# MOTIFSIM - MOTIF SIMilarity Detection Tool

**Version 2.0**

## INPUT

**Input Parameters**

| | |
|---|---|
| Number of files: | 2 |
| Number of top significant motifs: | 10 |
| Number of best matches: | 10 |
| Similarity cutoff >= | 0.75 |
| Output file type: | All |
| Output file format: | All |

**Input files and motif counts**

| File name | Count of motifs | Dataset number |
|---|---|---|
| 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

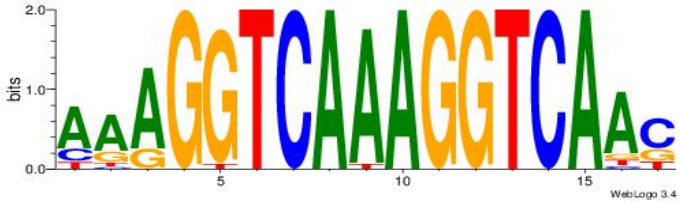
## Best Matches for Top Significant Motif ID 4 (Highest to Lowest)

| | |
|---|---|
| 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 |

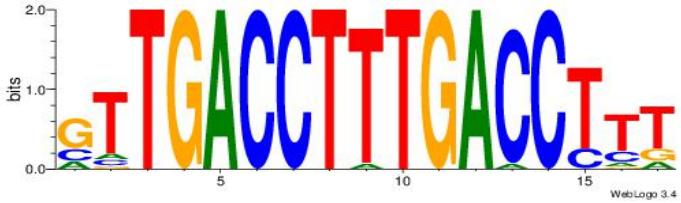
Alignment:

```
AAAGGTCAAAGGTCAAC
-----KCAGAG------
```

Original motif Consensus sequence: AAAGGTCAAAGGTCAAC




Reverse complement motif Consensus sequence: GTTGACCTTTGACCTTT

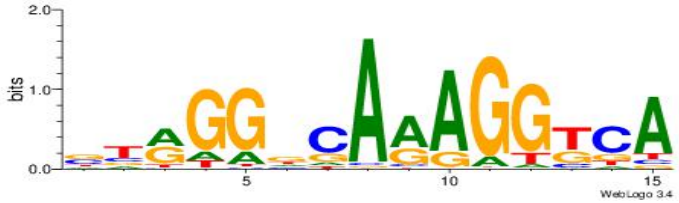


| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 20 |
| Motif name: | PPARGRXRA |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 6 |
| Number of overlap: | 6 |
| Similarity score: | 0.0140102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

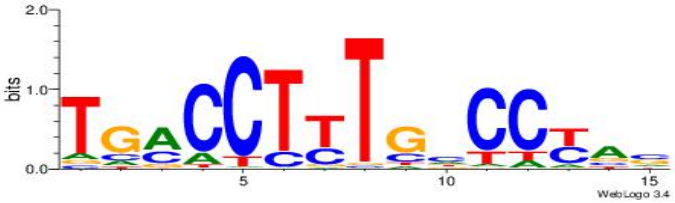
Alignment:

```
BTRGGDCARAGGKCA
-----KCAGAG----
```

Original motif Consensus sequence: BTRGGDCARAGGKCA




Reverse complement motif Consensus sequence: TGRCCTKTGHCCK

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| | |
|---|---|
| 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:
AKGYYCAAAGRTCA
----KCAGAG----

Original motif Consensus sequence: TGAMCTTTGMMCYT

Reverse complement motif Consensus sequence: AKGYYCAAAGRTCA

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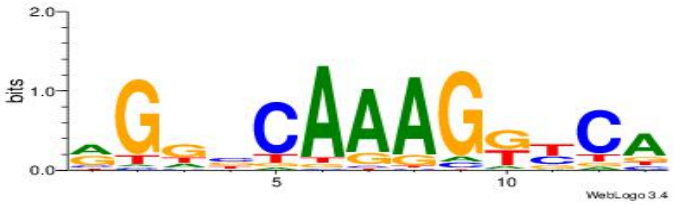
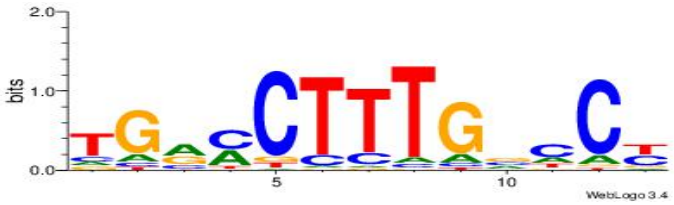
Dataset #: 2
Motif ID: 34
Motif name: HNF4A
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 4
Number of overlap: 6
Similarity score: 0.020602

Alignment:
RGGBCAAAGKYCA
---KCAGAG----

Original motif Consensus sequence: RGGBCAAAGKYCA

Reverse complement motif Consensus sequence: TGMYCTTTGBCCK

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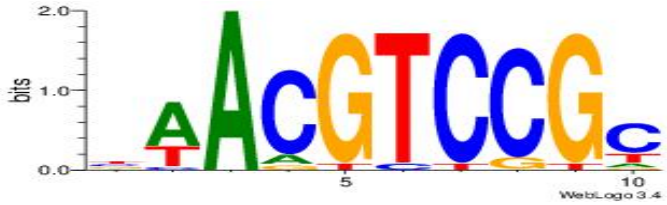
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 37 |
| Motif name: | MIZF |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 1 |
| Number of overlap: | 6 |
| Similarity score: | 0.0221665 |

Alignment:

```
BAACGTCCGC
----CTCTGY
```

Original motif Consensus sequence: BAACGTCCGC




Reverse complement motif Consensus sequence: GCGGACGTTV

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| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 35 |

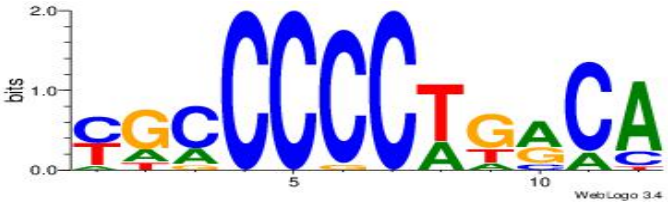
| | |
|---|---|
| Motif name: | INSM1 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 3 |
| Number of overlap: | 6 |
| Similarity score: | 0.0255256 |

Alignment:

```
TGYCAGGGGGCR
--KCAGAG----
```

Original motif Consensus sequence: TGYCAGGGGGCR

Reverse complement motif Consensus sequence: MGCCCCCTGMCA

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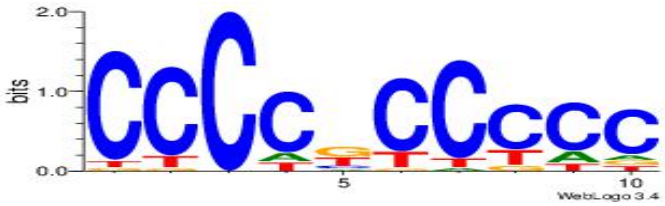
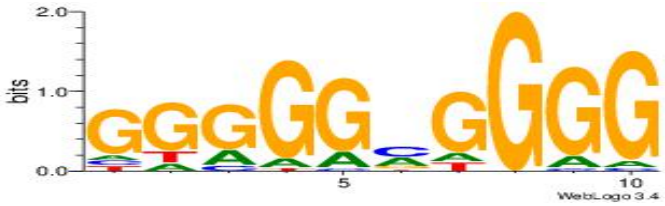
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 16 |
| Motif name: | SP1 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 5 |
| Number of overlap: | 6 |
| Similarity score: | 0.0349642 |

Alignment:
CCCCKCCCCC
CTCTGY----

Original motif Consensus sequence: CCCCKCCCCC




Reverse complement motif Consensus sequence: GGGGGYGGGG

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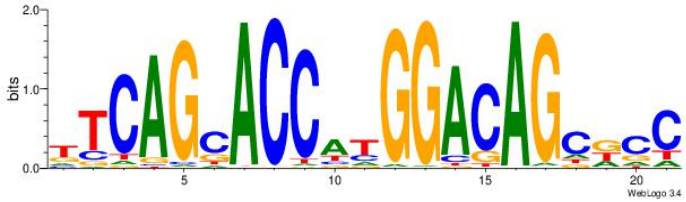
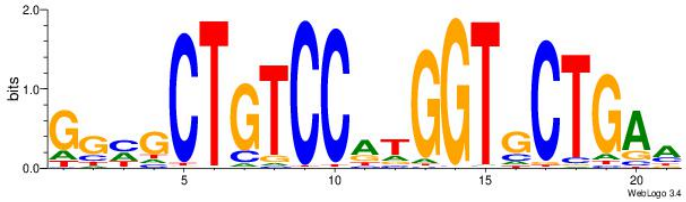
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 19 |
| Motif name: | REST |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Reverse Complement |
| Direction: | Forward |
| Position number: | 3 |
| Number of overlap: | 6 |
| Similarity score: | 0.0376108 |

Alignment:
GGYGCTGTCCATGGTGCTGAA
--CTCTGY----------

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC

Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA

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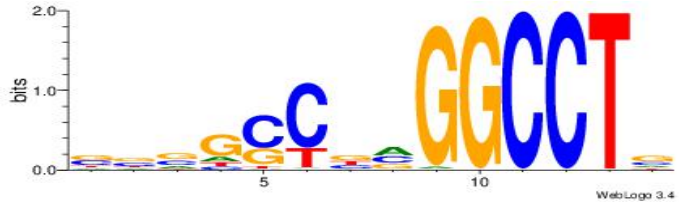
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 12 |
| Motif name: | Zfx |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 6 |
| Number of overlap: | 6 |
| Similarity score: | 0.0448449 |

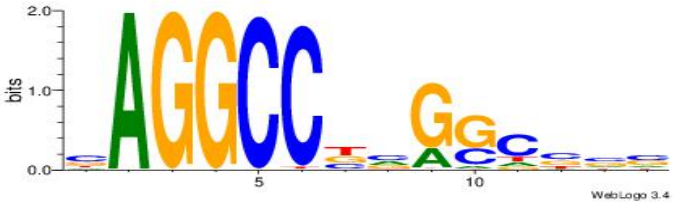
Alignment:

```
BBVGCCBVGGCCTV
---KCAGAG-----
```

Original motif Consensus sequence: BBVGCCBVGGCCTV




Reverse complement motif Consensus sequence: VAGGCCBBGGCVB

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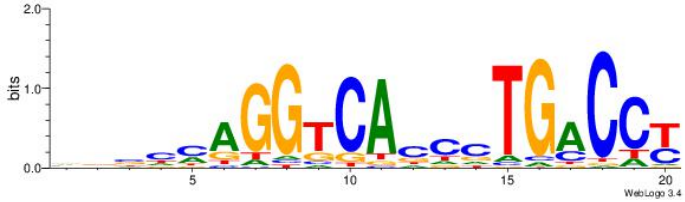
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 29 |

| | |
|---|---|
| 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 |

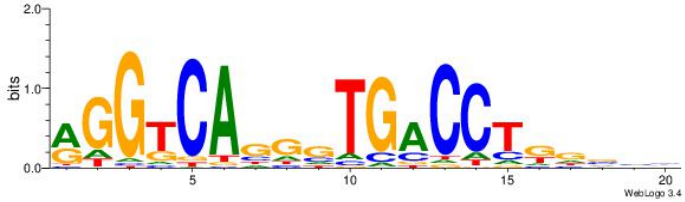
Alignment:

```
MGGTCAGGGTGACCTRDBHV
---KCAGAG-----------
```

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY




Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV

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

Original motif Consensus sequence: ATKTM

Reverse complement motif Consensus sequence: RARAT

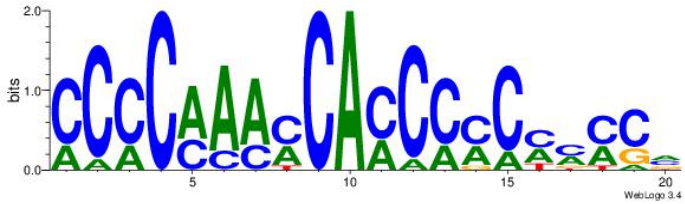
## Best Matches for Top Significant Motif ID 5 (Highest to Lowest)

| | |
|---|---|
| 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 |

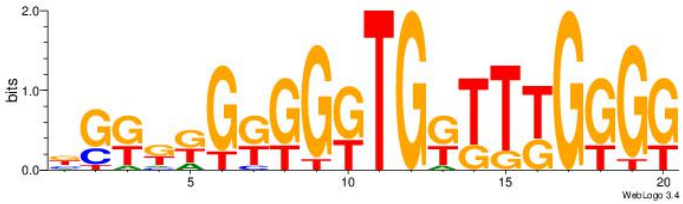
Alignment:

```
BGRRRGRGGRTGRTTYGGGG
------RARAT---------
```

Original motif Consensus sequence: CCCCMAAMCAMCCMCMMMCV




Reverse complement motif Consensus sequence: BGRRRGRGGRTGRTTYGGGG

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| | |
|---|---|
| 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

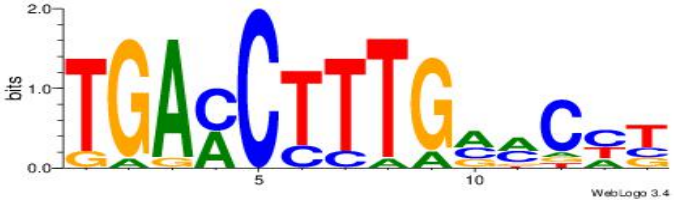
Reverse complement motif Consensus sequence: GTGACCTT

---

| | |
|---|---|
| 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:
AKGYYCAAAGRTCA
-------RARAT--

Original motif Consensus sequence: TGAMCTTTGMMCYT




Reverse complement motif Consensus sequence: AKGYYCAAAGRTCA

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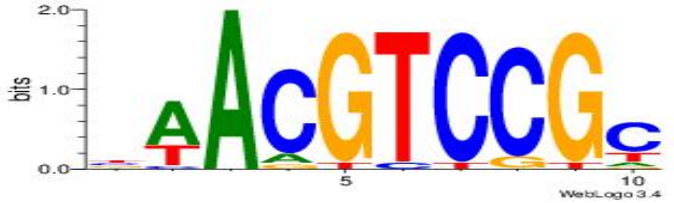
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 37 |
| Motif name: | MIZF |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 4 |
| Number of overlap: | 5 |
| Similarity score: | 0.0292478 |

Alignment:

```
BAACGTCCGC
--ATKTM---
```

Original motif Consensus sequence: BAACGTCCGC




Reverse complement motif Consensus sequence: GCGGACGTTV

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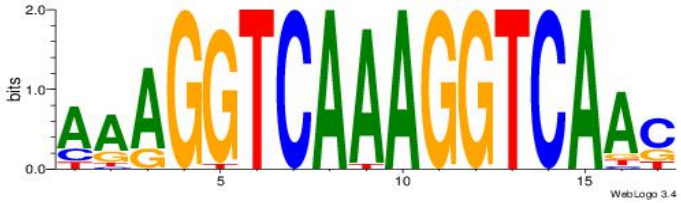
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 43 |
| Motif name: | NR1H2RXRA |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 10 |
| Number of overlap: | 5 |
| Similarity score: | 0.0292478 |

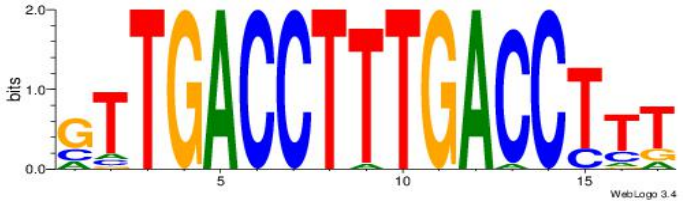
Alignment:

```
AAAGGTCAAAGGTCAAC
---------ATKTM---
```

Original motif Consensus sequence: AAAGGTCAAAGGTCAAC




Reverse complement motif Consensus sequence: GTTGACCTTTGACCTTT

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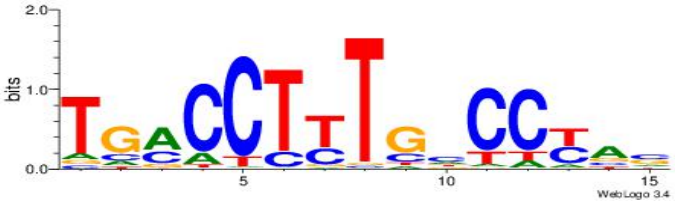
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 20 |
| Motif name: | PPARGRXRA |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Reverse Complement |
| Direction: | Backward |
| Position number: | 7 |

Number of overlap: 5
Similarity score: 0.0305369

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

Original motif Consensus sequence: BTRGGDCARAGGKCA

Reverse complement motif Consensus sequence: TGRCCTKTGHCCK

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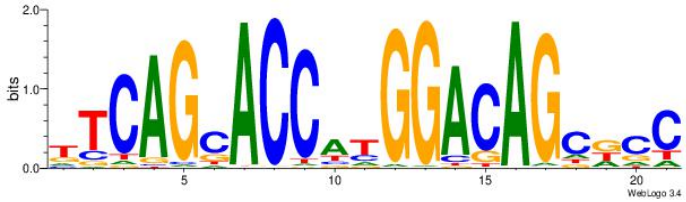
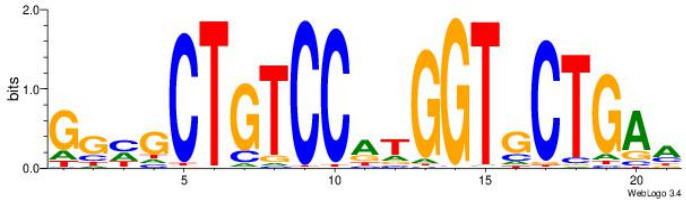
Dataset #: 2
Motif ID: 19
Motif name: REST
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 5
Number of overlap: 5
Similarity score: 0.0315454

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

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC

Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA

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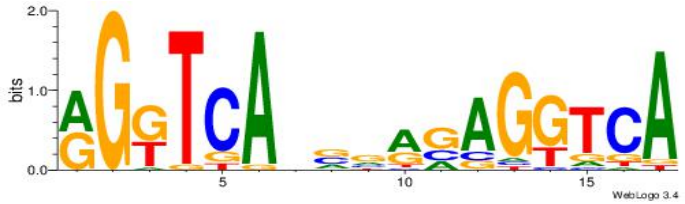
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 47 |
| Motif name: | RXRRAR_DR5 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 1 |
| Number of overlap: | 5 |
| Similarity score: | 0.0335956 |

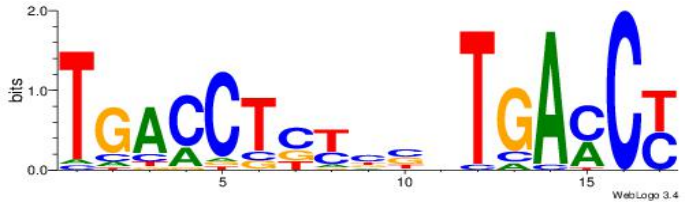
Alignment:

```
RGKTCABVVRGAGGTCA
ATKTM------------
```

Original motif Consensus sequence: RGKTCABVVRGAGGTCA




Reverse complement motif Consensus sequence: TGACCTCKVVBTGAYCK

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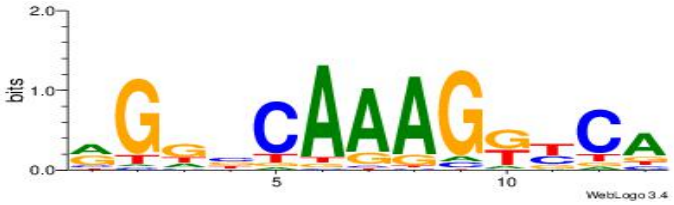
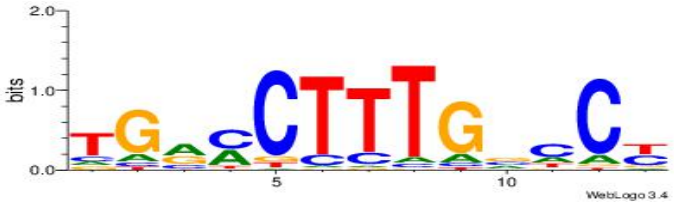
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 34 |
| Motif name: | HNF4A |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 2 |
| Number of overlap: | 5 |
| Similarity score: | 0.0367105 |

Alignment:
RGGBCAAAGKYCA
-------ATKTM-

Original motif Consensus sequence: RGGBCAAAGKYCA




Reverse complement motif Consensus sequence: TGMYCTTTGBCCK

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

Original motif Consensus sequence: CMGCRGC

Reverse complement motif Consensus sequence: GCKGCYG

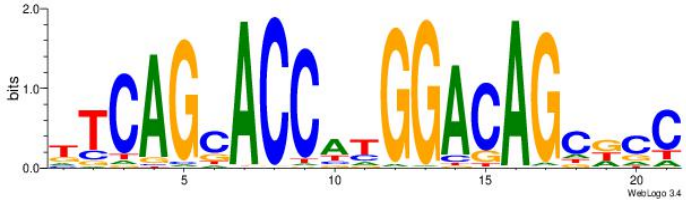
**Best Matches for Top Significant Motif ID 6 (Highest to Lowest)**

| | |
|---|---|
| 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 |

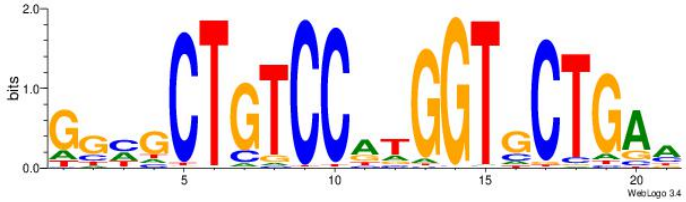
Number of overlap: 7
Similarity score: 0.0205607

Alignment:
TTCAGCACCATGGACAGCKCC
--CMGCRGC----------

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC




Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA

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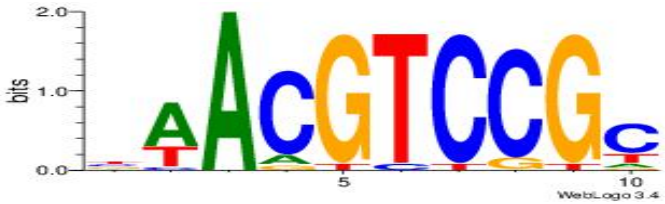
Dataset #: 2
Motif ID: 37
Motif name: MIZF
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 7
Similarity score: 0.0322623

Alignment:
GCGGACGTTV
GCKGCYG---

Original motif Consensus sequence: BAACGTCCGC

Reverse complement motif Consensus sequence: GCGGACGTTV



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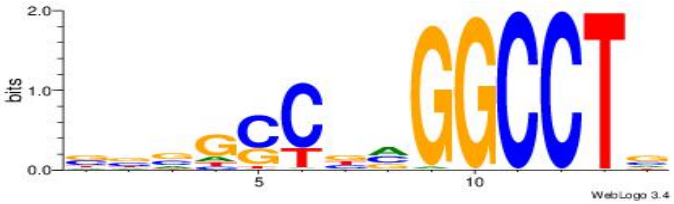
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 12 |
| Motif name: | Zfx |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 5 |
| Number of overlap: | 7 |
| Similarity score: | 0.038091 |

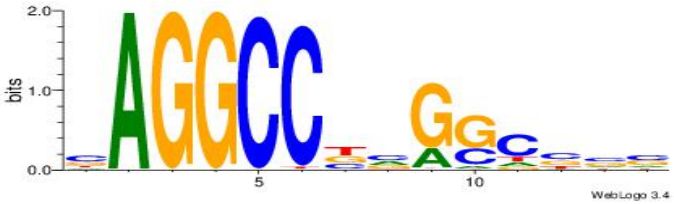
Alignment:

```
BBVGCCBVGGCCTV
----CMGCRGC---
```

Original motif Consensus sequence: BBVGCCBVGGCCTV




Reverse complement motif Consensus sequence: VAGGCCBBGGCVB

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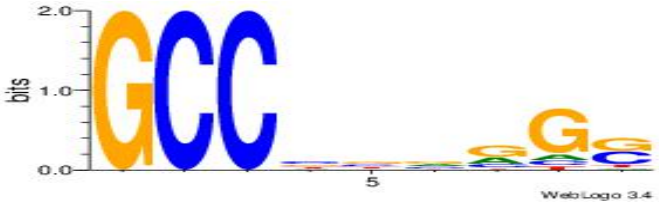
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 15 |

| | |
|---|---|
| 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 |

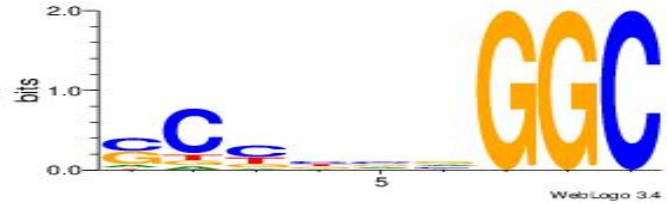
Alignment:

```
SCMVBBGGC
--CMGCRGC
```

Original motif Consensus sequence: GCCBBVRGS




Reverse complement motif Consensus sequence: SCMVBBGGC

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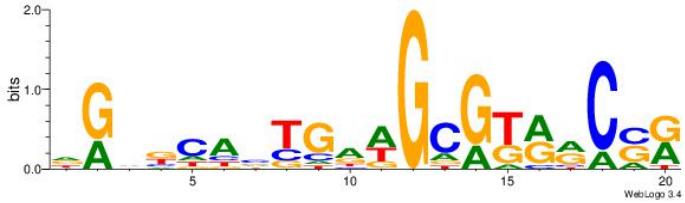
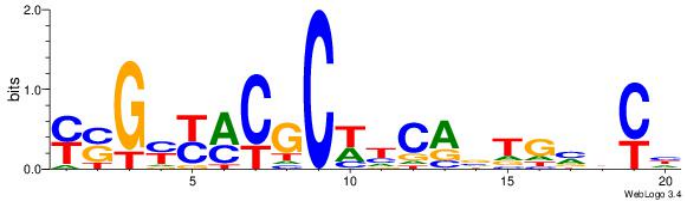
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 45 |
| Motif name: | Pax5 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction: | Backward |
| Position number: | 7 |
| Number of overlap: | 7 |
| Similarity score: | 0.0448462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

Alignment:
MSGKKRCGCWDCABTGBBCD
-------GCKGCYG------

Original motif Consensus sequence: DGVBCABTGDWGCGKRRCSR




Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD

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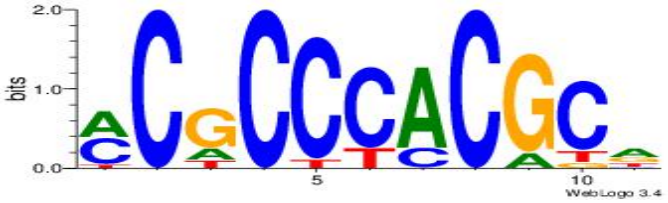
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 28 |
| Motif name: | Egr1 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 2 |
| Number of overlap: | 7 |
| Similarity score: | 0.0453576 |

Alignment:
HGCGTGGGCGK
---GCKGCYG-

Original motif Consensus sequence: HGCGTGGGCGK

Reverse complement motif Consensus sequence: YCGCCCACGCH

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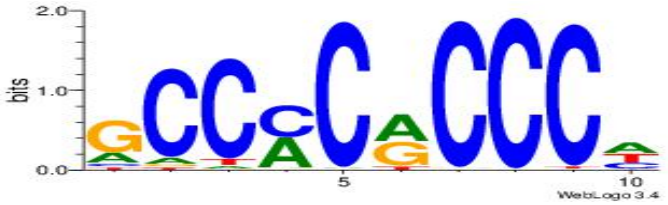
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 36 |
| Motif name: | Klf4 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Reverse Complement |
| Direction: | Forward |
| Position number: | 2 |
| Number of overlap: | 7 |
| Similarity score: | 0.0476958 |

Alignment:

```
GCCYCMCCCD
-CMGCRGC--
```

Original motif Consensus sequence: DGGGYGKGGC

Reverse complement motif Consensus sequence: GCCYCMCCCD

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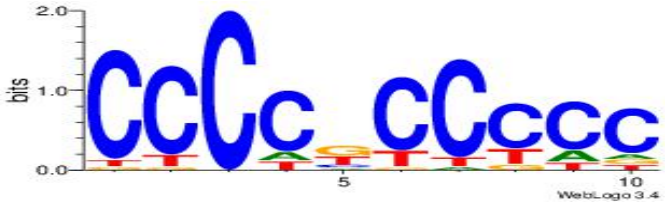
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 16 |

| | |
|---|---|
| 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 |

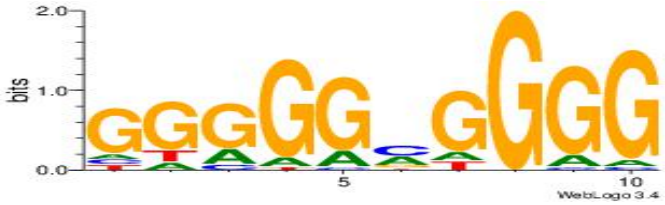
Alignment:

```
GGGGGYGGGG
GCKGCYG---
```

Original motif Consensus sequence: CCCCKCCCCC




Reverse complement motif Consensus sequence: GGGGGYGGGG

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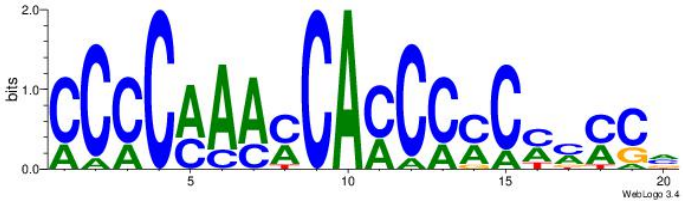
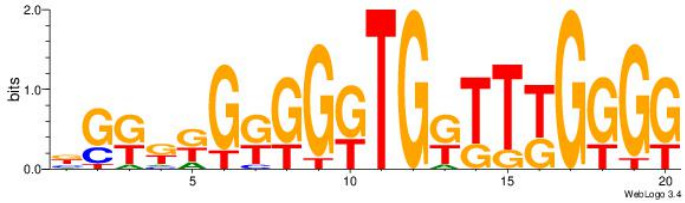
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 18 |
| Motif name: | RREB1 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction: | Forward |
| Position number: | 6 |
| Number of overlap: | 7 |
| Similarity score: | 0.0498726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

Alignment:
BGRRRGRGGRTGRTTYGGGG
-----GCKGCYG--------

Original motif Consensus sequence: CCCCMAAMCAMCCMCMMMCV




Reverse complement motif Consensus sequence: BGRRRGRGGRTGRTTYGGGG

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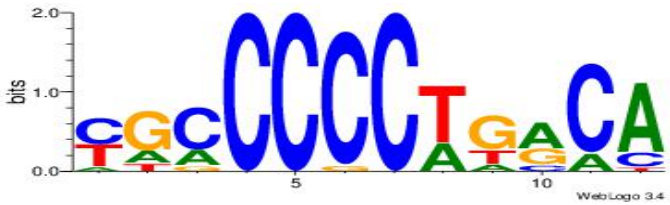
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 35 |
| Motif name: | INSM1 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Reverse Complement |
| Direction: | Forward |
| Position number: | 4 |
| Number of overlap: | 7 |
| Similarity score: | 0.0511926 |

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

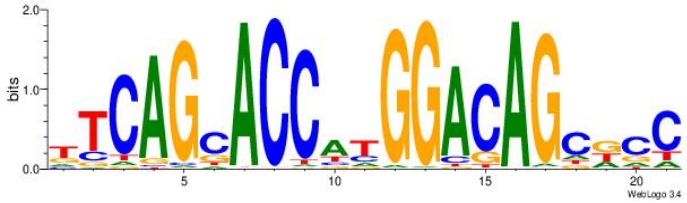
**Best Matches for Top Significant Motif ID 8 (Highest to Lowest)**

| | |
|---|---|
| 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 |

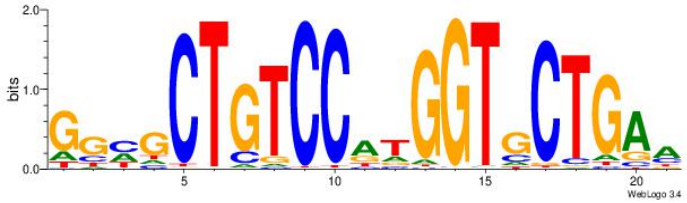
Alignment:

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

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC




Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA

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| | |
|---|---|
| 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

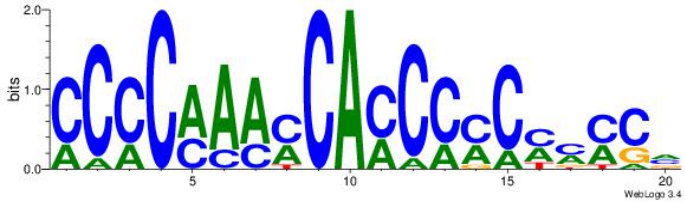
---

| | |
|---|---|
| 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 |

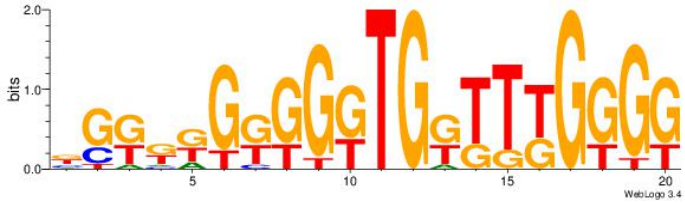
Alignment:

```
BGRRRGRGGRTGRTTYGGGG
--------------CTGGGA
```

Original motif Consensus sequence: CCCCMAAMCAMCCMCMMMCV




Reverse complement motif Consensus sequence: BGRRRGRGGRTGRTTYGGGG

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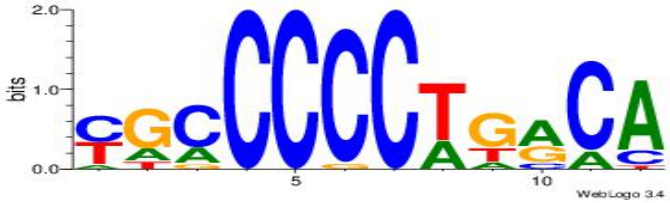
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 35 |
| Motif name: | INSM1 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 4 |

Number of overlap: 6
Similarity score: 0.0557857

Alignment:
TGYCAGGGGGCR
---CTGGGA---

Original motif Consensus sequence: TGYCAGGGGGCR

Reverse complement motif Consensus sequence: MGCCCCCTGMCA

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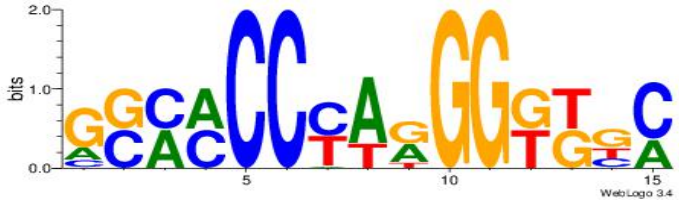
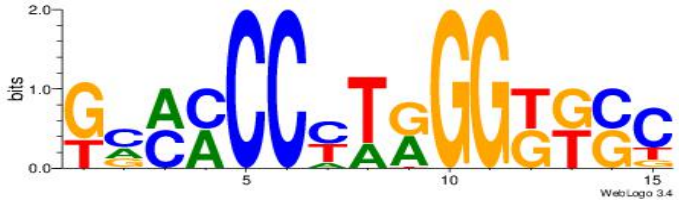
Dataset #: 2
Motif ID: 13
Motif name: Zfp423
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 7
Number of overlap: 6
Similarity score: 0.0624145

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

Original motif Consensus sequence: GSMMCCYARGGKKKC

Reverse complement motif Consensus sequence: GYRYCCMTKGGYR

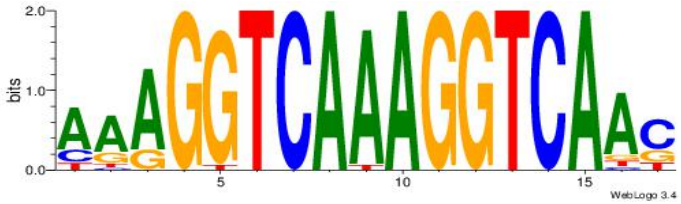


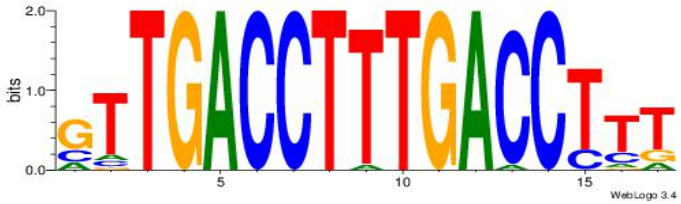

Dataset #: 2
Motif ID: 43
Motif name: NR1H2RXRA
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 6
Number of overlap: 6
Similarity score: 0.0650784

Alignment:
AAAGGTCAAAGGTCAAC
-----TCCCAG------

Original motif Consensus sequence: AAAGGTCAAAGGTCAAC




Reverse complement motif Consensus sequence: GTTGACCTTTGACCTTT



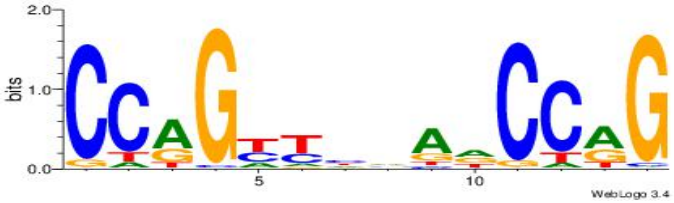

Dataset #: 2

| | |
|---|---|
| Motif ID: | 48 |
| Motif name: | Tcfcp2l1 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Reverse Complement |
| Direction: | Forward |
| Position number: | 1 |
| Number of overlap: | 6 |
| Similarity score: | 0.0663804 |

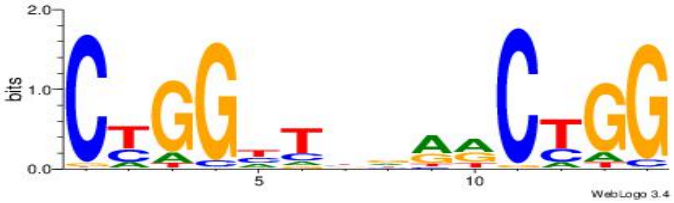
Alignment:

```
CKGGDTBDMMCTGG
CTGGGA--------
```

Original motif Consensus sequence: CCAGYYHVADCCRG




Reverse complement motif Consensus sequence: CKGGDTBDMMCTG

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| | |
|---|---|
| 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: HGCGTGGGCGK

Reverse complement motif Consensus sequence: YCGCCCACGCH

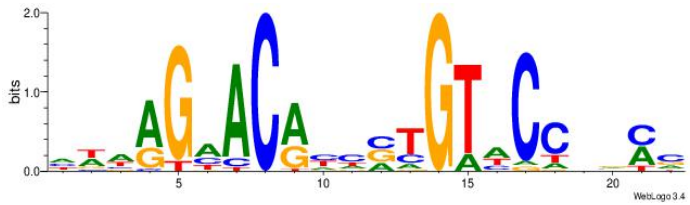
---

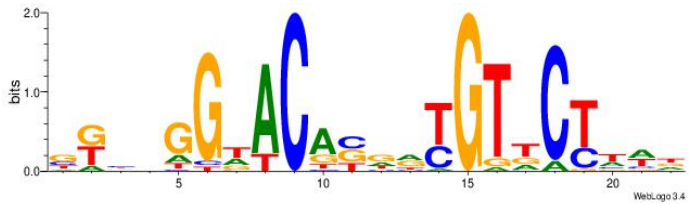
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 24 |
| Motif name: | Ar |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 3 |
| Number of overlap: | 6 |
| Similarity score: | 0.0714107 |

Alignment:
HWDAGHACRHHVTGTHCCHVMV
----------TCCCAG--

Original motif Consensus sequence: HWDAGHACRHHVTGTHCCHVMV

Reverse complement motif Consensus sequence: VRVDGGHACAVDDKGTHCTDWH



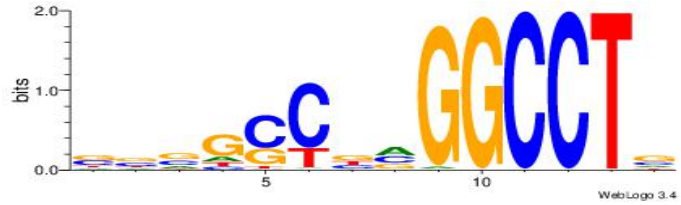




| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 12 |
| Motif name: | Zfx |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 4 |
| Number of overlap: | 6 |
| Similarity score: | 0.0718041 |

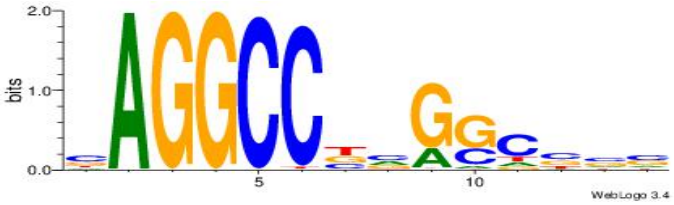
Alignment:

```
BBVGCCBVGGCCTV
-----CTGGGA---
```

Original motif Consensus sequence: BBVGCCBVGGCCTV




Reverse complement motif Consensus sequence: VAGGCCBBGGCVB




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

Original motif Consensus sequence: AMACA

Reverse complement motif Consensus sequence: TGTRT

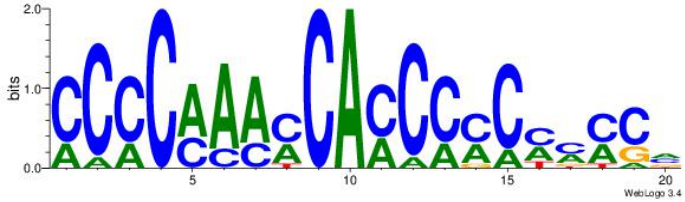
## Best Matches for Top Significant Motif ID 2 (Highest to Lowest)

| | |
|---|---|
| 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 |

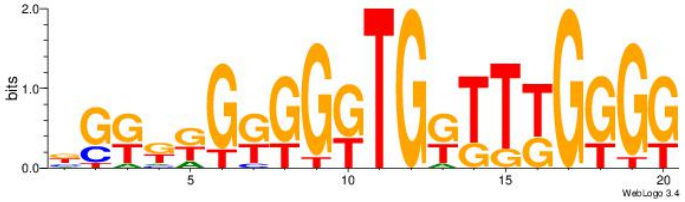
Alignment:

```
CCCCMAAMCAMCCMCMMMCV
-----AMACA----------
```

Original motif Consensus sequence: CCCCMAAMCAMCCMCMMMCV




Reverse complement motif Consensus sequence: BGRRRGRGGRTGRTTYGGGG

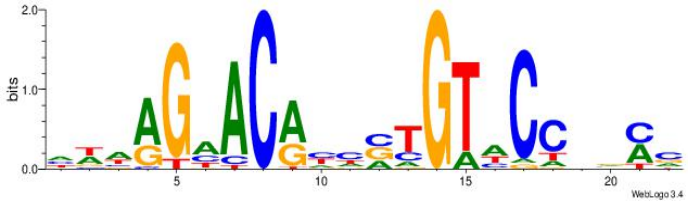


| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 24 |
| Motif name: | Ar |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 5 |
| Number of overlap: | 5 |
| Similarity score: | 0.0429089 |

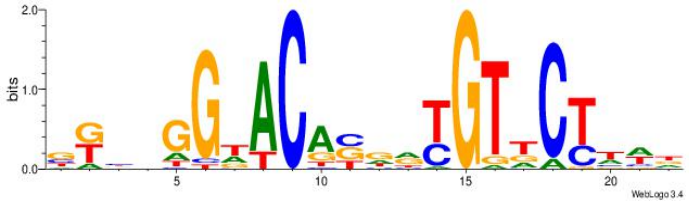
Alignment:

```
HWDAGHACRHHVTGTHCCHVMV
----AMACA-------------
```

Original motif Consensus sequence: HWDAGHACRHHVTGTHCCHVMV




Reverse complement motif Consensus sequence: VRVDGGHACAVDDKGTHCTDWH

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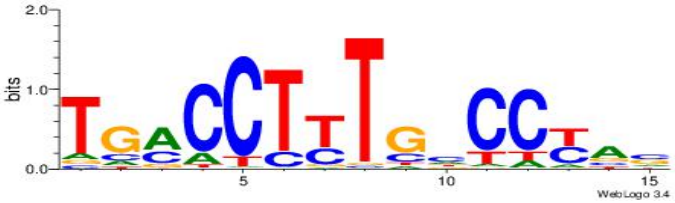
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 20 |
| Motif name: | PPARGRXRA |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction: | Backward |
| Position number: | 6 |

Number of overlap: 5
Similarity score: 0.0595073

Alignment:
TGRCCTKTGHCCKAB
-----TGTRT-----

Original motif Consensus sequence: BTRGGDCARAGGKCA

Reverse complement motif Consensus sequence: TGRCCTKTGHCCK




---

Dataset #: 2
Motif ID: 26
Motif name: ArntAhr
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: 0.0600161

Alignment:
YGCGTG
TGTRT-

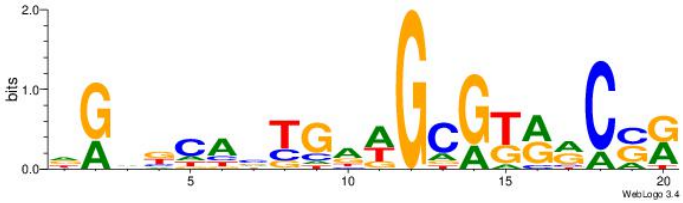
Original motif Consensus sequence: YGCGTG

Reverse complement motif Consensus sequence: CACGCM

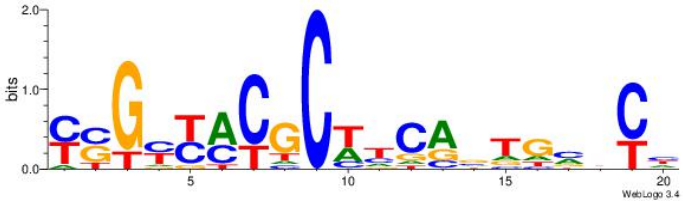
Dataset #: 2
Motif ID: 45
Motif name: Pax5
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 11
Number of overlap: 5
Similarity score: 0.0620995

Alignment:
MSGKKRCGCWDCABTGBBCD
-----AMACA----------

Original motif Consensus sequence: DGVBCABTGDWGCGKRRCSR




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:

```
AKGYYCAAAGRTCA
------AMACA---
```

Original motif Consensus sequence: TGAMCTTTGMMCYT

Reverse complement motif Consensus sequence: AKGYYCAAAGRTCA

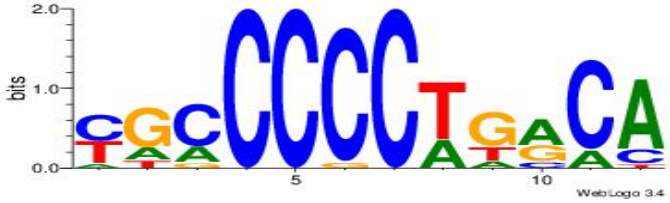
---

| | |
|---|---|
| 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

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| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 33 |
| Motif name: | HIF1AARNT |
| 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: | 0.0700905 |

Alignment:
VCACGTBV
AMACA---

Original motif Consensus sequence: VBACGTGV

Reverse complement motif Consensus sequence: VCACGTBV

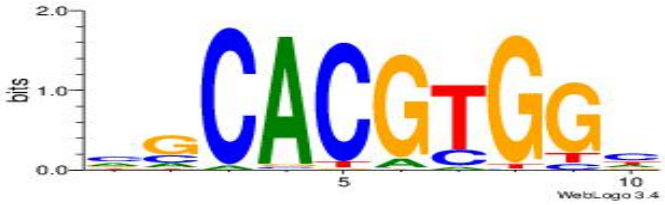
---

| | |
|---|---|
| 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

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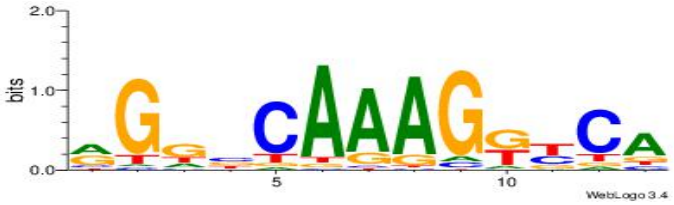
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 34 |

| | |
|---|---|
| Motif name: | HNF4A |
| 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: | 0.071574 |

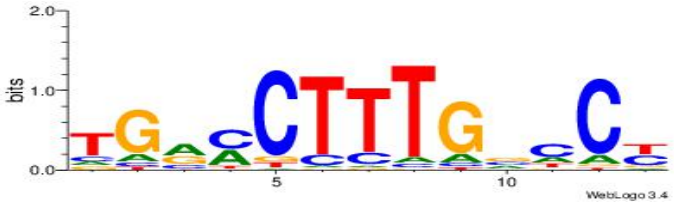
Alignment:

```
TGMYCTTTGBCCK
-----TGTRT---
```

Original motif Consensus sequence: RGGBCAAAGKYCA




Reverse complement motif Consensus sequence: TGMYCTTTGBCCK




---

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

Original motif Consensus sequence: AGSCWGG

Reverse complement motif Consensus sequence: CCWGSCT

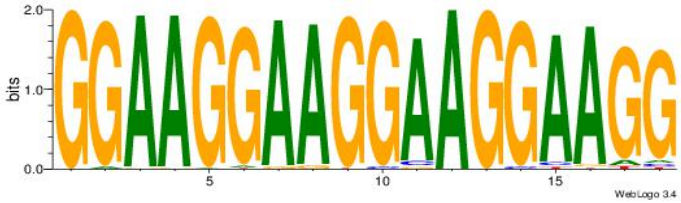
**Best Matches for Top Significant Motif ID 3 (Highest to Lowest)**

| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 32 |
| Motif name: | EWSR1-FLI1 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 8 |
| Number of overlap: | 7 |
| Similarity score: | 0.0395671 |

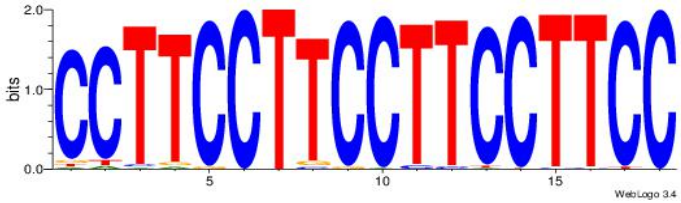
Alignment:

```
GGAAGGAAGGAAGGAAGG
-------AGSCWGG----
```

Original motif Consensus sequence: GGAAGGAAGGAAGGAAGG




Reverse complement motif Consensus sequence: CCTTCCTTCCTTCCTTCC

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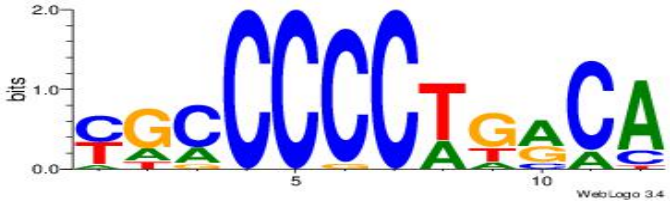
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 35 |
| Motif name: | INSM1 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction: | Backward |
| Position number: | 1 |

Number of overlap: 7
Similarity score: 0.0494688

Alignment:
MGCCCCCTGMCA
-----CCWGSCT

Original motif Consensus sequence: TGYCAGGGGGCR

Reverse complement motif Consensus sequence: MGCCCCCTGMCA



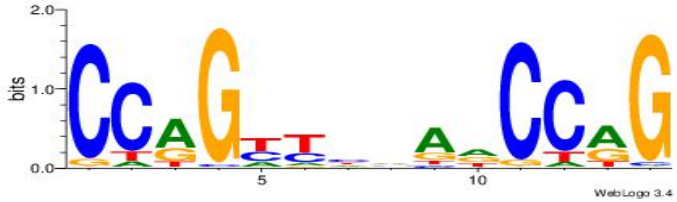

---

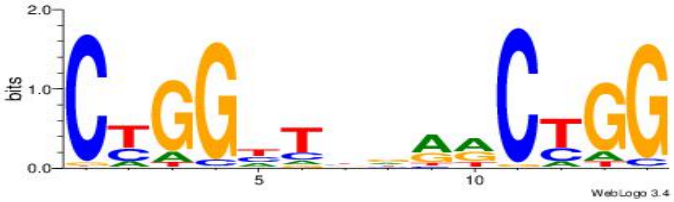
Dataset #: 2
Motif ID: 48
Motif name: Tcfcp2l1
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 7
Similarity score: 0.0669354

Alignment:
CCAGYYHVADCCRG
CCWGSCT-------

Original motif Consensus sequence: CCAGYYHVADCCRG

Reverse complement motif Consensus sequence: CKGGDTBDMMCT

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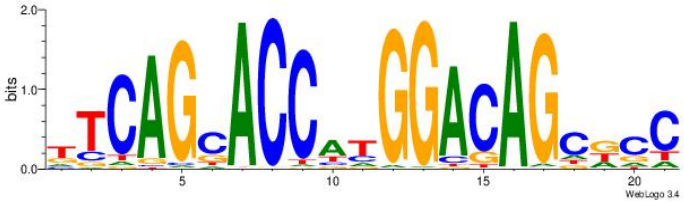
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 19 |
| Motif name: | REST |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 9 |
| Number of overlap: | 7 |
| Similarity score: | 0.0693747 |

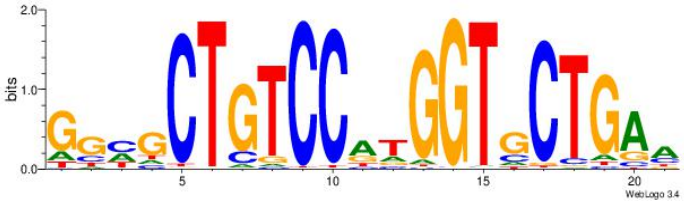
Alignment:

```
TTCAGCACCATGGACAGCKCC
------AGSCWGG--------
```

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC




Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA

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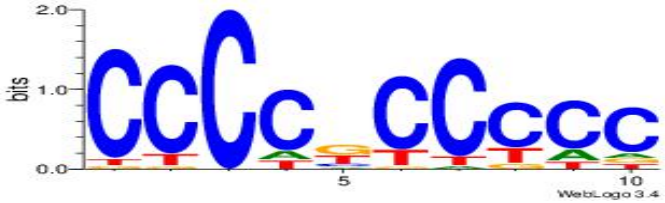
| | |
|---|---|
| Dataset #: | 2 |

| | |
|---|---|
| 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 |

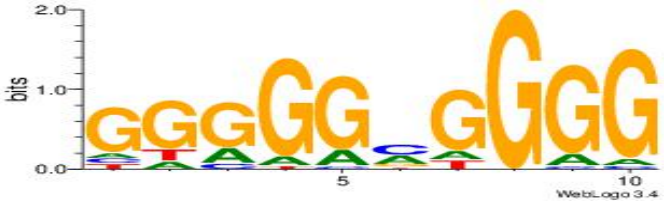
Alignment:

```
CCCCKCCCCC
-CCWGSCT--
```

Original motif Consensus sequence: CCCCKCCCCC




Reverse complement motif Consensus sequence: GGGGGYGGGG

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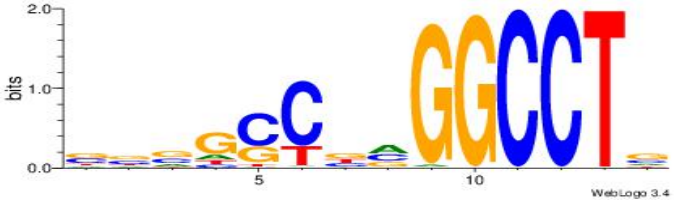
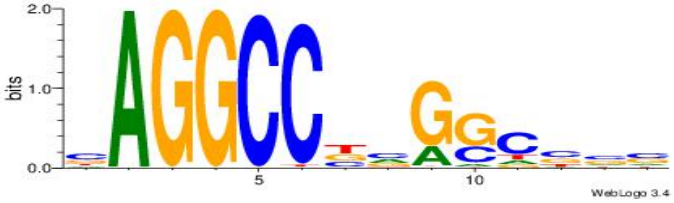
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 12 |
| Motif name: | Zfx |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 7 |
| Number of overlap: | 7 |
| Similarity score: | 0.0720685 |

Alignment:
BBVGCCBVGGCCTV
------CCWGSCT-

Original motif Consensus sequence: BBVGCCBVGGCCTV




Reverse complement motif Consensus sequence: VAGGCCBBGGCVB

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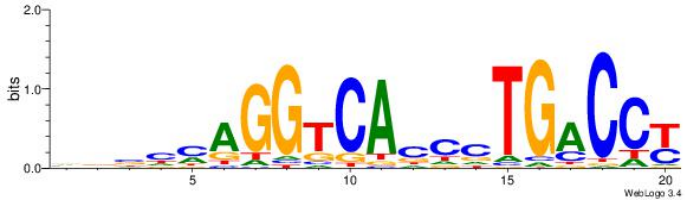
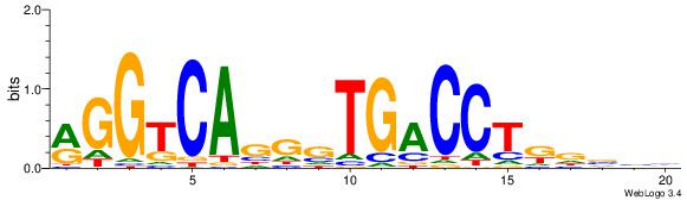
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 29 |
| Motif name: | ESR1 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction: | Forward |
| Position number: | 13 |
| Number of overlap: | 7 |
| Similarity score: | 0.0771405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

Alignment:
MGGTCAGGGTGACCTRDBHV
----------CCWGSCT-

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY

Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV

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| | |
|---|---|
| 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 |

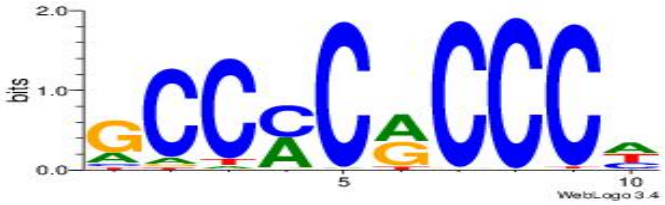
| | |
|---|---|
| Motif name: | Klf4 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction: | Backward |
| Position number: | 1 |
| Number of overlap: | 7 |
| Similarity score: | 0.0798994 |

Alignment:

```
GCCYCMCCCD
---CCWGSCT
```

Original motif Consensus sequence: DGGGYGKGGC

Reverse complement motif Consensus sequence: GCCYCMCCCD

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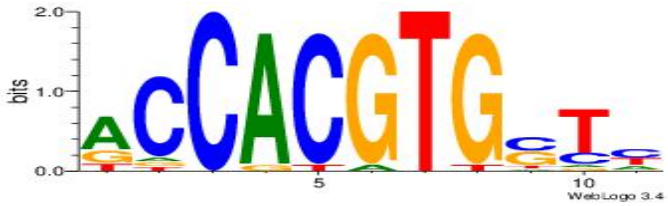
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 39 |
| Motif name: | MYCMAX |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 5 |
| Number of overlap: | 7 |
| Similarity score: | 0.0839075 |

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

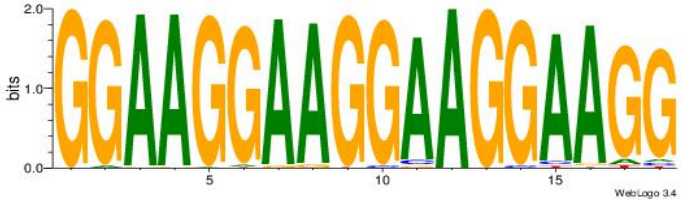
**Best Matches for Top Significant Motif ID 1 (Highest to Lowest)**

| | |
|---|---|
| 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 |

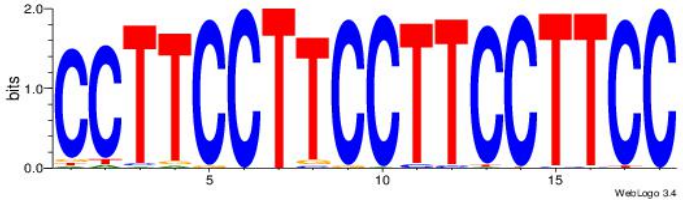
Number of overlap: 6
Similarity score: 0.0146511

Alignment:
GGAAGGAAGGAAGGAAGG
----------RGGAAR-

Original motif Consensus sequence: GGAAGGAAGGAAGGAAGG




Reverse complement motif Consensus sequence: CCTTCCTTCCTTCCTTCC

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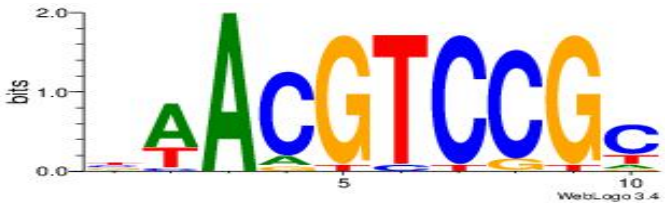
Dataset #: 2
Motif ID: 37
Motif name: MIZF
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 4
Number of overlap: 6
Similarity score: 0.0608243

Alignment:
BAACGTCCGC
---MTTCCK-

Original motif Consensus sequence: BAACGTCCGC

Reverse complement motif Consensus sequence: GCGGACGTTV



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| | |
|---|---|
| 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
----RGGAAR
```

Original motif Consensus sequence: BKAGGGGDAD

Reverse complement motif Consensus sequence: BTHCCCCTYB

---

| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 42 |

| | |
|---|---|
| Motif name: | NFKB1 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Reverse Complement |
| Direction: | Backward |
| Position number: | 5 |
| Number of overlap: | 6 |
| Similarity score: | 0.0757695 |

Alignment:

```
GGGGAAKCCCC
-RGGAAR----
```

Original motif Consensus sequence: GGGGRTTCCCC

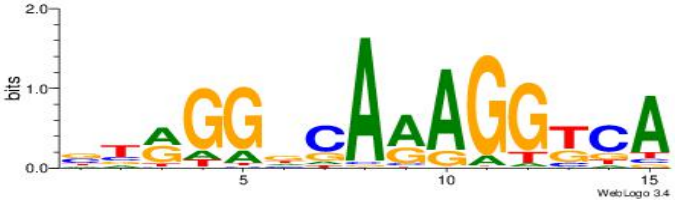
Reverse complement motif Consensus sequence: GGGGAAKCCCC

---

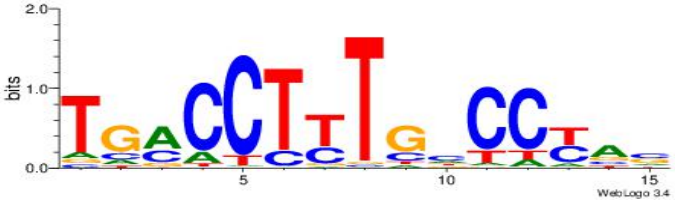
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 20 |
| Motif name: | PPARGRXRA |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 7 |
| Number of overlap: | 6 |
| Similarity score: | 0.0800484 |

Alignment:
BTRGGDCARAGGKCA
---RGGAAR------

Original motif Consensus sequence: BTRGGDCARAGGKCA




Reverse complement motif Consensus sequence: TGRCCTKTGHCCK

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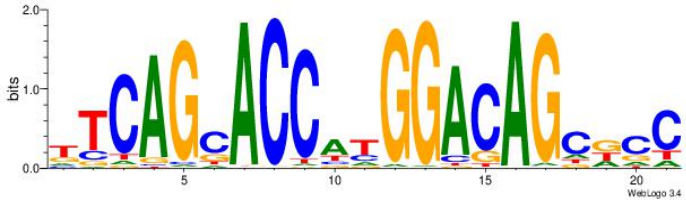
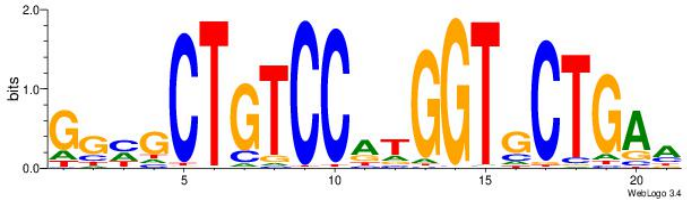
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 19 |
| Motif name: | REST |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 6 |
| Number of overlap: | 6 |
| Similarity score: | 0.0829223 |

Alignment:
TTCAGCACCATGGACAGCKCC
----------RGGAAR-----

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC

Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA

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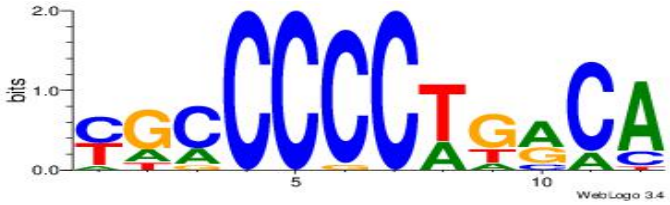
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 35 |
| Motif name: | INSM1 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 1 |
| Number of overlap: | 6 |
| Similarity score: | 0.0832926 |

Alignment:

```
TGYCAGGGGGCR
------RGGAAR
```

Original motif Consensus sequence: TGYCAGGGGGCR

Reverse complement motif Consensus sequence: MGCCCCCTGMCA

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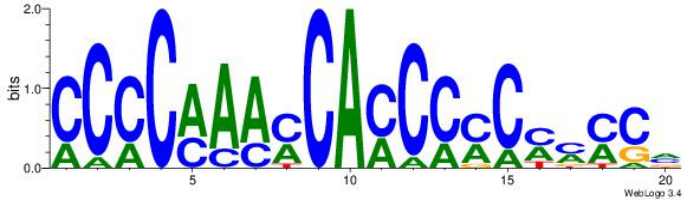
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 18 |

| | |
|---|---|
| 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 |

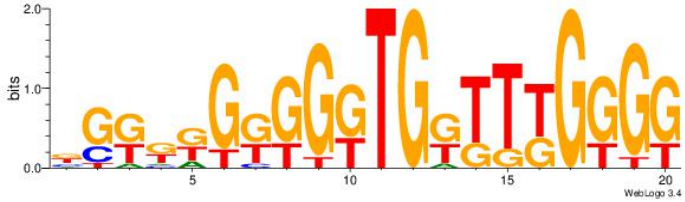
Alignment:

```
BGRRRGRGGRTGRTTYGGGG
----RGGAAR----------
```

Original motif Consensus sequence: CCCCMAAMCAMCCMCMMMCV




Reverse complement motif Consensus sequence: BGRRRGRGGRTGRTTYGGGG

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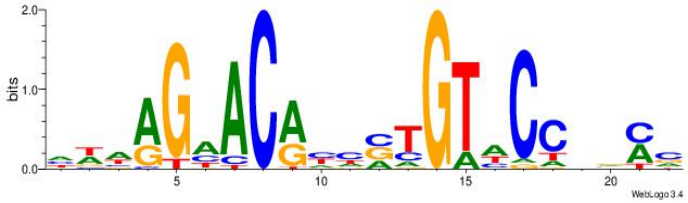
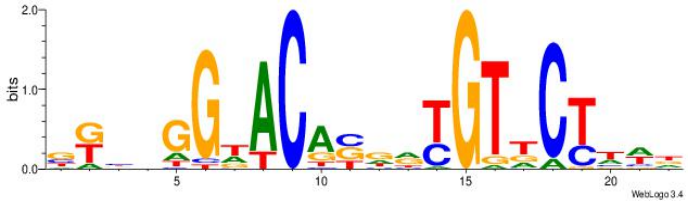
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 24 |
| Motif name: | Ar |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 4 |
| Number of overlap: | 6 |
| Similarity score: | 0.0836451 |

Alignment:
HWDAGHACRHHVTGTHCCHVMV
---RGGAAR----------

Original motif Consensus sequence: HWDAGHACRHHVTGTHCCHVMV




Reverse complement motif Consensus sequence: VRVDGGHACAVDDKGTHCTDWH

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| | |
|---|---|
| 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

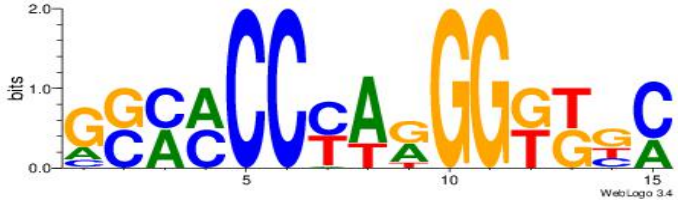
Reverse complement motif Consensus sequence: GCGCSAAA

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

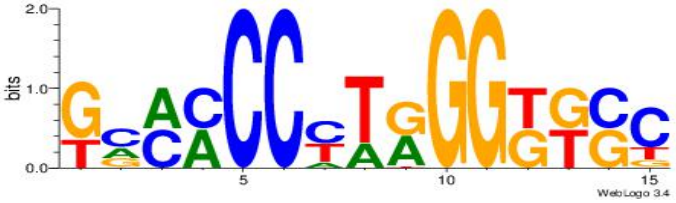
Alignment:

```
GYRYCCMTKGGYRSC
--------RGGAAR-
```

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

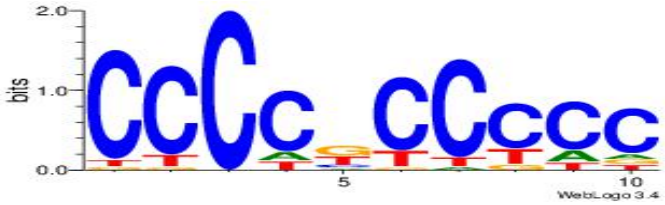
## Best Matches for Top Significant Motif ID 7 (Highest to Lowest)

| | |
|---|---|
| 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 |

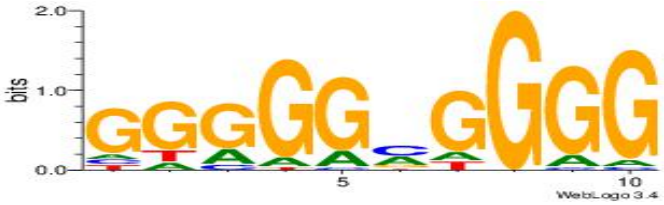
Alignment:

```
CCCCKCCCCC
-CCCRCCCC-
```

Original motif Consensus sequence: CCCCKCCCCC




Reverse complement motif Consensus sequence: GGGGGYGGGG



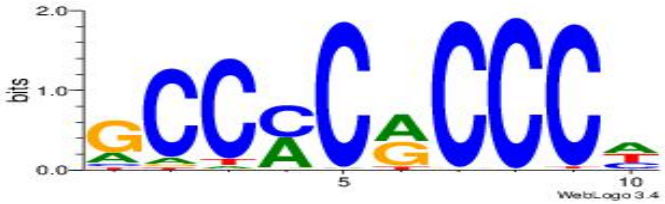
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 36 |
| Motif name: | Klf4 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 1 |
| Number of overlap: | 8 |
| Similarity score: | 0.0461644 |

Alignment:

```
DGGGYGKGGC
GGGGMGGG--
```

Original motif Consensus sequence: DGGGYGKGGC

Reverse complement motif Consensus sequence: GCCYCMCCCD

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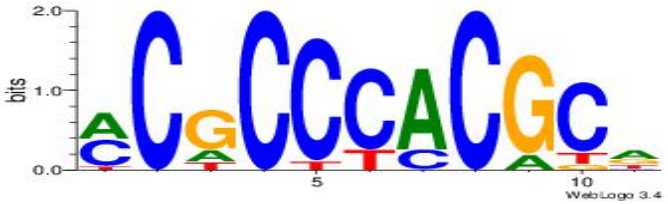
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 28 |
| Motif name: | Egr1 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Reverse Complement |
| Direction: | Backward |
| Position number: | 1 |
| Number of overlap: | 8 |

Similarity score: 0.0650374

Alignment:
YCGCCCACGCH
---CCCRCCCC

Original motif Consensus sequence: HGCGTGGGCGK

Reverse complement motif Consensus sequence: YCGCCCACGCH

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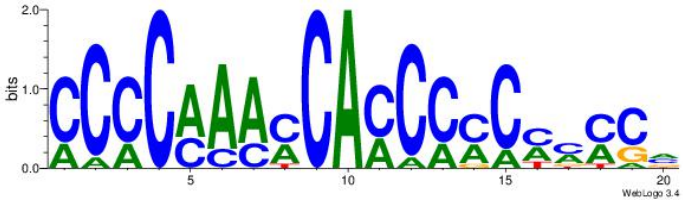
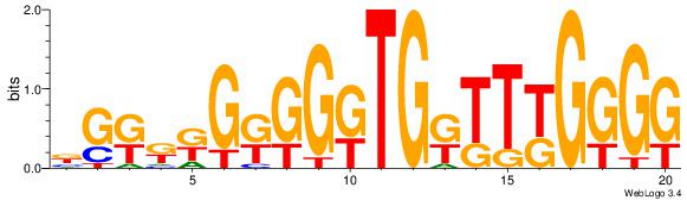
Dataset #: 2
Motif ID: 18
Motif name: RREB1
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 7
Number of overlap: 8
Similarity score: 0.076401

Alignment:
CCCCMAAMCAMCCMCMMMCV
------CCCRCCCC------

Original motif Consensus sequence: CCCCMAAMCAMCCMCMMMCV

Reverse complement motif Consensus sequence: BGRRRGRGGRTGRTTYGGGG

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| | |
|---|---|
| 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
GGGGMGGG---
```

Original motif Consensus sequence: GGGGRTTCCCC

Reverse complement motif Consensus sequence: GGGGAAKCCCC

---

| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 35 |

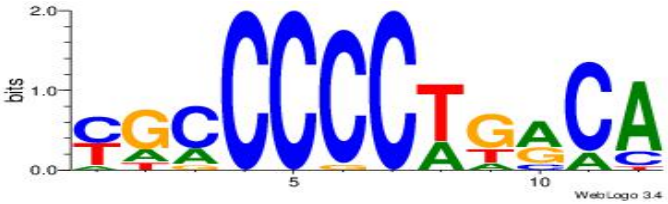
| | |
|---|---|
| Motif name: | INSM1 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 1 |
| Number of overlap: | 8 |
| Similarity score: | 0.0936832 |

Alignment:

```
TGYCAGGGGGCR
GGGGMGGG----
```

Original motif Consensus sequence: TGYCAGGGGGCR

Reverse complement motif Consensus sequence: MGCCCCCTGMCA

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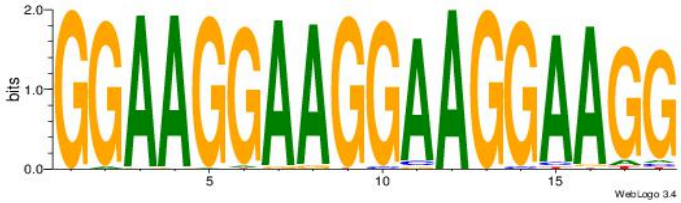
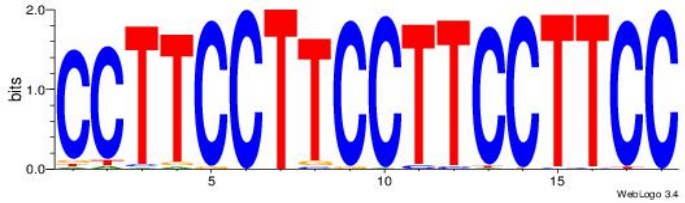
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 32 |
| Motif name: | EWSR1-FLI1 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 7 |
| Number of overlap: | 8 |
| Similarity score: | 0.0950969 |

Alignment:
GGAAGGAAGGAAGGAAGG
------GGGGMGGG----

Original motif Consensus sequence: GGAAGGAAGGAAGGAAGG




Reverse complement motif Consensus sequence: CCTTCCTTCCTTCCTTCC

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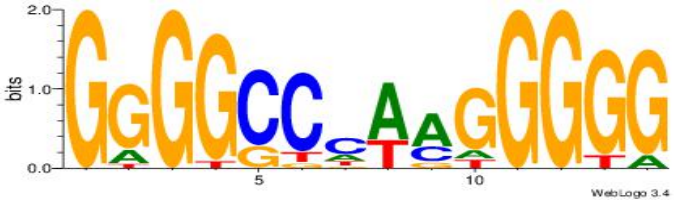
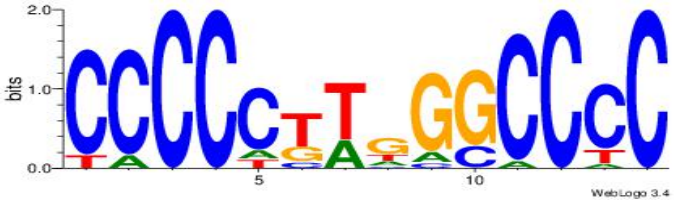
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 21 |
| Motif name: | PLAG1 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 1 |
| Number of overlap: | 8 |
| Similarity score: | 0.0998932 |

Alignment:
GGGGCCCAAGGGGG
GGGGMGGG------

Original motif Consensus sequence: GGGGCCCAAGGGGG

Reverse complement motif Consensus sequence: CCCCCTTGGGCCC

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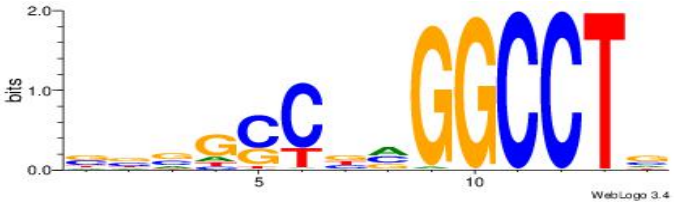
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 12 |
| Motif name: | Zfx |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 5 |
| Number of overlap: | 8 |
| Similarity score: | 0.10221 |

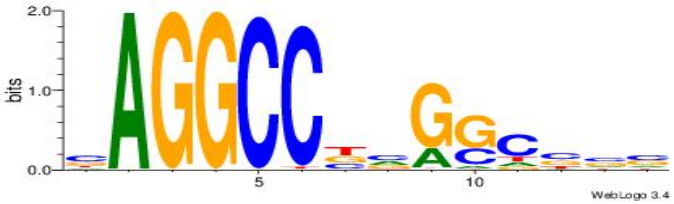
Alignment:

```
BBVGCCBVGGCCTV
----CCCRCCCC--
```

Original motif Consensus sequence: BBVGCCBVGGCCTV




Reverse complement motif Consensus sequence: VAGGCCBBGGCVB

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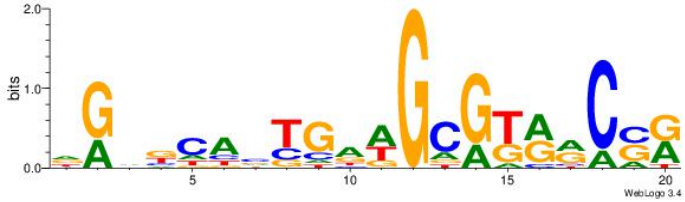
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 45 |

| | |
|---|---|
| Motif name: | Pax5 |
| 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: | 0.102497 |

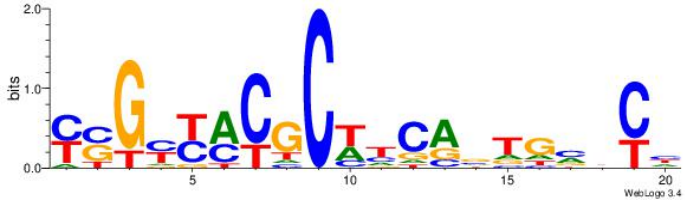
Alignment:

```
DGVBCABTGDWGCGKRRCSR
--------GGGGMGGG----
```

Original motif Consensus sequence: DGVBCABTGDWGCGKRRCSR




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

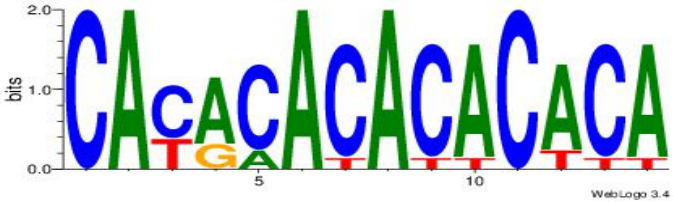
## Best Matches for Top Significant Motif ID 26 (Highest to Lowest)

| | |
|---|---|
| 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 |

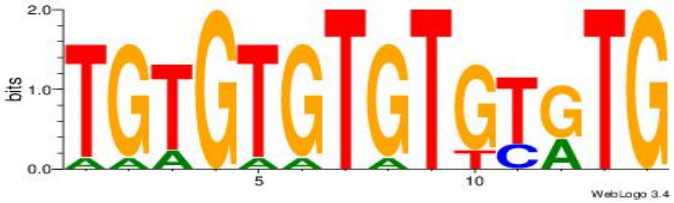
Alignment:

```
TGTGTGTGTGTKTG
------YGCGTG--
```

Original motif Consensus sequence: CAYACACACACACA




Reverse complement motif Consensus sequence: TGTGTGTGTGTKT




---

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

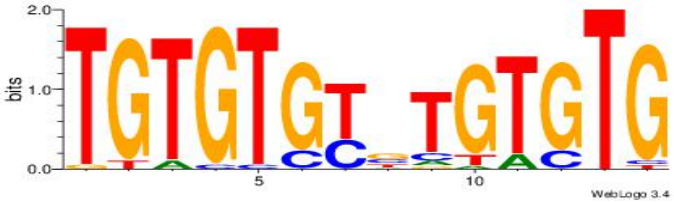
| | |
|---|---|
| Direction: | Backward |
| Position number: | 1 |
| Number of overlap: | 6 |
| Similarity score: | 0.0350575 |

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:
-GCKGCYG
YGCGTG--

Original motif Consensus sequence: CMGCRGC

Reverse complement motif Consensus sequence: GCKGCYG

---

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-
-YGCGTG

Original motif Consensus sequence: CTGGGA

Reverse complement motif Consensus sequence: TCCCAG

| | |
|---|---|
| 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)

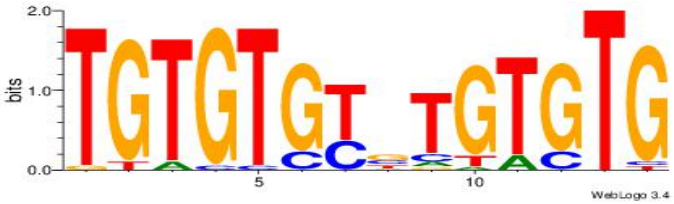
| | |
|---|---|
| Dataset #: | 1 |
| Motif ID: | 9 |
| Motif name: | Motif 9 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 2 |
| Number of overlap: | 8 |
| Similarity score: | 0.0745994 |

Alignment:

```
CACACAVRCACACA
-----VCACGTBV-
```

Original motif Consensus sequence: CACACAVRCACACA

Reverse complement motif Consensus sequence: TGTGTGKVTGTGT

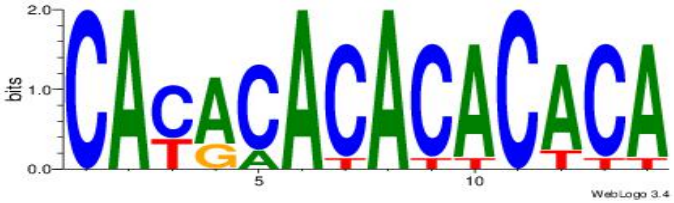


| | |
|---|---|
| Dataset #: | 1 |
| Motif ID: | 11 |
| Motif name: | Motif 11 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 4 |
| Number of overlap: | 8 |
| Similarity score: | 0.0850889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

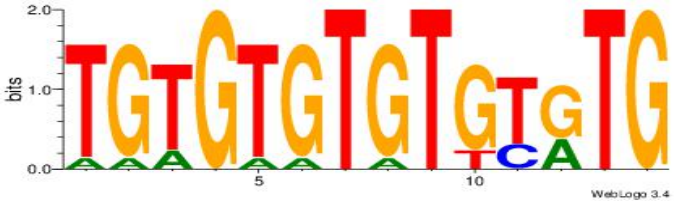
Alignment:

```
CAYACACACACACA
---VCACGTBV---
```

Original motif Consensus sequence: CAYACACACACACA




Reverse complement motif Consensus sequence: TGTGTGTGTGTKT




---

| | |
|---|---|
| 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

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

**Dataset #: 2 Motif ID: 14 Motif name: ZEB1**

Original motif Consensus sequence: CACCTD

Reverse complement motif Consensus sequence: HAGGTG

### Best Matches for Significant Motif ID 14 (Highest to Lowest)

| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 46 |
| Motif name: | RORA_1 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Reverse Complement |
| Direction: | Backward |
| Position number: | 4 |
| Number of overlap: | 6 |
| Similarity score: | 0.0141289 |

Alignment:

```
TGACCTDVWT
-CACCTD---
```

Original motif Consensus sequence: AWVDAGGTCA

Reverse complement motif Consensus sequence: TGACCTDVWT

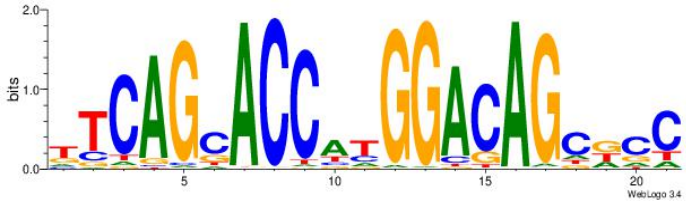
---

| | |
|---|---|
| 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: | 6 |
| Number of overlap: | 6 |
| Similarity score: | 0.0143133 |

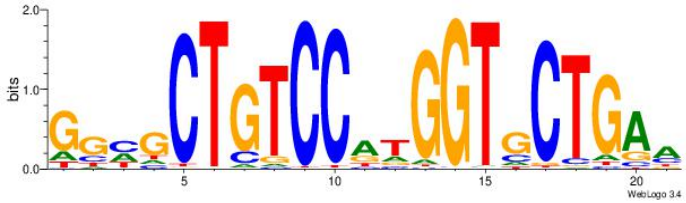
Alignment:

```
GGYGCTGTCCATGGTGCTGAA
----------HAGGTG-----
```

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC




Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA




---

Dataset #: 2

| | |
|---|---|
| Motif ID: | 25 |
| Motif name: | Arnt |
| 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: | 0.0207244 |

Alignment:

```
CACGTG
CACCTD
```

Original motif Consensus sequence: CACGTG

Reverse complement motif Consensus sequence: CACGTG

---

| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 31 |
| Motif name: | Esrrb |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 1 |
| Number of overlap: | 6 |
| Similarity score: | 0.0207244 |

Alignment:
CACGTG
HAGGTG

Original motif Consensus sequence: CACGTG

Reverse complement motif Consensus sequence: CACGTG

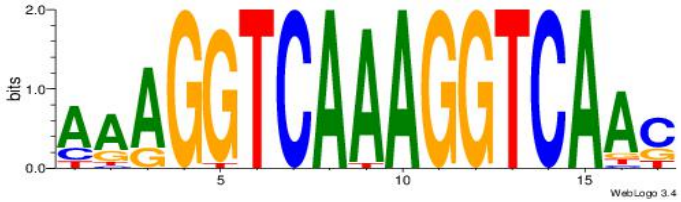
---

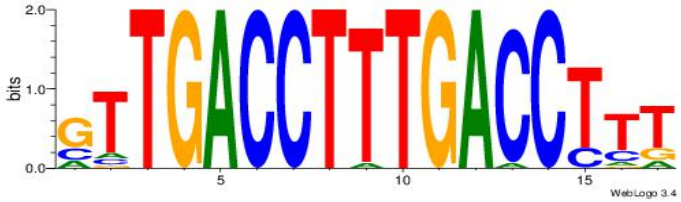
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 43 |
| Motif name: | NR1H2RXRA |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Reverse Complement |
| Direction: | Backward |
| Position number: | 2 |
| Number of overlap: | 6 |
| Similarity score: | 0.0232753 |

Alignment:
GTTGACCTTTGACCTTT
----------CACCTD-

Original motif Consensus sequence: AAAGGTCAAAGGTCAAC

Reverse complement motif Consensus sequence: GTTGACCTTTGACCTTT




---

| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 33 |
| Motif name: | HIF1AARNT |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Reverse Complement |
| Direction: | Backward |
| Position number: | 2 |
| Number of overlap: | 6 |
| Similarity score: | 0.0237889 |

Alignment:

```
VCACGTBV
-CACCTD-
```

Original motif Consensus sequence: VBACGTGV

Reverse complement motif Consensus sequence: VCACGTBV

---

| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 35 |

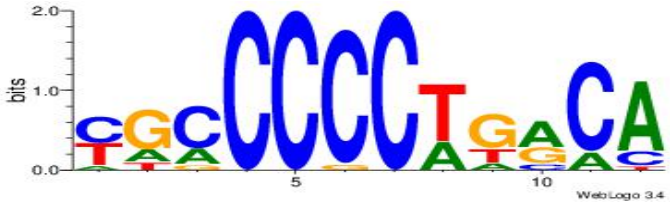
| | |
|---|---|
| Motif name: | INSM1 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 4 |
| Number of overlap: | 6 |
| Similarity score: | 0.0262123 |

Alignment:

```
TGYCAGGGGGCR
---HAGGTG---
```

Original motif Consensus sequence: TGYCAGGGGGCR

Reverse complement motif Consensus sequence: MGCCCCCTGMCA

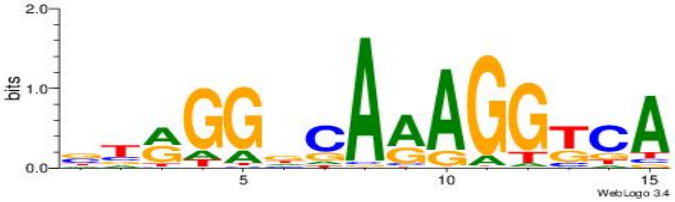



---

| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 20 |
| Motif name: | PPARGRXRA |
| 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: | 0.0264837 |

Alignment:
TGRCCTKTGHCCKAB
-CACCTD--------

Original motif Consensus sequence: BTRGGDCARAGGKCA




Reverse complement motif Consensus sequence: TGRCCTKTGHCCK

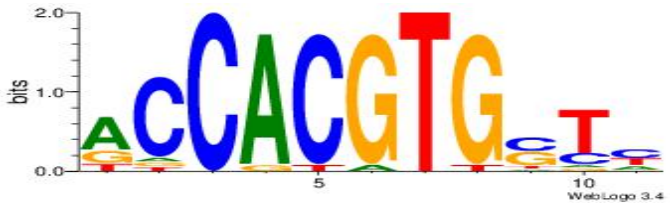
---

| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 39 |
| Motif name: | MYCMAX |
| 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: | 0.0269744 |

Alignment:
ACCACGTGSTM
--CACCTD---

Original motif Consensus sequence: RASCACGTGGT

Reverse complement motif Consensus sequence: ACCACGTGSTM

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| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 44 |
| Motif name: | NR4A2 |
| 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: | 0.0288897 |

Alignment:

```
GTGACCTT
--CACCTD
```

Original motif Consensus sequence: AAGGTCAC

Reverse complement motif Consensus sequence: GTGACCTT

---

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

Original motif Consensus sequence: CTCTGY

Reverse complement motif Consensus sequence: KCAGAG

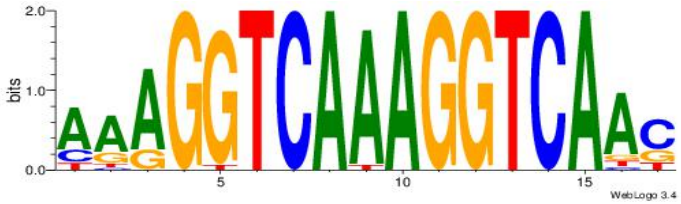
## Best Matches for Significant Motif ID 4 (Highest to Lowest)

| | |
|---|---|
| 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 |

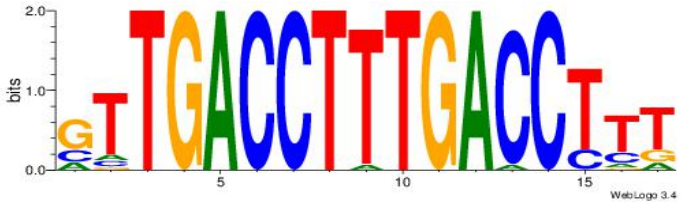
Alignment:

```
AAAGGTCAAAGGTCAAC
-----KCAGAG------
```

Original motif Consensus sequence: AAAGGTCAAAGGTCAAC




Reverse complement motif Consensus sequence: GTTGACCTTTGACCTTT

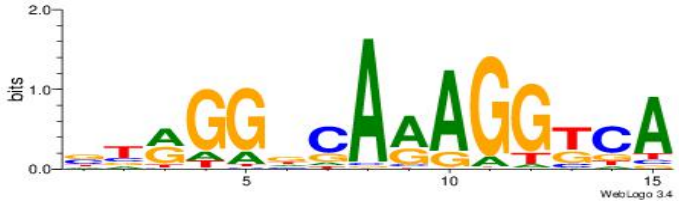


| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 20 |
| Motif name: | PPARGRXRA |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 5 |
| Number of overlap: | 6 |
| Similarity score: | 0.0140102 |

