



# MOTIFSIM - MOTIF SIMilarity Detection Tool

Version 2.1

## INPUT

### Input Parameters

|                                   |                       |
|-----------------------------------|-----------------------|
| Number of files:                  | 2                     |
| Number of top significant motifs: | 10                    |
| Number of best matches:           | 10                    |
| Similarity cutoff >=              | 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-ChIP_DM721.txt | 11              | 1              |
| PScanChIP_DM721.txt | 37              | 2              |

## RESULTS

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

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

Original motif      Consensus sequence: CTCTGY



Reverse complement motif      Consensus sequence: KCAGAG



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

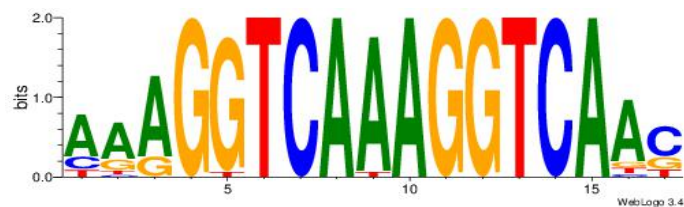
|                                  |                    |
|----------------------------------|--------------------|
| Dataset #:                       | 2                  |
| Motif ID:                        | 43                 |
| Motif name:                      | NR1H2RXRA          |
| Matching format of first motif:  | Reverse Complement |
| Matching format of second motif: | Original Motif     |
| Direction:                       | Forward            |
| Position number:                 | 6                  |
| Number of overlap:               | 6                  |
| Similarity score:                | 0.012269           |

Alignment:

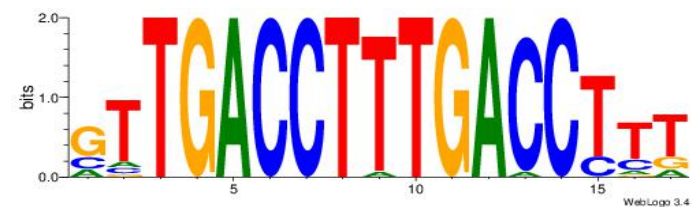
AAAGGTCAAAGGTCAAC

-----KCAGAG-----

Original motif      Consensus sequence: AAAGGTCAAAGGTCAAC



Reverse complement motif      Consensus sequence: GTTGACCTTTGACCTT



Dataset #: 2  
 Motif ID: 20  
 Motif name: PPARGRXRA  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 6  
 Number of overlap: 6  
 Similarity score: 0.0140102

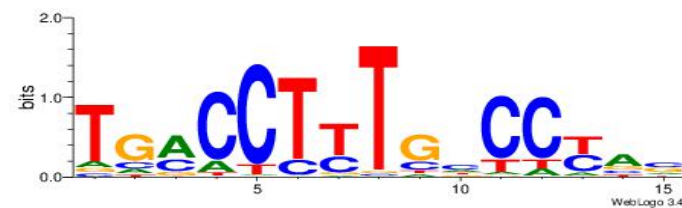
Alignment:

BTRGGDCARAGGKCA  
 -----KCAGAG-----

Original motif      Consensus sequence: BTRGGDCARAGGKCA



Reverse complement motif      Consensus sequence: TGRCCCTKTGHCCCK



Dataset #: 2  
 Motif ID: 22  
 Motif name: NR2F1  
 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: 0.0186793

Alignment:  
AKGYICAAAGRTCA  
----KCAGAG----

Original motif      Consensus sequence: TGAMCTTTGMMCYT



Reverse complement motif      Consensus sequence: AKGYICAAAGRTCA

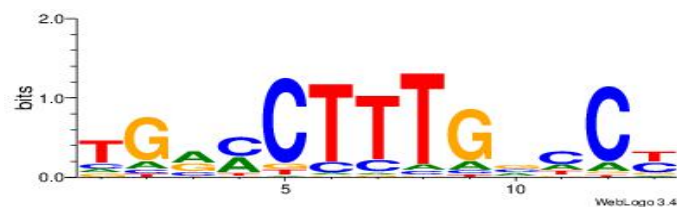
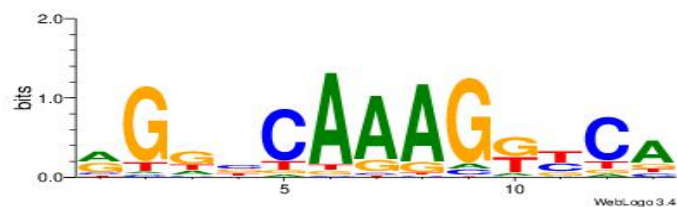


Dataset #: 2  
Motif ID: 34  
Motif name: HNF4A  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Original Motif  
Direction: Forward  
Position number: 4  
Number of overlap: 6  
Similarity score: 0.020602

Alignment:  
RGGBCAAAGKYCA  
---KCAGAG----

Original motif      Consensus sequence: RGGBCAAAGKYCA

Reverse complement motif      Consensus sequence: TGMYCTTTGBCCK



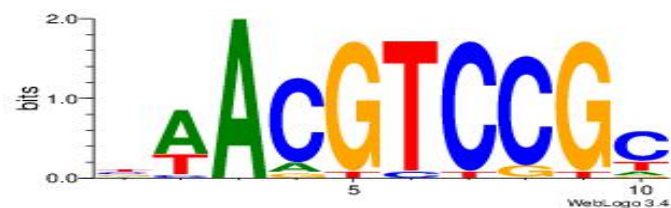
Dataset #: 2  
 Motif ID: 37  
 Motif name: MIZF  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 6  
 Similarity score: 0.0221665

#### Alignment:

BAACGTCCGC

----CTCTGY

Original motif      Consensus sequence: BAACGTCCGC



Reverse complement motif      Consensus sequence: GCGGACGTTT



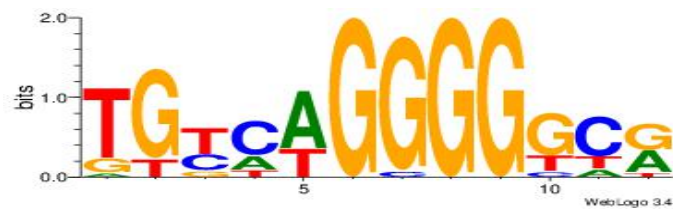
Dataset #: 2  
 Motif ID: 35

|                                  |                    |
|----------------------------------|--------------------|
| Motif name:                      | INSM1              |
| Matching format of first motif:  | Reverse Complement |
| Matching format of second motif: | Original Motif     |
| Direction:                       | Backward           |
| Position number:                 | 5                  |
| Number of overlap:               | 6                  |
| Similarity score:                | 0.0255256          |

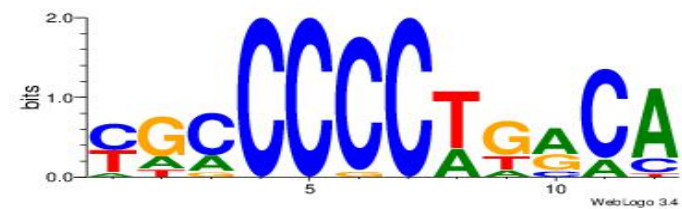
Alignment:

TGYCAGGGGGCR  
 --KCAGAG----

Original motif      Consensus sequence: TGYCAGGGGGCR



Reverse complement motif      Consensus sequence: MGCCCCCTGMCA



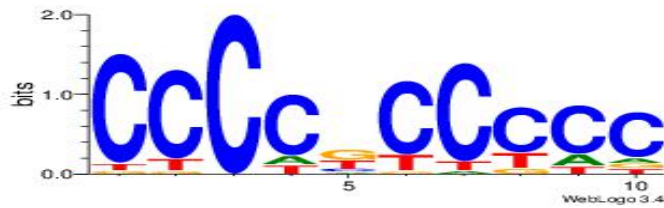
|                                  |                |
|----------------------------------|----------------|
| Dataset #:                       | 2              |
| Motif ID:                        | 16             |
| Motif name:                      | SP1            |
| Matching format of first motif:  | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction:                       | Backward       |
| Position number:                 | 5              |
| Number of overlap:               | 6              |
| Similarity score:                | 0.0349642      |

Alignment:

CCCCKCCCCC

CTCTGY----

Original motif      Consensus sequence: CCCCCKCCCCC



Reverse complement motif      Consensus sequence: GGGGGYGGGG



|                                  |                    |
|----------------------------------|--------------------|
| Dataset #:                       | 2                  |
| Motif ID:                        | 19                 |
| Motif name:                      | REST               |
| 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:                | 0.0376108          |

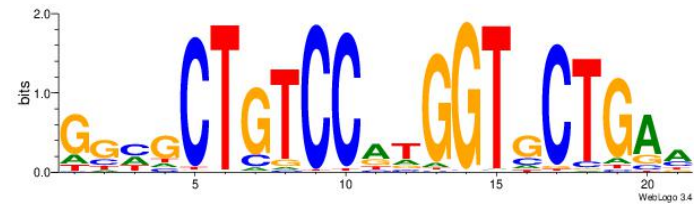
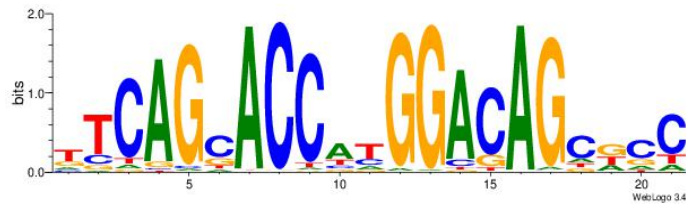
Alignment:

GGYGCTGTCCATGGTGCTGAA

--CTCTGY-----

Original motif      Consensus sequence: TTCAGCACCATGGACAGCKCC

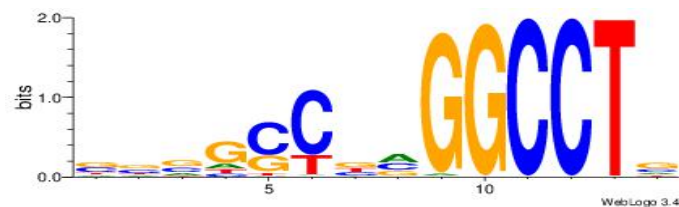
Reverse complement motif      Consensus sequence:  
GGYGCTGTCCATGGTGCTGAA



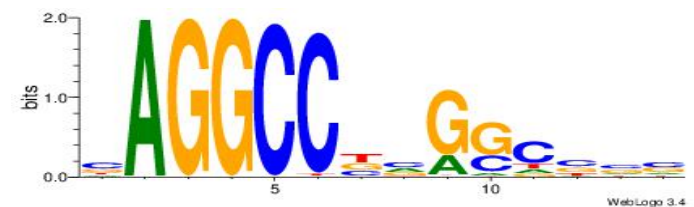
Dataset #: 2  
 Motif ID: 12  
 Motif name: Zfx  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 6  
 Number of overlap: 6  
 Similarity score: 0.0448449

Alignment:  
 BBVGCCBVGGCCTV  
 ---KCAGAG-----

Original motif      Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif      Consensus sequence: VAGGCCBBGGCV



Dataset #: 2  
 Motif ID: 29

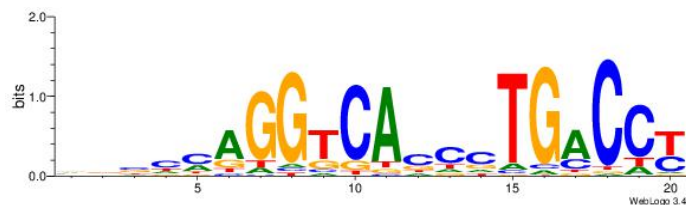


Motif name: ESR1  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 4  
 Number of overlap: 6  
 Similarity score: 0.0454269

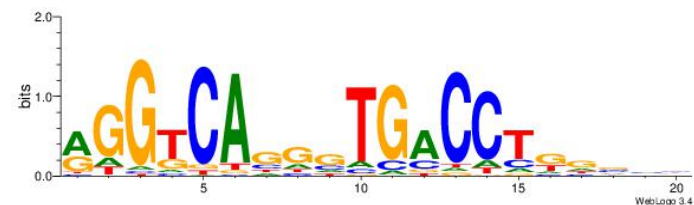
**Alignment:**

MGGTCAGGGTGACCTRDBHV  
 ---KCAGAG-----

Original motif      Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif      Consensus sequence: MGGTCAGGGTGACCTRDBHV



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

Original motif      Consensus sequence: ATKTM



Reverse complement motif      Consensus sequence: RARAT



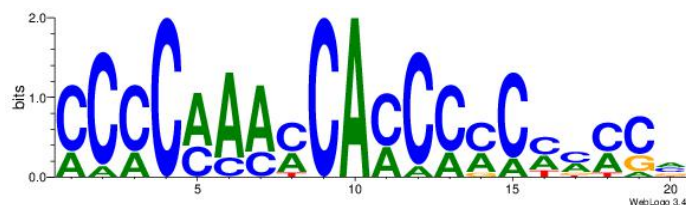
## Best Matches for Top Significant Motif ID 5 (Highest to Lowest)

