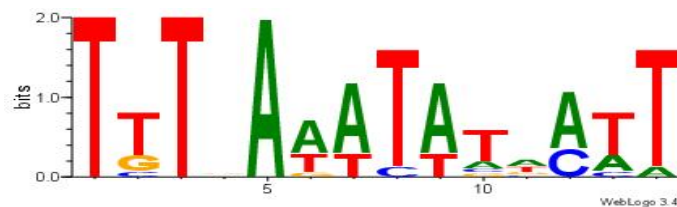
Alignment:

TTTDAWATATHATT
 AWWAAWTWAAASWA

Original motif Consensus sequence: AATHATATWTHAAA

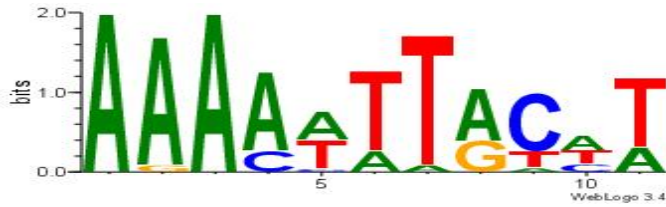


Reverse complement motif Consensus sequence: TTTDAWATATHATT



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

Original motif Consensus sequence: AAAAWTTRCWT



Reverse complement motif Consensus sequence: AWGKAAWTTTT



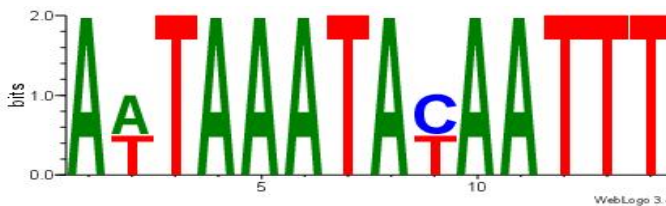
Best Matches for Motif ID 4 (Highest to Lowest)

Dataset #:	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

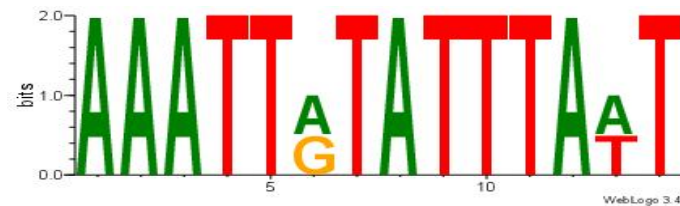
Alignment:

```
AAATTKTATTTAWT
AAAAWTTRCWT---
```

Original motif Consensus sequence: AWTAAATAYAATTT



Reverse complement motif Consensus sequence: AAATTKTATTTAW

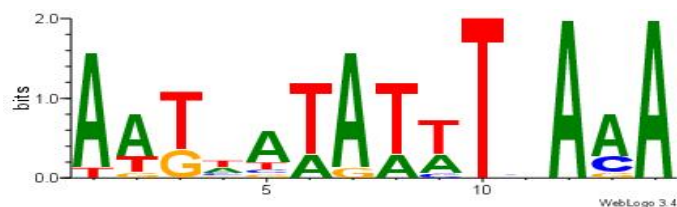


Dataset #: 2
 Motif ID: 9
 Motif name: Motif 9
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 4
 Number of overlap: 11
 Similarity score: 0.0820375

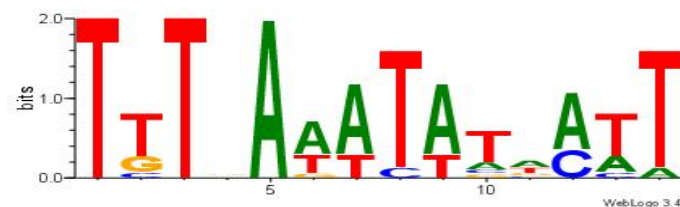
Alignment:

AATHATATWTHAAA
 AWGKAAWTTTT---

Original motif Consensus sequence: AATHATATWTHAAA



Reverse complement motif Consensus sequence: TTTDAWATATHAT



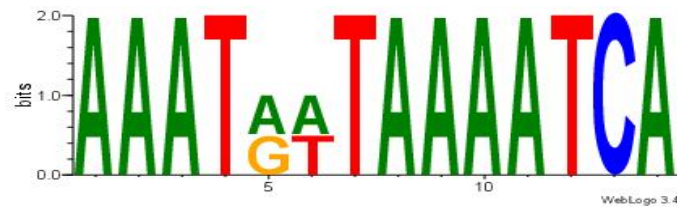
Dataset #: 2
 Motif ID: 8
 Motif name: Motif 8
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 4
 Number of overlap: 11

Similarity score: 0.083433

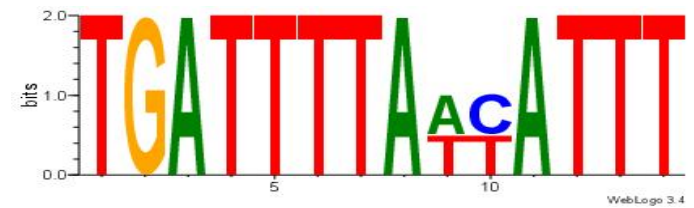
Alignment:

TGATTTTAWKATTT
---AWGKAAWTTTT

Original motif Consensus sequence: AAATRWAAAATCA



Reverse complement motif Consensus sequence: TGATTTTAWKATTT



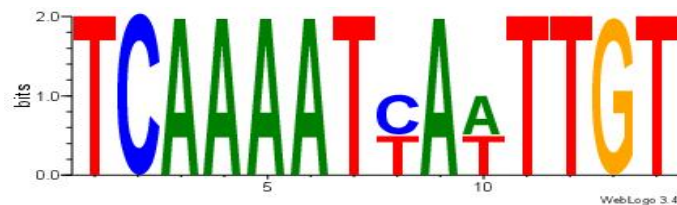
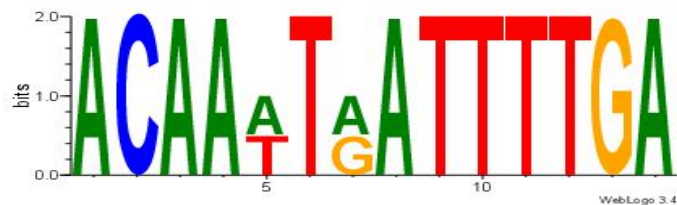
Dataset #: 2
Motif ID: 16
Motif name: Motif 16
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 11
Similarity score: 0.0852273

Alignment:

ACAAWTRATTTTGA
AAAATTRCWT---

Original motif Consensus sequence: ACAAWTRATTTTGA

Reverse complement motif Consensus sequence: TCAAAATKAWTTG



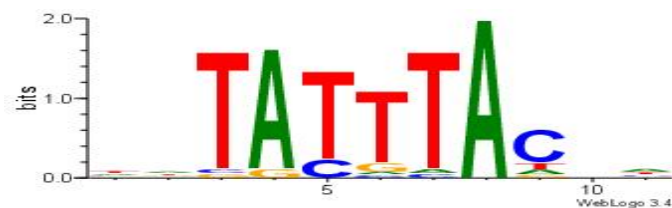
Dataset #: 4
 Motif ID: 45
 Motif name: wbgTAAATAww
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.086338

Alignment:
 DBGTAATAHD
 AWGKAATTTT

Original motif Consensus sequence: DBGTAATAHD

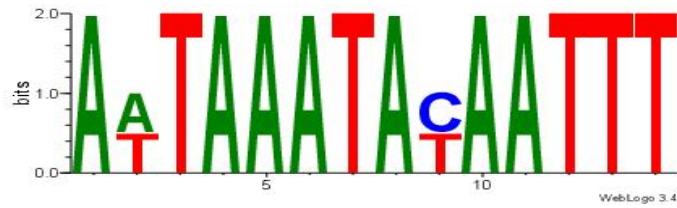


Reverse complement motif Consensus sequence: DHTATTTACBD

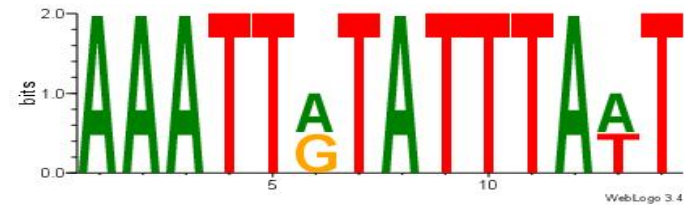


Dataset #: 2 Motif ID: 5 Motif name: Motif 5

Original motif Consensus sequence: AWTAAATAYAATTT



Reverse complement motif Consensus sequence: AAATTKTATTTAW



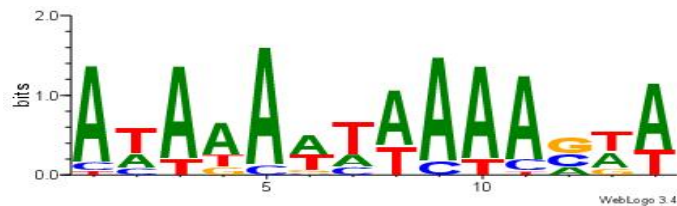
Best Matches for Motif ID 5 (Highest to Lowest)

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

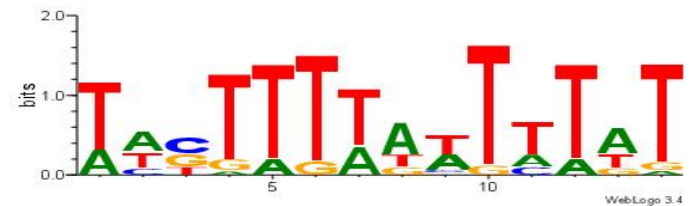
Alignment:

```
TWSTTTWAWTTTWT
AAATTKTATTTAWT
```

Original motif Consensus sequence: AWAAAWTWAASWA



Reverse complement motif Consensus sequence: TWSTTTWAWTTTWT

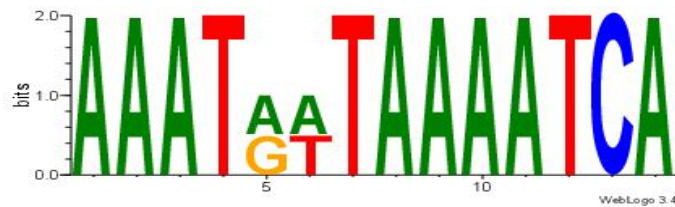


Dataset #: 2
 Motif ID: 8
 Motif name: Motif 8
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0.107143

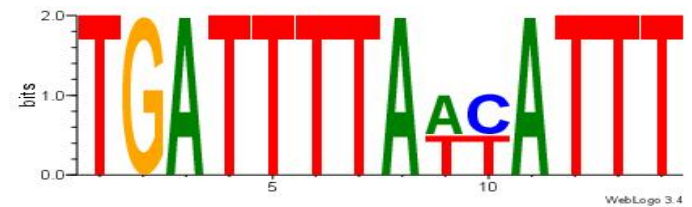
Alignment:

TGATTTTAWKATTT
 AAATTKTATTTAWT

Original motif Consensus sequence: AAATRWATAAATCA



Reverse complement motif Consensus sequence: TGATTTTAWKATTT



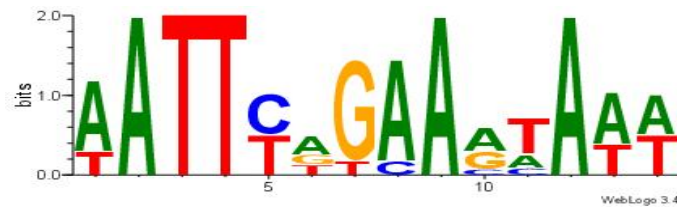
Dataset #: 2
 Motif ID: 6
 Motif name: Motif 6
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 14

Similarity score: 0.111607

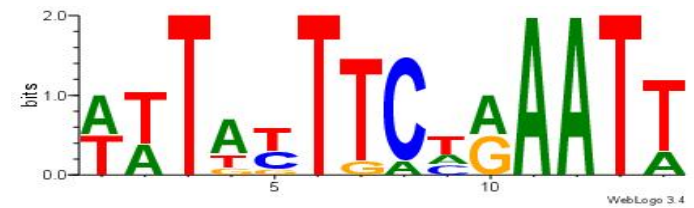
Alignment:

AATTYDGAARTAWW
AAATTKTATTTAWT

Original motif Consensus sequence: AATTYDGAARTAWW



Reverse complement motif Consensus sequence: WWTAKTTCDKAAAT



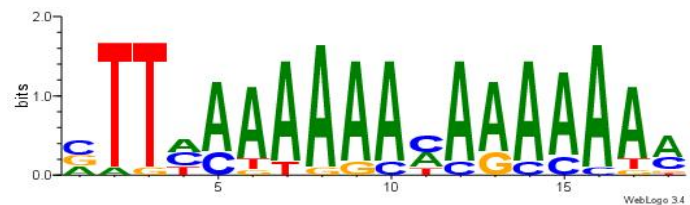
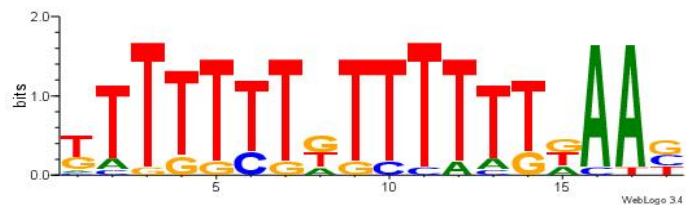
Dataset #: 5
Motif ID: 53
Motif name: TFM3
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 14
Similarity score: 0.113839

Alignment:

KTTTTTKTTTTTDAAB
AAATTKTATTTAWT----

Original motif Consensus sequence: KTTTTTKTTTTTDAAB

Reverse complement motif Consensus sequence:
BTTHAAAAAYAAAAAR



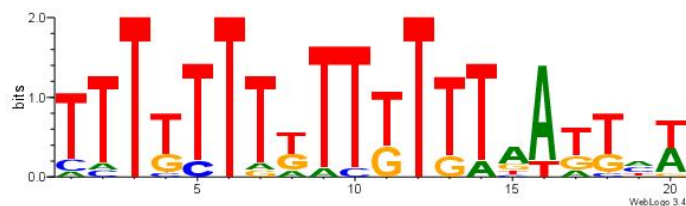
Dataset #: 5
 Motif ID: 56
 Motif name: TFM13
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 4
 Number of overlap: 14
 Similarity score: 0.121173

Alignment:

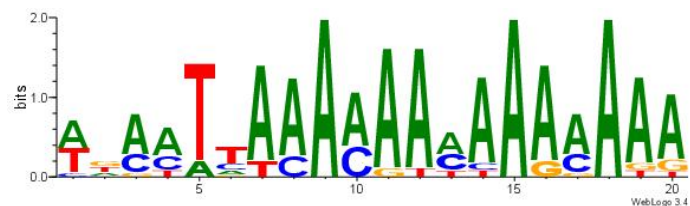
```

TTTTTTTKTTKTTTAATTHW
---AAATTKTATTTAWT---
  
```

Original motif Consensus sequence: TTTTTTKTTKTTTAATTHW



Reverse complement motif Consensus sequence: WHAATTAARAARAAAAA

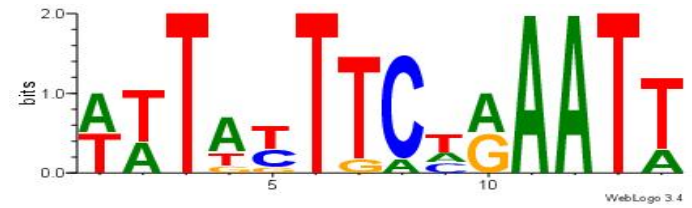


Dataset #: 2 Motif ID: 6 Motif name: Motif 6

Original motif Consensus sequence: AATTYDGAARTAWW



Reverse complement motif Consensus sequence: WWTAKTTCDKAAT



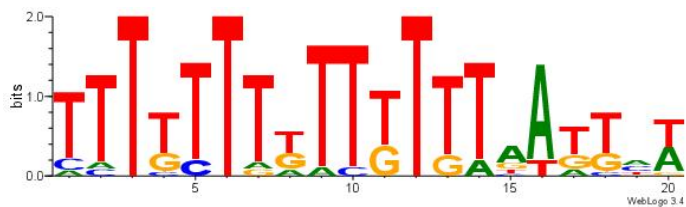
Best Matches for Motif ID 6 (Highest to Lowest)

Dataset #: 5
 Motif ID: 56
 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: 14
 Similarity score: 0.0619898

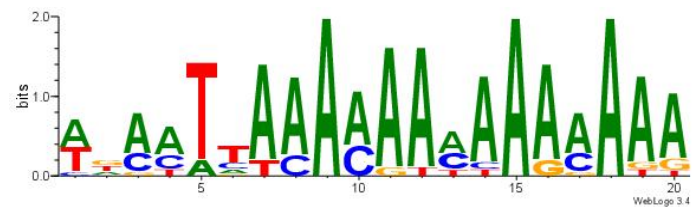
Alignment:

```
TTTTTTTKTTKTTTAATTHW
----WWTAKTTCDKAATT--
```

Original motif Consensus sequence: TTTTTTKTTKTTTAATTHW



Reverse complement motif Consensus sequence: WHAATTAARAARAAAAA

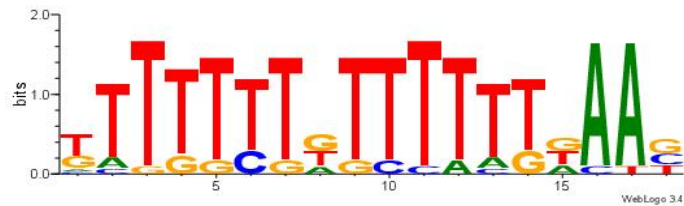


Dataset #: 5
 Motif ID: 53
 Motif name: TFM3
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0.071875

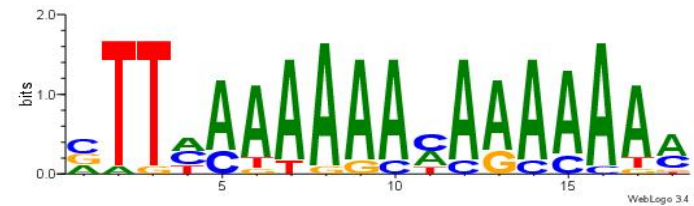
Alignment:

KTTTTTTKTTTTTTDAAB
 ----WWTAKTTCDKAATT

Original motif Consensus sequence: KTTTTTTKTTTTTTDAAB



Reverse complement motif Consensus sequence: BTTHAAAAAYAAAAAAR

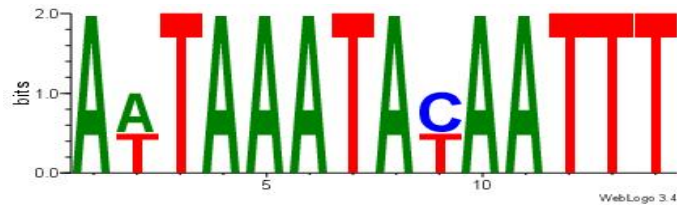


Dataset #: 2
 Motif ID: 5
 Motif name: Motif 5
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1

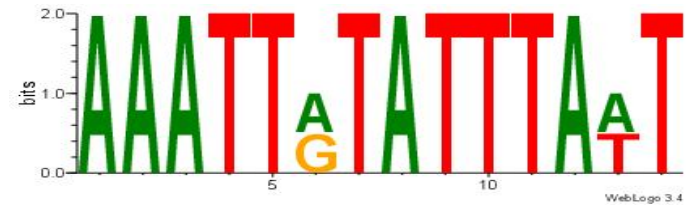
Number of overlap: 14
 Similarity score: 0.0741071

Alignment:
 AWTAAATAYAATTT
 WWTAKTTCDKAATT

Original motif Consensus sequence: AWTAAATAYAATTT



Reverse complement motif Consensus sequence: AAATTKTATTTAW

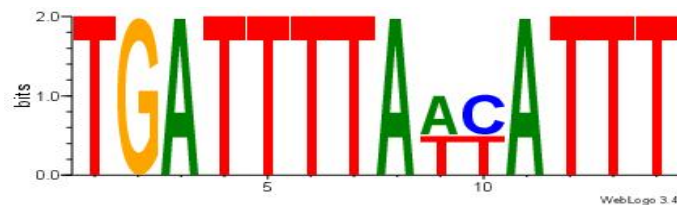
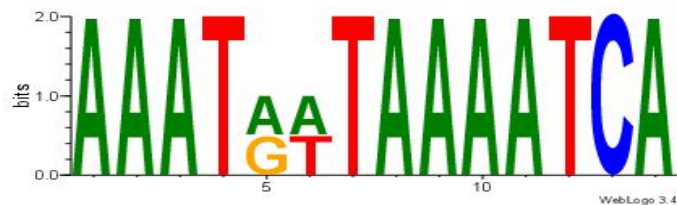


Dataset #: 2
 Motif ID: 8
 Motif name: Motif 8
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0.0763393

Alignment:
 TGATTTTAWKATTT
 WWTAKTTCDKAATT

Original motif Consensus sequence: AAATRWATAAATCA

Reverse complement motif Consensus sequence: TGATTTTAWKATTT

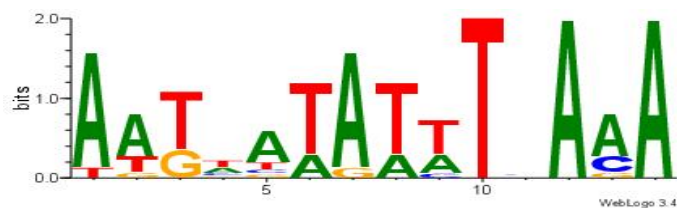


Dataset #: 2
 Motif ID: 9
 Motif name: Motif 9
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0.0852679

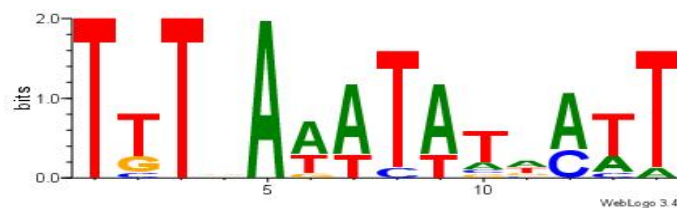
Alignment:

TTTDAWATATHATT
 WWTAKTTCDKAATT

Original motif Consensus sequence: AATHATATWTHAAA

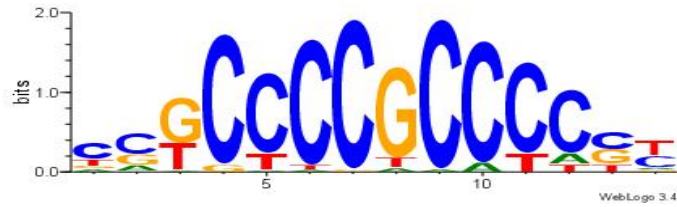


Reverse complement motif Consensus sequence: TTTDAWATATHATT

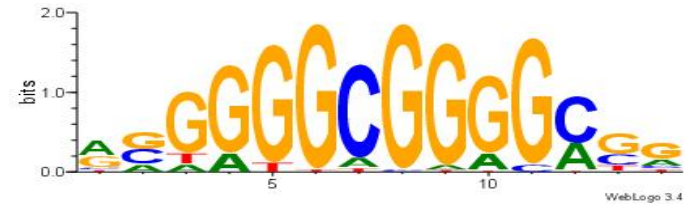


Dataset #: 2 Motif ID: 7 Motif name: Motif 7

Original motif Consensus sequence: CSKCCCCGCCCCSY



Reverse complement motif Consensus sequence: MSGGGGCGGGGY



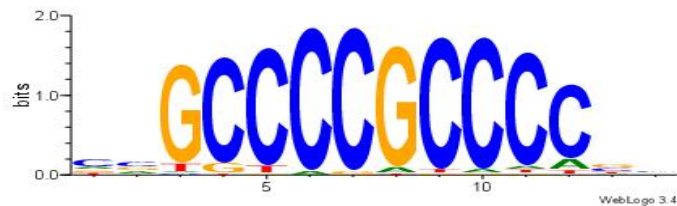
Best Matches for Motif ID 7 (Highest to Lowest)

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

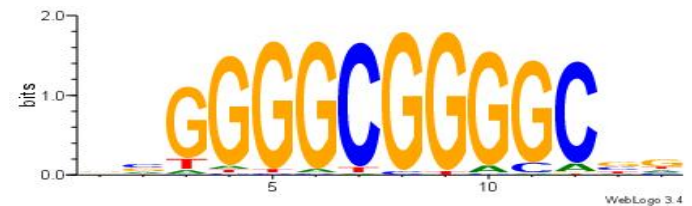
Alignment:

```
HVGCCCCGCCCCBB  
CSKCCCCGCCCCSY
```

Original motif Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGC

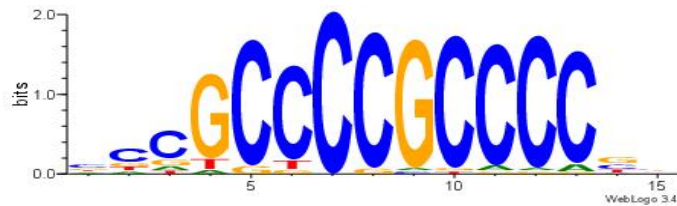


Dataset #: 4
 Motif ID: 38
 Motif name: cccGCCCCGCCCCsb
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0.0012818

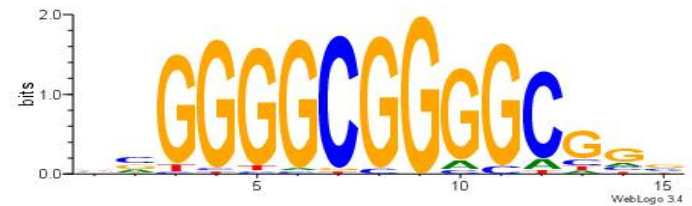
Alignment:

BCCGCCCCGCCCCBB
 -CSKCCCCGCCCCSY

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB



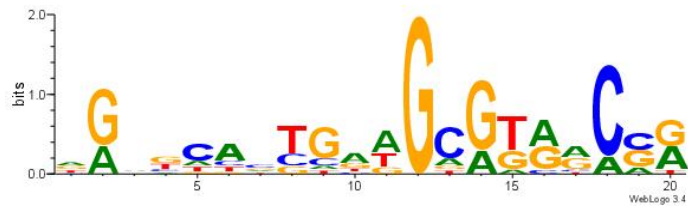
Dataset #: 3
 Motif ID: 31
 Motif name: Pax5
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 7

Number of overlap: 14
Similarity score: 0.0662825

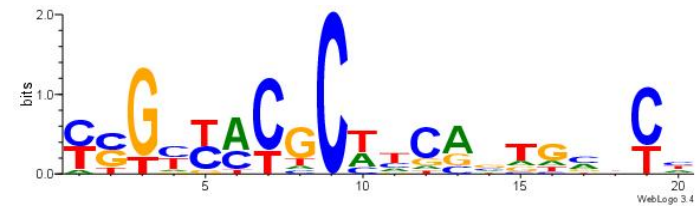
Alignment:

DGVBCABTGDWGCGRRCR
-----MSGGGGCGGGYSG

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR



Reverse complement motif Consensus sequence:
MSGKKRCGCWDCABTGBBCD

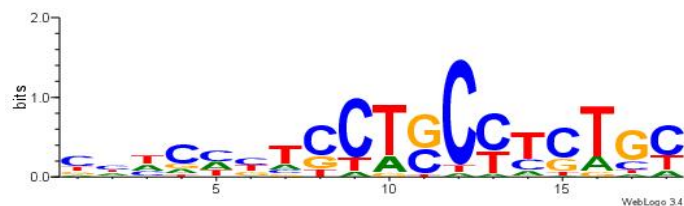


Dataset #: 5
Motif ID: 52
Motif name: TFM2
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 3
Number of overlap: 14
Similarity score: 0.0783913

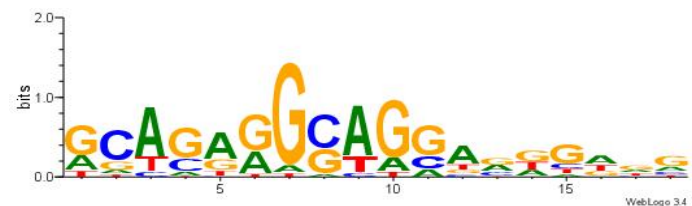
Alignment:

CHHCHBTCCTSCYTCTGC
--CSKCCCCGCCCSY--

Original motif Consensus sequence: CHHCHBTCCTSCYTCTGC



Reverse complement motif Consensus sequence:
GCAGAKGSAGGABDGH DG

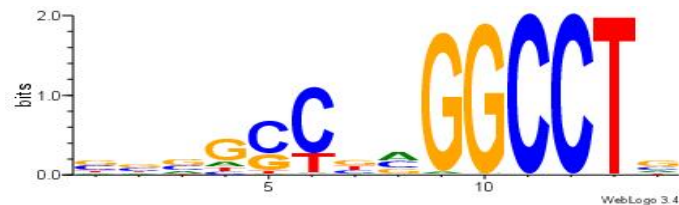


Dataset #: 3
Motif ID: 22
Motif name: Zfx
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 14
Similarity score: 0.0912118

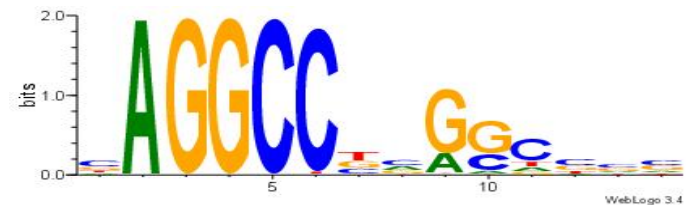
Alignment:

VAGGCCBBGGCVBB
CSKCCCCGCCCSY

Original motif Consensus sequence: BBVGCCBVGGCCTV

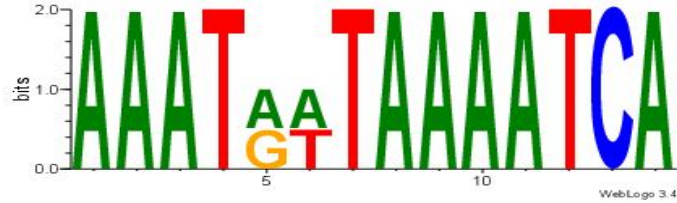


Reverse complement motif Consensus sequence: VAGGCCBBGGCVBB

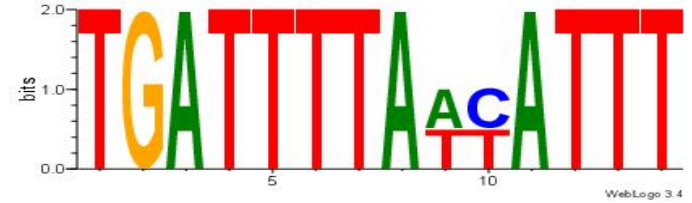


Dataset #: 2 Motif ID: 8 Motif name: Motif 8

Original motif Consensus sequence: AAATRWATAAATCA



Reverse complement motif Consensus sequence: TGATTTTAWKATTT



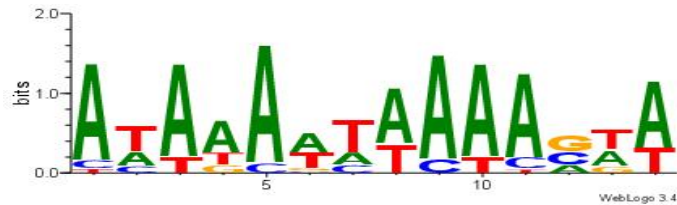
Best Matches for Motif ID 8 (Highest to Lowest)

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

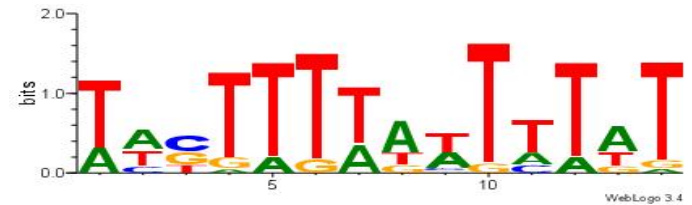
Alignment:

```
TWSTTTWAWTTTWT
TGATTTTAWKATTT
```

Original motif Consensus sequence: AWAAAWTWAAASWA



Reverse complement motif Consensus sequence: TWSTTTWAWTTTWT

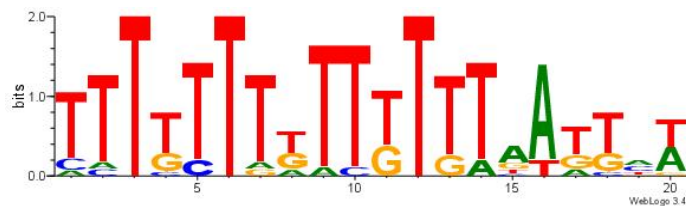


Dataset #: 5
 Motif ID: 56
 Motif name: TFM13
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 7
 Number of overlap: 14
 Similarity score: 0.105867

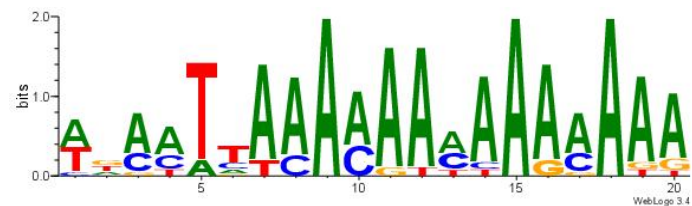
Alignment:

WHAATTAAARAARAAAAAAA
 -----AAATRWTA AAAATCA

Original motif Consensus sequence: TTTTTTKTTKTTTAATTHW



Reverse complement motif Consensus sequence: WHAATTAAARAARAAAAAAA



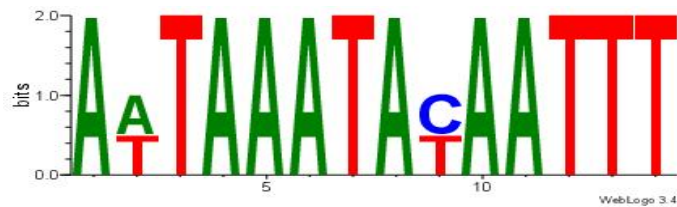
Dataset #: 2
 Motif ID: 5
 Motif name: Motif 5
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward

Position number: 1
 Number of overlap: 14
 Similarity score: 0.107143

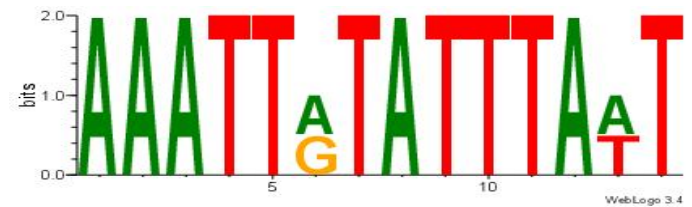
Alignment:

AAATTKTATTTAWT
 TGATTTTAWKATTT

Original motif Consensus sequence: AWTAAATAYAATTT



Reverse complement motif Consensus sequence: AAATTKTATTTAWT

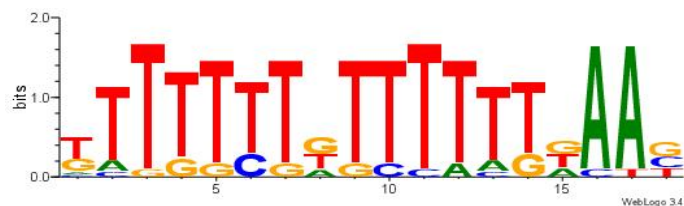


Dataset #: 5
 Motif ID: 53
 Motif name: TFM3
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 5
 Number of overlap: 14
 Similarity score: 0.111607

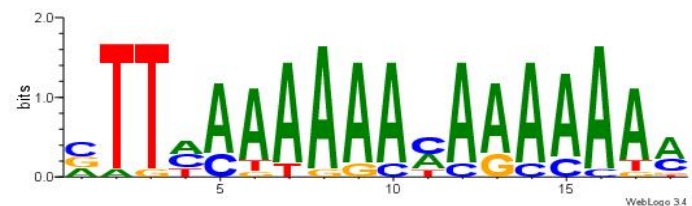
Alignment:

BTHAAAAAYAAAAAR
 ----AAATRWTAATCA

Original motif Consensus sequence: KTTTTTKTTTTTDAAB



Reverse complement motif Consensus sequence: BTTHAAAAAYAAAAAR



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: 0.113839

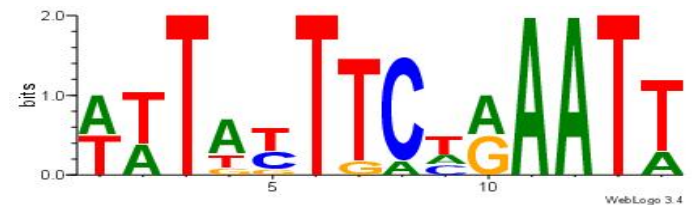
Alignment:

WWTAKTTCDKAATT
TGATTTTAWKATTT

Original motif Consensus sequence: AATTYDGAARTAWW

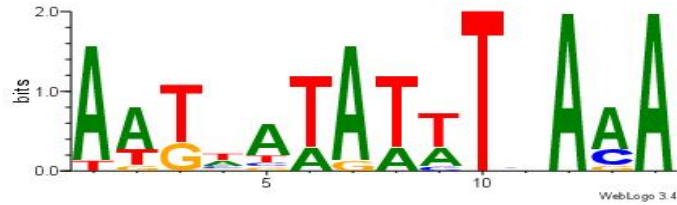


Reverse complement motif Consensus sequence: WWTAKTTCDKAATT

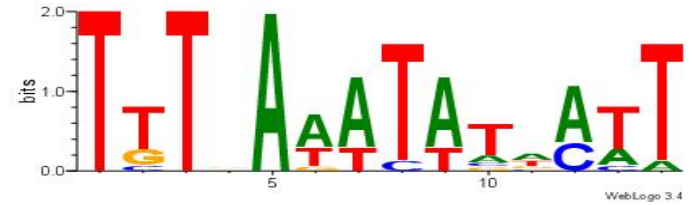


Dataset #: 2 Motif ID: 9 Motif name: Motif 9

Original motif Consensus sequence: AATHATATWTHAAA



Reverse complement motif Consensus sequence: TTTDAWATATHAT



Best Matches for Motif ID 9 (Highest to Lowest)

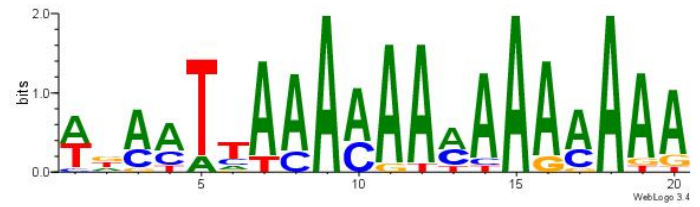
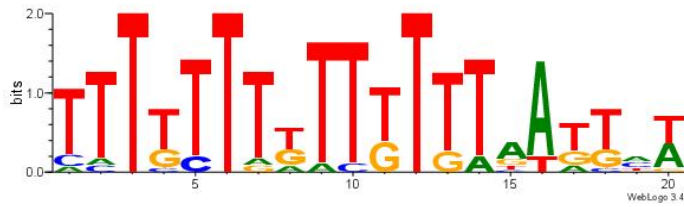
Dataset #:	5
Motif ID:	56
Motif name:	TFM13
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	5
Number of overlap:	14
Similarity score:	0.0472647

Alignment:

```
TTTTTTTKTTKTTTAATTHW
----TTTDAWATATHATT--
```

Original motif Consensus sequence: TTTTTTKTTKTTTAATTHW

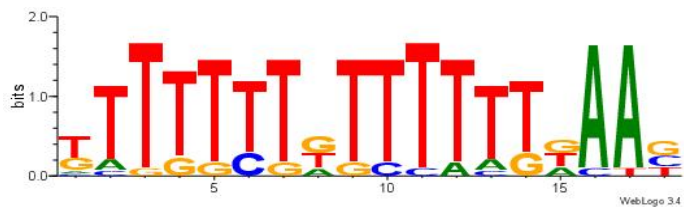
Reverse complement motif Consensus sequence: WHAATTAARAARAAAAAAA



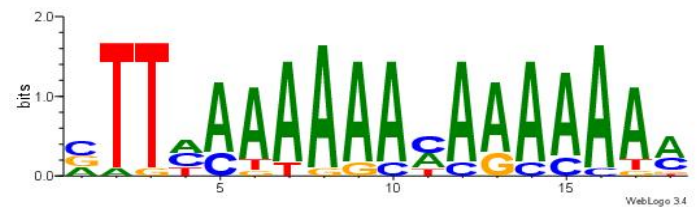
Dataset #: 5
 Motif ID: 53
 Motif name: TFM3
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 5
 Number of overlap: 14
 Similarity score: 0.0585318

Alignment:
 KTTTTTTKTTTTTTDAAB
 ----TTTDAWATATHATT

Original motif Consensus sequence: KTTTTTTKTTTTTTDAAB



Reverse complement motif Consensus sequence: BTTHAAAAAYAAAAAR



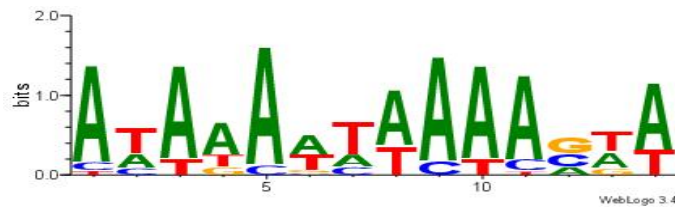
Dataset #: 2

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

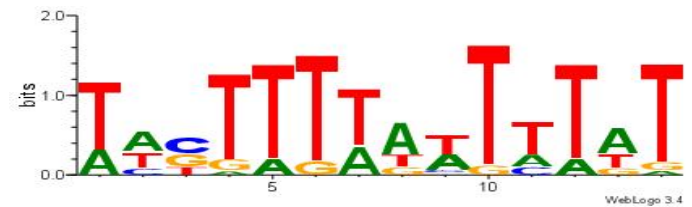
Alignment:

TWSTTTWAWTTTWT
 AATHATATWTHAAA

Original motif Consensus sequence: AWAAAWTWAASWA



Reverse complement motif Consensus sequence: TWSTTTWAWTTTWT



Dataset #: 2
 Motif ID: 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

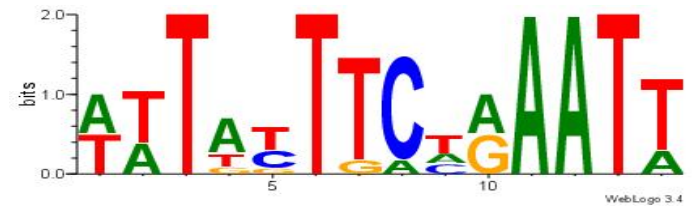
Alignment:

WWTAKTTCDKAATT
TTTDAWATATHATT

Original motif Consensus sequence: AATTYDGAARTAWW



Reverse complement motif Consensus sequence: WWTAKTTCDKAAT



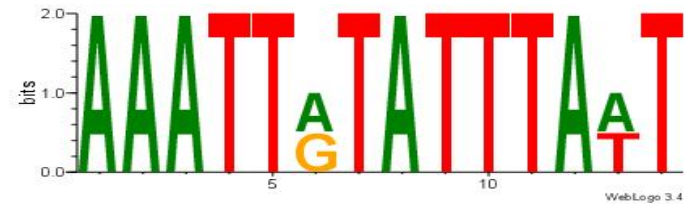
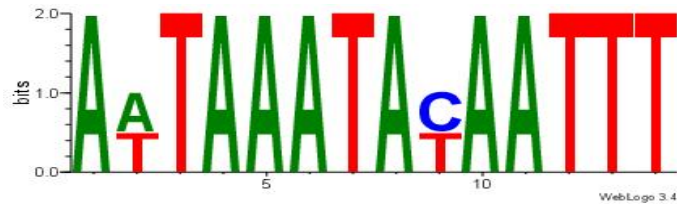
Dataset #:	2
Motif ID:	5
Motif name:	Motif 5
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	2
Number of overlap:	13
Similarity score:	0.547543

Alignment:

-AAATTKTATTTAWT
AATHATATWTHAAA-

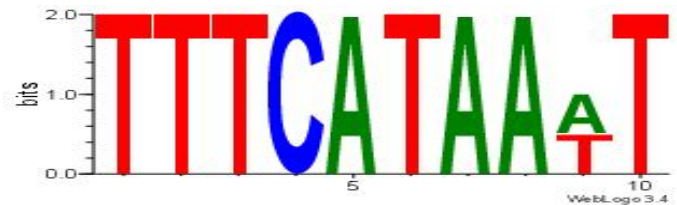
Original motif Consensus sequence: AWTAATAYAATTT

Reverse complement motif Consensus sequence: AAATTKTATTTAW

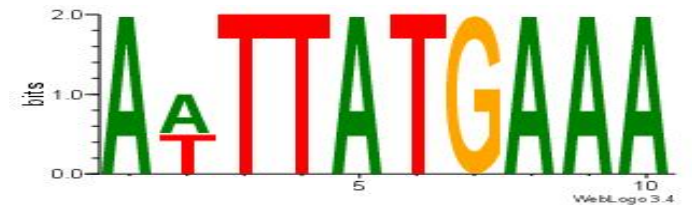


Dataset #: 2 Motif ID: 10 Motif name: Motif 10

Original motif Consensus sequence: TTTCATAAWT



Reverse complement motif Consensus sequence: AWTTATGAAA

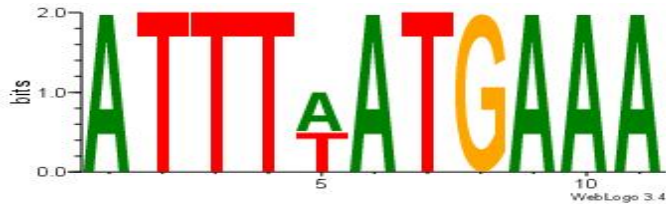


Best Matches for Motif ID 10 (Highest to Lowest)

