



MOTIFSIM - MOTIF SIMilarity Detection Tool

Version 2.1

INPUT

Input Parameters

Number of files:	4
Number of top significant motifs:	10
Number of best matches:	5
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
DREME_DM254.txt	45	1
MEME-CHIP_DM254.txt	24	2
PScanChIP_DM254.txt	63	3
RSAT_peak-motifs_DM254.txt	39	4

RESULTS

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

Dataset #: 2 Motif ID: 46 Motif name: Motif 46

Original motif Consensus sequence: AGRKGGCR



Reverse complement motif Consensus sequence: KGCCYKCT



Best Matches for Top Significant Motif ID 46 (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:	Forward
Position number:	1
Number of overlap:	8
Similarity score:	0

Alignment:
AGRKGGCR
AGRKGGCR

Original motif Consensus sequence: AGRKGGCR

Reverse complement motif Consensus sequence: KGCCYKCT



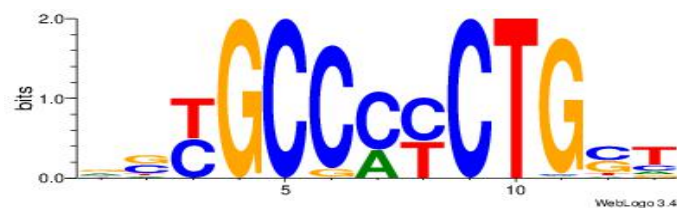
Dataset #: 4
 Motif ID: 147
 Motif name: asCAGrkGGCrSy
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 8
 Similarity score: 0.00651548

Alignment:
 ASCAGRGGGCRSB
 ---AGRKGCCR--

Original motif Consensus sequence: ASCAGRGGGCRSB



Reverse complement motif Consensus sequence: BSKGCCCMCTGST



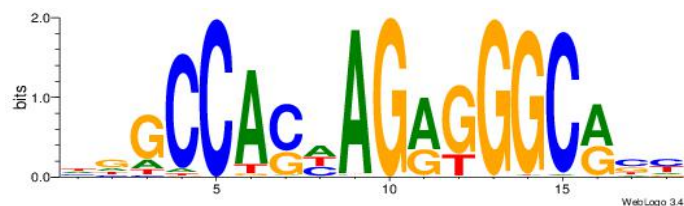
Dataset #: 4
 Motif ID: 165

Motif name: wgGCCAshAGrGGGCrSy
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 9
 Number of overlap: 8
 Similarity score: 0.0102443

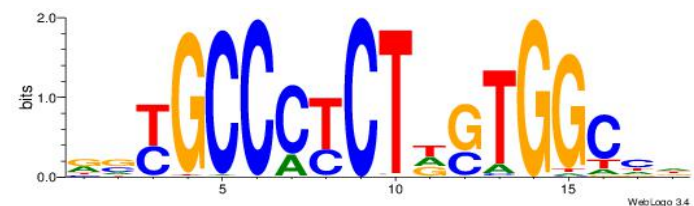
Alignment:

KBKGCCCKCTHGTGGCHH
 --KGCCYKCT-----

Original motif Consensus sequence: HDGCCACHAGRGGGCRBY



Reverse complement motif Consensus sequence: KBKGCCCKCTHGTGGCHH



Dataset #: 4
 Motif ID: 166
 Motif name: CasCAGrGGGCrSy
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3
 Number of overlap: 8
 Similarity score: 0.0104954

Alignment:

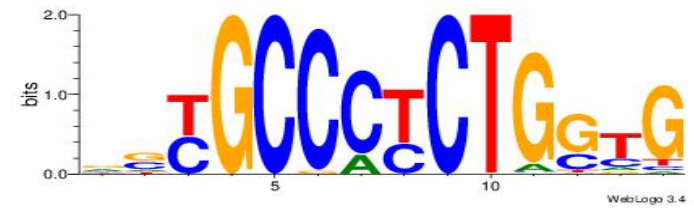
BSKGCCCKCTGGTG

--KGCCYKCT----

Original motif Consensus sequence: CACCAGRGGGCRSB



Reverse complement motif Consensus sequence: BSKGCCCKCTGGT



Dataset #:	4
Motif ID:	163
Motif name:	gwGGCCAGmAGAGGGCrby
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	3
Number of overlap:	8
Similarity score:	0.0165822

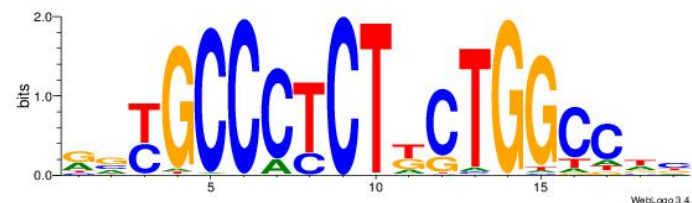
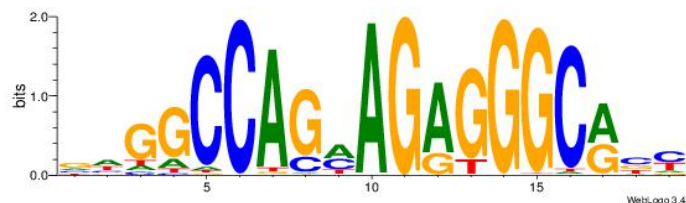
Alignment:

KBKGCCCTCTYCTGGCCHV

--KGCCYKCT-----

Original motif Consensus sequence: VHGGCCAGMAGAGGGCRBY

Reverse complement motif Consensus sequence:
KBKGCCCTCTYCTGGCCHV



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

Original motif Consensus sequence: AAATAH



Reverse complement motif Consensus sequence: DTATTT



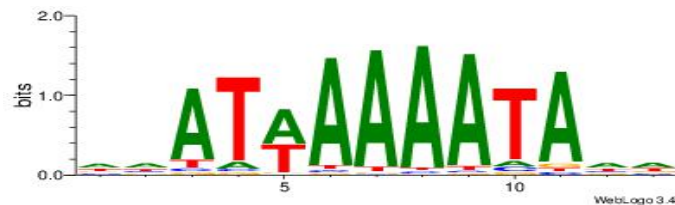
Best Matches for Top Significant Motif ID 8 (Highest to Lowest)

