



MOTIFSIM - MOTIF SIMilarity Detection Tool

Version 2.0

INPUT

Input Parameters

Number of files:	5
Number of top significant motifs:	10
Number of best matches:	10
Similarity cutoff $\geq$	0.75
Output file type:	All
Output file format:	All

Input files and motif counts

File name	Count of motifs	Dataset number
MEME_DM05.txt	46	1
MEME-CHIP_DM05.txt	4	2
PScanChIP_DM05.txt	16	3
RSAT_peak-motifs_DM05.txt	17	4
W-ChIPMotifs_DM05.txt	11	5

RESULTS

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

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

Original motif Consensus sequence: GCACTG



Reverse complement motif Consensus sequence: CAGTGC



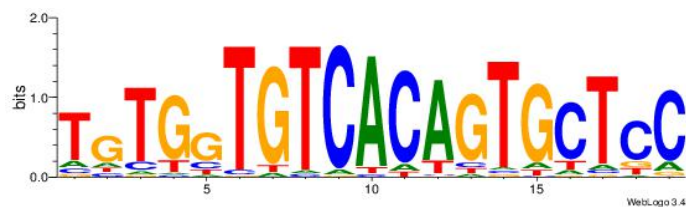
Best Matches for Top Significant Motif ID 84 (Highest to Lowest)

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

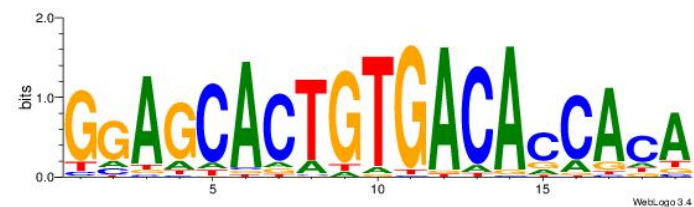
Alignment:

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

Original motif Consensus sequence: TGTGGTGTCACAGTGCTCC



Reverse complement motif Consensus sequence: GGAGCACTGTGACACCACA

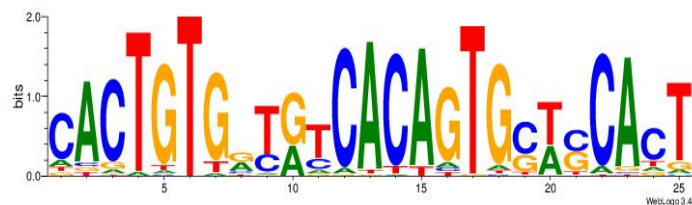


Dataset #: 4
 Motif ID: 72
 Motif name: CACTGTGrYrtCACAGTGswsCAcT
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 7
 Number of overlap: 6
 Similarity score: 0.000794289

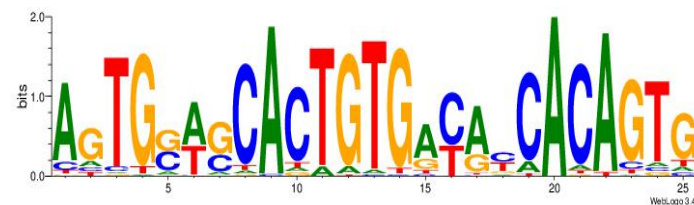
Alignment:

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

Original motif Consensus sequence:
 CACTGTGRTRTCACAGTGSWSCACT



Reverse complement motif Consensus sequence:
 AGTGSWSCACTGTGAMAMCACAGTG



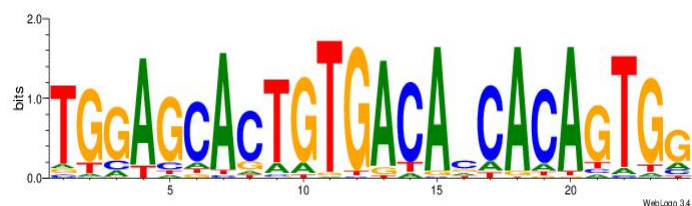
Dataset #: 4
 Motif ID: 73
 Motif name: TGGAGCACTGTGACAcCACAGTGg
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward

Position number: 5
 Number of overlap: 6
 Similarity score: 0.00482436

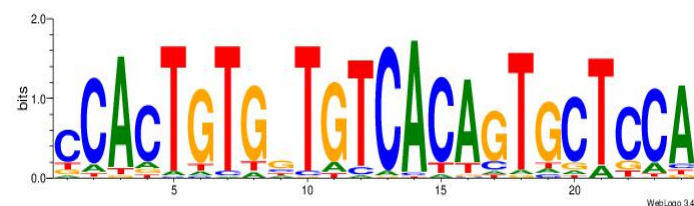
Alignment:

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

Original motif Consensus sequence: TGGAGCACTGTGACAVCACAGTGG



Reverse complement motif Consensus sequence: CCACTGTGVTGTCACAGTGCTCCA

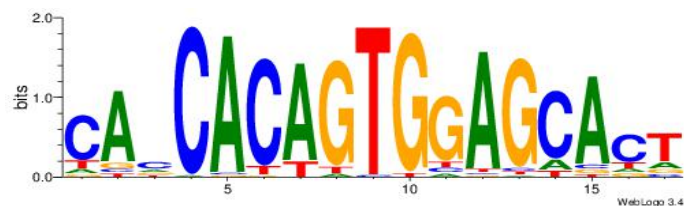


Dataset #: 4
 Motif ID: 76
 Motif name: CACACAGTGGAGCACT
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 7
 Number of overlap: 6
 Similarity score: 0.0201914

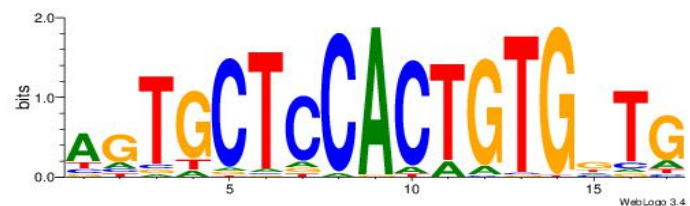
Alignment:

CAHCACAGTGGAGCACT
 -----CAGTGC-----

Original motif Consensus sequence: CAHCACAGTGGAGCACT



Reverse complement motif Consensus sequence: AGTGCTCCACTGTGDTG



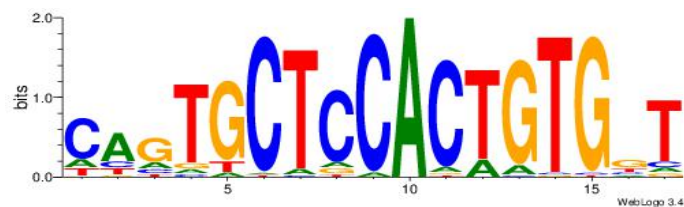
Dataset #: 4
Motif ID: 70
Motif name: CagTGCTCCACTGTGgT
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 5
Number of overlap: 6
Similarity score: 0.0205497

Alignment:

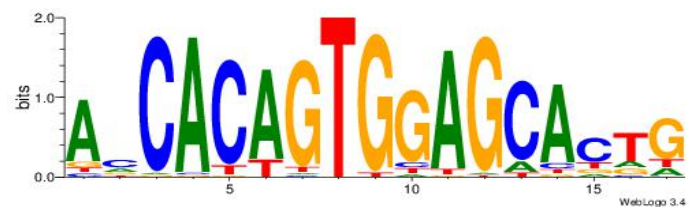
ABCACAGTGGAGCACTG

----CAGTGC-----

Original motif Consensus sequence: CAGTGCTCCACTGTGBT



Reverse complement motif Consensus sequence: ABCACAGTGGAGCACTG

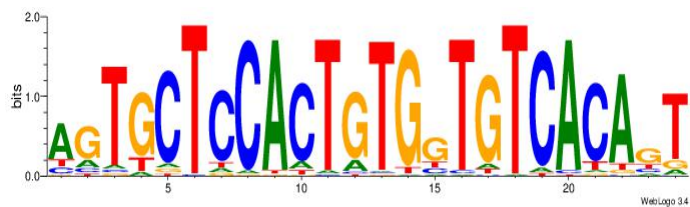


Dataset #: 4
 Motif ID: 77
 Motif name: AgTGCTCCACTGTGgTGTCACAgT
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 13
 Number of overlap: 6
 Similarity score: 0.0290883

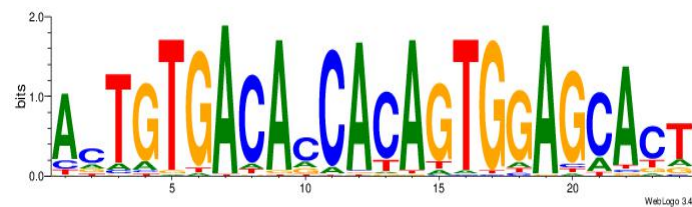
Alignment:

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

Original motif Consensus sequence: AGTGCTCCACTGTGGTGTTCACAGT



Reverse complement motif Consensus sequence: ACTGTGACACCACAGTGGAGCACT

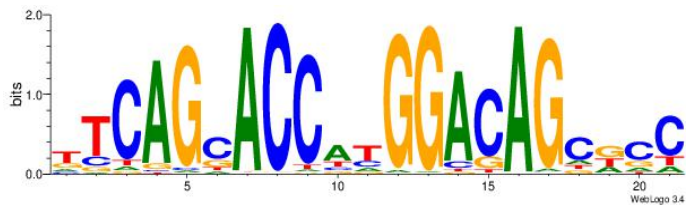


Dataset #: 3
 Motif ID: 57
 Motif name: REST
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 15

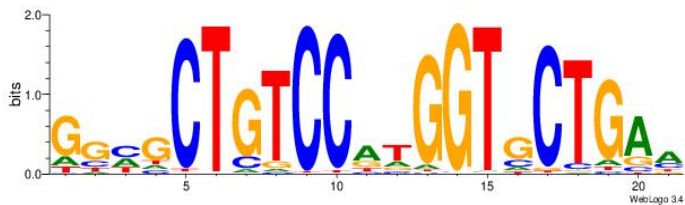
Number of overlap: 6
Similarity score: 0.039883

Alignment:
TTCAGCACCATGGACAGCKCC
-CAGTGC-----

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC



Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA

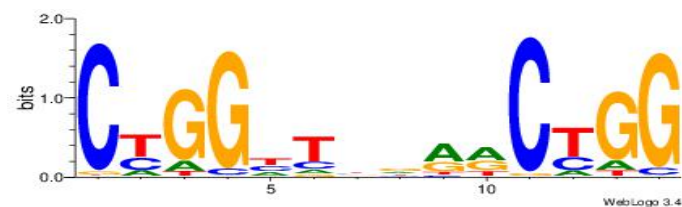
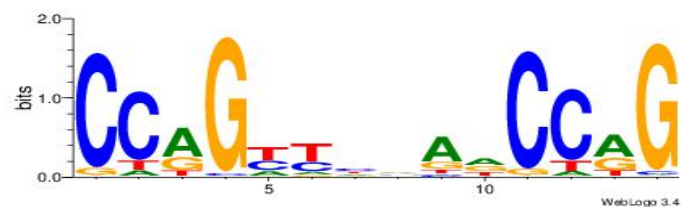


Dataset #: 3
Motif ID: 65
Motif name: Tcfcp2l1
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 8
Number of overlap: 6
Similarity score: 0.0447224

Alignment:
CCAGYYHVADCCRG
-----CAGTGC-

Original motif Consensus sequence: CCAGYYHVADCCRG

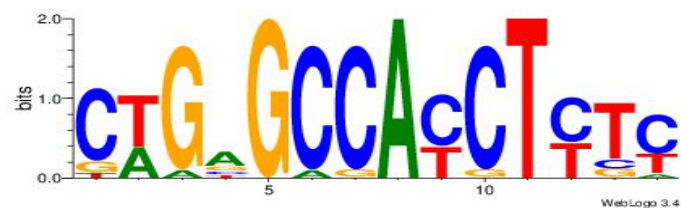
Reverse complement motif Consensus sequence: CKGGDTBDMMCTC



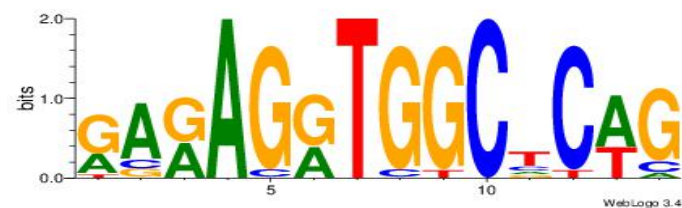
Dataset #: 1
 Motif ID: 5
 Motif name: Motif 5
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 9
 Number of overlap: 6
 Similarity score: 0.0459818

Alignment:
 CWGAGCCAYCTYTC
 -----CAGTGC

Original motif Consensus sequence: CWGAGCCAYCTYTC



Reverse complement motif Consensus sequence: GAKAGKTGGCTCV

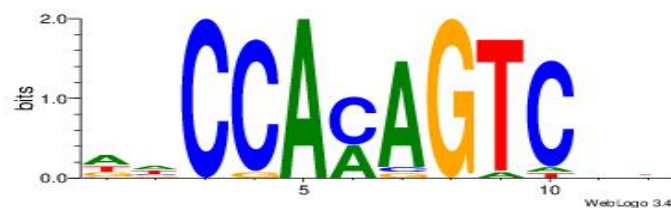


Dataset #: 4
 Motif ID: 75

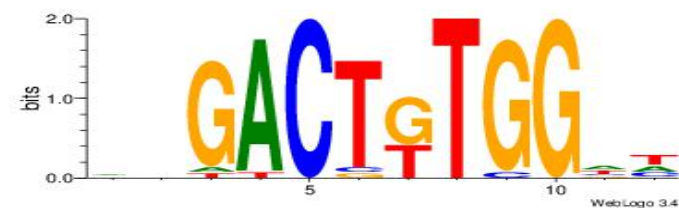
Motif name: wwCCAmAGTCmt
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 6
 Number of overlap: 6
 Similarity score: 0.0587933

Alignment:
 VDGA⁺CTRTGGDD
 -----GCACTG-

Original motif Consensus sequence: DDCCAMAGTCHB



Reverse complement motif Consensus sequence: VDGA⁺CTRTGGDD

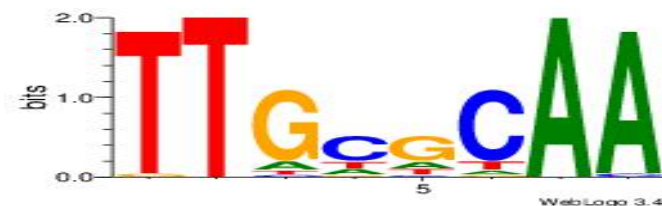


Dataset #: 5 Motif ID: 85 Motif name: TFW1

Original motif Consensus sequence: TTGCGCAA



Reverse complement motif Consensus sequence: TTGCGCAA



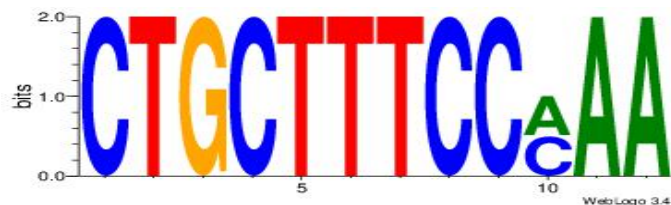
Best Matches for Top Significant Motif ID 85 (Highest to Lowest)

