



# MOTIFSIM - MOTIF SIMilarity Detection Tool

Version 2.1

## INPUT

### Input Parameters

|                                   |                       |
|-----------------------------------|-----------------------|
| Number of files:                  | 5                     |
| Number of top significant motifs: | 10                    |
| Number of best matches:           | 10                    |
| Similarity cutoff $\geq$          | 0.75                  |
| Matching motif database:          | UniProbe Mus Musculus |
| Phylogenetic tree:                | Yes                   |
| Combined similar motifs:          | Yes                   |
| Output file type:                 | All                   |
| Output file format:               | All                   |

### Input files and motif counts

| File name                 | Count of motifs | Dataset number |
|---------------------------|-----------------|----------------|
| MEME_DM05.txt             | 46              | 1              |
| MEME-ChIP_DM05.txt        | 4               | 2              |
| PScanChIP_DM05.txt        | 16              | 3              |
| RSAT_peak-motifs_DM05.txt | 17              | 4              |
| W-ChIPMotifs_DM05.txt     | 11              | 5              |

## RESULTS

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

**Dataset #: 5      Motif ID: 84      Motif name: TFW3**

Original motif      Consensus sequence: GCACTG



Reverse complement motif      Consensus sequence: CAGTGC



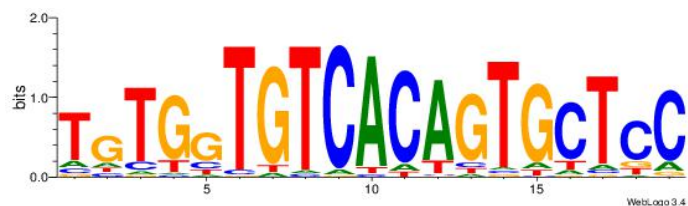
### Best Matches for Top Significant Motif ID 84 (Highest to Lowest)

|                                  |                     |
|----------------------------------|---------------------|
| Dataset #:                       | 4                   |
| Motif ID:                        | 67                  |
| Motif name:                      | TgTGgTGTCACAGTGCTCC |
| Matching format of first motif:  | Reverse Complement  |
| Matching format of second motif: | Original Motif      |
| Direction:                       | Backward            |
| Position number:                 | 11                  |
| Number of overlap:               | 6                   |
| Similarity score:                | 0                   |

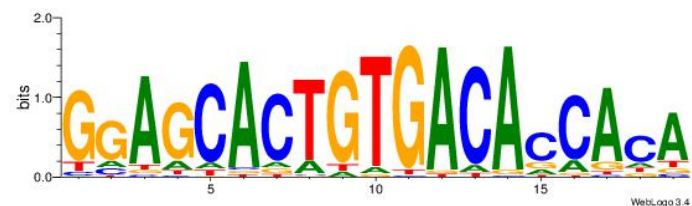
Alignment:

```
TGTGGTGTCACAGTGCTCC
---CAGTGC-----
```

Original motif      Consensus sequence: TGTGGTGTACAGTGCTCC



Reverse complement motif      Consensus sequence: GGAGCACTGTGACACCACA

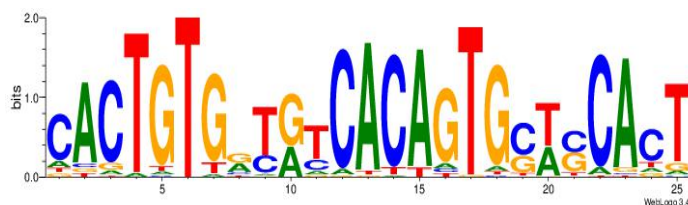


Dataset #: 4  
 Motif ID: 72  
 Motif name: CACTGTGrYrtCACAGTGswsCAcT  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 7  
 Number of overlap: 6  
 Similarity score: 0.000794289

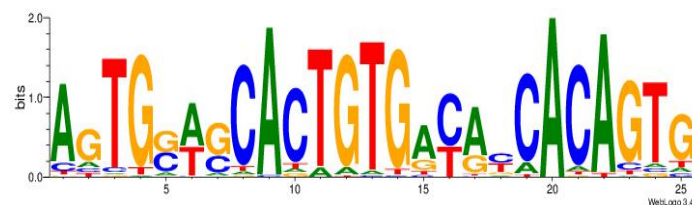
Alignment:

CACTGTGRTRTCACAGTGSWSCACT  
 -----CAGTGC-----

Original motif      Consensus sequence: CACTGTGRTRTCACAGTGSWSCACT



Reverse complement motif      Consensus sequence: AGTGSWSCACTGTGAMAMCACAGTG

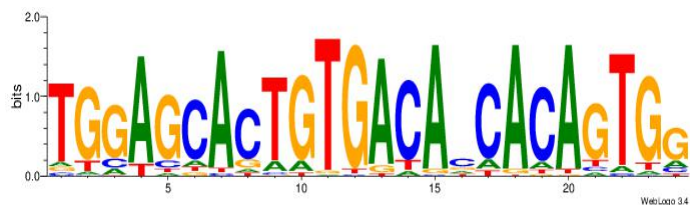


Dataset #: 4  
 Motif ID: 73  
 Motif name: TGGAGCACTGTGACAcCACAGTGg  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 5  
 Number of overlap: 6  
 Similarity score: 0.00482436

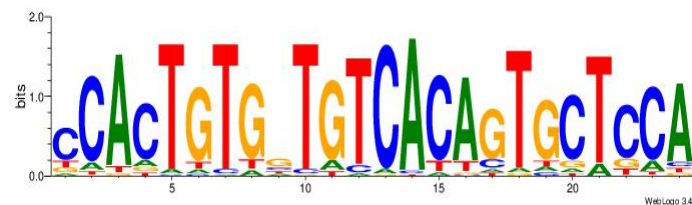
Alignment:

CCACTGTGVTGTCACAGTGCTCCA  
 -----CAGTGC-----

Original motif      Consensus sequence: TGGAGCACTGTGACAVCACAGTGG



Reverse complement motif      Consensus sequence: CCACTGTGVTGTCACAGTGCTCCA

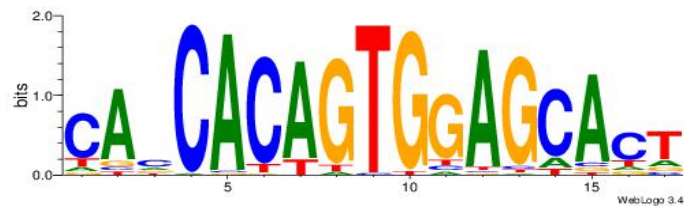


Dataset #: 4  
 Motif ID: 76  
 Motif name: CACcACAGTGGAGCAct  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 7

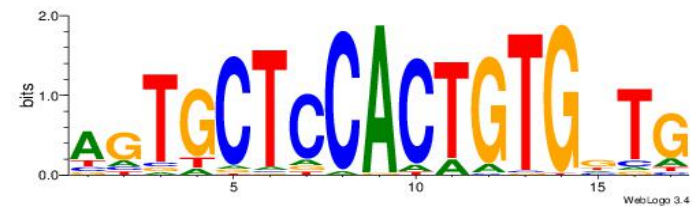
Number of overlap: 6  
Similarity score: 0.0201914

Alignment:  
CAHCACAGTGGAGCACT  
-----CAGTGC-----

Original motif      Consensus sequence: CAHCACAGTGGAGCACT



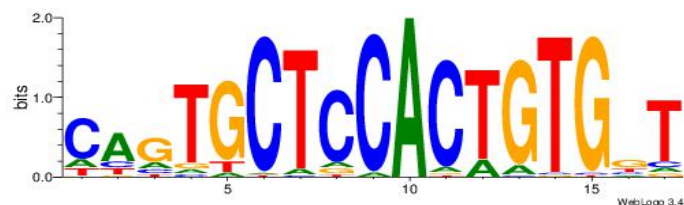
Reverse complement motif      Consensus sequence:  
AGTGCTCCACTGTGDTG



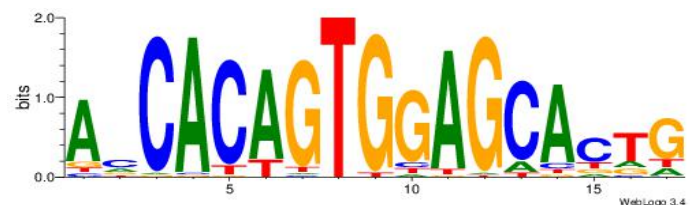
Dataset #: 4  
Motif ID: 70  
Motif name: CagTGCTCCACTGTGgT  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Reverse Complement  
Direction: Forward  
Position number: 5  
Number of overlap: 6  
Similarity score: 0.0205497

Alignment:  
ABCACAGTGGAGCACTG  
-----CAGTGC-----

Original motif      Consensus sequence: CAGTGCTCCACTGTGBT



Reverse complement motif      Consensus sequence: ABCACAGTGGAGCACTG

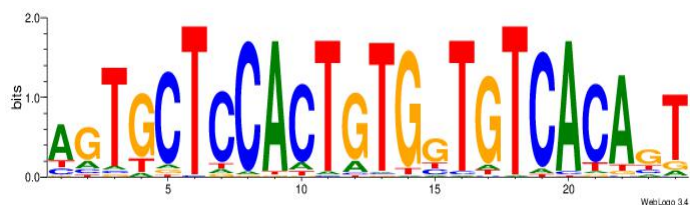


Dataset #: 4  
Motif ID: 77  
Motif name: AgTGCTCCACTGTGgTGTCACAgT  
Matching format of first motif: Original Motif  
Matching format of second motif: Original Motif  
Direction: Backward  
Position number: 13  
Number of overlap: 6  
Similarity score: 0.0290883

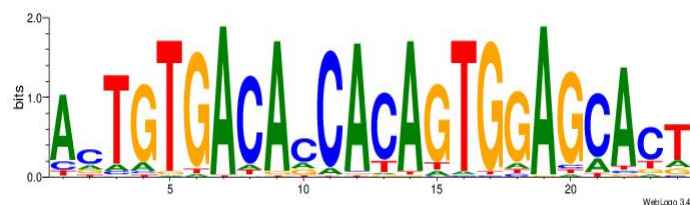
Alignment:

AGTGCTCCACTGTGGTGTTCACAGT  
-----GCACTG-----

Original motif      Consensus sequence: AGTGCTCCACTGTGGTGTTCACAGT



Reverse complement motif      Consensus sequence: ACTGTGACACCACAGTGGAGCACT

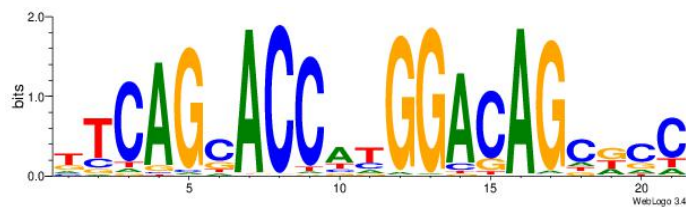


Dataset #: 3  
 Motif ID: 57  
 Motif name: REST  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 15  
 Number of overlap: 6  
 Similarity score: 0.039883

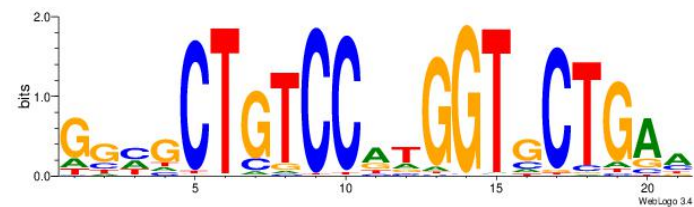
Alignment:

TTCAGCACCATGGACAGCKCC  
 -CAGTGC-----

Original motif      Consensus sequence: TTCAGCACCATGGACAGCKCC



Reverse complement motif      Consensus sequence: GGYGCTGTCCATGGTGCTGAA

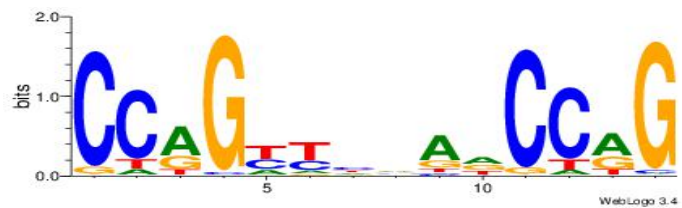


Dataset #: 3  
 Motif ID: 65  
 Motif name: Tcfcp2l1  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 8

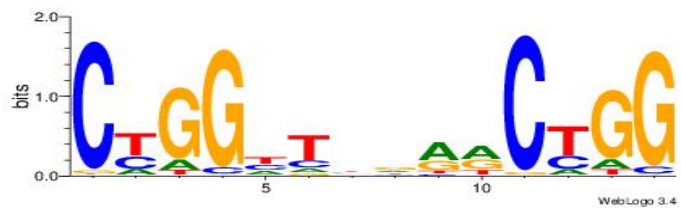
Number of overlap: 6  
Similarity score: 0.0447224

Alignment:  
CCAGYYHVADCCRG  
-----CAGTGC-

Original motif      Consensus sequence: CCAGYYHVADCCRG



Reverse complement motif      Consensus sequence: CKGGDTBDMMCTV



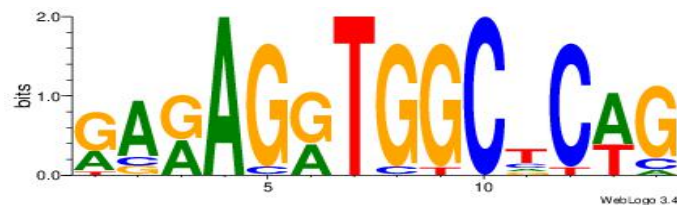
Dataset #: 1  
Motif ID: 5  
Motif name: Motif 5  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Original Motif  
Direction: Forward  
Position number: 9  
Number of overlap: 6  
Similarity score: 0.0459818

Alignment:  
CWGAGCCAYCTYTC  
-----CAGTGC

Original motif      Consensus sequence: CWGAGCCAYCTYTC

Reverse complement motif      Consensus sequence: GAKAGKTGGCTCV

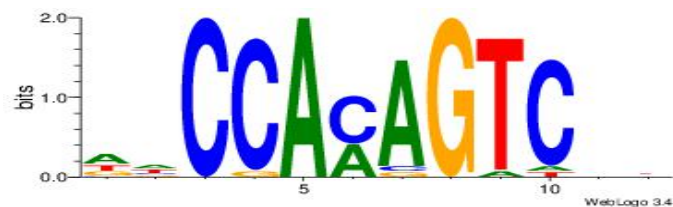




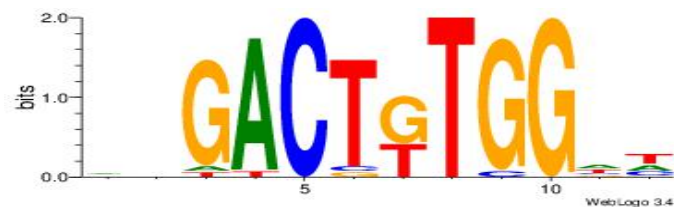
Dataset #: 4  
 Motif ID: 75  
 Motif name: wwCCAmAGTCmt  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 6  
 Number of overlap: 6  
 Similarity score: 0.0587933