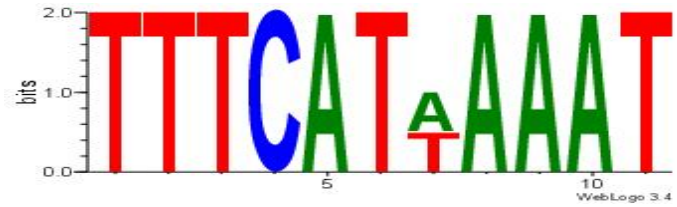
Dataset #:	2
Motif ID:	11
Motif name:	Motif 11
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	10
Similarity score:	0.01875

Alignment:
 ATTTWATGAAA
 -AWTTATGAAA

Original motif Consensus sequence: ATTTWATGAAA



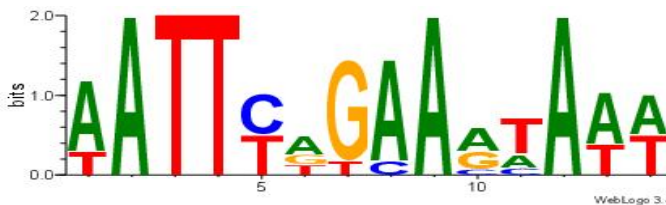
Reverse complement motif Consensus sequence: TTTTCATWAAAT



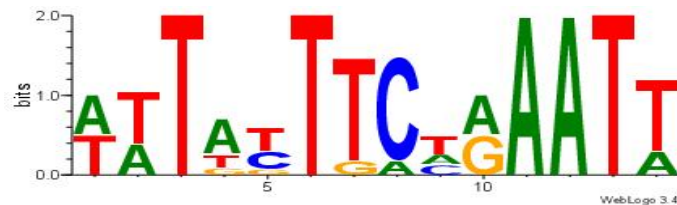
Dataset #: 2
 Motif ID: 6
 Motif name: Motif 6
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 5
 Number of overlap: 10
 Similarity score: 0.0375

Alignment:
 AATTYDGAARTAWW
 ----AWTTATGAAA

Original motif Consensus sequence: AATTYDGAARTAWW



Reverse complement motif Consensus sequence: WWTAKTTCDKAAT

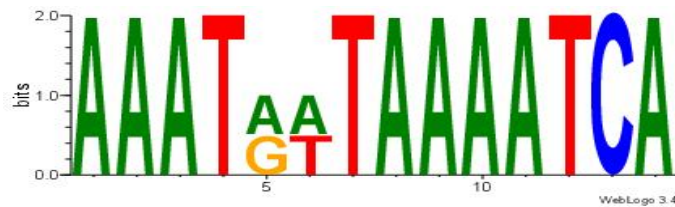


Dataset #: 2
 Motif ID: 8
 Motif name: Motif 8
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 10
 Similarity score: 0.04375

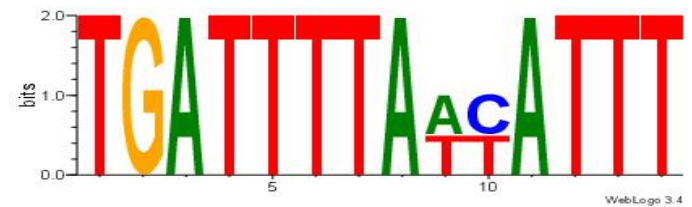
Alignment:

TGATTTTAWKATTT
 -TTCATAAWT---

Original motif Consensus sequence: AAATRWATAAATCA



Reverse complement motif Consensus sequence: TGATTTTAWKATTT



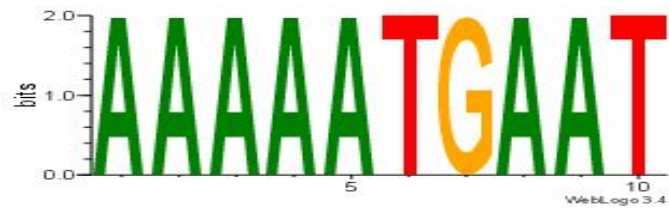
Dataset #: 2
 Motif ID: 17
 Motif name: Motif 17
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 10

Similarity score: 0.05625

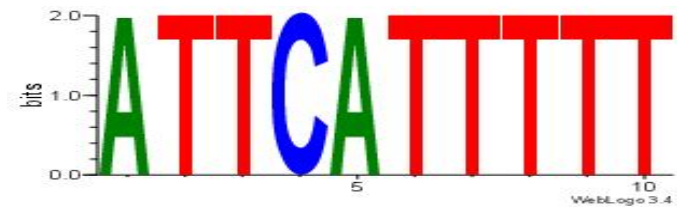
Alignment:

ATTCATTTTT
TTCATAAWT

Original motif Consensus sequence: AAAAATGAAT



Reverse complement motif Consensus sequence: ATTCATTTTT



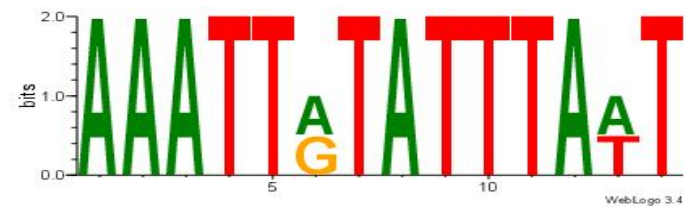
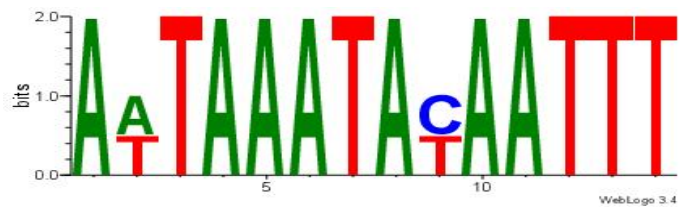
Dataset #: 2
Motif ID: 5
Motif name: Motif 5
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 10
Similarity score: 0.05625

Alignment:

AWTAAATAYAATTT
----AWTTATGAAA

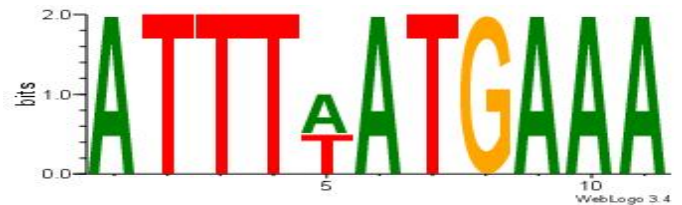
Original motif Consensus sequence: AWTAAATAYAATTT

Reverse complement motif Consensus sequence: AAATTKTATTTAW

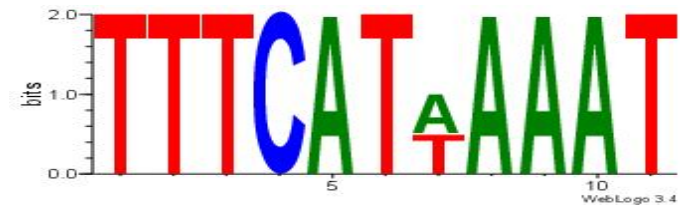


Dataset #: 2 Motif ID: 11 Motif name: Motif 11

Original motif Consensus sequence: ATTTWATGAAA



Reverse complement motif Consensus sequence: TTTTCATWAAAT

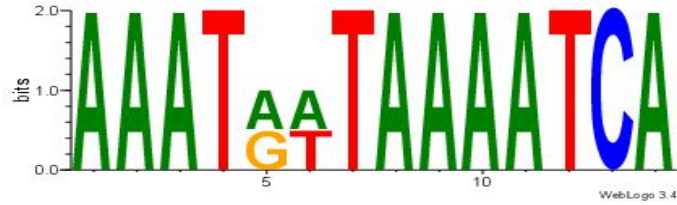


Best Matches for Motif ID 11 (Highest to Lowest)

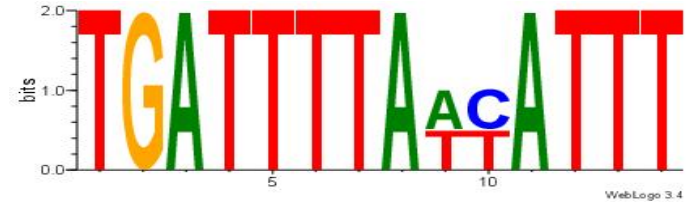
Dataset #:	2
Motif ID:	8
Motif name:	Motif 8
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	3
Number of overlap:	11
Similarity score:	0.0795455

Alignment:
AAATRWTA AAAATCA
--TTTCATWAAAT--

Original motif Consensus sequence: AAATRWTAATCA



Reverse complement motif Consensus sequence: TGATTTAWKATT

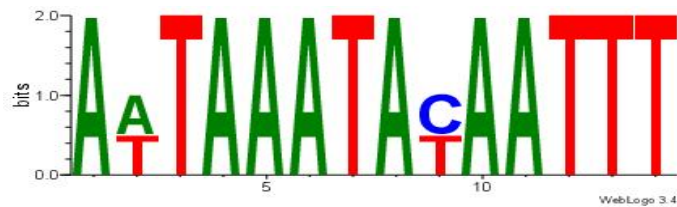


Dataset #: 2
 Motif ID: 5
 Motif name: Motif 5
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.0795455

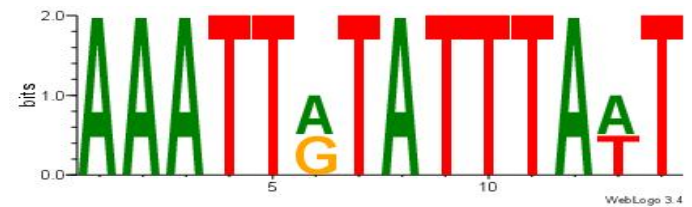
Alignment:

AAATTKTATTTAWT
 ---TTTCATWAAAT

Original motif Consensus sequence: AWTAAATAYAATTT



Reverse complement motif Consensus sequence: AAATTKTATTTAW

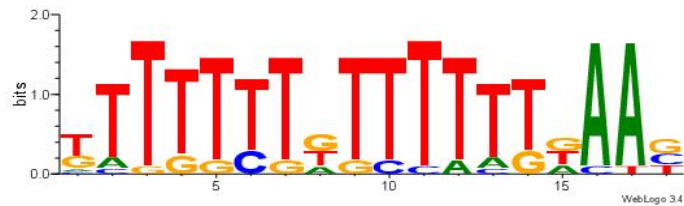


Dataset #: 5
 Motif ID: 53
 Motif name: TFM3
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 8
 Number of overlap: 11
 Similarity score: 0.0894886

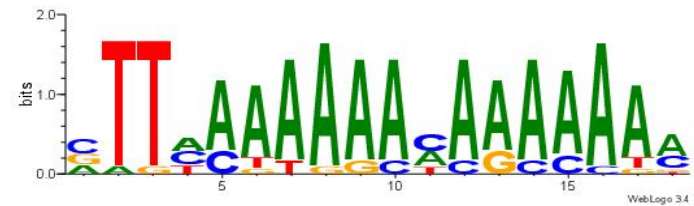
Alignment:

BTTHAAAAAYAAAAAR
 TTTCATWAAAT-----

Original motif Consensus sequence: KTTTTTKTTTTTDAAB



Reverse complement motif Consensus sequence: BTTHAAAAAYAAAAAR



Dataset #: 2
 Motif ID: 18
 Motif name: Motif 18
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1

Number of overlap: 11
Similarity score: 0.102273

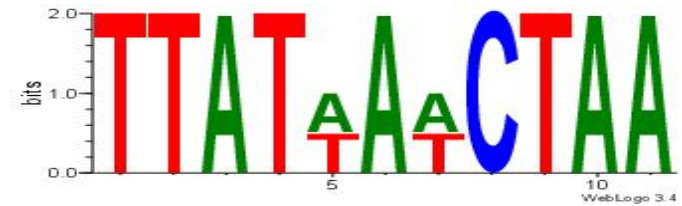
Alignment:

TTATWAWCTAA
ATTTWATGAAA

Original motif Consensus sequence: TTAGWTWATAA



Reverse complement motif Consensus sequence: TTATWAWCTAA



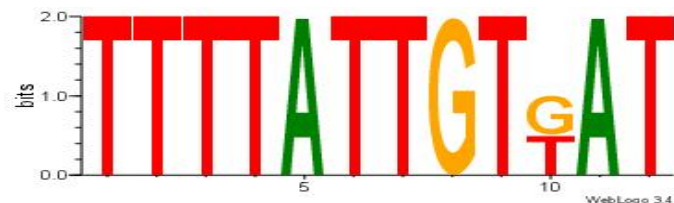
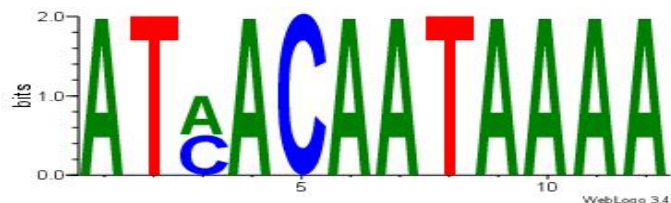
Dataset #: 2
Motif ID: 15
Motif name: Motif 15
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 11
Similarity score: 0.102273

Alignment:

TTTTATTGTYAT
ATTTWATGAAA-

Original motif Consensus sequence: ATMACAATAAAA

Reverse complement motif Consensus sequence: TTTTATTGTYAT



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

Original motif Consensus sequence: AAAACAAA



Reverse complement motif Consensus sequence: TTTGTTTT



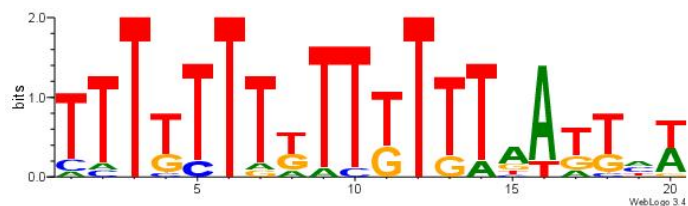
Best Matches for Motif ID 12 (Highest to Lowest)

Dataset #:	5
Motif ID:	56
Motif name:	TFM13
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	9
Number of overlap:	8
Similarity score:	0.0446429

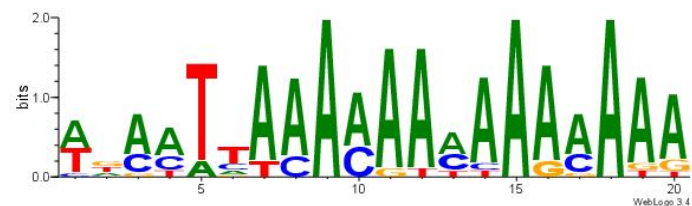
Alignment:

```
TTTTTTKTKTTTAATTHW
----TTTGTTTT-----
```


Original motif Consensus sequence: TTTTTTKTTKTTTAATTHW



Reverse complement motif Consensus sequence: WHAATTAARAARAAAAAA

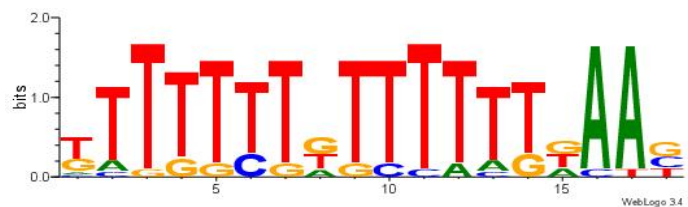


Dataset #: 5
Motif ID: 53
Motif name: TFM3
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 7
Number of overlap: 8
Similarity score: 0.046875

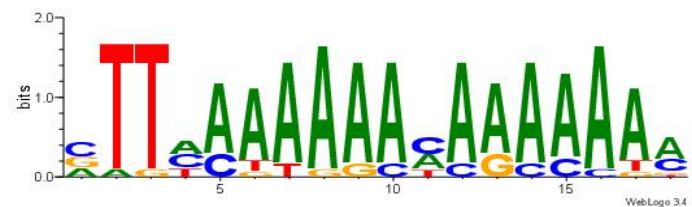
Alignment:

KTTTTTKTTTTTDAAB
----TTTGTTTT-----

Original motif Consensus sequence: KTTTTTKTTTTTDAAB



Reverse complement motif Consensus sequence: BTTHAAAAAYAAAAAAR

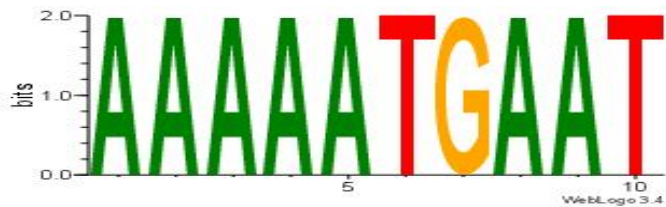


Dataset #: 2
 Motif ID: 17
 Motif name: Motif 17
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 8
 Similarity score: 0.0625

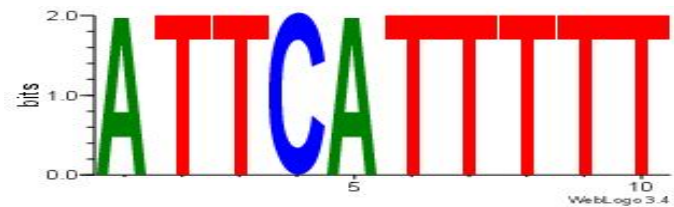
Alignment:

AAAAATGAAT
 -AAAACAAA-

Original motif Consensus sequence: AAAAATGAAT



Reverse complement motif Consensus sequence: ATTCA TTTT

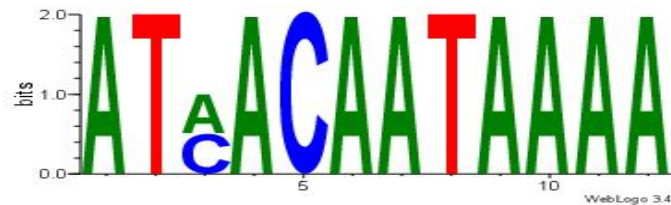


Dataset #: 2
 Motif ID: 15
 Motif name: Motif 15
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 8

Similarity score: 0.0625

Alignment:
ATMACAATAAAA
---AAAACAAA-

Original motif Consensus sequence: ATMACAATAAAA



Reverse complement motif Consensus sequence: TTTTATTGTYAT

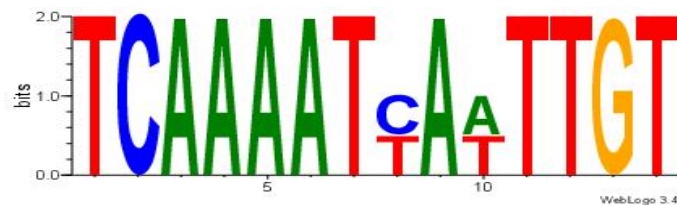
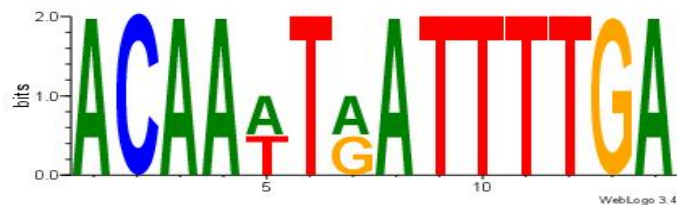


Dataset #: 2
Motif ID: 16
Motif name: Motif 16
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 3
Number of overlap: 8
Similarity score: 0.078125

Alignment:
ACAAWTRATTTTGA
----TTTGTTTT--

Original motif Consensus sequence: ACAAWTRATTTTGA

Reverse complement motif Consensus sequence: TCAAAATKAWTTG



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

Original motif Consensus sequence: AAAGATTT



Reverse complement motif Consensus sequence: AAATCTTT



Best Matches for Motif ID 13 (Highest to Lowest)

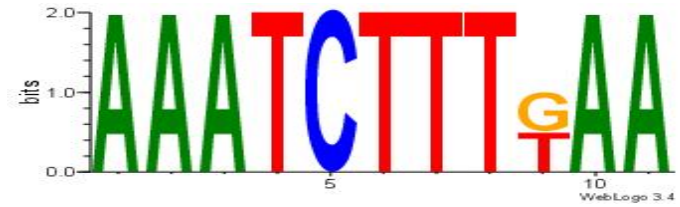
Dataset #:	2
Motif ID:	20
Motif name:	Motif 20
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	8
Similarity score:	0

Alignment:
 TTMAAAGATTT
 ---AAAGATTT

Original motif Consensus sequence: TTMAAAGATTT



Reverse complement motif Consensus sequence: AAATCTTYYAA

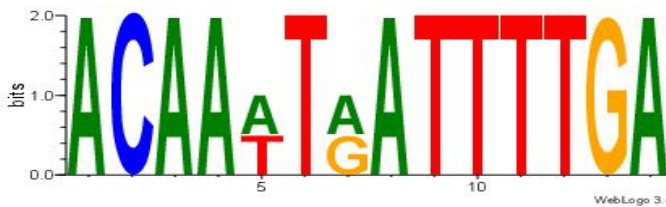


Dataset #: 2
 Motif ID: 16
 Motif name: Motif 16
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 8
 Similarity score: 0.0625

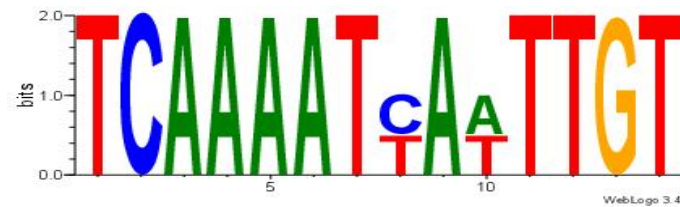
Alignment:

TCAAATKAWTTGT
 ----AAAGATTT--

Original motif Consensus sequence: ACAAWTRATTTTGA



Reverse complement motif Consensus sequence: TCAAATKAWTTG

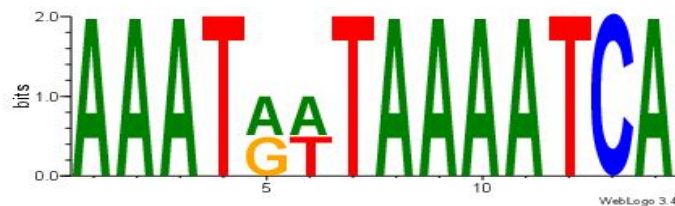


Dataset #: 2
 Motif ID: 8
 Motif name: Motif 8
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 7
 Number of overlap: 8
 Similarity score: 0.0625

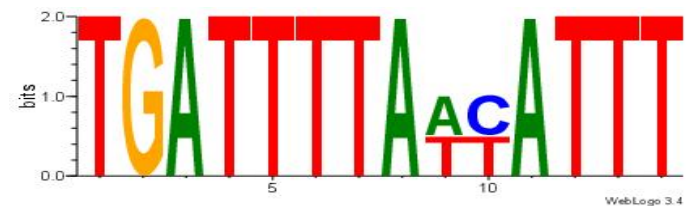
Alignment:

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

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



Reverse complement motif Consensus sequence: TGATTTAWKATT



Dataset #: 2
 Motif ID: 19
 Motif name: Motif 19
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3
 Number of overlap: 8

Similarity score: 0.078125

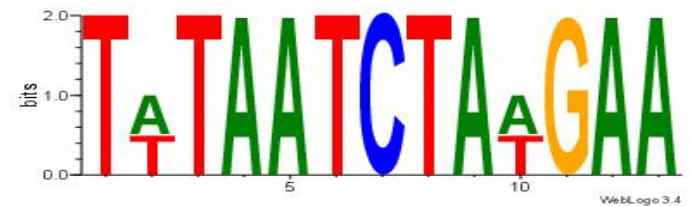
Alignment:

TWTAATCTAWGAA
--AAATCTTT---

Original motif Consensus sequence: TTCWTAGATTAWA



Reverse complement motif Consensus sequence: TWTAATCTAWGAA



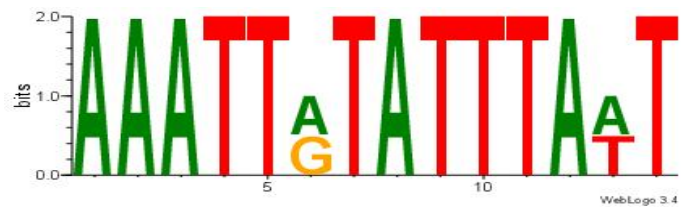
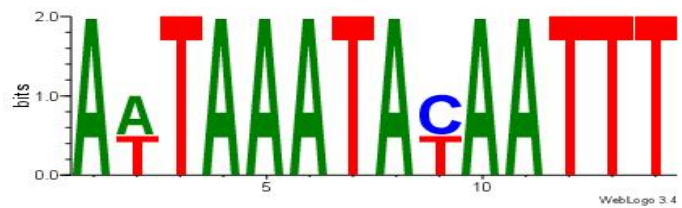
Dataset #: 2
Motif ID: 5
Motif name: Motif 5
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 7
Number of overlap: 8
Similarity score: 0.078125

Alignment:

AAATTKTATTTAWT
AAATCTTT-----

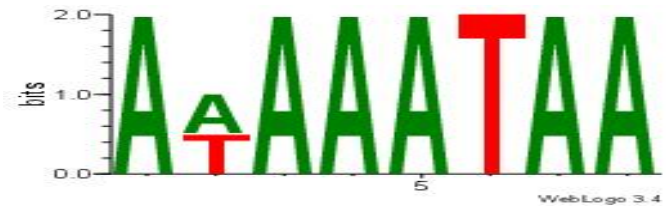
Original motif Consensus sequence: AWTAAATAYAATTT

Reverse complement motif Consensus sequence: AAATTKTATTTAWT

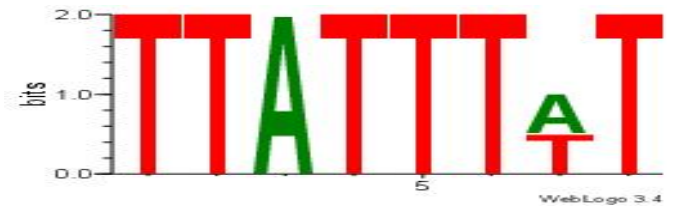


Dataset #: 2 Motif ID: 14 Motif name: Motif 14

Original motif Consensus sequence: AWAAATAA



Reverse complement motif Consensus sequence: TTATTTWT

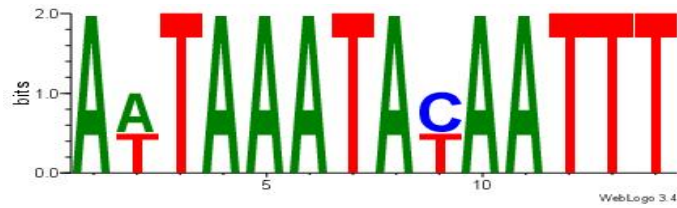


Best Matches for Motif ID 14 (Highest to Lowest)

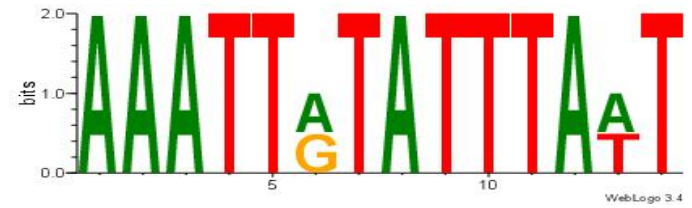
Dataset #:	2
Motif ID:	5
Motif name:	Motif 5
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	2
Number of overlap:	8
Similarity score:	0.046875

Alignment:
AAATTKTATTTAWT
-----TTATTTWT-

Original motif Consensus sequence: AWTAAATAYAATTT



Reverse complement motif Consensus sequence: AAATTKTATTTAW

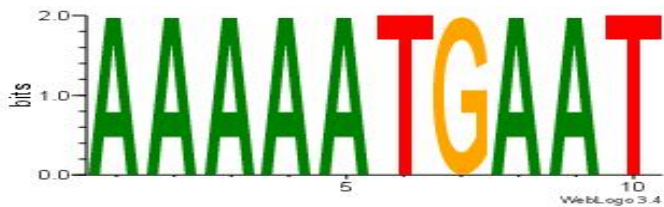


Dataset #: 2
Motif ID: 17
Motif name: Motif 17
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 8
Similarity score: 0.046875

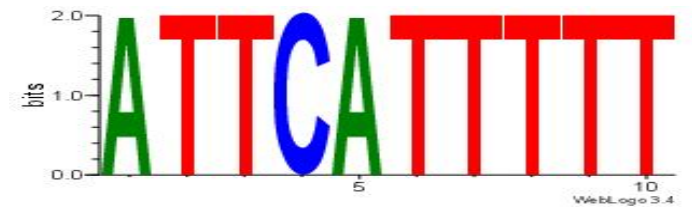
Alignment:

AAAAATGAAT
AWAAATAA--

Original motif Consensus sequence: AAAAATGAAT



Reverse complement motif Consensus sequence: ATTCAATTTT

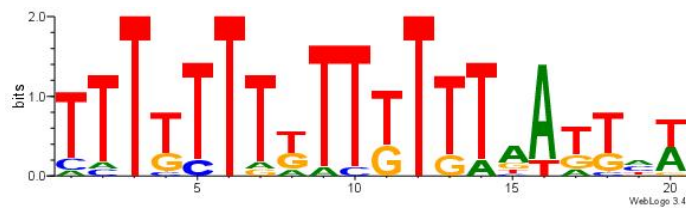


Dataset #: 5
 Motif ID: 56
 Motif name: TFM13
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 12
 Number of overlap: 8
 Similarity score: 0.0580357

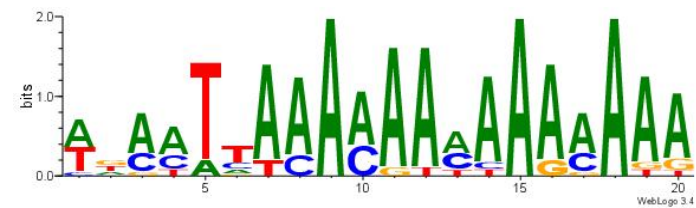
Alignment:

TTTTTTKTTKTTTAATTHW
 -TTATTTWT-----

Original motif Consensus sequence: TTTTTTKTTKTTTAATTHW



Reverse complement motif Consensus sequence: WHAATTAARAARAAAAAA



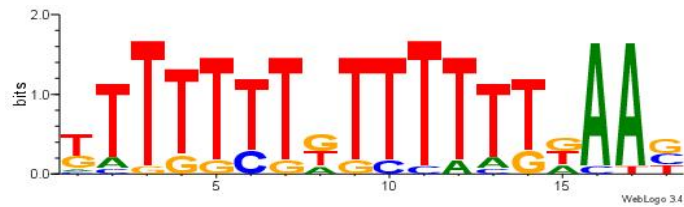
Dataset #: 5
 Motif ID: 53
 Motif name: TFM3
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 6

Number of overlap: 8
Similarity score: 0.0585938

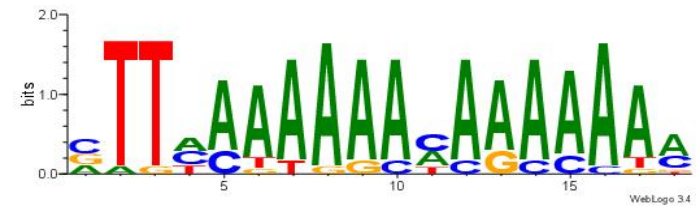
Alignment:

BTTHAAAAAYAAAAAR
-----AWAAATAA-----

Original motif Consensus sequence: KTTTTTKTTTTTDAAB



Reverse complement motif Consensus sequence:
BTTHAAAAAYAAAAAR



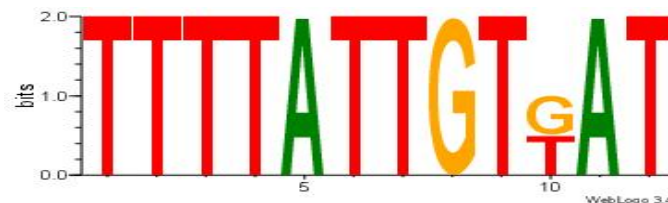
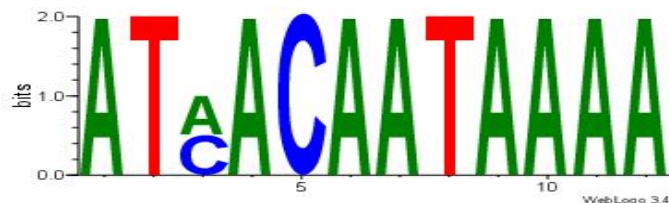
Dataset #: 2
Motif ID: 15
Motif name: Motif 15
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 3
Number of overlap: 8
Similarity score: 0.0625

Alignment:

ATMACAATAAAA
--AWAAATAA--

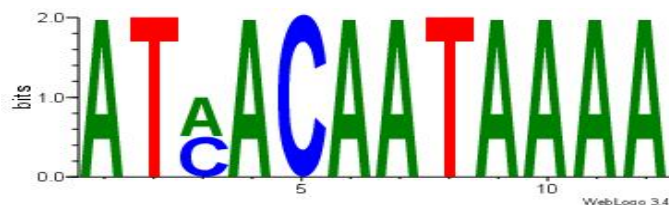
Original motif Consensus sequence: ATMACAATAAAA

Reverse complement motif Consensus sequence: TTTTATTGYAT

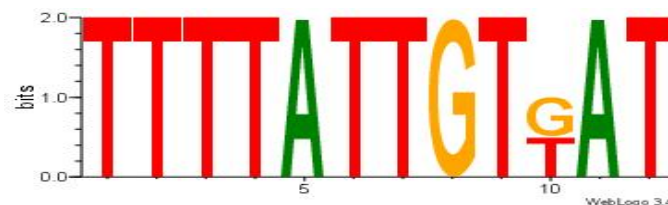


Dataset #: 2 Motif ID: 15 Motif name: Motif 15

Original motif Consensus sequence: ATMACAATAAAA



Reverse complement motif Consensus sequence: TTTTATTGTAT



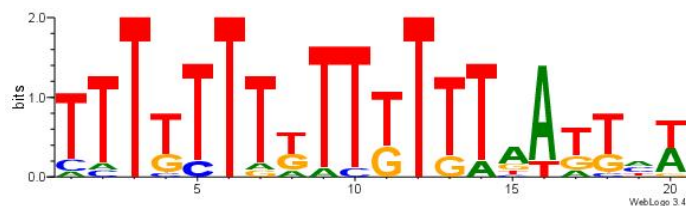
Best Matches for Motif ID 15 (Highest to Lowest)

Dataset #:	5
Motif ID:	56
Motif name:	TFM13
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	9
Number of overlap:	12
Similarity score:	0.0833333

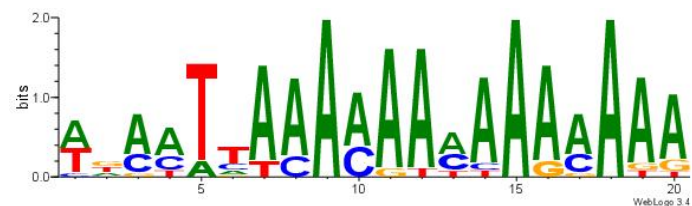
Alignment:

```
TTTTTTTKTTKTTTAATTHW
TTTTATTGTAT-----
```

Original motif Consensus sequence: TTTTTTKTTKTTTAATTHW



Reverse complement motif Consensus sequence: WHAATTAARAARAAAAA

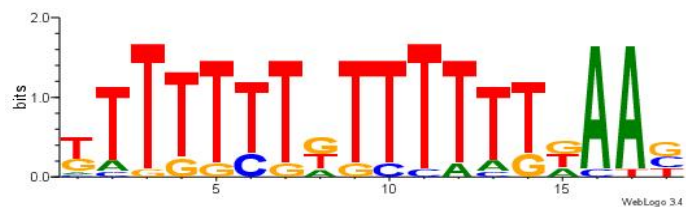


Dataset #: 5
Motif ID: 53
Motif name: TFM3
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 7
Number of overlap: 12
Similarity score: 0.0924479

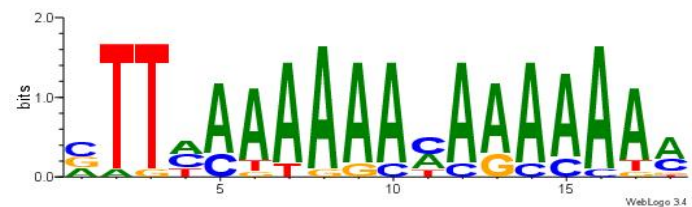
Alignment:

KTTTTTKTTTTTDAAB
TTTTATTGTYAT-----

Original motif Consensus sequence: KTTTTTKTTTTTDAAB



Reverse complement motif Consensus sequence: BTTHAAAAAYAAAAAAR

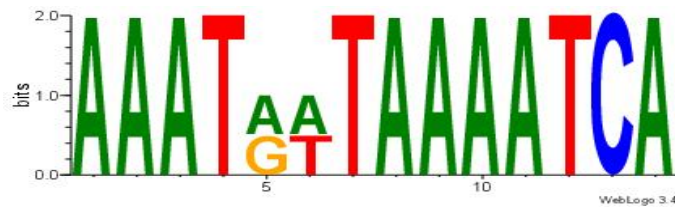


Dataset #: 2
 Motif ID: 8
 Motif name: Motif 8
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 12
 Similarity score: 0.104167

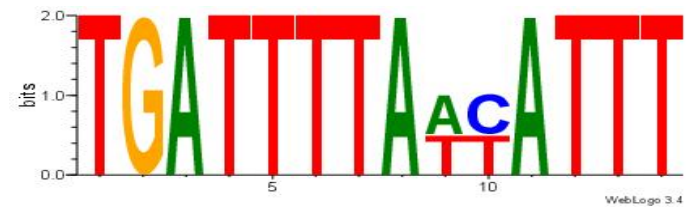
Alignment:

TGATTTTAWKATTT
 TTTTATTGTYAT--

Original motif Consensus sequence: AAATRWATAAATCA



Reverse complement motif Consensus sequence: TGATTTTAWKATTT



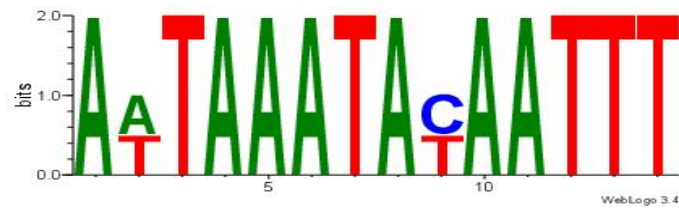
Dataset #: 2
 Motif ID: 5
 Motif name: Motif 5
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 12

Similarity score: 0.114583

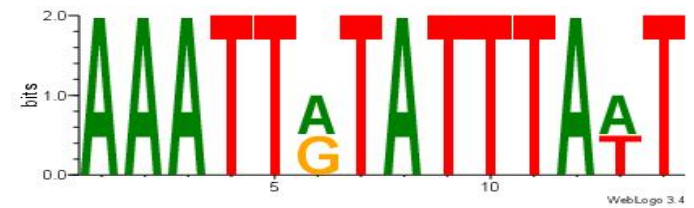
Alignment:

AWTAAATAYAATTT
-ATMACAATAAAA-

Original motif Consensus sequence: AWTAAATAYAATTT



Reverse complement motif Consensus sequence: AAATTKTATTTAW



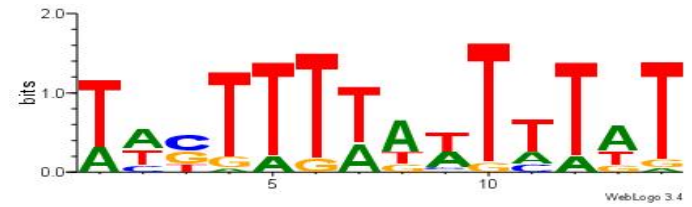
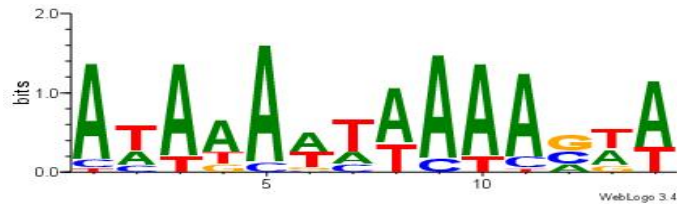
Dataset #: 2
Motif ID: 3
Motif name: Motif 3
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 3
Number of overlap: 12
Similarity score: 0.114583

Alignment:

AWAAAWTWAAASWA
ATMACAATAAAA--

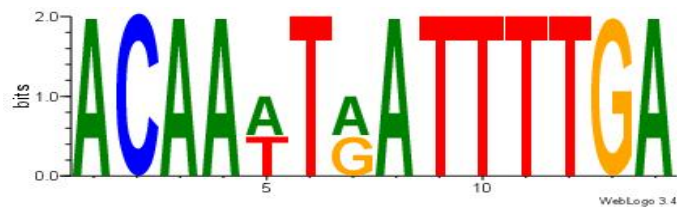
Original motif Consensus sequence: AWAAAWTWAAASWA

Reverse complement motif Consensus sequence: TWSTTTWAWTTT

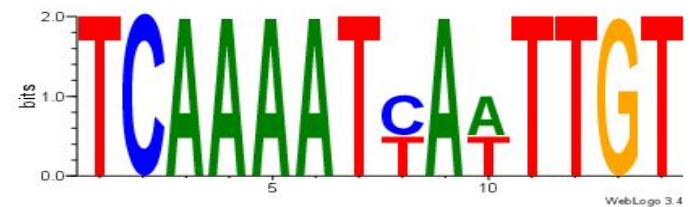


Dataset #: 2 Motif ID: 16 Motif name: Motif 16

Original motif Consensus sequence: ACAAWTRATTTTGA



Reverse complement motif Consensus sequence: TCAAATKAWTTG

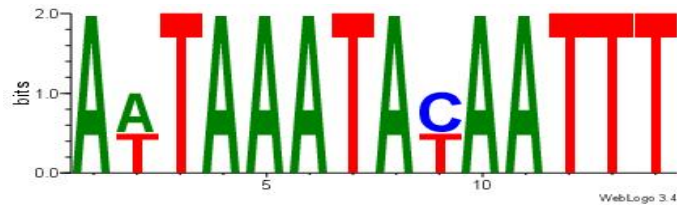


Best Matches for Motif ID 16 (Highest to Lowest)

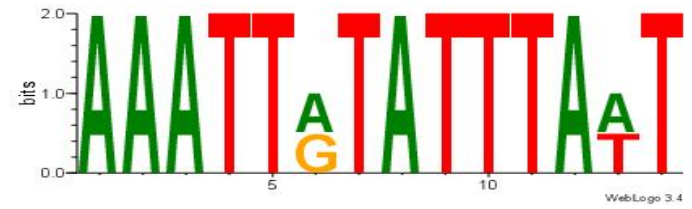
Dataset #:	2
Motif ID:	5
Motif name:	Motif 5
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	14
Similarity score:	0.1

Alignment:
 AWTAAATAYAATTT
 TCAAATKAWTTGT

Original motif Consensus sequence: AWTAAATAYAATTT



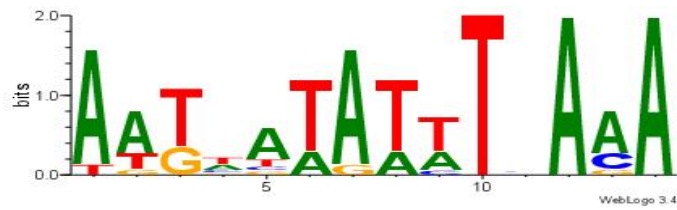
Reverse complement motif Consensus sequence: AAATTKTATTTAW



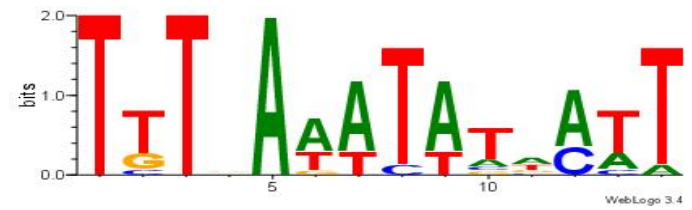
Dataset #: 2
 Motif ID: 9
 Motif name: Motif 9
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3
 Number of overlap: 12
 Similarity score: 1.08264

Alignment:
 TTTDAWATATHATT--
 --TCAAATKAWTTGT

Original motif Consensus sequence: AATHATATWTHAAA



Reverse complement motif Consensus sequence: TTTDAWATATHAT

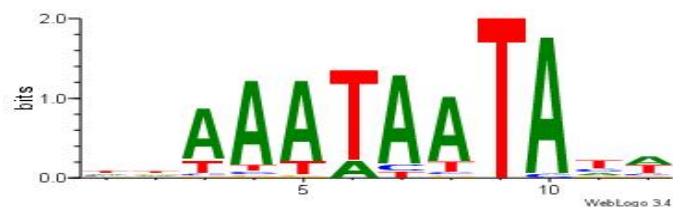


Dataset #: 4
 Motif ID: 37
 Motif name: tkAAATAATAtw
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 12
 Similarity score: 1.08403

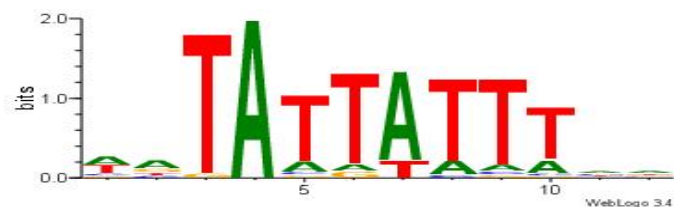
Alignment:

--WHTATTATTTDH
 TCAAATKAWTTGT

Original motif Consensus sequence: HDAAATAATAHW



Reverse complement motif Consensus sequence: WHTATTATTTDH



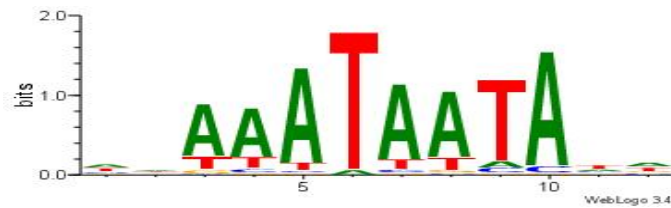
Dataset #: 4
 Motif ID: 41
 Motif name: wwAAATAATAtw
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 12