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

Alignment:

TTYGGAAAGCAG
 ----TTGCGCAA

Original motif Consensus sequence: CTGCTTTCCMAA



Reverse complement motif Consensus sequence: TTYGGAAAGCAG

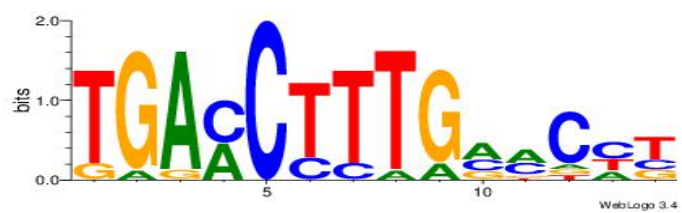


Dataset #: 3
 Motif ID: 52
 Motif name: NR2F1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 8

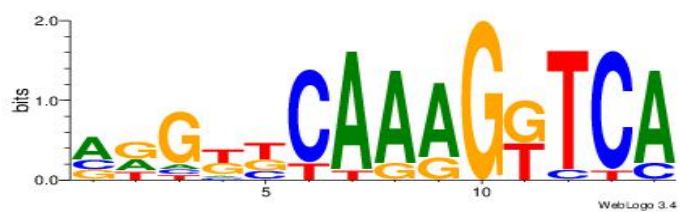
Similarity score: 0.0276442

Alignment:
AKGY YCAAAGRTCA
TTGCGCAA-----

Original motif Consensus sequence: TGAMCTTTGMMCYT



Reverse complement motif Consensus sequence: AKGY YCAAAGRTCA

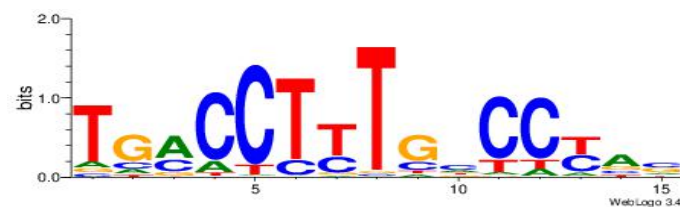
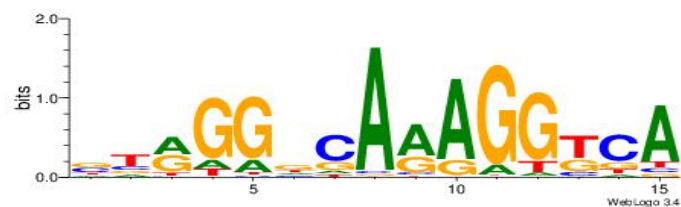


Dataset #: 3
Motif ID: 64
Motif name: PPARGRXRA
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 7
Number of overlap: 8
Similarity score: 0.0277567

Alignment:
BTRGGDCARAGGKCA
-----TTGCGCAA-

Original motif Consensus sequence: BTRGGDCARAGGKCA

Reverse complement motif Consensus sequence: TGRCC TKTGHCK



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

Alignment:

TTTACTAAAT

-TTGCGCAA-

Original motif Consensus sequence: ATTAGTAAA



Reverse complement motif Consensus sequence: TTTACTAAAT



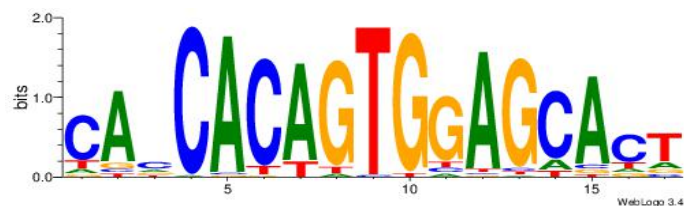
Dataset #: 4
 Motif ID: 76

Motif name:	CACACAGTGGAGCAct
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	8
Similarity score:	0.0336914

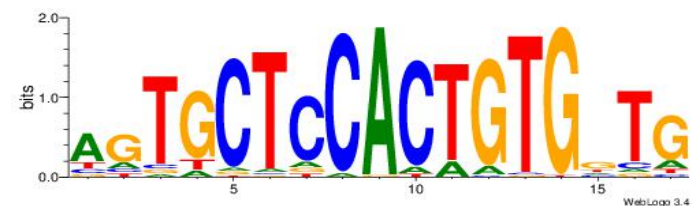
Alignment:

```
CAHCACAGTGGAGCACT
-TTGC GCAA-----
```

Original motif Consensus sequence: CAHCACAGTGGAGCACT



Reverse complement motif Consensus sequence: AGTGCTCCACTGTGDTG

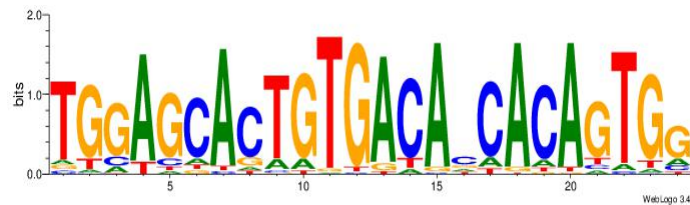


Dataset #:	4
Motif ID:	73
Motif name:	TGGAGCACTGTGACACACAGTGg
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	17
Number of overlap:	8
Similarity score:	0.0338471

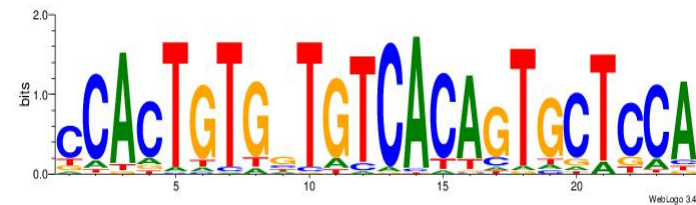
Alignment:

TGGAGCACTGTGACAVCACAGTGG
TTGCGCAA-----

Original motif Consensus sequence: TGGAGCACTGTGACAVCACAGTGG



Reverse complement motif Consensus sequence: CCACTGTGVTGTACAGTGCTCCA



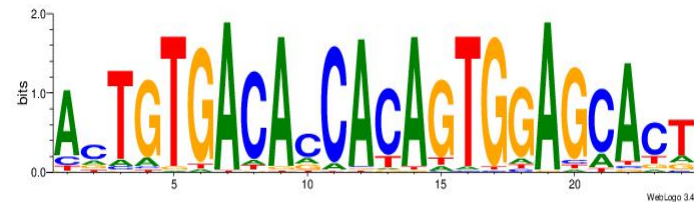
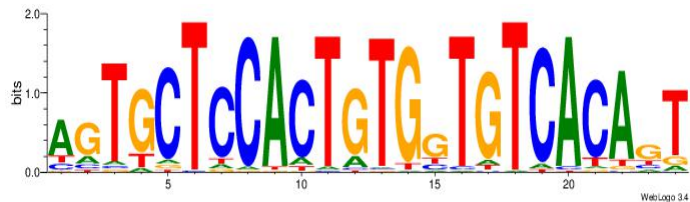
Dataset #:	4
Motif ID:	77
Motif name:	AgTGCTCCACTGTGgTGTCACAgT
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2
Number of overlap:	8
Similarity score:	0.034375

Alignment:

AGTGCTCCACTGTGGTGTACAGT
-----TTGCGCAA-

Original motif Consensus sequence: AGTGCTCCACTGTGGTGTACAGT

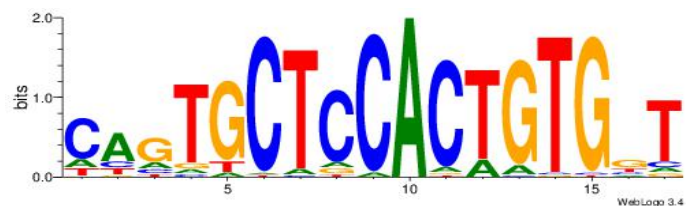
Reverse complement motif Consensus sequence: ACTGTGACACCACAGTGGAGCACT



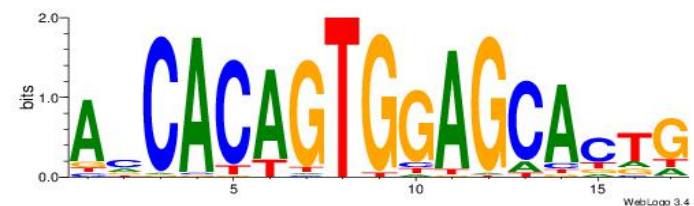
Dataset #: 4
 Motif ID: 70
 Motif name: CagTGCTCCACTGTGgT
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 8
 Similarity score: 0.0354167

Alignment:
 CAGTGCTCCACTGTGBT
 -----TTGCGCAA--

Original motif Consensus sequence: CAGTGCTCCACTGTGBT



Reverse complement motif Consensus sequence: ABCACAGTGGAGCACTG



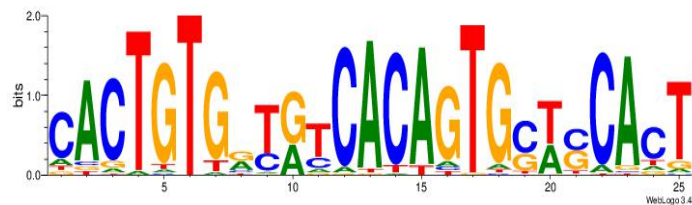
Dataset #: 4

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

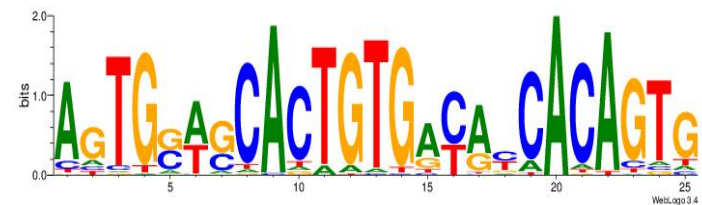
Alignment:

CACTGTGRTRTCACAGTGSWSCACT
 -----TTGCGCAA--

Original motif Consensus sequence:
 CACTGTGRTRTCACAGTGSWSCACT



Reverse complement motif Consensus sequence:
 AGTGSWSCACTGTGAMAMCACAGTG

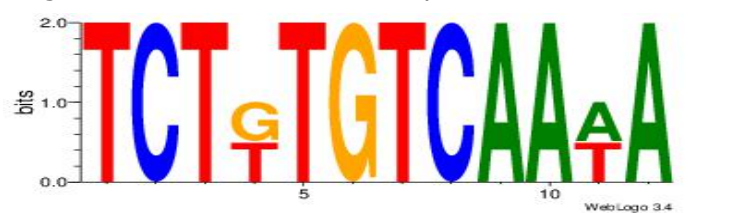


Dataset #: 1
 Motif ID: 16
 Motif name: Motif 16
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3
 Number of overlap: 8

Similarity score: 0.0421875

Alignment:
TWTGACAYAGA
--TTGCGCAA--

Original motif Consensus sequence: TCTKTGTCAAWA



Reverse complement motif Consensus sequence: TWTTGACAYAGA



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

Original motif Consensus sequence: CACCTD



Reverse complement motif Consensus sequence: HAGGTG



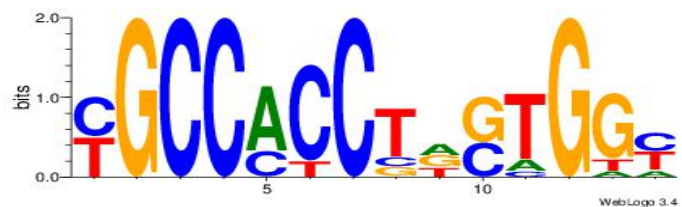
Best Matches for Top Significant Motif ID 55 (Highest to Lowest)

Dataset #:	2
Motif ID:	47
Motif name:	Motif 47
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward

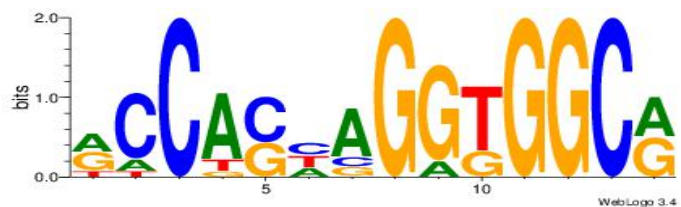
Position number: 4
Number of overlap: 6
Similarity score: 0

Alignment:
YGCCACCTDSTGGY
---CACCTD-----

Original motif Consensus sequence: YGCCACCTDSTGGY



Reverse complement motif Consensus sequence: KCCASDAGGTGGC

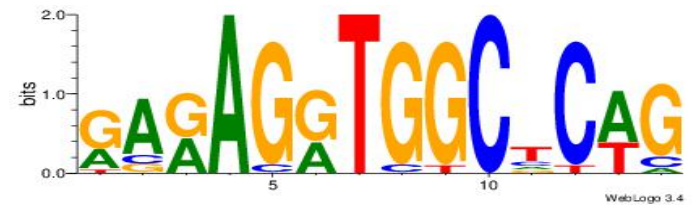
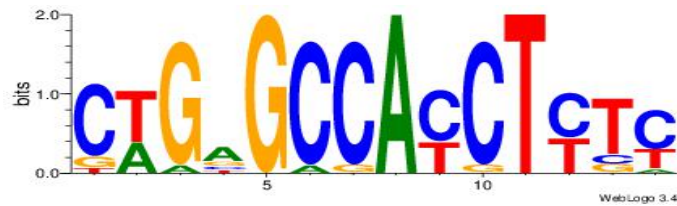


Dataset #: 1
Motif ID: 5
Motif name: Motif 5
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 7
Number of overlap: 6
Similarity score: 0.00902841

Alignment:
CWGAGCCAYCTYTC
-----CACCTD--

Original motif Consensus sequence: CWGAGCCAYCTYTC

Reverse complement motif Consensus sequence: GAKAGKTGGCTCV



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

Alignment:
 TATKCTAAACCTAT
 -CACCTD-----

Original motif Consensus sequence: ATAGGTTTAGYATA



Reverse complement motif Consensus sequence: TATKCTAAACCTAT



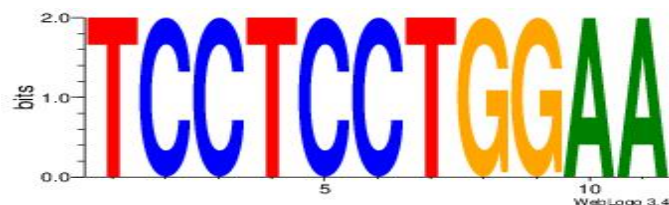
Dataset #: 1

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

Alignment:

TCCTCCTGGAA
 --CACCTD---

Original motif Consensus sequence: TCCTCCTGGAA



Reverse complement motif Consensus sequence: TTCCAGGAGGA



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

Alignment:

ACAACACATTT

----CACCTD-

Original motif Consensus sequence: ACAACACATTT



Reverse complement motif Consensus sequence: AAATGTGTTGT



Dataset #:	1
Motif ID:	34
Motif name:	Motif 34
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2
Number of overlap:	6
Similarity score:	0.0397068

Alignment:

AAAGATGA

-HAGGTG-

Original motif Consensus sequence: AAAGATGA

Reverse complement motif Consensus sequence: TCATCTTT



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

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

Original motif Consensus sequence: TTTATGGTGAGCAT



Reverse complement motif Consensus sequence: ATGCTCACCATAAA



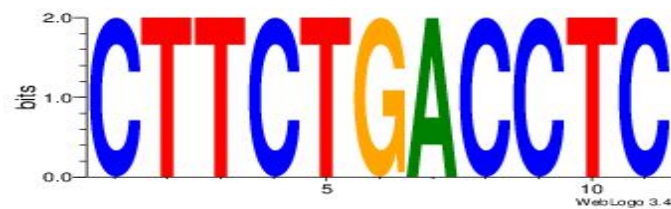
Dataset #: 1
 Motif ID: 17

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

Alignment:

GAGGTCAGAAG
HAGGTG-----

Original motif Consensus sequence: CTTCTGACCTC



Reverse complement motif Consensus sequence: GAGGTCAGAAG



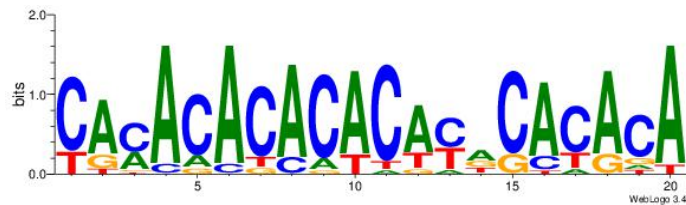
Dataset #:	5
Motif ID:	92
Motif name:	TFM11
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	7
Number of overlap:	6
Similarity score:	0.0461561

Alignment:

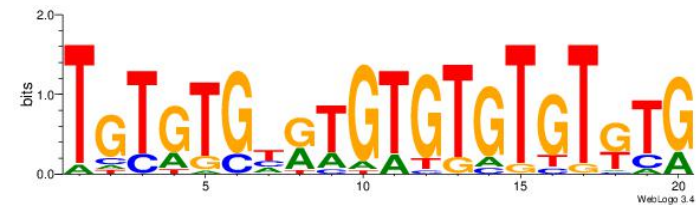
CAMACACACACAYDCACACA

-----CACCTD-----

Original motif Consensus sequence: CAMACACACACAYDCACACA



Reverse complement motif Consensus sequence:
TGTGTGDKTGTGTGTGTRTG



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

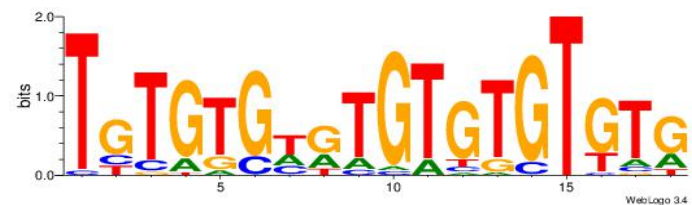
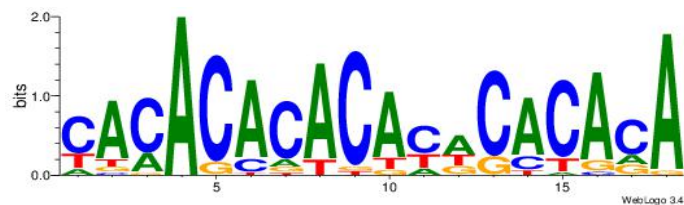
Alignment:

CACACACACACWCACACA

-----CACCTD-----

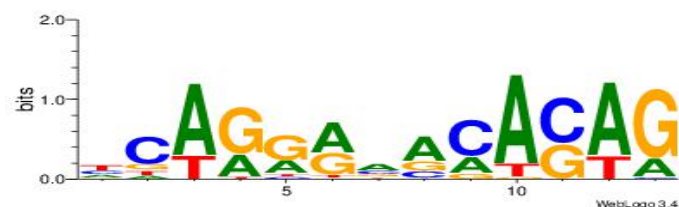
Original motif Consensus sequence: CACACACACACWCACACA

Reverse complement motif Consensus sequence:
TGTGTGWGTGTGTGTGTG

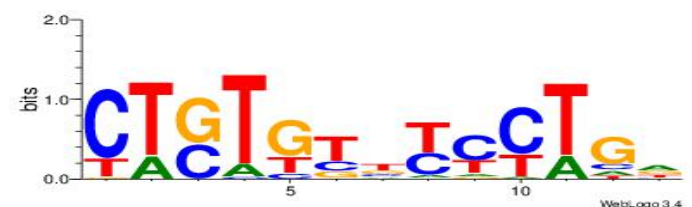


Dataset #: 1 Motif ID: 3 Motif name: Motif 3

Original motif Consensus sequence: HCAGRRVACASAG



Reverse complement motif Consensus sequence: CTSTGTBKMCTGH



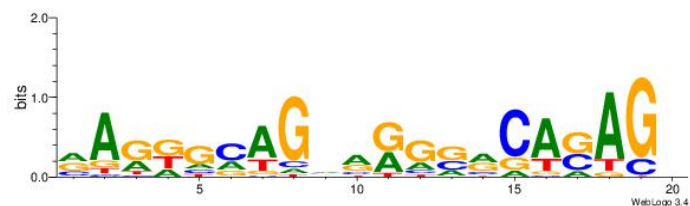
Best Matches for Top Significant Motif ID 3 (Highest to Lowest)

Dataset #:	5
Motif ID:	93
Motif name:	TFM12
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	7
Number of overlap:	13
Similarity score:	0.00926418

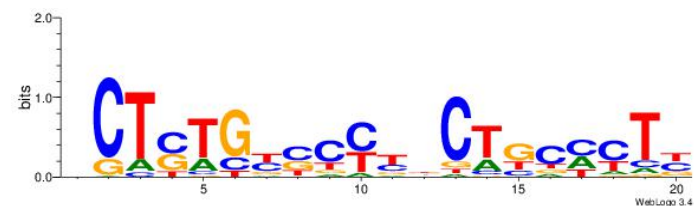
Alignment:

```
RAGKGMAGVRRGSRCASAGV
-----HCAGRRVACASAG--
```

Original motif Consensus sequence: RAGKGMAGVRRGSRCASAGV



Reverse complement motif Consensus sequence: VCTSTGKSCMKBCTRCYCTK

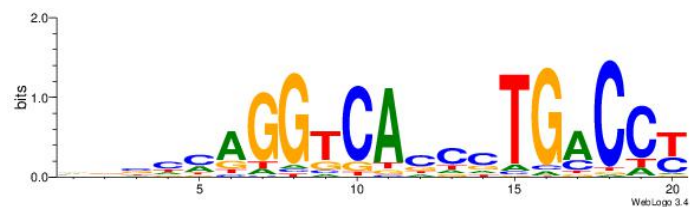


Dataset #: 3
 Motif ID: 53
 Motif name: ESR1
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 13
 Similarity score: 0.0328703

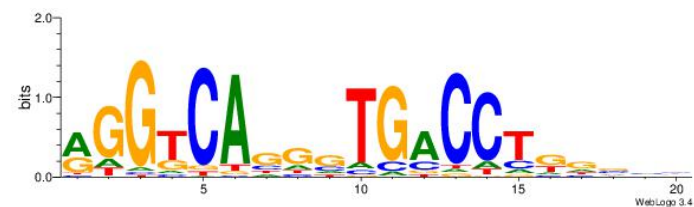
Alignment:

VDBHMAGGTCACCCTGACCY
 ---HCAGRRVACASAG----

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV

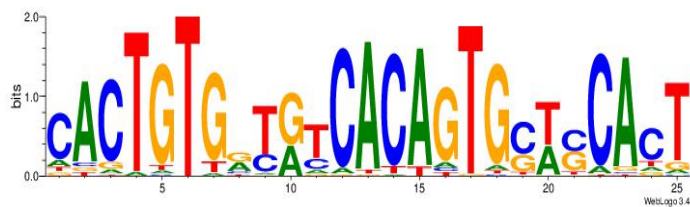


Dataset #: 4
 Motif ID: 72
 Motif name: CACTGTGrYrtCACAGTGswsCAcT
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 13
 Similarity score: 0.0400966

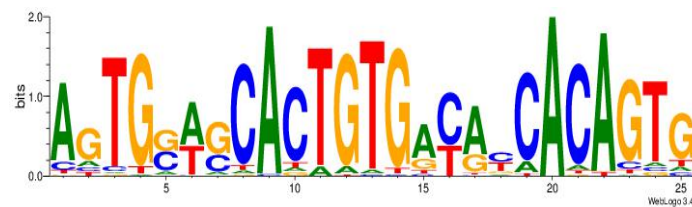
Alignment:

AGTGSWSCACTGTGAMAMCACAGTG
 -----HCAGRRVACASAG--

Original motif Consensus sequence:
 CACTGTGRTRTCACAGTGSWSCACT



Reverse complement motif Consensus sequence:
 AGTGSWSCACTGTGAMAMCACAGTG



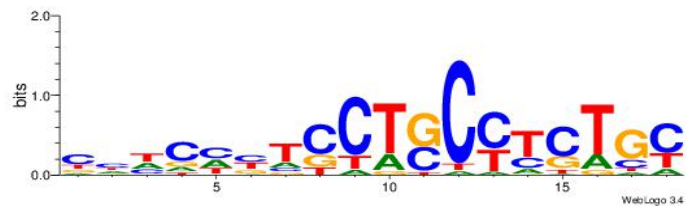
Dataset #: 5
 Motif ID: 90
 Motif name: TFM2
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3

Number of overlap: 13
Similarity score: 0.0435274

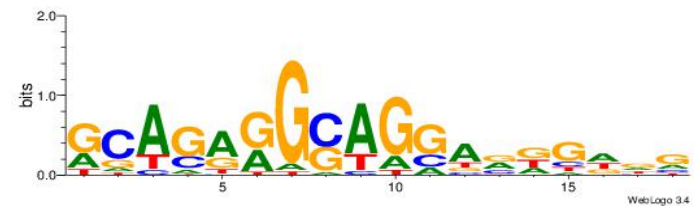
Alignment:

GCAGAKGSAGGABDGH
--HCAGRRVACASAG--

Original motif Consensus sequence: CHHCHBTCCTSCYTCTGC



Reverse complement motif Consensus sequence:
GCAGAKGSAGGABDGH

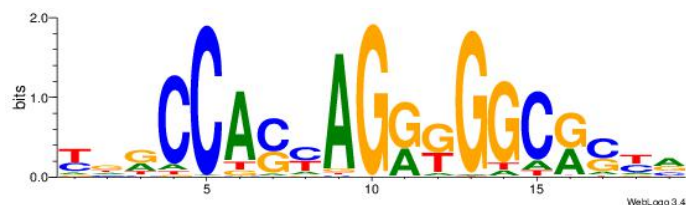


Dataset #: 3
Motif ID: 66
Motif name: CTCF
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 7
Number of overlap: 13
Similarity score: 0.0448341

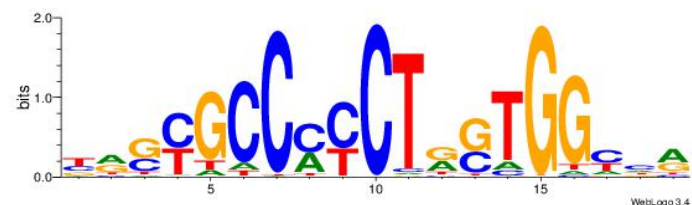
Alignment:

YDRCCASYAGRKGGRSYV
-----HCAGRRVACASAG

Original motif Consensus sequence: YDRCCASYAGRKGGCRSYV



Reverse complement motif Consensus sequence: BMSMGCCYMCTKSTGGMHM

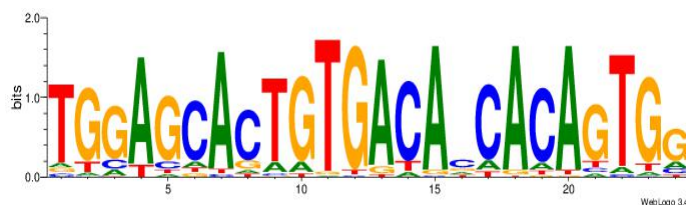


Dataset #: 4
 Motif ID: 73
 Motif name: TGGAGCACTGTGACAcCACAGTGg
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 4
 Number of overlap: 13
 Similarity score: 0.045698

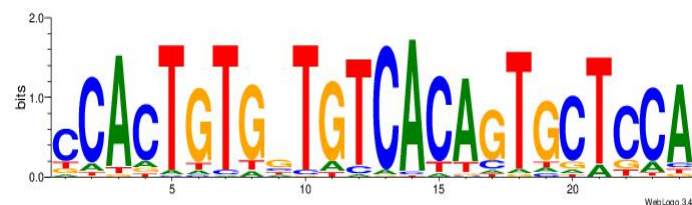
Alignment:

```
CCACTGTGVTGTGTCACAGTGCTCCA
---CTSTGTBKMCTGH-----
```

Original motif Consensus sequence: TGGAGCACTGTGACAVCACAGTGG



Reverse complement motif Consensus sequence: CCACTGTGVTGTGTCACAGTGCTCCA

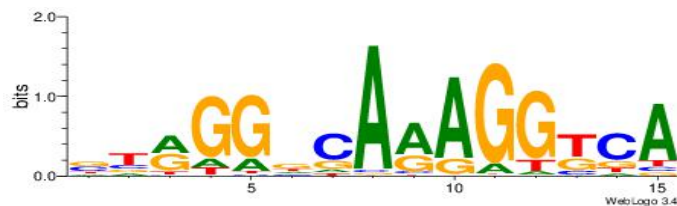


Dataset #: 3
 Motif ID: 64
 Motif name: PPARGRXRA
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 13
 Similarity score: 0.0457253