Alignment:  
 VDGACTRTGGDD  
 -----GCACTG-

Original motif      Consensus sequence: DDCCAMAGTCHB

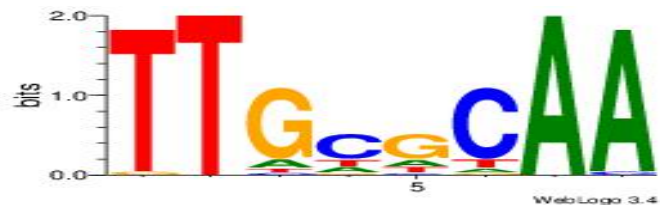


Reverse complement motif      Consensus sequence: VDGACTRTGGDD

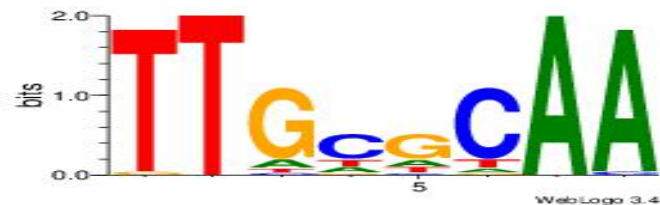


**Dataset #: 5      Motif ID: 85      Motif name: TFW1**

Original motif      Consensus sequence: TTGCGCAA



Reverse complement motif      Consensus sequence: TTGCGCAA



### Best Matches for Top Significant Motif ID 85 (Highest to Lowest)

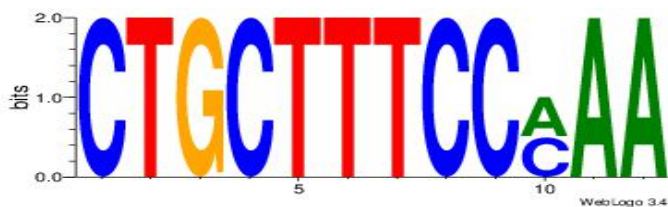
|                                  |                    |
|----------------------------------|--------------------|
| Dataset #:                       | 1                  |
| Motif ID:                        | 21                 |
| Motif name:                      | Motif 21           |
| Matching format of first motif:  | Original Motif     |
| Matching format of second motif: | Reverse Complement |
| Direction:                       | Backward           |
| Position number:                 | 1                  |
| Number of overlap:               | 8                  |
| Similarity score:                | 0.0195312          |

Alignment:

TTYGGAAAGCAG

----TTGCGCAA

Original motif      Consensus sequence: CTGCTTTCCMAA



Reverse complement motif      Consensus sequence: TTYGGAAAGCAG

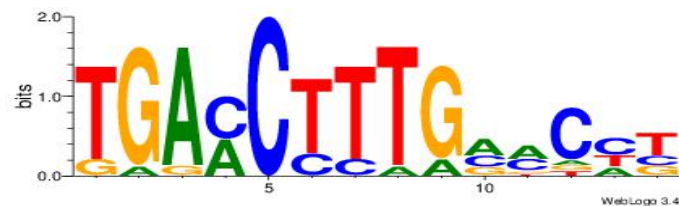


Dataset #: 3  
 Motif ID: 52  
 Motif name: NR2F1  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 8  
 Similarity score: 0.0276442

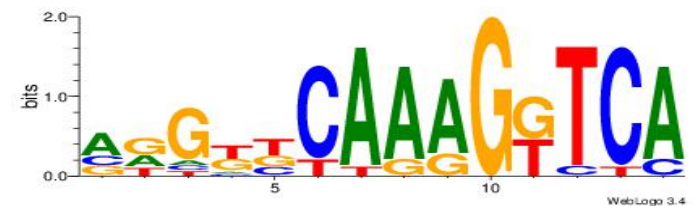
Alignment:

AKGYCAAAGRTCA  
 TTGCGCAA-----

Original motif      Consensus sequence: TGAMCTTTGMMCYT



Reverse complement motif      Consensus sequence: AKGYCAAAGRTCA

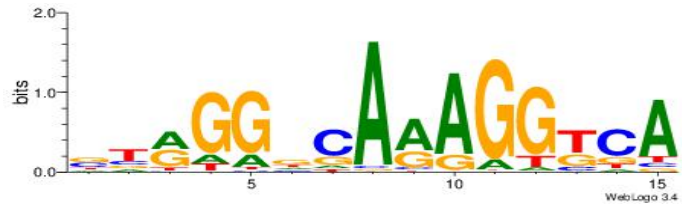


Dataset #: 3  
 Motif ID: 64  
 Motif name: PPARGRXRA  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 7  
 Number of overlap: 8

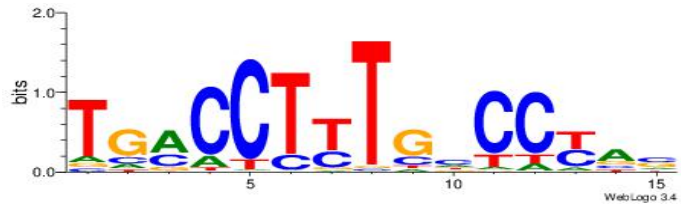
Similarity score: 0.0277567

Alignment:  
BTRGGDCARAGGKCA  
-----TTGCGCAA-

Original motif      Consensus sequence: BTRGGDCARAGGKCA



Reverse complement motif      Consensus sequence: TGRCCCTKTGHCCCK



Dataset #: 1  
Motif ID: 28  
Motif name: Motif 28  
Matching format of first motif: Original Motif  
Matching format of second motif: Reverse Complement  
Direction: Backward  
Position number: 2  
Number of overlap: 8  
Similarity score: 0.0328125

Alignment:  
TTTACTAAAT  
-TTGCGCAA-

Original motif      Consensus sequence: ATTAGTAAA

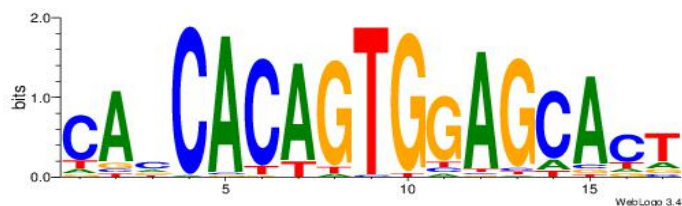
Reverse complement motif      Consensus sequence: TTTACTAAAT



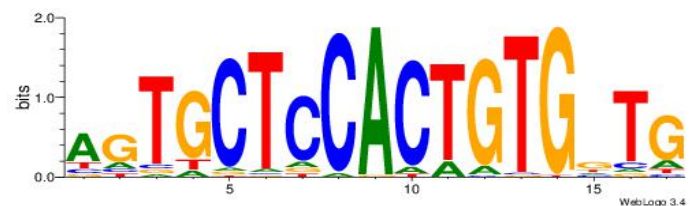
Dataset #: 4  
 Motif ID: 76  
 Motif name: CACACAGTGGAGCACT  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 2  
 Number of overlap: 8  
 Similarity score: 0.0336914

Alignment:  
 CAHCACAGTGGAGCACT  
 -TTGCGCAA-----

Original motif      Consensus sequence: CAHCACAGTGGAGCACT



Reverse complement motif      Consensus sequence: AGTGCTCCACTGTGDTG



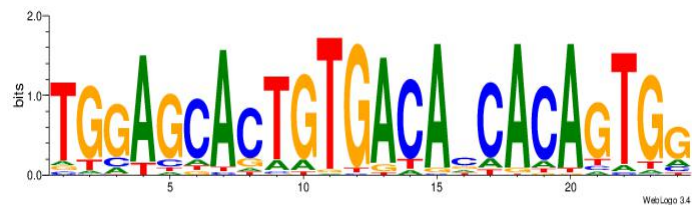
Dataset #: 4

Motif ID: 73  
 Motif name: TGGAGCACTGTGACAcCACAGTGg  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 17  
 Number of overlap: 8  
 Similarity score: 0.0338471

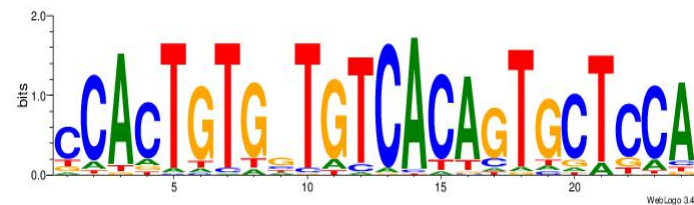
Alignment:

TGGAGCACTGTGACAVCACAGTGG  
 TTGCGCAA-----

Original motif    Consensus sequence: TGGAGCACTGTGACAVCACAGTGG



Reverse complement motif    Consensus sequence: CCACTGTGVTGTACAGTGCTCCA



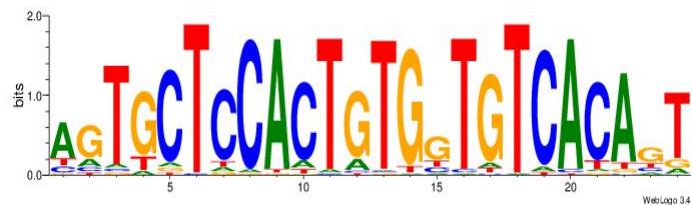
Dataset #: 4  
 Motif ID: 77  
 Motif name: AgTGCTCCACTGTGgTGTCACAgT  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 2  
 Number of overlap: 8

Similarity score: 0.034375

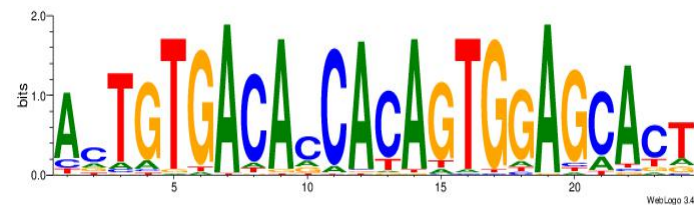
Alignment:

AGTGCTCCACTGTGGTGTACAGT  
-----TTGCGCAA-

Original motif      Consensus sequence: AGTGCTCCACTGTGGTGTACAGT



Reverse complement motif      Consensus sequence:  
ACTGTGACACCACAGTGGAGCACT



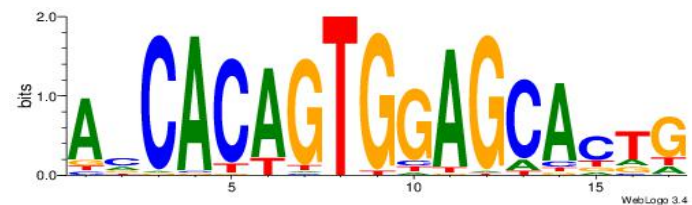
Dataset #: 4  
Motif ID: 70  
Motif name: CagTGCTCCACTGTGgT  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Original Motif  
Direction: Backward  
Position number: 3  
Number of overlap: 8  
Similarity score: 0.0354167

Alignment:

CAGTGCTCCACTGTGBT  
-----TTGCGCAA--

Original motif      Consensus sequence: CAGTGCTCCACTGTGBT

Reverse complement motif      Consensus sequence:  
ABCACAGTGGAGCACTG

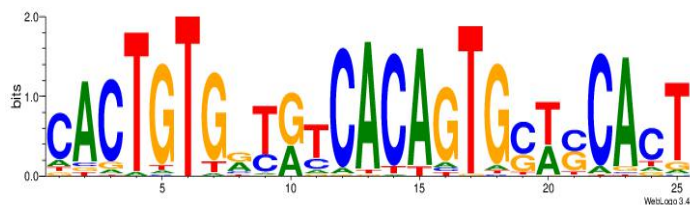


|                                  |                           |
|----------------------------------|---------------------------|
| Dataset #:                       | 4                         |
| Motif ID:                        | 72                        |
| Motif name:                      | CACTGTGrYrtCACAGTGswsCAcT |
| 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:                | 0.0407242                 |

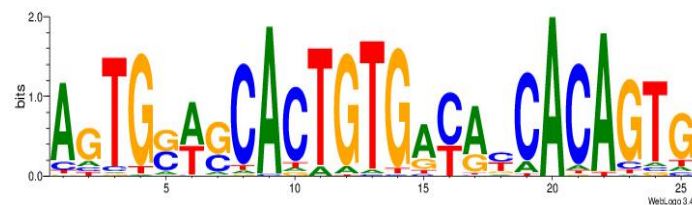
Alignment:

CACTGTGRTRTCACAGTGSWSCACT  
-----TTGCGCAA--

Original motif      Consensus sequence:  
CACTGTGRTRTCACAGTGSWSCACT



Reverse complement motif    Consensus sequence:  
AGTGSWSCACTGTGAMAMCACAGTG



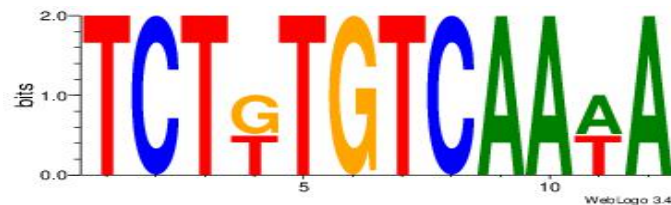
Dataset #: 1



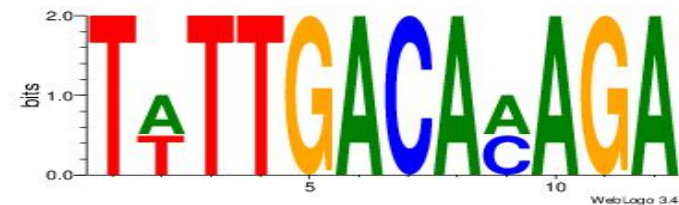
Motif ID: 16  
 Motif name: Motif 16  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 3  
 Number of overlap: 8  
 Similarity score: 0.0421875

Alignment:  
 TWTTGACAYAGA  
 --TTGCGCAA--

Original motif      Consensus sequence: TCTKTGTCAAWA



Reverse complement motif      Consensus sequence: TWTTGACAYAGA



**Dataset #: 3      Motif ID: 55      Motif name: ZEB1**

Original motif      Consensus sequence: CACCTD



Reverse complement motif      Consensus sequence: HAGGTG



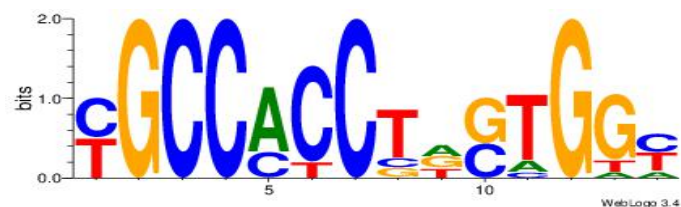
## Best Matches for Top Significant Motif ID 55 (Highest to Lowest)

Dataset #: 2  
 Motif ID: 47  
 Motif name: Motif 47  
 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

Alignment:

YGCCACCTDSTGGY  
 ---CACCTD-----

Original motif      Consensus sequence: YGCCACCTDSTGGY



Reverse complement motif      Consensus sequence: KCCASDAGGTGGC



Dataset #: 1  
 Motif ID: 5  
 Motif name: Motif 5  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif

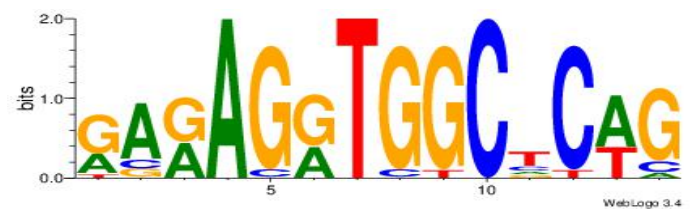
Direction: Forward  
 Position number: 7  
 Number of overlap: 6  
 Similarity score: 0.00902841

Alignment:  
 CWGAGCCAYCTYTC  
 -----CACCTD--

Original motif      Consensus sequence: CWGAGCCAYCTYTC



Reverse complement motif      Consensus sequence: GAKAGKTGGCTCV



Dataset #: 1  
 Motif ID: 46  
 Motif name: Motif 46  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 8  
 Number of overlap: 6  
 Similarity score: 0.0285279