Similarity score: 1.08881

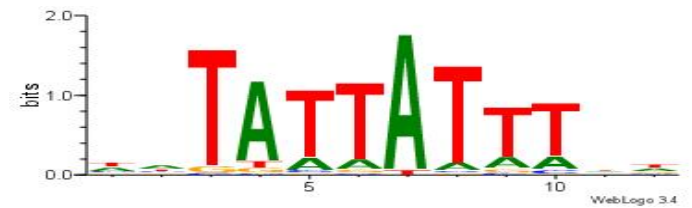
Alignment:

```
--DDTATTATTTDH  
TCAAATKAWTTGT
```

Original motif Consensus sequence: HDAAATAATADD



Reverse complement motif Consensus sequence: DDTATTATTTDH



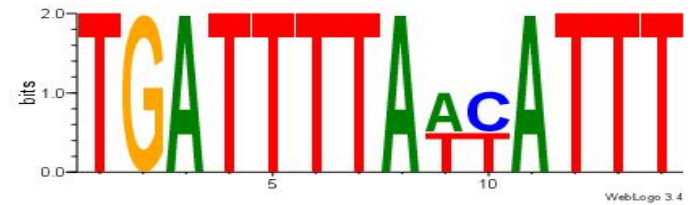
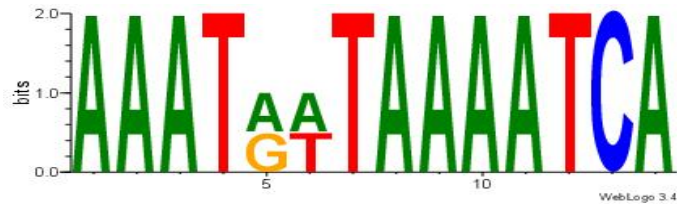
Dataset #: 2
Motif ID: 8
Motif name: Motif 8
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 3
Number of overlap: 12
Similarity score: 1.1

Alignment:

```
TGATTTTAWKATTT--  
--TCAAATKAWTTGT
```

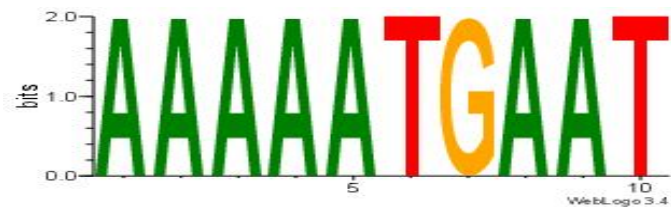
Original motif Consensus sequence: AAATRWATAAATCA

Reverse complement motif Consensus sequence: TGATTTTAWKATTT

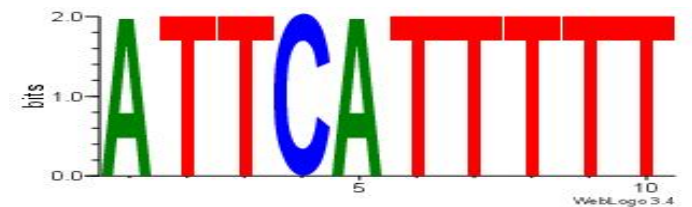


Dataset #: 2 Motif ID: 17 Motif name: Motif 17

Original motif Consensus sequence: AAAAATGAAT



Reverse complement motif Consensus sequence: ATTCATTTTT

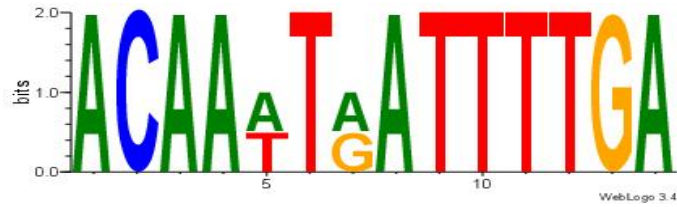


Best Matches for Motif ID 17 (Highest to Lowest)

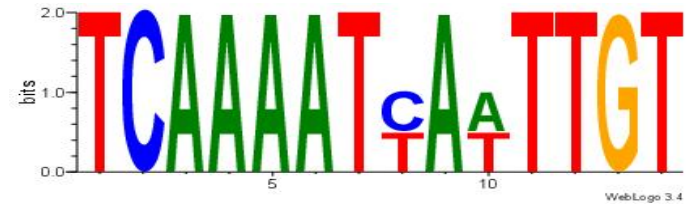
Dataset #:	2
Motif ID:	16
Motif name:	Motif 16
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	4
Number of overlap:	10
Similarity score:	0.05

Alignment:
 ACAAWTRATTTTGA
 -ATTCATTTTT---

Original motif Consensus sequence: ACAAWTRATTTTGA



Reverse complement motif Consensus sequence: TCAAAAATKAWTTG

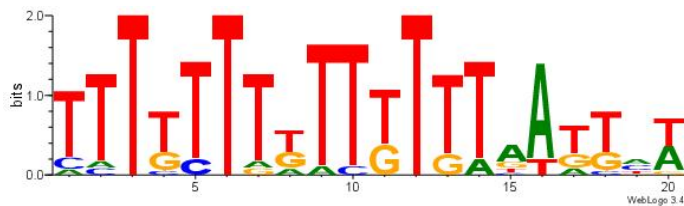


Dataset #: 5
 Motif ID: 56
 Motif name: TFM13
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 7
 Number of overlap: 10
 Similarity score: 0.0875

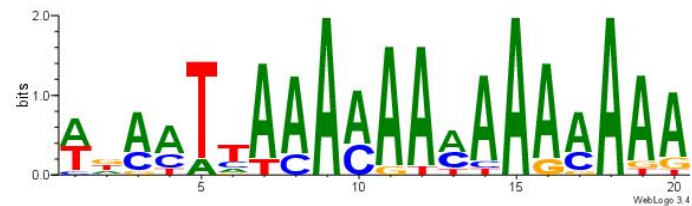
Alignment:

```
WHAATTAAARAARAAAAAAA
-----AAAAATGAAT-----
```

Original motif Consensus sequence: TTTTTTKTKTTTAATTHW



Reverse complement motif Consensus sequence: WHAATTAAARAARAAAAAAA

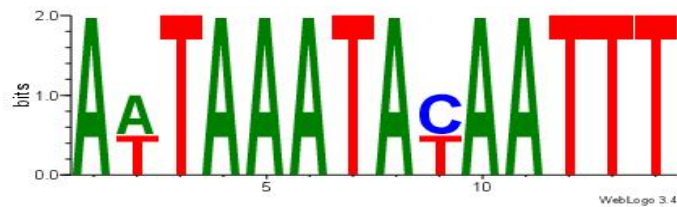


Dataset #: 2
 Motif ID: 5
 Motif name: Motif 5
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 10
 Similarity score: 0.0875

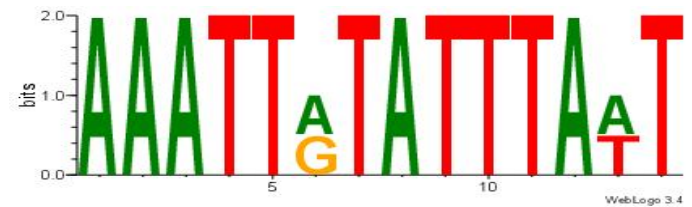
Alignment:

AWTAAATAYAATTT
 ---AAAAATGAAT-

Original motif Consensus sequence: AWTAAATAYAATTT



Reverse complement motif Consensus sequence: AAATTKTATTTAW

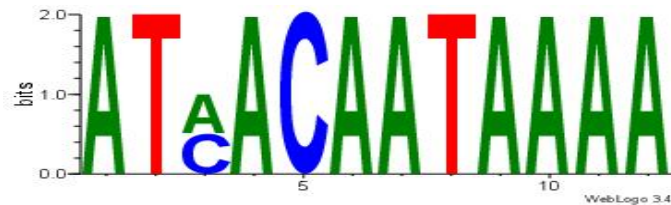


Dataset #: 2
 Motif ID: 15
 Motif name: Motif 15
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 10

Similarity score: 0.0875

Alignment:
TTTTATTGTYAT
ATTCATTTTT--

Original motif Consensus sequence: ATMACAATAAAA



Reverse complement motif Consensus sequence: TTTTATTGTYAT

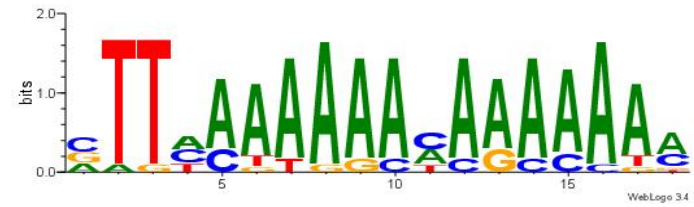
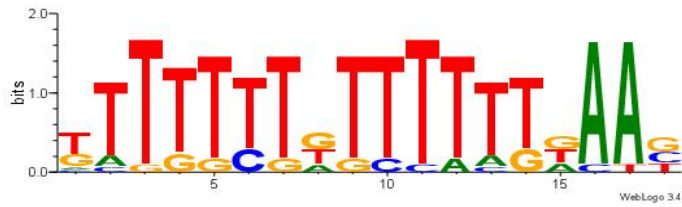


Dataset #: 5
Motif ID: 53
Motif name: TFM3
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 4
Number of overlap: 10
Similarity score: 0.0875

Alignment:
BTTHAAAAAYAAAAAR
-----AAAAATGAAT---

Original motif Consensus sequence: KTTTTTKTTTTTDAAB

Reverse complement motif Consensus sequence:
BTTHAAAAAYAAAAAR

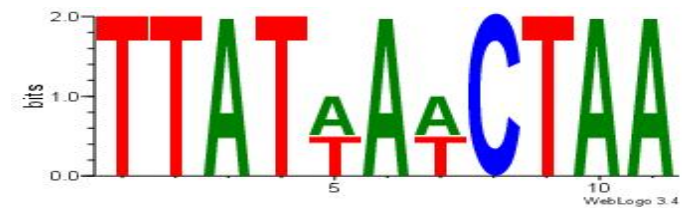


Dataset #: 2 Motif ID: 18 Motif name: Motif 18

Original motif Consensus sequence: TTAGWTWATAA



Reverse complement motif Consensus sequence: TTATWAWCTAA



Best Matches for Motif ID 18 (Highest to Lowest)

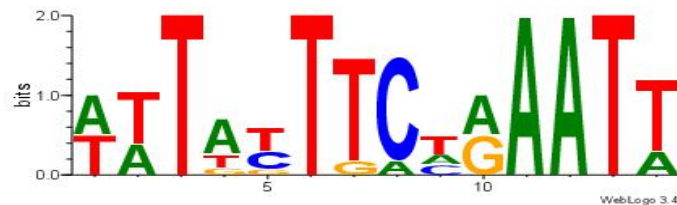
Dataset #:	2
Motif ID:	6
Motif name:	Motif 6
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	3
Number of overlap:	11
Similarity score:	0.09375

Alignment:
AATTYDGAARTAWW
-TTATWAWCTAA--

Original motif Consensus sequence: AATTYDGAARTAWW



Reverse complement motif Consensus sequence: WWTAKTTCDKAAAT

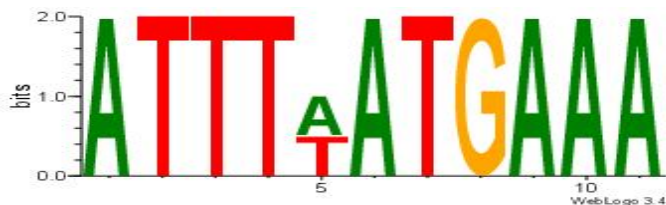


Dataset #: 2
Motif ID: 11
Motif name: Motif 11
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 11
Similarity score: 0.102273

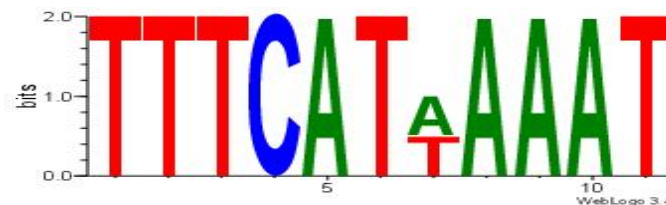
Alignment:

TTTCATWAAAT
TTAGWTWATAA

Original motif Consensus sequence: ATTTWATGAAA



Reverse complement motif Consensus sequence: TTTCATWAAAT

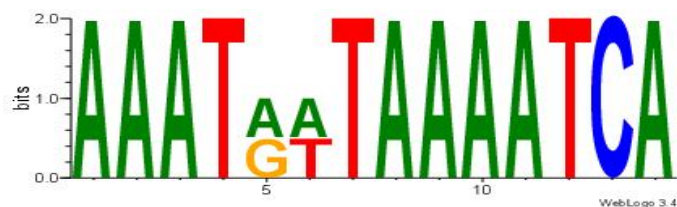


Dataset #: 2
 Motif ID: 8
 Motif name: Motif 8
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 4
 Number of overlap: 11
 Similarity score: 0.102273

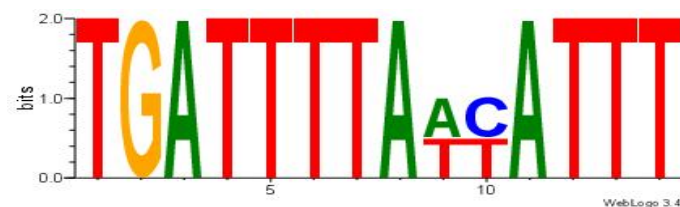
Alignment:

AAATRWTA~~AA~~ATCA
 TTATWAWCTAA---

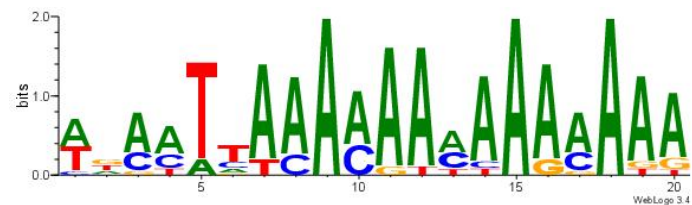
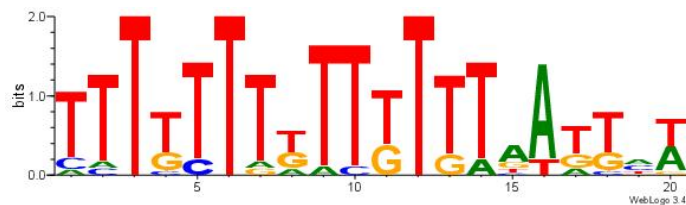
Original motif Consensus sequence: AAATRWTA~~AA~~ATCA



Reverse complement motif Consensus sequence: 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: 2
 Number of overlap: 11

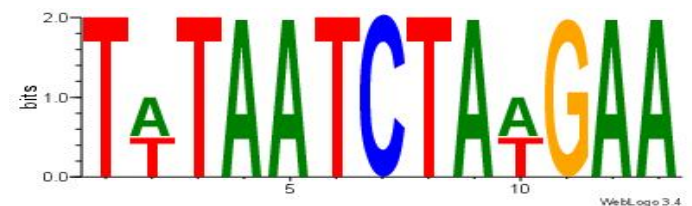


Dataset #: 2 Motif ID: 19 Motif name: Motif 19

Original motif Consensus sequence: TTCWTAGATTAWA



Reverse complement motif Consensus sequence: TWTAACTAWGAA

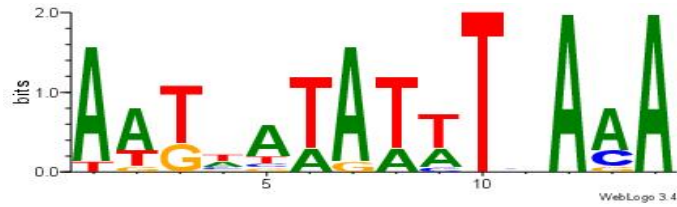


Best Matches for Motif ID 19 (Highest to Lowest)

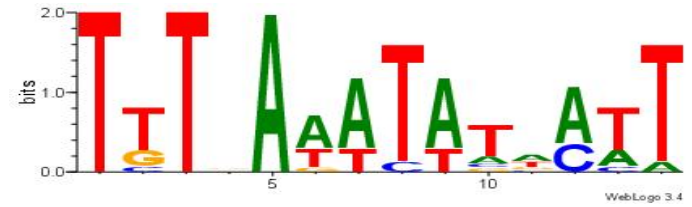
Dataset #:	2
Motif ID:	9
Motif name:	Motif 9
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	13
Similarity score:	0.0641025

Alignment:
AATHATATWTHAAA
-TTCWTAGATTAWA

Original motif Consensus sequence: AATHATATWTHAAA



Reverse complement motif Consensus sequence: TTTDAWATATHAT

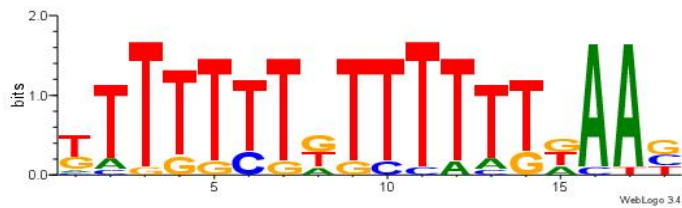


Dataset #: 5
 Motif ID: 53
 Motif name: TFM3
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 5
 Number of overlap: 13
 Similarity score: 0.0689103

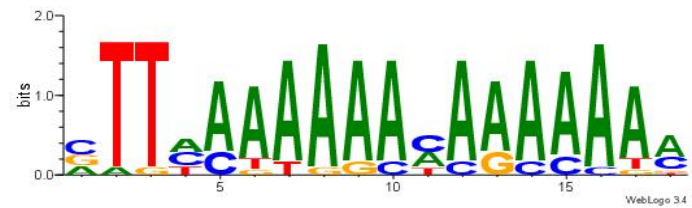
Alignment:

```
BTTHAAAAAYAAAAAR
-TTCWTAGATTAWA----
```

Original motif Consensus sequence: KTTTTTKTTTTTTDAAB



Reverse complement motif Consensus sequence: BTTHAAAAAYAAAAAR



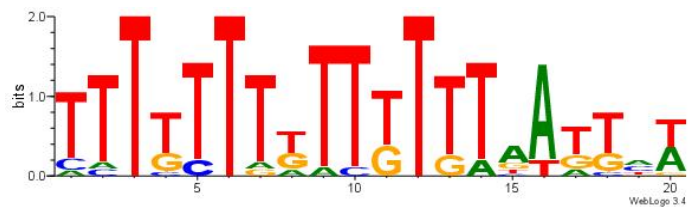
Dataset #: 5
 Motif ID: 56
 Motif name: TFM13
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 5
 Number of overlap: 13
 Similarity score: 0.0778388

Alignment:

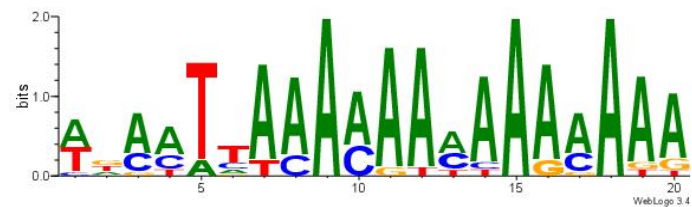
```

TTTTTTTKTTKTTTAATTHW
----TTCWTAGATTAWA----
  
```

Original motif Consensus sequence: TTTTTTKTTKTTTAATTHW



Reverse complement motif Consensus sequence: WHAATTAARAARAAAAAA

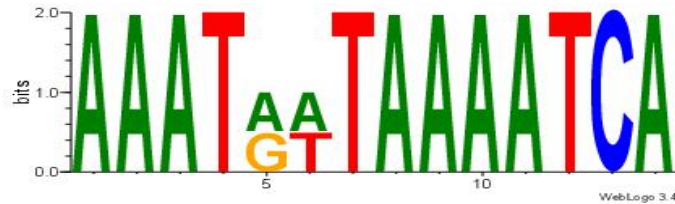


Dataset #: 2
 Motif ID: 8
 Motif name: Motif 8
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3

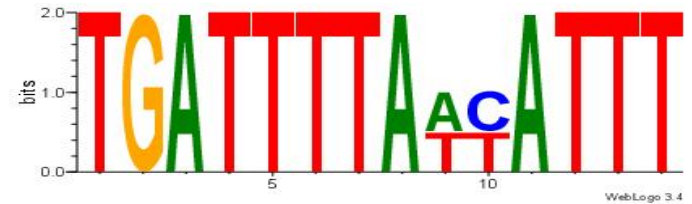
Number of overlap: 12
 Similarity score: 0.5625

Alignment:
 -TGATTTTAWKATTT
 TWTAACTAWGAA--

Original motif Consensus sequence: AAATRWTAATCA



Reverse complement motif Consensus sequence: TGATTTTAWKATTT

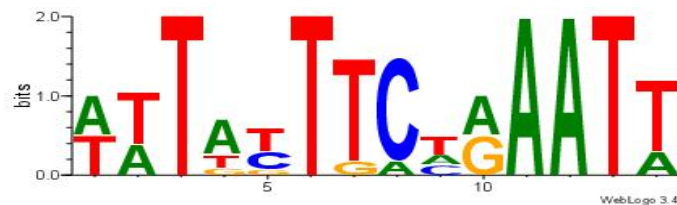


Dataset #: 2
 Motif ID: 6
 Motif name: Motif 6
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 12
 Similarity score: 0.5625

Alignment:
 AATTYDGAARTAWW-
 --TTCWTAGATTAWA

Original motif Consensus sequence: AATTYDGAARTAWW

Reverse complement motif Consensus sequence: WWTAKTTCDKAAAT

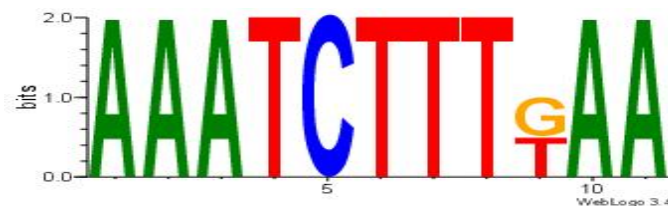


Dataset #: 2 Motif ID: 20 Motif name: Motif 20

Original motif Consensus sequence: TTMAAAGATTT



Reverse complement motif Consensus sequence: AAATCTTTYAA

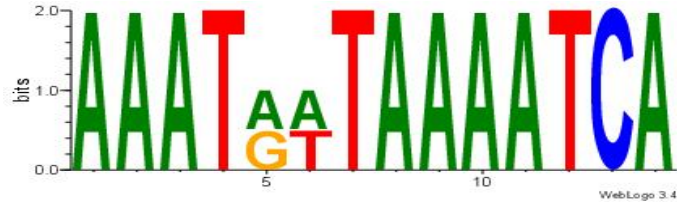


Best Matches for Motif ID 20 (Highest to Lowest)

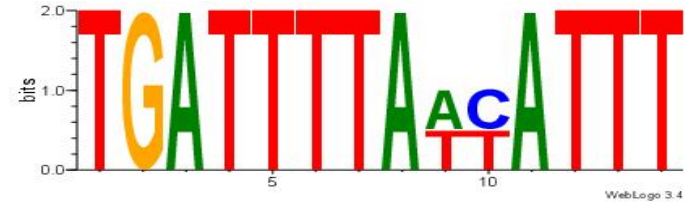
Dataset #:	2
Motif ID:	8
Motif name:	Motif 8
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	4
Number of overlap:	11
Similarity score:	0.0681818

Alignment:
AAATRWTAATAATCA
---AAATCTTTYAA

Original motif Consensus sequence: AAATRWTAATCA



Reverse complement motif Consensus sequence: TGATTTAWKATT



Dataset #: 2
Motif ID: 19
Motif name: Motif 19
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 3
Number of overlap: 11
Similarity score: 0.0681818

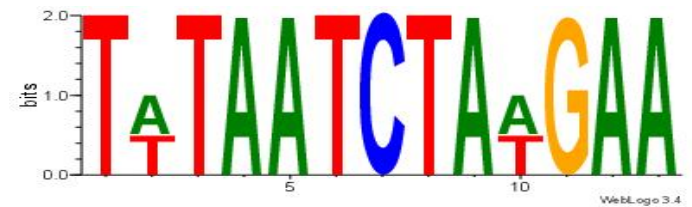
Alignment:

TTCWTAGATTAWA
TTMAAAGATTT--

Original motif Consensus sequence: TTCWTAGATTAWA



Reverse complement motif Consensus sequence: TWTAATCTAWGAA

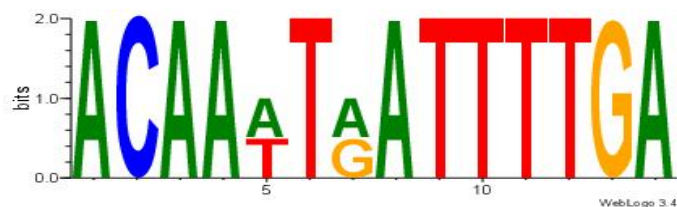


Dataset #: 2
 Motif ID: 16
 Motif name: Motif 16
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 11
 Similarity score: 0.102273

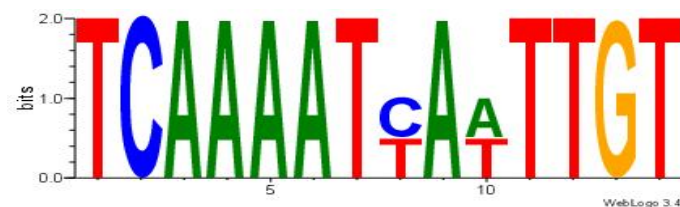
Alignment:

ACAAWTRATTTTGA
 -AAATCTTTYAA--

Original motif Consensus sequence: ACAAWTRATTTTGA



Reverse complement motif Consensus sequence: TCAAAATKAWTTG



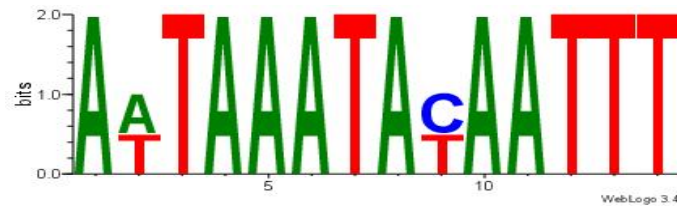
Dataset #: 2
 Motif ID: 5
 Motif name: Motif 5
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 11

Similarity score: 0.102273

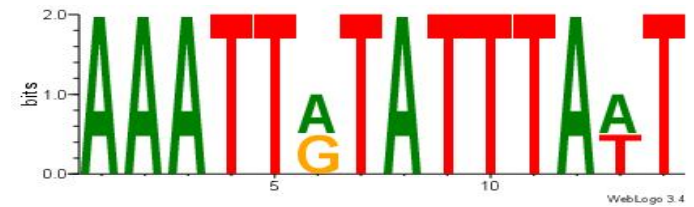
Alignment:

AWTAAATAYAATTT
--TTMAAAGATTT-

Original motif Consensus sequence: AWTAAATAYAATTT



Reverse complement motif Consensus sequence: AAATTKTATTTAW



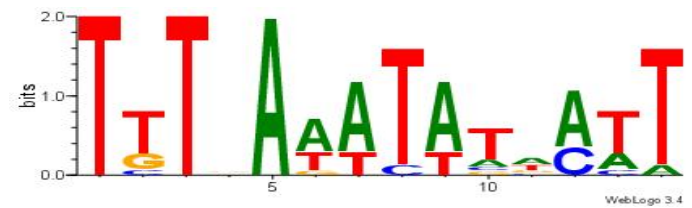
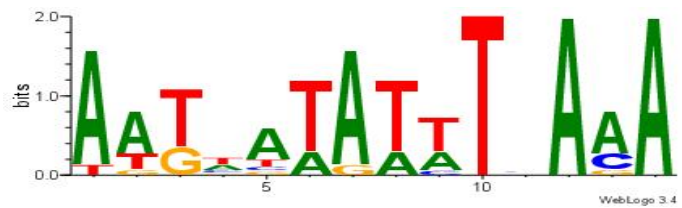
Dataset #: 2
Motif ID: 9
Motif name: Motif 9
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 2
Number of overlap: 11
Similarity score: 0.106061

Alignment:

TTTDAWATATHATT
--TTMAAAGATTT-

Original motif Consensus sequence: AATHATATWTHAAA

Reverse complement motif Consensus sequence: TTTDAWATATHATT

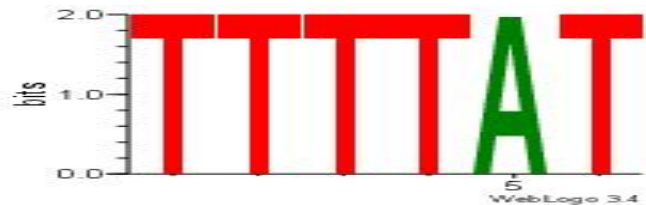


Dataset #: 2 Motif ID: 21 Motif name: Motif 21

Original motif Consensus sequence: ATAAAA



Reverse complement motif Consensus sequence: TTTTAT

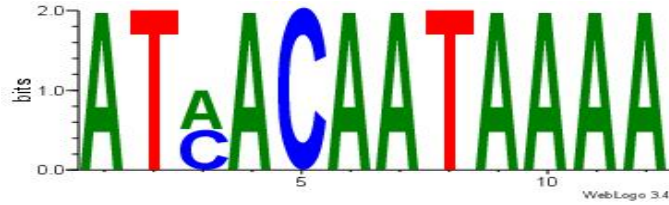


Best Matches for Motif ID 21 (Highest to Lowest)

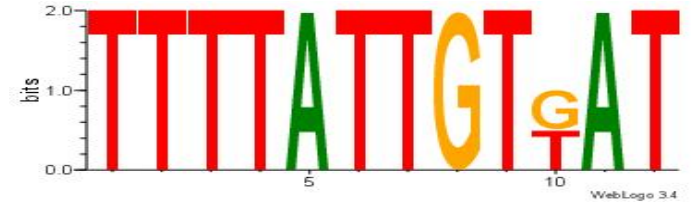
Dataset #:	2
Motif ID:	15
Motif name:	Motif 15
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	7
Number of overlap:	6
Similarity score:	0

Alignment:
 ATMACAATAAAA
 -----ATAAAA

Original motif Consensus sequence: ATMACAATAAAA



Reverse complement motif Consensus sequence: TTTTATTGTYAT

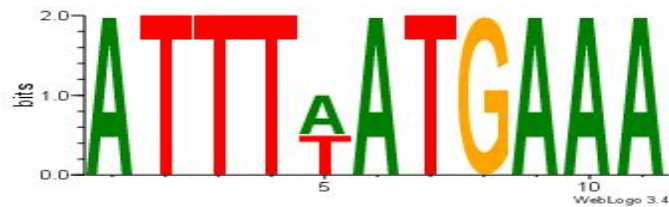


Dataset #: 2
Motif ID: 11
Motif name: Motif 11
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 5
Number of overlap: 6
Similarity score: 0.0208333

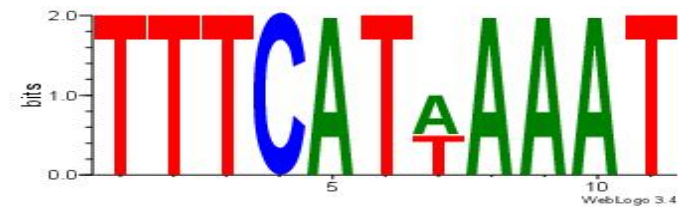
Alignment:

ATTTWATGAAA
----TTTAT-

Original motif Consensus sequence: ATTTWATGAAA



Reverse complement motif Consensus sequence: TTTCATWAAAT

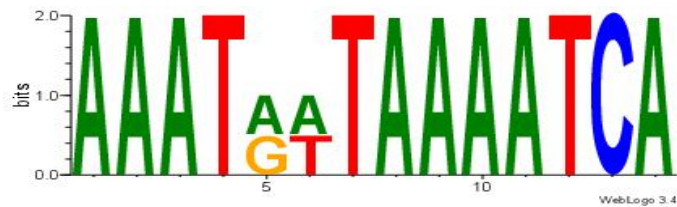


Dataset #: 2
 Motif ID: 8
 Motif name: Motif 8
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 6
 Number of overlap: 6
 Similarity score: 0.0208333

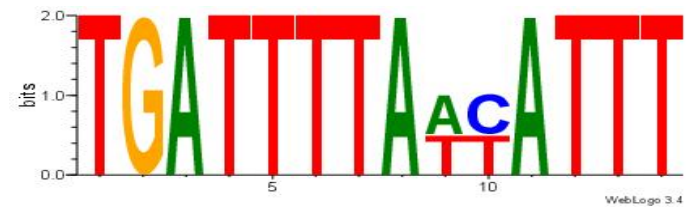
Alignment:

AAATRWTA~~AA~~ATCA
 -----ATAAAA-----

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



Reverse complement motif Consensus sequence: TGATTTTAWKATT



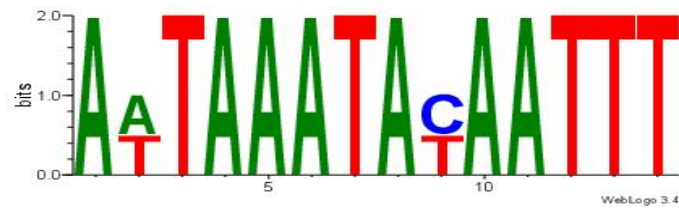
Dataset #: 2
 Motif ID: 5
 Motif name: Motif 5
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 4
 Number of overlap: 6

Similarity score: 0.0208333

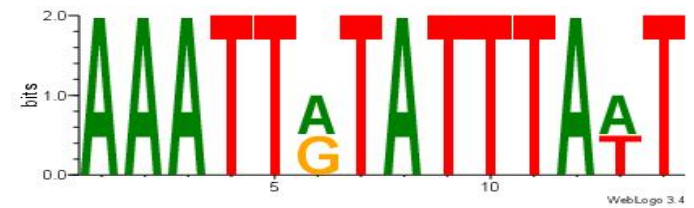
Alignment:

AAATTKTATTTAWT
---TTTTAT-----

Original motif Consensus sequence: AWTAAATAYAATTT



Reverse complement motif Consensus sequence: AAATTKTATTTAWT



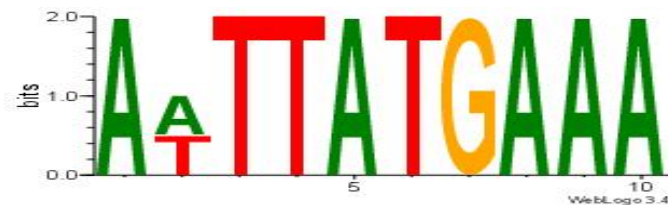
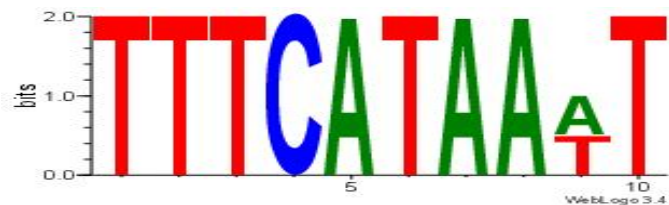
Dataset #: 2
Motif ID: 10
Motif name: Motif 10
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 5
Number of overlap: 6
Similarity score: 0.0416667

Alignment:

AWTTATGAAA
ATAAAA-----

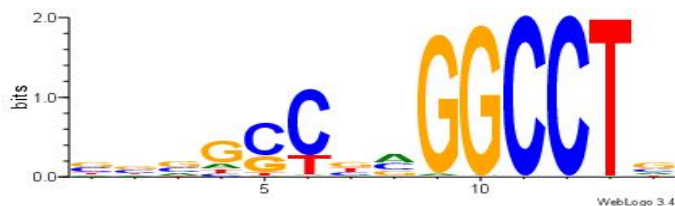
Original motif Consensus sequence: TTTCATAAWT

Reverse complement motif Consensus sequence: AWTTATGAAA



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

Original motif Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif Consensus sequence: VAGGCCBBGGCV



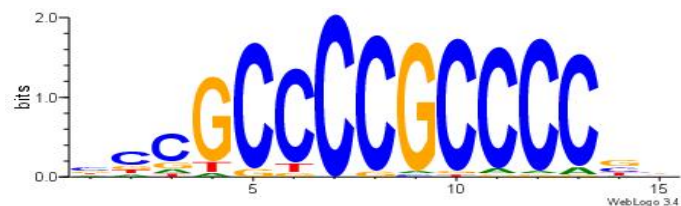
Best Matches for Motif ID 22 (Highest to Lowest)

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

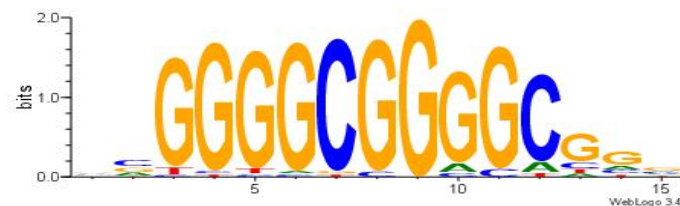
Alignment:

```
BCCGCCCCGCCCCBB
BBVGCCBVGGCCTV-
```


Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB

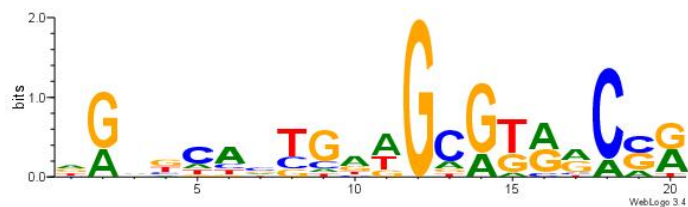


Dataset #: 3
Motif ID: 31
Motif name: Pax5
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 5
Number of overlap: 14
Similarity score: 0.0611182

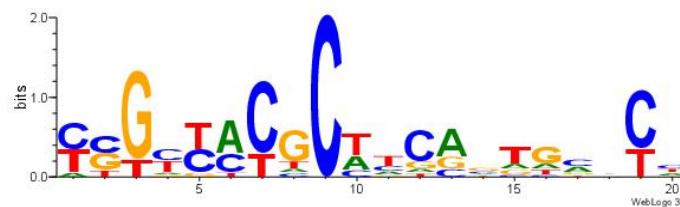
Alignment:

```
DGVBCABTGDWGCGRRCR  
--BBVGCCBVGGCCTV----
```

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBCD

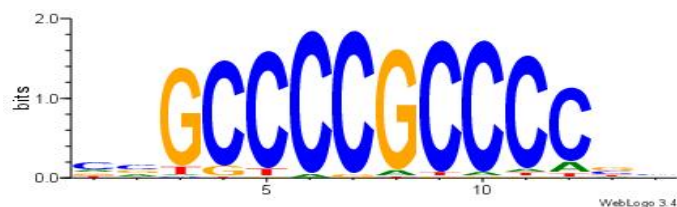


Dataset #: 4
 Motif ID: 36
 Motif name: csGCCCCGCCCCsc
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0.0654514

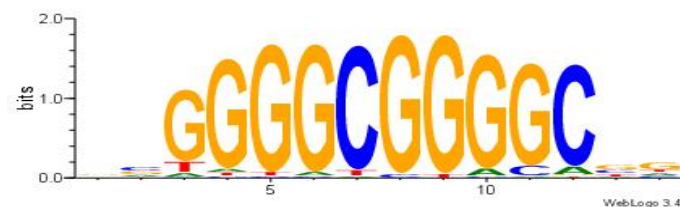
Alignment:

HVGCCCCGCCCCBB
 VAGGCCBBGGCVBB

Original motif Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGC



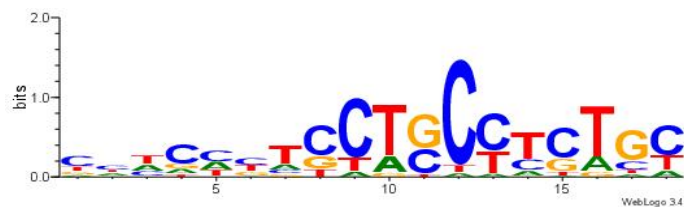
Dataset #: 5
 Motif ID: 52
 Motif name: TFM2
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 14

Similarity score: 0.0699096

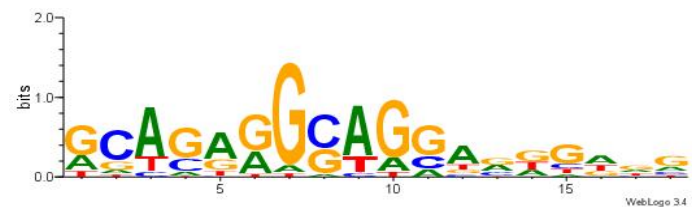
Alignment:

CHHCHBTCCTSCYTCTGC
-BBVGCCBVGGCCTV---

Original motif Consensus sequence: CHHCHBTCCTSCYTCTGC



Reverse complement motif Consensus sequence:
GCAGAKGSAGGABDGH DG



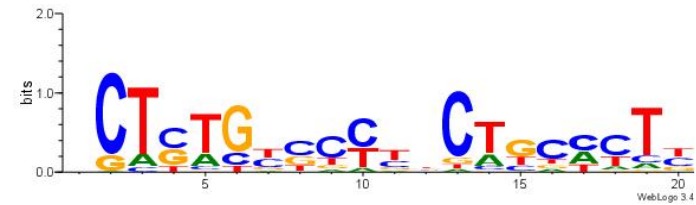
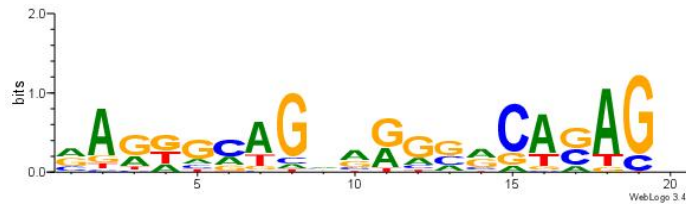
Dataset #: 5
Motif ID: 55
Motif name: TFM12
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 4
Number of overlap: 14
Similarity score: 0.071298

Alignment:

VCTSTGKSCMKBCTRCYCTK
---VAGGCCBBGGCVBB---

Original motif Consensus sequence: RAGKGMAGVRRGSR CASAGV

Reverse complement motif Consensus sequence:
VCTSTGKSCMKBCTRCYCTK

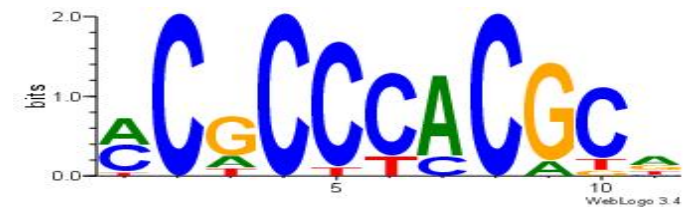


Dataset #: 3 Motif ID: 23 Motif name: Egr1

Original motif Consensus sequence: HGCGTGGGCGK



Reverse complement motif Consensus sequence: YCGCCACGCH

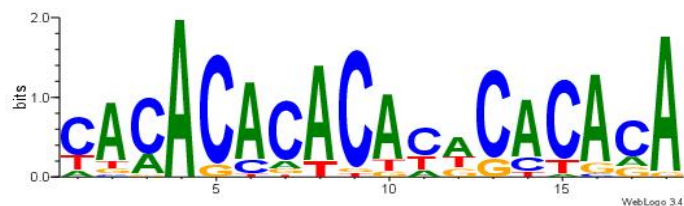


Best Matches for Motif ID 23 (Highest to Lowest)

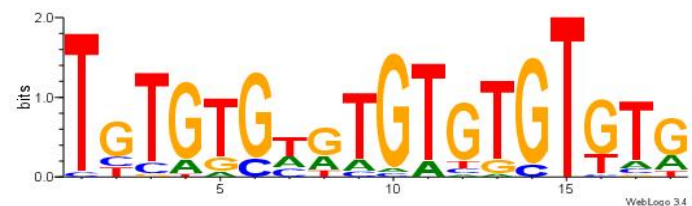
Dataset #:	5
Motif ID:	51
Motif name:	TFM1
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	2
Number of overlap:	11
Similarity score:	0.0650523

Alignment:
TGTGTGWTGTGTGTGTG
-----HGCGTGGGCGK-

Original motif Consensus sequence: CACACACACWCACACA



Reverse complement motif Consensus sequence: TGTGTGWGTGTGTGTGTG

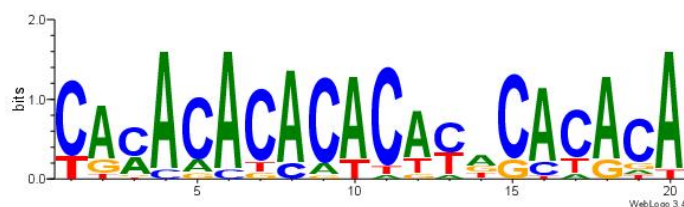


Dataset #: 5
Motif ID: 54
Motif name: TFM11
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 9
Number of overlap: 11
Similarity score: 0.0682449

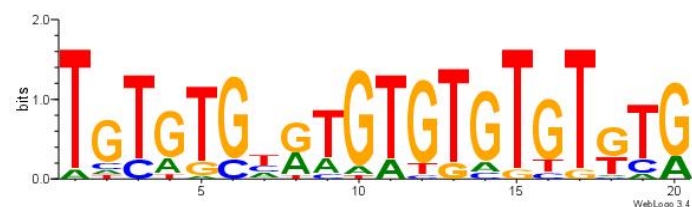
Alignment:

```
TGTGTGDKTGTGTGTGTRTG  
-----HGCGTGGGCGK--
```

Original motif Consensus sequence: CAMACACACACAYDCACACA



Reverse complement motif Consensus sequence: TGTGTGDKTGTGTGTGTRTG

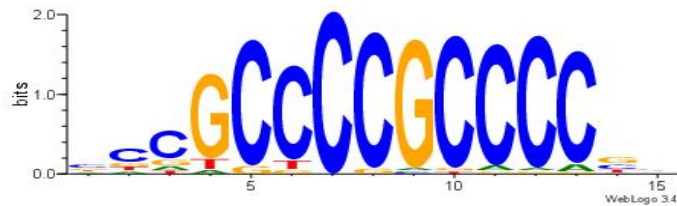


Dataset #: 4
 Motif ID: 38
 Motif name: cccGCCCCGCCCCsb
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 5
 Number of overlap: 11
 Similarity score: 0.0730967

