MOTIFSIM - MOTIF SIMilarity Detection Tool

Version 2.2

INPUT

Input Parameters

Number of files:	4
Number of top significant motifs:	10
Number of best matches:	5
Similarity cutoff >=	0.75
Matching motif database:	UniProbe Mus Musculus
Motif 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
---AGRKGGCR--
```

Original motif Consensus sequence: ASCAGRGGGCRSB

Reverse complement motif Consensus sequence: BSKGCCCMCTGST

Dataset #: 4

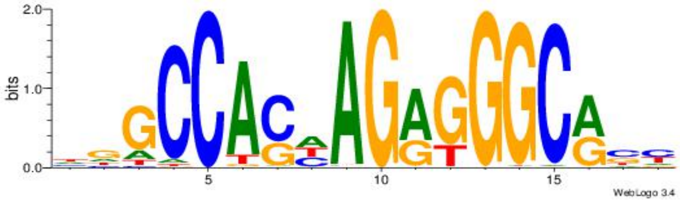
Motif ID: 165

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

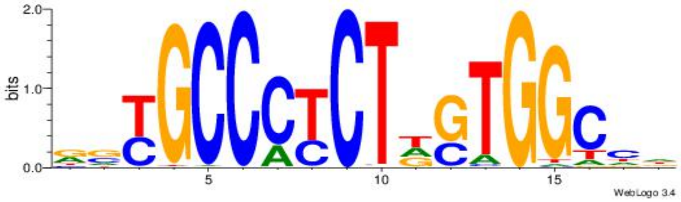
Alignment:

```
KBKGCCCKCTHGTGGCHH
--KGCCYKCT--------
```

Original motif Consensus sequence: HDGCCACHAGRGGGCRBY



Reverse complement motif Consensus sequence: KBKGCCCKCTHGTGGCHH

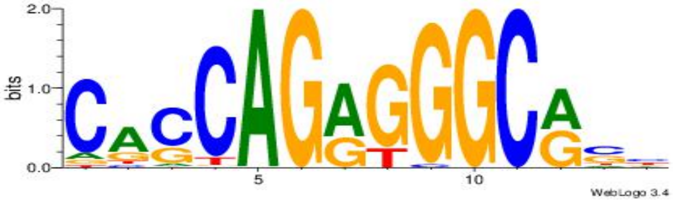


Dataset #:	4
Motif ID:	166
Motif name:	CasCAGrGGGCrsy
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	5
Number of overlap:	8
Similarity score:	0.0104954

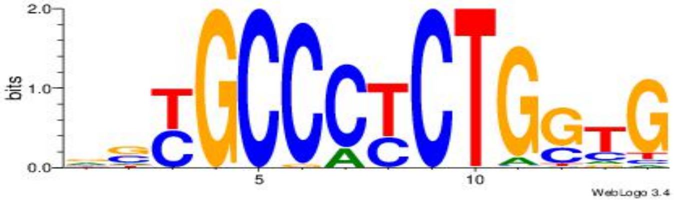
Alignment:

```
CACCAGRGGGCRSB
----AGRKGGCR--
```

Original motif Consensus sequence: CACCAGRGGGCRSB



Reverse complement motif Consensus sequence: BSKGCCCKCTGGT



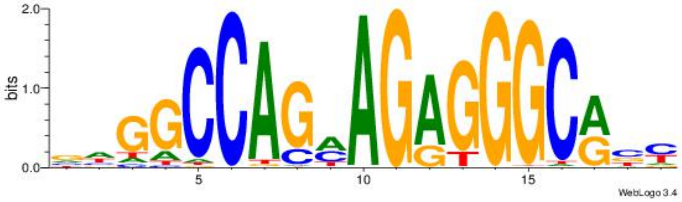
Dataset #:	4
Motif ID:	163
Motif name:	gwGGCCAGmAGAGGGCrby
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	3
Number of overlap:	8
Similarity score:	0.0165822

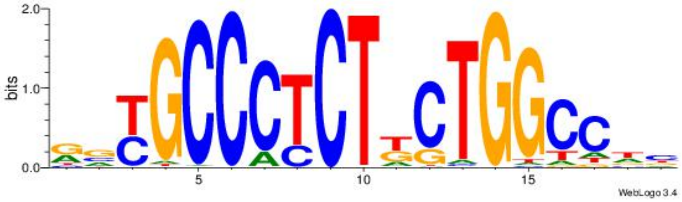
Alignment:

```
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

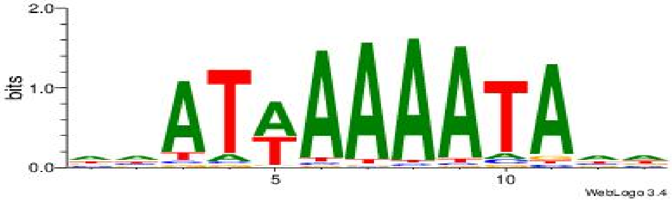
Best Matches for Top Significant Motif ID 8 (Highest to Lowest)

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

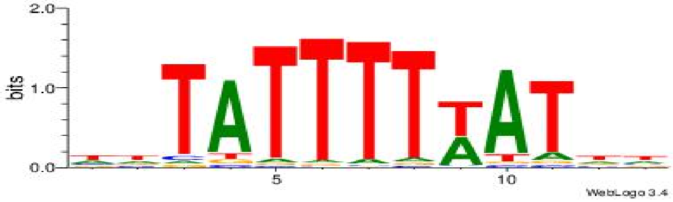
Alignment:

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

Original motif Consensus sequence: DHATWAAAATAHD



Reverse complement motif Consensus sequence: DHTATTTTWATHD

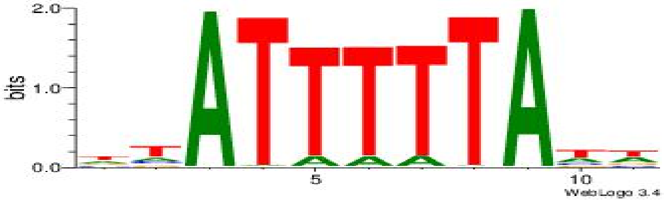


Dataset #:	4
Motif ID:	157
Motif name:	wtATTTTTAww
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	6
Similarity score:	0.00556446

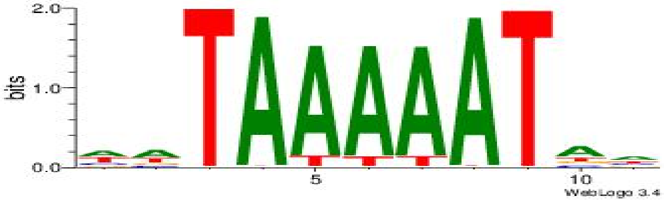
Alignment:

```
WWTAAAAATAD
-----AAATAH
```

Original motif Consensus sequence: DTATTTTTAWW



Reverse complement motif Consensus sequence: WWTAAAAATAD

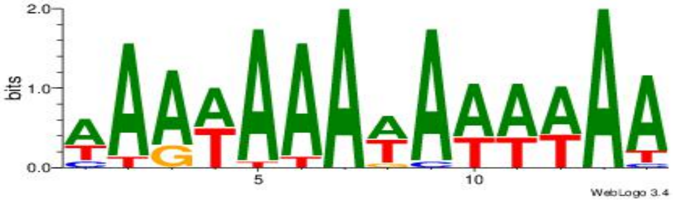


Dataset #: 2
Motif ID: 68
Motif name: Motif 68
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 5
Number of overlap: 6
Similarity score: 0.0128826

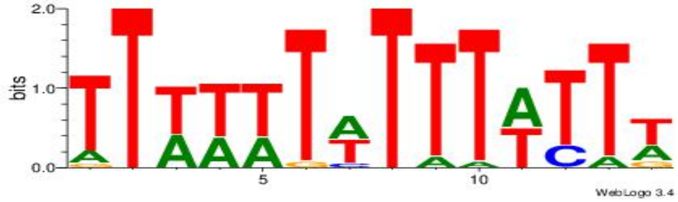
Alignment:

```
WAAWAAAWAWWWAA
----AAATAH----
```