Dataset #: 2  
 Motif ID: 18  
 Motif name: RREB1  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 10  
 Number of overlap: 5  
 Similarity score: 0.0256083

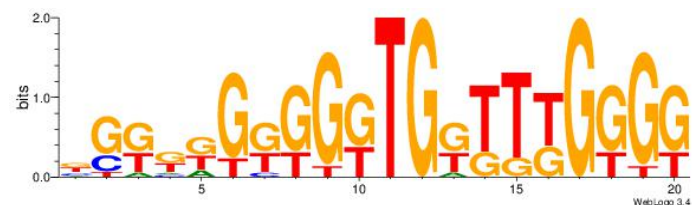
### Alignment:

BGRRRGRGGRTGRTTYGGGG  
 -----RARAT-----

Original motif      Consensus sequence: CCCMAAMCAMCCMCMMMC



Reverse complement motif      Consensus sequence: BGRRRGRGGRTGRTTYGGGG



Dataset #: 2  
 Motif ID: 44  
 Motif name: NR4A2  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif

Direction: Backward  
 Position number: 4  
 Number of overlap: 5  
 Similarity score: 0.0276382

Alignment:  
 AAGGTCAC  
 RARAT---

Original motif      Consensus sequence: AAGGTCAC



Reverse complement motif      Consensus sequence: GTGACCTT



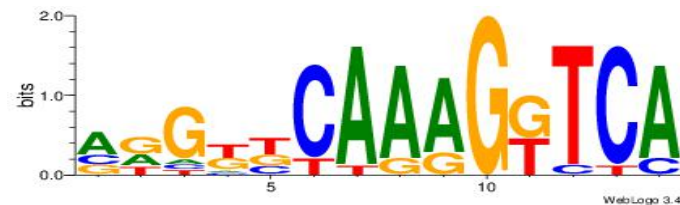
Dataset #: 2  
 Motif ID: 22  
 Motif name: NR2F1  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 3  
 Number of overlap: 5  
 Similarity score: 0.0279129

Alignment:  
 AKGY YCAAAGRTCA  
 -----RARAT--

Original motif      Consensus sequence: TGAMCTTTGMMCYT



Reverse complement motif      Consensus sequence: AKGYCAAAGRTC

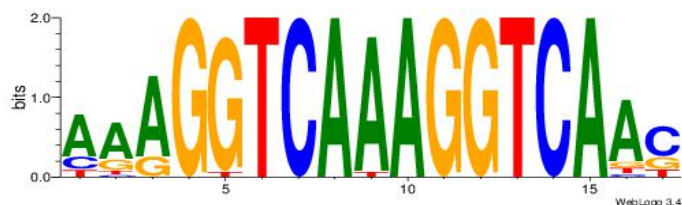


Dataset #: 2  
 Motif ID: 43  
 Motif name: NR1H2RXRA  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 10  
 Number of overlap: 5  
 Similarity score: 0.0292478

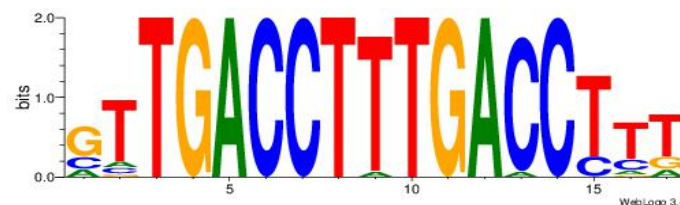
Alignment:

AAAGGTCAAAGGTCAAC  
 -----ATKTM----

Original motif      Consensus sequence: AAAGGTCAAAGGTCAAC



Reverse complement motif      Consensus sequence:  
 GTTGACCTTTGACCTT



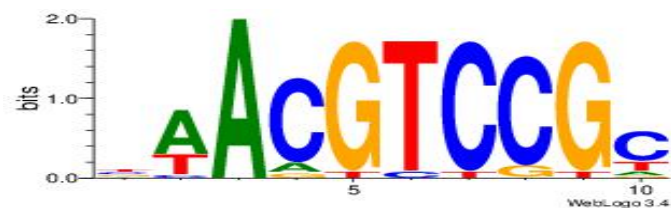
Dataset #: 2  
 Motif ID: 37  
 Motif name: MIZF  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 4  
 Number of overlap: 5  
 Similarity score: 0.0292478

Alignment:

BAACGTCCGC

--ATKTM---

Original motif      Consensus sequence: BAACGTCCGC



Reverse complement motif      Consensus sequence: GCGGACGTTT



Dataset #: 2  
 Motif ID: 20  
 Motif name: PPARGRXRA  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 5  
 Number of overlap: 5

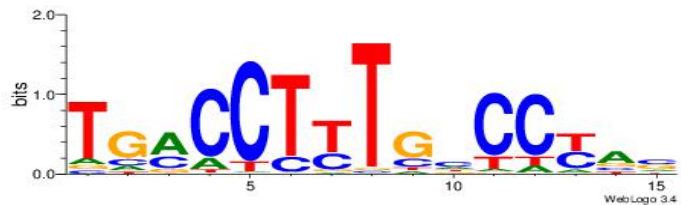
Similarity score: 0.0305369

Alignment:  
TGRCCTKTGHCCKAB  
-----ATKTM-----

Original motif      Consensus sequence: BTRGGDCARAGGKCA



Reverse complement motif      Consensus sequence: TGRCCTKTGHCCK

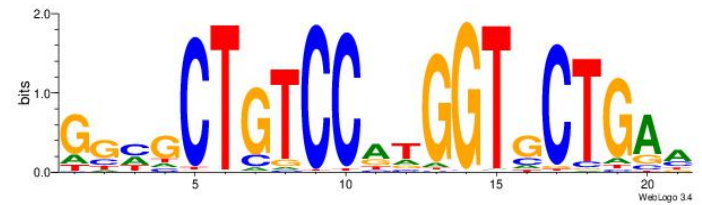
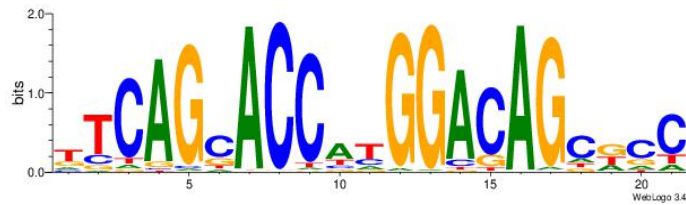


Dataset #: 2  
Motif ID: 19  
Motif name: REST  
Matching format of first motif: Original Motif  
Matching format of second motif: Reverse Complement  
Direction: Backward  
Position number: 13  
Number of overlap: 5  
Similarity score: 0.0315454

Alignment:  
GGYGCTGTCCATGGTGCTGAA  
-----ATKTM-----

Original motif      Consensus sequence: TTCAGCACCATGGACAGCKCC

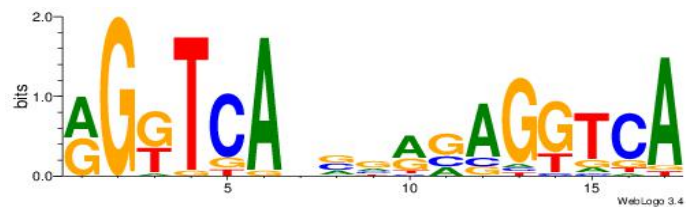
Reverse complement motif      Consensus sequence:  
GGYGCTGTCCATGGTGCTGAA



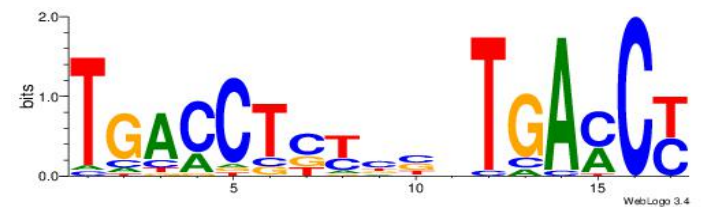
Dataset #: 2  
 Motif ID: 47  
 Motif name: RXRRAR\_DR5  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 5  
 Similarity score: 0.0335956

Alignment:  
 RGKTCABVVRGAGGTCA  
 ATKTM-----

Original motif      Consensus sequence: RGKTCABVVRGAGGTCA



Reverse complement motif      Consensus sequence: TGACCTCKVVB TGAYCK



Dataset #: 2

Motif ID: 46  
 Motif name: RORA\_1  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 3  
 Number of overlap: 5  
 Similarity score: 0.0336052

Alignment:

AWVDAGGTCA

---RARAT--

Original motif      Consensus sequence: AWVDAGGTCA



Reverse complement motif      Consensus sequence: TGACCTDVWT




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Dataset #: 2  
 Motif ID: 34  
 Motif name: HNF4A  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 2  
 Number of overlap: 5  
 Similarity score: 0.0367105

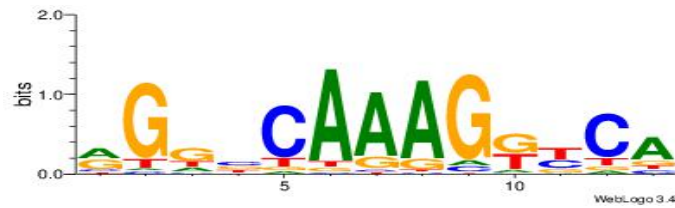


Alignment:

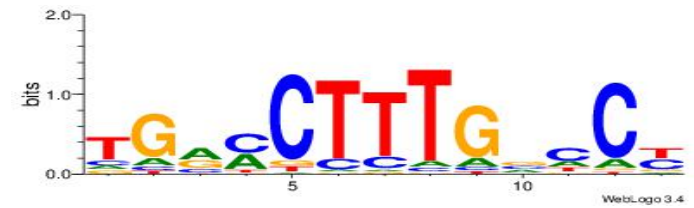
RGGBCAAAGKYCA

-----ATKTM-

Original motif      Consensus sequence: RGGBCAAAGKYCA



Reverse complement motif      Consensus sequence: TGM YCTTTGBCCK



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

Original motif      Consensus sequence: CMGCRGC



Reverse complement motif      Consensus sequence: GCKGCOYG



### Best Matches for Top Significant Motif ID 6 (Highest to Lowest)

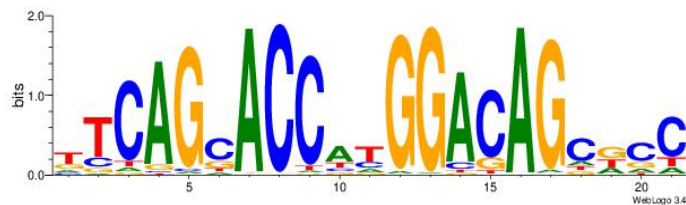
|                                  |                |
|----------------------------------|----------------|
| Dataset #:                       | 2              |
| Motif ID:                        | 19             |
| Motif name:                      | REST           |
| Matching format of first motif:  | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction:                       | Backward       |
| Position number:                 | 13             |

Number of overlap: 7  
Similarity score: 0.0205607

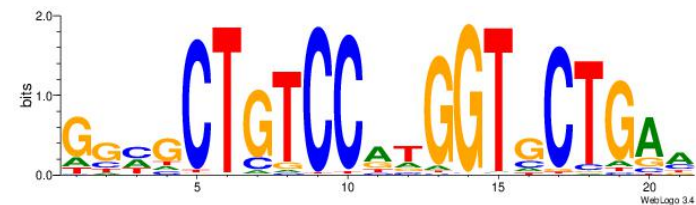
Alignment:

TTCAGCACCATGGACAGCKCC  
--CMGCRGC-----

Original motif      Consensus sequence: TTCAGCACCATGGACAGCKCC



Reverse complement motif      Consensus sequence: GGYGCTGTCCATGGTGCTGAA



Dataset #: 2  
Motif ID: 37  
Motif name: MIZF  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Reverse Complement  
Direction: Forward  
Position number: 1  
Number of overlap: 7  
Similarity score: 0.0322623

Alignment:

GCGGACGTTV  
GCKGCTG---

Original motif      Consensus sequence: BAACGTCCGC

Reverse complement motif      Consensus sequence: GCGGACGTTV



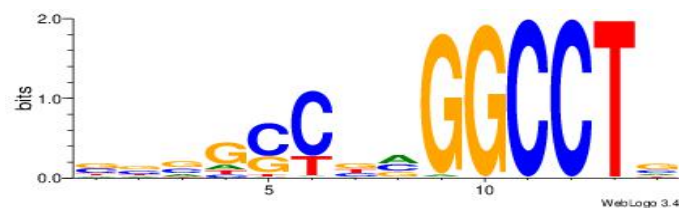
Dataset #: 2  
 Motif ID: 12  
 Motif name: Zfx  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 5  
 Number of overlap: 7  
 Similarity score: 0.038091

Alignment:

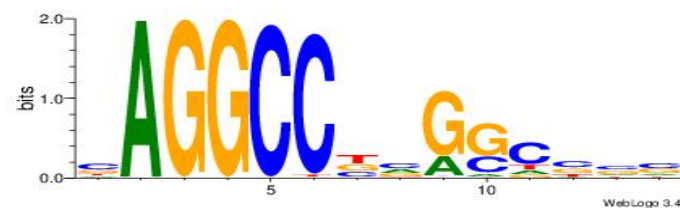
BBVGCCBVGGCCTV

----CMGCRGC---

Original motif      Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif      Consensus sequence: VAGGCCBBGGCV