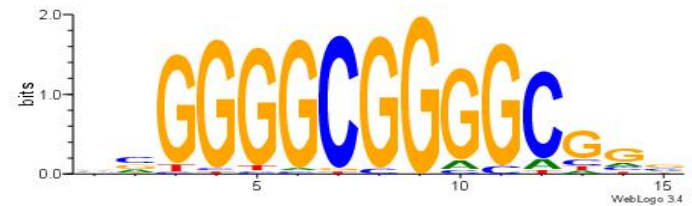
Alignment:

BBGGGGCGGGGCGGB
 ----HGCGTGGGCGK

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB



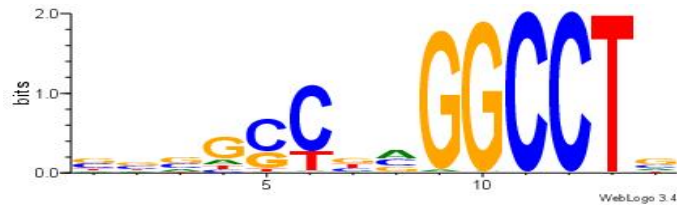
Dataset #: 3
 Motif ID: 22
 Motif name: Zfx
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2

Number of overlap: 11
Similarity score: 0.0764878

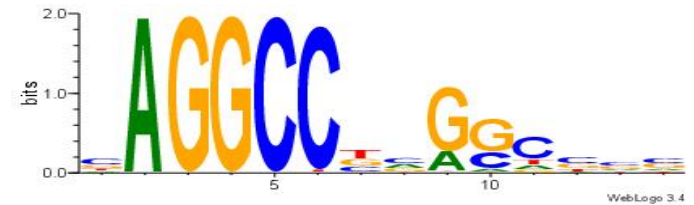
Alignment:

BBVGCCBVGGCCTV
--HGCGTGGGCGK--

Original motif Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif Consensus sequence: VAGGCCBBGGCV



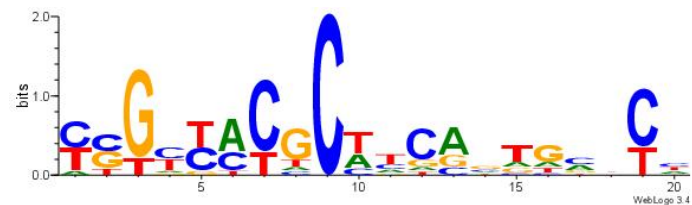
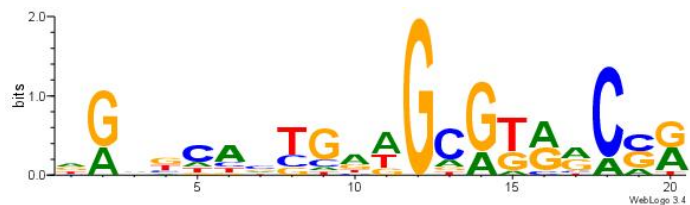
Dataset #: 3
Motif ID: 31
Motif name: Pax5
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 5
Number of overlap: 11
Similarity score: 0.0765783

Alignment:

DGVBCABTGDWGCGRCSR
----HGCGTGGGCGK-----

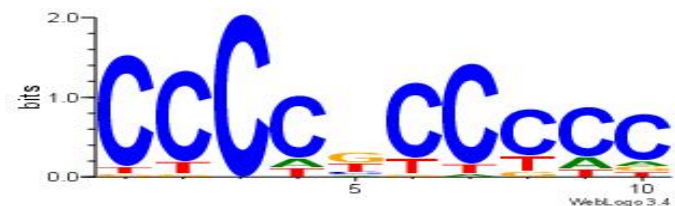
Original motif Consensus sequence: DGVBCABTGDWGCGRCSR

Reverse complement motif Consensus sequence:
MSGKKRCGCWDCABTGBBCD

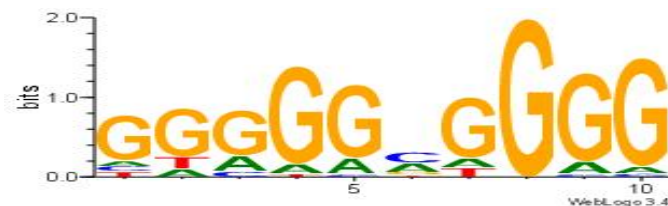


Dataset #: 3 Motif ID: 24 Motif name: SP1

Original motif Consensus sequence: CCCCKCCCC



Reverse complement motif Consensus sequence: GGGGYGGGG

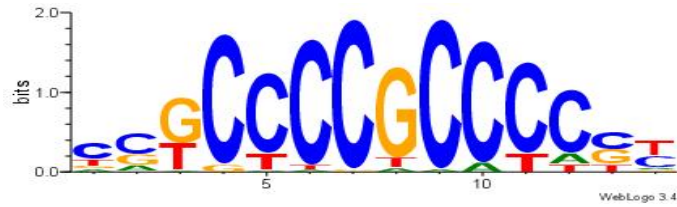


Best Matches for Motif ID 24 (Highest to Lowest)

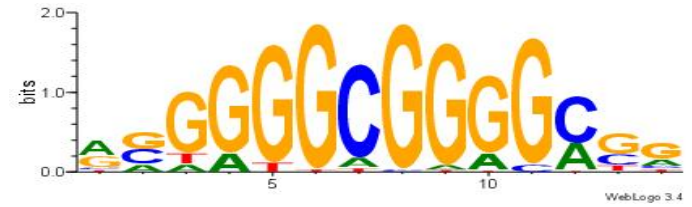
Dataset #:	2
Motif ID:	7
Motif name:	Motif 7
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	4
Number of overlap:	10
Similarity score:	0.00451594

Alignment:
 MSGGGGCGGGYSG
 -GGGGYGGGG---

Original motif Consensus sequence: CSKCCCCGCCCCSY



Reverse complement motif Consensus sequence: MSGGGGCGGGGY

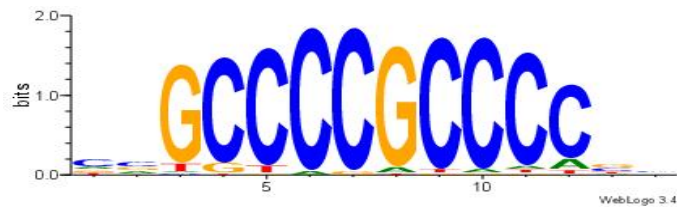


Dataset #: 4
Motif ID: 36
Motif name: csGCCCCGCCCCsc
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 4
Number of overlap: 10
Similarity score: 0.00965796

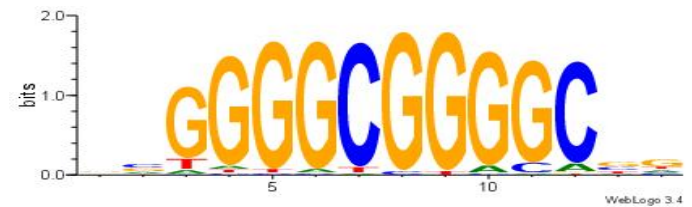
Alignment:

BBGGGGCGGGGCVD
-GGGGYGGGG---

Original motif Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGC

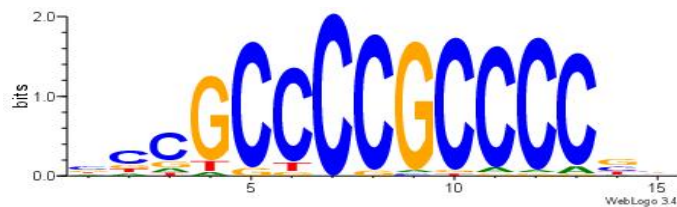


Dataset #: 4
 Motif ID: 38
 Motif name: cccGCCCCGCCCCsb
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 5
 Number of overlap: 10
 Similarity score: 0.0127292

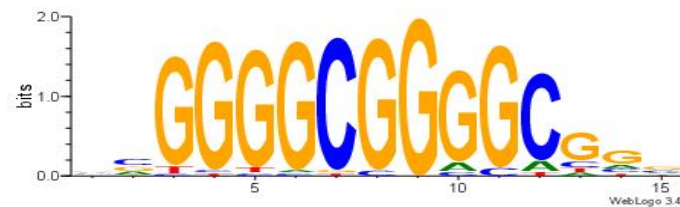
Alignment:

BBGGGGCGGGGCGGB
 -GGGGYGGGG-----

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB



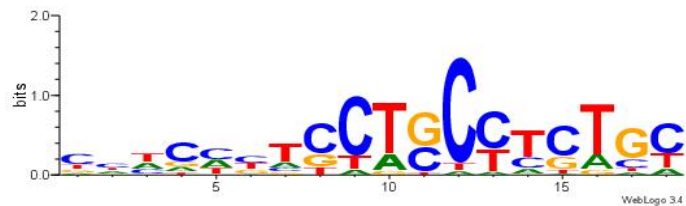
Dataset #: 5
 Motif ID: 52
 Motif name: TFM2
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 6

Number of overlap: 10
Similarity score: 0.0523047

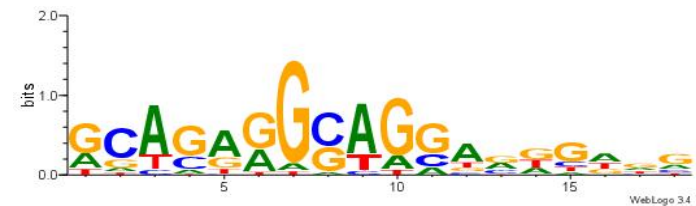
Alignment:

CHHCHBTCCTSCYTCTGC
-----CCCCKCCCC---

Original motif Consensus sequence: CHHCHBTCCTSCYTCTGC



Reverse complement motif Consensus sequence:
GCAGAKGSAGGABDGHG



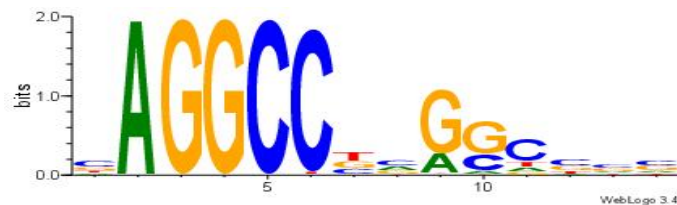
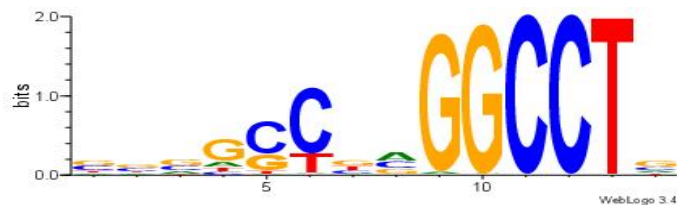
Dataset #: 3
Motif ID: 22
Motif name: Zfx
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 10
Similarity score: 0.0540825

Alignment:

BBVGCCBVGCCCTV
-----GGGGGYGGGG

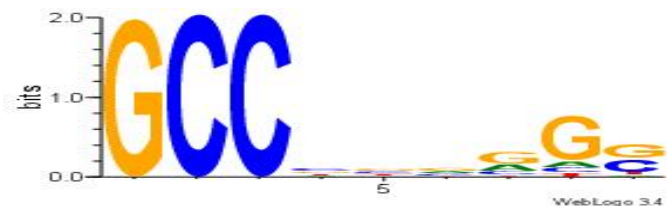
Original motif Consensus sequence: BBVGCCBVGCCCTV

Reverse complement motif Consensus sequence: VAGGCCBBGGCV

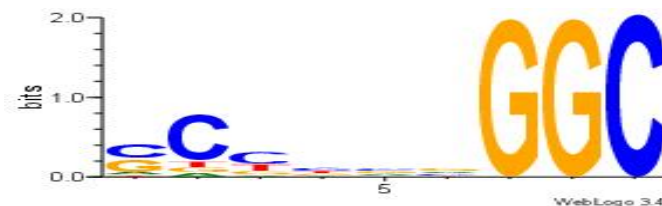


Dataset #: 3 Motif ID: 25 Motif name: TFAP2A

Original motif Consensus sequence: GCCBBVRGS



Reverse complement motif Consensus sequence: SCMVBGGC

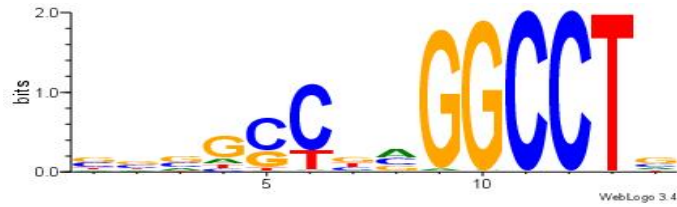


Best Matches for Motif ID 25 (Highest to Lowest)

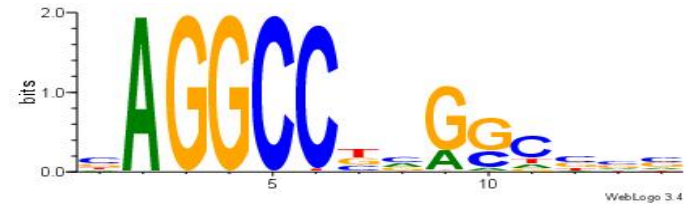
Dataset #:	3
Motif ID:	22
Motif name:	Zfx
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	3
Number of overlap:	9
Similarity score:	0.0131247

Alignment:
 BBVGCCBVGGCTV
 ---SCMVBBGGC--

Original motif Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif Consensus sequence: VAGGCCBBGGCV

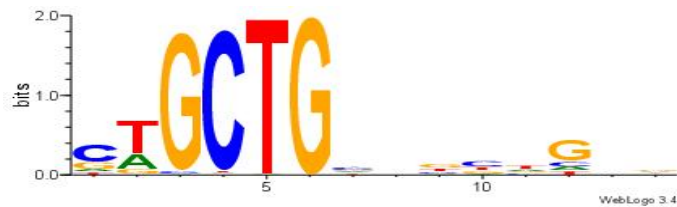


Dataset #: 5
Motif ID: 50
Motif name: TFF11
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 9
Similarity score: 0.0403253

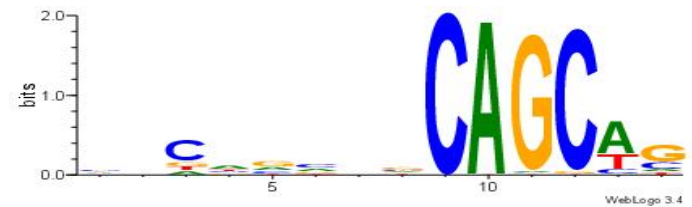
Alignment:

HVCDBBDBCAGCAG
SCMVBBGGC-----

Original motif Consensus sequence: CTGCTGBDBBDGBD



Reverse complement motif Consensus sequence: HVCDBBDBCAGCA

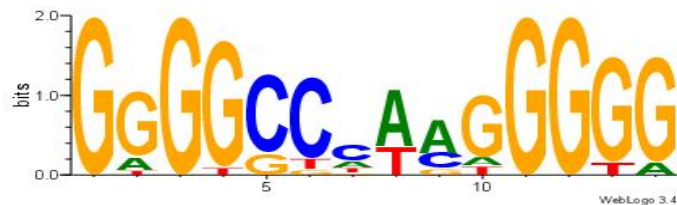


Dataset #: 3
 Motif ID: 30
 Motif name: PLAG1
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 9
 Similarity score: 0.0414588

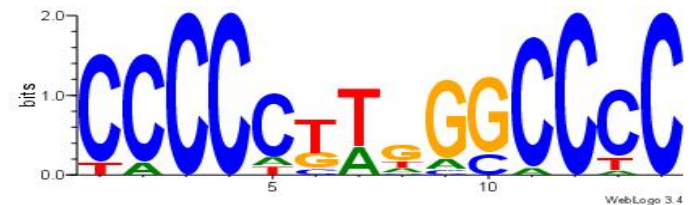
Alignment:

GGGGCCCAAGGGGG
 ---GCCBBVRGS--

Original motif Consensus sequence: GGGGCCCAAGGGGG



Reverse complement motif Consensus sequence: CCCCTTGGGCC



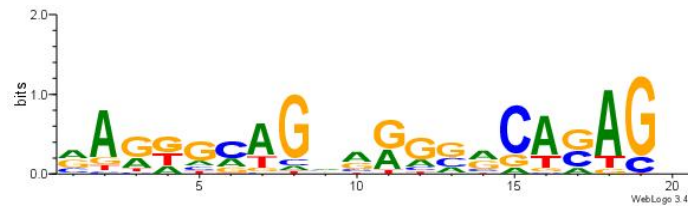
Dataset #: 5
 Motif ID: 55
 Motif name: TFM12
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 8
 Number of overlap: 9

Similarity score: 0.0542554

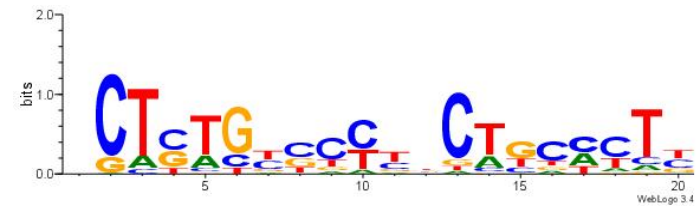
Alignment:

RAGKGMAGVRRGSRCASAGV
----GCCBBVRGS-----

Original motif Consensus sequence: RAGKGMAGVRRGSRCASAGV



Reverse complement motif Consensus sequence: VCTSTGKSCMKBCTRCYCTK



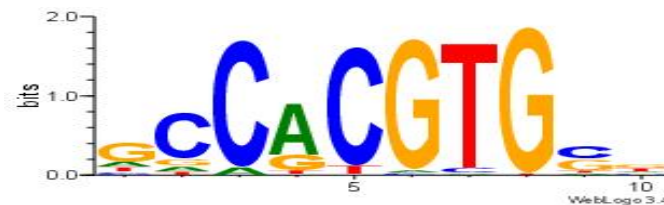
Dataset #: 3
Motif ID: 33
Motif name: Mycn
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 2
Number of overlap: 9
Similarity score: 0.0550803

Alignment:

HSCACGTGGC
-SCMVBBGGC

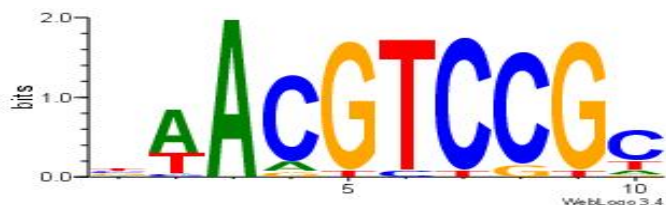
Original motif Consensus sequence: HSCACGTGGC

Reverse complement motif Consensus sequence: GCCACGTGSD



Dataset #: 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)

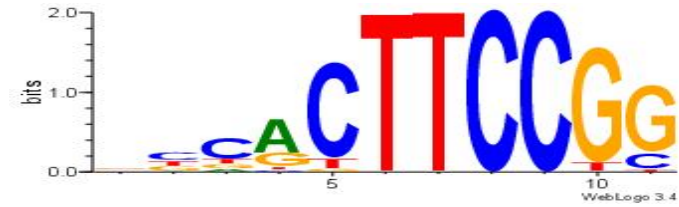
Dataset #:	3
Motif ID:	35
Motif name:	GABPA
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2
Number of overlap:	10
Similarity score:	0.00503821

Alignment:
 CCGGAAGTGVV
 GCGGACGTTV-

Original motif Consensus sequence: CCGGAAGTGVV



Reverse complement motif Consensus sequence: VVCACTTCCGG

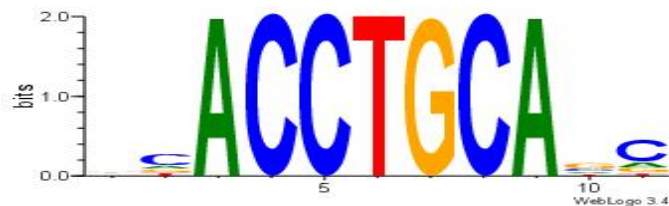


Dataset #: 4
Motif ID: 40
Motif name: kcACCTGCAGc
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2
Number of overlap: 10
Similarity score: 0.0369391

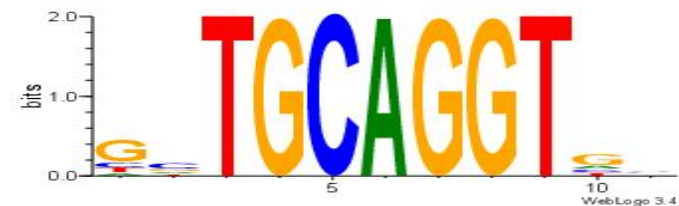
Alignment:

BCACCTGCABC
BAACGTCCGC-

Original motif Consensus sequence: BCACCTGCABC



Reverse complement motif Consensus sequence: GBTGCAGGTGB

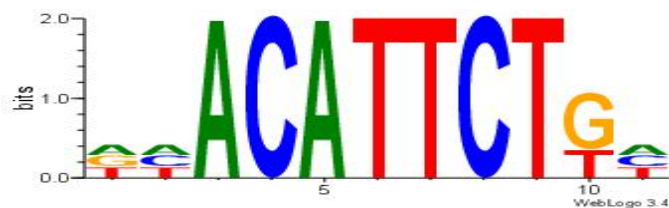


Dataset #: 4
 Motif ID: 44
 Motif name: dhACATTCTkh
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 10
 Similarity score: 0.0385417

Alignment:

DHACATTCTGH
 BAACGTCCGC-

Original motif Consensus sequence: DHACATTCTGH



Reverse complement motif Consensus sequence: HCAGAATGTHD



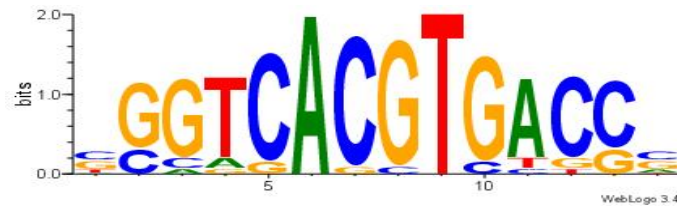
Dataset #: 4
 Motif ID: 42
 Motif name: sSGTCACGTGACSS
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 10

Similarity score: 0.0395139

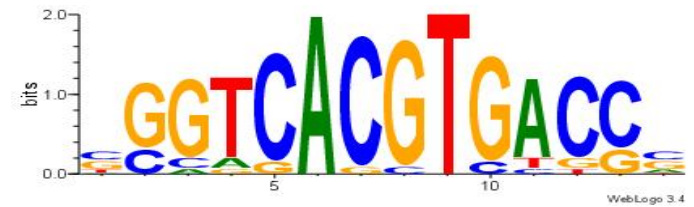
Alignment:

SGGTCACGTGACCS
---BAACGTCCGC-

Original motif Consensus sequence: SGGTCACGTGACCS



Reverse complement motif Consensus sequence: SGGTCACGTGACCS



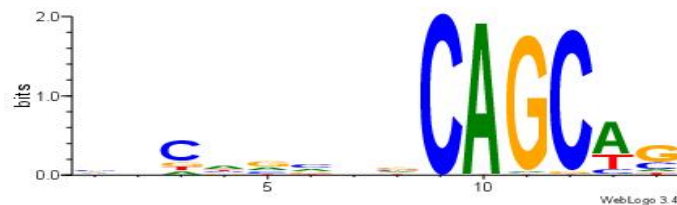
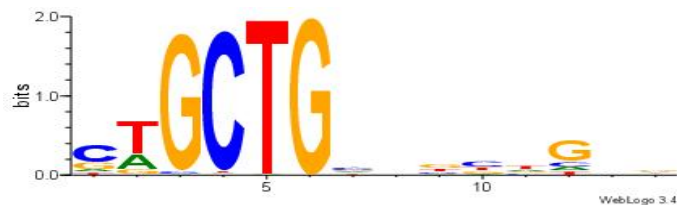
Dataset #: 5
Motif ID: 50
Motif name: TFF11
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 3
Number of overlap: 10
Similarity score: 0.0439583

Alignment:

CTGCTGBDBBDGDB
--GCGGACGTTV--

Original motif Consensus sequence: CTGCTGBDBBDGDB

Reverse complement motif Consensus sequence: HVCDBBDBCAGCA

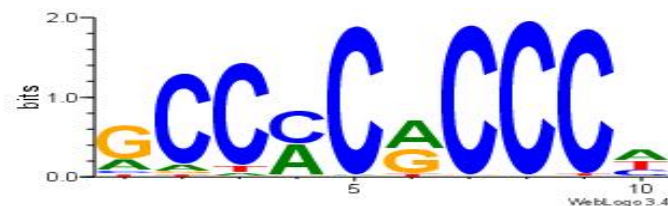


Dataset #: 3 Motif ID: 27 Motif name: Klf4

Original motif Consensus sequence: DGGYGKGGC



Reverse complement motif Consensus sequence: GCCYCMCCCD

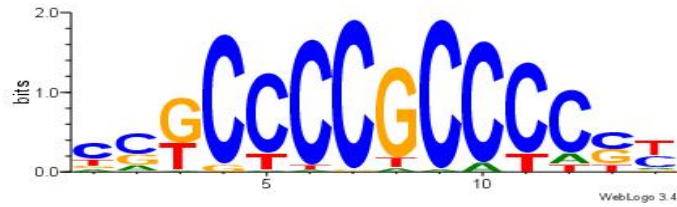


Best Matches for Motif ID 27 (Highest to Lowest)

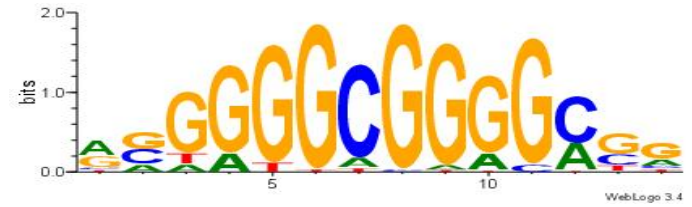
Dataset #:	2
Motif ID:	7
Motif name:	Motif 7
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	3
Number of overlap:	10
Similarity score:	0.0152457

Alignment:
 CSKCCCCGCCCSY
 --GCCYCMCCCD--

Original motif Consensus sequence: CSKCCCCGCCCSY



Reverse complement motif Consensus sequence: MSGGGCGGGGY

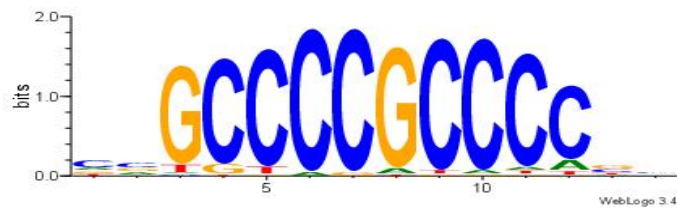


Dataset #: 4
Motif ID: 36
Motif name: csGCCCCGCCCSy
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 3
Number of overlap: 10
Similarity score: 0.0160185

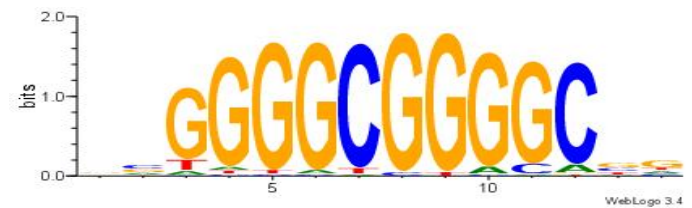
Alignment:

BBGGGGCGGGGCVD
--DGGGYGKGGC--

Original motif Consensus sequence: HVGCCCCGCCCB



Reverse complement motif Consensus sequence: BBGGGGCGGGGC

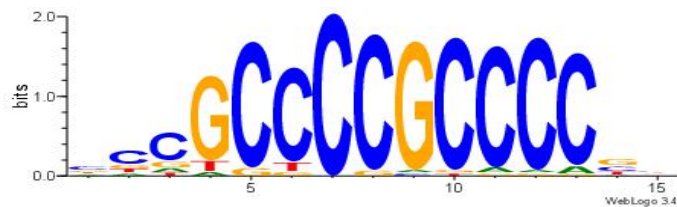


Dataset #: 4
 Motif ID: 38
 Motif name: cccGCCCCGCCCCsb
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3
 Number of overlap: 10
 Similarity score: 0.0194893

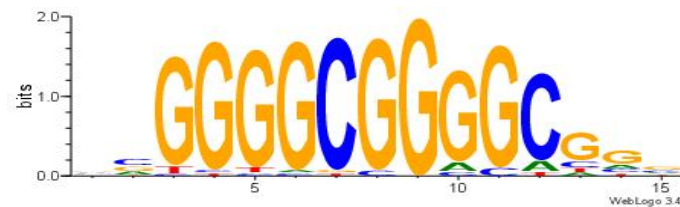
Alignment:

BBGGGGCGGGGCGGB
 --DGGGYGKGGC---

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB

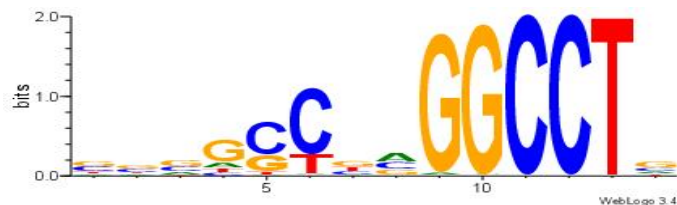


Dataset #: 3
 Motif ID: 22
 Motif name: Zfx
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 4

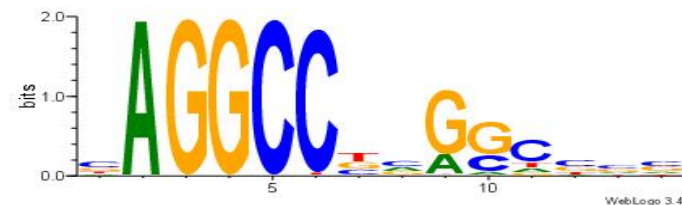
Number of overlap: 10
Similarity score: 0.0623591

Alignment:
BBVGCCBVGGCCTV
-GCCYCMCCCD---

Original motif Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif Consensus sequence: VAGGCCBBGGCV

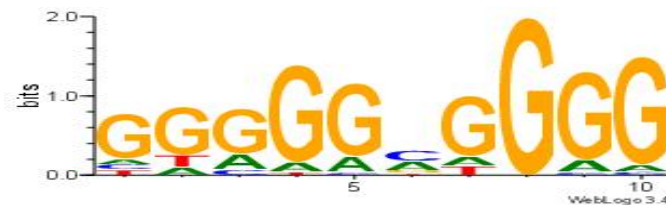
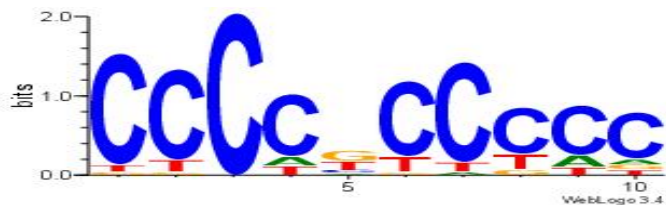


Dataset #: 3
Motif ID: 24
Motif name: SP1
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 10
Similarity score: 0.0663136

Alignment:
GGGGYGGGG
DGGYGKGGC

Original motif Consensus sequence: CCCCKCCCC

Reverse complement motif Consensus sequence: GGGGYGGGG



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

Original motif Consensus sequence: TTTSGCGC



Reverse complement motif Consensus sequence: GCGCSAAA

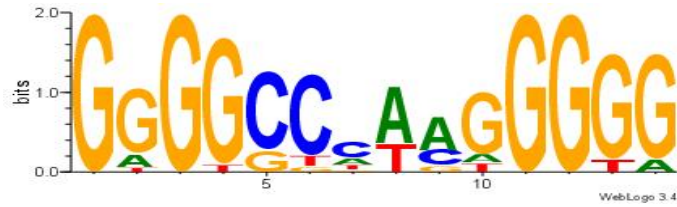


Best Matches for Motif ID 28 (Highest to Lowest)

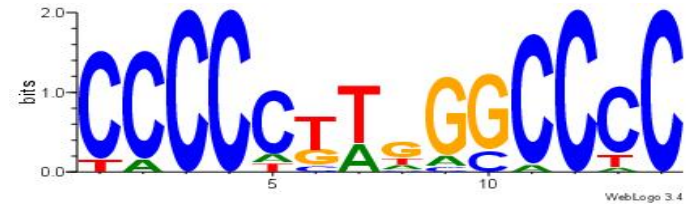
Dataset #:	3
Motif ID:	30
Motif name:	PLAG1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	8
Similarity score:	0.0357639

Alignment:
GGGGCCCAAGGGGG
-GCGCSAAA-----

Original motif Consensus sequence: GGGCCCAAGGGG



Reverse complement motif Consensus sequence: CCCCTTGGCC



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: 3
Number of overlap: 8
Similarity score: 0.0413603

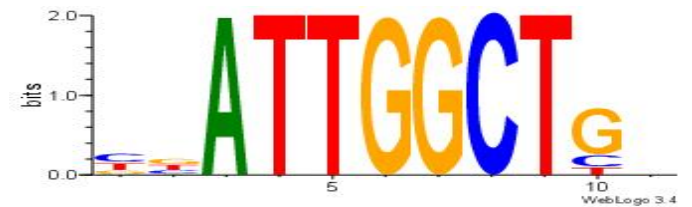
Alignment:

MBATTGGCTGH
--TTTSGCGC-

Original motif Consensus sequence: DCAGCCAATVR



Reverse complement motif Consensus sequence: MBATTGGCTGH



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: 0.0572917

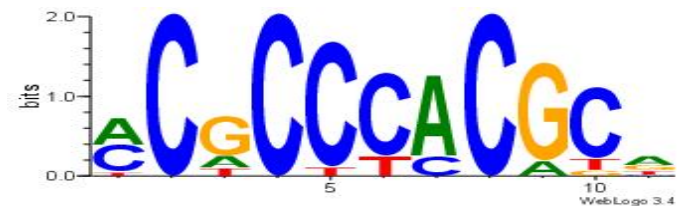
Alignment:

YGCCCCACGCH
 GCGCSAAA---

Original motif Consensus sequence: HGCGTGGGCGK



Reverse complement motif Consensus sequence: YGCCCCACGCH

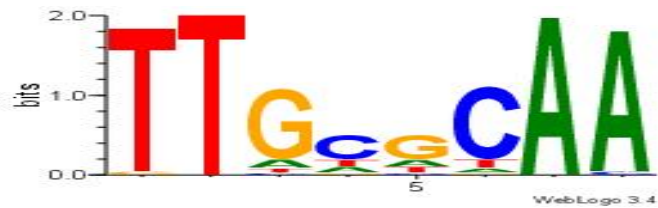


Dataset #: 5
 Motif ID: 47
 Motif name: TFW1
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 8

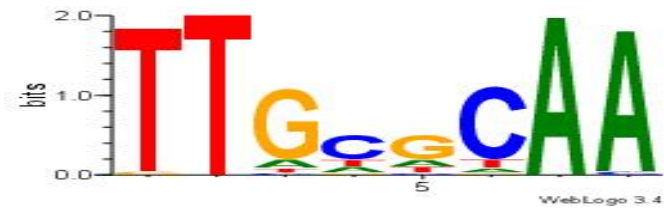
Similarity score: 0.0609375

Alignment:
TTGCGCAA
TTTSGCGC

Original motif Consensus sequence: TTGCGCAA



Reverse complement motif Consensus sequence: TTGCGCAA

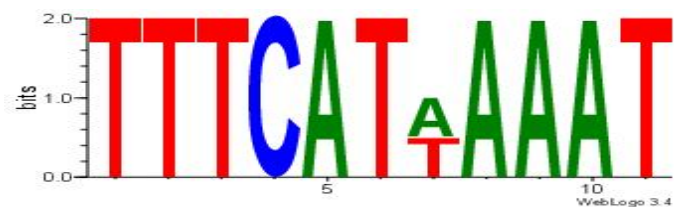
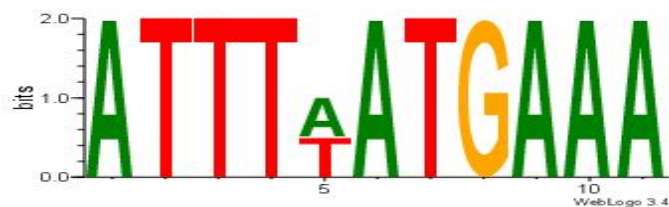


Dataset #: 2
Motif ID: 11
Motif name: Motif 11
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 2
Number of overlap: 8
Similarity score: 0.0625

Alignment:
ATTTWATGAAA
-TTTSGCGC--

Original motif Consensus sequence: ATTTWATGAAA

Reverse complement motif Consensus sequence: TTTCATWAAAT



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:	Forward
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

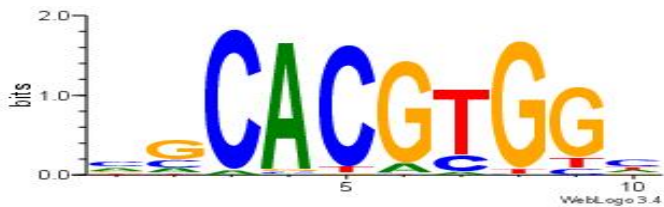


Dataset #: 3
Motif ID: 34
Motif name: Myc
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 2
Number of overlap: 8
Similarity score: 0.0144491

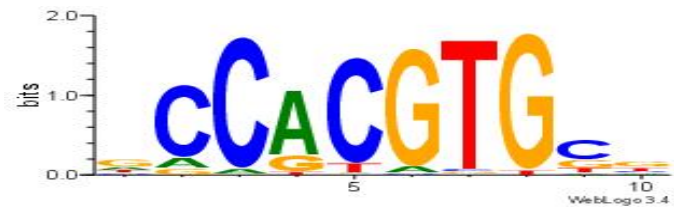
Alignment:

DCCACGTGCV
-VBACGTGV-

Original motif Consensus sequence: VGCACGTGGH



Reverse complement motif Consensus sequence: DCCACGTGCV

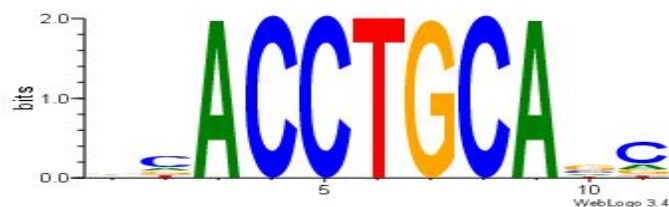


Dataset #: 4
 Motif ID: 40
 Motif name: kcACCTGCAGc
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 8
 Similarity score: 0.0295473

Alignment:

BCACCTGCABC
 VBACGTGV---

Original motif Consensus sequence: BCACCTGCABC



Reverse complement motif Consensus sequence: GBTGCAGGTGB



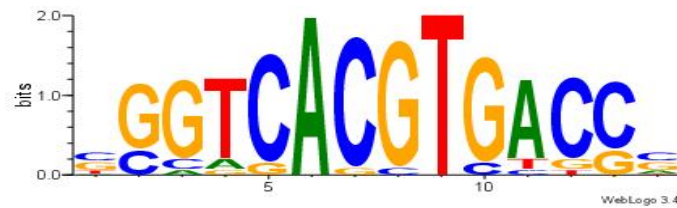
Dataset #: 4
 Motif ID: 42
 Motif name: sSGTCACGTGACSS
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 8

Similarity score: 0.0314837

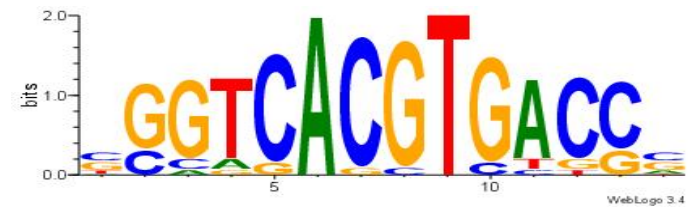
Alignment:

SGGTCACGTGACCS
---VCACGTBV---

Original motif Consensus sequence: SGGTCACGTGACCS



Reverse complement motif Consensus sequence: SGGTCACGTGACCS



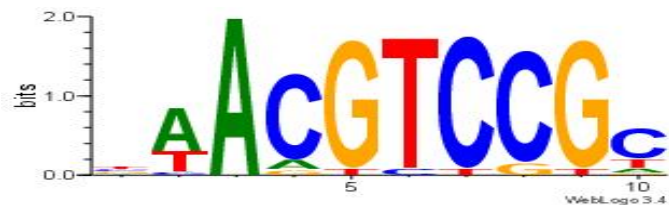
Dataset #: 3
Motif ID: 26
Motif name: MIZF
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 3
Number of overlap: 8
Similarity score: 0.0377204

Alignment:

GCGGACGTTV
--VCACGTBV

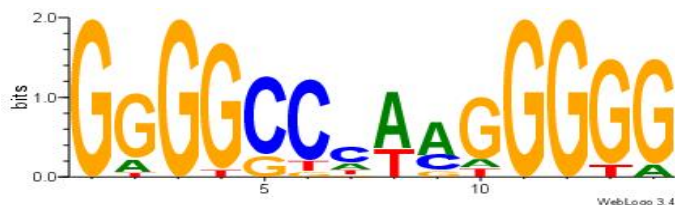
Original motif Consensus sequence: BAACGTCCGC

Reverse complement motif Consensus sequence: GCGGACGTTV

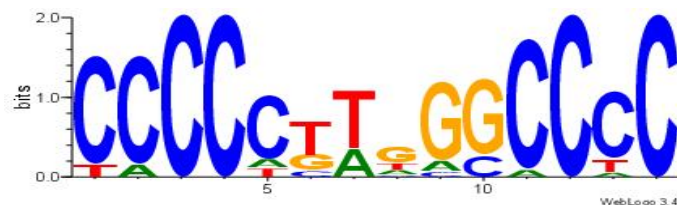


Dataset #: 3 Motif ID: 30 Motif name: PLAG1

Original motif Consensus sequence: GGGCCCAAGGGG



Reverse complement motif Consensus sequence: CCCCTTGGCC

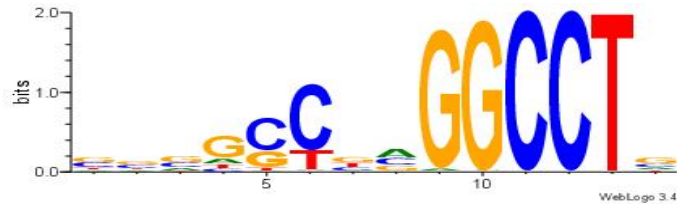


Best Matches for Motif ID 30 (Highest to Lowest)

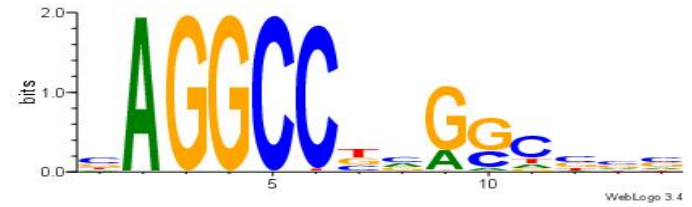
Dataset #:	3
Motif ID:	22
Motif name:	Zfx
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	14
Similarity score:	0.0886295

Alignment:
VAGGCCBBGGCVBB
GGGCCCAAGGGG

Original motif Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif Consensus sequence: VAGGCCBBGGCV

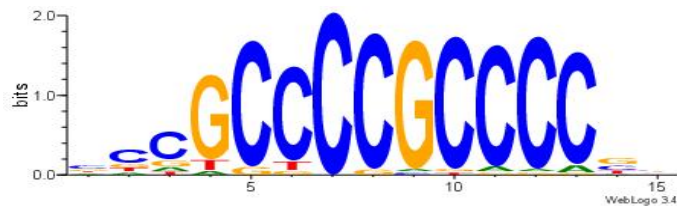


Dataset #: 4
Motif ID: 38
Motif name: cccGCCCCGCCCCsb
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2
Number of overlap: 14
Similarity score: 0.0904945

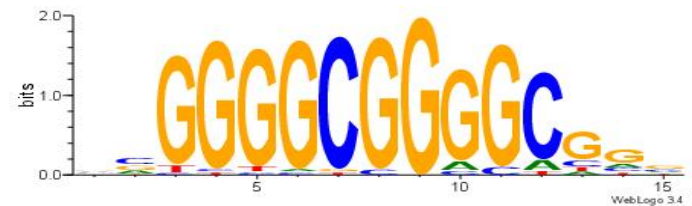
Alignment:

BCCGCCCCGCCCCBB
CCCCCTTGGGCCCC-

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB

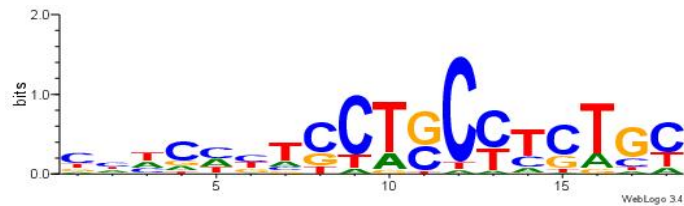


Dataset #: 5
 Motif ID: 52
 Motif name: TFM2
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 14
 Similarity score: 0.090969

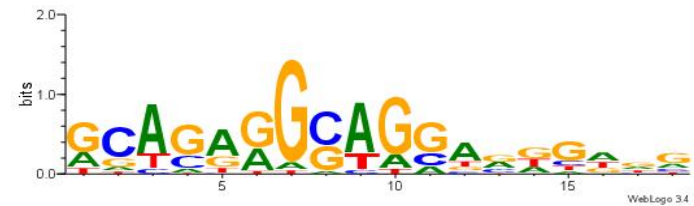
Alignment:

CHHCHBTCCTSCYTCTGC
 -CCCCCTTGGGCCCC---

Original motif Consensus sequence: CHHCHBTCCTSCYTCTGC



Reverse complement motif Consensus sequence: GCAGAKGSAGGABDGHDG



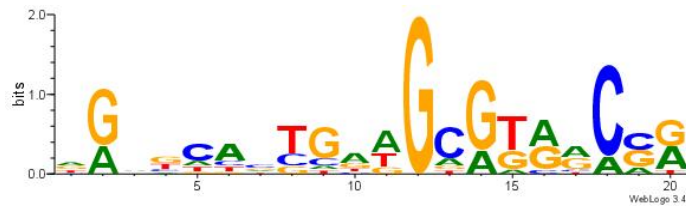
Dataset #: 3
 Motif ID: 31
 Motif name: Pax5
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1