Dataset #:	4
Motif ID:	150
Motif name:	waATwAAAATAww
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2
Number of overlap:	6
Similarity score:	0.00224204

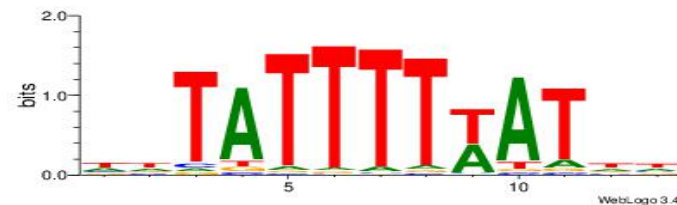
Alignment:

```
DHATWAAAATAHD
-----AAATAH-
```

Original motif Consensus sequence: DHATWAAAATAHD



Reverse complement motif Consensus sequence: DHTATTTTWATHD

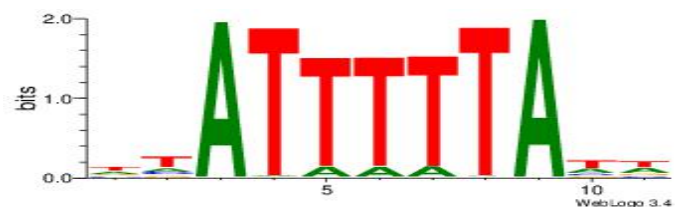


Dataset #: 4
 Motif ID: 157
 Motif name: wtATTTTAAww
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 6
 Number of overlap: 6
 Similarity score: 0.00556446

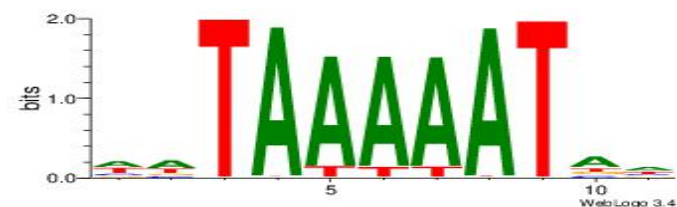
Alignment:

WWTAAAAATAD
 -----AAATAH

Original motif Consensus sequence: DTATTTTAAWW



Reverse complement motif Consensus sequence: WWTAAAAATAD

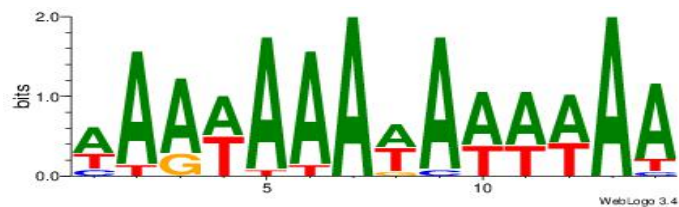


Dataset #: 2
 Motif ID: 68
 Motif name: Motif 68
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 5
 Number of overlap: 6
 Similarity score: 0.0128826

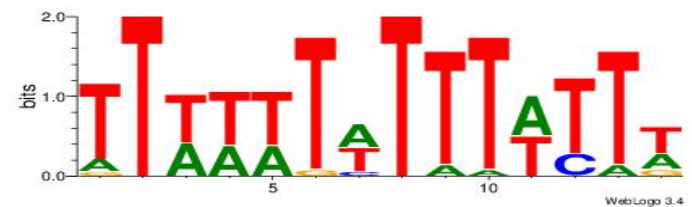
Alignment:

WAAWAAAWAWWWAA
 ----AAATAH-----

Original motif Consensus sequence: WAAWAAAWAWWWAA



Reverse complement motif Consensus sequence: TTWWWTWTTTWTTW



Dataset #: 2
 Motif ID: 52
 Motif name: Motif 52
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1

Number of overlap: 6
Similarity score: 0.0167304

Alignment:
AAATAAAW
AAATAH--

Original motif Consensus sequence: AAATAAAW



Reverse complement motif Consensus sequence: WTTTATTT

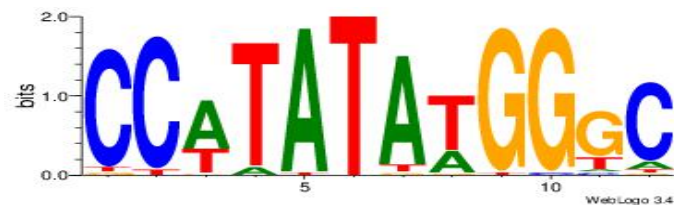
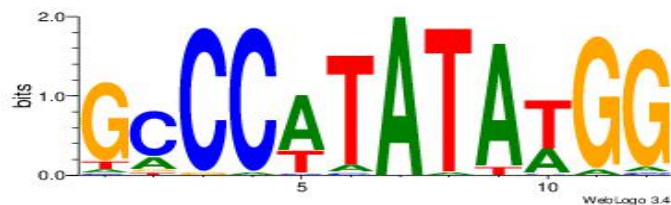


Dataset #: 3
Motif ID: 118
Motif name: SRF
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 3
Number of overlap: 6
Similarity score: 0.0210491

Alignment:
GCCCATATATGG
----AAATAH--

Original motif Consensus sequence: GCCCATATATGG

Reverse complement motif Consensus sequence: CCATATATGGGC



Dataset #: 1 Motif ID: 20 Motif name: Motif 20

Original motif Consensus sequence: CACGTR



Reverse complement motif Consensus sequence: MACGTG



Best Matches for Top Significant Motif ID 20 (Highest to Lowest)

Dataset #:	3
Motif ID:	71
Motif name:	Arnt
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	6
Similarity score:	0

Alignment:

CACGTG

CACGTR

Original motif Consensus sequence: CACGTG



Reverse complement motif Consensus sequence: CACGTG



Dataset #: 3
Motif ID: 95
Motif name: MYCMAX
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 3
Number of overlap: 6
Similarity score: 0.0102183

Alignment:

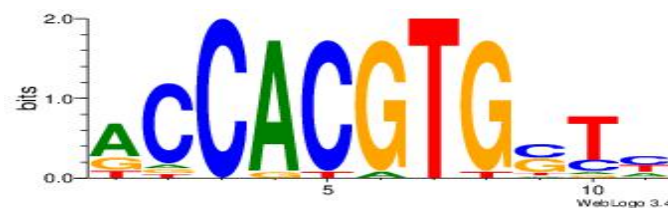
RASCACGTGGT

---MACGTG---

Original motif Consensus sequence: RASCACGTGGT



Reverse complement motif Consensus sequence: ACCACGTGSTM



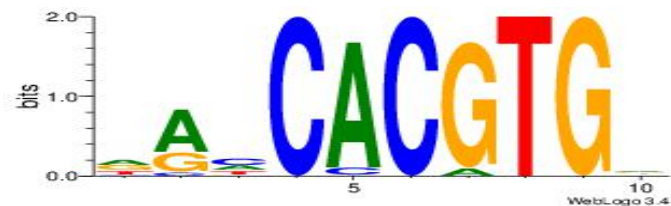
Dataset #: 3
 Motif ID: 91
 Motif name: MAX
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 4
 Number of overlap: 6
 Similarity score: 0.011152

Alignment:

BCACGTGDTD

-CACGTR---

Original motif Consensus sequence: DAHCACGTGD



Reverse complement motif Consensus sequence: BCACGTGDTD



Dataset #: 3
 Motif ID: 126
 Motif name: USF1
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 6

Similarity score: 0.0131944

Alignment:

MCACGTG

-CACGTR

Original motif Consensus sequence: CACGTGR



Reverse complement motif Consensus sequence: MCACGTG



Dataset #: 3
Motif ID: 94
Motif name: Myc
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 3
Number of overlap: 6
Similarity score: 0.0253396

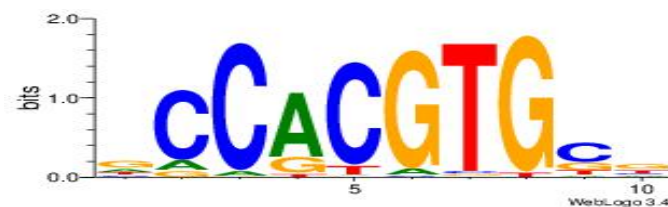
Alignment:

DCCACGTGCV

--CACGTR--

Original motif Consensus sequence: VGCACGTGGH

Reverse complement motif Consensus sequence: DCCACGTGCV



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

Original motif Consensus sequence: AGRKGGCR



Reverse complement motif Consensus sequence: KGCCYKCT



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

Dataset #:	2
Motif ID:	46
Motif name:	Motif 46
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	8
Similarity score:	0

Alignment:
 AGRKGGCR
 AGRKGGCR

Original motif Consensus sequence: AGRKGGCR



Reverse complement motif Consensus sequence: KGCCYKCT



Dataset #: 4
 Motif ID: 147
 Motif name: asCAGrkGGCrSy
 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: 0.00628523

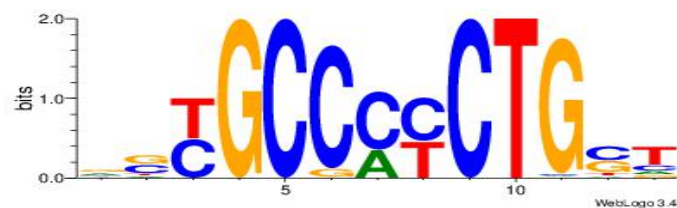
Alignment:

ASCAGRGGGCRSB
 ---AGRKGGCR---

Original motif Consensus sequence: ASCAGRGGGCRSB



Reverse complement motif Consensus sequence: BSKGCCCMCTGST

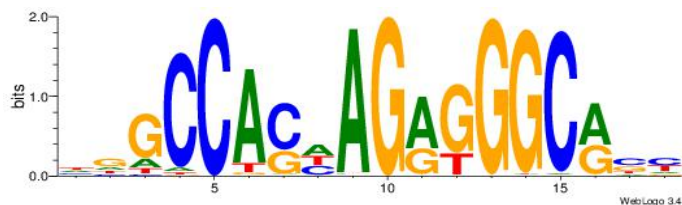


Dataset #: 4
 Motif ID: 165
 Motif name: wgGCCAshAGrGGGCrSy
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3
 Number of overlap: 8
 Similarity score: 0.0102152

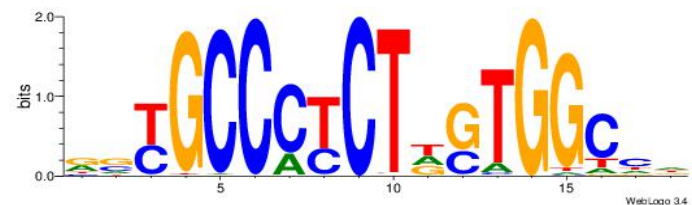
Alignment:

KBKGCCCKCTHGTGGCHH
 --KGCCYKCT-----

Original motif Consensus sequence: HDGCCACHAGRGGGCRBY



Reverse complement motif Consensus sequence: KBKGCCCKCTHGTGGCHH



Dataset #: 4
 Motif ID: 166
 Motif name: CasCAGrGGGCrSy
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3

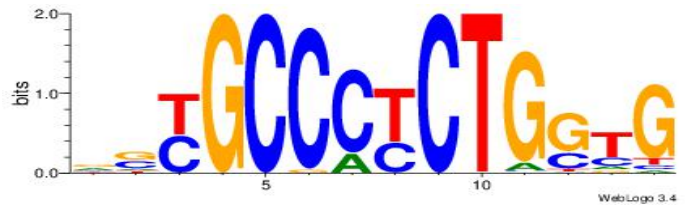
Number of overlap: 8
Similarity score: 0.0106761