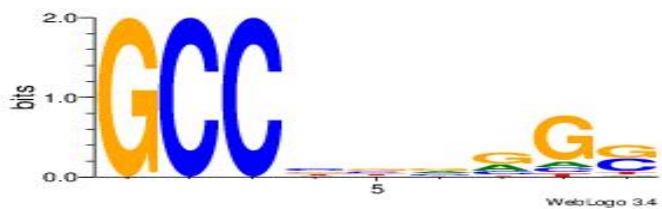
Dataset #: 2  
 Motif ID: 15

|                                  |                    |
|----------------------------------|--------------------|
| Motif name:                      | TFAP2A             |
| Matching format of first motif:  | Original Motif     |
| Matching format of second motif: | Reverse Complement |
| Direction:                       | Backward           |
| Position number:                 | 1                  |
| Number of overlap:               | 7                  |
| Similarity score:                | 0.0393168          |

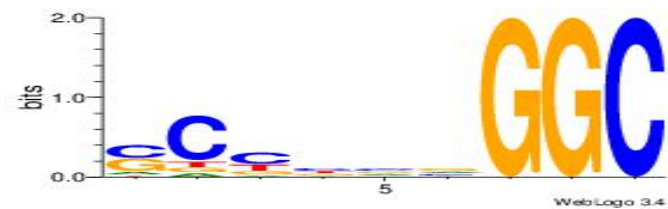
Alignment:

SCMVBBGGC  
 --CMGCRGC

Original motif    Consensus sequence: GCCBBVRGS



Reverse complement motif    Consensus sequence: SCMVBBGGC



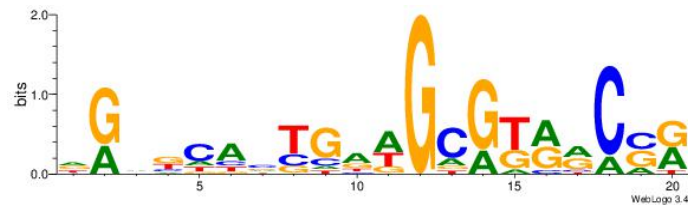
|                                  |                    |
|----------------------------------|--------------------|
| Dataset #:                       | 2                  |
| Motif ID:                        | 45                 |
| Motif name:                      | Pax5               |
| Matching format of first motif:  | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction:                       | Backward           |
| Position number:                 | 7                  |
| Number of overlap:               | 7                  |
| Similarity score:                | 0.0448462          |

Alignment:

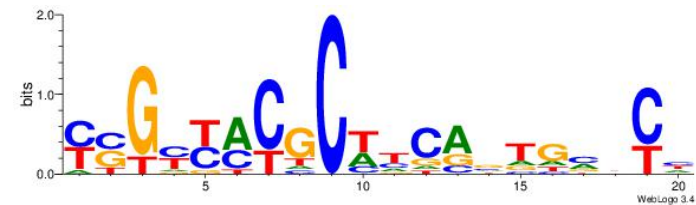
MSGKKRCGCWDCABTGBB CD

-----GCKGCG-----

Original motif      Consensus sequence: DGVBCABTGDWGCGRCSR



Reverse complement motif      Consensus sequence: MSGKKRCGCWDCABTGBB CD



|                                  |                    |
|----------------------------------|--------------------|
| Dataset #:                       | 2                  |
| Motif ID:                        | 28                 |
| Motif name:                      | Egr1               |
| Matching format of first motif:  | Reverse Complement |
| Matching format of second motif: | Original Motif     |
| Direction:                       | Backward           |
| Position number:                 | 2                  |
| Number of overlap:               | 7                  |
| Similarity score:                | 0.0453576          |

Alignment:

HGCGTGGGCGK

---GCKGCG---

Original motif      Consensus sequence: HGCGTGGGCGK

Reverse complement motif      Consensus sequence: YGCCCCACGCH



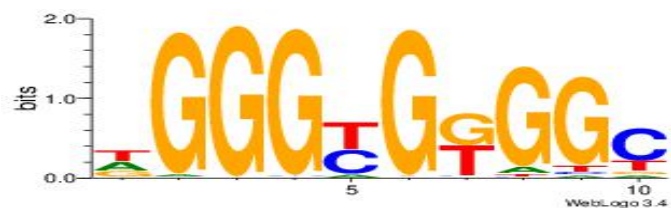
Dataset #: 2  
 Motif ID: 36  
 Motif name: Klf4  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 2  
 Number of overlap: 7  
 Similarity score: 0.0476958

Alignment:

GCCYCMCCCD

-CMGCRGC--

Original motif      Consensus sequence: DGGGYGKGGC



Reverse complement motif      Consensus sequence: GCCYCMCCCD



Dataset #: 2  
 Motif ID: 16

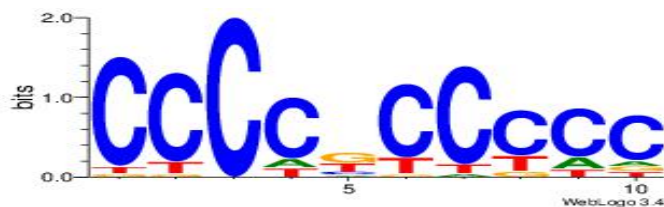
|                                  |                    |
|----------------------------------|--------------------|
| Motif name:                      | SP1                |
| Matching format of first motif:  | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction:                       | Forward            |
| Position number:                 | 1                  |
| Number of overlap:               | 7                  |
| Similarity score:                | 0.0490991          |

Alignment:

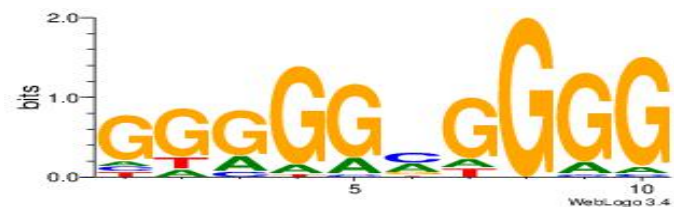
GGGGGYGGGG

GCKGCG---

Original motif      Consensus sequence: CCCCKCCCC



Reverse complement motif      Consensus sequence: GGGGGYGGGG

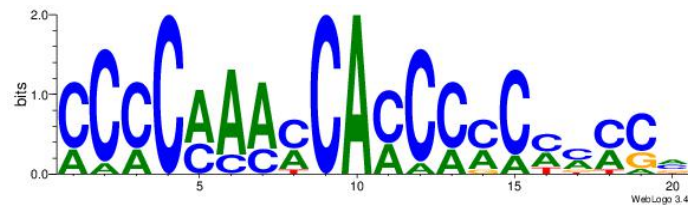


|                                  |                    |
|----------------------------------|--------------------|
| Dataset #:                       | 2                  |
| Motif ID:                        | 18                 |
| Motif name:                      | RREB1              |
| Matching format of first motif:  | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction:                       | Forward            |
| Position number:                 | 6                  |
| Number of overlap:               | 7                  |
| Similarity score:                | 0.0498726          |

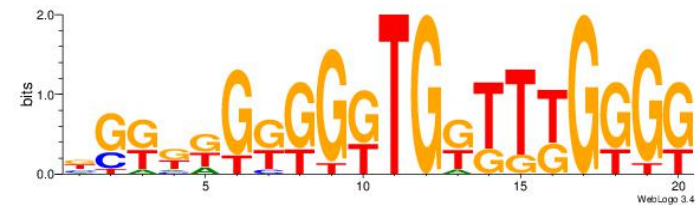
Alignment:

BGRRRGRGGRTGRTTYGGGG  
-----GCKGCTY-----

Original motif      Consensus sequence: CCCMAAMCAMCCMCMMMC



Reverse complement motif      Consensus sequence:  
BGRRRGRGGRTGRTTYGGGG



|                                  |                    |
|----------------------------------|--------------------|
| Dataset #:                       | 2                  |
| Motif ID:                        | 35                 |
| Motif name:                      | INSM1              |
| Matching format of first motif:  | Original Motif     |
| Matching format of second motif: | Reverse Complement |
| Direction:                       | Backward           |
| Position number:                 | 3                  |
| Number of overlap:               | 7                  |
| Similarity score:                | 0.0511926          |

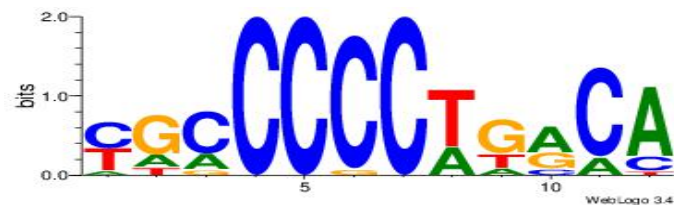
Alignment:

MGCCCCCTGMCA  
---CMGCRGC---

Original motif      Consensus sequence: TGYCAGGGGGCR

Reverse complement motif      Consensus sequence: MGCCCCCTGMCA





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

Original motif      Consensus sequence: CTGGGA



Reverse complement motif      Consensus sequence: TCCCAG



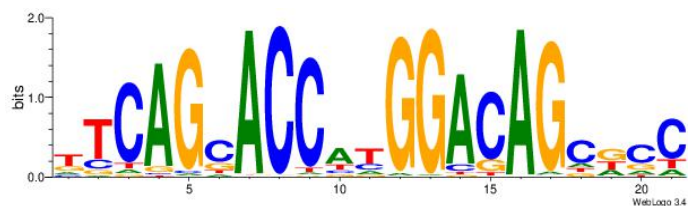
### Best Matches for Top Significant Motif ID 8 (Highest to Lowest)

|                                  |                    |
|----------------------------------|--------------------|
| Dataset #:                       | 2                  |
| Motif ID:                        | 19                 |
| Motif name:                      | REST               |
| Matching format of first motif:  | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction:                       | Backward           |
| Position number:                 | 9                  |
| Number of overlap:               | 6                  |
| Similarity score:                | 0.0392549          |

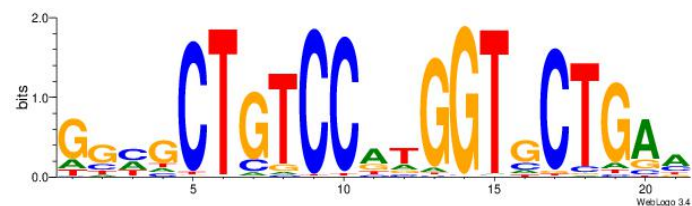
Alignment:

```
GGYGCTGTCCATGGTGCTGAA
-----TCCCAG-----
```

Original motif      Consensus sequence: TTCAGCACCATGGACAGCKCC



Reverse complement motif      Consensus sequence: GGYGCTGTCCATGGTGCTGAA



Dataset #: 2  
Motif ID: 23  
Motif name: MZF1\_1-4  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Reverse Complement  
Direction: Forward  
Position number: 1  
Number of overlap: 6  
Similarity score: 0.0416319

Alignment:

TCCCCV

TCCCAG

Original motif      Consensus sequence: BGGGGA



Reverse complement motif      Consensus sequence: TCCCCV

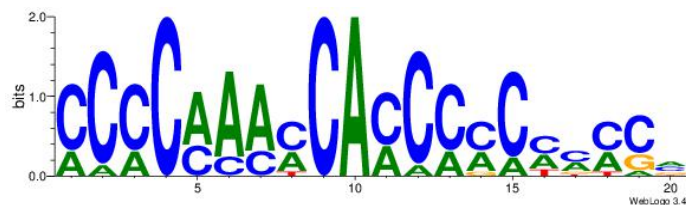


Dataset #: 2  
 Motif ID: 18  
 Motif name: RREB1  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 6  
 Similarity score: 0.0509122

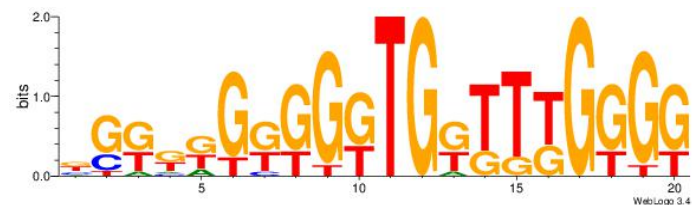
Alignment:

BGRRRGRGGRTGRTTYGGGG  
 -----CTGGGA

Original motif      Consensus sequence: CCCMAAMCAMCCMCMMMC



Reverse complement motif      Consensus sequence: BGRRRGRGGRTGRTTYGGGG

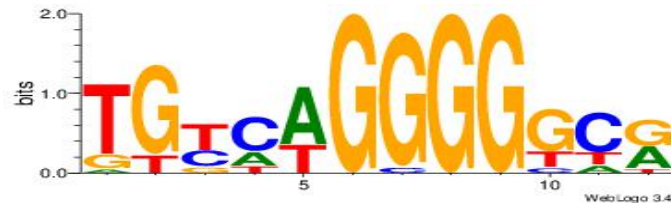


Dataset #: 2  
 Motif ID: 35  
 Motif name: INSM1  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 4