Number of overlap: 14
 Similarity score: 0.0943783

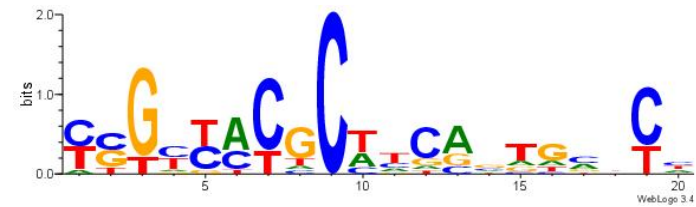
Alignment:

DGVBCABTGDWGCGRRCR
 GGGGCCCAAGGGG-----

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR



Reverse complement motif Consensus sequence:
 MSGKKRCGCWDCABTGGBCD



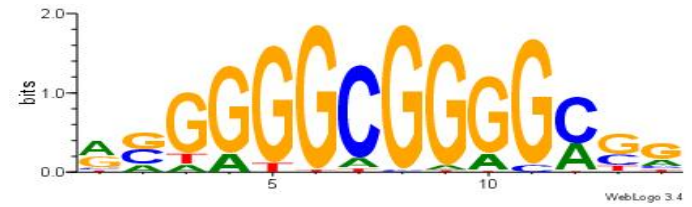
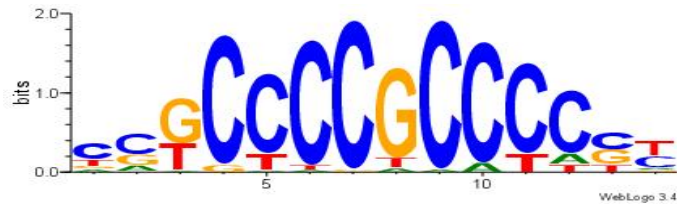
Dataset #: 2
 Motif ID: 7
 Motif name: Motif 7
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 13
 Similarity score: 0.588053

Alignment:

-MSGGGGCGGGGYSG
 GGGGCCCAAGGGG-

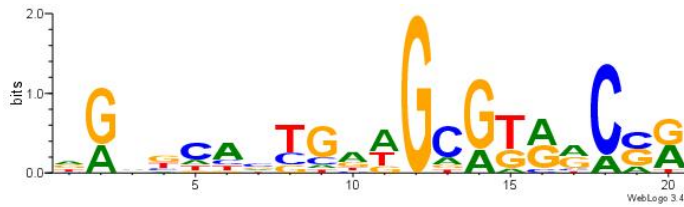
Original motif Consensus sequence: CSKCCCCGCCCSY

Reverse complement motif Consensus sequence: MSGGGGCGGGGY

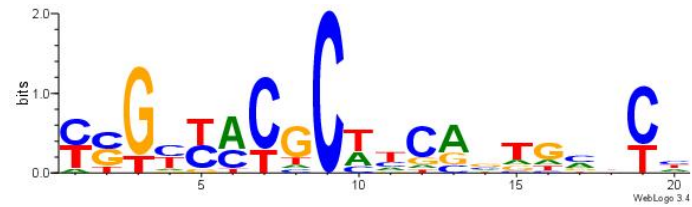


Dataset #: 3 Motif ID: 31 Motif name: Pax5

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBCD



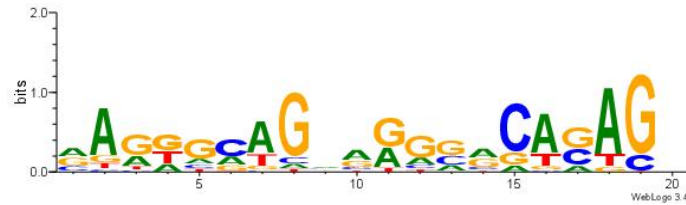
Best Matches for Motif ID 31 (Highest to Lowest)

Dataset #:	5
Motif ID:	55
Motif name:	TFM12
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:	0.0575851

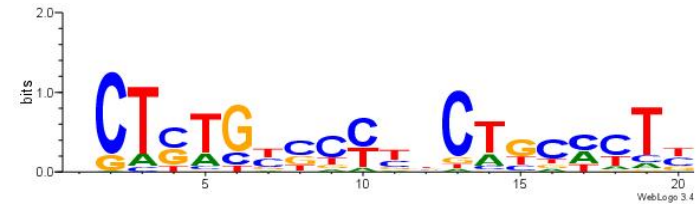
Alignment:

RAGKGMAGVRRGSRCASAGV
DGVBCABTGDWGCGRRCR

Original motif Consensus sequence: RAGKGMAGVRRGSRCASAGV



Reverse complement motif Consensus sequence:
VCTSTGKSCMKBCTRCYCTK



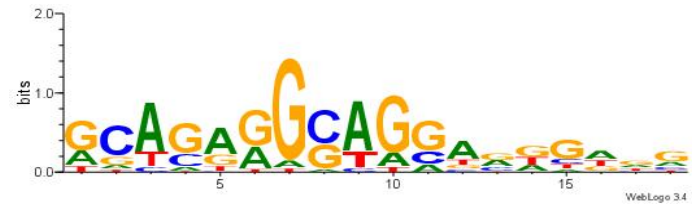
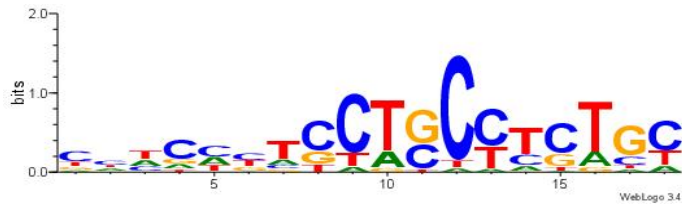
Dataset #:	5
Motif ID:	52
Motif name:	TFM2
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	18
Similarity score:	1.05466

Alignment:

--GCAGAKGSAGGABDGH
DGVBCABTGDWGCGRRCR

Original motif Consensus sequence: CHHCHBTCCTSCYTCTGC

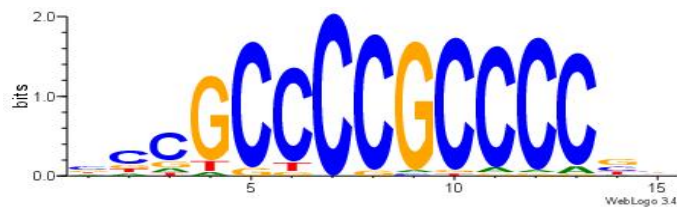
Reverse complement motif Consensus sequence:
GCAGAKGSAGGABDGH



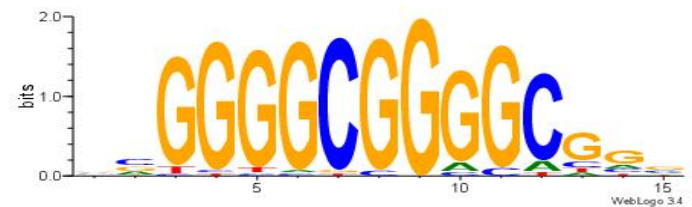
Dataset #: 4
 Motif ID: 38
 Motif name: cccGCCCCGCCCCsb
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 15
 Similarity score: 2.56328

Alignment:
 BBGGGGCGGGGCGGB-----
 MSGKKRCGCWDCABTGBBCD

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB



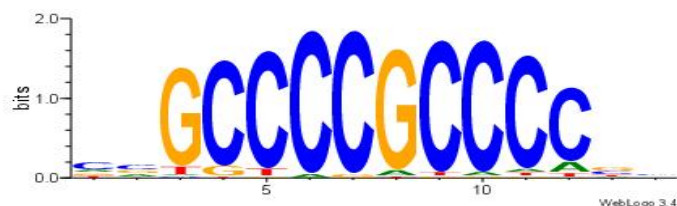
Dataset #: 4

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: 3.03874

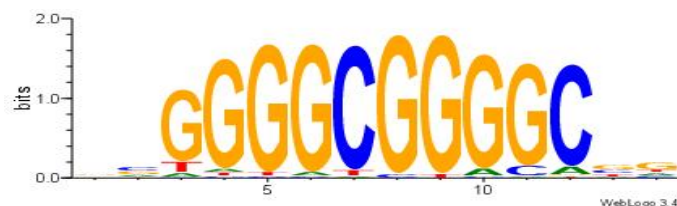
Alignment:

-----BBGGGGCGGGGCVD
 DGVBCABTGDWCGCKRRCR

Original motif Consensus sequence: HVGCCCCGCCCB



Reverse complement motif Consensus sequence: BBGGGGCGGGGC

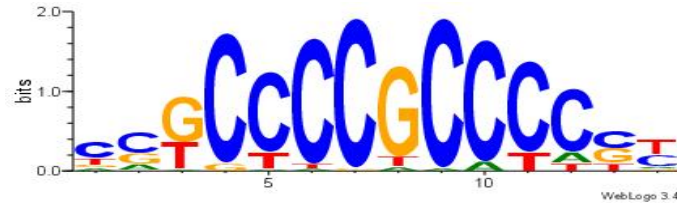


Dataset #: 2
 Motif ID: 7
 Motif name: Motif 7
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 14
 Similarity score: 3.04206

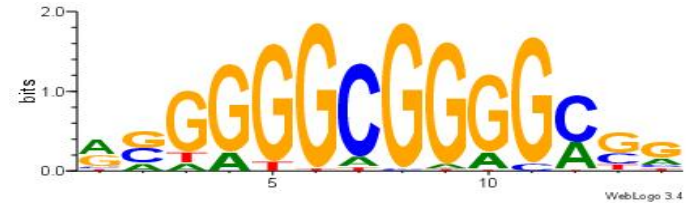
Alignment:

```
-----CSKCCCCGCCCCSY  
MSGKKRCGCWDCABTGBBCD
```

Original motif Consensus sequence: CSKCCCCGCCCCSY



Reverse complement motif Consensus sequence: MSGGGGCGGGGY



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

Original motif Consensus sequence: YGCGTG



Reverse complement motif Consensus sequence: CACGCM



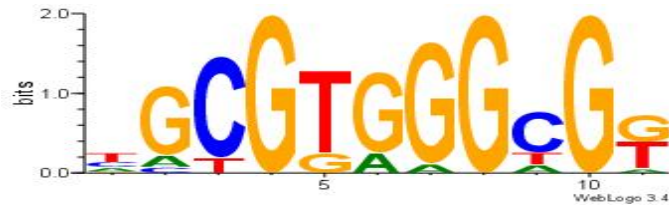
Best Matches for Motif ID 32 (Highest to Lowest)

Dataset #:	3
Motif ID:	23
Motif name:	Egr1
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1

Number of overlap: 6
Similarity score: 0

Alignment:
HGCGTGGGCGK
YGCGTG-----

Original motif Consensus sequence: HGCGTGGGCGK



Reverse complement motif Consensus sequence: YGCCCCACGCH



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

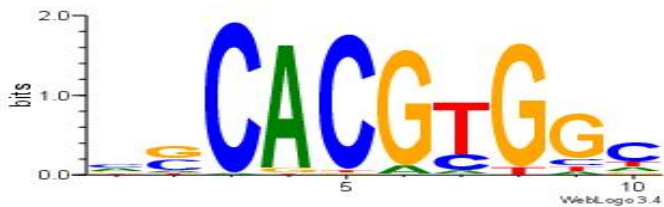
Reverse complement motif Consensus sequence: VCACGTBV



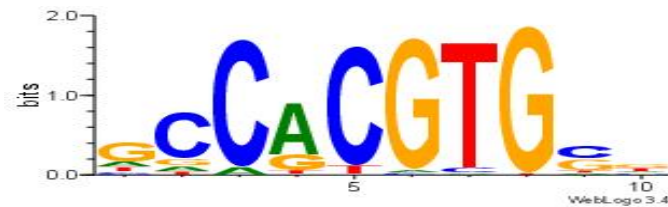
Dataset #: 3
 Motif ID: 33
 Motif name: Mycn
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3
 Number of overlap: 6
 Similarity score: 0.0377949

Alignment:
 GCCACGTGSD
 --YGCCGTG--

Original motif Consensus sequence: HSCACGTGGC



Reverse complement motif Consensus sequence: GCCACGTGSD

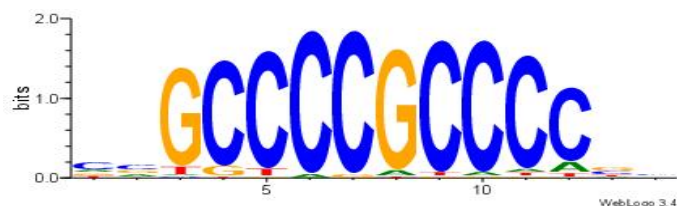


Dataset #: 4
 Motif ID: 36

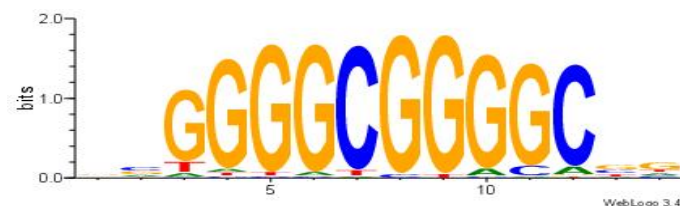
Motif name: csGCCCCGCCCCsc
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 5
 Number of overlap: 6
 Similarity score: 0.0396403

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

Original motif Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGCGGGGC

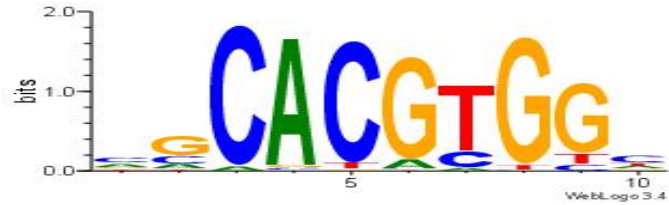


Dataset #: 3
 Motif ID: 34
 Motif name: Myc
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3
 Number of overlap: 6
 Similarity score: 0.0399214

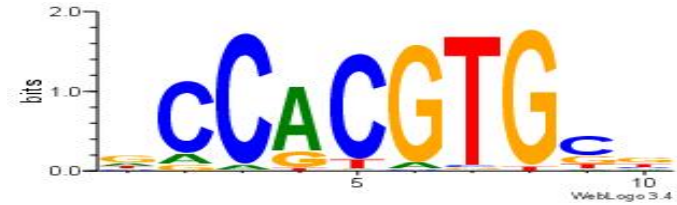
Alignment:

DCCACGTGCV
--YGCGTG--

Original motif Consensus sequence: VGCACGTGGH

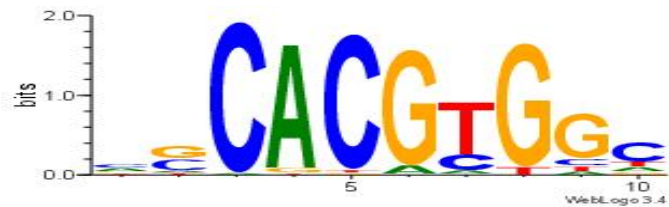


Reverse complement motif Consensus sequence: DCCACGTGCV



Dataset #: 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)

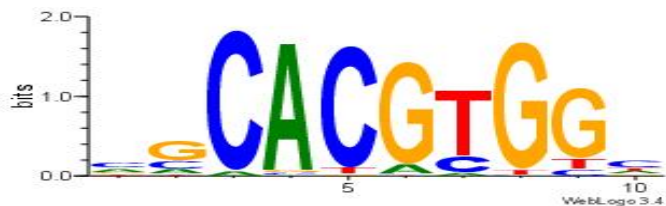
Dataset #:	3
Motif ID:	34
Motif name:	Myc
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1

Number of overlap: 10
Similarity score: 0

Alignment:

DCCACGTGCV
GCCACGTGSD

Original motif Consensus sequence: VGCACGTGGH



Reverse complement motif Consensus sequence: DCCACGTGCV



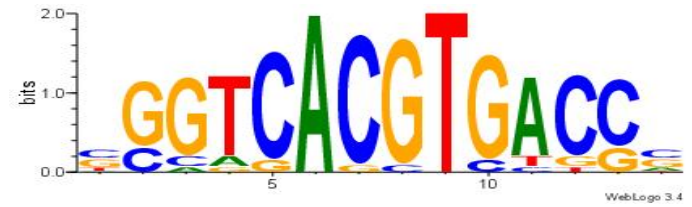
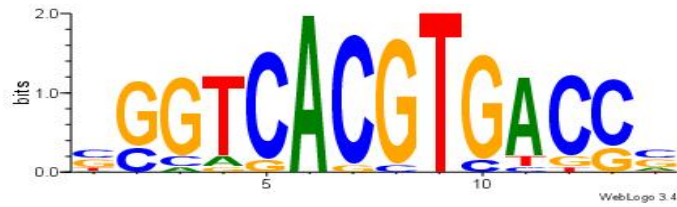
Dataset #: 4
Motif ID: 42
Motif name: sSGTCACGTGACSS
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 3
Number of overlap: 10
Similarity score: 0.0628441

Alignment:

SGGTCACGTGACCS
--GCCACGTGSD--

Original motif Consensus sequence: SGGTCACGTGACCS

Reverse complement motif Consensus sequence: SGGTCACGTGACCS



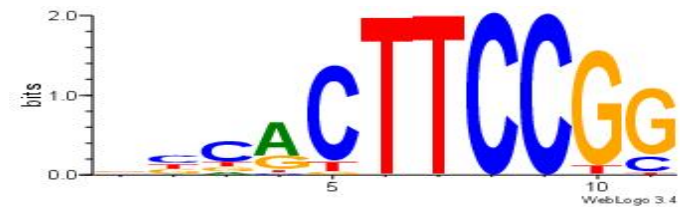
Dataset #: 3
 Motif ID: 35
 Motif name: GABPA
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 10
 Similarity score: 0.0884396

Alignment:
 VVCACTTCCGG
 GCCACGTGSD-

Original motif Consensus sequence: CCGGAAGTGVV



Reverse complement motif Consensus sequence: VVCACTTCCGG



Dataset #: 3
 Motif ID: 27

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

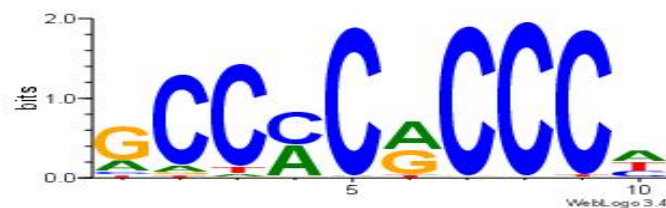
Alignment:

DGGGYGKGGC
 HSCACGTGGC

Original motif Consensus sequence: DGGGYGKGGC



Reverse complement motif Consensus sequence: GCCYCMCCCD

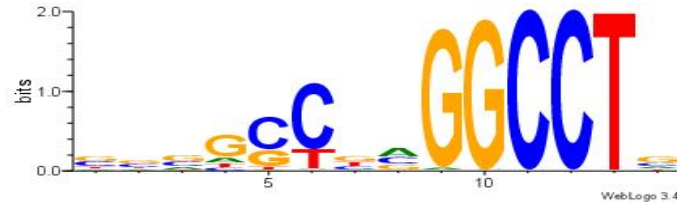


Dataset #: 3
 Motif ID: 22
 Motif name: Zfx
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 4
 Number of overlap: 10
 Similarity score: 0.0899944

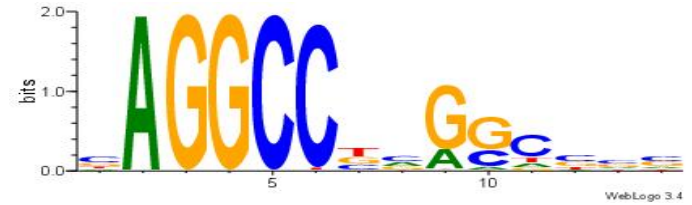
Alignment:

VAGGCCBBGGCVBB
---GCCACGTGSD-

Original motif Consensus sequence: BBVGCCBVGGCCTV

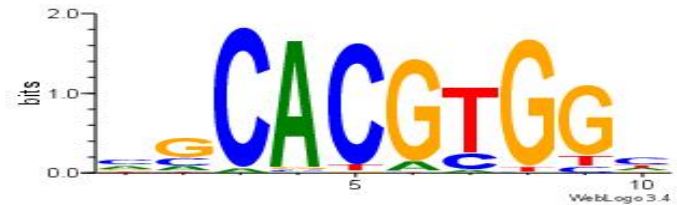


Reverse complement motif Consensus sequence: VAGGCCBBGGCVBB

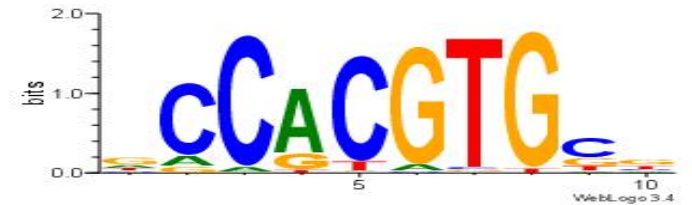


Dataset #: 3 Motif ID: 34 Motif name: Myc

Original motif Consensus sequence: VGCACGTGGH



Reverse complement motif Consensus sequence: DCCACGTGCV



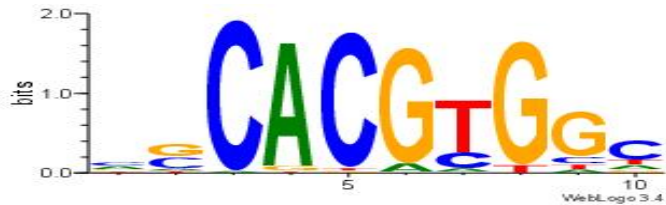
Best Matches for Motif ID 34 (Highest to Lowest)

Dataset #:	3
Motif ID:	33
Motif name:	Mycn
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1

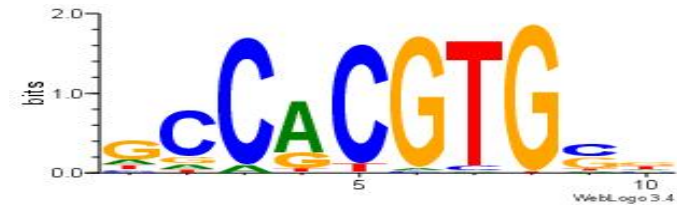
Number of overlap: 10
 Similarity score: 0

Alignment:
 GCCACGTGSD
 DCCACGTGCV

Original motif Consensus sequence: HSCACGTGGC



Reverse complement motif Consensus sequence: GCCACGTGSD

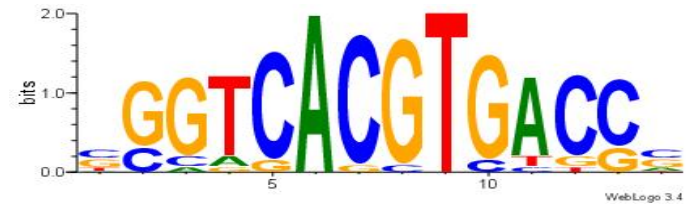
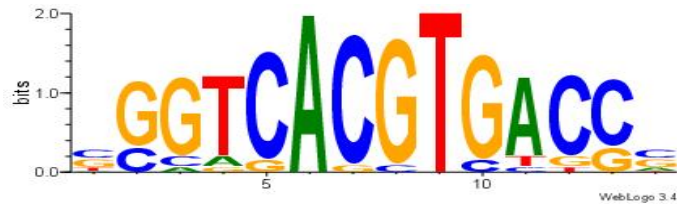


Dataset #: 4
 Motif ID: 42
 Motif name: sSGTCACGTGACSS
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 10
 Similarity score: 0.0646601

Alignment:
 SGGTCACGTGACCS
 --DCCACGTGCV--

Original motif Consensus sequence: SGGTCACGTGACCS

Reverse complement motif Consensus sequence: SGGTCACGTGACCS



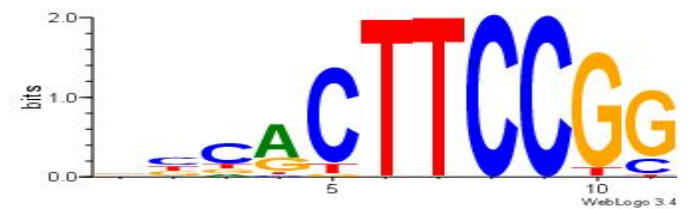
Dataset #: 3
 Motif ID: 35
 Motif name: GABPA
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 10
 Similarity score: 0.0840341

Alignment:
 VVCACTTCCGG
 DCCACGTGCV-

Original motif Consensus sequence: CCGGAAGTGVV



Reverse complement motif Consensus sequence: VVCACTTCCGG



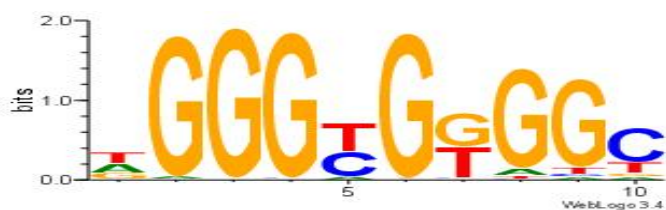
Dataset #: 3
 Motif ID: 27

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

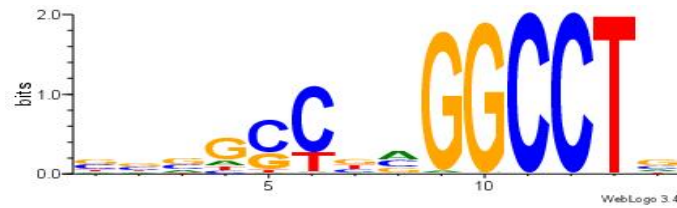


Dataset #: 3
 Motif ID: 22
 Motif name: Zfx
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 10
 Similarity score: 0.0925451

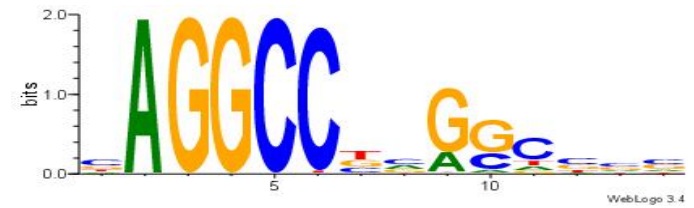
Alignment:

VAGGCCBBGGCVBB
---DCCACGTGCV-

Original motif Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif Consensus sequence: VAGGCCBBGGCVBB

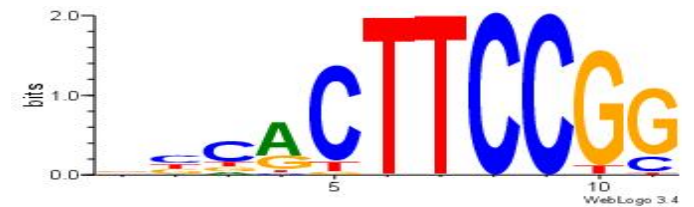


Dataset #: 3 Motif ID: 35 Motif name: GABPA

Original motif Consensus sequence: CCGAAGTGVV



Reverse complement motif Consensus sequence: VVCACTTCCGG



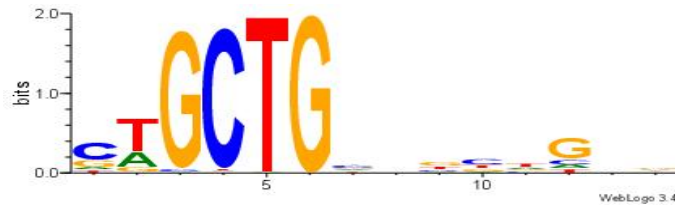
Best Matches for Motif ID 35 (Highest to Lowest)

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

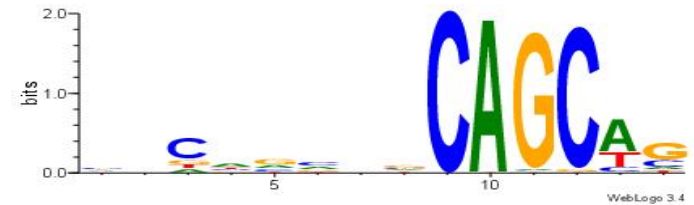
Number of overlap: 11
Similarity score: 0.0293518

Alignment:
HVCDBBDBCAGCAG
VVCACTTCCGG---

Original motif Consensus sequence: CTGCTGBDBBDGBD



Reverse complement motif Consensus sequence: HVCDBBDBCAGCA

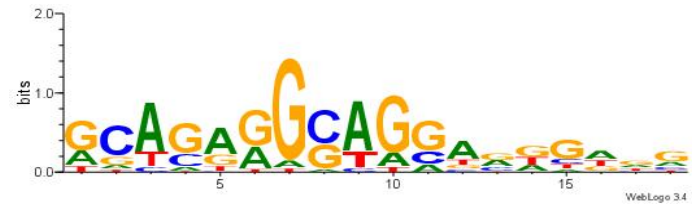
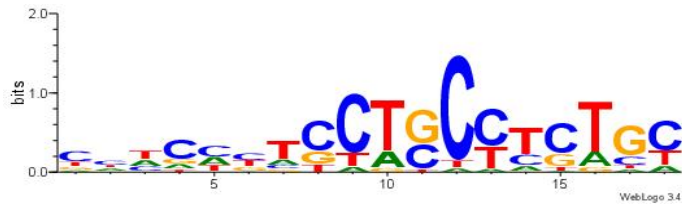


Dataset #: 5
Motif ID: 52
Motif name: TFM2
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 11
Similarity score: 0.0304867

Alignment:
CHHCHBTCCTSCYTCTGC
VVCACTTCCGG-----

Original motif Consensus sequence: CHHCHBTCCTSCYTCTGC

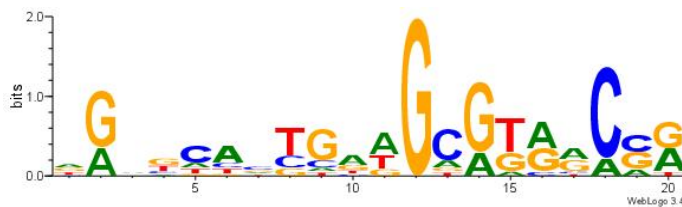
Reverse complement motif Consensus sequence:
GCAGAKGSAGGABDGHDG



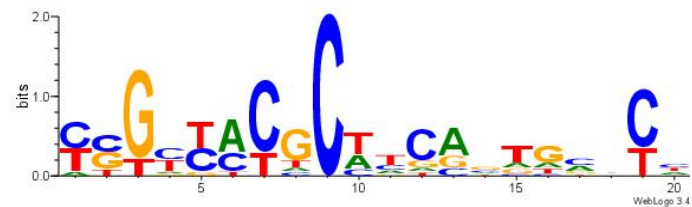
Dataset #: 3
 Motif ID: 31
 Motif name: Pax5
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 8
 Number of overlap: 11
 Similarity score: 0.0353243

Alignment:
 DGVCABTGDWCGKRRCSR
 -----VVCACTTCCGG--

Original motif Consensus sequence: DGVCABTGDWCGKRRCSR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD



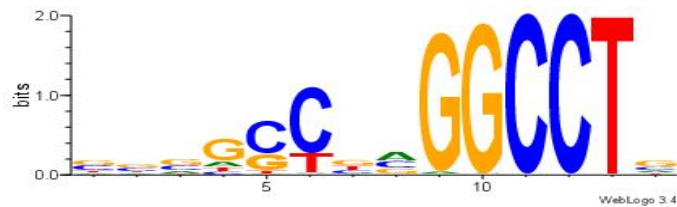
Dataset #: 3

Motif ID: 22
 Motif name: Zfx
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 4
 Number of overlap: 11
 Similarity score: 0.0364314

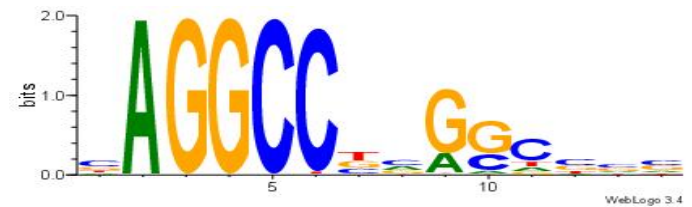
Alignment:

BBVGCCBVGGCCTV
 VVCACTTCCGG---

Original motif Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif Consensus sequence: VAGGCCBBGGCV

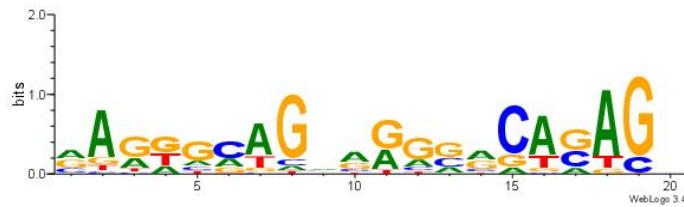


Dataset #: 5
 Motif ID: 55
 Motif name: TFM12
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 5
 Number of overlap: 11
 Similarity score: 0.037633

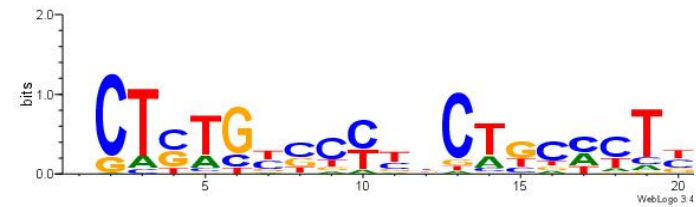
Alignment:

RAGKGMAGVRRGSRCASAGV
-----CCGGAAGTGTV-----

Original motif Consensus sequence: RAGKGMAGVRRGSRCASAGV

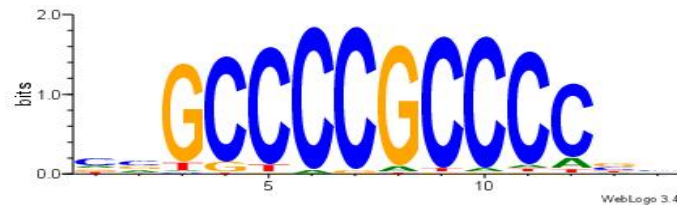


Reverse complement motif Consensus sequence: VCTSTGKSCMKBCTRCYCTK

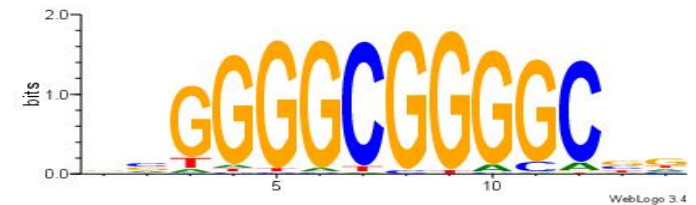


Dataset #: 4 Motif ID: 36 Motif name: csGCCCCGCCCCsc

Original motif Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGC



Best Matches for Motif ID 36 (Highest to Lowest)

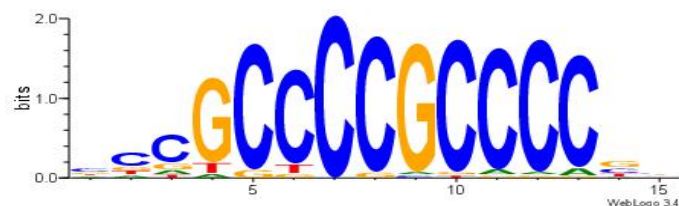
Dataset #:	4
Motif ID:	38
Motif name:	cccGCCCCGCCCCsb
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward

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

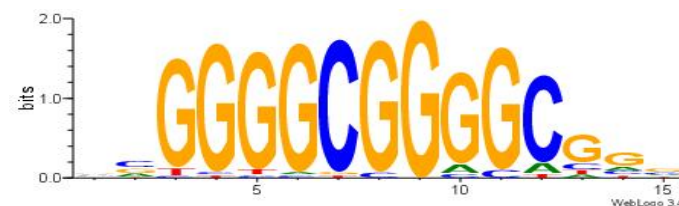
Alignment:

BCCGCCCCGCCCCBB
-HVGCCCCGCCCCBB

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB

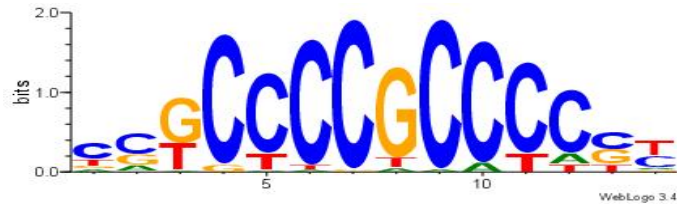


Dataset #: 2
Motif ID: 7
Motif name: Motif 7
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 14
Similarity score: 0.0117332

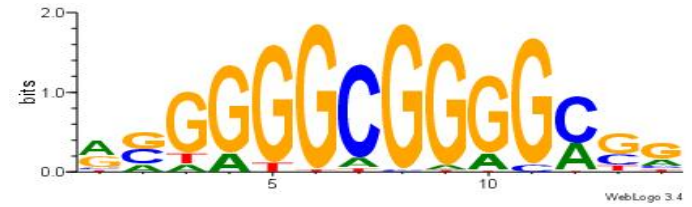
Alignment:

CSKCCCCGCCCCSY
HVGCCCCGCCCCBB

Original motif Consensus sequence: CSKCCCCGCCCSY



Reverse complement motif Consensus sequence: MSGGGCGGGGY

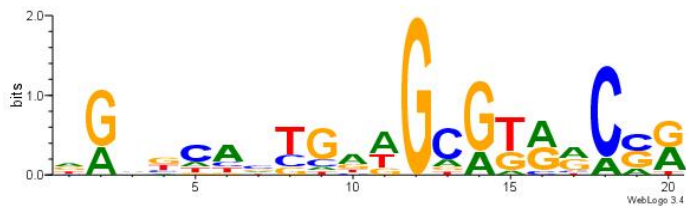


Dataset #: 3
 Motif ID: 31
 Motif name: Pax5
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0.0747029

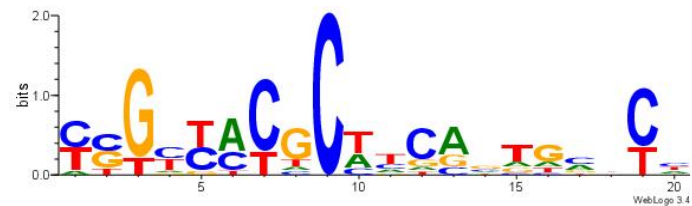
Alignment:

```
MSGKKRCGCWDCABTGBBCD
-----HVGCCCCGCCCB
```

Original motif Consensus sequence: DGVBCABTGDWGCGRCSR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD

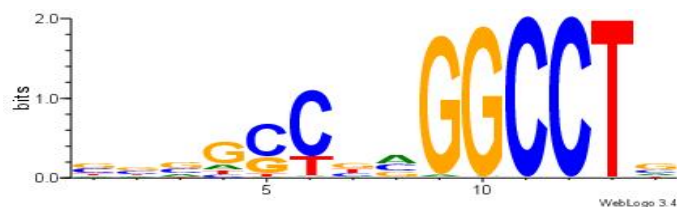


Dataset #: 3
 Motif ID: 22
 Motif name: Zfx
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0.0884848

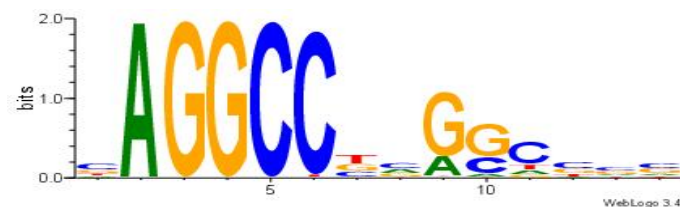
Alignment:

BBVGCCBVGGCCTV
 BBGGGGCGGGGCVD

Original motif Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif Consensus sequence: VAGGCCBBGGCCTV



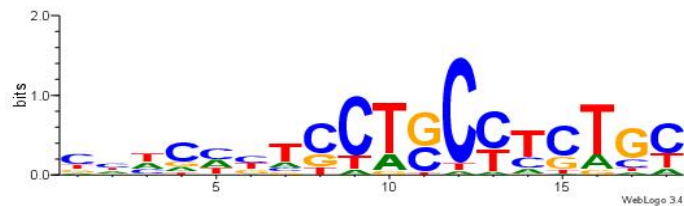
Dataset #: 5
 Motif ID: 52
 Motif name: TFM2
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 14

Similarity score: 0.095556

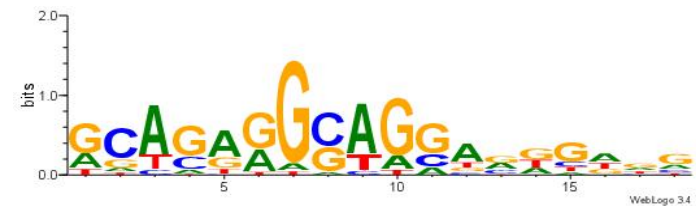
Alignment:

```
CHHCHBTCCTSCYTCTGC  
---HVGCCCCGCCCCBB-
```

Original motif Consensus sequence: CHHCHBTCCTSCYTCTGC

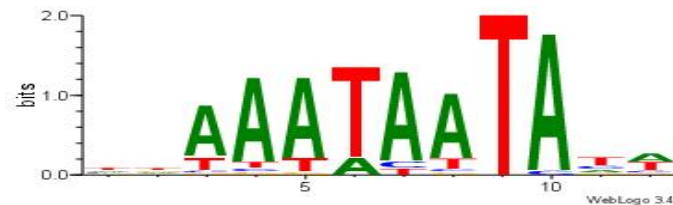


Reverse complement motif Consensus sequence:
GCAGAKGSAGGABDGH DG

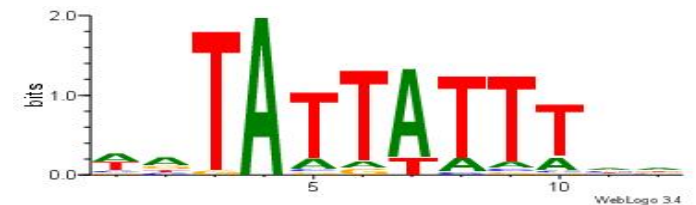


Dataset #: 4 Motif ID: 37 Motif name: tkAAATAATAtw

Original motif Consensus sequence: HDAAATAATAHW



Reverse complement motif Consensus sequence: WHTATTATTTDH



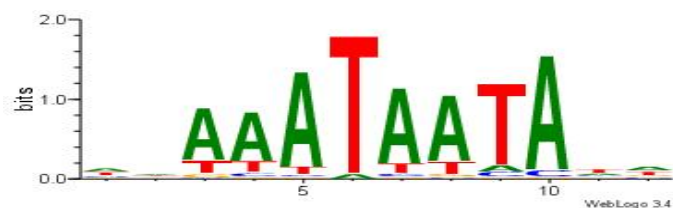
Best Matches for Motif ID 37 (Highest to Lowest)

Dataset #:	4
Motif ID:	41
Motif name:	wwAAATAATAtw
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif

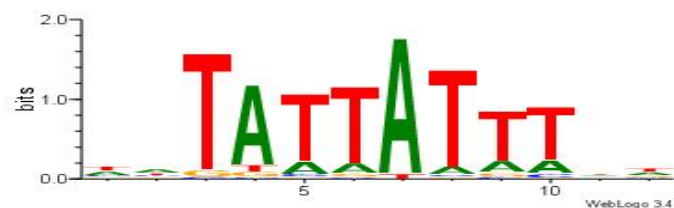
Direction: Forward
 Position number: 1
 Number of overlap: 12
 Similarity score: 0

Alignment:
 HDAAATAATADD
 HDAAATAATAHW

Original motif Consensus sequence: HDAAATAATADD



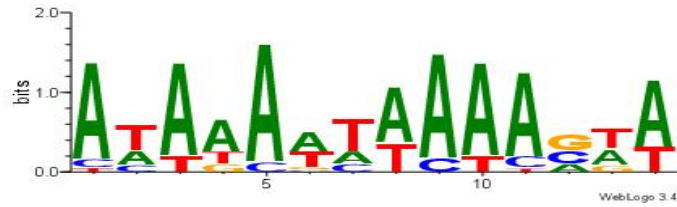
Reverse complement motif Consensus sequence: DDTATTATTTDH



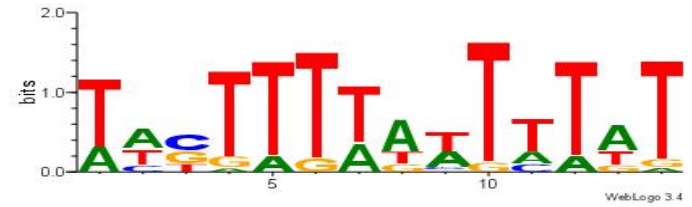
Dataset #: 2
 Motif ID: 3
 Motif name: Motif 3
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 12
 Similarity score: 0.0522317

Alignment:
 TWSTTTWAWTTTWT
 -WHTATTATTTDH-

Original motif Consensus sequence: AWAAAWTWAAASWA



Reverse complement motif Consensus sequence: TWSTTTWAWTTTVA



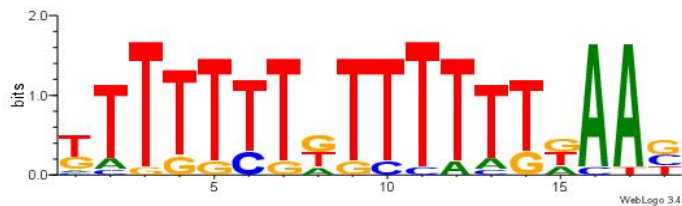
Dataset #: 5
 Motif ID: 53
 Motif name: TFM3
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3
 Number of overlap: 12
 Similarity score: 0.0631559

Alignment:

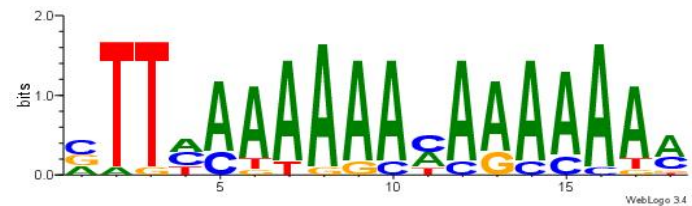
```

BTTHAAAAAYAAAAAR
--HDAAATAATAHW----
    
```