Alignment:
CACCAGRGGGCRSB
-----AGRKGCCR--

Original motif Consensus sequence: CACCAGRGGGCRSB



Reverse complement motif Consensus sequence: BSKGCCCKCTGGT

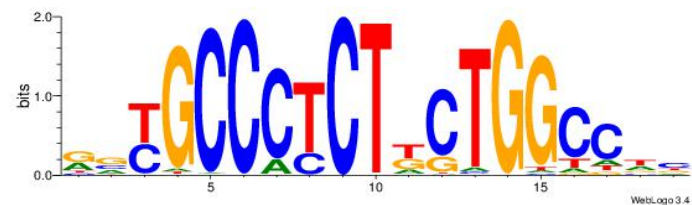
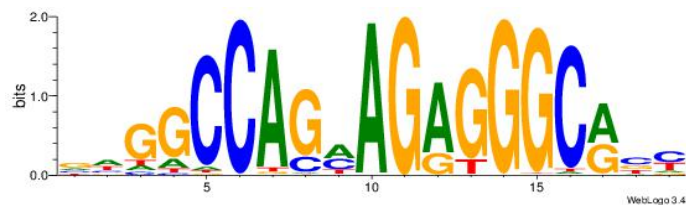


Dataset #: 4
Motif ID: 163
Motif name: gwGGCCAGmAGAGGGCrby
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 3
Number of overlap: 8
Similarity score: 0.016658

Alignment:
KBKGCCCTCTYCTGGCCHV
--KGCCYKCT-----

Original motif Consensus sequence: VHGGCCAGMAGAGGGCRBY

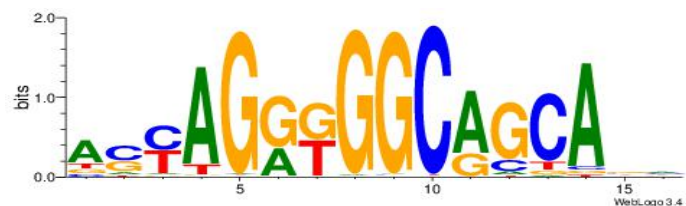
Reverse complement motif Consensus sequence:
KBKGCCCTCTYCTGGCCHV



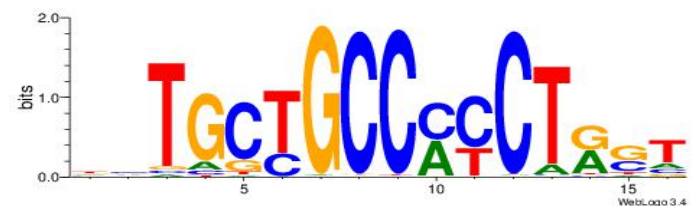
Dataset #: 4
 Motif ID: 164
 Motif name: asyAGrkGGCRGCa
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 8
 Similarity score: 0.0201849

Alignment:
 ASYAGRKGGCAGCABH
 ---AGRKGGCR-----

Original motif Consensus sequence: ASYAGRKGGCAGCABH



Reverse complement motif Consensus sequence: HBTGCTGCCYMCTKST



Dataset #: 3 Motif ID: 127 Motif name: YY1

Original motif Consensus sequence: RCCATB



Reverse complement motif Consensus sequence: BATGGM



Best Matches for Top Significant Motif ID 127 (Highest to Lowest)

Dataset #:	2
Motif ID:	61
Motif name:	Motif 61
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:	0.00122549

Alignment:

AGATGGY

BATGGM-

Original motif Consensus sequence: AGATGGY



Reverse complement motif Consensus sequence: KCCATCT



Dataset #: 1
 Motif ID: 12
 Motif name: Motif 12
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 6
 Similarity score: 0.00857843

Alignment:
 GAGCCATC
 RCCATB--

Original motif Consensus sequence: GATGGCTC



Reverse complement motif Consensus sequence: GAGCCATC

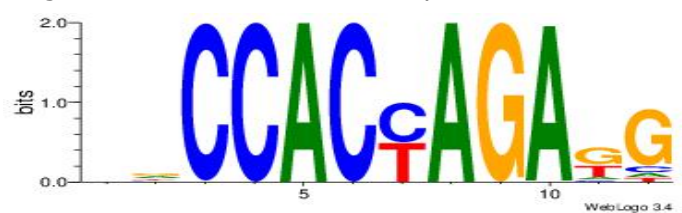


Dataset #: 4
 Motif ID: 145
 Motif name: grCCACyAGAkG
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 6

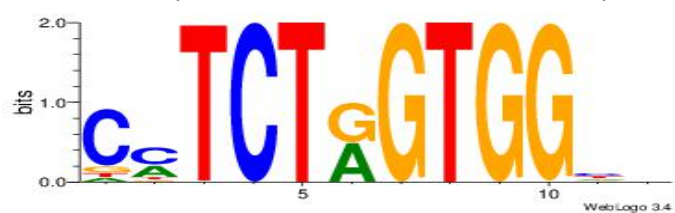
Similarity score: 0.022036

Alignment:
CYTCTKGTGGHH
-----BATGGM-

Original motif Consensus sequence: DDCCACYAGAKG



Reverse complement motif Consensus sequence: CYTCTKGTGGHH

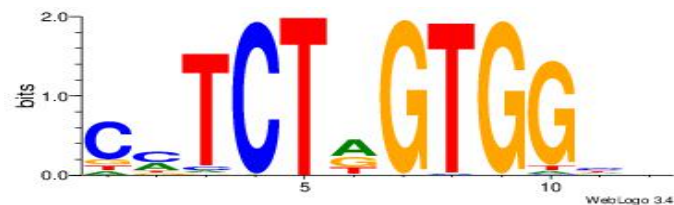
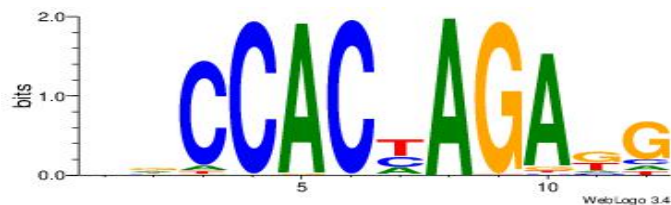