Number of overlap: 6  
Similarity score: 0.0557857

Alignment:  
TGYCAGGGGGCR  
---CTGGGA---

Original motif      Consensus sequence: TGYCAGGGGGCR



Reverse complement motif      Consensus sequence: MGCCCCCTGMCA

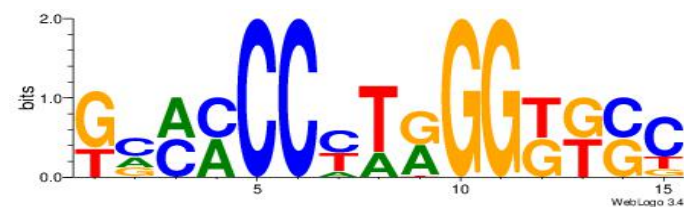
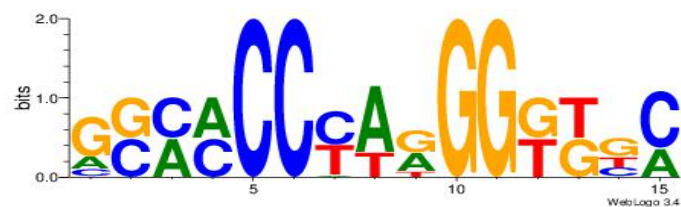


Dataset #: 2  
Motif ID: 13  
Motif name: Zfp423  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Reverse Complement  
Direction: Forward  
Position number: 4  
Number of overlap: 6  
Similarity score: 0.0624145

Alignment:  
GYRYCCMTKGGYRSC  
---TCCCAG-----

Original motif      Consensus sequence: GSMCCYARGGKKKC

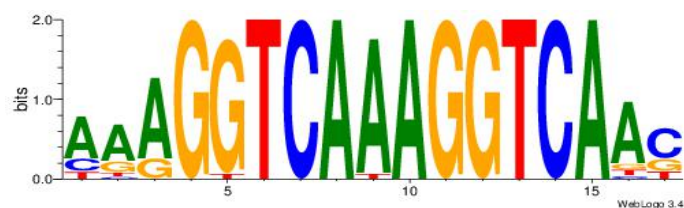
Reverse complement motif      Consensus sequence: GYRYCCMTKGGYR



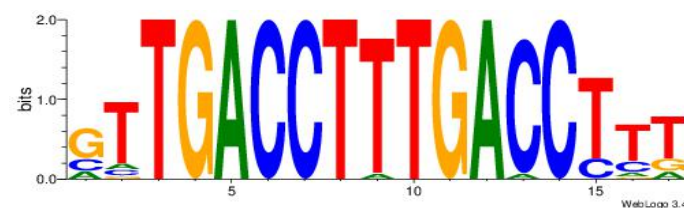
Dataset #: 2  
 Motif ID: 43  
 Motif name: NR1H2RXRA  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 6  
 Number of overlap: 6  
 Similarity score: 0.0650784

Alignment:  
 GTTGACCTTTGACCTTT  
 -----CTGGGA-----

Original motif      Consensus sequence: AAAGGTCAAAGGTCAAC



Reverse complement motif      Consensus sequence: GTTGACCTTTGACCTTT

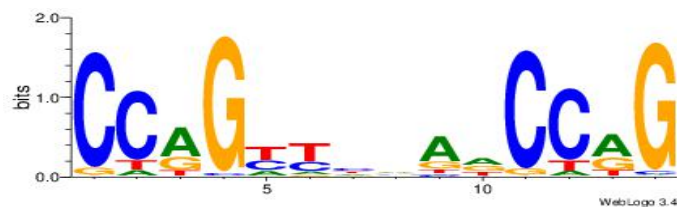


Dataset #: 2

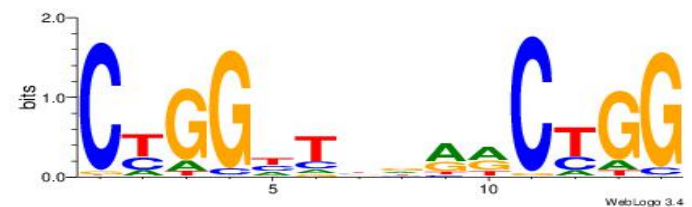
Motif ID: 48  
 Motif name: Tcfcp2l1  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 9  
 Number of overlap: 6  
 Similarity score: 0.0663804

Alignment:  
 CKGGDTBDMMCTGG  
 CTGGGA-----

Original motif      Consensus sequence: CCAGYYHVADCCRG



Reverse complement motif      Consensus sequence: CKGGDTBDMMCTGG



Dataset #: 2  
 Motif ID: 28  
 Motif name: Egr1  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 3  
 Number of overlap: 6  
 Similarity score: 0.0678562

Alignment:

YCGCCCACGCH

--TCCCAG---

Original motif      Consensus sequence: HCGTG GGGCGK



Reverse complement motif      Consensus sequence: YCGCCCACGCH



|                                  |                    |
|----------------------------------|--------------------|
| Dataset #:                       | 2                  |
| Motif ID:                        | 24                 |
| Motif name:                      | Ar                 |
| Matching format of first motif:  | Reverse Complement |
| Matching format of second motif: | Original Motif     |
| Direction:                       | Backward           |
| Position number:                 | 3                  |
| Number of overlap:               | 6                  |
| Similarity score:                | 0.0714107          |

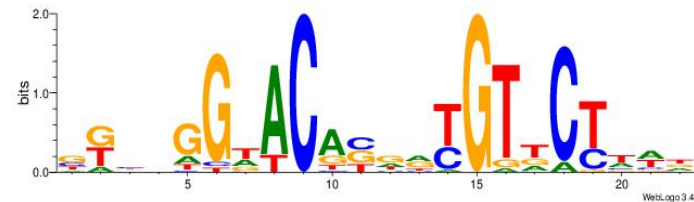
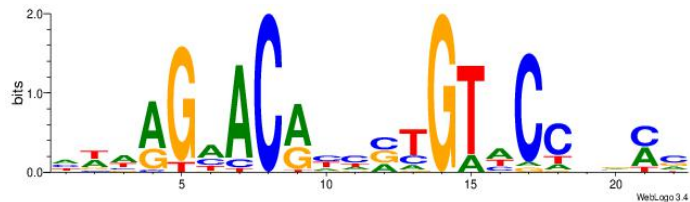
Alignment:

HWDAGHACRHHVTGTHCCHVMV

-----TCCCAG--

Original motif      Consensus sequence: HWDAGHACRHHVTGTHCCHVMV

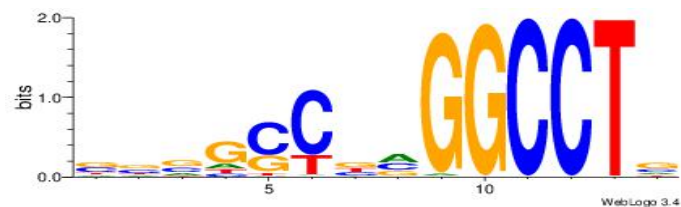
Reverse complement motif      Consensus sequence:  
VRVDGGHACAVDDKGTHCTDWH



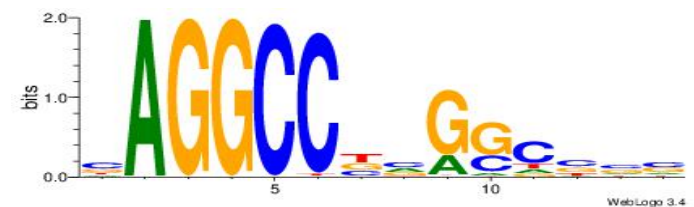
Dataset #: 2  
 Motif ID: 12  
 Motif name: Zfx  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 4  
 Number of overlap: 6  
 Similarity score: 0.0718041

Alignment:  
 BBVGCCBVGGCCTV  
 -----CTGGGA---

Original motif      Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif      Consensus sequence: VAGGCCBBGGCV



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



Original motif      Consensus sequence: AMACA



Reverse complement motif      Consensus sequence: TGTRT



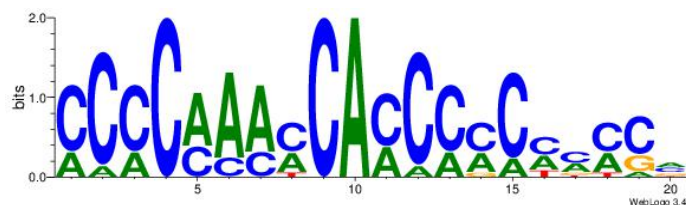
## Best Matches for Top Significant Motif ID 2 (Highest to Lowest)

Dataset #: 2  
 Motif ID: 18  
 Motif name: RREB1  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 11  
 Number of overlap: 5  
 Similarity score: 0.0243918

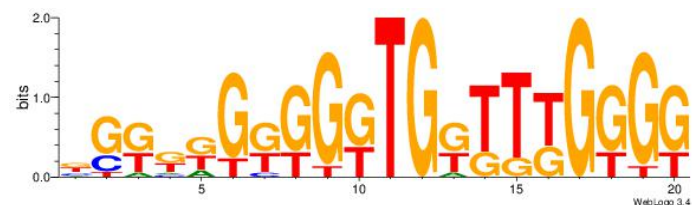
Alignment:

CCCCMAAMCAMECCMMMCV  
 -----AMACA-----

Original motif      Consensus sequence: CCCCMAAMCAMECCMMMCV



Reverse complement motif      Consensus sequence: BGGRRGRGGRTGRTTYGGGG

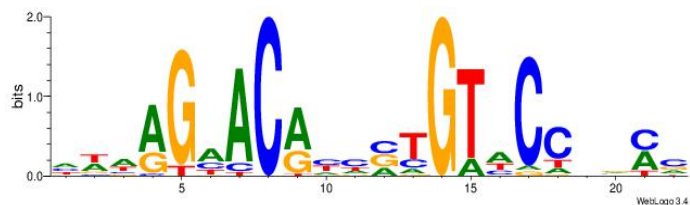


Dataset #: 2  
 Motif ID: 24  
 Motif name: Ar  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 5  
 Number of overlap: 5  
 Similarity score: 0.0429089

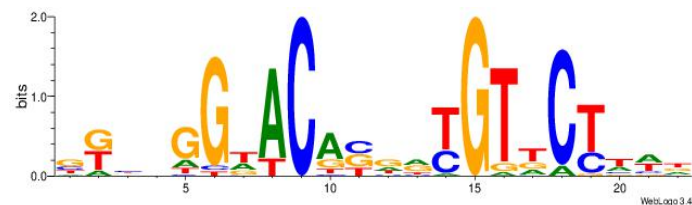
Alignment:

HWDAGHACRHHVTGTHCCHVMV  
 ----AMACA-----

Original motif      Consensus sequence: HWDAGHACRHHVTGTHCCHVMV



Reverse complement motif      Consensus sequence: VRVDGGHACA VDDKGTCTDWH

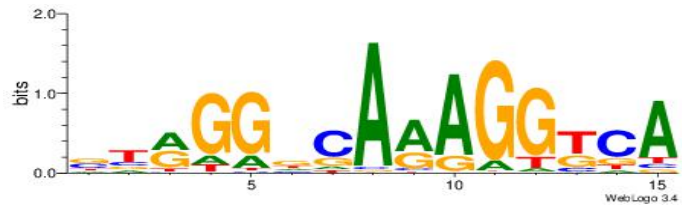


Dataset #: 2  
 Motif ID: 20  
 Motif name: PPARGRXRA  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 6

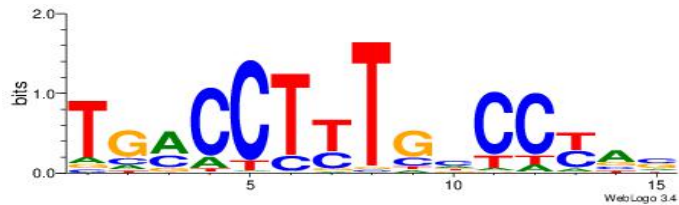
Number of overlap: 5  
Similarity score: 0.0595073

Alignment:  
TGRCCCTKTGHCCCKAB  
-----TGTRT-----

Original motif      Consensus sequence: BTRGGDCARAGGKCA



Reverse complement motif      Consensus sequence: TGRCCCTKTGHCCCK



Dataset #: 2  
Motif ID: 26  
Motif name: ArntAhr  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Original Motif  
Direction: Backward  
Position number: 2  
Number of overlap: 5  
Similarity score: 0.0600161

Alignment:  
YGCGTG  
TGTRT-

Original motif      Consensus sequence: YGCGTG

Reverse complement motif      Consensus sequence: CACGCM

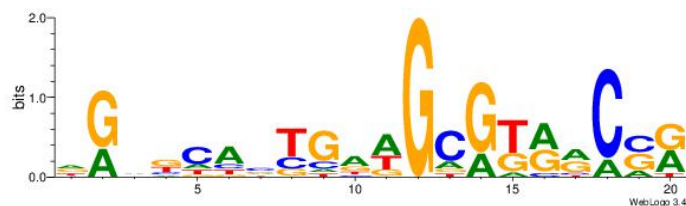


Dataset #: 2  
 Motif ID: 45  
 Motif name: Pax5  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 11  
 Number of overlap: 5  
 Similarity score: 0.0620995