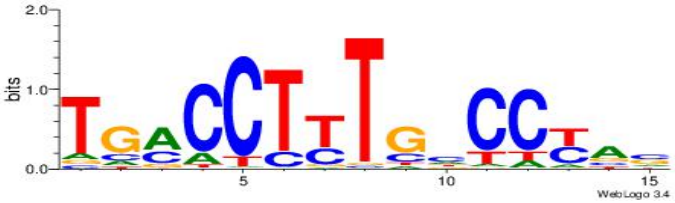
Alignment:

```
BTRGGDCARAGGKCA
-----KCAGAG----
```

Original motif Consensus sequence: BTRGGDCARAGGKCA




Reverse complement motif Consensus sequence: TGRCCTKTGHCCK

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

Alignment:
AKGYYCAAAGRTCA
----KCAGAG----

Original motif Consensus sequence: TGAMCTTTGMMCYT

Reverse complement motif Consensus sequence: AKGYYCAAAGRTCA

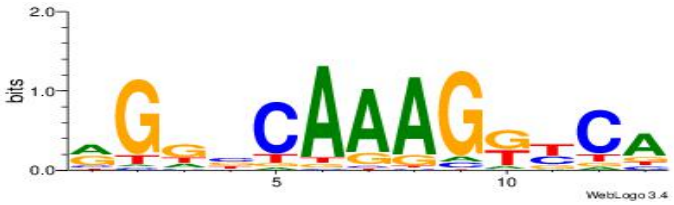
---

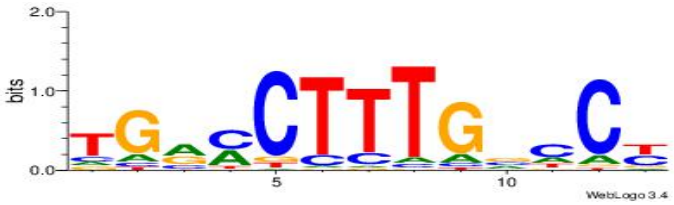
Dataset #: 2
Motif ID: 34
Motif name: HNF4A
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 4
Number of overlap: 6
Similarity score: 0.020602

Alignment:
RGGBCAAAGKYCA
---KCAGAG----

Original motif Consensus sequence: RGGBCAAAGKYCA

Reverse complement motif Consensus sequence: TGMYCTTTGBCCK

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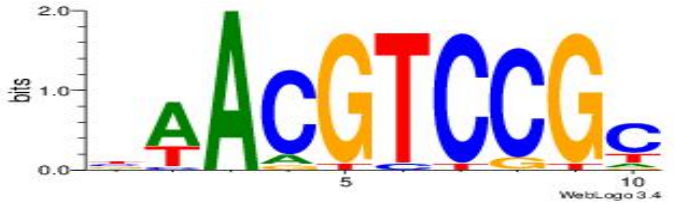
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 37 |
| Motif name: | MIZF |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 5 |
| Number of overlap: | 6 |
| Similarity score: | 0.0221665 |

Alignment:

```
BAACGTCCGC
----CTCTGY
```

Original motif Consensus sequence: BAACGTCCGC




Reverse complement motif Consensus sequence: GCGGACGTTV

---

| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 35 |

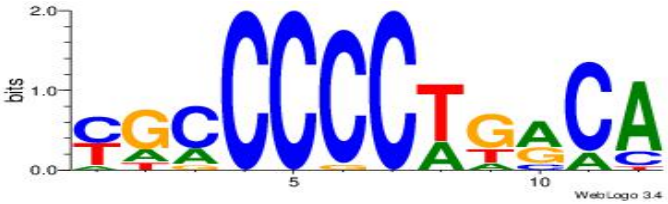
| | |
|---|---|
| Motif name: | INSM1 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 3 |
| Number of overlap: | 6 |
| Similarity score: | 0.0255256 |

Alignment:

```
TGYCAGGGGGCR
--KCAGAG----
```

Original motif Consensus sequence: TGYCAGGGGGCR

Reverse complement motif Consensus sequence: MGCCCCCTGMCA

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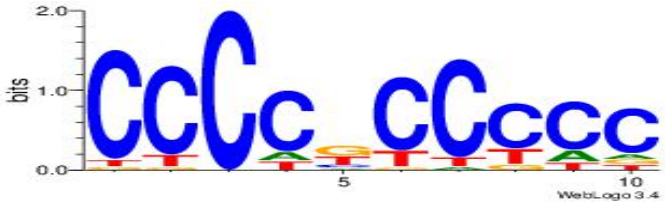
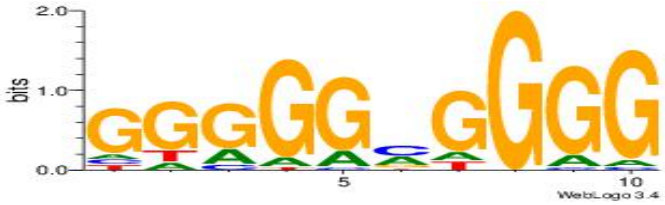
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 16 |
| Motif name: | SP1 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 5 |
| Number of overlap: | 6 |
| Similarity score: | 0.0349642 |

Alignment:
CCCCKCCCCC
CTCTGY----

Original motif Consensus sequence: CCCCKCCCCC




Reverse complement motif Consensus sequence: GGGGGYGGGG

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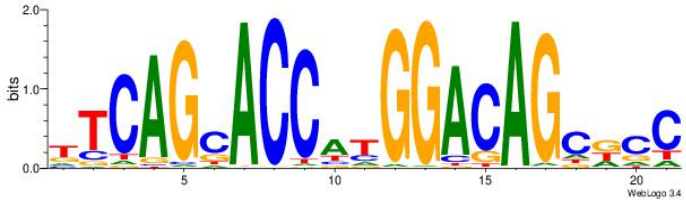
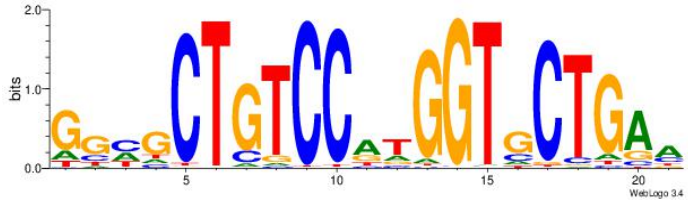
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 19 |
| Motif name: | REST |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Reverse Complement |
| Direction: | Forward |
| Position number: | 3 |
| Number of overlap: | 6 |
| Similarity score: | 0.0376108 |

Alignment:
GGYGCTGTCCATGGTGCTGAA
--CTCTGY----------

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC

Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA




---

| | |
|---|---|
| Dataset #: | 1 |
| Motif ID: | 8 |
| Motif name: | Motif 8 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction: | Backward |
| Position number: | 1 |
| Number of overlap: | 6 |
| Similarity score: | 0.0446026 |

Alignment:

```
TCCCAG
KCAGAG
```

Original motif Consensus sequence: CTGGGA

Reverse complement motif Consensus sequence: TCCCAG

---

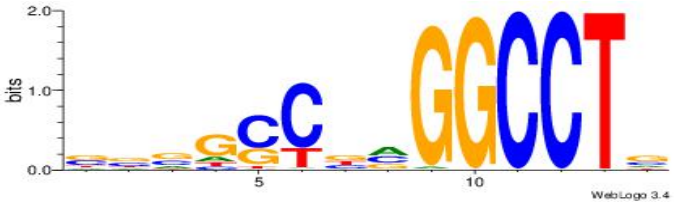
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 12 |

| | |
|---|---|
| Motif name: | Zfx |
| 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: | 0.0448449 |

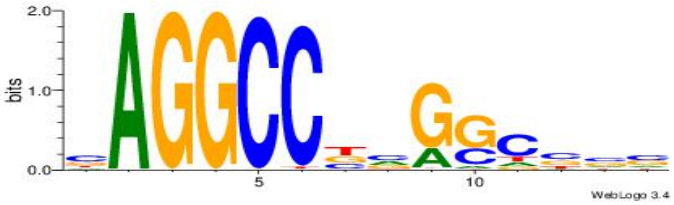
Alignment:

```
BBVGCCBVGGCCTV
---KCAGAG-----
```

Original motif Consensus sequence: BBVGCCBVGGCCTV




Reverse complement motif Consensus sequence: VAGGCCBBGGCVB




---

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

Original motif Consensus sequence: ATKTM

Reverse complement motif Consensus sequence: RARAT

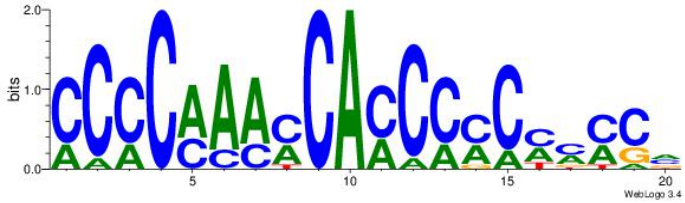
**Best Matches for Significant Motif ID 5 (Highest to Lowest)**

| | |
|---|---|
| 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 |

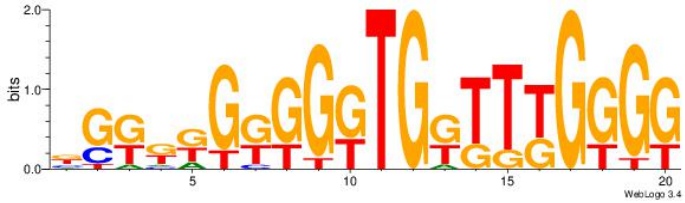
Alignment:

```
BGRRRGRGGRTGRTTYGGGG
------RARAT---------
```

Original motif Consensus sequence: CCCCMAAMCAMCCMCMMMCV




Reverse complement motif Consensus sequence: BGRRRGRGGRTGRTTYGGGG



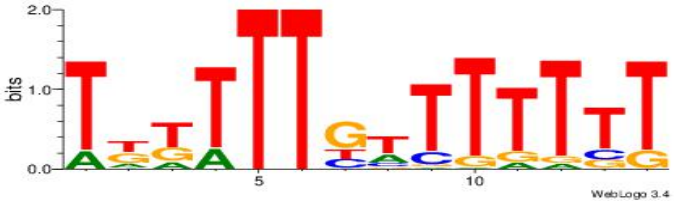

---

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

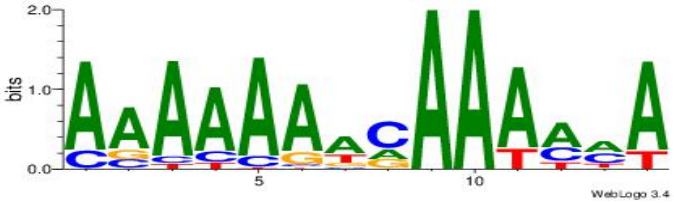
Number of overlap: 5
Similarity score: 0.0260117

Alignment:
AAAAAAACAAARRA
-RARAT--------

Original motif Consensus sequence: TKKTTTGTTTTTTT




Reverse complement motif Consensus sequence: AAAAAAACAAARR




---

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:

```
AKGYYCAAAGRTCA
-------RARAT--
```

Original motif Consensus sequence: TGAMCTTTGMMCYT

Reverse complement motif Consensus sequence: AKGYYCAAAGRTCA

---

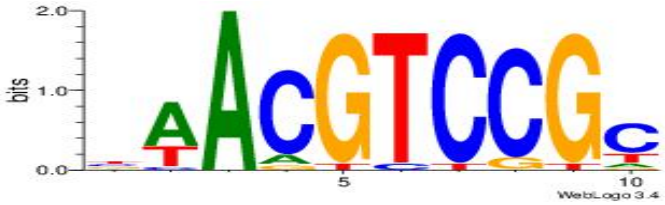
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 37 |

| | |
|---|---|
| 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



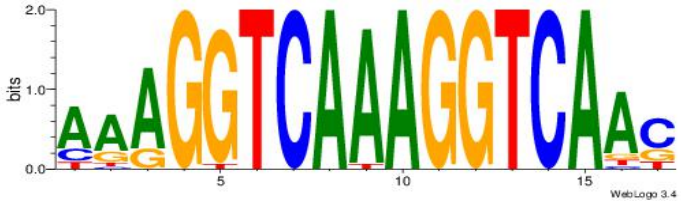

Reverse complement motif Consensus sequence: GCGGACGTTV

---

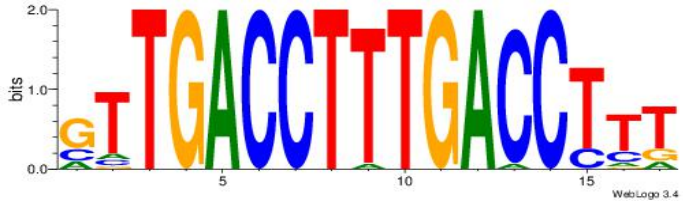
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 43 |
| Motif name: | NR1H2RXRA |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 10 |
| Number of overlap: | 5 |
| Similarity score: | 0.0292478 |

Alignment:
AAAGGTCAAAGGTCAAC
---------ATKTM---

Original motif Consensus sequence: AAAGGTCAAAGGTCAAC




Reverse complement motif Consensus sequence: GTTGACCTTTGACCTTT

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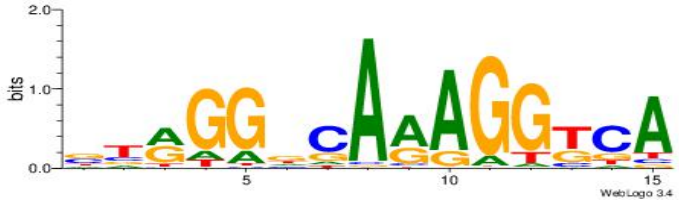
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 20 |
| Motif name: | PPARGRXRA |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Reverse Complement |
| Direction: | Forward |
| Position number: | 5 |
| Number of overlap: | 5 |
| Similarity score: | 0.0305369 |

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

Original motif Consensus sequence: BTRGGDCARAGGKCA

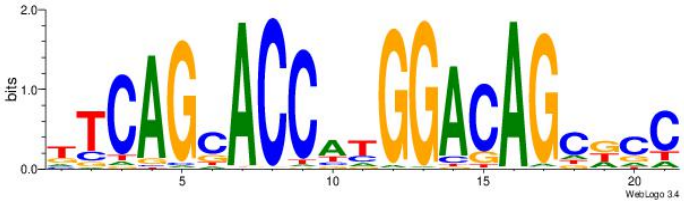
Reverse complement motif Consensus sequence: TGRCCTKTGHCCK



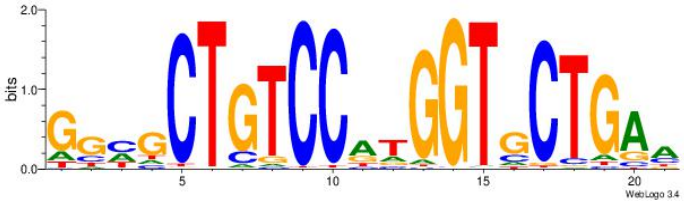
Dataset #: 2
Motif ID: 19
Motif name: REST
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 5
Number of overlap: 5
Similarity score: 0.0315454

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

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC




Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA



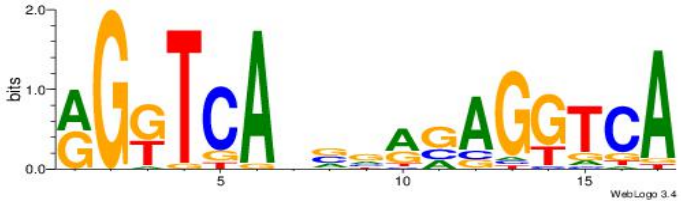

Dataset #: 2

| | |
|---|---|
| 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 |

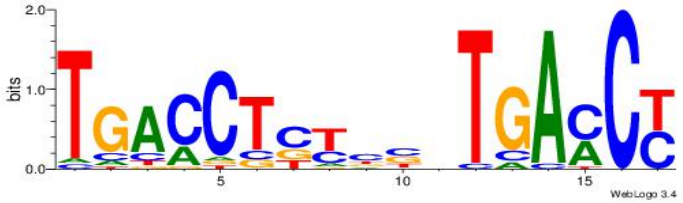
Alignment:

```
RGKTCABVVRGAGGTCA
ATKTM------------
```

Original motif Consensus sequence: RGKTCABVVRGAGGTCA




Reverse complement motif Consensus sequence: TGACCTCKVVBTGAYCK

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| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 46 |
| Motif name: | RORA_1 |
| 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: 0.0336052

Alignment:
AWVDAGGTCA
---RARAT--

Original motif Consensus sequence: AWVDAGGTCA

Reverse complement motif Consensus sequence: TGACCTDVWT

---

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

Original motif Consensus sequence: YGCGTG

Reverse complement motif Consensus sequence: CACGCM

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

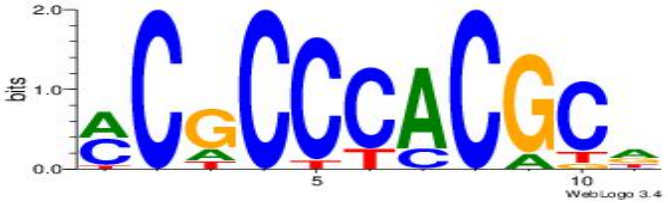
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 28 |
| Motif name: | Egr1 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction: | Backward |

| | |
|---|---|
| Position number: | 1 |
| Number of overlap: | 6 |
| Similarity score: | 0 |

Alignment:
YCGCCCACGCH
-----CACGCM

Original motif Consensus sequence: HGCGTGGGCGK

Reverse complement motif Consensus sequence: YCGCCCACGCH

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| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 33 |
| Motif name: | HIF1AARNT |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 2 |
| Number of overlap: | 6 |
| Similarity score: | 0.0112447 |

Alignment:
VBACGTGV
-YGCGTG-

Original motif Consensus sequence: VBACGTGV

Reverse complement motif Consensus sequence: VCACGTBV

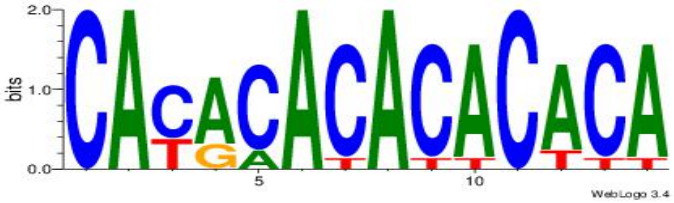
---

| | |
|---|---|
| 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 |

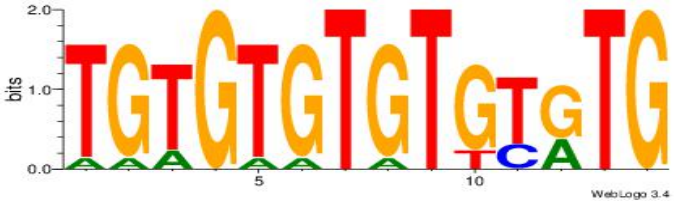
Alignment:

```
TGTGTGTGTGTKTG
------YGCGTG--
```

Original motif Consensus sequence: CAYACACACACACA




Reverse complement motif Consensus sequence: TGTGTGTGTGTKT

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| | |
|---|---|
| Dataset #: | 2 |

| | |
|---|---|
| Motif ID: | 31 |
| Motif name: | Esrrb |
| 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: | 0.0315972 |

Alignment:

CACGTG

YGCGTG

Original motif Consensus sequence: CACGTG

Reverse complement motif Consensus sequence: CACGTG

---

| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 25 |
| Motif name: | Arnt |
| 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: | 0.0315972 |

Alignment:
CACGTG
YGCGTG

Original motif Consensus sequence: CACGTG

Reverse complement motif Consensus sequence: CACGTG

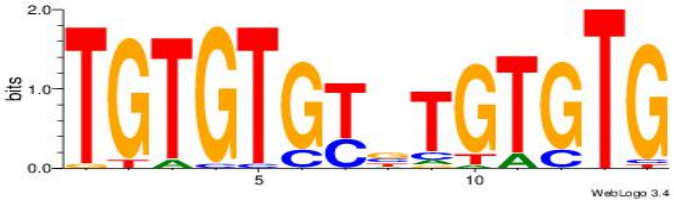
---

| | |
|---|---|
| Dataset #: | 1 |
| Motif ID: | 9 |
| Motif name: | Motif 9 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Reverse Complement |
| Direction: | Backward |
| Position number: | 9 |
| Number of overlap: | 6 |
| Similarity score: | 0.0350575 |

Alignment:
TGTGTGKVTGTGTG
YGCGTG--------

Original motif Consensus sequence: CACACAVRCACACA

Reverse complement motif Consensus sequence: TGTGTGKVTGTGT

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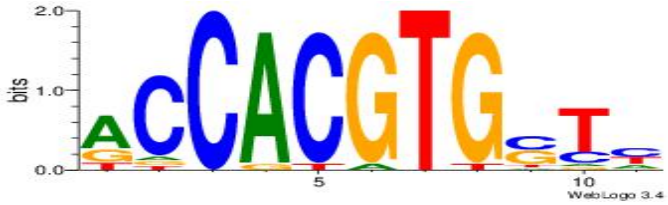
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 39 |
| Motif name: | MYCMAX |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 3 |
| Number of overlap: | 6 |
| Similarity score: | 0.0376488 |

Alignment:

```
RASCACGTGGT
---YGCGTG--
```

Original motif Consensus sequence: RASCACGTGGT

Reverse complement motif Consensus sequence: ACCACGTGSTM

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| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 40 |

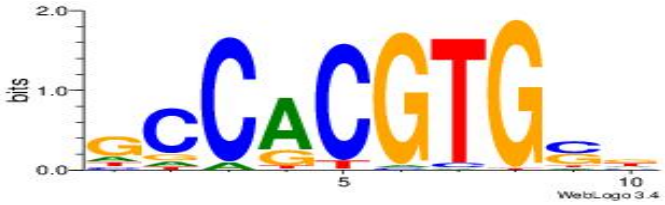
| | |
|---|---|
| Motif name: | Mycn |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Reverse Complement |
| Direction: | Forward |
| Position number: | 3 |
| Number of overlap: | 6 |
| Similarity score: | 0.0377949 |

Alignment:

```
GCCACGTGSD
--YGCGTG--
```

Original motif Consensus sequence: HSCACGTGGC

Reverse complement motif Consensus sequence: GCCACGTGSD

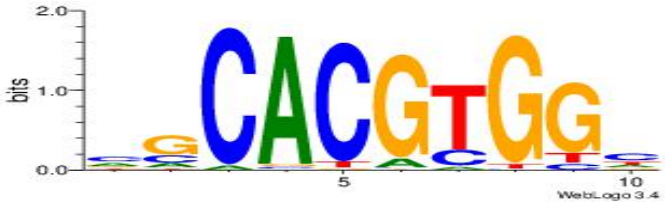



---

| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 38 |
| Motif name: | Myc |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Reverse Complement |
| Direction: | Forward |
| Position number: | 3 |
| Number of overlap: | 6 |
| Similarity score: | 0.0399214 |

Alignment:
DCCACGTGCV
--YGCGTG--

Original motif Consensus sequence: VGCACGTGGH




Reverse complement motif Consensus sequence: DCCACGTGCV

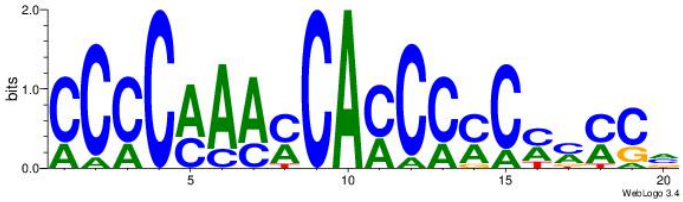
---

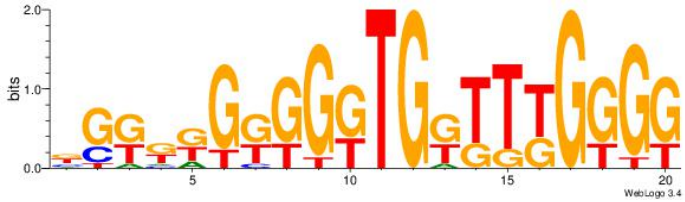
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 18 |
| Motif name: | RREB1 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Reverse Complement |
| Direction: | Backward |
| Position number: | 7 |
| Number of overlap: | 6 |
| Similarity score: | 0.0433081 |

Alignment:
BGRRRGRGGRTGRTTYGGGG
--------YGCGTG------

Original motif Consensus sequence: CCCCMAAMCAMCCMCMMMCV

Reverse complement motif Consensus sequence: BGRRRGRGGRTGRTTYGGGG




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

Original motif Consensus sequence: CMGCRGC

Reverse complement motif Consensus sequence: GCKGCYG

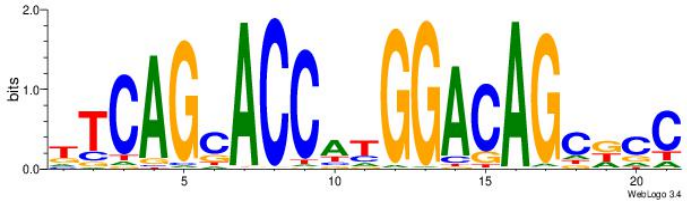
**Best Matches for Significant Motif ID 6 (Highest to Lowest)**

| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 19 |
| Motif name: | REST |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction: | Forward |
| Position number: | 13 |
| Number of overlap: | 7 |
| Similarity score: | 0.0205607 |

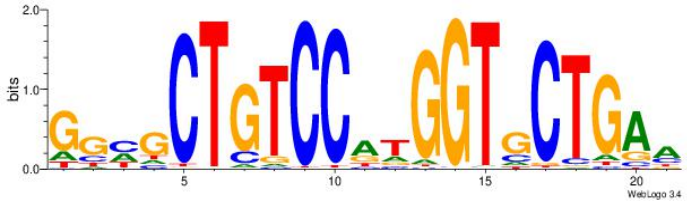
Alignment:

```
GGYGCTGTCCATGGTGCTGAA
------------GCKGCYG--
```

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC




Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA

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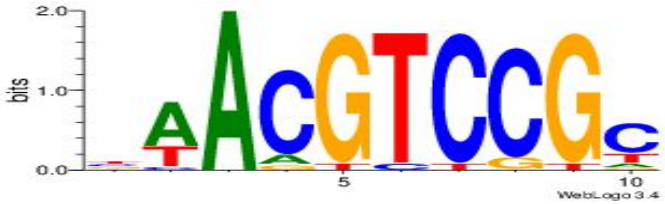
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 37 |
| Motif name: | MIZF |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction: | Forward |
| Position number: | 1 |
| Number of overlap: | 7 |
| Similarity score: | 0.0322623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

Alignment:

```
GCGGACGTTV
GCKGCYG---
```

Original motif Consensus sequence: BAACGTCCGC




Reverse complement motif Consensus sequence: GCGGACGTTV

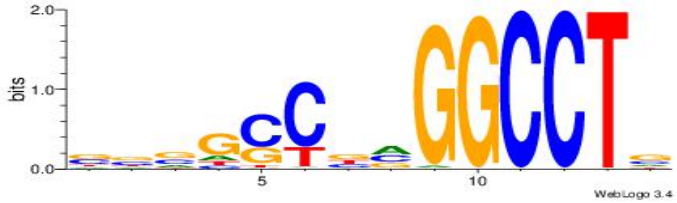
---

| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 12 |
| Motif name: | Zfx |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 4 |
| Number of overlap: | 7 |
| Similarity score: | 0.038091 |

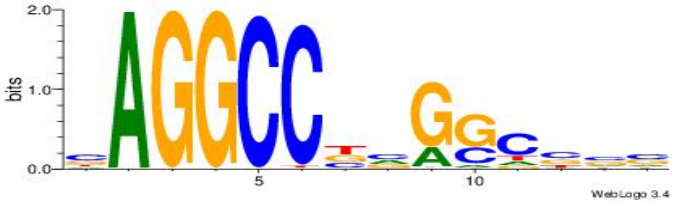
Alignment:

```
BBVGCCBVGGCCTV
----CMGCRGC---
```

Original motif Consensus sequence: BBVGCCBVGGCCTV




Reverse complement motif Consensus sequence: VAGGCCBBGGCVB

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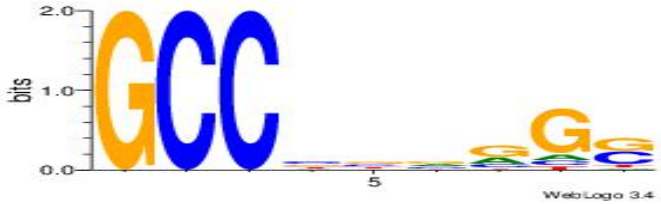
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 15 |
| Motif name: | TFAP2A |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Reverse Complement |
| Direction: | Forward |
| Position number: | 3 |
| Number of overlap: | 7 |

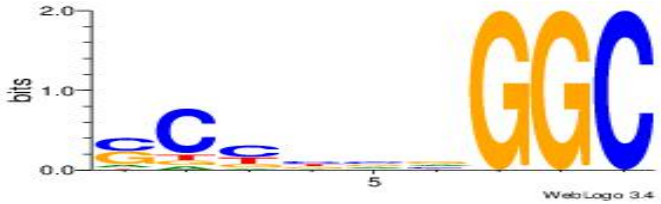
Similarity score: 0.0393168

Alignment:
SCMVBBGGC
--CMGCRGC

Original motif Consensus sequence: GCCBBVRGS




Reverse complement motif Consensus sequence: SCMVBBGGC




---

Dataset #: 1
Motif ID: 7
Motif name: Motif 7
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 2
Number of overlap: 7
Similarity score: 0.0443244

Alignment:
CCCRCCCC
-CMGCRGC

Original motif Consensus sequence: CCCRCCCC

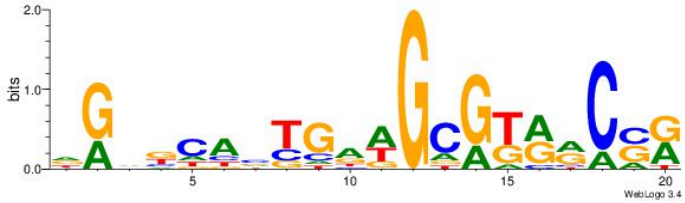
Reverse complement motif Consensus sequence: GGGGMGGG

| | |
|---|---|
| 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 |

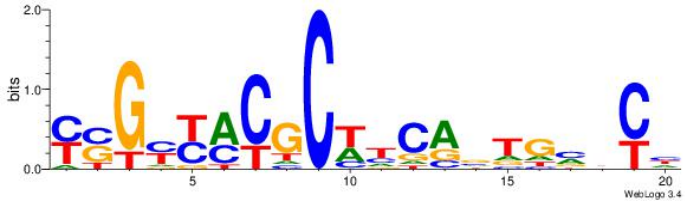
Alignment:

```
MSGKKRCGCWDCABTGBBCD
-------GCKGCYG------
```

Original motif Consensus sequence: DGVBCABTGDWGCGKRRCSR




Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD




| | |
|---|---|
| Dataset #: | 2 |

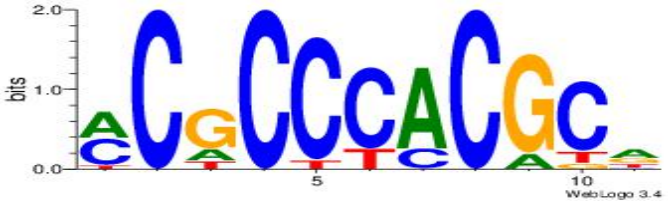
| | |
|---|---|
| Motif ID: | 28 |
| Motif name: | Egr1 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 2 |
| Number of overlap: | 7 |
| Similarity score: | 0.0453576 |

Alignment:

```
HGCGTGGGCGK
---GCKGCYG-
```

Original motif Consensus sequence: HGCGTGGGCGK

Reverse complement motif Consensus sequence: YCGCCCACGCH

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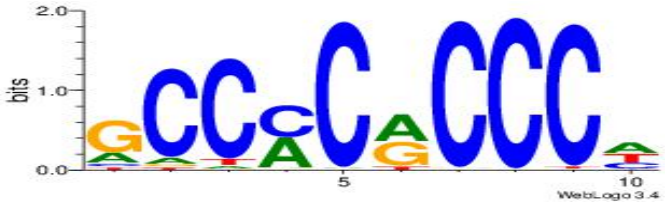
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 36 |
| Motif name: | Klf4 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Reverse Complement |
| Direction: | Forward |
| Position number: | 2 |
| Number of overlap: | 7 |
| Similarity score: | 0.0476958 |

Alignment:
GCCYCMCCCD
-CMGCRGC--

Original motif Consensus sequence: DGGGYGKGGC

Reverse complement motif Consensus sequence: GCCYCMCCCD

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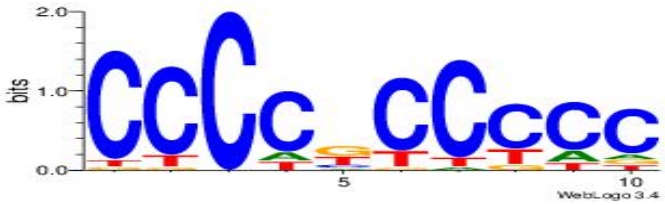
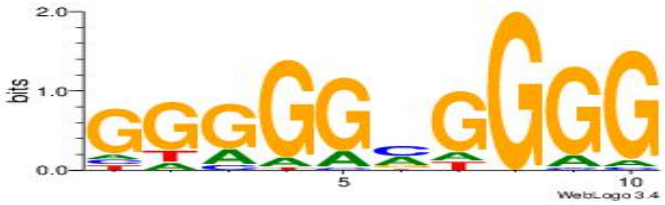
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 16 |
| Motif name: | SP1 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction: | Forward |
| Position number: | 1 |
| Number of overlap: | 7 |
| Similarity score: | 0.0490991 |

Alignment:
GGGGGYGGGG
GCKGCYG---

Original motif Consensus sequence: CCCCKCCCCC

Reverse complement motif Consensus sequence: GGGGGYGGGG



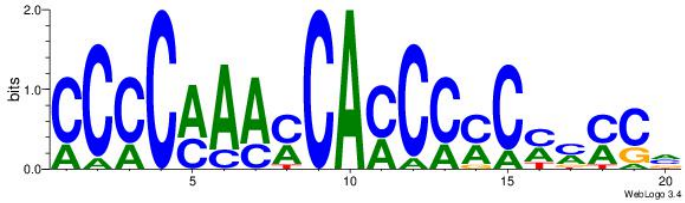




| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 18 |
| Motif name: | RREB1 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction: | Forward |
| Position number: | 6 |
| Number of overlap: | 7 |
| Similarity score: | 0.0498726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

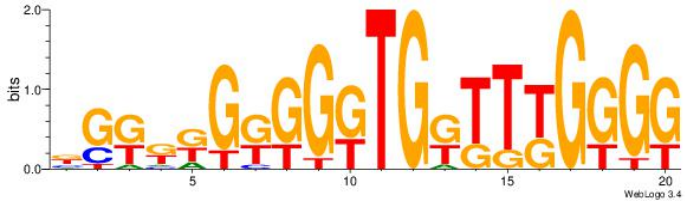
Alignment:

```
BGRRRGRGGRTGRTTYGGGG
-----GCKGCYG--------
```

Original motif Consensus sequence: CCCCMAAMCAMCCMCMMMCV




Reverse complement motif Consensus sequence: BGRRRGRGGRTGRTTYGGGG




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

Original motif Consensus sequence: AMACA

Reverse complement motif Consensus sequence: TGTRT

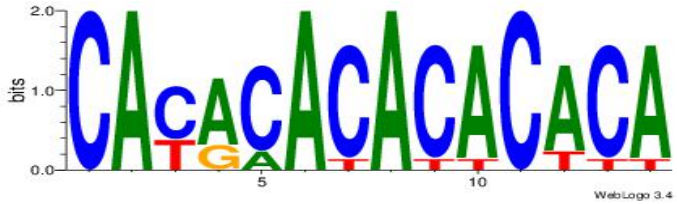
## Best Matches for Significant Motif ID 2 (Highest to Lowest)

| | |
|---|---|
| Dataset #: | 1 |
| Motif ID: | 11 |
| Motif name: | Motif 11 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction: | Forward |
| Position number: | 5 |
| Number of overlap: | 5 |
| Similarity score: | 0 |

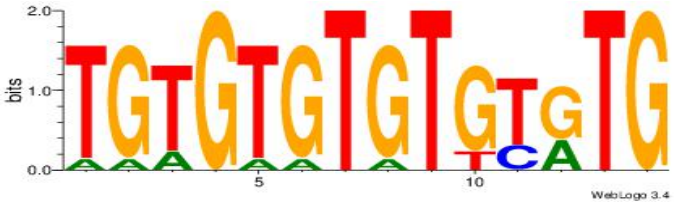
Alignment:

```
TGTGTGTGTGTKTG
----TGTRT-----
```

Original motif Consensus sequence: CAYACACACACACA




Reverse complement motif Consensus sequence: TGTGTGTGTGTKT



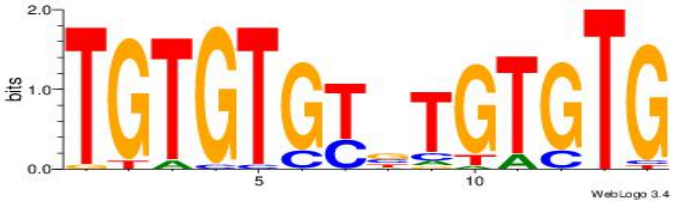
| | |
|---|---|
| Dataset #: | 1 |
| Motif ID: | 9 |
| Motif name: | Motif 9 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 10 |
| Number of overlap: | 5 |
| Similarity score: | 0.0040753 |

Alignment:

```
CACACAVRCACACA
---------AMACA
```

Original motif Consensus sequence: CACACAVRCACACA

Reverse complement motif Consensus sequence: TGTGTGKVTGTGT

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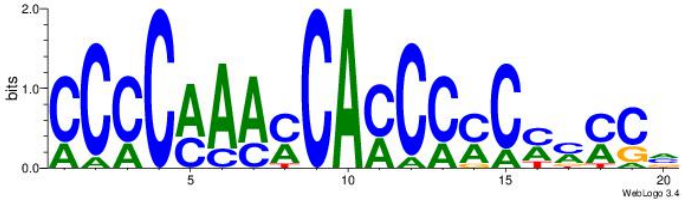
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 18 |
| Motif name: | RREB1 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 11 |
| Number of overlap: | 5 |

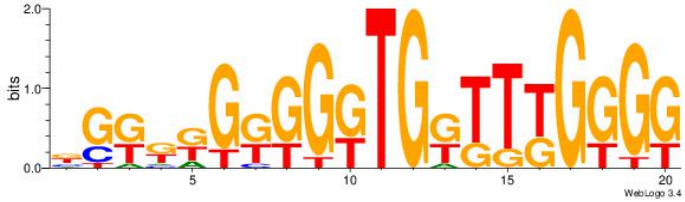
Similarity score: 0.0243918

Alignment:
CCCCMAAMCAMCCMCMMMCV
-----AMACA----------

Original motif Consensus sequence: CCCCMAAMCAMCCMCMMMCV




Reverse complement motif Consensus sequence: BGRRRGRGGRTGRTTYGGGG



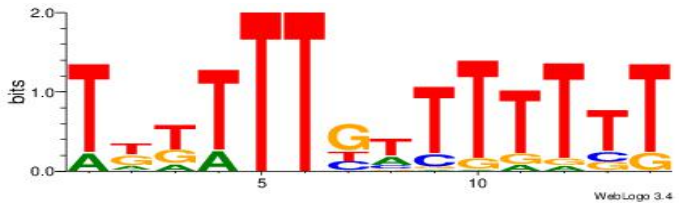

---

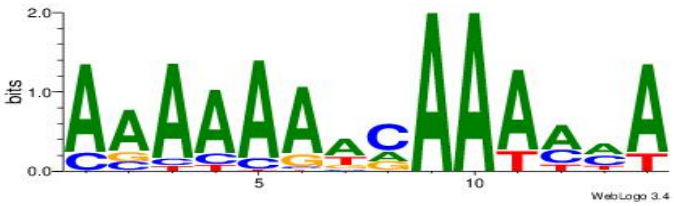
Dataset #: 1
Motif ID: 10
Motif name: Motif 10
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 6
Number of overlap: 5
Similarity score: 0.0394919

Alignment:
AAAAAAACAAARRA
----AMACA-----

Original motif Consensus sequence: TKKTTTGTTTTTTT

Reverse complement motif Consensus sequence: AAAAAAACAAARR

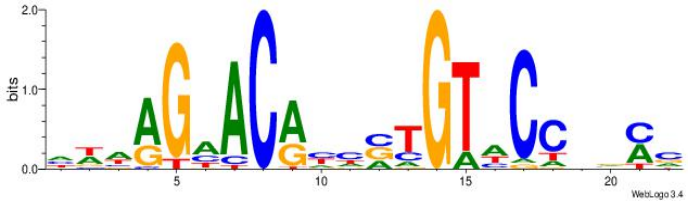


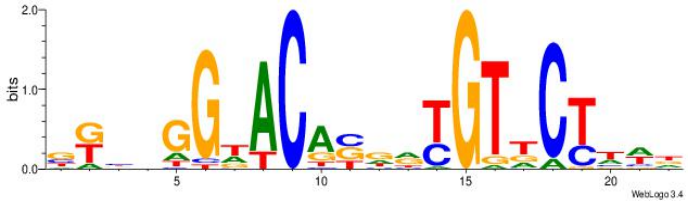

Dataset #: 2
Motif ID: 24
Motif name: Ar
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 5
Number of overlap: 5
Similarity score: 0.0429089

Alignment:
HWDAGHACRHHVTGTHCCHVMV
----AMACA----------

Original motif Consensus sequence: HWDAGHACRHHVTGTHCCHVMV




Reverse complement motif Consensus sequence: VRVDGGHACAVDDKGTHCTDWH



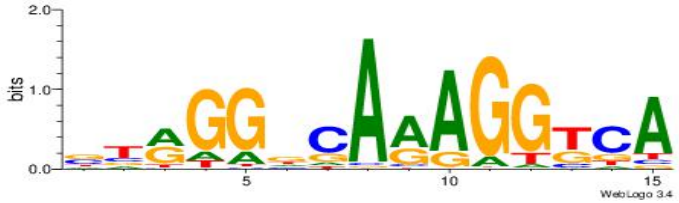

Dataset #: 2

| | |
|---|---|
| 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 |

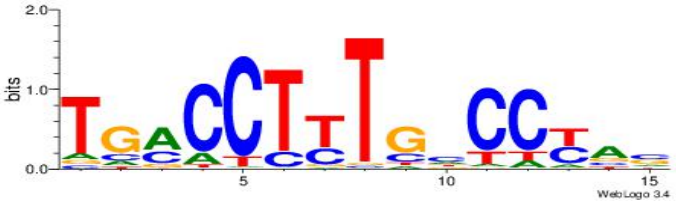
Alignment:

```
TGRCCTKTGHCCKAB
-----TGTRT-----
```

Original motif Consensus sequence: BTRGGDCARAGGKCA




Reverse complement motif Consensus sequence: TGRCCTKTGHCCK

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| | |
|---|---|
| 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

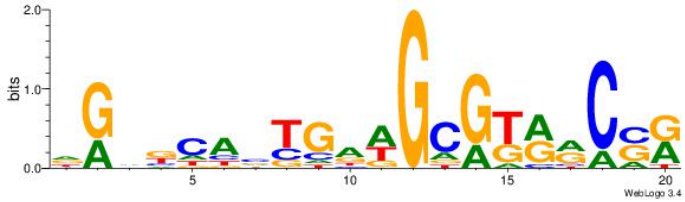
---

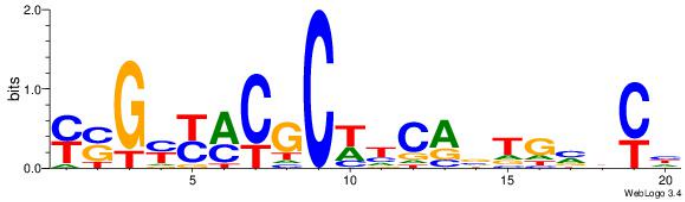
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 45 |
| Motif name: | Pax5 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Reverse Complement |
| Direction: | Forward |
| Position number: | 6 |
| Number of overlap: | 5 |
| Similarity score: | 0.0620995 |

Alignment:
MSGKKRCGCWDCABTGBBCD
-----AMACA----------

Original motif Consensus sequence: DGVBCABTGDWGCGKRRCSR

Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD

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| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 22 |
| Motif name: | NR2F1 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Reverse Complement |
| Direction: | Forward |
| Position number: | 7 |
| Number of overlap: | 5 |
| Similarity score: | 0.0650242 |

Alignment:

```
AKGYYCAAAGRTCA
------AMACA---
```

Original motif Consensus sequence: TGAMCTTTGMMCYT

Reverse complement motif Consensus sequence: AKGYYCAAAGRTCA

---

| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 35 |

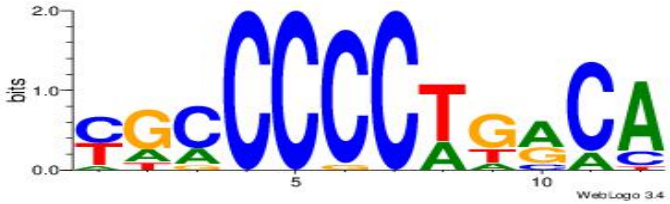
| | |
|---|---|
| Motif name: | INSM1 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 8 |
| Number of overlap: | 5 |
| Similarity score: | 0.0670984 |

Alignment:

```
TGYCAGGGGGCR
TGTRT-------
```

Original motif Consensus sequence: TGYCAGGGGGCR

Reverse complement motif Consensus sequence: MGCCCCCTGMCA




---

**Dataset #: 2 Motif ID: 23 Motif name: MZF1_1-4**

Original motif Consensus sequence: BGGGGA

Reverse complement motif Consensus sequence: TCCCCV

**Best Matches for Significant Motif ID 23 (Highest to Lowest)**

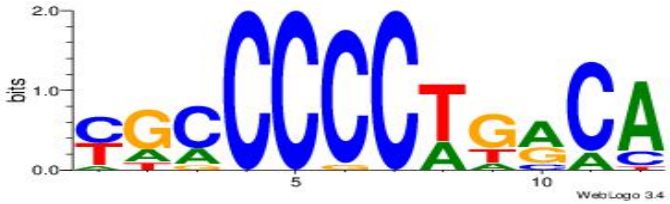
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 35 |
| Motif name: | INSM1 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction: | Backward |
| Position number: | 5 |
| Number of overlap: | 6 |
| Similarity score: | 0.0276389 |

Alignment:

```
MGCCCCCTGMCA
--TCCCCV----
```

Original motif Consensus sequence: TGYCAGGGGGCR

Reverse complement motif Consensus sequence: MGCCCCCTGMCA

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| | |
|---|---|
| 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: | Forward |
| Position number: | 4 |
| Number of overlap: | 6 |

Similarity score: 0.0314583

Alignment:
BKAGGGGDAD
---BGGGGA-

Original motif Consensus sequence: BKAGGGGDAD

Reverse complement motif Consensus sequence: BTHCCCCTYB

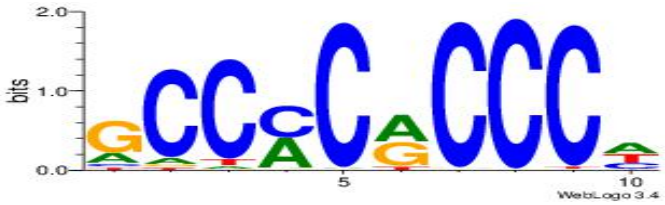
---

Dataset #: 2
Motif ID: 36
Motif name: Klf4
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: 0.0406514

Alignment:
GCCYCMCCCD
TCCCCV----

Original motif Consensus sequence: DGGGYGKGGC

Reverse complement motif Consensus sequence: GCCYCMCCCD

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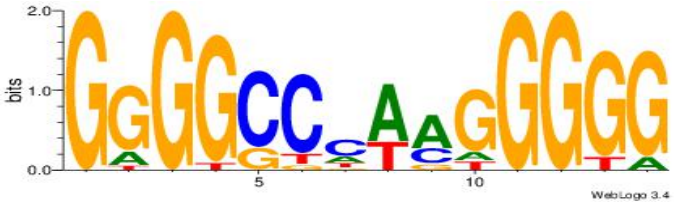
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 21 |
| Motif name: | PLAG1 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 9 |
| Number of overlap: | 6 |
| Similarity score: | 0.0412963 |

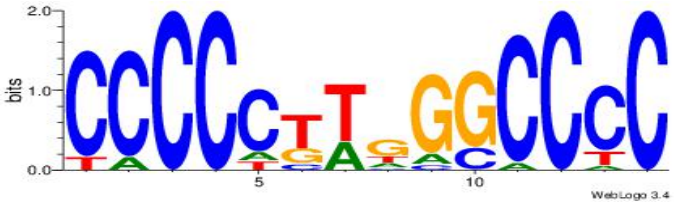
Alignment:

```
GGGGCCCAAGGGGG
--------BGGGGA
```

Original motif Consensus sequence: GGGGCCCAAGGGGG




Reverse complement motif Consensus sequence: CCCCCTTGGGCCC

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| | |
|---|---|
| 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: | 1 |
| Number of overlap: | 6 |
| Similarity score: | 0.0426517 |

Alignment:

```
TCCCAG
TCCCCV
```

Original motif Consensus sequence: CTGGGA

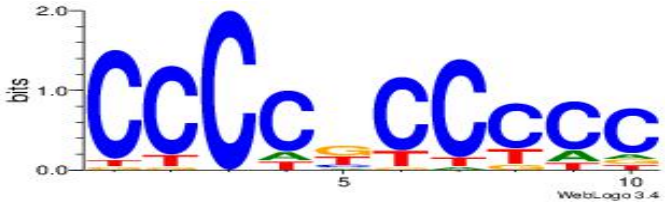
Reverse complement motif Consensus sequence: TCCCAG

---

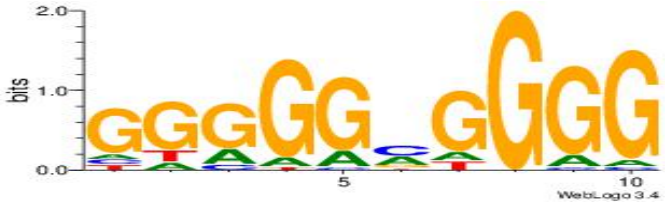
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 16 |
| Motif name: | SP1 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Reverse Complement |
| Direction: | Forward |
| Position number: | 5 |
| Number of overlap: | 6 |
| Similarity score: | 0.0464881 |

Alignment:
GGGGGYGGGG
----BGGGGA

Original motif Consensus sequence: CCCCKCCCCC




Reverse complement motif Consensus sequence: GGGGGYGGGG

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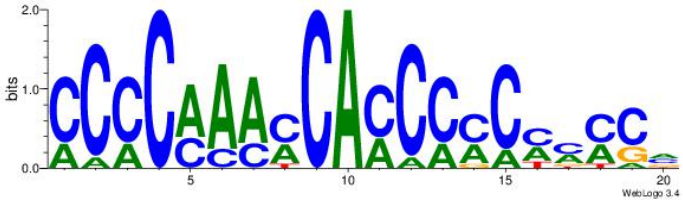
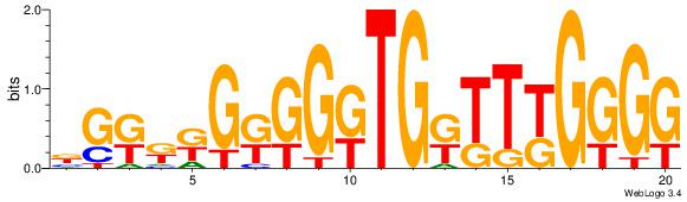
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 18 |
| Motif name: | RREB1 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 5 |
| Number of overlap: | 6 |
| Similarity score: | 0.0493561 |

Alignment:
CCCCMAAMCAMCCMCMMMCV
----TCCCCV----------

Original motif Consensus sequence: CCCCMAAMCAMCCMCMMMCV

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: | Original Motif |
| Direction: | Backward |
| Position number: | 1 |
| Number of overlap: | 6 |
| Similarity score: | 0.0521759 |

Alignment:

```
GGGGRTTCCCC
-----TCCCCV
```

Original motif Consensus sequence: GGGGRTTCCCC

Reverse complement motif Consensus sequence: GGGGAAKCCCC

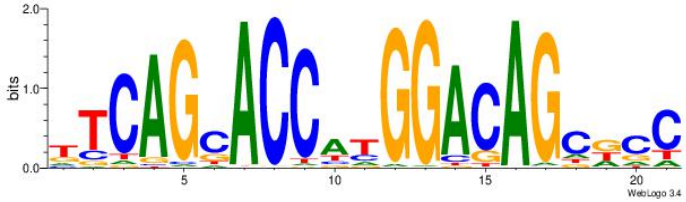
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 19 |

| | |
|---|---|
| Motif name: | REST |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction: | Backward |
| Position number: | 11 |
| Number of overlap: | 6 |
| Similarity score: | 0.0581528 |

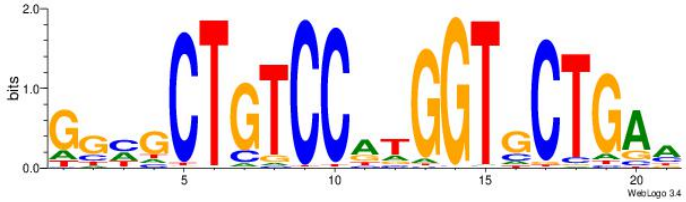
Alignment:

```
GGYGCTGTCCATGGTGCTGAA
-----TCCCCV----------
```

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC




Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA

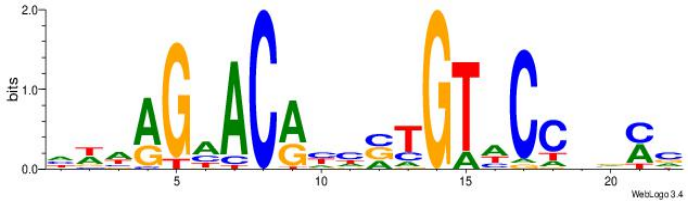



---

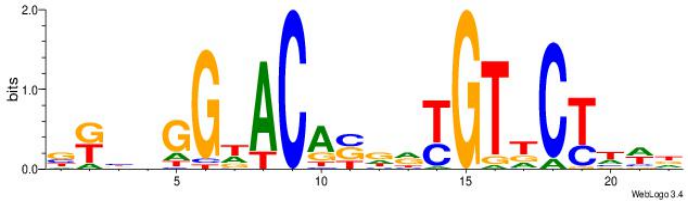
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 24 |
| Motif name: | Ar |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 3 |
| Number of overlap: | 6 |
| Similarity score: | 0.0585417 |

Alignment:
HWDAGHACRHHVTGTHCCHVMV
----------TCCCCV--

Original motif Consensus sequence: HWDAGHACRHHVTGTHCCHVMV



Reverse complement motif Consensus sequence: VRVDGGHACAVDDKGTHCTDWH



**Dataset #: 2 Motif ID: 44 Motif name: NR4A2**

Original motif Consensus sequence: AAGGTCAC

Reverse complement motif Consensus sequence: GTGACCTT

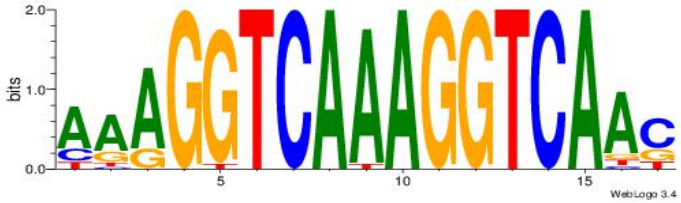
**Best Matches for Significant Motif ID 44 (Highest to Lowest)**

| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 43 |
| Motif name: | NR1H2RXRA |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |

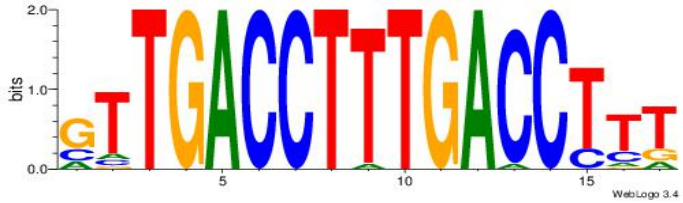
Position number: 2
Number of overlap: 8
Similarity score: 0.0167759

Alignment:
AAAGGTCAAAGGTCAAC
-AAGGTCAC--------

Original motif Consensus sequence: AAAGGTCAAAGGTCAAC




Reverse complement motif Consensus sequence: GTTGACCTTTGACCTTT

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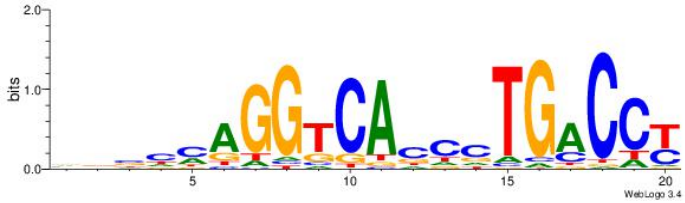
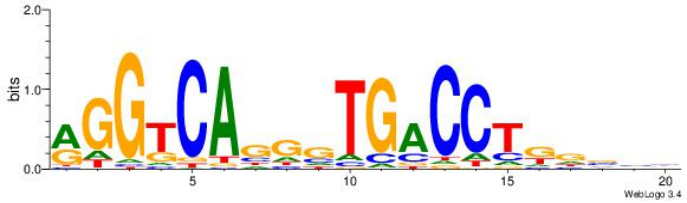
Dataset #: 2
Motif ID: 29
Motif name: ESR1
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 5
Number of overlap: 8
Similarity score: 0.0195235

Alignment:
VDBHMAGGTCACCCTGACCY
----AAGGTCAC--------

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV

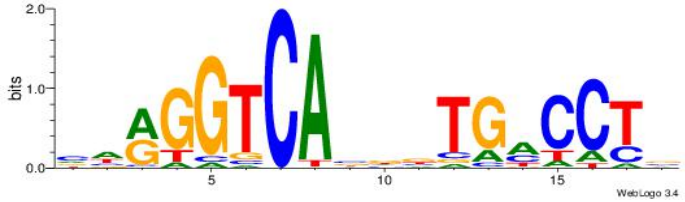


| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 30 |
| Motif name: | ESR2 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 2 |
| Number of overlap: | 8 |
| Similarity score: | 0.0198372 |

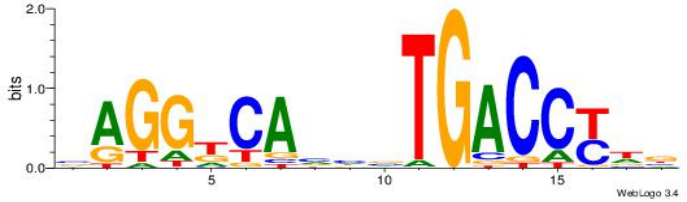
Alignment:

```
VHRGGTCABDBTGMCCTB
-AAGGTCAC---------
```

Original motif Consensus sequence: VHRGGTCABDBTGMCCTB



Reverse complement motif Consensus sequence: BAGGYCABHBTGACCKHV

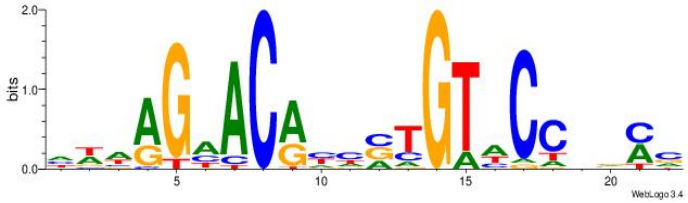


| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 24 |
| Motif name: | Ar |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction: | Forward |
| Position number: | 13 |
| Number of overlap: | 8 |
| Similarity score: | 0.0487608 |

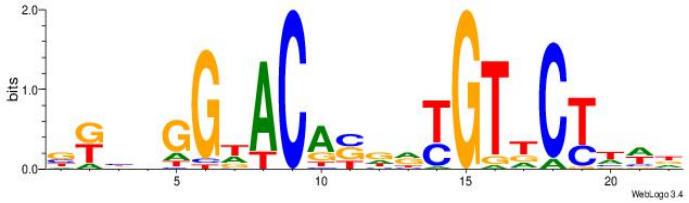
Alignment:

```
VRVDGGHACAVDDKGTHCTDWH
------------GTGACCTT--
```

Original motif Consensus sequence: HWDAGHACRHHVTGTHCCHVMV




Reverse complement motif Consensus sequence: VRVDGGHACAVDDKGTHCTDWH

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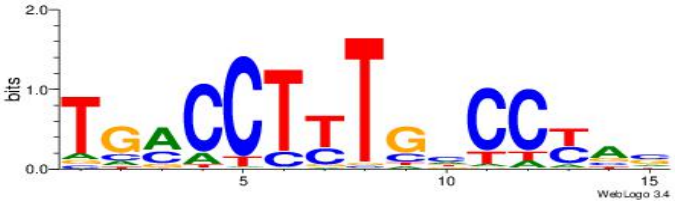
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 20 |
| Motif name: | PPARGRXRA |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 7 |

Number of overlap: 8
Similarity score: 0.0495607

Alignment:
BTRGGDCARAGGKCA
-AAGGTCAC------

Original motif Consensus sequence: BTRGGDCARAGGKCA

Reverse complement motif Consensus sequence: TGRCCTKTGHCCK

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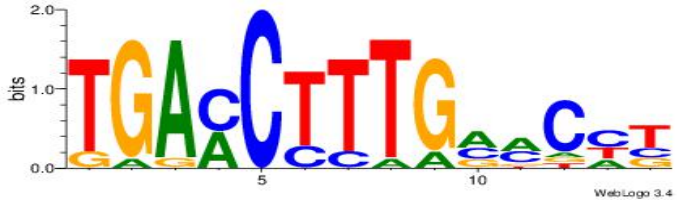
Dataset #: 2
Motif ID: 22
Motif name: NR2F1
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 7
Number of overlap: 8
Similarity score: 0.0564874

Alignment:
AKGYYCAAAGRTCA
------AAGGTCAC

Original motif Consensus sequence: TGAMCTTTGMMCYT

Reverse complement motif Consensus sequence: AKGYYCAAAGRTC



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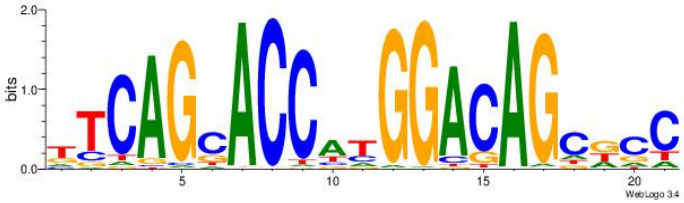
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 19 |
| Motif name: | REST |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 5 |
| Number of overlap: | 8 |
| Similarity score: | 0.0594649 |

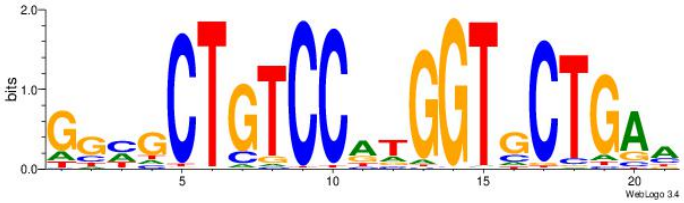
Alignment:

```
TTCAGCACCATGGACAGCKCC
---------AAGGTCAC----
```

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC




Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA

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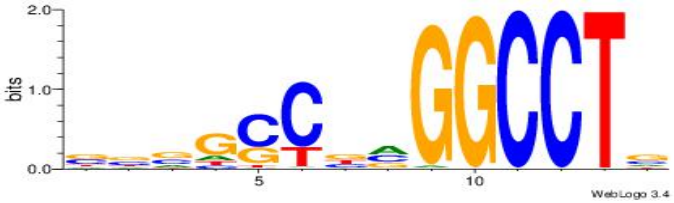
Dataset #: 2

| | |
|---|---|
| Motif ID: | 12 |
| Motif name: | Zfx |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 1 |
| Number of overlap: | 8 |
| Similarity score: | 0.0631514 |

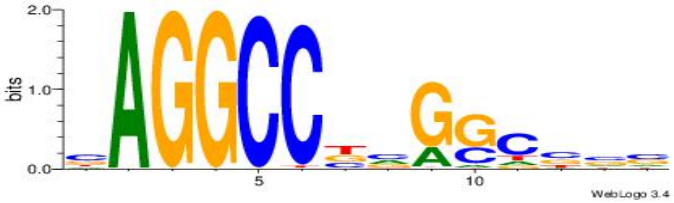
Alignment:

```
BBVGCCBVGGCCTV
GTGACCTT------
```

Original motif Consensus sequence: BBVGCCBVGGCCTV




Reverse complement motif Consensus sequence: VAGGCCBBGGCVB

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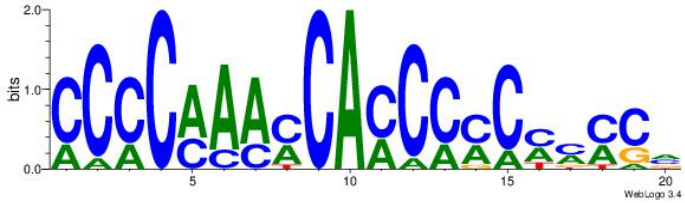
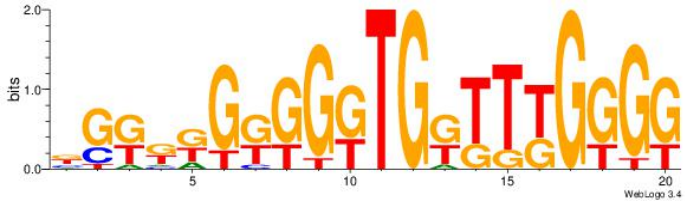
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 18 |
| Motif name: | RREB1 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction: | Backward |
| Position number: | 4 |
| Number of overlap: | 8 |
| Similarity score: | 0.0720656 |

Alignment:
BGRRRGRGGRTGRTTYGGGG
---------GTGACCTT---

Original motif Consensus sequence: CCCCMAAMCAMCCMCMMMCV




Reverse complement motif Consensus sequence: BGRRRGRGGRTGRTTYGGGG

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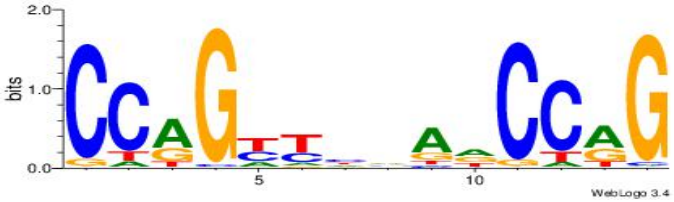
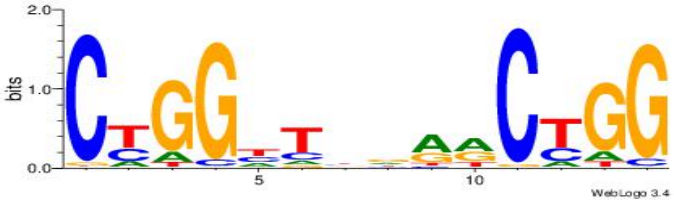
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 48 |
| Motif name: | Tcfcp2l1 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction: | Backward |
| Position number: | 2 |
| Number of overlap: | 8 |
| Similarity score: | 0.0740998 |

Alignment:
CKGGDTBDMMCTGG
-----GTGACCTT-

Original motif Consensus sequence: CCAGYYHVADCCRG

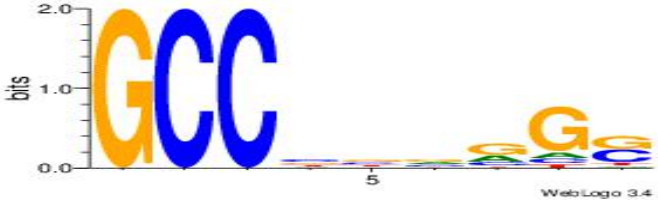
Reverse complement motif Consensus sequence: CKGGDTBDMMCT



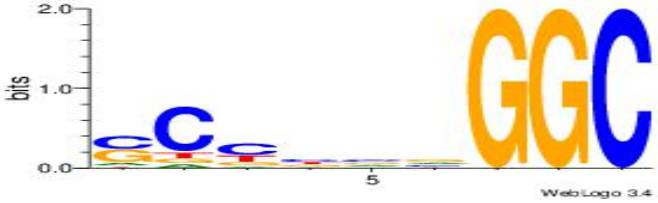




**Dataset #: 2** **Motif ID: 15** **Motif name: TFAP2A**

Original motif Consensus sequence: GCCBBVRGS




Reverse complement motif Consensus sequence: SCMVBBGGC



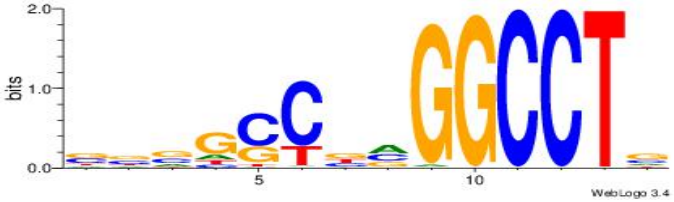

## Best Matches for Significant Motif ID 15 (Highest to Lowest)

| | |
|---|---|
| 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: | 3 |
| Number of overlap: | 9 |
| Similarity score: | 0.0131247 |

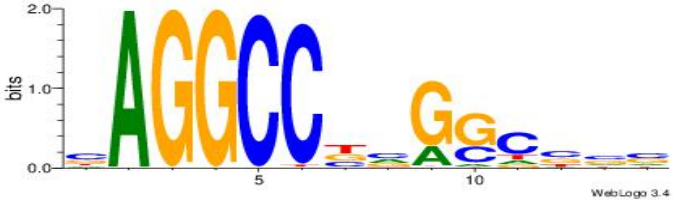
Alignment:

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

Original motif Consensus sequence: BBVGCCBVGGCCTV




Reverse complement motif Consensus sequence: VAGGCCBBGGCVB

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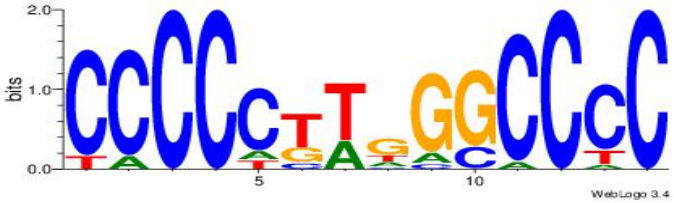
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 21 |
| Motif name: | PLAG1 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 4 |
| Number of overlap: | 9 |
| Similarity score: | 0.0414588 |

Alignment:

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

Original motif Consensus sequence: GGGGCCCAAGGGGG

Reverse complement motif Consensus sequence: CCCCCTTGGGCCC

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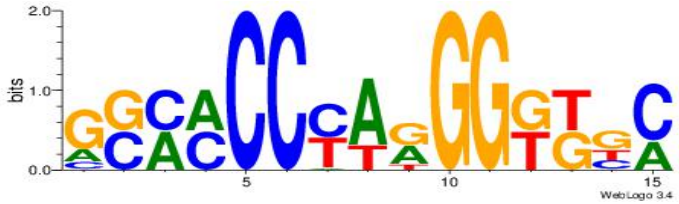
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 13 |
| Motif name: | Zfp423 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction: | Backward |
| Position number: | 4 |
| Number of overlap: | 9 |
| Similarity score: | 0.0438157 |

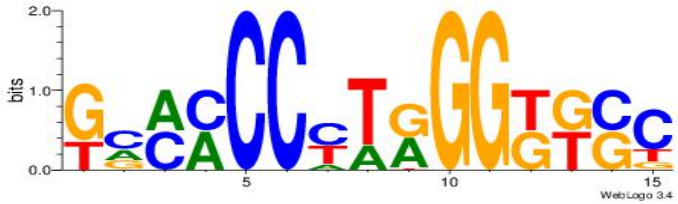
Alignment:

```
GYRYCCMTKGGYRSC
---SCMVBBGGC---
```

Original motif Consensus sequence: GSMMCCYARGGKKKC




Reverse complement motif Consensus sequence: GYRYCCMTKGGYR

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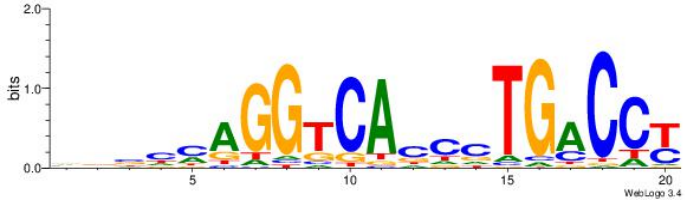
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 29 |
| Motif name: | ESR1 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Reverse Complement |
| Direction: | Backward |
| Position number: | 2 |
| Number of overlap: | 9 |

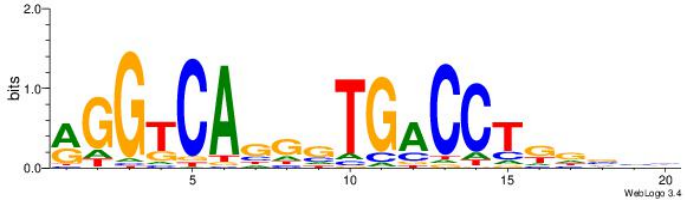
Similarity score: 0.0450672

Alignment:
MGGTCAGGGTGACCTRDBHV
----------GCCBBVRGS-

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY




Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV

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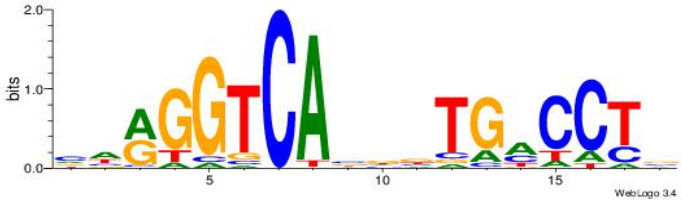
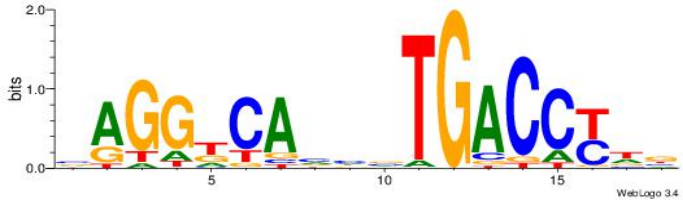
Dataset #: 2
Motif ID: 30
Motif name: ESR2
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 6
Number of overlap: 9
Similarity score: 0.0531668

Alignment:
BAGGYCABHBTGACCKHV
-----SCMVBBGGC----

Original motif Consensus sequence: VHRGGTCABDBTGMCCTB

Reverse complement motif Consensus sequence: BAGGYCABHBTGACCKHV

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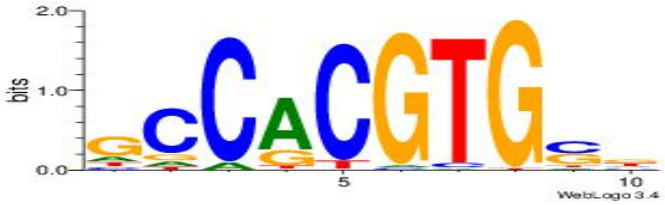
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 40 |
| Motif name: | Mycn |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 2 |
| Number of overlap: | 9 |
| Similarity score: | 0.0550803 |

Alignment:

```
HSCACGTGGC
-SCMVBBGGC
```

Original motif Consensus sequence: HSCACGTGGC

Reverse complement motif Consensus sequence: GCCACGTGSD




---

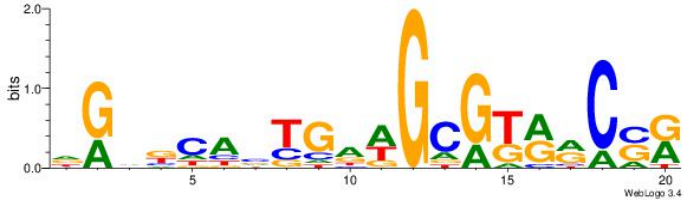
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 45 |

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

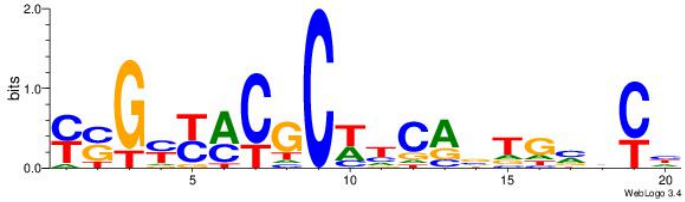
Alignment:

```
MSGKKRCGCWDCABTGBBCD
-------GCCBBVRGS----
```

Original motif Consensus sequence: DGVBCABTGDWGCGKRRCSR




Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD

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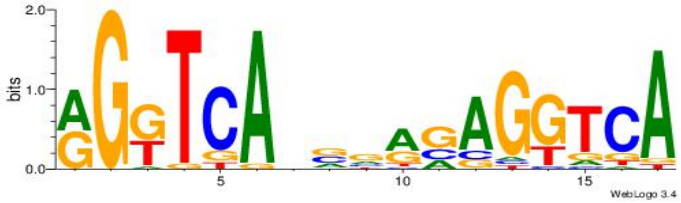
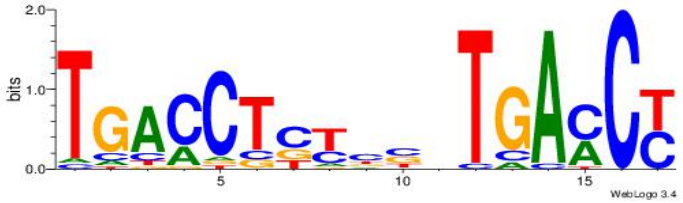
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 47 |
| Motif name: | RXRRAR_DR5 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 7 |
| Number of overlap: | 9 |
| Similarity score: | 0.0606062 |

Alignment:
RGKTCABVVRGAGGTCA
--GCCBBVRGS------

Original motif Consensus sequence: RGKTCABVVRGAGGTCA




Reverse complement motif Consensus sequence: TGACCTCKVVBTGAYCK

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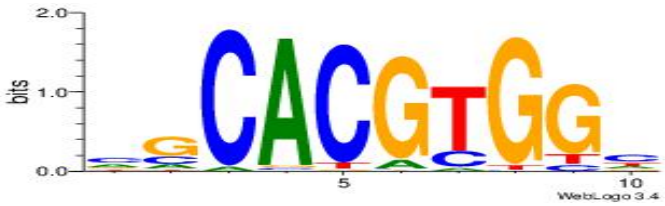
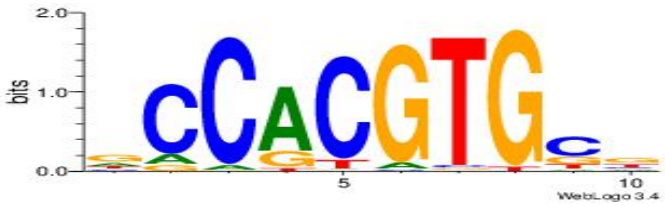
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 38 |
| Motif name: | Myc |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 2 |
| Number of overlap: | 9 |
| Similarity score: | 0.0613455 |

Alignment:
VGCACGTGGH
-SCMVBBGGC

Original motif Consensus sequence: VGCACGTGGH

Reverse complement motif Consensus sequence: DCCACGTGCV

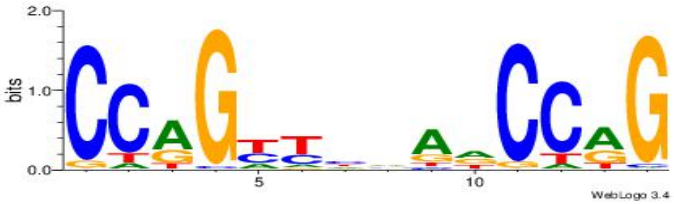


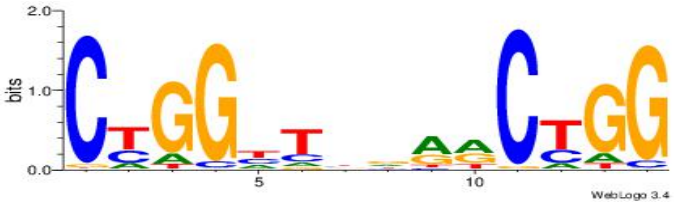

Dataset #: 2
Motif ID: 48
Motif name: Tcfcp2l1
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 3
Number of overlap: 9
Similarity score: 0.0631412

Alignment:
CCAGYYHVADCCRG
---GCCBBVRGS--

Original motif Consensus sequence: CCAGYYHVADCCRG




Reverse complement motif Consensus sequence: CKGGDTBDMMCTG




**Dataset #: 2 Motif ID: 25 Motif name: Arnt**

Original motif Consensus sequence: CACGTG

Reverse complement motif Consensus sequence: CACGTG

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

| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 31 |
| Motif name: | Esrrb |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 1 |
| Number of overlap: | 6 |
| Similarity score: | 0 |

Alignment:

```
CACGTG
CACGTG
```

Original motif Consensus sequence: CACGTG

Reverse complement motif Consensus sequence: CACGTG

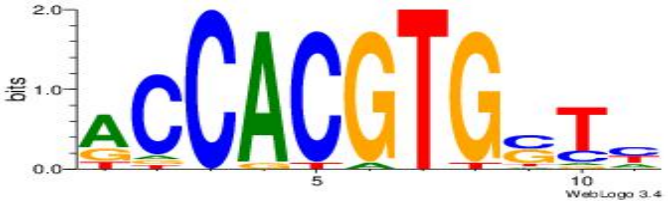
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 39 |
| Motif name: | MYCMAX |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction: | Forward |
| Position number: | 3 |
| Number of overlap: | 6 |
| Similarity score: | 0.0143849 |

Alignment:

```
ACCACGTGSTM
--CACGTG---
```

Original motif Consensus sequence: RASCACGTGGT

Reverse complement motif Consensus sequence: ACCACGTGSTM



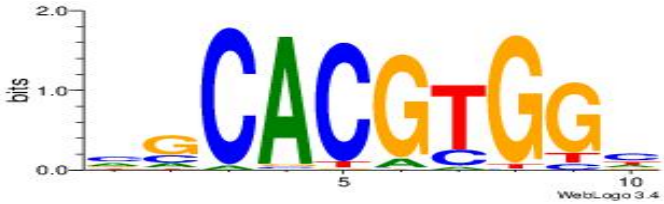

---

| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 38 |
| Motif name: | Myc |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction: | Backward |
| Position number: | 3 |
| Number of overlap: | 6 |

Similarity score: 0.0267529

Alignment:
DCCACGTGCV
--CACGTG--

Original motif Consensus sequence: VGCACGTGGH




Reverse complement motif Consensus sequence: DCCACGTGCV

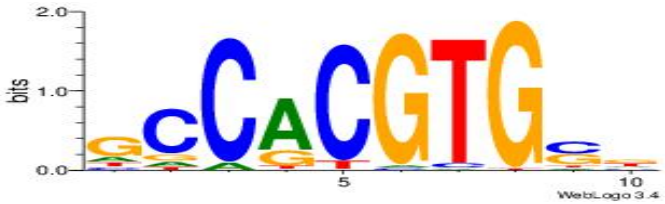
---

Dataset #: 2
Motif ID: 40
Motif name: Mycn
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: 0.0272641

Alignment:
HSCACGTGGC
--CACGTG--

Original motif Consensus sequence: HSCACGTGGC

Reverse complement motif Consensus sequence: GCCACGTGSD




---

| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 33 |
| Motif name: | HIF1AARNT |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 2 |
| Number of overlap: | 6 |
| Similarity score: | 0.0347756 |

Alignment:

```
VBACGTGV
-CACGTG-
```

Original motif Consensus sequence: VBACGTGV

Reverse complement motif Consensus sequence: VCACGTBV

---

| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 26 |

| | |
|---|---|
| Motif name: | ArntAhr |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 1 |
| Number of overlap: | 6 |
| Similarity score: | 0.065625 |

Alignment:

```
YGCGTG
CACGTG
```

Original motif Consensus sequence: YGCGTG

Reverse complement motif Consensus sequence: CACGCM

---

| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 14 |
| Motif name: | ZEB1 |
| 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: | 0.0689533 |

Alignment:
HAGGTG
CACGTG

Original motif Consensus sequence: CACCTD

Reverse complement motif Consensus sequence: HAGGTG

---

| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 28 |
| Motif name: | Egr1 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 1 |
| Number of overlap: | 6 |
| Similarity score: | 0.0784722 |

Alignment:
HGCGTGGGCGK
CACGTG-----

Original motif Consensus sequence: HGCGTGGGCGK

Reverse complement motif Consensus sequence: YCGCCCACGCH

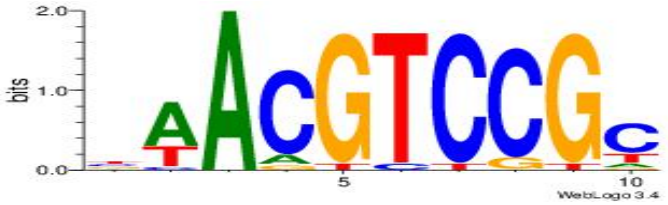
---

| | |
|---|---|
| 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: | 6 |
| Similarity score: | 0.0854167 |

Alignment:

```
BAACGTCCGC
-CACGTG---
```

Original motif Consensus sequence: BAACGTCCGC




Reverse complement motif Consensus sequence: GCGGACGTTV

---

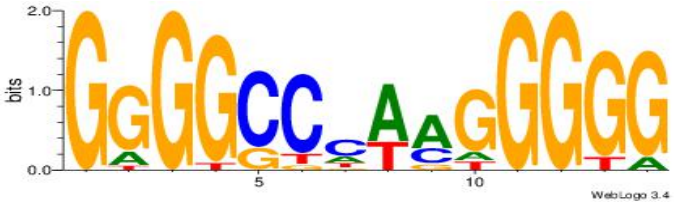
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 21 |

| | |
|---|---|
| Motif name: | PLAG1 |
| 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: | 0.105093 |

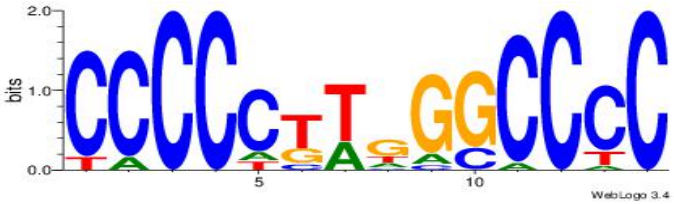
Alignment:

```
GGGGCCCAAGGGGG
------CACGTG--
```

Original motif Consensus sequence: GGGGCCCAAGGGGG




Reverse complement motif Consensus sequence: CCCCCTTGGGCCC




## Best Matches for Each Motif (Highest to Lowest)

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

Original motif Consensus sequence: RGGAAR Reverse complement motif Consensus sequence: MTTCCK

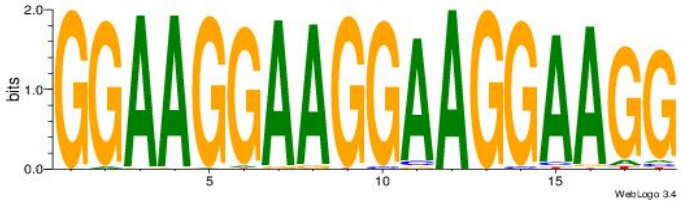
## Best Matches for Motif ID 1 (Highest to Lowest)

| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 32 |
| Motif name: | EWSR1-FLI1 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction: | Backward |
| Position number: | 12 |
| Number of overlap: | 6 |
| Similarity score: | 0.0146511 |

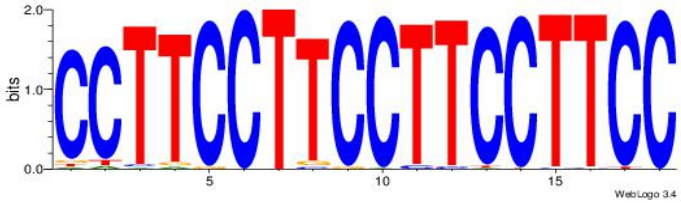
Alignment:

```
CCTTCCTTCCTTCCTTCC
-MTTCCK-----------
```

Original motif Consensus sequence: GGAAGGAAGGAAGGAAGG




Reverse complement motif Consensus sequence: CCTTCCTTCCTTCCTTCC

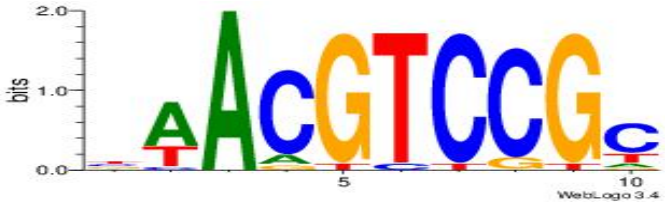


| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 37 |
| Motif name: | MIZF |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 4 |
| Number of overlap: | 6 |
| Similarity score: | 0.0608243 |

Alignment:

```
BAACGTCCGC
---MTTCCK-
```

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
----RGGAAR

Original motif Consensus sequence: BKAGGGGDAD

Reverse complement motif Consensus sequence: BTHCCCCTYB

---

Dataset #: 2
Motif ID: 42
Motif name: NFKB1
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 5
Number of overlap: 6
Similarity score: 0.0757695

Alignment:
GGGGAAKCCCC
-RGGAAR----

Original motif Consensus sequence: GGGGRTTCCCC

Reverse complement motif Consensus sequence: GGGGAAKCCCC

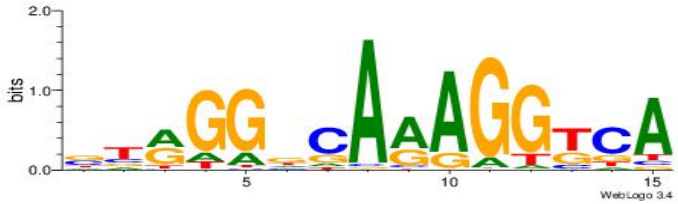
---

| | |
|---|---|
| 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 |

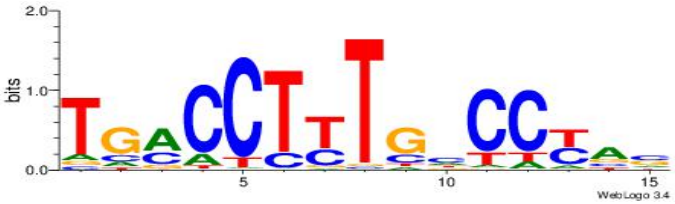
Alignment:

```
BTRGGDCARAGGKCA
---RGGAAR------
```

Original motif Consensus sequence: BTRGGDCARAGGKCA




Reverse complement motif Consensus sequence: TGRCCTKTGHCCK

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| | |
|---|---|
| Dataset #: | 1 |
| Motif ID: | 7 |

| | |
|---|---|
| Motif name: | Motif 7 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Reverse Complement |
| Direction: | Backward |
| Position number: | 3 |
| Number of overlap: | 6 |
| Similarity score: | 0.0827261 |

Alignment:

```
GGGGMGGG
RGGAAR--
```

Original motif Consensus sequence: CCCRCCCC

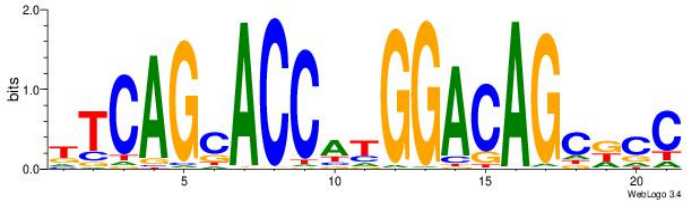
Reverse complement motif Consensus sequence: GGGGMGGG

---

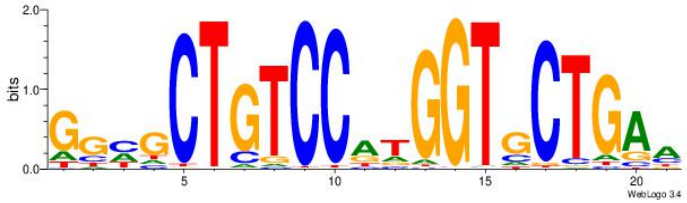
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 19 |
| Motif name: | REST |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 6 |
| Number of overlap: | 6 |
| Similarity score: | 0.0829223 |

