



MOTIFSIM - MOTIF SIMilarity Detection Tool

Version 2.1

INPUT

Input Parameters

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

Input files and motif counts

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

RESULTS

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

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

Original motif Consensus sequence: GCACTG



Reverse complement motif Consensus sequence: CAGTGC



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

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

Alignment:

```
GGAGCACTGTGACACCACA
-----GCACTG----
```

Alignment:

```
CACTGTGRTRTCACAGTGSWSCACT
-----CAGTGC-----
```

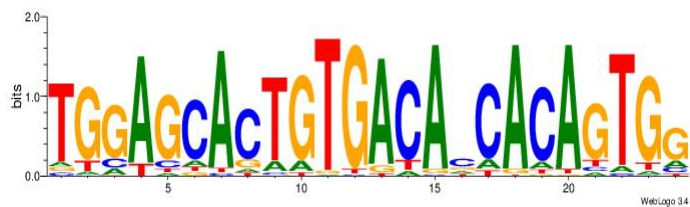
Sequence logo for the 25 bp motif. The y-axis is 'bits' (0.0 to 2.0) and the x-axis is 'West.coop 3.4' (0 to 25). The sequence is approximately AGTGGAGGCACTGTGACACAGTG.

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

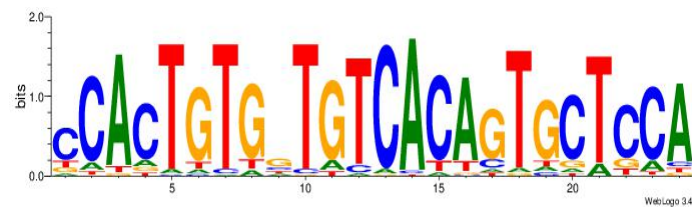
Alignment:

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

Original motif Consensus sequence: TGGAGCACTGTGACAVCACAGTGG



Reverse complement motif Consensus sequence: CCACTGTGVTGTCACAGTGCTCCA

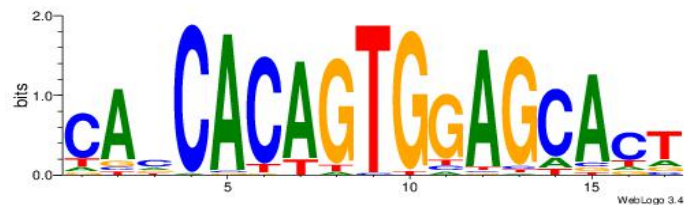


Dataset #: 4
 Motif ID: 76
 Motif name: CACcACAGTGGAGCAct
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 7

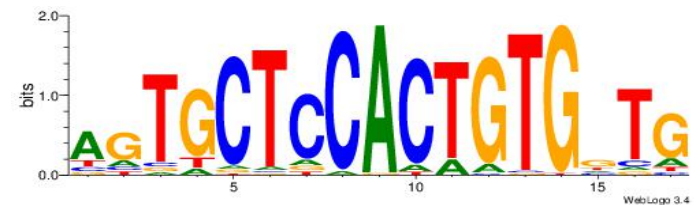
Number of overlap: 6
Similarity score: 0.0201914

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

Original motif Consensus sequence: CAHCACAGTGGAGCACT



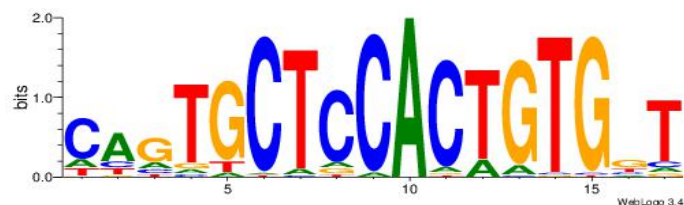
Reverse complement motif Consensus sequence:
AGTGCTCCACTGTGDTG



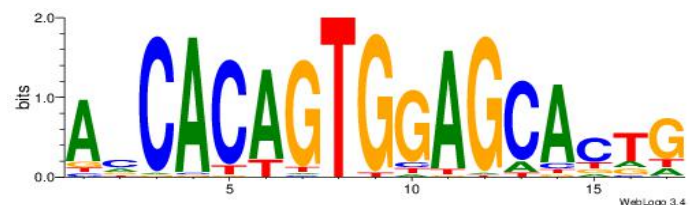
Dataset #: 4
Motif ID: 70
Motif name: CagTGCTCCACTGTGgT
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 8
Number of overlap: 6
Similarity score: 0.0205497

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

Original motif Consensus sequence: CAGTGCTCCACTGTGBT



Reverse complement motif Consensus sequence: ABCACAGTGGAGCACTG

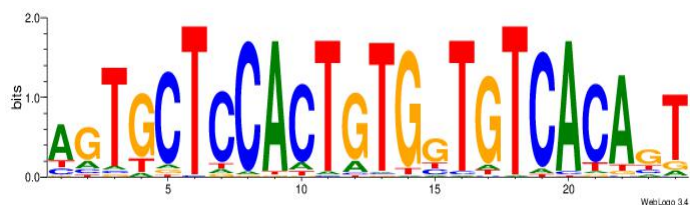


Dataset #: 4
Motif ID: 77
Motif name: AgTGCTCCACTGTGgTGTCACAgT
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 13
Number of overlap: 6
Similarity score: 0.0290883

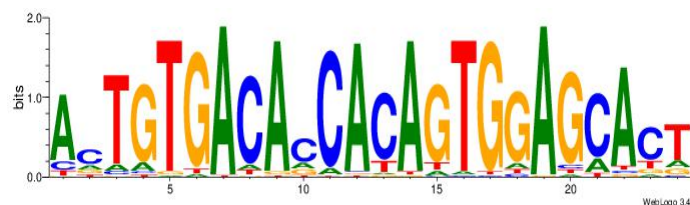
Alignment:

ACTGTGACACCACAGTGGAGCACT
-----CAGTGC-----

Original motif Consensus sequence: AGTGCTCCACTGTGGTGTTCACAGT



Reverse complement motif Consensus sequence: ACTGTGACACCACAGTGGAGCACT

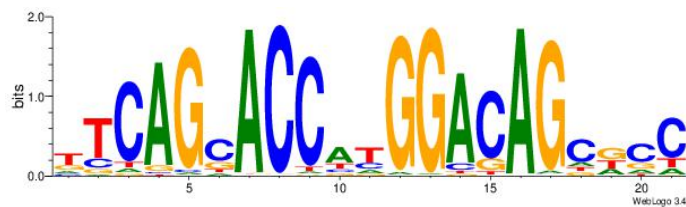


Dataset #: 3
 Motif ID: 57
 Motif name: REST
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 15
 Number of overlap: 6
 Similarity score: 0.039883

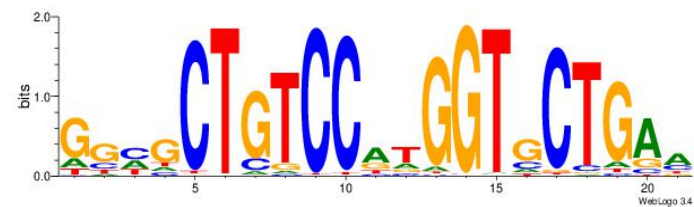
Alignment:

TTCAGCACCATGGACAGCKCC
 -CAGTGC-----

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC



Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA

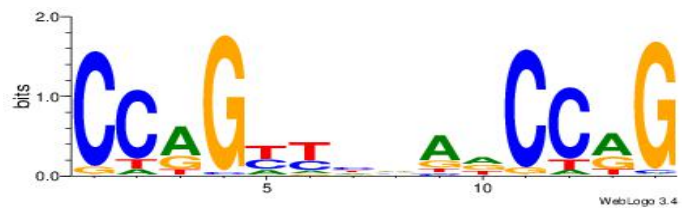


Dataset #: 3
 Motif ID: 65
 Motif name: Tcfcp2l1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 8

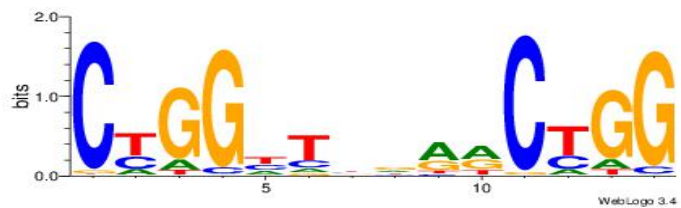
Number of overlap: 6
Similarity score: 0.0447224

Alignment:
CCAGYYHVADCCRG
-----CAGTGC-

Original motif Consensus sequence: CCAGYYHVADCCRG



Reverse complement motif Consensus sequence: CKGGDTBDMMCTV

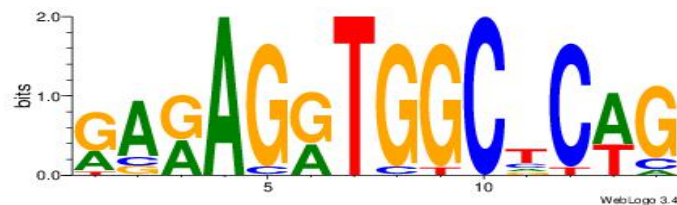


Dataset #: 2
Motif ID: 9
Motif name: Motif 9
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 9
Number of overlap: 6
Similarity score: 0.0459818

Alignment:
GAKAGKTGGCTCWG
GCACTG-----

Original motif Consensus sequence: CWGAGCCAYCTYTC

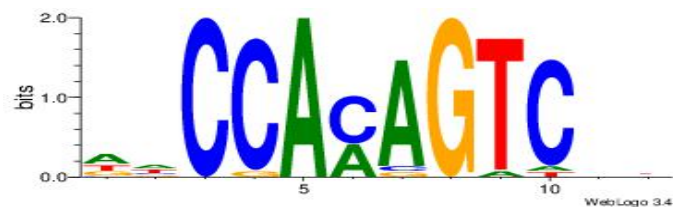
Reverse complement motif Consensus sequence: GAKAGKTGGCTCV



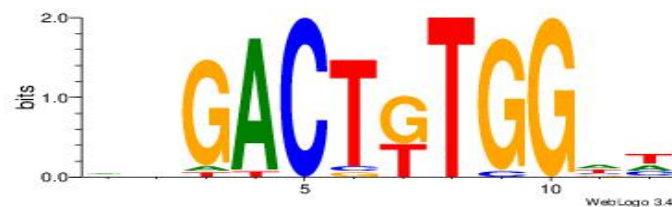
Dataset #: 4
 Motif ID: 75
 Motif name: wwCCAmAGTCmt
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 6
 Number of overlap: 6
 Similarity score: 0.0587933

Alignment:
 VDGACTRTGGDD
 -----GCACTG-

Original motif Consensus sequence: DDCCAMAGTCHB

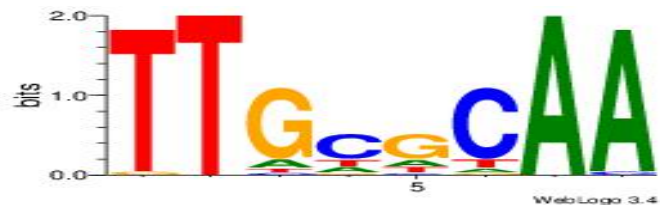


Reverse complement motif Consensus sequence: VDGACTRTGGDD

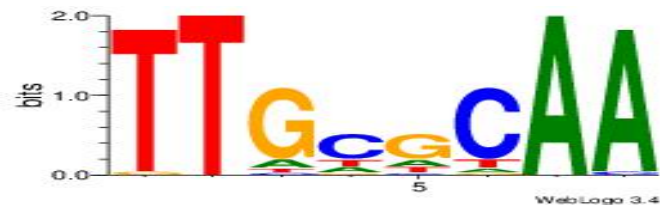


Dataset #: 5 Motif ID: 85 Motif name: TFW1

Original motif Consensus sequence: TTGCGCAA



Reverse complement motif Consensus sequence: TTGCGCAA



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

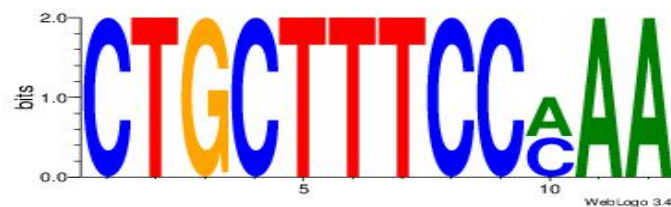
Dataset #:	2
Motif ID:	25
Motif name:	Motif 25
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	8
Similarity score:	0.0195312

Alignment:

TTYGGAAAGCAG

----TTGCGCAA

Original motif Consensus sequence: CTGCTTTCCMAA



Reverse complement motif Consensus sequence: TTYGGAAAGCAG

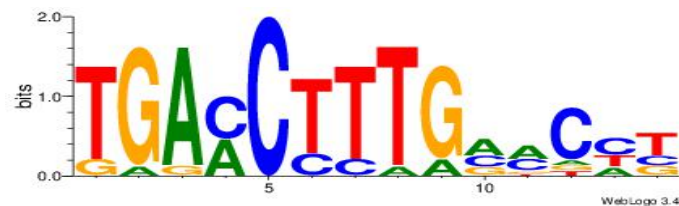


Dataset #: 3
 Motif ID: 52
 Motif name: NR2F1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 8
 Similarity score: 0.0276442

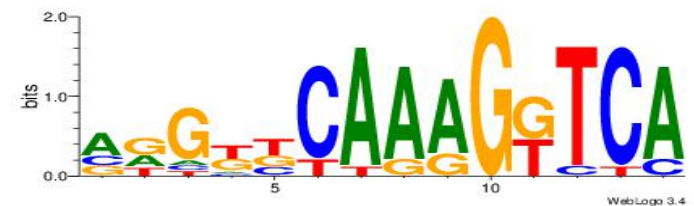
Alignment:

AKGYCAAAGRTCA
 TTGCGCAA-----

Original motif Consensus sequence: TGAMCTTTGMMCYT



Reverse complement motif Consensus sequence: AKGYCAAAGRTCA

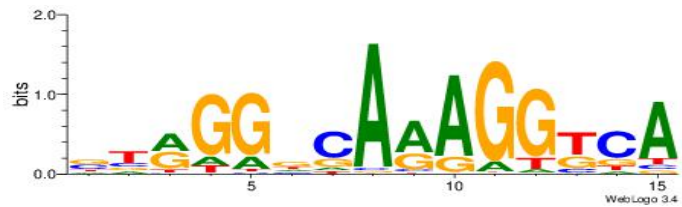


Dataset #: 3
 Motif ID: 64
 Motif name: PPARGRXRA
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 7
 Number of overlap: 8

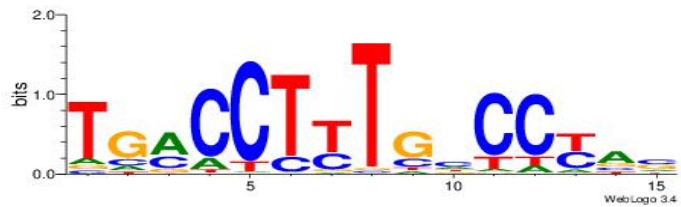
Similarity score: 0.0277567

Alignment:
BTRGGDCARAGGKCA
-----TTGCGCAA-

Original motif Consensus sequence: BTRGGDCARAGGKCA



Reverse complement motif Consensus sequence: TGRCCCTKTGHCCCK



Dataset #: 2
Motif ID: 32
Motif name: Motif 32
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 2
Number of overlap: 8
Similarity score: 0.0328125

Alignment:
TTTACTAAAT
-TTGCGCAA-

Original motif Consensus sequence: ATTAGTAAA

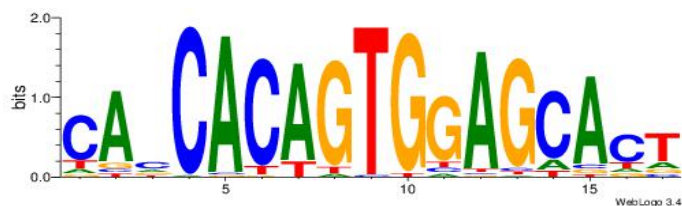
Reverse complement motif Consensus sequence: TTTACTAAAT



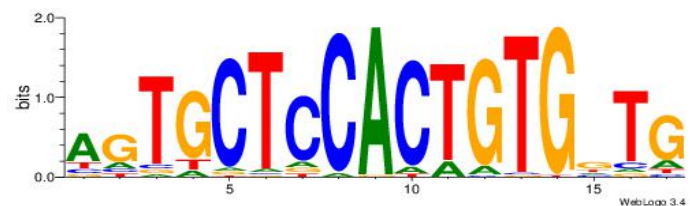
Dataset #: 4
 Motif ID: 76
 Motif name: CACACAGTGGAGCACT
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 8
 Similarity score: 0.0336914

Alignment:
 CAHCACAGTGGAGCACT
 -TTGCGCAA-----

Original motif Consensus sequence: CAHCACAGTGGAGCACT



Reverse complement motif Consensus sequence: AGTGCTCCACTGTGDTG



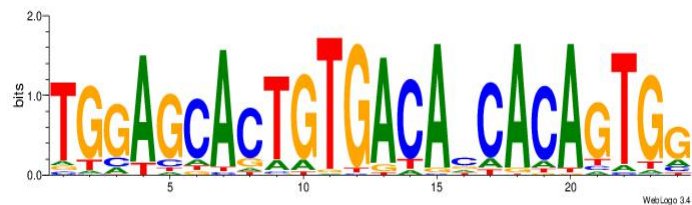
Dataset #: 4

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

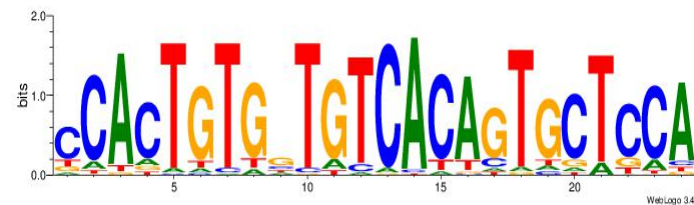
Alignment:

TGGAGCACTGTGACAVCACAGTGG
 TTGCGCAA-----

Original motif Consensus sequence: TGGAGCACTGTGACAVCACAGTGG



Reverse complement motif Consensus sequence: CCACTGTGVTGTACAGTGCTCCA



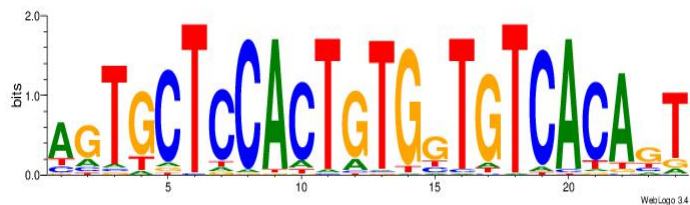
Dataset #: 4
 Motif ID: 77
 Motif name: AgTGCTCCACTGTGgTGTCACAgT
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 8

Similarity score: 0.034375

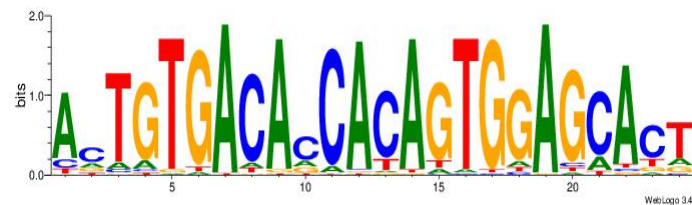
Alignment:

AGTGCTCCACTGTGGTGTACAGT
-----TTGCGCAA-

Original motif Consensus sequence: AGTGCTCCACTGTGGTGTACAGT



Reverse complement motif Consensus sequence:
ACTGTGACACCACAGTGGAGCACT



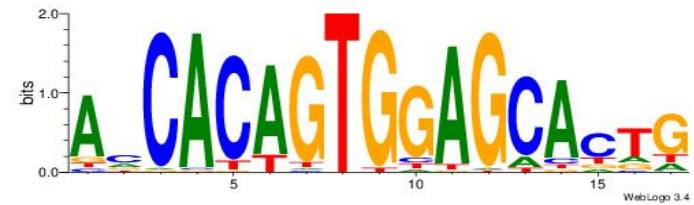
Dataset #: 4
Motif ID: 70
Motif name: CagTGCTCCACTGTGgT
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 3
Number of overlap: 8
Similarity score: 0.0354167

Alignment:

CAGTGCTCCACTGTGBT
-----TTGCGCAA--

Original motif Consensus sequence: CAGTGCTCCACTGTGBT

Reverse complement motif Consensus sequence:
ABCACAGTGGAGCACTG

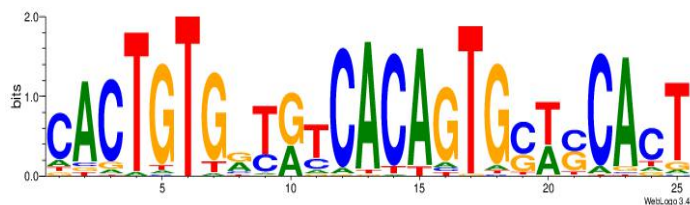


Dataset #:	4
Motif ID:	72
Motif name:	CACTGTGrYrtCACAGTGswsCAcT
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	3
Number of overlap:	8
Similarity score:	0.0407242

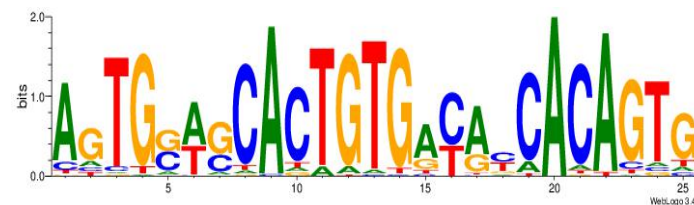
Alignment:

CACTGTGRTRTCACAGTGSWSCACT
-----TTGCGCAA--

Original motif Consensus sequence:
CACTGTGRTRTCACAGTGSWSCACT



Reverse complement motif Consensus sequence:
AGTGSWSCACTGTGAMAMCACAGTG

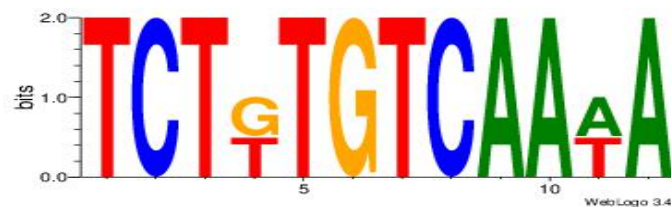


Dataset #: 2

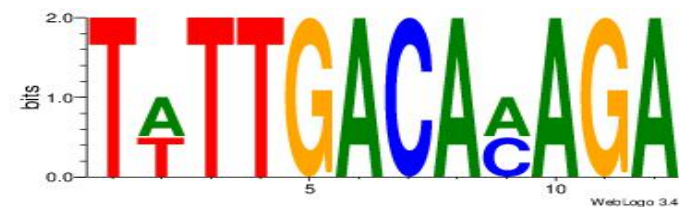
Motif ID: 20
 Motif name: Motif 20
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3
 Number of overlap: 8
 Similarity score: 0.0421875

Alignment:
 TWTTGACAYAGA
 --TTGCGCAA--

Original motif Consensus sequence: TCTKTGTCAAWA



Reverse complement motif Consensus sequence: TWTTGACAYAGA



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

Original motif Consensus sequence: CACCTD



Reverse complement motif Consensus sequence: HAGGTG



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

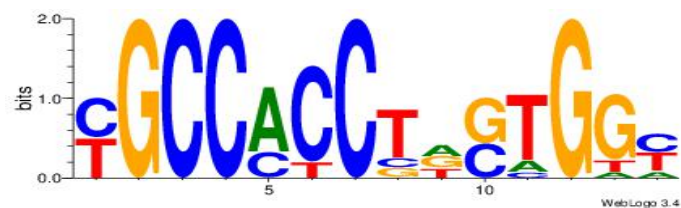
Dataset #: 1
 Motif ID: 1
 Motif name: Motif 1
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 6
 Number of overlap: 6
 Similarity score: 0

Alignment:

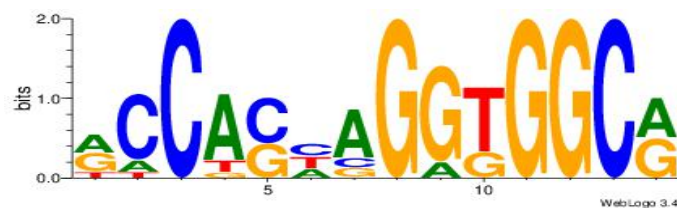
YGCCACCTDSTGGY

---CACCTD-----

Original motif Consensus sequence: YGCCACCTDSTGGY



Reverse complement motif Consensus sequence: KCCASDAGGTGGC



Dataset #: 2
 Motif ID: 9
 Motif name: Motif 9
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif

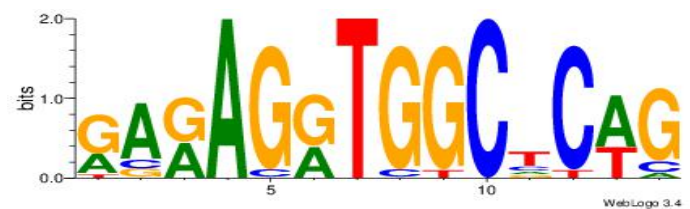
Direction: Backward
 Position number: 3
 Number of overlap: 6
 Similarity score: 0.00902841

Alignment:
 CWGAGCCAYCTYTC
 -----CACCTD--

Original motif Consensus sequence: CWGAGCCAYCTYTC



Reverse complement motif Consensus sequence: GAKAGKTGGCTCV



Dataset #: 2
 Motif ID: 50
 Motif name: Motif 50
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 8
 Number of overlap: 6
 Similarity score: 0.0285279

Alignment:
 TATKCTAAACCTAT
 -CACCTD-----

Original motif Consensus sequence: ATAGGTTTAGYATA



Reverse complement motif Consensus sequence: TATKCTAAACCTAT



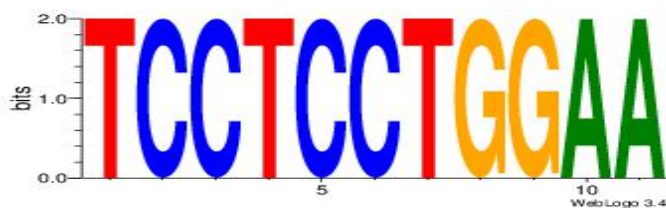
Dataset #: 2
 Motif ID: 24
 Motif name: Motif 24
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 4
 Number of overlap: 6
 Similarity score: 0.0346255

Alignment:

TTCCAGGAGGA

---HAGGTG---

Original motif Consensus sequence: TCCTCCTGGAA



Reverse complement motif Consensus sequence: TTCCAGGAGGA



Dataset #: 2
 Motif ID: 16
 Motif name: Motif 16
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 5
 Number of overlap: 6
 Similarity score: 0.0376742

Alignment:

ACAACACATTT
 ----CACCTD-

Original motif Consensus sequence: ACAACACATTT



Reverse complement motif Consensus sequence: AAATGTGTTGT



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

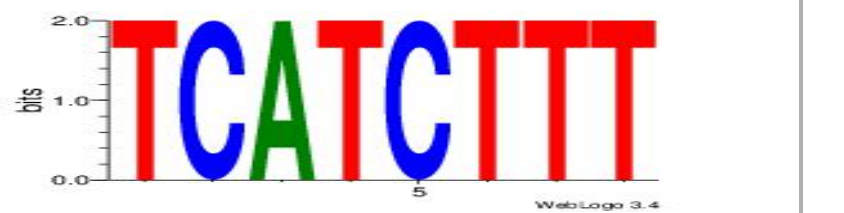
Similarity score: 0.0397068

Alignment:
AAAGATGA
-HAGGTG-

Original motif Consensus sequence: AAAGATGA



Reverse complement motif Consensus sequence: TCATCTTT



Dataset #: 2
Motif ID: 26
Motif name: Motif 26
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: 0.0397068