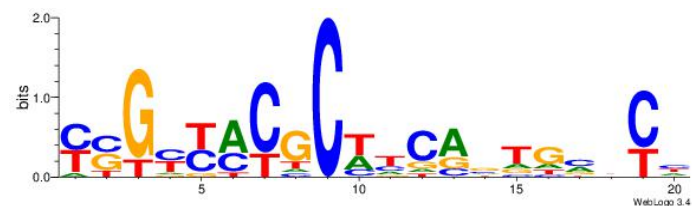
#### Alignment:

MSGKKRCGCWDCABTGBBCD  
 -----AMACA-----

Original motif      Consensus sequence: DGVBCABTGDWGCGRRCR



Reverse complement motif      Consensus sequence: MSGKKRCGCWDCABTGBBCD



Dataset #: 2

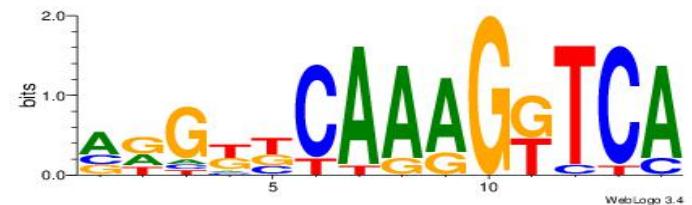
Motif ID: 22  
 Motif name: NR2F1  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 4  
 Number of overlap: 5  
 Similarity score: 0.0650242

Alignment:  
 AKGYCAAAGRTCA  
 -----AMACA---

Original motif      Consensus sequence: TGAMCTTTGMMCYT



Reverse complement motif      Consensus sequence: AKGYCAAAGRTCA



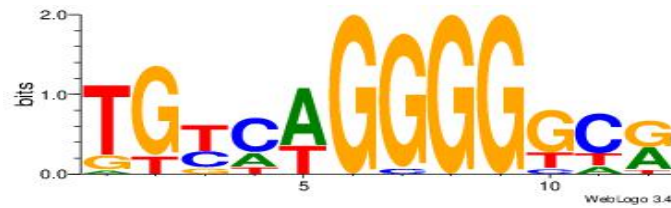
Dataset #: 2  
 Motif ID: 35  
 Motif name: INSM1  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 8  
 Number of overlap: 5  
 Similarity score: 0.0670984

Alignment:

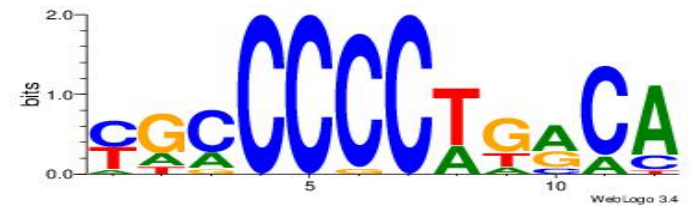
MGCCCCCTGMCA

-----AMACA

Original motif      Consensus sequence: TGYCAGGGGGCR



Reverse complement motif      Consensus sequence: MGCCCCCTGMCA



|                                  |                    |
|----------------------------------|--------------------|
| Dataset #:                       | 2                  |
| Motif ID:                        | 33                 |
| Motif name:                      | HIF1AARNT          |
| Matching format of first motif:  | Original Motif     |
| Matching format of second motif: | Reverse Complement |
| Direction:                       | Forward            |
| Position number:                 | 1                  |
| Number of overlap:               | 5                  |
| Similarity score:                | 0.0700905          |

Alignment:

VCACGTBV

AMACA---

Original motif      Consensus sequence: VBACGTGV

Reverse complement motif      Consensus sequence: VCACGTBV



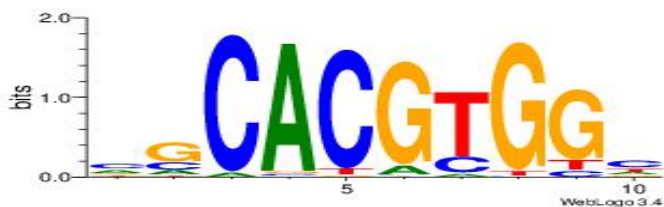
Dataset #: 2  
 Motif ID: 38  
 Motif name: Myc  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 5  
 Number of overlap: 5  
 Similarity score: 0.0708148

Alignment:

VGCACGTGGH

-AMACA----

Original motif      Consensus sequence: VGCACGTGGH



Reverse complement motif      Consensus sequence: DCCACGTGCV



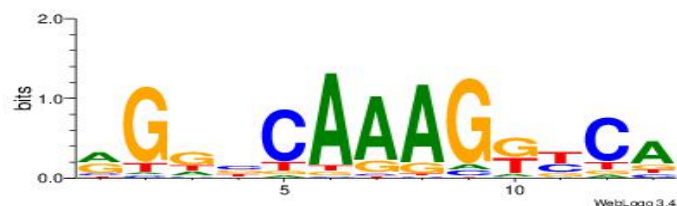
Dataset #: 2  
 Motif ID: 34

Motif name: HNF4A  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 4  
 Number of overlap: 5  
 Similarity score: 0.071574

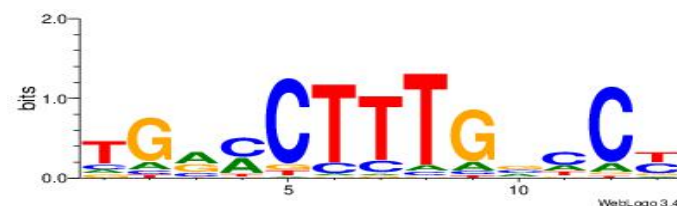
Alignment:

TGM YCTTTGBCCK  
 -----TGTRT-----

Original motif      Consensus sequence: RGGBCAAAGKYCA



Reverse complement motif      Consensus sequence: TGM YCTTTGBCCK



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

Original motif      Consensus sequence: AGSCWGG



Reverse complement motif      Consensus sequence: CCWGSCT



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

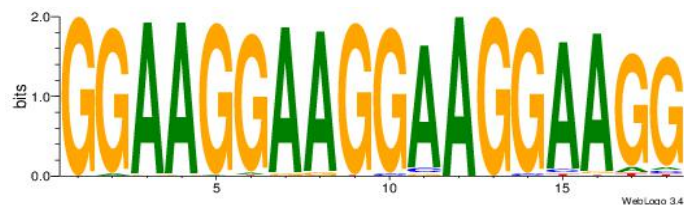


Dataset #: 2  
 Motif ID: 32  
 Motif name: EWSR1-FLI1  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 5  
 Number of overlap: 7  
 Similarity score: 0.0395671

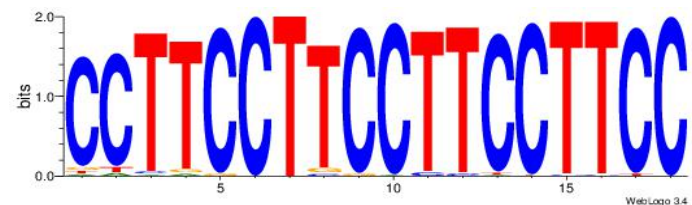
Alignment:

GGAAGGAAGGAAGGAAGG  
 -----AGSCWGG-----

Original motif      Consensus sequence: GGAAGGAAGGAAGGAAGG



Reverse complement motif      Consensus sequence: CCTTCCTTCCTTCCTTC

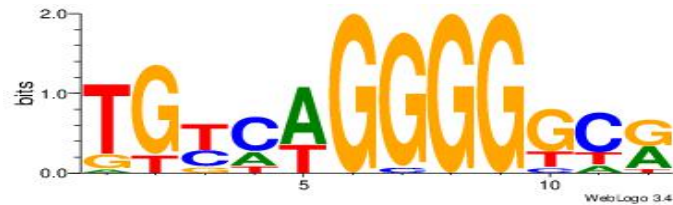


Dataset #: 2  
 Motif ID: 35  
 Motif name: INSM1  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 1

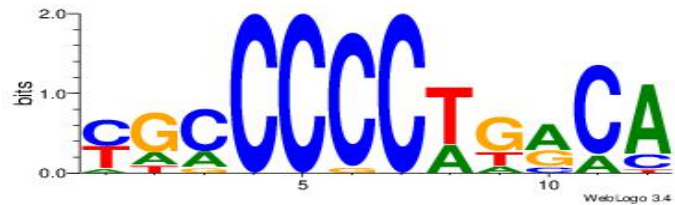
Number of overlap: 7  
Similarity score: 0.0494688

Alignment:  
MGCCCCCTGMCA  
-----CCWGSCT

Original motif      Consensus sequence: TGYCAGGGGGCR



Reverse complement motif      Consensus sequence: MGCCCCCTGMCA

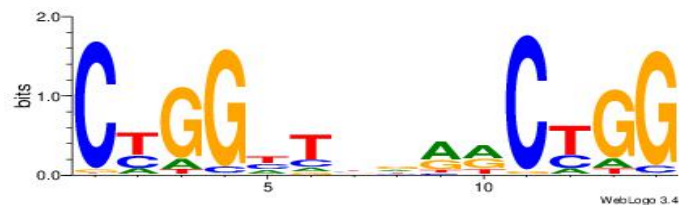
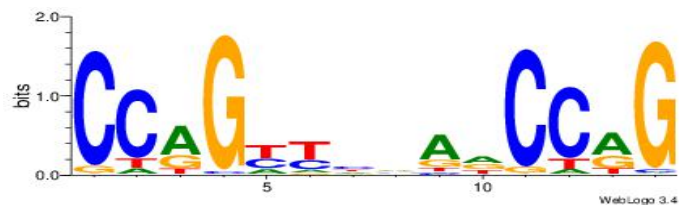


Dataset #: 2  
Motif ID: 48  
Motif name: Tcfcp2l1  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Original Motif  
Direction: Forward  
Position number: 1  
Number of overlap: 7  
Similarity score: 0.0669354

Alignment:  
CCAGYYHVADCCRG  
CCWGSCT-----

Original motif      Consensus sequence: CCAGYYHVADCCRG

Reverse complement motif      Consensus sequence: CKGGDTBDMMCTC

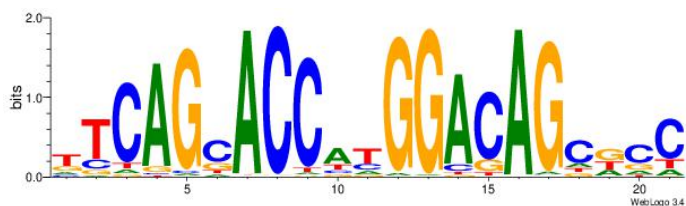


Dataset #: 2  
 Motif ID: 19  
 Motif name: REST  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 9  
 Number of overlap: 7  
 Similarity score: 0.0693747

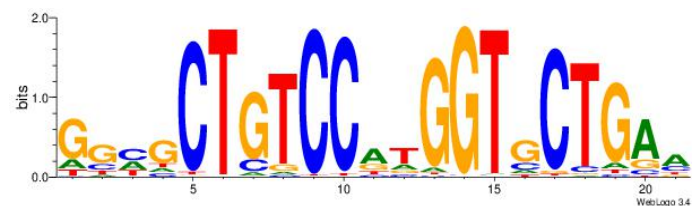
#### Alignment:

TTCAGCACCATGGACAGCKCC  
 -----AGSCWGG-----

Original motif      Consensus sequence: TTCAGCACCATGGACAGCKCC



Reverse complement motif      Consensus sequence: GGYGCTGTCCATGGTGCTGAA

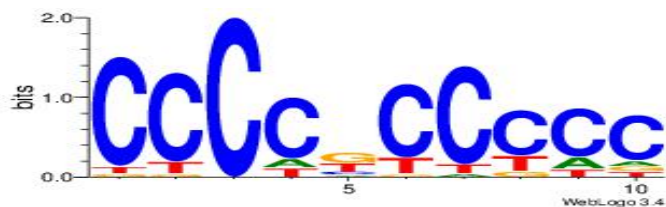


Dataset #: 2

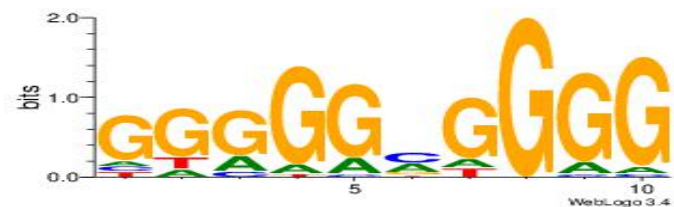
Motif ID: 16  
 Motif name: SP1  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 3  
 Number of overlap: 7  
 Similarity score: 0.0695377