Alignment:
TTCAGCACCATGGACAGCKCC
----------RGGAAR-----

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC




Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA

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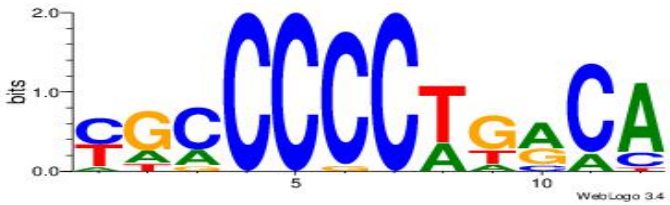
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 35 |
| Motif name: | INSM1 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 7 |
| Number of overlap: | 6 |
| Similarity score: | 0.0832926 |

Alignment:
TGYCAGGGGGCR
------RGGAAR

Original motif Consensus sequence: TGYCAGGGGGCR

Reverse complement motif Consensus sequence: MGCCCCCTGMCA

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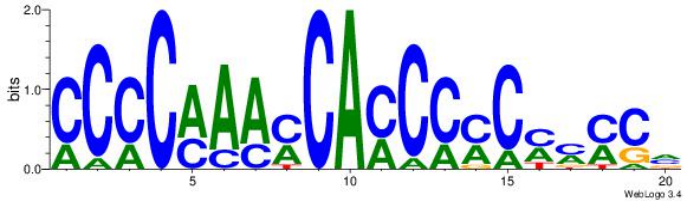
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 18 |
| Motif name: | RREB1 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Reverse Complement |
| Direction: | Forward |
| Position number: | 5 |
| Number of overlap: | 6 |
| Similarity score: | 0.0835516 |

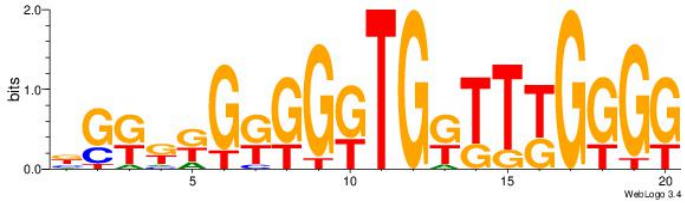
Alignment:

```
BGRRRGRGGRTGRTTYGGGG
----RGGAAR----------
```

Original motif Consensus sequence: CCCCMAAMCAMCCMCMMMCV




Reverse complement motif Consensus sequence: BGRRRGRGGRTGRTTYGGGG

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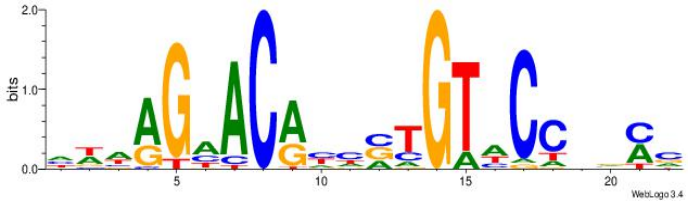
Dataset #: 2

| | |
|---|---|
| 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 |

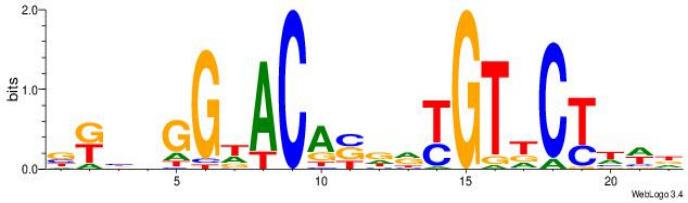
Alignment:

```
HWDAGHACRHHVTGTHCCHVMV
---RGGAAR-------------
```

Original motif Consensus sequence: HWDAGHACRHHVTGTHCCHVMV




Reverse complement motif Consensus sequence: VRVDGGHACAVDDKGTHCTDWH

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| | |
|---|---|
| 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 #: 1 Motif ID: 2 Motif name: Motif 2**

Original motif Consensus sequence: AMACA

Reverse complement motif Consensus sequence: TGTRT

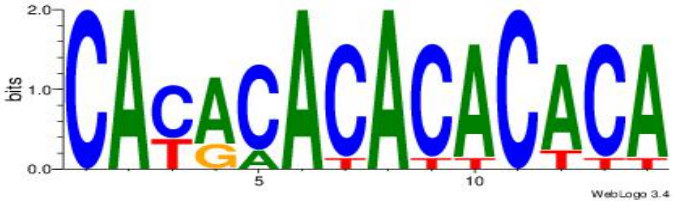
**Best Matches for Motif ID 2 (Highest to Lowest)**

| | |
|---|---|
| Dataset #: | 1 |
| Motif ID: | 11 |
| Motif name: | Motif 11 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction: | Forward |

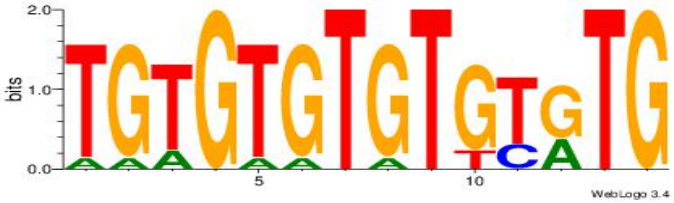
Position number: 5
Number of overlap: 5
Similarity score: 0

Alignment:
TGTGTGTGTGTKTG
----TGTRT-----

Original motif Consensus sequence: CAYACACACACACA




Reverse complement motif Consensus sequence: TGTGTGTGTGTKT



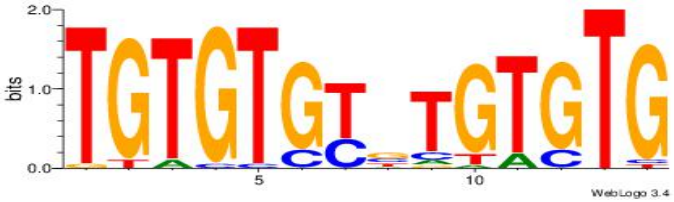

---

Dataset #: 1
Motif ID: 9
Motif name: Motif 9
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 10
Number of overlap: 5
Similarity score: 0.0040753

Alignment:
CACACAVRCACACA
---------AMACA

Original motif Consensus sequence: CACACAVRCACACA

Reverse complement motif Consensus sequence: TGTGTGKVTGTGT

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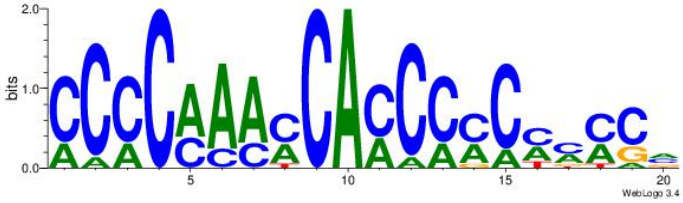
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 18 |
| Motif name: | RREB1 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 11 |
| Number of overlap: | 5 |
| Similarity score: | 0.0243918 |

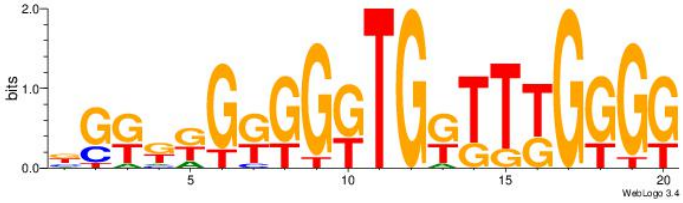
Alignment:

```
CCCCMAAMCAMCCMCMMMCV
-----AMACA----------
```

Original motif Consensus sequence: CCCCMAAMCAMCCMCMMMCV




Reverse complement motif Consensus sequence: BGRRRGRGGRTGRTTYGGGG

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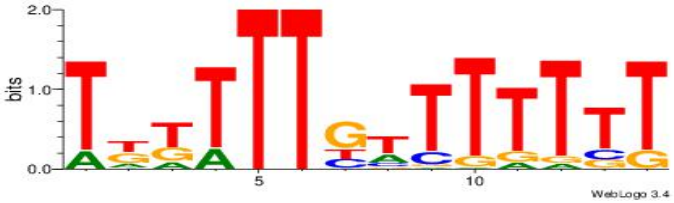
Dataset #: 1

| | |
|---|---|
| Motif ID: | 10 |
| Motif name: | Motif 10 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Reverse Complement |
| Direction: | Backward |
| Position number: | 6 |
| Number of overlap: | 5 |
| Similarity score: | 0.0394919 |

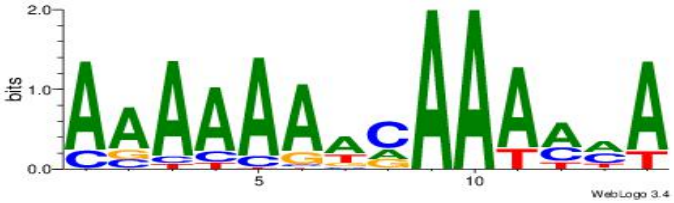
Alignment:

```
AAAAAAACAAARRA
----AMACA-----
```

Original motif Consensus sequence: TKKTTTGTTTTTTT




Reverse complement motif Consensus sequence: AAAAAAACAAARR

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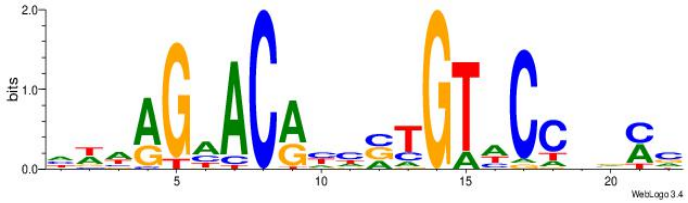
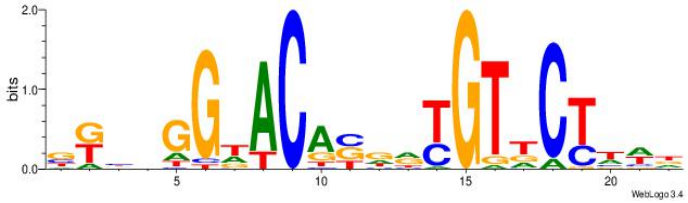
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 24 |
| Motif name: | Ar |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 5 |
| Number of overlap: | 5 |
| Similarity score: | 0.0429089 |

Alignment:
HWDAGHACRHHVTGTHCCHVMV
----AMACA----------

Original motif Consensus sequence: HWDAGHACRHHVTGTHCCHVMV




Reverse complement motif Consensus sequence: VRVDGGHACAVDDKGTHCTDWH

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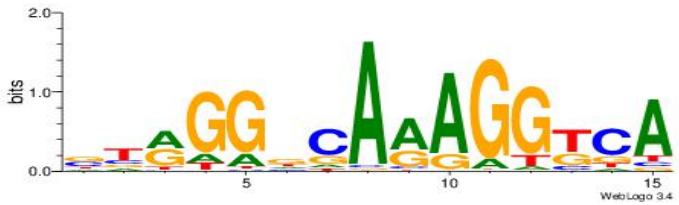
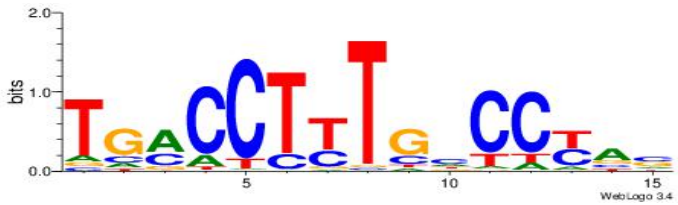
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 20 |
| Motif name: | PPARGRXRA |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction: | Backward |
| Position number: | 6 |
| Number of overlap: | 5 |
| Similarity score: | 0.0595073 |

Alignment:
TGRCCTKTGHCCKAB
-----TGTRT-----

Original motif Consensus sequence: BTRGGDCARAGGKCA

Reverse complement motif Consensus sequence: TGRCCTKTGHCCK

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| | |
|---|---|
| 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

---

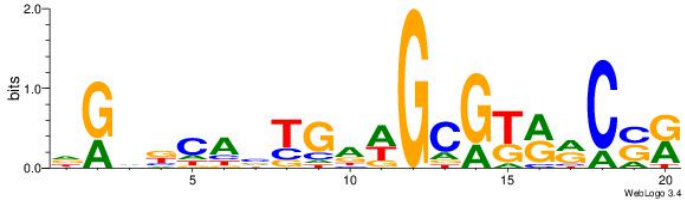
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 45 |

| | |
|---|---|
| Motif name: | Pax5 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Reverse Complement |
| Direction: | Forward |
| Position number: | 6 |
| Number of overlap: | 5 |
| Similarity score: | 0.0620995 |

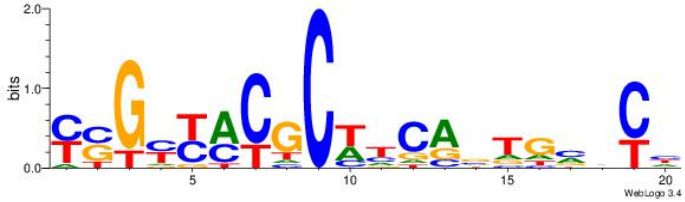
Alignment:

```
MSGKKRCGCWDCABTGBBCD
-----AMACA----------
```

Original motif Consensus sequence: DGVBCABTGDWGCGKRRCSR




Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD

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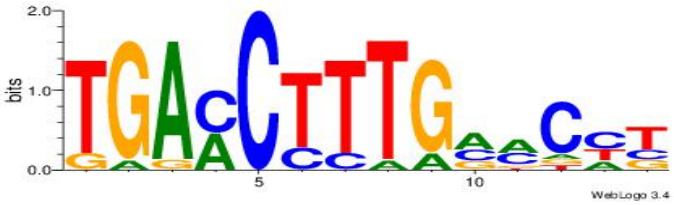
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 22 |
| Motif name: | NR2F1 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Reverse Complement |
| Direction: | Forward |
| Position number: | 7 |
| Number of overlap: | 5 |
| Similarity score: | 0.0650242 |

Alignment:
AKGYYCAAAGRTCA
------AMACA---

Original motif Consensus sequence: TGAMCTTTGMMCYT




Reverse complement motif Consensus sequence: AKGYYCAAAGRTCA

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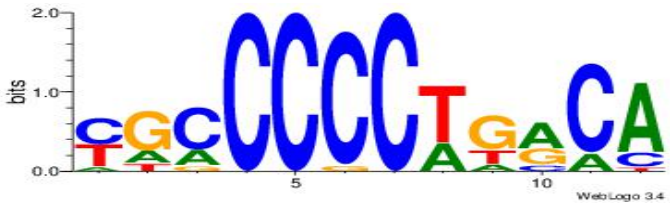
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 35 |
| Motif name: | INSM1 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 8 |
| Number of overlap: | 5 |
| Similarity score: | 0.0670984 |

Alignment:
TGYCAGGGGGCR
TGTRT-------

Original motif Consensus sequence: TGYCAGGGGGCR

Reverse complement motif Consensus sequence: MGCCCCCTGMCA




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

Original motif Consensus sequence: AGSCWGG

Reverse complement motif Consensus sequence: CCWGSCT

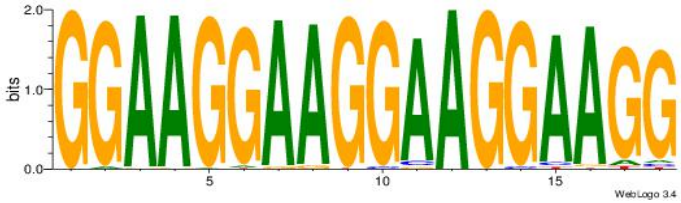
**Best Matches for Motif ID 3 (Highest to Lowest)**

| | |
|---|---|
| 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 |

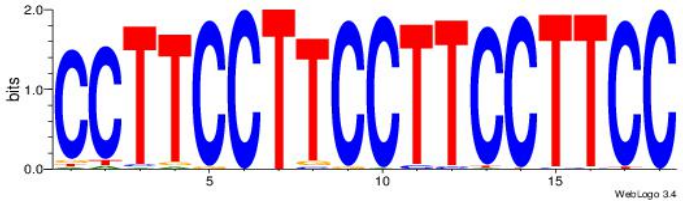
Alignment:

```
GGAAGGAAGGAAGGAAGG
-------AGSCWGG----
```

Original motif Consensus sequence: GGAAGGAAGGAAGGAAGG




Reverse complement motif Consensus sequence: CCTTCCTTCCTTCCTTCC

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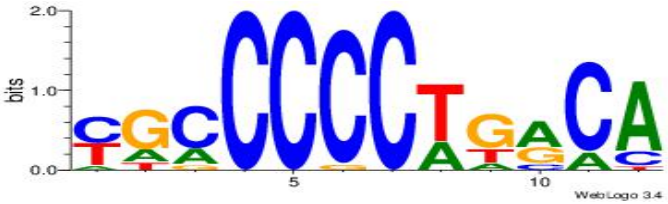
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 35 |
| Motif name: | INSM1 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction: | Backward |
| Position number: | 1 |
| Number of overlap: | 7 |
| Similarity score: | 0.0494688 |

Alignment:

```
MGCCCCCTGMCA
-----CCWGSCT
```

Original motif Consensus sequence: TGYCAGGGGGCR

Reverse complement motif Consensus sequence: MGCCCCCTGMCA

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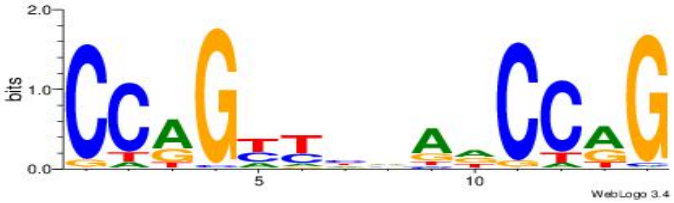
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 48 |
| Motif name: | Tcfcp2l1 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 1 |
| Number of overlap: | 7 |
| Similarity score: | 0.0669354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

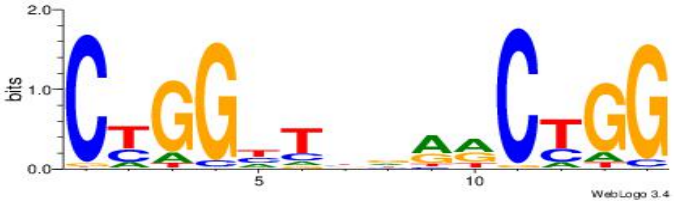
Alignment:

```
CCAGYYHVADCCRG
CCWGSCT-------
```

Original motif Consensus sequence: CCAGYYHVADCCRG




Reverse complement motif Consensus sequence: CKGGDTBDMMCT

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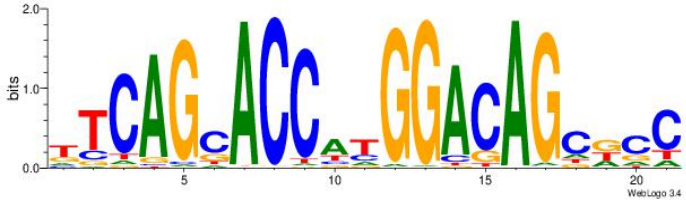
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 19 |
| Motif name: | REST |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 7 |
| Number of overlap: | 7 |

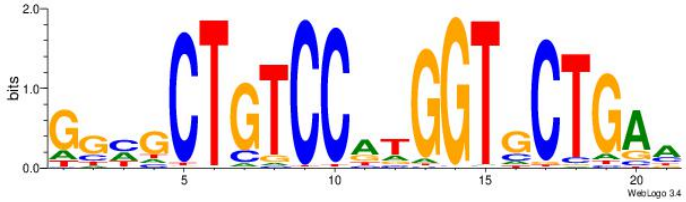
Similarity score: 0.0693747

Alignment:
TTCAGCACCATGGACAGCKCC
------AGSCWGG--------

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC




Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA



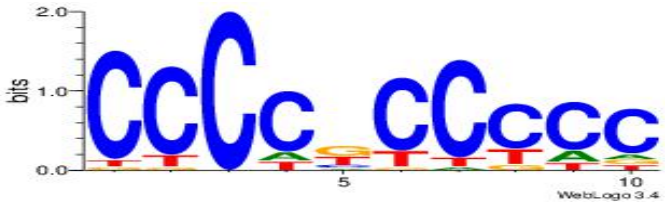

---

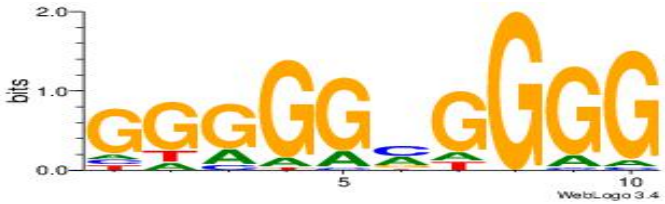
Dataset #: 2
Motif ID: 16
Motif name: SP1
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 3
Number of overlap: 7
Similarity score: 0.0695377

Alignment:
CCCCKCCCCC
-CCWGSCT--

Original motif Consensus sequence: CCCCKCCCCC

Reverse complement motif Consensus sequence: GGGGGYGGGG

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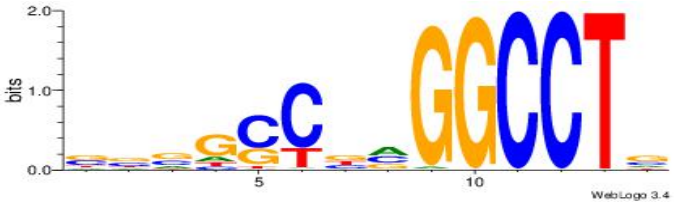
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 12 |
| Motif name: | Zfx |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 7 |
| Number of overlap: | 7 |
| Similarity score: | 0.0720685 |

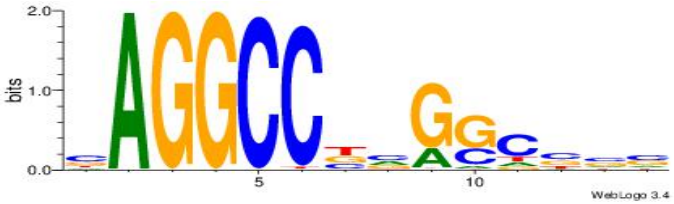
Alignment:

```
BBVGCCBVGGCCTV
------CCWGSCT-
```

Original motif Consensus sequence: BBVGCCBVGGCCTV




Reverse complement motif Consensus sequence: VAGGCCBBGGCVB

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| | |
|---|---|
| Dataset #: | 1 |
| Motif ID: | 7 |

| | |
|---|---|
| Motif name: | Motif 7 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 2 |
| Number of overlap: | 7 |
| Similarity score: | 0.0742342 |

Alignment:

```
CCCRCCCC
CCWGSCT-
```

Original motif Consensus sequence: CCCRCCCC

Reverse complement motif Consensus sequence: GGGGMGGG

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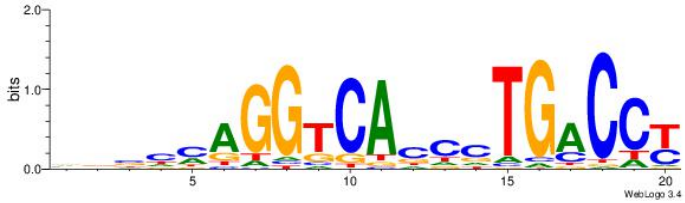
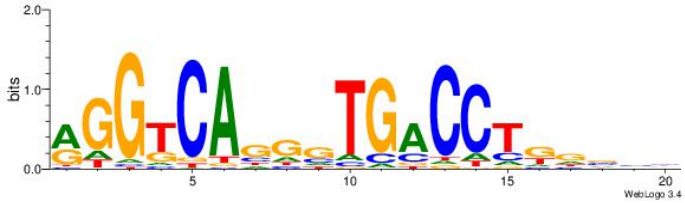
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 29 |
| Motif name: | ESR1 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction: | Backward |
| Position number: | 2 |
| Number of overlap: | 7 |
| Similarity score: | 0.0771405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

Alignment:
MGGTCAGGGTGACCTRDBHV
----------CCWGSCT-

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY




Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV

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| | |
|---|---|
| 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

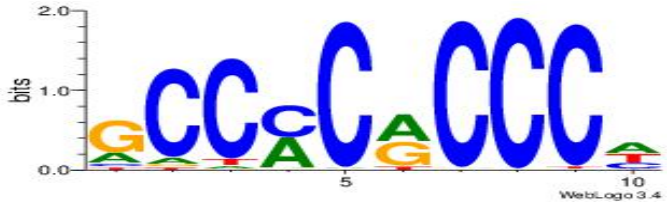
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 36 |
| Motif name: | Klf4 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction: | Backward |
| Position number: | 1 |
| Number of overlap: | 7 |
| Similarity score: | 0.0798994 |

Alignment:

```
GCCYCMCCCD
---CCWGSCT
```

Original motif Consensus sequence: DGGGYGKGGC

Reverse complement motif Consensus sequence: GCCYCMCCCD




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

Original motif Consensus sequence: CTCTGY

Reverse complement motif Consensus sequence: KCAGAG

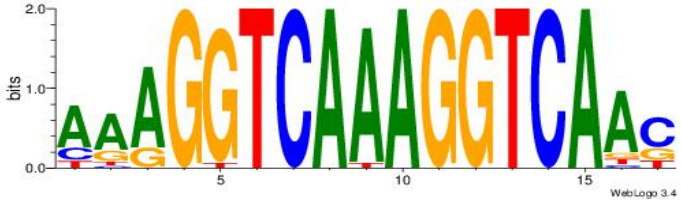
## Best Matches for Motif ID 4 (Highest to Lowest)

| | |
|---|---|
| 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 |

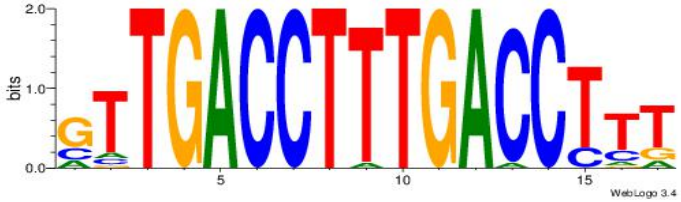
Alignment:

```
AAAGGTCAAAGGTCAAC
-----KCAGAG------
```

Original motif Consensus sequence: AAAGGTCAAAGGTCAAC




Reverse complement motif Consensus sequence: GTTGACCTTTGACCTTT

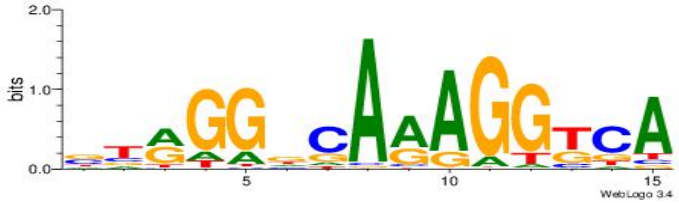


| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 20 |
| Motif name: | PPARGRXRA |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 5 |
| Number of overlap: | 6 |
| Similarity score: | 0.0140102 |

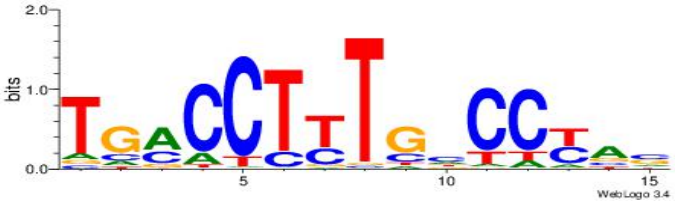
Alignment:

```
BTRGGDCARAGGKCA
-----KCAGAG----
```

Original motif Consensus sequence: BTRGGDCARAGGKCA




Reverse complement motif Consensus sequence: TGRCCTKTGHCCK

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

Alignment:
AKGYYCAAAGRTCA
----KCAGAG----

Original motif Consensus sequence: TGAMCTTTGMMCYT

Reverse complement motif Consensus sequence: AKGYYCAAAGRTCA

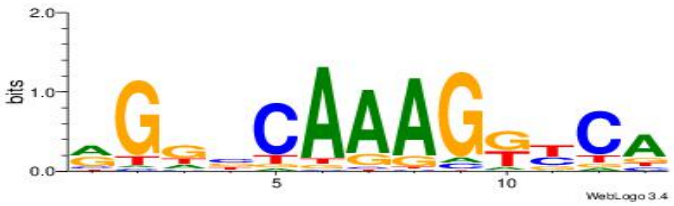
---

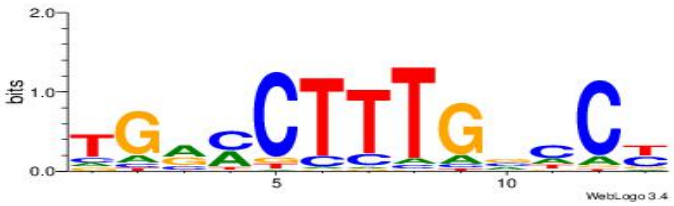
Dataset #: 2
Motif ID: 34
Motif name: HNF4A
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 4
Number of overlap: 6
Similarity score: 0.020602

Alignment:
RGGBCAAAGKYCA
---KCAGAG----

Original motif Consensus sequence: RGGBCAAAGKYCA

Reverse complement motif Consensus sequence: TGMYCTTTGBCCK

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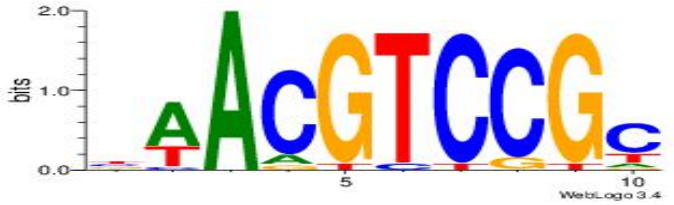
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 37 |
| Motif name: | MIZF |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 5 |
| Number of overlap: | 6 |
| Similarity score: | 0.0221665 |

Alignment:

```
BAACGTCCGC
----CTCTGY
```

Original motif Consensus sequence: BAACGTCCGC




Reverse complement motif Consensus sequence: GCGGACGTTV

---

| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 35 |

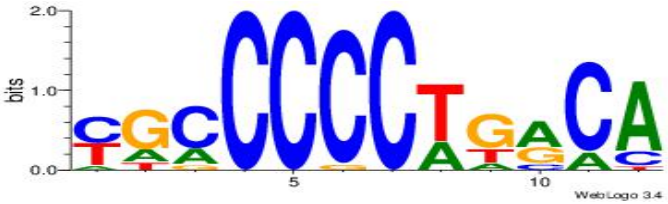
| | |
|---|---|
| Motif name: | INSM1 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 3 |
| Number of overlap: | 6 |
| Similarity score: | 0.0255256 |

Alignment:

```
TGYCAGGGGGCR
--KCAGAG----
```

Original motif Consensus sequence: TGYCAGGGGGCR

Reverse complement motif Consensus sequence: MGCCCCCTGMCA

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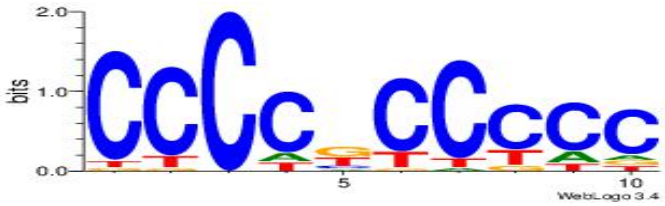
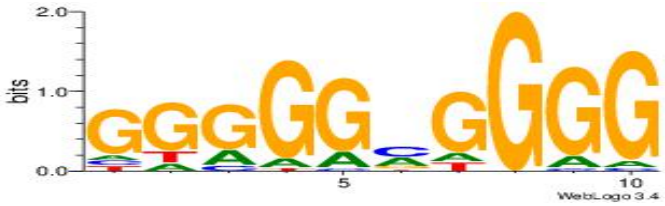
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 16 |
| Motif name: | SP1 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 5 |
| Number of overlap: | 6 |
| Similarity score: | 0.0349642 |

Alignment:
CCCCKCCCCC
CTCTGY----

Original motif Consensus sequence: CCCCKCCCCC




Reverse complement motif Consensus sequence: GGGGGYGGGG

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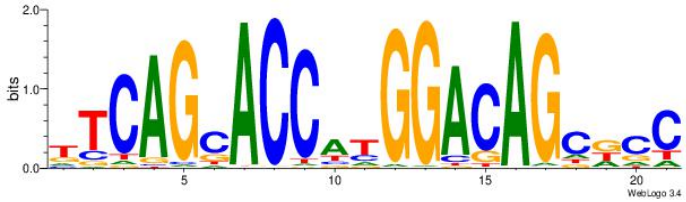
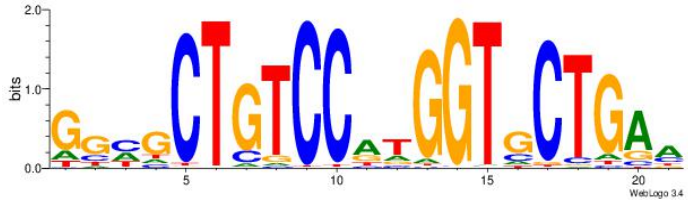
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 19 |
| Motif name: | REST |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Reverse Complement |
| Direction: | Forward |
| Position number: | 3 |
| Number of overlap: | 6 |
| Similarity score: | 0.0376108 |

Alignment:
GGYGCTGTCCATGGTGCTGAA
--CTCTGY----------

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC

Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA

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| | |
|---|---|
| Dataset #: | 1 |
| Motif ID: | 8 |
| Motif name: | Motif 8 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction: | Backward |
| Position number: | 1 |
| Number of overlap: | 6 |
| Similarity score: | 0.0446026 |

Alignment:

```
TCCCAG
KCAGAG
```

Original motif Consensus sequence: CTGGGA

Reverse complement motif Consensus sequence: TCCCAG

---

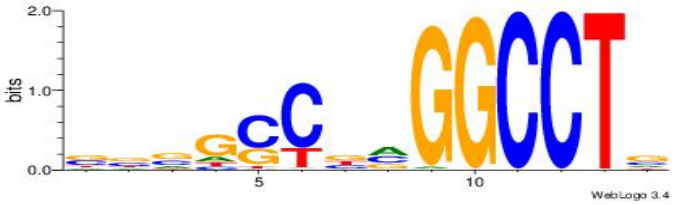
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 12 |

| | |
|---|---|
| Motif name: | Zfx |
| 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: | 0.0448449 |

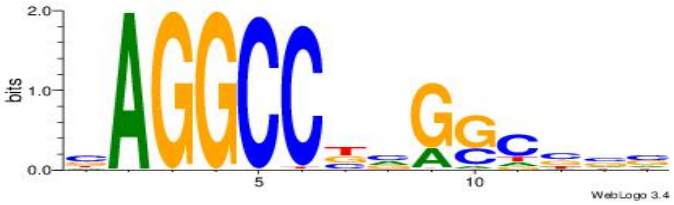
Alignment:

```
BBVGCCBVGGCCTV
---KCAGAG-----
```

Original motif Consensus sequence: BBVGCCBVGGCCTV




Reverse complement motif Consensus sequence: VAGGCCBBGGCVB




---

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

Original motif Consensus sequence: ATKTM

Reverse complement motif Consensus sequence: RARAT

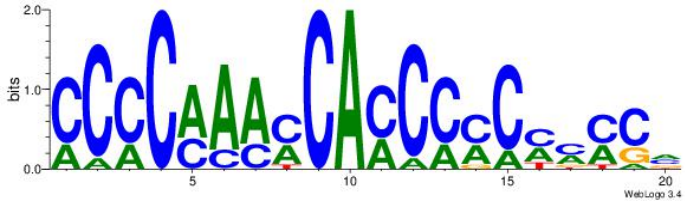
**Best Matches for Motif ID 5 (Highest to Lowest)**

| | |
|---|---|
| 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 |

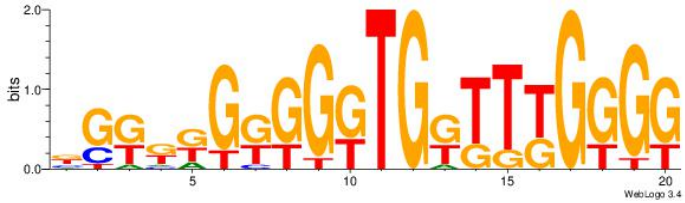
Alignment:

```
BGRRRGRGGRTGRTTYGGGG
------RARAT---------
```

Original motif Consensus sequence: CCCCMAAMCAMCCMCMMMCV




Reverse complement motif Consensus sequence: BGRRRGRGGRTGRTTYGGGG



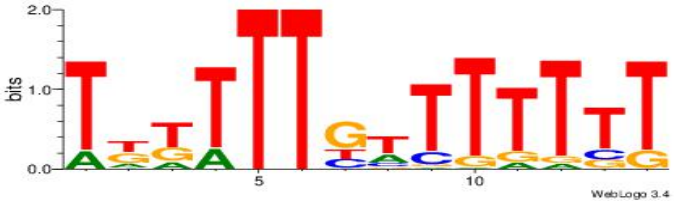

---

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

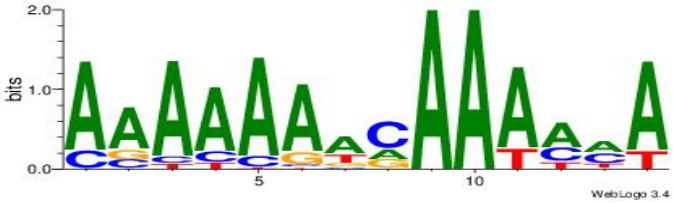
Number of overlap: 5
Similarity score: 0.0260117

Alignment:
AAAAAAACAAARRA
-RARAT--------

Original motif Consensus sequence: TKKTTTGTTTTTTT




Reverse complement motif Consensus sequence: AAAAAAACAAARR




---

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:

```
AKGYYCAAAGRTCA
-------RARAT--
```

Original motif Consensus sequence: TGAMCTTTGMMCYT

Reverse complement motif Consensus sequence: AKGYYCAAAGRTCA

---

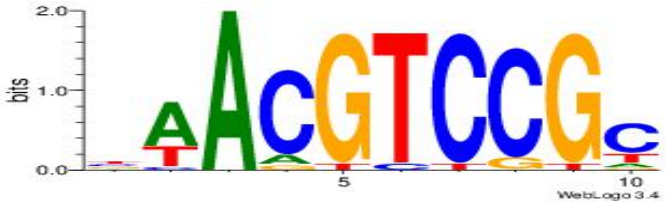
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 37 |

| | |
|---|---|
| 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



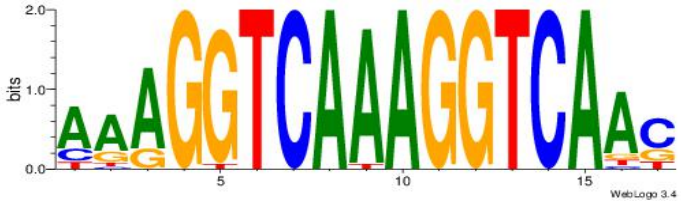

Reverse complement motif Consensus sequence: GCGGACGTTV

---

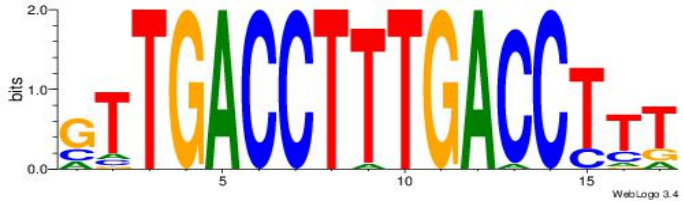
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 43 |
| Motif name: | NR1H2RXRA |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 10 |
| Number of overlap: | 5 |
| Similarity score: | 0.0292478 |

Alignment:
AAAGGTCAAAGGTCAAC
---------ATKTM---

Original motif Consensus sequence: AAAGGTCAAAGGTCAAC




Reverse complement motif Consensus sequence: GTTGACCTTTGACCTTT

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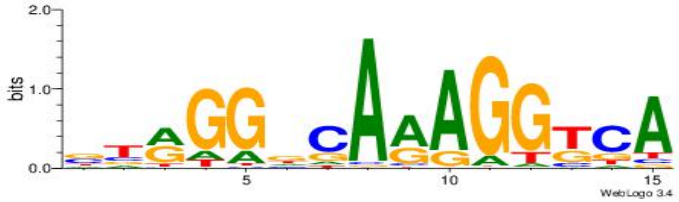
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 20 |
| Motif name: | PPARGRXRA |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Reverse Complement |
| Direction: | Forward |
| Position number: | 5 |
| Number of overlap: | 5 |
| Similarity score: | 0.0305369 |

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

Original motif Consensus sequence: BTRGGDCARAGGKCA

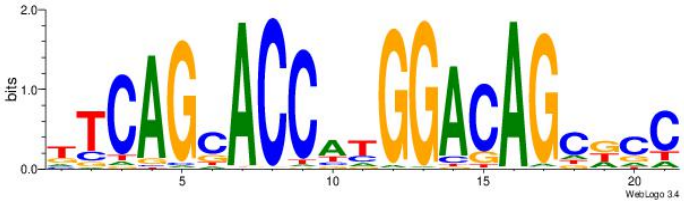
Reverse complement motif Consensus sequence: TGRCCTKTGHCCK



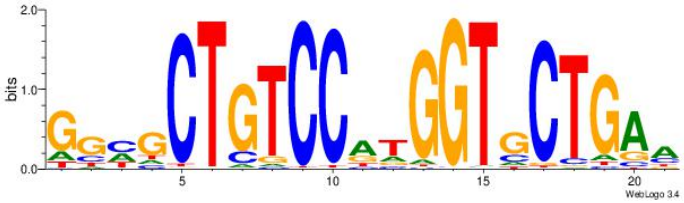
Dataset #: 2
Motif ID: 19
Motif name: REST
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 5
Number of overlap: 5
Similarity score: 0.0315454

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

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC




Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA



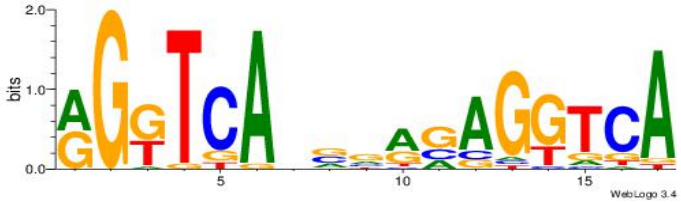

Dataset #: 2

| | |
|---|---|
| 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 |

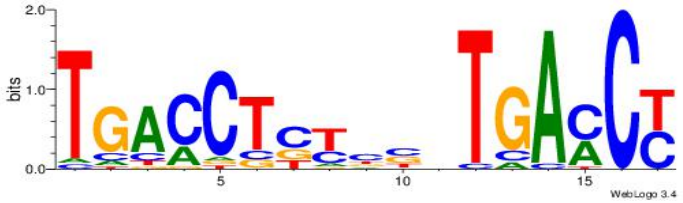
Alignment:

```
RGKTCABVVRGAGGTCA
ATKTM------------
```

Original motif Consensus sequence: RGKTCABVVRGAGGTCA




Reverse complement motif Consensus sequence: TGACCTCKVVBTGAYCK

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| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 46 |
| Motif name: | RORA_1 |
| 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: 0.0336052

Alignment:
AWVDAGGTCA
---RARAT--

Original motif Consensus sequence: AWVDAGGTCA

Reverse complement motif Consensus sequence: TGACCTDVWT

---

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

Original motif Consensus sequence: CMGCRGC

Reverse complement motif Consensus sequence: GCKGCYG

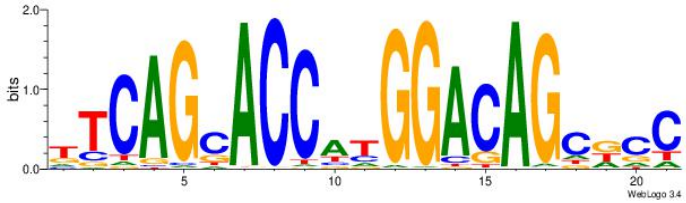
**Best Matches for Motif ID 6 (Highest to Lowest)**

| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 19 |
| Motif name: | REST |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction: | Forward |

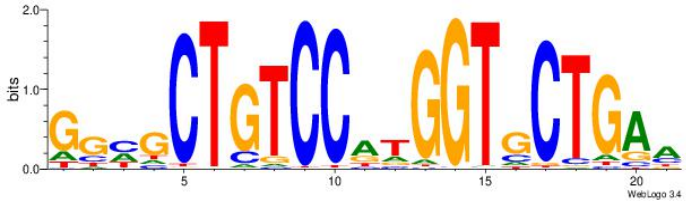
Position number: 13
Number of overlap: 7
Similarity score: 0.0205607

Alignment:
GGYGCTGTCCATGGTGCTGAA
----------GCKGCYG--

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC




Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA

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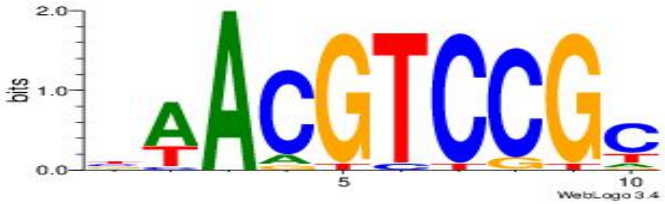
Dataset #: 2
Motif ID: 37
Motif name: MIZF
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 7
Similarity score: 0.0322623

Alignment:
GCGGACGTTV
GCKGCYG---

Original motif Consensus sequence: BAACGTCCGC




Reverse complement motif Consensus sequence: GCGGACGTTV

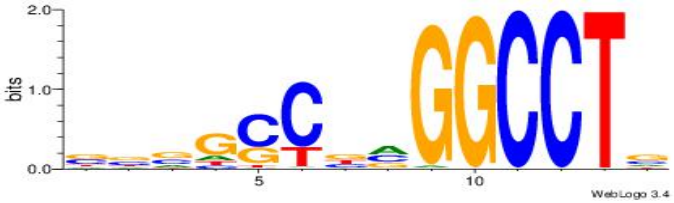
---

| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 12 |
| Motif name: | Zfx |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 4 |
| Number of overlap: | 7 |
| Similarity score: | 0.038091 |

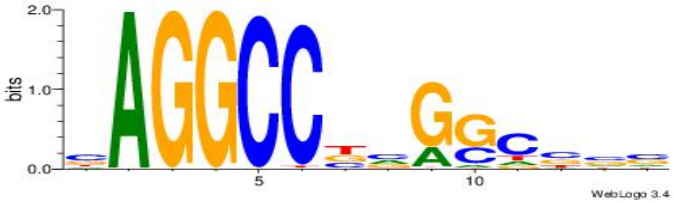
Alignment:

```
BBVGCCBVGGCCTV
----CMGCRGC---
```

Original motif Consensus sequence: BBVGCCBVGGCCTV




Reverse complement motif Consensus sequence: VAGGCCBBGGCVB

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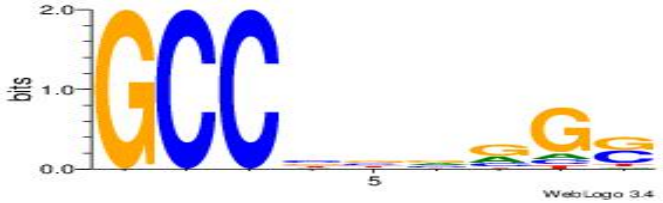
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 15 |
| Motif name: | TFAP2A |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Reverse Complement |
| Direction: | Forward |
| Position number: | 3 |
| Number of overlap: | 7 |
| Similarity score: | 0.0393168 |

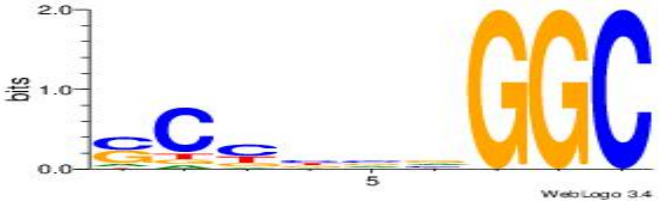
Alignment:

```
SCMVBBGGC
--CMGCRGC
```

Original motif Consensus sequence: GCCBBVRGS




Reverse complement motif Consensus sequence: SCMVBBGGC

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| | |
|---|---|
| Dataset #: | 1 |
| Motif ID: | 7 |
| Motif name: | Motif 7 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 2 |
| Number of overlap: | 7 |

Similarity score: 0.0443244

Alignment:
CCCRCCCC
-CMGCRGC

Original motif Consensus sequence: CCCRCCCC

Reverse complement motif Consensus sequence: GGGGMGGG

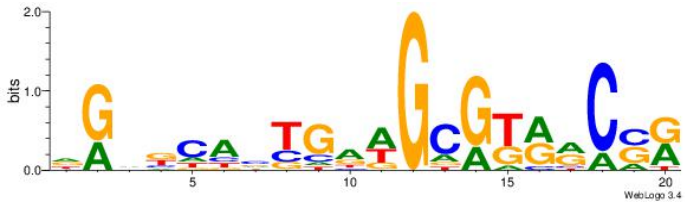
---

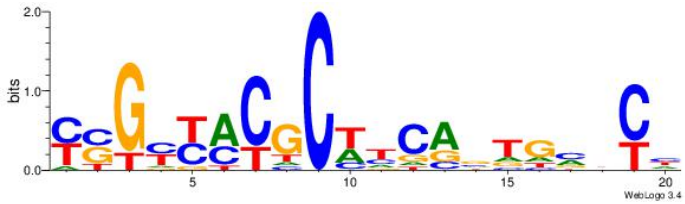
Dataset #: 2
Motif ID: 45
Motif name: Pax5
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 7
Number of overlap: 7
Similarity score: 0.0448462

Alignment:
MSGKKRCGCWDCABTGBBCD
-------GCKGCYG------

Original motif Consensus sequence: DGVBCABTGDWGCGKRRCSR

Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD

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| | |
|---|---|
| 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
---GCKGCYG-
```

Original motif Consensus sequence: HGCGTGGGCGK

Reverse complement motif Consensus sequence: YCGCCCACGCH

---

| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 36 |

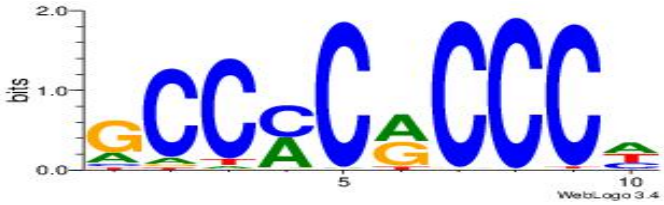
| | |
|---|---|
| Motif name: | Klf4 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Reverse Complement |
| Direction: | Forward |
| Position number: | 2 |
| Number of overlap: | 7 |
| Similarity score: | 0.0476958 |

Alignment:

```
GCCYCMCCCD
-CMGCRGC--
```

Original motif Consensus sequence: DGGGYGKGGC

Reverse complement motif Consensus sequence: GCCYCMCCCD

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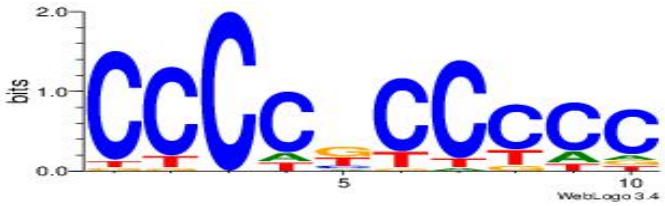
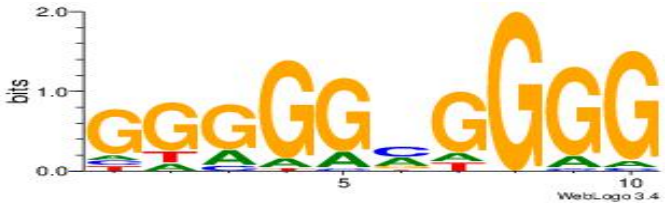
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 16 |
| Motif name: | SP1 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction: | Forward |
| Position number: | 1 |
| Number of overlap: | 7 |
| Similarity score: | 0.0490991 |

Alignment:
GGGGGYGGGG
GCKGCYG---

Original motif Consensus sequence: CCCCKCCCCC




Reverse complement motif Consensus sequence: GGGGGYGGGG

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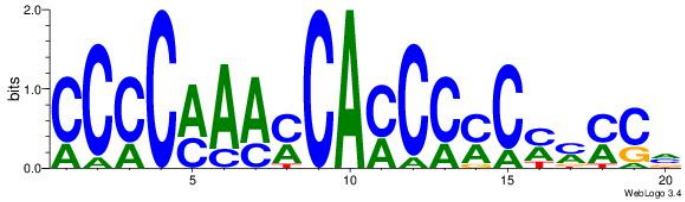
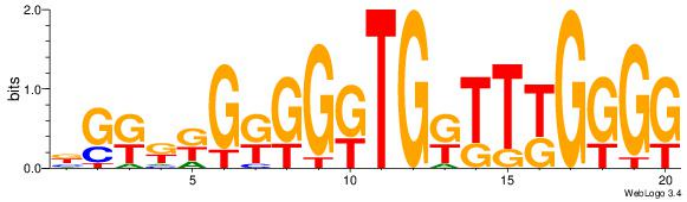
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 18 |
| Motif name: | RREB1 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction: | Forward |
| Position number: | 6 |
| Number of overlap: | 7 |
| Similarity score: | 0.0498726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

Alignment:
BGRRRGRGGRTGRTTYGGGG
-----GCKGCYG--------

Original motif Consensus sequence: CCCCMAAMCAMCCMCMMMCV

Reverse complement motif Consensus sequence: BGRRRGRGGRTGRTTYGGGG




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

Original motif Consensus sequence: CCCRCCCC

Reverse complement motif Consensus sequence: GGGGMGGG

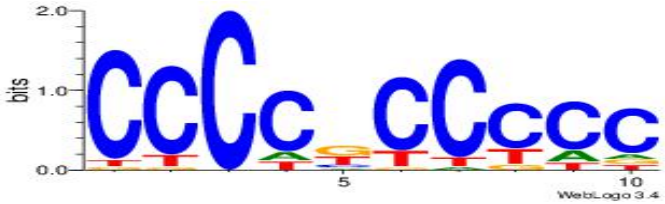
## Best Matches for Motif ID 7 (Highest to Lowest)

| | |
|---|---|
| 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 |

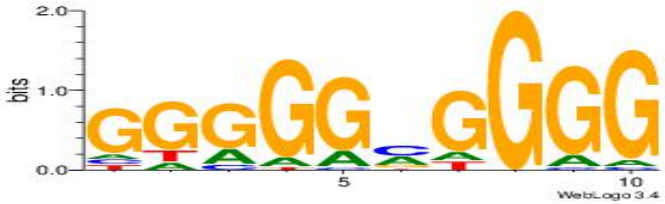
Alignment:

```
CCCCKCCCCC
-CCCRCCCC-
```

Original motif Consensus sequence: CCCCKCCCCC




Reverse complement motif Consensus sequence: GGGGGYGGGG

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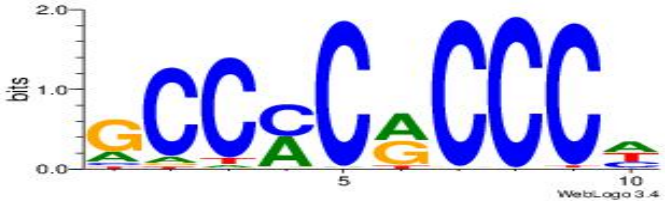
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 36 |
| Motif name: | Klf4 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 1 |
| Number of overlap: | 8 |
| Similarity score: | 0.0461644 |

Alignment:

```
DGGGYGKGGC
GGGGMGGG--
```

Original motif Consensus sequence: DGGGYGKGGC

Reverse complement motif Consensus sequence: GCCYCMCCCD

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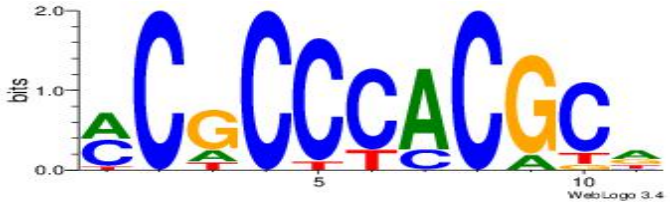
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 28 |
| Motif name: | Egr1 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Reverse Complement |
| Direction: | Forward |
| Position number: | 4 |
| Number of overlap: | 8 |
| Similarity score: | 0.0650374 |

Alignment:

```
YCGCCCACGCH
---CCCRCCCC
```

Original motif Consensus sequence: HGCGTGGGCGK

Reverse complement motif Consensus sequence: YCGCCCACGCH

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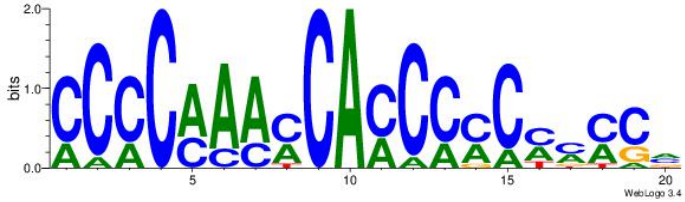
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 18 |
| Motif name: | RREB1 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 2 |
| Number of overlap: | 8 |

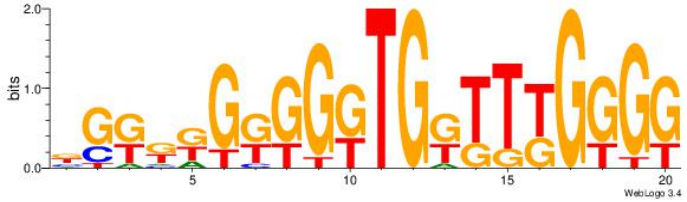
Similarity score: 0.076401

Alignment:
CCCCMAAMCAMCCMCMMMCV
-CCCRCCCC----------

Original motif Consensus sequence: CCCCMAAMCAMCCMCMMMCV




Reverse complement motif Consensus sequence: BGRRRGRGGRTGRTTYGGGG

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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
GGGGMGGG---

Original motif Consensus sequence: GGGGRTTCCCC

Reverse complement motif Consensus sequence: GGGGAAKCCCC

---

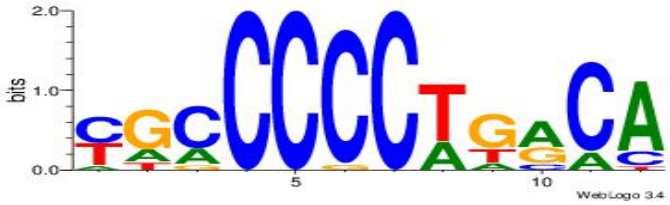
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 35 |
| Motif name: | INSM1 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 1 |
| Number of overlap: | 8 |
| Similarity score: | 0.0936832 |

Alignment:

```
TGYCAGGGGGCR
GGGGMGGG----
```

Original motif Consensus sequence: TGYCAGGGGGCR

Reverse complement motif Consensus sequence: MGCCCCCTGMCA




---

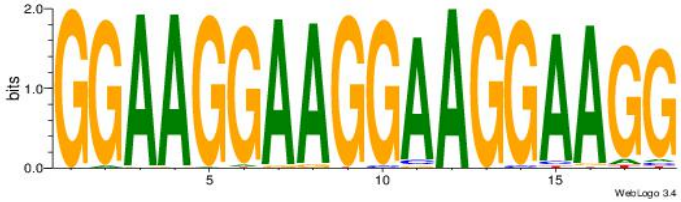
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 32 |

| | |
|---|---|
| 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 |

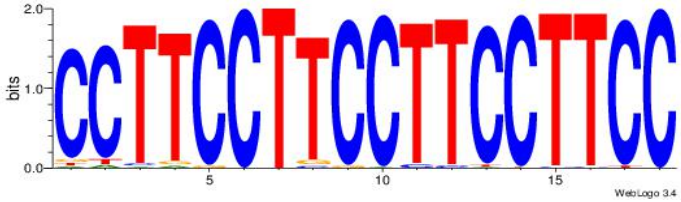
Alignment:

```
GGAAGGAAGGAAGGAAGG
------GGGGMGGG----
```

Original motif Consensus sequence: GGAAGGAAGGAAGGAAGG




Reverse complement motif Consensus sequence: CCTTCCTTCCTTCCTTCC

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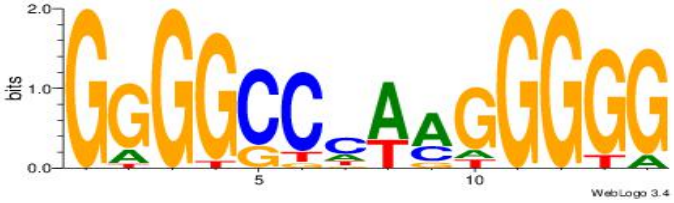
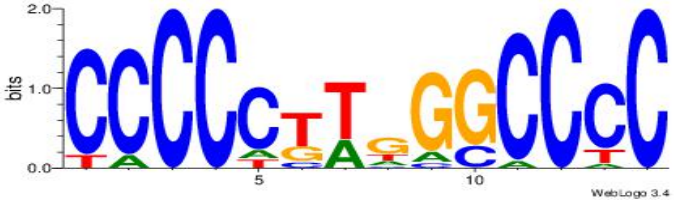
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 21 |
| Motif name: | PLAG1 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 1 |
| Number of overlap: | 8 |
| Similarity score: | 0.0998932 |

Alignment:
GGGGCCCAAGGGGG
GGGGMGGG------

Original motif Consensus sequence: GGGGCCCAAGGGGG




Reverse complement motif Consensus sequence: CCCCCTTGGGCCC

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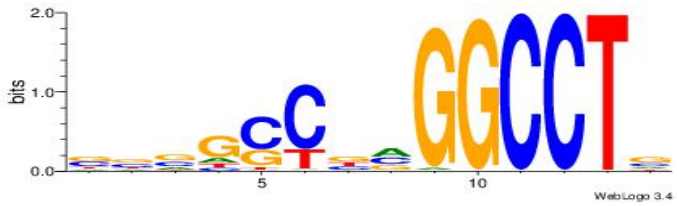
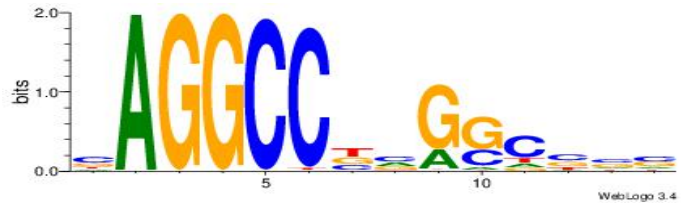
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 12 |
| Motif name: | Zfx |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 5 |
| Number of overlap: | 8 |
| Similarity score: | 0.10221 |

Alignment:
BBVGCCBVGGCCTV
----CCCRCCCC--

Original motif Consensus sequence: BBVGCCBVGGCCTV

Reverse complement motif Consensus sequence: VAGGCCBBGGCVE



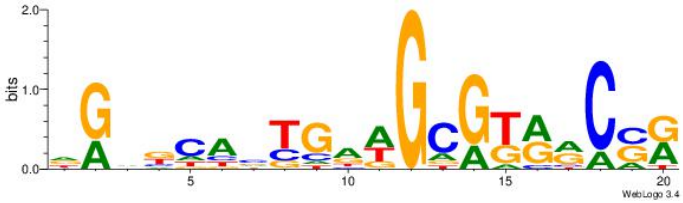




| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 45 |
| Motif name: | Pax5 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 5 |
| Number of overlap: | 8 |
| Similarity score: | 0.102497 |

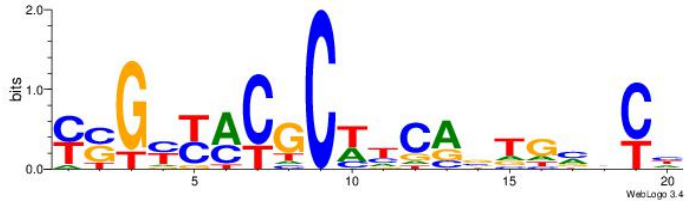
Alignment:

```
DGVBCABTGDWGCGKRRCSR
--------GGGGMGGG----
```

Original motif Consensus sequence: DGVBCABTGDWGCGKRRCSR




Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD




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

Original motif Consensus sequence: CTGGGA

Reverse complement motif Consensus sequence: TCCCAG

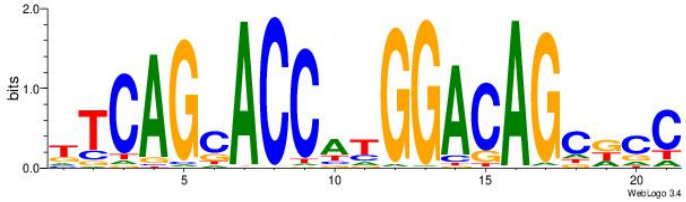
## Best Matches for Motif ID 8 (Highest to Lowest)

| | |
|---|---|
| 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 |

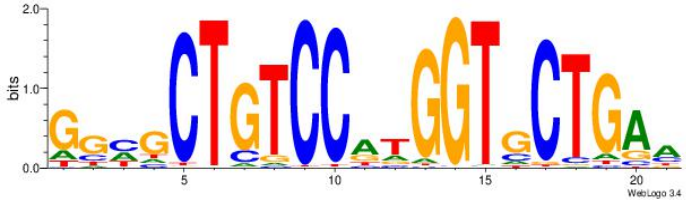
Alignment:

```
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

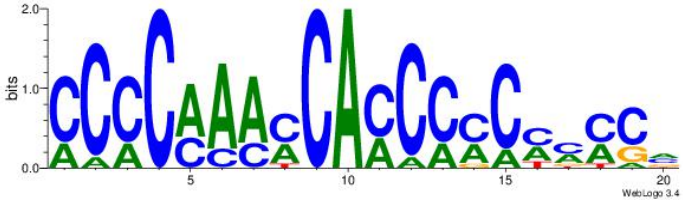
---

| | |
|---|---|
| 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 |

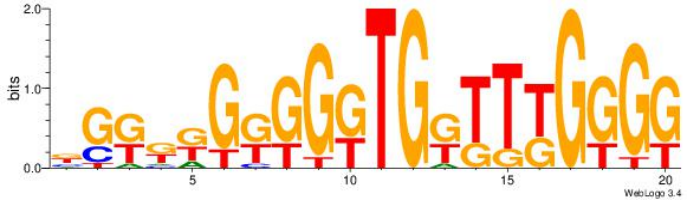
Similarity score: 0.0509122

Alignment:
BGRRRGRGGRTGRTTYGGGG
----------CTGGGA

Original motif Consensus sequence: CCCCMAAMCAMCCMCMMMCV




Reverse complement motif Consensus sequence: BGRRRGRGGRTGRTTYGGGG

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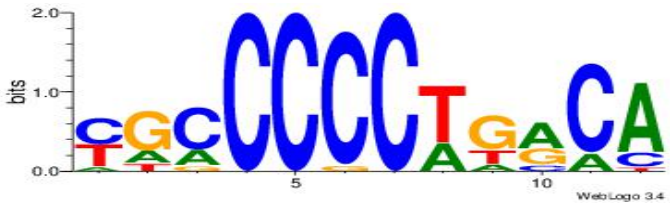
Dataset #: 2
Motif ID: 35
Motif name: INSM1
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 4
Number of overlap: 6
Similarity score: 0.0557857

Alignment:
TGYCAGGGGGCR
---CTGGGA---

Original motif Consensus sequence: TGYCAGGGGGCR

Reverse complement motif Consensus sequence: MGCCCCCTGMCA

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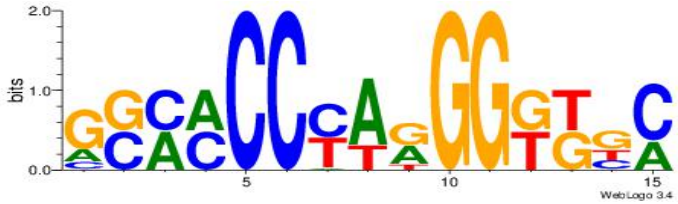
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 13 |
| Motif name: | Zfp423 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction: | Backward |
| Position number: | 7 |
| Number of overlap: | 6 |
| Similarity score: | 0.0624145 |

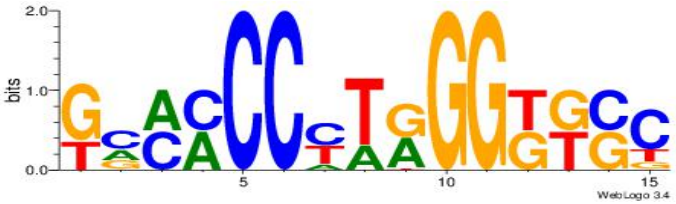
Alignment:

```
GYRYCCMTKGGYRSC
---TCCCAG------
```

Original motif Consensus sequence: GSMMCCYARGGKKKC




Reverse complement motif Consensus sequence: GYRYCCMTKGGYR

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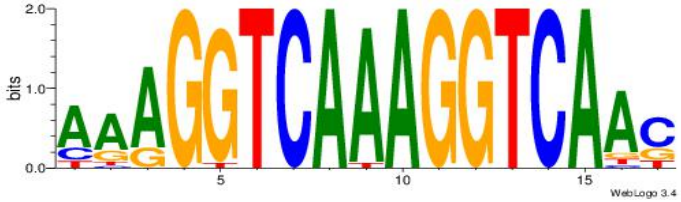
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 43 |

| | |
|---|---|
| Motif name: | NR1H2RXRA |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 7 |
| Number of overlap: | 6 |
| Similarity score: | 0.0650784 |

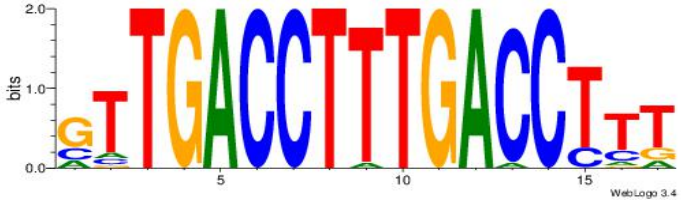
Alignment:

```
AAAGGTCAAAGGTCAAC
-----TCCCAG------
```

Original motif Consensus sequence: AAAGGTCAAAGGTCAAC




Reverse complement motif Consensus sequence: GTTGACCTTTGACCTTT

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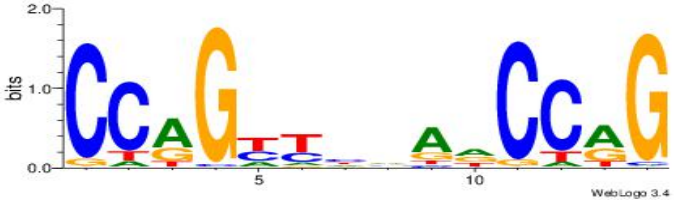
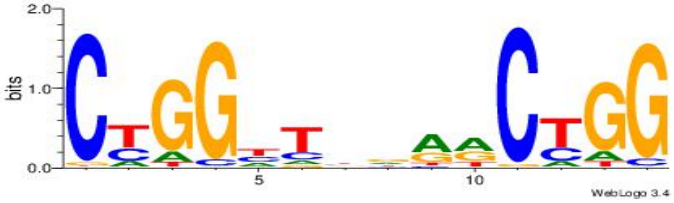
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 48 |
| Motif name: | Tcfcp2l1 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Reverse Complement |
| Direction: | Backward |
| Position number: | 9 |
| Number of overlap: | 6 |
| Similarity score: | 0.0663804 |

Alignment:
CKGGDTBDMMCTGG
CTGGGA--------

Original motif Consensus sequence: CCAGYYHVADCCRG




Reverse complement motif Consensus sequence: CKGGDTBDMMCT

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| | |
|---|---|
| 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: HGCGTGGGCGK

Reverse complement motif Consensus sequence: YCGCCCACGCH

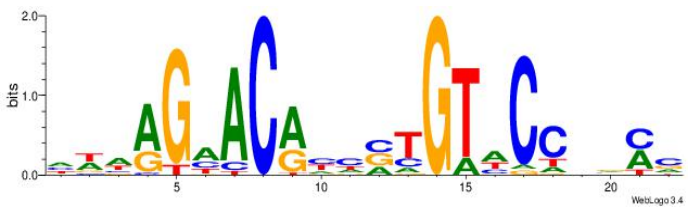
---

| | |
|---|---|
| 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 |

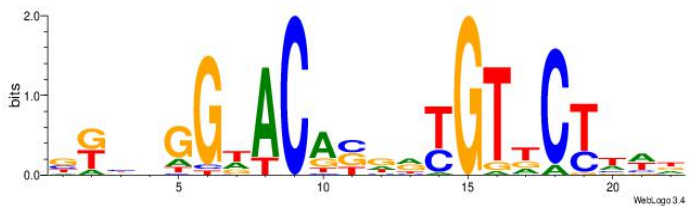
Alignment:

```
HWDAGHACRHHVTGTHCCHVMV
--------------TCCCAG--
```

Original motif Consensus sequence: HWDAGHACRHHVTGTHCCHVMV




Reverse complement motif Consensus sequence: VRVDGGHACAVDDKGTHCTDWH

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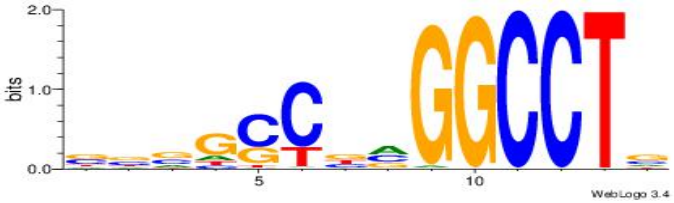
| | |
|---|---|
| Dataset #: | 2 |

| | |
|---|---|
| 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 |

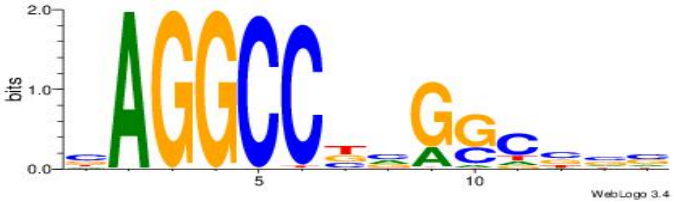
Alignment:

```
BBVGCCBVGGCCTV
-----CTGGGA---
```

Original motif Consensus sequence: BBVGCCBVGGCCTV




Reverse complement motif Consensus sequence: VAGGCCBBGGCVB

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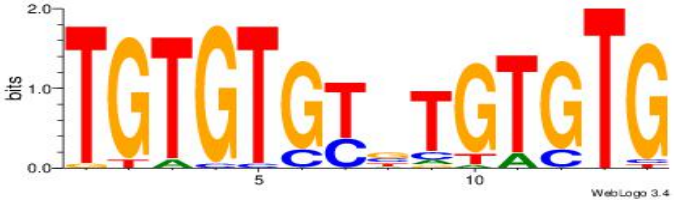
**Dataset #: 1 Motif ID: 9 Motif name: Motif 9**

Original motif Consensus sequence: CACACAVRCACACA

Reverse complement motif Consensus sequence: TGTGTGKVTGTGT

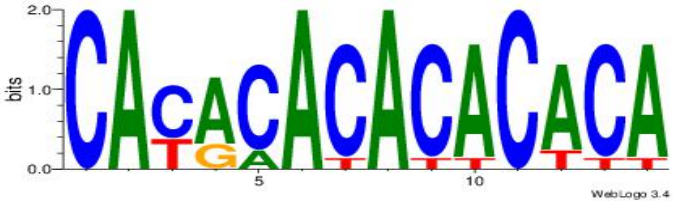


## Best Matches for Motif ID 9 (Highest to Lowest)

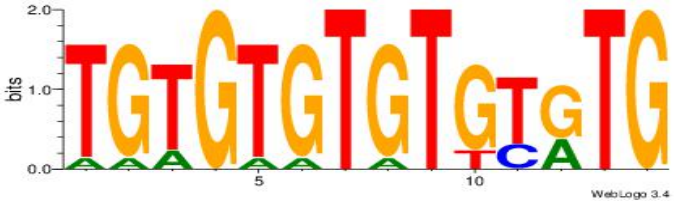
| | |
|---|---|
| Dataset #: | 1 |
| Motif ID: | 11 |
| Motif name: | Motif 11 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 1 |
| Number of overlap: | 14 |
| Similarity score: | 0.0170175 |

Alignment:
CAYACACACACACA
CACACAVRCACACA

Original motif Consensus sequence: CAYACACACACACA




Reverse complement motif Consensus sequence: TGTGTGTGTGTKT

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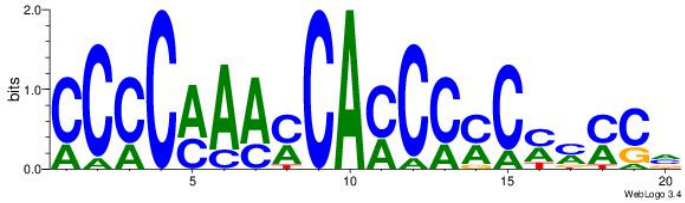
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 18 |
| Motif name: | RREB1 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |

| | |
|---|---|
| Direction: | Backward |
| Position number: | 3 |
| Number of overlap: | 14 |
| Similarity score: | 0.0868786 |

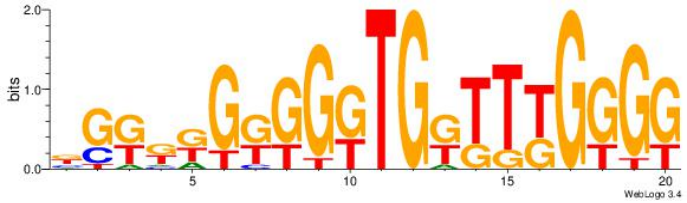
Alignment:

```
CCCCMAAMCAMCCMCMMMCV
----CACACAVRCACACA--
```

Original motif Consensus sequence: CCCCMAAMCAMCCMCMMMCV




Reverse complement motif Consensus sequence: BGRRRGRGGRTGRTTYGGGG

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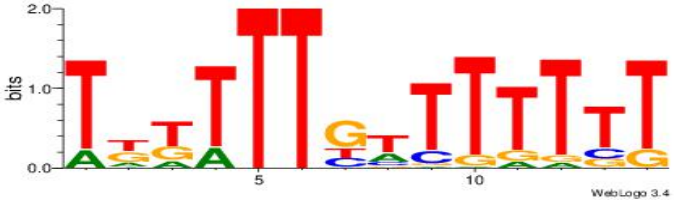
| | |
|---|---|
| Dataset #: | 1 |
| Motif ID: | 10 |
| Motif name: | Motif 10 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 2 |
| Number of overlap: | 13 |
| Similarity score: | 0.578949 |

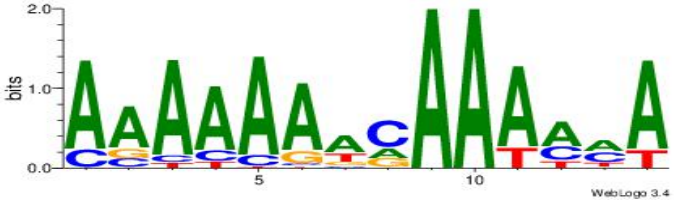
Alignment:

```
TKKTTTGTTTTTTT-
-TGTGTGKVTGTGTG
```

Original motif Consensus sequence: TKKTTTGTTTTTTT




Reverse complement motif Consensus sequence: AAAAAAACAAARR



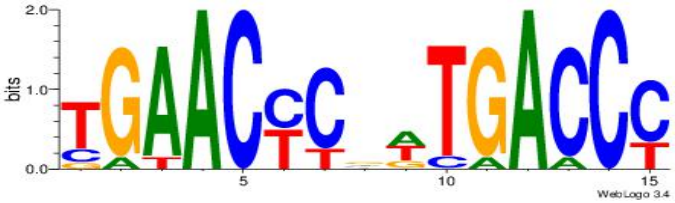

| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 17 |
| Motif name: | RXRAVDR |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Reverse Complement |
| Direction: | Forward |
| Position number: | 3 |
| Number of overlap: | 13 |
| Similarity score: | 0.593978 |

Alignment:

```
TGAACKCBWTGACCC-
--CACACAVRCACACA
```

Original motif Consensus sequence: GGGTCAWBGRGTTCA

Reverse complement motif Consensus sequence: TGAACKCBWTGAC

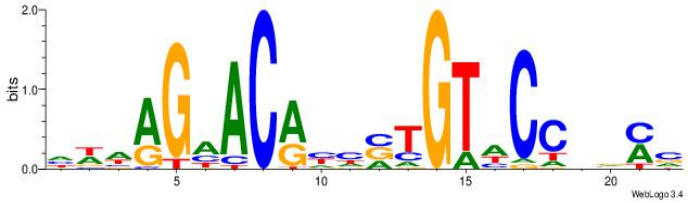


| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 24 |
| Motif name: | Ar |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Reverse Complement |
| Direction: | Backward |
| Position number: | 11 |
| Number of overlap: | 12 |
| Similarity score: | 1.09291 |

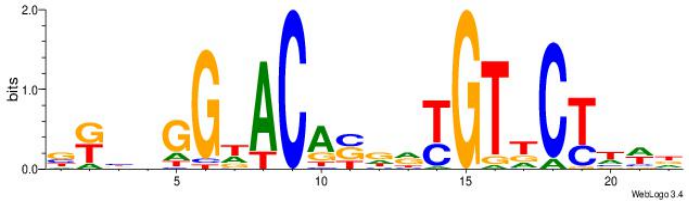
Alignment:

```
--VRVDGGHACAVDDKGTHCTDWH
CACACAVRCACACA----------
```

Original motif Consensus sequence: HWDAGHACRHHVTGTHCCHVMV




Reverse complement motif Consensus sequence: VRVDGGHACAVDDKGTHCTDWH

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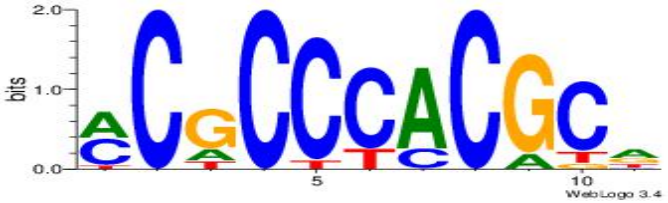
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 28 |
| Motif name: | Egr1 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 1 |

Number of overlap: 11
Similarity score: 1.57424

Alignment:
HGCGTGGGCGK---
TGTGTGKVTGTGTG

Original motif Consensus sequence: HGCGTGGGCGK

Reverse complement motif Consensus sequence: YCGCCCACGCH

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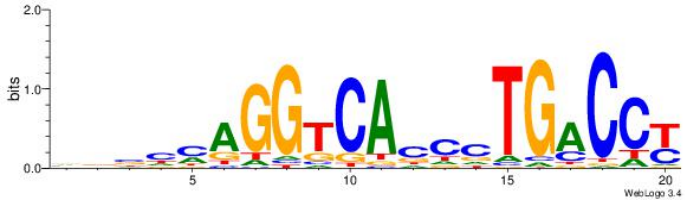
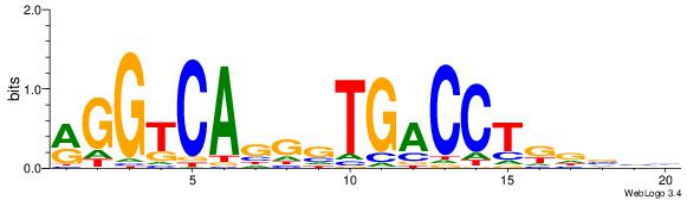
Dataset #: 2
Motif ID: 29
Motif name: ESR1
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 10
Number of overlap: 11
Similarity score: 1.58704

Alignment:
VDBHMAGGTCACCCTGACCY---
---------CACACAVRCACACA

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY

Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV

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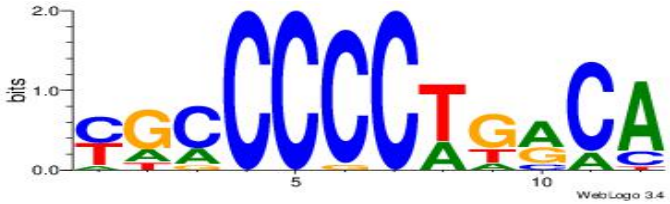
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 35 |
| Motif name: | INSM1 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 3 |
| Number of overlap: | 10 |
| Similarity score: | 2.08086 |

Alignment:

```
----TGYCAGGGGGCR
TGTGTGKVTGTGTG--
```

Original motif Consensus sequence: TGYCAGGGGGCR

Reverse complement motif Consensus sequence: MGCCCCCTGMCA

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| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 36 |

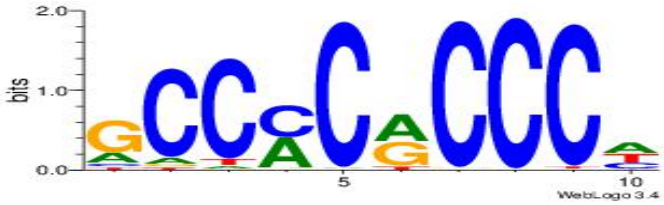
| | |
|---|---|
| Motif name: | Klf4 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 1 |
| Number of overlap: | 10 |
| Similarity score: | 2.0884 |

Alignment:

```
DGGGYGKGGC----
TGTGTGKVTGTGTG
```

Original motif Consensus sequence: DGGGYGKGGC

Reverse complement motif Consensus sequence: GCCYCMCCCD

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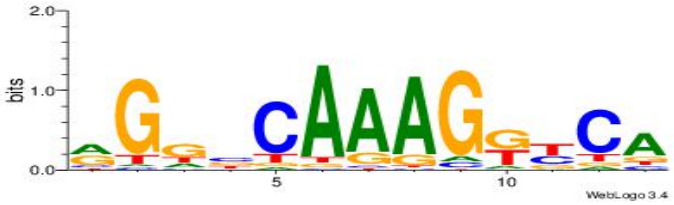
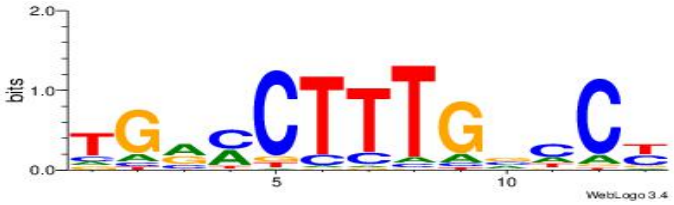
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 34 |
| Motif name: | HNF4A |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction: | Forward |
| Position number: | 4 |
| Number of overlap: | 10 |
| Similarity score: | 2.09226 |

Alignment:
TGMYCTTTGBCCK----
---TGTGTGKVTGTGTG

Original motif Consensus sequence: RGGBCAAAGKYCA




Reverse complement motif Consensus sequence: TGMYCTTTGBCCK

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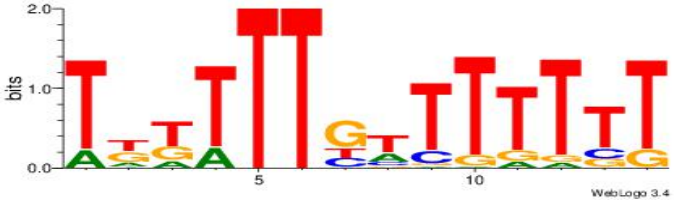
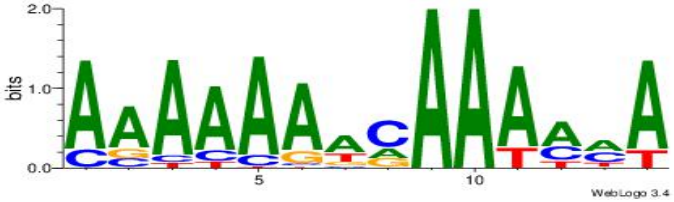
**Dataset #: 1 Motif ID: 10 Motif name: Motif 10**

Original motif Consensus sequence: TKKTTTGTTTTTT




Reverse complement motif Consensus sequence: AAAAAAACAAARR



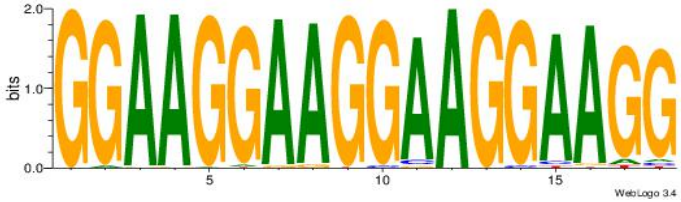

**Best Matches for Motif ID 10 (Highest to Lowest)**

| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 32 |
| Motif name: | EWSR1-FLI1 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 3 |

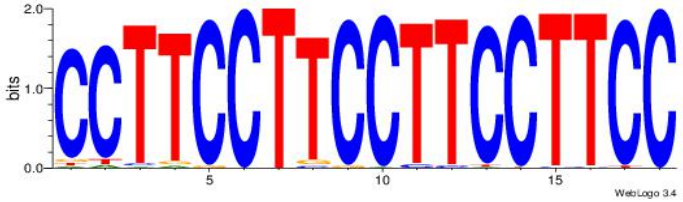
Number of overlap: 14
Similarity score: 0.0424269

Alignment:
GGAAGGAAGGAAGGAAGG
--AAAAAAACAAARRA--

Original motif Consensus sequence: GGAAGGAAGGAAGGAAGG




Reverse complement motif Consensus sequence: CCTTCCTTCCTTCCTTCC

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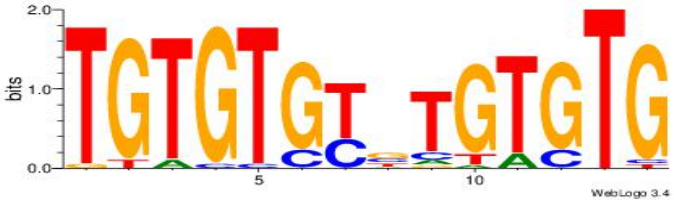
Dataset #: 1
Motif ID: 9
Motif name: Motif 9
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2
Number of overlap: 13
Similarity score: 0.529035

Alignment:
-CACACAVRCACACA
AAAAAAACAAARRA-

Original motif Consensus sequence: CACACAVRCACACA

Reverse complement motif Consensus sequence: TGTGTGKVTGTGT

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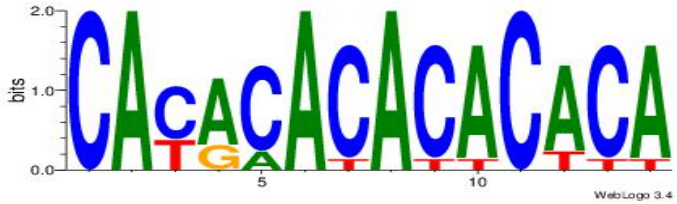
| | |
|---|---|
| Dataset #: | 1 |
| Motif ID: | 11 |
| Motif name: | Motif 11 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Reverse Complement |
| Direction: | Backward |
| Position number: | 2 |
| Number of overlap: | 13 |
| Similarity score: | 0.531594 |

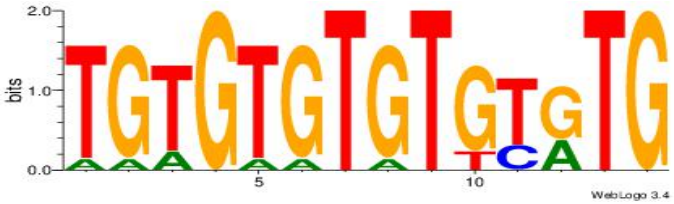
Alignment:

```
-TGTGTGTGTGTKTG
TKKTTTGTTTTTTT-
```

Original motif Consensus sequence: CAYACACACACACA




Reverse complement motif Consensus sequence: TGTGTGTGTGTKT

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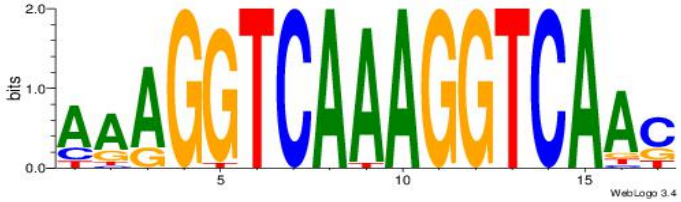
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 43 |

| | |
|---|---|
| Motif name: | NR1H2RXRA |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 5 |
| Number of overlap: | 13 |
| Similarity score: | 0.535643 |

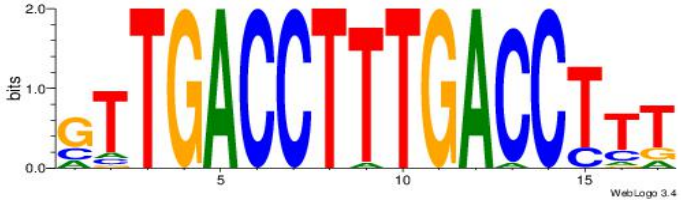
Alignment:

```
-AAAGGTCAAAGGTCAAC
AAAAAAACAAARRA----
```

Original motif Consensus sequence: AAAGGTCAAAGGTCAAC




Reverse complement motif Consensus sequence: GTTGACCTTTGACCTTT

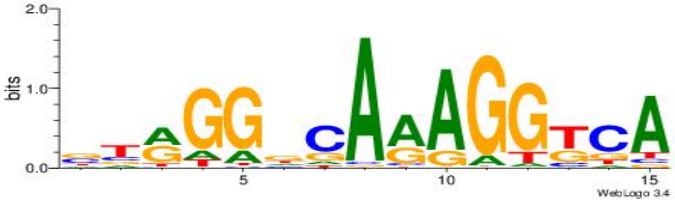



---

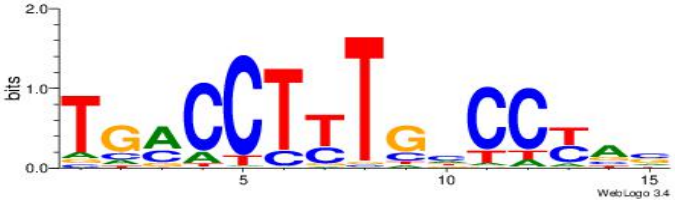
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 20 |
| Motif name: | PPARGRXRA |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 3 |
| Number of overlap: | 13 |
| Similarity score: | 0.543043 |