Dataset #: 4
Motif ID: 138
Motif name: grCCACyAGAkG
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 2
Number of overlap: 6
Similarity score: 0.0223679

Alignment:
DDCCACYAGAKG
-RCCATB-----

Original motif Consensus sequence: DDCCACYAGAKG

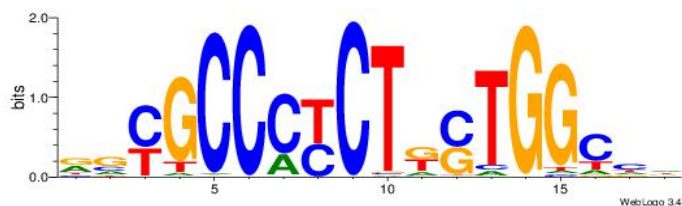
Reverse complement motif Consensus sequence: CYTCTMGTGGHH



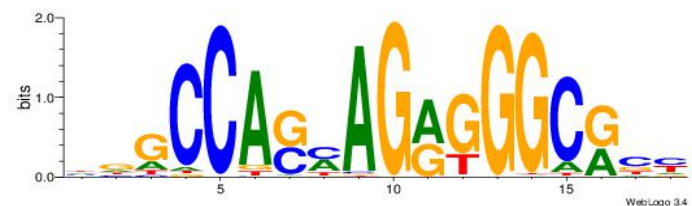
Dataset #: 4
 Motif ID: 156
 Motif name: rgyGCCMyCTksTGGccd
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3
 Number of overlap: 6
 Similarity score: 0.0275501

Alignment:
 DDGCCASYAGMGGGCKVM
 --RCCATB-----

Original motif Consensus sequence: RVYGCCCYCTKSTGGCHD

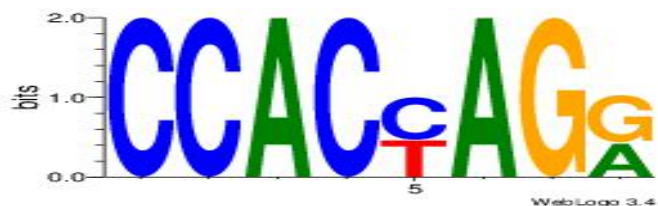


Reverse complement motif Consensus sequence: DDGCCASYAGMGGGCKVM



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

Original motif Consensus sequence: CCACYAGR



Reverse complement motif Consensus sequence: MCTKGTGG

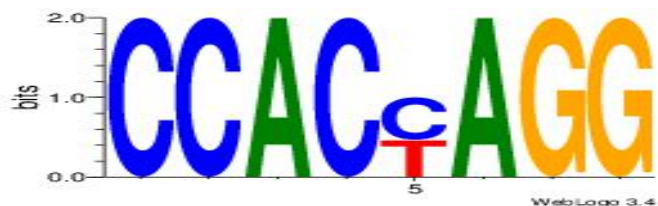


Best Matches for Top Significant Motif ID 48 (Highest to Lowest)

Dataset #:	1
Motif ID:	21
Motif name:	Motif 21
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	8
Similarity score:	0.00903109

Alignment:
CCACYAGG
CCACYAGR

Original motif Consensus sequence: CCACYAGG



Reverse complement motif Consensus sequence: CCTKGTGG

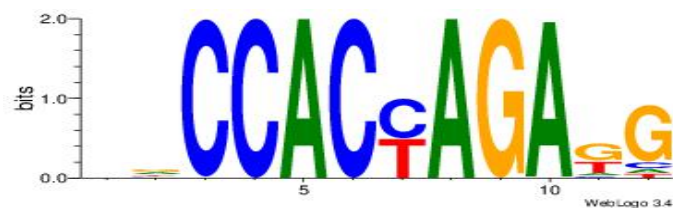


Dataset #: 4
 Motif ID: 145
 Motif name: grCCACyAGAkG
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 8
 Similarity score: 0.0155354

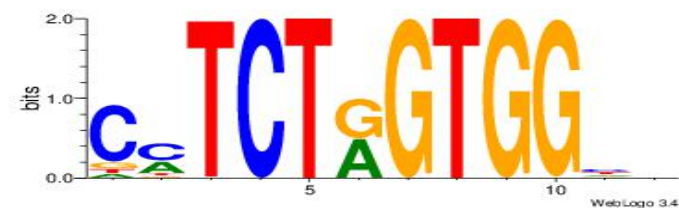
Alignment:

DDCCACYAGAKG
 --CCACYAGR--

Original motif Consensus sequence: DDCCACYAGAKG



Reverse complement motif Consensus sequence: CYTCTKGTGGHH



Dataset #: 4
 Motif ID: 158
 Motif name: grCCACwAGrk
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 8

Similarity score: 0.0192652

Alignment:
DDCCACWAGRK
--CCACYAGR--

Original motif Consensus sequence: DDCCACWAGRK



Reverse complement motif Consensus sequence: YMCTWGTGGHH

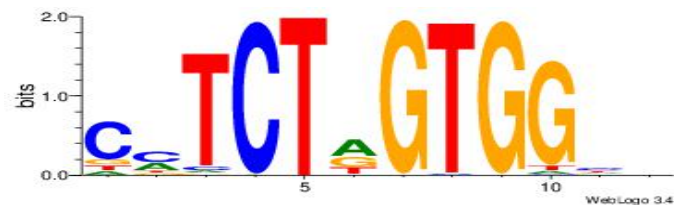
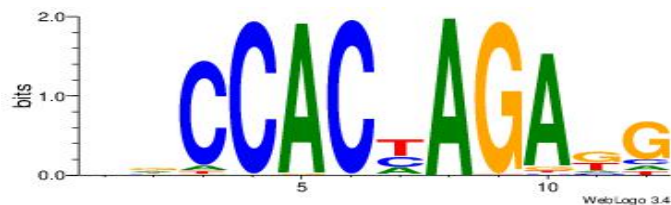