Alignment:  
 TATKCTAAACCTAT  
 -CACCTD-----

Original motif      Consensus sequence: ATAGGTTTAGYATA



Reverse complement motif      Consensus sequence: TATKCTAAACCTAT

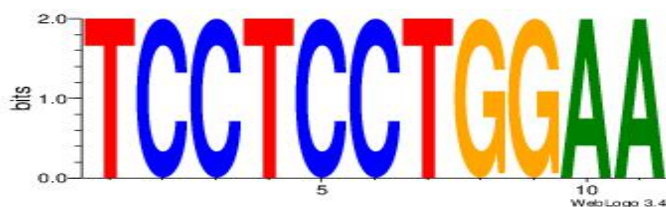


Dataset #: 1  
 Motif ID: 20  
 Motif name: Motif 20  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 3  
 Number of overlap: 6  
 Similarity score: 0.0346255

Alignment:

TCCTCCTGGAA  
 --CACCTD---

Original motif      Consensus sequence: TCCTCCTGGAA



Reverse complement motif      Consensus sequence: TTCCAGGAGGA



Dataset #: 1  
 Motif ID: 12  
 Motif name: Motif 12  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 5  
 Number of overlap: 6  
 Similarity score: 0.0376742

Alignment:

ACAACACATTT  
 ----CACCTD-

Original motif      Consensus sequence: ACAACACATTT



Reverse complement motif      Consensus sequence: AAATGTGTTGT



Dataset #: 1  
 Motif ID: 34  
 Motif name: Motif 34  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 2  
 Number of overlap: 6

Similarity score: 0.0397068

Alignment:  
AAAGATGA  
-HAGGTG-

Original motif      Consensus sequence: AAAGATGA



Reverse complement motif      Consensus sequence: TCATCTTT



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Dataset #: 1  
Motif ID: 22  
Motif name: Motif 22  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Original Motif  
Direction: Backward  
Position number: 4  
Number of overlap: 6  
Similarity score: 0.0397068

Alignment:  
TTTATGGTGAGCAT  
-----HAGGTG---

Original motif      Consensus sequence: TTTATGGTGAGCAT

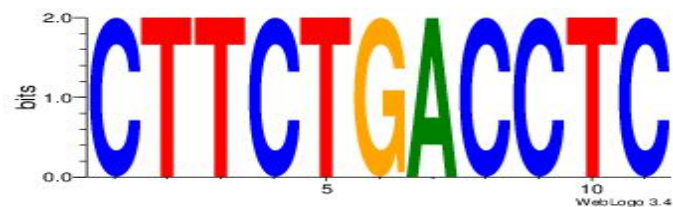
Reverse complement motif      Consensus sequence: ATGCTCACCATAA



Dataset #: 1  
 Motif ID: 17  
 Motif name: Motif 17  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 6  
 Number of overlap: 6  
 Similarity score: 0.0458043

Alignment:  
 GAGGTCAGAAG  
 HAGGTG-----

Original motif      Consensus sequence: CTTCTGACCTC



Reverse complement motif      Consensus sequence: GAGGTCAGAAG



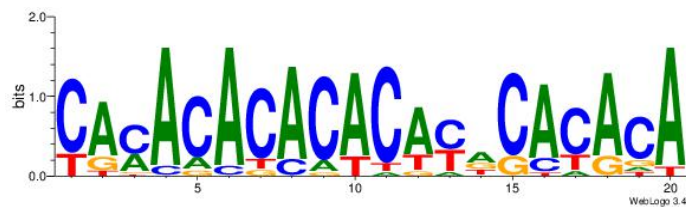
Dataset #: 5  
 Motif ID: 92

Motif name: TFM11  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 7  
 Number of overlap: 6  
 Similarity score: 0.0461561

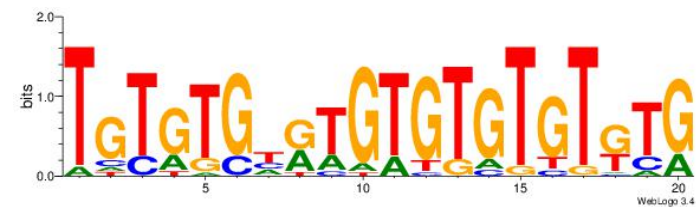
Alignment:

CAMACACACACAYDCACACA  
 -----CACCTD-----

Original motif      Consensus sequence: CAMACACACACAYDCACACA



Reverse complement motif      Consensus sequence: TGTGTGDKTGTGTGTGTRTG



Dataset #: 5  
 Motif ID: 89  
 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: 6  
 Similarity score: 0.0467843

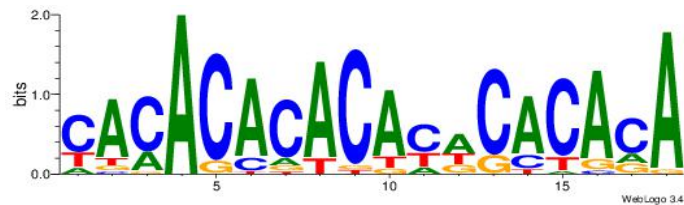


Alignment:

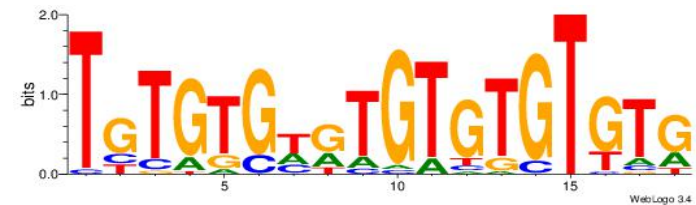
CACACACACACWCACACA

-----CACCTD-----

Original motif      Consensus sequence: CACACACACACWCACACA

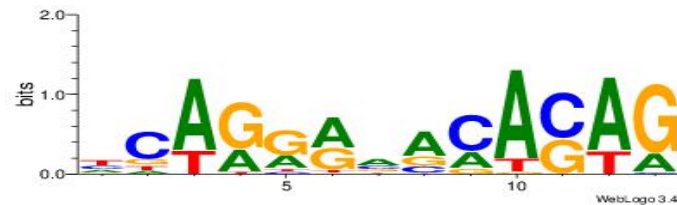


Reverse complement motif      Consensus sequence: TGTGTGWGTGTGTGTGTG

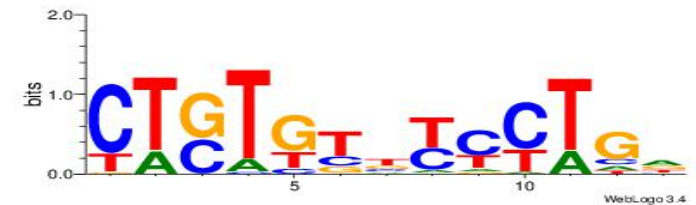


**Dataset #: 1      Motif ID: 3      Motif name: Motif 3**

Original motif      Consensus sequence: HCAGRRVACASAG



Reverse complement motif      Consensus sequence: CTSTGTBKMCTGHH



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

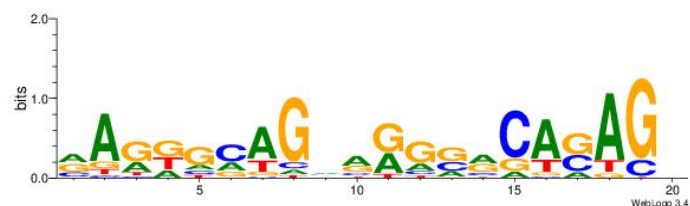
|                                  |                |
|----------------------------------|----------------|
| Dataset #:                       | 5              |
| Motif ID:                        | 93             |
| Motif name:                      | TFM12          |
| Matching format of first motif:  | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction:                       | Forward        |

Position number: 7  
 Number of overlap: 13  
 Similarity score: 0.00926418

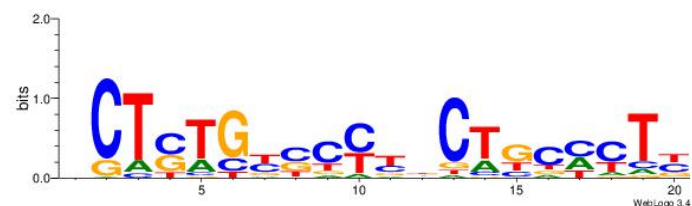
Alignment:

RAGKGMAGVRRGSRCASAGV  
 -----HCAGRRVACASAG--

Original motif Consensus sequence: RAGKGMAGVRRGSRCASAGV



Reverse complement motif Consensus sequence:  
 VCTSTGKSCMKBCTRCYCTK

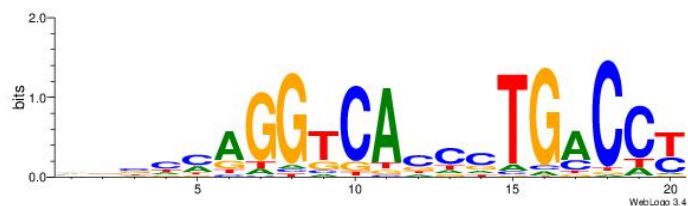


Dataset #: 3  
 Motif ID: 53  
 Motif name: ESR1  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 4  
 Number of overlap: 13  
 Similarity score: 0.0328703

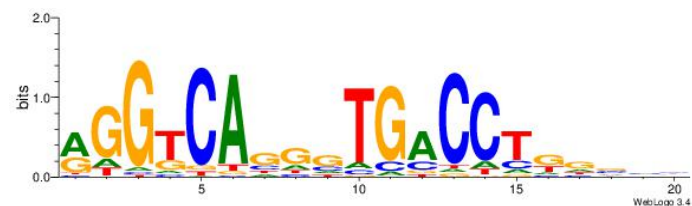
Alignment:

VDBHMAGGTCACCCTGACCY  
 ---HCAGRRVACASAG----

Original motif      Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif      Consensus sequence: MGGTCAGGGTGACCTRDBHV

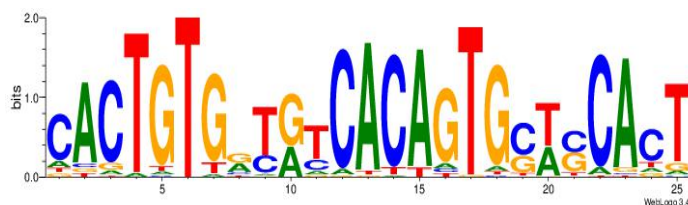


Dataset #: 4  
Motif ID: 72  
Motif name: CACTGTGrYrtCACAGTGswsCAcT  
Matching format of first motif: Original Motif  
Matching format of second motif: Reverse Complement  
Direction: Backward  
Position number: 3  
Number of overlap: 13  
Similarity score: 0.0400966

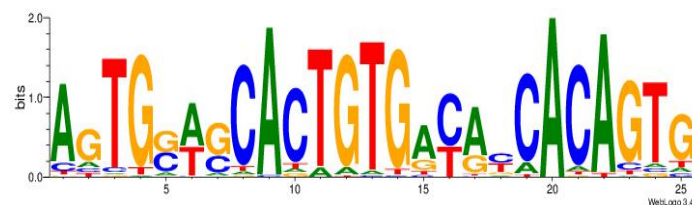
Alignment:

AGTGSWSCACTGTGAMAMCACAGTG  
-----HCAGRRVACASAG--

Original motif      Consensus sequence:  
CACTGTGRTRTCACAGTGSWSCACT



Reverse complement motif      Consensus sequence:  
AGTGSWSCACTGTGAMAMCACAGTG

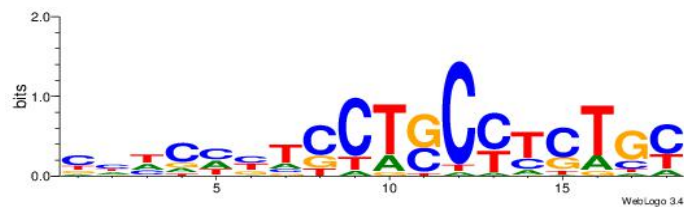


Dataset #: 5  
 Motif ID: 90  
 Motif name: TFM2  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 3  
 Number of overlap: 13  
 Similarity score: 0.0435274

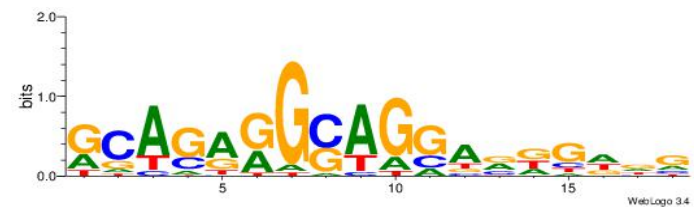
Alignment:

GCAGAKGSAGGABDGHG  
 --HCAGRRVACASAG---

Original motif      Consensus sequence: CHHCHBTCCTSCYTCTGC



Reverse complement motif      Consensus sequence: GCAGAKGSAGGABDGHG



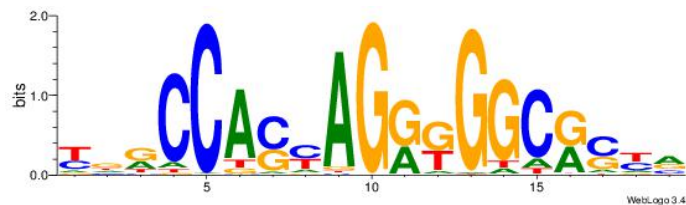
Dataset #: 3  
 Motif ID: 66  
 Motif name: CTCF  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 7

Number of overlap: 13  
Similarity score: 0.0448341

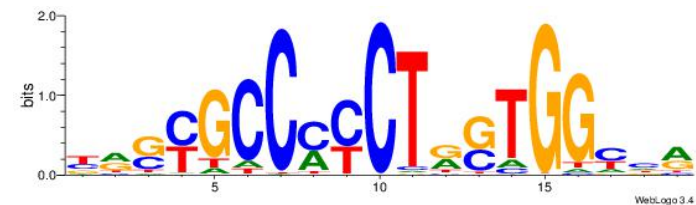
Alignment:

YDRCCASYAGRKGGRSYV  
-----HCAGRRVACASAG

Original motif      Consensus sequence: YDRCCASYAGRKGGRSYV



Reverse complement motif      Consensus sequence:  
BMSMGCCYMCTKSTGGMHM

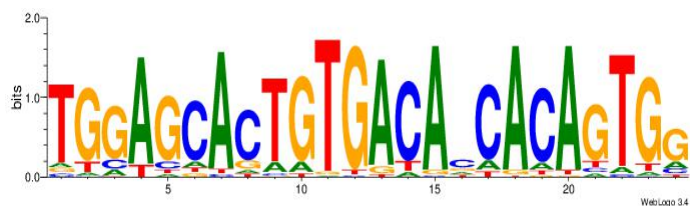


Dataset #: 4  
Motif ID: 73  
Motif name: TGGAGCACTGTGACAcCACAGTGg  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Reverse Complement  
Direction: Forward  
Position number: 4  
Number of overlap: 13  
Similarity score: 0.045698

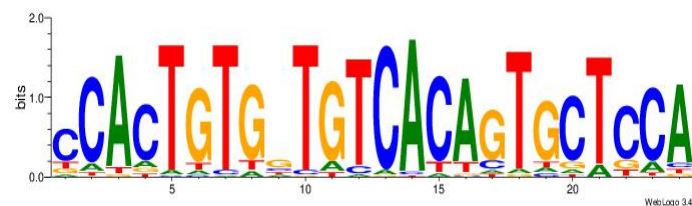
Alignment:

CCACTGTGVTGTCACAGTGCTCCA  
---CTSTGTBKMCTGH-----

Original motif      Consensus sequence: TGGAGCACTGTGACAVCACAGTGG



Reverse complement motif      Consensus sequence: CCACTGTGVTGTACAGTGCTCCA

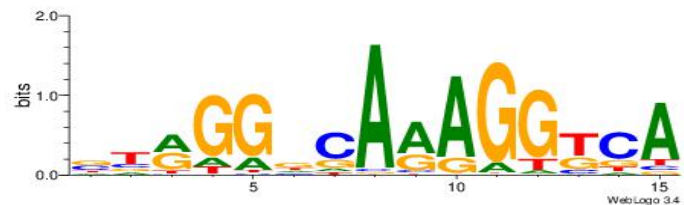


Dataset #: 3  
 Motif ID: 64  
 Motif name: PPARGRXRA  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 13  
 Similarity score: 0.0457253