Alignment:
-BTRGGDCARAGGKCA
AAAAAAACAAARRA--

Original motif Consensus sequence: BTRGGDCARAGGKCA




Reverse complement motif Consensus sequence: TGRCCTKTGHCCK



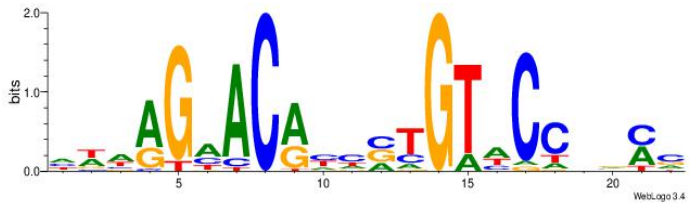

---

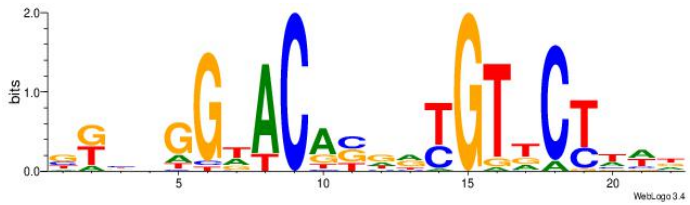
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 24 |
| Motif name: | Ar |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Reverse Complement |
| Direction: | Forward |
| Position number: | 10 |
| Number of overlap: | 13 |
| Similarity score: | 0.544053 |

Alignment:
VRVDGGHACAVDDKGTHCTDWH-
---------TKKTTTGTTTTTTT

Original motif Consensus sequence: HWDAGHACRHHVTGTHCCHVMV

Reverse complement motif Consensus sequence: VRVDGGHACAVDDKGTHCTDWH

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| | |
|---|---|
| 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: | 12 |
| Similarity score: | 1.04059 |

Alignment:

```
--AKGYYCAAAGRTCA
AAAAAAACAAARRA--
```

Original motif Consensus sequence: TGAMCTTTGMMCYT

Reverse complement motif Consensus sequence: AKGYYCAAAGRTCA

---

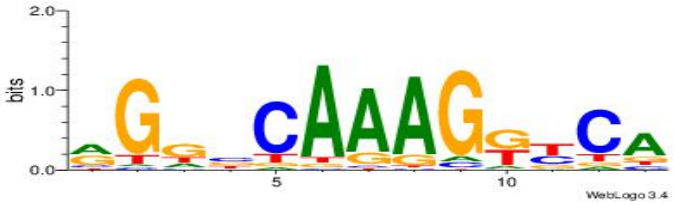
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 34 |

| | |
|---|---|
| Motif name: | HNF4A |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 3 |
| Number of overlap: | 11 |
| Similarity score: | 1.53429 |

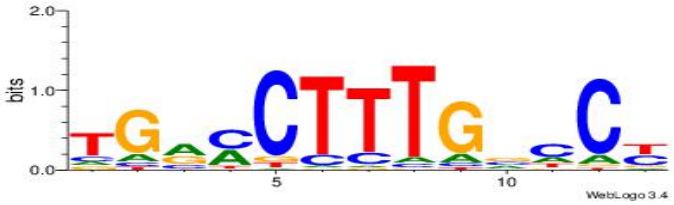
Alignment:

```
---RGGBCAAAGKYCA
AAAAAAACAAARRA--
```

Original motif Consensus sequence: RGGBCAAAGKYCA




Reverse complement motif Consensus sequence: TGMYCTTTGBCCK

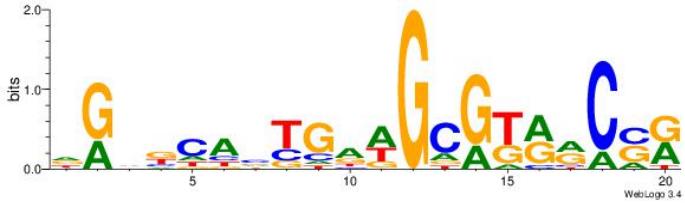



---

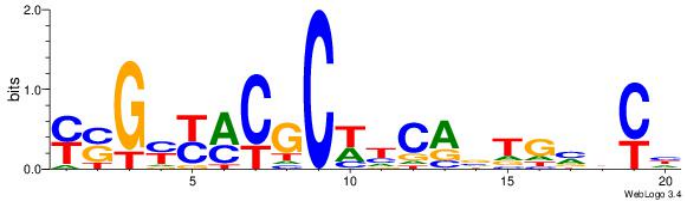
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 45 |
| Motif name: | Pax5 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 10 |
| Number of overlap: | 11 |
| Similarity score: | 1.54022 |

Alignment:
```
---DGVBCABTGDWGCGKRRCSR
AAAAAAACAAARRA---------
```

Original motif Consensus sequence: DGVBCABTGDWGCGKRRCSR




Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD

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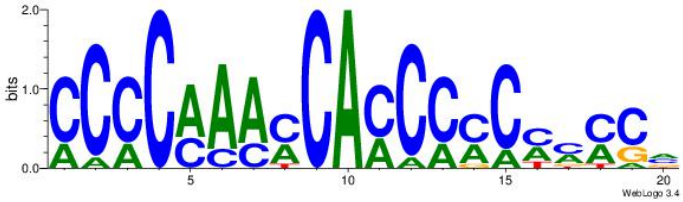
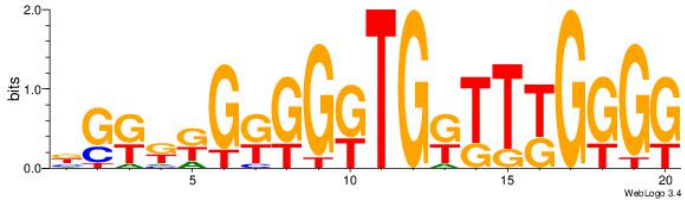
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 18 |
| Motif name: | RREB1 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 11 |
| Number of overlap: | 10 |
| Similarity score: | 2.0484 |

Alignment:
```
----CCCCMAAMCAMCCMCMMMCV
AAAAAAACAAARRA----------
```

Original motif Consensus sequence: CCCCMAAMCAMCCMCMMMCV

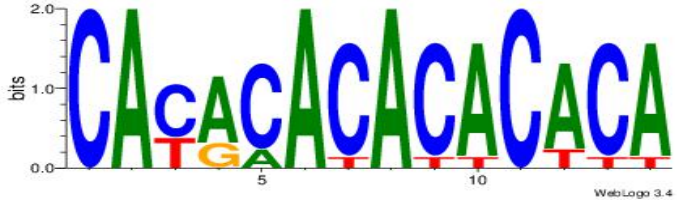
Reverse complement motif Consensus sequence: BGRRRGRGGRTGRTTYGGGG



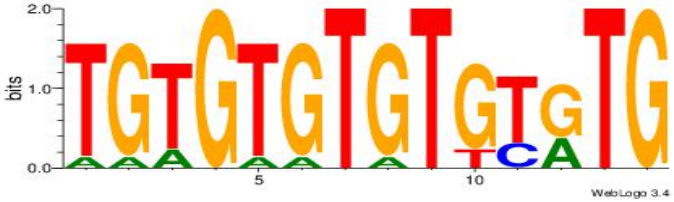




**Dataset #: 1** **Motif ID: 11** **Motif name: Motif 11**

Original motif Consensus sequence: CAYACACACACACA




Reverse complement motif Consensus sequence: TGTGTGTGTGTKT




## Best Matches for Motif ID 11 (Highest to Lowest)

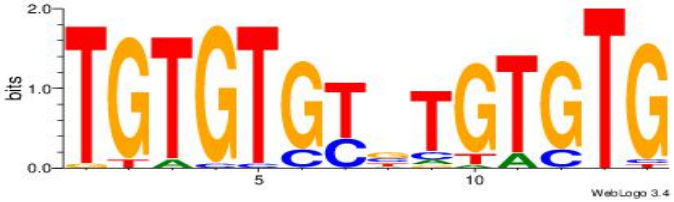
| | |
|---|---|
| Dataset #: | 1 |
| Motif ID: | 9 |
| Motif name: | Motif 9 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 1 |
| Number of overlap: | 14 |
| Similarity score: | 0.0170175 |

Alignment:

```
CACACAVRCACACA
CAYACACACACACA
```

Original motif Consensus sequence: CACACAVRCACACA

Reverse complement motif Consensus sequence: TGTGTGKVTGTGT

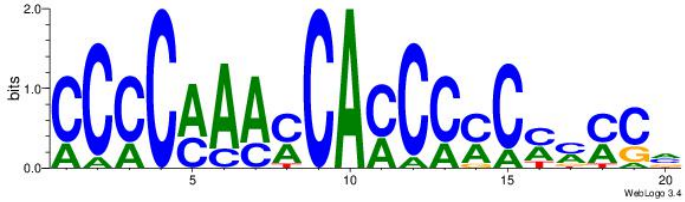



| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 18 |
| Motif name: | RREB1 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 3 |
| Number of overlap: | 14 |
| Similarity score: | 0.0837439 |

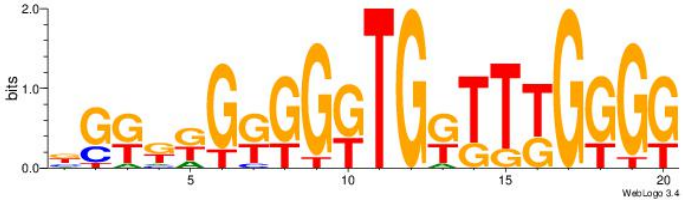
Alignment:

```
CCCCMAAMCAMCCMCMMMCV
----CAYACACACACACA--
```

Original motif Consensus sequence: CCCCMAAMCAMCCMCMMMCV



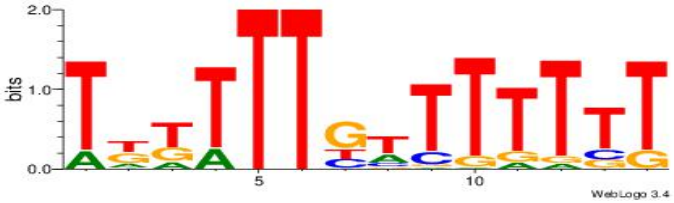

Reverse complement motif Consensus sequence: BGRRRGRGGRTGRTTYGGGG



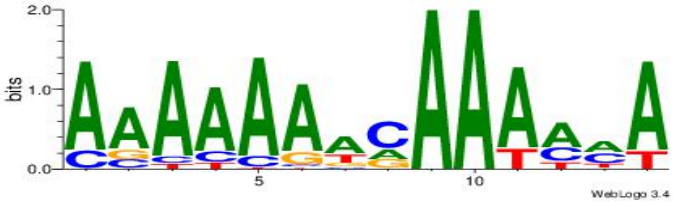
| | |
|---|---|
| Dataset #: | 1 |
| Motif ID: | 10 |
| Motif name: | Motif 10 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Reverse Complement |
| Direction: | Forward |
| Position number: | 2 |
| Number of overlap: | 13 |
| Similarity score: | 0.581509 |

Alignment:
AAAAAAACAAARRA-
-CAYACACACACACA

Original motif Consensus sequence: TKKTTTGTTTTTT




Reverse complement motif Consensus sequence: AAAAAAACAAARR

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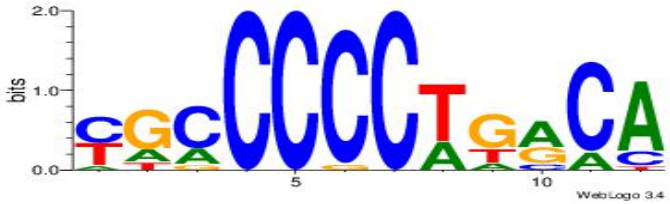
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 35 |
| Motif name: | INSM1 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 1 |
| Number of overlap: | 12 |

Similarity score: 1.09362

Alignment:
--TGYCAGGGGGCR
TGTGTGTGTGTKTG

Original motif Consensus sequence: TGYCAGGGGGCR

Reverse complement motif Consensus sequence: MGCCCCCTGMCA




---

Dataset #: 2
Motif ID: 28
Motif name: Egr1
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 11
Similarity score: 1.56977

Alignment:
HGCGTGGGCGK---
TGTGTGTGTGTKTG

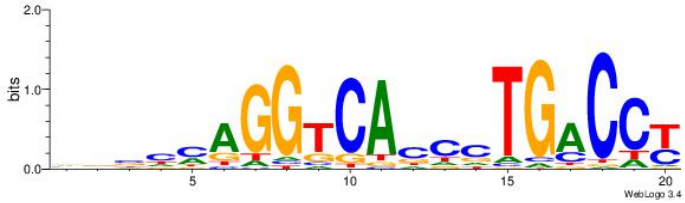
Original motif Consensus sequence: HGCGTGGGCGK

Reverse complement motif Consensus sequence: YCGCCCACGCH

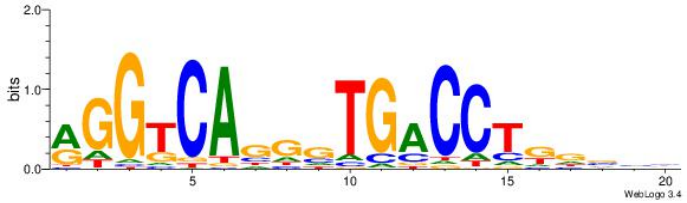
Dataset #: 2
Motif ID: 29
Motif name: ESR1
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 10
Number of overlap: 11
Similarity score: 1.59795

Alignment:
VDBHMAGGTCACCCTGACCY---
---------CAYACACACACACA

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY




Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV




Dataset #: 2

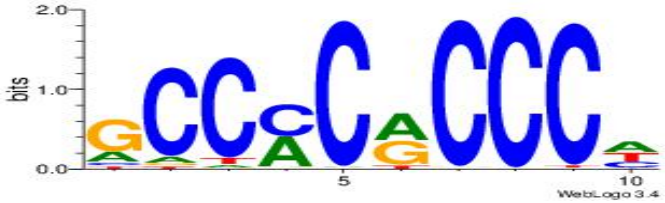
| | |
|---|---|
| Motif ID: | 36 |
| Motif name: | Klf4 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 1 |
| Number of overlap: | 10 |
| Similarity score: | 2.08683 |

Alignment:

```
DGGGYGKGGC----
TGTGTGTGTGTKTG
```

Original motif Consensus sequence: DGGGYGKGGC

Reverse complement motif Consensus sequence: GCCYCMCCCD

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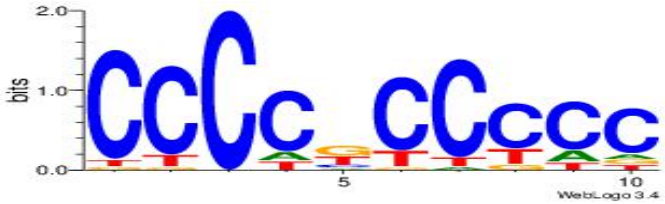
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 16 |
| Motif name: | SP1 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction: | Backward |
| Position number: | 2 |
| Number of overlap: | 9 |
| Similarity score: | 2.59204 |

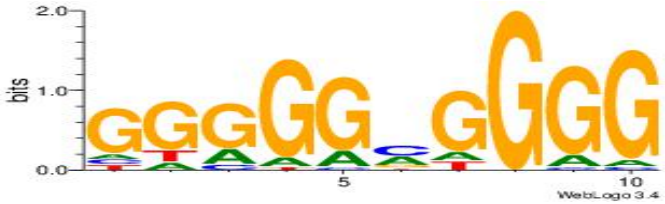
Alignment:

```
-----GGGGGYGGGG
TGTGTGTGTGTKTG-
```

Original motif Consensus sequence: CCCCKCCCCC




Reverse complement motif Consensus sequence: GGGGGYGGGG

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| | |
|---|---|
| Dataset #: | 1 |
| Motif ID: | 7 |
| Motif name: | Motif 7 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 1 |
| Number of overlap: | 8 |
| Similarity score: | 3.09205 |

Alignment:

```
------CCCRCCCC
CAYACACACACACA
```

Original motif Consensus sequence: CCCRCCCC

Reverse complement motif Consensus sequence: GGGGMGGG

| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 33 |
| Motif name: | HIF1AARNT |
| 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: | 3.58699 |

Alignment:

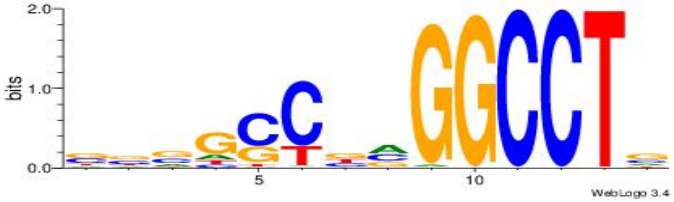
```
-------VBACGTGV
TGTGTGTGTGTKTG-
```

Original motif Consensus sequence: VBACGTGV

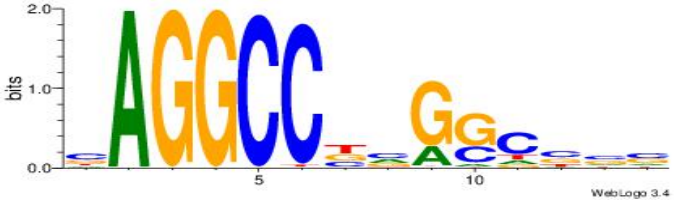
Reverse complement motif Consensus sequence: VCACGTBV

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

Original motif Consensus sequence: BBVGCCBVGGCCTV




Reverse complement motif Consensus sequence: VAGGCCBBGGCVB



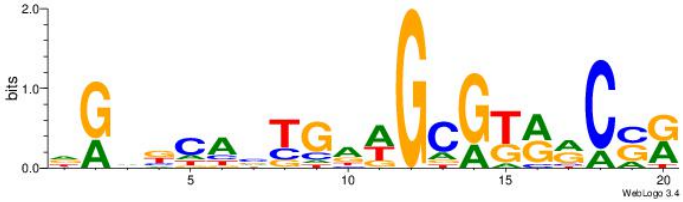

## Best Matches for Motif ID 12 (Highest to Lowest)

| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 45 |
| Motif name: | Pax5 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 5 |
| Number of overlap: | 14 |
| Similarity score: | 0.0611182 |

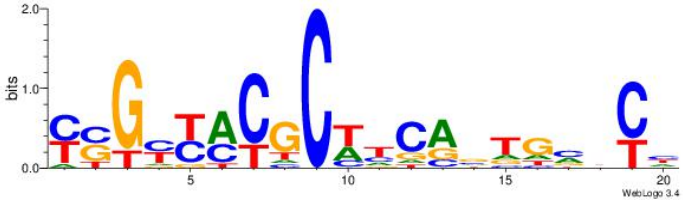
Alignment:

```
DGVBCABTGDWGCGKRRCSR
--BBVGCCBVGGCCTV----
```

Original motif Consensus sequence: DGVBCABTGDWGCGKRRCSR




Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD

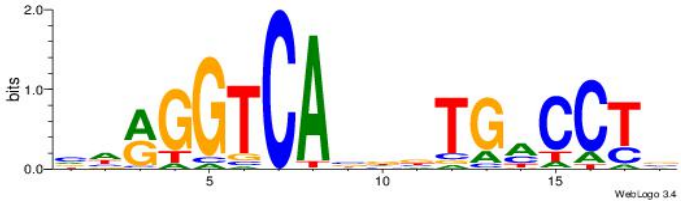


| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 30 |
| Motif name: | ESR2 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Reverse Complement |
| Direction: | Backward |
| Position number: | 2 |
| Number of overlap: | 14 |
| Similarity score: | 0.0635714 |

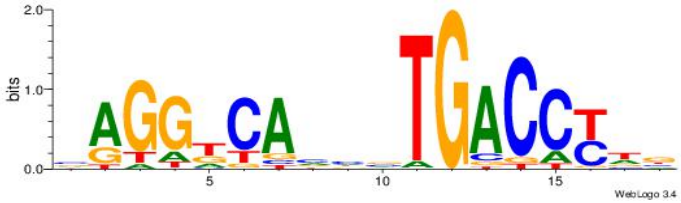
Alignment:

```
BAGGYCABHBTGACCKHV
---BBVGCCBVGGCCTV-
```

Original motif Consensus sequence: VHRGGTCABDBTGMCCTB




Reverse complement motif Consensus sequence: BAGGYCABHBTGACCKHV



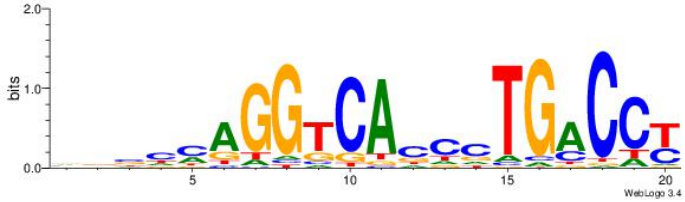

---

| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 29 |
| Motif name: | ESR1 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Reverse Complement |
| Direction: | Backward |
| Position number: | 5 |

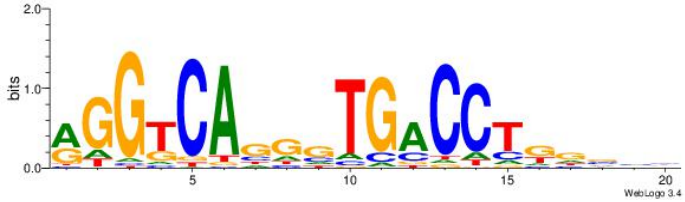
Number of overlap: 14
Similarity score: 0.0722733

Alignment:
MGGTCAGGGTGACCTRDBHV
--BBVGCCBVGGCCTV----

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY




Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV

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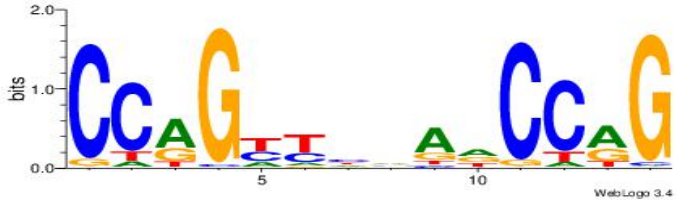
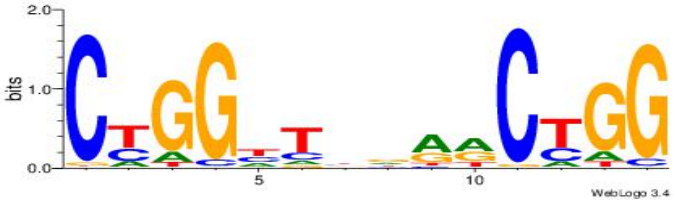
Dataset #: 2
Motif ID: 48
Motif name: Tcfcp2l1
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 14
Similarity score: 0.0732898

Alignment:
CCAGYYHVADCCRG
BBVGCCBVGGCCTV

Original motif Consensus sequence: CCAGYYHVADCCRG

Reverse complement motif Consensus sequence: CKGGDTBDMMCT

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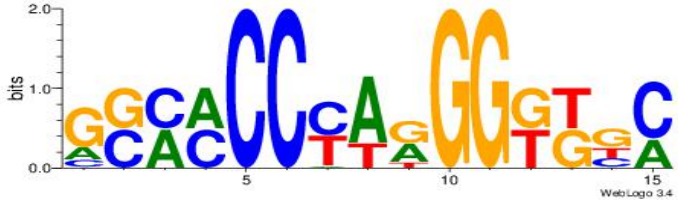
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 13 |
| Motif name: | Zfp423 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction: | Forward |
| Position number: | 2 |
| Number of overlap: | 14 |
| Similarity score: | 0.0747812 |

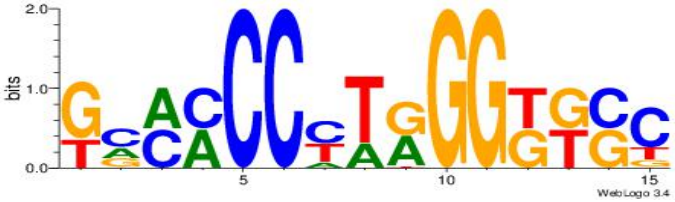
Alignment:

```
GYRYCCMTKGGYRSC
-VAGGCCBBGGCVBB
```

Original motif Consensus sequence: GSMMCCYARGGKKKC




Reverse complement motif Consensus sequence: GYRYCCMTKGGYR

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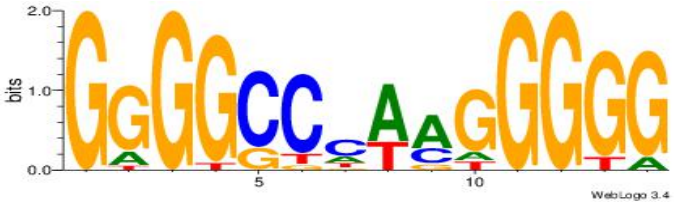
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 21 |

| | |
|---|---|
| Motif name: | PLAG1 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Reverse Complement |
| Direction: | Forward |
| Position number: | 1 |
| Number of overlap: | 14 |
| Similarity score: | 0.0796879 |

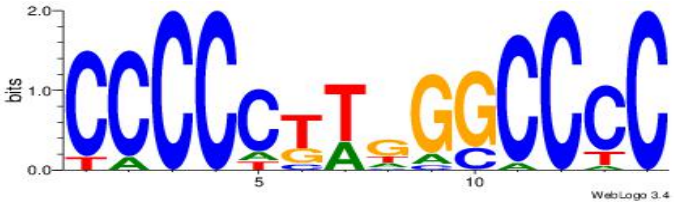
Alignment:

```
CCCCCTTGGGCCCC
BBVGCCBVGGCCTV
```

Original motif Consensus sequence: GGGGCCCAAGGGGG




Reverse complement motif Consensus sequence: CCCCCTTGGGCCC

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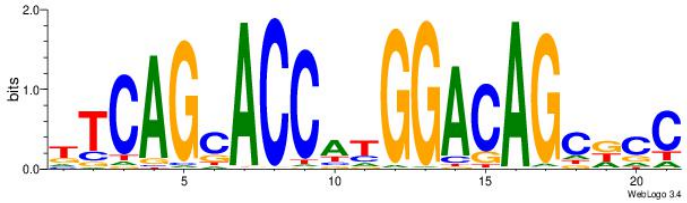
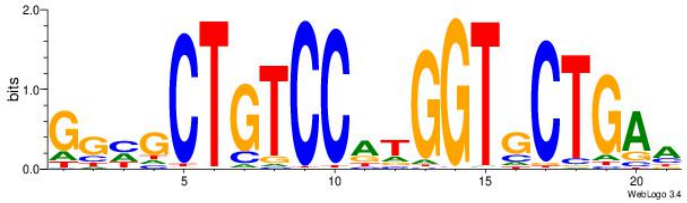
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 19 |
| Motif name: | REST |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction: | Forward |
| Position number: | 5 |
| Number of overlap: | 14 |
| Similarity score: | 0.0812253 |

Alignment:
GGYGCTGTCCATGGTGCTGAA
----VAGGCCBBGGCVBB---

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC




Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA

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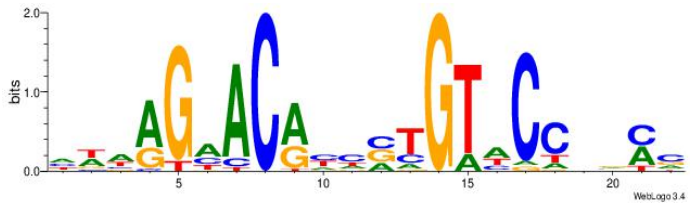
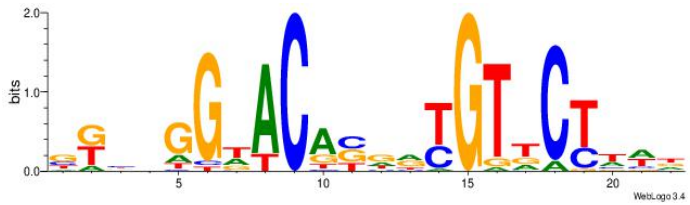
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 24 |
| Motif name: | Ar |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 4 |
| Number of overlap: | 14 |
| Similarity score: | 0.0832838 |

Alignment:
HWDAGHACRHHVTGTHCCHVMV
-----VAGGCCBBGGCVBB---

Original motif Consensus sequence: HWDAGHACRHHVTGTHCCHVMV

Reverse complement motif Consensus sequence: VRVDGGHACAVDDKGTHCTDWH

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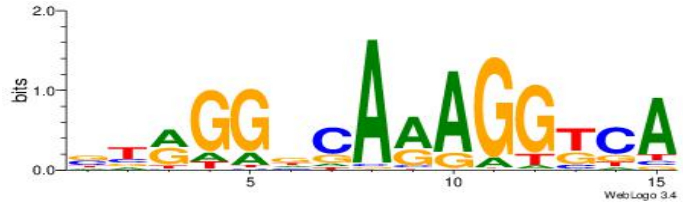
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 20 |
| Motif name: | PPARGRXRA |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Reverse Complement |
| Direction: | Forward |
| Position number: | 1 |
| Number of overlap: | 14 |
| Similarity score: | 0.0836605 |

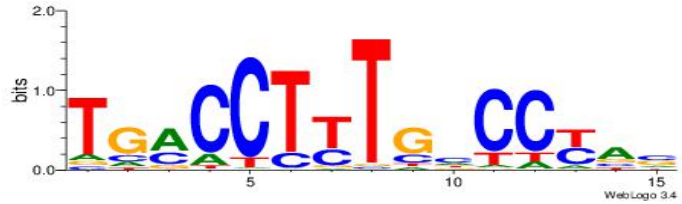
Alignment:

```
TGRCCTKTGHCCKAB
BBVGCCBVGGCCTV-
```

Original motif Consensus sequence: BTRGGDCARAGGKCA




Reverse complement motif Consensus sequence: TGRCCTKTGHCCK

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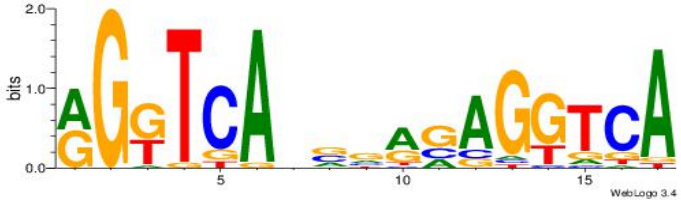
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 47 |

| | |
|---|---|
| Motif name: | RXRRAR_DR5 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Reverse Complement |
| Direction: | Forward |
| Position number: | 5 |
| Number of overlap: | 13 |
| Similarity score: | 0.570818 |

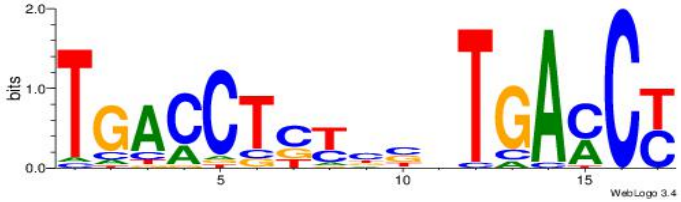
Alignment:

```
TGACCTCKVVBTGAYCK-
----BBVGCCBVGGCCTV
```

Original motif Consensus sequence: RGKTCABVVRGAGGTCA




Reverse complement motif Consensus sequence: TGACCTCKVVBTGAYCK

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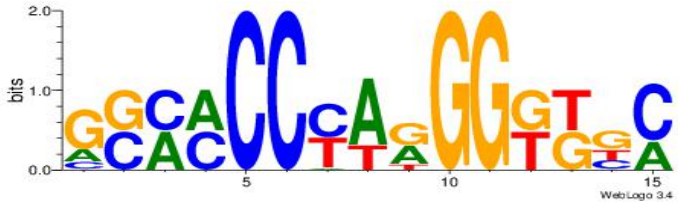
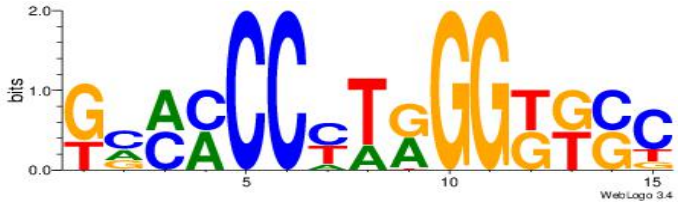
**Dataset #: 2 Motif ID: 13 Motif name: Zfp423**

Original motif Consensus sequence: GSMMCCYARGGKKKC




Reverse complement motif Consensus sequence: GYRYCCMTKGGYR



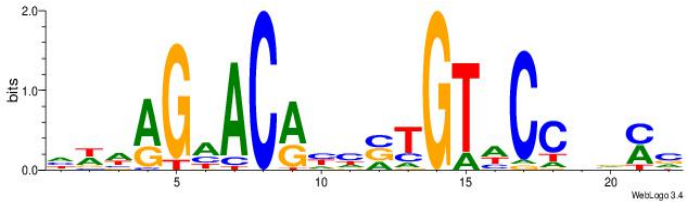
## Best Matches for Motif ID 13 (Highest to Lowest)

| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 24 |
| Motif name: | Ar |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 5 |
| Number of overlap: | 15 |
| Similarity score: | 0.0400042 |

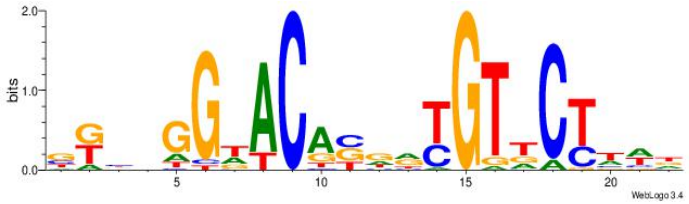
Alignment:

```
HWDAGHACRHHVTGTHCCHVMV
---GSMMCCYARGGKKKC----
```

Original motif Consensus sequence: HWDAGHACRHHVTGTHCCHVMV




Reverse complement motif Consensus sequence: VRVDGGHACAVDDKGTHCTDWH

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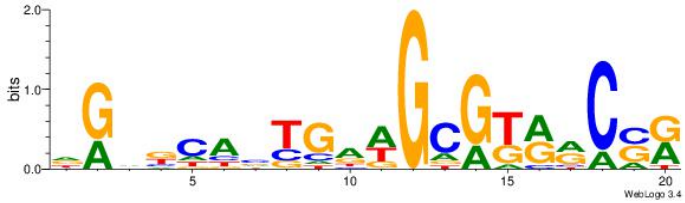
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 45 |
| Motif name: | Pax5 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |

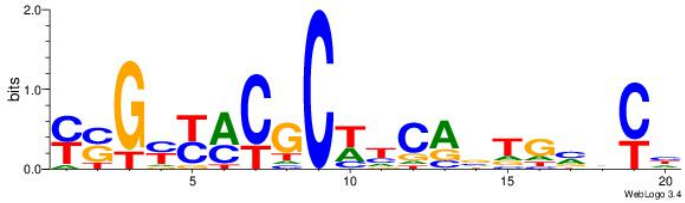
| | |
|---|---|
| Direction: | Forward |
| Position number: | 3 |
| Number of overlap: | 15 |
| Similarity score: | 0.0400673 |

Alignment:
DGVBCABTGDWGCGKRRCSR
--GSMMCCYARGGKKKC---

Original motif Consensus sequence: DGVBCABTGDWGCGKRRCSR




Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD

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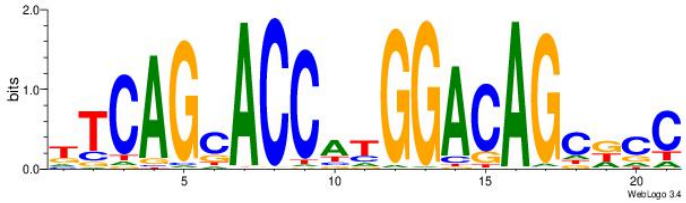
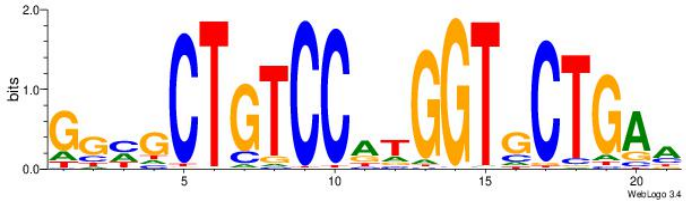
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 19 |
| Motif name: | REST |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 4 |
| Number of overlap: | 15 |
| Similarity score: | 0.0410001 |

Alignment:
TTCAGCACCATGGACAGCKCC
---GYRYCCMTKGGYRSC---

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC



Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA



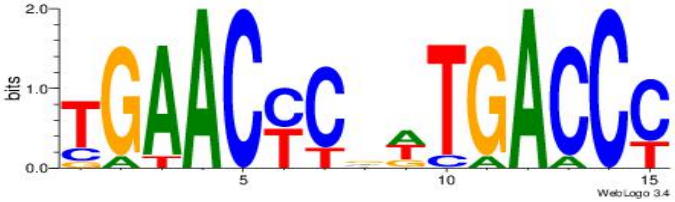
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 17 |
| Motif name: | RXRAVDR |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 1 |
| Number of overlap: | 15 |
| Similarity score: | 0.0465067 |

Alignment:

```
GGGTCAWBGRGTTCA
GYRYCCMTKGGYRSC
```

Original motif Consensus sequence: GGGTCAWBGRGTTCA

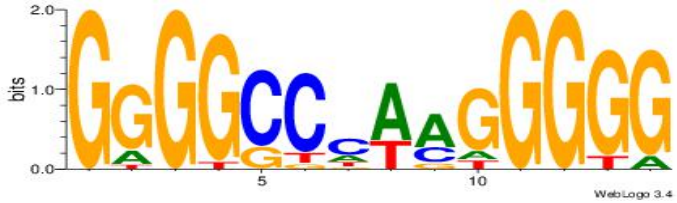
Reverse complement motif Consensus sequence: TGAACKCBWTGAC



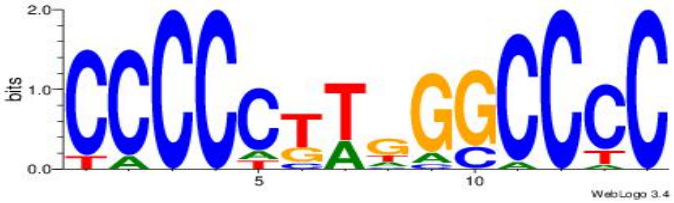
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 21 |
| Motif name: | PLAG1 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 1 |
| Number of overlap: | 14 |
| Similarity score: | 0.527928 |

Alignment:
GGGGCCCAAGGGGG-
GSMMCCYARGGKKKC

Original motif Consensus sequence: GGGGCCCAAGGGGG




Reverse complement motif Consensus sequence: CCCCCTTGGGCCC

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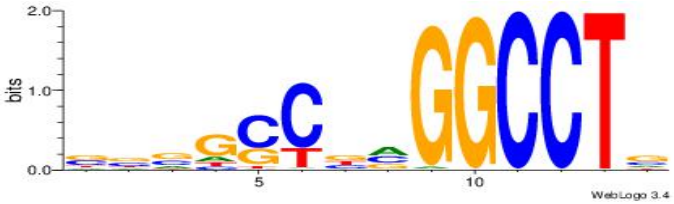
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 12 |
| Motif name: | Zfx |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction: | Backward |
| Position number: | 1 |
| Number of overlap: | 14 |

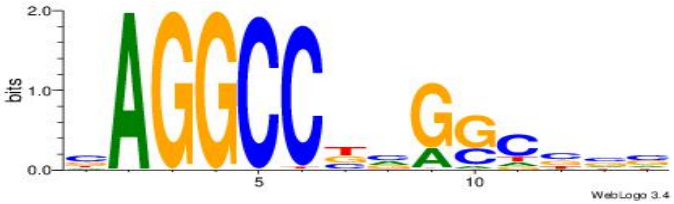
Similarity score: 0.53991

Alignment:
-VAGGCCBBGGCVBB
GYRYCCMTKGGYRSC

Original motif Consensus sequence: BBVGCCBVGGCCTV




Reverse complement motif Consensus sequence: VAGGCCBBGGCVB

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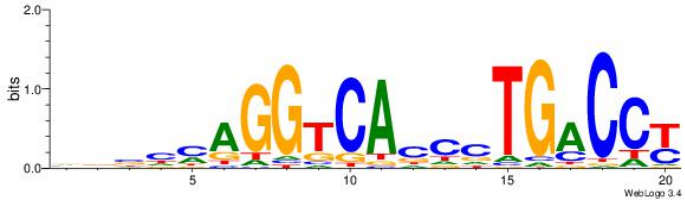
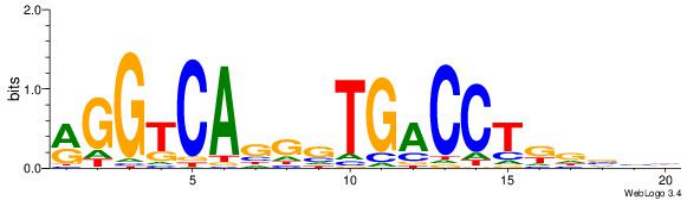
Dataset #: 2
Motif ID: 29
Motif name: ESR1
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 8
Number of overlap: 13
Similarity score: 1.03254

Alignment:
--VDBHMAGGTCACCCTGACCY
GYRYCCMTKGGYRSC-------

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY

Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV

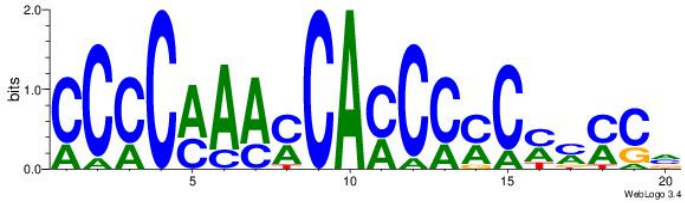


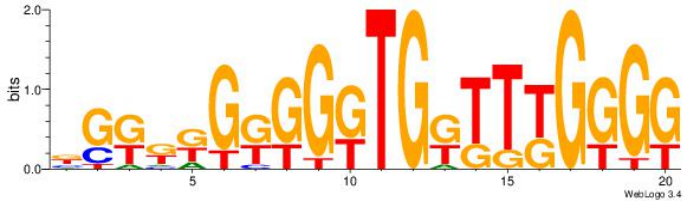

Dataset #: 2
Motif ID: 18
Motif name: RREB1
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 8
Number of overlap: 13
Similarity score: 1.04952

Alignment:
BGRRRGRGGRTGRTTYGGGG--
-------GYRYCCMTKGGYRSC

Original motif Consensus sequence: CCCCMAAMCAMCCMCMMMCV




Reverse complement motif Consensus sequence:
BGRRRGRGGRTGRTTYGGGG




Dataset #: 2

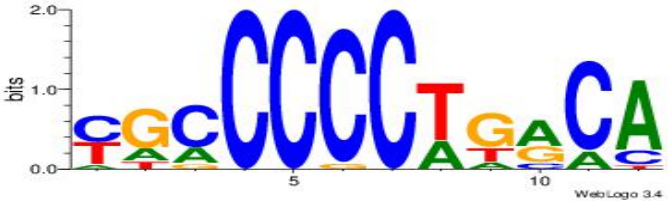
| | |
|---|---|
| Motif ID: | 35 |
| Motif name: | INSM1 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 1 |
| Number of overlap: | 12 |
| Similarity score: | 1.54193 |

Alignment:

```
---TGYCAGGGGGCR
GSMMCCYARGGKKKC
```

Original motif Consensus sequence: TGYCAGGGGGCR

Reverse complement motif Consensus sequence: MGCCCCCTGMCA

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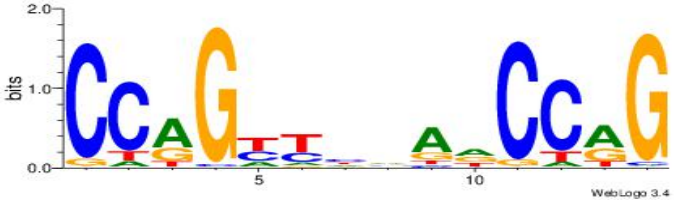
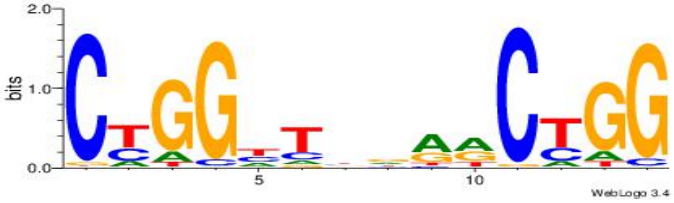
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 48 |
| Motif name: | Tcfcp2l1 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction: | Forward |
| Position number: | 4 |
| Number of overlap: | 11 |
| Similarity score: | 2.04218 |

Alignment:
CKGGDTBDMMCTGG----
---GYRYCCMTKGGYRSC

Original motif Consensus sequence: CCAGYYHVADCCRG




Reverse complement motif Consensus sequence: CKGGDTBDMMCT




---

**Dataset #: 2 Motif ID: 14 Motif name: ZEB1**

Original motif Consensus sequence: CACCTD

Reverse complement motif Consensus sequence: HAGGTG

**Best Matches for Motif ID 14 (Highest to Lowest)**

| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 46 |
| Motif name: | RORA_1 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Reverse Complement |
| Direction: | Backward |
| Position number: | 4 |

Number of overlap: 6
Similarity score: 0.0141289

Alignment:
TGACCTDVWT
-CACCTD---

Original motif Consensus sequence: AWVDAGGTCA

Reverse complement motif Consensus sequence: TGACCTDVWT

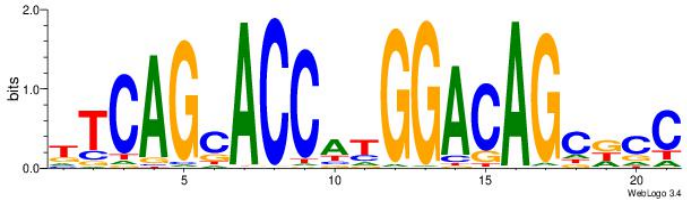
---

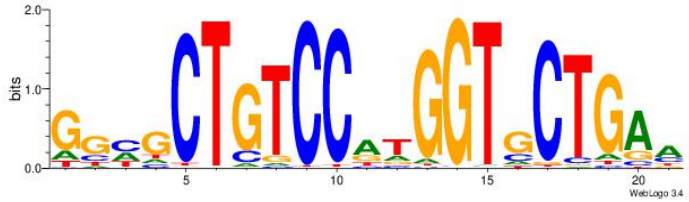
Dataset #: 2
Motif ID: 19
Motif name: REST
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 6
Number of overlap: 6
Similarity score: 0.0143133

Alignment:
GGYGCTGTCCATGGTGCTGAA
----------HAGGTG-----

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC

Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA

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| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 25 |
| Motif name: | Arnt |
| 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: | 0.0207244 |

Alignment:

```
CACGTG
CACCTD
```

Original motif Consensus sequence: CACGTG

Reverse complement motif Consensus sequence: CACGTG

---

| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 31 |

| | |
|---|---|
| Motif name: | Esrrb |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 1 |
| Number of overlap: | 6 |
| Similarity score: | 0.0207244 |

Alignment:

```
CACGTG
HAGGTG
```

Original motif Consensus sequence: CACGTG

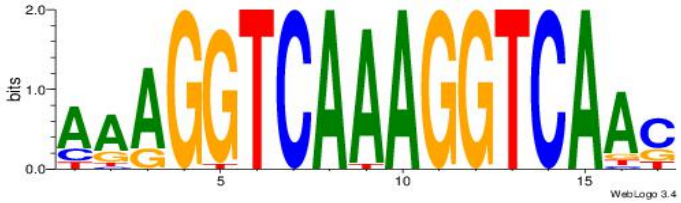
Reverse complement motif Consensus sequence: CACGTG

---

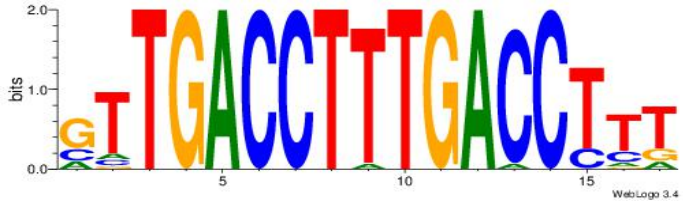
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 43 |
| Motif name: | NR1H2RXRA |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Reverse Complement |
| Direction: | Backward |
| Position number: | 2 |
| Number of overlap: | 6 |
| Similarity score: | 0.0232753 |

Alignment:
GTTGACCTTTGACCTTT
----------CACCTD-

Original motif Consensus sequence: AAAGGTCAAAGGTCAAC




Reverse complement motif Consensus sequence: GTTGACCTTTGACCTTT

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| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 33 |
| Motif name: | HIF1AARNT |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Reverse Complement |
| Direction: | Backward |
| Position number: | 2 |
| Number of overlap: | 6 |
| Similarity score: | 0.0237889 |

Alignment:
VCACGTBV
-CACCTD-

Original motif Consensus sequence: VBACGTGV

Reverse complement motif Consensus sequence: VCACGTBV

---

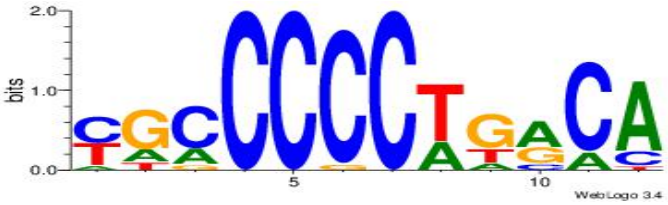
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 35 |
| Motif name: | INSM1 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 4 |
| Number of overlap: | 6 |
| Similarity score: | 0.0262123 |

Alignment:

```
TGYCAGGGGGCR
---HAGGTG---
```

Original motif Consensus sequence: TGYCAGGGGGCR

Reverse complement motif Consensus sequence: MGCCCCCTGMCA

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| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 20 |

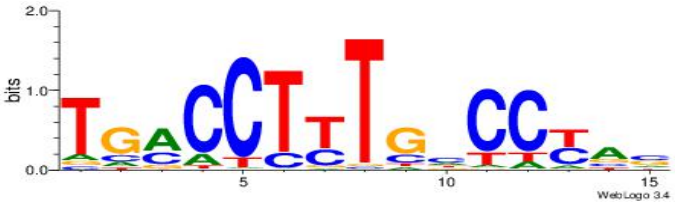
| | |
|---|---|
| Motif name: | PPARGRXRA |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Reverse Complement |
| Direction: | Backward |
| Position number: | 9 |
| Number of overlap: | 6 |
| Similarity score: | 0.0264837 |

Alignment:

```
TGRCCTKTGHCCKAB
-CACCTD--------
```

Original motif Consensus sequence: BTRGGDCARAGGKCA

Reverse complement motif Consensus sequence: TGRCCTKTGHCCK

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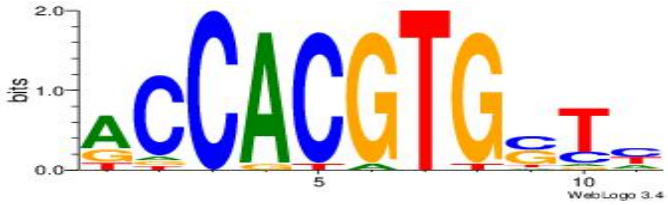
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 39 |
| Motif name: | MYCMAX |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Reverse Complement |
| Direction: | Forward |
| Position number: | 3 |
| Number of overlap: | 6 |
| Similarity score: | 0.0269744 |

Alignment:
ACCACGTGSTM
--CACCTD---

Original motif Consensus sequence: RASCACGTGGT

Reverse complement motif Consensus sequence: ACCACGTGSTM

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| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 44 |
| Motif name: | NR4A2 |
| 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: | 0.0288897 |

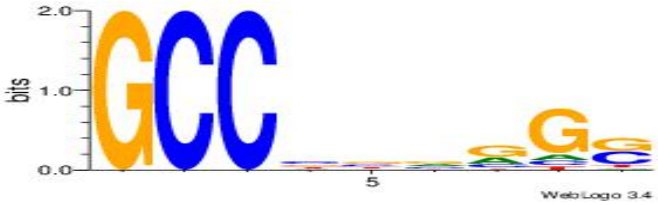
Alignment:
GTGACCTT
--CACCTD

Original motif Consensus sequence: AAGGTCAC

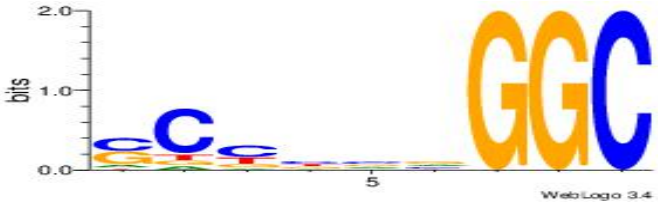
Reverse complement motif Consensus sequence: GTGACCTT

**Dataset #: 2 Motif ID: 15 Motif name: TFAP2A**

Original motif Consensus sequence: GCCBBVRGS




Reverse complement motif Consensus sequence: SCMVBBGGC



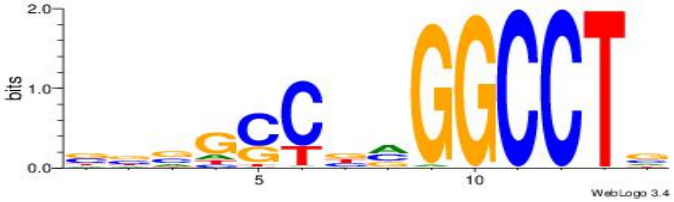

## Best Matches for Motif ID 15 (Highest to Lowest)

| | |
|---|---|
| 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: | 3 |
| Number of overlap: | 9 |
| Similarity score: | 0.0131247 |

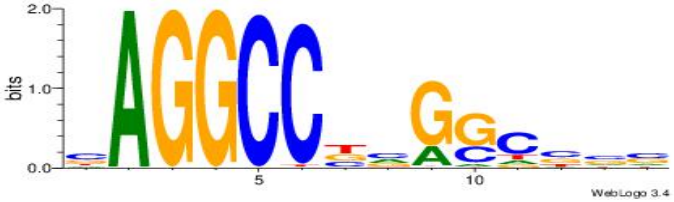
Alignment:

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

Original motif Consensus sequence: BBVGCCBVGGCCTV




Reverse complement motif Consensus sequence: VAGGCCBBGGCVB

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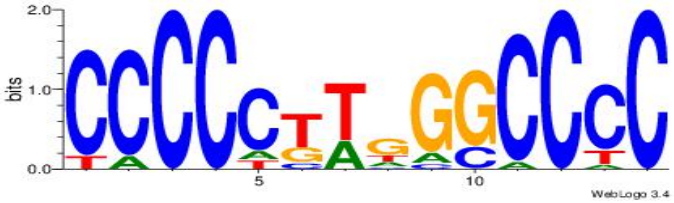
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 21 |
| Motif name: | PLAG1 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 4 |
| Number of overlap: | 9 |
| Similarity score: | 0.0414588 |

Alignment:

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

Original motif Consensus sequence: GGGGCCCAAGGGGG

Reverse complement motif Consensus sequence: CCCCCTTGGGCCC

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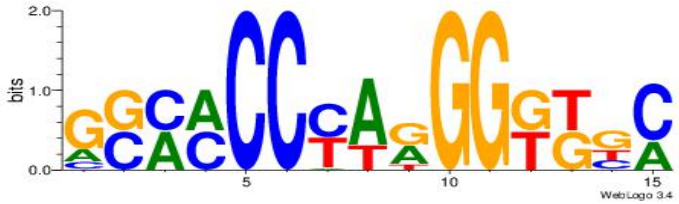
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 13 |
| Motif name: | Zfp423 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction: | Backward |
| Position number: | 4 |
| Number of overlap: | 9 |
| Similarity score: | 0.0438157 |

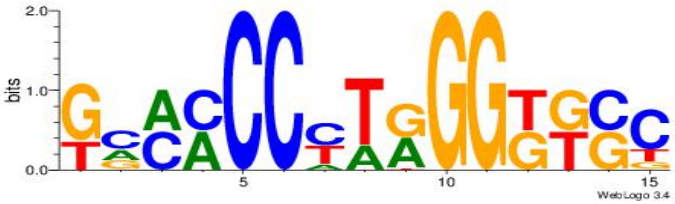
Alignment:

```
GYRYCCMTKGGYRSC
---SCMVBBGGC---
```

Original motif Consensus sequence: GSMMCCYARGGKKKC




Reverse complement motif Consensus sequence: GYRYCCMTKGGYR

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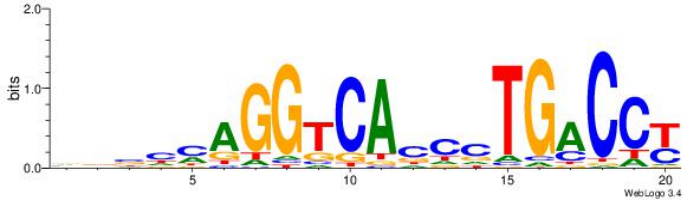
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 29 |
| Motif name: | ESR1 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Reverse Complement |
| Direction: | Backward |
| Position number: | 2 |
| Number of overlap: | 9 |

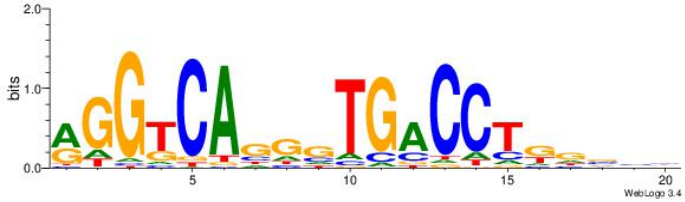
Similarity score: 0.0450672

Alignment:
MGGTCAGGGTGACCTRDBHV
----------GCCBBVRGS-

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY




Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV



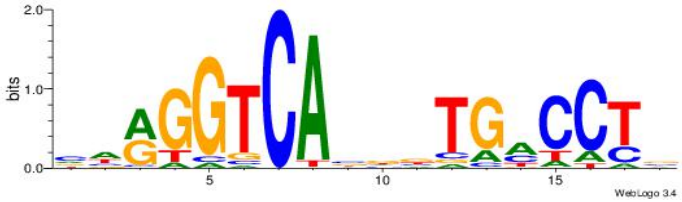

---

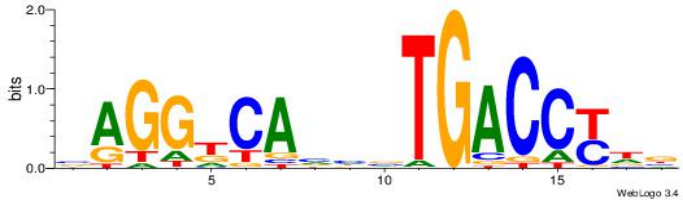
Dataset #: 2
Motif ID: 30
Motif name: ESR2
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 6
Number of overlap: 9
Similarity score: 0.0531668

Alignment:
BAGGYCABHBTGACCKHV
-----SCMVBBGGC----

Original motif Consensus sequence: VHRGGTCABDBTGMCCTB

Reverse complement motif Consensus sequence: BAGGYCABHBTGACCKHV

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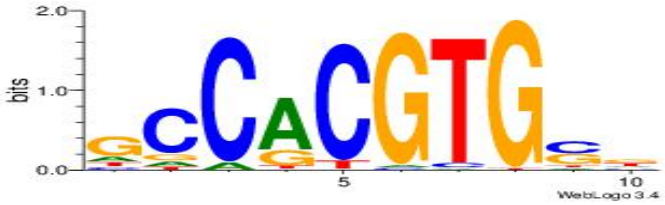
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 40 |
| Motif name: | Mycn |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 2 |
| Number of overlap: | 9 |
| Similarity score: | 0.0550803 |

Alignment:

```
HSCACGTGGC
-SCMVBBGGC
```

Original motif Consensus sequence: HSCACGTGGC

Reverse complement motif Consensus sequence: GCCACGTGSD

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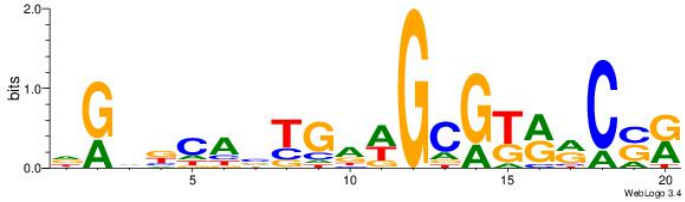
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 45 |

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

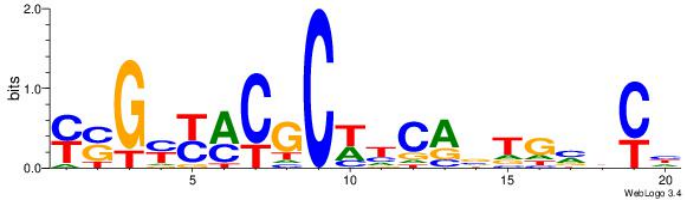
Alignment:

```
MSGKKRCGCWDCABTGBBCD
-------GCCBBVRGS----
```

Original motif Consensus sequence: DGVBCABTGDWGCGKRRCSR




Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD

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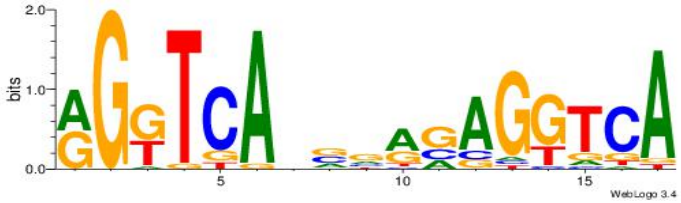
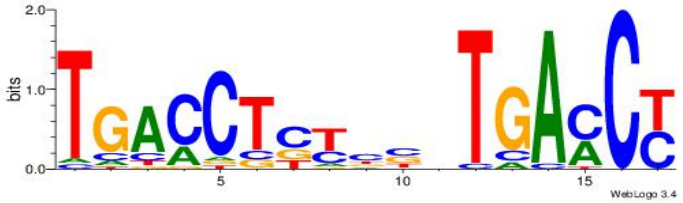
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 47 |
| Motif name: | RXRRAR_DR5 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 7 |
| Number of overlap: | 9 |
| Similarity score: | 0.0606062 |

Alignment:
RGKTCABVVRGAGGTCA
--GCCBBVRGS------

Original motif Consensus sequence: RGKTCABVVRGAGGTCA




Reverse complement motif Consensus sequence: TGACCTCKVVBTGAYCK

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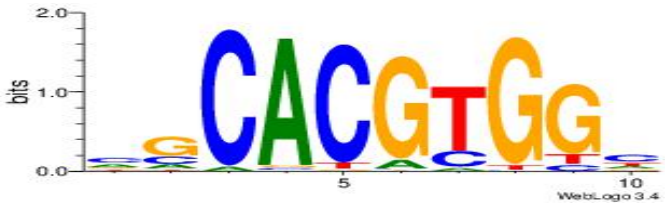
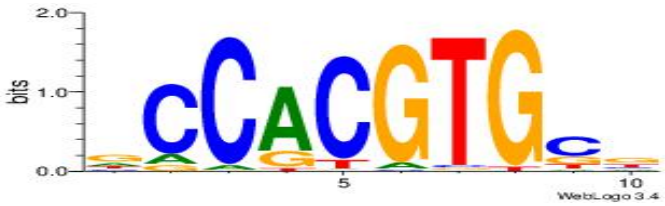
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 38 |
| Motif name: | Myc |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 2 |
| Number of overlap: | 9 |
| Similarity score: | 0.0613455 |

Alignment:
VGCACGTGGH
-SCMVBBGGC

Original motif Consensus sequence: VGCACGTGGH

Reverse complement motif Consensus sequence: DCCACGTGCV



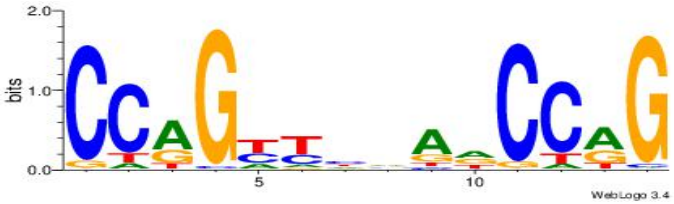




| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 48 |
| Motif name: | Tcfcp2l1 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 3 |
| Number of overlap: | 9 |
| Similarity score: | 0.0631412 |

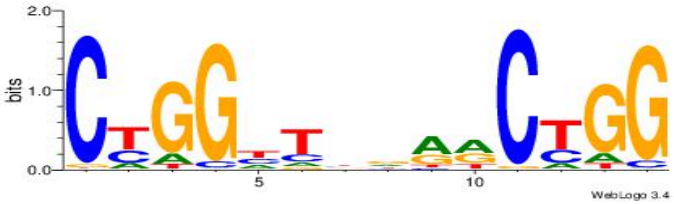
Alignment:

```
CCAGYYHVADCCRG
---GCCBBVRGS--
```

Original motif Consensus sequence: CCAGYYHVADCCRG

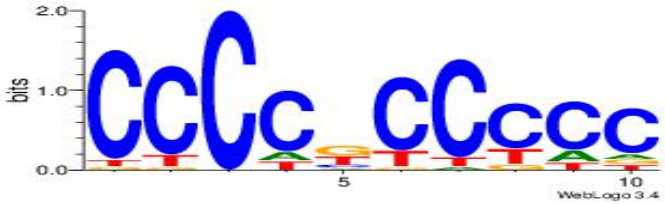



Reverse complement motif Consensus sequence: CKGGDTBDMMCTG

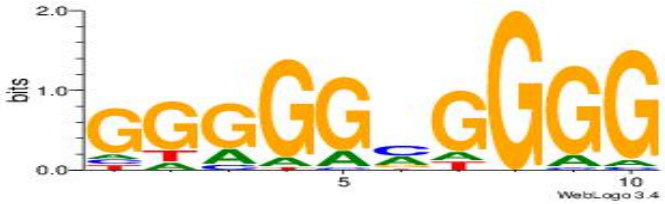



**Dataset #: 2 Motif ID: 16 Motif name: SP1**

Original motif Consensus sequence: CCCCKCCCCC




Reverse complement motif Consensus sequence: GGGGGYGGGG



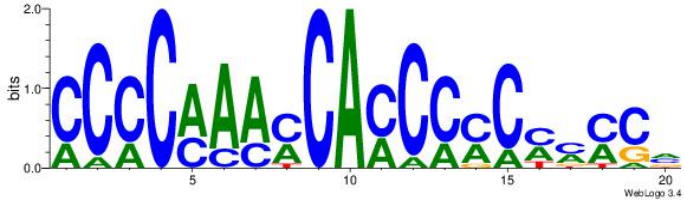

## Best Matches for Motif ID 16 (Highest to Lowest)

| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 18 |
| Motif name: | RREB1 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction: | Forward |
| Position number: | 2 |
| Number of overlap: | 10 |
| Similarity score: | 0.0646465 |

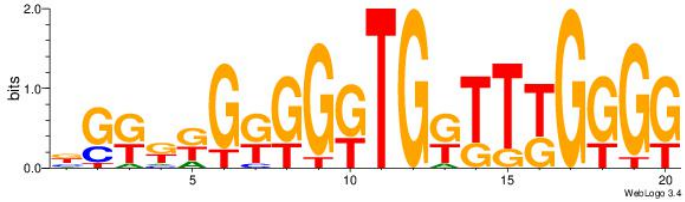
Alignment:

```
BGRRRGRGGRTGRTTYGGGG
-GGGGGYGGGG---------
```

Original motif Consensus sequence: CCCCMAAMCAMCCMCMMMCV




Reverse complement motif Consensus sequence: BGRRRGRGGRTGRTTYGGGG

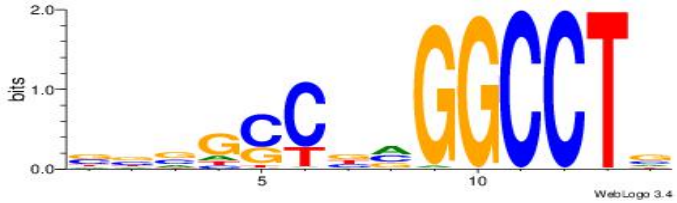


| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 12 |
| Motif name: | Zfx |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 5 |
| Number of overlap: | 10 |
| Similarity score: | 0.0664832 |

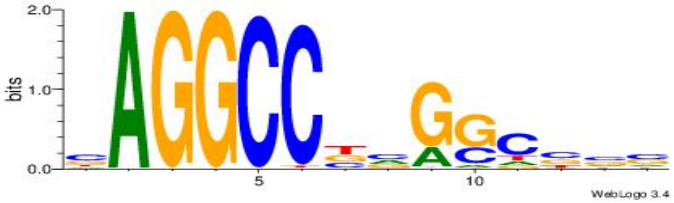
Alignment:

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

Original motif Consensus sequence: BBVGCCBVGGCCTV




Reverse complement motif Consensus sequence: VAGGCCBBGGCVB

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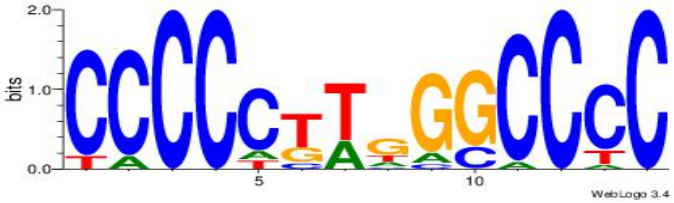
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 21 |
| Motif name: | PLAG1 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Reverse Complement |
| Direction: | Backward |
| Position number: | 4 |
| Number of overlap: | 10 |

Similarity score: 0.0725

Alignment:
CCCCCTTGGGCCCC
-CCCCKCCCCC---

Original motif Consensus sequence: GGGGCCCAAGGGGG

Reverse complement motif Consensus sequence: CCCCCTTGGGCCC



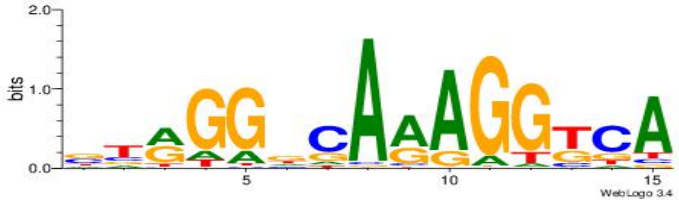

---

Dataset #: 2
Motif ID: 20
Motif name: PPARGRXRA
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 4
Number of overlap: 10
Similarity score: 0.0731995

Alignment:
TGRCCTKTGHCCKAB
--CCCCKCCCCC---

Original motif Consensus sequence: BTRGGDCARAGGKCA

Reverse complement motif Consensus sequence: TGRCCTKTGHCCK



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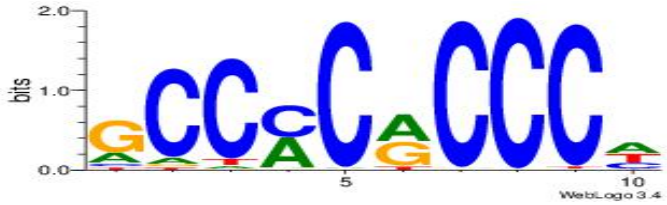
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 36 |
| Motif name: | Klf4 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Reverse Complement |
| Direction: | Backward |
| Position number: | 1 |
| Number of overlap: | 10 |
| Similarity score: | 0.0761191 |

Alignment:

```
GCCYCMCCCD
CCCCKCCCCC
```

Original motif Consensus sequence: DGGGYGKGGC

Reverse complement motif Consensus sequence: GCCYCMCCCD

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| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 28 |

| | |
|---|---|
| Motif name: | Egr1 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 1 |
| Number of overlap: | 10 |
| Similarity score: | 0.0798413 |

Alignment:

```
HGCGTGGGCGK
GGGGGYGGGG-
```

Original motif Consensus sequence: HGCGTGGGCGK

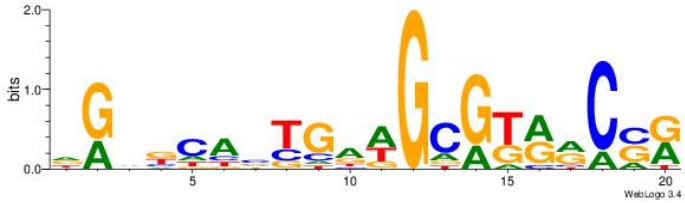
Reverse complement motif Consensus sequence: YCGCCCACGCH

---

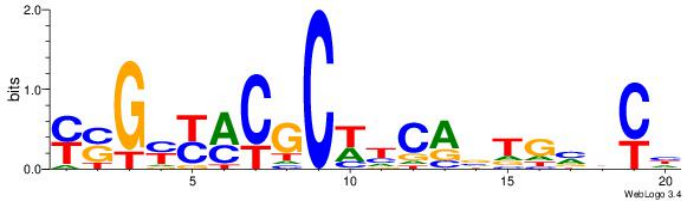
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 45 |
| Motif name: | Pax5 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 8 |
| Number of overlap: | 10 |
| Similarity score: | 0.0846627 |

Alignment:
DGVBCABTGDWGCGKRRCSR
-------GGGGGYGGGG---

Original motif Consensus sequence: DGVBCABTGDWGCGKRRCSR




Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD

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| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 41 |
| Motif name: | MZF1_5-13 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 1 |
| Number of overlap: | 10 |
| Similarity score: | 0.0884127 |

Alignment:
BKAGGGGDAD
GGGGGYGGGG

Original motif Consensus sequence: BKAGGGGDAD

Reverse complement motif Consensus sequence: BTHCCCCTYB

---

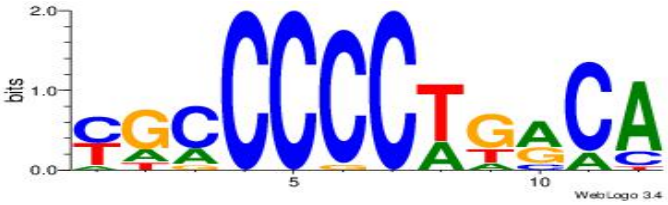
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 35 |
| Motif name: | INSM1 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 3 |
| Number of overlap: | 10 |
| Similarity score: | 0.089127 |

Alignment:

```
TGYCAGGGGGCR
GGGGGYGGGG--
```

Original motif Consensus sequence: TGYCAGGGGGCR

Reverse complement motif Consensus sequence: MGCCCCCTGMCA

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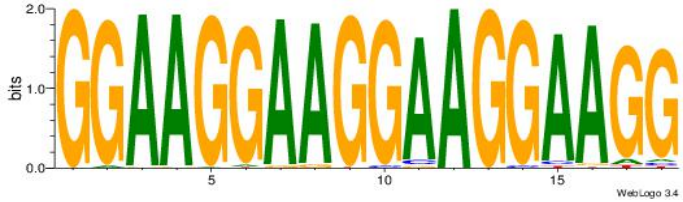
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 32 |

| | |
|---|---|
| Motif name: | EWSR1-FLI1 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Reverse Complement |
| Direction: | Backward |
| Position number: | 6 |
| Number of overlap: | 10 |
| Similarity score: | 0.0893651 |

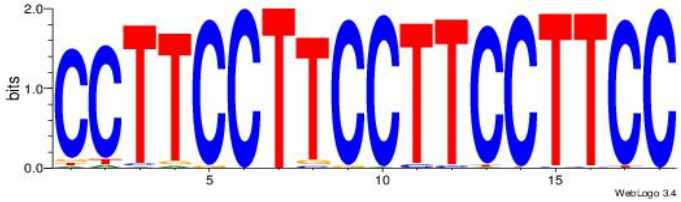
Alignment:

```
CCTTCCTTCCTTCCTTCC
---CCCCKCCCCC-----
```

Original motif Consensus sequence: GGAAGGAAGGAAGGAAGG




Reverse complement motif Consensus sequence: CCTTCCTTCCTTCCTTCC

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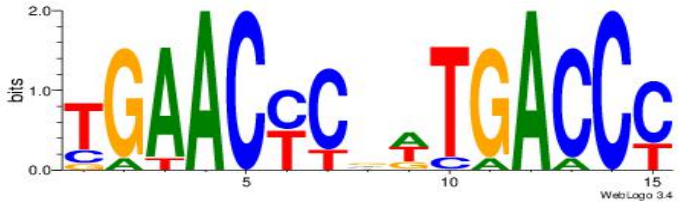
**Dataset #: 2 Motif ID: 17 Motif name: RXRAVDR**

Original motif Consensus sequence: GGGTCAWBGRGTTCA

Reverse complement motif Consensus sequence: TGAACKCBWTGAC



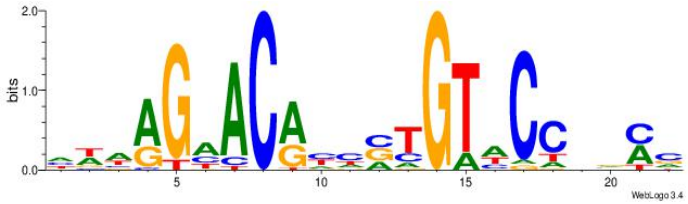
## Best Matches for Motif ID 17 (Highest to Lowest)

| | |
|---|---|
| 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: | 5 |
| Number of overlap: | 15 |
| Similarity score: | 0.0566667 |

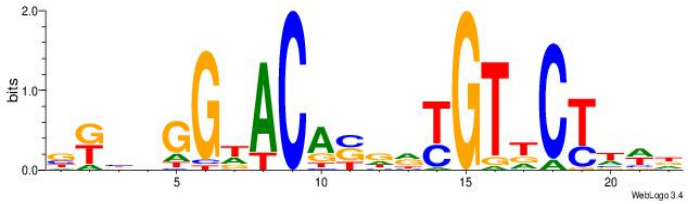
Alignment:

```
HWDAGHACRHHVTGTHCCHVMV
---TGAACKCBWTGACCC----
```

Original motif Consensus sequence: HWDAGHACRHHVTGTHCCHVMV




Reverse complement motif Consensus sequence: VRVDGGHACAVDDKGTHCTDWH

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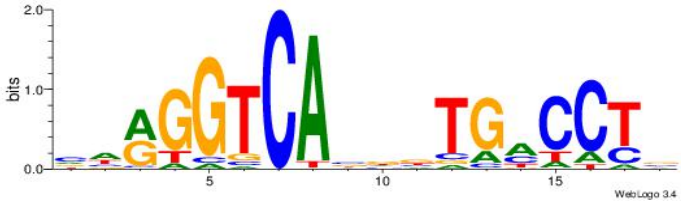
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 30 |
| Motif name: | ESR2 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |

| | |
|---|---|
| Direction: | Forward |
| Position number: | 3 |
| Number of overlap: | 15 |
| Similarity score: | 0.0617507 |

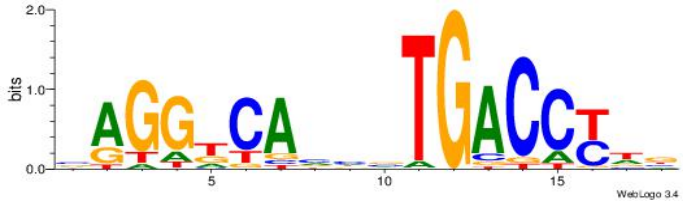
Alignment:

```
VHRGGTCABDBTGMCCTB
--GGGTCAWBGRGTTCA-
```

Original motif Consensus sequence: VHRGGTCABDBTGMCCTB




Reverse complement motif Consensus sequence: BAGGYCABHBTGACCKHV

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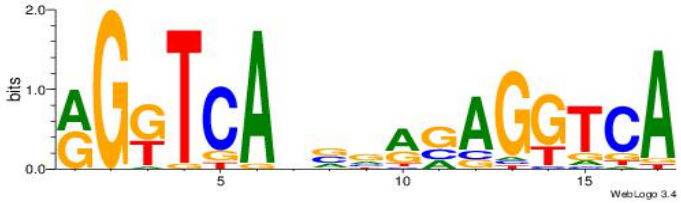
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 47 |
| Motif name: | RXRRAR_DR5 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 3 |
| Number of overlap: | 15 |
| Similarity score: | 0.062029 |

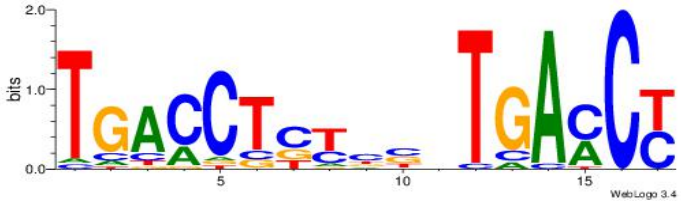
Alignment:

```
RGKTCABVVRGAGGTCA
GGGTCAWBGRGTTCA--
```

Original motif Consensus sequence: RGKTCABVVRGAGGTCA



Reverse complement motif Consensus sequence: TGACCTCKVVBTGAYCK

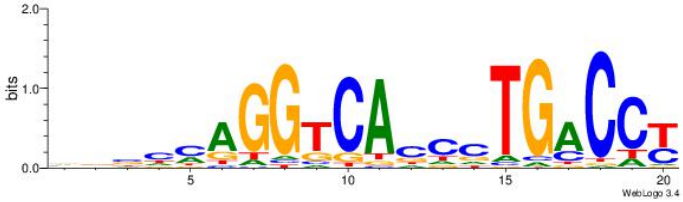


| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 29 |
| Motif name: | ESR1 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 1 |
| Number of overlap: | 15 |
| Similarity score: | 0.0714525 |

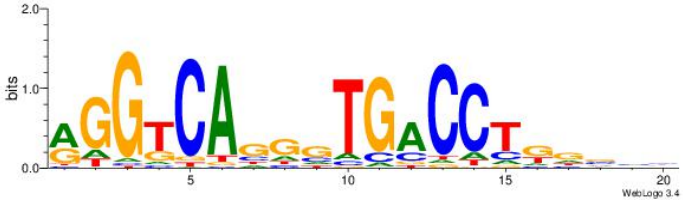
Alignment:

```
VDBHMAGGTCACCCTGACCY
-----TGAACKCBWTGACCC
```

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV

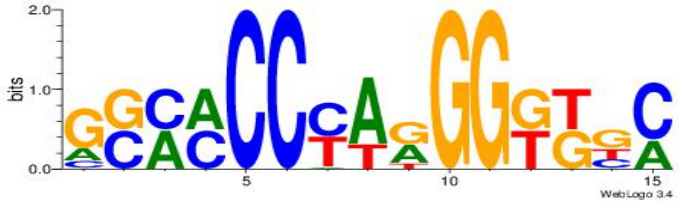


| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 13 |
| Motif name: | Zfp423 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 1 |
| Number of overlap: | 15 |
| Similarity score: | 0.0849495 |

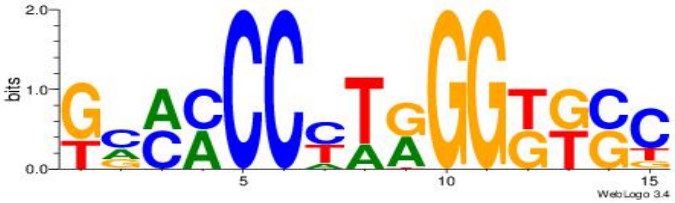
Alignment:

```
GSMMCCYARGGKKKC
TGAACKCBWTGACCC
```

Original motif Consensus sequence: GSMMCCYARGGKKKC




Reverse complement motif Consensus sequence: GYRYCCMTKGGYR

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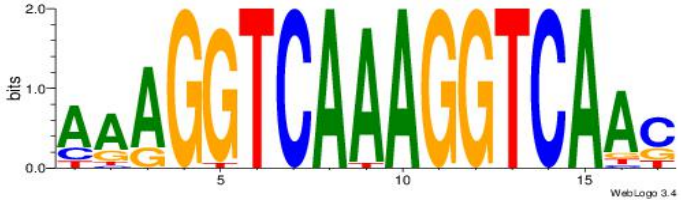
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 43 |
| Motif name: | NR1H2RXRA |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 3 |
| Number of overlap: | 15 |

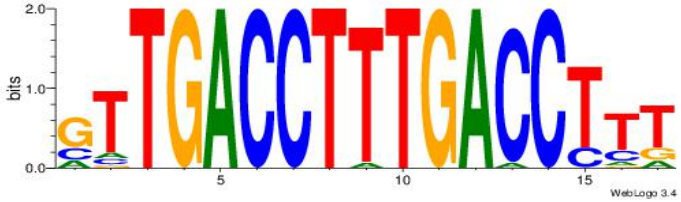
Similarity score: 0.0866667

Alignment:
AAAGGTCAAAGGTCAAC
--GGGTCAWBGRGTTCA

Original motif Consensus sequence: AAAGGTCAAAGGTCAAC




Reverse complement motif Consensus sequence: GTTGACCTTTGACCTTT

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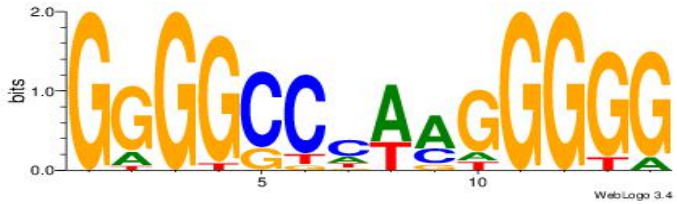
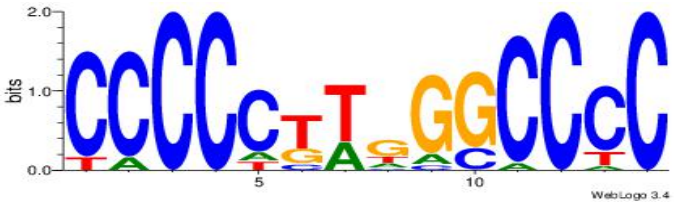
Dataset #: 2
Motif ID: 21
Motif name: PLAG1
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 2
Number of overlap: 13
Similarity score: 1.06201

Alignment:
GGGGCCCAAGGGGG--
-GGGTCAWBGRGTTCA

Original motif Consensus sequence: GGGGCCCAAGGGGG

Reverse complement motif Consensus sequence: CCCCCTTGGGCCC



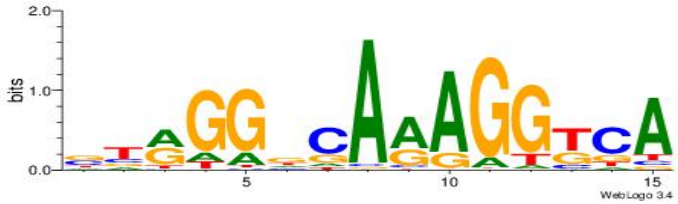




| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 20 |
| Motif name: | PPARGRXRA |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 3 |
| Number of overlap: | 13 |
| Similarity score: | 1.07837 |

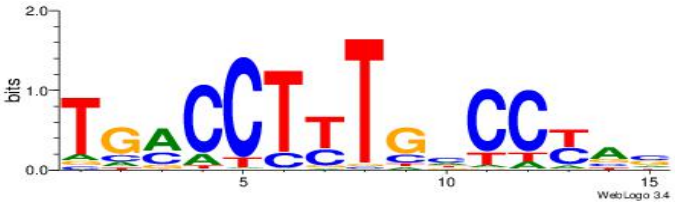
Alignment:

```
BTRGGDCARAGGKCA--
--GGGTCAWBGRGTTCA
```

Original motif Consensus sequence: BTRGGDCARAGGKCA




Reverse complement motif Consensus sequence: TGRCCTKTGHCCK



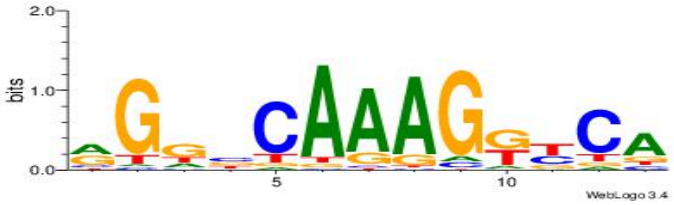

| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 34 |

| | |
|---|---|
| Motif name: | HNF4A |
| 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: | 1.0801 |

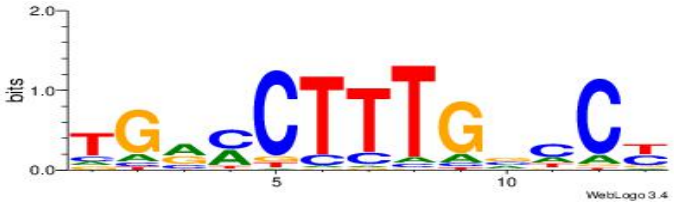
Alignment:

```
RGGBCAAAGKYCA--
GGGTCAWBGRGTTCA
```

Original motif Consensus sequence: RGGBCAAAGKYCA




Reverse complement motif Consensus sequence: TGMYCTTTGBCCK

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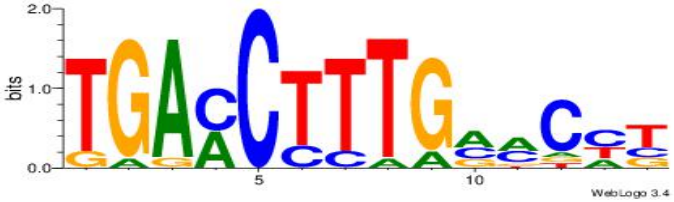
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 22 |
| Motif name: | NR2F1 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Reverse Complement |
| Direction: | Forward |
| Position number: | 2 |
| Number of overlap: | 13 |
| Similarity score: | 1.08482 |

Alignment:
AKGYYCAAAGRTCA--
-GGGTCAWBGRGTTCA

Original motif Consensus sequence: TGAMCTTTGMMCYT

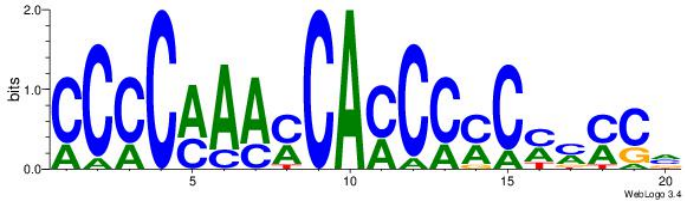



Reverse complement motif Consensus sequence: AKGYYCAAAGRTCA

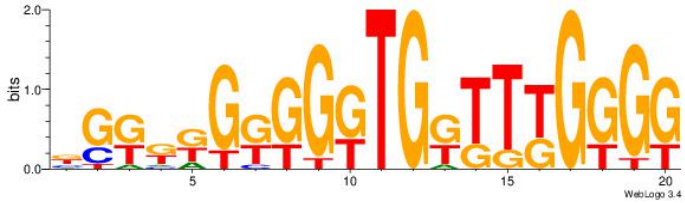
---

**Dataset #: 2 Motif ID: 18 Motif name: RREB1**

Original motif Consensus sequence: CCCCMAAMCAMCCMCMMMCV




Reverse complement motif Consensus sequence: BGRRRGRGGRTGRTTYGGGG



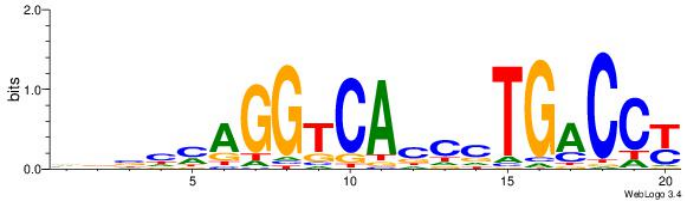

**Best Matches for Motif ID 18 (Highest to Lowest)**

| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 29 |
| Motif name: | ESR1 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction: | Backward |

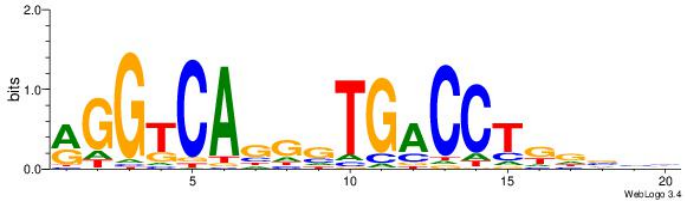
Position number: 2
Number of overlap: 19
Similarity score: 0.0874679