Original motif Consensus sequence: KTTTTTKTTTTTDAAB



Reverse complement motif Consensus sequence: BTTHAAAAAYAAAAAR

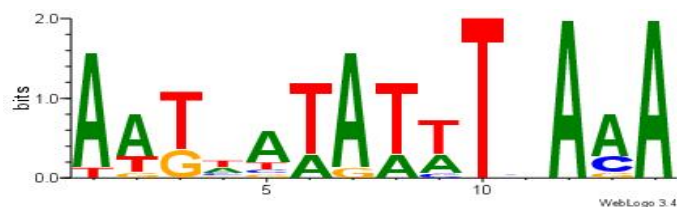


Dataset #: 2
 Motif ID: 9
 Motif name: Motif 9
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 12
 Similarity score: 0.0641975

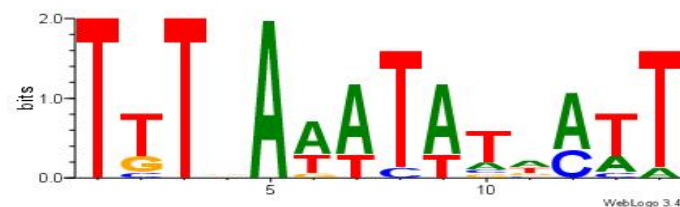
Alignment:

AATHATATWTHAAA
 --WHTATTATTTDH

Original motif Consensus sequence: AATHATATWTHAAA



Reverse complement motif Consensus sequence: TTTDAWATATHAT



Dataset #: 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

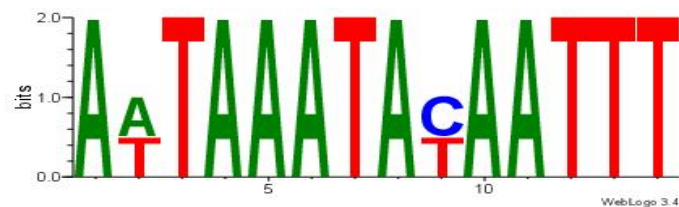
Similarity score: 0.0704475

Alignment:

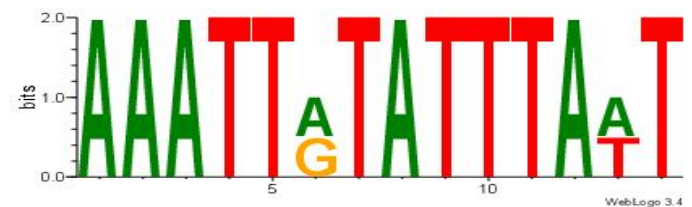
AAATTKTATTTAWT

-WHTATTATTTDH-

Original motif Consensus sequence: AWTAAATAYAATTT

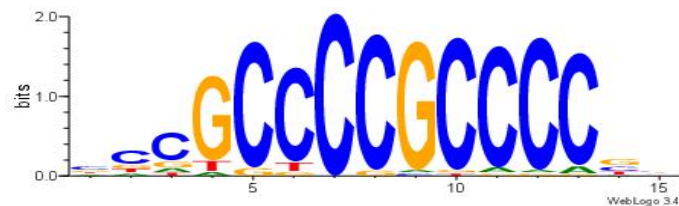


Reverse complement motif Consensus sequence: AAATTKTATTTAWT

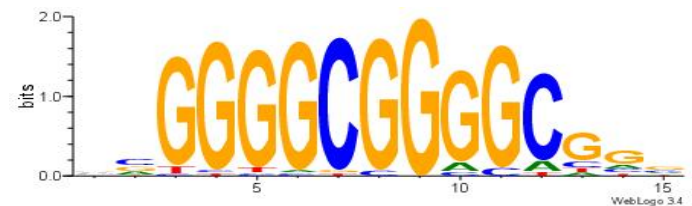


Dataset #: 4 Motif ID: 38 Motif name: cccGCCCGCCCCsb

Original motif Consensus sequence: BCCGCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGCGGB



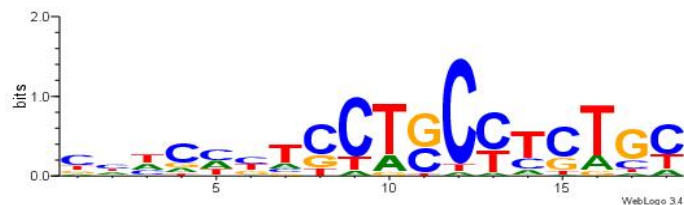
Best Matches for Motif ID 38 (Highest to Lowest)

Dataset #:	5
Motif ID:	52
Motif name:	TFM2
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif

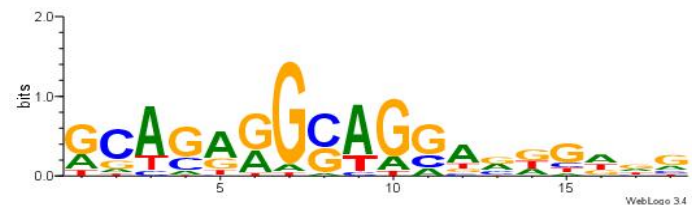
Direction: Forward
Position number: 3
Number of overlap: 15
Similarity score: 0.09558

Alignment:
CHHCHBTCCTSCYTCTGC
--BCCGCCCCGCCCCBB--

Original motif Consensus sequence: CHHCHBTCCTSCYTCTGC



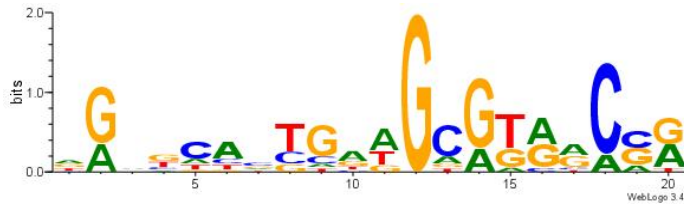
Reverse complement motif Consensus sequence: GCAGAKGSAGGABDGHG



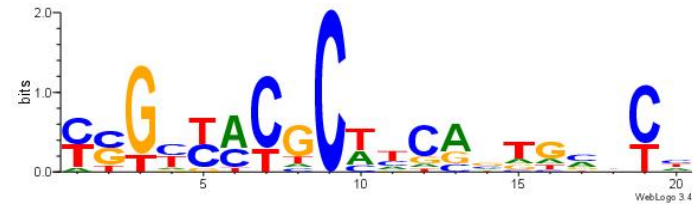
Dataset #: 3
Motif ID: 31
Motif name: Pax5
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 15
Similarity score: 0.0992376

Alignment:
MSGKKRCGCWDCABTGBBCD
BBGGGGCGGGCGGB-----

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD

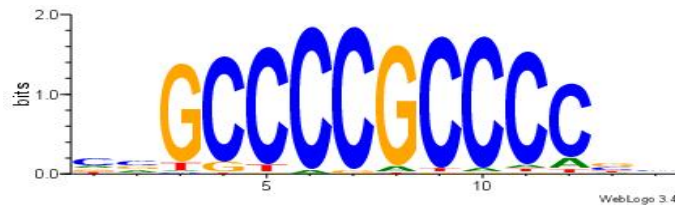


Dataset #: 4
Motif ID: 36
Motif name: csGCCCCGCCCCsc
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 14
Similarity score: 0.5

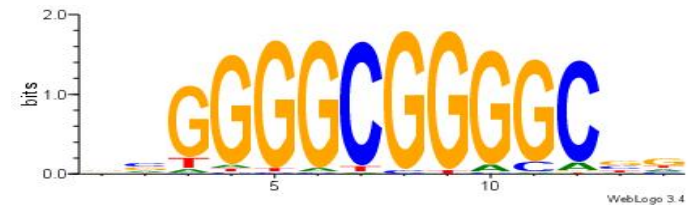
Alignment:

BBGGGGCGGGGCVD-
BBGGGGCGGGGCGB

Original motif Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif Consensus sequence: BBGGGGCGGGGC

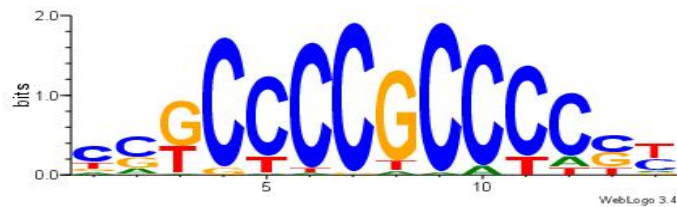


Dataset #: 2
 Motif ID: 7
 Motif name: Motif 7
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0.513015

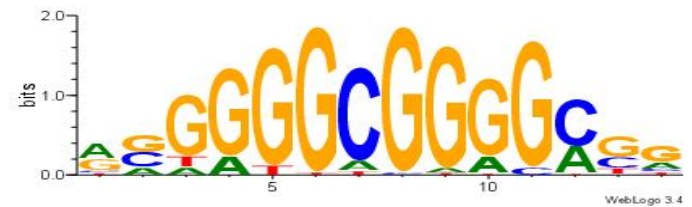
Alignment:

-CSKCCCCGCCCCSY
 BCCGCCCCGCCCCBB

Original motif Consensus sequence: CSKCCCCGCCCCSY



Reverse complement motif Consensus sequence: MSGGGGCGGGGY



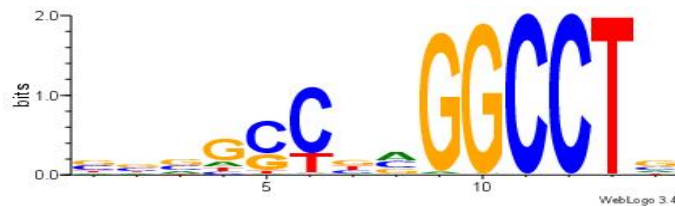
Dataset #: 3
 Motif ID: 22
 Motif name: Zfx
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 14

Similarity score: 0.574434

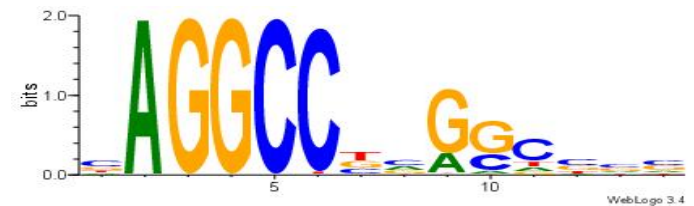
Alignment:

BBVGCCBVGCCCTV-
BCCGCCCCGCCCCBB

Original motif Consensus sequence: BBVGCCBVGCCCTV



Reverse complement motif Consensus sequence: VAGGCCBBGGCV



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

Original motif Consensus sequence: DCAGCCAATVR



Reverse complement motif Consensus sequence: MBATTGGCTGH



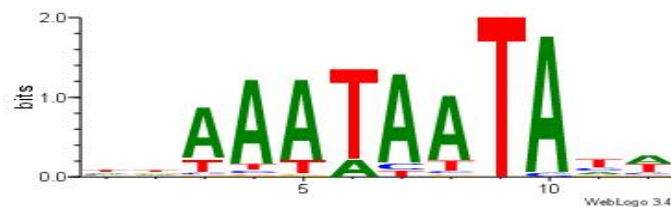
Best Matches for Motif ID 39 (Highest to Lowest)

Dataset #:	4
Motif ID:	37
Motif name:	tkAAATAATAtw
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward

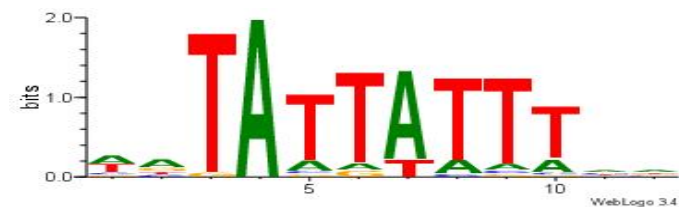
Position number: 2
 Number of overlap: 11
 Similarity score: 0.0559269

Alignment:
 WHTATTATTTDH
 -MBATTGGCTGH

Original motif Consensus sequence: HDAAATAATAHW



Reverse complement motif Consensus sequence: WHTATTATTTDH

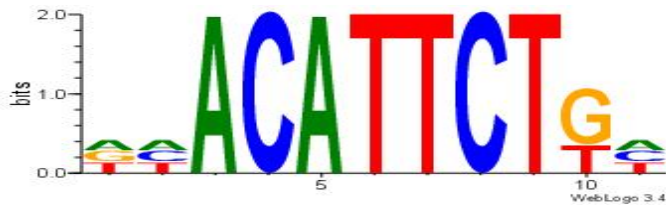


Dataset #: 4
 Motif ID: 44
 Motif name: dhACATTCTkh
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.0588235

Alignment:
 HCAGAATGTHD
 DCAGCCAATVR

Original motif Consensus sequence: DHACATTCTGH

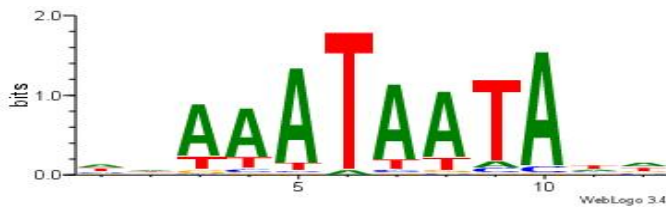
Reverse complement motif Consensus sequence: HCAGAATGTHD



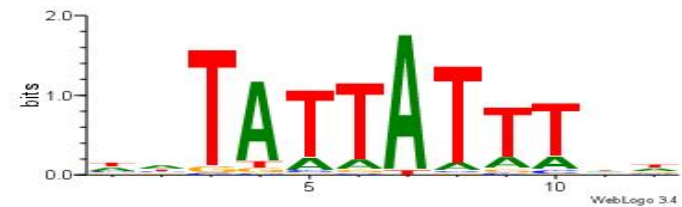
Dataset #: 4
 Motif ID: 41
 Motif name: wwAAATAATAtw
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 11
 Similarity score: 0.0597643

Alignment:
 DDTATTATTTDH
 -MBATTGGCTGH

Original motif Consensus sequence: HDAAATAATADD



Reverse complement motif Consensus sequence: DDTATTATTTDH

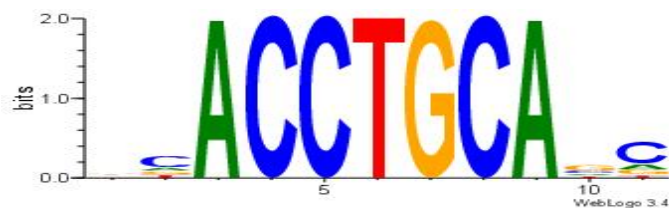


Dataset #: 4

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

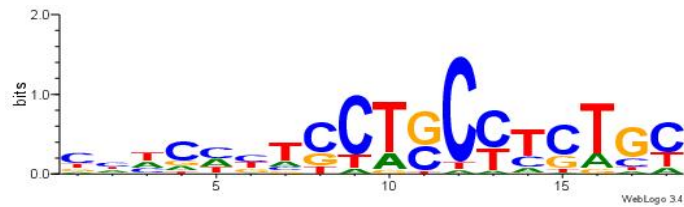


Dataset #: 5
 Motif ID: 52
 Motif name: TFM2
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.0635874

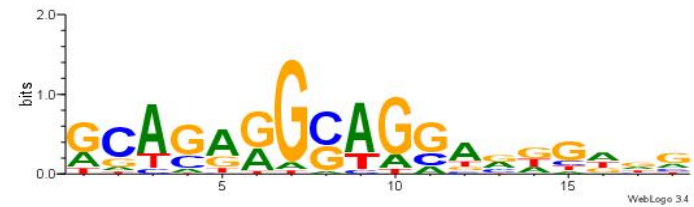
Alignment:

GCAGAKGSAGGABDGH
MBATTGGCTGH-----

Original motif Consensus sequence: CHHCHBTCCTSCYTCTGC

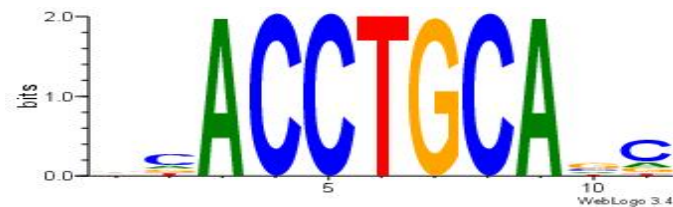


Reverse complement motif Consensus sequence:
GCAGAKGSAGGABDGH

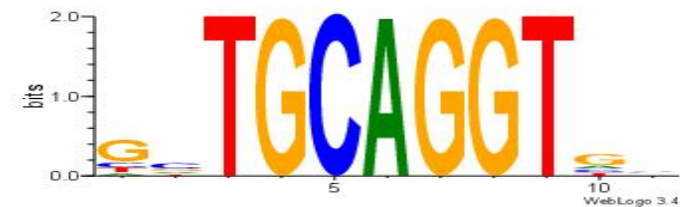


Dataset #: 4 Motif ID: 40 Motif name: kcACCTGCAGc

Original motif Consensus sequence: BCACCTGCABC



Reverse complement motif Consensus sequence: GBTGCAGGTGB



Best Matches for Motif ID 40 (Highest to Lowest)

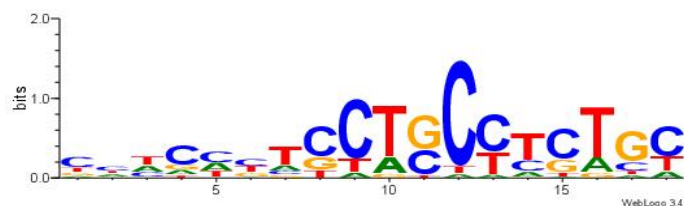
Dataset #:	5
Motif ID:	52
Motif name:	TFM2
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward

Position number: 4
Number of overlap: 11
Similarity score: 0.0194012

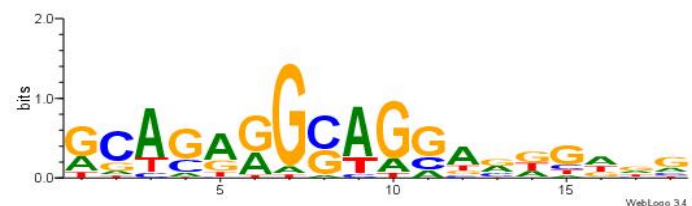
Alignment:

GCAGAKGSAGGABDGH
---GBTGCAGGTGB---

Original motif Consensus sequence: CHHCHBTCCTSCYTCTGC



Reverse complement motif Consensus sequence:
GCAGAKGSAGGABDGH



Dataset #: 4
Motif ID: 43
Motif name: wTACwGTAsw
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: HVTACWGATABD



Reverse complement motif Consensus sequence: DBTACWGTAHVH

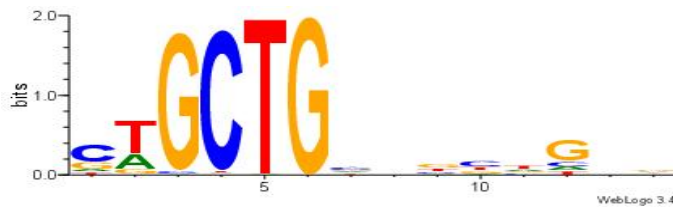


Dataset #: 5
Motif ID: 50
Motif name: TFF11
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 3
Number of overlap: 11
Similarity score: 0.0222944

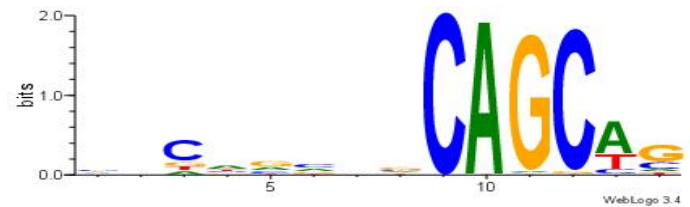
Alignment:

CTGCTGBDBBDGDB
--GBTGCAGGTGB--

Original motif Consensus sequence: CTGCTGBDBBDGDB



Reverse complement motif Consensus sequence: HVCDBBDBCAGCA

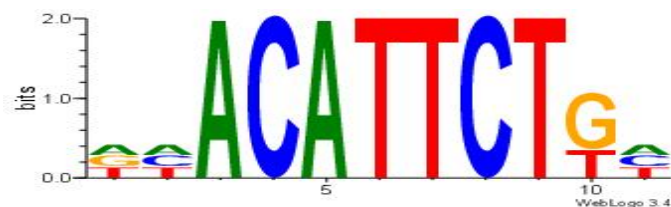


Dataset #: 4
 Motif ID: 44
 Motif name: dhACATTCTkh
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.0254134

Alignment:

DHACATTCTGH
 BCACCTGCABC

Original motif Consensus sequence: DHACATTCTGH



Reverse complement motif Consensus sequence: HCAGAATGTHD



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

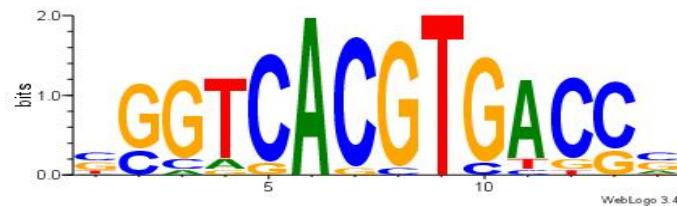
Similarity score: 0.031338

Alignment:

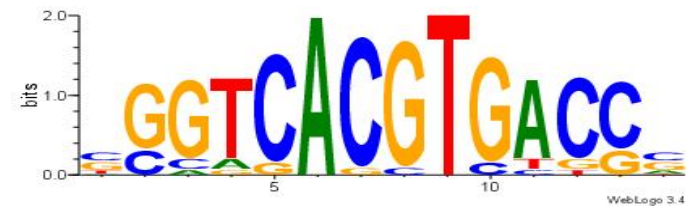
SGGTCACGTGACCS

---BCACCTGCABC

Original motif Consensus sequence: SGGTCACGTGACCS

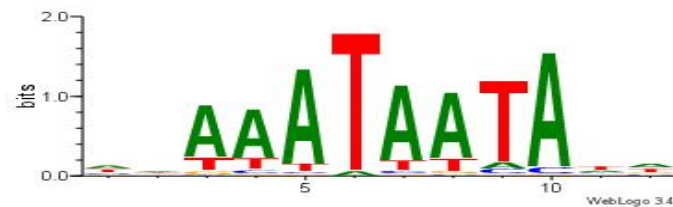


Reverse complement motif Consensus sequence: SGGTCACGTGACCS

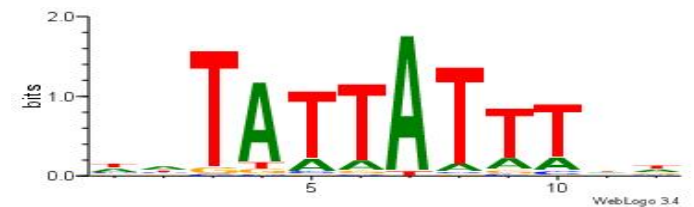


Dataset #: 4 Motif ID: 41 Motif name: wwAAATAATAtw

Original motif Consensus sequence: HDAAATAATADD



Reverse complement motif Consensus sequence: DDTATTATTTDH



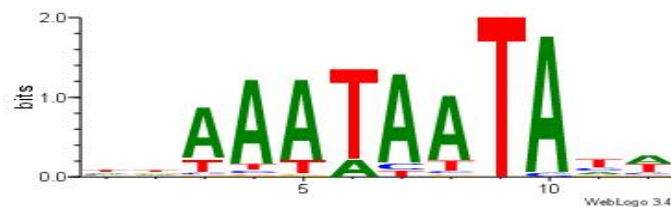
Best Matches for Motif ID 41 (Highest to Lowest)

Dataset #:	4
Motif ID:	37
Motif name:	tkAAATAATAtw
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward

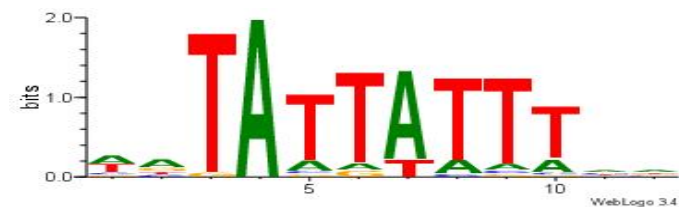
Position number: 1
 Number of overlap: 12
 Similarity score: 0

Alignment:
 HDAAATAATAHW
 HDAAATAATADD

Original motif Consensus sequence: HDAAATAATAHW



Reverse complement motif Consensus sequence: WHTATTATTTDH

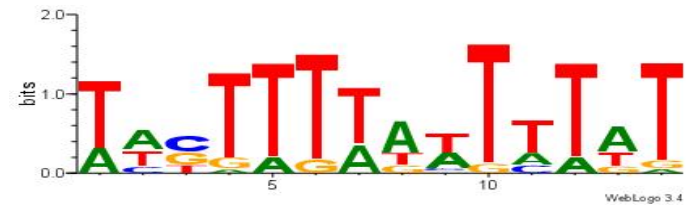
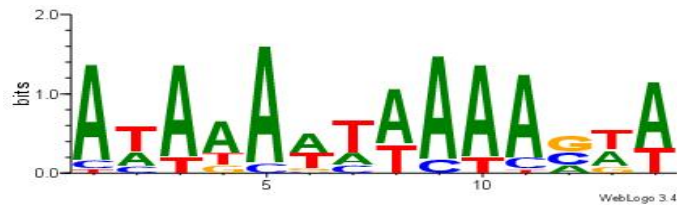


Dataset #: 2
 Motif ID: 3
 Motif name: Motif 3
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 12
 Similarity score: 0.0536028

Alignment:
 AWAAAWTWAAASWA
 -HDAAATAATADD-

Original motif Consensus sequence: AWAAAWTWAAASWA

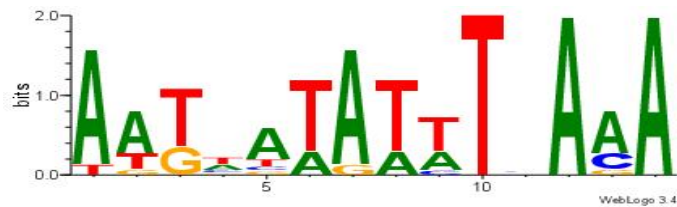
Reverse complement motif Consensus sequence: TWSTTTWAWTTT



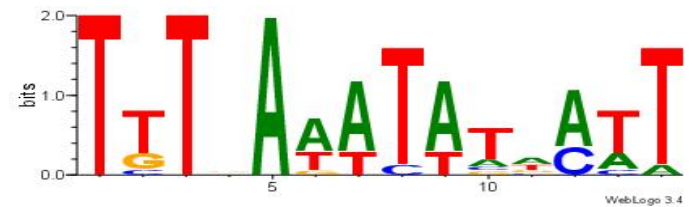
Dataset #: 2
 Motif ID: 9
 Motif name: Motif 9
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 12
 Similarity score: 0.0591821

Alignment:
 AATHATATWTHAAA
 --DDTATTATTTDH

Original motif Consensus sequence: AATHATATWTHAAA



Reverse complement motif Consensus sequence: TTTDAWATATHAT



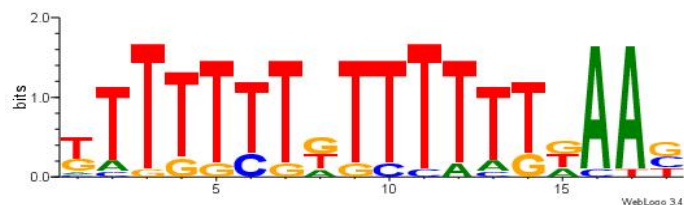
Dataset #: 5

Motif ID: 53
 Motif name: TFM3
 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: 0.0645351

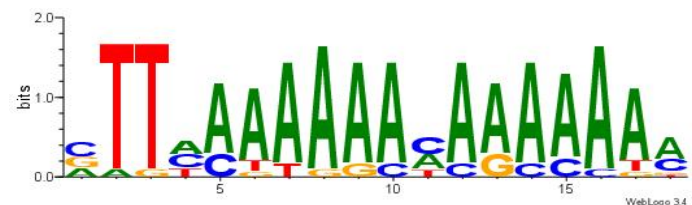
Alignment:

BTTHAAAAAYAAAAAR
 --HDAAATAATADD----

Original motif Consensus sequence: KTTTTTKTTTTTDAAB



Reverse complement motif Consensus sequence: BTTHAAAAAYAAAAAR



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

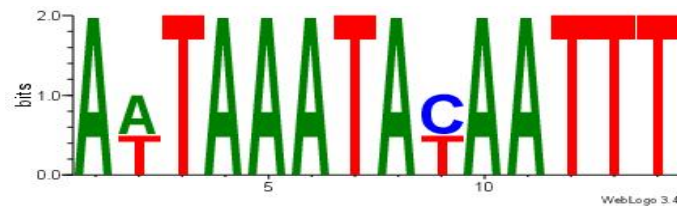
Similarity score: 0.0715278

Alignment:

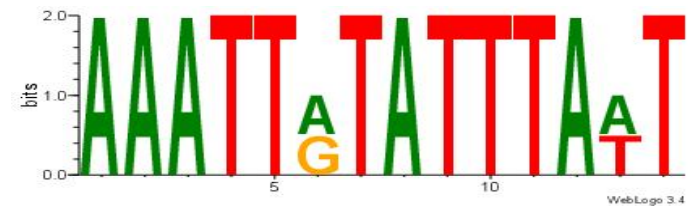
AAATTKTATTTAWT

-DDTATTATTTDH-

Original motif Consensus sequence: AWTAAATAYAATTT

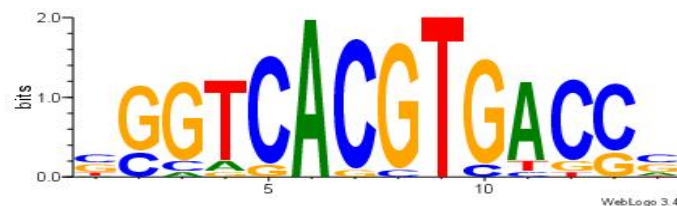


Reverse complement motif Consensus sequence: AAATTKTATTTAWT

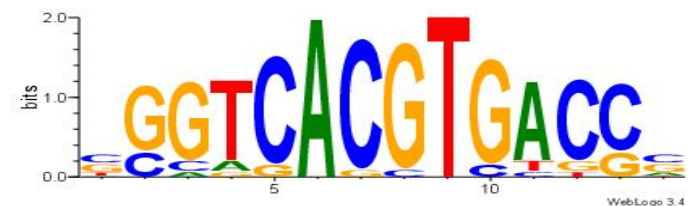


Dataset #: 4 Motif ID: 42 Motif name: sSGTCACGTGACCS

Original motif Consensus sequence: SGGTCACGTGACCS



Reverse complement motif Consensus sequence: SGGTCACGTGACCS



Best Matches for Motif ID 42 (Highest to Lowest)

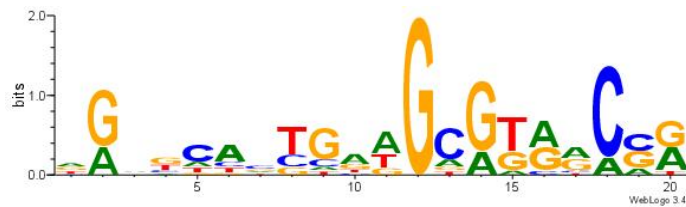
Dataset #:	3
Motif ID:	31
Motif name:	Pax5
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward

Position number: 7
 Number of overlap: 14
 Similarity score: 0.0353836

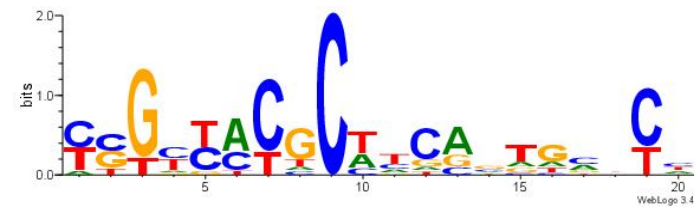
Alignment:

DGVBCABTGDWGCGRRCR
 -----SSGTCACGTGACCS

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD

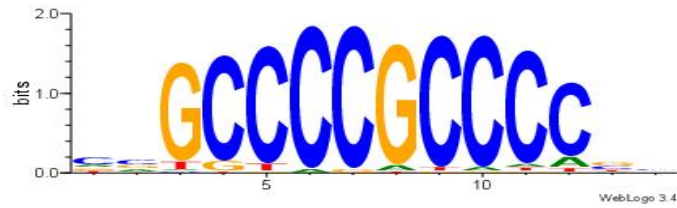


Dataset #: 4
 Motif ID: 36
 Motif name: csGCCCCGCCCCsc
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0.0374195

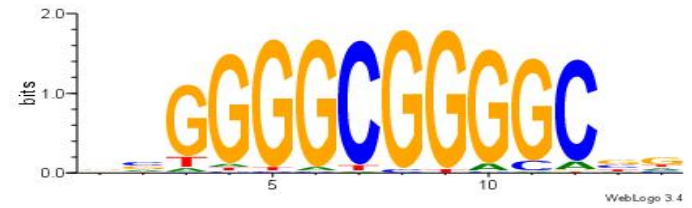
Alignment:

BBGGGGCGGGCVD
 SSGTCACGTGACCS

Original motif Consensus sequence: HVGCCCCGCCCB



Reverse complement motif Consensus sequence: BBGGGCGGGGC

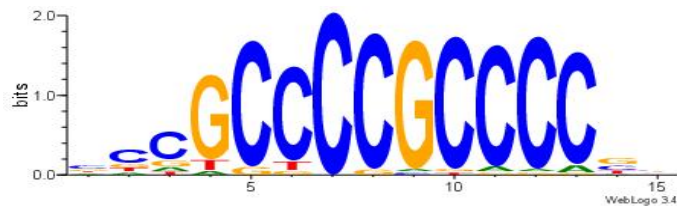


Dataset #: 4
Motif ID: 38
Motif name: cccGCCCCGCCCBsb
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 14
Similarity score: 0.0417054

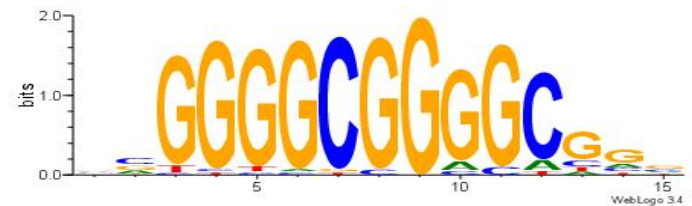
Alignment:

BCCGCCCCGCCCB
SGGTCACGTGACCS-

Original motif Consensus sequence: BCCGCCCCGCCCB



Reverse complement motif Consensus sequence: BBGGGCGGGGCGGB

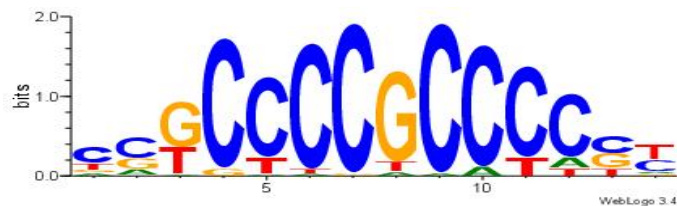


Dataset #: 2
 Motif ID: 7
 Motif name: Motif 7
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0.0469233

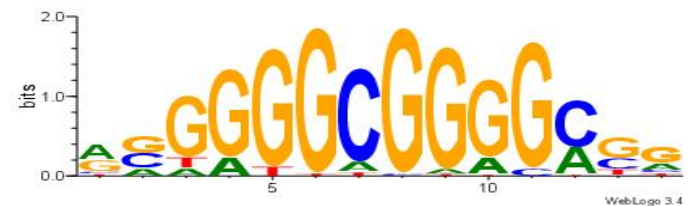
Alignment:

MSGGGGCGGGYSG
 SGGTCACGTGACCS

Original motif Consensus sequence: CSKCCCCGCCCSY



Reverse complement motif Consensus sequence: MSGGGGCGGGY



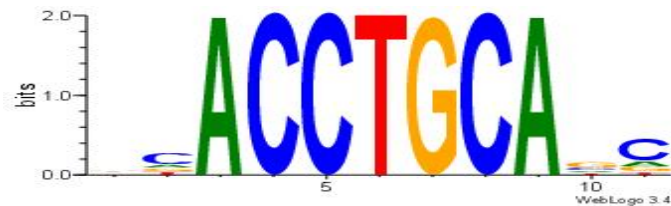
Dataset #: 4
 Motif ID: 40
 Motif name: kcACCTGCAGc
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 11

Similarity score: 1.53093

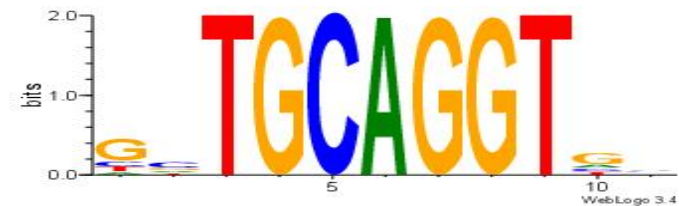
Alignment:

---BCACCTGCABC
SGGTCACGTGACCS

Original motif Consensus sequence: BCACCTGCABC



Reverse complement motif Consensus sequence: GBTGCAGGTGB



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

Original motif Consensus sequence: HVTACWGATABD



Reverse complement motif Consensus sequence: DBTACWGTAVH



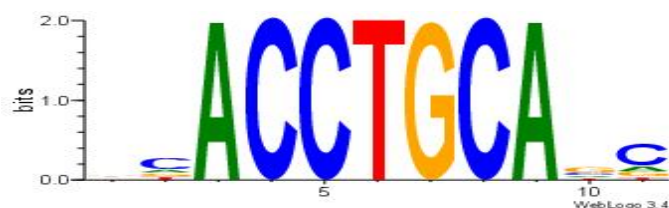
Best Matches for Motif ID 43 (Highest to Lowest)

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: 0.0137367

Alignment:
GBTGCAGGTGB
HVTACWG TABD

Original motif Consensus sequence: BCACCTGCABC



Reverse complement motif Consensus sequence: GBTGCAGGTGB

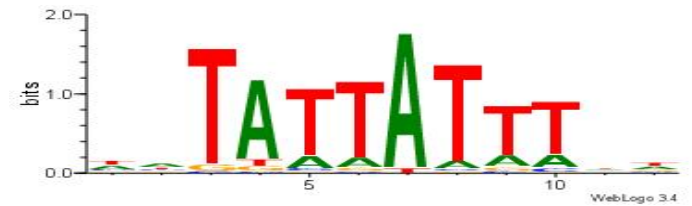
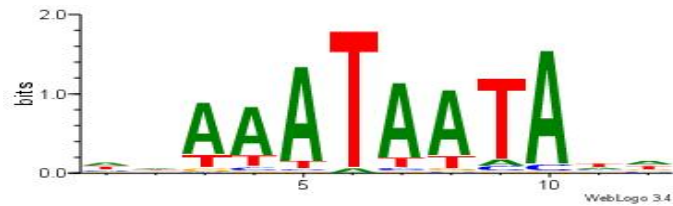


Dataset #: 4
Motif ID: 41
Motif name: wwAAATAATAtw
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 11
Similarity score: 0.0247119

Alignment:
DDTATTATTTDH
-HVTACWG TABD

Original motif Consensus sequence: HDAAATAATADD

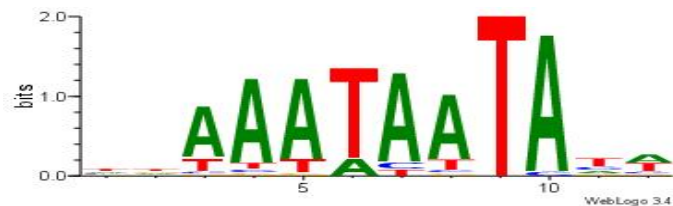
Reverse complement motif Consensus sequence: DDTATTATTTDH



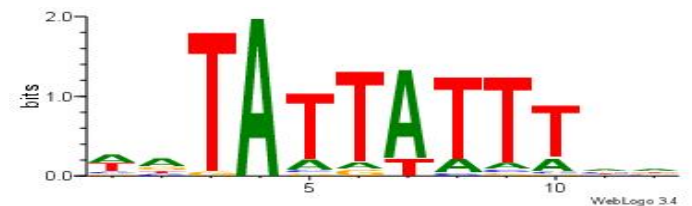
Dataset #: 4
 Motif ID: 37
 Motif name: tkAAATAATAtw
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.0274897

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: 0.0291311

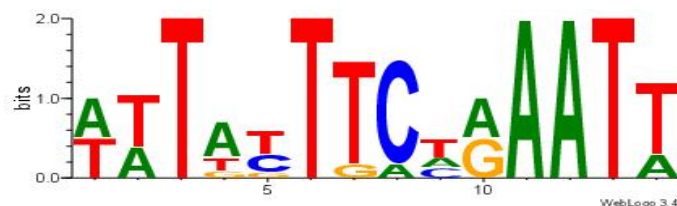
Alignment:

AATTYDGAARTAWW
 HVTACWGTABD---

Original motif Consensus sequence: AATTYDGAARTAWW



Reverse complement motif Consensus sequence: WWTAKTTCDKAAAT



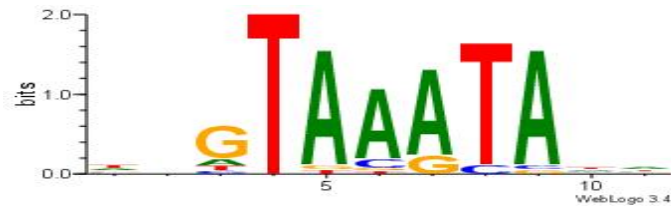
Dataset #: 4
 Motif ID: 45
 Motif name: wbgTAAATAww
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.0312956

Alignment:

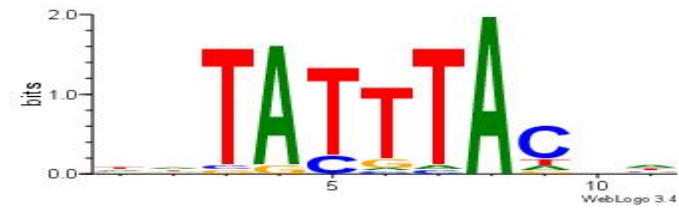
DBGTAAATAHD

DBTACWGTAVH

Original motif Consensus sequence: DBGTAAATAHD

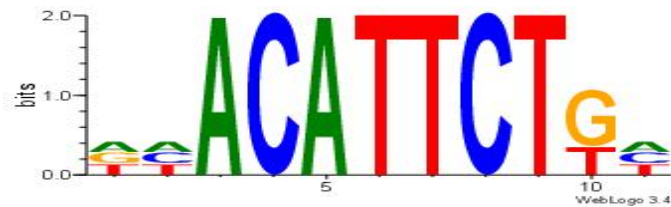


Reverse complement motif Consensus sequence: DHTATTTACBD



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

Original motif Consensus sequence: DHACATTCTGH



Reverse complement motif Consensus sequence: HCAGAATGTHD



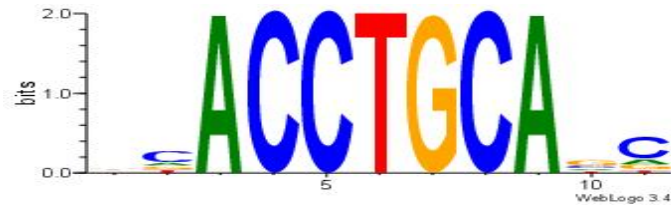
Best Matches for Motif ID 44 (Highest to Lowest)

Dataset #:	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

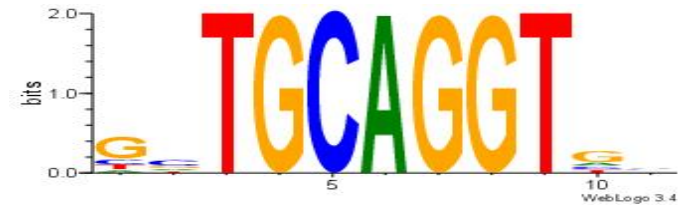
Number of overlap: 11
Similarity score: 0.023951

Alignment:
BCACCTGCABC
DHACATTCTGH

Original motif Consensus sequence: BCACCTGCABC



Reverse complement motif Consensus sequence: GBTGCAGGTGB

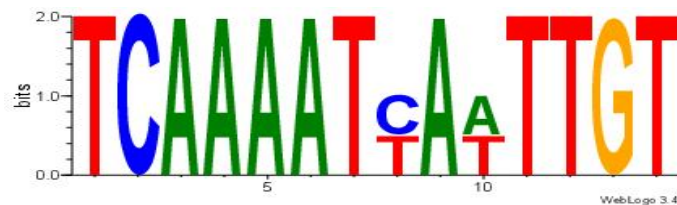
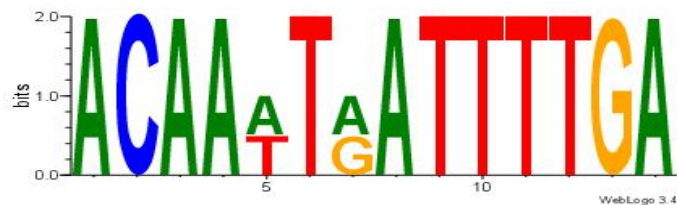


Dataset #: 2
Motif ID: 16
Motif name: Motif 16
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 4
Number of overlap: 11
Similarity score: 0.0259907

Alignment:
TCAAAATKAWTTGT
HCAGAATGTHD---

Original motif Consensus sequence: ACAAWTRATTTTGA

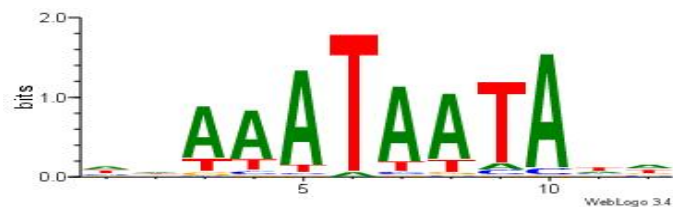
Reverse complement motif Consensus sequence: TCAAAATKAWTTG