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

Original motif Consensus sequence: TTTATGGTGAGCAT

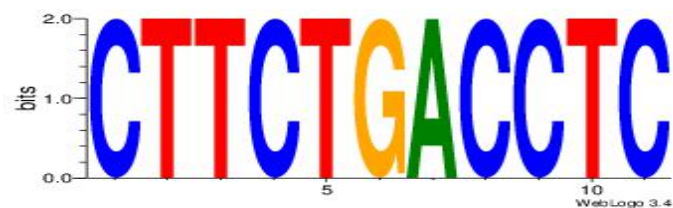
Reverse complement motif Consensus sequence: ATGCTCACCATAA



Dataset #: 2
 Motif ID: 21
 Motif name: Motif 21
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 6
 Number of overlap: 6
 Similarity score: 0.0458043

Alignment:
 CTTCTGACCTC
 -----CACCTD

Original motif Consensus sequence: CTTCTGACCTC



Reverse complement motif Consensus sequence: GAGGTCAGAAG



Dataset #: 5
 Motif ID: 92

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

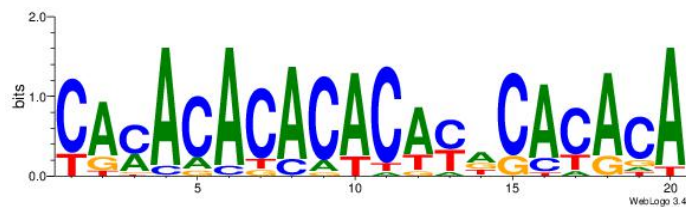
Alignment:

```

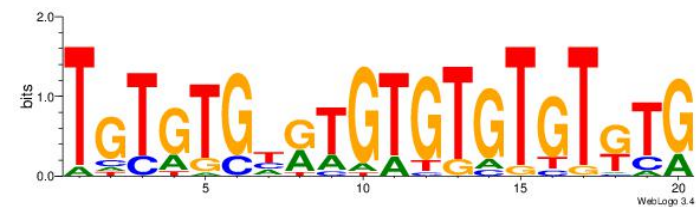
CAMACACACACAYDCACACA
-----CACCTD-----

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Original motif Consensus sequence: CAMACACACACAYDCACACA



Reverse complement motif Consensus sequence: TGTGTGDKTGTGTGTGTRTG



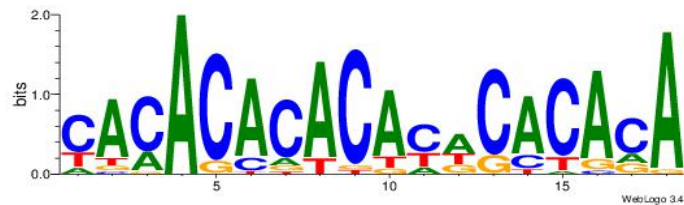
Dataset #:	5
Motif ID:	89
Motif name:	TFM1
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	7
Number of overlap:	6
Similarity score:	0.0467843

Alignment:

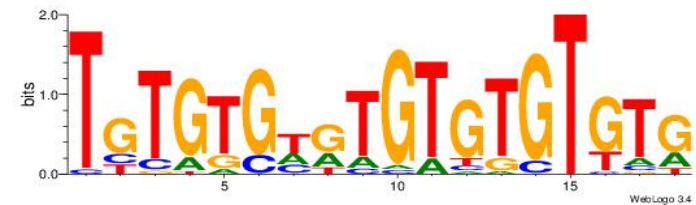
CACACACACACWCACACA

-----CACCTD-----

Original motif Consensus sequence: CACACACACACWCACACA

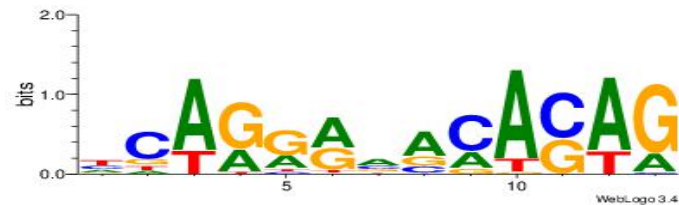


Reverse complement motif Consensus sequence: TGTGTGWGTGTGTGTGTG

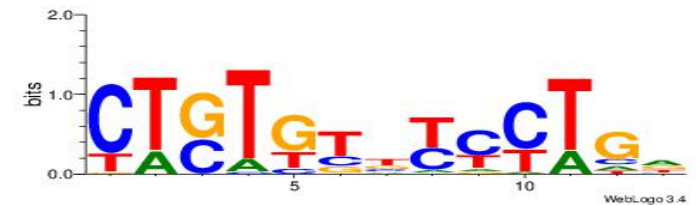


Dataset #: 2 Motif ID: 7 Motif name: Motif 7

Original motif Consensus sequence: HCAGRRVACASAG



Reverse complement motif Consensus sequence: CTSTGTBKMCTGHH



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

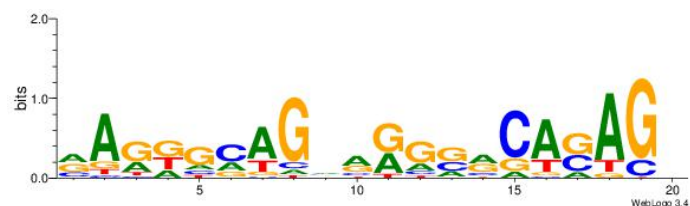
Dataset #:	5
Motif ID:	93
Motif name:	TFM12
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward

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

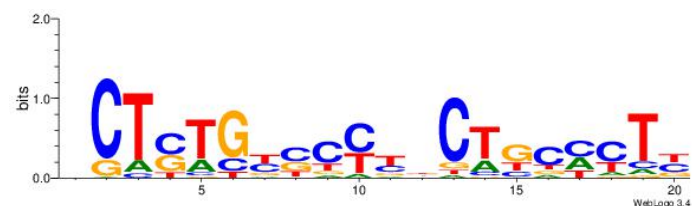
Alignment:

RAGKGMAGVRRGSRCASAGV
 -----HCAGRRVACASAG--

Original motif Consensus sequence: RAGKGMAGVRRGSRCASAGV



Reverse complement motif Consensus sequence:
 VCTSTGKSCMKBCTRCYCTK

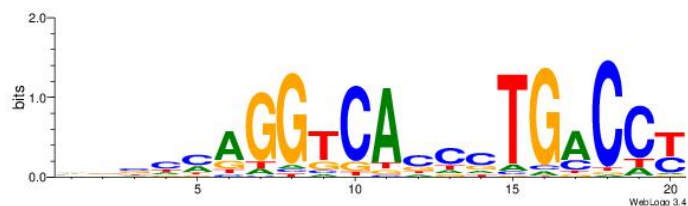


Dataset #: 3
 Motif ID: 53
 Motif name: ESR1
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 13
 Similarity score: 0.0328703

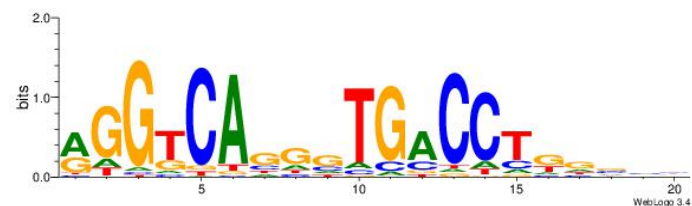
Alignment:

VDBHMAGGTCACCCTGACCY
 ---HCAGRRVACASAG----

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV

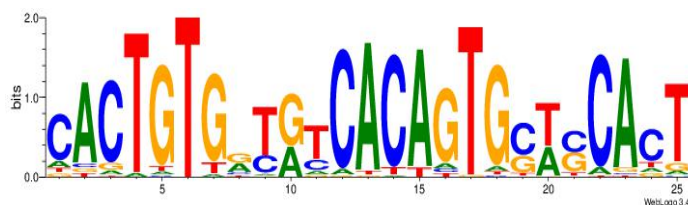


Dataset #: 4
Motif ID: 72
Motif name: CACTGTGrYrtCACAGTGswsCAcT
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 3
Number of overlap: 13
Similarity score: 0.0400966

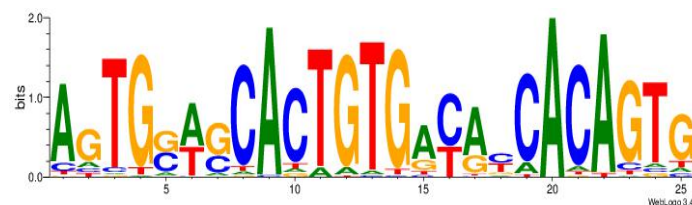
Alignment:

AGTGSWSCACTGTGAMAMCACAGTG
-----HCAGRRVACASAG--

Original motif Consensus sequence:
CACTGTGRTRTCACAGTGSWSCACT



Reverse complement motif Consensus sequence:
AGTGSWSCACTGTGAMAMCACAGTG

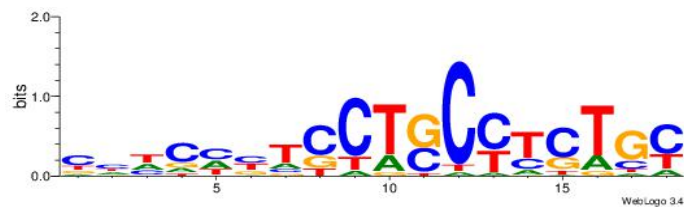


Dataset #: 5
 Motif ID: 90
 Motif name: TFM2
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3
 Number of overlap: 13
 Similarity score: 0.0435274

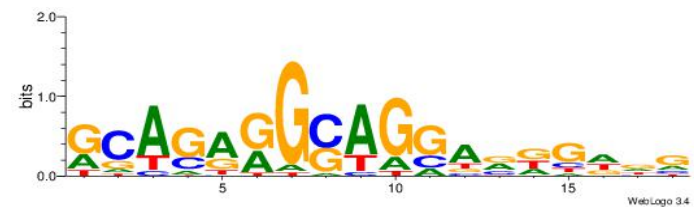
Alignment:

GCAGAKGSAGGABDGHG
 --HCAGRRVACASAG---

Original motif Consensus sequence: CHHCHBTCCTSCYTCTGC



Reverse complement motif Consensus sequence: GCAGAKGSAGGABDGHG



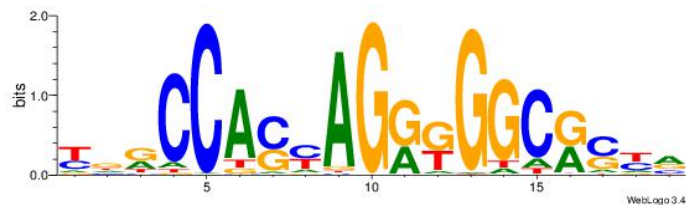
Dataset #: 3
 Motif ID: 66
 Motif name: CTCF
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 7

Number of overlap: 13
Similarity score: 0.0448341

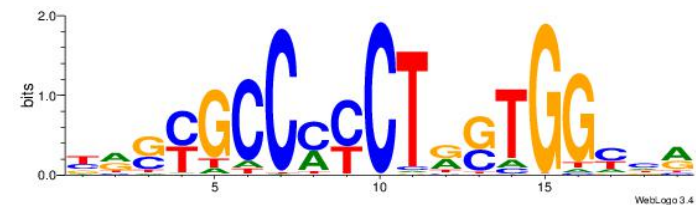
Alignment:

YDRCCASYAGRKGGRSYV
-----HCAGRRVACASAG

Original motif Consensus sequence: YDRCCASYAGRKGGRSYV



Reverse complement motif Consensus sequence:
BMSMGCCYMCTKSTGGMHM

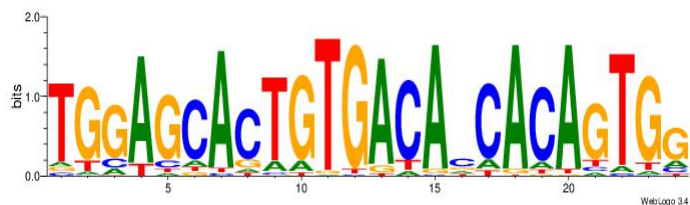


Dataset #: 4
Motif ID: 73
Motif name: TGGAGCACTGTGACAcCACAGTGg
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 4
Number of overlap: 13
Similarity score: 0.045698

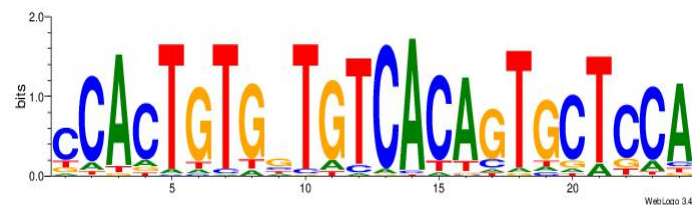