Alignment:
-MGGTCAGGGTGACCTRDBHV
BGRRRGRGGRTGRTTYGGGG-

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY




Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV

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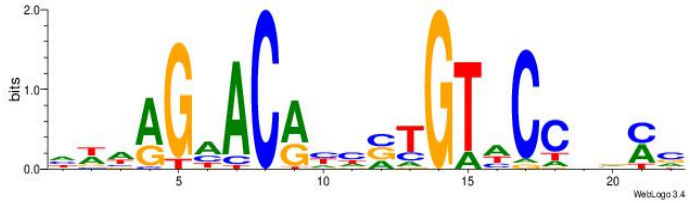
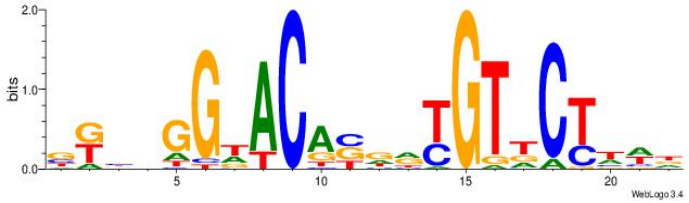
Dataset #: 2
Motif ID: 24
Motif name: Ar
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 4
Number of overlap: 19
Similarity score: 0.0927532

Alignment:
-HWDAGHACRHHVTGTHCCHVMV
CCCCMAAMCAMCCMCMMMCV---

Original motif Consensus sequence: HWDAGHACRHHVTGTHCCHVMV



Reverse complement motif Consensus sequence: VRVDGGHACAVDDKGTHCTDWH

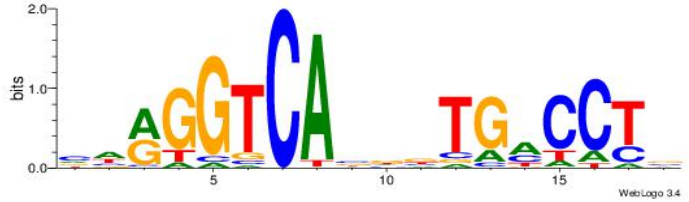


| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 30 |
| Motif name: | ESR2 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction: | Forward |
| Position number: | 1 |
| Number of overlap: | 18 |
| Similarity score: | 0.593122 |

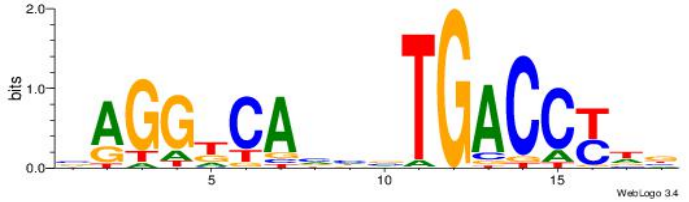
Alignment:

```
BAGGYCABHBTGACCKHV--
BGRRRGRGGRTGRTTYGGGG
```

Original motif Consensus sequence: VHRGGTCABDBTGMCCTB



Reverse complement motif Consensus sequence: BAGGYCABHBTGACCKHV

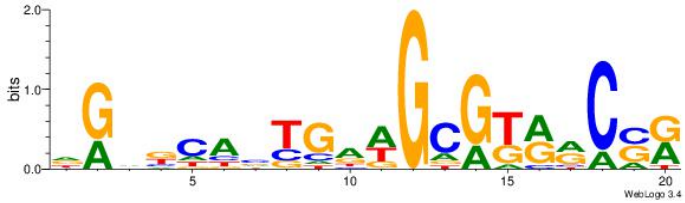


| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 45 |
| Motif name: | Pax5 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 4 |
| Number of overlap: | 17 |
| Similarity score: | 1.09431 |

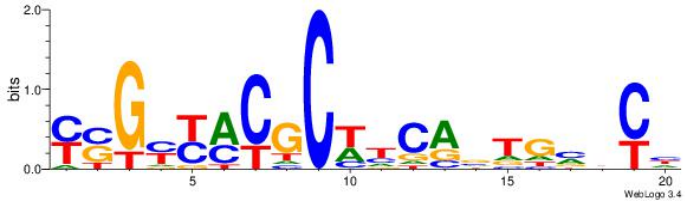
Alignment:

```
---DGVBCABTGDWGCGKRRCSR
BGRRRGRGGRTGRTTYGGGG---
```

Original motif Consensus sequence: DGVBCABTGDWGCGKRRCSR




Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD

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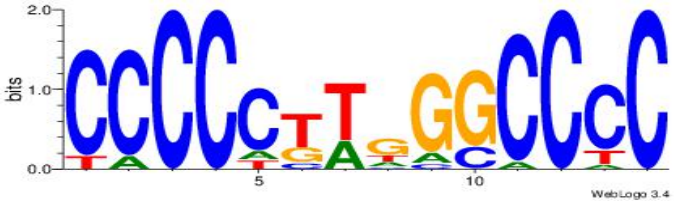
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 21 |
| Motif name: | PLAG1 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Reverse Complement |
| Direction: | Forward |
| Position number: | 1 |

Number of overlap: 14
Similarity score: 2.5804

Alignment:
CCCCCTTGGGCCCC------
CCCCMAAMCAMCCMCMMMCV

Original motif Consensus sequence: GGGGCCCAAGGGGG

Reverse complement motif Consensus sequence: CCCCCTTGGGCCC

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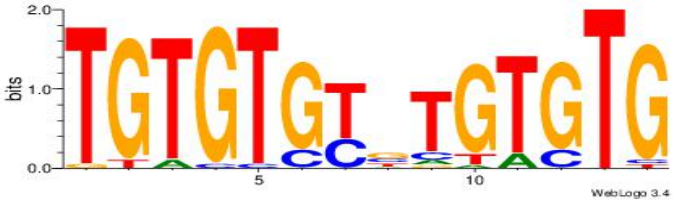
Dataset #: 1
Motif ID: 9
Motif name: Motif 9
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 14
Similarity score: 2.58596

Alignment:
------CACACAVRCACACA
CCCCMAAMCAMCCMCMMMCV

Original motif Consensus sequence: CACACAVRCACACA

Reverse complement motif Consensus sequence: TGTGTGKVTGTGT



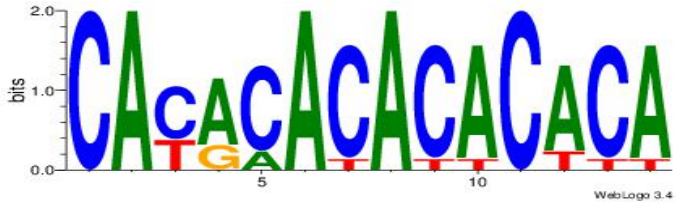

---

| | |
|---|---|
| Dataset #: | 1 |
| Motif ID: | 11 |
| Motif name: | Motif 11 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 1 |
| Number of overlap: | 14 |
| Similarity score: | 2.59077 |

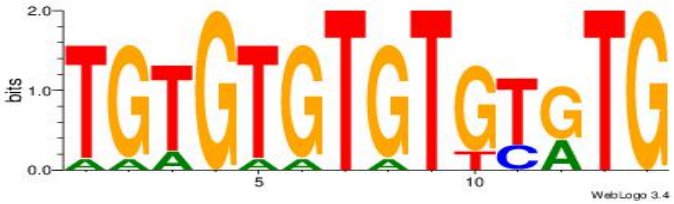
Alignment:

```
------CAYACACACACACA
CCCCMAAMCAMCCMCMMMCV
```

Original motif Consensus sequence: CAYACACACACACA




Reverse complement motif Consensus sequence: TGTGTGTGTGTKT

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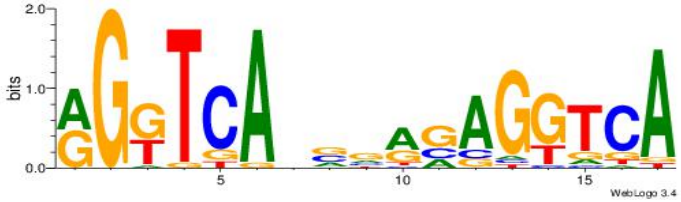
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 47 |

| | |
|---|---|
| Motif name: | RXRRAR_DR5 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 5 |
| Number of overlap: | 13 |
| Similarity score: | 3.07964 |

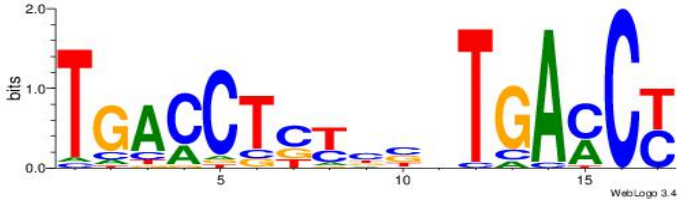
Alignment:

```
RGKTCABVVRGAGGTCA-------
----BGRRRGRGGRTGRTTYGGGG
```

Original motif Consensus sequence: RGKTCABVVRGAGGTCA




Reverse complement motif Consensus sequence: TGACCTCKVVBTGAYCK

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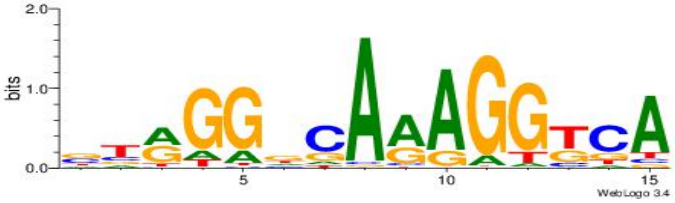
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 20 |
| Motif name: | PPARGRXRA |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 3 |
| Number of overlap: | 13 |
| Similarity score: | 3.08033 |

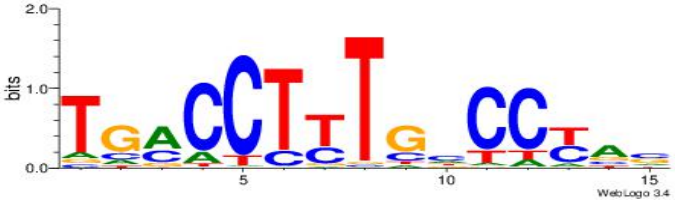
Alignment:

```
BTRGGDCARAGGKCA-------
--BGRRRGRGGRTGRTTYGGGG
```

Original motif Consensus sequence: BTRGGDCARAGGKCA




Reverse complement motif Consensus sequence: TGRCCTKTGHCCK

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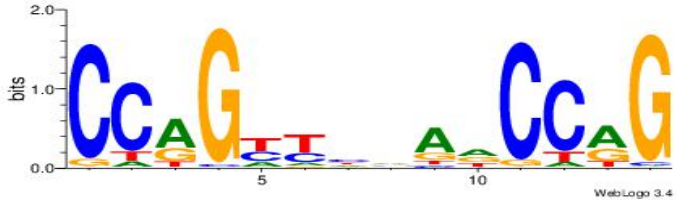
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 48 |
| Motif name: | Tcfcp2l1 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 2 |
| Number of overlap: | 13 |
| Similarity score: | 3.08771 |

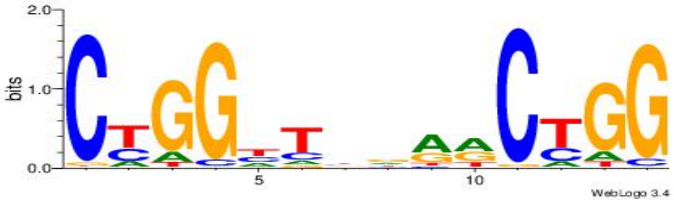
Alignment:

```
-------CCAGYYHVADCCRG
CCCCMAAMCAMCCMCMMMCV-
```

Original motif Consensus sequence: CCAGYYHVADCCRG

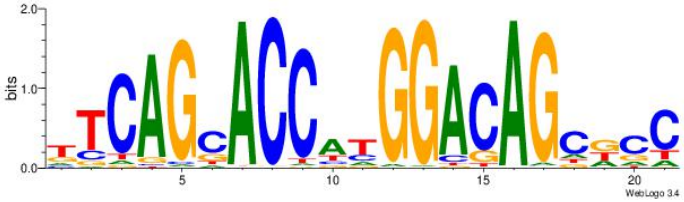
Reverse complement motif Consensus sequence: CKGGDTBDMMCT



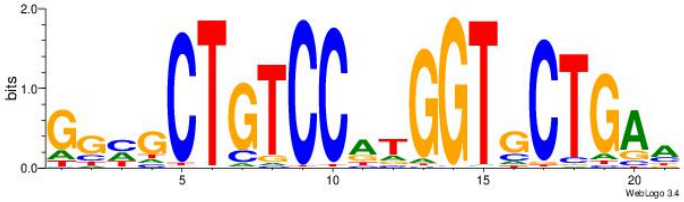




**Dataset #: 2 Motif ID: 19 Motif name: REST**

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC




Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA



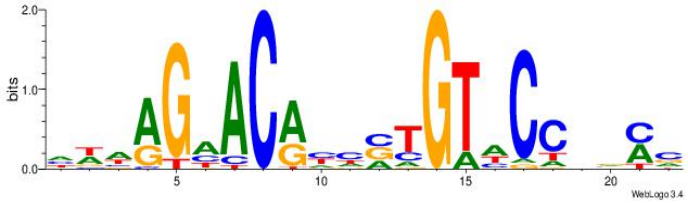

## Best Matches for Motif ID 19 (Highest to Lowest)

| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 24 |
| Motif name: | Ar |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction: | Backward |
| Position number: | 1 |
| Number of overlap: | 21 |
| Similarity score: | 0.0685835 |

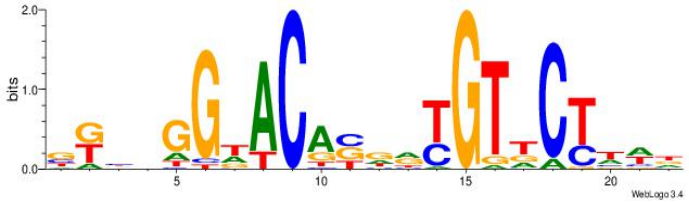
Alignment:

VRVDGGHACAVDDKGTHCTDWH
-GGYGCTGTCCATGGTGCTGAA

Original motif Consensus sequence: HWDAGHACRHHVTGTHCCHVMV




Reverse complement motif Consensus sequence: VRVDGGHACAVDDKGTHCTDWH

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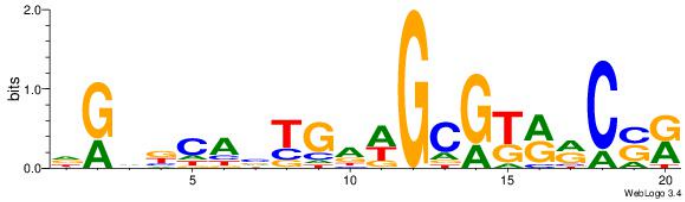
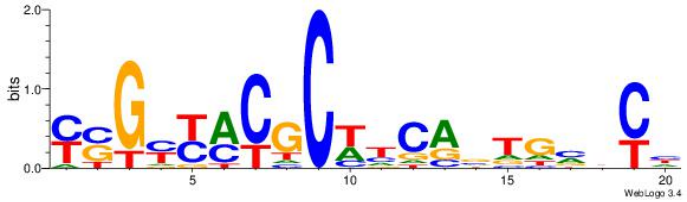
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 45 |
| Motif name: | Pax5 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction: | Forward |
| Position number: | 3 |
| Number of overlap: | 18 |
| Similarity score: | 1.577 |

Alignment:
MSGKKRCGCWDCABTGBBCD---
--GGYGCTGTCCATGGTGCTGAA

Original motif Consensus sequence: DGVBCABTGDWGCGKRRCSR

Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD



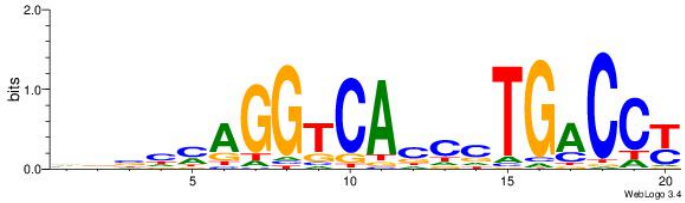




| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 29 |
| Motif name: | ESR1 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 5 |
| Number of overlap: | 16 |
| Similarity score: | 2.56863 |

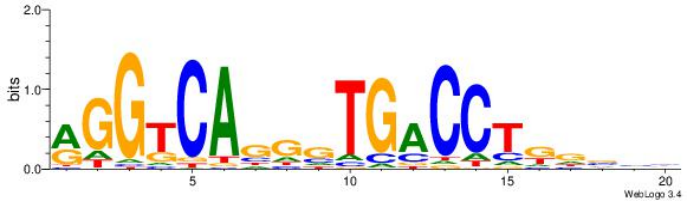
Alignment:

```
-----VDBHMAGGTCACCCTGACCY
TTCAGCACCATGGACAGCKCC----
```

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY




Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV



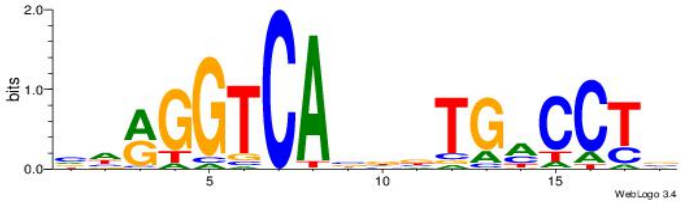

| | |
|---|---|
| Dataset #: | 2 |

| | |
|---|---|
| Motif ID: | 30 |
| Motif name: | ESR2 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction: | Forward |
| Position number: | 6 |
| Number of overlap: | 13 |
| Similarity score: | 4.05754 |

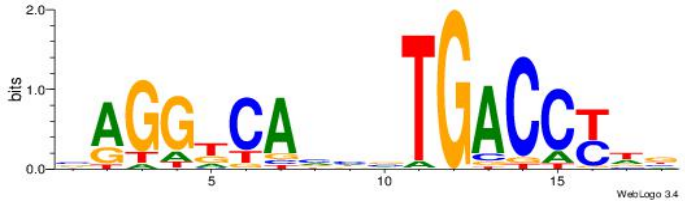
Alignment:

```
BAGGYCABHBTGACCKHV--------
-----GGYGCTGTCCATGGTGCTGAA
```

Original motif Consensus sequence: VHRGGTCABDBTGMCCTB




Reverse complement motif Consensus sequence: BAGGYCABHBTGACCKHV

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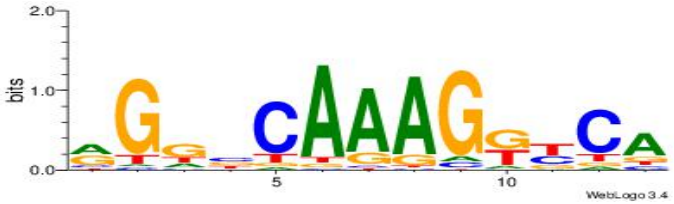
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 34 |
| Motif name: | HNF4A |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction: | Forward |
| Position number: | 1 |
| Number of overlap: | 13 |

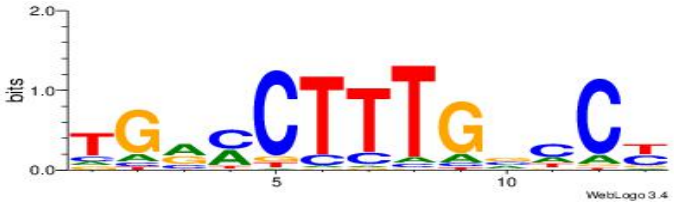
Similarity score: 4.06973

Alignment:
TGMYCTTTGBCCK--------
GGYGCTGTCCATGGTGCTGAA

Original motif Consensus sequence: RGGBCAAAGKYCA




Reverse complement motif Consensus sequence: TGMYCTTTGBCCK

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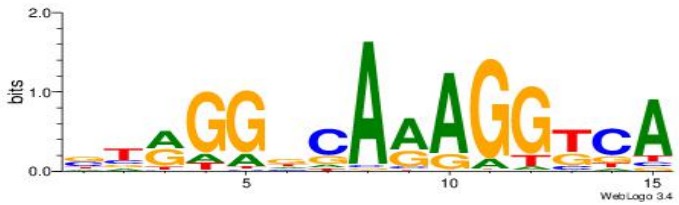
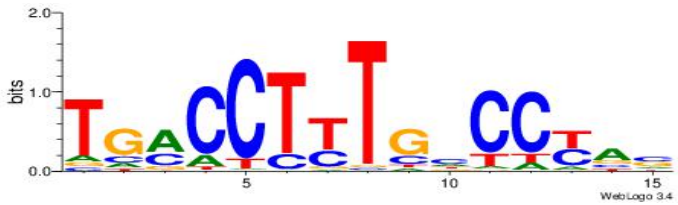
Dataset #: 2
Motif ID: 20
Motif name: PPARGRXRA
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 3
Number of overlap: 13
Similarity score: 4.07172

Alignment:
--------BTRGGDCARAGGKCA
TTCAGCACCATGGACAGCKCC--

Original motif Consensus sequence: BTRGGDCARAGGKCA

Reverse complement motif Consensus sequence: TGRCCTKTGHCCK

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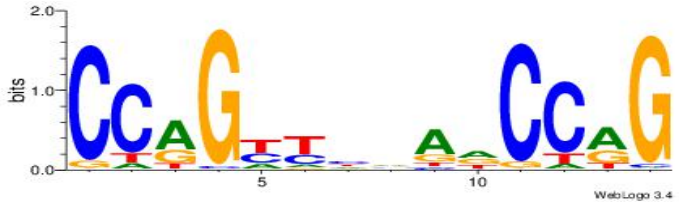
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 48 |
| Motif name: | Tcfcp2l1 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 3 |
| Number of overlap: | 12 |
| Similarity score: | 4.57098 |

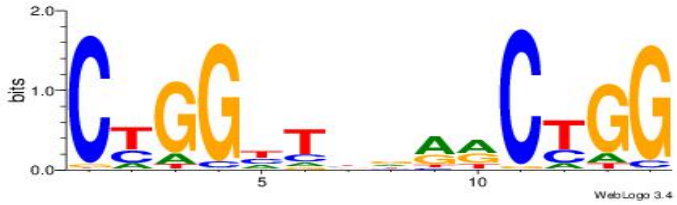
Alignment:

```
CCAGYYHVADCCRG---------
--GGYGCTGTCCATGGTGCTGAA
```

Original motif Consensus sequence: CCAGYYHVADCCRG




Reverse complement motif Consensus sequence: CKGGDTBDMMCT




---

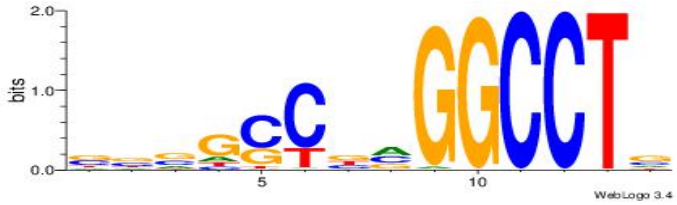
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 12 |

| | |
|---|---|
| Motif name: | Zfx |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 3 |
| Number of overlap: | 12 |
| Similarity score: | 4.57482 |

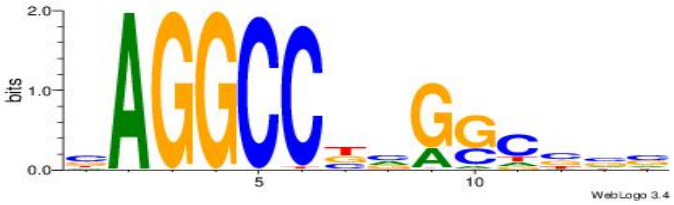
Alignment:

```
---------BBVGCCBVGGCCTV
GGYGCTGTCCATGGTGCTGAA--
```

Original motif Consensus sequence: BBVGCCBVGGCCTV




Reverse complement motif Consensus sequence: VAGGCCBBGGCVB

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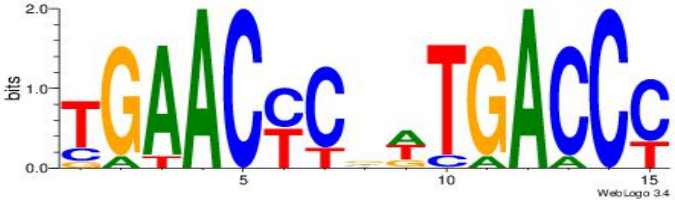
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 17 |
| Motif name: | RXRAVDR |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction: | Forward |
| Position number: | 5 |
| Number of overlap: | 11 |
| Similarity score: | 5.05758 |

Alignment:
TGAACKCBWTGACCC----------
----GGYGCTGTCCATGGTGCTGAA

Original motif Consensus sequence: GGGTCAWBGRGTTCA

Reverse complement motif Consensus sequence: TGAACKCBWTGAC

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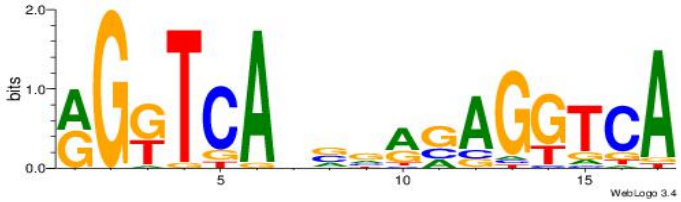
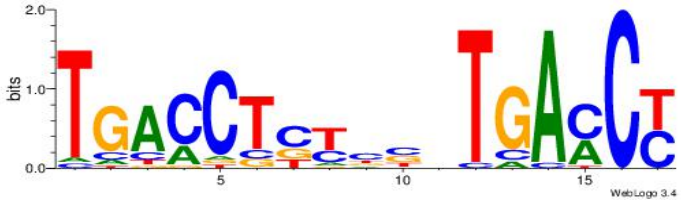
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 47 |
| Motif name: | RXRRAR_DR5 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction: | Forward |
| Position number: | 7 |
| Number of overlap: | 11 |
| Similarity score: | 5.05947 |

Alignment:
TGACCTCKVVBTGAYCK----------
------GGYGCTGTCCATGGTGCTGAA

Original motif Consensus sequence: RGKTCABVVRGAGGTCA

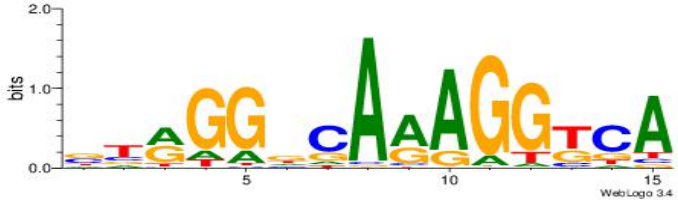
Reverse complement motif Consensus sequence: TGACCTCKVVBTGAYCK




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

Original motif Consensus sequence: BTRGGDCARAGGKCA




Reverse complement motif Consensus sequence: TGRCCTKTGHCCK

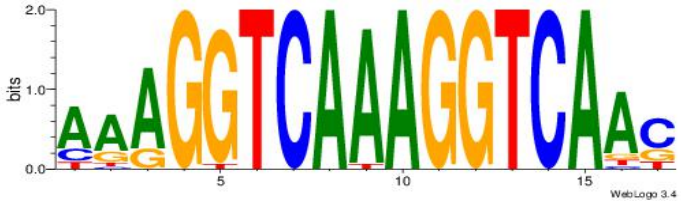
## Best Matches for Motif ID 20 (Highest to Lowest)

| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 43 |
| Motif name: | NR1H2RXRA |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 3 |
| Number of overlap: | 15 |
| Similarity score: | 0.0442974 |

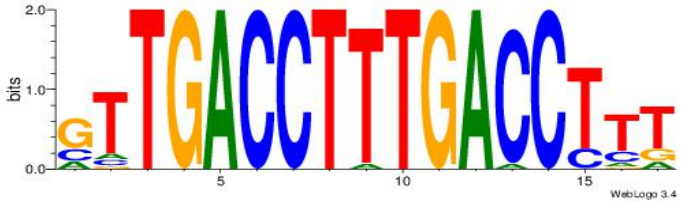
Alignment:

```
AAAGGTCAAAGGTCAAC
BTRGGDCARAGGKCA--
```

Original motif Consensus sequence: AAAGGTCAAAGGTCAAC




Reverse complement motif Consensus sequence: GTTGACCTTTGACCTTT

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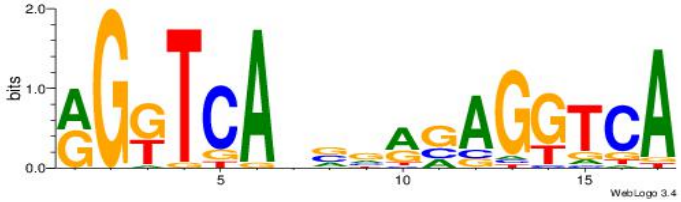
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 47 |
| Motif name: | RXRRAR_DR5 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 1 |
| Number of overlap: | 15 |
| Similarity score: | 0.0500583 |

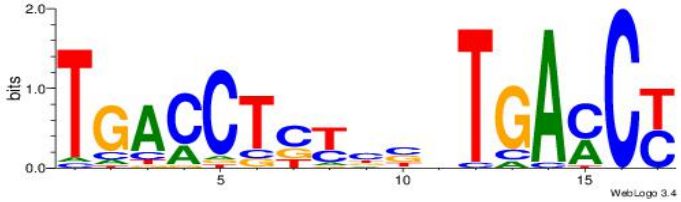
Alignment:

```
RGKTCABVVRGAGGTCA
--BTRGGDCARAGGKCA
```

Original motif Consensus sequence: RGKTCABVVRGAGGTCA




Reverse complement motif Consensus sequence: TGACCTCKVVBTGAYCK

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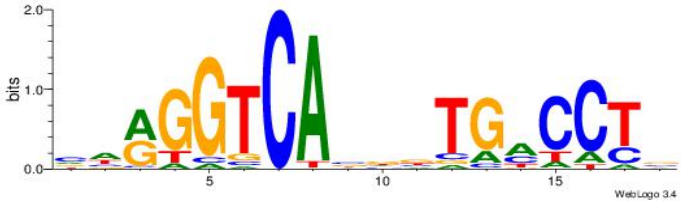
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 30 |
| Motif name: | ESR2 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 4 |
| Number of overlap: | 15 |
| Similarity score: | 0.0602408 |

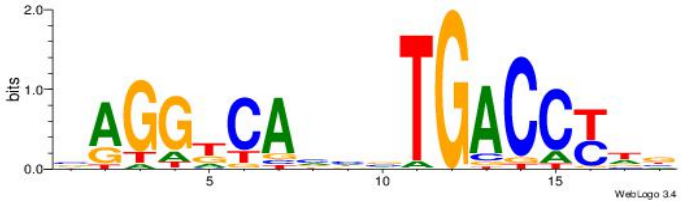
Alignment:

```
VHRGGTCABDBTGMCCTB
BTRGGDCARAGGKCA---
```

Original motif Consensus sequence: VHRGGTCABDBTGMCCTB




Reverse complement motif Consensus sequence: BAGGYCABHBTGACCKHV

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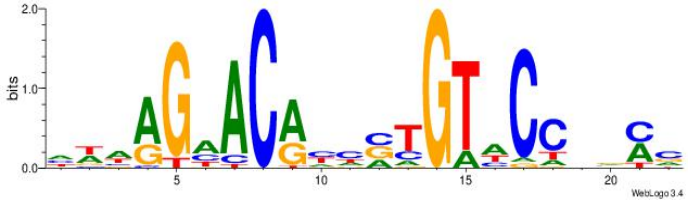
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 24 |
| Motif name: | Ar |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 8 |

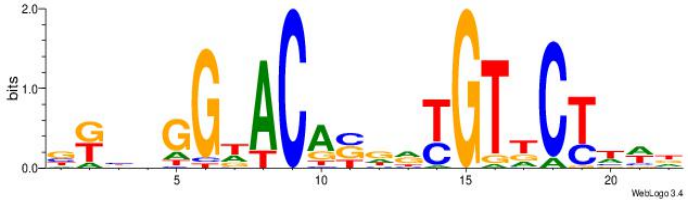
Number of overlap: 15
Similarity score: 0.0714981

Alignment:
HWDAGHACRHHVTGTHCCHVMV
-------TGRCCTKTGHCCKAB

Original motif Consensus sequence: HWDAGHACRHHVTGTHCCHVMV




Reverse complement motif Consensus sequence: VRVDGGHACAVDDKGTHCTDWH

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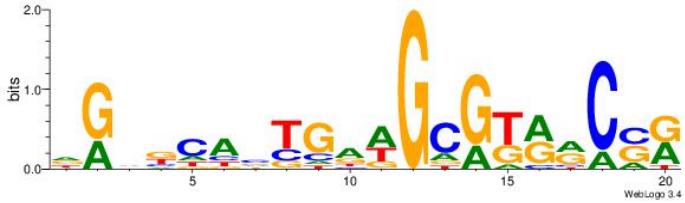
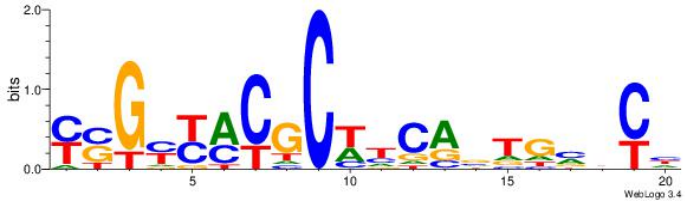
Dataset #: 2
Motif ID: 45
Motif name: Pax5
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 4
Number of overlap: 15
Similarity score: 0.0720255

Alignment:
MSGKKRCGCWDCABTGBBCD
---TGRCCTKTGHCCKAB--

Original motif Consensus sequence: DGVBCABTGDWGCGKRRCSR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD

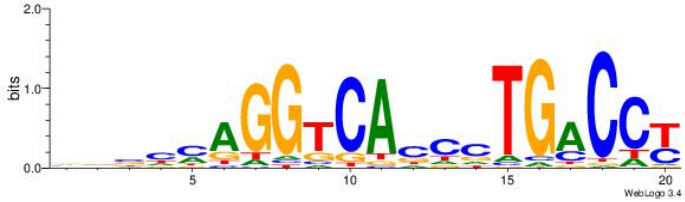


| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 29 |
| Motif name: | ESR1 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 3 |
| Number of overlap: | 15 |
| Similarity score: | 0.0723092 |

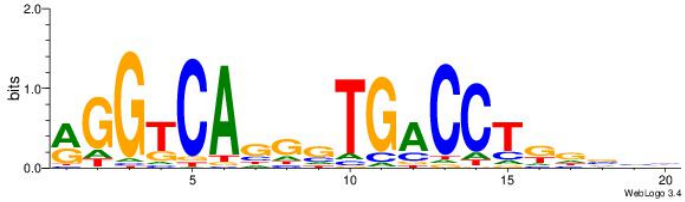
Alignment:

```
VDBHMAGGTCACCCTGACCY
---BTRGGDCARAGGKCA--
```

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV

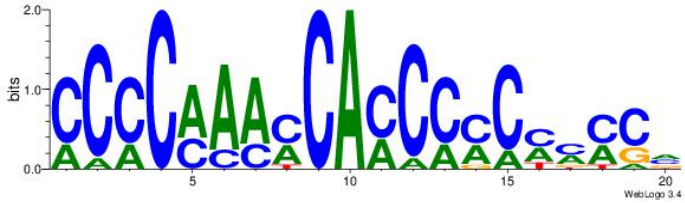


| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 18 |
| Motif name: | RREB1 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 2 |
| Number of overlap: | 15 |
| Similarity score: | 0.0755648 |

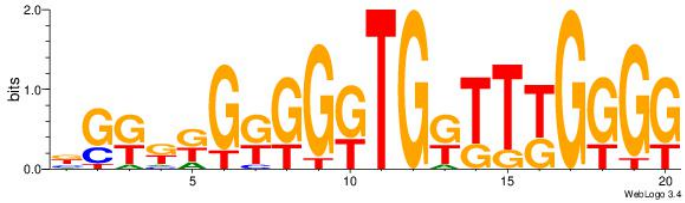
Alignment:

```
CCCCMAAMCAMCCMCMMMCV
-TGRCCTKTGHCCKAB----
```

Original motif Consensus sequence: CCCCMAAMCAMCCMCMMMCV




Reverse complement motif Consensus sequence: BGRRRGRGGRTGRTTYGGGG

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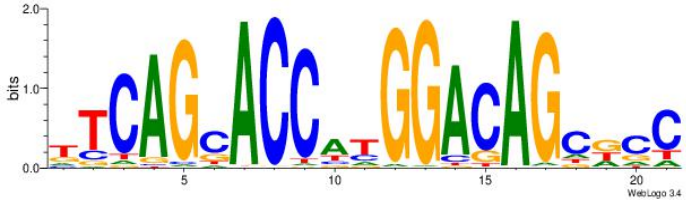
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 19 |
| Motif name: | REST |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 2 |

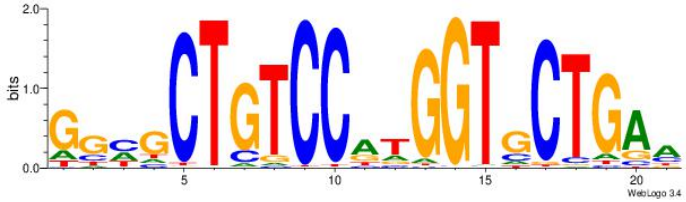
Number of overlap: 15
Similarity score: 0.0796159

Alignment:
TTCAGCACCATGGACAGCKCC
-BTRGGDCARAGGKCA-----

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC




Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA

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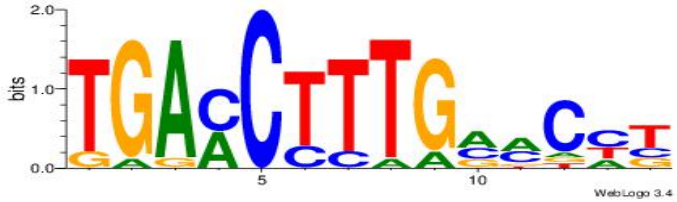
Dataset #: 2
Motif ID: 22
Motif name: NR2F1
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 14
Similarity score: 0.536521

Alignment:
TGAMCTTTGMMCYT-
TGRCCTKTGHCCKAB

Original motif Consensus sequence: TGAMCTTTGMMCYT

Reverse complement motif Consensus sequence: AKGYYCAAAGRTC

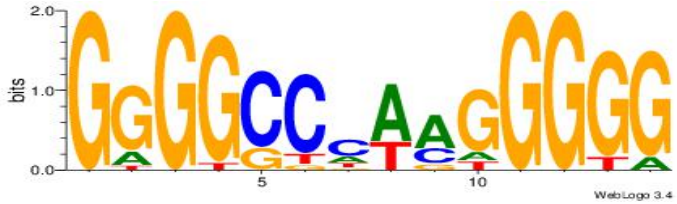


| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 21 |
| Motif name: | PLAG1 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 1 |
| Number of overlap: | 14 |
| Similarity score: | 0.575248 |

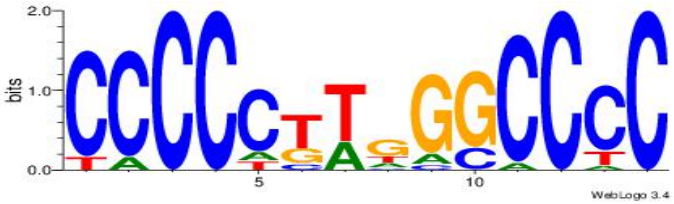
Alignment:

```
-GGGGCCCAAGGGGG
BTRGGDCARAGGKCA
```

Original motif Consensus sequence: GGGGCCCAAGGGGG

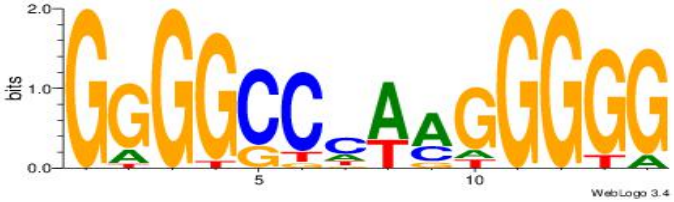



Reverse complement motif Consensus sequence: CCCCCTTGGGCCC

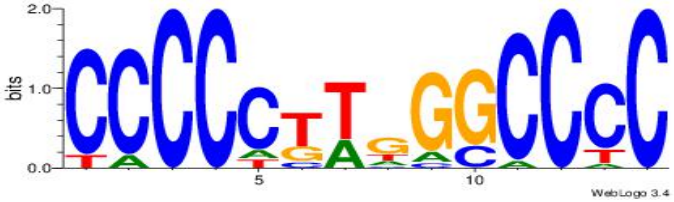



**Dataset #: 2 Motif ID: 21 Motif name: PLAG1**

Original motif Consensus sequence: GGGGCCCAAGGGGG




Reverse complement motif Consensus sequence: CCCCCTTGGGCCC



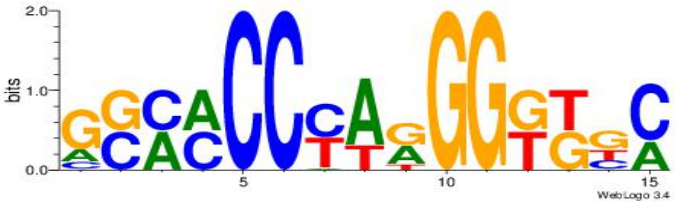

## Best Matches for Motif ID 21 (Highest to Lowest)

| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 13 |
| Motif name: | Zfp423 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 1 |
| Number of overlap: | 14 |
| Similarity score: | 0.0944264 |

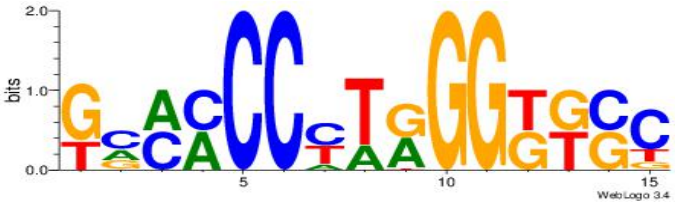
Alignment:

```
GSMMCCYARGGKKKC
GGGGCCCAAGGGGG-
```

Original motif Consensus sequence: GSMMCCYARGGKKKC




Reverse complement motif Consensus sequence: GYRYCCMTKGGYR

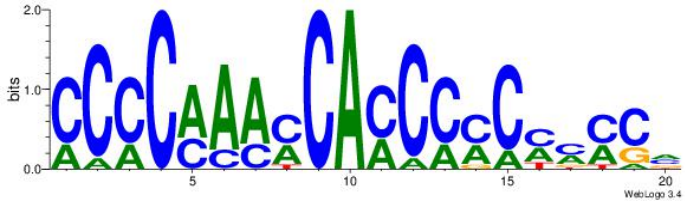


| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 18 |
| Motif name: | RREB1 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Reverse Complement |
| Direction: | Backward |
| Position number: | 7 |
| Number of overlap: | 14 |
| Similarity score: | 0.102814 |

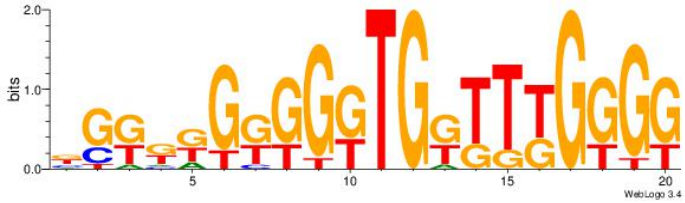
Alignment:

```
BGRRRGRGGRTGRTTYGGGG
GGGGCCCAAGGGGG------
```

Original motif Consensus sequence: CCCCMAAMCAMCCMCMMMCV




Reverse complement motif Consensus sequence: BGRRRGRGGRTGRTTYGGGG

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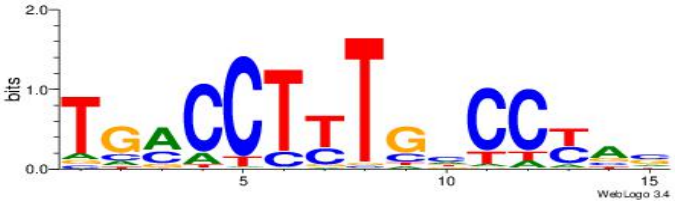
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 20 |
| Motif name: | PPARGRXRA |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 2 |

Number of overlap: 14
Similarity score: 0.107206

Alignment:
BTRGGDCARAGGKCA
-GGGGCCCAAGGGGG

Original motif Consensus sequence: BTRGGDCARAGGKCA

Reverse complement motif Consensus sequence: TGRCCTKTGHCCK

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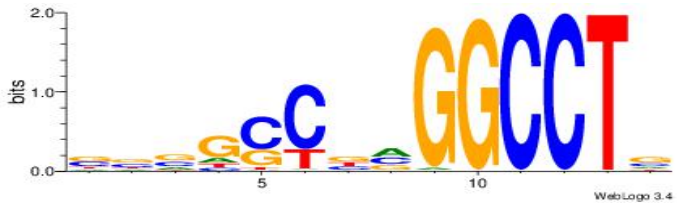
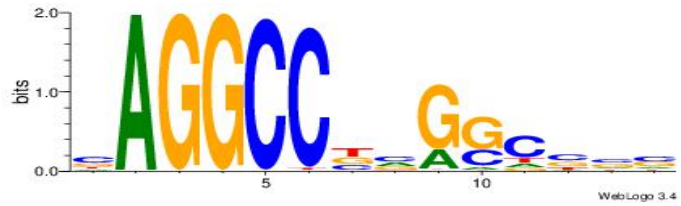
Dataset #: 2
Motif ID: 12
Motif name: Zfx
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 14
Similarity score: 0.111315

Alignment:
VAGGCCBBGGCVBB
GGGGCCCAAGGGGG

Original motif Consensus sequence: BBVGCCBVGGCCTV

Reverse complement motif Consensus sequence: VAGGCCBBGGCVB

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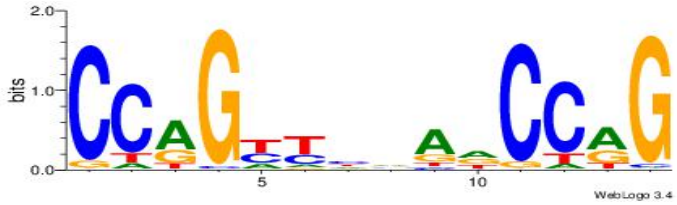
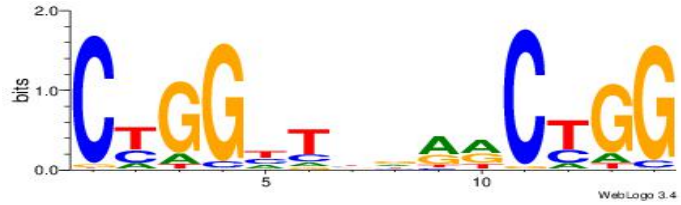
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 48 |
| Motif name: | Tcfcp2l1 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 1 |
| Number of overlap: | 14 |
| Similarity score: | 0.115151 |

Alignment:
CCAGYYHVADCCRG
CCCCCTTGGGCCCC

Original motif Consensus sequence: CCAGYYHVADCCRG




Reverse complement motif Consensus sequence: CKGGDTBDMMCT

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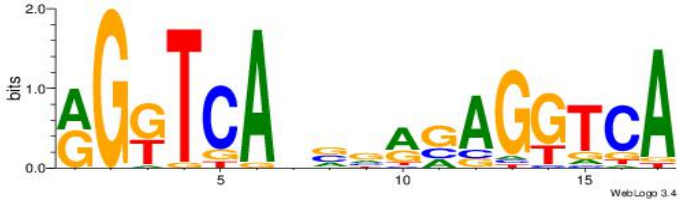
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 47 |

| | |
|---|---|
| Motif name: | RXRRAR_DR5 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 4 |
| Number of overlap: | 14 |
| Similarity score: | 0.116287 |

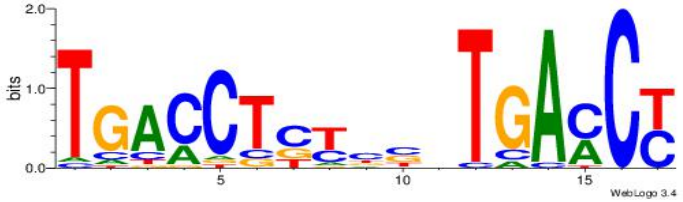
Alignment:

```
RGKTCABVVRGAGGTCA
GGGGCCCAAGGGGG---
```

Original motif Consensus sequence: RGKTCABVVRGAGGTCA




Reverse complement motif Consensus sequence: TGACCTCKVVBTGAYCK

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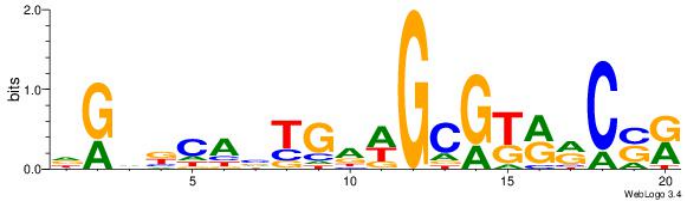
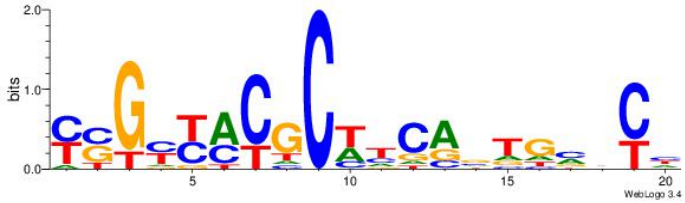
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 45 |
| Motif name: | Pax5 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 1 |
| Number of overlap: | 14 |
| Similarity score: | 0.117063 |

Alignment:
DGVBCABTGDWGCGKRRCSR
GGGGCCCAAGGGGG------

Original motif Consensus sequence: DGVBCABTGDWGCGKRRCSR




Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD

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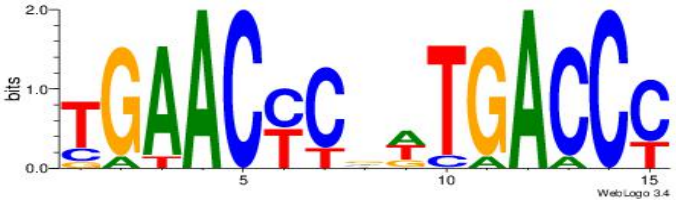
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 17 |
| Motif name: | RXRAVDR |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 3 |
| Number of overlap: | 13 |
| Similarity score: | 0.590064 |

Alignment:
-GGGTCAWBGRGTTCA
GGGGCCCAAGGGGG--

Original motif Consensus sequence: GGGTCAWBGRGTTCA

Reverse complement motif Consensus sequence: TGAACKCBWTGAC

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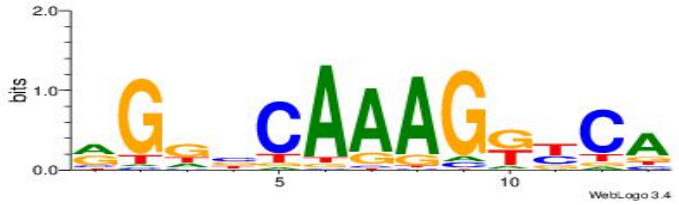
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 34 |
| Motif name: | HNF4A |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 1 |
| Number of overlap: | 13 |
| Similarity score: | 0.603385 |

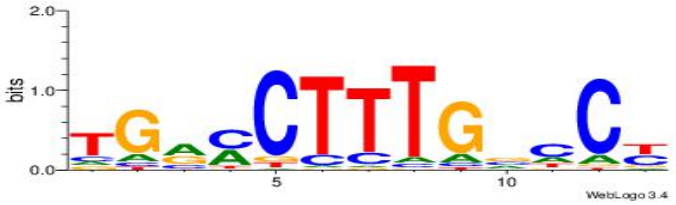
Alignment:

```
-RGGBCAAAGKYCA
GGGGCCCAAGGGGG
```

Original motif Consensus sequence: RGGBCAAAGKYCA




Reverse complement motif Consensus sequence: TGMYCTTTGBCCK

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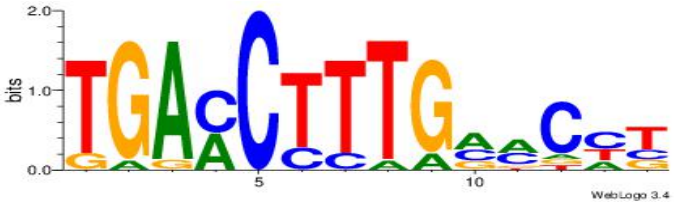
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 22 |

| | |
|---|---|
| Motif name: | NR2F1 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Reverse Complement |
| Direction: | Backward |
| Position number: | 2 |
| Number of overlap: | 13 |
| Similarity score: | 0.613207 |

Alignment:

```
-AKGYYCAAAGRTCA
GGGGCCCAAGGGGG-
```

Original motif Consensus sequence: TGAMCTTTGMMCYT




Reverse complement motif Consensus sequence: AKGYYCAAAGRTCA

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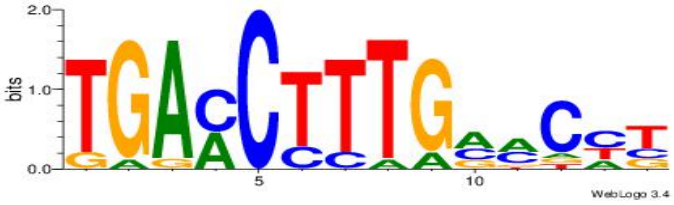
**Dataset #: 2 Motif ID: 22 Motif name: NR2F1**

Original motif Consensus sequence: TGAMCTTTGMMCYT




Reverse complement motif Consensus sequence: AKGYYCAAAGRTCA

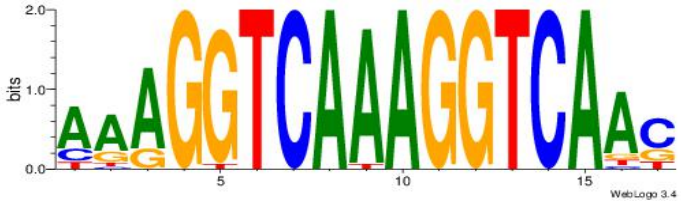
**Best Matches for Motif ID 22 (Highest to Lowest)**

| | |
|---|---|
| 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: | 2 |
| Number of overlap: | 14 |
| Similarity score: | 0.0174588 |

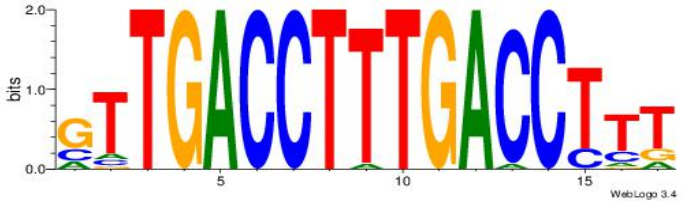
Alignment:

```
GTTGACCTTTGACCTTT
--TGAMCTTTGMMCYT-
```

Original motif Consensus sequence: AAAGGTCAAAGGTCAAC




Reverse complement motif Consensus sequence: GTTGACCTTTGACCTTT

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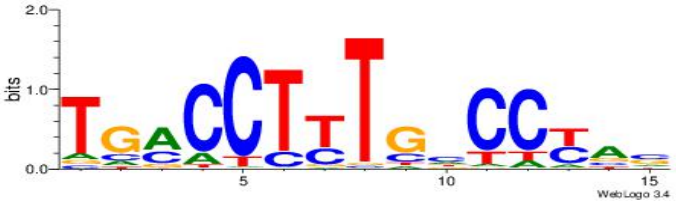
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 20 |
| Motif name: | PPARGRXRA |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 2 |

Number of overlap: 14
Similarity score: 0.0278283

Alignment:
BTRGGDCARAGGKCA
AKGYYCAAAGRTCA-

Original motif Consensus sequence: BTRGGDCARAGGKCA

Reverse complement motif Consensus sequence: TGRCCTKTGHCCK

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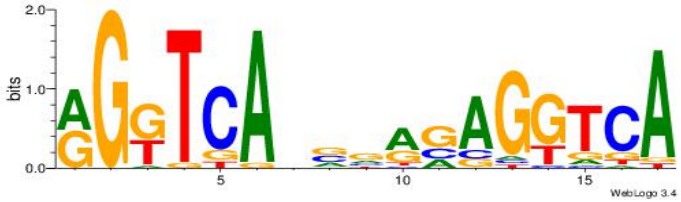
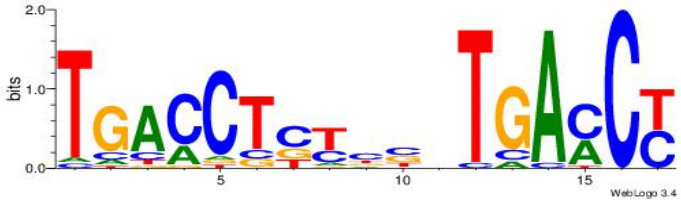
Dataset #: 2
Motif ID: 47
Motif name: RXRRAR_DR5
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 4
Number of overlap: 14
Similarity score: 0.0625328

Alignment:
RGKTCABVVRGAGGTCA
---AKGYYCAAAGRTCA

Original motif Consensus sequence: RGKTCABVVRGAGGTCA

Reverse complement motif Consensus sequence: TGACCTCKVVBTGAYCK

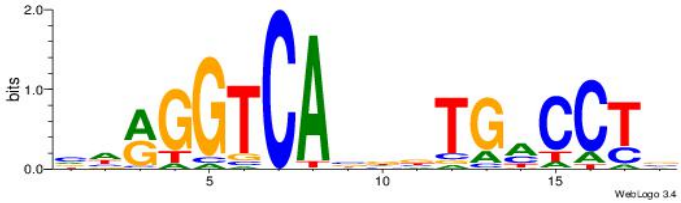


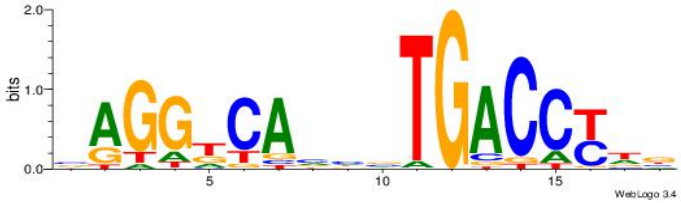

Dataset #: 2
Motif ID: 30
Motif name: ESR2
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 2
Number of overlap: 14
Similarity score: 0.0710475

Alignment:
BAGGYCABHBTGACCKHV
---TGAMCTTTGMMCYT-

Original motif Consensus sequence: VHRGGTCABDBTGMCCTB




Reverse complement motif Consensus sequence:
BAGGYCABHBTGACCKHV



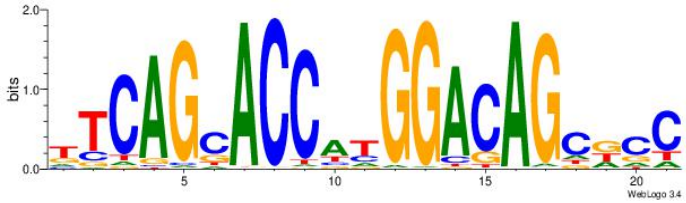

Dataset #: 2

| | |
|---|---|
| Motif ID: | 19 |
| Motif name: | REST |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Reverse Complement |
| Direction: | Backward |
| Position number: | 6 |
| Number of overlap: | 14 |
| Similarity score: | 0.071796 |

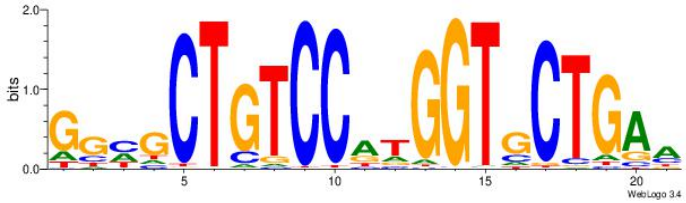
Alignment:

```
GGYGCTGTCCATGGTGCTGAA
--TGAMCTTTGMMCYT-----
```

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC




Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA

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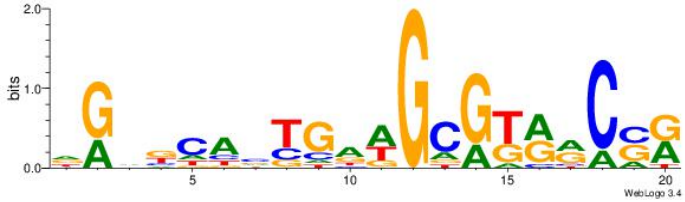
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 45 |
| Motif name: | Pax5 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Reverse Complement |
| Direction: | Forward |
| Position number: | 5 |
| Number of overlap: | 14 |

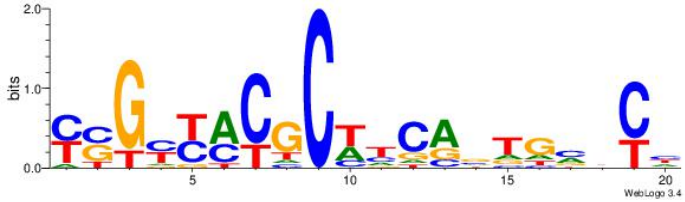
Similarity score: 0.0741987

Alignment:
MSGKKRCGCWDCABTGBBCD
----TGAMCTTTGMMCYT--

Original motif Consensus sequence: DGVBCABTGDWGCGKRRCSR




Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD

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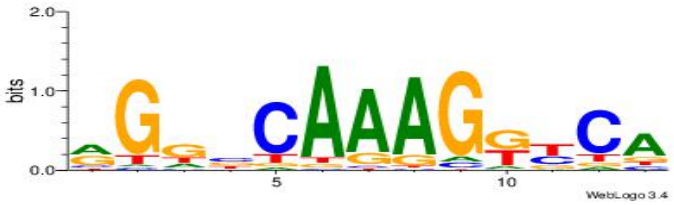
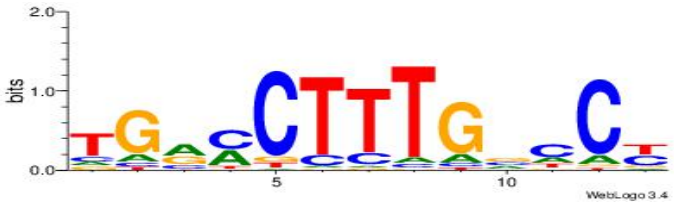
Dataset #: 2
Motif ID: 34
Motif name: HNF4A
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 13
Similarity score: 0.514048

Alignment:
-RGGBCAAAGKYCA
AKGYYCAAAGRTCA

Original motif Consensus sequence: RGGBCAAAGKYCA

Reverse complement motif Consensus sequence: TGMYCTTTGBCCK

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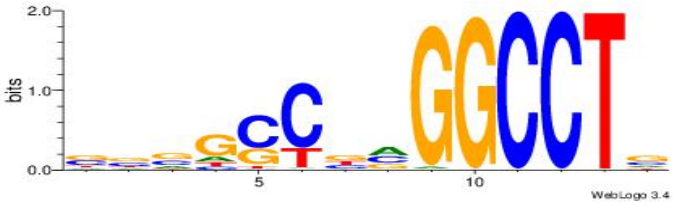
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 12 |
| Motif name: | Zfx |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 2 |
| Number of overlap: | 13 |
| Similarity score: | 0.568042 |

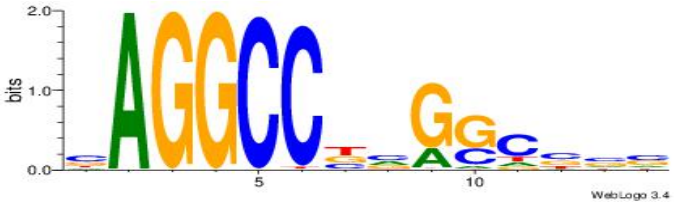
Alignment:

```
BBVGCCBVGGCCTV-
-AKGYYCAAAGRTCA
```

Original motif Consensus sequence: BBVGCCBVGGCCTV




Reverse complement motif Consensus sequence: VAGGCCBBGGCVB

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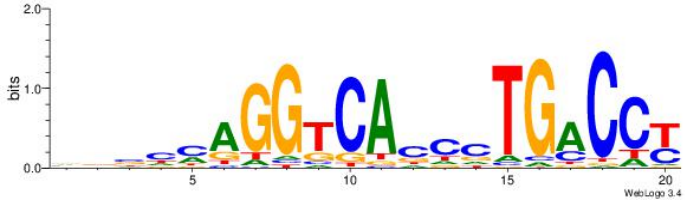
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 29 |

| | |
|---|---|
| Motif name: | ESR1 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 8 |
| Number of overlap: | 13 |
| Similarity score: | 0.569869 |

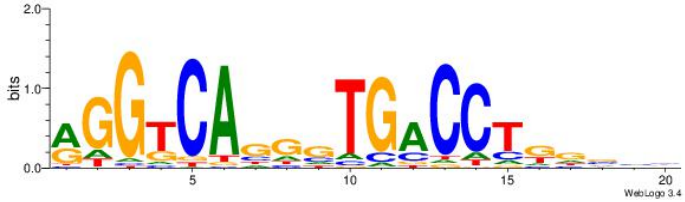
Alignment:

```
VDBHMAGGTCACCCTGACCY-
-------TGAMCTTTGMMCYT
```

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY




Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV

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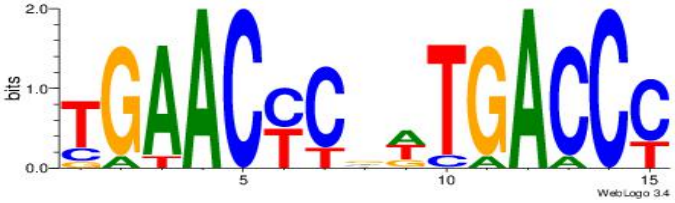
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 17 |
| Motif name: | RXRAVDR |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Reverse Complement |
| Direction: | Backward |
| Position number: | 3 |
| Number of overlap: | 13 |
| Similarity score: | 0.572226 |

Alignment:
-TGAACKCBWTGACCC
TGAMCTTTGMMCYT--

Original motif Consensus sequence: GGGTCAWBGRGTTCA

Reverse complement motif Consensus sequence: TGAACKCBWTGAC




---

**Dataset #: 2 Motif ID: 23 Motif name: MZF1_1-4**

Original motif Consensus sequence: BGGGGA

Reverse complement motif Consensus sequence: TCCCCV

**Best Matches for Motif ID 23 (Highest to Lowest)**

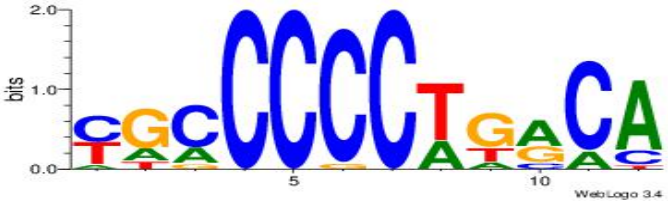
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 35 |
| Motif name: | INSM1 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction: | Backward |
| Position number: | 5 |

Number of overlap: 6
Similarity score: 0.0276389

Alignment:
MGCCCCCTGMCA
--TCCCCV----

Original motif Consensus sequence: TGYCAGGGGGCR

Reverse complement motif Consensus sequence: MGCCCCCTGMCA




---

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: Forward
Position number: 4
Number of overlap: 6
Similarity score: 0.0314583

Alignment:
BKAGGGGDAD
---BGGGGA-

Original motif Consensus sequence: BKAGGGGDAD

Reverse complement motif Consensus sequence: BTHCCCCTYB

---

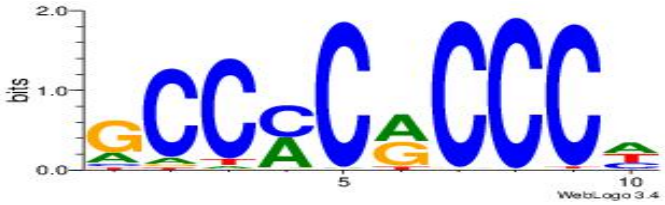
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 36 |
| Motif name: | Klf4 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction: | Forward |
| Position number: | 1 |
| Number of overlap: | 6 |
| Similarity score: | 0.0406514 |

Alignment:

```
GCCYCMCCCD
TCCCCV----
```

Original motif Consensus sequence: DGGGYGKGGC

Reverse complement motif Consensus sequence: GCCYCMCCCD

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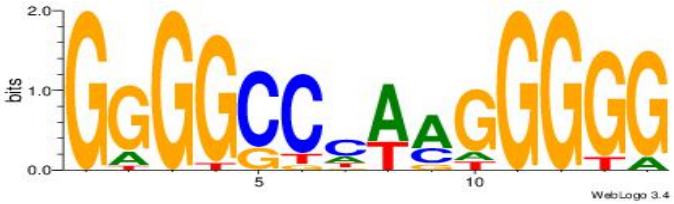
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 21 |

| | |
|---|---|
| Motif name: | PLAG1 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 9 |
| Number of overlap: | 6 |
| Similarity score: | 0.0412963 |

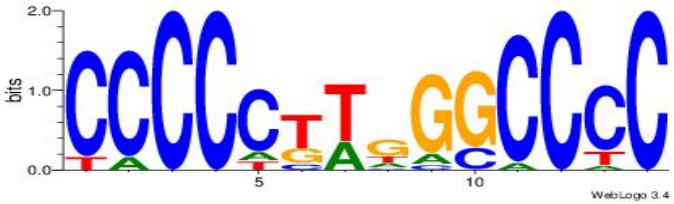
Alignment:

```
GGGGCCCAAGGGGG
--------BGGGGA
```

Original motif Consensus sequence: GGGGCCCAAGGGGG




Reverse complement motif Consensus sequence: CCCCCTTGGGCCC




---

| | |
|---|---|
| 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: | 1 |
| Number of overlap: | 6 |
| Similarity score: | 0.0426517 |

Alignment:
TCCCAG
TCCCCV

Original motif Consensus sequence: CTGGGA

Reverse complement motif Consensus sequence: TCCCAG

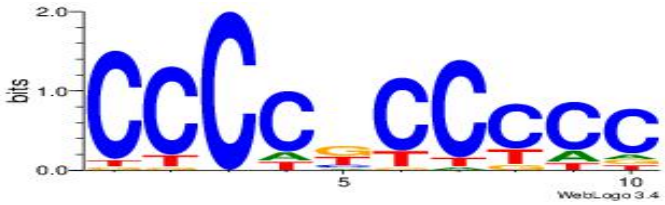
---

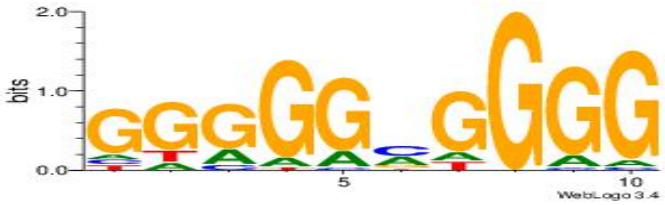
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 16 |
| Motif name: | SP1 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Reverse Complement |
| Direction: | Forward |
| Position number: | 5 |
| Number of overlap: | 6 |
| Similarity score: | 0.0464881 |

Alignment:
GGGGGYGGGG
----BGGGGA

Original motif Consensus sequence: CCCCKCCCCC

Reverse complement motif Consensus sequence: GGGGGYGGGG

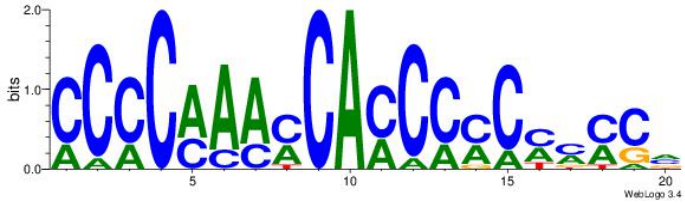


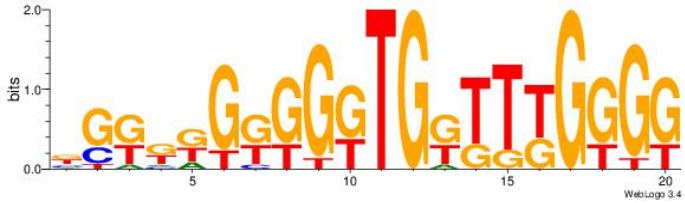

Dataset #: 2
Motif ID: 18
Motif name: RREB1
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 5
Number of overlap: 6
Similarity score: 0.0493561

Alignment:
CCCCMAAMCAMCCMCMMMCV
----TCCCCV----------

Original motif Consensus sequence: CCCCMAAMCAMCCMCMMMCV




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: | Original Motif |
| Direction: | Backward |
| Position number: | 1 |
| Number of overlap: | 6 |
| Similarity score: | 0.0521759 |

Alignment:

```
GGGGRTTCCCC
-----TCCCCV
```

Original motif Consensus sequence: GGGGRTTCCCC

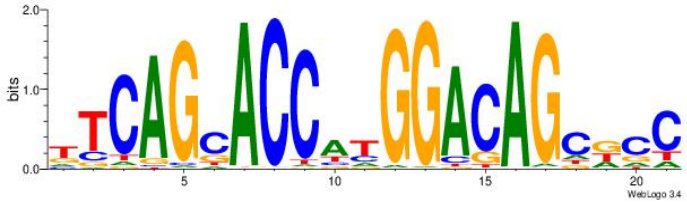
Reverse complement motif Consensus sequence: GGGGAAKCCCC

---

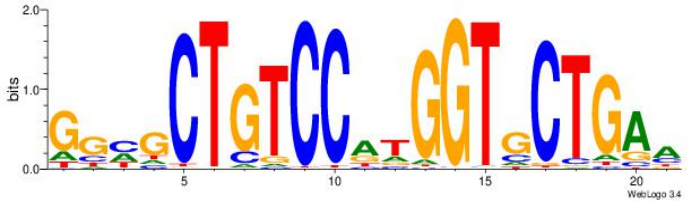
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 19 |
| Motif name: | REST |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction: | Backward |
| Position number: | 11 |
| Number of overlap: | 6 |
| Similarity score: | 0.0581528 |

Alignment:
GGYGCTGTCCATGGTGCTGAA
-----TCCCCV----------

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC




Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA



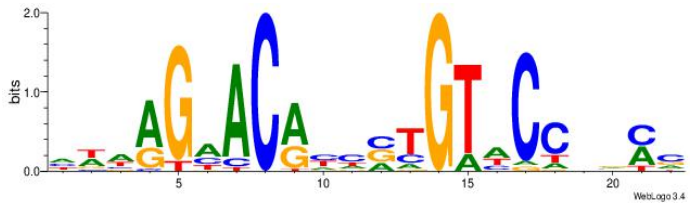

---

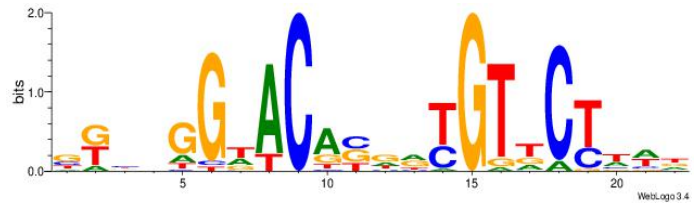
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 24 |
| Motif name: | Ar |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 3 |
| Number of overlap: | 6 |
| Similarity score: | 0.0585417 |

Alignment:
HWDAGHACRHHVTGTHCCHVMV
--------------TCCCCV--

Original motif Consensus sequence: HWDAGHACRHHVTGTHCCHVMV

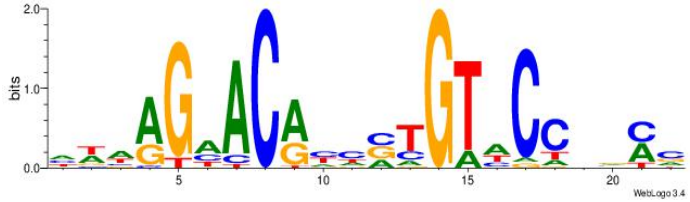
Reverse complement motif Consensus sequence: VRVDGGHACAVDDKGTHCTDWH



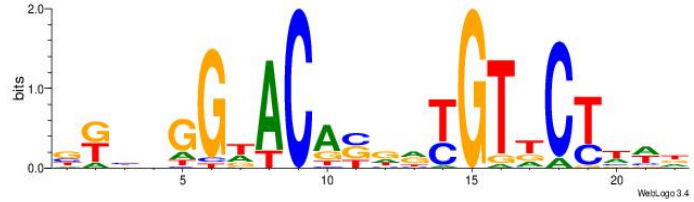




**Dataset #: 2** **Motif ID: 24** **Motif name: Ar**

Original motif Consensus sequence: HWDAGHACRHHVTGTHCCHVMV




Reverse complement motif Consensus sequence: VRVDGGHACAVDDKGTHCTDWH



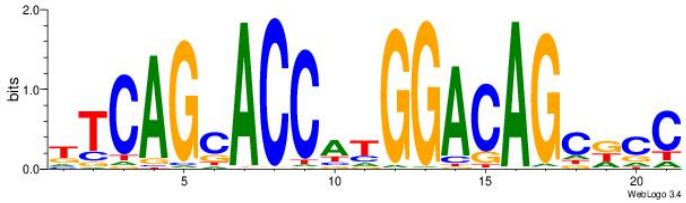

## Best Matches for Motif ID 24 (Highest to Lowest)

| | |
|---|---|
| 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: | 1 |
| Number of overlap: | 21 |
| Similarity score: | 0.0696331 |

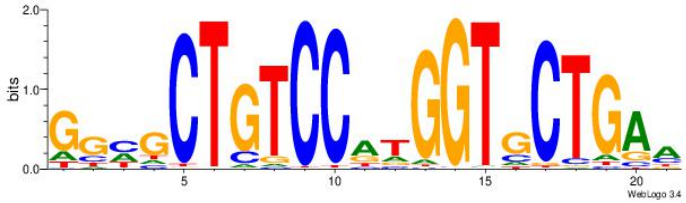
Alignment:

-GGYGCTGTCCATGGTGCTGAA
VRVDGGHACAVDDKGTHCTDWH

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC




Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA

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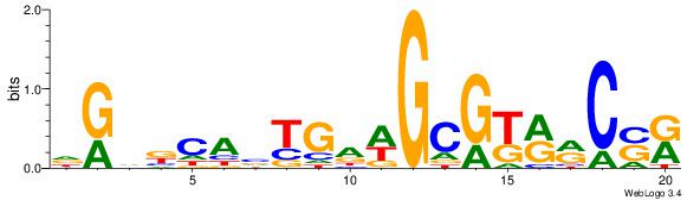
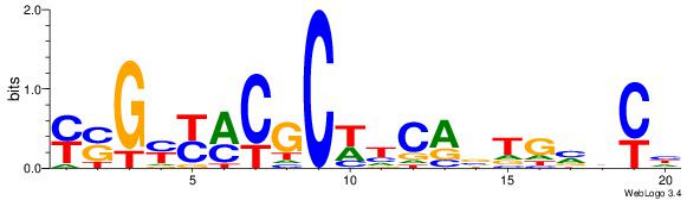
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 45 |
| Motif name: | Pax5 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction: | Backward |
| Position number: | 1 |
| Number of overlap: | 20 |
| Similarity score: | 0.564914 |

Alignment:
--MSGKKRCGCWDCABTGBBCD
VRVDGGHACAVDDKGTHCTDWH

Original motif Consensus sequence: DGVBCABTGDWGCGKRRCSR

Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD



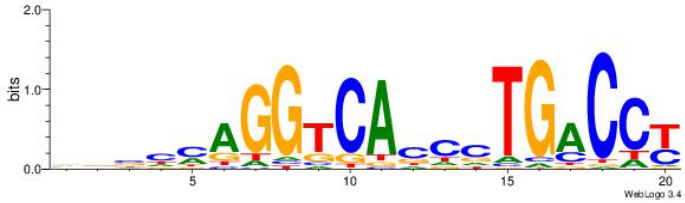




| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 29 |
| Motif name: | ESR1 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 2 |
| Number of overlap: | 19 |
| Similarity score: | 1.05195 |

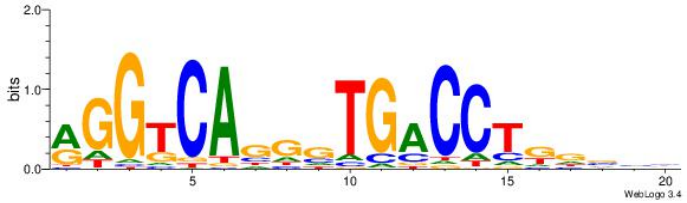
Alignment:

```
VDBHMAGGTCACCCTGACCY---
-VRVDGGHACAVDDKGTHCTDWH
```

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY




Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV



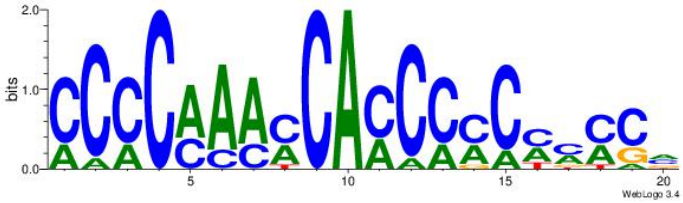

Dataset #: 2

| | |
|---|---|
| Motif ID: | 18 |
| Motif name: | RREB1 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 2 |
| Number of overlap: | 19 |
| Similarity score: | 1.07661 |

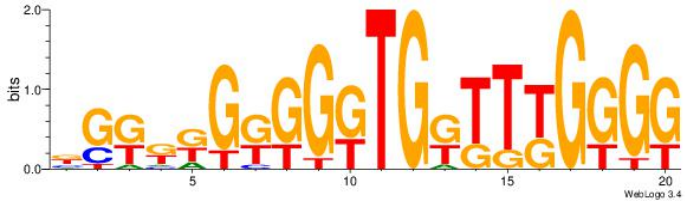
Alignment:

```
CCCCMAAMCAMCCMCMMMCV---
-HWDAGHACRHHVTGTHCCHVMV
```

Original motif Consensus sequence: CCCCMAAMCAMCCMCMMMCV




Reverse complement motif Consensus sequence: BGRRRGRGGRTGRTTYGGGG

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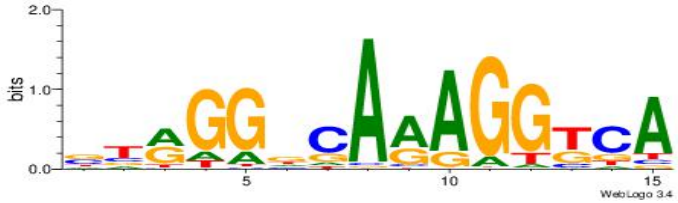
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 20 |
| Motif name: | PPARGRXRA |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 1 |
| Number of overlap: | 15 |

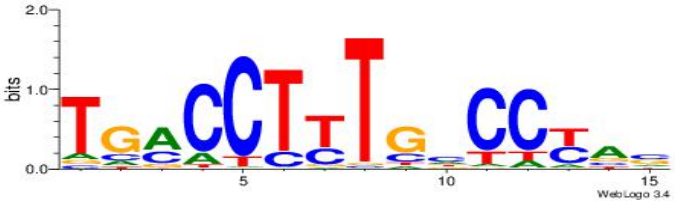
Similarity score: 3.0649

Alignment:
-------BTRGGDCARAGGKCA
VRVDGGHACAVDDKGTHCTDWH

Original motif Consensus sequence: BTRGGDCARAGGKCA




Reverse complement motif Consensus sequence: TGRCCTKTGHCCK

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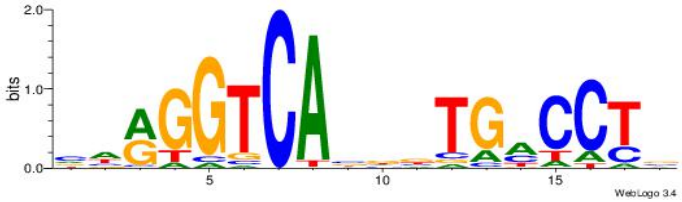
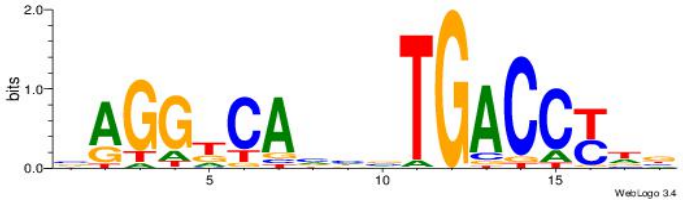
Dataset #: 2
Motif ID: 30
Motif name: ESR2
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 5
Number of overlap: 14
Similarity score: 3.57597

Alignment:
--------VHRGGTCABDBTGMCCTB
VRVDGGHACAVDDKGTHCTDWH----

Original motif Consensus sequence: VHRGGTCABDBTGMCCTB

Reverse complement motif Consensus sequence: BAGGYCABHBTGACCKHV

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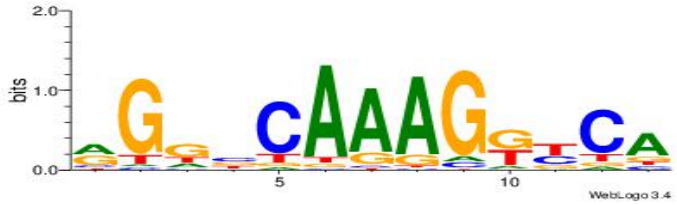
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 34 |
| Motif name: | HNF4A |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Reverse Complement |
| Direction: | Backward |
| Position number: | 1 |
| Number of overlap: | 13 |
| Similarity score: | 4.07506 |

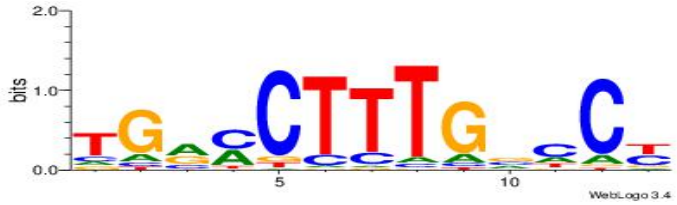
Alignment:

```
---------TGMYCTTTGBCCK
HWDAGHACRHHVTGTHCCHVMV
```

Original motif Consensus sequence: RGGBCAAAGKYCA




Reverse complement motif Consensus sequence: TGMYCTTTGBCCK

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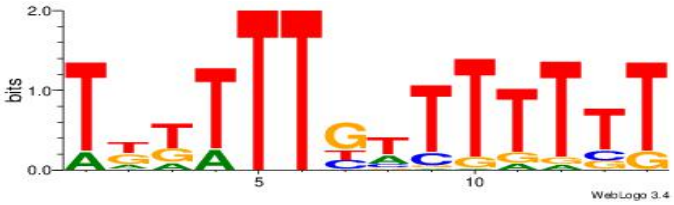
| | |
|---|---|
| Dataset #: | 1 |
| Motif ID: | 10 |

| | |
|---|---|
| Motif name: | Motif 10 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Reverse Complement |
| Direction: | Backward |
| Position number: | 2 |
| Number of overlap: | 13 |
| Similarity score: | 4.07511 |

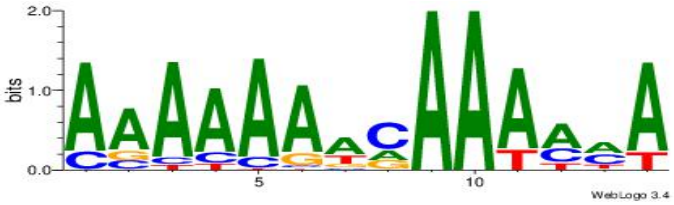
Alignment:

```
---------AAAAAAACAAARRA
HWDAGHACRHHVTGTHCCHVMV-
```

Original motif Consensus sequence: TKKTTTGTTTTTTT




Reverse complement motif Consensus sequence: AAAAAAACAAARR

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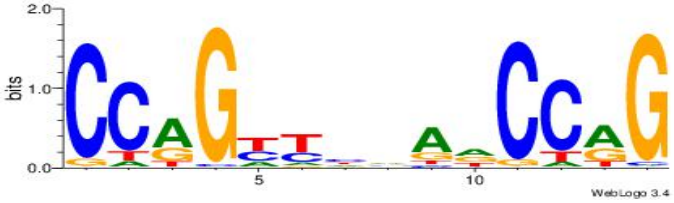
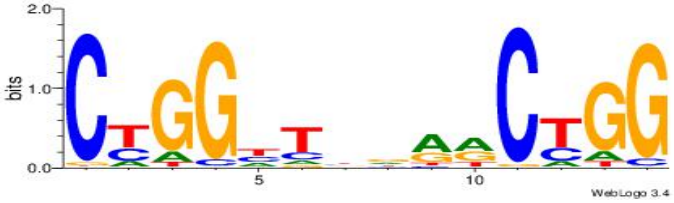
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 48 |
| Motif name: | Tcfcp2l1 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction: | Forward |
| Position number: | 2 |
| Number of overlap: | 13 |
| Similarity score: | 4.0791 |

Alignment:
CKGGDTBDMMCTGG---------
-VRVDGGHACAVDDKGTHCTDWH

Original motif Consensus sequence: CCAGYYHVADCCRG




Reverse complement motif Consensus sequence: CKGGDTBDMMCT



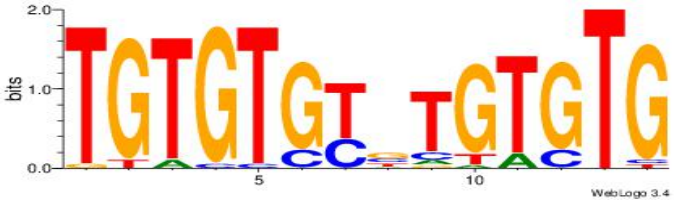

---

| | |
|---|---|
| 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: | 3 |
| Number of overlap: | 12 |
| Similarity score: | 4.57405 |

Alignment:
TGTGTGKVTGTGTG----------
--HWDAGHACRHHVTGTHCCHVMV

Original motif Consensus sequence: CACACAVRCACACA

Reverse complement motif Consensus sequence: TGTGTGKVTGTGT




**Dataset #: 2** **Motif ID: 25** **Motif name: Arnt**

Original motif Consensus sequence: CACGTG

Reverse complement motif Consensus sequence: CACGTG

## Best Matches for Motif ID 25 (Highest to Lowest)

| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 31 |
| Motif name: | Esrrb |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 1 |
| Number of overlap: | 6 |
| Similarity score: | 0 |

Alignment:

```
CACGTG
CACGTG
```

Original motif Consensus sequence: CACGTG

Reverse complement motif Consensus sequence: CACGTG

---

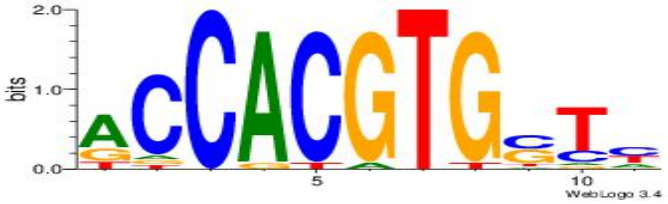
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 39 |
| Motif name: | MYCMAX |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction: | Forward |
| Position number: | 3 |
| Number of overlap: | 6 |
| Similarity score: | 0.0143849 |

Alignment:

```
ACCACGTGSTM
--CACGTG---
```

Original motif Consensus sequence: RASCACGTGGT

Reverse complement motif Consensus sequence: ACCACGTGSTM

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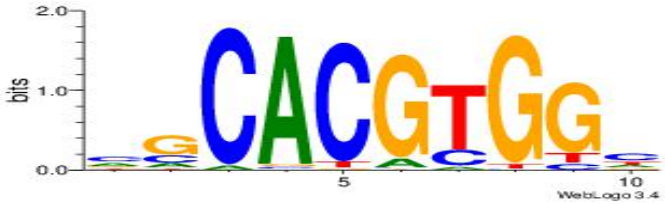
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 38 |
| Motif name: | Myc |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction: | Backward |
| Position number: | 3 |
| Number of overlap: | 6 |
| Similarity score: | 0.0267529 |

Alignment:

```
DCCACGTGCV
--CACGTG--
```

Original motif Consensus sequence: VGCACGTGGH




Reverse complement motif Consensus sequence: DCCACGTGCV

---

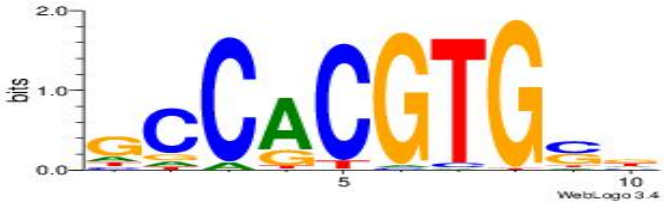
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 40 |
| Motif name: | Mycn |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 3 |
| Number of overlap: | 6 |

Similarity score: 0.0272641

Alignment:
HSCACGTGGC
--CACGTG--

Original motif Consensus sequence: HSCACGTGGC

Reverse complement motif Consensus sequence: GCCACGTGSD




---

Dataset #: 2
Motif ID: 33
Motif name: HIF1AARNT
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2
Number of overlap: 6
Similarity score: 0.0347756

Alignment:
VBACGTGV
-CACGTG-

Original motif Consensus sequence: VBACGTGV

Reverse complement motif Consensus sequence: VCACGTBV

---

| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 26 |
| Motif name: | ArntAhr |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 1 |
| Number of overlap: | 6 |
| Similarity score: | 0.065625 |

Alignment:
YGCGTG
CACGTG

Original motif Consensus sequence: YGCGTG

Reverse complement motif Consensus sequence: CACGCM

---

| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 14 |

| | |
|---|---|
| Motif name: | ZEB1 |
| 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: | 0.0689533 |