Original motif Consensus sequence: WAAWAAAWAWWWAA



Reverse complement motif Consensus sequence: TTWWWTWTTTWTTW



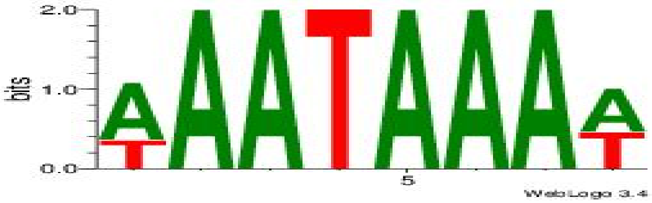
Dataset #: 2
Motif ID: 52
Motif name: Motif 52
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1

Number of overlap:	6
Similarity score:	0.0167304

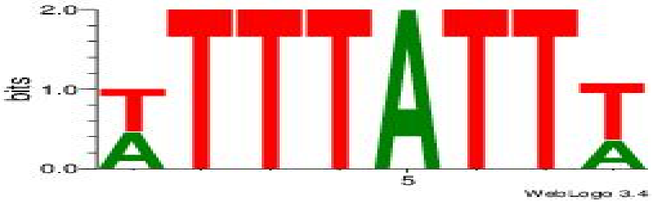
Alignment:

AAATAAAW
AAATAH--

Original motif Consensus sequence: AAATAAAW



Reverse complement motif Consensus sequence: WTTTATTT



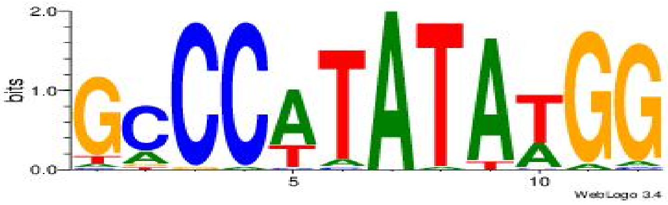
Dataset #:	3
Motif ID:	118
Motif name:	SRF
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	3
Number of overlap:	6
Similarity score:	0.0210491

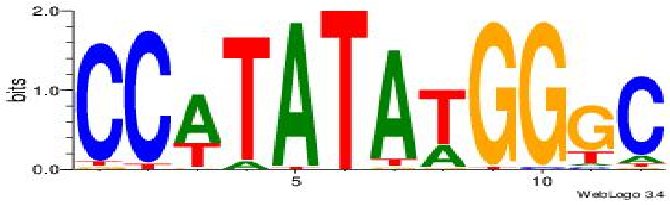
Alignment:

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

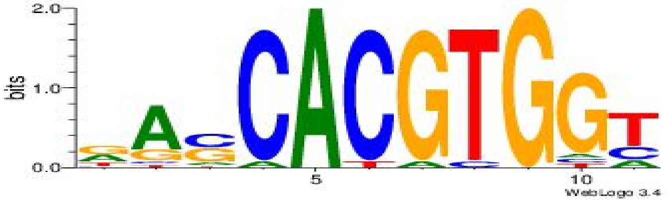
Reverse complement motif Consensus sequence: CACGTG

Dataset #:	3
Motif ID:	95
Motif name:	MYCMAX
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	4
Number of overlap:	6
Similarity score:	0.0102183

Alignment:

```
RASCACGTGGT
---MACGTG--
```

Original motif Consensus sequence: RASCACGTGGT



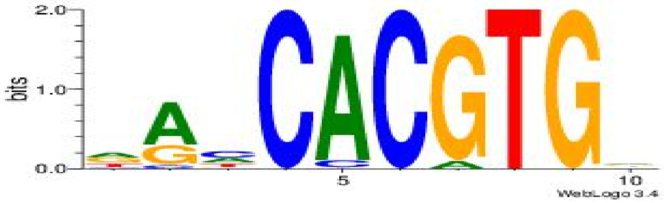
Reverse complement motif Consensus sequence: ACCACGTGSTM