Alignment:

CCACTGTGVTGTCACAGTGCTCCA
---CTSTGTBKMCTGH-----

Original motif Consensus sequence: TGGAGCACTGTGACAVCACAGTGG



Reverse complement motif Consensus sequence: CCACTGTGVTGTCACAGTGCTCCA

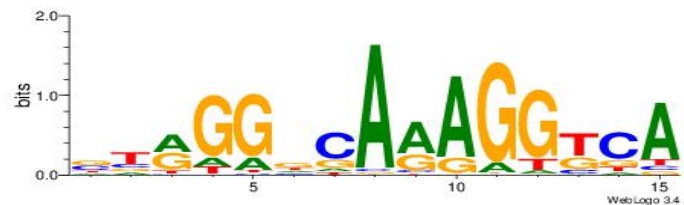


Dataset #: 3
 Motif ID: 64
 Motif name: PPARGRXRA
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 13
 Similarity score: 0.0457253

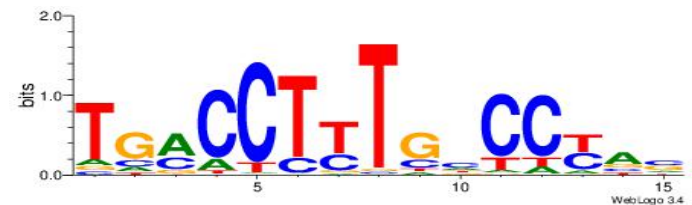
Alignment:

BTRGGDCARAGGKCA
 HCAGRRVACASAG--

Original motif Consensus sequence: BTRGGDCARAGGKCA



Reverse complement motif Consensus sequence: TGRCCCTKTGHCCK

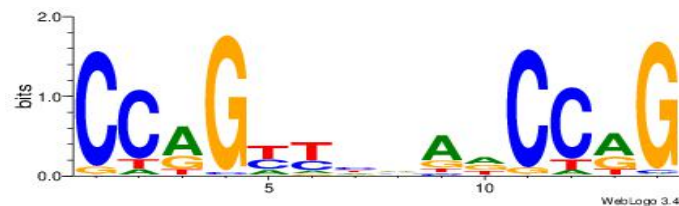


Dataset #: 3
 Motif ID: 65
 Motif name: Tcfcp2l1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 13
 Similarity score: 0.0477557

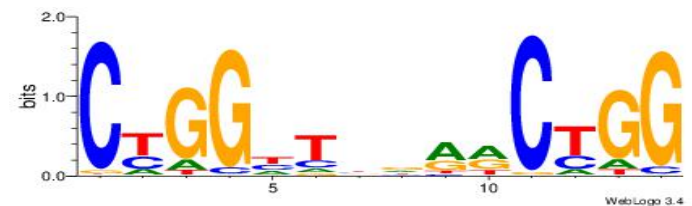
Alignment:

CKGGDTBDMMCTGG
 CTSTGTBKMCTGH-

Original motif Consensus sequence: CCAGYYHVADCCRG



Reverse complement motif Consensus sequence: CKGGDTBDMMCTGG

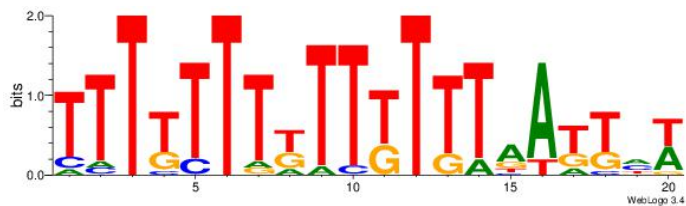


Dataset #: 5
 Motif ID: 94
 Motif name: TFM13
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 4
 Number of overlap: 13

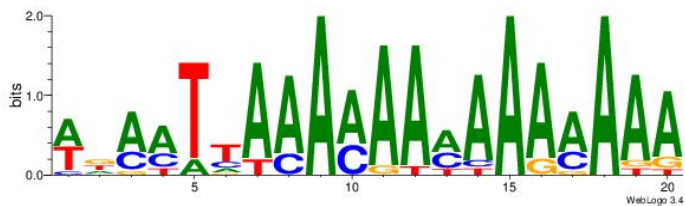
Similarity score: 0.0478998

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

Original motif Consensus sequence: TTTTTTKTTKTTTAATTHW



Reverse complement motif Consensus sequence: WHAATTAAARAARAAAAAAA

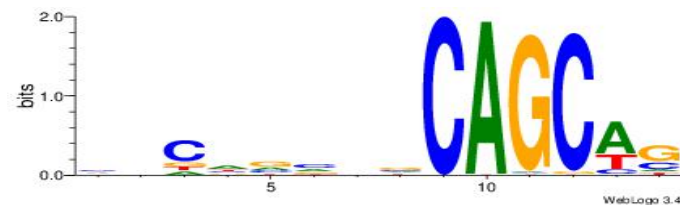
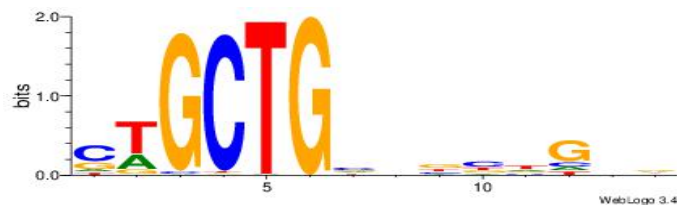


Dataset #: 5
Motif ID: 88
Motif name: TFF11
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 2
Number of overlap: 13
Similarity score: 0.048132

Alignment:
HVCDBBDBCAGCAG
-HCAGRRVACASAG

Original motif Consensus sequence: CTGCTGBDBBDGBD

Reverse complement motif Consensus sequence: HVCDBBDBCAGCA

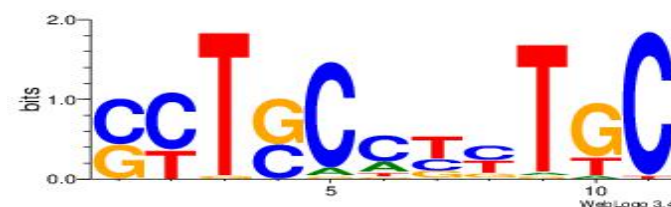


Dataset #: 1 Motif ID: 2 Motif name: Motif 2

Original motif Consensus sequence: GCARRGGSAGS



Reverse complement motif Consensus sequence: SCTSCCKMTGC

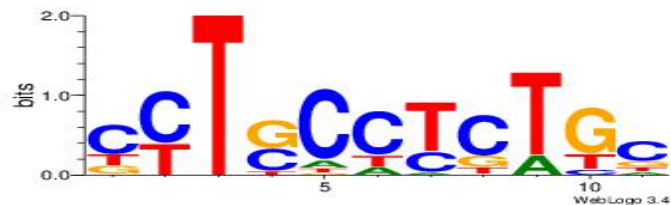


Best Matches for Top Significant Motif ID 2 (Highest to Lowest)

Dataset #:	2
Motif ID:	5
Motif name:	Motif 5
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	11
Similarity score:	0

Alignment:
CYTSCCTCTGC
SCTSCCKMTGC

Original motif Consensus sequence: CYTSCCTCTGC



Reverse complement motif Consensus sequence: GCAGAGGSAKG

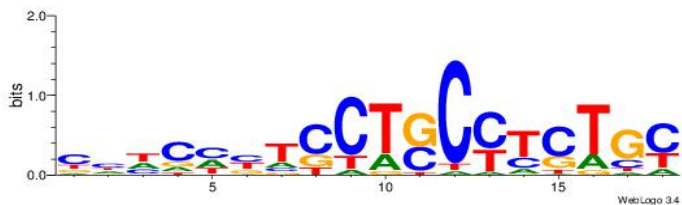


Dataset #: 5
 Motif ID: 90
 Motif name: TFM2
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.000952693

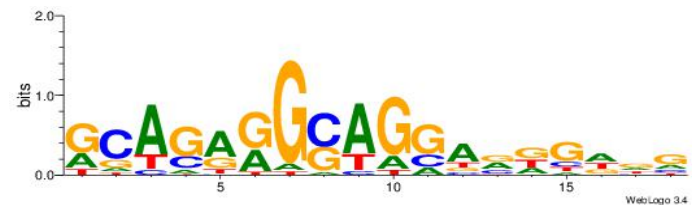
Alignment:

GCAGAKGSAGGABDGHG
 GCARRGGSAGS-----

Original motif Consensus sequence: CHHCHBTCCTSCYTCTGC



Reverse complement motif Consensus sequence: GCAGAKGSAGGABDGHG

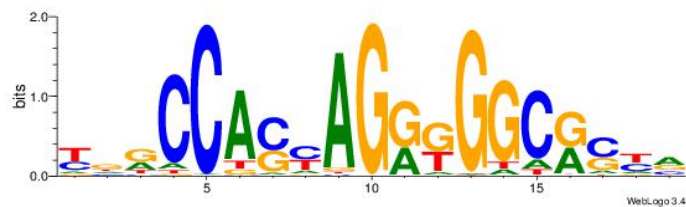


Dataset #: 3
 Motif ID: 66
 Motif name: CTCF
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 11
 Similarity score: 0.033658

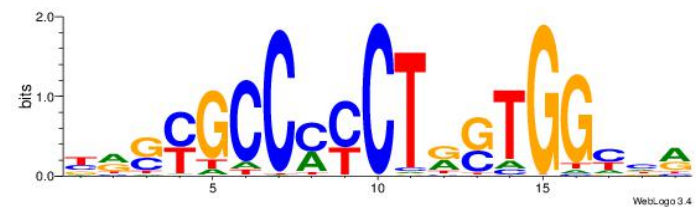
Alignment:

YDRCCASYAGRKGGRSYV
 -----GCARRGGSAGS--

Original motif Consensus sequence: YDRCCASYAGRKGGRSYV



Reverse complement motif Consensus sequence: BMSMGCCYMCTKSTGGMHM

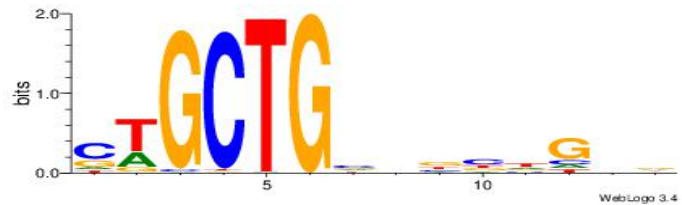


Dataset #: 5
 Motif ID: 88
 Motif name: TFF11
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3

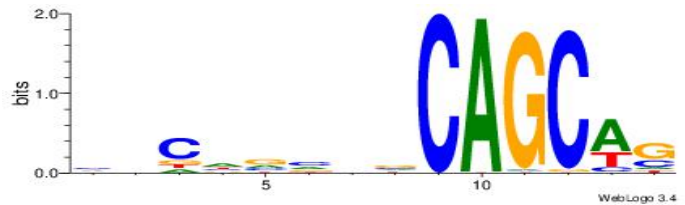
Number of overlap: 11
Similarity score: 0.0410341

Alignment:
CTGCTGBDBBDGBD
--SCTSCCKMTGC--

Original motif Consensus sequence: CTGCTGBDBBDGBD



Reverse complement motif Consensus sequence: HVCDBBDBCAGCA

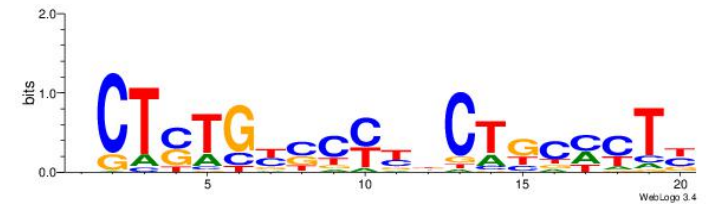


Dataset #: 5
Motif ID: 93
Motif name: TFM12
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 6
Number of overlap: 11
Similarity score: 0.0422459

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

Original motif Consensus sequence: RAGKGMAGVRRGSRCASAGV

Reverse complement motif Consensus sequence:
VCTSTGKSCMKBCTRCYCTK



Alignment:

```
CCAGYYHVADCCRG
SCTSCCKMTGC---
```

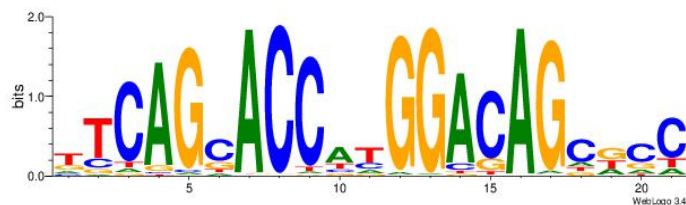
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Motif name:	REST
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	4
Number of overlap:	11
Similarity score:	0.0578944

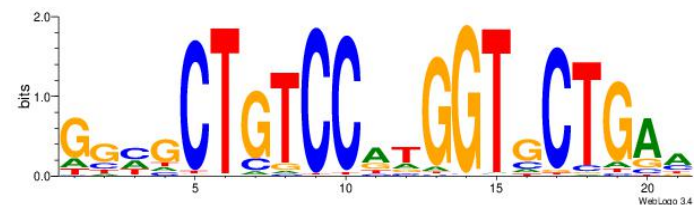
Alignment:

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

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC



Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA

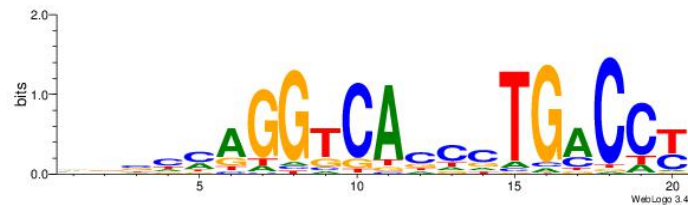


Dataset #:	3
Motif ID:	53
Motif name:	ESR1
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	3
Number of overlap:	11
Similarity score:	0.0620615

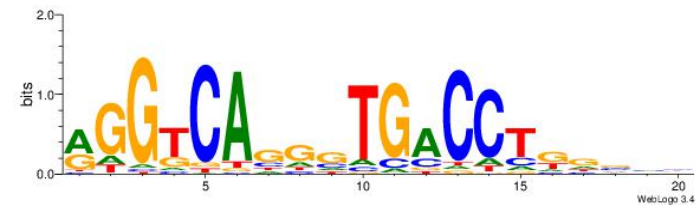
Alignment:

VDBHMAGGTCACCCTGACCY
--GCARRGGSAGS-----

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif Consensus sequence:
MGGTCAGGGTGACCTRDBHV



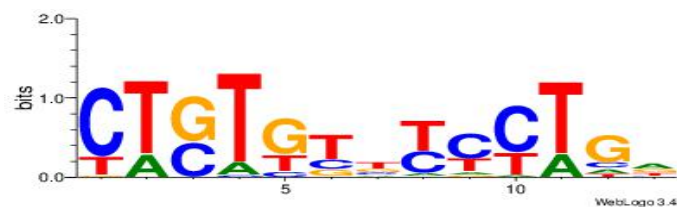
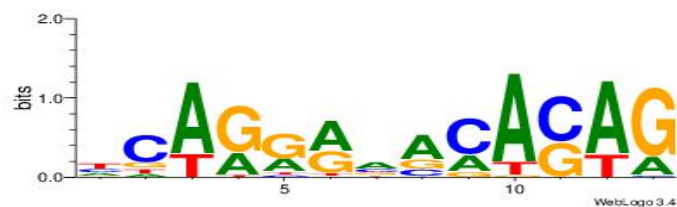
Dataset #:	2
Motif ID:	7
Motif name:	Motif 7
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	11
Similarity score:	0.0627554

Alignment:

HCAGRRVACASAG
GCARRGGSAGS--

Original motif Consensus sequence: HCAGRRVACASAG

Reverse complement motif Consensus sequence: CTSTGTBKMCTGHH

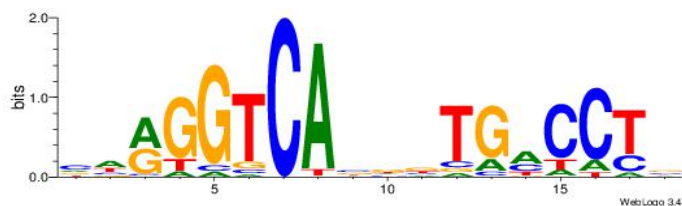


Dataset #: 3
 Motif ID: 59
 Motif name: ESR2
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 5
 Number of overlap: 11
 Similarity score: 0.0646979

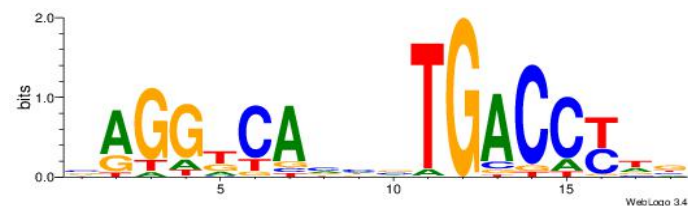
Alignment:

VHRGGTCABDBTGMCTB
 ---SCTSCCKMTGC----

Original motif Consensus sequence: VHRGGTCABDBTGMCTB

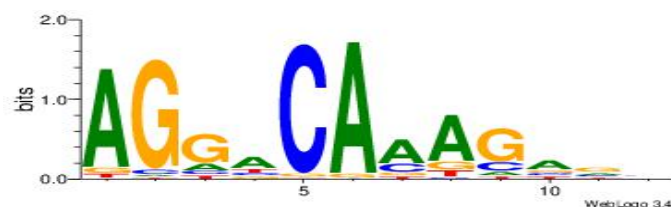


Reverse complement motif Consensus sequence: BAGGYCABHBTGACCKHV

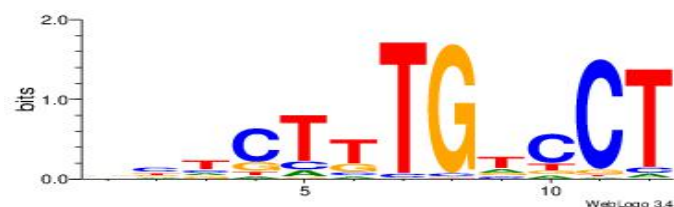


Dataset #: 5 Motif ID: 87 Motif name: TFF1

Original motif Consensus sequence: AGGACAAAGAVV



Reverse complement motif Consensus sequence: VVTCTTTGTCCT



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

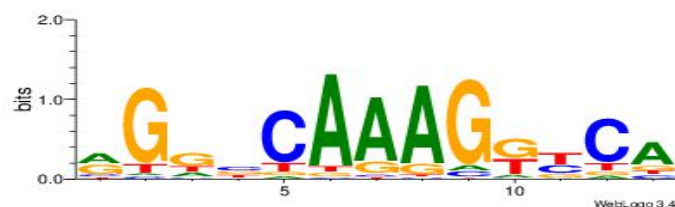
Dataset #:	3
Motif ID:	51
Motif name:	HNF4A
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	2
Number of overlap:	12
Similarity score:	0.0111472

Alignment:

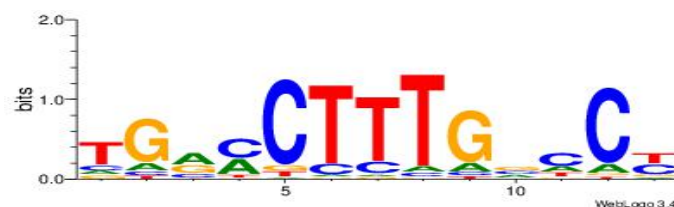
TGMYCTTTGBCCK

-VVTCTTTGTCCT

Original motif Consensus sequence: RGGBCAAAGKYCA



Reverse complement motif Consensus sequence: TGMYCTTTGBCCK

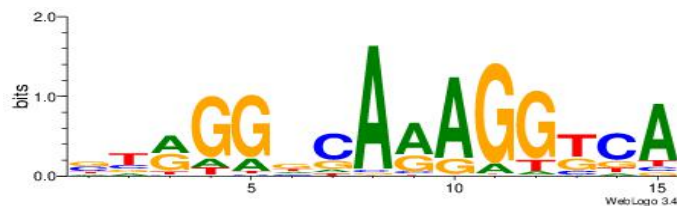


Dataset #: 3
 Motif ID: 64
 Motif name: PPARGRXRA
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 12
 Similarity score: 0.0210867

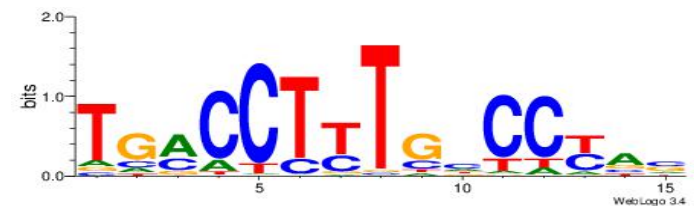
Alignment:

BTRGGDCARAGGKCA
 --AGGACAAAGAVV--

Original motif Consensus sequence: BTRGGDCARAGGKCA



Reverse complement motif Consensus sequence: TGRCCCTKTGHCCCK



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

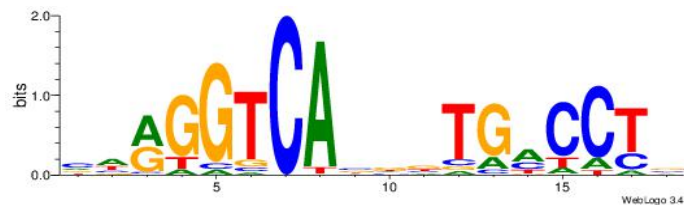
Similarity score: 0.0351633

Alignment:

BAGGYCABHBTGACCKHV

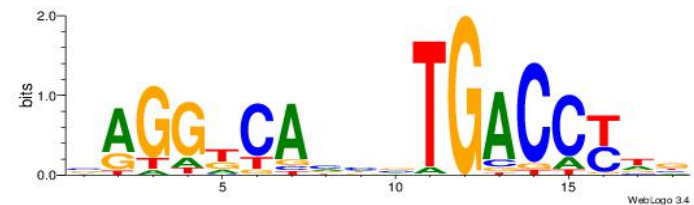
----VVTCTTTGTCCT--

Original motif Consensus sequence: VHRGGTCABDBTGMCTB



Reverse complement motif
BAGGYCABHBTGACCKHV

Consensus sequence:



Dataset #: 3
Motif ID: 53
Motif name: ESR1
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 9
Number of overlap: 12
Similarity score: 0.039773

Alignment:

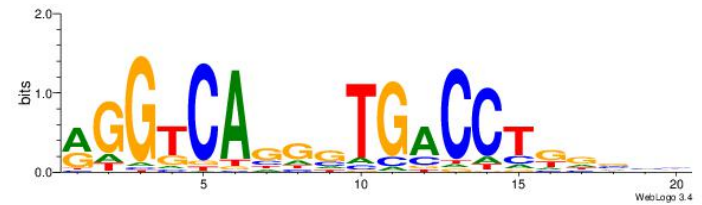
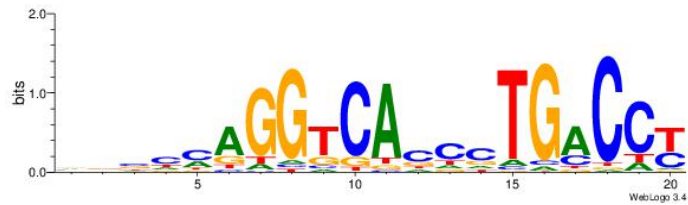
VDBHMAGGTCACCCTGACCY

VVTCTTTGTCCT-----

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY

Reverse complement motif
MGGTCAGGGTGACCTRDBHV

Consensus sequence:



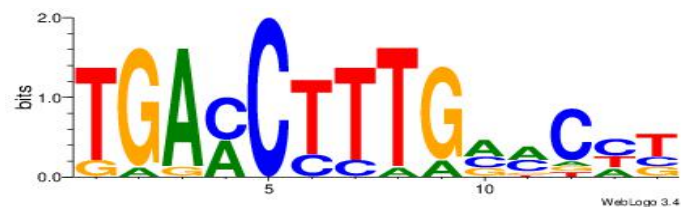
Dataset #: 3
 Motif ID: 52
 Motif name: NR2F1
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 12
 Similarity score: 0.0472374

Alignment:

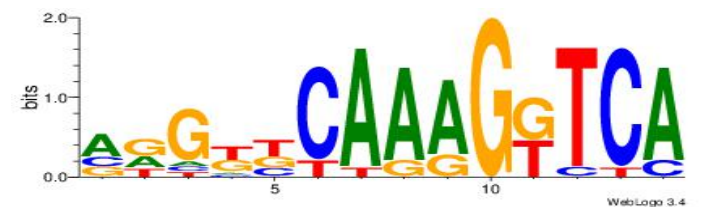
AKGYCAAAGRTCA

-AGGACAAAGAVV-

Original motif Consensus sequence: TGAMCTTTGMMCYT



Reverse complement motif Consensus sequence: AKGYCAAAGRTCA



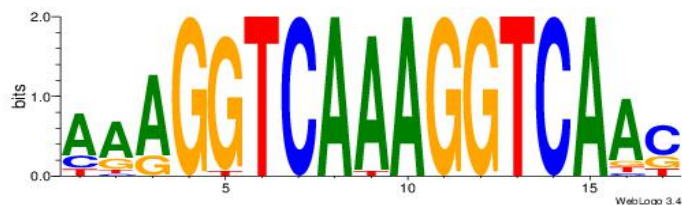
Dataset #: 3
 Motif ID: 60

Motif name: NR1H2RXRA
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 12
 Similarity score: 0.0472884

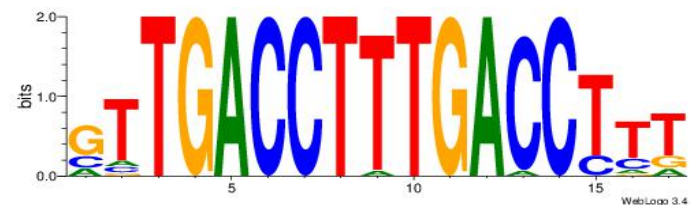
Alignment:

GTTGACCTTTGACCTTT
 ---VVTCTTTGTCCT--

Original motif Consensus sequence: AAAGGTCAAAGGTCAAC



Reverse complement motif Consensus sequence: GTTGACCTTTGACCTTT

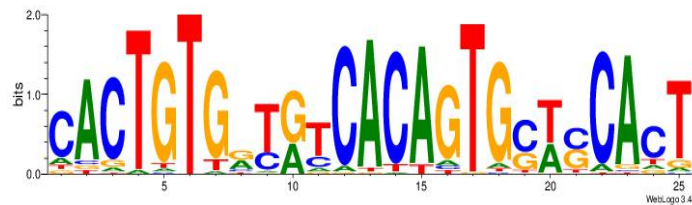


Dataset #: 4
 Motif ID: 72
 Motif name: CACTGTGrYrtCACAGTGswsCAcT
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 7
 Number of overlap: 12
 Similarity score: 0.0530556

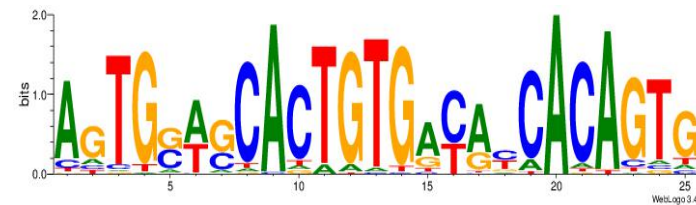
Alignment:

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

Original motif Consensus sequence:
CACTGTGRTRTCACAGTGSWSCACT



Reverse complement motif Consensus sequence:
AGTGSWSCACTGTGAMAMCACAGTG

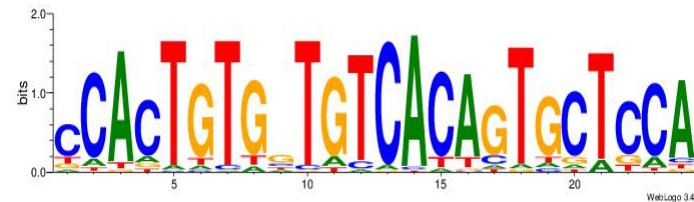
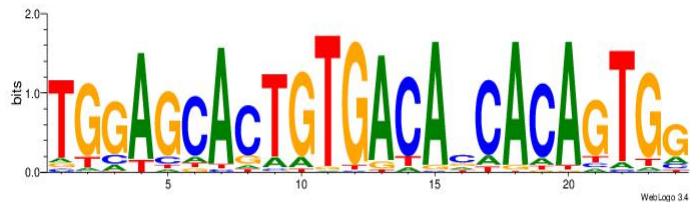


Dataset #:	4
Motif ID:	73
Motif name:	TGGAGCACTGTGACAcCACAGTGg
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	13
Number of overlap:	12
Similarity score:	0.0539204

Alignment:

TGGAGCACTGTGACAVCACAGTGG
-----AGGACAAAGAVV

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

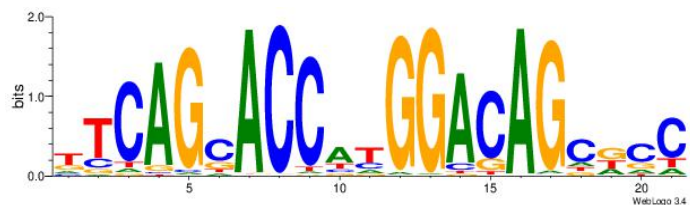


Dataset #: 3
 Motif ID: 57
 Motif name: REST
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 7
 Number of overlap: 12
 Similarity score: 0.0558379

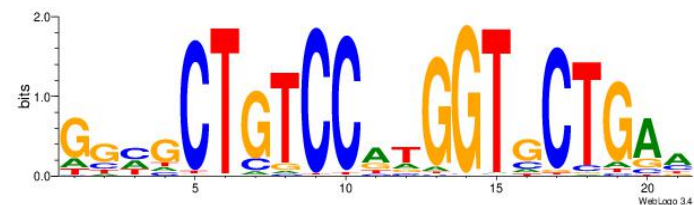
Alignment:

TTCAGCACCATGGACAGCKCC