Alignment:

```
HAGGTG
CACGTG
```

Original motif Consensus sequence: CACCTD

Reverse complement motif Consensus sequence: HAGGTG

---

| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 28 |
| Motif name: | Egr1 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 1 |
| Number of overlap: | 6 |
| Similarity score: | 0.0784722 |

Alignment:
HGCGTGGGCGK
CACGTG-----

Original motif Consensus sequence: HGCGTGGGCGK

Reverse complement motif Consensus sequence: YCGCCCACGCH

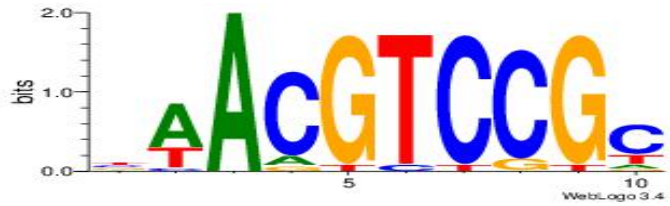
---

| | |
|---|---|
| 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: | 6 |
| Similarity score: | 0.0854167 |

Alignment:
BAACGTCCGC
-CACGTG---

Original motif Consensus sequence: BAACGTCCGC

Reverse complement motif Consensus sequence: GCGGACGTTV

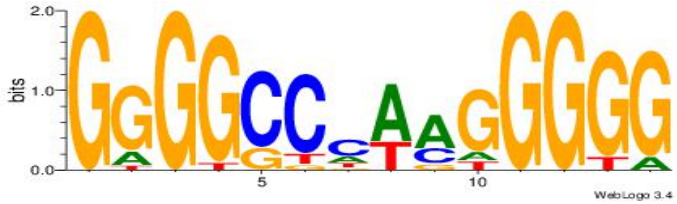


| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 21 |
| Motif name: | PLAG1 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 7 |
| Number of overlap: | 6 |
| Similarity score: | 0.105093 |

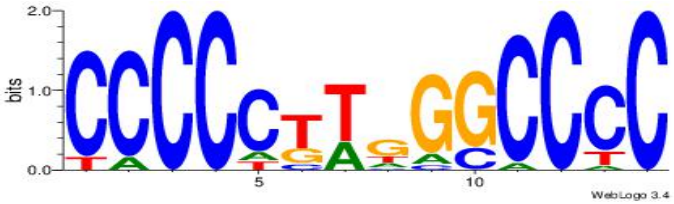
Alignment:

```
GGGGCCCAAGGGGG
------CACGTG--
```

Original motif Consensus sequence: GGGGCCCAAGGGGG




Reverse complement motif Consensus sequence: CCCCCTTGGGCCC




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

Original motif Consensus sequence: YGCGTG

Reverse complement motif Consensus sequence: CACGCM

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

| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 28 |
| Motif name: | Egr1 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction: | Backward |
| Position number: | 1 |
| Number of overlap: | 6 |
| Similarity score: | 0 |

Alignment:

```
YCGCCCACGCH
-----CACGCM
```

Original motif Consensus sequence: HGCGTGGGCGK

Reverse complement motif Consensus sequence: YCGCCCACGCH

| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 33 |
| Motif name: | HIF1AARNT |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 2 |
| Number of overlap: | 6 |
| Similarity score: | 0.0112447 |

Alignment:

```
VBACGTGV
-YGCGTG-
```

Original motif Consensus sequence: VBACGTGV

Reverse complement motif Consensus sequence: VCACGTBV

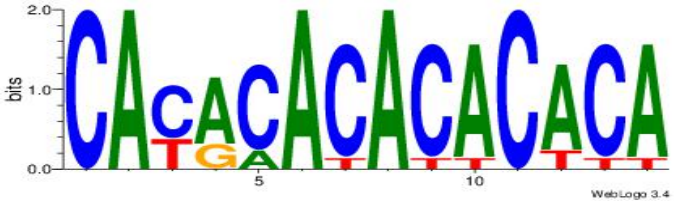
---

| | |
|---|---|
| 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 |

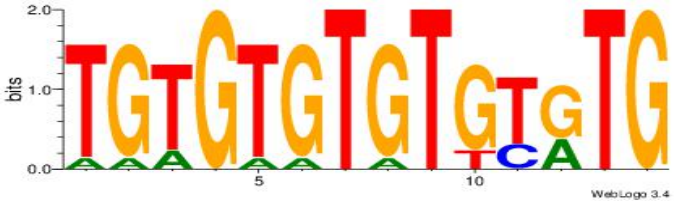
Similarity score: 0.0308396

Alignment:
TGTGTGTGTGTKTG
------YGCGTG--

Original motif Consensus sequence: CAYACACACACACA




Reverse complement motif Consensus sequence: TGTGTGTGTGTKT




---

Dataset #: 2
Motif ID: 31
Motif name: Esrrb
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: 0.0315972

Alignment:
CACGTG
YGCGTG

Original motif Consensus sequence: CACGTG

Reverse complement motif Consensus sequence: CACGTG

---

| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 25 |
| Motif name: | Arnt |
| 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: | 0.0315972 |

Alignment:

```
CACGTG
YGCGTG
```

Original motif Consensus sequence: CACGTG

Reverse complement motif Consensus sequence: CACGTG

---

| | |
|---|---|
| Dataset #: | 1 |
| Motif ID: | 9 |

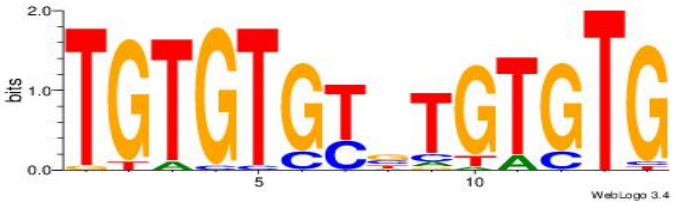
| | |
|---|---|
| Motif name: | Motif 9 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Reverse Complement |
| Direction: | Backward |
| Position number: | 9 |
| Number of overlap: | 6 |
| Similarity score: | 0.0350575 |

Alignment:

```
TGTGTGKVTGTGTG
YGCGTG--------
```

Original motif Consensus sequence: CACACAVRCACACA

Reverse complement motif Consensus sequence: TGTGTGKVTGTGT

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| | |
|---|---|
| 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: | 3 |
| Number of overlap: | 6 |
| Similarity score: | 0.0376488 |

Alignment:
RASCACGTGGT
---YGCGTG--

Original motif Consensus sequence: RASCACGTGGT

Reverse complement motif Consensus sequence: ACCACGTGSTM

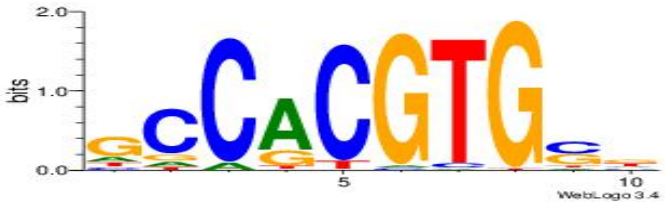
---

| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 40 |
| Motif name: | Mycn |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Reverse Complement |
| Direction: | Forward |
| Position number: | 3 |
| Number of overlap: | 6 |
| Similarity score: | 0.0377949 |

Alignment:
GCCACGTGSD
--YGCGTG--

Original motif Consensus sequence: HSCACGTGGC

Reverse complement motif Consensus sequence: GCCACGTGSD

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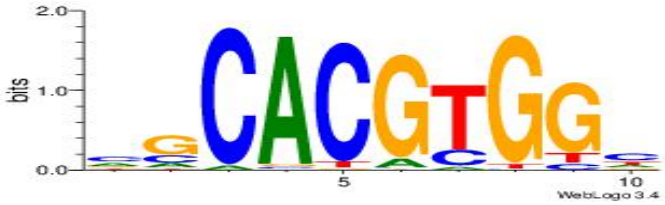
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 38 |
| Motif name: | Myc |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Reverse Complement |
| Direction: | Forward |
| Position number: | 3 |
| Number of overlap: | 6 |
| Similarity score: | 0.0399214 |

Alignment:

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

Original motif Consensus sequence: VGCACGTGGH




Reverse complement motif Consensus sequence: DCCACGTGCV

---

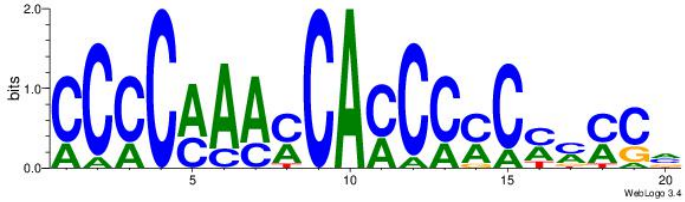
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 18 |

| | |
|---|---|
| Motif name: | RREB1 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Reverse Complement |
| Direction: | Backward |
| Position number: | 7 |
| Number of overlap: | 6 |
| Similarity score: | 0.0433081 |

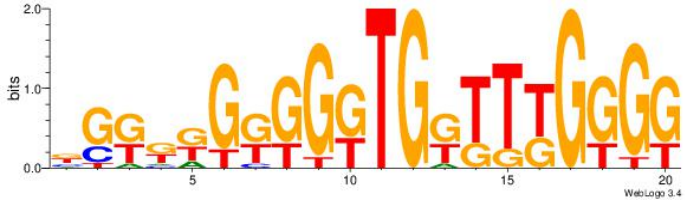
Alignment:

```
BGRRRGRGGRTGRTTYGGGG
--------YGCGTG------
```

Original motif Consensus sequence: CCCCMAAMCAMCCMCMMMCV




Reverse complement motif Consensus sequence: BGRRRGRGGRTGRTTYGGGG




---

**Dataset #: 2 Motif ID: 27 Motif name: E2F1**

Original motif Consensus sequence: TTTSGCGC

Reverse complement motif Consensus sequence: GCGCSAAA

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

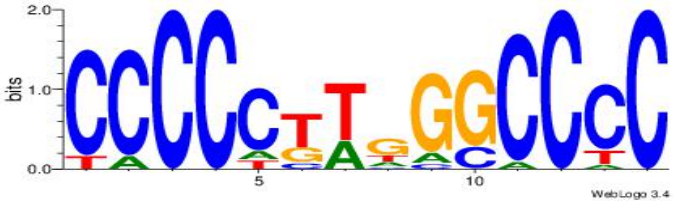
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 21 |
| Motif name: | PLAG1 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Reverse Complement |
| Direction: | Forward |
| Position number: | 2 |
| Number of overlap: | 8 |
| Similarity score: | 0.0255644 |

Alignment:

```
CCCCCTTGGGCCCC
-TTTSGCGC-----
```

Original motif Consensus sequence: GGGGCCCAAGGGGG

Reverse complement motif Consensus sequence: CCCCCTTGGGCCC




---

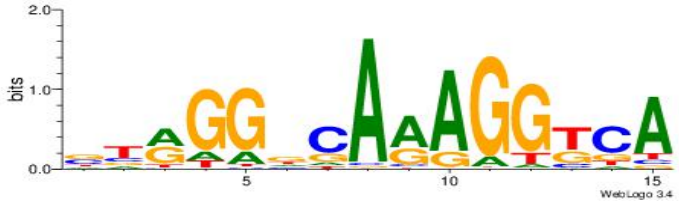
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 20 |
| Motif name: | PPARGRXRA |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Reverse Complement |

| | |
|---|---|
| Direction: | Backward |
| Position number: | 6 |
| Number of overlap: | 8 |
| Similarity score: | 0.0280436 |

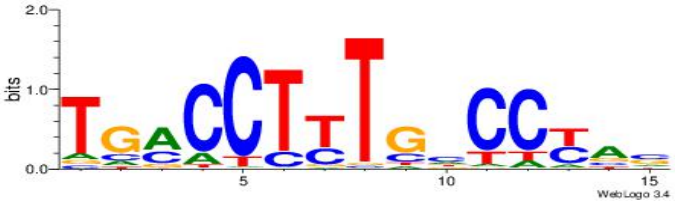
Alignment:

```
TGRCCTKTGHCCKAB
--TTTSGCGC-----
```

Original motif Consensus sequence: BTRGGDCARAGGKCA




Reverse complement motif Consensus sequence: TGRCCTKTGHCCK

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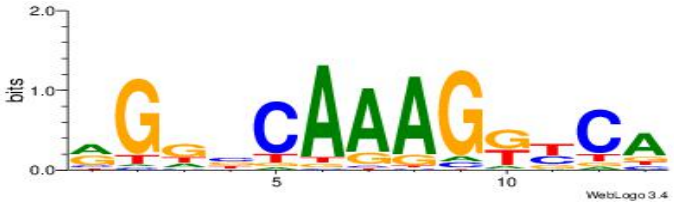
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 34 |
| Motif name: | HNF4A |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 1 |
| Number of overlap: | 8 |
| Similarity score: | 0.0283733 |

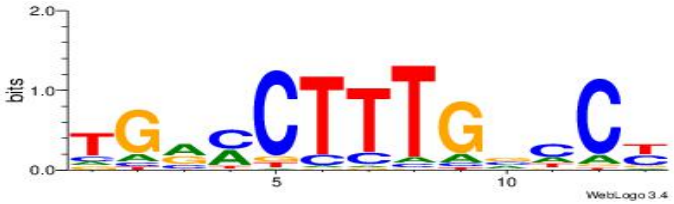
Alignment:

```
RGGBCAAAGKYCA
GCGCSAAA-----
```

Original motif Consensus sequence: RGGBCAAAGKYCA




Reverse complement motif Consensus sequence: TGMYCTTTGBCCK

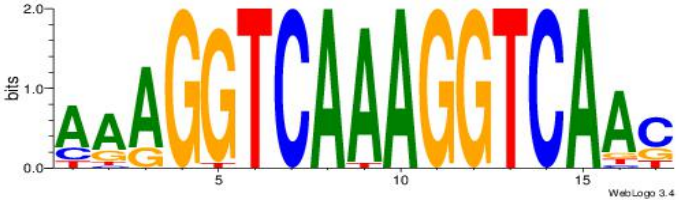



| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 43 |
| Motif name: | NR1H2RXRA |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 3 |
| Number of overlap: | 8 |
| Similarity score: | 0.0298005 |

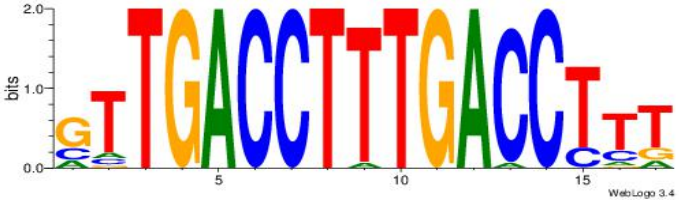
Alignment:

```
AAAGGTCAAAGGTCAAC
--GCGCSAAA-------
```

Original motif Consensus sequence: AAAGGTCAAAGGTCAAC




Reverse complement motif Consensus sequence: GTTGACCTTTGACCTTT

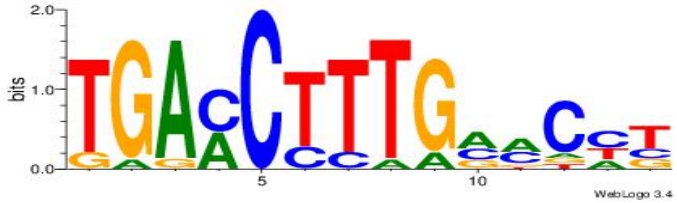


| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 22 |
| Motif name: | NR2F1 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 2 |
| Number of overlap: | 8 |
| Similarity score: | 0.0369159 |

Alignment:

```
TGAMCTTTGMMCYT
-----TTTSGCGC-
```

Original motif Consensus sequence: TGAMCTTTGMMCYT




Reverse complement motif Consensus sequence: AKGYYCAAAGRTCA

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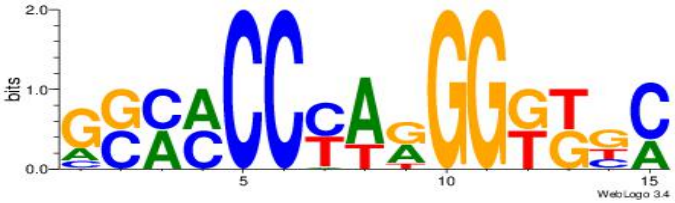
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 13 |
| Motif name: | Zfp423 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 7 |
| Number of overlap: | 8 |

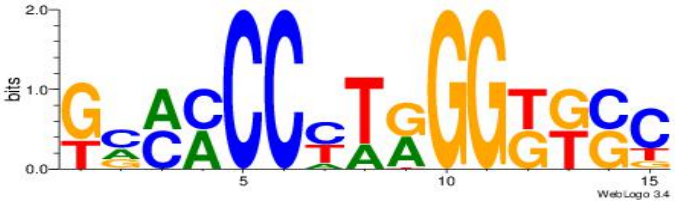
Similarity score: 0.0423573

Alignment:
GSMMCCYARGGKKKC
------GCGCSAAA-

Original motif Consensus sequence: GSMMCCYARGGKKKC




Reverse complement motif Consensus sequence: GYRYCCMTKGGYR



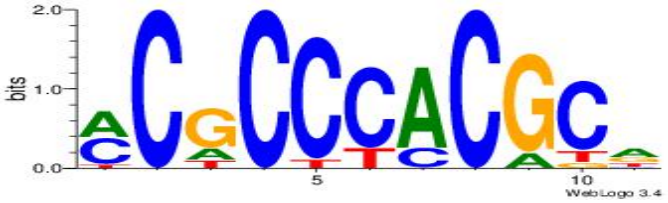

---

Dataset #: 2
Motif ID: 28
Motif name: Egr1
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 4
Number of overlap: 8
Similarity score: 0.0470922

Alignment:
YCGCCCACGCH
GCGCSAAA---

Original motif Consensus sequence: HGCGTGGGCGK

Reverse complement motif Consensus sequence: YCGCCCACGCH



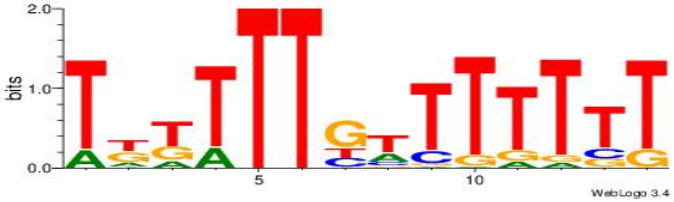

---

| | |
|---|---|
| Dataset #: | 1 |
| Motif ID: | 10 |
| Motif name: | Motif 10 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 4 |
| Number of overlap: | 8 |
| Similarity score: | 0.0486459 |

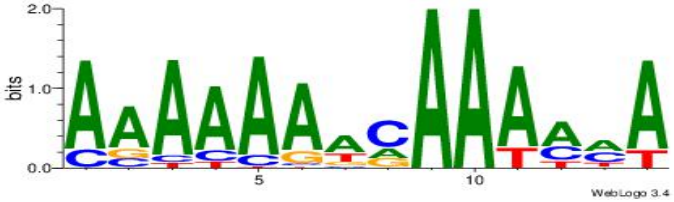
Alignment:

```
TKKTTTGTTTTTTT
---TTTSGCGC---
```

Original motif Consensus sequence: TKKTTTGTTTTTTT




Reverse complement motif Consensus sequence: AAAAAAACAAARR




---

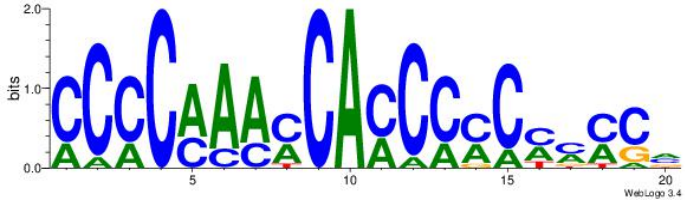
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 18 |

| | |
|---|---|
| Motif name: | RREB1 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Reverse Complement |
| Direction: | Backward |
| Position number: | 13 |
| Number of overlap: | 8 |
| Similarity score: | 0.0497437 |

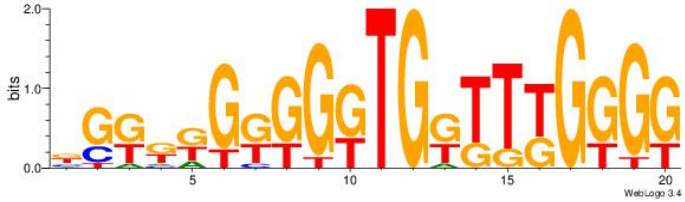
Alignment:

```
BGRRRGRGGRTGRTTYGGGG
TTTSGCGC------------
```

Original motif Consensus sequence: CCCCMAAMCAMCCMCMMMCV




Reverse complement motif Consensus sequence: BGRRRGRGGRTGRTTYGGGG

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| | |
|---|---|
| Dataset #: | 1 |
| Motif ID: | 1 |
| Motif name: | Motif 1 |
| 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: | 1.03392 |

Alignment:
--MTTCCK
TTTSGCGC

Original motif Consensus sequence: RGGAAR

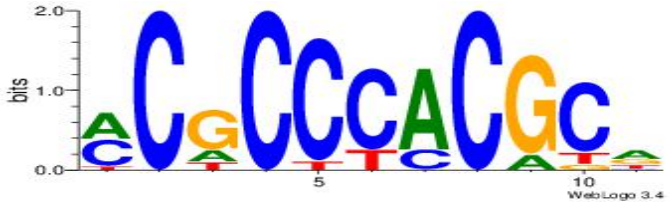
Reverse complement motif Consensus sequence: MTTCCK

---

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

Original motif Consensus sequence: HGCGTGGGCGK

Reverse complement motif Consensus sequence: YCGCCCACGCH



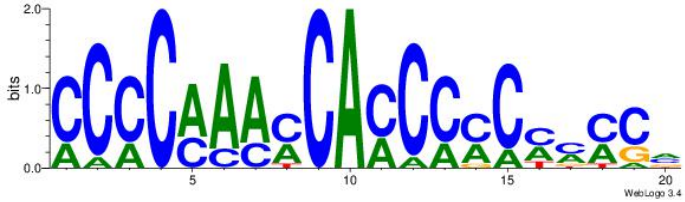

**Best Matches for Motif ID 28 (Highest to Lowest)**

| | |
|---|---|
| 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: | 3 |

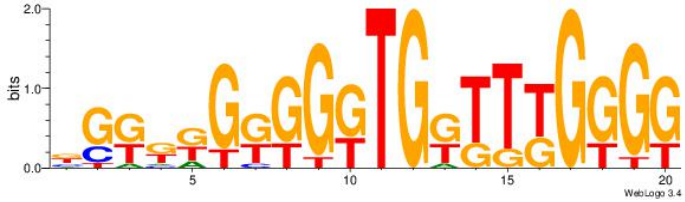
Number of overlap: 11
Similarity score: 0.0550907

Alignment:
BGRRRGRGGRTGRTTYGGGG
-------HGCGTGGGCGK--

Original motif Consensus sequence: CCCCMAAMCAMCCMCMMMCV




Reverse complement motif Consensus sequence: BGRRRGRGGRTGRTTYGGGG

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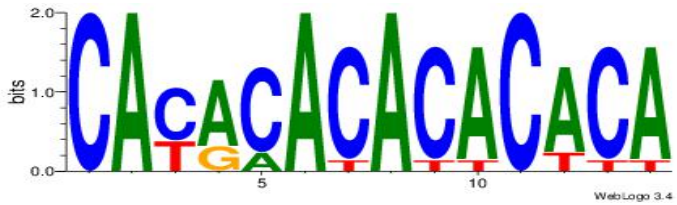
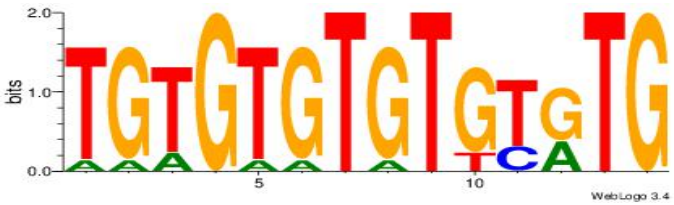
Dataset #: 1
Motif ID: 11
Motif name: Motif 11
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 11
Similarity score: 0.062391

Alignment:
CAYACACACACACA
YCGCCCACGCH---

Original motif Consensus sequence: CAYACACACACACA

Reverse complement motif Consensus sequence: TGTGTGTGTGTKT

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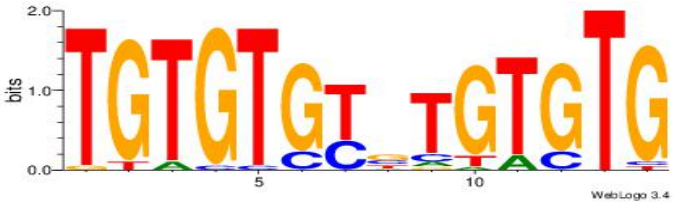
| | |
|---|---|
| Dataset #: | 1 |
| Motif ID: | 9 |
| Motif name: | Motif 9 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 1 |
| Number of overlap: | 11 |
| Similarity score: | 0.0668604 |

Alignment:

```
CACACAVRCACACA
YCGCCCACGCH---
```

Original motif Consensus sequence: CACACAVRCACACA

Reverse complement motif Consensus sequence: TGTGTGKVTGTGT

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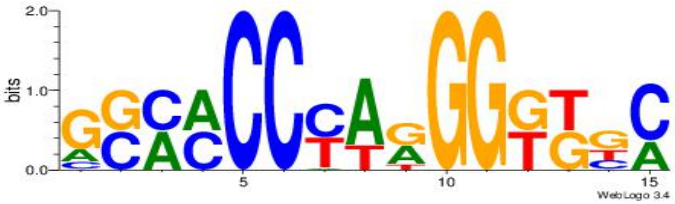
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 13 |

| | |
|---|---|
| Motif name: | Zfp423 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 2 |
| Number of overlap: | 11 |
| Similarity score: | 0.0673496 |

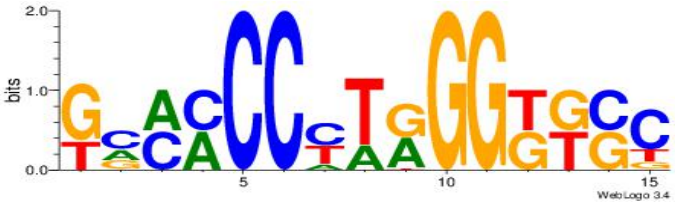
Alignment:

```
GSMMCCYARGGKKKC
---YCGCCCACGCH-
```

Original motif Consensus sequence: GSMMCCYARGGKKKC




Reverse complement motif Consensus sequence: GYRYCCMTKGGYR

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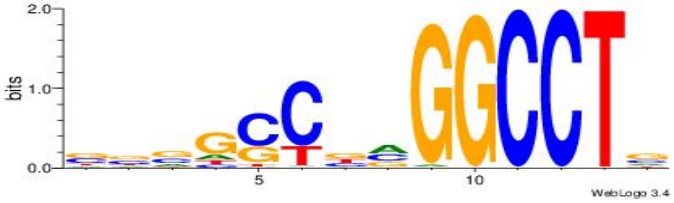
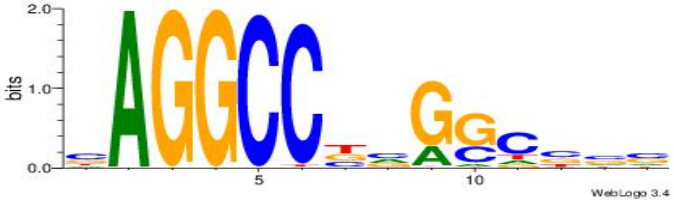
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 12 |
| Motif name: | Zfx |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 2 |
| Number of overlap: | 11 |
| Similarity score: | 0.0764878 |

Alignment:
BBVGCCBVGGCCTV
--HGCGTGGGCGK-

Original motif Consensus sequence: BBVGCCBVGGCCTV




Reverse complement motif Consensus sequence: VAGGCCBBGGCVB

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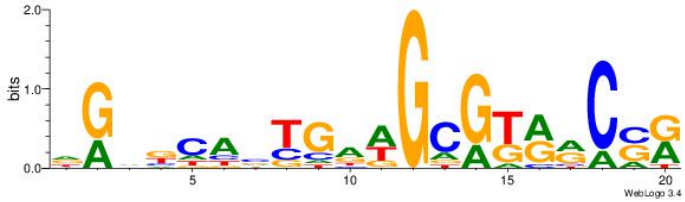
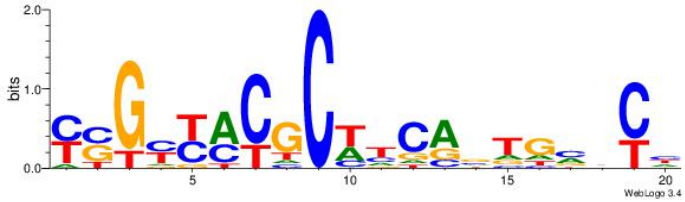
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 45 |
| Motif name: | Pax5 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 6 |
| Number of overlap: | 11 |
| Similarity score: | 0.0765783 |

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

Original motif Consensus sequence: DGVBCABTGDWGCGKRRCSR

Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD

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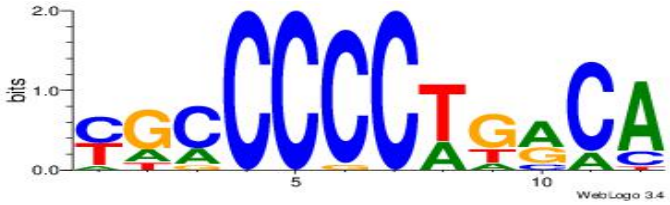
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 35 |
| Motif name: | INSM1 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 1 |
| Number of overlap: | 11 |
| Similarity score: | 0.0830177 |

Alignment:

```
TGYCAGGGGGCR
HGCGTGGGCGK-
```

Original motif Consensus sequence: TGYCAGGGGGCR

Reverse complement motif Consensus sequence: MGCCCCCTGMCA

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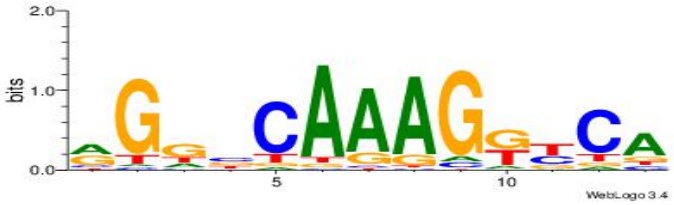
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 34 |

| | |
|---|---|
| Motif name: | HNF4A |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Reverse Complement |
| Direction: | Backward |
| Position number: | 1 |
| Number of overlap: | 11 |
| Similarity score: | 0.0857144 |

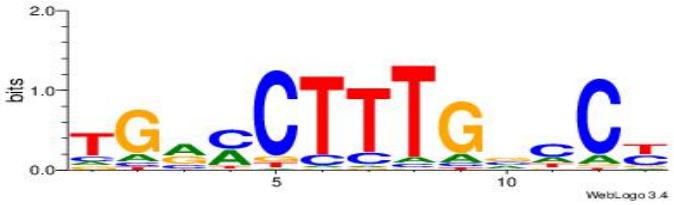
Alignment:

```
TGMYCTTTGBCCK
--HGCGTGGGCGK
```

Original motif Consensus sequence: RGGBCAAAGKYCA




Reverse complement motif Consensus sequence: TGMYCTTTGBCCK

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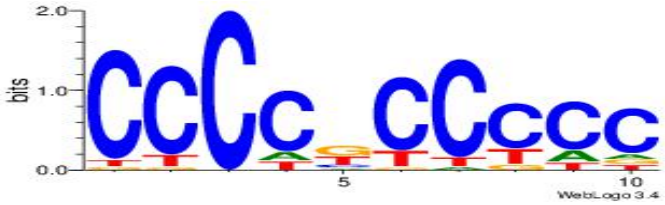
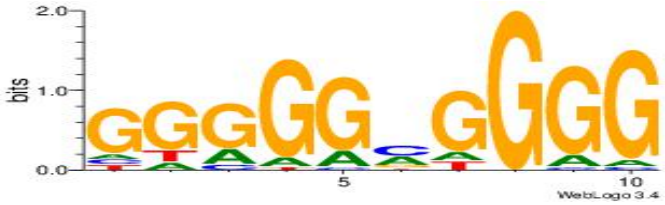
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 16 |
| Motif name: | SP1 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 1 |
| Number of overlap: | 10 |
| Similarity score: | 0.572401 |

Alignment:
CCCCKCCCCC-
YCGCCCACGCH

Original motif Consensus sequence: CCCCKCCCCC




Reverse complement motif Consensus sequence: GGGGGYGGGG

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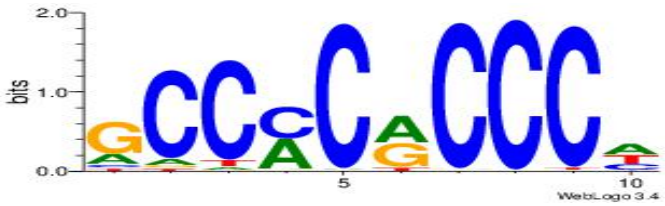
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 36 |
| Motif name: | Klf4 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 1 |
| Number of overlap: | 10 |
| Similarity score: | 0.580823 |

Alignment:
DGGGYGKGGC-
HGCGTGGGCGK

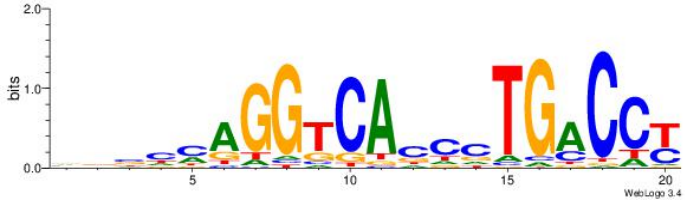
Original motif Consensus sequence: DGGGYGKGGC

Reverse complement motif Consensus sequence: GCCYCMCCCD

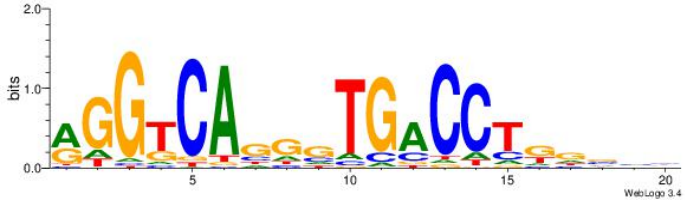



**Dataset #: 2** **Motif ID: 29** **Motif name: ESR1**

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY




Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV



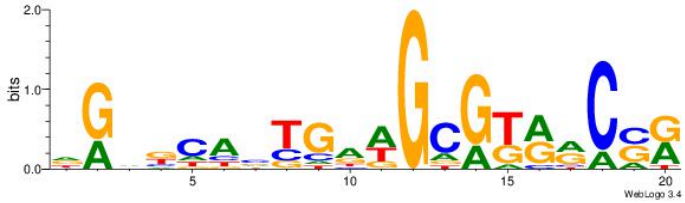

## Best Matches for Motif ID 29 (Highest to Lowest)

| | |
|---|---|
| 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: | 1 |
| Number of overlap: | 20 |
| Similarity score: | 0.0624908 |

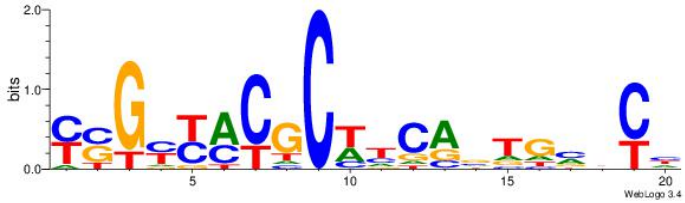
Alignment:

MSGKKRCGCWDCABTGBBCD
MGGTCAGGGTGACCTRDBHV

Original motif Consensus sequence: DGVBCABTGDWGCGKRRCSR




Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD

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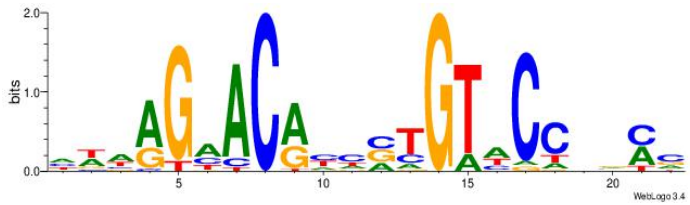
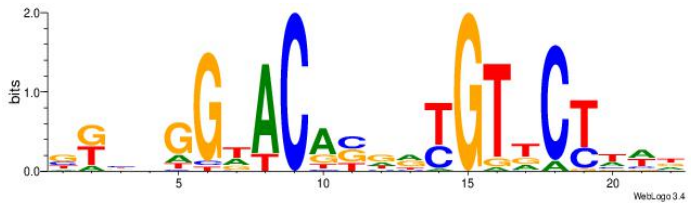
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 24 |
| Motif name: | Ar |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 4 |
| Number of overlap: | 19 |
| Similarity score: | 0.556363 |

Alignment:
-HWDAGHACRHHVTGTHCCHVMV
MGGTCAGGGTGACCTRDBHV---

Original motif Consensus sequence: HWDAGHACRHHVTGTHCCHVMV

Reverse complement motif Consensus sequence: VRVDGGHACAVDDKGTHCTDWH

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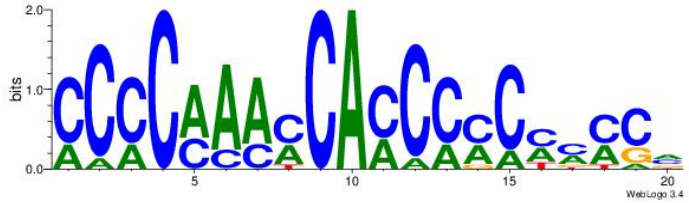
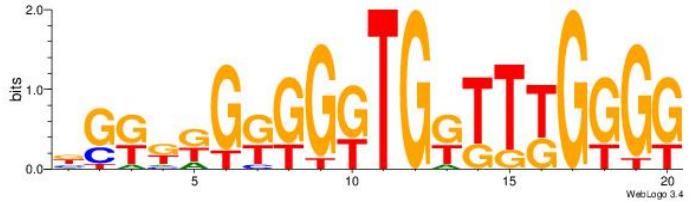
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 18 |
| Motif name: | RREB1 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction: | Forward |
| Position number: | 2 |
| Number of overlap: | 19 |
| Similarity score: | 0.575732 |

Alignment:
BGRRRGRGGRTGRTTYGGGG-
-MGGTCAGGGTGACCTRDBHV

Original motif Consensus sequence: CCCCMAAMCAMCCMCMMMCV




Reverse complement motif Consensus sequence:
BGRRRGRGGRTGRTTYGGGG

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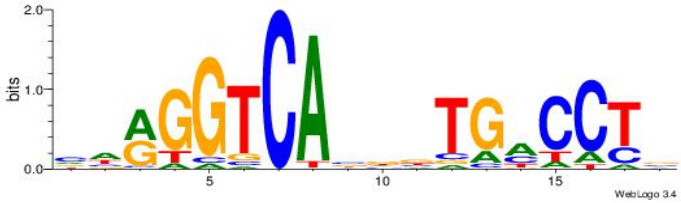
| | |
|---|---|
| Dataset #: | 2 |

| | |
|---|---|
| Motif ID: | 30 |
| Motif name: | ESR2 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 2 |
| Number of overlap: | 17 |
| Similarity score: | 1.50287 |

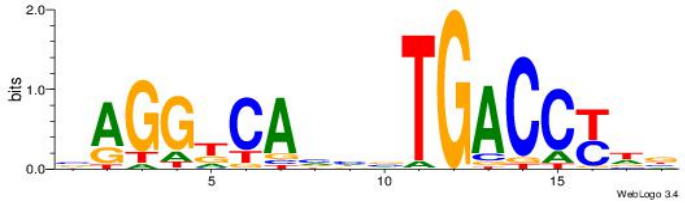
Alignment:

```
---VHRGGTCABDBTGMCCTB
VDBHMAGGTCACCCTGACCY-
```

Original motif Consensus sequence: VHRGGTCABDBTGMCCTB




Reverse complement motif Consensus sequence: BAGGYCABHBTGACCKHV

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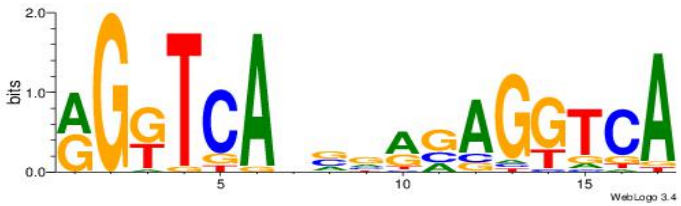
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 47 |
| Motif name: | RXRRAR_DR5 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Reverse Complement |
| Direction: | Backward |
| Position number: | 1 |
| Number of overlap: | 17 |

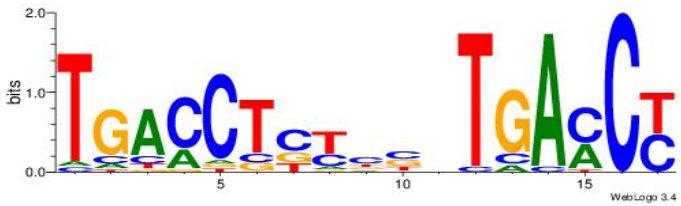
Similarity score: 1.55839

Alignment:
```
---TGACCTCKVVBTGAYCK
VDBHMAGGTCACCCTGACCY
```

Original motif Consensus sequence: RGKTCABVVRGAGGTCA




Reverse complement motif Consensus sequence: TGACCTCKVVBTGAYCK

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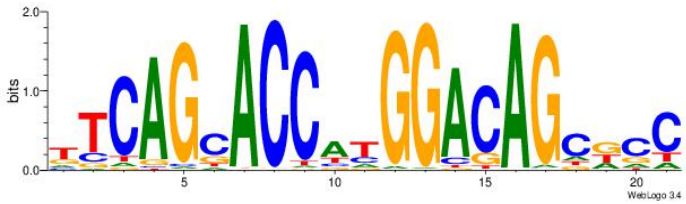
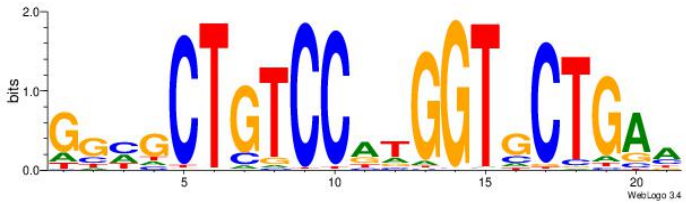
Dataset #: 2
Motif ID: 19
Motif name: REST
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 6
Number of overlap: 16
Similarity score: 2.07409

Alignment:
```
TTCAGCACCATGGACAGCKCC----
-----VDBHMAGGTCACCCTGACCY
```

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC

Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA

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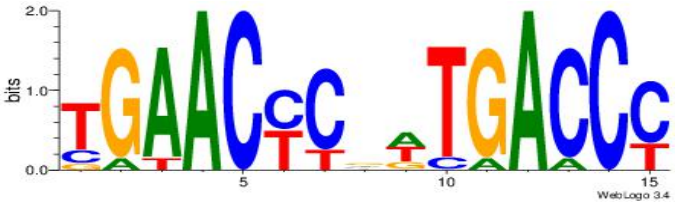
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 17 |
| Motif name: | RXRAVDR |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 1 |
| Number of overlap: | 15 |
| Similarity score: | 2.56536 |

Alignment:

```
-----GGGTCAWBGRGTTCA
MGGTCAGGGTGACCTRDBHV
```

Original motif Consensus sequence: GGGTCAWBGRGTTCA

Reverse complement motif Consensus sequence: TGAACKCBWTGAC

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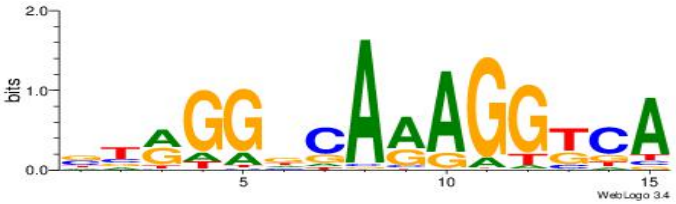
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 20 |

| | |
|---|---|
| Motif name: | PPARGRXRA |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Reverse Complement |
| Direction: | Backward |
| Position number: | 2 |
| Number of overlap: | 14 |
| Similarity score: | 3.07055 |

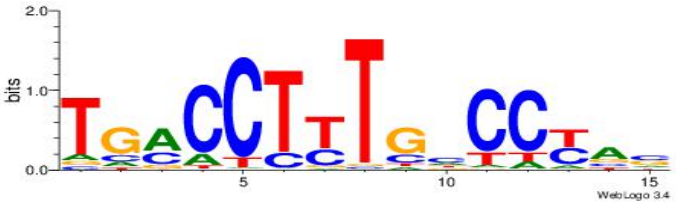
Alignment:

```
------TGRCCTKTGHCCKAB
VDBHMAGGTCACCCTGACCY-
```

Original motif Consensus sequence: BTRGGDCARAGGKCA




Reverse complement motif Consensus sequence: TGRCCTKTGHCCK

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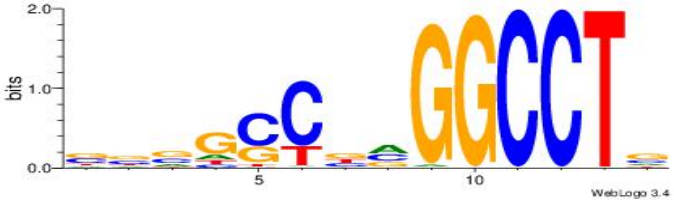
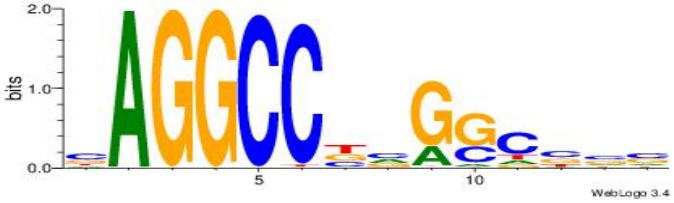
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 12 |
| Motif name: | Zfx |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction: | Forward |
| Position number: | 2 |
| Number of overlap: | 13 |
| Similarity score: | 3.56429 |

Alignment:
VAGGCCBBGGCVBB-------
-MGGTCAGGGTGACCTRDBHV

Original motif Consensus sequence: BBVGCCBVGGCCTV




Reverse complement motif Consensus sequence: VAGGCCBBGGCVB

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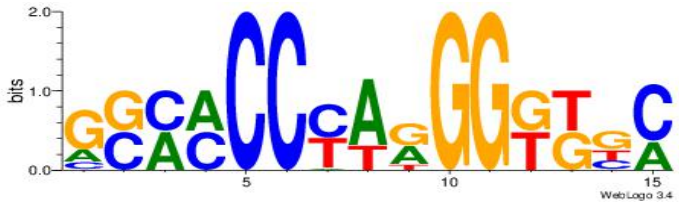
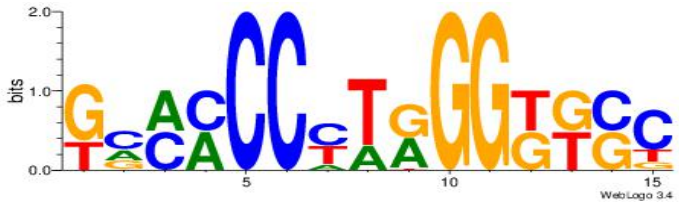
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 13 |
| Motif name: | Zfp423 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 3 |
| Number of overlap: | 13 |
| Similarity score: | 3.56489 |

Alignment:
GSMMCCYARGGKKKC-------
--MGGTCAGGGTGACCTRDBHV

Original motif Consensus sequence: GSMMCCYARGGKKKC

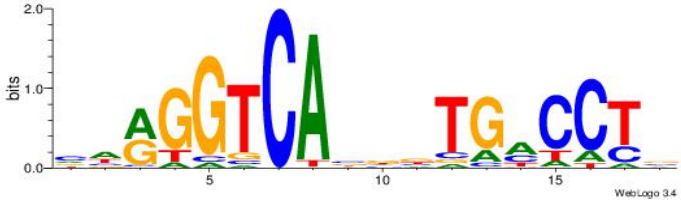
Reverse complement motif Consensus sequence: GYRYCCMTKGGYR



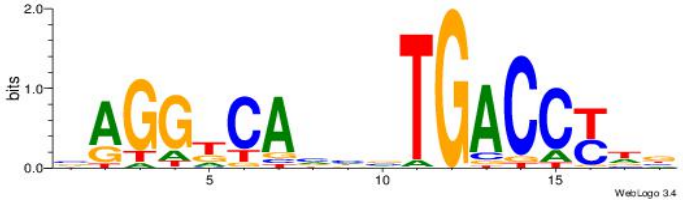




**Dataset #: 2** **Motif ID: 30** **Motif name: ESR2**

Original motif Consensus sequence: VHRGGTCABDBTGMCCTB




Reverse complement motif Consensus sequence: BAGGYCABHBTGACCKHV



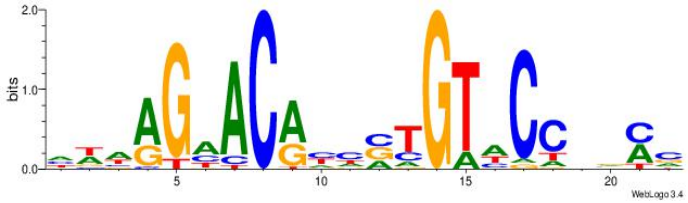

## Best Matches for Motif ID 30 (Highest to Lowest)

| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 24 |
| Motif name: | Ar |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 3 |
| Number of overlap: | 18 |
| Similarity score: | 0.0488603 |

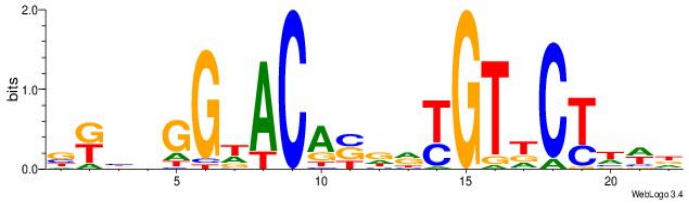
Alignment:

HWDAGHACRHHVTGTHCCHVMV
--BAGGYCABHBTGACCKHV--

Original motif Consensus sequence: HWDAGHACRHHVTGTHCCHVMV




Reverse complement motif Consensus sequence: VRVDGGHACAVDDKGTHCTDWH

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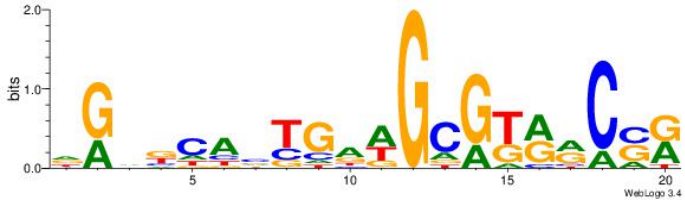
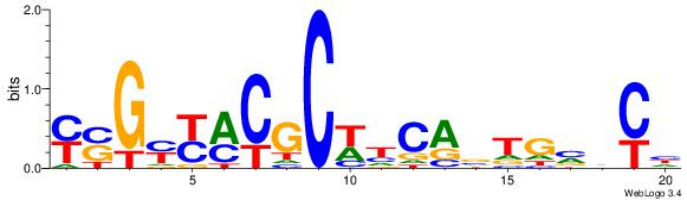
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 45 |
| Motif name: | Pax5 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction: | Backward |
| Position number: | 3 |
| Number of overlap: | 18 |
| Similarity score: | 0.0851144 |

Alignment:
MSGKKRCGCWDCABTGBBCD
BAGGYCABHBTGACCKHV--

Original motif Consensus sequence: DGVBCABTGDWGCGKRRCSR

Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD

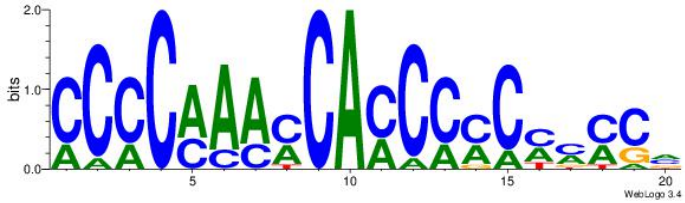


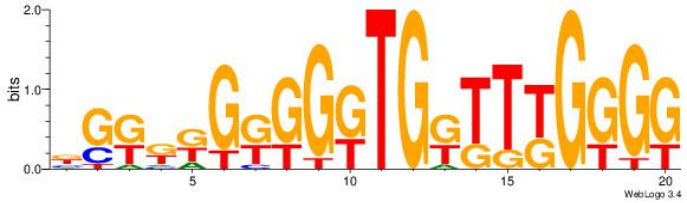

| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 18 |
| Motif name: | RREB1 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction: | Forward |
| Position number: | 1 |
| Number of overlap: | 18 |
| Similarity score: | 0.0903249 |

Alignment:
BGRRRGRGGRTGRTTYGGGG
BAGGYCABHBTGACCKHV--

Original motif Consensus sequence: CCCCMAAMCAMCCMCMMMCV




Reverse complement motif Consensus sequence:
BGRRRGRGGRTGRTTYGGGG



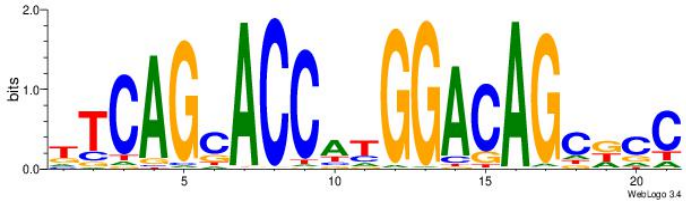

| | |
|---|---|
| Dataset #: | 2 |

| | |
|---|---|
| Motif ID: | 19 |
| Motif name: | REST |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Reverse Complement |
| Direction: | Backward |
| Position number: | 3 |
| Number of overlap: | 18 |
| Similarity score: | 0.0916961 |

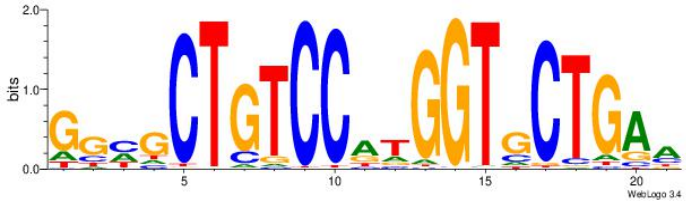
Alignment:

```
GGYGCTGTCCATGGTGCTGAA
-VHRGGTCABDBTGMCCTB--
```

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC




Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA

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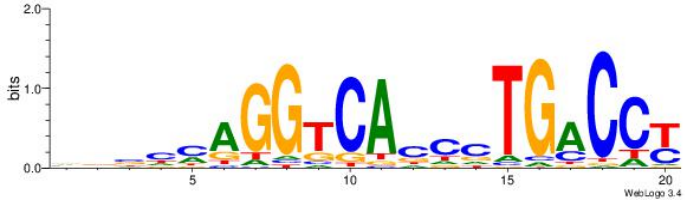
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 29 |
| Motif name: | ESR1 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 4 |
| Number of overlap: | 17 |

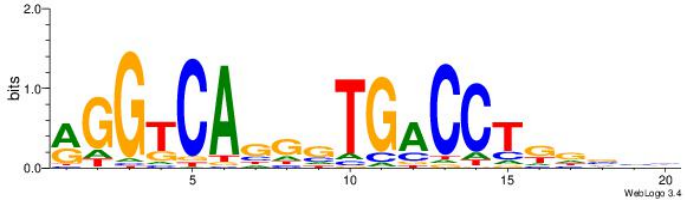
Similarity score: 0.511812

Alignment:
VDBHMAGGTCACCCTGACCY-
---VHRGGTCABDBTGMCCTB

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY




Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV



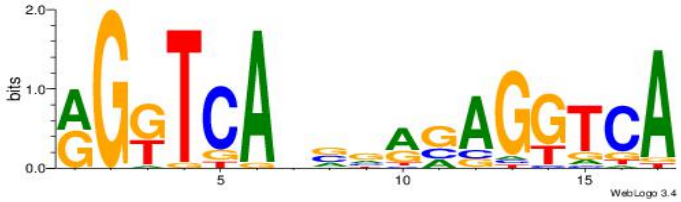

---

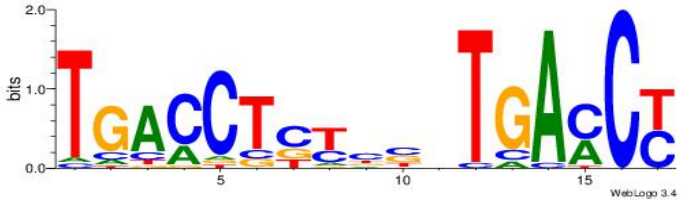
Dataset #: 2
Motif ID: 47
Motif name: RXRRAR_DR5
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 17
Similarity score: 0.570972

Alignment:
-RGKTCABVVRGAGGTCA
BAGGYCABHBTGACCKHV

Original motif Consensus sequence: RGKTCABVVRGAGGTCA

Reverse complement motif Consensus sequence: TGACCTCKVVBTGAYCK



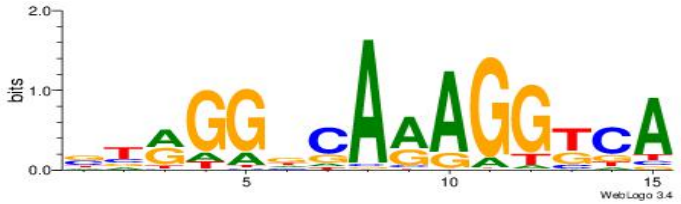

---

| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 20 |
| 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: | 15 |
| Similarity score: | 1.56699 |

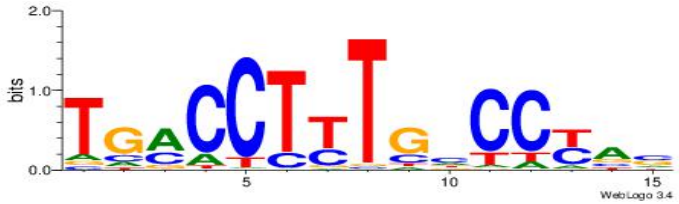
Alignment:

```
BTRGGDCARAGGKCA---
VHRGGTCABDBTGMCCTB
```

Original motif Consensus sequence: BTRGGDCARAGGKCA




Reverse complement motif Consensus sequence: TGRCCTKTGHCCK




---

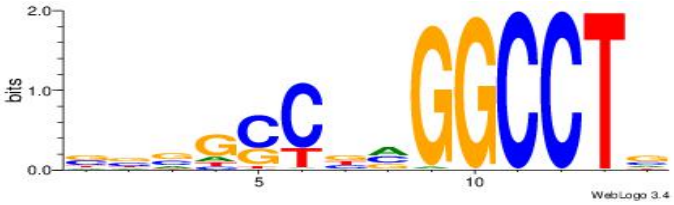
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 12 |

| | |
|---|---|
| Motif name: | Zfx |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction: | Forward |
| Position number: | 1 |
| Number of overlap: | 14 |
| Similarity score: | 2.07891 |

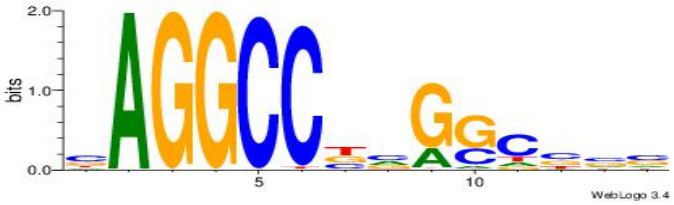
Alignment:

```
VAGGCCBBGGCVBB----
BAGGYCABHBTGACCKHV
```

Original motif Consensus sequence: BBVGCCBVGGCCTV




Reverse complement motif Consensus sequence: VAGGCCBBGGCVB

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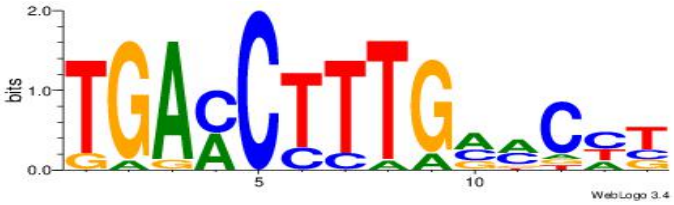
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 22 |
| Motif name: | NR2F1 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 1 |
| Number of overlap: | 14 |
| Similarity score: | 2.08921 |

Alignment:

```
----TGAMCTTTGMMCYT
VHRGGTCABDBTGMCCTB
```

Original motif Consensus sequence: TGAMCTTTGMMCYT




Reverse complement motif Consensus sequence: AKGYYCAAAGRTCA

---

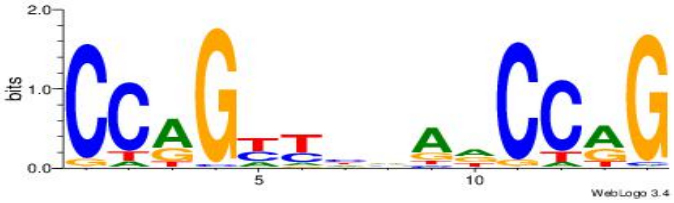
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 48 |
| Motif name: | Tcfcp2l1 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 1 |
| Number of overlap: | 14 |
| Similarity score: | 2.09109 |

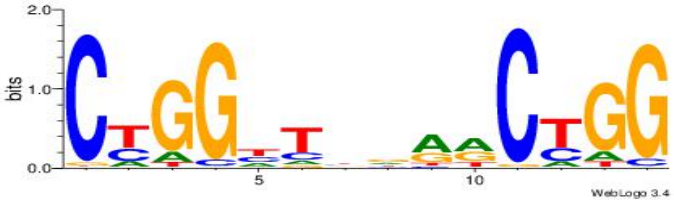
Alignment:

```
----CCAGYYHVADCCRG
BAGGYCABHBTGACCKHV
```

Original motif Consensus sequence: CCAGYYHVADCCRG

Reverse complement motif Consensus sequence: CKGGDTBDMMCT




**Dataset #: 2** **Motif ID: 31** **Motif name: Esrrb**

Original motif Consensus sequence: CACGTG

Reverse complement motif Consensus sequence: CACGTG

**Best Matches for Motif ID 31 (Highest to Lowest)**

| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 25 |
| Motif name: | Arnt |
| 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 |

Alignment:

```
CACGTG
CACGTG
```

Original motif Consensus sequence: CACGTG

Reverse complement motif Consensus sequence: CACGTG

---

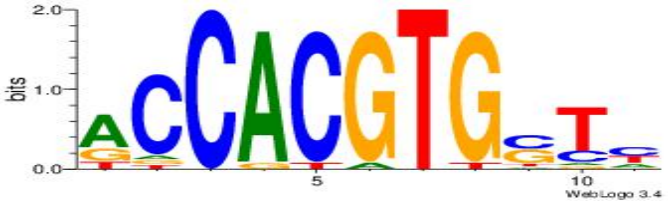
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 39 |
| Motif name: | MYCMAX |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction: | Forward |
| Position number: | 3 |
| Number of overlap: | 6 |
| Similarity score: | 0.0143849 |

Alignment:

```
ACCACGTGSTM
--CACGTG---
```

Original motif Consensus sequence: RASCACGTGGT

Reverse complement motif Consensus sequence: ACCACGTGSTM

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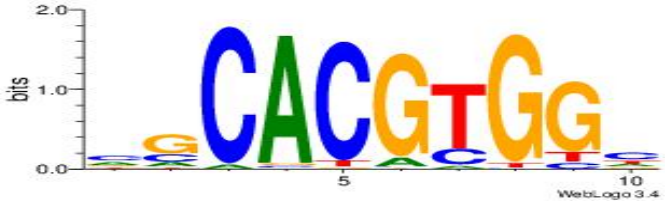
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 38 |
| Motif name: | Myc |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 3 |
| Number of overlap: | 6 |
| Similarity score: | 0.0267529 |

Alignment:

```
VGCACGTGGH
--CACGTG--
```

Original motif Consensus sequence: VGCACGTGGH




Reverse complement motif Consensus sequence: DCCACGTGCV

---

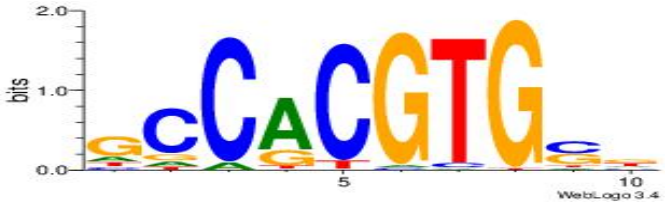
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 40 |
| Motif name: | Mycn |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction: | Backward |
| Position number: | 3 |
| Number of overlap: | 6 |

Similarity score: 0.0272641

Alignment:
GCCACGTGSD
--CACGTG--

Original motif Consensus sequence: HSCACGTGGC

Reverse complement motif Consensus sequence: GCCACGTGSD




---

Dataset #: 2
Motif ID: 33
Motif name: HIF1AARNT
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: 0.0347756

Alignment:
VCACGTBV
-CACGTG-

Original motif Consensus sequence: VBACGTGV

Reverse complement motif Consensus sequence: VCACGTBV

---

| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 26 |
| Motif name: | ArntAhr |
| 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: | 0.065625 |

Alignment:
YGCGTG
CACGTG

Original motif Consensus sequence: YGCGTG

Reverse complement motif Consensus sequence: CACGCM

---

| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 14 |

| | |
|---|---|
| Motif name: | ZEB1 |
| 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: | 0.0689533 |

Alignment:

```
HAGGTG
CACGTG
```

Original motif Consensus sequence: CACCTD

Reverse complement motif Consensus sequence: HAGGTG

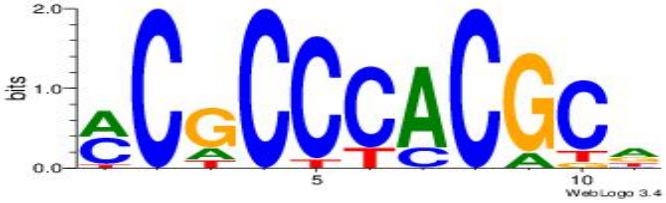
---

| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 28 |
| Motif name: | Egr1 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 1 |
| Number of overlap: | 6 |
| Similarity score: | 0.0784722 |

Alignment:
HGCGTGGGCGK
CACGTG-----

Original motif Consensus sequence: HGCGTGGGCGK

Reverse complement motif Consensus sequence: YCGCCCACGCH



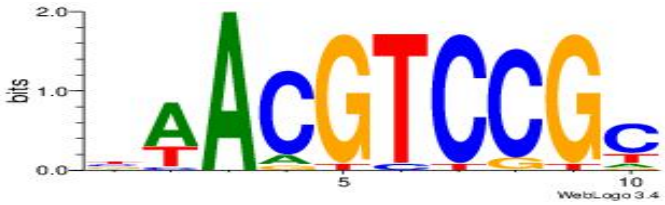

---

| | |
|---|---|
| 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: | 6 |
| Similarity score: | 0.0854167 |

Alignment:
BAACGTCCGC
-CACGTG---

Original motif Consensus sequence: BAACGTCCGC

Reverse complement motif Consensus sequence: GCGGACGTTV

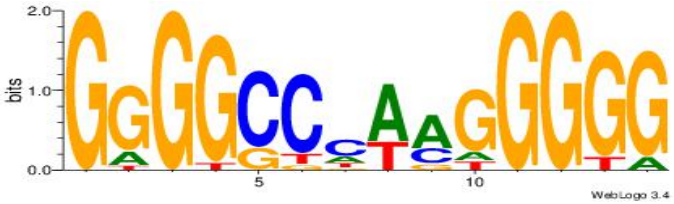


| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 21 |
| Motif name: | PLAG1 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 3 |
| Number of overlap: | 6 |
| Similarity score: | 0.105093 |

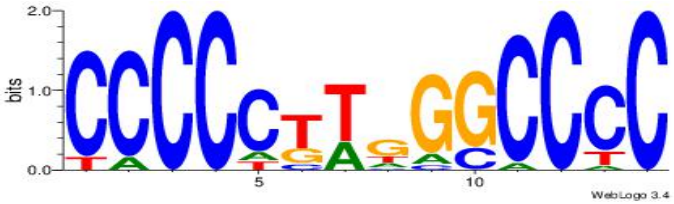
Alignment:

```
GGGGCCCAAGGGGG
------CACGTG--
```

Original motif Consensus sequence: GGGGCCCAAGGGGG

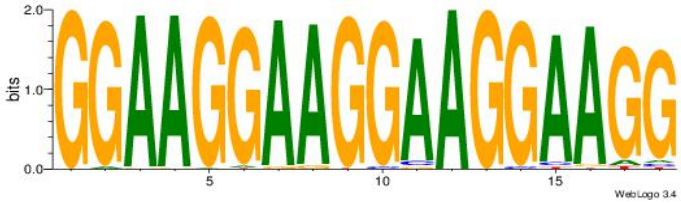



Reverse complement motif Consensus sequence: CCCCCTTGGGCCC

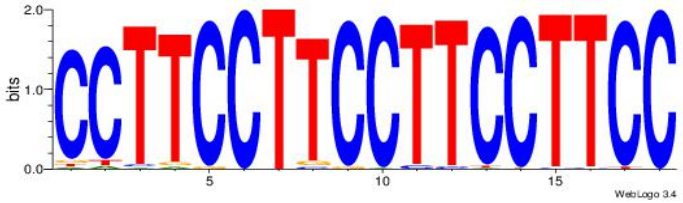



**Dataset #: 2 Motif ID: 32 Motif name: EWSR1-FLI1**

Original motif Consensus sequence: GGAAGGAAGGAAGGAAGG




Reverse complement motif Consensus sequence: CCTTCCTTCCTTCCTTCC



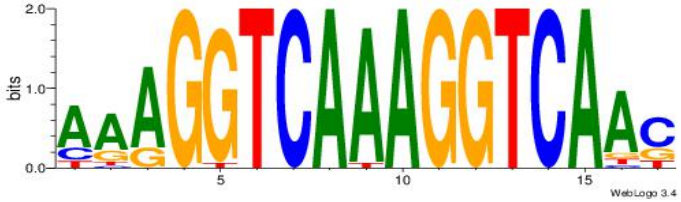

## Best Matches for Motif ID 32 (Highest to Lowest)

| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 43 |
| Motif name: | NR1H2RXRA |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 6 |
| Number of overlap: | 12 |
| Similarity score: | 1.09472 |

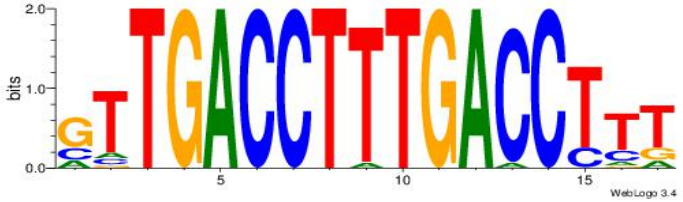
Alignment:

```
------AAAGGTCAAAGGTCAAC
GGAAGGAAGGAAGGAAGG-----
```

Original motif Consensus sequence: AAAGGTCAAAGGTCAAC




Reverse complement motif Consensus sequence: GTTGACCTTTGACCTTT

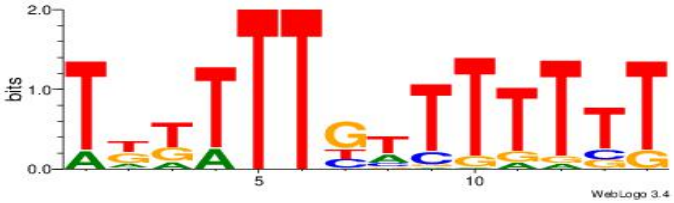


| | |
|---|---|
| Dataset #: | 1 |
| Motif ID: | 10 |
| Motif name: | Motif 10 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 3 |
| Number of overlap: | 12 |
| Similarity score: | 1.1007 |

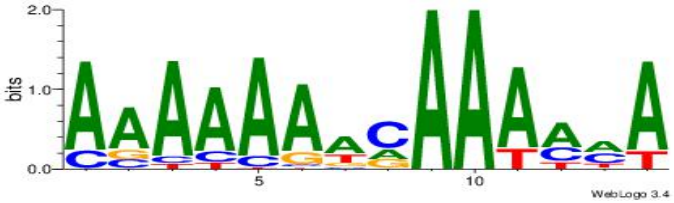
Alignment:

```
------TKKTTTGTTTTTTT
CCTTCCTTCCTTCCTTCC--
```

Original motif Consensus sequence: TKKTTTGTTTTTTT




Reverse complement motif Consensus sequence: AAAAAAACAAARR

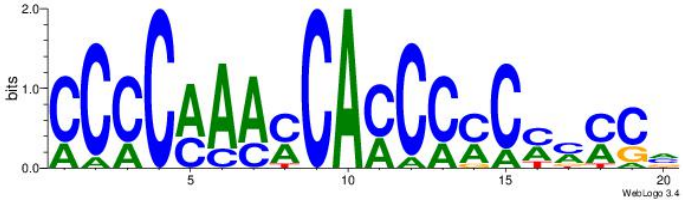



| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 18 |
| Motif name: | RREB1 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 11 |

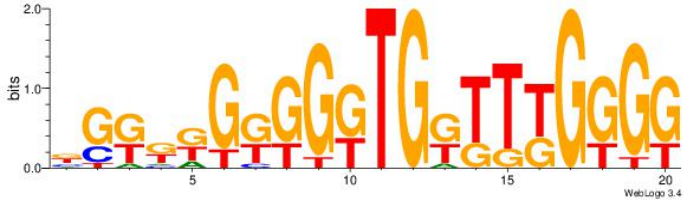
Number of overlap: 10
Similarity score: 2.09833

Alignment:
```
--------CCCCMAAMCAMCCMCMMMCV
CCTTCCTTCCTTCCTTCC----------
```

Original motif Consensus sequence: CCCCMAAMCAMCCMCMMMCV




Reverse complement motif Consensus sequence: BGRRRGRGGRTGRTTYGGGG



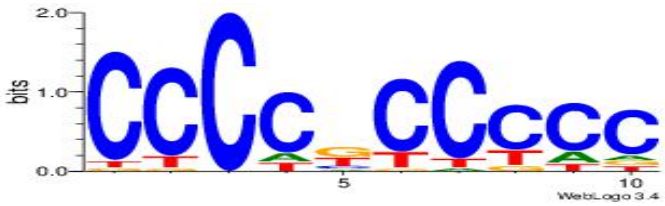

---

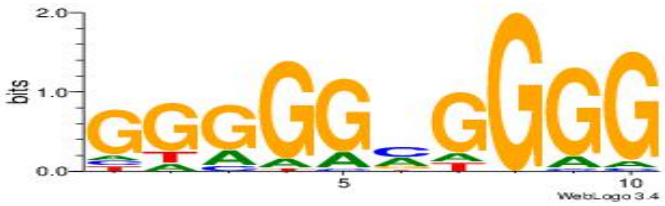
Dataset #: 2
Motif ID: 16
Motif name: SP1
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 2
Number of overlap: 9
Similarity score: 2.58264

Alignment:
```
GGGGGYGGGG---------
-GGAAGGAAGGAAGGAAGG
```

Original motif Consensus sequence: CCCCKCCCCC

Reverse complement motif Consensus sequence: GGGGGYGGGG



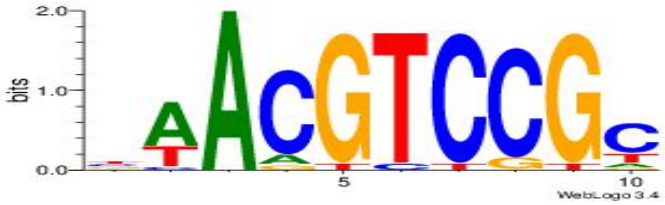

---

| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 37 |
| Motif name: | MIZF |
| 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: | 3.0896 |

Alignment:

```
----------BAACGTCCGC
CCTTCCTTCCTTCCTTCC--
```

Original motif Consensus sequence: BAACGTCCGC




Reverse complement motif Consensus sequence: GCGGACGTTV

---

| | |
|---|---|
| Dataset #: | 1 |
| Motif ID: | 7 |

| | |
|---|---|
| Motif name: | Motif 7 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 1 |
| Number of overlap: | 8 |
| Similarity score: | 3.09107 |

Alignment:

```
----------CCCRCCCC
CCTTCCTTCCTTCCTTCC
```

Original motif Consensus sequence: CCCRCCCC

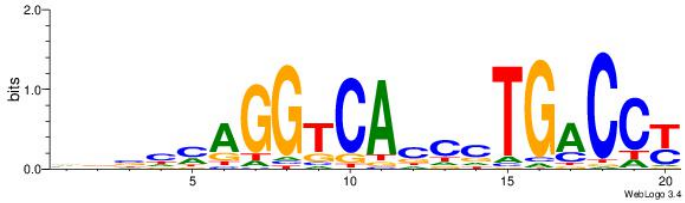
Reverse complement motif Consensus sequence: GGGGMGGG

---

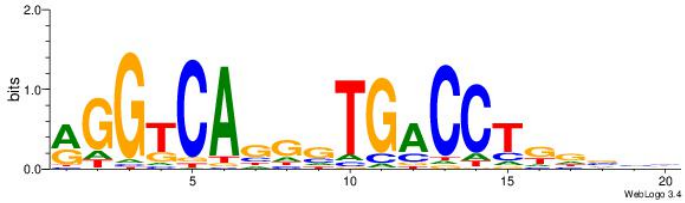
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 29 |
| Motif name: | ESR1 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Reverse Complement |
| Direction: | Forward |
| Position number: | 13 |
| Number of overlap: | 8 |
| Similarity score: | 3.09836 |

Alignment:
MGGTCAGGGTGACCTRDBHV----------
----------GGAAGGAAGGAAGGAAGG

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY




Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV

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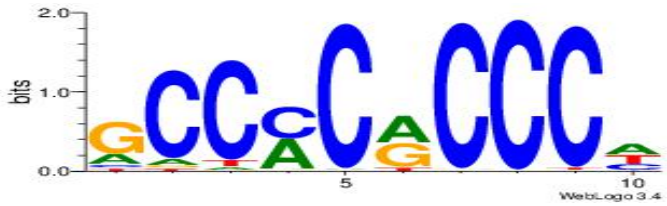
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 36 |
| Motif name: | Klf4 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 3 |
| Number of overlap: | 8 |
| Similarity score: | 3.10206 |

Alignment:
----------DGGGYGKGGC
GGAAGGAAGGAAGGAAGG--

Original motif Consensus sequence: DGGGYGKGGC

Reverse complement motif Consensus sequence: GCCYCMCCCD

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| | |
|---|---|
| Dataset #: | 1 |
| Motif ID: | 3 |
| Motif name: | Motif 3 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 1 |
| Number of overlap: | 7 |
| Similarity score: | 3.55161 |

Alignment:

```
-----------AGSCWGG
GGAAGGAAGGAAGGAAGG
```

Original motif Consensus sequence: AGSCWGG

Reverse complement motif Consensus sequence: CCWGSCT

---

| | |
|---|---|
| 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: | 3.58428 |

Alignment:

```
TGACCTDVWT-----------
---CCTTCCTTCCTTCCTTCC
```

Original motif Consensus sequence: AWVDAGGTCA

Reverse complement motif Consensus sequence: TGACCTDVWT

---

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

Original motif Consensus sequence: VBACGTGV

Reverse complement motif Consensus sequence: VCACGTBV

**Best Matches for Motif ID 33 (Highest to Lowest)**

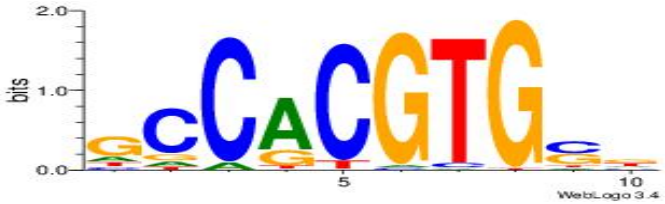
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 40 |
| Motif name: | Mycn |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Reverse Complement |
| Direction: | Forward |
| Position number: | 2 |
| Number of overlap: | 8 |
| Similarity score: | 0.0228069 |

Alignment:

```
GCCACGTGSD
-VBACGTGV-
```

Original motif Consensus sequence: HSCACGTGGC

Reverse complement motif Consensus sequence: GCCACGTGSD

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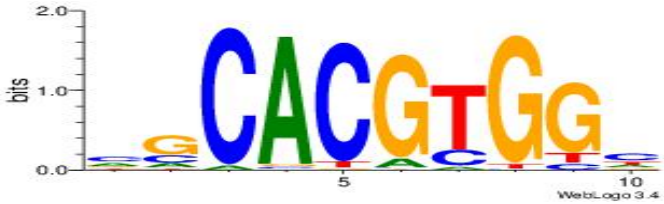
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 38 |
| Motif name: | Myc |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Reverse Complement |
| Direction: | Forward |
| Position number: | 2 |
| Number of overlap: | 8 |

Similarity score: 0.0249459

Alignment:
DCCACGTGCV
-VBACGTGV-

Original motif Consensus sequence: VGCACGTGGH




Reverse complement motif Consensus sequence: DCCACGTGCV

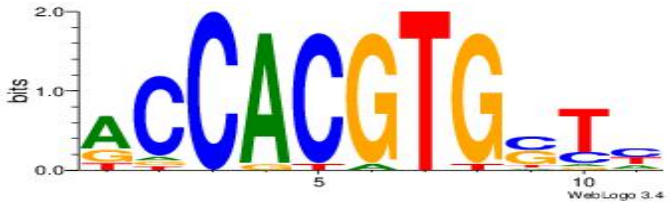
---

Dataset #: 2
Motif ID: 39
Motif name: MYCMAX
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: 0.0254922

Alignment:
ACCACGTGSTM
-VCACGTBV--

Original motif Consensus sequence: RASCACGTGGT

Reverse complement motif Consensus sequence: ACCACGTGSTM



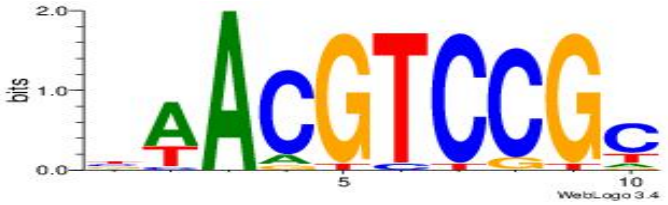

---

| | |
|---|---|
| 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: | 3 |
| Number of overlap: | 8 |
| Similarity score: | 0.0482171 |

Alignment:

```
GCGGACGTTV
--VCACGTBV
```

Original motif Consensus sequence: BAACGTCCGC




Reverse complement motif Consensus sequence: GCGGACGTTV

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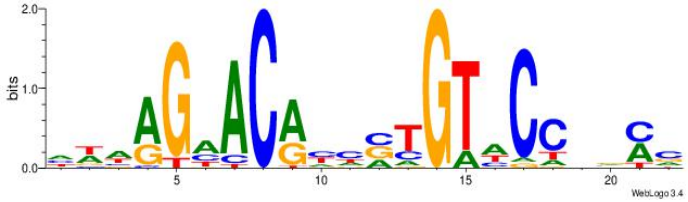
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 24 |

| | |
|---|---|
| Motif name: | Ar |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Reverse Complement |
| Direction: | Forward |
| Position number: | 5 |
| Number of overlap: | 8 |
| Similarity score: | 0.0533654 |

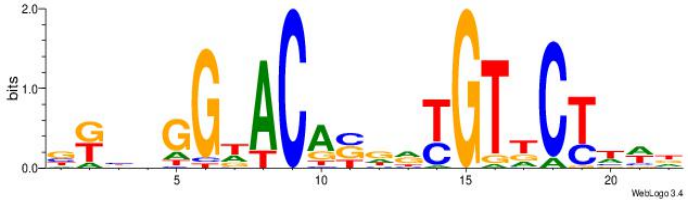
Alignment:

```
VRVDGGHACAVDDKGTHCTDWH
----VBACGTGV----------
```

Original motif Consensus sequence: HWDAGHACRHHVTGTHCCHVMV




Reverse complement motif Consensus sequence: VRVDGGHACAVDDKGTHCTDWH

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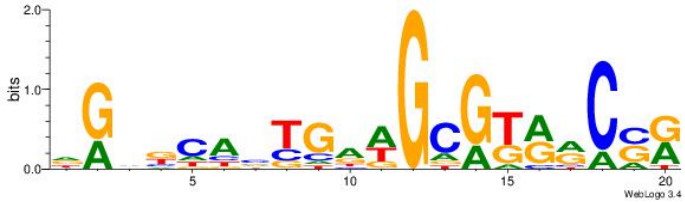
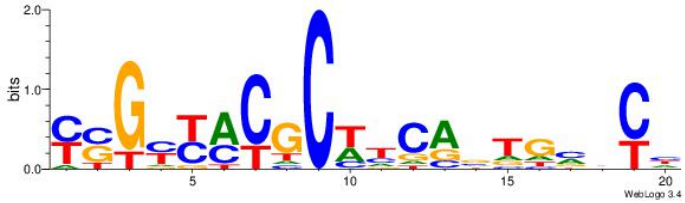
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 45 |
| Motif name: | Pax5 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction: | Backward |
| Position number: | 8 |
| Number of overlap: | 8 |
| Similarity score: | 0.0661859 |

Alignment:
MSGKKRCGCWDCABTGBBCD
-----VCACGTBV-------

Original motif Consensus sequence: DGVBCABTGDWGCGKRRCSR




Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD

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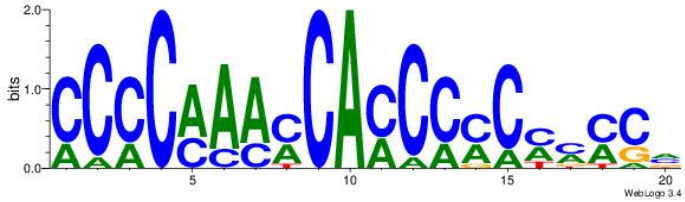
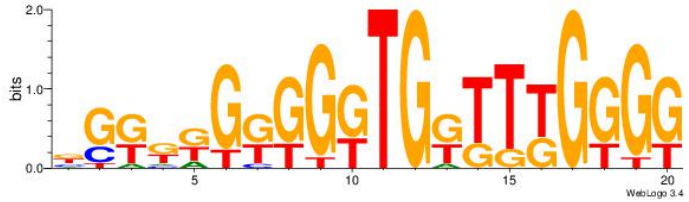
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 18 |
| Motif name: | RREB1 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 8 |
| Number of overlap: | 8 |
| Similarity score: | 0.0666776 |

Alignment:
CCCCMAAMCAMCCMCMMMCV
-----VCACGTBV-------

Original motif Consensus sequence: CCCCMAAMCAMCCMCMMMCV

Reverse complement motif Consensus sequence: BGRRRGRGGRTGRTTYGGGG




| | |
|---|---|
| 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: | 3 |
| Number of overlap: | 8 |
| Similarity score: | 0.0703926 |

Alignment:

```
BKAGGGGDAD
VBACGTGV--
```

Original motif Consensus sequence: BKAGGGGDAD

Reverse complement motif Consensus sequence: BTHCCCCTYB

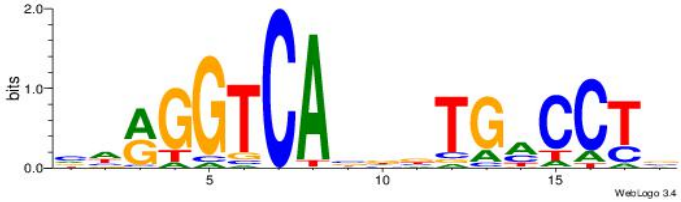
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 30 |

| | |
|---|---|
| Motif name: | ESR2 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Reverse Complement |
| Direction: | Backward |
| Position number: | 6 |
| Number of overlap: | 8 |
| Similarity score: | 0.0716055 |

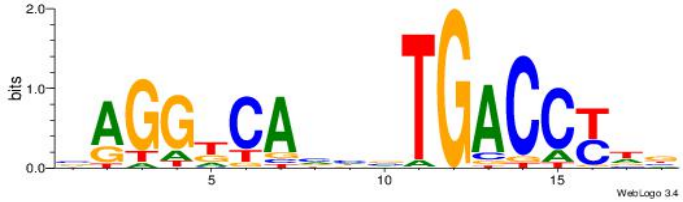
Alignment:

```
BAGGYCABHBTGACCKHV
-----VBACGTGV-----
```

Original motif Consensus sequence: VHRGGTCABDBTGMCCTB




Reverse complement motif Consensus sequence: BAGGYCABHBTGACCKHV

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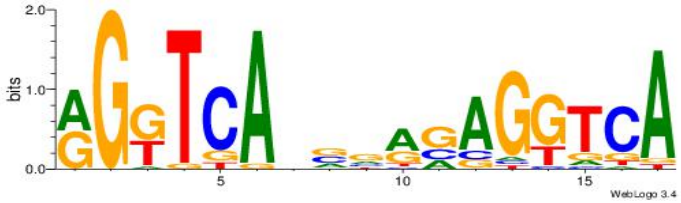
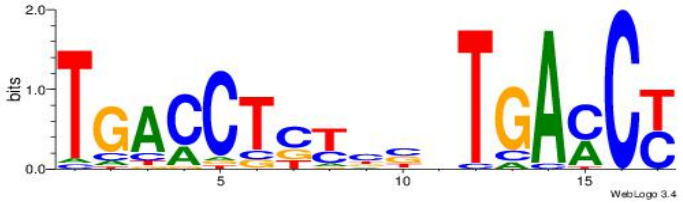
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 47 |
| Motif name: | RXRRAR_DR5 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Reverse Complement |
| Direction: | Backward |
| Position number: | 4 |
| Number of overlap: | 8 |
| Similarity score: | 0.0726789 |

Alignment:
TGACCTCKVVBTGAYCK
------VBACGTGV---

Original motif Consensus sequence: RGKTCABVVRGAGGTCA



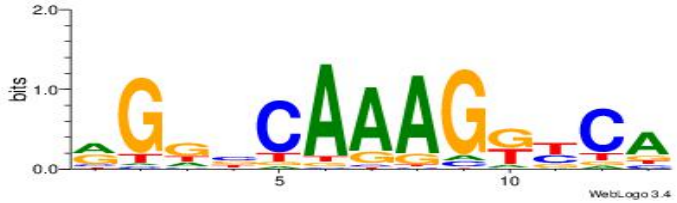

Reverse complement motif Consensus sequence:
TGACCTCKVVBTGAYCK



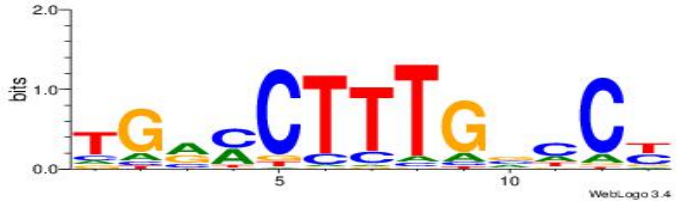

---

**Dataset #: 2 Motif ID: 34 Motif name: HNF4A**

Original motif Consensus sequence: RGGBCAAAGKYCA




Reverse complement motif Consensus sequence: TGMYCTTTGBCCK




**Best Matches for Motif ID 34 (Highest to Lowest)**

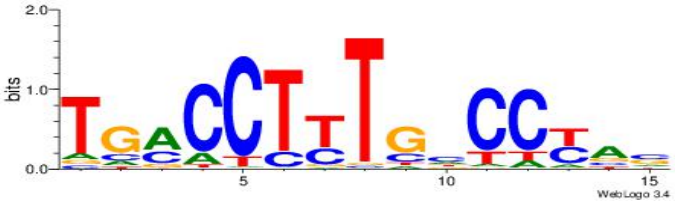
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 20 |
| Motif name: | PPARGRXRA |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |

| | |
|---|---|
| Position number: | 3 |
| Number of overlap: | 13 |
| Similarity score: | 0 |

Alignment:
BTRGGDCARAGGKCA
--RGGBCAAAGKYCA

Original motif Consensus sequence: BTRGGDCARAGGKCA

Reverse complement motif Consensus sequence: TGRCCTKTGHCCK

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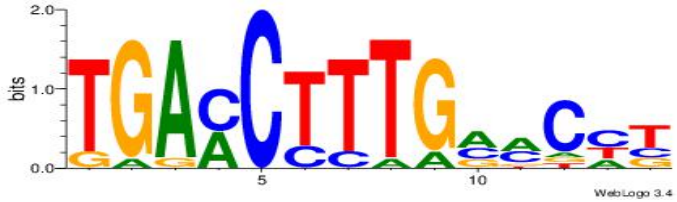
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 22 |
| Motif name: | NR2F1 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 2 |
| Number of overlap: | 13 |
| Similarity score: | 0.0227413 |

Alignment:
TGAMCTTTGMMCYT
-TGMYCTTTGBCCK

Original motif Consensus sequence: TGAMCTTTGMMCYT

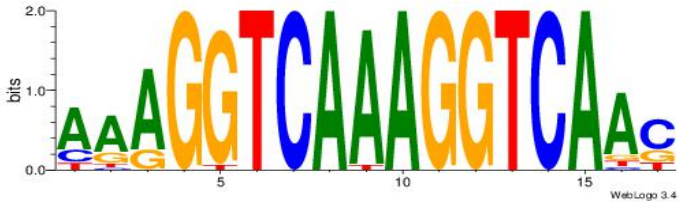
Reverse complement motif Consensus sequence: AKGYYCAAAGRTC