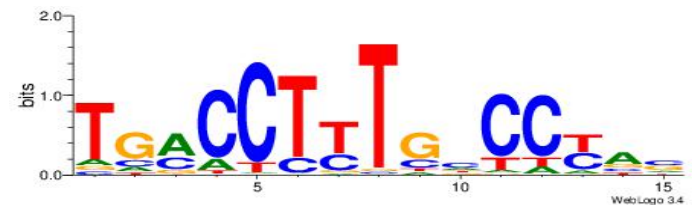
Alignment:

BTRGGDCARAGGKCA  
 HCAGRRVACASAG--

Original motif      Consensus sequence: BTRGGDCARAGGKCA



Reverse complement motif      Consensus sequence: TGRCCCTKTGHCCK

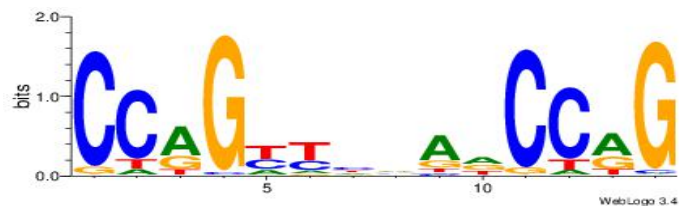


Dataset #: 3  
 Motif ID: 65  
 Motif name: Tcfcp2l1  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 13  
 Similarity score: 0.0477557

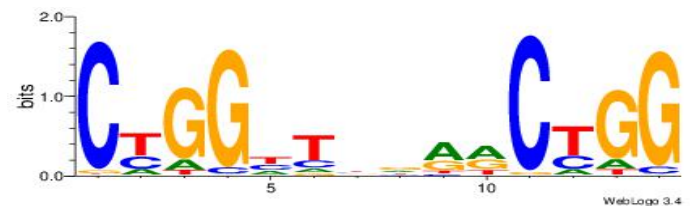
Alignment:

CKGGDTBDMMCTGG  
 CTSTGTBKMCTGH-

Original motif      Consensus sequence: CCAGYYHVADCCRG



Reverse complement motif      Consensus sequence: CKGGDTBDMMCTGG

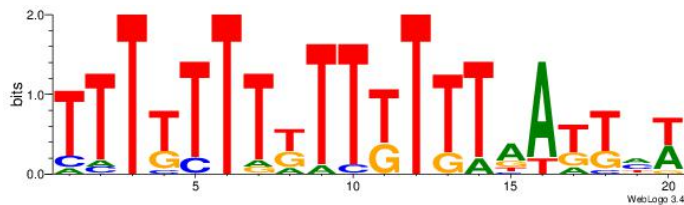


Dataset #: 5  
 Motif ID: 94  
 Motif name: TFM13  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 4  
 Number of overlap: 13

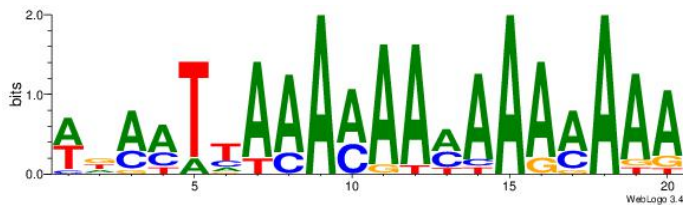
Similarity score: 0.0478998

Alignment:  
WHAATTAAARAARAAAAAAA  
----HCAGRRVACASAG----

Original motif      Consensus sequence: TTTTTTKTTKTTTAATTHW



Reverse complement motif      Consensus sequence: WHAATTAAARAARAAAAAAA



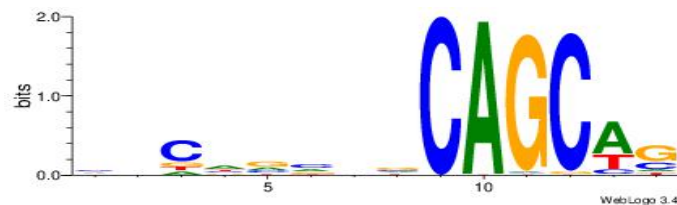
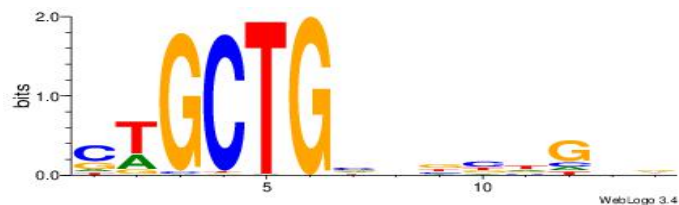
Dataset #: 5  
Motif ID: 88  
Motif name: TFF11  
Matching format of first motif: Original Motif  
Matching format of second motif: Reverse Complement  
Direction: Backward  
Position number: 1  
Number of overlap: 13  
Similarity score: 0.048132

Alignment:  
HVCDBBDBCAGCAG  
-HCAGRRVACASAG

Original motif      Consensus sequence: CTGCTGBDBBDGBD

Reverse complement motif      Consensus sequence: HVCDBBDBCAGCA



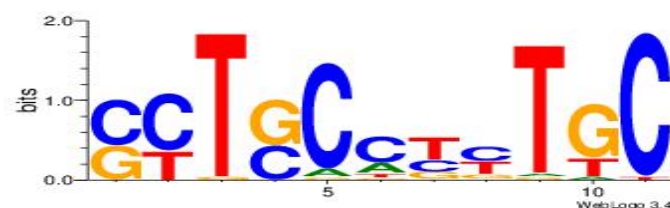


**Dataset #: 2      Motif ID: 48      Motif name: Motif 48**

Original motif      Consensus sequence: GCARRGGSAGS



Reverse complement motif      Consensus sequence: SCTSCCKMTGC

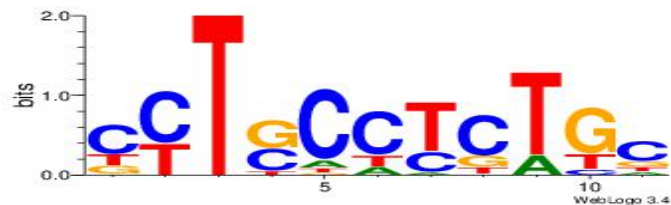


### Best Matches for Top Significant Motif ID 48 (Highest to Lowest)

|                                  |                    |
|----------------------------------|--------------------|
| Dataset #:                       | 1                  |
| Motif ID:                        | 1                  |
| Motif name:                      | Motif 1            |
| 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                  |

Alignment:  
CYTSCCTCTGC  
SCTSCCKMTGC

Original motif      Consensus sequence: CYTSCCTCTGC



Reverse complement motif      Consensus sequence: GCAGAGGSAKG

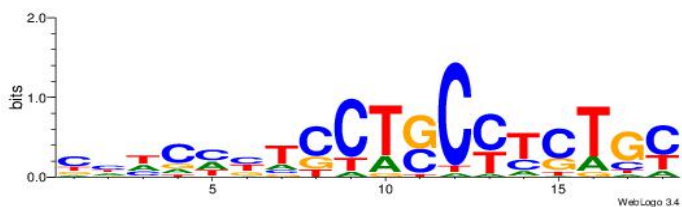


Dataset #: 5  
 Motif ID: 90  
 Motif name: TFM2  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 11  
 Similarity score: 0.000952693

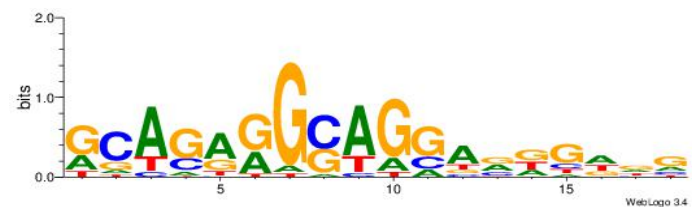
Alignment:

GCAGAKGSAGGABDGHG  
 GCARRGGSAGS-----

Original motif      Consensus sequence: CHHCHBTCCTSCYTCTGC



Reverse complement motif      Consensus sequence: GCAGAKGSAGGABDGHG

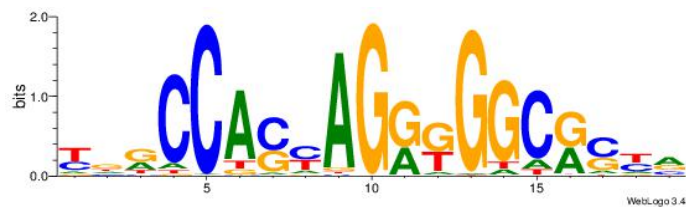


Dataset #: 3  
 Motif ID: 66  
 Motif name: CTCF  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 3  
 Number of overlap: 11  
 Similarity score: 0.033658

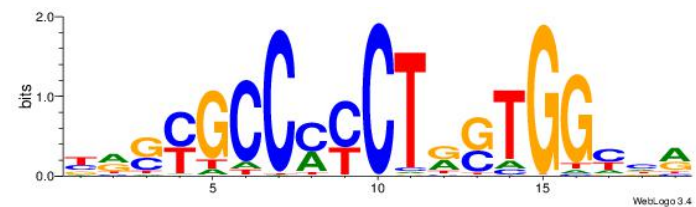
Alignment:

YDRCCASYAGRKGGRSYV  
 -----GCARRGGSAGS--

Original motif      Consensus sequence: YDRCCASYAGRKGGRSYV



Reverse complement motif      Consensus sequence: BMSMGCCYMCTKSTGGMHM

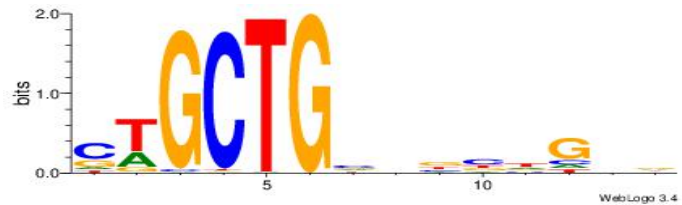


Dataset #: 5  
 Motif ID: 88  
 Motif name: TFF11  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 3

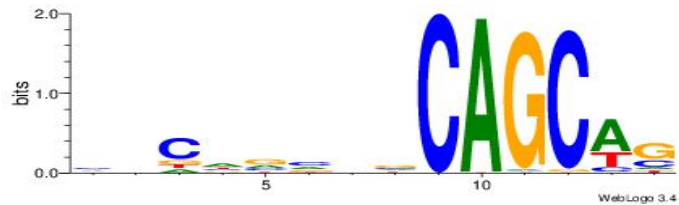
Number of overlap: 11  
Similarity score: 0.0410341

Alignment:  
CTGCTGBDBBDGBD  
--SCTSCCKMTGC--

Original motif      Consensus sequence: CTGCTGBDBBDGBD



Reverse complement motif      Consensus sequence: HVCDBBDBCAGCA

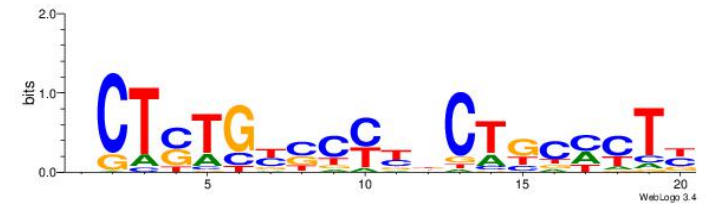


Dataset #: 5  
Motif ID: 93  
Motif name: TFM12  
Matching format of first motif: Original Motif  
Matching format of second motif: Original Motif  
Direction: Backward  
Position number: 6  
Number of overlap: 11  
Similarity score: 0.0422459

Alignment:  
RAGKGMAGVRRGSRCASAGV  
----GCARRGGSAGS-----

Original motif      Consensus sequence: RAGKGMAGVRRGSRCASAGV

Reverse complement motif      Consensus sequence:  
VCTSTGKSCMKBCTRCYCTK



Alignment:

```
CCAGYYHVADCCRG
SCTSCCKMTGC---
```

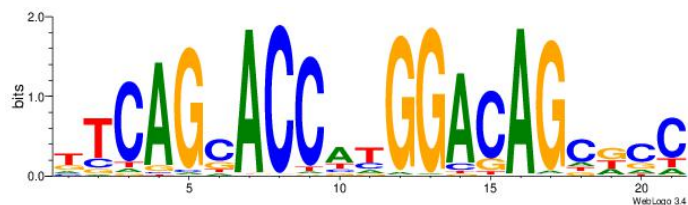
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|                                  |                    |
|----------------------------------|--------------------|
| Motif name:                      | REST               |
| Matching format of first motif:  | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction:                       | Forward            |
| Position number:                 | 4                  |
| Number of overlap:               | 11                 |
| Similarity score:                | 0.0578944          |

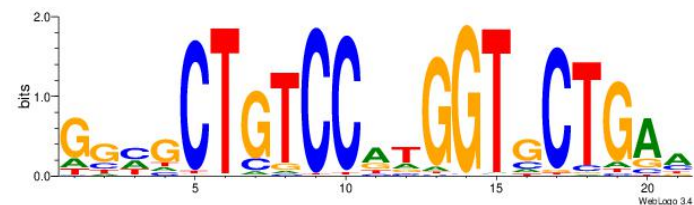
**Alignment:**

```
GGYGCTGTCCATGGTGCTGAA
---SCTSCCKMTGC-----
```

Original motif      Consensus sequence: TTCAGCACCATGGACAGCKCC



Reverse complement motif      Consensus sequence: GGYGCTGTCCATGGTGCTGAA

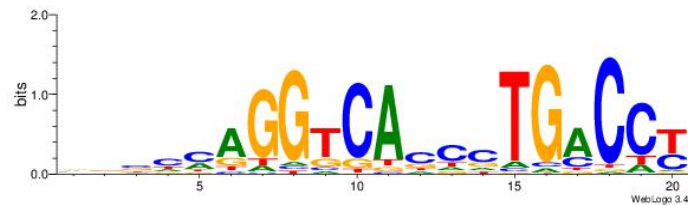


|                                  |                |
|----------------------------------|----------------|
| Dataset #:                       | 3              |
| Motif ID:                        | 53             |
| Motif name:                      | ESR1           |
| Matching format of first motif:  | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction:                       | Forward        |
| Position number:                 | 3              |
| Number of overlap:               | 11             |
| Similarity score:                | 0.0620615      |

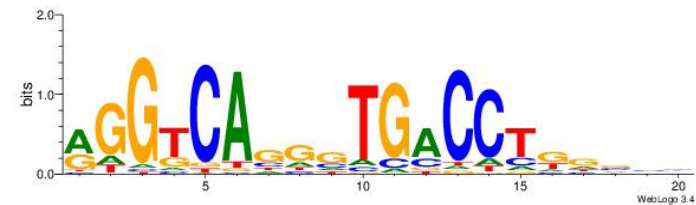
Alignment:

VDBHMAGGTCACCCTGACCY  
--GCARRGGSAGS-----

Original motif      Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif      Consensus sequence:  
MGGTCAGGGTGACCTRDBHV