 ---AGGACAAAGAVV-----

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC



Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA



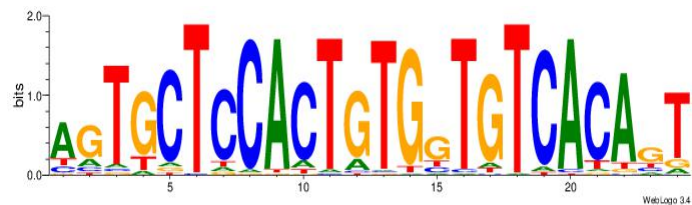
Dataset #: 4

Motif ID: 77
 Motif name: AgTGCTCCACTGTGgTGTCACAgT
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 7
 Number of overlap: 12
 Similarity score: 0.0609269

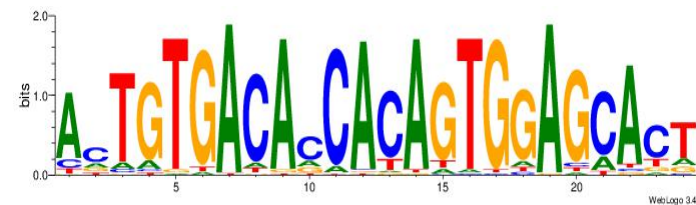
Alignment:

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

Original motif Consensus sequence: AGTGCTCCACTGTGGTGTTCACAGT



Reverse complement motif Consensus sequence: ACTGTGACACCACAGTGGAGCACT



Dataset #: 2 Motif ID: 41 Motif name: Motif 41

Original motif Consensus sequence: ACTTTGG



Reverse complement motif Consensus sequence: CCAAAGT



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

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

Alignment:

GCCAAAGTAT

-CCAAAGT--

Original motif Consensus sequence: ATACTTTGGC



Reverse complement motif Consensus sequence: GCCAAAGTAT



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

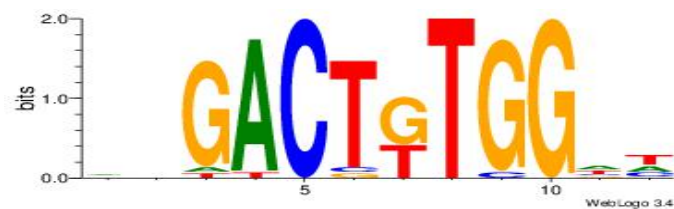
Direction: Backward
 Position number: 4
 Number of overlap: 7
 Similarity score: 0.0275974

Alignment:
 DDCCAMAGTCHB
 --CCAAAGT---

Original motif Consensus sequence: DDCCAMAGTCHB



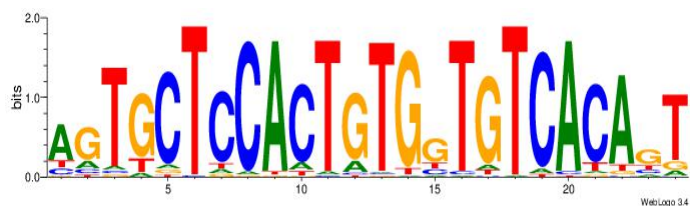
Reverse complement motif Consensus sequence: VDGACTRTGGDD



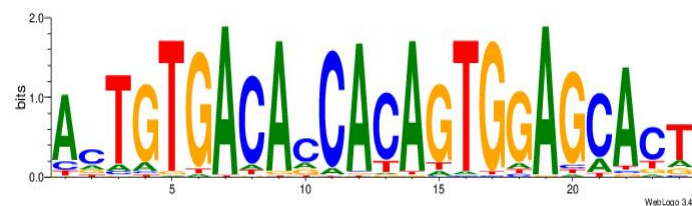
Dataset #: 4
 Motif ID: 77
 Motif name: AgTGCTCCACTGTGgTGTCACAgT
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 10
 Number of overlap: 7
 Similarity score: 0.056841

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

Original motif Consensus sequence: AGTGCTCCACTGTGGTGTACAGT



Reverse complement motif Consensus sequence: ACTGTGACACCACAGTGGAGCACT



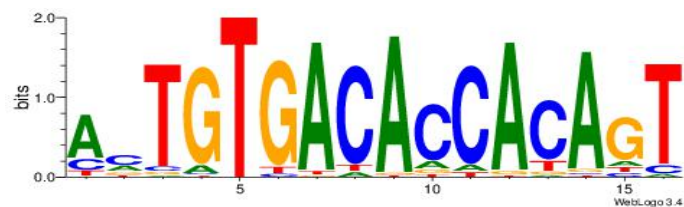
Dataset #: 4
Motif ID: 71
Motif name: AmTGTGACACCACAGT
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 7
Similarity score: 0.0597098

Alignment:

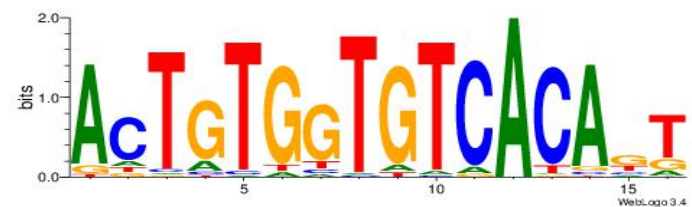
ACTGTGGTGTACART

ACTTTGG-----

Original motif Consensus sequence: AMTGTGACACCACAGT



Reverse complement motif Consensus sequence: ACTGTGGTGTACART

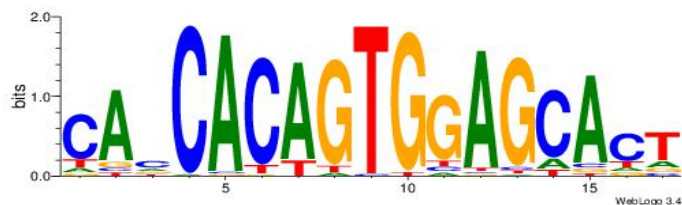


Dataset #: 4
 Motif ID: 76
 Motif name: CACACAGTGGAGCAct
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 7
 Similarity score: 0.061942

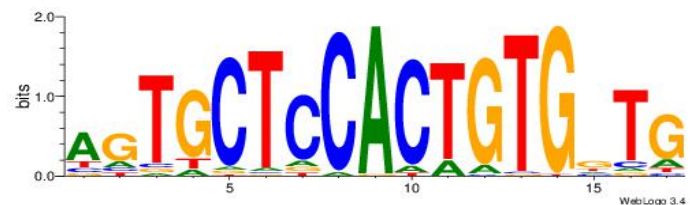
Alignment:

AGTGCTCCACTGTGDTG
 -----ACTTTGG--

Original motif Consensus sequence: CAHCACAGTGGAGCACT



Reverse complement motif Consensus sequence: AGTGCTCCACTGTGDTG

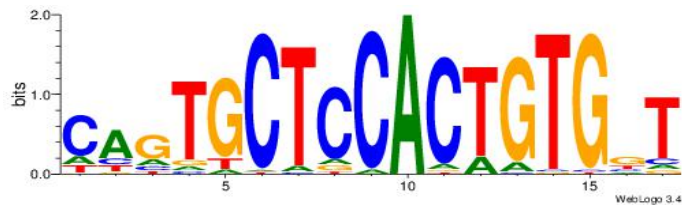


Dataset #: 4
 Motif ID: 70
 Motif name: CagTGCTCCACTGTGgT
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2

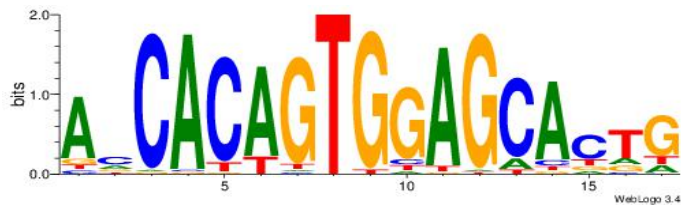
Number of overlap: 7
Similarity score: 0.0625

Alignment:
ABCACAGTGGAGCACTG
-CCAAAGT-----

Original motif Consensus sequence: CAGTGCTCCACTGTGBT



Reverse complement motif Consensus sequence:
ABCACAGTGGAGCACTG

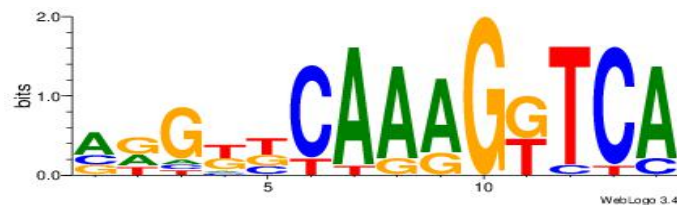


Dataset #: 3
Motif ID: 52
Motif name: NR2F1
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 4
Number of overlap: 7
Similarity score: 0.0686813

Alignment:
TGAMCTTTGMMCYT
---ACTTTGG----

Original motif Consensus sequence: TGAMCTTTGMMCYT

Reverse complement motif Consensus sequence: AKGYCAAAGRTC

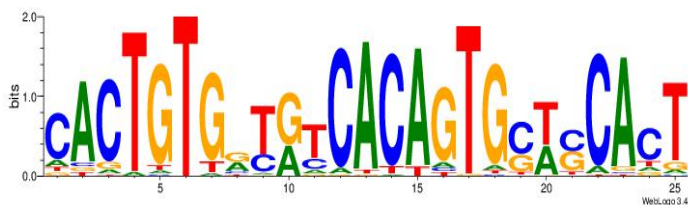


Dataset #: 4
 Motif ID: 72
 Motif name: CACTGTGrYrtCACAGTGswsCACT
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 7
 Similarity score: 0.0714286

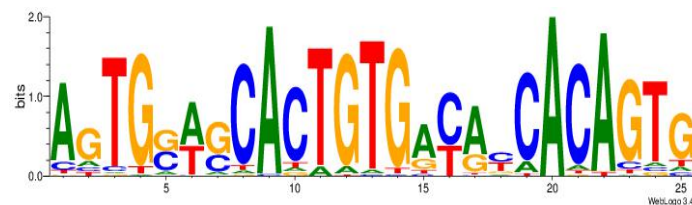
Alignment:

CACTGTGRTRTCACAGTGSWSCACT
 -ACTTTGG-----

Original motif Consensus sequence:
 CACTGTGRTRTCACAGTGSWSCACT



Reverse complement motif Consensus sequence:
 AGTGSWSCACTGTGAMAMCACAGTG

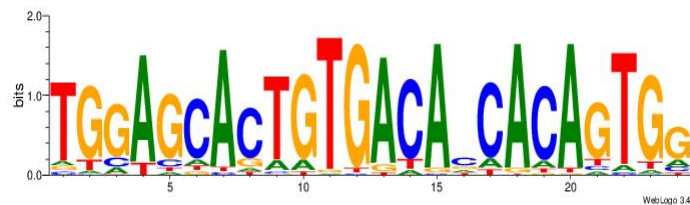


Dataset #: 4

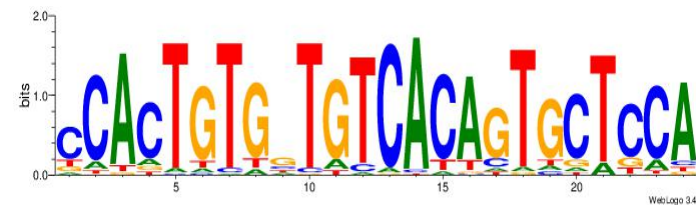
Motif ID: 73
 Motif name: TGGAGCACTGTGACAcCACAGTGg
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 7
 Similarity score: 0.0714286

Alignment:
 TGGAGCACTGTGACAVCACAGTGG
 -----CCAAAGT--

Original motif Consensus sequence: TGGAGCACTGTGACAVCACAGTGG



Reverse complement motif Consensus sequence: CCACTGTGVTGTACAGTGCTCCA



Dataset #: 3
 Motif ID: 60
 Motif name: NR1H2RXRA
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 6
 Number of overlap: 7

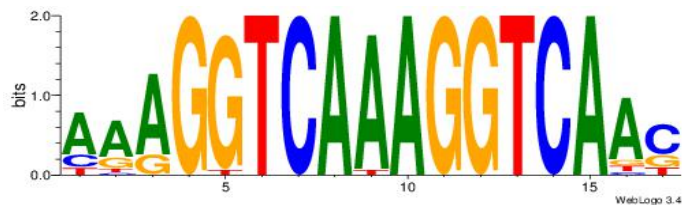
Similarity score: 0.0728571

Alignment:

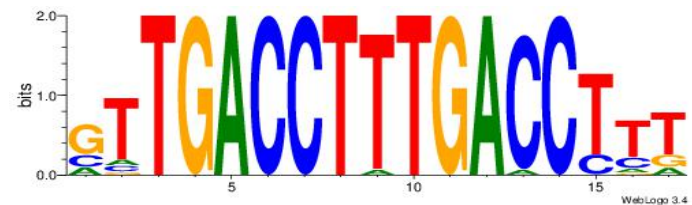
GTGACCTTTGACCTTT

-----ACTTTGG-----

Original motif Consensus sequence: AAAGGTCAAAGGTCAAC



Reverse complement motif Consensus sequence: GTTGACCTTTGACCTTT



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

Original motif Consensus sequence: GGAAM



Reverse complement motif Consensus sequence: YTTCC



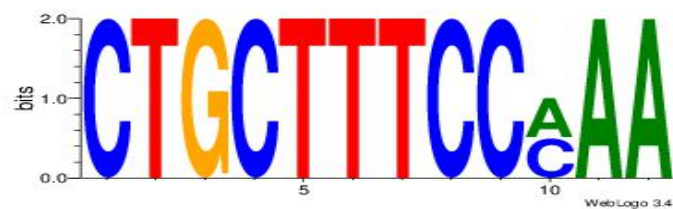
Best Matches for Top Significant Motif ID 4 (Highest to Lowest)

Dataset #:	2
Motif ID:	25
Motif name:	Motif 25
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif

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

Alignment:
 CTGCTTTCCMAA
 ----YTTCC---

Original motif Consensus sequence: CTGCTTTCCMAA



Reverse complement motif Consensus sequence: TTYGGAAAGCAG



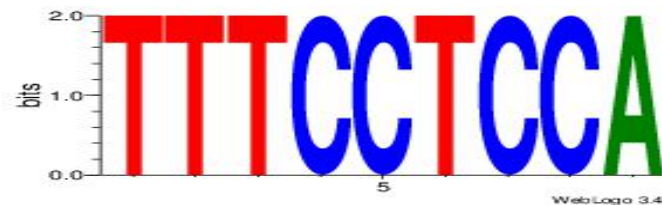
Dataset #: 2
 Motif ID: 45
 Motif name: Motif 45
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 5