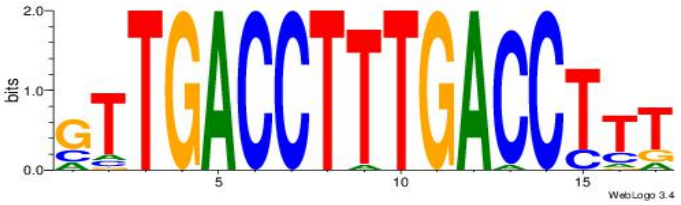
Dataset #: 2
Motif ID: 43
Motif name: NR1H2RXRA
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 3
Number of overlap: 13
Similarity score: 0.0423023

Alignment:
AAAGGTCAAAGGTCAAC
--RGGBCAAAGKYCA--

Original motif Consensus sequence: AAAGGTCAAAGGTCAAC




Reverse complement motif Consensus sequence: GTTGACCTTTGACCTTT



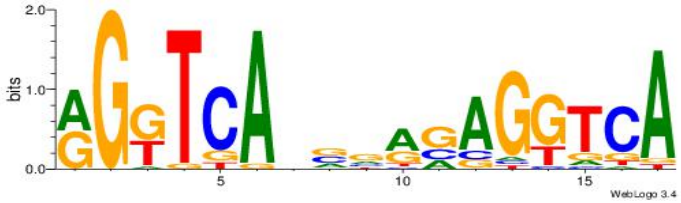

Dataset #: 2

| | |
|---|---|
| Motif ID: | 47 |
| Motif name: | RXRRAR_DR5 |
| 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: | 0.048852 |

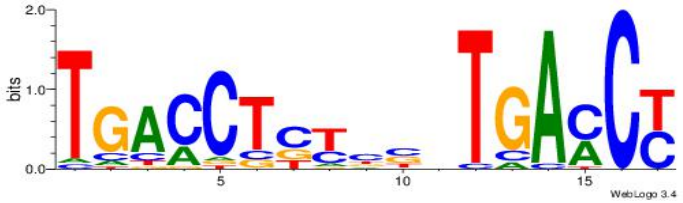
Alignment:

```
TGACCTCKVVBTGAYCK
TGMYCTTTGBCCK----
```

Original motif Consensus sequence: RGKTCABVVRGAGGTCA




Reverse complement motif Consensus sequence: TGACCTCKVVBTGAYCK

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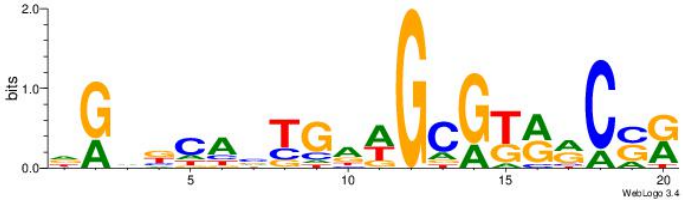
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 45 |
| Motif name: | Pax5 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Reverse Complement |
| Direction: | Forward |
| Position number: | 8 |
| Number of overlap: | 13 |

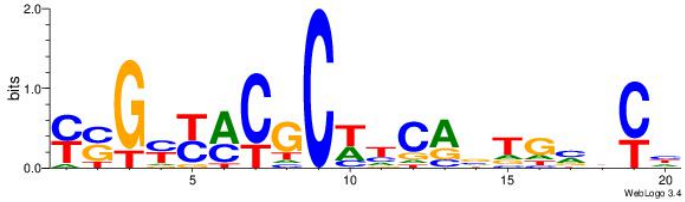
Similarity score: 0.063924

Alignment:
MSGKKRCGCWDCABTGBBCD
-------RGGBCAAAGKYCA

Original motif Consensus sequence: DGVBCABTGDWGCGKRRCSR




Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD



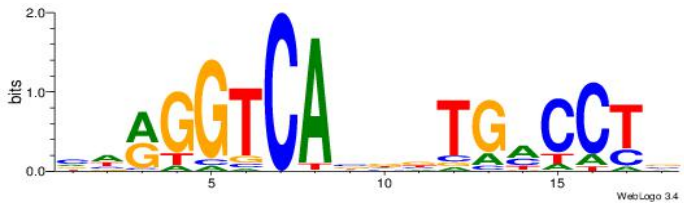

---

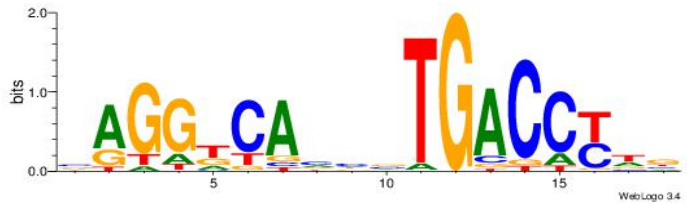
Dataset #: 2
Motif ID: 30
Motif name: ESR2
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 3
Number of overlap: 13
Similarity score: 0.0671615

Alignment:
VHRGGTCABDBTGMCCTB
--RGGBCAAAGKYCA---

Original motif Consensus sequence: VHRGGTCABDBTGMCCTB

Reverse complement motif Consensus sequence: BAGGYCABHBTGACCKHV

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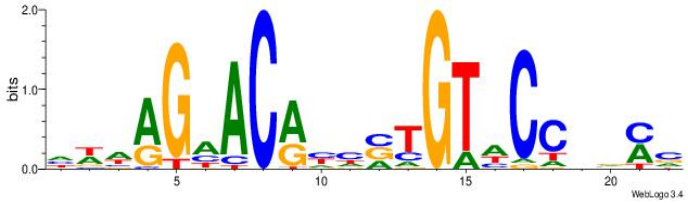
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 24 |
| Motif name: | Ar |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction: | Forward |
| Position number: | 7 |
| Number of overlap: | 13 |
| Similarity score: | 0.067775 |

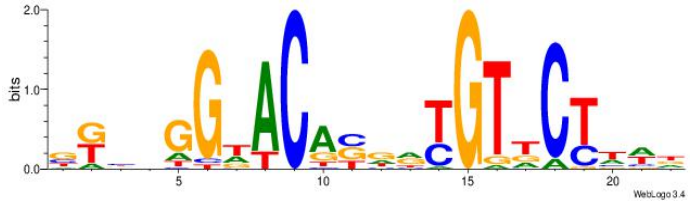
Alignment:

```
VRVDGGHACAVDDKGTHCTDWH
------TGMYCTTTGBCCK---
```

Original motif Consensus sequence: HWDAGHACRHHVTGTHCCHVMV




Reverse complement motif Consensus sequence: VRVDGGHACAVDDKGTHCTDWH

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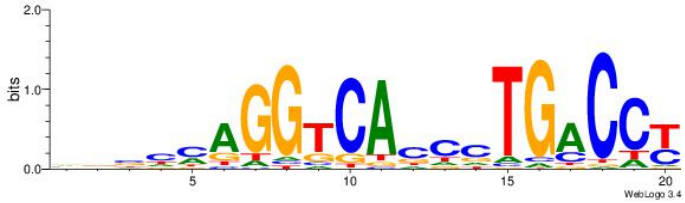
Dataset #: 2

| | |
|---|---|
| Motif ID: | 29 |
| Motif name: | ESR1 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 1 |
| Number of overlap: | 13 |
| Similarity score: | 0.0711137 |

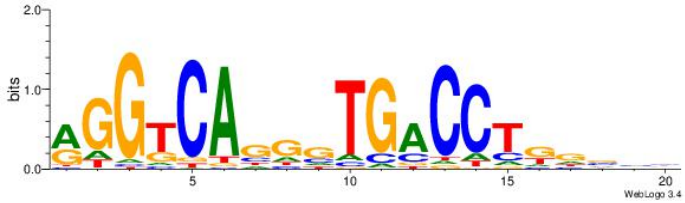
Alignment:

```
VDBHMAGGTCACCCTGACCY
TGMYCTTTGBCCK-------
```

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY




Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV

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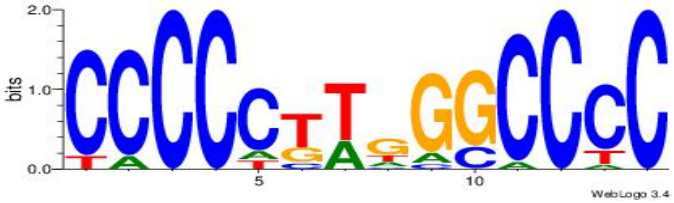
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 21 |
| Motif name: | PLAG1 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 1 |
| Number of overlap: | 13 |

Similarity score: 0.0714266

Alignment:
GGGGCCCAAGGGGG
-RGGBCAAAGKYCA

Original motif Consensus sequence: GGGGCCCAAGGGGG

Reverse complement motif Consensus sequence: CCCCCTTGGGCCC

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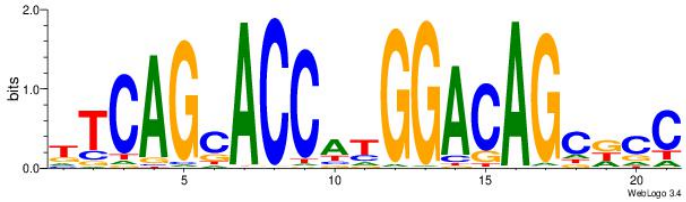
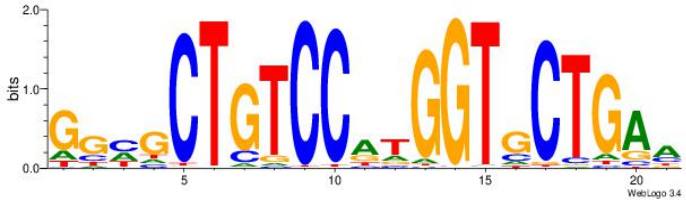
Dataset #: 2
Motif ID: 19
Motif name: REST
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 4
Number of overlap: 13
Similarity score: 0.0741922

Alignment:
GGYGCTGTCCATGGTGCTGAA
-----TGMYCTTTGBCCK---

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC

Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA

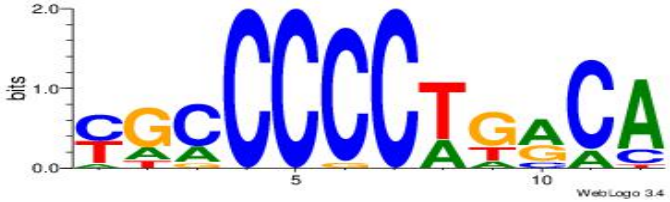



**Dataset #: 2** **Motif ID: 35** **Motif name: INSM1**

Original motif Consensus sequence: TGYCAGGGGGCR

Reverse complement motif Consensus sequence: MGCCCCCTGMCA



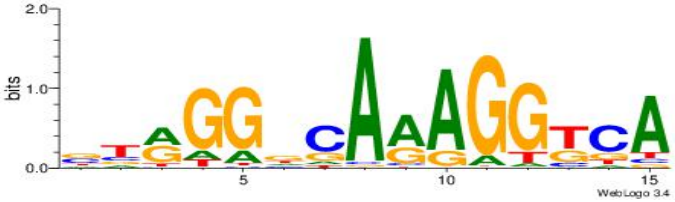

## Best Matches for Motif ID 35 (Highest to Lowest)

| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 20 |
| Motif name: | PPARGRXRA |
| 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: | 0.0472454 |

Alignment:

```
BTRGGDCARAGGKCA
---TGYCAGGGGGCR
```

Original motif Consensus sequence: BTRGGDCARAGGKCA




Reverse complement motif Consensus sequence: TGRCCTKTGHCCK

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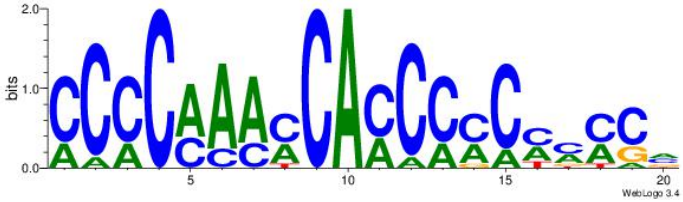
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 18 |
| Motif name: | RREB1 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Reverse Complement |
| Direction: | Backward |
| Position number: | 1 |
| Number of overlap: | 12 |
| Similarity score: | 0.0499162 |

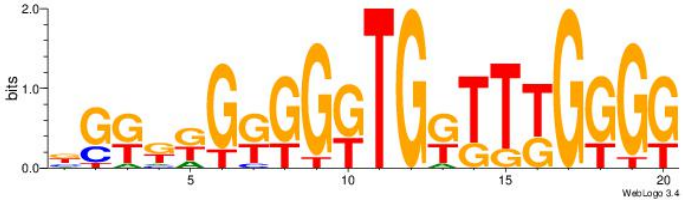
Alignment:

```
BGRRRGRGGRTGRTTYGGGG
--------TGYCAGGGGGCR
```

Original motif Consensus sequence: CCCCMAAMCAMCCMCMMMCV




Reverse complement motif Consensus sequence: BGRRRGRGGRTGRTTYGGGG

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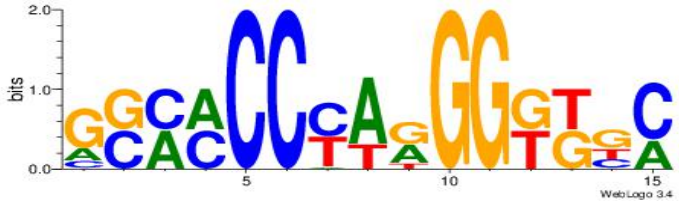
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 13 |
| Motif name: | Zfp423 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction: | Backward |
| Position number: | 3 |
| Number of overlap: | 12 |
| Similarity score: | 0.0538619 |

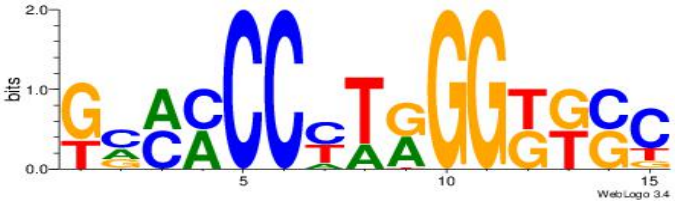
Alignment:

```
GYRYCCMTKGGYRSC
-MGCCCCCTGMCA--
```

Original motif Consensus sequence: GSMMCCYARGGKKKC




Reverse complement motif Consensus sequence: GYRYCCMTKGGYR

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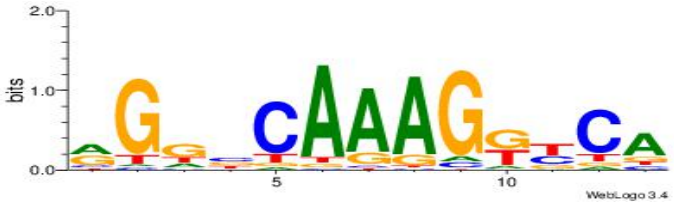
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 34 |
| Motif name: | HNF4A |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 2 |
| Number of overlap: | 12 |

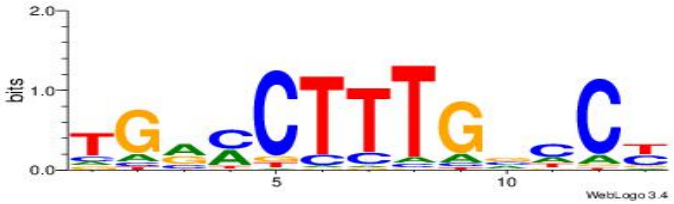
Similarity score: 0.0551858

Alignment:
RGGBCAAAGKYCA
-TGYCAGGGGGCR

Original motif Consensus sequence: RGGBCAAAGKYCA




Reverse complement motif Consensus sequence: TGMYCTTTGBCCK

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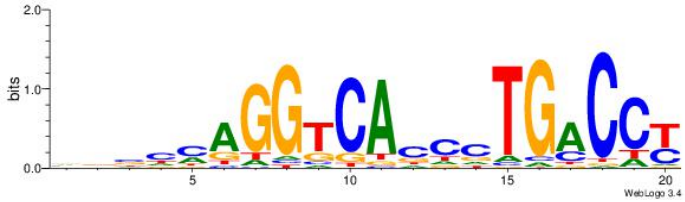
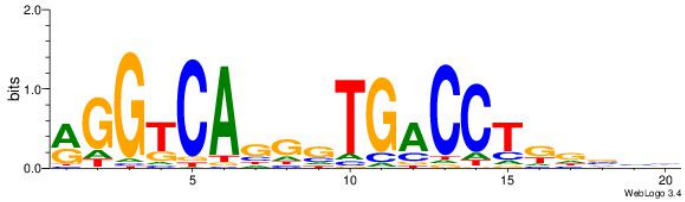
Dataset #: 2
Motif ID: 29
Motif name: ESR1
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 2
Number of overlap: 12
Similarity score: 0.0630846

Alignment:
VDBHMAGGTCACCCTGACCY
-TGYCAGGGGGCR-------

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY

Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV

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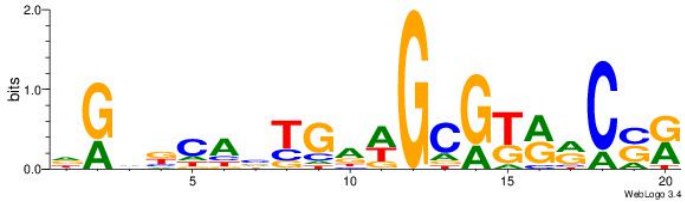
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 45 |
| Motif name: | Pax5 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 6 |
| Number of overlap: | 12 |
| Similarity score: | 0.0679087 |

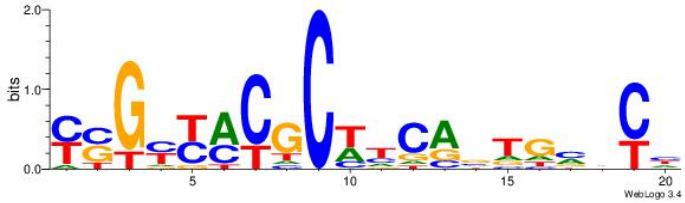
Alignment:

```
DGVBCABTGDWGCGKRRCSR
-----TGYCAGGGGGCR---
```

Original motif Consensus sequence: DGVBCABTGDWGCGKRRCSR




Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD

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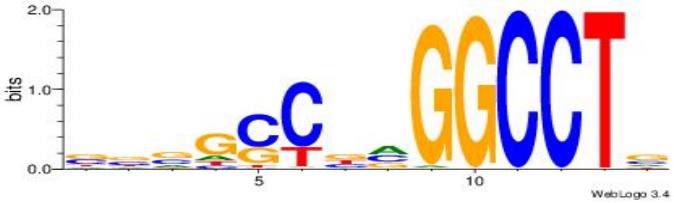
| | |
|---|---|
| Dataset #: | 2 |

| | |
|---|---|
| Motif ID: | 12 |
| Motif name: | Zfx |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction: | Backward |
| Position number: | 2 |
| Number of overlap: | 12 |
| Similarity score: | 0.069037 |

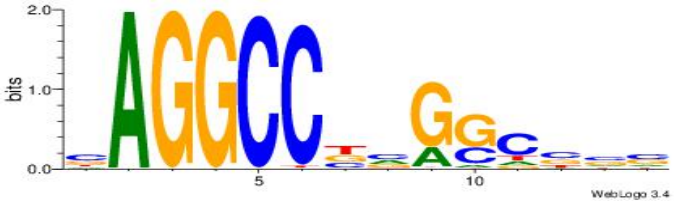
Alignment:

```
VAGGCCBBGGCVBB
-MGCCCCCTGMCA-
```

Original motif Consensus sequence: BBVGCCBVGGCCTV




Reverse complement motif Consensus sequence: VAGGCCBBGGCVB

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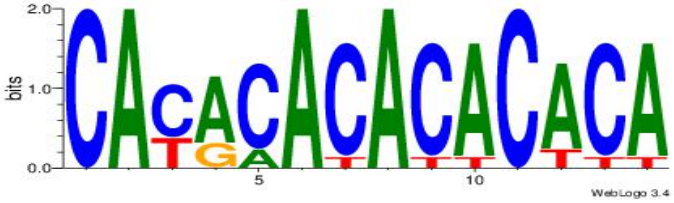
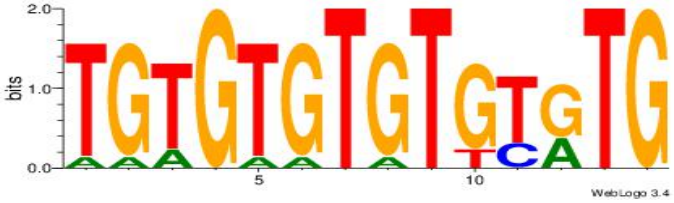
| | |
|---|---|
| Dataset #: | 1 |
| Motif ID: | 11 |
| Motif name: | Motif 11 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 3 |
| Number of overlap: | 12 |
| Similarity score: | 0.0692502 |

Alignment:
CAYACACACACACA
--MGCCCCCTGMCA

Original motif Consensus sequence: CAYACACACACACA




Reverse complement motif Consensus sequence: TGTGTGTGTGTKT

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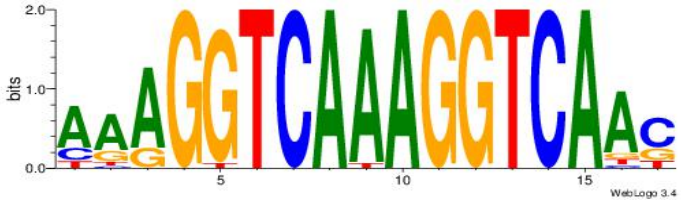
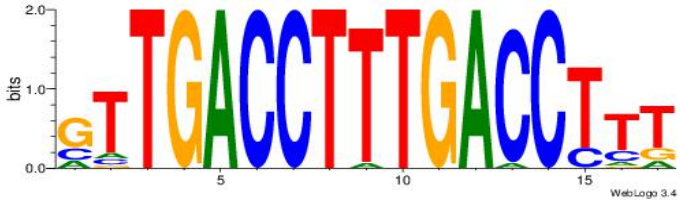
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 43 |
| Motif name: | NR1H2RXRA |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 3 |
| Number of overlap: | 12 |
| Similarity score: | 0.0696795 |

Alignment:
AAAGGTCAAAGGTCAAC
---TGYCAGGGGGCR--

Original motif Consensus sequence: AAAGGTCAAAGGTCAAC

Reverse complement motif Consensus sequence: GTTGACCTTTGACCTTT



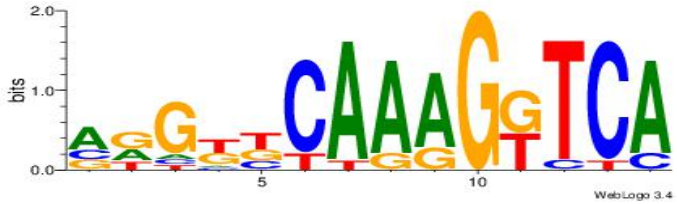

| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 22 |
| Motif name: | NR2F1 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 1 |
| Number of overlap: | 12 |
| Similarity score: | 0.0705128 |

Alignment:

```
TGAMCTTTGMMCYT
--MGCCCCCTGMCA
```

Original motif Consensus sequence: TGAMCTTTGMMCYT

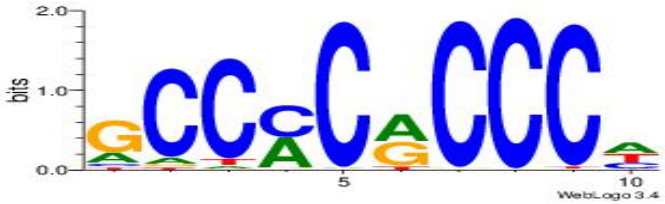
Reverse complement motif Consensus sequence: AKGYYCAAAGRTCA




**Dataset #: 2 Motif ID: 36 Motif name: Klf4**

Original motif Consensus sequence: DGGGYGKGGC

Reverse complement motif Consensus sequence: GCCYCMCCCD



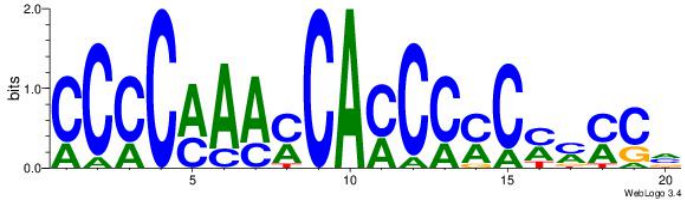

## Best Matches for Motif ID 36 (Highest to Lowest)

| | |
|---|---|
| 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: | 10 |
| Similarity score: | 0.065355 |

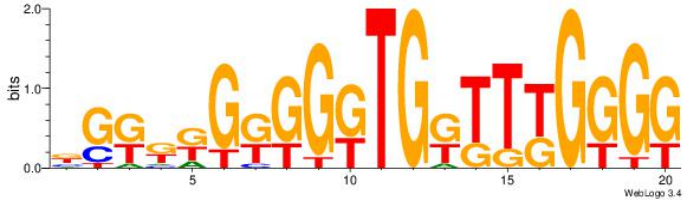
Alignment:

```
BGRRRGRGGRTGRTTYGGGG
----------DGGGYGKGGC
```

Original motif Consensus sequence: CCCCMAAMCAMCCMCMMMCV




Reverse complement motif Consensus sequence: BGRRRGRGGRTGRTTYGGGG

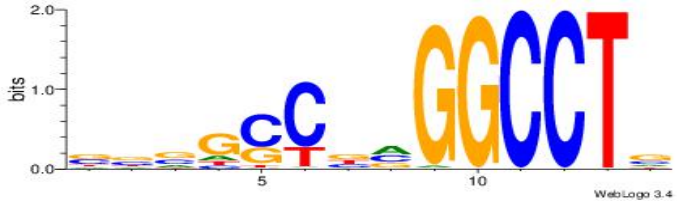


| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 12 |
| Motif name: | Zfx |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 4 |
| Number of overlap: | 10 |
| Similarity score: | 0.0734166 |

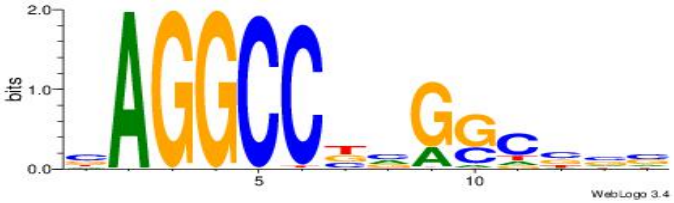
Alignment:

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

Original motif Consensus sequence: BBVGCCBVGGCCTV




Reverse complement motif Consensus sequence: VAGGCCBBGGCVB

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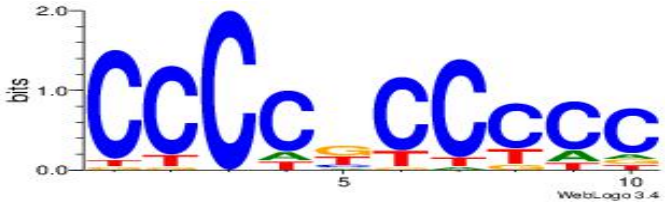
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 16 |
| Motif name: | SP1 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Reverse Complement |
| Direction: | Backward |
| Position number: | 1 |
| Number of overlap: | 10 |

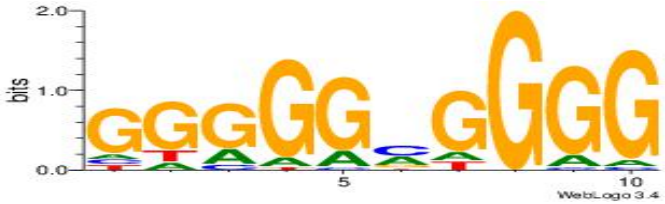
Similarity score: 0.0773711

Alignment:
GGGGGYGGGG
DGGGYGKGGC

Original motif Consensus sequence: CCCCKCCCCC




Reverse complement motif Consensus sequence: GGGGGYGGGG



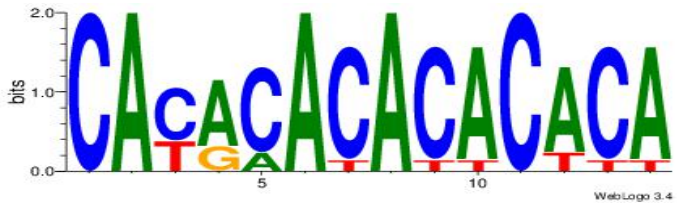

---

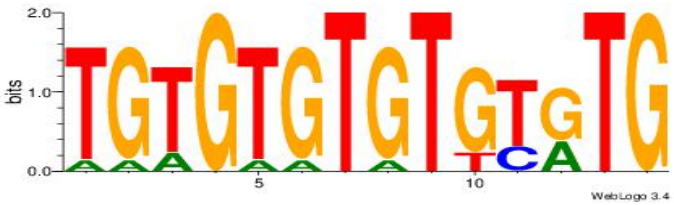
Dataset #: 1
Motif ID: 11
Motif name: Motif 11
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 3
Number of overlap: 10
Similarity score: 0.0781179

Alignment:
CAYACACACACACA
--GCCYCMCCCD--

Original motif Consensus sequence: CAYACACACACACA

Reverse complement motif Consensus sequence: TGTGTGTGTGTKT

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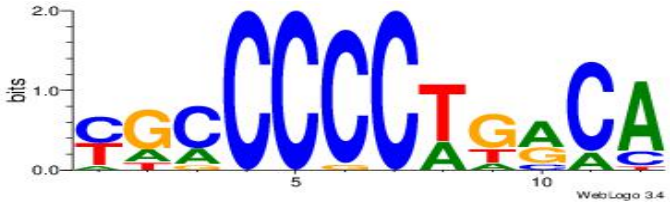
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 35 |
| Motif name: | INSM1 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction: | Backward |
| Position number: | 1 |
| Number of overlap: | 10 |
| Similarity score: | 0.0785684 |

Alignment:

```
MGCCCCCTGMCA
--GCCYCMCCCD
```

Original motif Consensus sequence: TGYCAGGGGGCR

Reverse complement motif Consensus sequence: MGCCCCCTGMCA

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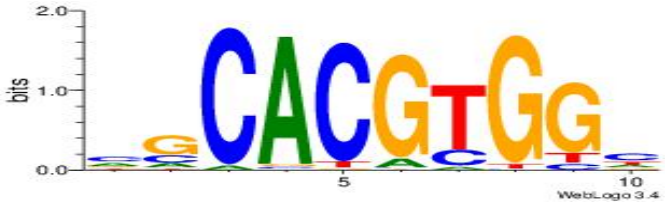
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 38 |

| | |
|---|---|
| Motif name: | Myc |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 1 |
| Number of overlap: | 10 |
| Similarity score: | 0.0797423 |

Alignment:

```
VGCACGTGGH
DGGGYGKGGC
```

Original motif Consensus sequence: VGCACGTGGH




Reverse complement motif Consensus sequence: DCCACGTGCV

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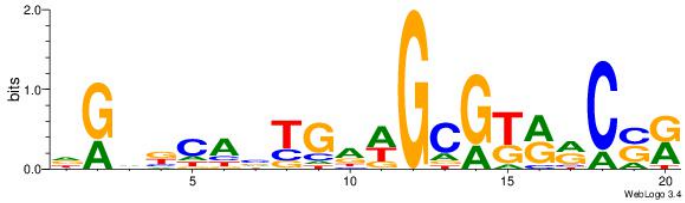
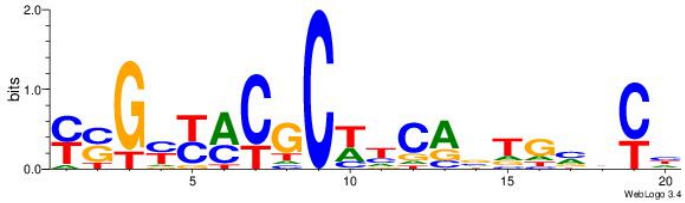
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 45 |
| Motif name: | Pax5 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 9 |
| Number of overlap: | 10 |
| Similarity score: | 0.0806175 |

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

Original motif Consensus sequence: DGVBCABTGDWGCGKRRCSR




Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD

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| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 40 |
| Motif name: | Mycn |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 1 |
| Number of overlap: | 10 |
| Similarity score: | 0.080695 |

Alignment:
HSCACGTGGC
DGGGYGKGGC

Original motif Consensus sequence: HSCACGTGGC

Reverse complement motif Consensus sequence: GCCACGTGSD

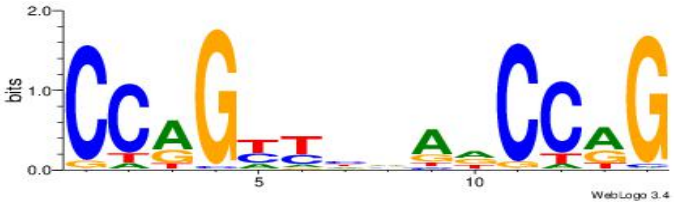
---

| | |
|---|---|
| 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: | 4 |
| Number of overlap: | 10 |
| Similarity score: | 0.0807235 |

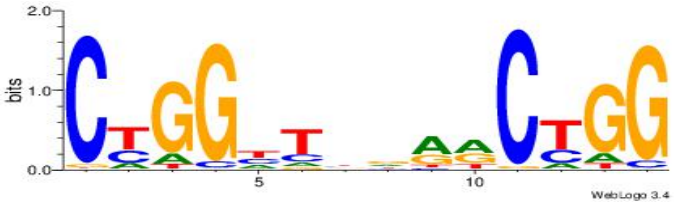
Alignment:

```
CCAGYYHVADCCRG
---GCCYCMCCCD-
```

Original motif Consensus sequence: CCAGYYHVADCCRG




Reverse complement motif Consensus sequence: CKGGDTBDMMCT

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| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 28 |

| | |
|---|---|
| Motif name: | Egr1 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction: | Backward |
| Position number: | 1 |
| Number of overlap: | 10 |
| Similarity score: | 0.089515 |

Alignment:

```
YCGCCCACGCH
-GCCYCMCCCD
```

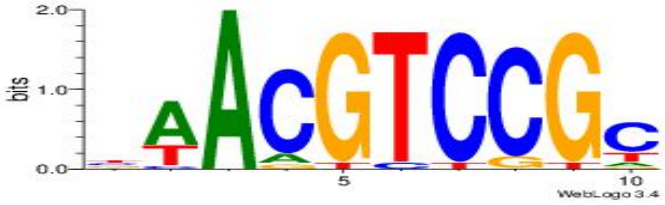
Original motif Consensus sequence: HGCGTGGGCGK

Reverse complement motif Consensus sequence: YCGCCCACGCH

---

**Dataset #: 2 Motif ID: 37 Motif name: MIZF**

Original motif Consensus sequence: BAACGTCCGC




Reverse complement motif Consensus sequence: GCGGACGTTV

**Best Matches for Motif ID 37 (Highest to Lowest)**

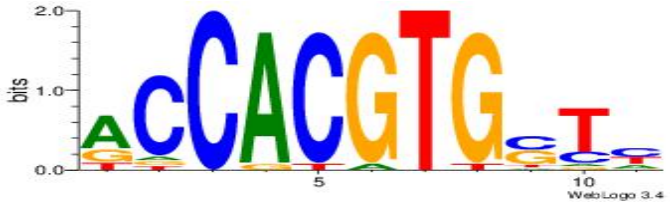
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 39 |
| Motif name: | MYCMAX |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Reverse Complement |
| Direction: | Forward |
| Position number: | 2 |
| Number of overlap: | 10 |
| Similarity score: | 0.0390724 |

Alignment:

```
ACCACGTGSTM
-BAACGTCCGC
```

Original motif Consensus sequence: RASCACGTGGT

Reverse complement motif Consensus sequence: ACCACGTGSTM

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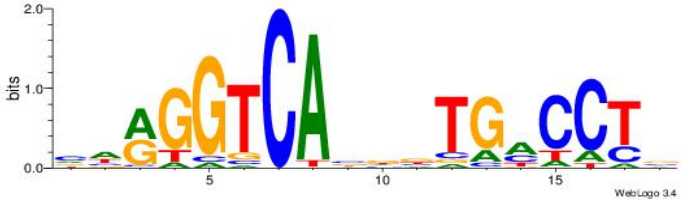
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 30 |
| Motif name: | ESR2 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction: | Backward |
| Position number: | 1 |
| Number of overlap: | 10 |

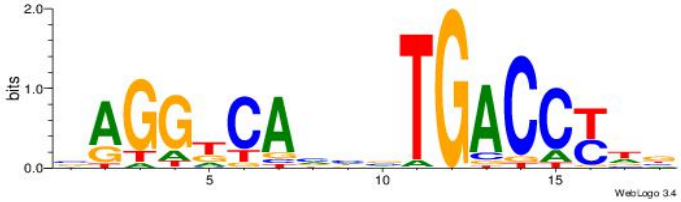
Similarity score: 0.0399477

Alignment:
BAGGYCABHBTGACCKHV
--------GCGGACGTTV

Original motif Consensus sequence: VHRGGTCABDBTGMCCTB




Reverse complement motif Consensus sequence:
BAGGYCABHBTGACCKHV

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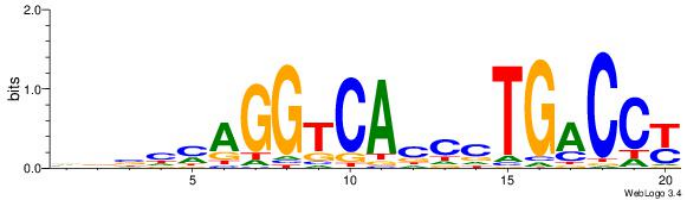
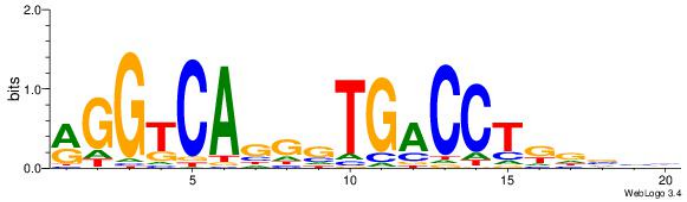
Dataset #: 2
Motif ID: 29
Motif name: ESR1
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 8
Number of overlap: 10
Similarity score: 0.0408267

Alignment:
VDBHMAGGTCACCCTGACCY
---BAACGTCCGC-------

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY

Reverse complement motif Consensus sequence:
MGGTCAGGGTGACCTRDBHV

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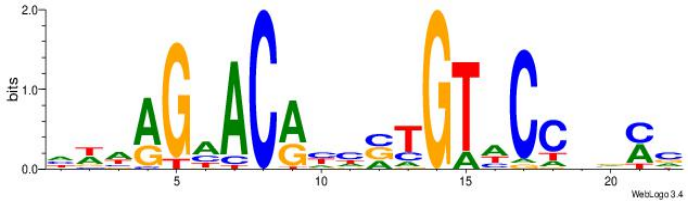
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 24 |
| Motif name: | Ar |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 4 |
| Number of overlap: | 10 |
| Similarity score: | 0.0432688 |

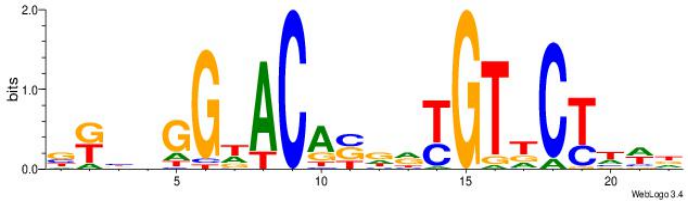
Alignment:

```
HWDAGHACRHHVTGTHCCHVMV
---------BAACGTCCGC---
```

Original motif Consensus sequence: HWDAGHACRHHVTGTHCCHVMV




Reverse complement motif Consensus sequence: VRVDGGHACAVDDKGTHCTDWH

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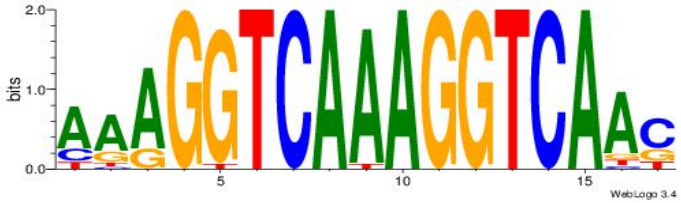
| | |
|---|---|
| Dataset #: | 2 |

| | |
|---|---|
| Motif ID: | 43 |
| Motif name: | NR1H2RXRA |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 1 |
| Number of overlap: | 10 |
| Similarity score: | 0.0439771 |

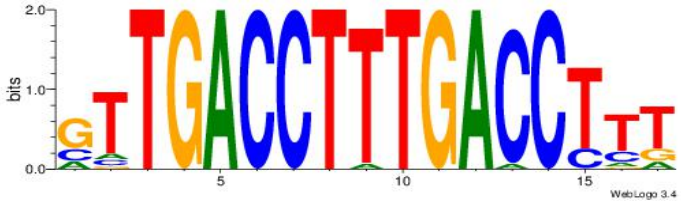
Alignment:

```
AAAGGTCAAAGGTCAAC
-------BAACGTCCGC
```

Original motif Consensus sequence: AAAGGTCAAAGGTCAAC




Reverse complement motif Consensus sequence: GTTGACCTTTGACCTTT

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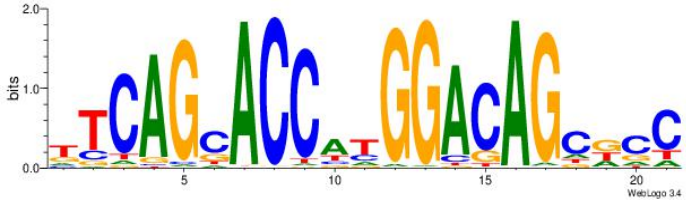
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 19 |
| Motif name: | REST |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Reverse Complement |
| Direction: | Backward |
| Position number: | 3 |
| Number of overlap: | 10 |

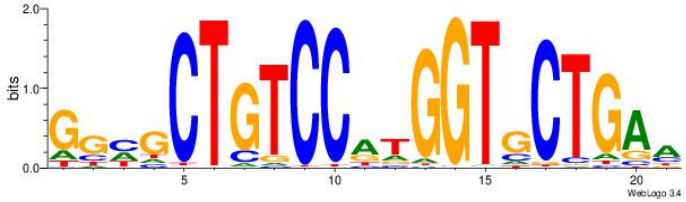
Similarity score: 0.0501848

Alignment:
GGYGCTGTCCATGGTGCTGAA
---------BAACGTCCGC--

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC




Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA



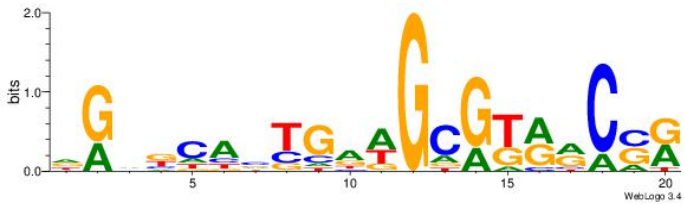

---

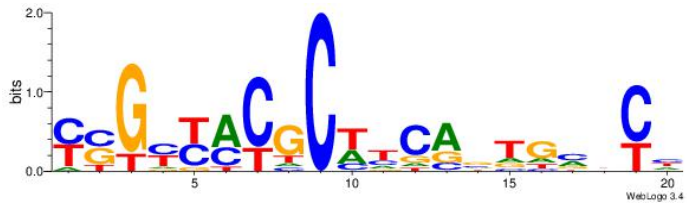
Dataset #: 2
Motif ID: 45
Motif name: Pax5
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 2
Number of overlap: 10
Similarity score: 0.0576438

Alignment:
MSGKKRCGCWDCABTGBBCD
-GCGGACGTTV---------

Original motif Consensus sequence: DGVBCABTGDWGCGKRRCSR

Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD

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| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 38 |
| Motif name: | Myc |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Reverse Complement |
| Direction: | Forward |
| Position number: | 2 |
| Number of overlap: | 9 |
| Similarity score: | 0.535015 |

Alignment:

```
DCCACGTGCV-
-BAACGTCCGC
```

Original motif Consensus sequence: VGCACGTGGH

Reverse complement motif Consensus sequence: DCCACGTGCV

---

| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 28 |

| | |
|---|---|
| Motif name: | Egr1 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 3 |
| Number of overlap: | 9 |
| Similarity score: | 0.537968 |

Alignment:

```
-HGCGTGGGCGK
BAACGTCCGC--
```

Original motif Consensus sequence: HGCGTGGGCGK

Reverse complement motif Consensus sequence: YCGCCCACGCH

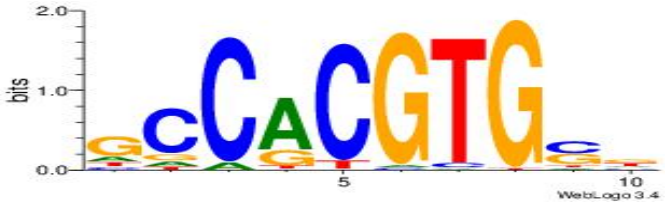
---

| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 40 |
| Motif name: | Mycn |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Reverse Complement |
| Direction: | Forward |
| Position number: | 2 |
| Number of overlap: | 9 |
| Similarity score: | 0.540549 |

Alignment:
GCCACGTGSD-
-BAACGTCCGC

Original motif Consensus sequence: HSCACGTGGC

Reverse complement motif Consensus sequence: GCCACGTGSD

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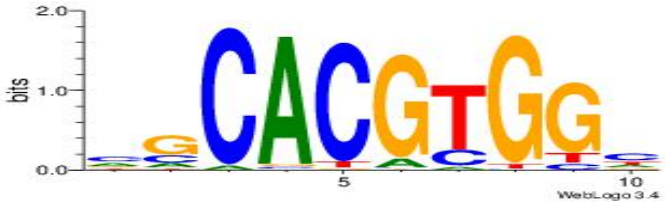
**Dataset #: 2 Motif ID: 38 Motif name: Myc**

Original motif Consensus sequence: VGCACGTGGH




Reverse complement motif Consensus sequence: DCCACGTGCV

**Best Matches for Motif ID 38 (Highest to Lowest)**

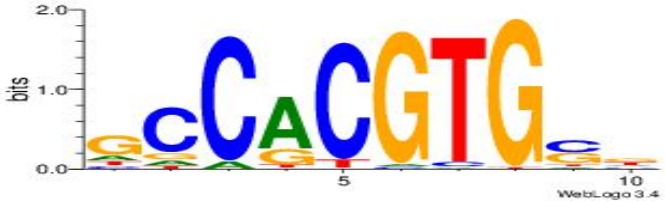
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 40 |
| Motif name: | Mycn |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 1 |

Number of overlap: 10
Similarity score: 0

Alignment:
HSCACGTGGC
VGCACGTGGH

Original motif Consensus sequence: HSCACGTGGC

Reverse complement motif Consensus sequence: GCCACGTGSD

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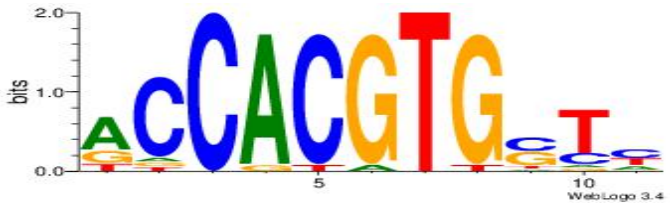
Dataset #: 2
Motif ID: 39
Motif name: MYCMAX
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 10
Similarity score: 0.0209359

Alignment:
RASCACGTGGT
-VGCACGTGGH

Original motif Consensus sequence: RASCACGTGGT

Reverse complement motif Consensus sequence: ACCACGTGSTM

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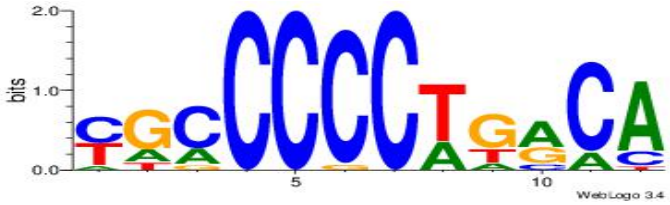
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 35 |
| Motif name: | INSM1 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction: | Backward |
| Position number: | 2 |
| Number of overlap: | 10 |
| Similarity score: | 0.0844808 |

Alignment:

```
MGCCCCCTGMCA
-DCCACGTGCV-
```

Original motif Consensus sequence: TGYCAGGGGGCR

Reverse complement motif Consensus sequence: MGCCCCCTGMCA

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| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 36 |

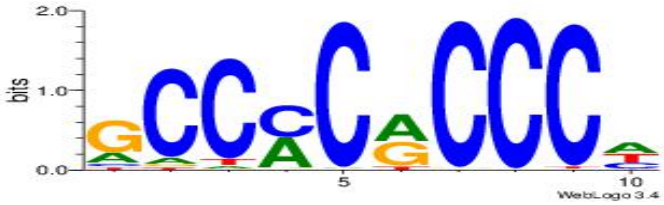
| | |
|---|---|
| Motif name: | Klf4 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 1 |
| Number of overlap: | 10 |
| Similarity score: | 0.0883745 |

Alignment:

```
DGGGYGKGGC
VGCACGTGGH
```

Original motif Consensus sequence: DGGGYGKGGC

Reverse complement motif Consensus sequence: GCCYCMCCCD

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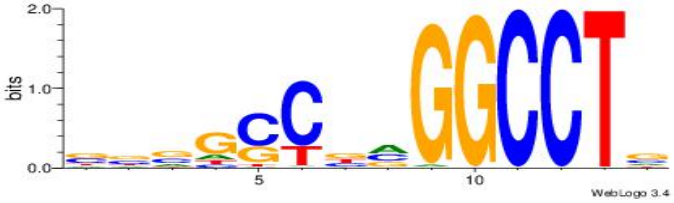
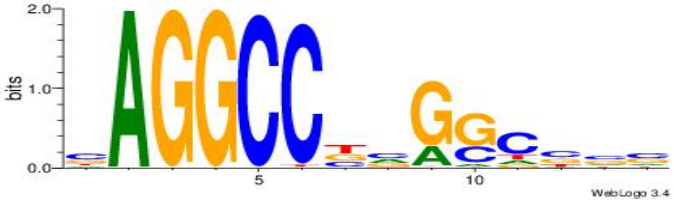
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 12 |
| Motif name: | Zfx |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction: | Backward |
| Position number: | 2 |
| Number of overlap: | 10 |
| Similarity score: | 0.0925451 |

Alignment:
VAGGCCBBGGCVBB
---DCCACGTGCV-

Original motif Consensus sequence: BBVGCCBVGGCCTV




Reverse complement motif Consensus sequence: VAGGCCBBGGCVB

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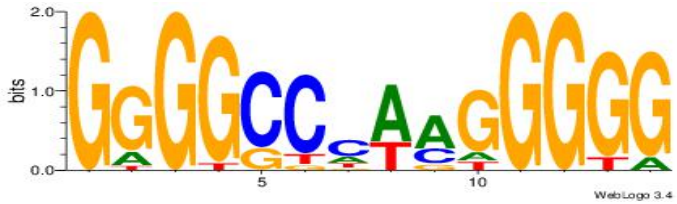
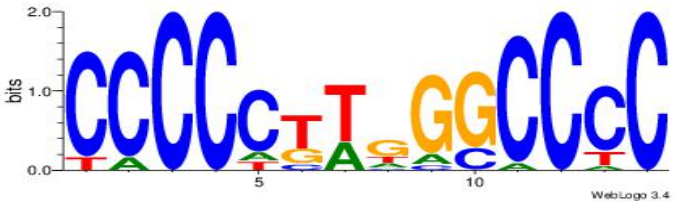
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 21 |
| Motif name: | PLAG1 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Reverse Complement |
| Direction: | Forward |
| Position number: | 5 |
| Number of overlap: | 10 |
| Similarity score: | 0.0930375 |

Alignment:
CCCCCTTGGGCCCC
----VGCACGTGGH

Original motif Consensus sequence: GGGGCCCAAGGGGG

Reverse complement motif Consensus sequence: CCCCCTTGGGCCC



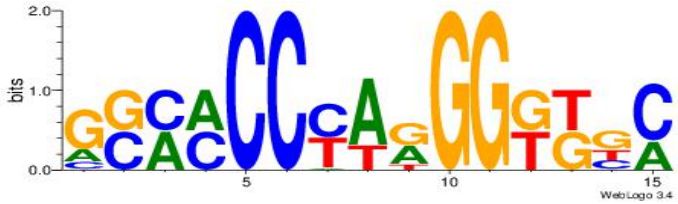




| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 13 |
| Motif name: | Zfp423 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction: | Backward |
| Position number: | 3 |
| Number of overlap: | 10 |
| Similarity score: | 0.0930519 |

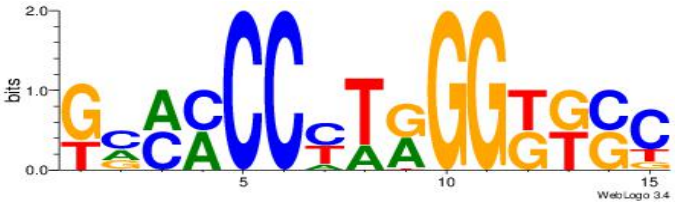
Alignment:

```
GYRYCCMTKGGYRSC
---DCCACGTGCV--
```

Original motif Consensus sequence: GSMMCCYARGGKKKC




Reverse complement motif Consensus sequence: GYRYCCMTKGGYR



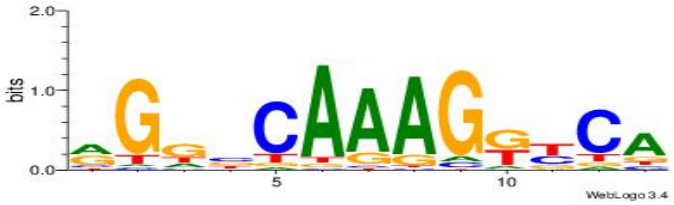

| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 34 |

| | |
|---|---|
| Motif name: | HNF4A |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Reverse Complement |
| Direction: | Backward |
| Position number: | 1 |
| Number of overlap: | 10 |
| Similarity score: | 0.0934488 |

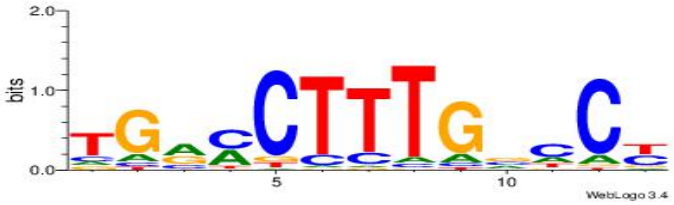
Alignment:

```
TGMYCTTTGBCCK
---VGCACGTGGH
```

Original motif Consensus sequence: RGGBCAAAGKYCA




Reverse complement motif Consensus sequence: TGMYCTTTGBCCK

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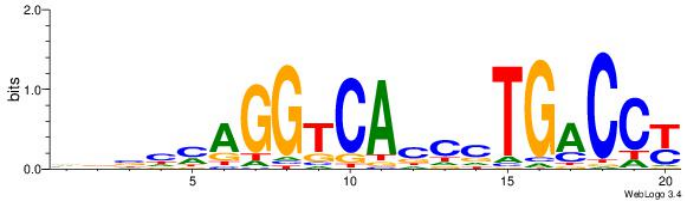
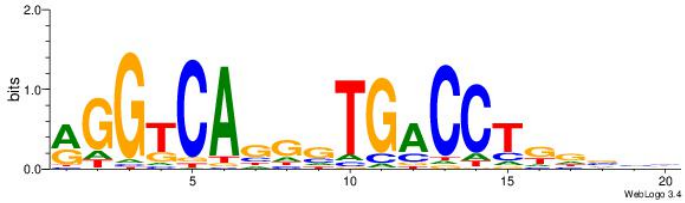
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 29 |
| Motif name: | ESR1 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction: | Backward |
| Position number: | 3 |
| Number of overlap: | 10 |
| Similarity score: | 0.0940438 |

Alignment:
MGGTCAGGGTGACCTRDBHV
--------DCCACGTGCV--

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY




Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV

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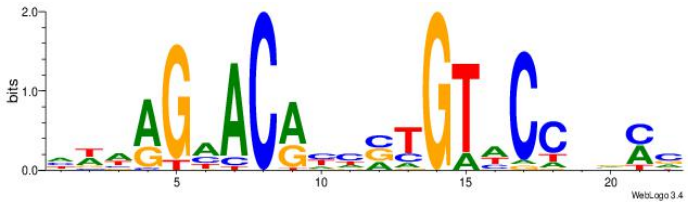
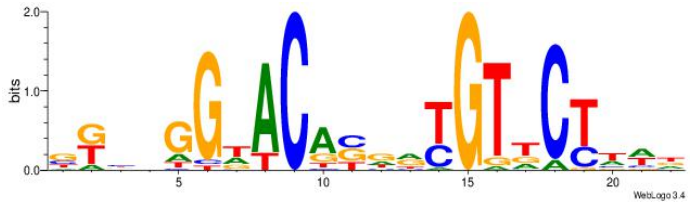
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 24 |
| Motif name: | Ar |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 7 |
| Number of overlap: | 10 |
| Similarity score: | 0.0966137 |

Alignment:
HWDAGHACRHHVTGTHCCHVMV
------DCCACGTGCV------

Original motif Consensus sequence: HWDAGHACRHHVTGTHCCHVMV

Reverse complement motif Consensus sequence: VRVDGGHACAVDDKGTHCTDWH

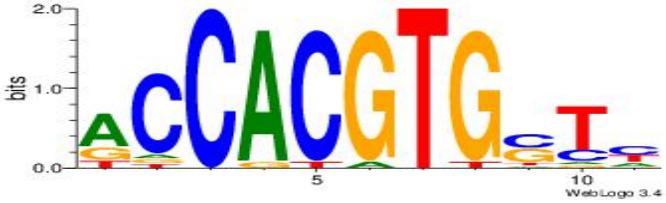




**Dataset #: 2** **Motif ID: 39** **Motif name: MYCMAX**

Original motif Consensus sequence: RASCACGTGGT

Reverse complement motif Consensus sequence: ACCACGTGSTM



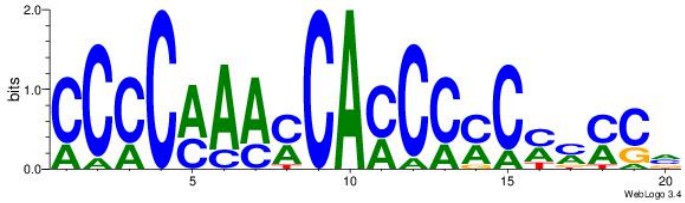
## Best Matches for Motif ID 39 (Highest to Lowest)

| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 18 |
| Motif name: | RREB1 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 7 |
| Number of overlap: | 11 |
| Similarity score: | 0.0862644 |

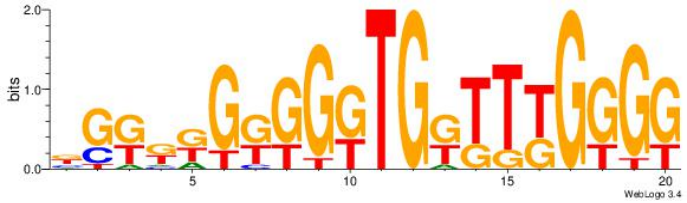
Alignment:

```
CCCCMAAMCAMCCMCMMMCV
---ACCACGTGSTM------
```

Original motif Consensus sequence: CCCCMAAMCAMCCMCMMMCV



Reverse complement motif Consensus sequence: BGRRRGRGGRTGRTTYGGGG

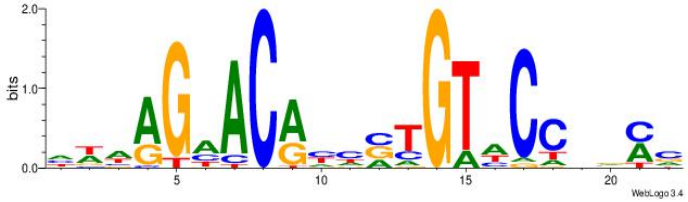


| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 24 |
| Motif name: | Ar |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 10 |
| Number of overlap: | 11 |
| Similarity score: | 0.0877525 |

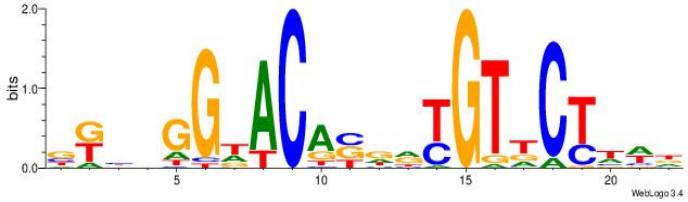
Alignment:

```
HWDAGHACRHHVTGTHCCHVMV
--RASCACGTGGT---------
```

Original motif Consensus sequence: HWDAGHACRHHVTGTHCCHVMV



Reverse complement motif Consensus sequence: VRVDGGHACAVDDKGTHCTDWH

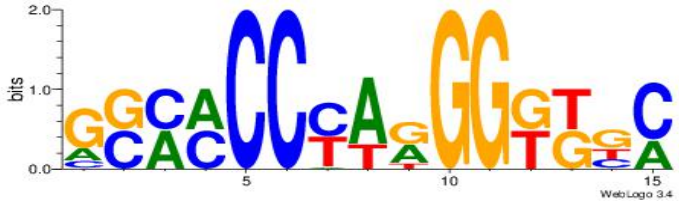


| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 13 |
| Motif name: | Zfp423 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 4 |
| Number of overlap: | 11 |
| Similarity score: | 0.0933483 |

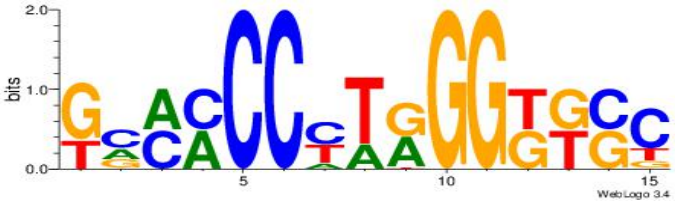
Alignment:

```
GSMMCCYARGGKKKC
-ACCACGTGSTM---
```

Original motif Consensus sequence: GSMMCCYARGGKKKC




Reverse complement motif Consensus sequence: GYRYCCMTKGGYR

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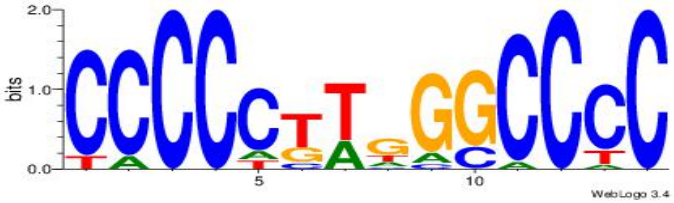
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 21 |
| Motif name: | PLAG1 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction: | Forward |
| Position number: | 1 |
| Number of overlap: | 11 |

Similarity score: 0.10358

Alignment:
CCCCCTTGGGCCCC
ACCACGTGSTM---

Original motif Consensus sequence: GGGGCCCAAGGGGG

Reverse complement motif Consensus sequence: CCCCCTTGGGCCC

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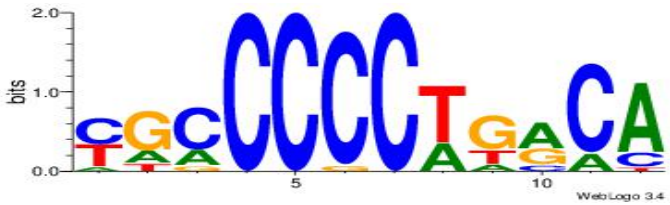
Dataset #: 2
Motif ID: 35
Motif name: INSM1
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2
Number of overlap: 11
Similarity score: 0.104527

Alignment:
TGYCAGGGGGCR
RASCACGTGGT-

Original motif Consensus sequence: TGYCAGGGGGCR

Reverse complement motif Consensus sequence: MGCCCCCTGMCA

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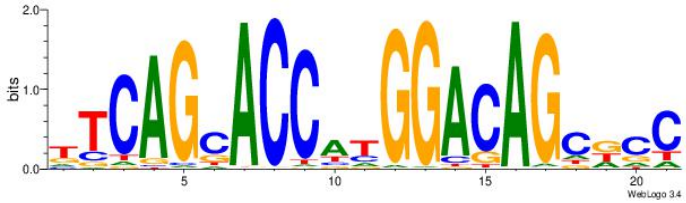
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 19 |
| Motif name: | REST |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction: | Backward |
| Position number: | 3 |
| Number of overlap: | 11 |
| Similarity score: | 0.105174 |

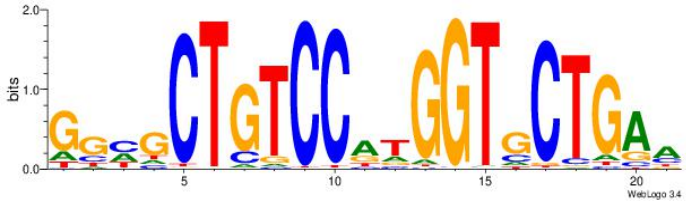
Alignment:

```
GGYGCTGTCCATGGTGCTGAA
--------ACCACGTGSTM--
```

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC




Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA




---

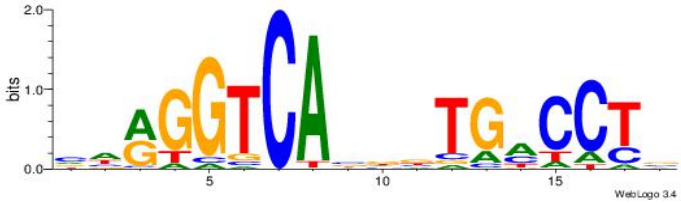
Dataset #: 2

| | |
|---|---|
| Motif ID: | 30 |
| Motif name: | ESR2 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 4 |
| Number of overlap: | 11 |
| Similarity score: | 0.105681 |

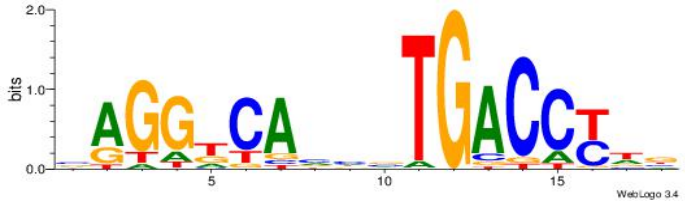
Alignment:

```
VHRGGTCABDBTGMCCTB
---RASCACGTGGT----
```

Original motif Consensus sequence: VHRGGTCABDBTGMCCTB




Reverse complement motif Consensus sequence: BAGGYCABHBTGACCKHV

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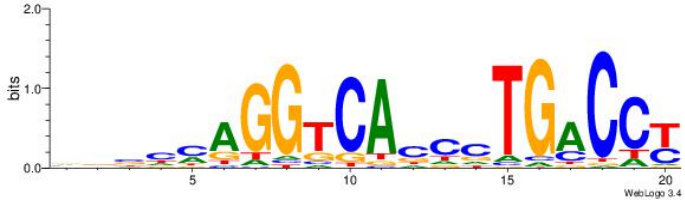
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 29 |
| Motif name: | ESR1 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction: | Backward |
| Position number: | 2 |
| Number of overlap: | 11 |

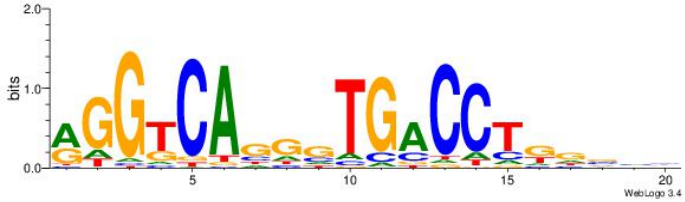
Similarity score: 0.107782

Alignment:
MGGTCAGGGTGACCTRDBHV
--------ACCACGTGSTM-

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY




Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV



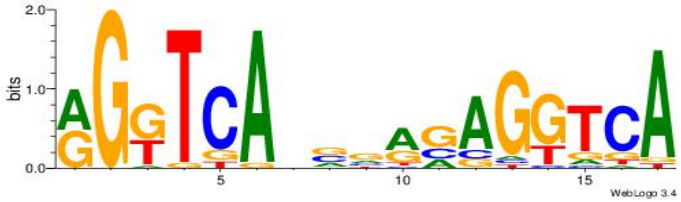

---

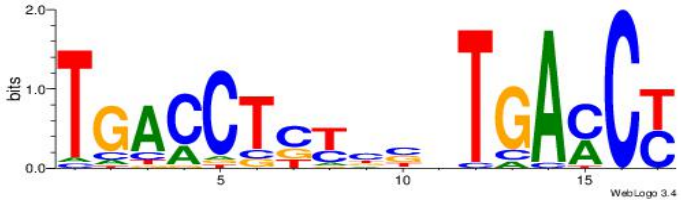
Dataset #: 2
Motif ID: 47
Motif name: RXRRAR_DR5
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 3
Number of overlap: 11
Similarity score: 0.108615

Alignment:
TGACCTCKVVBTGAYCK
--ACCACGTGSTM----

Original motif Consensus sequence: RGKTCABVVRGAGGTCA

Reverse complement motif Consensus sequence: TGACCTCKVVBTGAYCK



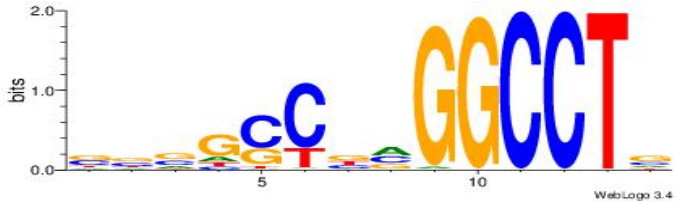




| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 12 |
| Motif name: | Zfx |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 1 |
| Number of overlap: | 11 |
| Similarity score: | 0.110189 |

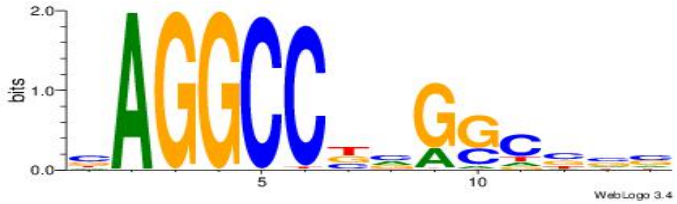
Alignment:

```
BBVGCCBVGGCCTV
RASCACGTGGT---
```

Original motif Consensus sequence: BBVGCCBVGGCCTV



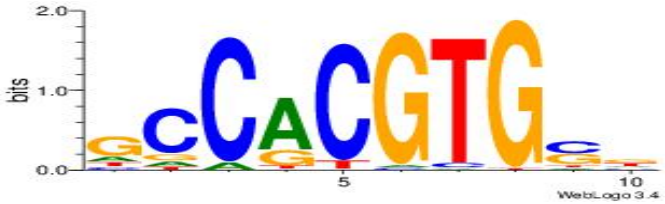

Reverse complement motif Consensus sequence: VAGGCCBBGGCVB




**Dataset #: 2 Motif ID: 40 Motif name: Mycn**

Original motif Consensus sequence: HSCACGTGGC

Reverse complement motif Consensus sequence: GCCACGTGSD



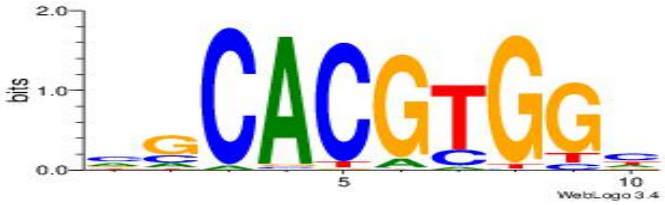

## Best Matches for Motif ID 40 (Highest to Lowest)

| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 38 |
| Motif name: | Myc |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction: | Forward |
| Position number: | 1 |
| Number of overlap: | 10 |
| Similarity score: | 0 |

Alignment:

```
DCCACGTGCV
GCCACGTGSD
```

Original motif Consensus sequence: VGCACGTGGH




Reverse complement motif Consensus sequence: DCCACGTGCV

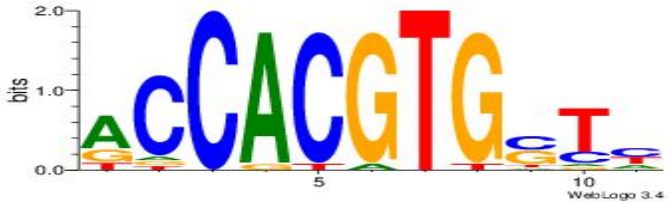
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 39 |
| Motif name: | MYCMAX |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 2 |
| Number of overlap: | 10 |
| Similarity score: | 0.0200467 |

Alignment:

```
RASCACGTGGT
-HSCACGTGGC
```

Original motif Consensus sequence: RASCACGTGGT

Reverse complement motif Consensus sequence: ACCACGTGSTM

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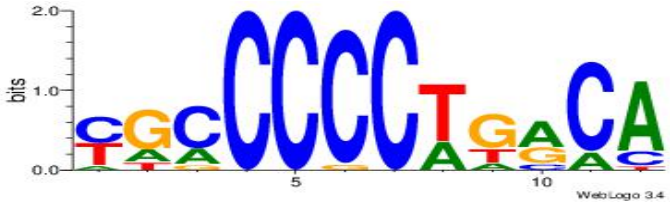
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 35 |
| Motif name: | INSM1 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction: | Backward |
| Position number: | 2 |
| Number of overlap: | 10 |

Similarity score: 0.0834824

Alignment:
MGCCCCCTGMCA
-GCCACGTGSD-

Original motif Consensus sequence: TGYCAGGGGGCR

Reverse complement motif Consensus sequence: MGCCCCCTGMCA



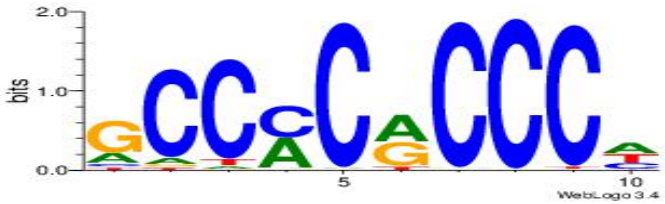

---

Dataset #: 2
Motif ID: 36
Motif name: Klf4
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 10
Similarity score: 0.0893272

Alignment:
DGGGYGKGGC
HSCACGTGGC

Original motif Consensus sequence: DGGGYGKGGC

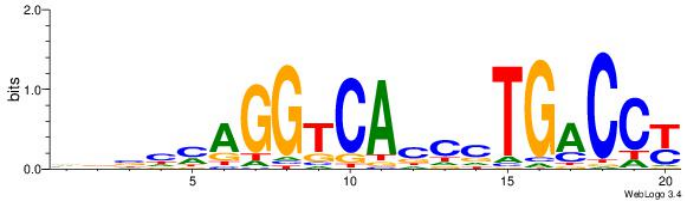
Reverse complement motif Consensus sequence: GCCYCMCCCD



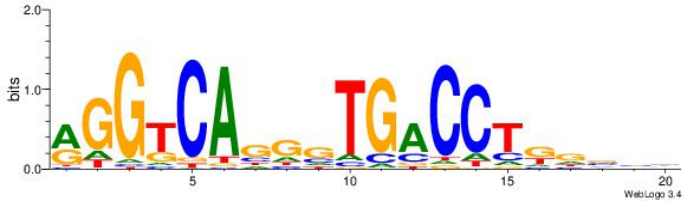

Dataset #: 2
Motif ID: 29
Motif name: ESR1
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 3
Number of overlap: 10
Similarity score: 0.089863

Alignment:
MGGTCAGGGTGACCTRDBHV
--------GCCACGTGSD--

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY




Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV



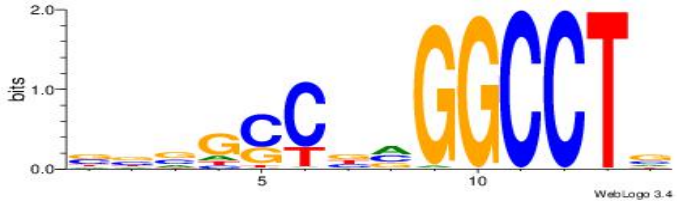

Dataset #: 2

| | |
|---|---|
| Motif ID: | 12 |
| Motif name: | Zfx |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction: | Forward |
| Position number: | 4 |
| Number of overlap: | 10 |
| Similarity score: | 0.0899944 |

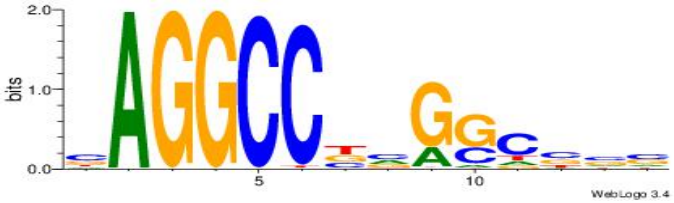
Alignment:

```
VAGGCCBBGGCVBB
---GCCACGTGSD-
```

Original motif Consensus sequence: BBVGCCBVGGCCTV




Reverse complement motif Consensus sequence: VAGGCCBBGGCVB

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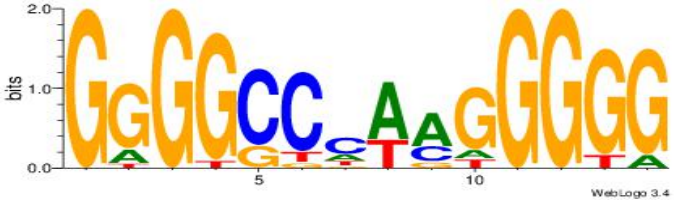
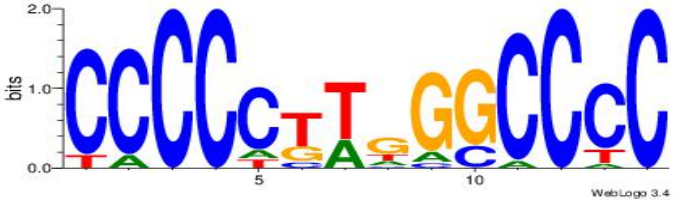
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 21 |
| Motif name: | PLAG1 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Reverse Complement |
| Direction: | Backward |
| Position number: | 1 |
| Number of overlap: | 10 |
| Similarity score: | 0.0921439 |

Alignment:
CCCCCTTGGGCCCC
----HSCACGTGGC

Original motif Consensus sequence: GGGGCCCAAGGGGG




Reverse complement motif Consensus sequence: CCCCCTTGGGCCC

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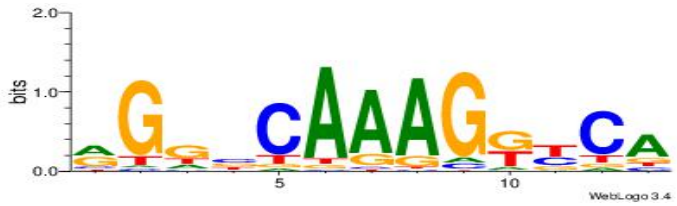
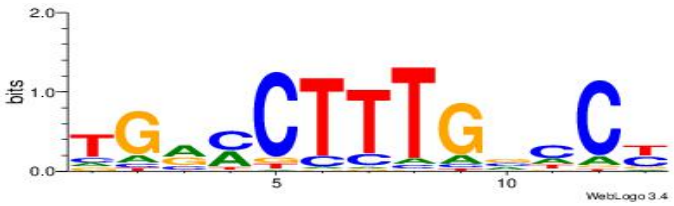
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 34 |
| Motif name: | HNF4A |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction: | Forward |
| Position number: | 2 |
| Number of overlap: | 10 |
| Similarity score: | 0.0947124 |

Alignment:
TGMYCTTTGBCCK
-GCCACGTGSD--

Original motif Consensus sequence: RGGBCAAAGKYCA

Reverse complement motif Consensus sequence: TGMYCTTTGBCCK

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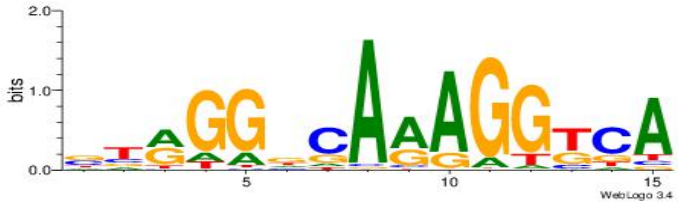
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 20 |
| Motif name: | PPARGRXRA |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction: | Backward |
| Position number: | 5 |
| Number of overlap: | 10 |
| Similarity score: | 0.0954444 |

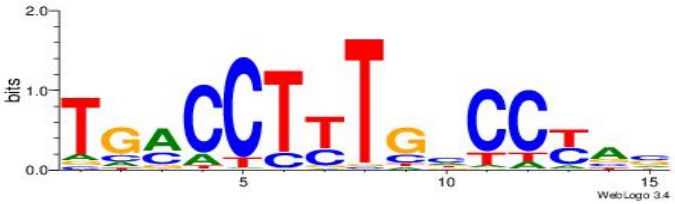
Alignment:

```
TGRCCTKTGHCCKAB
-GCCACGTGSD----
```

Original motif Consensus sequence: BTRGGDCARAGGKCA




Reverse complement motif Consensus sequence: TGRCCTKTGHCCK

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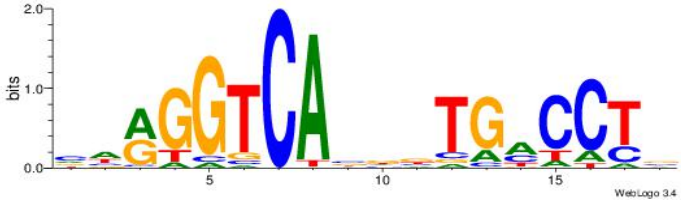
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 30 |

| | |
|---|---|
| Motif name: | ESR2 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 5 |
| Number of overlap: | 10 |
| Similarity score: | 0.0964708 |

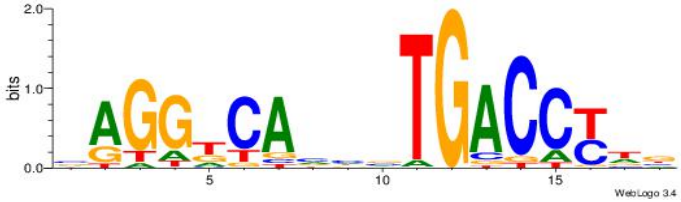
Alignment:

```
VHRGGTCABDBTGMCCTB
----HSCACGTGGC----
```

Original motif Consensus sequence: VHRGGTCABDBTGMCCTB




Reverse complement motif Consensus sequence: BAGGYCABHBTGACCKHV

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**Dataset #: 2 Motif ID: 41 Motif name: MZF1_5-13**

Original motif Consensus sequence: BKAGGGGDAD

Reverse complement motif Consensus sequence: BTHCCCCTYB

## Best Matches for Motif ID 41 (Highest to Lowest)

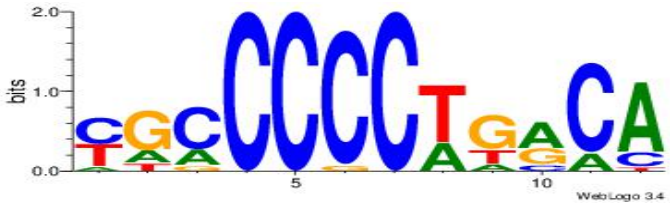
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 35 |
| Motif name: | INSM1 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 1 |
| Number of overlap: | 10 |
| Similarity score: | 0.0360532 |

Alignment:

```
TGYCAGGGGGCR
--BKAGGGGDAD
```

Original motif Consensus sequence: TGYCAGGGGGCR

Reverse complement motif Consensus sequence: MGCCCCCTGMCA

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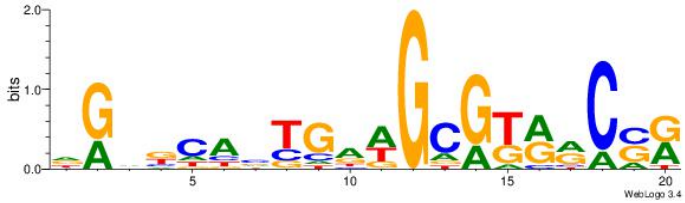
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 45 |
| Motif name: | Pax5 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |

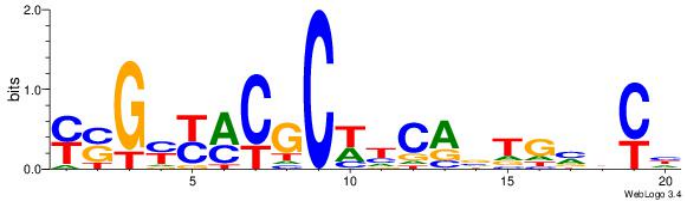
| | |
|---|---|
| Direction: | Backward |
| Position number: | 4 |
| Number of overlap: | 10 |
| Similarity score: | 0.0428241 |

Alignment:
DGVBCABTGDWGCGKRRCSR
-------BKAGGGGDAD---

Original motif Consensus sequence: DGVBCABTGDWGCGKRRCSR




Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD

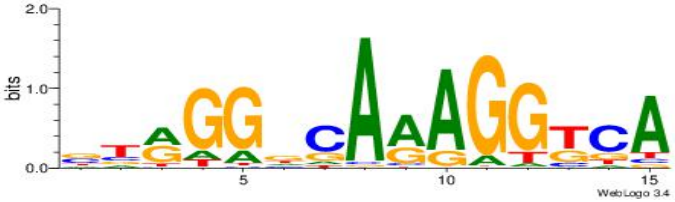



---

| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 20 |
| 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: | 10 |
| Similarity score: | 0.0470779 |

Alignment:
BTRGGDCARAGGKCA
BKAGGGGDAD-----

Original motif Consensus sequence: BTRGGDCARAGGKCA




Reverse complement motif Consensus sequence: TGRCCTKTGHCCK

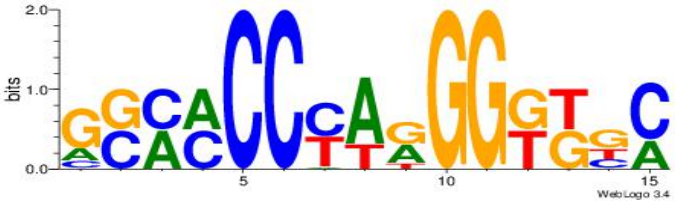
---

| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 13 |
| Motif name: | Zfp423 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 1 |
| Number of overlap: | 10 |
| Similarity score: | 0.0524832 |

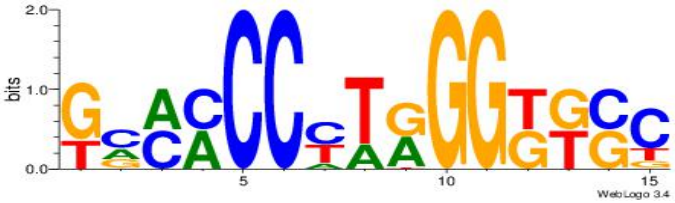
Alignment:

```
GSMMCCYARGGKKKC
-----BKAGGGGDAD
```

Original motif Consensus sequence: GSMMCCYARGGKKKC




Reverse complement motif Consensus sequence: GYRYCCMTKGGYR

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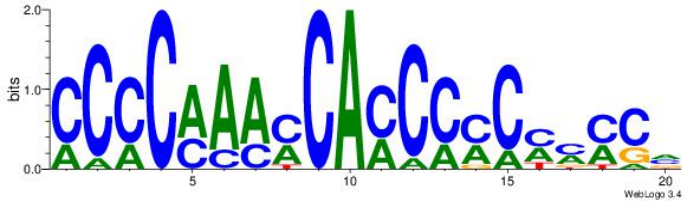
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 18 |
| Motif name: | RREB1 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 2 |
| Number of overlap: | 10 |
| Similarity score: | 0.0548506 |

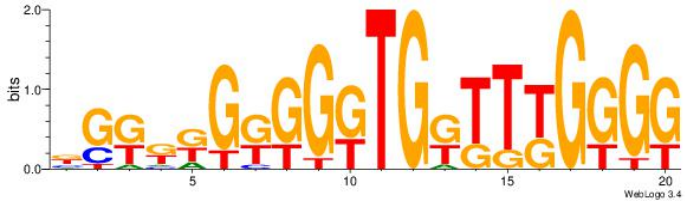
Alignment:

```
CCCCMAAMCAMCCMCMMMCV
-BTHCCCCTYB---------
```

Original motif Consensus sequence: CCCCMAAMCAMCCMCMMMCV




Reverse complement motif Consensus sequence: BGRRRGRGGRTGRTTYGGGG

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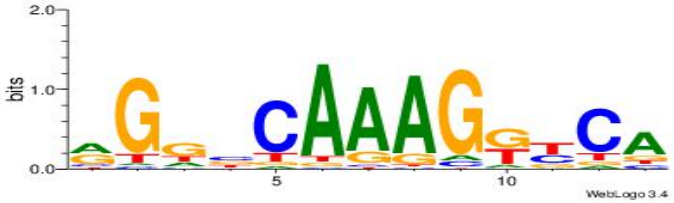
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 34 |
| Motif name: | HNF4A |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction: | Forward |
| Position number: | 1 |

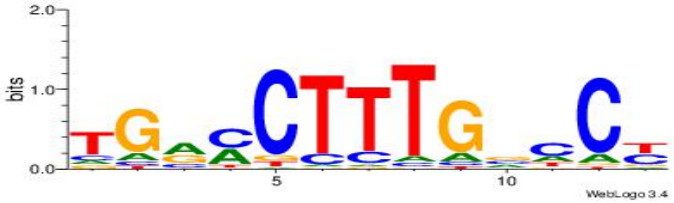
Number of overlap: 10
Similarity score: 0.0568244

Alignment:
TGMYCTTTGBCCK
BTHCCCCTYB---

Original motif Consensus sequence: RGGBCAAAGKYCA




Reverse complement motif Consensus sequence: TGMYCTTTGBCCK

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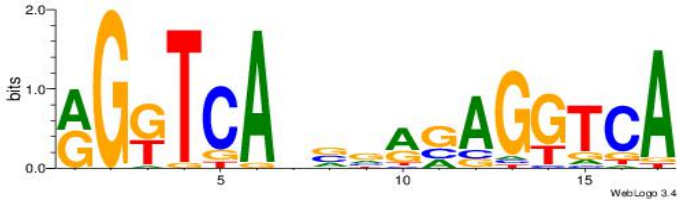
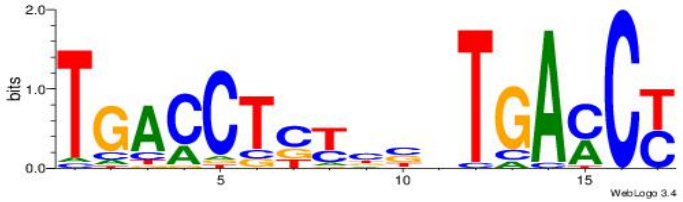
Dataset #: 2
Motif ID: 47
Motif name: RXRRAR_DR5
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 10
Similarity score: 0.0581547

Alignment:
TGACCTCKVVBTGAYCK
BTHCCCCTYB-------

Original motif Consensus sequence: RGKTCABVVRGAGGTCA

Reverse complement motif Consensus sequence: TGACCTCKVVBTGAYCK

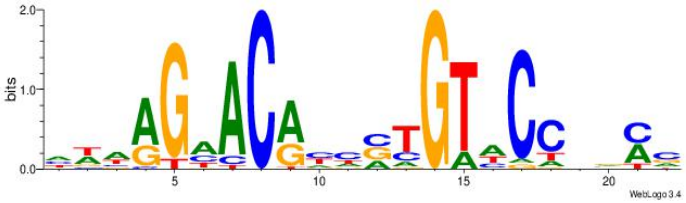


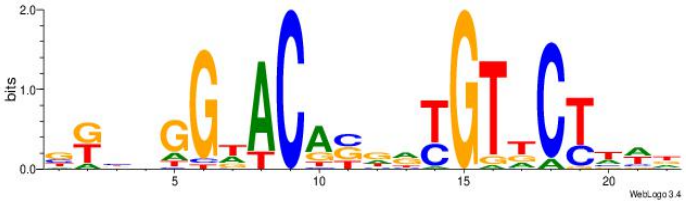

Dataset #: 2
Motif ID: 24
Motif name: Ar
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 13
Number of overlap: 10
Similarity score: 0.0610532

Alignment:
VRVDGGHACAVDDKGTHCTDWH
----------BKAGGGGDAD

Original motif Consensus sequence: HWDAGHACRHHVTGTHCCHVMV




Reverse complement motif Consensus sequence: VRVDGGHACAVDDKGTHCTDWH



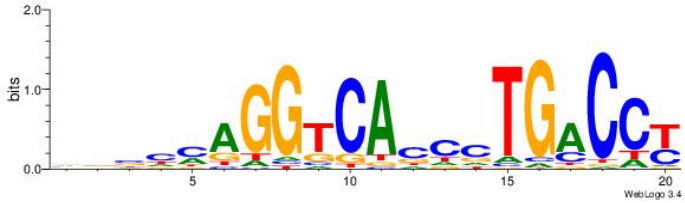

Dataset #: 2

| | |
|---|---|
| Motif ID: | 29 |
| Motif name: | ESR1 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 9 |
| Number of overlap: | 10 |
| Similarity score: | 0.0642057 |