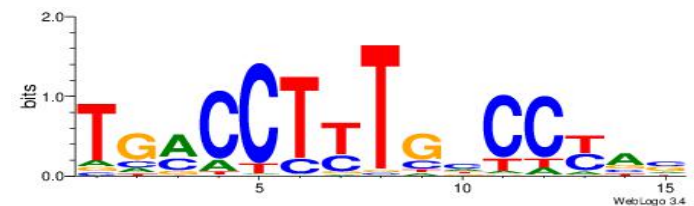
Alignment:

BTRGGDCARAGGKCA
 HCAGRRVACASAG--

Original motif Consensus sequence: BTRGGDCARAGGKCA



Reverse complement motif Consensus sequence: TGRCCCTKGHCCK

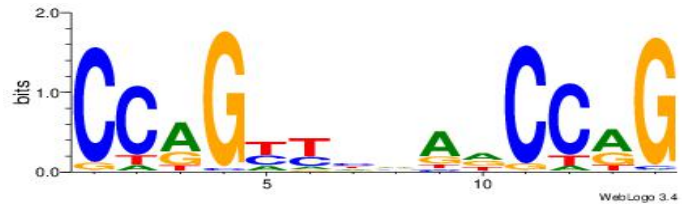


Dataset #: 3
 Motif ID: 65
 Motif name: Tcfcp2l1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 13

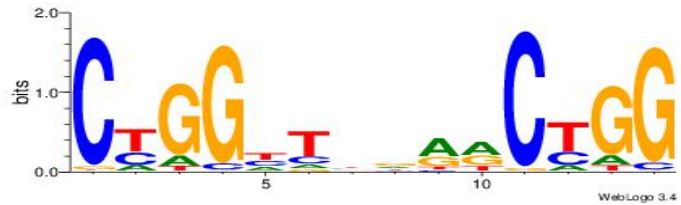
Similarity score: 0.0477557

Alignment:
CKGGDTBDMMCTGG
CTSTGTBKMCTGH-

Original motif Consensus sequence: CCAGYYHVADCCRG



Reverse complement motif Consensus sequence: CKGGDTBDMMCTGG

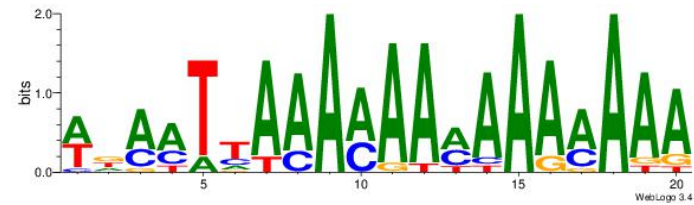
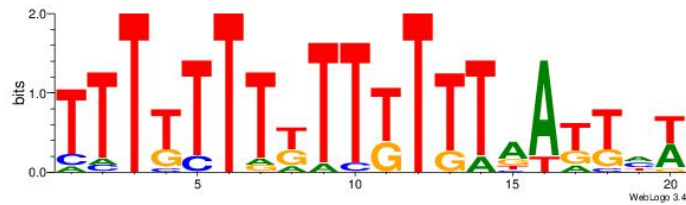


Dataset #: 5
Motif ID: 94
Motif name: TFM13
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 4
Number of overlap: 13
Similarity score: 0.0478998

Alignment:
WHAATTAAARAARAAAAAAA
----HCAGR RVACASAG----

Original motif Consensus sequence: TTTTTTKTTKTTTAATTHW

Reverse complement motif Consensus sequence:
WHAATTAAARAARAAAAAAA



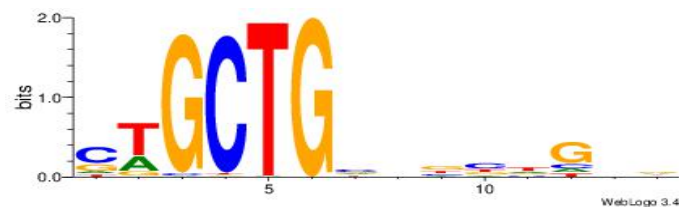
Dataset #: 5
 Motif ID: 88
 Motif name: TFF11
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 13
 Similarity score: 0.048132

Alignment:

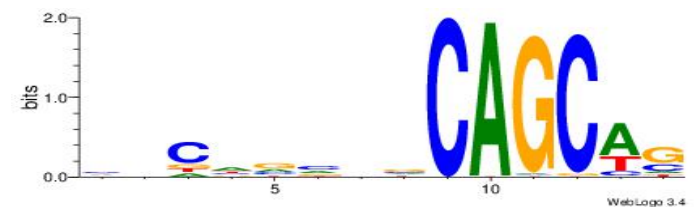
HVCDBBDBCAGCAG

–HCAGRRVACASAG

Original motif Consensus sequence: CTGCTGBDBBDGBD



Reverse complement motif Consensus sequence: HVCDBBDBCAGCA

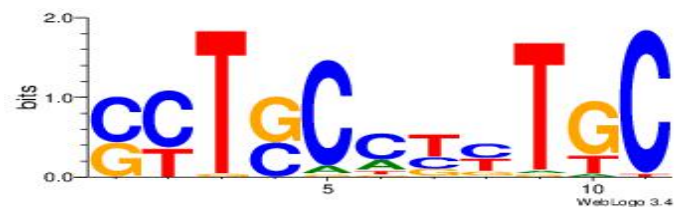


Dataset #: 2 Motif ID: 48 Motif name: Motif 48

Original motif Consensus sequence: GCARRGGSAGS



Reverse complement motif Consensus sequence: SCTSCCKMTGC



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

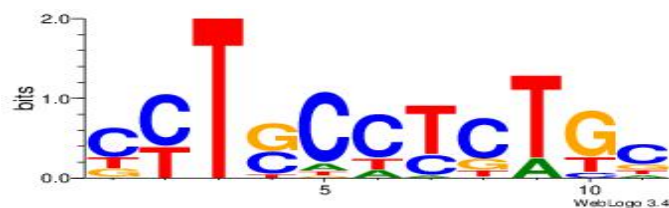
Dataset #:	1
Motif ID:	1
Motif name:	Motif 1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	11
Similarity score:	0

Alignment:

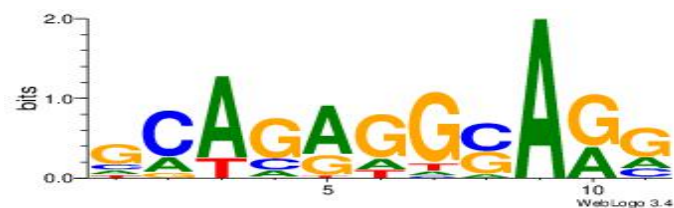
CYTSCCTCTGC

SCTSCCKMTGC

Original motif Consensus sequence: CYTSCCTCTGC



Reverse complement motif Consensus sequence: GCAGAGGSAKG

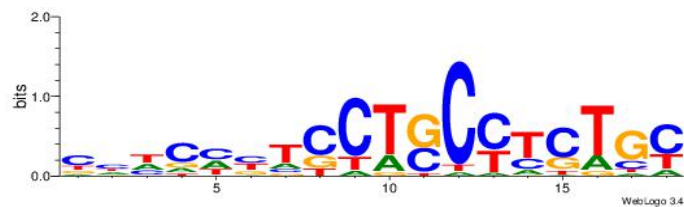


Dataset #: 5
 Motif ID: 90
 Motif name: TFM2
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.000952693

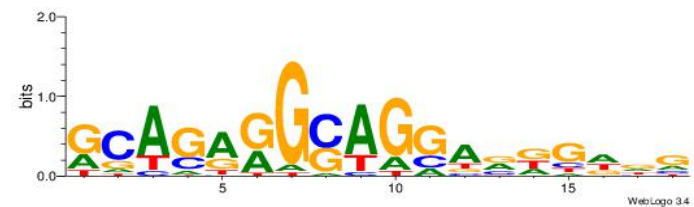
Alignment:

GCAGAKGSAGGABDGHG
 GCARRGGSAGS-----

Original motif Consensus sequence: CHHCHBTCCTSCYTCTGC



Reverse complement motif Consensus sequence: GCAGAKGSAGGABDGHG

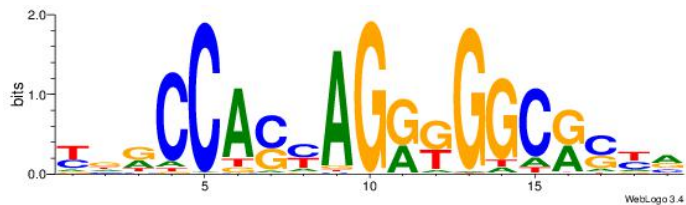


Dataset #: 3
 Motif ID: 66
 Motif name: CTCF
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3

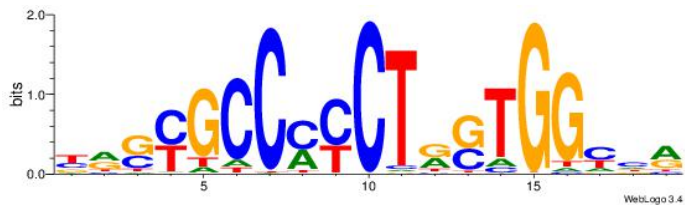
Number of overlap: 11
Similarity score: 0.033658

Alignment:
YDRCCASYAGRKGGCRSYV
-----GCARRGGSAGS--

Original motif Consensus sequence: YDRCCASYAGRKGGCRSYV



Reverse complement motif Consensus sequence:
BMSMGCCYMCTKSTGGMHM

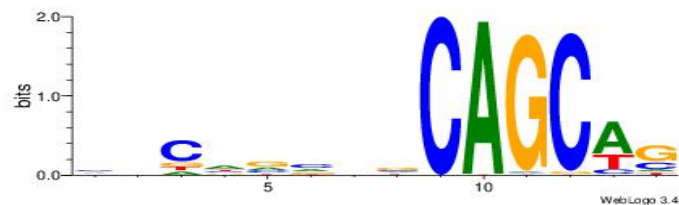
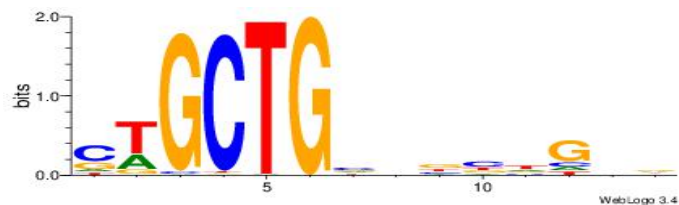


Dataset #: 5
Motif ID: 88
Motif name: TFF11
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 3
Number of overlap: 11
Similarity score: 0.0410341

Alignment:
CTGCTGBDBBDGBD
--SCTSCCKMTGC--

Original motif Consensus sequence: CTGCTGBDBBDGBD

Reverse complement motif Consensus sequence: HVCDBBDBCAGCA

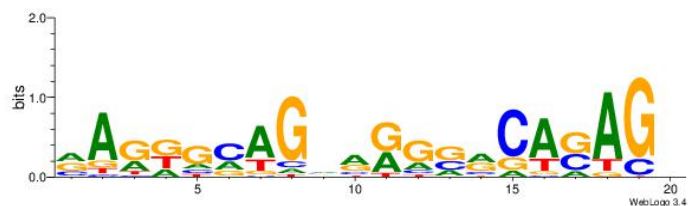


Dataset #: 5
 Motif ID: 93
 Motif name: TFM12
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 6
 Number of overlap: 11
 Similarity score: 0.0422459

Alignment:

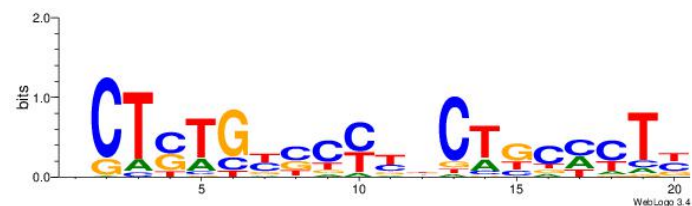
RAGKGMAGVRRGSRCASAGV
 ----GCARRGGSAGS-----

Original motif Consensus sequence: RAGKGMAGVRRGSRCASAGV



Reverse complement motif
VCTSTGKSCMKBCTRCYCTK

Consensus sequence:

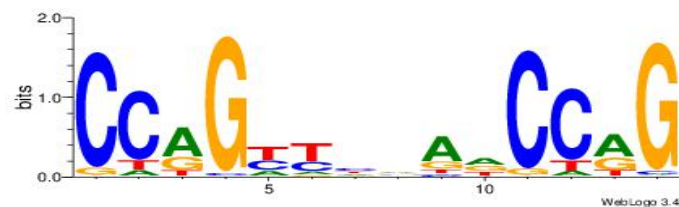


Dataset #: 3

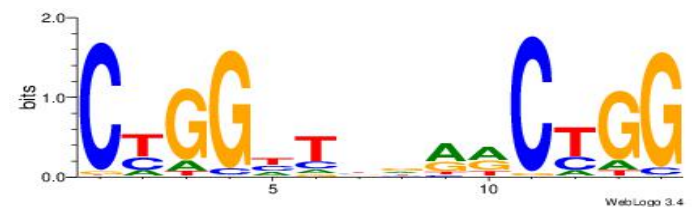
Motif ID: 65
 Motif name: Tcfcp2l1
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.0533531

Alignment:
 CCAGYYHVADCCRG
 SCTSCCKMTGC---

Original motif Consensus sequence: CCAGYYHVADCCRG



Reverse complement motif Consensus sequence: CKGGDTBDMMCTG



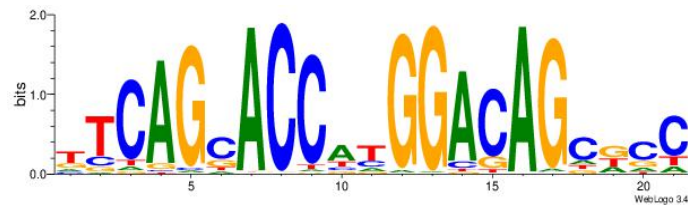
Dataset #: 3
 Motif ID: 57
 Motif name: REST
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 4
 Number of overlap: 11
 Similarity score: 0.0578944

Alignment:

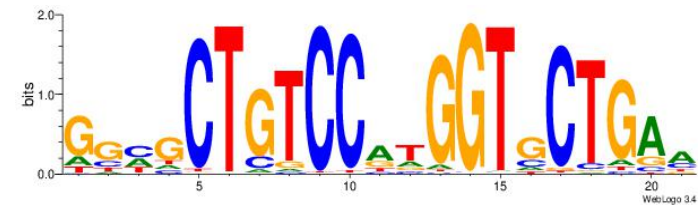
GGYGCTGTCCATGGTGCTGAA

---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

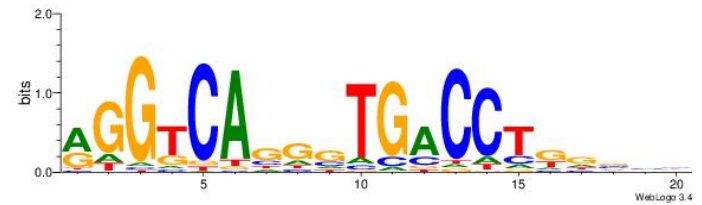
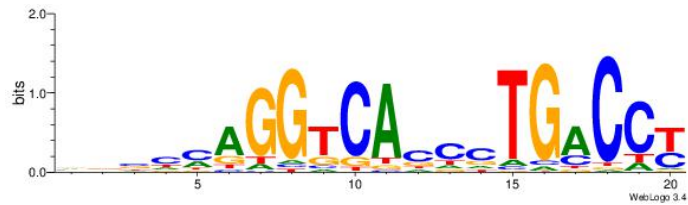
Alignment:

VDBHMAGGTCACCCTGACCY

--GCARRGGSAGS-----

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY

Reverse complement motif Consensus sequence:
MGGTCAGGGTGACCTGDBHV



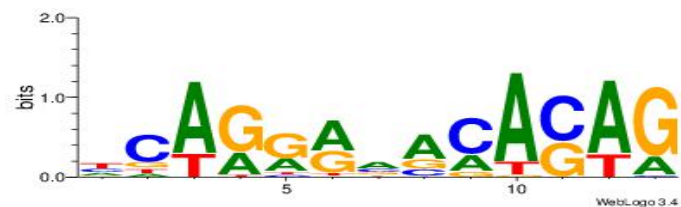
Dataset #: 1
 Motif ID: 3
 Motif name: Motif 3
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 11
 Similarity score: 0.0627554

Alignment:

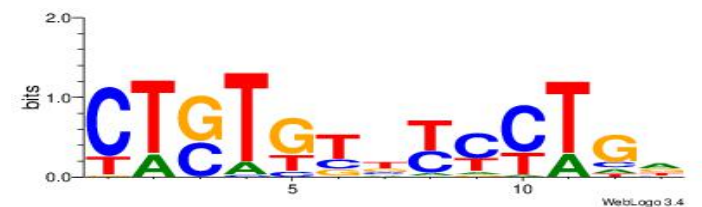
HCAGRRVACASAG

GCARRGGSAGS--

Original motif Consensus sequence: HCAGRRVACASAG



Reverse complement motif Consensus sequence: CTSTGTBKMCTGH



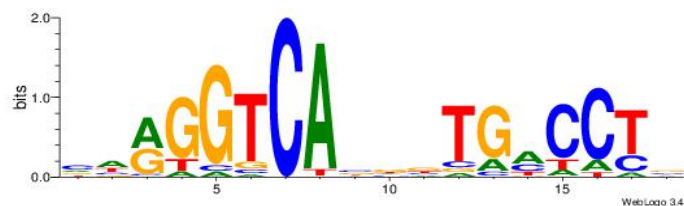
Dataset #: 3
 Motif ID: 59

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

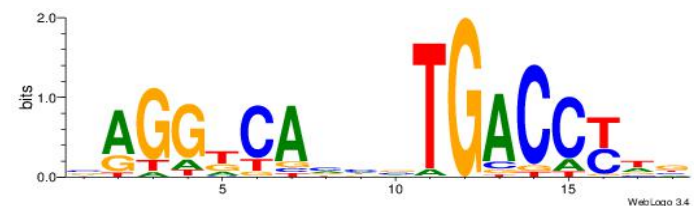
Alignment:

VHRGGTCABDBTGMCTB
 ---SCTSCCKMTGC-----

Original motif Consensus sequence: VHRGGTCABDBTGMCTB

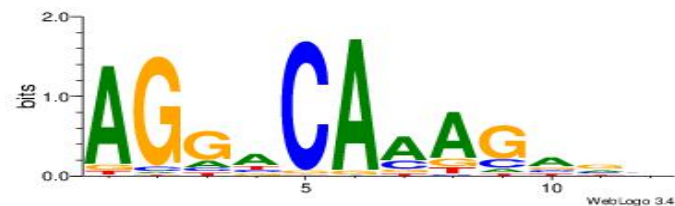


Reverse complement motif Consensus sequence: BAGGYCABHBTGACCKHV

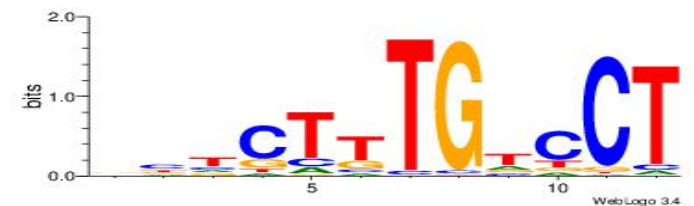


Dataset #: 5 Motif ID: 87 Motif name: TFF1

Original motif Consensus sequence: AGGACAAAGAVV



Reverse complement motif Consensus sequence: VVTCTTTGTCCT



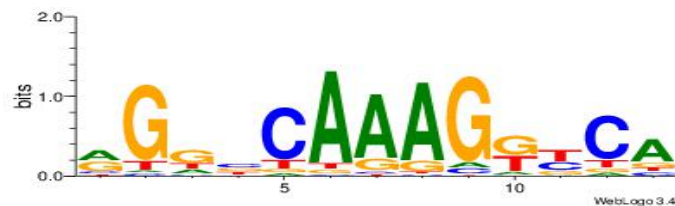
Best Matches for Top Significant Motif ID 87 (Highest to Lowest)

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

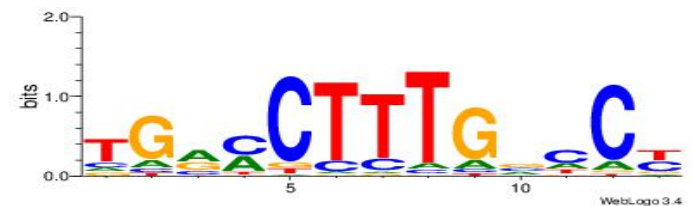
Alignment:

TGMYCTTTGBCK
-VVTCTTTGTCCT

Original motif Consensus sequence: RGGBCAAAGKYCA



Reverse complement motif Consensus sequence: TGMYCTTTGBCK

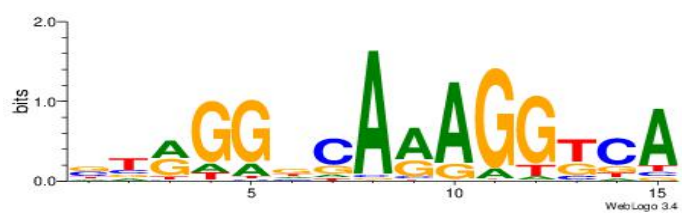


Dataset #: 3
Motif ID: 64
Motif name: PPARGRXRA
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif

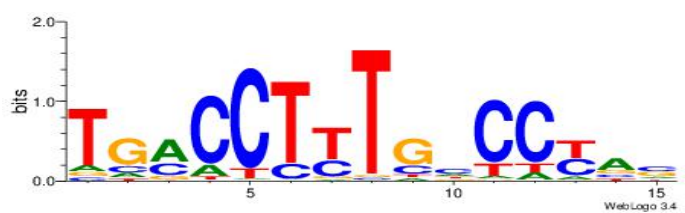
Direction: Forward
Position number: 3
Number of overlap: 12
Similarity score: 0.0210867

Alignment:
BTRGGDCARAGGKCA
--AGGACAAAGAVV--

Original motif Consensus sequence: BTRGGDCARAGGKCA



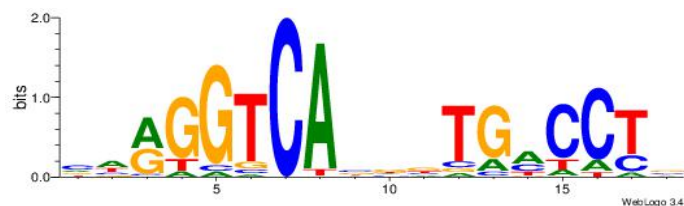
Reverse complement motif Consensus sequence: TGRCCCTKGHCKK



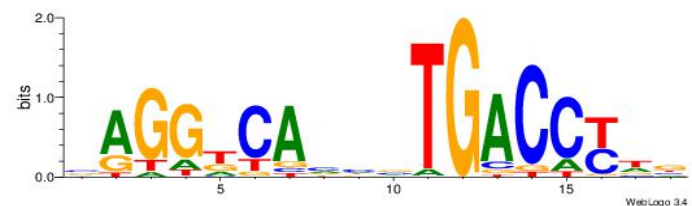
Dataset #: 3
Motif ID: 59
Motif name: ESR2
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 5
Number of overlap: 12
Similarity score: 0.0351633

Alignment:
BAGGYCABHBTGACCKHV
----VVTCTTTGTCCT--

Original motif Consensus sequence: VHRGGTCABDBTGMCTB



Reverse complement motif Consensus sequence: BAGGYCABHBTGACCKHV

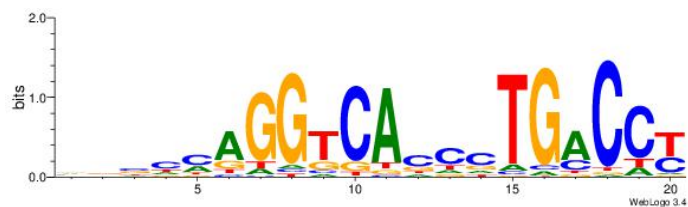


Dataset #: 3
Motif ID: 53
Motif name: ESR1
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 9
Number of overlap: 12
Similarity score: 0.039773

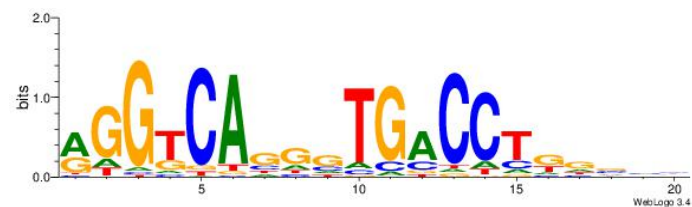
Alignment:

VDBHMAGGTCACCCTGACCY
VVTCTTTGTCCT-----

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV



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

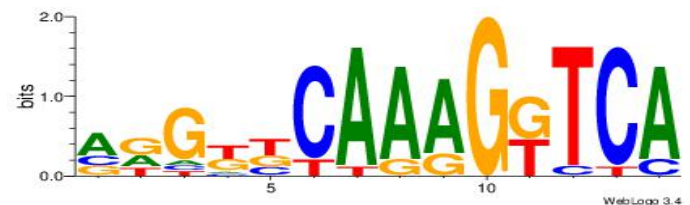
Alignment:

AKGYCAAAGRTCA
 -AGGACAAAGAVV-

Original motif Consensus sequence: TGAMCTTTGMMCYT



Reverse complement motif Consensus sequence: AKGYCAAAGRTCA



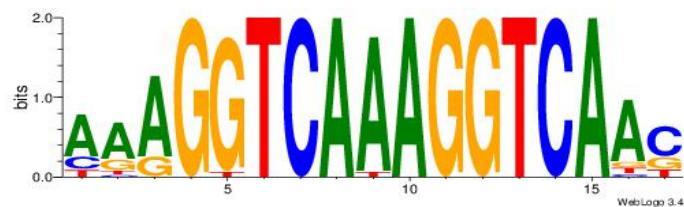
Dataset #: 3
 Motif ID: 60
 Motif name: NR1H2RXRA
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 12

Similarity score: 0.0472884

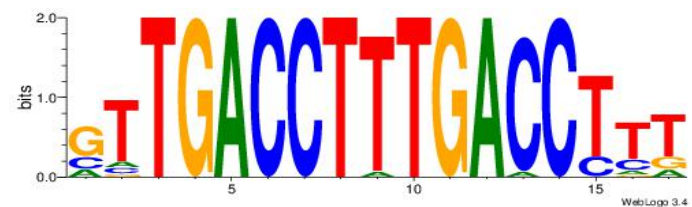
Alignment:

GTGACCTTTGACCTTT
---VVTCTTTGTCCT--

Original motif Consensus sequence: AAAGGTCAAAGGTCAAC



Reverse complement motif Consensus sequence: GTTGACCTTTGACCTTT



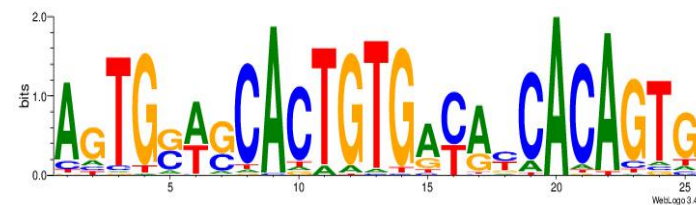
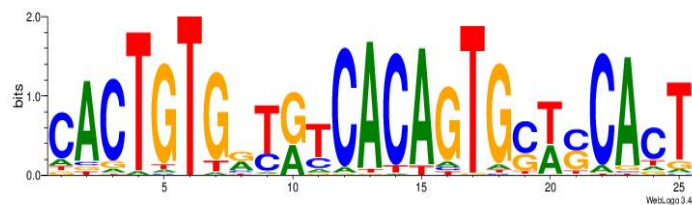
Dataset #: 4
Motif ID: 72
Motif name: CACTGTGrYrtCACAGTGswsCAcT
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 7
Number of overlap: 12
Similarity score: 0.0530556

Alignment:

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

Original motif Consensus sequence:
CACTGTGRTRTCACAGTGSWSCACT

Reverse complement motif Consensus sequence:
AGTGSWSCACTGTGAMAMCACAGTG

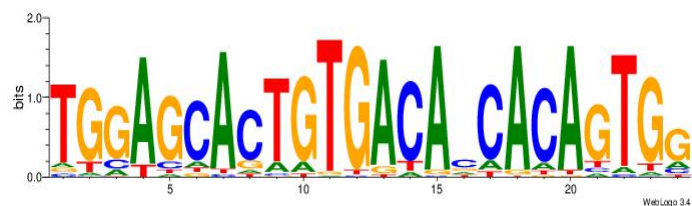


Dataset #: 4
 Motif ID: 73
 Motif name: TGGAGCACTGTGACAcCACAGTGg
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 13
 Number of overlap: 12
 Similarity score: 0.0539204

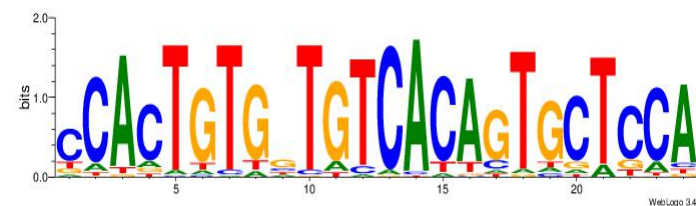
Alignment:

TGGAGCACTGTGACAVCACAGTGG
 -----AGGACAAAGAVV

Original motif Consensus sequence: TGGAGCACTGTGACAVCACAGTGG



Reverse complement motif Consensus sequence: CCACTGTGVTGTCACAGTGCTCCA



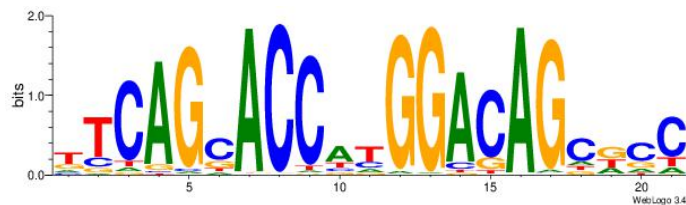
Dataset #: 3

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

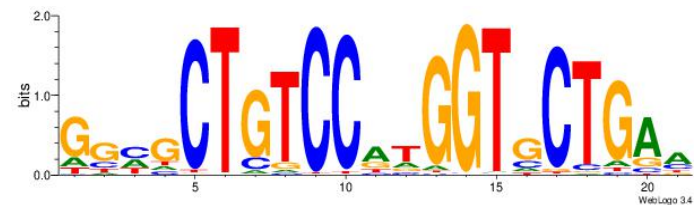
Alignment:

TTCAGCACCATGGACAGCKCC
 ---AGGACAAAGAVV-----

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC



Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA

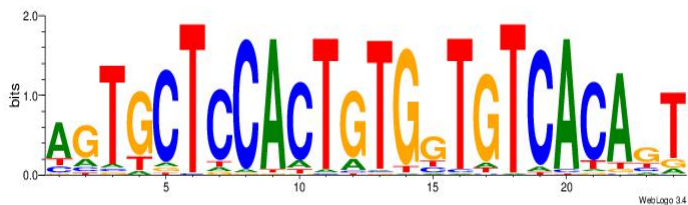


Dataset #: 4
 Motif ID: 77
 Motif name: AgTGCTCCACTGTGgTGTCACAgT
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 7
 Number of overlap: 12

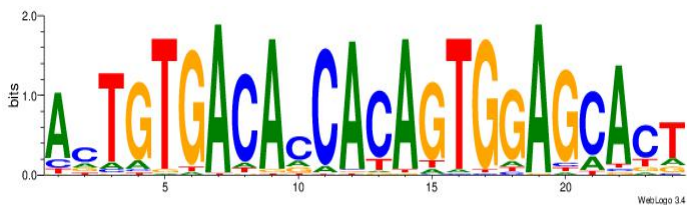
Similarity score: 0.0609269

Alignment:
AGTGCTCCACTGTGGTGTCACAGT
-----VVTCTTTGTCCT-----

Original motif Consensus sequence: AGTGCTCCACTGTGGTGTCACAGT



Reverse complement motif Consensus sequence: ACTGTGACACCACAGTGGAGCACT



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

Original motif Consensus sequence: ACTTTGG



Reverse complement motif Consensus sequence: CCAAAGT



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

Dataset #:	4
Motif ID:	69
Motif name:	atactttggc
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement

Direction: Forward
 Position number: 2
 Number of overlap: 7
 Similarity score: 0

Alignment:
 GCCAAAGTAT
 -CCAAAGT--

Original motif Consensus sequence: ATACTTTGGC



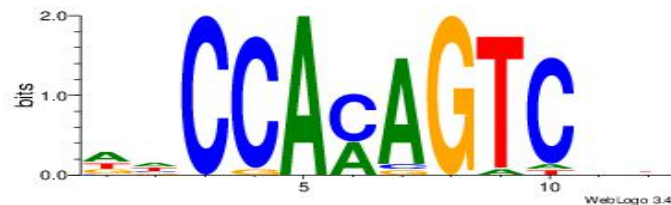
Reverse complement motif Consensus sequence: GCCAAAGTAT



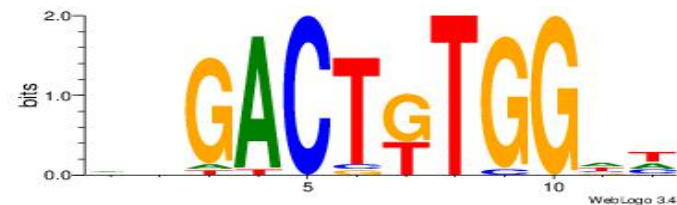
Dataset #: 4
 Motif ID: 75
 Motif name: wwCCAmAGTCmt
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 4
 Number of overlap: 7
 Similarity score: 0.0275974

Alignment:
 DDCCAMAGTCHB
 --CCAAAGT---

Original motif Consensus sequence: DDCCAMAGTCHB



Reverse complement motif Consensus sequence: VDGACTRTGGDD

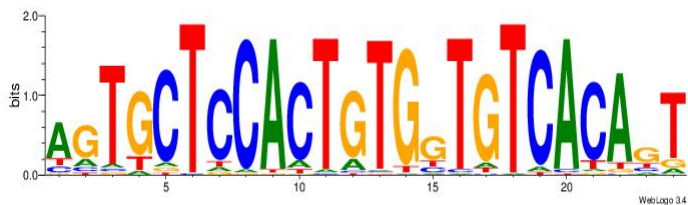


Dataset #: 4
 Motif ID: 77
 Motif name: AgTGCTCCACTGTGgTGTCACAgT
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 10
 Number of overlap: 7
 Similarity score: 0.056841

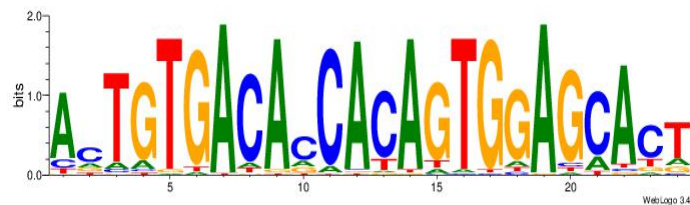
Alignment:

```
ACTGTGACACCACAGTGGAGCACT
-----CCAAAGT-----
```

Original motif Consensus sequence: AGTGCTCCACTGTGGTGTACAGT



Reverse complement motif Consensus sequence: ACTGTGACACCACAGTGGAGCACT

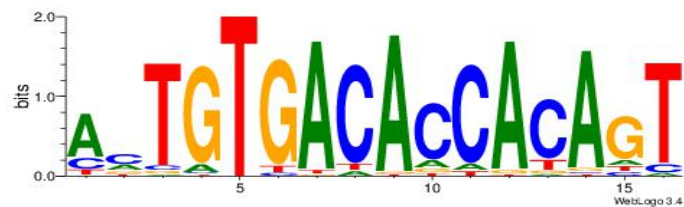


Dataset #: 4
 Motif ID: 71
 Motif name: AmTGTGACACCACAGT
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 10
 Number of overlap: 7
 Similarity score: 0.0597098

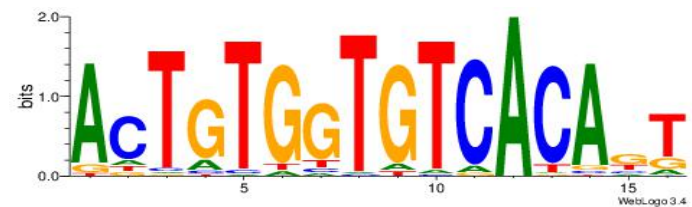
Alignment:

ACTGTGGTGTACART
 ACTTTGG-----

Original motif Consensus sequence: AMTGTGACACCACAGT



Reverse complement motif Consensus sequence: ACTGTGGTGTACART



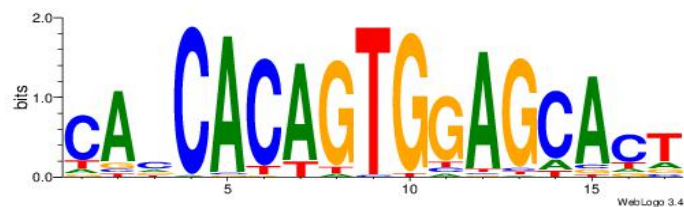
Dataset #: 4
 Motif ID: 76
 Motif name: CACACAGTGGAGCACT
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 9

Number of overlap: 7
Similarity score: 0.061942

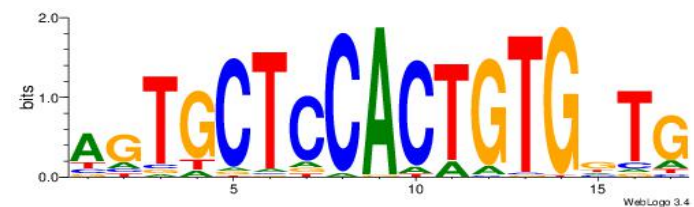
Alignment:

AGTGCTCCACTGTGDTG
-----ACTTTGG--

Original motif Consensus sequence: CAHCACAGTGGAGCACT



Reverse complement motif Consensus sequence:
AGTGCTCCACTGTGDTG

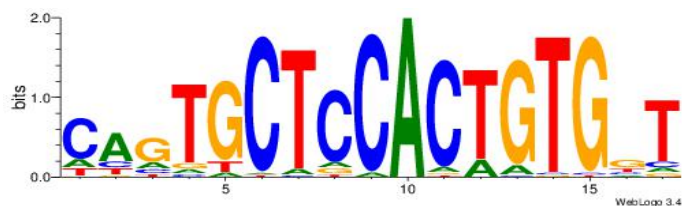


Dataset #: 4
Motif ID: 70
Motif name: CagTGCTCCACTGTGgT
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 2
Number of overlap: 7
Similarity score: 0.0625

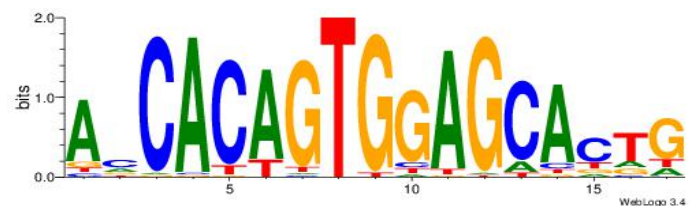
Alignment:

ABCACAGTGGAGCACTG
-CCAAAGT-----

Original motif Consensus sequence: CAGTGCTCCACTGTGBT



Reverse complement motif Consensus sequence: ABCACAGTGGAGCACTG



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

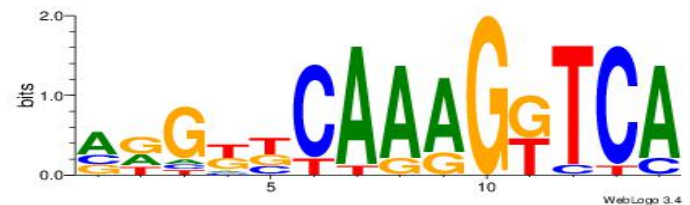
Alignment:

TGAMCTTTGMMCYT
---ACTTTGG----

Original motif Consensus sequence: TGAMCTTTGMMCYT



Reverse complement motif Consensus sequence: AKGYCAAAGRTC

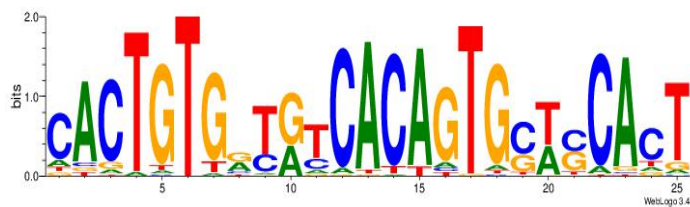


Dataset #: 4
 Motif ID: 72
 Motif name: CACTGTGrYrtCACAGTGswsCAcT
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 7
 Similarity score: 0.0714286

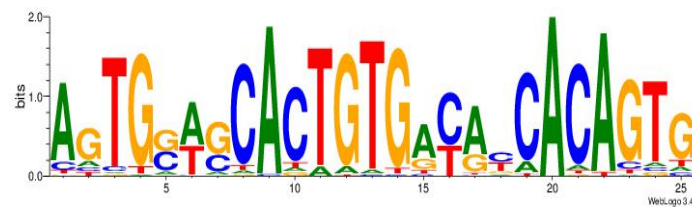
Alignment:

CACTGTGRTRTCACAGTGSWSCACT
 -ACTTTGG-----

Original motif Consensus sequence:
 CACTGTGRTRTCACAGTGSWSCACT



Reverse complement motif Consensus sequence:
 AGTGSWSCACTGTGAMAMCACAGTG



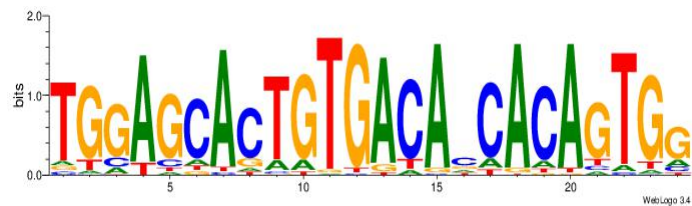
Dataset #: 4
 Motif ID: 73
 Motif name: TGGAGCACTGTGACAcCACAGTGg
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3

Number of overlap: 7
Similarity score: 0.0714286

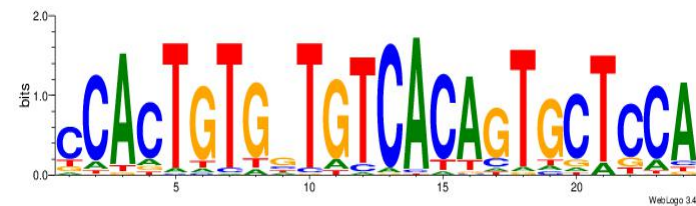
Alignment:

TGGAGCACTGTGACAVCACAGTGG
-----CCAAAGT--

Original motif Consensus sequence: TGGAGCACTGTGACAVCACAGTGG



Reverse complement motif Consensus sequence: CCAGTGTGTCACAGTGCTCCA

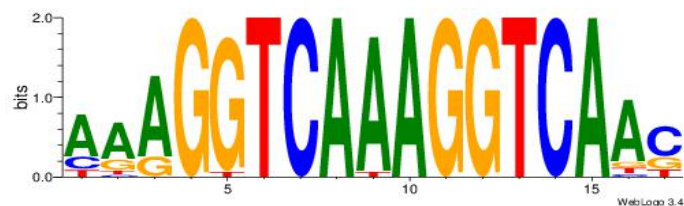


Dataset #: 3
Motif ID: 60
Motif name: NR1H2RXRA
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 5
Number of overlap: 7
Similarity score: 0.0728571