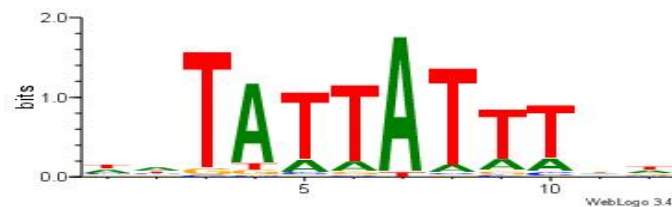
Dataset #: 4
 Motif ID: 41
 Motif name: wwAAATAATAtw
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.0293577

Alignment:
 DDTATTATTTDH
 -HCAGAATGTHD

Original motif Consensus sequence: HDAAATAATADD



Reverse complement motif Consensus sequence: DDTATTATTTDH



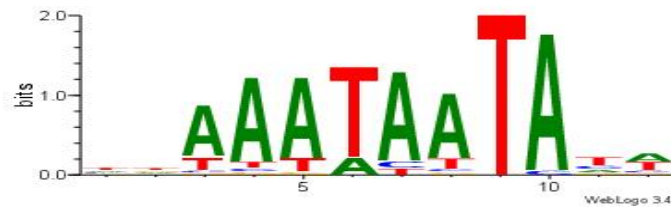
Dataset #: 4
 Motif ID: 37

Motif name: tkAAATAATAtw
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.0365967

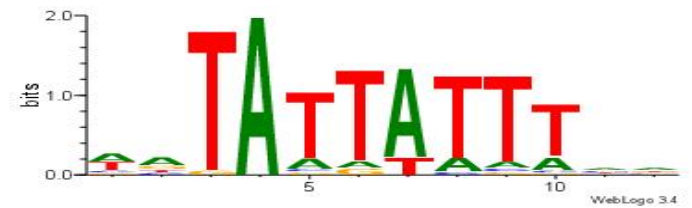
Alignment:

WHTATTATTTDH
 -HCAGAAATGTHD

Original motif Consensus sequence: HDAAATAATAHW



Reverse complement motif Consensus sequence: WHTATTATTTDH

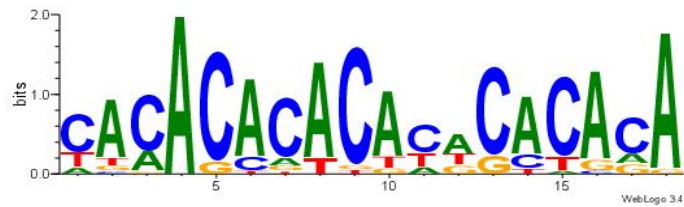


Dataset #: 5
 Motif ID: 51
 Motif name: TFM1
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 7
 Number of overlap: 11
 Similarity score: 0.038166

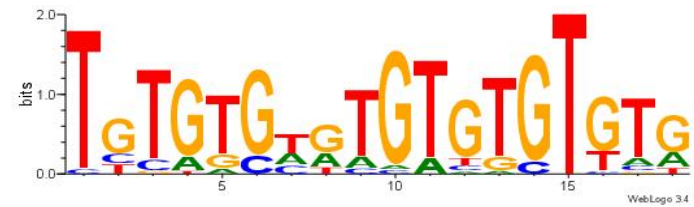
Alignment:

CACACACACACWCACACA
-DHACATTCTGH-----

Original motif Consensus sequence: CACACACACACWCACACA

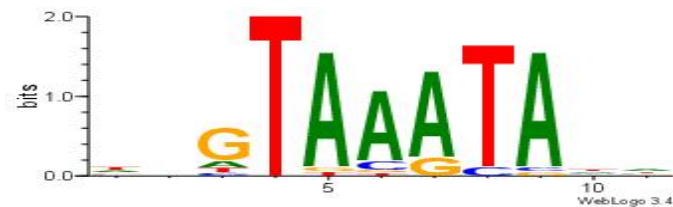


Reverse complement motif Consensus sequence:
TGTGTGWGTGTGTGTGTG

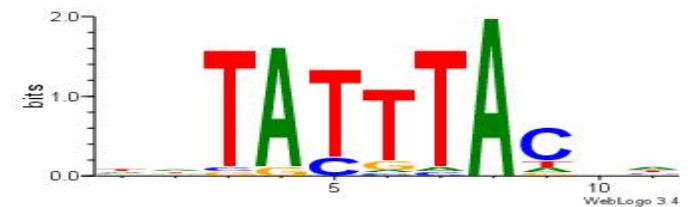


Dataset #: 4 Motif ID: 45 Motif name: wbgTAAATAww

Original motif Consensus sequence: DBGTAATAHD



Reverse complement motif Consensus sequence: DHTATTTACBD



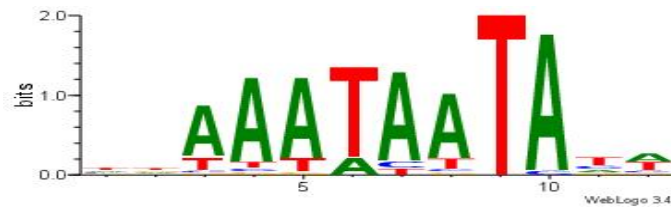
Best Matches for Motif ID 45 (Highest to Lowest)

Dataset #:	4
Motif ID:	37
Motif name:	tkAAATAATAtw
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward

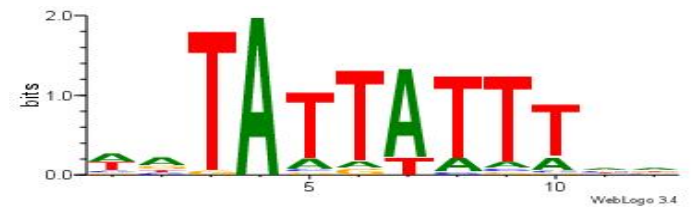
Position number: 1
Number of overlap: 11
Similarity score: 0.00892084

Alignment:
HDAAATAATAHW
-DBGTAAATAHD

Original motif Consensus sequence: HDAAATAATAHW



Reverse complement motif Consensus sequence: WHTATTATTTDH

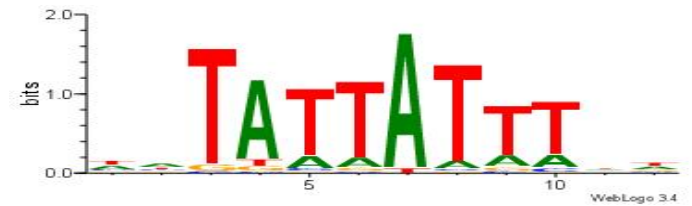
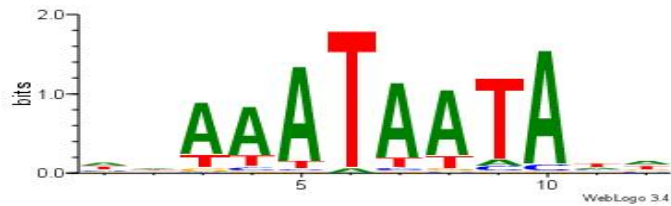


Dataset #: 4
Motif ID: 41
Motif name: wwAAATAATAtw
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 2
Number of overlap: 11
Similarity score: 0.00917337

Alignment:
DDTATTATTTDH
DHTATTTACBD-

Original motif Consensus sequence: HDAAATAATADD

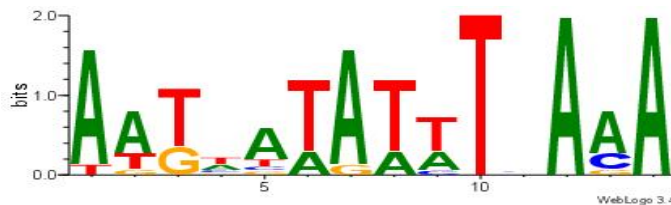
Reverse complement motif Consensus sequence: DDTATTATTTDH



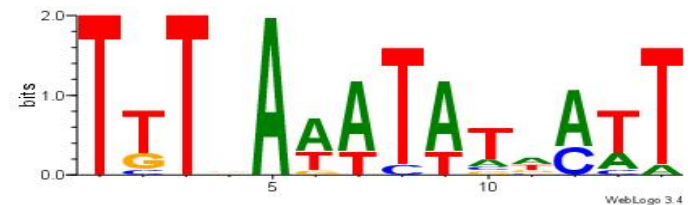
Dataset #: 2
 Motif ID: 9
 Motif name: Motif 9
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 4
 Number of overlap: 11
 Similarity score: 0.0177412

Alignment:
 AATHATATWTHAAA
 DHTATTTACBD---

Original motif Consensus sequence: AATHATATWTHAAA



Reverse complement motif Consensus sequence: TTTDAWATATHAT



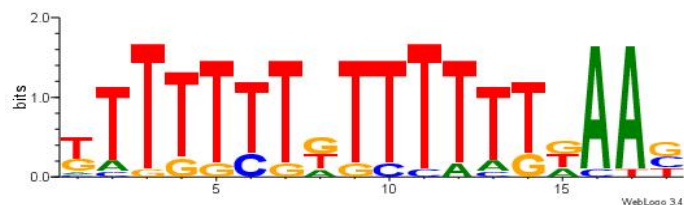
Dataset #: 5

Motif ID: 53
 Motif name: TFM3
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 4
 Number of overlap: 11
 Similarity score: 0.0203792

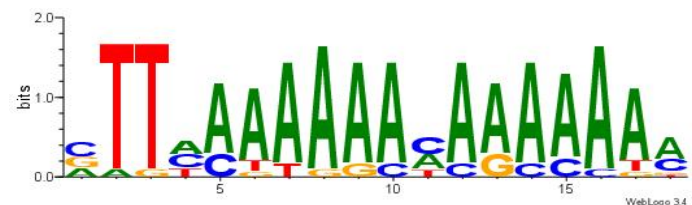
Alignment:

BTTHAAAAAYAAAAAR
 ---DBGTAATAHD----

Original motif Consensus sequence: KTTTTTKTTTTTDAAB



Reverse complement motif Consensus sequence: BTTHAAAAAYAAAAAR



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:

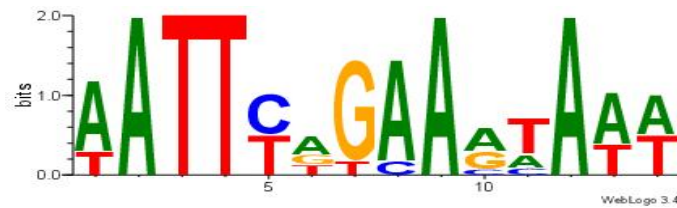
0.0205821

Alignment:

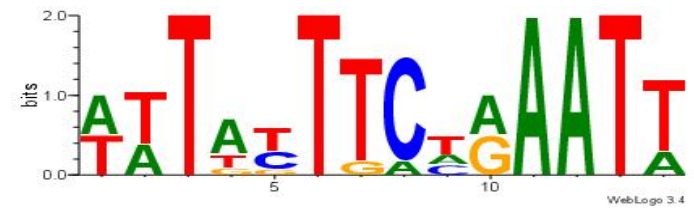
AATTYDGAARTAWW

---DBGTAAATAHD

Original motif Consensus sequence: AATTYDGAARTAWW



Reverse complement motif Consensus sequence: WWTAKTTCDKAAT



Dataset #: 5

Motif ID: 46

Motif name: TFW3

Original motif Consensus sequence: GCACTG



Reverse complement motif Consensus sequence: CAGTGC



Best Matches for Motif ID 46 (Highest to Lowest)

Dataset #:

4

Motif ID:

43

Motif name:

wsTACwGTAsw

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: 0.00773193

Alignment:
DBTACWGTAVH
----CAGTGC-

Original motif Consensus sequence: HVTACWG TABD



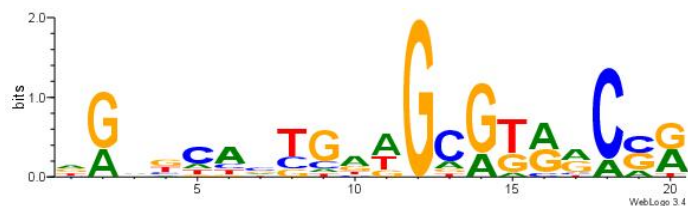
Reverse complement motif Consensus sequence: DBTACWGTAVH



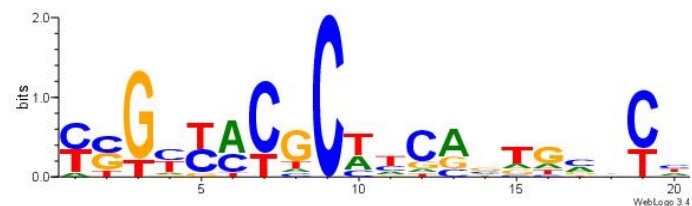
Dataset #: 3
Motif ID: 31
Motif name: Pax5
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 4
Number of overlap: 6
Similarity score: 0.0111111

Alignment:
DGVBCABTGDWCGKRRCSR
---GCACTG-----

Original motif Consensus sequence: DGVBCABTGDWGCGRRCRCSR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBBCD

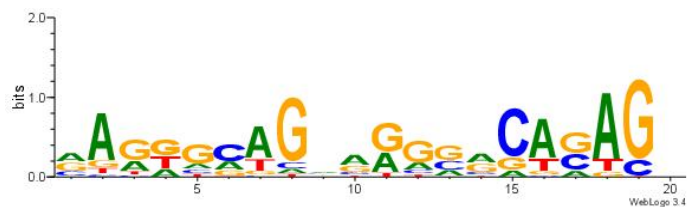


Dataset #: 5
Motif ID: 55
Motif name: TFM12
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 14
Number of overlap: 6
Similarity score: 0.0147489

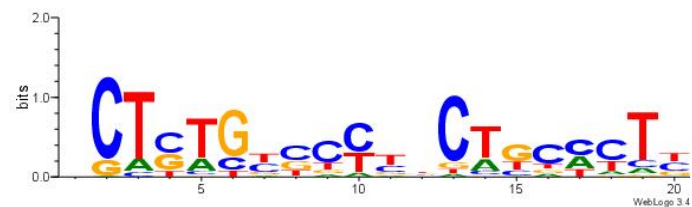
Alignment:

RAGKGMAGVRRGSRCASAGV
-----GCACTG--

Original motif Consensus sequence: RAGKGMAGVRRGSRCASAGV



Reverse complement motif Consensus sequence: VCTSTGKSCMKBCTRCYCTK

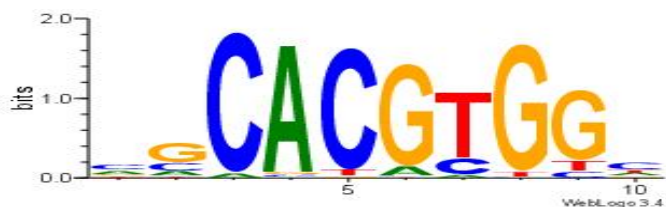


Dataset #: 3
 Motif ID: 34
 Motif name: Myc
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 4
 Number of overlap: 6
 Similarity score: 0.0148473

Alignment:

DCCACGTGCV
 ---CAGTGC-

Original motif Consensus sequence: VGCACGTGGH



Reverse complement motif Consensus sequence: DCCACGTGCV



Dataset #: 3
 Motif ID: 35
 Motif name: GABPA
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 6

Similarity score: 0.0156785

Alignment:

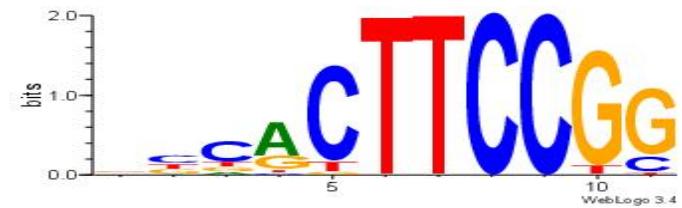
VVCACTTCCGG

----GCACTG--

Original motif Consensus sequence: CCGGAAGTGVV

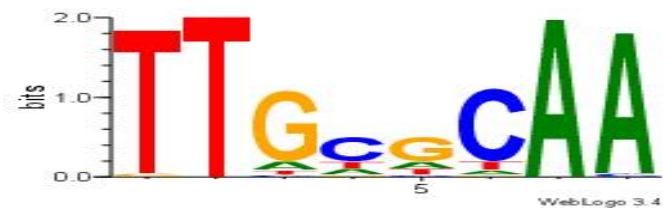


Reverse complement motif Consensus sequence: VVCACTTCCGG

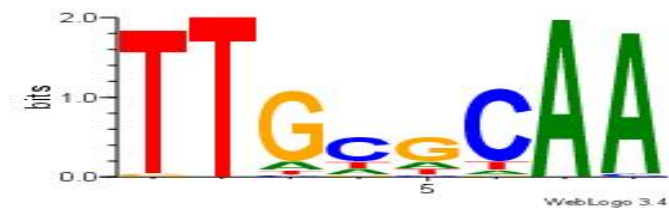


Dataset #: 5 Motif ID: 47 Motif name: TFW1

Original motif Consensus sequence: TTGCGCAA



Reverse complement motif Consensus sequence: TTGCGCAA



Best Matches for Motif ID 47 (Highest to Lowest)

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

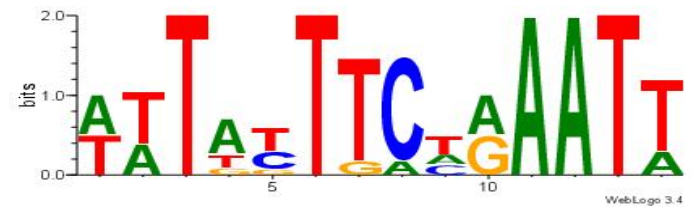
Position number: 5
 Number of overlap: 8
 Similarity score: 0.0289062

Alignment:
 AATTYDGAARTAWW
 ----TTGCGCAA--

Original motif Consensus sequence: AATTYDGAARTAWW



Reverse complement motif Consensus sequence: WWTAKTTCDKAAAT

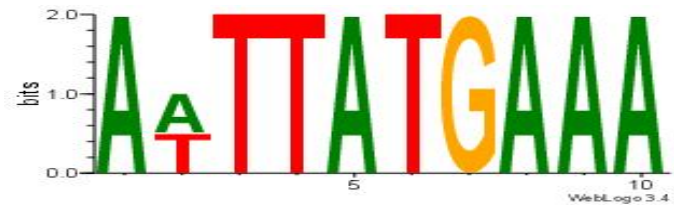
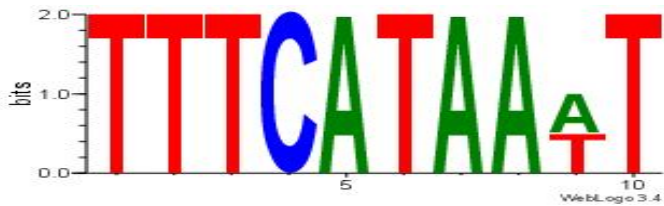


Dataset #: 2
 Motif ID: 10
 Motif name: Motif 10
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 8
 Similarity score: 0.0328125

Alignment:
 TTCATAAWT
 TTGCGCAA--

Original motif Consensus sequence: TTCATAAWT

Reverse complement motif Consensus sequence: AWTTATGAAA



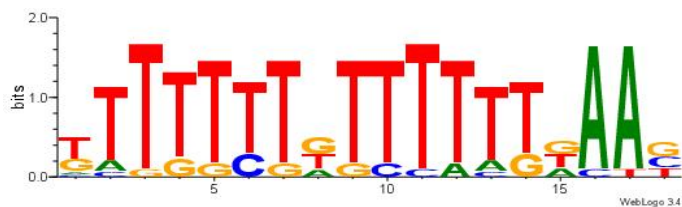
Dataset #: 5
 Motif ID: 53
 Motif name: TFM3
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 8
 Similarity score: 0.0359375

Alignment:

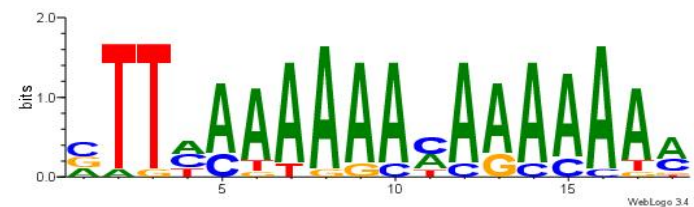
```

KTTTTTTKTTTTTTDAAB
-----TTGCGCAA-
  
```

Original motif Consensus sequence: KTTTTTTKTTTTTTDAAB



Reverse complement motif Consensus sequence: BTTHAAAAAYAAAAAAR



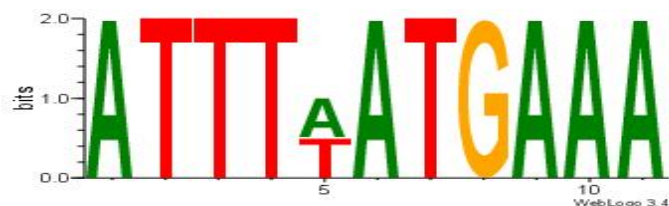
Dataset #: 2

Motif ID: 11
 Motif name: Motif 11
 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: 0.0460937

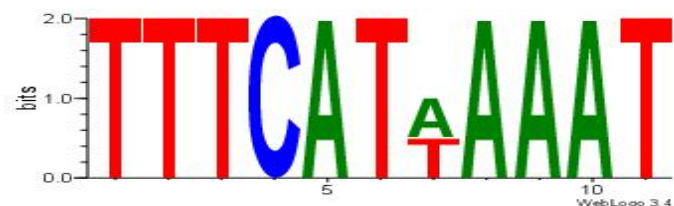
Alignment:

TTTCATWAAAT
 -TTGCGCAA--

Original motif Consensus sequence: ATTTWATGAAA



Reverse complement motif Consensus sequence: TTTCATWAAAT

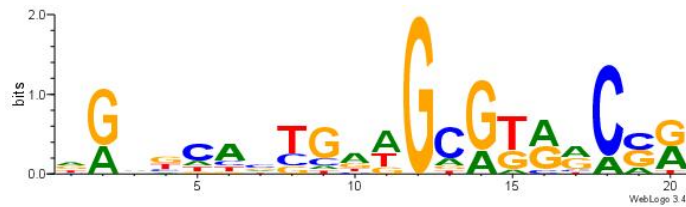


Dataset #: 3
 Motif ID: 31
 Motif name: Pax5
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 10
 Number of overlap: 8
 Similarity score: 0.0460937

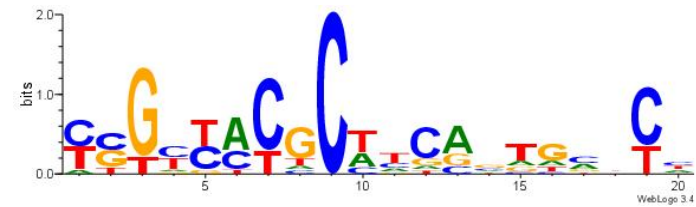
Alignment:

DGVBCABTGDWGCGRRCR
---TTGCGCAA-----

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR

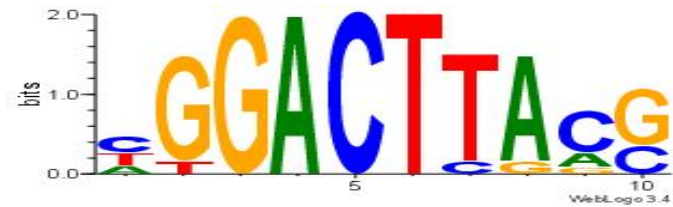


Reverse complement motif Consensus sequence:
MSGKKRCGCWDCABTGBCD



Dataset #: 5 Motif ID: 48 Motif name: TFW2

Original motif Consensus sequence: YGGACTTACG



Reverse complement motif Consensus sequence: CGTAAGTCCK



Best Matches for Motif ID 48 (Highest to Lowest)

Dataset #:	4
Motif ID:	45
Motif name:	wbgTAAATAww
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: 0.025377

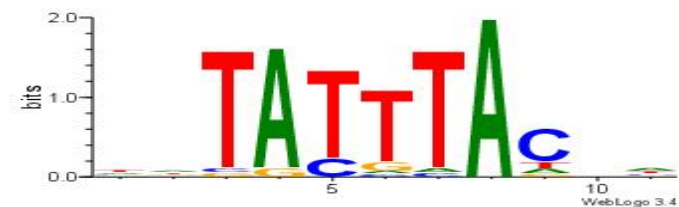
Alignment:

DHTATTTACBD
-YGGACTTACG

Original motif Consensus sequence: DBGTAATAHD



Reverse complement motif Consensus sequence: DHTATTTACBD



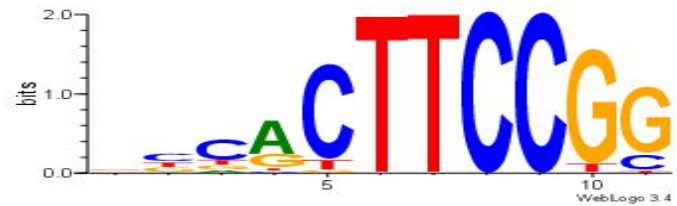
Dataset #: 3
Motif ID: 35
Motif name: GABPA
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 10
Similarity score: 0.0305272

Alignment:

VVCACTTCCGG
-YGGACTTACG

Original motif Consensus sequence: CCGGAAGTGVV

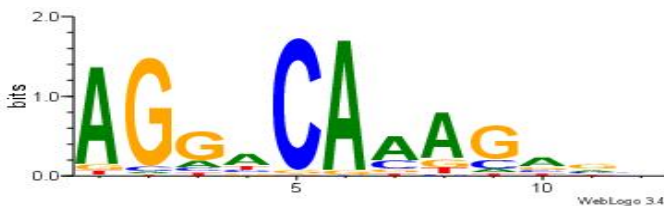
Reverse complement motif Consensus sequence: VVCACTTCCGG



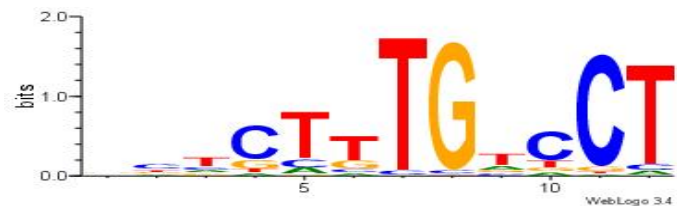
Dataset #: 5
 Motif ID: 49
 Motif name: TFF1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3
 Number of overlap: 10
 Similarity score: 0.0481358

Alignment:
 VVTCTTTGTCCT
 --CGTAAGTCCK

Original motif Consensus sequence: AGGACAAAGAVV



Reverse complement motif Consensus sequence: VVTCTTTGTCCT



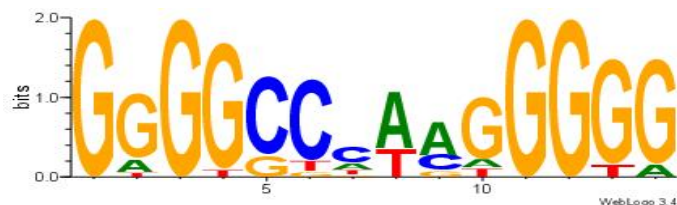
Dataset #: 3

Motif ID: 30
 Motif name: PLAG1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 4
 Number of overlap: 10
 Similarity score: 0.0523611

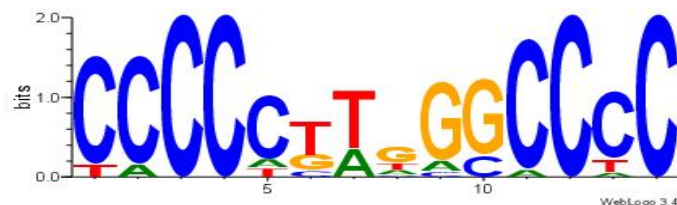
Alignment:

CCCCCTTGGGCCCC
 ---CGTAAGTCK-

Original motif Consensus sequence: GGGGCCCAAGGGG



Reverse complement motif Consensus sequence: CCCCCTTGGGCCCC

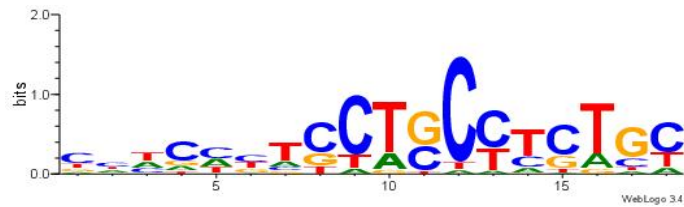


Dataset #: 5
 Motif ID: 52
 Motif name: TFM2
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 9
 Number of overlap: 10
 Similarity score: 0.0530849

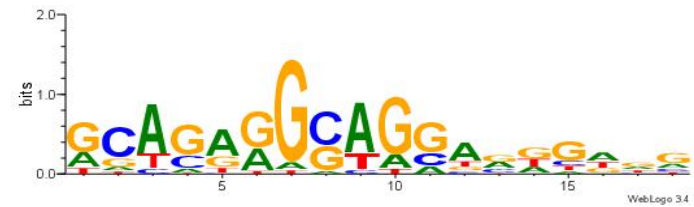
Alignment:

```
CHHCHBTCCTSCYTCTGC
CGTAAGTCK-----
```

Original motif Consensus sequence: CHHCHBTCCTSCYTCTGC

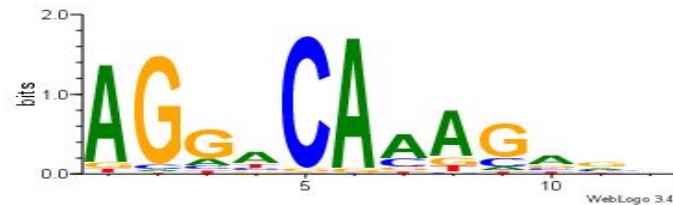


Reverse complement motif Consensus sequence:
GCAGAKGSAGGABDGHDG

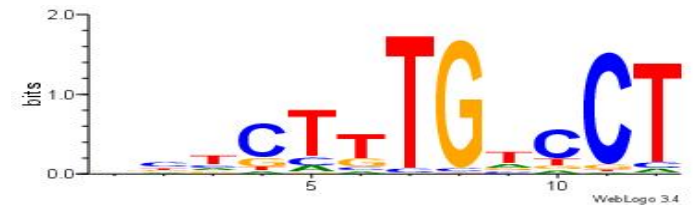


Dataset #: 5 Motif ID: 49 Motif name: TFF1

Original motif Consensus sequence: AGGACAAAGAVV



Reverse complement motif Consensus sequence: VVTCTTGTCTCT



Best Matches for Motif ID 49 (Highest to Lowest)

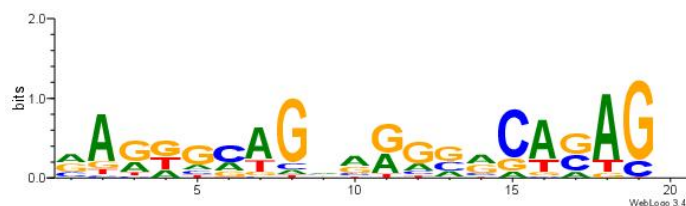
Dataset #:	5
Motif ID:	55
Motif name:	TFM12
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward

Position number: 8
 Number of overlap: 12
 Similarity score: 0.0365317

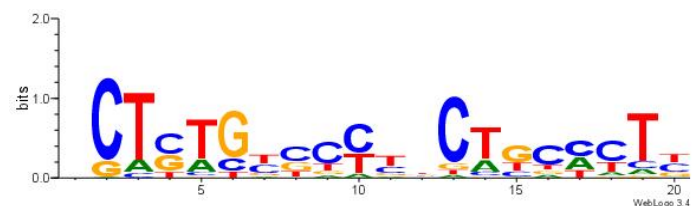
Alignment:

RAGKGMAGVRRGSRCASAGV
 -AGGACAAAGAVV-----

Original motif Consensus sequence: RAGKGMAGVRRGSRCASAGV



Reverse complement motif Consensus sequence: VCTSTGKSCMKBCTRCYCTK

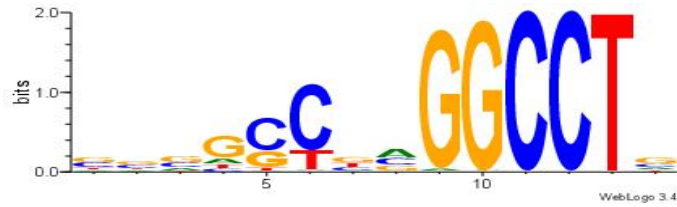


Dataset #: 3
 Motif ID: 22
 Motif name: Zfx
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 12
 Similarity score: 0.0365998

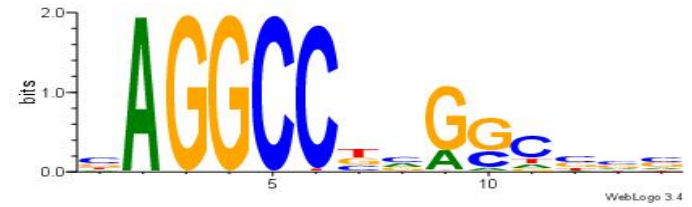
Alignment:

VAGGCCBBGGCVBB
 -AGGACAAAGAVV-

Original motif Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif Consensus sequence: VAGGCCBBGGCV

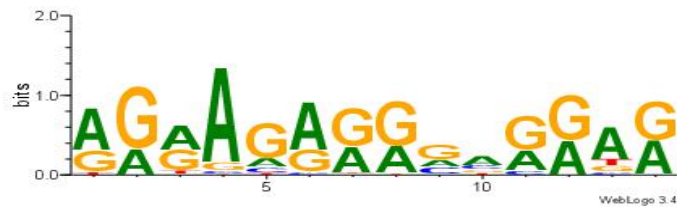


Dataset #: 2
Motif ID: 2
Motif name: Motif 2
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 12
Similarity score: 0.0390077

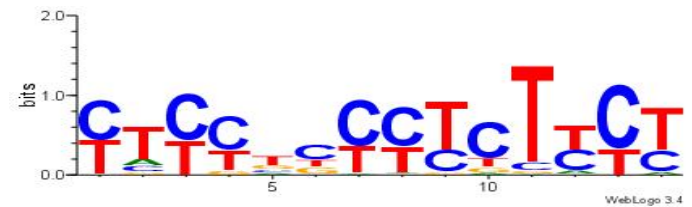
Alignment:

RGRAGARRGARRAR
AGGACAAAGAVV--

Original motif Consensus sequence: RGRAGARRGARRAR



Reverse complement motif Consensus sequence: MTMMTCMMTCTK

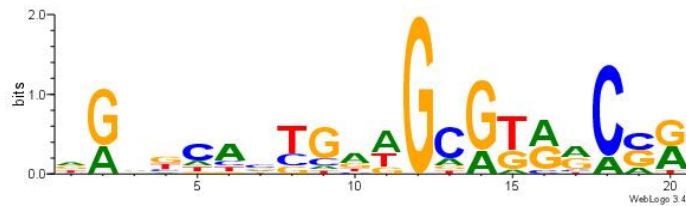


Dataset #: 3
 Motif ID: 31
 Motif name: Pax5
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 12
 Similarity score: 0.0484644

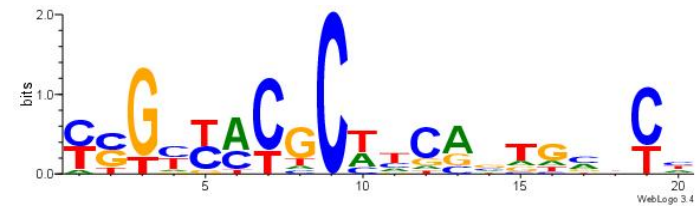
Alignment:

MSGKKRCGCWDCABTGBBCD
 -----VVTCTTTGTCCT

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD



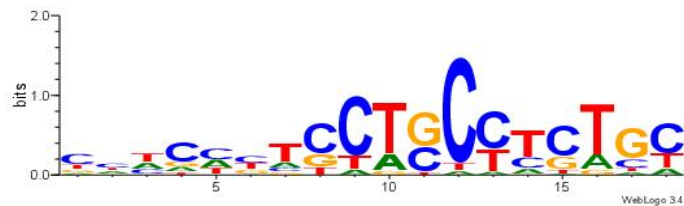
Dataset #: 5
 Motif ID: 52
 Motif name: TFM2
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 6

Number of overlap: 12
 Similarity score: 0.053257

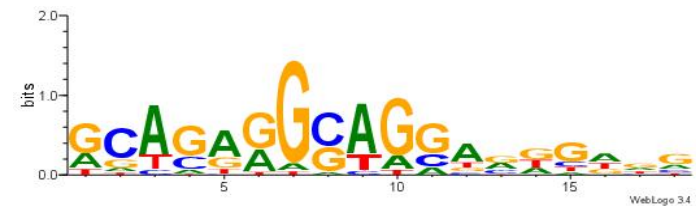
Alignment:

CHHCHBTCCTSCYTCTGC
 -VVTCTTTGTCCT-----

Original motif Consensus sequence: CHHCHBTCCTSCYTCTGC

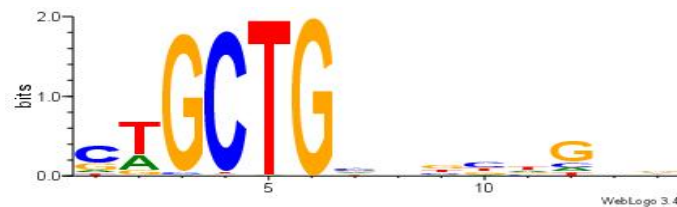


Reverse complement motif Consensus sequence:
 GCAGAKGSAGGABDGHG

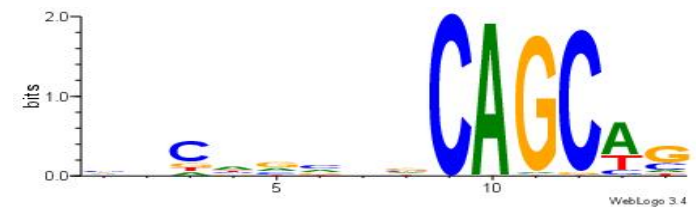


Dataset #: 5 Motif ID: 50 Motif name: TFF11

Original motif Consensus sequence: CTGCTGBDBBDGBD



Reverse complement motif Consensus sequence: HVCDBBDBCAGCA



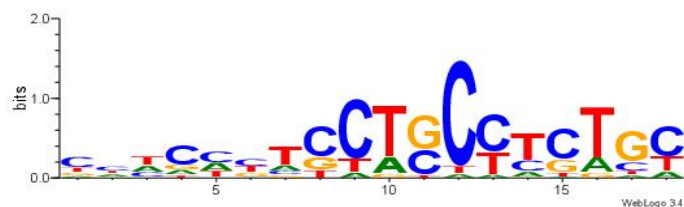
Best Matches for Motif ID 50 (Highest to Lowest)

Dataset #: 5
 Motif ID: 52
 Motif name: TFM2
 Matching format of first motif: Original Motif

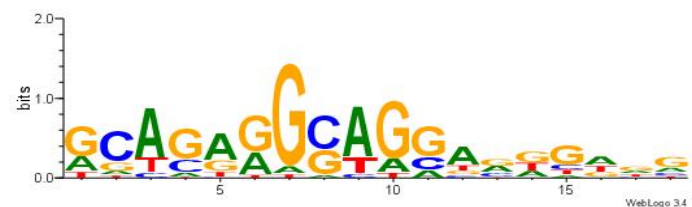
Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 14
 Similarity score: 0.038418

Alignment:
 GCAGAKGSAGGABDGHGDG
 -CTGCTGBDBBDGBD---

Original motif Consensus sequence: CHHCHBTCCTSCYTCTGC



Reverse complement motif Consensus sequence:
 GCAGAKGSAGGABDGHGDG

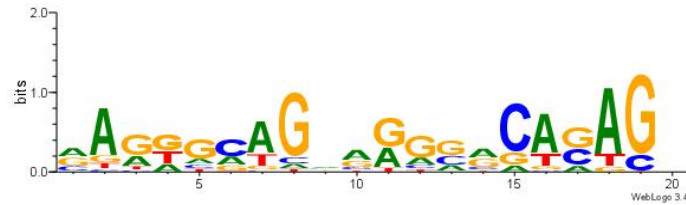


Dataset #: 5
 Motif ID: 55
 Motif name: TFM12
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 14
 Similarity score: 0.0408073

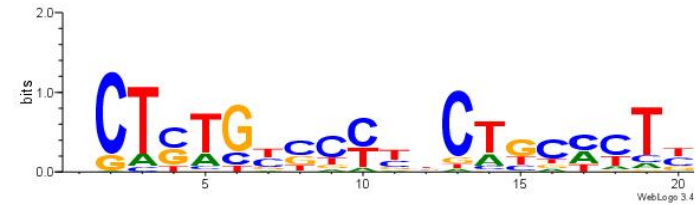
Alignment:

RAGKGMAGVRRGSRCASAGV
 ---HVCDBBDBCAGCAG---

Original motif Consensus sequence: RAGKGMAGVRRGSRCASAGV



Reverse complement motif Consensus sequence:
 VCTSTGKSCMKBCTRCYCTK

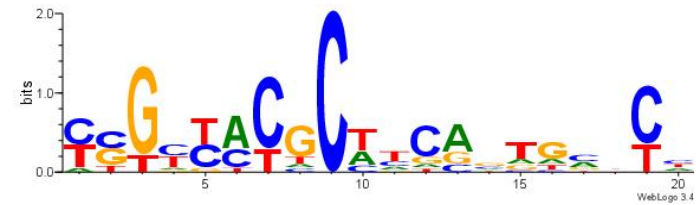
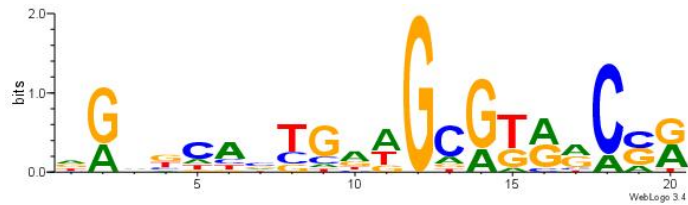


Dataset #: 3
 Motif ID: 31
 Motif name: Pax5
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 6
 Number of overlap: 14
 Similarity score: 0.0480382

Alignment:
 DGVBCABTGDWGCGRCSR
 -----HVCDBBDBCAGCAG-

Original motif Consensus sequence: DGVBCABTGDWGCGRCSR

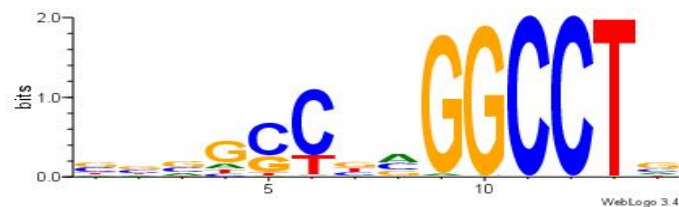
Reverse complement motif Consensus sequence:
 MSGKKRCGCWDCABTGBBCD



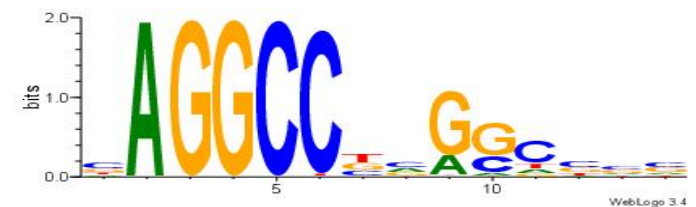
Dataset #: 3
 Motif ID: 22
 Motif name: Zfx
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0.0601959

Alignment:
 BBVGCCBVGGCCTV
 HVCDBBDBCAGCAG

Original motif Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif Consensus sequence: VAGGCCBBGGCV



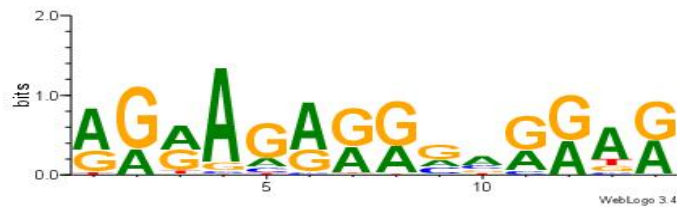
Dataset #: 2
 Motif ID: 2

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: 0.0646528

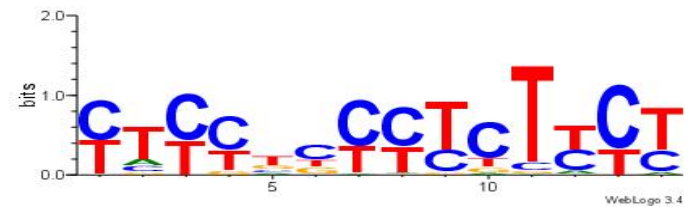
Alignment:

RGRAGARRGARRAR
 HVCDBBDBCAGCAG

Original motif Consensus sequence: RGRAGARRGARRAR

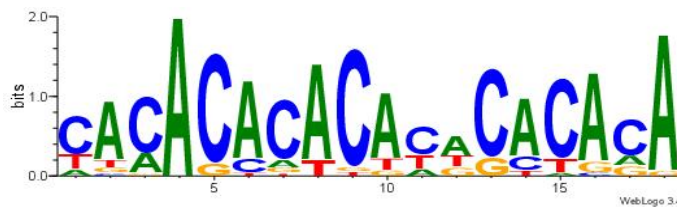


Reverse complement motif Consensus sequence: MTMMTCMMTCTK

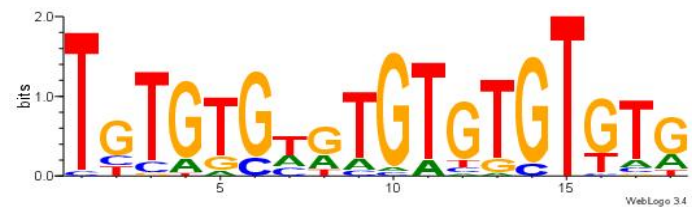


Dataset #: 5 Motif ID: 51 Motif name: TFM1

Original motif Consensus sequence: CACACACACWCACACA



Reverse complement motif Consensus sequence: TGTGTGWGTGTGTGTGTG



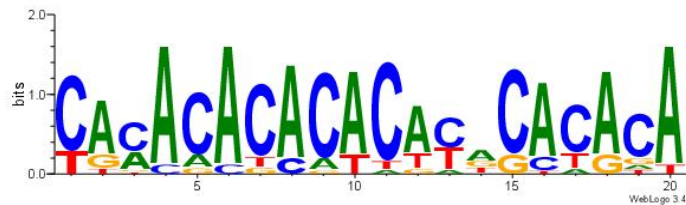
Best Matches for Motif ID 51 (Highest to Lowest)