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

Alignment:

```
DAHCACGTGD
---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

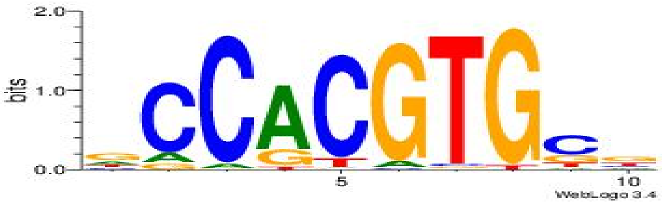
Similarity score: 0.0253396

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

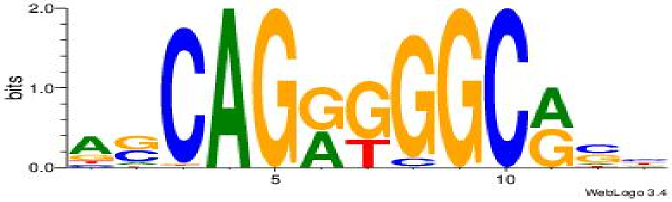
Reverse complement motif Consensus sequence: KGCCYKCT

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



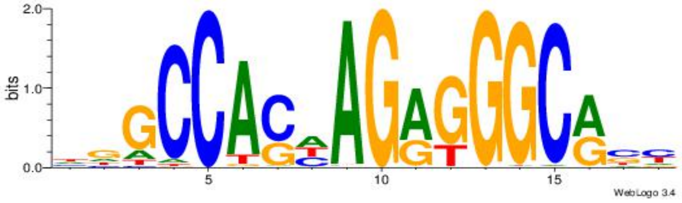
Reverse complement motif Consensus sequence: BSKGCCCMCTGST

Dataset #:	4
Motif ID:	165
Motif name:	wgGCCAshAGrGGGCrsy
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	3
Number of overlap:	8
Similarity score:	0.0102152

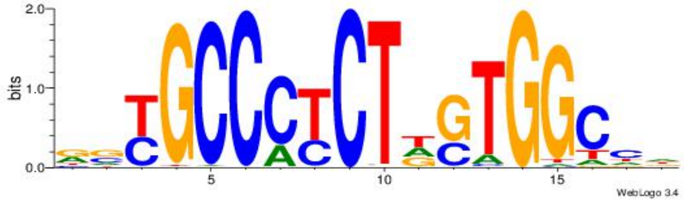
Alignment:

```
HDGCCACHAGRGGGCRBY
--------AGRKGGCR--
```

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

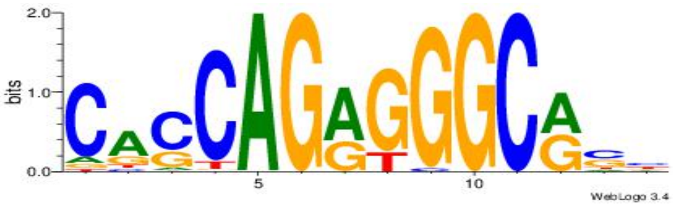
Number of overlap: 8

Similarity score: 0.0106761

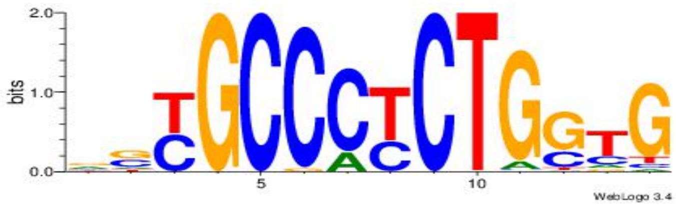
Alignment:

```
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

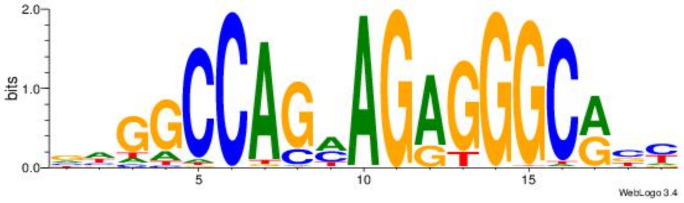
Similarity score: 0.016658

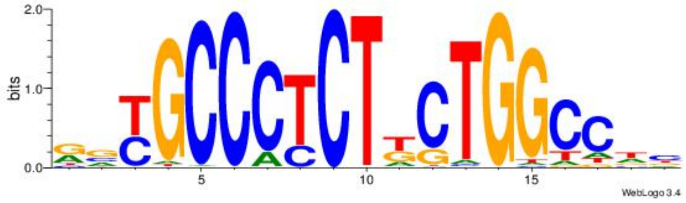
Alignment:

```
KBKGCCCTCTYCTGGCCHV
--KGCCYKCT---------
```