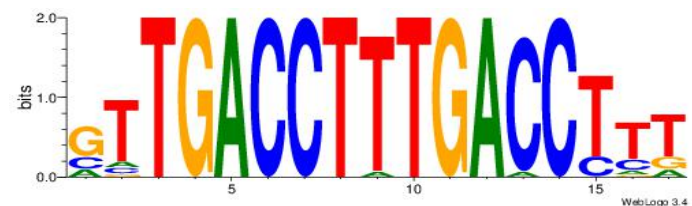
Alignment:

GTTGACCTTTGACCTTT
----ACTTTGG-----

Original motif Consensus sequence: AAAGGTCAAAGGTCAAC



Reverse complement motif Consensus sequence: GTTGACCTTTGACCTTT



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

Original motif Consensus sequence: GGAAM



Reverse complement motif Consensus sequence: YTTCC



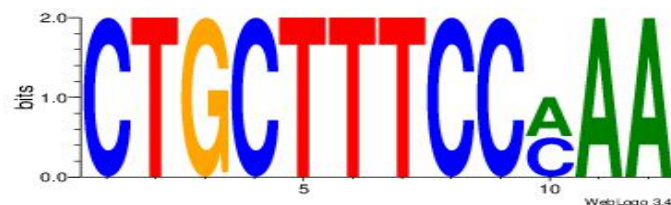
Best Matches for Top Significant Motif ID 50 (Highest to Lowest)

Dataset #:	1
Motif ID:	21
Motif name:	Motif 21
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	4
Number of overlap:	5
Similarity score:	0.01875

Alignment:

CTGCTTTCCMAA
---YTTCC----

Original motif Consensus sequence: CTGCTTTCCMAA



Reverse complement motif Consensus sequence: TTYGGAAAGCAG



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

Alignment:

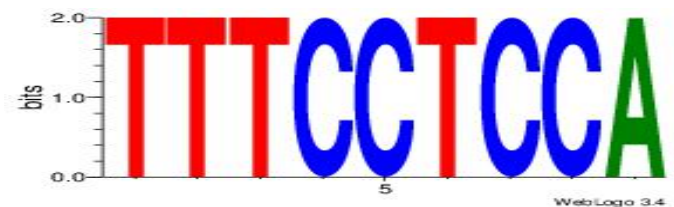
TTTCCTCCA

YTTCC----

Original motif Consensus sequence: TGGAGGAAA



Reverse complement motif Consensus sequence: TTTCCTCCA



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

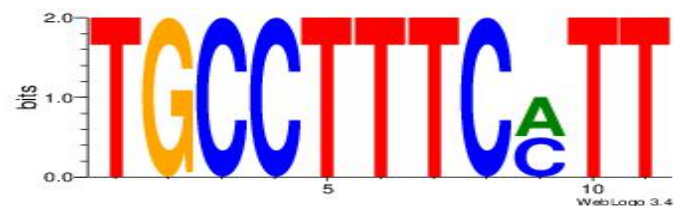
Alignment:

TGCCTTTCYTT
 ----YTTCC--

Original motif Consensus sequence: AAKGAAAGGCA



Reverse complement motif Consensus sequence: TGCCTTTCYTT



Dataset #: 1
 Motif ID: 44
 Motif name: Motif 44
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3

Number of overlap: 5
Similarity score: 0.05625

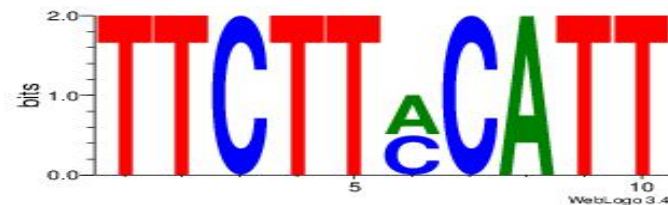
Alignment:

TTCTTYCATT
--YTTCC---

Original motif Consensus sequence: AATGKAAGAA



Reverse complement motif Consensus sequence: TTCTTYCATT



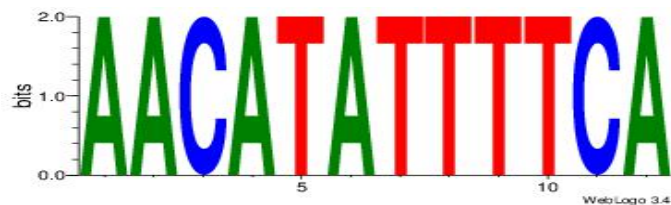
Dataset #: 1
Motif ID: 9
Motif name: Motif 9
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 8
Number of overlap: 5
Similarity score: 0.06875

Alignment:

TGAAAATATGTT
-----GGAAM

Original motif Consensus sequence: AACATATTTTCA

Reverse complement motif Consensus sequence: TGAAAATATGTT



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

Alignment:
 CTTTCTCT
 -YTTCC--

Original motif Consensus sequence: AGAGAAAG



Reverse complement motif Consensus sequence: CTTTCTCT



Dataset #: 1
 Motif ID: 28

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

Alignment:

ATTTAGTAAA
 -----GGAAM

Original motif Consensus sequence: ATTTAGTAAA



Reverse complement motif Consensus sequence: TTTACTAAAT



Dataset #:	1
Motif ID:	8
Motif name:	Motif 8
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	7
Number of overlap:	5
Similarity score:	0.06875

Alignment:

AAGSATTTTCA

-----YTTCC

Original motif Consensus sequence: TGAAAATCCTT



Reverse complement motif Consensus sequence: AAGSATTTTCA



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

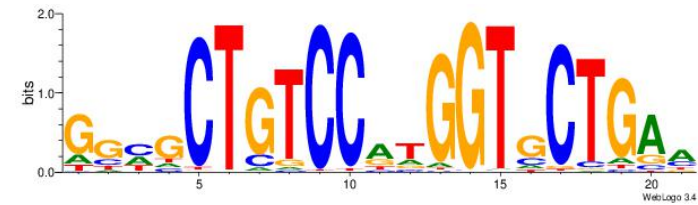
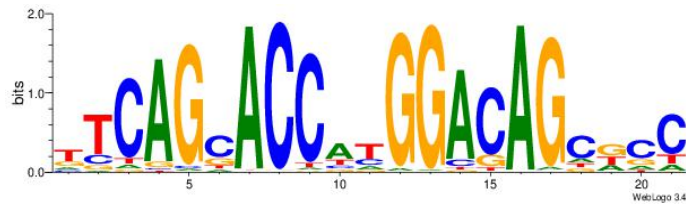
Alignment:

GGYGCTGTCCATGGTGCTGAA

-----YTTCC-----

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC

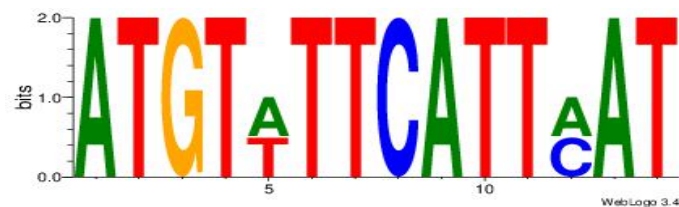
Reverse complement motif Consensus sequence:
GGYGCTGTCCATGGTGCTGAA



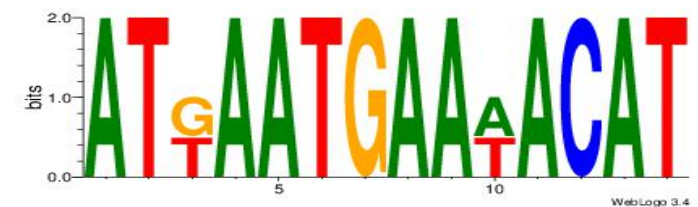
Dataset #: 1
 Motif ID: 23
 Motif name: Motif 23
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 5
 Number of overlap: 5
 Similarity score: 0.075

Alignment:
 ATGTW TTCATTMAT
 -----YTTCC-----

Original motif Consensus sequence: ATGTW TTCATTMAT



Reverse complement motif Consensus sequence: ATYAATGAAWACA



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

Original motif Consensus sequence: AAGGTCAC



Reverse complement motif Consensus sequence: GTGACCTT



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

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

Alignment:

CTTCTGACCTC

GTGACCTT---

Original motif Consensus sequence: CTTCTGACCTC



Reverse complement motif Consensus sequence: GAGGTCAGAAG



Dataset #: 1
 Motif ID: 15
 Motif name: Motif 15
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 8
 Similarity score: 0.040519

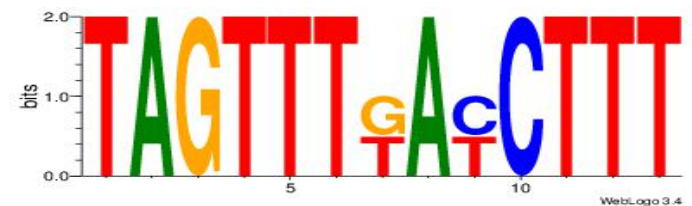
Alignment:

AAAGRTMAAACTA
 -AAGGTCAC-----

Original motif Consensus sequence: AAAGRTMAAACTA



Reverse complement motif Consensus sequence: TAGTTTYAKCTTT



Dataset #: 1
 Motif ID: 24
 Motif name: Motif 24
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 4
 Number of overlap: 8

Similarity score: 0.0539119

Alignment:

TTWATGWCTTT

---GTGACCTT

Original motif Consensus sequence: AAAGWCATWAA



Reverse complement motif Consensus sequence: TTWATGWCTTT



Dataset #: 4
Motif ID: 72
Motif name: CACTGTGrYrtCACAGTGswsCAcT
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 7
Number of overlap: 8
Similarity score: 0.0557243

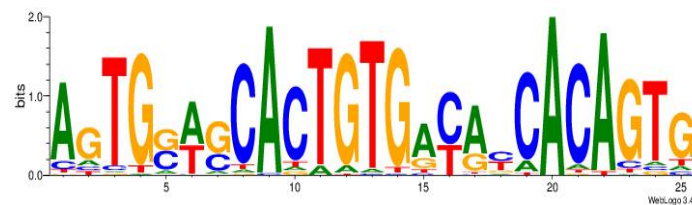
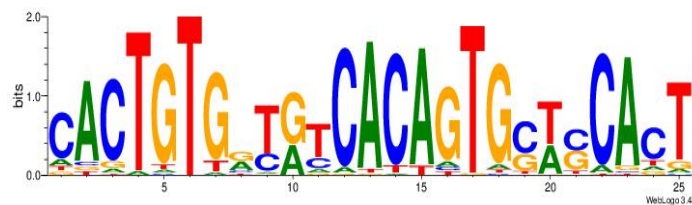
Alignment:

CACTGTGRTRTCACAGTGSWSCACT

-----AAGGTCAC-----

Original motif Consensus sequence:
CACTGTGRTRTCACAGTGSWSCACT

Reverse complement motif Consensus sequence:
AGTGSWSCACTGTGAMAMCACAGTG



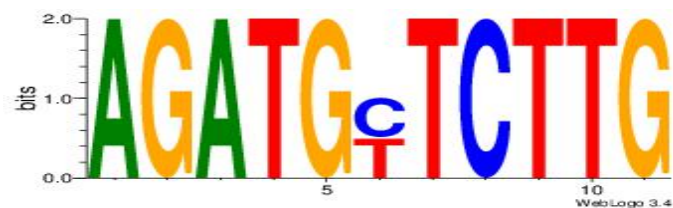
Dataset #: 1
 Motif ID: 35
 Motif name: Motif 35
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 8
 Similarity score: 0.0566591

Alignment:

AGATGYTCTTG

-GTGACCTT--

Original motif Consensus sequence: AGATGYTCTTG



Reverse complement motif Consensus sequence: CAAGAKCATCT



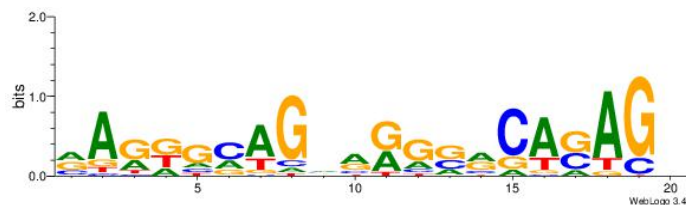
Dataset #: 5
 Motif ID: 93

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

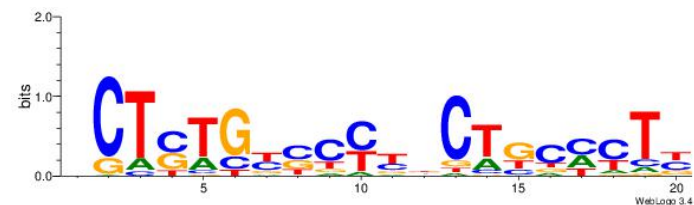
Alignment:

RAGKGMAGVRRGSRASAGV
 -----AAGGTCAC---

Original motif Consensus sequence: RAGKGMAGVRRGSRASAGV



Reverse complement motif Consensus sequence: VCTSTGKSCMKBCTRCYCTK



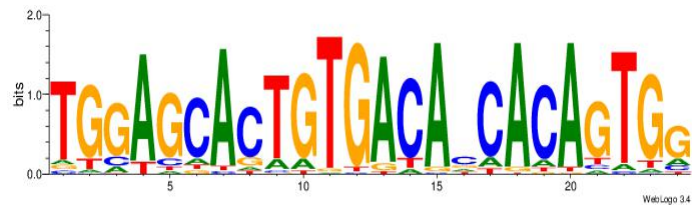
Dataset #: 4
 Motif ID: 73
 Motif name: TGGAGCACTGTGACACACAGTGg
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 8
 Number of overlap: 8
 Similarity score: 0.060729

Alignment:

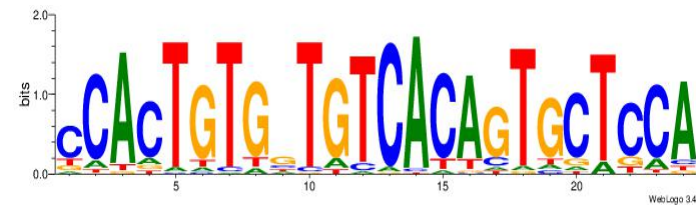
CCACTGTGVTGTCACAGTGCTCCA

-----AAGGTCAC-----

Original motif Consensus sequence: TGGAGCACTGTGACAVCACAGTGG



Reverse complement motif Consensus sequence:
CCACTGTGVTGTCACAGTGCTCCA



Dataset #:	4
Motif ID:	71
Motif name:	AmTGTGACACCACAGT
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	6
Number of overlap:	8
Similarity score:	0.0645146