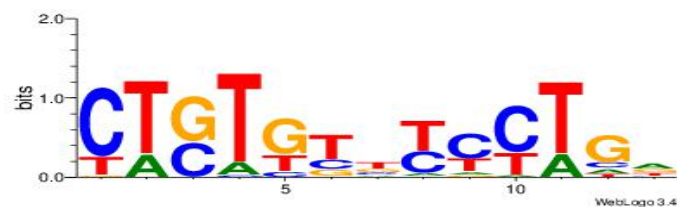
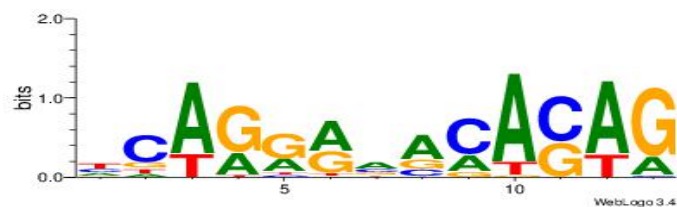
|                                  |                |
|----------------------------------|----------------|
| Dataset #:                       | 1              |
| Motif ID:                        | 3              |
| Motif name:                      | Motif 3        |
| Matching format of first motif:  | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction:                       | Forward        |
| Position number:                 | 1              |
| Number of overlap:               | 11             |
| Similarity score:                | 0.0627554      |

Alignment:

HCAGRRVACASAG  
GCARRGGSAGS--

Original motif      Consensus sequence: HCAGRRVACASAG

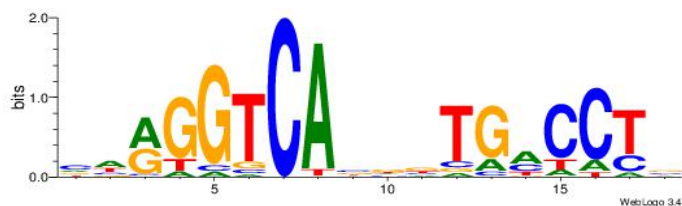
Reverse complement motif      Consensus sequence: CTSTGTBKMCTGHH



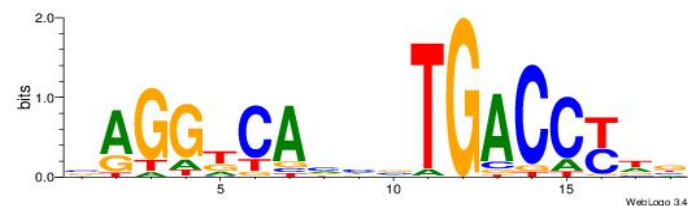
Dataset #: 3  
 Motif ID: 59  
 Motif name: ESR2  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 5  
 Number of overlap: 11  
 Similarity score: 0.0646979

Alignment:  
 VHRGGTCABDBTGMCTB  
 ---SCTSCCKMTGC----

Original motif      Consensus sequence: VHRGGTCABDBTGMCTB



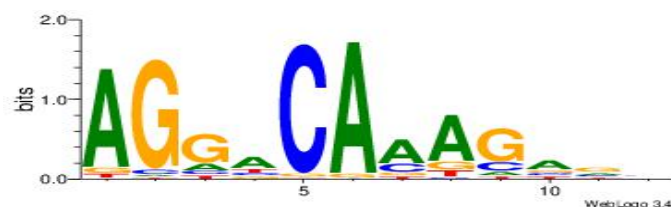
Reverse complement motif      Consensus sequence: BAGGYCABHBTGACCKHV



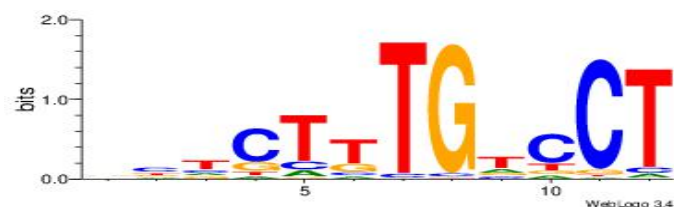
**Dataset #: 5      Motif ID: 87      Motif name: TFF1**



Original motif      Consensus sequence: AGGACAAAGAVV



Reverse complement motif      Consensus sequence: VVTCTTTGTCCT



### Best Matches for Top Significant Motif ID 87 (Highest to Lowest)

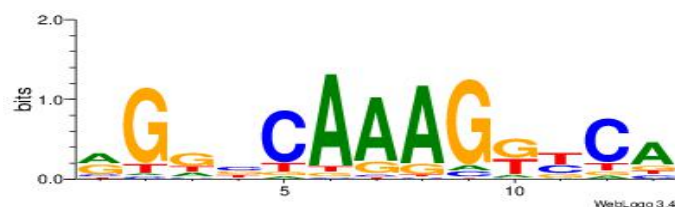
|                                  |                    |
|----------------------------------|--------------------|
| Dataset #:                       | 3                  |
| Motif ID:                        | 51                 |
| Motif name:                      | HNF4A              |
| Matching format of first motif:  | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction:                       | Forward            |
| Position number:                 | 2                  |
| Number of overlap:               | 12                 |
| Similarity score:                | 0.0111472          |

Alignment:

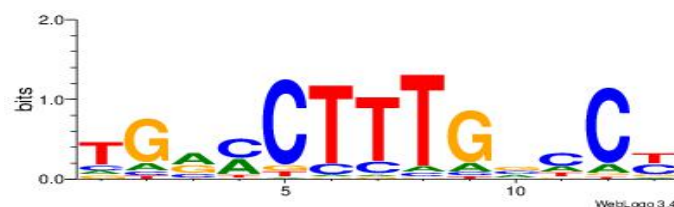
TGMYCTTTGBCCK

-VVTCTTTGTCCT

Original motif      Consensus sequence: RGGBCAAAGKYCA



Reverse complement motif      Consensus sequence: TGMYCTTTGBCCK

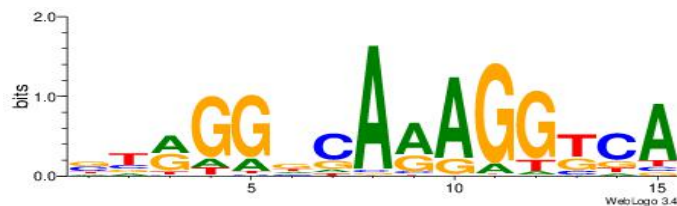


Dataset #: 3  
 Motif ID: 64  
 Motif name: PPARGRXRA  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 3  
 Number of overlap: 12  
 Similarity score: 0.0210867

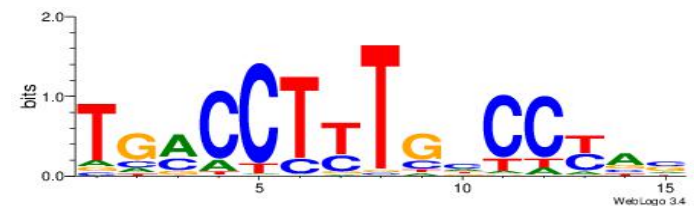
Alignment:

BTRGGDCARAGGKCA  
 --AGGACAAAGAVV--

Original motif      Consensus sequence: BTRGGDCARAGGKCA



Reverse complement motif      Consensus sequence: TGRCCCTKGHCCK



Dataset #: 3  
 Motif ID: 59  
 Motif name: ESR2  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 5  
 Number of overlap: 12

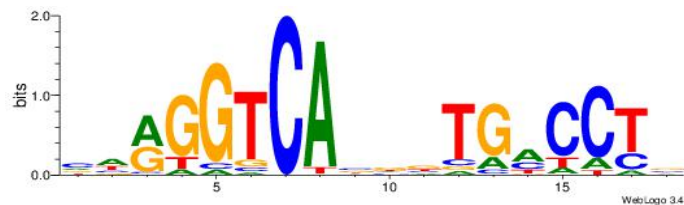
Similarity score: 0.0351633

Alignment:

BAGGYCABHBTGACCKHV

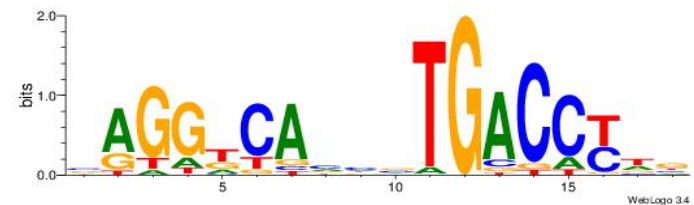
----VVTCTTTGTCCT--

Original motif      Consensus sequence: VHRGGTCABDBTGMCTB



Reverse complement motif  
BAGGYCABHBTGACCKHV

Consensus sequence:



Dataset #: 3  
Motif ID: 53  
Motif name: ESR1  
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: 0.039773

Alignment:

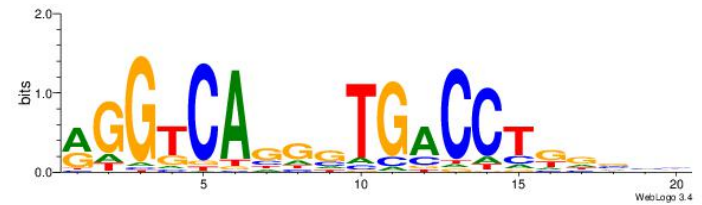
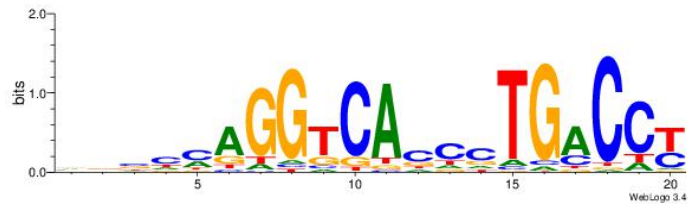
VDBHMAGGTCACCCTGACCY

VVTCTTTGTCCT-----

Original motif      Consensus sequence: VDBHMAGGTCACCCTGACCY

Reverse complement motif  
MGGTCAGGGTGACCTRDBHV

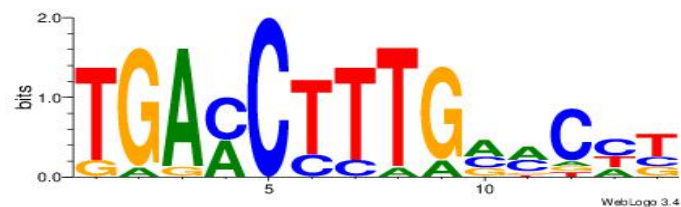
Consensus sequence:



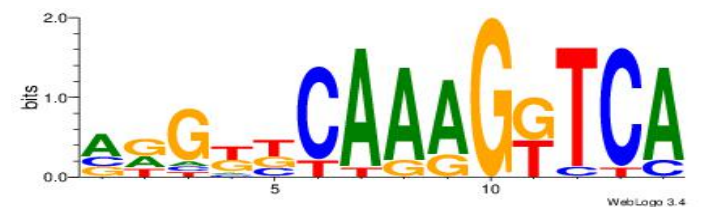
Dataset #: 3  
 Motif ID: 52  
 Motif name: NR2F1  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 2  
 Number of overlap: 12  
 Similarity score: 0.0472374

Alignment:  
 AKGYCAAAGRTCA  
 -AGGACAAAGAVV-

Original motif      Consensus sequence: TGAMCTTTGMMCYT



Reverse complement motif      Consensus sequence: AKGYCAAAGRTCA



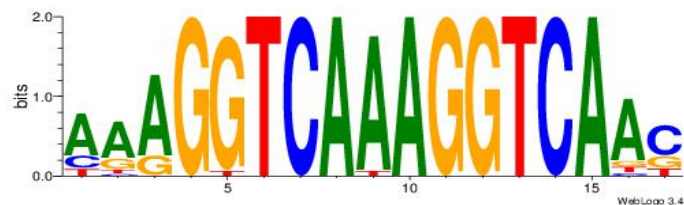
Dataset #: 3  
 Motif ID: 60

|                                  |                    |
|----------------------------------|--------------------|
| Motif name:                      | NR1H2RXRA          |
| 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:                | 0.0472884          |

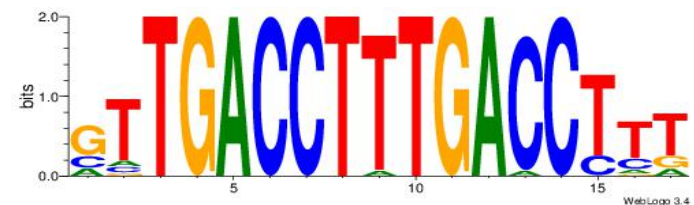
Alignment:

```
GTTGACCTTTGACCTTT
---VVTCTTTGTCCT--
```

Original motif      Consensus sequence: AAAGGTCAAAGGTCAAC



Reverse complement motif      Consensus sequence: GTTGACCTTTGACCTTT

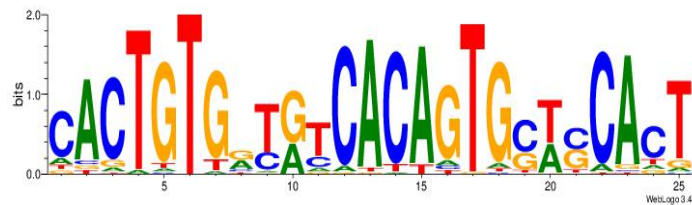


|                                  |                           |
|----------------------------------|---------------------------|
| Dataset #:                       | 4                         |
| Motif ID:                        | 72                        |
| Motif name:                      | CACTGTGrYrtCACAGTGswsCAcT |
| Matching format of first motif:  | Original Motif            |
| Matching format of second motif: | Original Motif            |
| Direction:                       | Backward                  |
| Position number:                 | 7                         |
| Number of overlap:               | 12                        |
| Similarity score:                | 0.0530556                 |

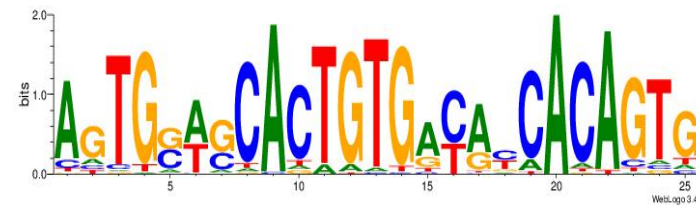
Alignment:

CACTGTGRTRTCACAGTGSWSCACT  
-----AGGACAAAGAVV-----

Original motif    Consensus sequence:  
CACTGTGRTRTCACAGTGSWSCACT



Reverse complement motif    Consensus sequence:  
AGTGSWSCACTGTGAMAMCACAGTG

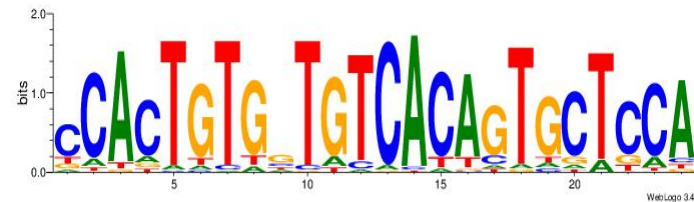
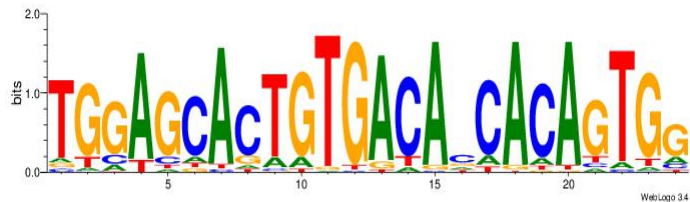


|                                  |                          |
|----------------------------------|--------------------------|
| Dataset #:                       | 4                        |
| Motif ID:                        | 73                       |
| Motif name:                      | TGGAGCACTGTGACAcCACAGTGg |
| Matching format of first motif:  | Original Motif           |
| Matching format of second motif: | Original Motif           |
| Direction:                       | Forward                  |
| Position number:                 | 13                       |
| Number of overlap:               | 12                       |
| Similarity score:                | 0.0539204                |

Alignment:

TGGAGCACTGTGACAVCACAGTGG  
-----AGGACAAAGAVV

|                |                                              |                          |                                             |
|----------------|----------------------------------------------|--------------------------|---------------------------------------------|
| Original motif | Consensus sequence: TGGAGCACTGTGACAVCACAGTGG | Reverse complement motif | Consensus sequence: CCACTGTGVTGTACAGTGCTCCA |
|----------------|----------------------------------------------|--------------------------|---------------------------------------------|