 Number of overlap: 5
 Similarity score: 0.01875

Alignment:
 TGGAGGAAA
 ----GGAAM

Original motif Consensus sequence: TGGAGGAAA



Reverse complement motif Consensus sequence: TTTCTCCA



Dataset #: 2
Motif ID: 47
Motif name: Motif 47
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 5
Number of overlap: 5
Similarity score: 0.04375

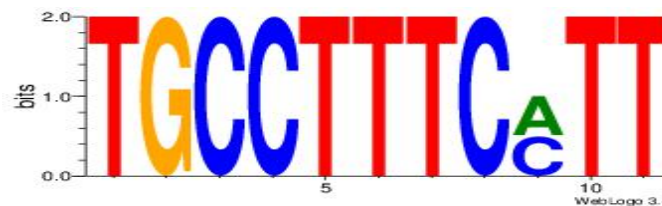
Alignment:

TGCCTTTCYTT
----YTTCC--

Original motif Consensus sequence: AAKGAAAGGCA



Reverse complement motif Consensus sequence: TGCCTTTCYTT



Dataset #: 2
 Motif ID: 48
 Motif name: Motif 48
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3
 Number of overlap: 5
 Similarity score: 0.05625

Alignment:

TTCTTYCATT
 --YTTCC--

Original motif Consensus sequence: AATGKAAGAA



Reverse complement motif Consensus sequence: TTCTTYCATT



Dataset #: 2
 Motif ID: 32
 Motif name: Motif 32
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 5

Similarity score: 0.06875

Alignment:
TTTACTAAAT
YTTCC-----

Original motif Consensus sequence: ATTAGTAAA



Reverse complement motif Consensus sequence: TTTACTAAAT



Dataset #: 2
Motif ID: 12
Motif name: Motif 12
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 7
Number of overlap: 5
Similarity score: 0.06875

Alignment:
TGAAAATSCTT
GGAAM-----

Original motif Consensus sequence: TGAAAATSCTT

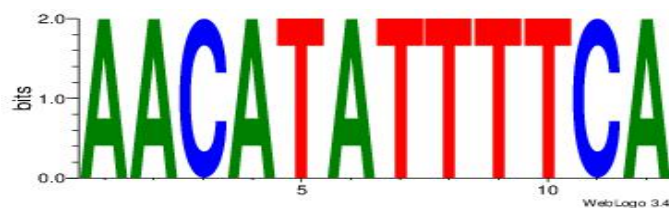
Reverse complement motif Consensus sequence: AAGSATTTTCA



Dataset #: 2
 Motif ID: 13
 Motif name: Motif 13
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 8
 Number of overlap: 5
 Similarity score: 0.06875

Alignment:
 TGAAAATATGTT
 GGAAM-----

Original motif Consensus sequence: AACATATTTTCA



Reverse complement motif Consensus sequence: TGAAAATATGTT



Dataset #: 2
 Motif ID: 23

Motif name:	Motif 23
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:	0.06875

Alignment:
CTTTCTCT
-YTTCC--

Original motif Consensus sequence: AGAGAAAG



Reverse complement motif Consensus sequence: CTTTCTCT



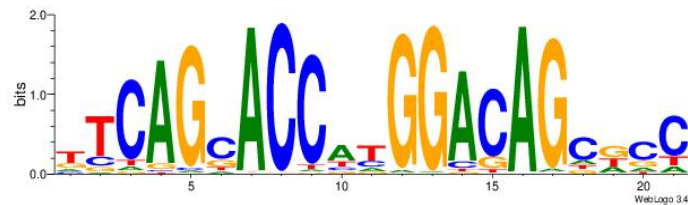
Dataset #:	3
Motif ID:	57
Motif name:	REST
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	12
Number of overlap:	5
Similarity score:	0.0747947

Alignment:

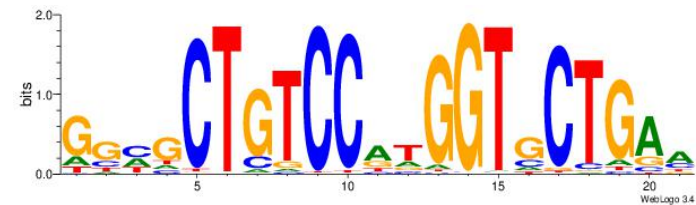
GGYGCTGTCCATGGTGCTGAA

-----YTTCC-----

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC



Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA



Dataset #:	2
Motif ID:	27
Motif name:	Motif 27
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	6
Number of overlap:	5
Similarity score:	0.075

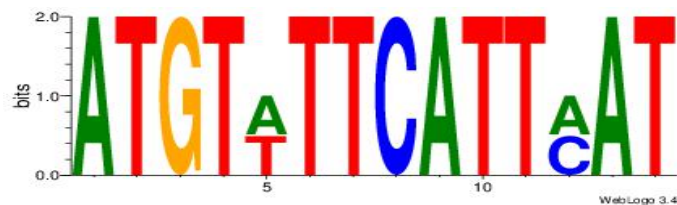
Alignment:

ATGTW TTCATTMAT

-----YTTCC-----

Original motif Consensus sequence: ATGTW TTCATTMAT

Reverse complement motif Consensus sequence: ATYAATGA AWACA



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

Original motif Consensus sequence: AAGGTCAC



Reverse complement motif Consensus sequence: GTGACCTT

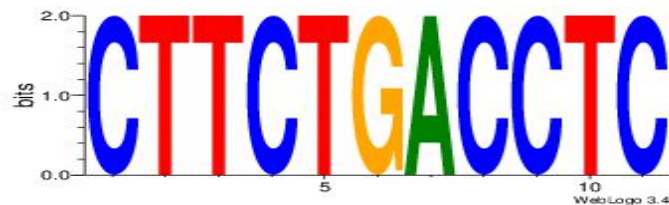


Best Matches for Top Significant Motif ID 61 (Highest to Lowest)

Dataset #:	2
Motif ID:	21
Motif name:	Motif 21
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	8
Similarity score:	0.0393171

Alignment:
 CTTCTGACCTC
 GTGACCTT---

Original motif Consensus sequence: CTTCTGACCTC



Reverse complement motif Consensus sequence: GAGGTCAGAAG



Dataset #: 2
 Motif ID: 19
 Motif name: Motif 19
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 8
 Similarity score: 0.040519

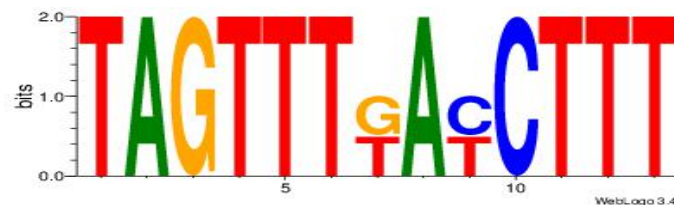
Alignment:

AAAGRTMAAACTA
 -AAGGTCAC-----

Original motif Consensus sequence: AAAGRTMAAACTA



Reverse complement motif Consensus sequence: TAGTTTAACTTT



Dataset #: 2
 Motif ID: 28
 Motif name: Motif 28
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 4
 Number of overlap: 8
 Similarity score: 0.0539119

Alignment:

TTWATGWCTTT
 ---GTGACCTT

Original motif Consensus sequence: AAAGWCATWAA



Reverse complement motif Consensus sequence: TTWATGWCTTT

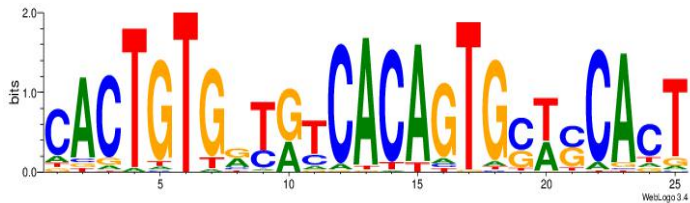


Dataset #: 4
 Motif ID: 72
 Motif name: CACTGTGrYrtCACAGTGswsCAcT
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 7
 Number of overlap: 8

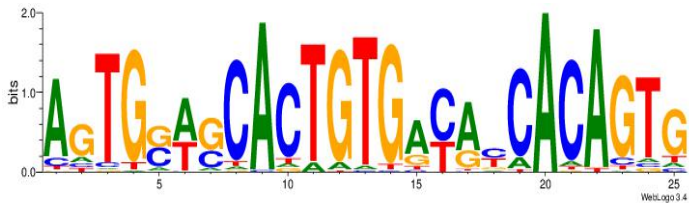
Similarity score: 0.0557243

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

Original motif Consensus sequence:
CACTGTGRTRTCACAGTGSWSCACT



Reverse complement motif Consensus sequence:
AGTGSWSCACTGTGAMAMCACAGTG



Dataset #: 2
Motif ID: 39
Motif name: Motif 39
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 2
Number of overlap: 8
Similarity score: 0.0566591

Alignment:
AGATGYTCTTG
-GTGACCTT--

Original motif Consensus sequence: AGATGYTCTTG

Reverse complement motif Consensus sequence: CAAGAKCATCT

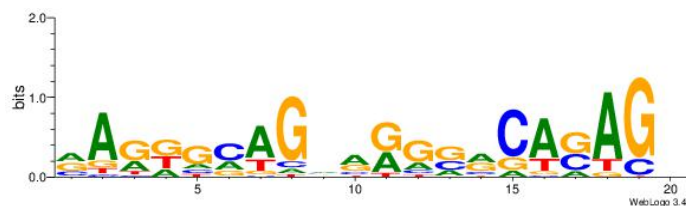


Dataset #: 5
 Motif ID: 93
 Motif name: TFM12
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 10
 Number of overlap: 8
 Similarity score: 0.0584971

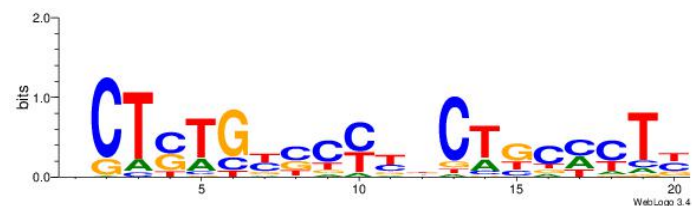
Alignment:

RAGKMAGVRRGSRCASAGV
 -----AAGGTCAC----

Original motif Consensus sequence: RAGKMAGVRRGSRCASAGV



Reverse complement motif Consensus sequence: VCTSTGKSCMKBCTRCYCTK



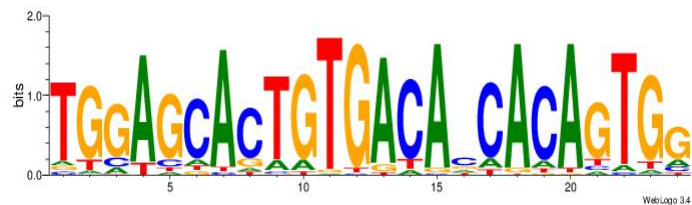
Dataset #: 4

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

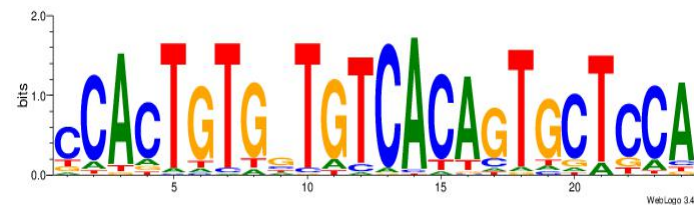
Alignment:

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