Dataset #: 4
Motif ID: 138
Motif name: grCCACyAGAkG
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 3
Number of overlap: 8
Similarity score: 0.0244381

Alignment:
DDCCACYAGAKG
--CCACYAGR--

Original motif Consensus sequence: DDCCACYAGAKG

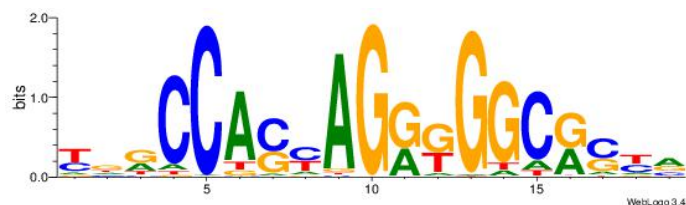
Reverse complement motif Consensus sequence: CYTCTMGTGGHH



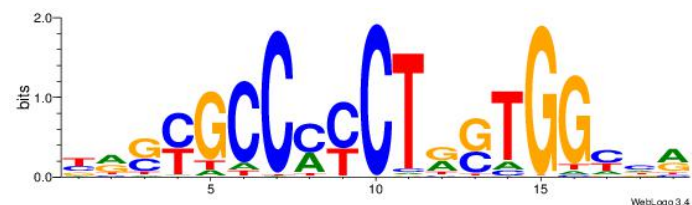
Dataset #: 3
 Motif ID: 74
 Motif name: CTCF
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 9
 Number of overlap: 8
 Similarity score: 0.0284404

Alignment:
 BSMGCCYMCTKSTGGMHM
 -----MCTKGTGG---

Original motif Consensus sequence: YDRCCASYAGRKGGCRSYV



Reverse complement motif Consensus sequence: BSMGCCYMCTKSTGGMHM



Dataset #: 2 Motif ID: 65 Motif name: Motif 65

Original motif Consensus sequence: ARAACA



Reverse complement motif Consensus sequence: TGTTMT



Best Matches for Top Significant Motif ID 65 (Highest to Lowest)

Dataset #:	4
Motif ID:	141
Motif name:	raCAAAACam
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:	0.00122368

Alignment:

DACAAAACAH

---ARAACA-

Original motif Consensus sequence: DACAAAACAH



Reverse complement motif Consensus sequence: HTGTTTTGTD



Dataset #: 1
 Motif ID: 44
 Motif name: Motif 44
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 6
 Similarity score: 0.0101983

Alignment:
 GDAAACA
 -ARAACA

Original motif Consensus sequence: GDAAACA



Reverse complement motif Consensus sequence: TGTTTDC



Dataset #: 4
 Motif ID: 159
 Motif name: kkAAGAGCAsy
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 6

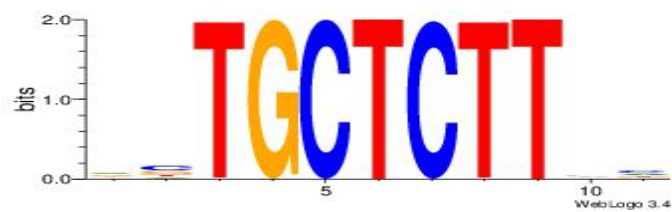
Similarity score: 0.0232212

Alignment:
DBAAGAGCAVH
---ARAACA--

Original motif Consensus sequence: DBAAGAGCAVH



Reverse complement motif Consensus sequence: HVTGCTCTTBH

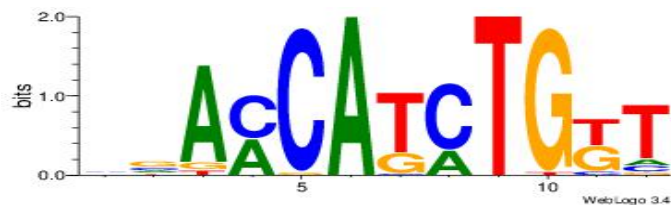


Dataset #: 3
Motif ID: 121
Motif name: TAL1TCF3
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 7
Number of overlap: 6
Similarity score: 0.0330056

Alignment:
HVAMCATCTGKT
ARAACA-----

Original motif Consensus sequence: HVAMCATCTGKT

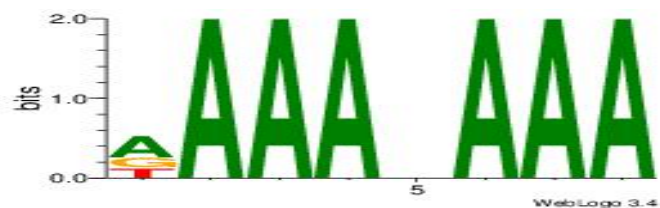
Reverse complement motif Consensus sequence: ARCAGATGRTVD



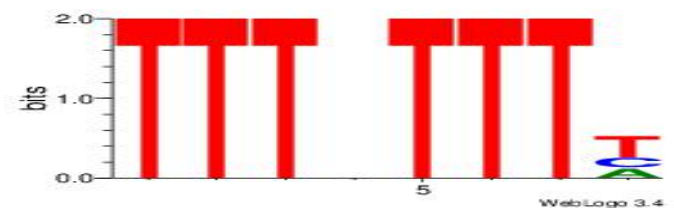
Dataset #: 1
 Motif ID: 2
 Motif name: Motif 2
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 6
 Similarity score: 0.0333069