Original motif Consensus sequence: VHGGCCAGMAGAGGGCRBY

Reverse complement motif Consensus sequence: KBKGCCCTCTYCTGGCCHV



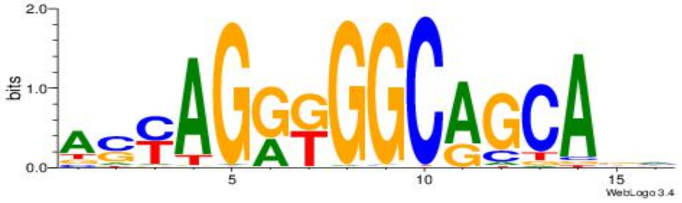


Dataset #:	4
Motif ID:	164
Motif name:	asyAGrkGGCRGCAga
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	4
Number of overlap:	8
Similarity score:	0.0201849

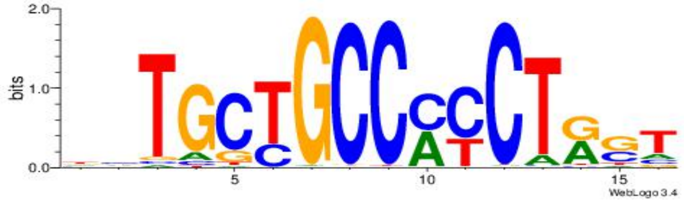
Alignment:

```
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:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	6
Similarity score:	0.00857843

Alignment:

```
GATGGCTC
--BATGGM
```

Original motif Consensus sequence: GATGGCTC

Reverse complement motif Consensus sequence: GAGCCATC

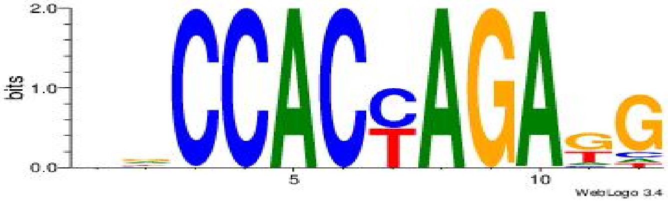
Dataset #:	4
Motif ID:	145
Motif name:	grCCACyAGAkG
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	2
Number of overlap:	6

Similarity score: 0.022036

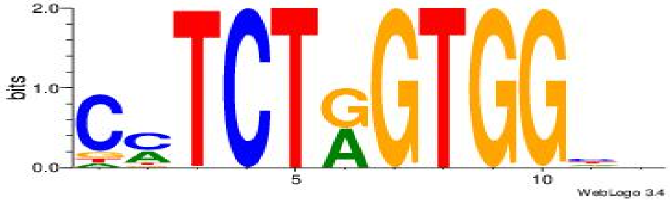
Alignment:

```
CYTCTKGTGGHH
-----BATGGM-
```

Original motif Consensus sequence: DDCCACYAGAKG



Reverse complement motif Consensus sequence: CYTCTKGTGGHH



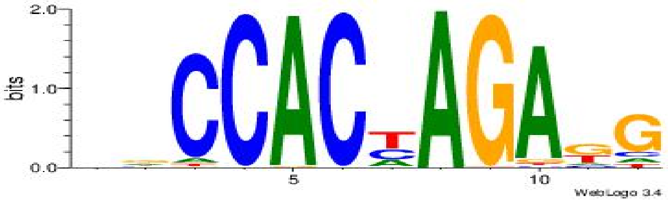
Dataset #:	4
Motif ID:	138
Motif name:	grCCACyAGAkG
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	6
Similarity score:	0.0223679

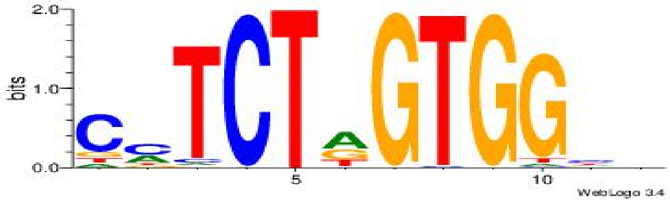
Alignment:

```
DDCCACYAGAKG
-RCCATB-----
```

Original motif Consensus sequence: DDCCACYAGAKG

Reverse complement motif Consensus sequence: CYTCTMGTGGHH



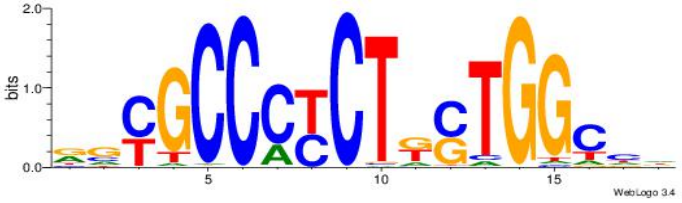


Dataset #:	4
Motif ID:	156
Motif name:	rgyGCCMyCTksTGGccd
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	3
Number of overlap:	6
Similarity score:	0.0275501

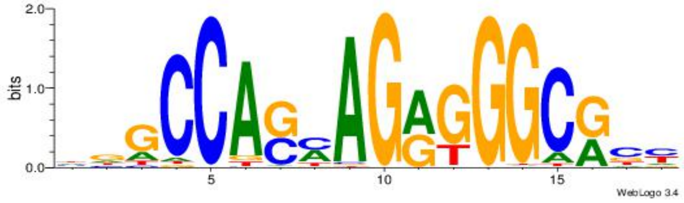
Alignment:

```
DDGCCASYAGMGGGCKVM
--RCCATB----------
```

Original motif Consensus sequence: RVYGCCCYCTKSTGGCHD

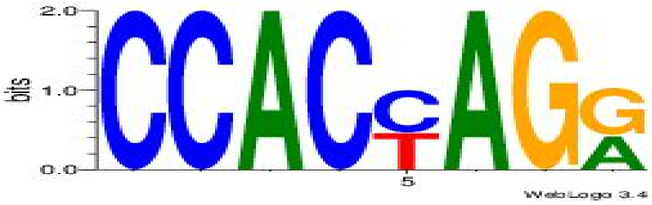


Reverse complement motif Consensus sequence: DDGCCASYAGMGGGCKVM



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

Original motif Consensus sequence: CCACYAGR



Reverse complement motif Consensus sequence: MCTKGTGG

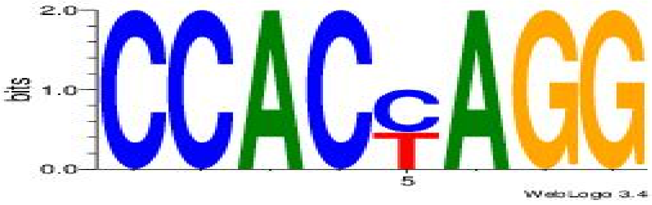
Best Matches for Top Significant Motif ID 48 (Highest to Lowest)

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



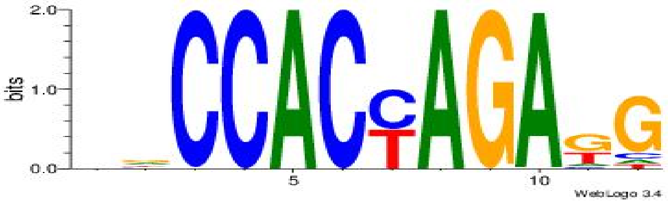
Reverse complement motif Consensus sequence: CCTKGTGG

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

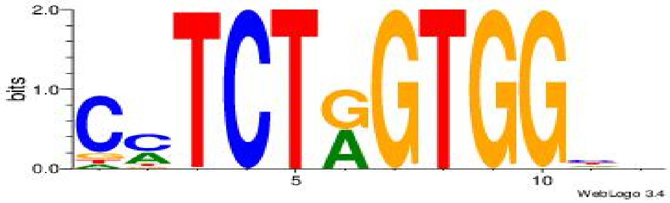
Alignment:

```
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

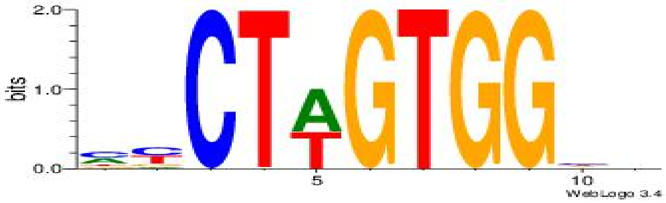
Similarity score: 0.0192652

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

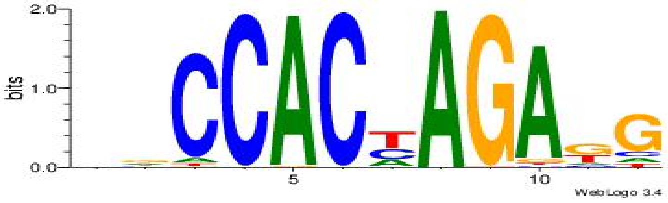
Similarity score: 0.0244381

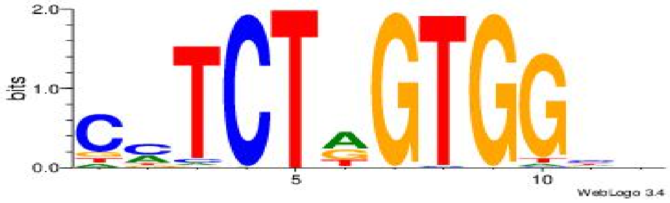
Alignment:

```
DDCCACYAGAKG
--CCACYAGR--
```

Original motif Consensus sequence: DDCCACYAGAKG

Reverse complement motif Consensus sequence: CYTCTMGTGGHH



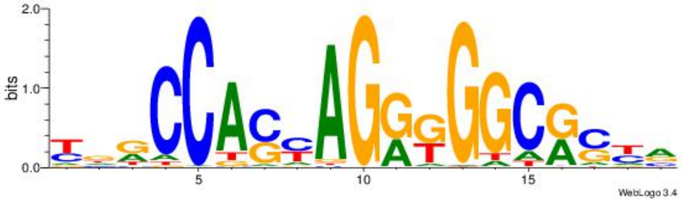


Dataset #:	3
Motif ID:	74
Motif name:	CTCF
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	9
Number of overlap:	8
Similarity score:	0.0284404

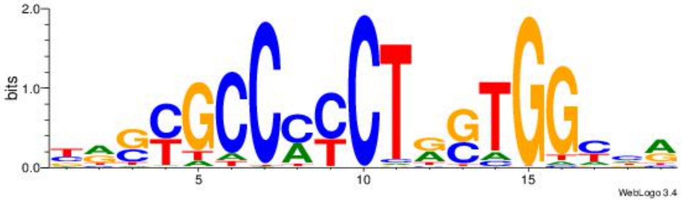
Alignment:

```
BMSMGCCYMCTKSTGGMHM
--------MCTKGTGG---
```

Original motif Consensus sequence: YDRCCASYAGRKGGCRSYV



Reverse complement motif Consensus sequence: BMSMGCCYMCTKSTGGMHM



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: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 3
Number of overlap: 6

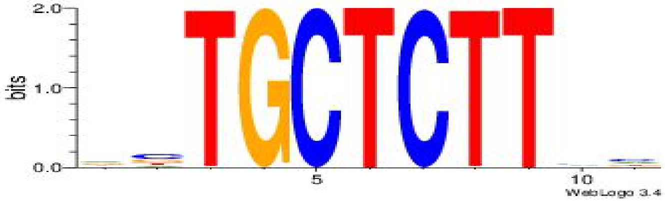
Similarity score: 0.0232212

Alignment:

```
HVTGCTCTTBH
--TGTTMT---
```

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

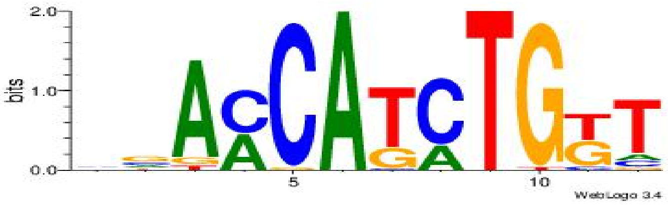
Similarity score: 0.0330056

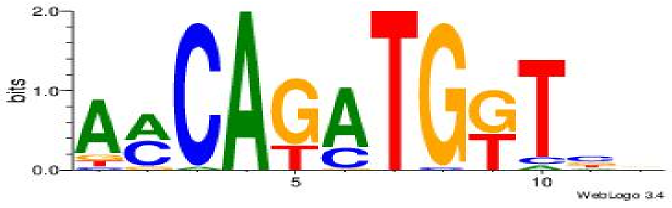
Alignment:

```
HVAMCATCTGKT
ARAACA------
```