Original motif Consensus sequence: TGGAGCACTGTGACAVCACAGTGG



Reverse complement motif Consensus sequence: CCACTGTGVTGTCACAGTGCTCCA



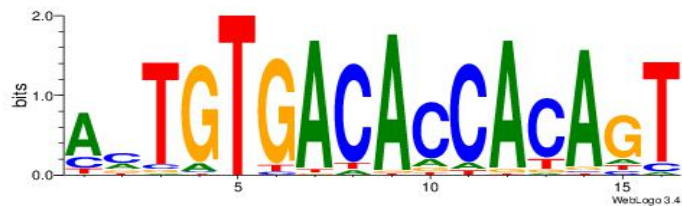
Dataset #: 4
 Motif ID: 71
 Motif name: AmTGTGACACCACAGT
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 4
 Number of overlap: 8

Similarity score: 0.0645146

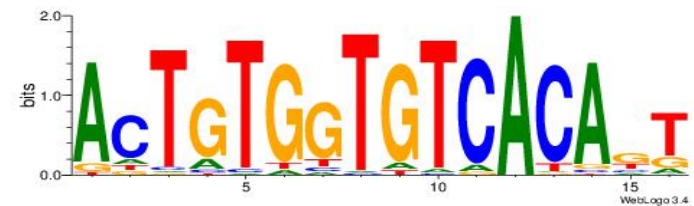
Alignment:

ACTGTGGTGTACART
-----AAGGTCAC---

Original motif Consensus sequence: AMTGTGACACCACAGT



Reverse complement motif Consensus sequence:
ACTGTGGTGTACART



Dataset #: 2
Motif ID: 26
Motif name: Motif 26
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: 0.0664462

Alignment:

ATGCTCACCATAAA
-----AAGGTCAC

Original motif Consensus sequence: TTTATGGTGAGCAT

Reverse complement motif Consensus sequence: ATGCTCACCATAAA



Dataset #: 2
 Motif ID: 22
 Motif name: Motif 22
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 8
 Similarity score: 0.0674765

Alignment:
 GCTGGACTTTG
 -GTGACCTT--

Original motif Consensus sequence: CAAAGTCCAGC



Reverse complement motif Consensus sequence: GCTGGACTTTG



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

Original motif Consensus sequence: CCGCGGRCACG



Reverse complement motif Consensus sequence: CGTGKCCGCGG



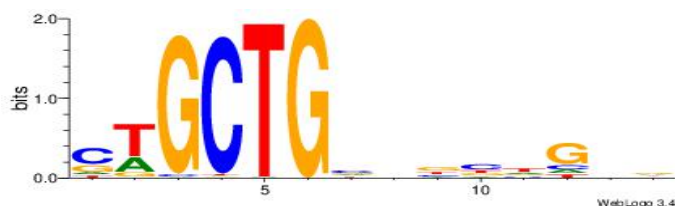
Best Matches for Top Significant Motif ID 79 (Highest to Lowest)

Dataset #: 5
 Motif ID: 88
 Motif name: TFF11
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.0478408

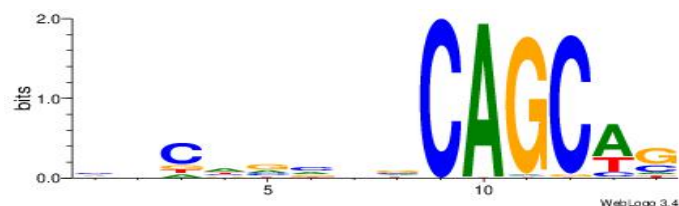
Alignment:

HVCDBBDBCAGCAG
 ---CGTGKCCGCGG

Original motif Consensus sequence: CTGCTGBDBBDGBD



Reverse complement motif Consensus sequence: HVCDBBDBCAGCAG

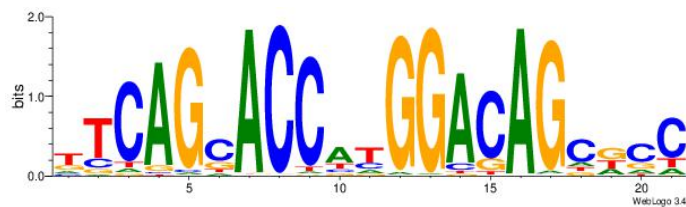


Dataset #: 3
 Motif ID: 57
 Motif name: REST
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 4
 Number of overlap: 11
 Similarity score: 0.0484441

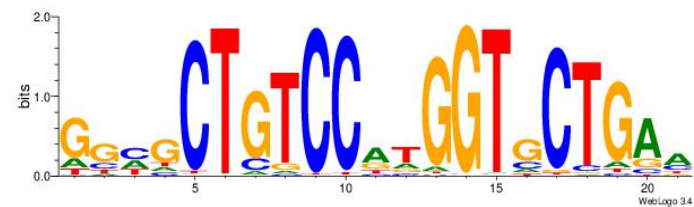
Alignment:

TTCAGCACCATGGACAGCKCC
 -----CCGCGGRCACG---

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC



Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA



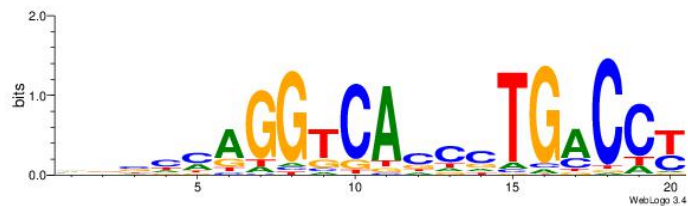
Dataset #: 3
 Motif ID: 53
 Motif name: ESR1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3

Number of overlap: 11
Similarity score: 0.0486581

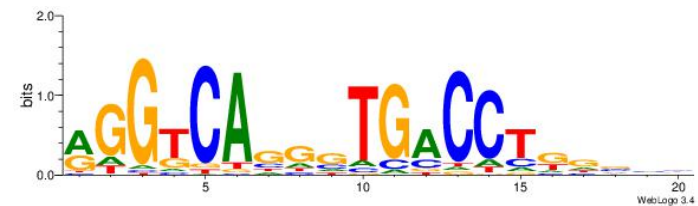
Alignment:

MGGTCAGGGTGACCTRDBHV
-----CGTGKCCGCGG--

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV

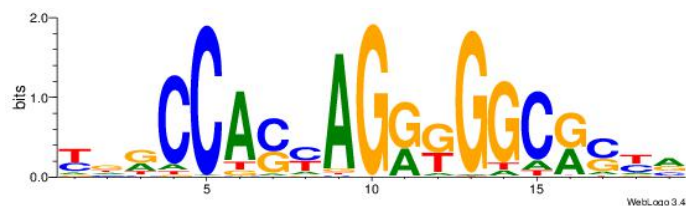


Dataset #: 3
Motif ID: 66
Motif name: CTCF
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 8
Number of overlap: 11
Similarity score: 0.0588663

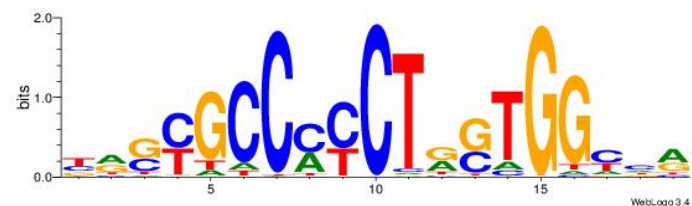
Alignment:

YDRCCASYAGRKGGCRSYV
-----CCGCGGRCACG--

Original motif Consensus sequence: YDRCCASYAGRKGGCRSYV



Reverse complement motif Consensus sequence: BMSMGCCYMCTKSTGGMHM

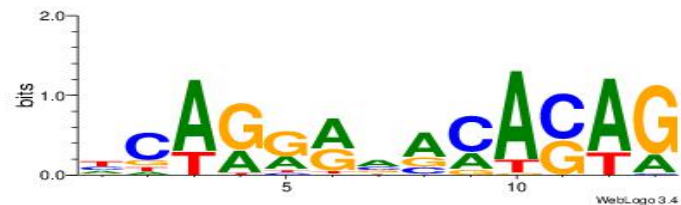


Dataset #: 2
Motif ID: 7
Motif name: Motif 7
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 2
Number of overlap: 11
Similarity score: 0.0597806

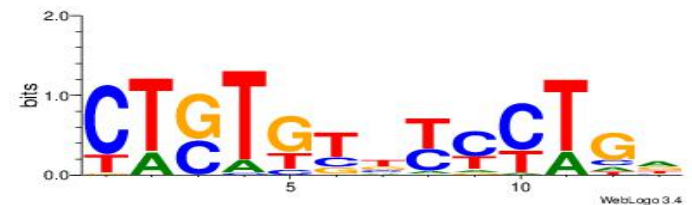
Alignment:

HCAGRRVACASAG
-CCGCGGRCACG-

Original motif Consensus sequence: HCAGRRVACASAG



Reverse complement motif Consensus sequence: CTSTGTBKMCTGH

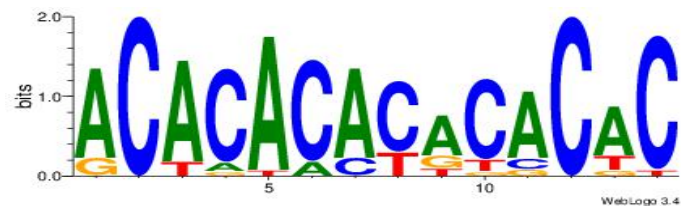


Dataset #: 2
 Motif ID: 6
 Motif name: Motif 6
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 11
 Similarity score: 0.0624268

Alignment:

GTGTGTGTGTGTGT
 -CGTGKCCGCGG--

Original motif Consensus sequence: ACACACACACAC



Reverse complement motif Consensus sequence: GTGTGTGTGTGT

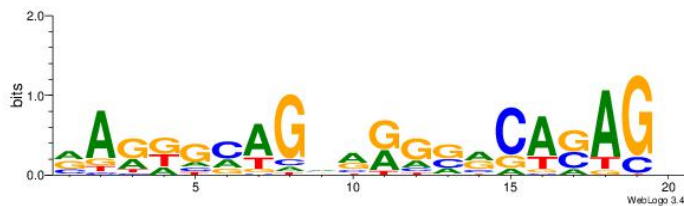


Dataset #: 5
 Motif ID: 93
 Motif name: TFM12
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 5
 Number of overlap: 11

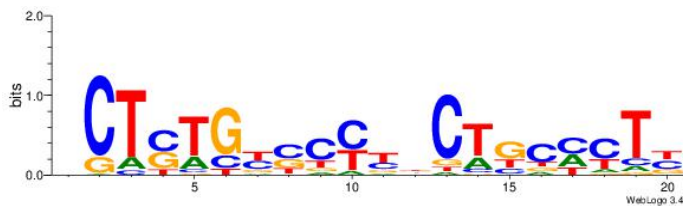
Similarity score: 0.0625015

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

Original motif Consensus sequence: RAGKGMAGVRRGSRCASAGV



Reverse complement motif Consensus sequence: VCTSTGKSCMKBCTRCYCTK

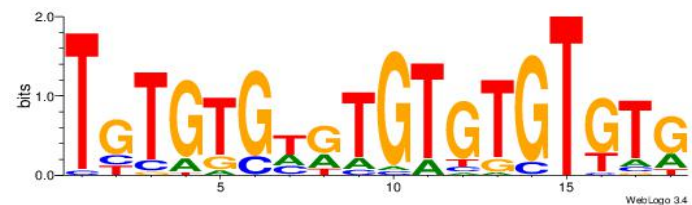
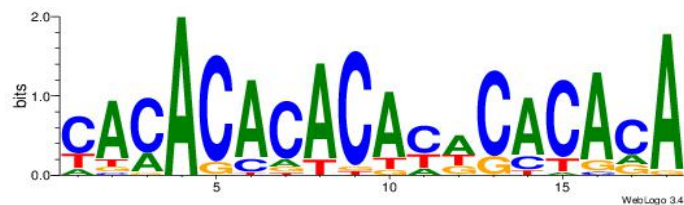


Dataset #: 5
Motif ID: 89
Motif name: TFM1
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 3
Number of overlap: 11
Similarity score: 0.0628056

Alignment:
CACACACACWCACACA
-----CCGCGGRCACG--

Original motif Consensus sequence: CACACACACACWCACACA

Reverse complement motif Consensus sequence: TGTGTGWGTGTGTGTGTG

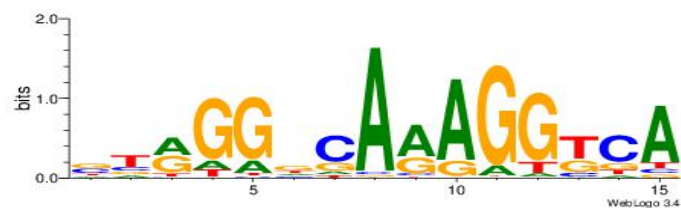


Dataset #: 3
 Motif ID: 64
 Motif name: PPARGRXRA
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 11
 Similarity score: 0.0629476

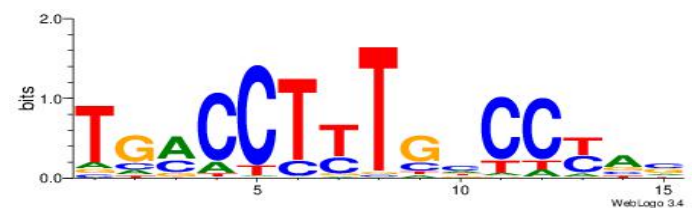
Alignment:

TGRCCCTKTGHCCCKAB
 ---CGTGKCCGCGG-

Original motif Consensus sequence: BTRGGDCARAGGKCA



Reverse complement motif Consensus sequence: TGRCCCTKTGHCCCKAB



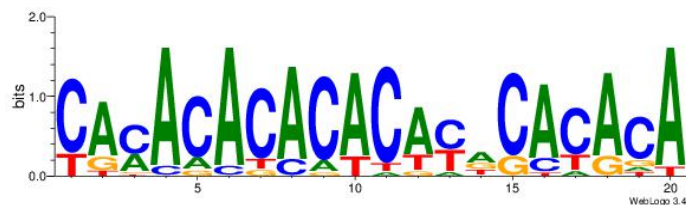
Dataset #: 5
 Motif ID: 92

Motif name: TFM11
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 11
 Similarity score: 0.0634175

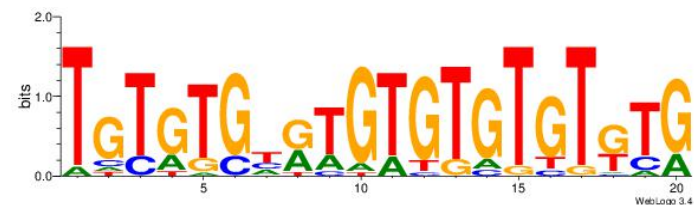
Alignment:

CAMACACACACAYDCACACA
 -----CCGCGGRCACG--

Original motif Consensus sequence: CAMACACACACAYDCACACA



Reverse complement motif Consensus sequence: TGTGTGDKTGTGTGTGTRTG



Results created by MOTIFSIM on 11-19-2016 20:57:29

Runtime: 853.531 seconds

MOTIFSIM is written by Ngoc Tam L. Tran

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