Alignment:
 AAAAHAAA
 ARAACA--

Original motif Consensus sequence: AAAAHAAA



Reverse complement motif Consensus sequence: TTTDTTTT



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

Original motif Consensus sequence: CCCCDCCC



Reverse complement motif Consensus sequence: GGGDGGGG



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

Dataset #:	2
Motif ID:	59
Motif name:	Motif 59
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	8
Similarity score:	0.00363191

Alignment:
 CCCCRCRCC
 CCCCDCCC

Original motif Consensus sequence: CCCCRCRCC



Reverse complement motif Consensus sequence: GGGKGGGG

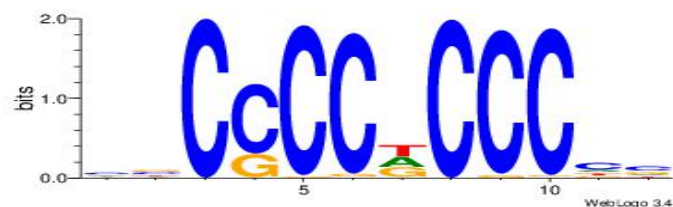


Dataset #: 4
 Motif ID: 155
 Motif name: csCSCCdCCCcs
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 8
 Similarity score: 0.00464015

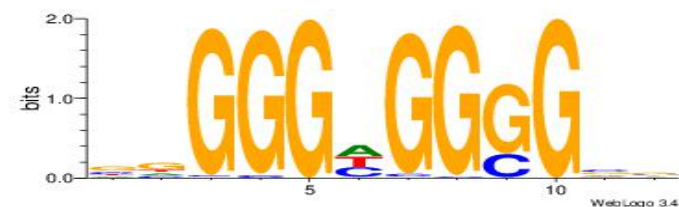
Alignment:

VBCCCCDCCCHV
 --CCCCDCCC--

Original motif Consensus sequence: VBCCCCDCCCHV



Reverse complement motif Consensus sequence: VDGGGDGGGGBV



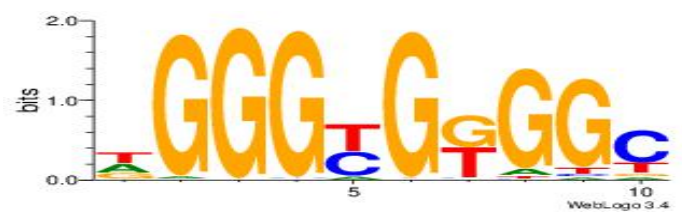
Dataset #: 3
 Motif ID: 89
 Motif name: Klf4
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 8

Similarity score: 0.0352587

Alignment:

GCCYCMCCCD
-CCCCDCCC-

Original motif Consensus sequence: DGGYGKGGC



Reverse complement motif Consensus sequence: GCCYCMCCCD



Dataset #: 4
Motif ID: 154
Motif name: csCsCCTCCcc
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 3
Number of overlap: 8
Similarity score: 0.0361349

Alignment:

VBCCCCTCCHB
--CCCCDCCC-

Original motif Consensus sequence: VBCCCCTCCHB

Reverse complement motif Consensus sequence: BDGGAGGGGBV



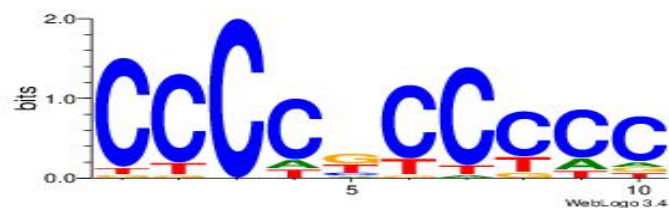
Dataset #: 3
 Motif ID: 116
 Motif name: SP1
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 8
 Similarity score: 0.0368066

Alignment:

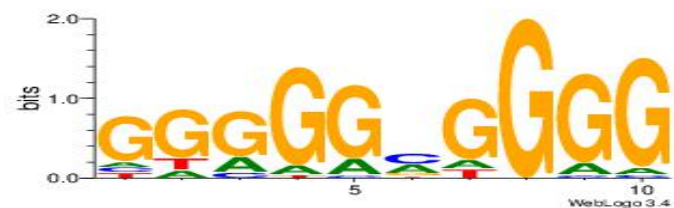
CCCCKCCCCC

CCCDCCC--

Original motif Consensus sequence: CCCCKCCCCC



Reverse complement motif Consensus sequence: GGGGYGGGG



Dataset #: 3 Motif ID: 72 Motif name: ArntAhr

Original motif Consensus sequence: YGCGTG



Reverse complement motif Consensus sequence: CACGCM



Best Matches for Top Significant Motif ID 72 (Highest to Lowest)

Dataset #: 4
 Motif ID: 134
 Motif name: ssCGwGCGss
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 5
 Number of overlap: 6
 Similarity score: 0.0128947

Alignment:

BSCGWGCGBV
 YGCGTG----

Original motif Consensus sequence: BSCGWGCGBV



Reverse complement motif Consensus sequence: VBCGCWCGSB



Dataset #: 1
 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: 1
 Number of overlap: 6
 Similarity score: 0.0206428

Alignment:

MACGTG

YGCGTG

Original motif Consensus sequence: CACGTR



Reverse complement motif Consensus sequence: MACGTG



Dataset #: 1
 Motif ID: 42
 Motif name: Motif 42
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 6

Similarity score: 0.0259081

Alignment:
CSGCGCG
YGCGTG-

Original motif Consensus sequence: CGCGCSG



Reverse complement motif Consensus sequence: CSGCGCG



Dataset #: 4
Motif ID: 152
Motif name: yrCATGCAyr
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 3
Number of overlap: 6
Similarity score: 0.0279287

Alignment:
BRCATGCABD
--CACGCM--

Original motif Consensus sequence: BRCATGCABD

Reverse complement motif Consensus sequence: HVTGCATGKV



Dataset #: 2
 Motif ID: 57
 Motif name: Motif 57
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 6
 Similarity score: 0.0315171