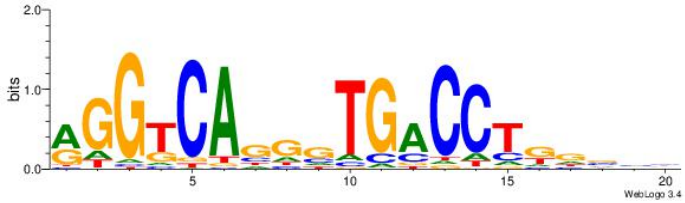
Alignment:

```
VDBHMAGGTCACCCTGACCY
--BKAGGGGDAD--------
```

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY




Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV

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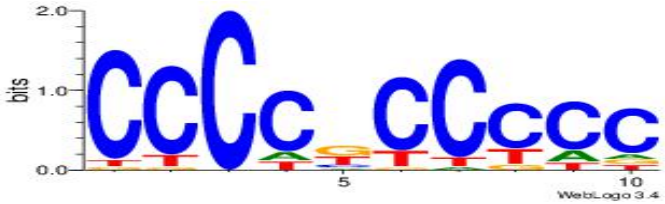
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 16 |
| Motif name: | SP1 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 1 |
| Number of overlap: | 10 |

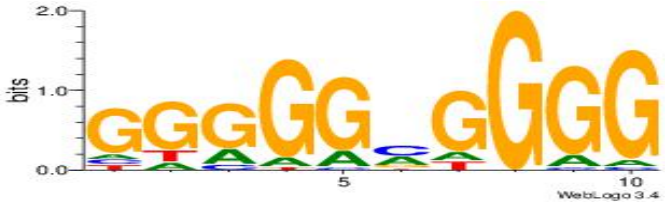
Similarity score: 0.0692824

Alignment:
CCCCKCCCCC
BTHCCCCTYB

Original motif Consensus sequence: CCCCKCCCCC




Reverse complement motif Consensus sequence: GGGGGYGGGG




---

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

Original motif Consensus sequence: GGGGRTTCCCC

Reverse complement motif Consensus sequence: GGGGAAKCCCC

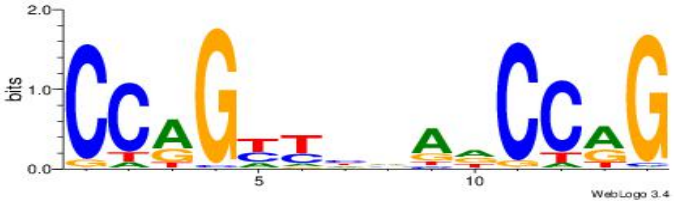
**Best Matches for Motif ID 42 (Highest to Lowest)**

| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 48 |
| Motif name: | Tcfcp2l1 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Reverse Complement |
| Direction: | Backward |

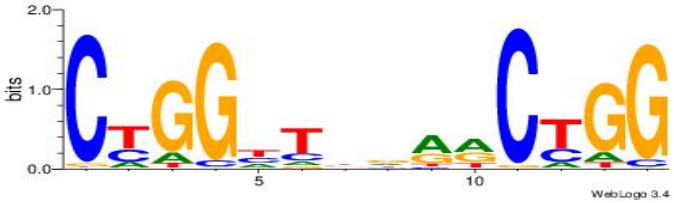
Position number: 4
Number of overlap: 11
Similarity score: 0.103405

Alignment:
CKGGDTBDMMCTGG
GGGGRTTCCCC---

Original motif Consensus sequence: CCAGYYHVADCCRG




Reverse complement motif Consensus sequence: CKGGDTBDMMCT

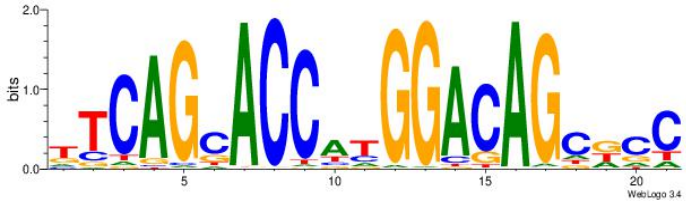



---

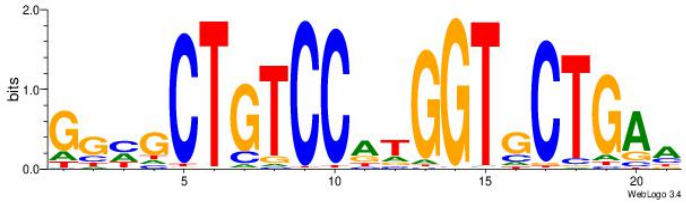
Dataset #: 2
Motif ID: 19
Motif name: REST
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 11
Similarity score: 0.112926

Alignment:
TTCAGCACCATGGACAGCKCC
GGGGAAKCCCC----------

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC



Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA

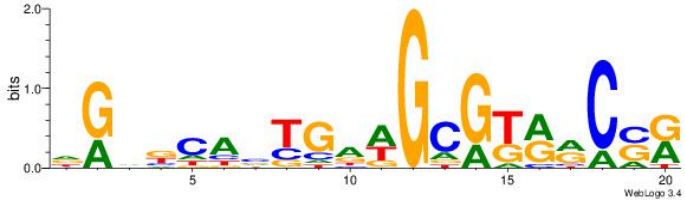


| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 45 |
| Motif name: | Pax5 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction: | Backward |
| Position number: | 9 |
| Number of overlap: | 11 |
| Similarity score: | 0.116162 |

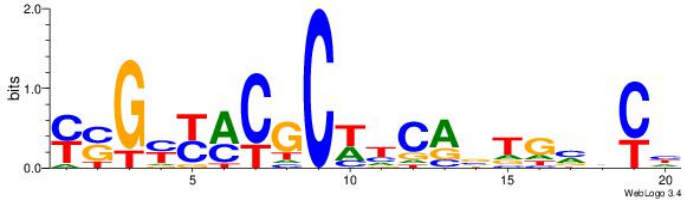
Alignment:

```
MSGKKRCGCWDCABTGBBCD
-GGGGAAKCCCC--------
```

Original motif Consensus sequence: DGVBCABTGDWGCGKRRCSR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD

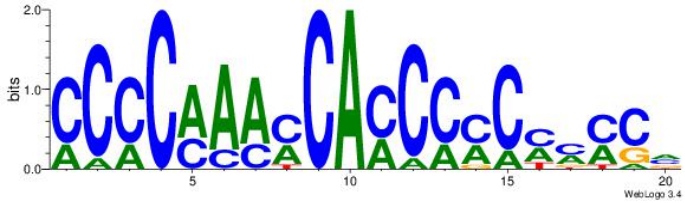


| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 18 |
| Motif name: | RREB1 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 5 |
| Number of overlap: | 11 |
| Similarity score: | 0.117826 |

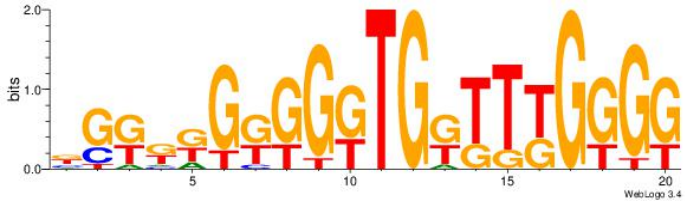
Alignment:

```
CCCCMAAMCAMCCMCMMMCV
-----GGGGAAKCCCC----
```

Original motif Consensus sequence: CCCCMAAMCAMCCMCMMMCV




Reverse complement motif Consensus sequence: BGRRRGRGGRTGRTTYGGGG

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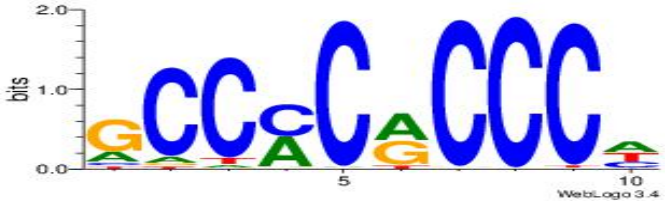
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 36 |
| Motif name: | Klf4 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Reverse Complement |
| Direction: | Forward |
| Position number: | 1 |

Number of overlap: 10
Similarity score: 0.616368

Alignment:
GCCYCMCCCD-
GGGGRTTCCCC

Original motif Consensus sequence: DGGGYGKGGC

Reverse complement motif Consensus sequence: GCCYCMCCCD

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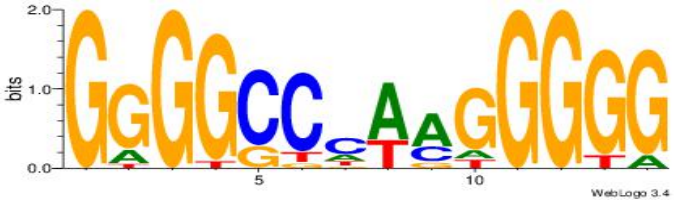
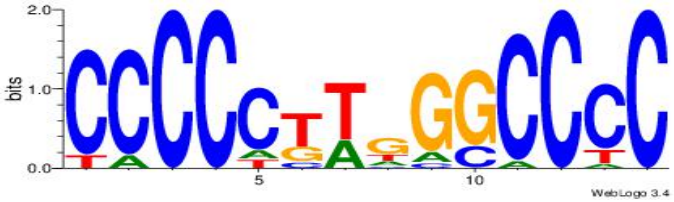
Dataset #: 2
Motif ID: 21
Motif name: PLAG1
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 6
Number of overlap: 9
Similarity score: 1.11497

Alignment:
--GGGGCCCAAGGGGG
GGGGRTTCCCC-----

Original motif Consensus sequence: GGGGCCCAAGGGGG

Reverse complement motif Consensus sequence: CCCCCTTGGGCCC

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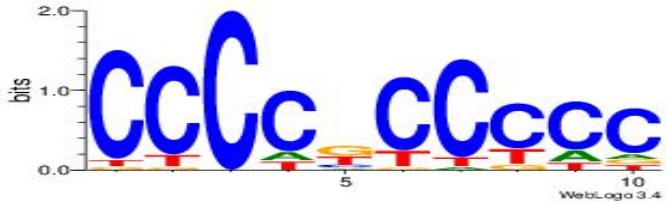
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 16 |
| Motif name: | SP1 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Reverse Complement |
| Direction: | Backward |
| Position number: | 2 |
| Number of overlap: | 9 |
| Similarity score: | 1.11585 |

Alignment:

```
--GGGGGYGGGG
GGGGRTTCCCC-
```

Original motif Consensus sequence: CCCCKCCCCC




Reverse complement motif Consensus sequence: GGGGGYGGGG

---

| | |
|---|---|
| Dataset #: | 1 |
| Motif ID: | 7 |

| | |
|---|---|
| Motif name: | Motif 7 |
| 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: | 1.59629 |

Alignment:

```
GGGGMGGG---
GGGGAAKCCCC
```

Original motif Consensus sequence: CCCRCCCC

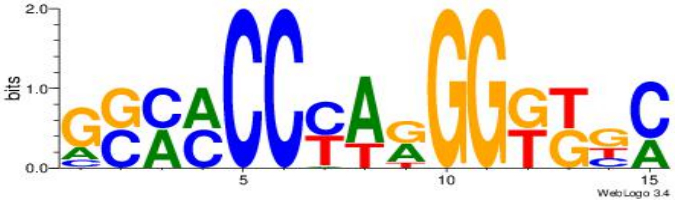
Reverse complement motif Consensus sequence: GGGGMGGG

---

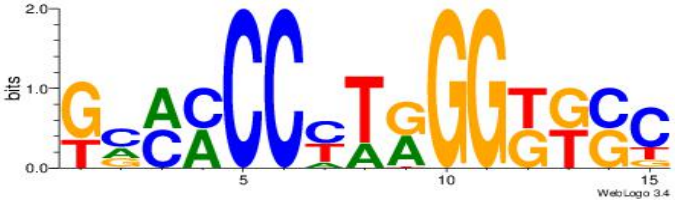
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 13 |
| Motif name: | Zfp423 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 8 |
| Number of overlap: | 8 |
| Similarity score: | 1.59848 |

Alignment:
GSMMCCYARGGKKKC---
-------GGGGRTTCCCC

Original motif Consensus sequence: GSMMCCYARGGKKKC




Reverse complement motif Consensus sequence: GYRYCCMTKGGYR

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| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 41 |
| Motif name: | MZF1_5-13 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 3 |
| Number of overlap: | 8 |
| Similarity score: | 1.61306 |

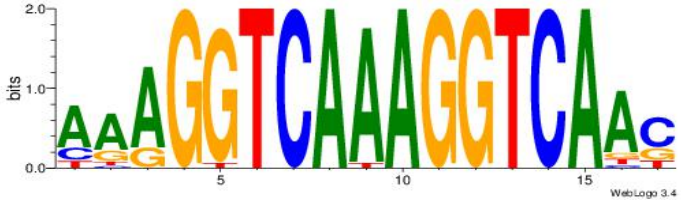
Alignment:
---BKAGGGGDAD
GGGGAAKCCCC--

Original motif Consensus sequence: BKAGGGGDAD

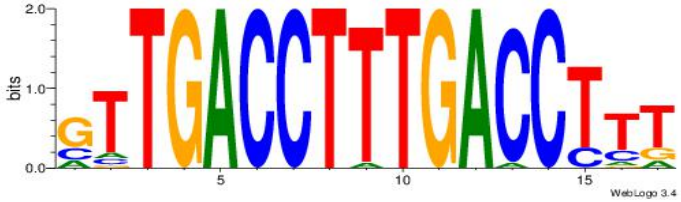
Reverse complement motif Consensus sequence: BTHCCCCTYB

**Dataset #: 2 Motif ID: 43 Motif name: NR1H2RXRA**

Original motif Consensus sequence: AAAGGTCAAAGGTCAAC




Reverse complement motif Consensus sequence: GTTGACCTTTGACCTTT



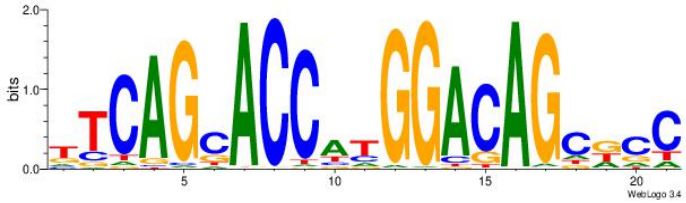

## Best Matches for Motif ID 43 (Highest to Lowest)

| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 19 |
| Motif name: | REST |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction: | Forward |
| Position number: | 4 |
| Number of overlap: | 17 |
| Similarity score: | 0.0911991 |

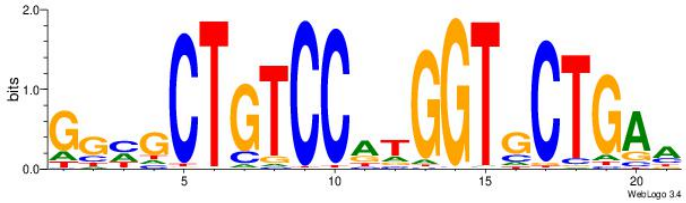
Alignment:

GGYGCTGTCCATGGTGCTGAA
---GTTGACCTTTGACCTTT-

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC




Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA

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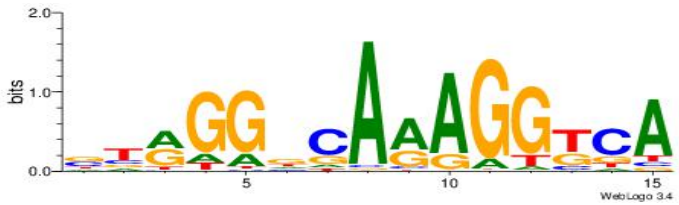
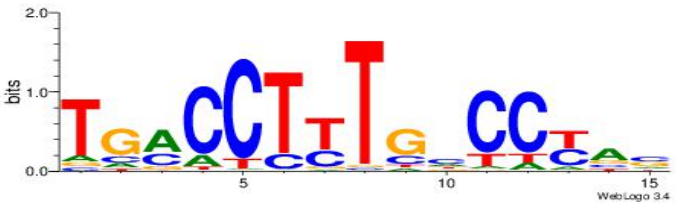
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 20 |
| Motif name: | PPARGRXRA |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 1 |
| Number of overlap: | 15 |
| Similarity score: | 1.05945 |

Alignment:
BTRGGDCARAGGKCA--
AAAGGTCAAAGGTCAAC

Original motif Consensus sequence: BTRGGDCARAGGKCA

Reverse complement motif Consensus sequence: TGRCCTKTGHCCK

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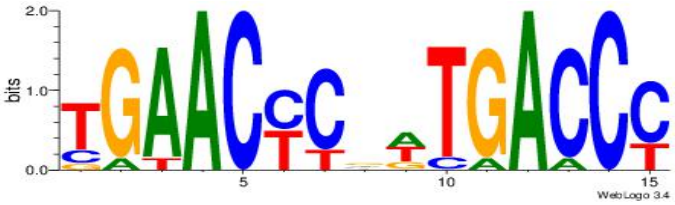
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 17 |
| Motif name: | RXRAVDR |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 1 |
| Number of overlap: | 15 |
| Similarity score: | 1.09792 |

Alignment:

```
--GGGTCAWBGRGTTCA
AAAGGTCAAAGGTCAAC
```

Original motif Consensus sequence: GGGTCAWBGRGTTCA

Reverse complement motif Consensus sequence: TGAACKCBWTGAC




---

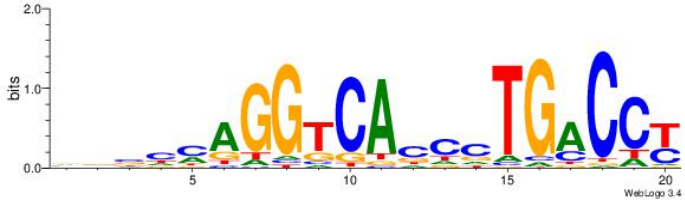
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 29 |

| | |
|---|---|
| Motif name: | ESR1 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 8 |
| Number of overlap: | 13 |
| Similarity score: | 2.08514 |

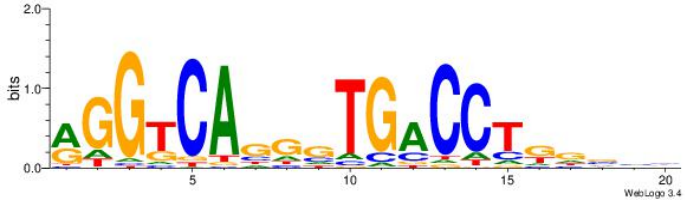
Alignment:

```
----VDBHMAGGTCACCCTGACCY
AAAGGTCAAAGGTCAAC-------
```

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY




Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV

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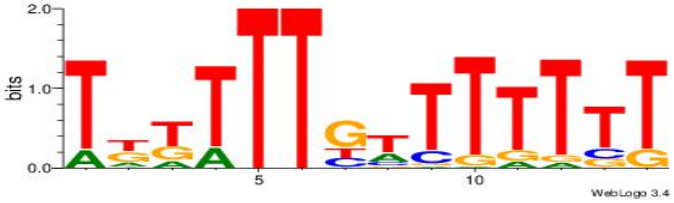
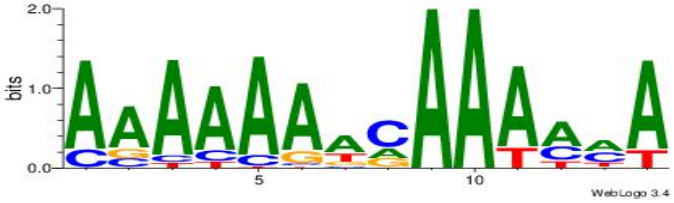
| | |
|---|---|
| Dataset #: | 1 |
| Motif ID: | 10 |
| Motif name: | Motif 10 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 2 |
| Number of overlap: | 13 |
| Similarity score: | 2.08845 |

Alignment:
TKKTTTGTTTTTTT----
-GTTGACCTTTGACCTTT

Original motif Consensus sequence: TKKTTTGTTTTTTT




Reverse complement motif Consensus sequence: AAAAAAACAAARR

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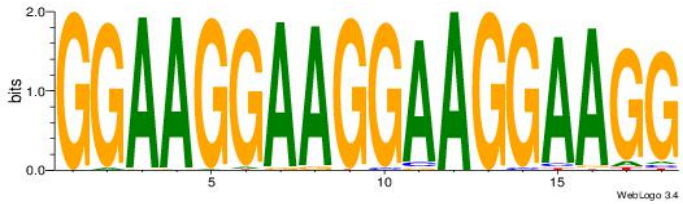
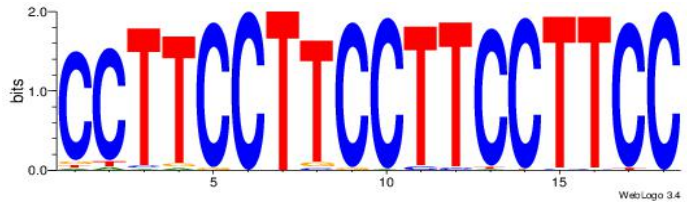
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 32 |
| Motif name: | EWSR1-FLI1 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 7 |
| Number of overlap: | 12 |
| Similarity score: | 2.59335 |

Alignment:
GGAAGGAAGGAAGGAAGG-----
------AAAGGTCAAAGGTCAAC

Original motif Consensus sequence: GGAAGGAAGGAAGGAAGG

Reverse complement motif Consensus sequence: CCTTCCTTCCTTCCTTCC



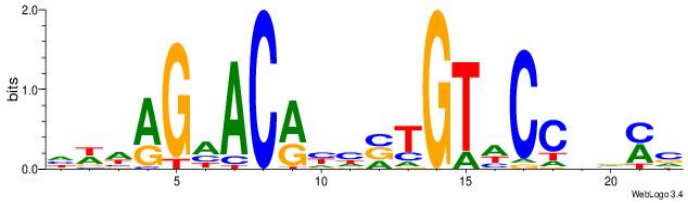




| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 24 |
| Motif name: | Ar |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction: | Forward |
| Position number: | 12 |
| Number of overlap: | 11 |
| Similarity score: | 3.09595 |

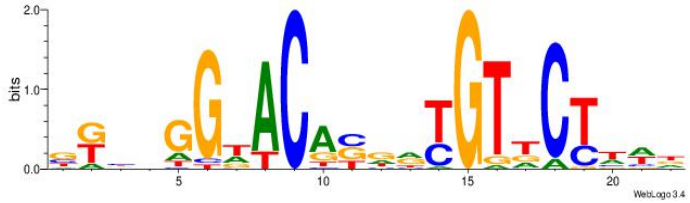
Alignment:

```
VRVDGGHACAVDDKGTHCTDWH------
-----------GTTGACCTTTGACCTTT
```

Original motif Consensus sequence: HWDAGHACRHHVTGTHCCHVMV




Reverse complement motif Consensus sequence: VRVDGGHACAVDDKGTHCTDWH



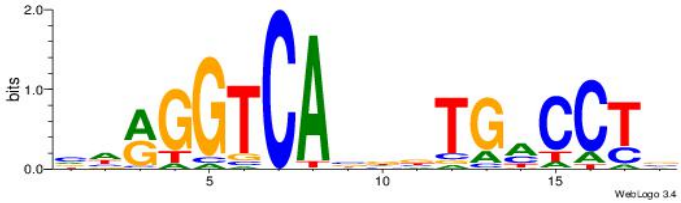

| | |
|---|---|
| Dataset #: | 2 |

| | |
|---|---|
| Motif ID: | 30 |
| Motif name: | ESR2 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction: | Forward |
| Position number: | 9 |
| Number of overlap: | 10 |
| Similarity score: | 3.56221 |

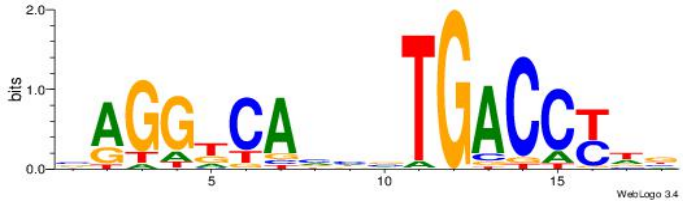
Alignment:

```
BAGGYCABHBTGACCKHV-------
--------GTTGACCTTTGACCTTT
```

Original motif Consensus sequence: VHRGGTCABDBTGMCCTB




Reverse complement motif Consensus sequence: BAGGYCABHBTGACCKHV

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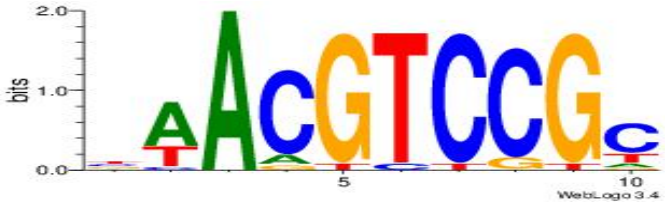
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 37 |
| Motif name: | MIZF |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 1 |
| Number of overlap: | 10 |

Similarity score: 3.5855

Alignment:
-------BAACGTCCGC
AAAGGTCAAAGGTCAAC

Original motif Consensus sequence: BAACGTCCGC




Reverse complement motif Consensus sequence: GCGGACGTTV

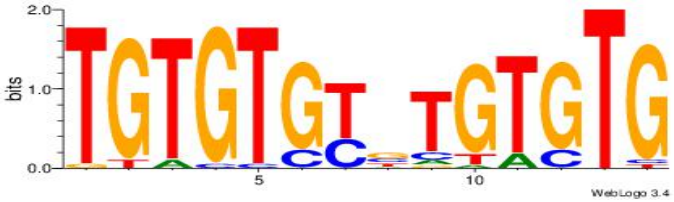
---

Dataset #: 1
Motif ID: 9
Motif name: Motif 9
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 5
Number of overlap: 10
Similarity score: 3.59839

Alignment:
CACACAVRCACACA-------
----AAAGGTCAAAGGTCAAC

Original motif Consensus sequence: CACACAVRCACACA

Reverse complement motif Consensus sequence: TGTGTGKVTGTGT




**Dataset #: 2 Motif ID: 44 Motif name: NR4A2**

Original motif Consensus sequence: AAGGTCAC

Reverse complement motif Consensus sequence: GTGACCTT

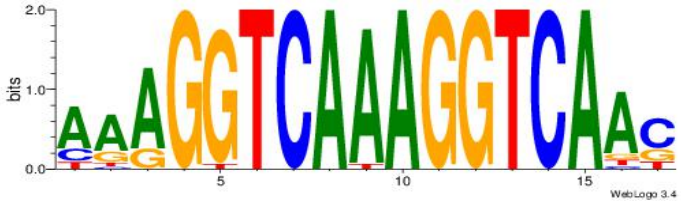
**Best Matches for Motif ID 44 (Highest to Lowest)**

| | |
|---|---|
| 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: | 2 |
| Number of overlap: | 8 |
| Similarity score: | 0.0167759 |

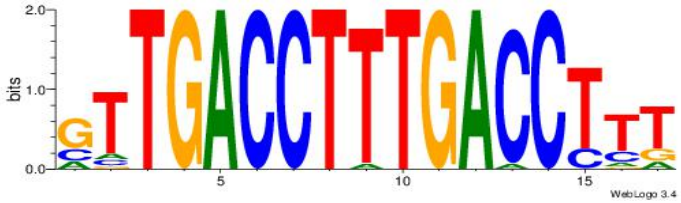
Alignment:

```
AAAGGTCAAAGGTCAAC
-AAGGTCAC--------
```

Original motif Consensus sequence: AAAGGTCAAAGGTCAAC




Reverse complement motif Consensus sequence: GTTGACCTTTGACCTTT

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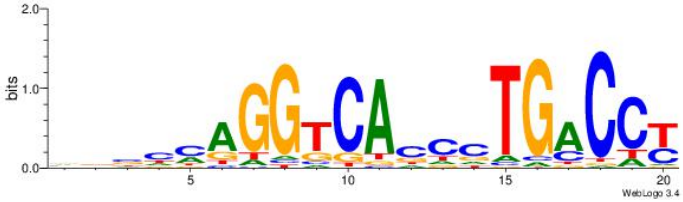
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 29 |
| Motif name: | ESR1 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 5 |
| Number of overlap: | 8 |
| Similarity score: | 0.0195235 |

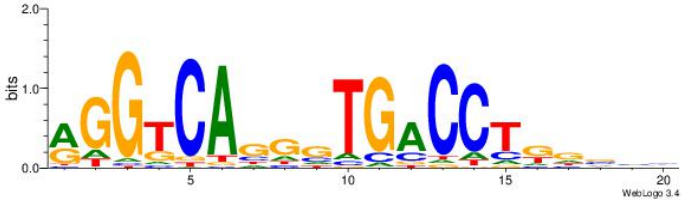
Alignment:

```
VDBHMAGGTCACCCTGACCY
----AAGGTCAC--------
```

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY




Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV

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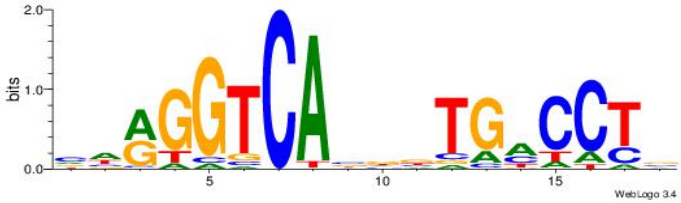
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 30 |
| Motif name: | ESR2 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 2 |
| Number of overlap: | 8 |
| Similarity score: | 0.0198372 |

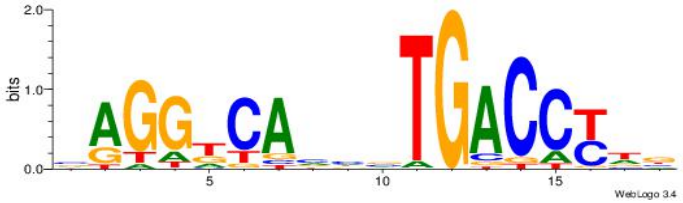
Alignment:

```
VHRGGTCABDBTGMCCTB
-AAGGTCAC---------
```

Original motif Consensus sequence: VHRGGTCABDBTGMCCTB




Reverse complement motif Consensus sequence: BAGGYCABHBTGACCKHV

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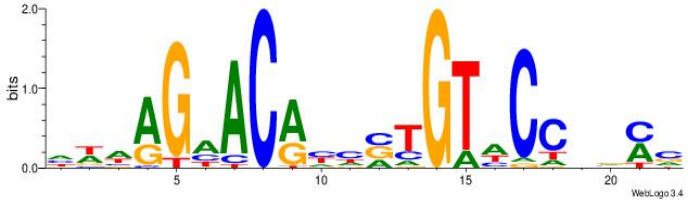
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 24 |
| Motif name: | Ar |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction: | Forward |
| Position number: | 13 |

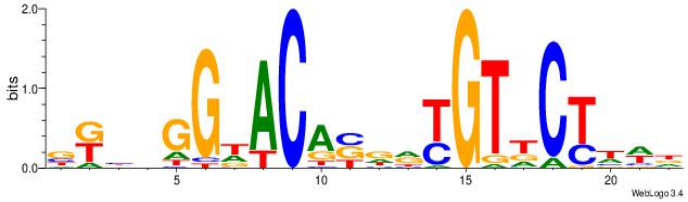
Number of overlap: 8
Similarity score: 0.0487608

Alignment:
VRVDGGHACAVDDKGTHCTDWH
----------GTGACCTT--

Original motif Consensus sequence: HWDAGHACRHHVTGTHCCHVMV




Reverse complement motif Consensus sequence: VRVDGGHACAVDDKGTHCTDWH

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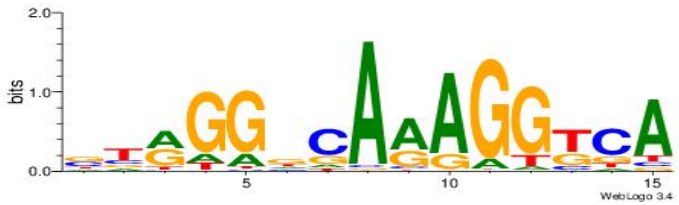
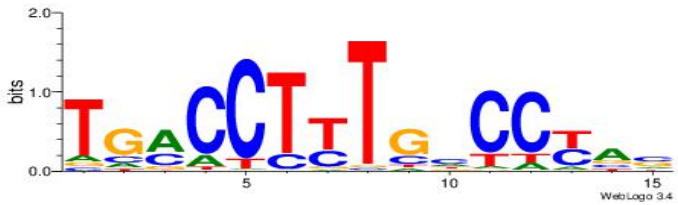
Dataset #: 2
Motif ID: 20
Motif name: PPARGRXRA
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 7
Number of overlap: 8
Similarity score: 0.0495607

Alignment:
BTRGGDCARAGGKCA
-AAGGTCAC------

Original motif Consensus sequence: BTRGGDCARAGGKCA

Reverse complement motif Consensus sequence: TGRCCTKTGHCCK

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| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 22 |
| Motif name: | NR2F1 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Reverse Complement |
| Direction: | Forward |
| Position number: | 7 |
| Number of overlap: | 8 |
| Similarity score: | 0.0564874 |

Alignment:

```
AKGYYCAAAGRTCA
------AAGGTCAC
```

Original motif Consensus sequence: TGAMCTTTGMMCYT

Reverse complement motif Consensus sequence: AKGYYCAAAGRTCA

---

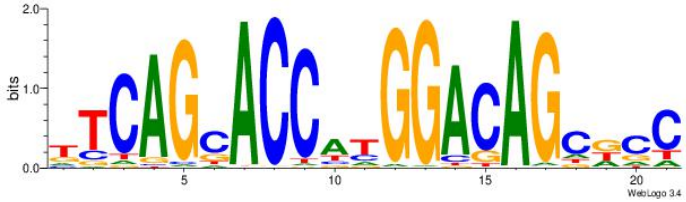
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 19 |

| | |
|---|---|
| Motif name: | REST |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 5 |
| Number of overlap: | 8 |
| Similarity score: | 0.0594649 |

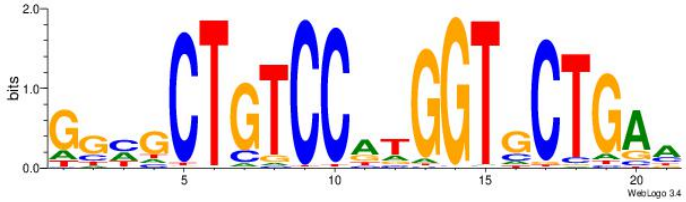
Alignment:

```
TTCAGCACCATGGACAGCKCC
---------AAGGTCAC----
```

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC




Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA

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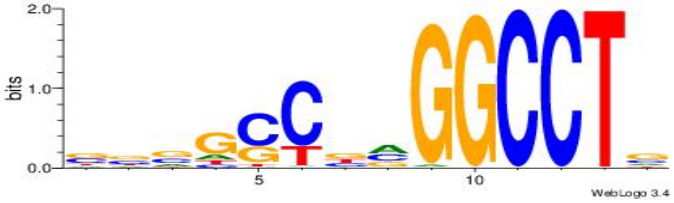
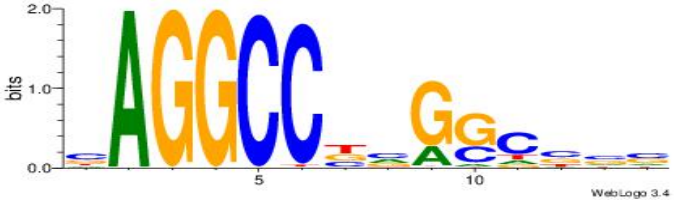
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 12 |
| Motif name: | Zfx |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 1 |
| Number of overlap: | 8 |
| Similarity score: | 0.0631514 |

Alignment:
BBVGCCBVGGCCTV
GTGACCTT------

Original motif Consensus sequence: BBVGCCBVGGCCTV




Reverse complement motif Consensus sequence: VAGGCCBBGGCVB

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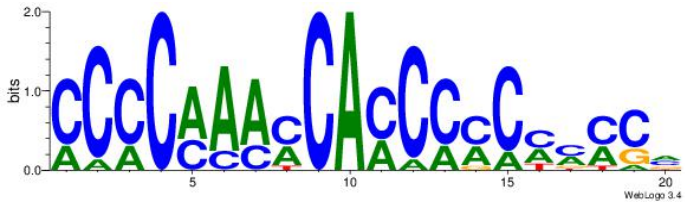
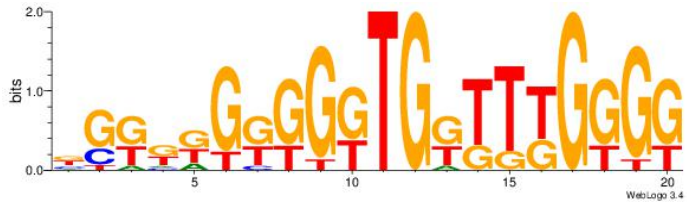
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 18 |
| Motif name: | RREB1 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction: | Backward |
| Position number: | 4 |
| Number of overlap: | 8 |
| Similarity score: | 0.0720656 |

Alignment:
BGRRRGRGGRTGRTTYGGGG
---------GTGACCTT---

Original motif Consensus sequence: CCCCMAAMCAMCCMCMMMCV

Reverse complement motif Consensus sequence: BGRRRGRGGRTGRTTYGGGG



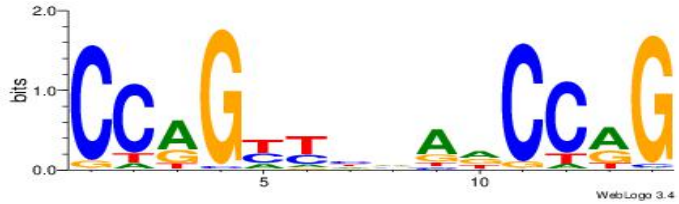




| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 48 |
| Motif name: | Tcfcp2l1 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction: | Backward |
| Position number: | 2 |
| Number of overlap: | 8 |
| Similarity score: | 0.0740998 |

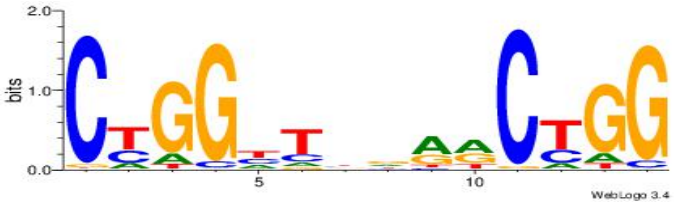
Alignment:

```
CKGGDTBDMMCTGG
-----GTGACCTT-
```

Original motif Consensus sequence: CCAGYYHVADCCRG

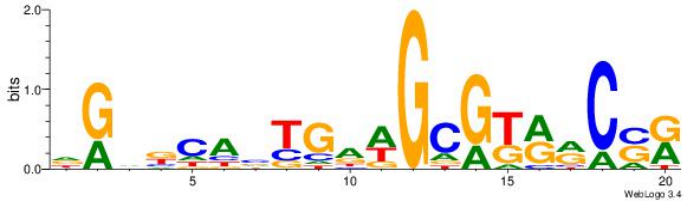



Reverse complement motif Consensus sequence: CKGGDTBDMMCT

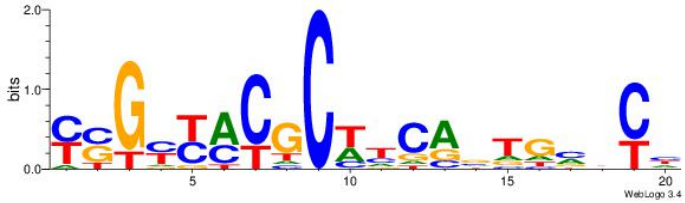



**Dataset #: 2 Motif ID: 45 Motif name: Pax5**

Original motif Consensus sequence: DGVBCABTGDWGCGKRRCSR




Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD

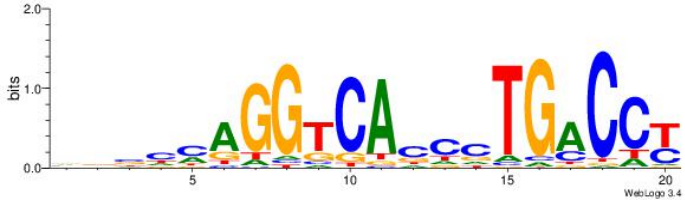



## Best Matches for Motif ID 45 (Highest to Lowest)

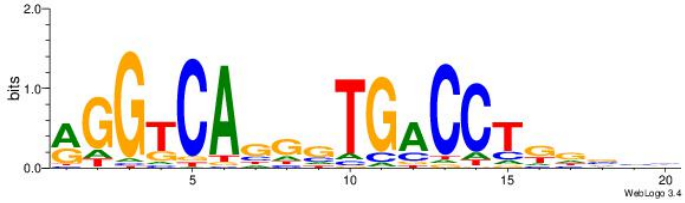
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 29 |
| Motif name: | ESR1 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction: | Backward |
| Position number: | 1 |
| Number of overlap: | 20 |
| Similarity score: | 0.0382347 |

Alignment:
MGGTCAGGGTGACCTRDBHV
MSGKKRCGCWDCABTGBBCD

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



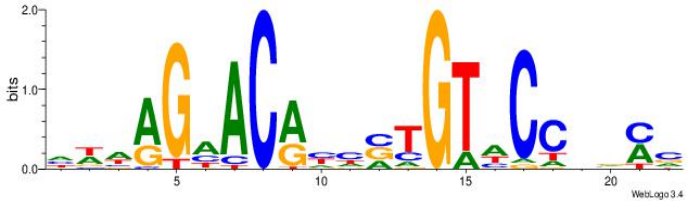

Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV



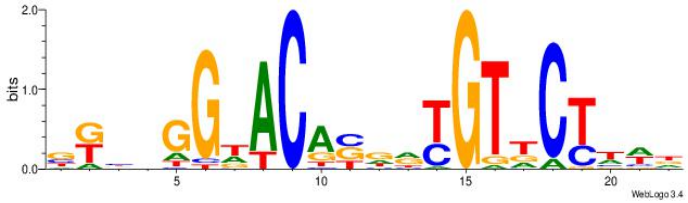
Dataset #: 2
Motif ID: 24
Motif name: Ar
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 20
Similarity score: 0.0450685

Alignment:
VRVDGGHACAVDDKGTHCTDWH
--MSGKKRCGCWDCABTGBBCD

Original motif Consensus sequence: HWDAGHACRHHVTGTHCCHVMV




Reverse complement motif Consensus sequence: VRVDGGHACAVDDKGTHCTDWH

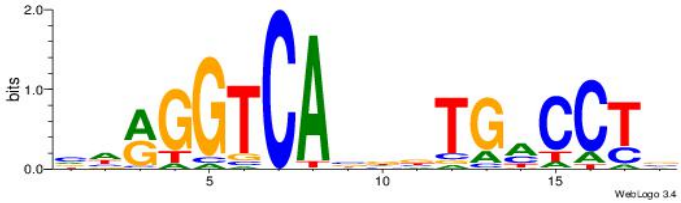



Dataset #: 2
Motif ID: 30
Motif name: ESR2
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward

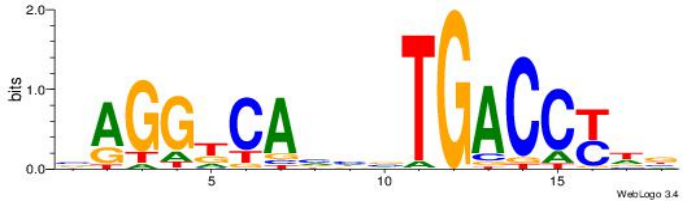
Position number: 1
Number of overlap: 18
Similarity score: 1.05192

Alignment:
BAGGYCABHBTGACCKHV--
MSGKKRCGCWDCABTGBBCD

Original motif Consensus sequence: VHRGGTCABDBTGMCCTB




Reverse complement motif Consensus sequence: BAGGYCABHBTGACCKHV

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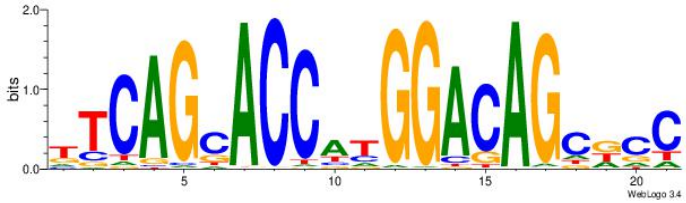
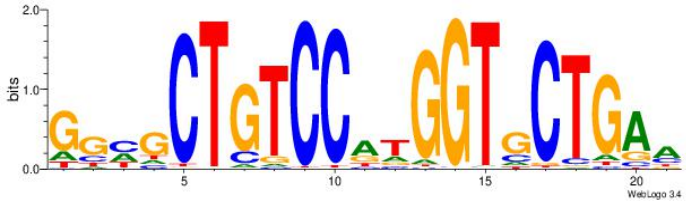
Dataset #: 2
Motif ID: 19
Motif name: REST
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 4
Number of overlap: 18
Similarity score: 1.0582

Alignment:
--GGYGCTGTCCATGGTGCTGAA
MSGKKRCGCWDCABTGBBCD---

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC



Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA

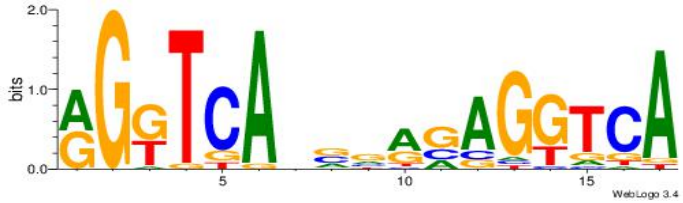


| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 47 |
| Motif name: | RXRRAR_DR5 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction: | Backward |
| Position number: | 1 |
| Number of overlap: | 17 |
| Similarity score: | 1.53818 |

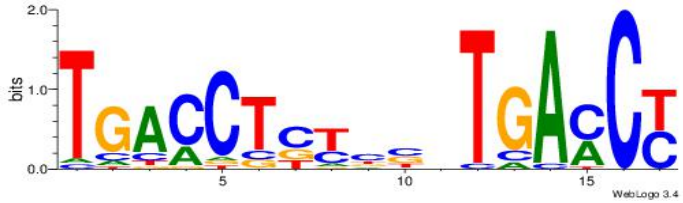
Alignment:

```
---TGACCTCKVVBTGAYCK
MSGKKRCGCWDCABTGBBCD
```

Original motif Consensus sequence: RGKTCABVVRGAGGTCA



Reverse complement motif Consensus sequence: TGACCTCKVVBTGAYCK

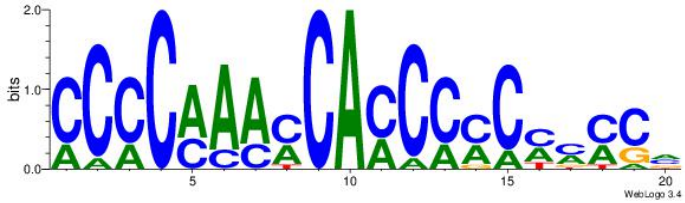


| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 18 |
| Motif name: | RREB1 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 4 |
| Number of overlap: | 17 |
| Similarity score: | 1.55831 |

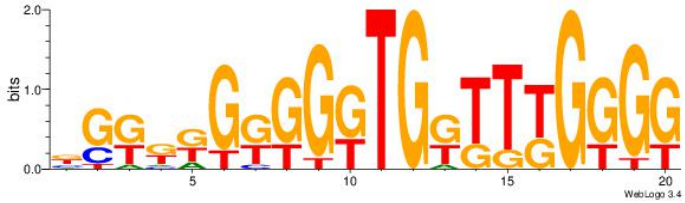
Alignment:

```
CCCCMAAMCAMCCMCMMMCV---
---MSGKKRCGCWDCABTGBBCD
```

Original motif Consensus sequence: CCCCMAAMCAMCCMCMMMCV




Reverse complement motif Consensus sequence: BGRRRGRGGRTGRTTYGGGG

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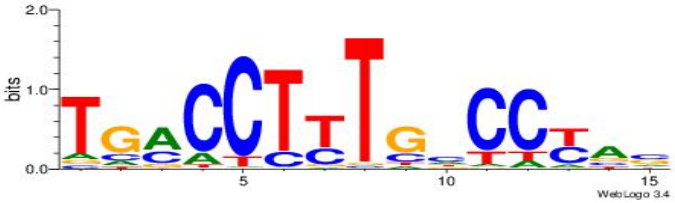
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 20 |
| Motif name: | PPARGRXRA |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Reverse Complement |
| Direction: | Backward |
| Position number: | 1 |

Number of overlap: 15
Similarity score: 2.55126

Alignment:
```
-----TGRCCTKTGHCCKAB
DGVBCABTGDWGCGKRRCSR
```

Original motif Consensus sequence: BTRGGDCARAGGKCA

Reverse complement motif Consensus sequence: TGRCCTKTGHCCK

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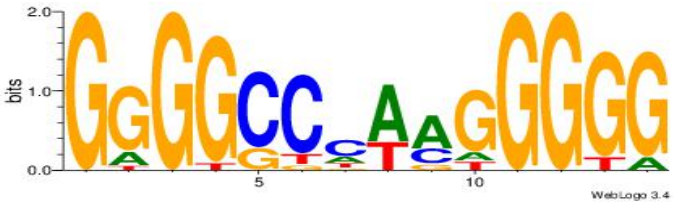
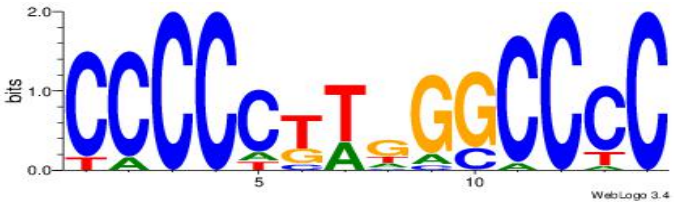
Dataset #: 2
Motif ID: 21
Motif name: PLAG1
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 14
Similarity score: 3.05866

Alignment:
```
GGGGCCCAAGGGGG------
DGVBCABTGDWGCGKRRCSR
```

Original motif Consensus sequence: GGGGCCCAAGGGGG

Reverse complement motif Consensus sequence: CCCCCTTGGGCCC

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| | |
|---|---|
| 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: | 1 |
| Number of overlap: | 14 |
| Similarity score: | 3.05897 |

Alignment:

```
------AKGYYCAAAGRTCA
MSGKKRCGCWDCABTGBBCD
```

Original motif Consensus sequence: TGAMCTTTGMMCYT

Reverse complement motif Consensus sequence: AKGYYCAAAGRTCA

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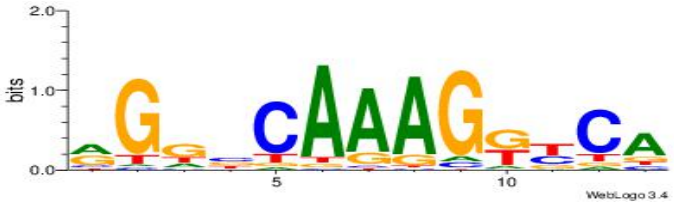
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 34 |

| | |
|---|---|
| Motif name: | HNF4A |
| 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: | 3.53748 |

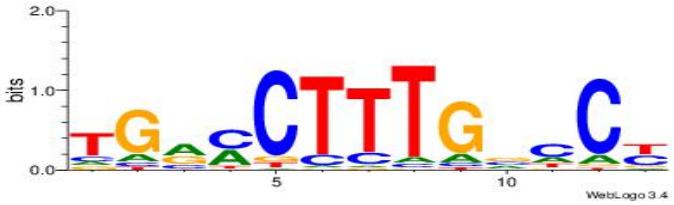
Alignment:

```
-------TGMYCTTTGBCCK
DGVBCABTGDWGCGKRRCSR
```

Original motif Consensus sequence: RGGBCAAAGKYCA




Reverse complement motif Consensus sequence: TGMYCTTTGBCCK

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**Dataset #: 2 Motif ID: 46 Motif name: RORA_1**

Original motif Consensus sequence: AWVDAGGTCA

Reverse complement motif Consensus sequence: TGACCTDVWT

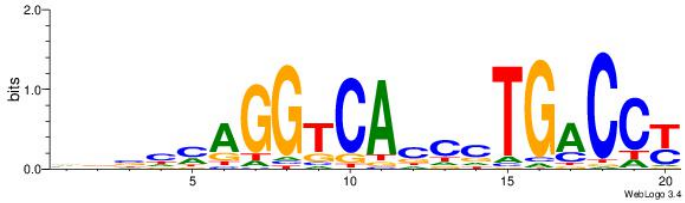
**Best Matches for Motif ID 46 (Highest to Lowest)**

| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 29 |
| Motif name: | ESR1 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction: | Backward |
| Position number: | 2 |
| Number of overlap: | 10 |
| Similarity score: | 0.0417851 |

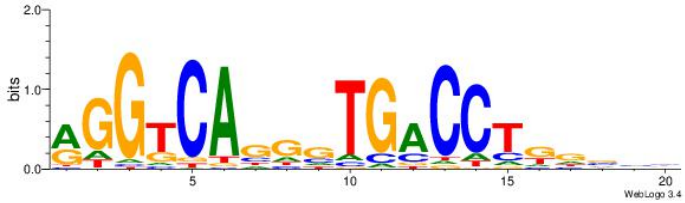
Alignment:

```
MGGTCAGGGTGACCTRDBHV
---------TGACCTDVWT-
```

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY




Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV

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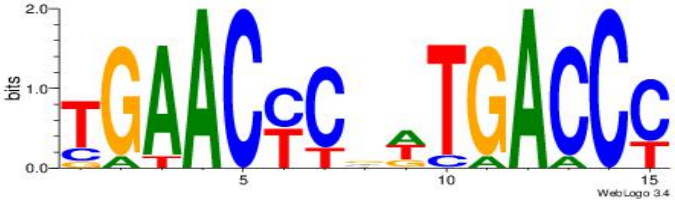
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 17 |
| Motif name: | RXRAVDR |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 1 |

Number of overlap: 10
Similarity score: 0.05325

Alignment:
GGGTCAWBGRGTTCA
-----AWVDAGGTCA

Original motif Consensus sequence: GGGTCAWBGRGTTCA

Reverse complement motif Consensus sequence: TGAACKCBWTGAC

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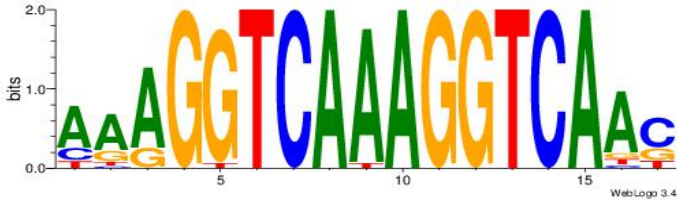
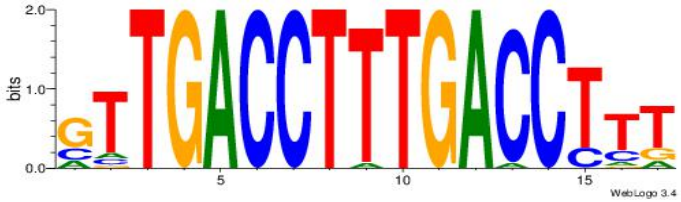
Dataset #: 2
Motif ID: 43
Motif name: NR1H2RXRA
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 3
Number of overlap: 10
Similarity score: 0.05425

Alignment:
AAAGGTCAAAGGTCAAC
-----AWVDAGGTCA--

Original motif Consensus sequence: AAAGGTCAAAGGTCAAC

Reverse complement motif Consensus sequence: GTTGACCTTTGACCTTT

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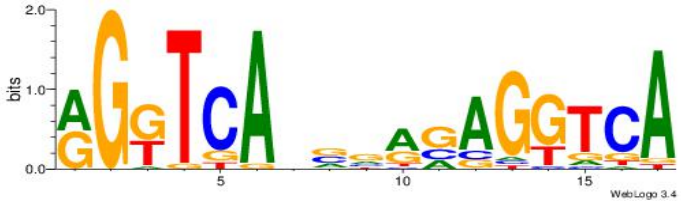
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 47 |
| Motif name: | RXRRAR_DR5 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction: | Forward |
| Position number: | 1 |
| Number of overlap: | 10 |
| Similarity score: | 0.0600761 |

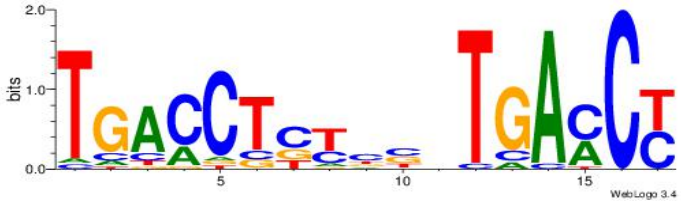
Alignment:

```
TGACCTCKVVBTGAYCK
TGACCTDVWT-------
```

Original motif Consensus sequence: RGKTCABVVRGAGGTCA




Reverse complement motif Consensus sequence: TGACCTCKVVBTGAYCK

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| | |
|---|---|
| Dataset #: | 2 |

| | |
|---|---|
| Motif ID: | 22 |
| Motif name: | NR2F1 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 5 |
| Number of overlap: | 10 |
| Similarity score: | 0.0654808 |

Alignment:

```
TGAMCTTTGMMCYT
----TGACCTDVWT
```

Original motif Consensus sequence: TGAMCTTTGMMCYT

Reverse complement motif Consensus sequence: AKGYYCAAAGRTCA

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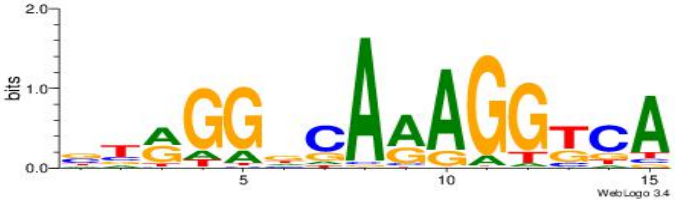
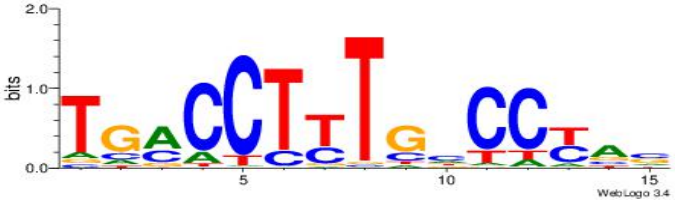
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 20 |
| Motif name: | PPARGRXRA |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 1 |
| Number of overlap: | 10 |
| Similarity score: | 0.06668 |

Alignment:
BTRGGDCARAGGKCA
-----AWVDAGGTCA

Original motif Consensus sequence: BTRGGDCARAGGKCA




Reverse complement motif Consensus sequence: TGRCCTKTGHCCK

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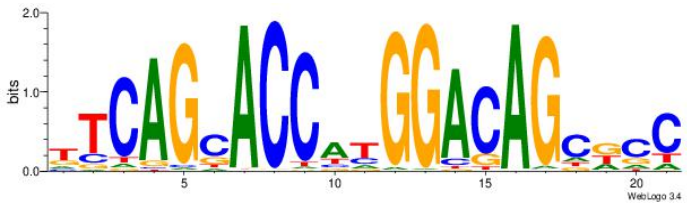
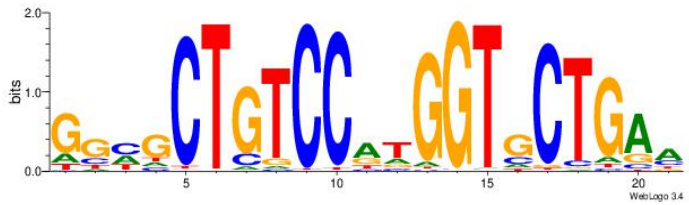
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 19 |
| Motif name: | REST |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 7 |
| Number of overlap: | 10 |
| Similarity score: | 0.0755608 |

Alignment:
TTCAGCACCATGGACAGCKCC
------AWVDAGGTCA-----

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC

Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA

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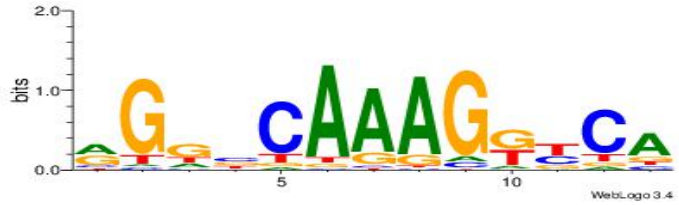
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 34 |
| Motif name: | HNF4A |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 4 |
| Number of overlap: | 10 |
| Similarity score: | 0.0803396 |

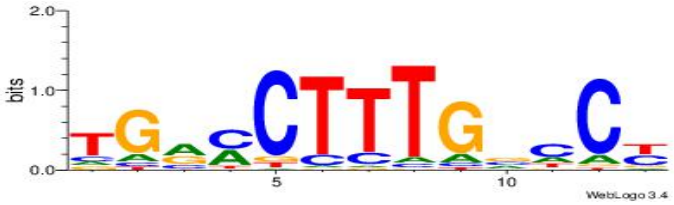
Alignment:

```
RGGBCAAAGKYCA
---AWVDAGGTCA
```

Original motif Consensus sequence: RGGBCAAAGKYCA




Reverse complement motif Consensus sequence: TGMYCTTTGBCCK

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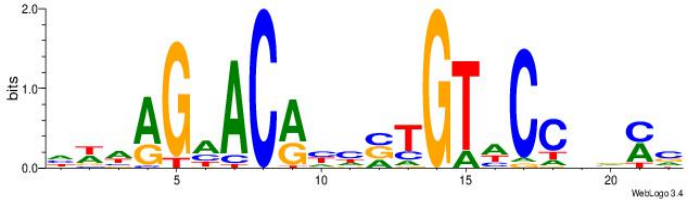
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 24 |

| | |
|---|---|
| Motif name: | Ar |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Reverse Complement |
| Direction: | Forward |
| Position number: | 13 |
| Number of overlap: | 10 |
| Similarity score: | 0.0814167 |

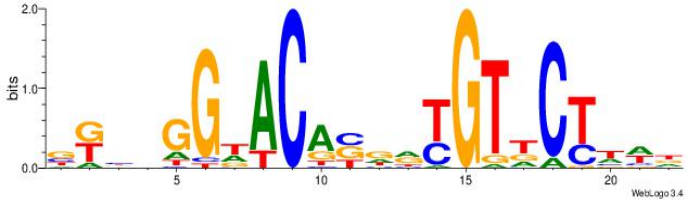
Alignment:

```
VRVDGGHACAVDDKGTHCTDWH
------------AWVDAGGTCA
```

Original motif Consensus sequence: HWDAGHACRHHVTGTHCCHVMV




Reverse complement motif Consensus sequence: VRVDGGHACAVDDKGTHCTDWH

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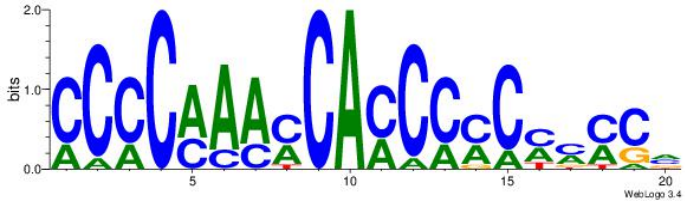
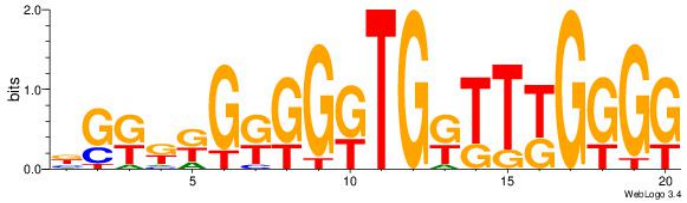
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 18 |
| Motif name: | RREB1 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 8 |
| Number of overlap: | 10 |
| Similarity score: | 0.0901591 |

Alignment:
CCCCMAAMCAMCCMCMMMCV
---TGACCTDVWT-------

Original motif Consensus sequence: CCCCMAAMCAMCCMCMMMCV




Reverse complement motif Consensus sequence: BGRRRGRGGRTGRTTYGGGG

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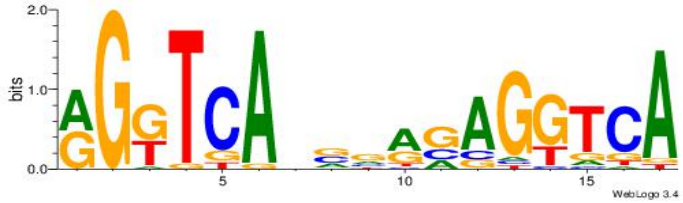
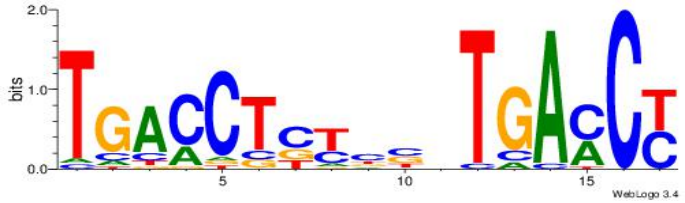
**Dataset #: 2 Motif ID: 47 Motif name: RXRRAR_DR5**

Original motif Consensus sequence: RGKTCABVVRGAGGTCA




Reverse complement motif Consensus sequence: TGACCTCKVVBTGAYCK




**Best Matches for Motif ID 47 (Highest to Lowest)**

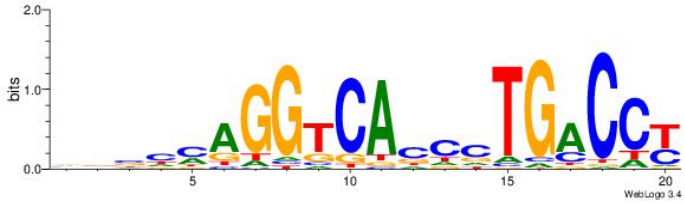
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 29 |
| Motif name: | ESR1 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Reverse Complement |

| | |
|---|---|
| Direction: | Backward |
| Position number: | 1 |
| Number of overlap: | 17 |
| Similarity score: | 0.0554256 |

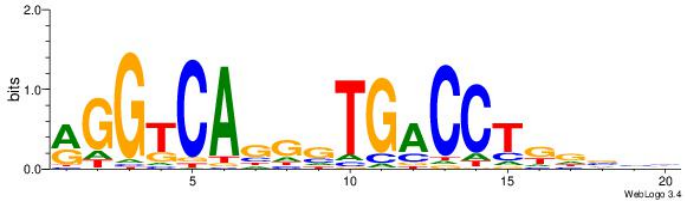
Alignment:

```
MGGTCAGGGTGACCTRDBHV
---RGKTCABVVRGAGGTCA
```

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY




Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV

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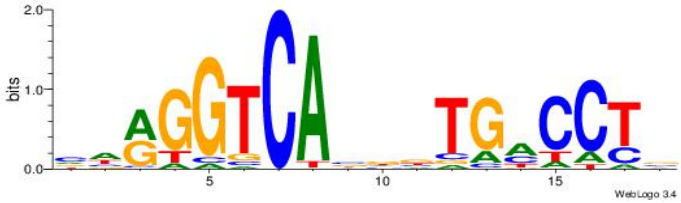
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 30 |
| Motif name: | ESR2 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 2 |
| Number of overlap: | 17 |
| Similarity score: | 0.0590677 |

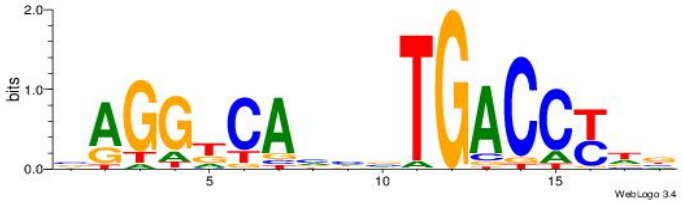
Alignment:

```
VHRGGTCABDBTGMCCTB
-TGACCTCKVVBTGAYCK
```

Original motif Consensus sequence: VHRGGTCABDBTGMCCTB




Reverse complement motif Consensus sequence: BAGGYCABHBTGACCKHV

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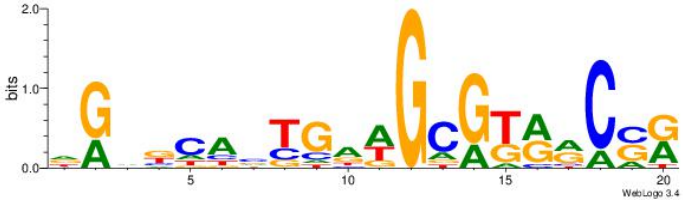
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 45 |
| Motif name: | Pax5 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction: | Backward |
| Position number: | 1 |
| Number of overlap: | 17 |
| Similarity score: | 0.0594693 |

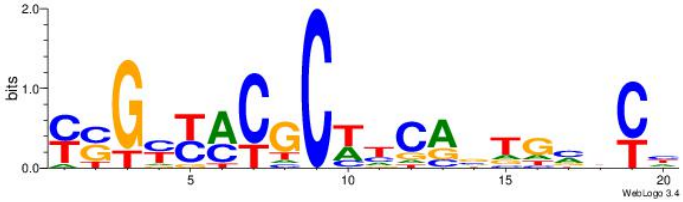
Alignment:

```
MSGKKRCGCWDCABTGBBCD
---TGACCTCKVVBTGAYCK
```

Original motif Consensus sequence: DGVBCABTGDWGCGKRRCSR




Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD

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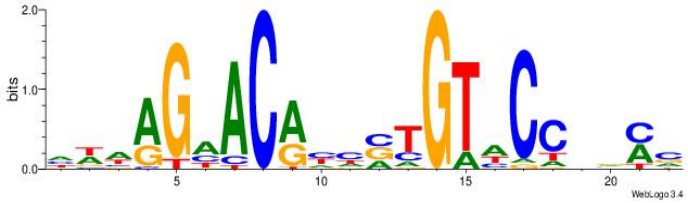
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 24 |
| Motif name: | Ar |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 2 |
| Number of overlap: | 17 |
| Similarity score: | 0.0751876 |

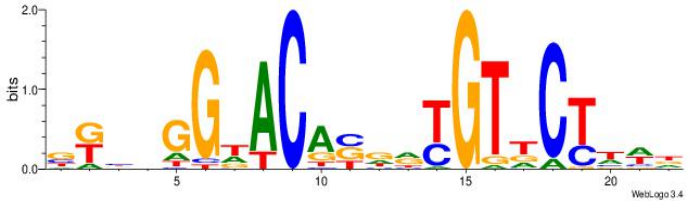
Alignment:

```
HWDAGHACRHHVTGTHCCHVMV
----TGACCTCKVVBTGAYCK-
```

Original motif Consensus sequence: HWDAGHACRHHVTGTHCCHVMV




Reverse complement motif Consensus sequence: VRVDGGHACAVDDKGTHCTDWH

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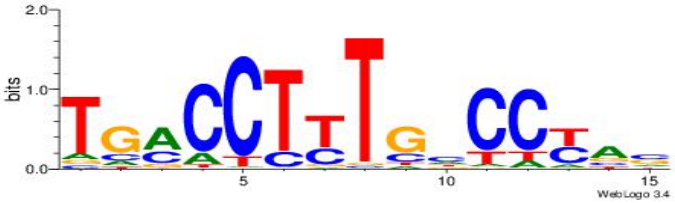
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 20 |
| Motif name: | PPARGRXRA |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 1 |

Number of overlap: 15
Similarity score: 1.0449

Alignment:
--BTRGGDCARAGGKCA
RGKTCABVVRGAGGTCA

Original motif Consensus sequence: BTRGGDCARAGGKCA

Reverse complement motif Consensus sequence: TGRCCTKTGHCCK

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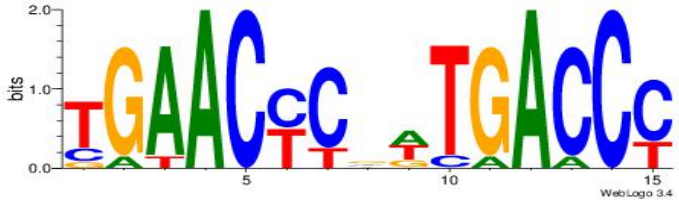
Dataset #: 2
Motif ID: 17
Motif name: RXRAVDR
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 15
Similarity score: 1.05297

Alignment:
GGGTCAWBGRGTTCA--
RGKTCABVVRGAGGTCA

Original motif Consensus sequence: GGGTCAWBGRGTTCA

Reverse complement motif Consensus sequence: TGAACKCBWTGAC

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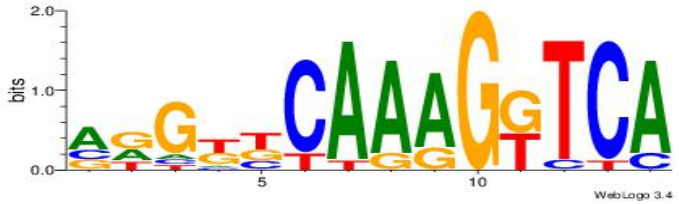
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 22 |
| Motif name: | NR2F1 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 1 |
| Number of overlap: | 14 |
| Similarity score: | 1.56607 |

Alignment:

```
---TGAMCTTTGMMCYT
TGACCTCKVVBTGAYCK
```

Original motif Consensus sequence: TGAMCTTTGMMCYT

Reverse complement motif Consensus sequence: AKGYYCAAAGRTCA

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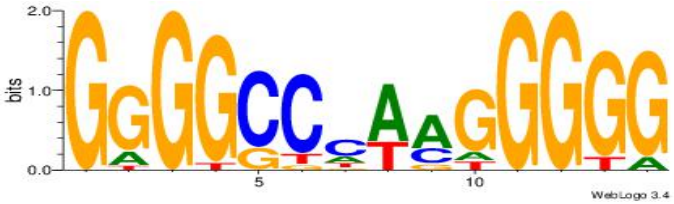
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 21 |

| | |
|---|---|
| Motif name: | PLAG1 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 1 |
| Number of overlap: | 14 |
| Similarity score: | 1.57917 |

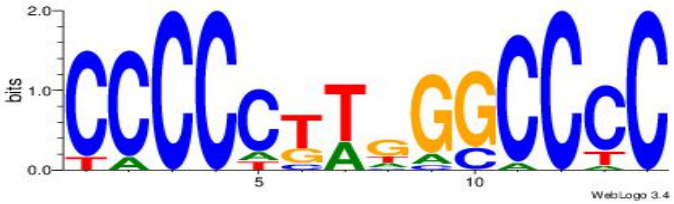
Alignment:

```
GGGGCCCAAGGGGG---
RGKTCABVVRGAGGTCA
```

Original motif Consensus sequence: GGGGCCCAAGGGGG




Reverse complement motif Consensus sequence: CCCCCTTGGGCCC

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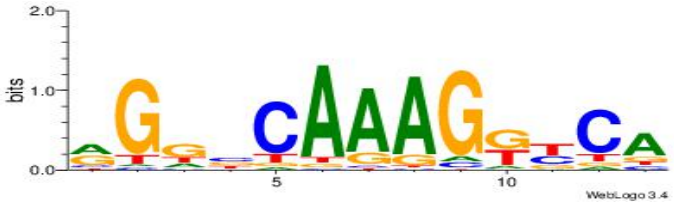
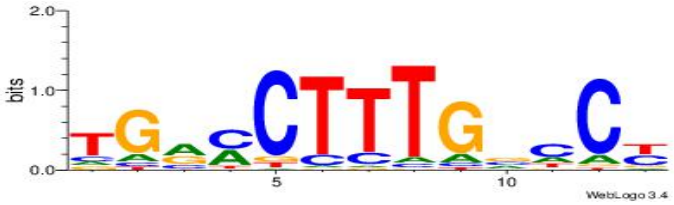
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 34 |
| Motif name: | HNF4A |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction: | Forward |
| Position number: | 1 |
| Number of overlap: | 13 |
| Similarity score: | 2.0437 |

Alignment:
TGMYCTTTGBCCK----
TGACCTCKVVBTGAYCK

Original motif Consensus sequence: RGGBCAAAGKYCA




Reverse complement motif Consensus sequence: TGMYCTTTGBCCK

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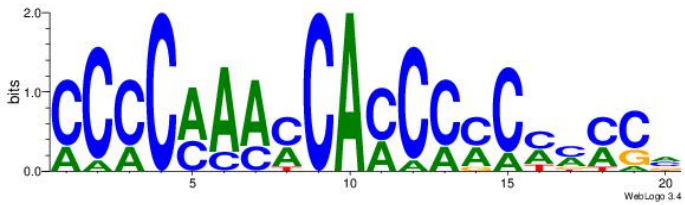
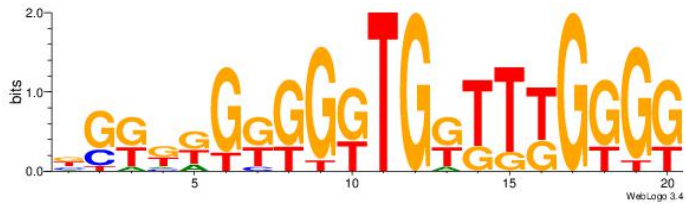
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 18 |
| Motif name: | RREB1 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 8 |
| Number of overlap: | 13 |
| Similarity score: | 2.06494 |

Alignment:
----CCCCMAAMCAMCCMCMMMCV
TGACCTCKVVBTGAYCK-------

Original motif Consensus sequence: CCCCMAAMCAMCCMCMMMCV

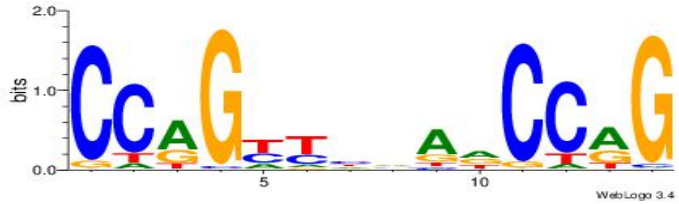
Reverse complement motif Consensus sequence: BGRRRGRGGRTGRTTYGGGG



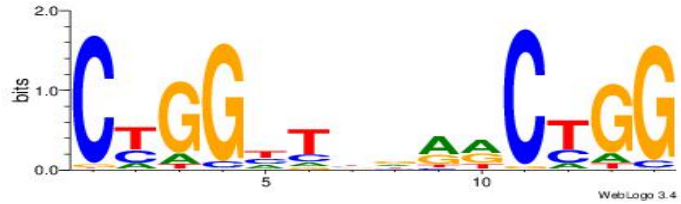




**Dataset #: 2 Motif ID: 48 Motif name: Tcfcp2l1**

Original motif Consensus sequence: CCAGYYHVADCCRG




Reverse complement motif Consensus sequence: CKGGDTBDMMCT



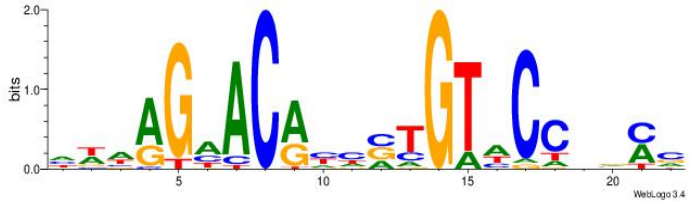

## Best Matches for Motif ID 48 (Highest to Lowest)

| | |
|---|---|
| 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: | 7 |
| Number of overlap: | 14 |
| Similarity score: | 0.0679942 |

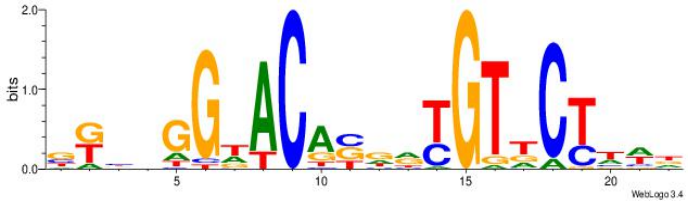
Alignment:

```
HWDAGHACRHHVTGTHCCHVMV
------CCAGYYHVADCCRG--
```

Original motif Consensus sequence: HWDAGHACRHHVTGTHCCHVMV



Reverse complement motif Consensus sequence: VRVDGGHACAVDDKGTHCTDWH

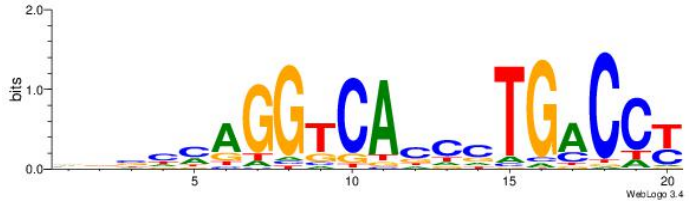


| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 29 |
| Motif name: | ESR1 |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Reverse Complement |
| Direction: | Forward |
| Position number: | 4 |
| Number of overlap: | 14 |
| Similarity score: | 0.0713928 |

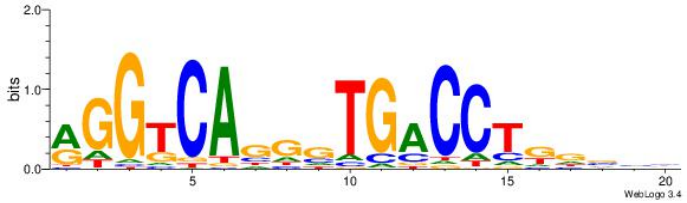
Alignment:

```
MGGTCAGGGTGACCTRDBHV
---CCAGYYHVADCCRG---
```

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV

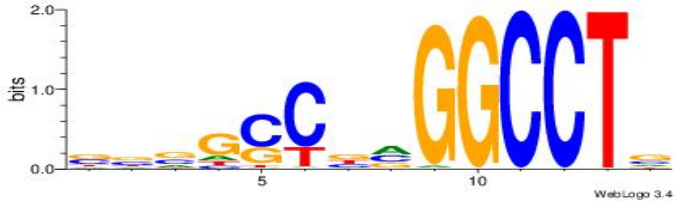


| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 12 |
| Motif name: | Zfx |
| Matching format of first motif: | Original Motif |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 1 |
| Number of overlap: | 14 |
| Similarity score: | 0.0714852 |

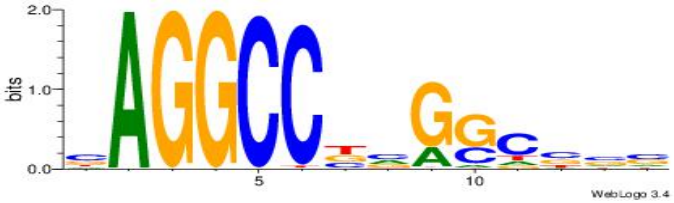
Alignment:

```
BBVGCCBVGGCCTV
CCAGYYHVADCCRG
```

Original motif Consensus sequence: BBVGCCBVGGCCTV




Reverse complement motif Consensus sequence: VAGGCCBBGGCVB

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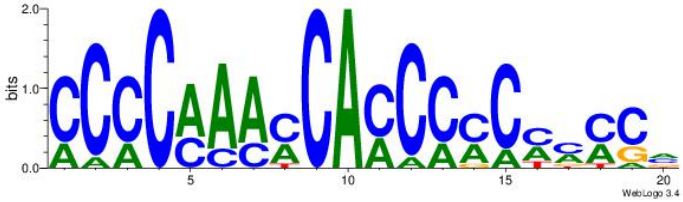
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 18 |
| Motif name: | RREB1 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction: | Backward |
| Position number: | 2 |
| Number of overlap: | 14 |

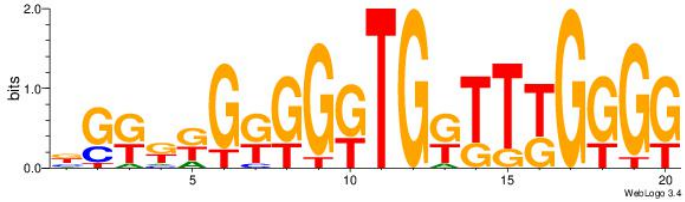
Similarity score: 0.0777364

Alignment:
BGRRRGRGGRTGRTTYGGGG
-----CKGGDTBDMMCTGG-

Original motif Consensus sequence: CCCCMAAMCAMCCMCMMMCV




Reverse complement motif Consensus sequence: BGRRRGRGGRTGRTTYGGGG

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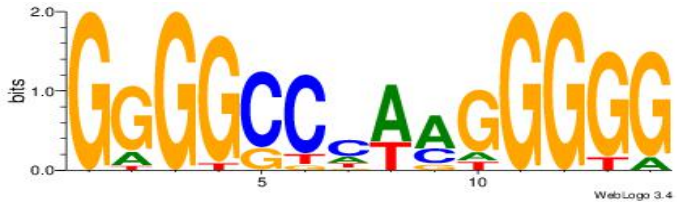
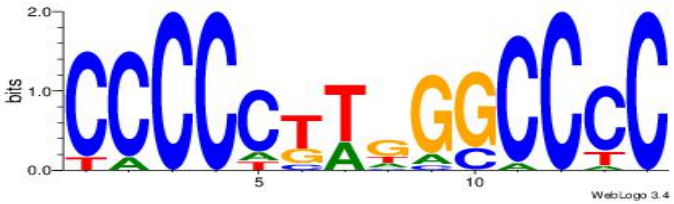
Dataset #: 2
Motif ID: 21
Motif name: PLAG1
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 14
Similarity score: 0.0817193

Alignment:
GGGGCCCAAGGGGG
CKGGDTBDMMCTGG

Original motif Consensus sequence: GGGGCCCAAGGGGG

Reverse complement motif Consensus sequence: CCCCCTTGGGCCC

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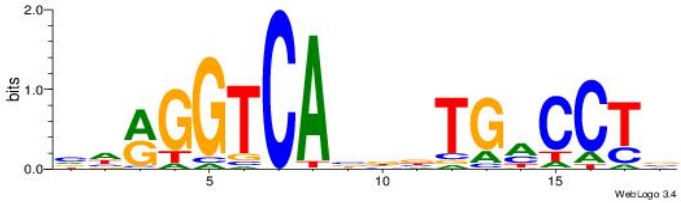
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 30 |
| Motif name: | ESR2 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 1 |
| Number of overlap: | 14 |
| Similarity score: | 0.0828703 |

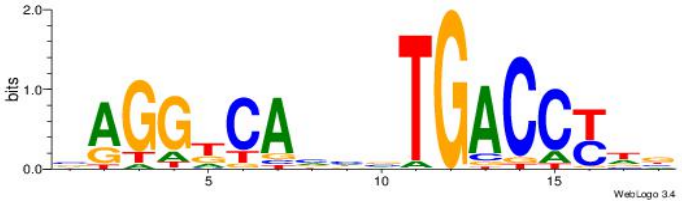
Alignment:

```
VHRGGTCABDBTGMCCTB
----CKGGDTBDMMCTGG
```

Original motif Consensus sequence: VHRGGTCABDBTGMCCTB




Reverse complement motif Consensus sequence: BAGGYCABHBTGACCKHV

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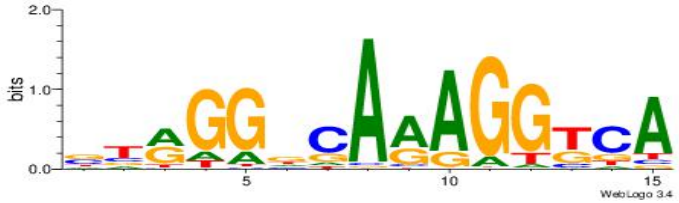
Dataset #: 2

| | |
|---|---|
| Motif ID: | 20 |
| Motif name: | PPARGRXRA |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Reverse Complement |
| Direction: | Backward |
| Position number: | 1 |
| Number of overlap: | 14 |
| Similarity score: | 0.0829929 |

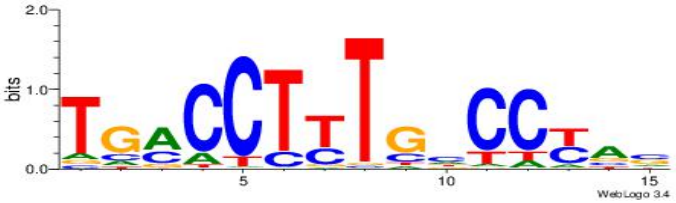
Alignment:

```
TGRCCTKTGHCCKAB
-CKGGDTBDMMCTGG
```

Original motif Consensus sequence: BTRGGDCARAGGKCA




Reverse complement motif Consensus sequence: TGRCCTKTGHCCK

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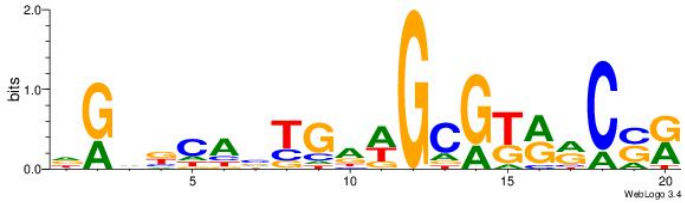
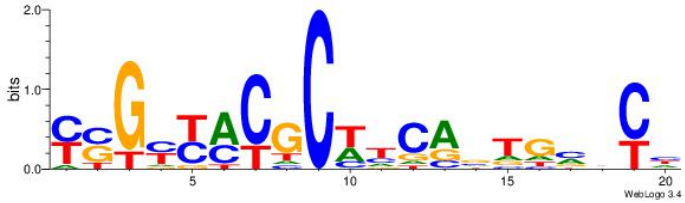
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 45 |
| Motif name: | Pax5 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 8 |
| Number of overlap: | 13 |
| Similarity score: | 0.575635 |

Alignment:
DGVBCABTGDWGCGKRRCSR-
-------CKGGDTBDMMCTGG

Original motif Consensus sequence: DGVBCABTGDWGCGKRRCSR




Reverse complement motif Consensus sequence:
MSGKKRCGCWDCABTGBBCD

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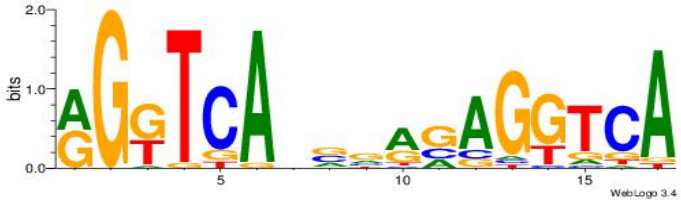
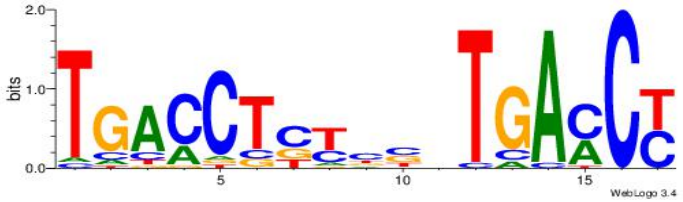
| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 47 |
| Motif name: | RXRRAR_DR5 |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Forward |
| Position number: | 5 |
| Number of overlap: | 13 |
| Similarity score: | 0.578477 |

Alignment:
RGKTCABVVRGAGGTCA-
----CKGGDTBDMMCTGG

Original motif Consensus sequence: RGKTCABVVRGAGGTCA

Reverse complement motif Consensus sequence:
TGACCTCKVVBTGAYCK



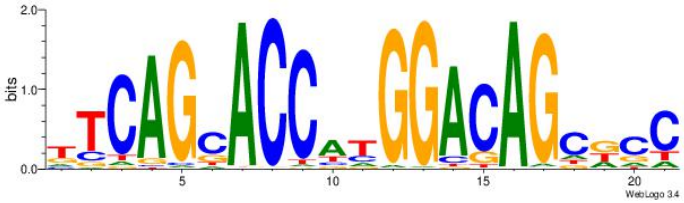




| | |
|---|---|
| Dataset #: | 2 |
| Motif ID: | 19 |
| Motif name: | REST |
| Matching format of first motif: | Reverse Complement |
| Matching format of second motif: | Original Motif |
| Direction: | Backward |
| Position number: | 10 |
| Number of overlap: | 12 |
| Similarity score: | 1.07716 |

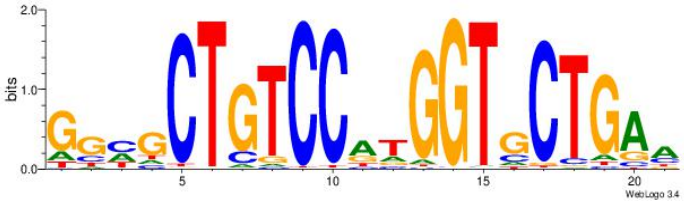
Alignment:

```
--TTCAGCACCATGGACAGCKCC
CKGGDTBDMMCTGG---------
```

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC




Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA



Results created by MOTIFSIM on 09-23-2015 12:30:58
Runtime: 62.6699 seconds.

MOTIFSIM is written by Ngoc Tam L. Tran
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