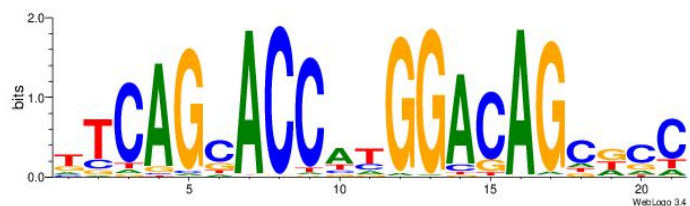


Dataset #: 3  
 Motif ID: 57  
 Motif name: REST  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 4  
 Number of overlap: 12  
 Similarity score: 0.0558379

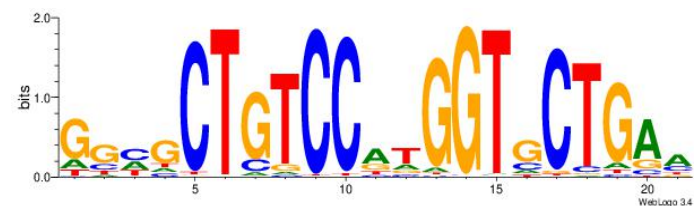
Alignment:

TTCAGCACCATGGACAGCKCC  
 ---AGGACAAAGAVV-----

Original motif      Consensus sequence: TTCAGCACCATGGACAGCKCC



Reverse complement motif      Consensus sequence: GGYGCTGTCCATGGTGCTGAA



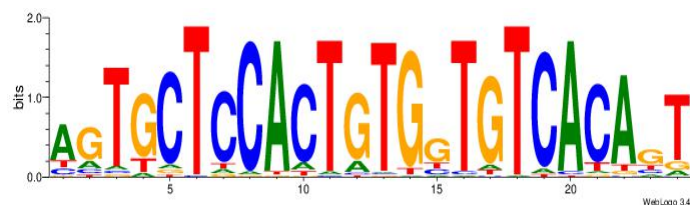
Dataset #: 4

Motif ID: 77  
 Motif name: AgTGCTCCACTGTGgTGTCACAgT  
 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: 0.0609269

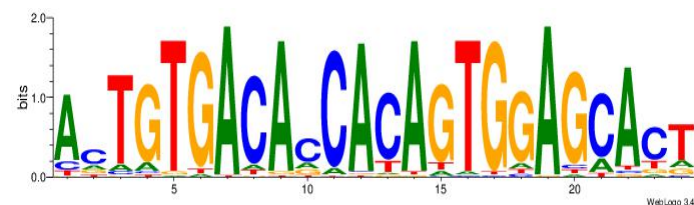
**Alignment:**

AGTGCTCCACTGTGGTGTTCACAGT  
 -----VVTCTTTGTCCT-----

Original motif      Consensus sequence: AGTGCTCCACTGTGGTGTTCACAGT



Reverse complement motif      Consensus sequence: ACTGTGACACCACAGTGGAGCACT



**Dataset #: 1      Motif ID: 37      Motif name: Motif 37**

Original motif      Consensus sequence: ACTTTGG



Reverse complement motif      Consensus sequence: CCAAAGT





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

Dataset #: 4  
 Motif ID: 69  
 Motif name: atactttggc  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 2  
 Number of overlap: 7  
 Similarity score: 0

Alignment:

GCCAAAGTAT

-CCAAAGT--

Original motif      Consensus sequence: ATACTTTGGC



Reverse complement motif      Consensus sequence: GCCAAAGTAT



Dataset #: 4  
 Motif ID: 75  
 Motif name: wwCCAmAGTCmt  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif

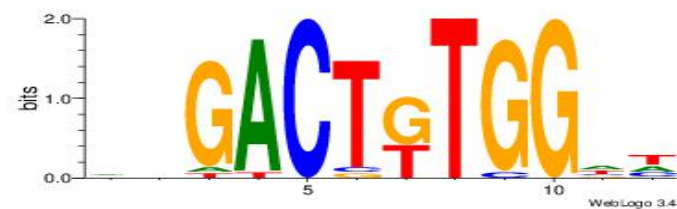
Direction: Backward  
 Position number: 4  
 Number of overlap: 7  
 Similarity score: 0.0275974

Alignment:  
 DDCCAMAGTCHB  
 --CCAAAGT---

Original motif      Consensus sequence: DDCCAMAGTCHB



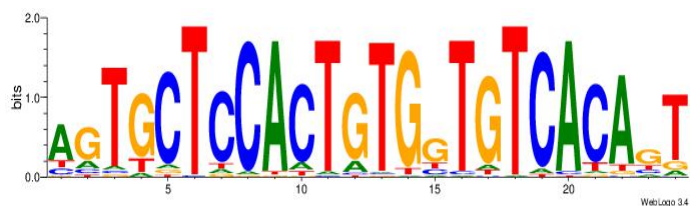
Reverse complement motif      Consensus sequence: VDGACTRTGGDD



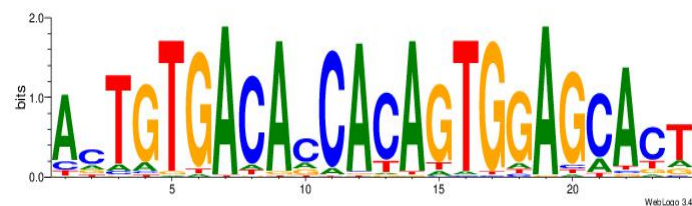
Dataset #: 4  
 Motif ID: 77  
 Motif name: AgTGCTCCACTGTGgTGTCACAgT  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 10  
 Number of overlap: 7  
 Similarity score: 0.056841

Alignment:  
 ACTGTGACACCACAGTGGAGCACT  
 -----CCAAAGT-----

Original motif      Consensus sequence: AGTGCTCCACTGTGGTGTACAGT



Reverse complement motif      Consensus sequence: ACTGTGACACCACAGTGGAGCACT



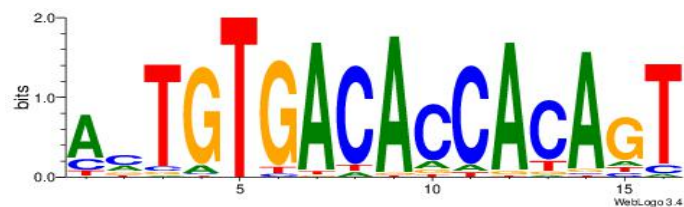
Dataset #: 4  
Motif ID: 71  
Motif name: AmTGTGACACCACAGT  
Matching format of first motif: Original Motif  
Matching format of second motif: Reverse Complement  
Direction: Backward  
Position number: 10  
Number of overlap: 7  
Similarity score: 0.0597098

Alignment:

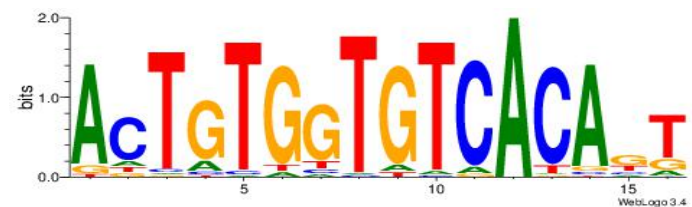
ACTGTGGTGTACART

ACTTTGG-----

Original motif      Consensus sequence: AMTGTGACACCACAGT



Reverse complement motif      Consensus sequence: ACTGTGGTGTACART

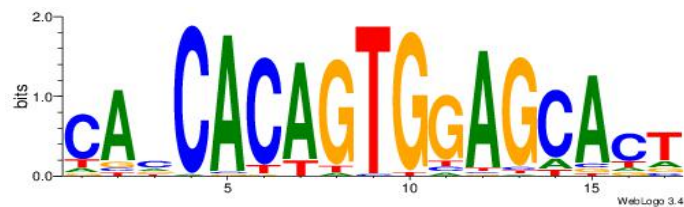


Dataset #: 4  
 Motif ID: 76  
 Motif name: CACACAGTGGAGCAct  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 9  
 Number of overlap: 7  
 Similarity score: 0.061942

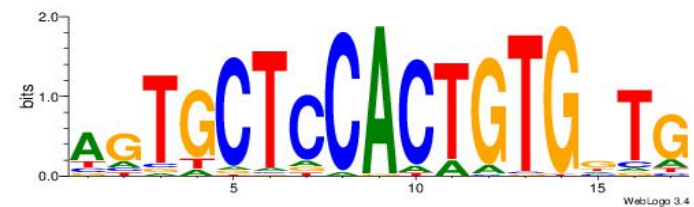
Alignment:

AGTGCTCCACTGTGDTG  
 -----ACTTTGG--

Original motif      Consensus sequence: CAHCACAGTGGAGCACT



Reverse complement motif      Consensus sequence: AGTGCTCCACTGTGDTG

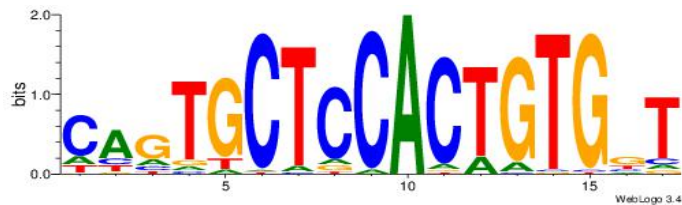


Dataset #: 4  
 Motif ID: 70  
 Motif name: CagTGCTCCACTGTGgT  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 2

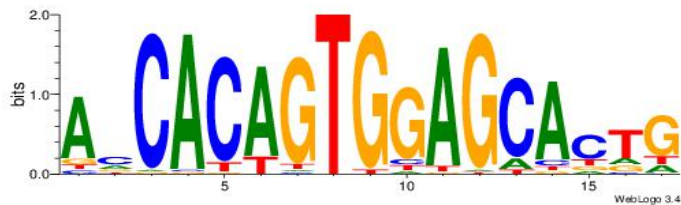
Number of overlap: 7  
Similarity score: 0.0625

Alignment:  
ABCACAGTGGAGCACTG  
-CCAAAGT-----

Original motif      Consensus sequence: CAGTGCTCCACTGTGBT



Reverse complement motif      Consensus sequence:  
ABCACAGTGGAGCACTG

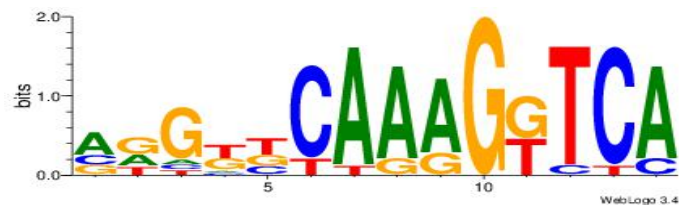


Dataset #: 3  
Motif ID: 52  
Motif name: NR2F1  
Matching format of first motif: Original Motif  
Matching format of second motif: Original Motif  
Direction: Forward  
Position number: 4  
Number of overlap: 7  
Similarity score: 0.0686813

Alignment:  
TGAMCTTTGMMCYT  
---ACTTTGG----

Original motif      Consensus sequence: TGAMCTTTGMMCYT

Reverse complement motif      Consensus sequence: AKGYCAAAGRTC

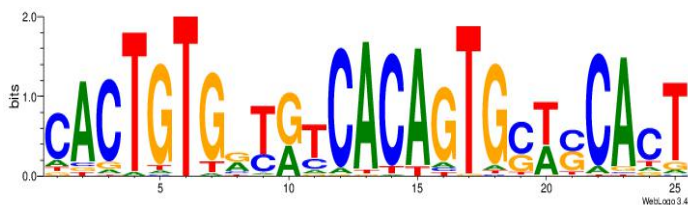


Dataset #: 4  
 Motif ID: 72  
 Motif name: CACTGTGrYrtCACAGTGswsCACT  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 2  
 Number of overlap: 7  
 Similarity score: 0.0714286

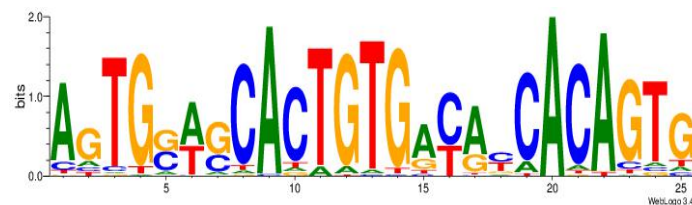
#### Alignment:

CACTGTGRTRTCACAGTGSWSCACT  
 -ACTTTGG-----

Original motif    Consensus sequence:  
 CACTGTGRTRTCACAGTGSWSCACT



Reverse complement motif    Consensus sequence:  
 AGTGSWSCACTGTGAMAMCACAGTG

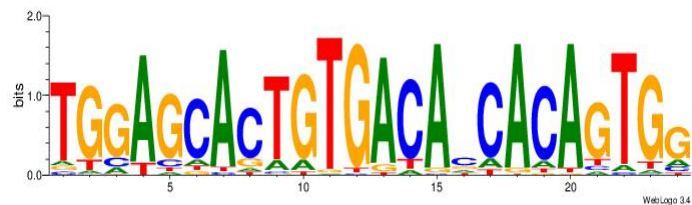


Dataset #: 4

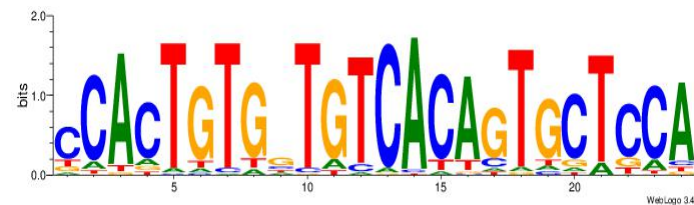
Motif ID: 73  
 Motif name: TGGAGCACTGTGACAcCACAGTGg  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 3  
 Number of overlap: 7  
 Similarity score: 0.0714286

Alignment:  
 TGGAGCACTGTGACAVCACAGTGG  
 -----CCAAAGT--

Original motif      Consensus sequence: TGGAGCACTGTGACAVCACAGTGG



Reverse complement motif      Consensus sequence: CCACTGTGVTGTACAGTGCTCCA



Dataset #: 3  
 Motif ID: 60  
 Motif name: NR1H2RXRA  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 5  
 Number of overlap: 7

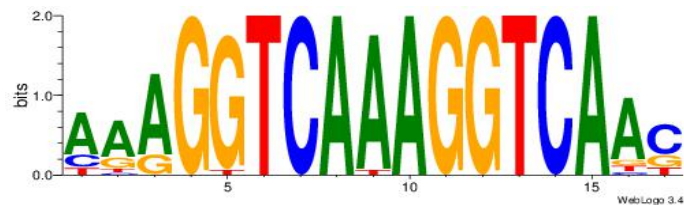
Similarity score: 0.0728571

Alignment:

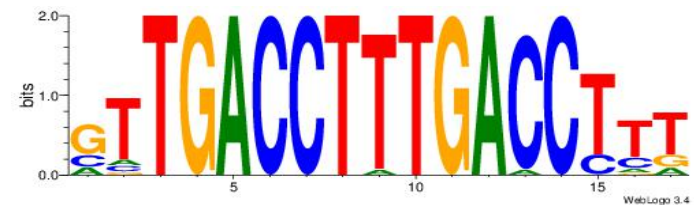
GTGACCTTTGACCTTT

----ACTTTGG-----

Original motif      Consensus sequence: AAAGGTCAAAGGTCAAC



Reverse complement motif      Consensus sequence: GTTGACCTTTGACCTTT



**Dataset #: 2      Motif ID: 50      Motif name: Motif 50**

Original motif      Consensus sequence: GGAAM



Reverse complement motif      Consensus sequence: YTTCC



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

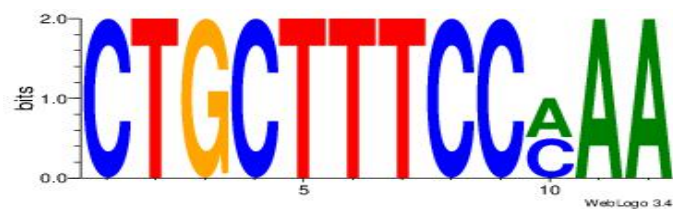
|                                  |                    |
|----------------------------------|--------------------|
| Dataset #:                       | 1                  |
| Motif ID:                        | 21                 |
| Motif name:                      | Motif 21           |
| Matching format of first motif:  | Reverse Complement |
| Matching format of second motif: | Original Motif     |