Alignment:
 ACACACAY
 -CACGCM-

Original motif Consensus sequence: ACACACAY



Reverse complement motif Consensus sequence: KTGTGTGT



Dataset #: 3 Motif ID: 101 Motif name: NFIC

Original motif Consensus sequence: TTGGCD



Reverse complement motif Consensus sequence: DGCCAA



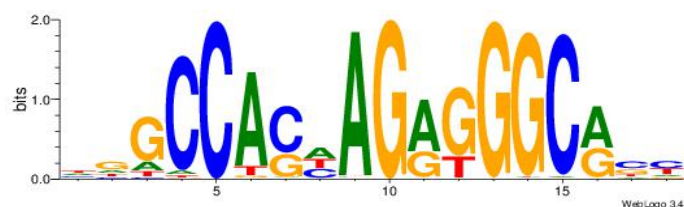
Best Matches for Top Significant Motif ID 101 (Highest to Lowest)

Dataset #: 4
 Motif ID: 165
 Motif name: wgGCCAshAGrGGGCrSy
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 12
 Number of overlap: 6
 Similarity score: 0.0215379

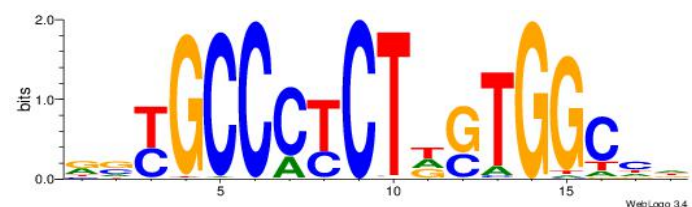
Alignment:

HDGCCACHAGRGGGCRBY
 -DGCCAA-----

Original motif Consensus sequence: HDGCCACHAGRGGGCRBY



Reverse complement motif Consensus sequence: KBKGCCCKCTHGTGGCHH

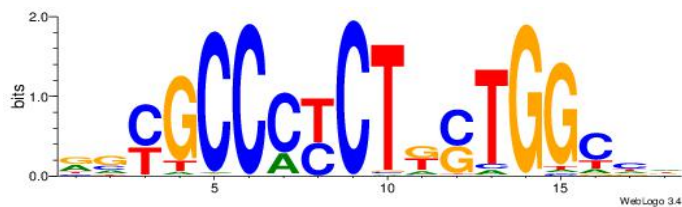


Dataset #: 4
 Motif ID: 156
 Motif name: rgyGCCMyCTksTGGccd
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 6
 Similarity score: 0.026631

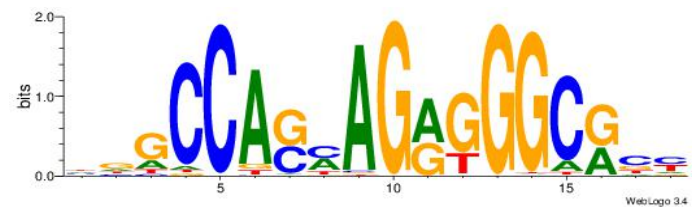
Alignment:

DDGCCASYAGMGGGCKVM
 -DGCCAA-----

Original motif Consensus sequence: RYVGCCCYCTKSTGGCHD



Reverse complement motif Consensus sequence: DDGCCASYAGMGGGCKVM



Dataset #: 4
 Motif ID: 151
 Motif name: agrCCAGmAGrg
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2

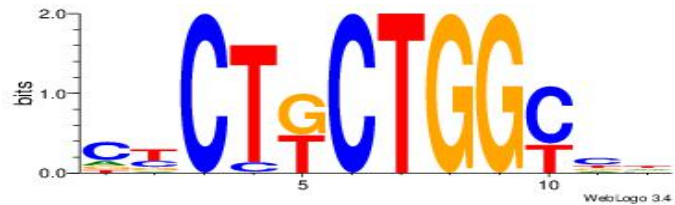
Number of overlap: 6
Similarity score: 0.0273632

Alignment:
CKCTRCTGGCVH
-----TTGGCD-

Original motif Consensus sequence: HVGCCAGMAGRG



Reverse complement motif Consensus sequence: CKCTRCTGGCVH



Dataset #: 1
Motif ID: 9
Motif name: Motif 9
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 2
Number of overlap: 6
Similarity score: 0.0280507

Alignment:
SWGCCACC
-DGCCAA-

Original motif Consensus sequence: GGTGGCWS

Reverse complement motif Consensus sequence: SWGCCACC

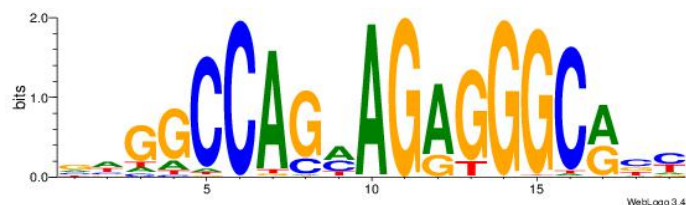


Dataset #: 4
 Motif ID: 163
 Motif name: gwGGCCAGmAGAGGGCrby
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 6
 Similarity score: 0.0280858

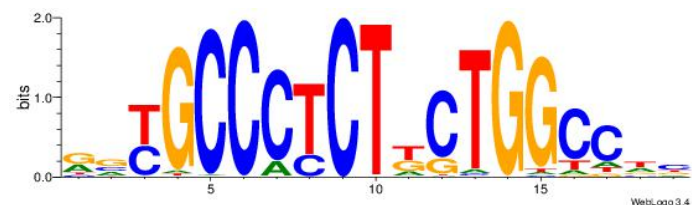
Alignment:

KBKGCCCTCTYCTGGCCHV
 -----TTGGCD--

Original motif Consensus sequence: VHGGCCAGMAGAGGGCRBY



Reverse complement motif Consensus sequence: KBKGCCCTCTYCTGGCCHV



Results created by MOTIFSIM on 11-19-2016 22:45:25
Runtime: 1028.98 seconds

MOTIFSIM is written by Ngoc Tam L. Tran
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