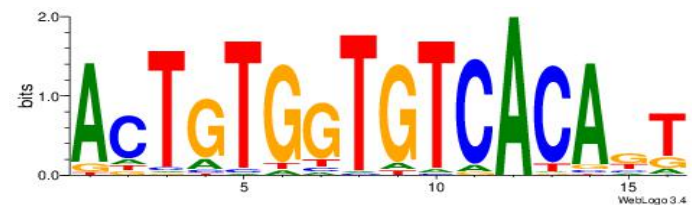
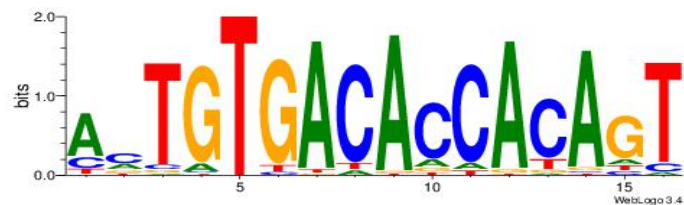
Alignment:

ACTGTGGTGTACART

-----AAGGTCAC---

Original motif Consensus sequence: AMTGTGACACCACAGT

Reverse complement motif Consensus sequence:
ACTGTGGTGTACART

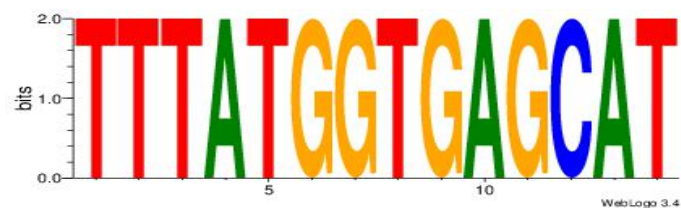


Dataset #: 1
 Motif ID: 22
 Motif name: Motif 22
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 7
 Number of overlap: 8
 Similarity score: 0.0664462

Alignment:

TTTATGGTGAGCAT
 GTGACCTT-----

Original motif Consensus sequence: TTTATGGTGAGCAT



Reverse complement motif Consensus sequence: ATGCTCACCATAAA



Dataset #: 1
 Motif ID: 18

Motif name:	Motif 18
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	2
Number of overlap:	8
Similarity score:	0.0674765

Alignment:

GCTGGACTTTG

-GTGACCTT--

Original motif Consensus sequence: CAAAGTCCAGC



Reverse complement motif Consensus sequence: GCTGGACTTTG



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

Original motif Consensus sequence: CCGCGGRCACG



Reverse complement motif Consensus sequence: CGTGKCCGCGG



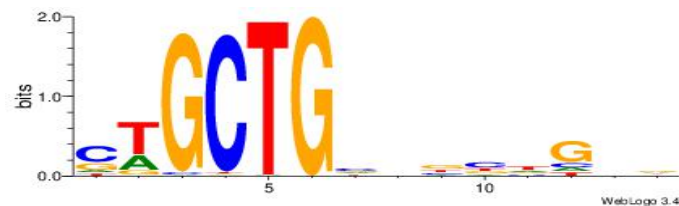
Best Matches for Top Significant Motif ID 79 (Highest to Lowest)

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

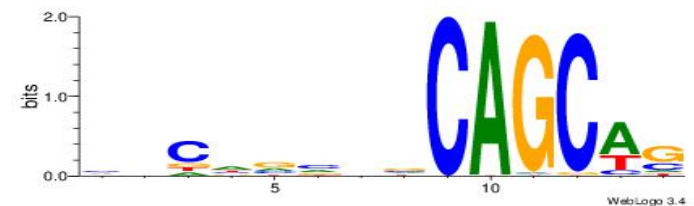
Alignment:

HVCDBBDBCAGCAG
 ---CGTGKCCGCGG

Original motif Consensus sequence: CTGCTGBDBBDGBD



Reverse complement motif Consensus sequence: HVCDBBDBCAGCA



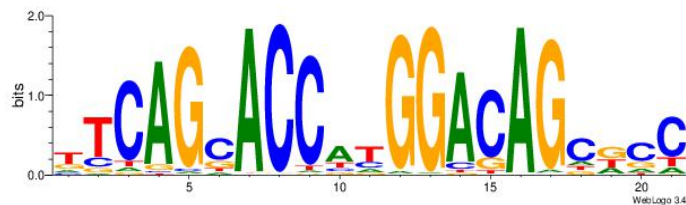
Dataset #: 3
 Motif ID: 57
 Motif name: REST
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 4
 Number of overlap: 11

Similarity score: 0.0484441

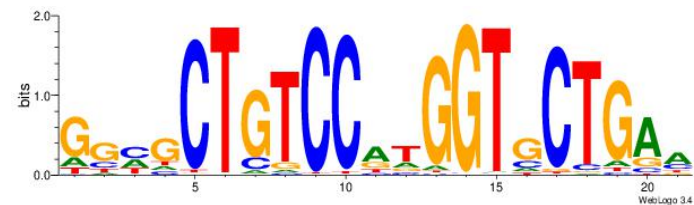
Alignment:

TTCAGCACCATGGACAGCKCC
-----CCGCGGRCACG---

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC



Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA



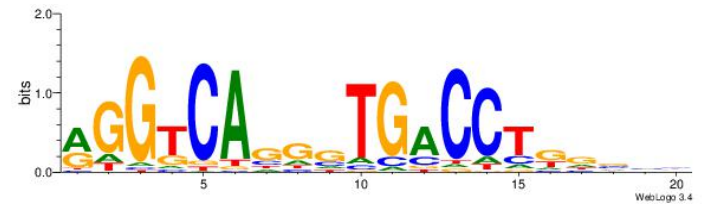
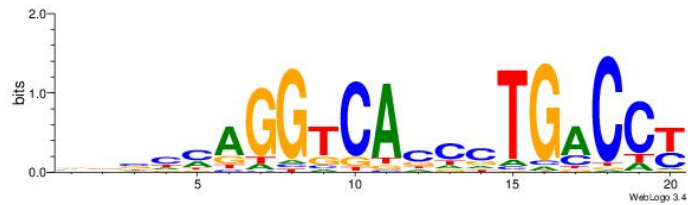
Dataset #: 3
Motif ID: 53
Motif name: ESR1
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 3
Number of overlap: 11
Similarity score: 0.0486581

Alignment:

MGGTCAGGGTGACCTRDBHV
-----CGTGKCCGCGG---

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY

Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV

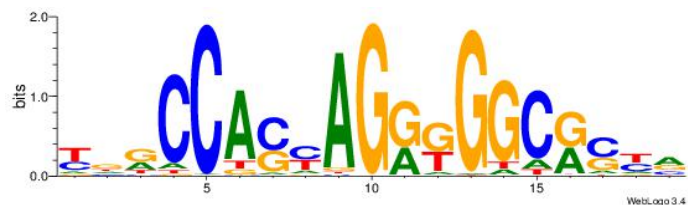


Dataset #: 3
 Motif ID: 66
 Motif name: CTCF
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 11
 Similarity score: 0.0588663

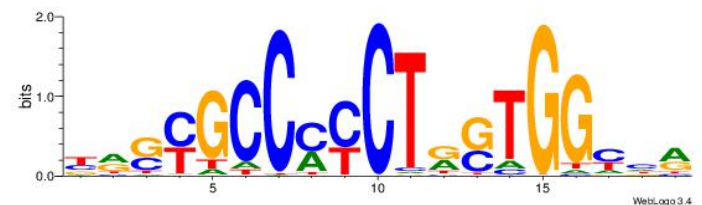
Alignment:

YDRCCASYAGRKGGRSYV
 -----CCGCGGRCACG-

Original motif Consensus sequence: YDRCCASYAGRKGGRSYV



Reverse complement motif Consensus sequence: BMSMGCCYMCTKSTGGMHM



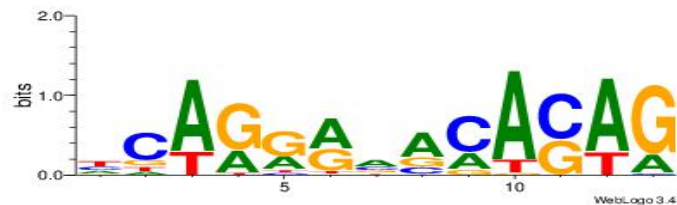
Dataset #: 1

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

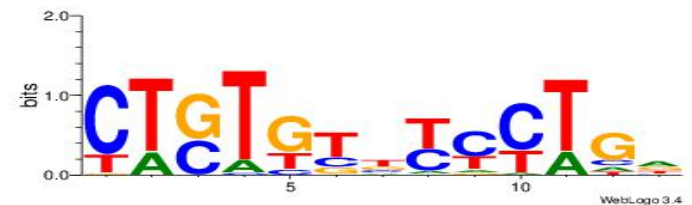
Alignment:

HCAGRRVACASAG
 -CCGCGGRCACG-

Original motif Consensus sequence: HCAGRRVACASAG



Reverse complement motif Consensus sequence: CTSTGTBKMCTGH



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

Alignment:

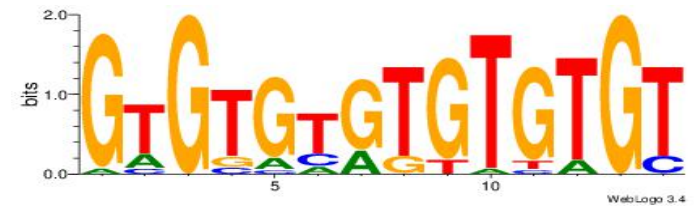
GTGTGTGTGTGTGT

-CGTGKCCGCGG--

Original motif Consensus sequence: ACACACACACAC



Reverse complement motif Consensus sequence: GTGTGTGTGTGT



Dataset #:	5
Motif ID:	93
Motif name:	TFM12
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	5
Number of overlap:	11
Similarity score:	0.0625015

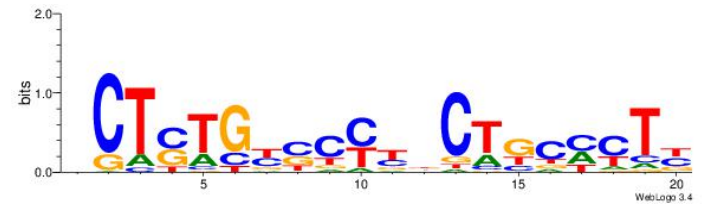
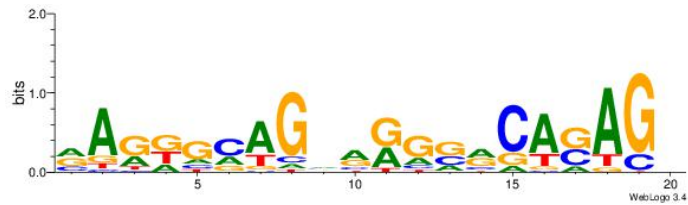
Alignment:

RAGKGMAGVRRGSRCASAGV

-----CCGCGGRCACG-----

Original motif Consensus sequence: RAGKGMAGVRRGSRCASAGV

Reverse complement motif Consensus sequence:
VCTSTGKSCMKBCTRCYCTK

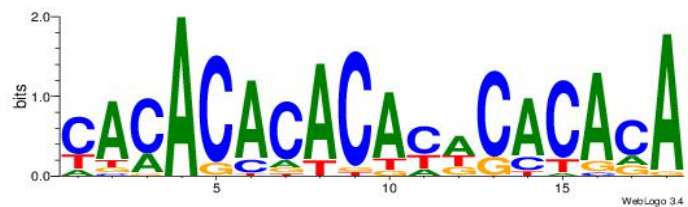


Dataset #: 5
 Motif ID: 89
 Motif name: TFM1
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 11
 Similarity score: 0.0628056

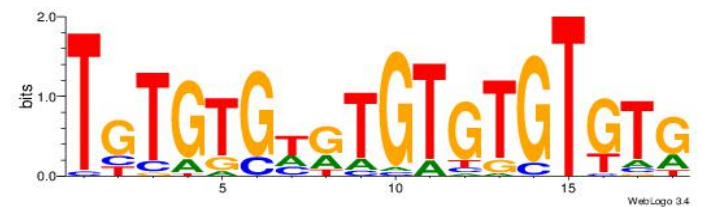
Alignment:

CACACACACACWCACACA
 -----CCGCGGRCACG--

Original motif Consensus sequence: CACACACACACWCACACA



Reverse complement motif Consensus sequence: TGTGTGWGTGTGTGTGTG



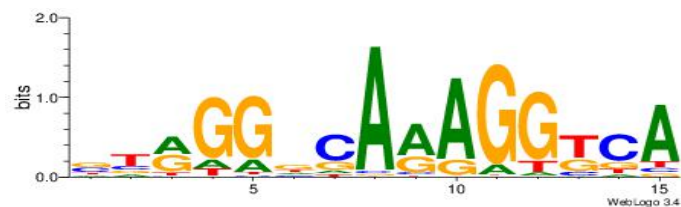
Dataset #: 3

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

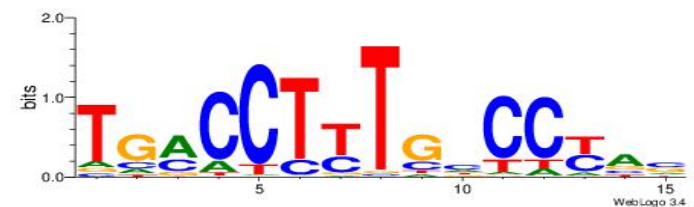
Alignment:

TGRCCTKTGHCKAB
 ---CGTGKCCGCGG-

Original motif Consensus sequence: BTRGGDCARAGGKCA



Reverse complement motif Consensus sequence: TGRCCTKTGHCKAB



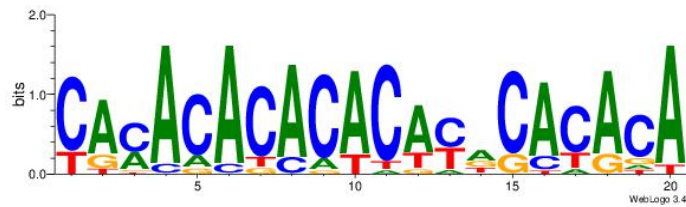
Dataset #: 5
 Motif ID: 92
 Motif name: TFM11
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 8
 Number of overlap: 11
 Similarity score: 0.0634175

Alignment:

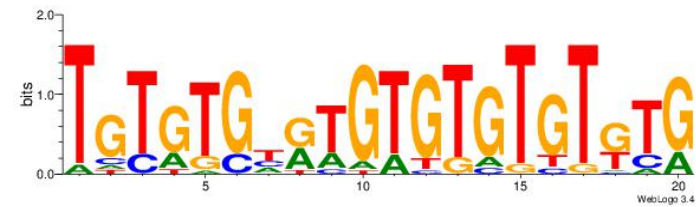
CAMACACACACAYDCACACA

-----CCGCGGRCACG--

Original motif Consensus sequence: CAMACACACACAYDCACACA



Reverse complement motif Consensus sequence: TGTGTGDKTGTGTGTGTRTG



Results created by MOTIFSIM on 09-23-2015 12:07:36

Runtime: 137.654 seconds.

MOTIFSIM is written by Ngoc Tam L. Tran

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