Direction: Forward  
 Position number: 4  
 Number of overlap: 5  
 Similarity score: 0.01875

Alignment:  
 CTGCTTTCCMAA  
 ---YTTCC----

Original motif      Consensus sequence: CTGCTTTCCMAA



Reverse complement motif      Consensus sequence: TTYGGAAAGCAG



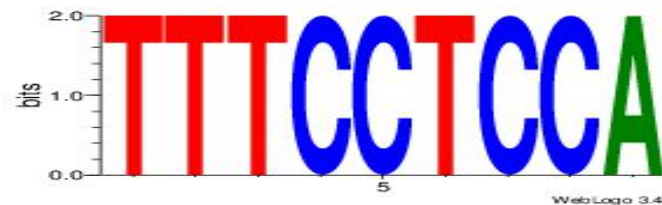
Dataset #: 1  
 Motif ID: 41  
 Motif name: Motif 41  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 5  
 Number of overlap: 5  
 Similarity score: 0.01875

Alignment:  
 TTCCTCCA  
 YTTCC----

Original motif      Consensus sequence: TGGAGGAAA



Reverse complement motif      Consensus sequence: TTTCTCCA



Dataset #: 1  
 Motif ID: 43  
 Motif name: Motif 43  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 5  
 Number of overlap: 5  
 Similarity score: 0.04375

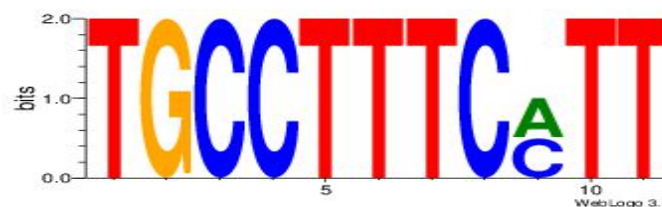
Alignment:

TGCCTTTCYTT  
 ----YTTCC--

Original motif      Consensus sequence: AAKGAAAGGCA



Reverse complement motif      Consensus sequence: TGCCTTTCYTT



Dataset #: 1  
 Motif ID: 44  
 Motif name: Motif 44  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 3  
 Number of overlap: 5  
 Similarity score: 0.05625

Alignment:

TTCTTYCATT  
 --YTTCC--

Original motif      Consensus sequence: AATGKAAGAA



Reverse complement motif      Consensus sequence: TTCTTYCATT



Dataset #: 1  
 Motif ID: 9  
 Motif name: Motif 9  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 8  
 Number of overlap: 5

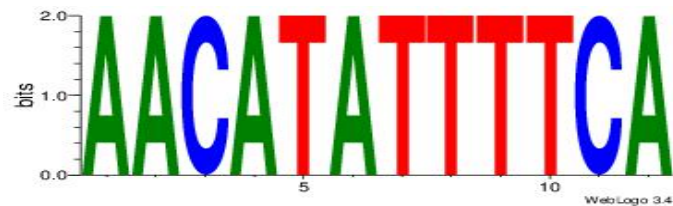
Similarity score: 0.06875

Alignment:

TGAAAATATGTT

-----GGAAM

Original motif      Consensus sequence: AACATATTTTCA



Reverse complement motif      Consensus sequence: TGAAAATATGTT



---

Dataset #: 1  
Motif ID: 19  
Motif name: Motif 19  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Reverse Complement  
Direction: Backward  
Position number: 3  
Number of overlap: 5  
Similarity score: 0.06875

Alignment:

CTTTCTCT

-YTTCC--

Original motif      Consensus sequence: AGAGAAAG

Reverse complement motif      Consensus sequence: CTTTCTCT



Dataset #: 1  
 Motif ID: 28  
 Motif name: Motif 28  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 6  
 Number of overlap: 5  
 Similarity score: 0.06875

Alignment:

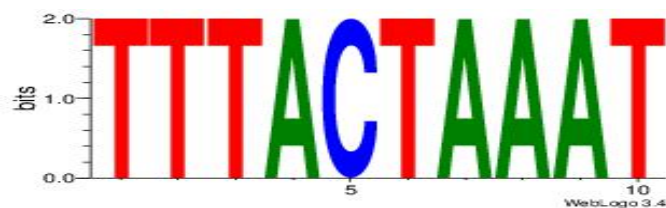
ATTTAGTAAA

-----GGAAM

Original motif      Consensus sequence: ATTTAGTAAA



Reverse complement motif      Consensus sequence: TTTACTAAAT



Dataset #: 1  
 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:                 | 7                  |
| Number of overlap:               | 5                  |
| Similarity score:                | 0.06875            |

Alignment:

```
AAGSATTTCA
-----YTTCC
```

Original motif      Consensus sequence: TGAAAATCCTT



Reverse complement motif      Consensus sequence: AAGSATTTTCA



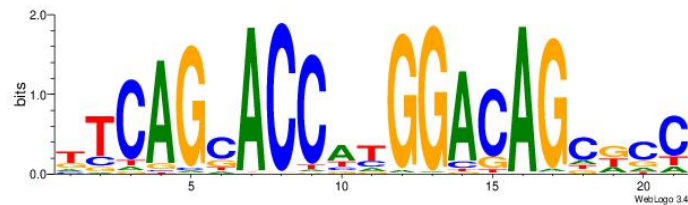
|                                  |                    |
|----------------------------------|--------------------|
| Dataset #:                       | 3                  |
| Motif ID:                        | 57                 |
| Motif name:                      | REST               |
| Matching format of first motif:  | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction:                       | Forward            |
| Position number:                 | 6                  |
| Number of overlap:               | 5                  |
| Similarity score:                | 0.0747947          |

Alignment:

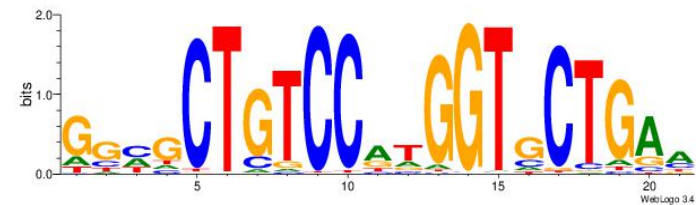
GGYGCTGTCCATGGTGCTGAA

-----YTTCC-----

Original motif      Consensus sequence: TTCAGCACCATGGACAGCKCC



Reverse complement motif      Consensus sequence: GGYGCTGTCCATGGTGCTGAA



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|                                  |                    |
|----------------------------------|--------------------|
| Dataset #:                       | 1                  |
| Motif ID:                        | 23                 |
| Motif name:                      | Motif 23           |
| Matching format of first motif:  | Reverse Complement |
| Matching format of second motif: | Original Motif     |
| Direction:                       | Backward           |
| Position number:                 | 5                  |
| Number of overlap:               | 5                  |
| Similarity score:                | 0.075              |

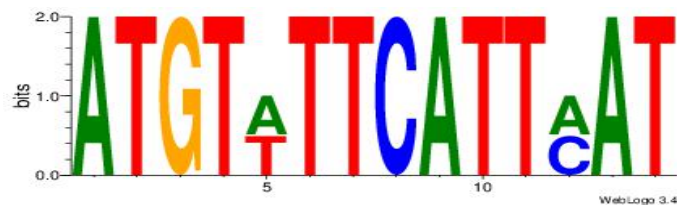
Alignment:

ATGTW TTCATTMAT

-----YTTCC-----

Original motif      Consensus sequence: ATGTW TTCATTMAT

Reverse complement motif      Consensus sequence: ATYAATGA AWACA



**Dataset #: 3      Motif ID: 61      Motif name: NR4A2**

Original motif      Consensus sequence: AAGGTCAC



Reverse complement motif      Consensus sequence: GTGACCTT



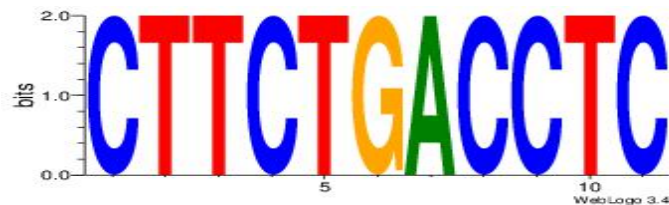
### Best Matches for Top Significant Motif ID 61 (Highest to Lowest)

|                                  |                    |
|----------------------------------|--------------------|
| Dataset #:                       | 1                  |
| Motif ID:                        | 17                 |
| Motif name:                      | Motif 17           |
| Matching format of first motif:  | Reverse Complement |
| Matching format of second motif: | Original Motif     |
| Direction:                       | Forward            |
| Position number:                 | 1                  |
| Number of overlap:               | 8                  |
| Similarity score:                | 0.0393171          |

Alignment:  
 CTTCTGACCTC  
 GTGACCTT---



Original motif      Consensus sequence: CTTCTGACCTC



Reverse complement motif      Consensus sequence: GAGGTCAGAAG



Dataset #: 1  
 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: 2  
 Number of overlap: 8  
 Similarity score: 0.040519

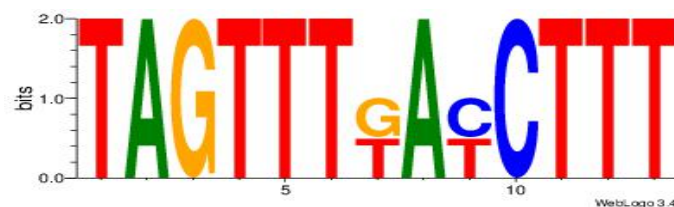
Alignment:

AAAGRTMAAACTA  
 -AAGGTCAC-----

Original motif      Consensus sequence: AAAGRTMAAACTA



Reverse complement motif      Consensus sequence: TAGTTTAACTTT



Dataset #: 1  
 Motif ID: 24  
 Motif name: Motif 24  
 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: 0.0539119

Alignment:

TTWATGWCTTT  
 ---GTGACCTT

Original motif      Consensus sequence: AAAGWCATWAA



Reverse complement motif      Consensus sequence: TTWATGWCTTT

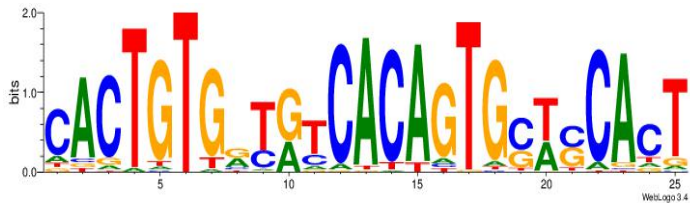


Dataset #: 4  
 Motif ID: 72  
 Motif name: CACTGTGrYrtCACAGTGswsCAcT  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 7  
 Number of overlap: 8

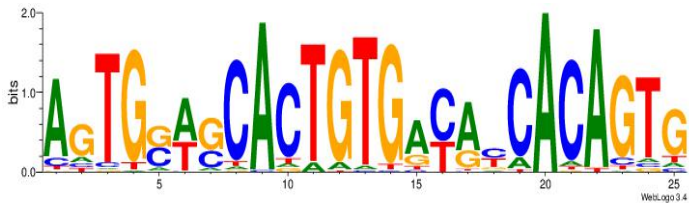
Similarity score: 0.0557243

Alignment:  
CACTGTGRTRTCACAGTGSWSCACT  
-----AAGGTCAC-----

Original motif    Consensus sequence:  
CACTGTGRTRTCACAGTGSWSCACT



Reverse complement motif    Consensus sequence:  
AGTGSWSCACTGTGAMAMCACAGTG



Dataset #: 1  
Motif ID: 35  
Motif name: Motif 35  
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: 0.0566591

Alignment:  
AGATGYTCTTG  
-GTGACCTT--

Original motif    Consensus sequence: AGATGYTCTTG

Reverse complement motif    Consensus sequence: CAAGAKCATCT

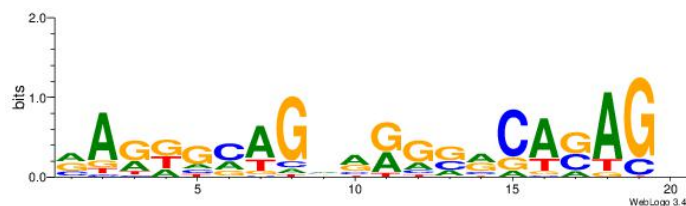


Dataset #: 5  
 Motif ID: 93  
 Motif name: TFM12  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 10  
 Number of overlap: 8  
 Similarity score: 0.0584971

#### Alignment:

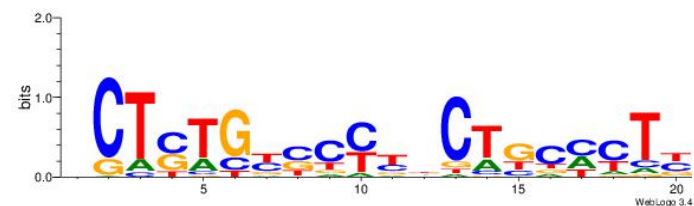
RAGKGMAGVRRGSRCASAGV  
 -----AAGGTCAC----

Original motif      Consensus sequence: RAGKGMAGVRRGSRCASAGV



Reverse complement motif  
VCTSTGKSCMKBCTRCYCTK

Consensus sequence:



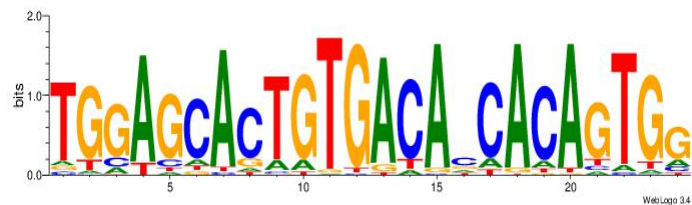
Dataset #: 4

Motif ID: 73  
 Motif name: TGGAGCACTGTGACAcCACAGTGg  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 8  
 Number of overlap: 8  
 Similarity score: 0.060729

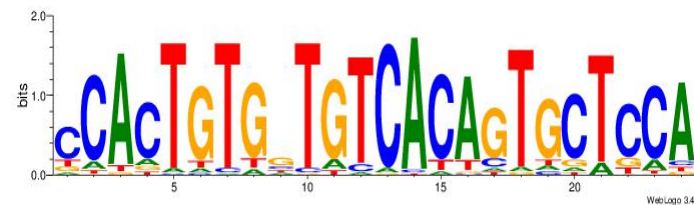
Alignment:

CCACTGTGVTGTCACAGTGCTCCA  
 -----AAGGTCAC-----

Original motif      Consensus sequence: TGGAGCACTGTGACAVCACAGTGG



Reverse complement motif      Consensus sequence: CCACTGTGVTGTCACAGTGCTCCA



Dataset #: 4  
 Motif ID: 71  
 Motif name: AmTGTGACACCACAGT  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 6  
 Number of overlap: 8

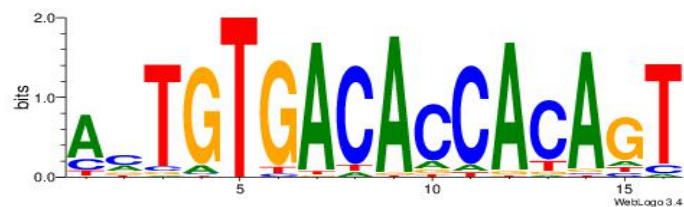
Similarity score: 0.0645146

Alignment:

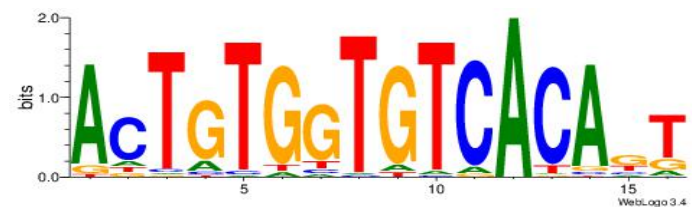
ACTGTGGTGTACART

-----AAGGTCAC---

Original motif      Consensus sequence: AMTGTGACACCACAGT



Reverse complement motif      Consensus sequence: ACTGTGGTGTACART



Dataset #: 1

Motif ID: 22

Motif name: Motif 22

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: 0.0664462

Alignment:

TTTATGGTGAGCAT

GTGACCTT-----

Original motif      Consensus sequence: TTTATGGTGAGCAT

Reverse complement motif      Consensus sequence: ATGCTCACCATAA



Dataset #: 1  
 Motif ID: 18  
 Motif name: Motif 18  
 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: 0.0674765

Alignment:  
 GCTGGACTTTG  
 -GTGACCTT--

Original motif      Consensus sequence: CAAAGTCCAGC



Reverse complement motif      Consensus sequence: GCTGGACTTTG



**Dataset #: 4      Motif ID: 79      Motif name: cCGCGGrCACG**

Original motif      Consensus sequence: CCGCGGRCACG



Reverse complement motif      Consensus sequence: CGTGKCCGCGG



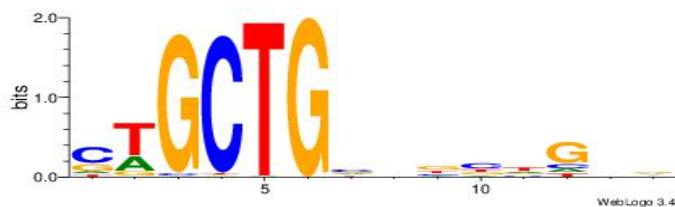
### Best Matches for Top Significant Motif ID 79 (Highest to Lowest)

Dataset #: 5  
 Motif ID: 88  
 Motif name: TFF11  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 4  
 Number of overlap: 11  
 Similarity score: 0.0478408

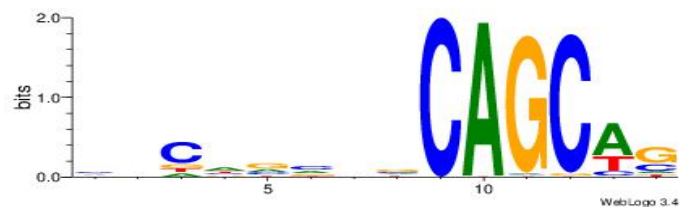
Alignment:

HVCDBBDBCAGCAG  
 ---CGTGKCCGCGG

Original motif      Consensus sequence: CTGCTGBDBBDGBD



Reverse complement motif      Consensus sequence: HVCDBBDBCAGCAG



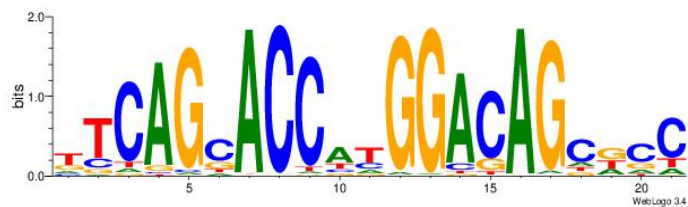


Dataset #: 3  
 Motif ID: 57  
 Motif name: REST  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 4  
 Number of overlap: 11  
 Similarity score: 0.0484441

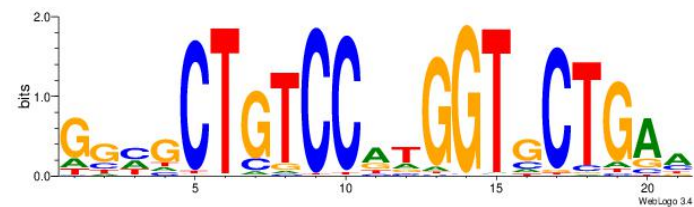
Alignment:

TTCAGCACCATGGACAGCKCC  
 -----CCGCGGRCACG---

Original motif      Consensus sequence: TTCAGCACCATGGACAGCKCC



Reverse complement motif      Consensus sequence: GGYGCTGTCCATGGTGCTGAA



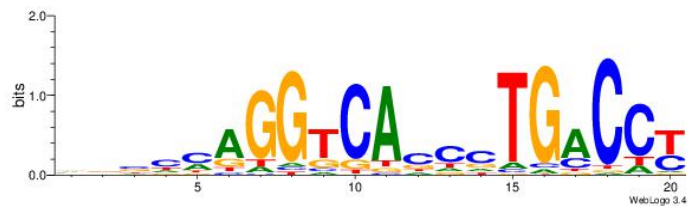
Dataset #: 3  
 Motif ID: 53  
 Motif name: ESR1  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 3

Number of overlap: 11  
Similarity score: 0.0486581

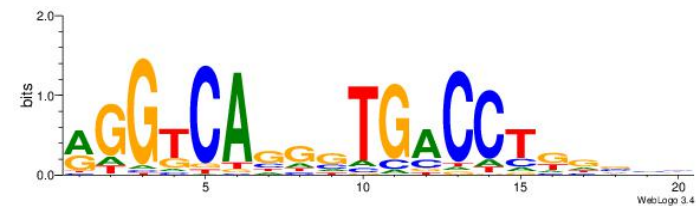
Alignment:

MGGTCAGGGTGACCTRDBHV  
-----CGTGKCCGCGG--

Original motif      Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif      Consensus sequence: MGGTCAGGGTGACCTRDBHV

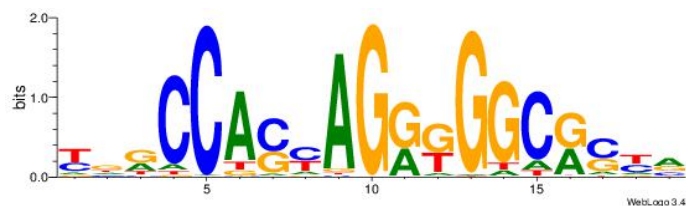


Dataset #: 3  
Motif ID: 66  
Motif name: CTCF  
Matching format of first motif: Original Motif  
Matching format of second motif: Original Motif  
Direction: Backward  
Position number: 2  
Number of overlap: 11  
Similarity score: 0.0588663

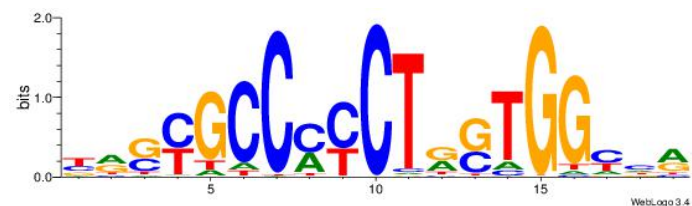
Alignment:

YDRCCASYAGRKGGCRSYV  
-----CCGCGGRCACG--

Original motif      Consensus sequence: YDRCCASYAGRKGGCRSYV



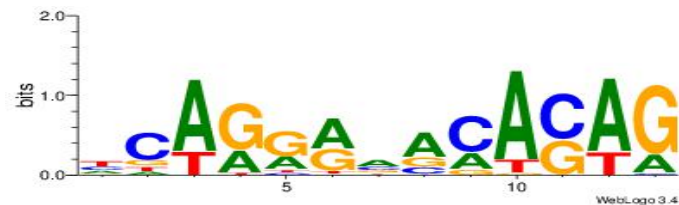
Reverse complement motif      Consensus sequence: BMSMGCCYMCTKSTGGMHM



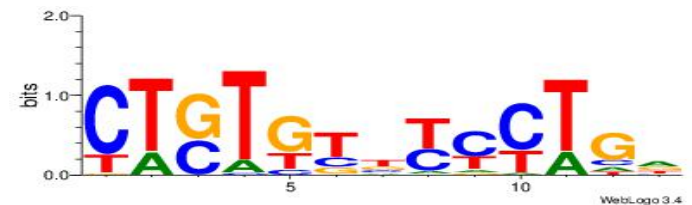
Dataset #: 1  
 Motif ID: 3  
 Motif name: Motif 3  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 2  
 Number of overlap: 11  
 Similarity score: 0.0597806

Alignment:  
 HCAGRRVACASAG  
 -CCGCGGRCACG-

Original motif      Consensus sequence: HCAGRRVACASAG



Reverse complement motif      Consensus sequence: CTSTGTBKMCTGH

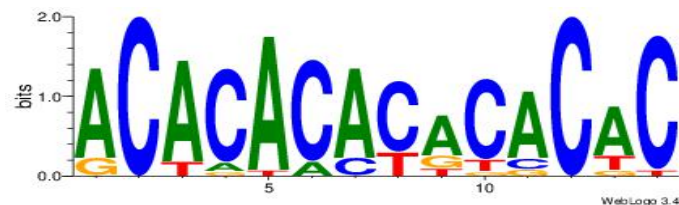


Dataset #: 1  
 Motif ID: 2  
 Motif name: Motif 2  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 3  
 Number of overlap: 11  
 Similarity score: 0.0624268

Alignment:

GTGTGTGTGTGTGT  
 -CGTGKCCGCGG--

Original motif      Consensus sequence: ACACACACACAC



Reverse complement motif      Consensus sequence: GTGTGTGTGTGT

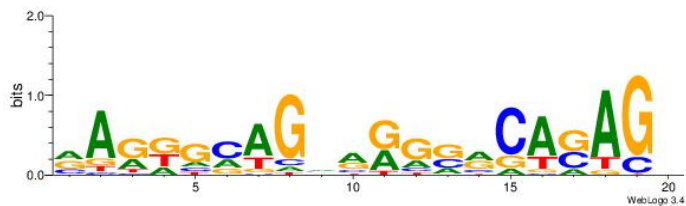


Dataset #: 5  
 Motif ID: 93  
 Motif name: TFM12  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 5  
 Number of overlap: 11

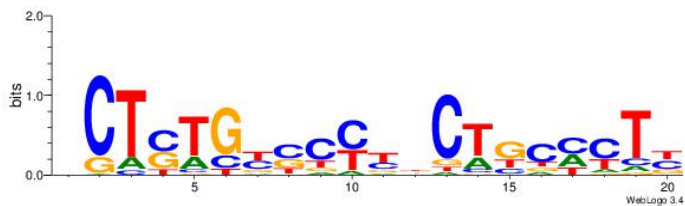
Similarity score: 0.0625015

Alignment:  
RAGKGMAGVRRGSRCASAGV  
-----CCGCGGRCACG-----

Original motif      Consensus sequence: RAGKGMAGVRRGSRCASAGV



Reverse complement motif      Consensus sequence:  
VCTSTGKSCMKBCTRCYCTK

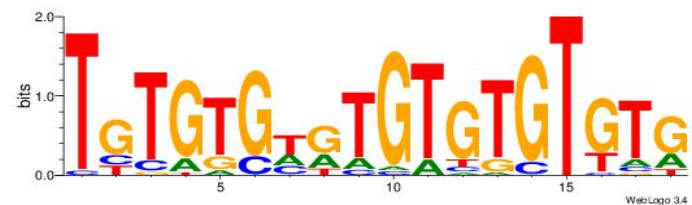
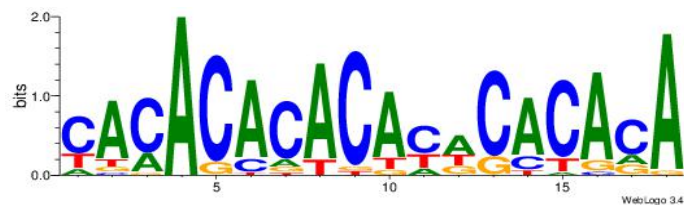


Dataset #: 5  
Motif ID: 89  
Motif name: TFM1  
Matching format of first motif: Original Motif  
Matching format of second motif: Original Motif  
Direction: Backward  
Position number: 3  
Number of overlap: 11  
Similarity score: 0.0628056

Alignment:  
CACACACACWCACACA  
-----CCGCGGRCACG--

Original motif      Consensus sequence: CACACACACACWCACACA

Reverse complement motif      Consensus sequence:  
TGTGTGWGTGTGTGTGTG

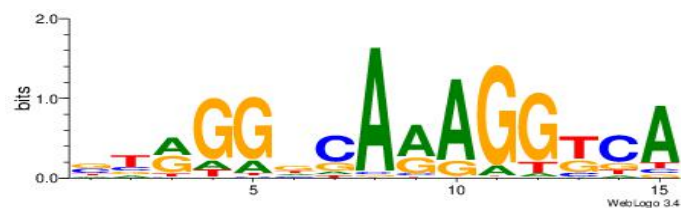


Dataset #: 3  
 Motif ID: 64  
 Motif name: PPARGRXRA  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 4  
 Number of overlap: 11  
 Similarity score: 0.0629476

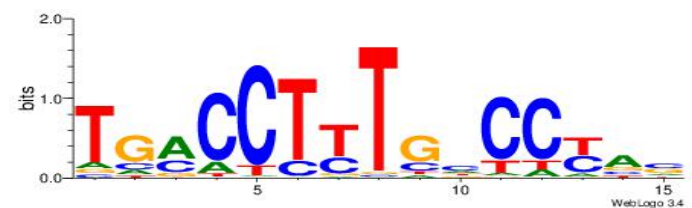
#### Alignment:

TGRCCCTKTGHCCCKAB  
 ---CGTGKCCGCGG-

Original motif      Consensus sequence: BTRGGDCARAGGKCA



Reverse complement motif      Consensus sequence: TGRCCCTKTGHCCCK



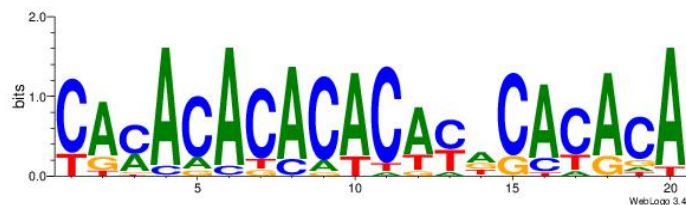
Dataset #: 5  
 Motif ID: 92

|                                  |                |
|----------------------------------|----------------|
| Motif name:                      | TFM11          |
| Matching format of first motif:  | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction:                       | Forward        |
| Position number:                 | 8              |
| Number of overlap:               | 11             |
| Similarity score:                | 0.0634175      |

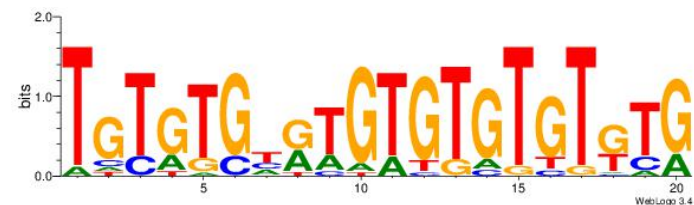
**Alignment:**

```
CAMACACACACAYDCACACA
-----CCGCGGRCACG--
```

Original motif      Consensus sequence: CAMACACACACAYDCACACA



Reverse complement motif      Consensus sequence: TGTGTGDKTGTGTGTGTRTG



Results created by MOTIFSIM on 11-20-2016 22:58:31

Runtime: 1057.23 seconds

MOTIFSIM is written by Ngoc Tam L. Tran

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