Alignment:  
 CCCCKCCCC  
 -CCWGSCT--

Original motif      Consensus sequence: CCCCKCCCC



Reverse complement motif      Consensus sequence: GGGGGYGGGG




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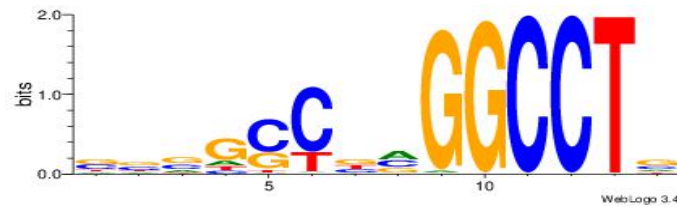
Dataset #: 2  
 Motif ID: 12  
 Motif name: Zfx  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 2  
 Number of overlap: 7  
 Similarity score: 0.0720685

Alignment:

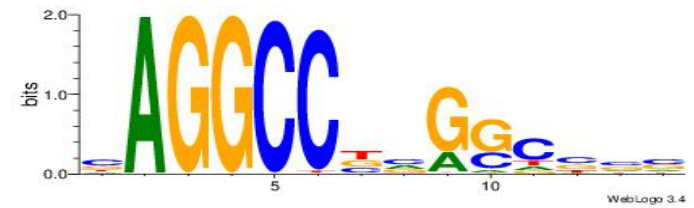
BBVGCCBVGGCCTV

-----CCWGSCT-

Original motif      Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif      Consensus sequence: VAGGCCBBGGCVB



|                                  |                    |
|----------------------------------|--------------------|
| Dataset #:                       | 2                  |
| Motif ID:                        | 29                 |
| Motif name:                      | ESR1               |
| Matching format of first motif:  | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction:                       | Forward            |
| Position number:                 | 13                 |
| Number of overlap:               | 7                  |
| Similarity score:                | 0.0771405          |

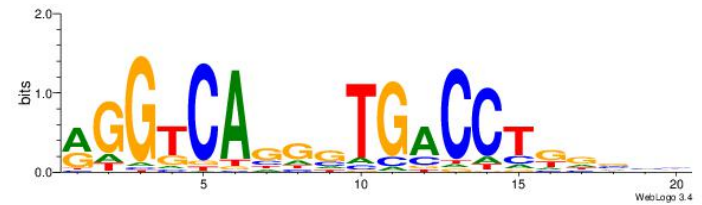
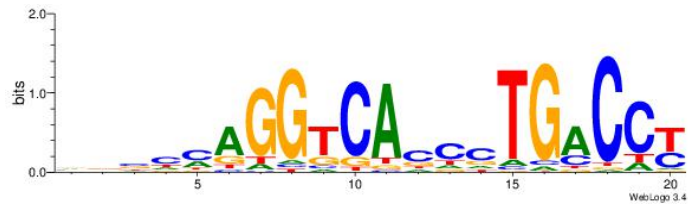
Alignment:

MGGTCAGGGTGACCTRDBHV

-----CCWGSCT-

Original motif      Consensus sequence: VDBHMAGGTCACCCTGACCY

Reverse complement motif      Consensus sequence:  
MGGTCAGGGTGACCTRDBHV



Dataset #: 2  
 Motif ID: 46  
 Motif name: RORA\_1  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 4  
 Number of overlap: 7  
 Similarity score: 0.0772276

#### Alignment:

TGACCTDVWT  
 ---CCWGSCT

Original motif      Consensus sequence: AWVDAGGTCA



Reverse complement motif      Consensus sequence: TGACCTDVWT



Dataset #: 2  
 Motif ID: 36

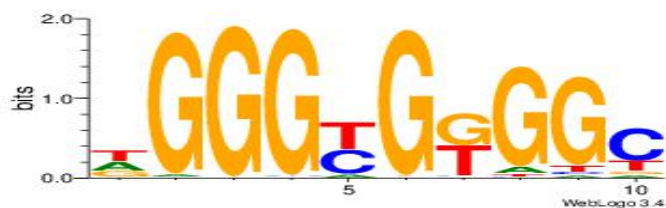
|                                  |                    |
|----------------------------------|--------------------|
| Motif name:                      | Klf4               |
| Matching format of first motif:  | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction:                       | Backward           |
| Position number:                 | 1                  |
| Number of overlap:               | 7                  |
| Similarity score:                | 0.0798994          |

Alignment:

GCCYCMCCCD

---CCWGSCT

Original motif      Consensus sequence: DGGGYGKGGC



Reverse complement motif      Consensus sequence: GCCYCMCCCD



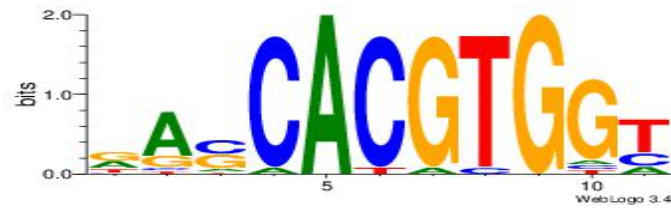
|                                  |                |
|----------------------------------|----------------|
| Dataset #:                       | 2              |
| Motif ID:                        | 39             |
| Motif name:                      | MYCMAX         |
| Matching format of first motif:  | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction:                       | Backward       |
| Position number:                 | 5              |
| Number of overlap:               | 7              |
| Similarity score:                | 0.0839075      |

Alignment:

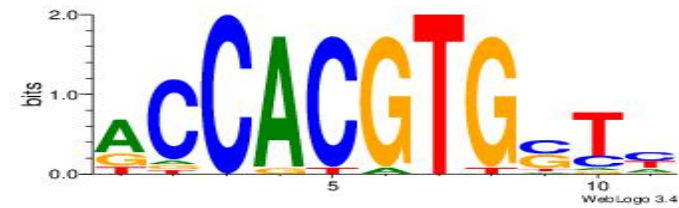
RASCACGTGGT

AGSCWGG----

Original motif      Consensus sequence: RASCACGTGGT



Reverse complement motif      Consensus sequence: ACCACGTGSTM



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

Original motif      Consensus sequence: RGGAAR



Reverse complement motif      Consensus sequence: MTTCCK



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

|                                  |                |
|----------------------------------|----------------|
| Dataset #:                       | 2              |
| Motif ID:                        | 32             |
| Motif name:                      | EWSR1-FLI1     |
| Matching format of first motif:  | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction:                       | Forward        |
| Position number:                 | 12             |

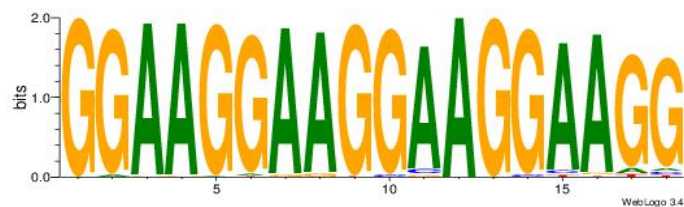


Number of overlap: 6  
Similarity score: 0.0146511

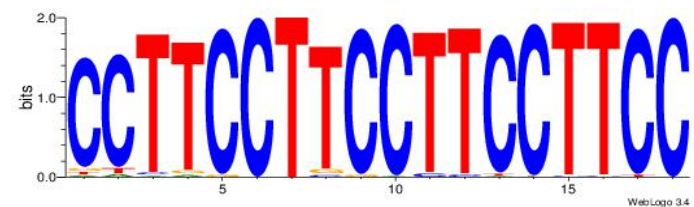
Alignment:

GGAAGGAAGGAAGGAAGG  
-----RGGAAR-

Original motif      Consensus sequence: GGAAGGAAGGAAGGAAGG



Reverse complement motif      Consensus sequence:  
CCTTCCTTCCTTCCTTCC



Dataset #: 2  
Motif ID: 37  
Motif name: MIZF  
Matching format of first motif: Reverse Complement  
Matching format of second motif: Original Motif  
Direction: Forward  
Position number: 4  
Number of overlap: 6  
Similarity score: 0.0608243

Alignment:

BAACGTCCGC  
---MTTCK-

Original motif      Consensus sequence: BAACGTCCGC

Reverse complement motif      Consensus sequence: GCGGACGTTV



Dataset #: 2  
 Motif ID: 41  
 Motif name: MZF1\_5-13  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 6  
 Similarity score: 0.0753789

#### Alignment:

BKAGGGGDAD

----RGAAR

Original motif      Consensus sequence: BKAGGGGDAD



Reverse complement motif      Consensus sequence: BTHCCCTYB



Dataset #: 2  
 Motif ID: 42

|                                  |                    |
|----------------------------------|--------------------|
| Motif name:                      | NFKB1              |
| Matching format of first motif:  | Original Motif     |
| Matching format of second motif: | Reverse Complement |
| Direction:                       | Forward            |
| Position number:                 | 2                  |
| Number of overlap:               | 6                  |
| Similarity score:                | 0.0757695          |

Alignment:

GGGGAAKCCCC

-RGGGAAR----

Original motif      Consensus sequence: GGGGRTTCCCC



Reverse complement motif      Consensus sequence: GGGGAAKCCCC



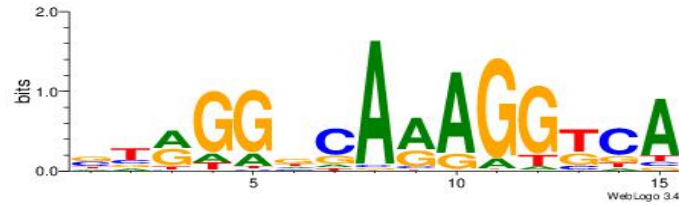
|                                  |                |
|----------------------------------|----------------|
| Dataset #:                       | 2              |
| Motif ID:                        | 20             |
| Motif name:                      | PPARGRXRA      |
| Matching format of first motif:  | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction:                       | Backward       |
| Position number:                 | 7              |
| Number of overlap:               | 6              |
| Similarity score:                | 0.0800484      |

Alignment:

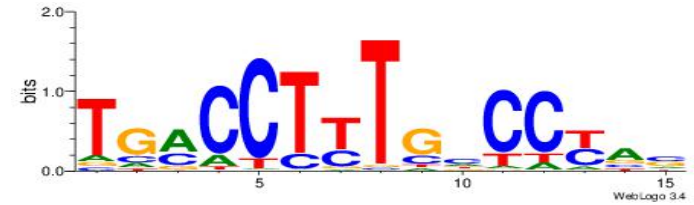
BTRGGDCARAGGKCA

---RGGAAR-----

Original motif      Consensus sequence: BTRGGDCARAGGKCA



Reverse complement motif      Consensus sequence: TGRCCTKTGHCCCK



|                                  |                |
|----------------------------------|----------------|
| Dataset #:                       | 2              |
| Motif ID:                        | 19             |
| Motif name:                      | REST           |
| Matching format of first motif:  | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction:                       | Backward       |
| Position number:                 | 6              |
| Number of overlap:               | 6              |
| Similarity score:                | 0.0829223      |

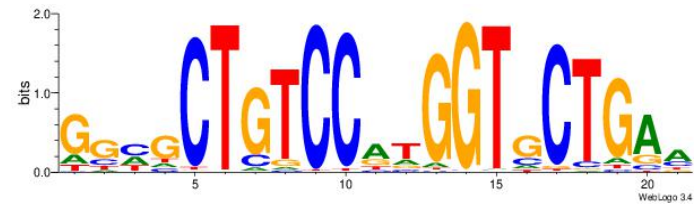
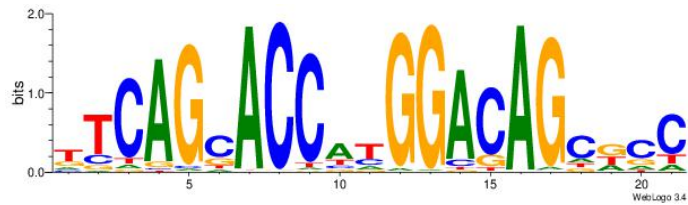
Alignment:

TTCAGCACCATGGACAGCKCC

-----RGGAAR-----

Original motif      Consensus sequence: TTCAGCACCATGGACAGCKCC

Reverse complement motif      Consensus sequence:  
GGYGCTGTCCATGGTGCTGAA

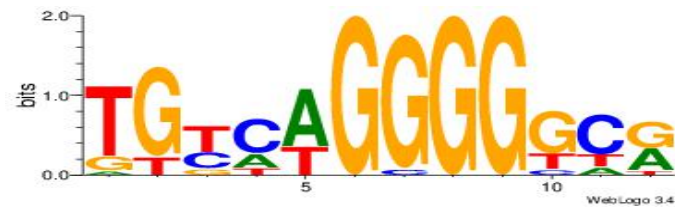


Dataset #: 2  
 Motif ID: 35  
 Motif name: INSM1  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Backward  
 Position number: 1  
 Number of overlap: 6  
 Similarity score: 0.0832926

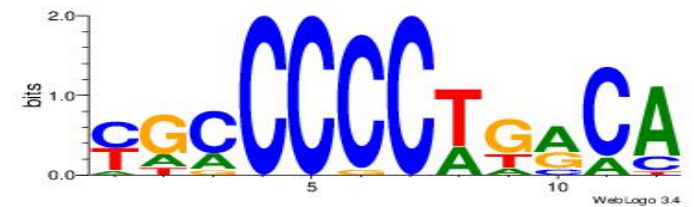
#### Alignment:

TGYCAGGGGGCR  
 -----RGAAR

Original motif      Consensus sequence: TGYCAGGGGGCR



Reverse complement motif      Consensus sequence: MGCCCCCTGMCA



Dataset #: 2  
 Motif ID: 18

|                                  |                    |
|----------------------------------|--------------------|
| Motif name:                      | RREB1              |
| Matching format of first motif:  | Original Motif     |
| Matching format of second motif: | Reverse Complement |
| Direction:                       | Forward            |
| Position number:                 | 5                  |
| Number of overlap:               | 6                  |
| Similarity score:                | 0.0835516          |

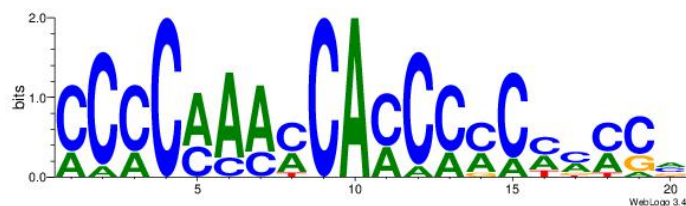
#### Alignment:

```

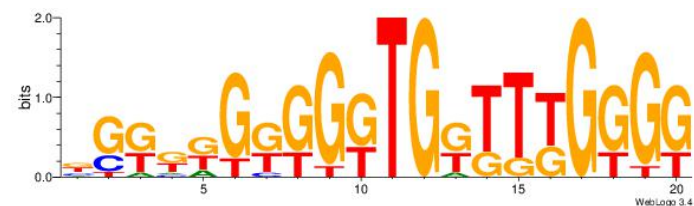
BGRRRGRGGRTGRTTYGGGG
----RGGAAR-----

```

Original motif      Consensus sequence: CCCCMAAMCAMCCMCMMMC



Reverse complement motif      Consensus sequence: BGRRRGRGGRTGRTTYGGGG



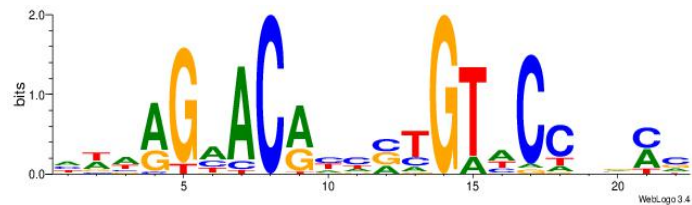
|                                  |                |
|----------------------------------|----------------|
| Dataset #:                       | 2              |
| Motif ID:                        | 24             |
| Motif name:                      | Ar             |
| Matching format of first motif:  | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction:                       | Forward        |
| Position number:                 | 4              |
| Number of overlap:               | 6              |
| Similarity score:                | 0.0836451      |

Alignment:

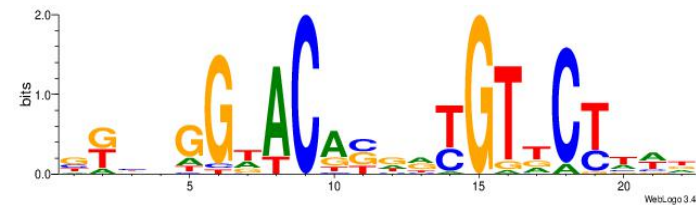
HWDAGHACRHHVTGTHCCHVMV

---RGGAAR-----

Original motif      Consensus sequence: HWDAGHACRHHVTGTHCCHVMV



Reverse complement motif      Consensus sequence: VRVDGGHACAVDDKGTHCTDWH



---

|                                  |                    |
|----------------------------------|--------------------|
| Dataset #:                       | 2                  |
| Motif ID:                        | 27                 |
| Motif name:                      | E2F1               |
| Matching format of first motif:  | Original Motif     |
| Matching format of second motif: | Reverse Complement |
| Direction:                       | Backward           |
| Position number:                 | 1                  |
| Number of overlap:               | 6                  |
| Similarity score:                | 0.0842331          |

Alignment:

GCGCSAAA

--RGGAAR

Original motif      Consensus sequence: TTTSGCGC

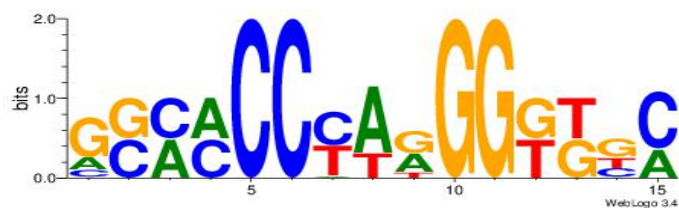
Reverse complement motif      Consensus sequence: GCGCSAAA



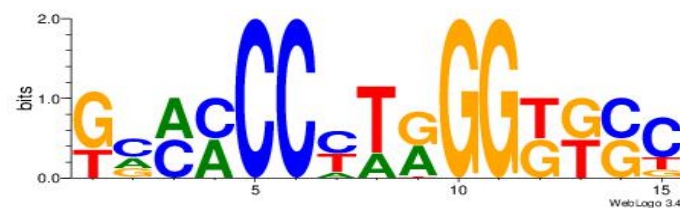
Dataset #: 2  
 Motif ID: 13  
 Motif name: Zfp423  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 9  
 Number of overlap: 6  
 Similarity score: 0.0850287

Alignment:  
 GYRYCCMTKGGYRSC  
 -----RGAAR-

Original motif      Consensus sequence: GSMMCCYARGGKKKC



Reverse complement motif      Consensus sequence: GYRYCCMTKGGYR



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



Original motif      Consensus sequence: CCCRCCCC



Reverse complement motif      Consensus sequence: GGGGMGGG



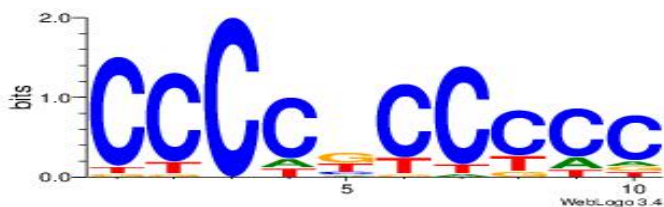
### Best Matches for Top Significant Motif ID 7 (Highest to Lowest)

|                                  |                |
|----------------------------------|----------------|
| Dataset #:                       | 2              |
| Motif ID:                        | 16             |
| Motif name:                      | SP1            |
| 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:                | 0.0423611      |

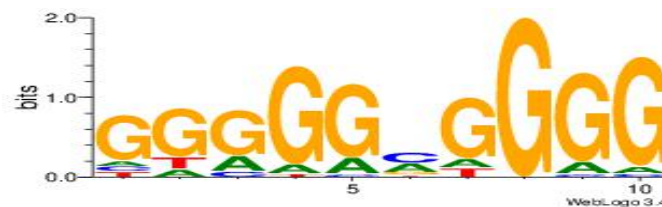
Alignment:

CCCCKCCCCC  
-CCRCRCCCC-

Original motif      Consensus sequence: CCCCKCCCCC



Reverse complement motif      Consensus sequence: GGGGGYGGGG



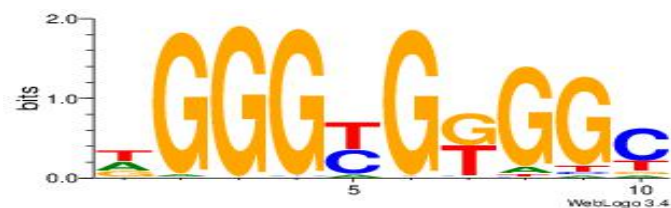
Dataset #: 2  
 Motif ID: 36  
 Motif name: Klf4  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 8  
 Similarity score: 0.0461644

Alignment:

DGGGYGKGGC

GGGGMGGG--

Original motif      Consensus sequence: DGGGYGKGGC



Reverse complement motif      Consensus sequence: GCCYCMCCCD



Dataset #: 2  
 Motif ID: 28  
 Motif name: Egr1  
 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: 0.0650374

Alignment:  
YCGCCACGCH  
---CCCRCCCC

Original motif      Consensus sequence: HCGTG GGGCGK



Reverse complement motif      Consensus sequence: YCGCCACGCH

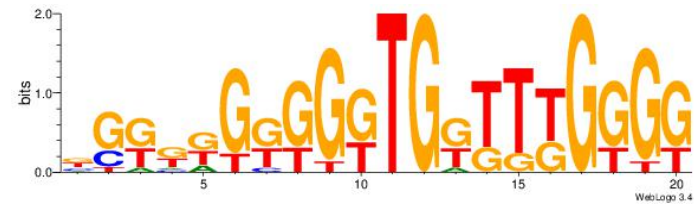
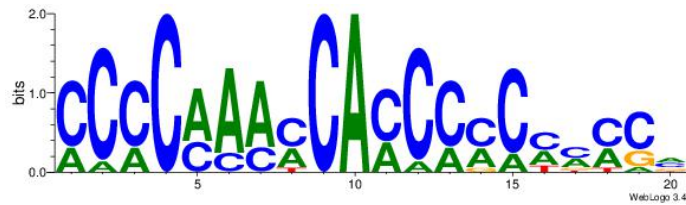


Dataset #: 2  
Motif ID: 18  
Motif name: RREB1  
Matching format of first motif: Original Motif  
Matching format of second motif: Original Motif  
Direction: Forward  
Position number: 7  
Number of overlap: 8  
Similarity score: 0.076401

Alignment:  
CCCCMAAMCAMCCMCMMMC  
-----CCCRCCCC-----

Original motif      Consensus sequence: CCCCMAAMCAMCCMCMMMC

Reverse complement motif      Consensus sequence:  
BGRRRGRGGRTGRTTYGGGG



Dataset #: 2  
 Motif ID: 42  
 Motif name: NFKB1  
 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: 0.0893429

#### Alignment:

GGGGAAKCCCC

GGGGMGG---

Original motif      Consensus sequence: GGGGRTTCCCC



Reverse complement motif      Consensus sequence: GGGGAAKCCCC



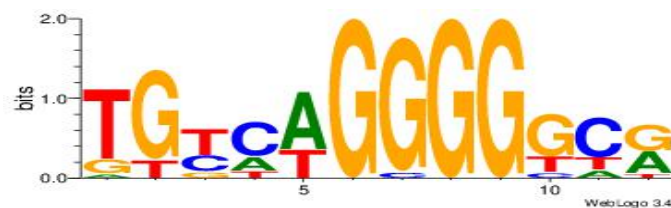
Dataset #: 2  
 Motif ID: 35

|                                  |                    |
|----------------------------------|--------------------|
| Motif name:                      | INSM1              |
| 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:                | 0.0936832          |

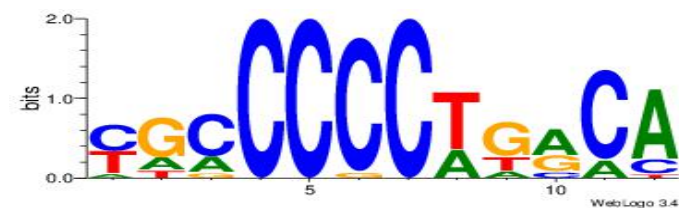
Alignment:

TGYCAGGGGGCR  
GGGGMGGG----

Original motif      Consensus sequence: TGYCAGGGGGCR



Reverse complement motif      Consensus sequence: MGCCCCCTGMCA



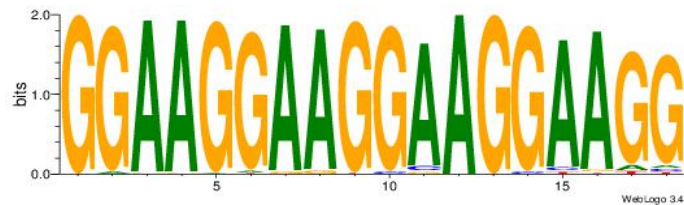
|                                  |                    |
|----------------------------------|--------------------|
| Dataset #:                       | 2                  |
| Motif ID:                        | 32                 |
| Motif name:                      | EWSR1-FLI1         |
| Matching format of first motif:  | Reverse Complement |
| Matching format of second motif: | Original Motif     |
| Direction:                       | Backward           |
| Position number:                 | 5                  |
| Number of overlap:               | 8                  |
| Similarity score:                | 0.0950969          |

Alignment:

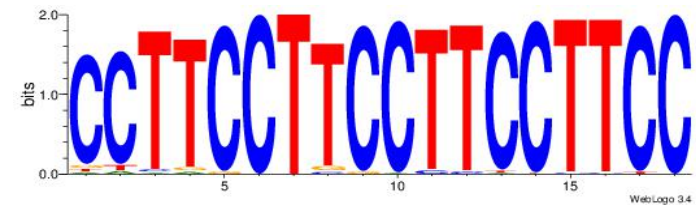
GGAAGGAAGGAAGGAAGG

-----GGGGMGGG-----

Original motif      Consensus sequence: GGAAGGAAGGAAGGAAGG



Reverse complement motif      Consensus sequence:  
CCTTCCTTCCTTCCTTCC



|                                  |                    |
|----------------------------------|--------------------|
| Dataset #:                       | 2                  |
| Motif ID:                        | 21                 |
| Motif name:                      | PLAG1              |
| Matching format of first motif:  | Reverse Complement |
| Matching format of second motif: | Original Motif     |
| Direction:                       | Forward            |
| Position number:                 | 1                  |
| Number of overlap:               | 8                  |
| Similarity score:                | 0.0998932          |