Dataset #: 5
 Motif ID: 54
 Motif name: TFM11
 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

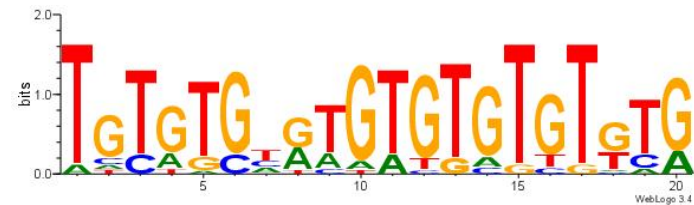
Alignment:

CAMACACACACAYDCACACA
 --CACACACACACWCACACA

Original motif Consensus sequence: CAMACACACACAYDCACACA



Reverse complement motif Consensus sequence: TGTGTGDKTGTGTGTGTRTG



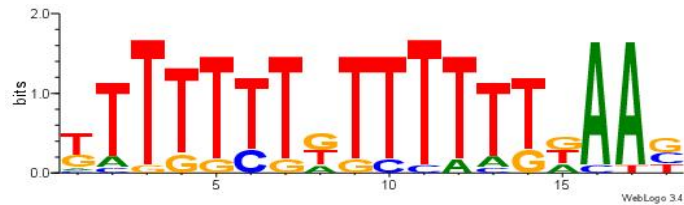
Dataset #: 5
 Motif ID: 53
 Motif name: TFM3
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif

Direction: Backward
 Position number: 1
 Number of overlap: 18
 Similarity score: 0.099254

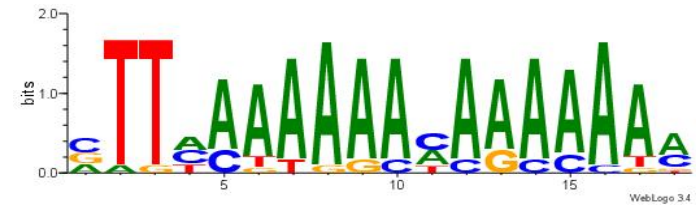
Alignment:

KTTTTTTKTTTTTTDAAB
 TGTGTGWGTGTGTGTGTG

Original motif Consensus sequence: KTTTTTTKTTTTTTDAAB



Reverse complement motif Consensus sequence: BTTHAAAAAYAAAAAAR

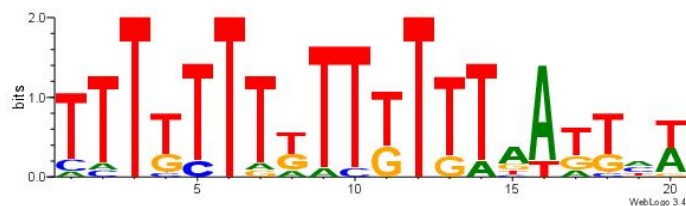


Dataset #: 5
 Motif ID: 56
 Motif name: TFM13
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 6
 Number of overlap: 15
 Similarity score: 1.59953

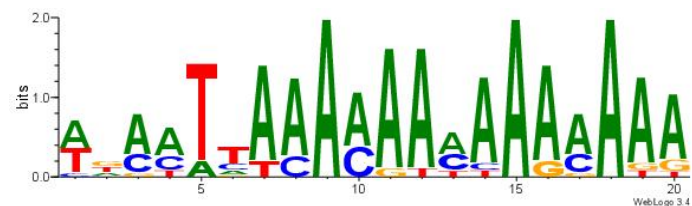
Alignment:

---TTTTTTTKTTKTTTAATTHW
 TGTGTGWGTGTGTGTGTG-----

Original motif Consensus sequence: TTTTTTKTTKTTTAATTHW



Reverse complement motif Consensus sequence: WHAATTAARAARAAAAAA

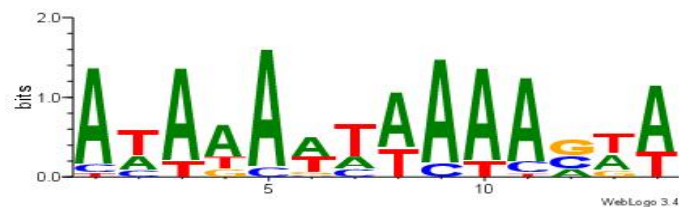


Dataset #: 2
Motif ID: 3
Motif name: Motif 3
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 2
Number of overlap: 13
Similarity score: 2.58697

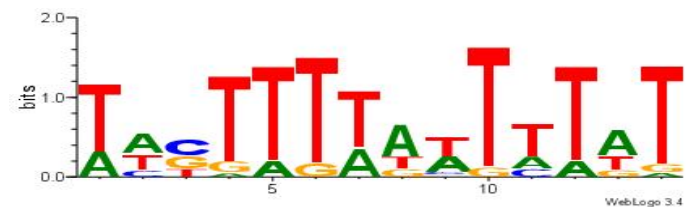
Alignment:

```
TWSTTTWAWTTTWT-----  
-TGTGTGWGTGTGTGTGTG
```

Original motif Consensus sequence: AWAAAWTWAASWA



Reverse complement motif Consensus sequence: TWSTTTWAWTTTWT

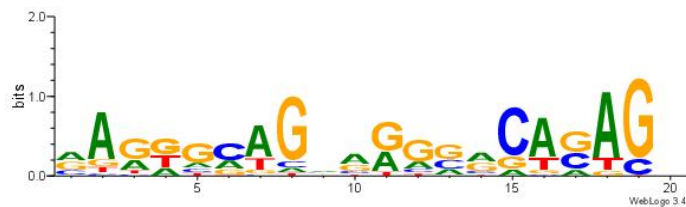


Dataset #: 5
 Motif ID: 55
 Motif name: TFM12
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 9
 Number of overlap: 12
 Similarity score: 3.08676

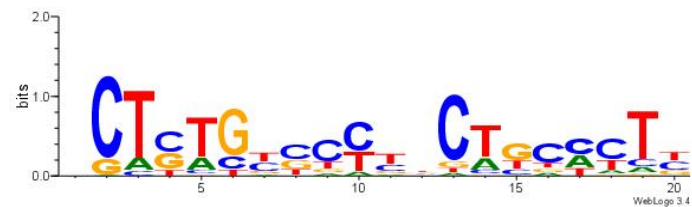
Alignment:

RAGKGMAGVRRGSRCASAGV-----
 -----CACACACACACWCACACA

Original motif Consensus sequence: RAGKGMAGVRRGSRCASAGV



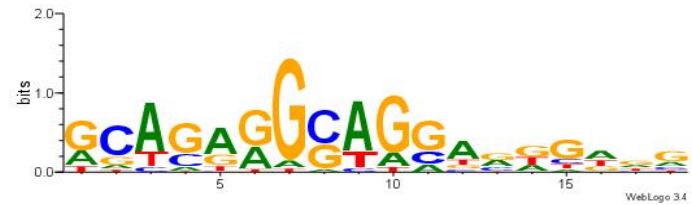
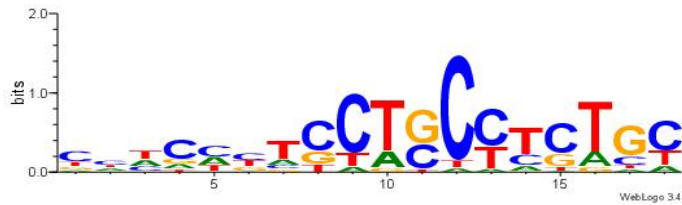
Reverse complement motif Consensus sequence: VCTSTGKSCMKBCTRCYCTK



Dataset #: 5 Motif ID: 52 Motif name: TFM2

Original motif Consensus sequence: CHHCHBTCCTSCYTCTGC

Reverse complement motif Consensus sequence: GCAGAKGSAGGABDGH DG

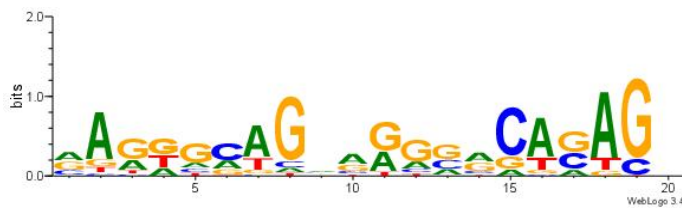


Best Matches for Motif ID 52 (Highest to Lowest)

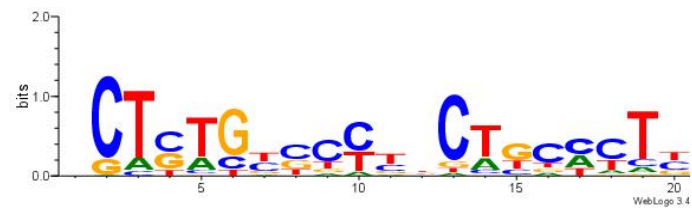
Dataset #: 5
 Motif ID: 55
 Motif name: TFM12
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 18
 Similarity score: 0.0461659

Alignment:
 RAGKGMAGVRRGSRCASAGV
 --GCAGAKGSAGGABDGH DG

Original motif Consensus sequence: RAGKGMAGVRRGSRCASAGV



Reverse complement motif Consensus sequence: VCTSTGKSCMKBCTRCYCTK

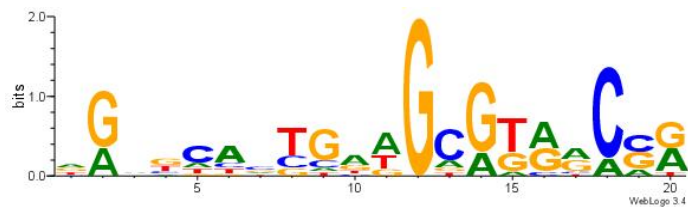


Dataset #: 3
 Motif ID: 31
 Motif name: Pax5
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 18
 Similarity score: 0.0506977

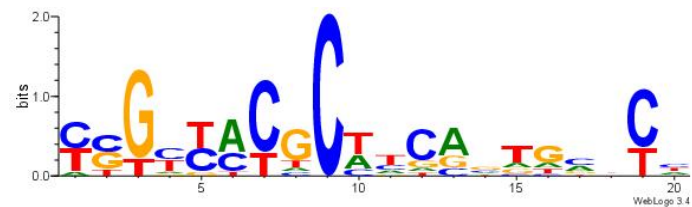
Alignment:

MSGKKRCGCWDCABTGBBCD
 --CHHCHBTCCTSCYTCTGC

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD



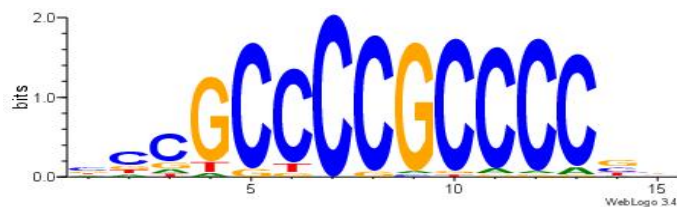
Dataset #: 4
 Motif ID: 38
 Motif name: cccGCCCCGCCCCsb
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1

Number of overlap: 15
Similarity score: 1.56819

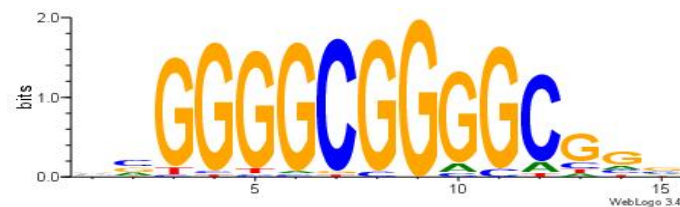
Alignment:

---BCCGCCCCGCCCCBB
CHHCHBTCCTSCYTCTGC

Original motif Consensus sequence: BCCGCCCCGCCCCBB



Reverse complement motif Consensus sequence:
BBGGGGCGGGGCGGB



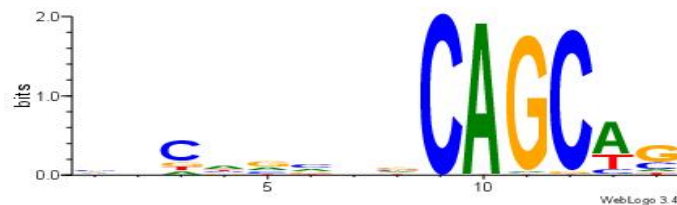
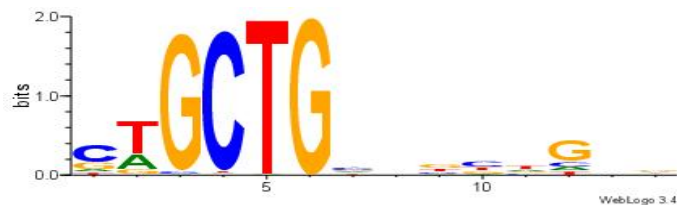
Dataset #: 5
Motif ID: 50
Motif name: TFF11
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 14
Similarity score: 2.03634

Alignment:

---HVCDBBDBCAGCAG
CHHCHBTCCTSCYTCTGC

Original motif Consensus sequence: CTGCTGBDBBDGBD

Reverse complement motif Consensus sequence: HVCDBBDBCAGCA



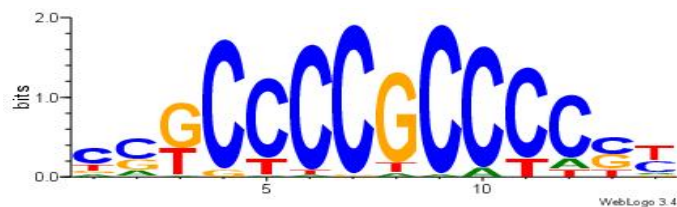
Dataset #: 2
 Motif ID: 7
 Motif name: Motif 7
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 14
 Similarity score: 2.05115

Alignment:

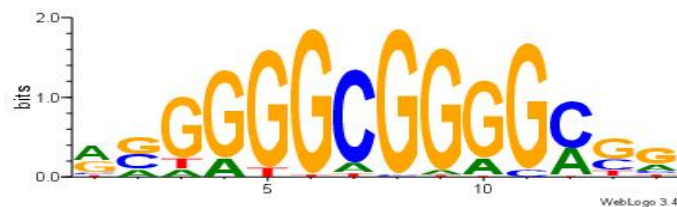
```

----MSGGGGCGGGYSG
GCAGAKGSAGGABDGHG
  
```

Original motif Consensus sequence: CSKCCCCGCCCSY

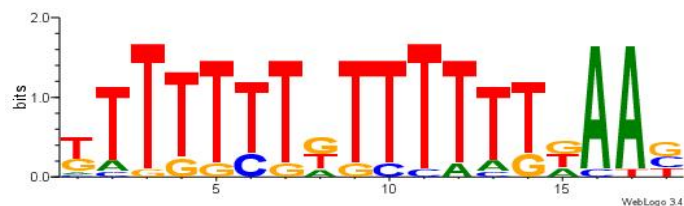


Reverse complement motif Consensus sequence: MSGGGGCGGGY

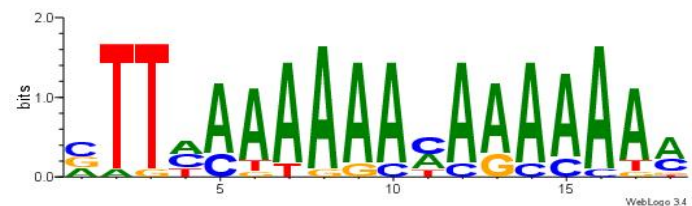


Dataset #: 5 Motif ID: 53 Motif name: TFM3

Original motif Consensus sequence: KTTTTTKTTTTTDAAB



Reverse complement motif Consensus sequence: BTTHAAAAAYAAAAAR



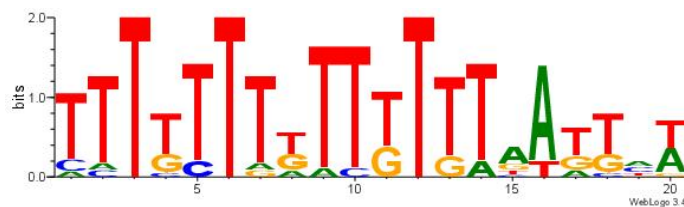
Best Matches for Motif ID 53 (Highest to Lowest)

Dataset #:	5
Motif ID:	56
Motif name:	TFM13
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	18
Similarity score:	0.0119727

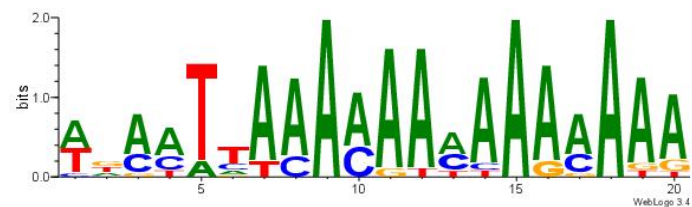
Alignment:

```
TTTTTTTKTTKTTTAATTHW
KTTTTTTKTTTTTTDAAB--
```

Original motif Consensus sequence: TTTTTTKTTKTTTAATTHW



Reverse complement motif Consensus sequence: WHAATTAARAARAAAAAA

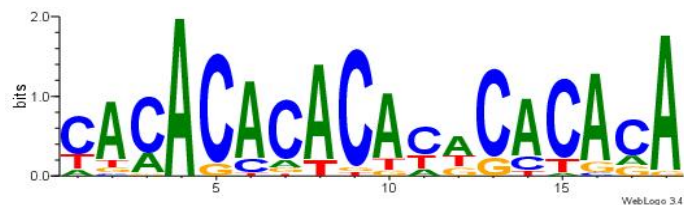


Dataset #: 5
 Motif ID: 51
 Motif name: TFM1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 18
 Similarity score: 0.080053

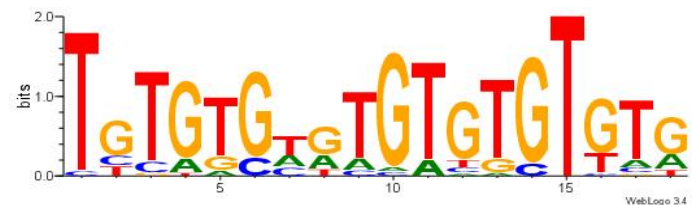
Alignment:

CACACACACACWCACACA
 BTTHAAAAAYAAAAAR

Original motif Consensus sequence: CACACACACWCACACA



Reverse complement motif Consensus sequence: TGTGTGWGTGTGTGTGTG



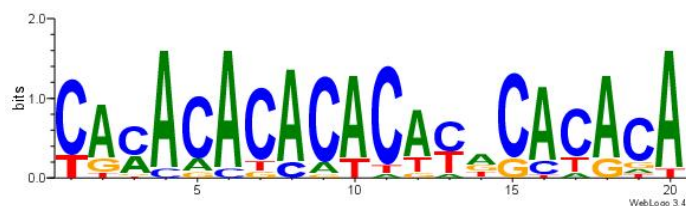
Dataset #: 5
 Motif ID: 54
 Motif name: TFM11
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward

Position number: 6
 Number of overlap: 15
 Similarity score: 1.58044

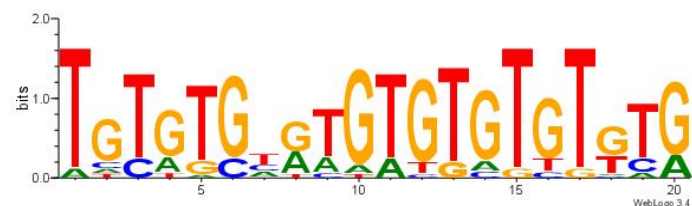
Alignment:

TGTGTGDKTGTGTGTGTRTG---
 -----KTTTTTTKTTTTTTDAAB

Original motif Consensus sequence: CAMACACACACAYDCACACA



Reverse complement motif Consensus sequence: TGTGTGDKTGTGTGTGTRTG

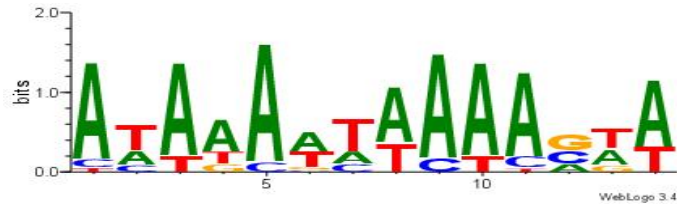


Dataset #: 2
 Motif ID: 3
 Motif name: Motif 3
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 14
 Similarity score: 2.03302

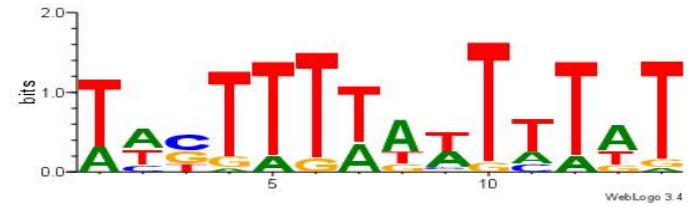
Alignment:

----TWSTTTWAWTTTWT
 KTTTTTTKTTTTTTDAAB

Original motif Consensus sequence: AWAAAWTWAAASWA



Reverse complement motif Consensus sequence: TWSTTTWAWTTTV

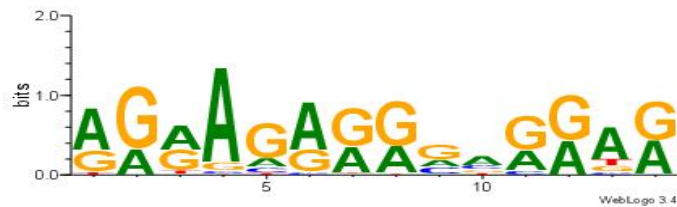


Dataset #: 2
Motif ID: 2
Motif name: Motif 2
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 14
Similarity score: 2.06009

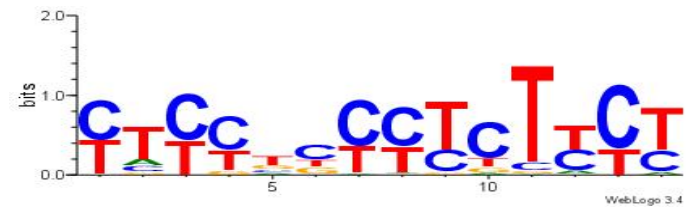
Alignment:

```
----MTMMTCMMTCTKCK  
KTTTTTTKTTTTTTDAAB
```

Original motif Consensus sequence: RGRAGARRGARRAR

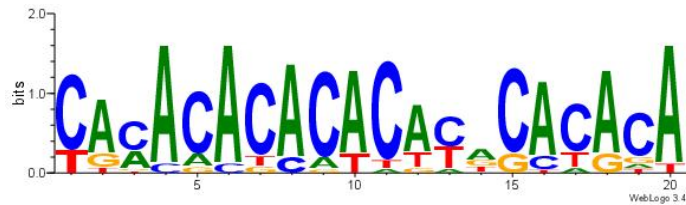


Reverse complement motif Consensus sequence: MTMMTCMMTCTKCK

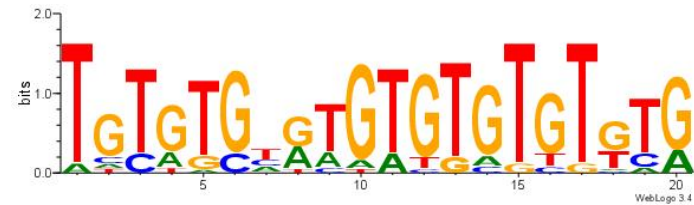


Dataset #: 5 Motif ID: 54 Motif name: TFM11

Original motif Consensus sequence: CAMACACACACAYDCACACA



Reverse complement motif Consensus sequence: TGTGTGDKTGTGTGTGTRTG



Best Matches for Motif ID 54 (Highest to Lowest)

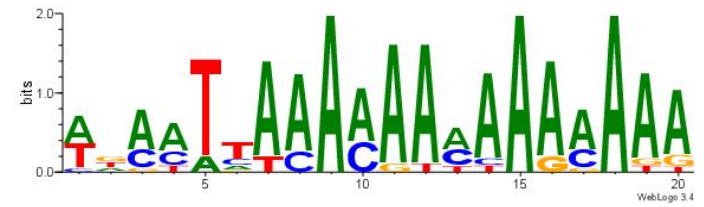
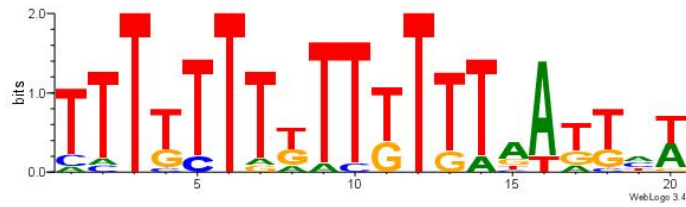
Dataset #:	5
Motif ID:	56
Motif name:	TFM13
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	19
Similarity score:	0.0921695

Alignment:

```
TTTTTTTKTTKTTTAATTHW-  
-TGTGTGDKTGTGTGTGTRTG
```

Original motif Consensus sequence: TTTTTTKTTKTTTAATTHW

Reverse complement motif Consensus sequence: WHAATTAARAARAAAAAAA



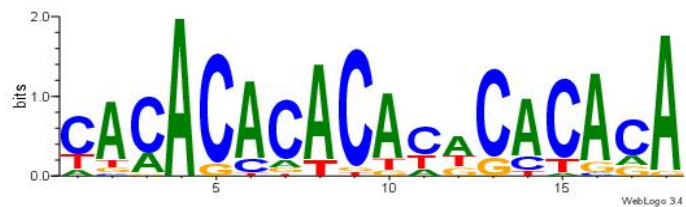
Dataset #: 5
 Motif ID: 51
 Motif name: TFM1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 18
 Similarity score: 0.5

Alignment:

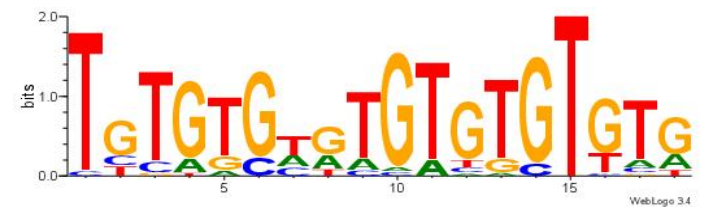
```

TGTGTGWGTGTGTGTGTG--
TGTGTGDKTGTGTGTGTRTG
  
```

Original motif Consensus sequence: CACACACACWCACACA



Reverse complement motif Consensus sequence: TGTGTGWGTGTGTGTGTG



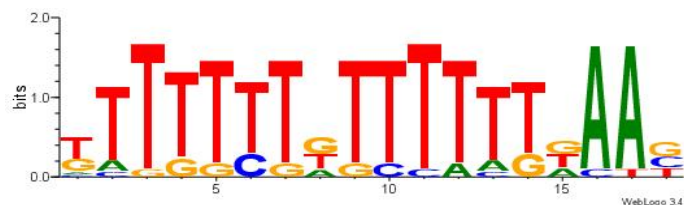
Dataset #: 5

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: 15
 Similarity score: 2.09964

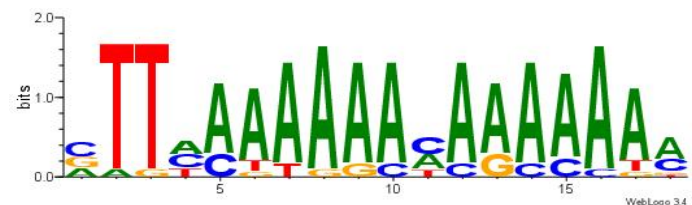
Alignment:

-----BTTHAAAAAYAAAAAR
 CAMACACACACAYDCACACA---

Original motif Consensus sequence: KTTTTTKTTTTTDAAB



Reverse complement motif Consensus sequence: BTTHAAAAAYAAAAAR



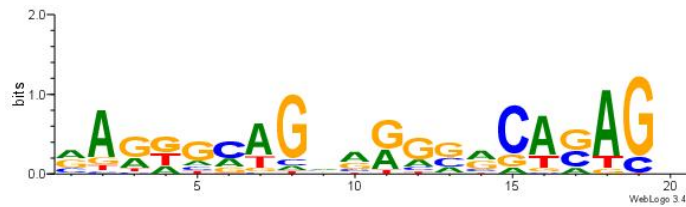
Dataset #: 5
 Motif ID: 55
 Motif name: TFM12
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 7
 Number of overlap: 14

Similarity score: 2.59651

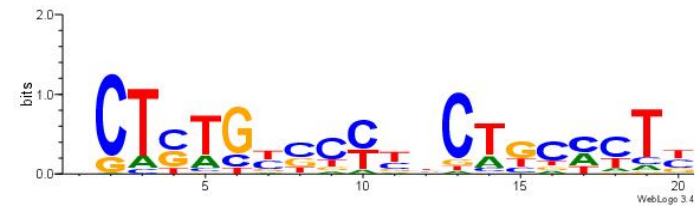
Alignment:

```
RAGKGMAGVRRGSRCASAGV-----  
-----CAMACACACACAYDCACACA
```

Original motif Consensus sequence: RAGKGMAGVRRGSRCASAGV



Reverse complement motif Consensus sequence: VCTSTGKSCMKBCTRCYCTK



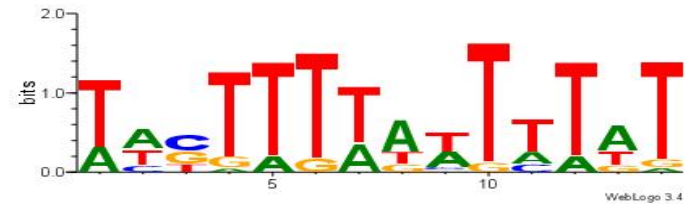
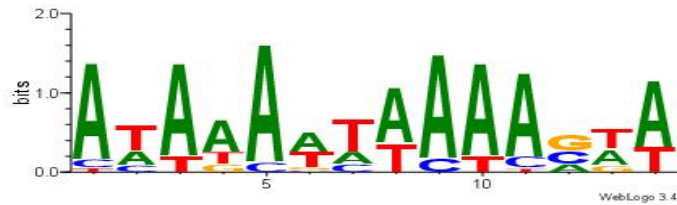
Dataset #: 2
Motif ID: 3
Motif name: Motif 3
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 2
Number of overlap: 13
Similarity score: 3.08903

Alignment:

```
TWSTTTWAWTTTWT-----  
-TGTGTGDKTGTGTGTGTRTG
```

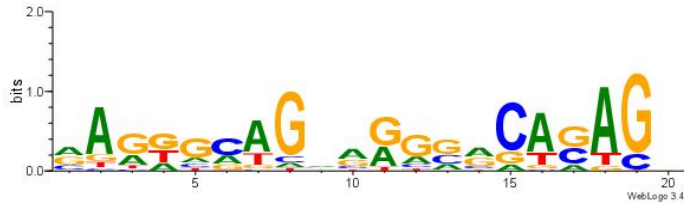
Original motif Consensus sequence: AWAAAWTWAAASWA

Reverse complement motif Consensus sequence: TWSTTTWAWTTTWT

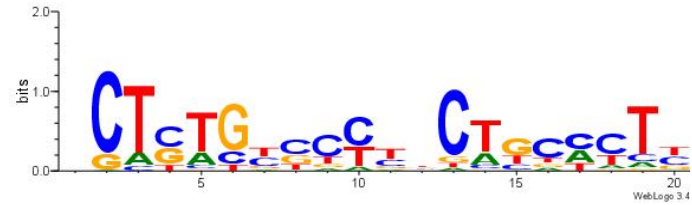


Dataset #: 5 Motif ID: 55 Motif name: TFM12

Original motif Consensus sequence: RAGKGMAGVRRGSRCASAGV



Reverse complement motif Consensus sequence: VCTSTGKSCMKBCTRCYCTK



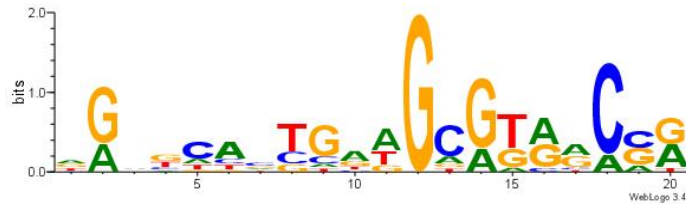
Best Matches for Motif ID 55 (Highest to Lowest)

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:	1
Number of overlap:	20
Similarity score:	0.0559712

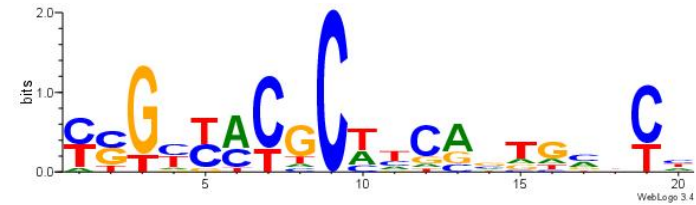
Alignment:

DGVBCABTGDWGCGRRCR
RAGKGMAGVRRGSRCASAGV

Original motif Consensus sequence: DGVBCABTGDWGCGRRCR



Reverse complement motif Consensus sequence:
MSGKKRCGCWDCABTGBBCD



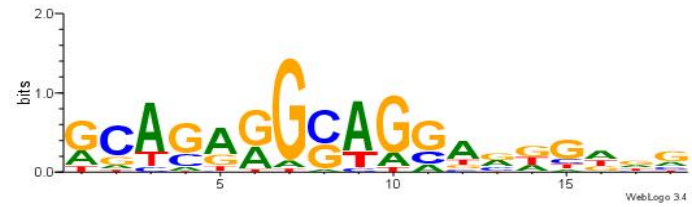
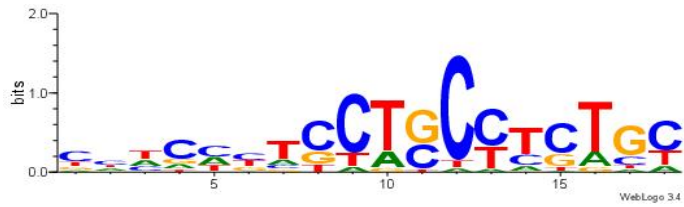
Dataset #: 5
Motif ID: 52
Motif name: TFM2
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 18
Similarity score: 1.04851

Alignment:

--CHHCHBTCCTSCYTCTGC
VCTSTGKSCMKBCTRCYCTK

Original motif Consensus sequence: CHHCHBTCCTSCYTCTGC

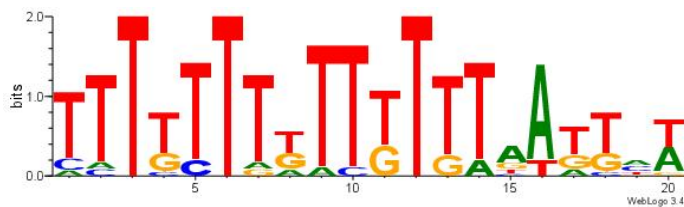
Reverse complement motif Consensus sequence:
GCAGAKGSAGGABDGHG



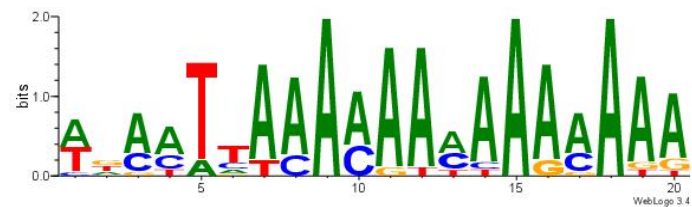
Dataset #: 5
 Motif ID: 56
 Motif name: TFM13
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3
 Number of overlap: 18
 Similarity score: 1.06828

Alignment:
 WHAATTAAARAARAAAAA--
 --RAGKGMAGVRRGSRCASAGV

Original motif Consensus sequence: TTTTTTKTKTTTAATTHW



Reverse complement motif Consensus sequence: WHAATTAAARAARAAAAA



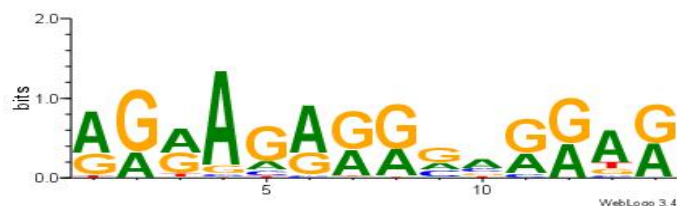
Dataset #: 2

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: 3.03181

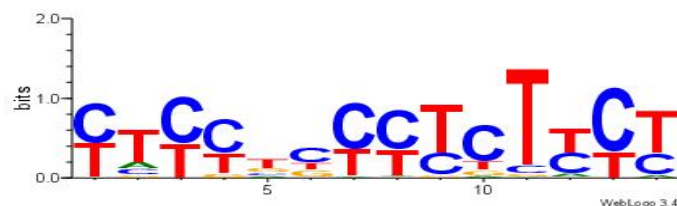
Alignment:

RGRAGARRGARRAR-----
 RAGKGMAGVRRGSRCASAGV

Original motif Consensus sequence: RGRAGARRGARRAR



Reverse complement motif Consensus sequence: MTMMTCMMTCTK

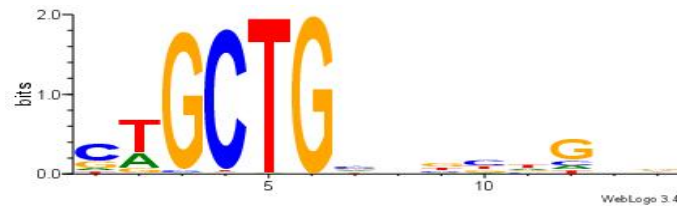


Dataset #: 5
 Motif ID: 50
 Motif name: TFF11
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 14
 Similarity score: 3.05894

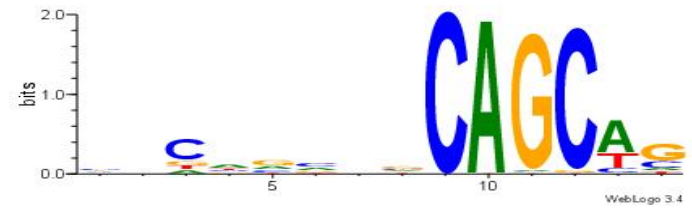
Alignment:

-----CTGCTGBDBBDGBD
VCTSTGKSCMKBCTRCYCTK

Original motif Consensus sequence: CTGCTGBDBBDGBD

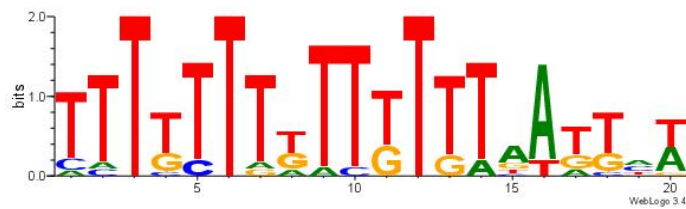


Reverse complement motif Consensus sequence: HVCDBBDBCAGCA

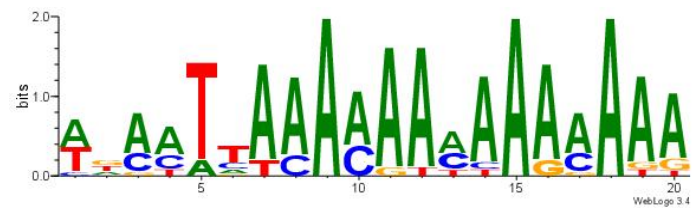


Dataset #: 5 Motif ID: 56 Motif name: TFM13

Original motif Consensus sequence: TTTTTTKTTKTTTAATTHW



Reverse complement motif Consensus sequence: WHAATTAARAARAAAAAA



Best Matches for Motif ID 56 (Highest to Lowest)

Dataset #:	5
Motif ID:	54
Motif name:	TFM11
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward

Position number: 2
 Number of overlap: 19
 Similarity score: 0.0780436

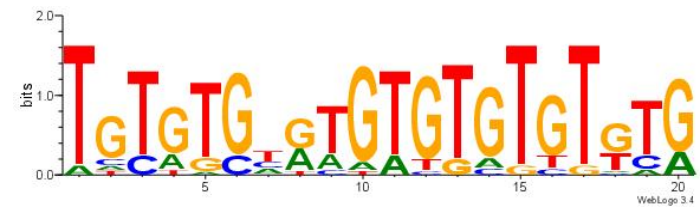
Alignment:

-CAMACACACACAYDCACACA
 WHAATTAAARAARAAAAA-

Original motif Consensus sequence: CAMACACACACAYDCACACA



Reverse complement motif Consensus sequence: TGTGTGDKTGTGTGTRTG

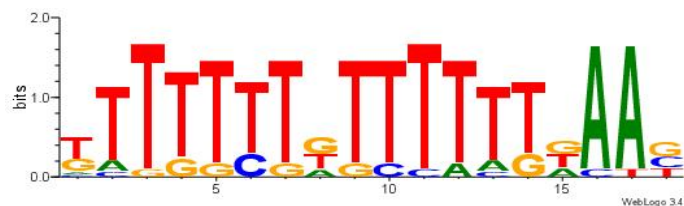


Dataset #: 5
 Motif ID: 53
 Motif name: TFM3
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 18
 Similarity score: 0.517048

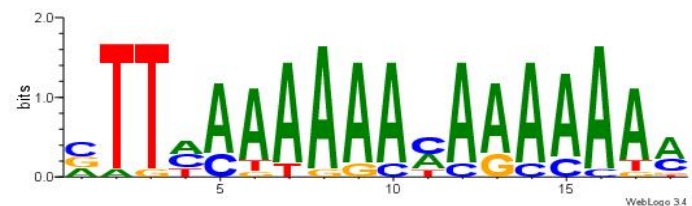
Alignment:

KTTTTTTKTTTTTTDAAB--
 TTTTTTTKTTKTTTAATHW

Original motif Consensus sequence: KTTTTTKTTTTTDAAB



Reverse complement motif Consensus sequence: BTTHAAAAAYAAAAAAR

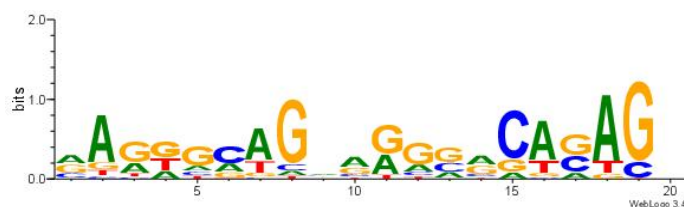


Dataset #: 5
Motif ID: 55
Motif name: TFM12
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 3
Number of overlap: 18
Similarity score: 0.582391

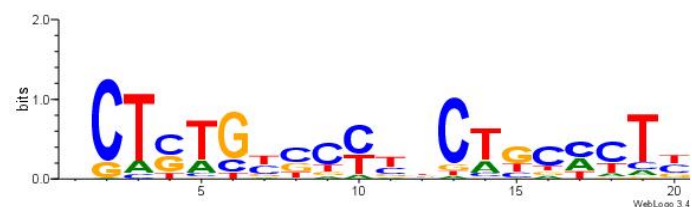
Alignment:

--VCTSTGKSCMKBCTRCYCTK
TTTTTTTTKTTKTTTAATTHW--

Original motif Consensus sequence: RAGKGMAGVRRGSRCASAGV



Reverse complement motif Consensus sequence: VCTSTGKSCMKBCTRCYCTK

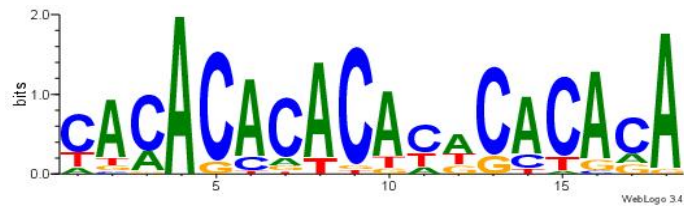


Dataset #: 5
 Motif ID: 51
 Motif name: TFM1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 15
 Similarity score: 2.0854

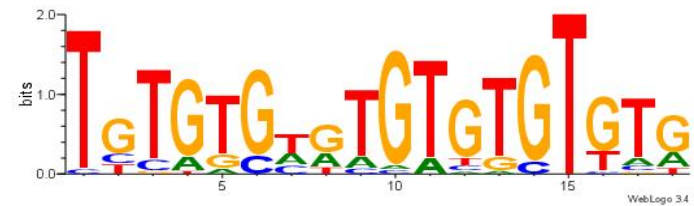
Alignment:

CACACACACACWCACACA-----
 ---WHAATTAAARAARAAAAAAA

Original motif Consensus sequence: CACACACACACWCACACA



Reverse complement motif Consensus sequence: TGTGTGWGTGTGTGTGTG



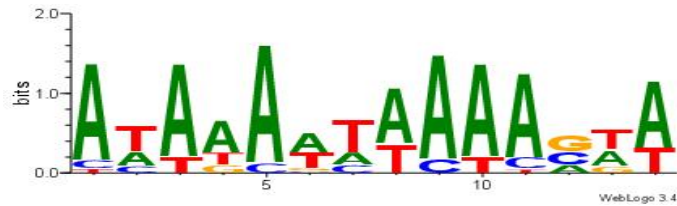
Dataset #: 2
 Motif ID: 3
 Motif name: Motif 3
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1

Number of overlap: 14
Similarity score: 2.54283

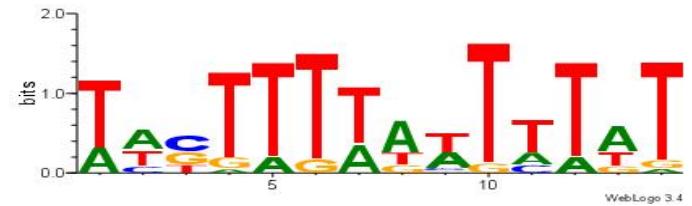
Alignment:

```
-----TWSTTTWAWTTTWT  
TTTTTTTKTTKTTTAATTHW
```

Original motif Consensus sequence: AWAAAWTWAASWA



Reverse complement motif Consensus sequence: TWSTTTWAWTTTWT



Results created by MOTIFSIM on 06-24-2023 16:08:01

Runtime: 118.467 seconds

MOTIFSIM is written by Ngoc Tam L. Tran

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