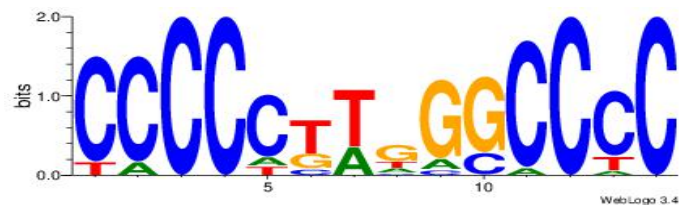
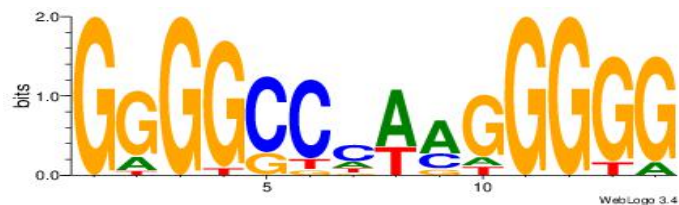
Alignment:

GGGGCCCAAGGGGG

GGGGMGGG-----

Original motif      Consensus sequence: GGGGCCCAAGGGGG

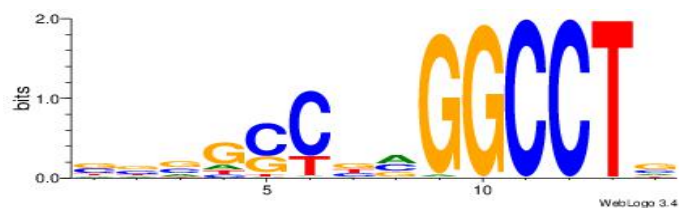
Reverse complement motif      Consensus sequence: CCCCCTTGGGCC



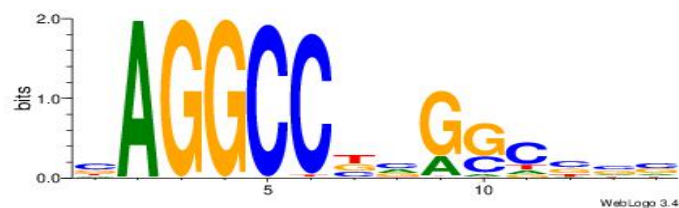
Dataset #: 2  
 Motif ID: 12  
 Motif name: Zfx  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 5  
 Number of overlap: 8  
 Similarity score: 0.10221

Alignment:  
 BBVGCCBVGGCCTV  
 ----CCCRCCCC--

Original motif      Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif      Consensus sequence: VAGGCCBBGGCV



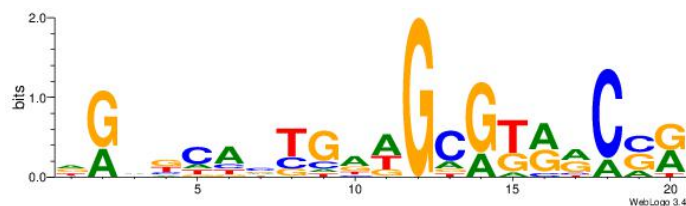
Dataset #: 2  
 Motif ID: 45

|                                  |                    |
|----------------------------------|--------------------|
| Motif name:                      | Pax5               |
| Matching format of first motif:  | Reverse Complement |
| Matching format of second motif: | Original Motif     |
| Direction:                       | Forward            |
| Position number:                 | 9                  |
| Number of overlap:               | 8                  |
| Similarity score:                | 0.102497           |

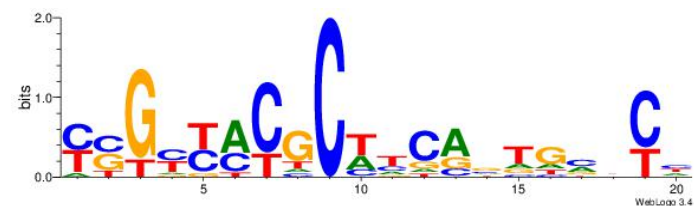
**Alignment:**

```
DGVBCABTGDWGCGRRCR
-----GGGGMGGG-----
```

Original motif      Consensus sequence: DGVBCABTGDWGCGRRCR



Reverse complement motif      Consensus sequence: MSGKKRCGCWDCABTGBBCD



**Dataset #: 2      Motif ID: 26      Motif name: ArntAhr**

Original motif      Consensus sequence: YGCGTG



Reverse complement motif      Consensus sequence: CACGCM





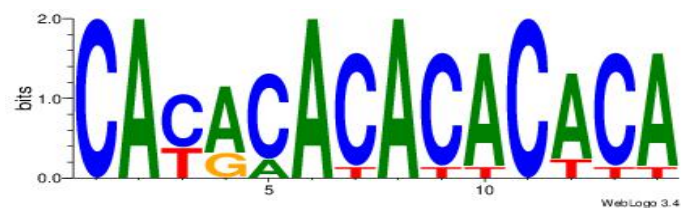
## Best Matches for Top Significant Motif ID 26 (Highest to Lowest)

Dataset #: 1  
 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: 7  
 Number of overlap: 6  
 Similarity score: 0.0308396

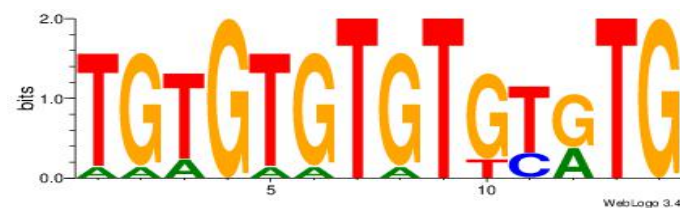
### Alignment:

TGTGTGTGTGKTG  
 -----YGCGTG--

Original motif      Consensus sequence: CAYACACACACACA



Reverse complement motif      Consensus sequence: TGTGTGTGTGKTG



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

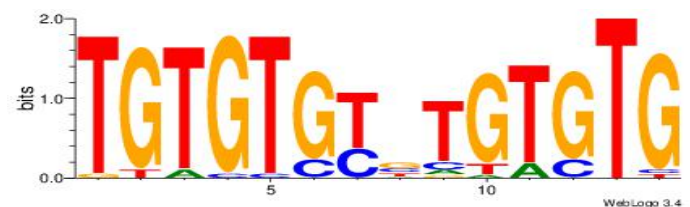
Direction: Forward  
 Position number: 9  
 Number of overlap: 6  
 Similarity score: 0.0350575

Alignment:  
 CACACAVRCACACA  
 -----CACGCM

Original motif Consensus sequence: CACACAVRCACACA



Reverse complement motif Consensus sequence: TGTGTGKVTGTGT



Dataset #: 1  
 Motif ID: 7  
 Motif name: Motif 7  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 6  
 Similarity score: 0.0586538

Alignment:  
 GGGGMGGG  
 YGCGTG--

Original motif      Consensus sequence: CCCRCCCC



Reverse complement motif      Consensus sequence: GGGGMGGG



Dataset #: 1  
 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: 6  
 Similarity score: 0.0884818

Alignment:  
 CCWGSCT  
 -CACGCM

Original motif      Consensus sequence: AGSCWGG



Reverse complement motif      Consensus sequence: CCWGSCT



Dataset #: 1  
 Motif ID: 2  
 Motif name: Motif 2  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 5  
 Similarity score: 0.563057

Alignment:  
 AMACA-  
 CACGCM

Original motif      Consensus sequence: AMACA



Reverse complement motif      Consensus sequence: TGTRT



Dataset #: 1  
 Motif ID: 6  
 Motif name: Motif 6  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Backward  
 Position number: 3  
 Number of overlap: 5

Similarity score: 0.572774

Alignment:

-GCKGCTG

YGCCTG--

Original motif Consensus sequence: CMGCRGC



Reverse complement motif Consensus sequence: GCKGCTG



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Dataset #: 1  
Motif ID: 8  
Motif name: Motif 8  
Matching format of first motif: Original Motif  
Matching format of second motif: Original Motif  
Direction: Forward  
Position number: 2  
Number of overlap: 5  
Similarity score: 0.581904

Alignment:

CTGGGA-

-YGCCTG

Original motif Consensus sequence: CTGGGA

Reverse complement motif Consensus sequence: TCCAG



Dataset #: 1  
 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: 3  
 Number of overlap: 4  
 Similarity score: 1.06919

Alignment:  
 --KCAGAG  
 YGCGTG--

Original motif      Consensus sequence: CTCTGY



Reverse complement motif      Consensus sequence: KCAGAG



**Dataset #: 2      Motif ID: 33      Motif name: HIF1AARNT**

Original motif      Consensus sequence: VBACGTGV



Reverse complement motif      Consensus sequence: VCACGTBV



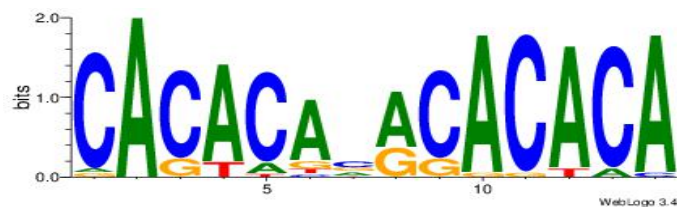
### Best Matches for Top Significant Motif ID 33 (Highest to Lowest)

Dataset #: 1  
 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: 2  
 Number of overlap: 8  
 Similarity score: 0.0745994

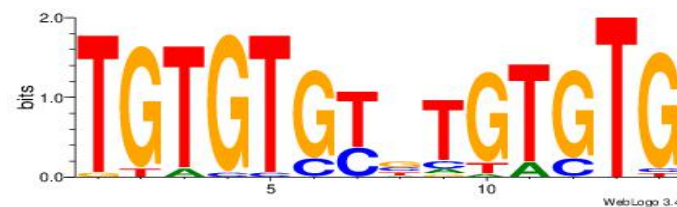
Alignment:

CACACAVRCACACA  
 -----VCACGTBV--

Original motif      Consensus sequence: CACACAVRCACACA



Reverse complement motif      Consensus sequence: TGTGTGKVTGTGT

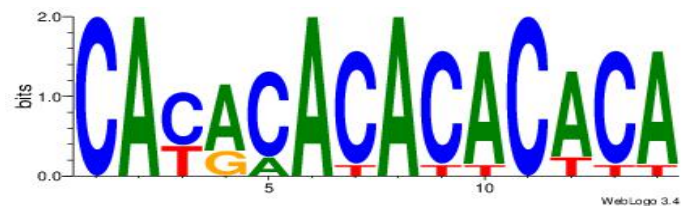


Dataset #: 1  
 Motif ID: 11  
 Motif name: Motif 11  
 Matching format of first motif: Reverse Complement  
 Matching format of second motif: Original Motif  
 Direction: Forward  
 Position number: 4  
 Number of overlap: 8  
 Similarity score: 0.0850889

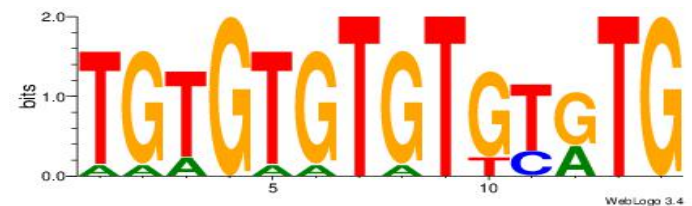
Alignment:

CAYACACACACACA  
 ---VCACGTBV---

Original motif      Consensus sequence: CAYACACACACACA



Reverse complement motif      Consensus sequence: TGTGTGTGTGKT



Dataset #: 1  
 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: 2  
 Number of overlap: 7



Similarity score: 0.588622

Alignment:  
CCCRCCCC-  
-VCACGTBV

Original motif      Consensus sequence: CCCRCCCC



Reverse complement motif      Consensus sequence: GGGGMGGG



Dataset #: 1  
Motif ID: 3  
Motif name: Motif 3  
Matching format of first motif: Original Motif  
Matching format of second motif: Reverse Complement  
Direction: Forward  
Position number: 3  
Number of overlap: 5  
Similarity score: 1.55675

Alignment:  
CCWGSCT---  
--VBACGTGV

Original motif      Consensus sequence: AGSCWGG

Reverse complement motif      Consensus sequence: CCWGSCT



Dataset #: 1  
 Motif ID: 2  
 Motif name: Motif 2  
 Matching format of first motif: Original Motif  
 Matching format of second motif: Reverse Complement  
 Direction: Forward  
 Position number: 1  
 Number of overlap: 5  
 Similarity score: 1.57238

Alignment:  
 TGTRT---  
 VBACGTGV

Original motif      Consensus sequence: AMACA



Reverse complement motif      Consensus sequence: TGTRT



Results created by MOTIFSIM on 11-20-2016 13:44:02  
Runtime: 673.485 seconds

MOTIFSIM is written by Ngoc Tam L. Tran  
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