Original motif Consensus sequence: HVAMCATCTGKT

Reverse complement motif Consensus sequence: ARCAGATGRTVD



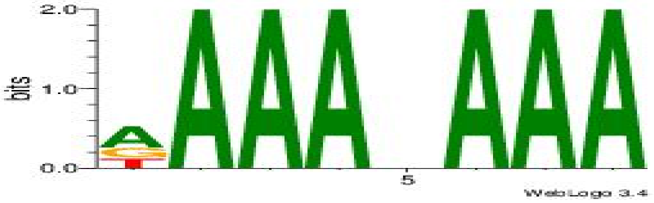


Dataset #: 1
Motif ID: 2
Motif name: Motif 2
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 3
Number of overlap: 6
Similarity score: 0.0333069

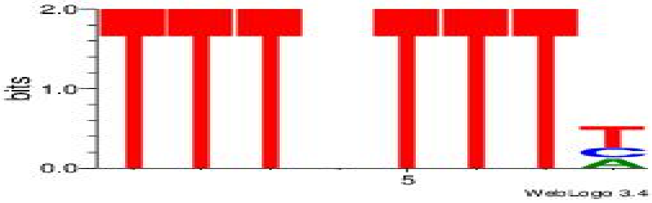
Alignment:

```
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:

```
CCCCRCCC
CCCCDCCC
```

Original motif Consensus sequence: CCCCRCCC

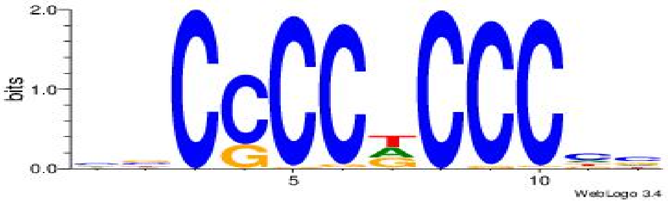
Reverse complement motif Consensus sequence: GGGKGGGG

Dataset #:	4
Motif ID:	155
Motif name:	csCSCCdCCCcs
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:	0.00464015

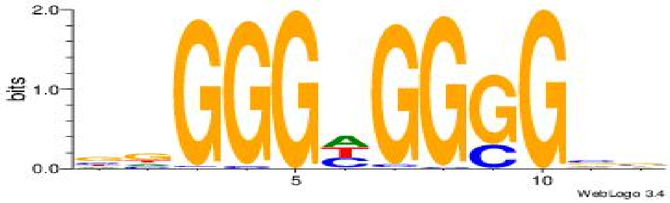
Alignment:

```
VDGGGDGGGGBV
--GGGDGGGG--
```

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: DGGGYGKGGC

Reverse complement motif Consensus sequence: GCCYCMCCCD

Dataset #:	4
Motif ID:	154
Motif name:	csCsCCTCCcc
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:	0.0361349

Alignment:

```
BDGGAGGGGBV
-GGGDGGGG--
```

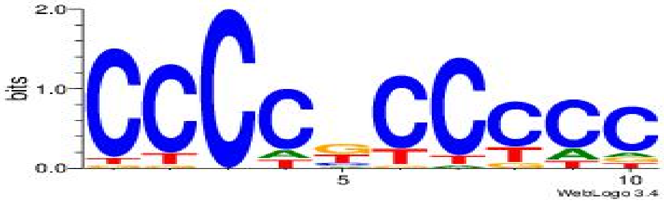
Original motif Consensus sequence: VBCCCCTCCHB

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
CCCCDCCC--
```

Original motif   Consensus sequence: CCCCKCCCCC



Reverse complement motif   Consensus sequence: GGGGGYGGGG

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:	Backward
Position number:	2
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

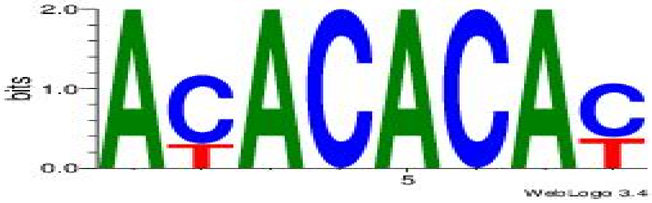
Reverse complement motif Consensus sequence: HVTGCATGKV

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

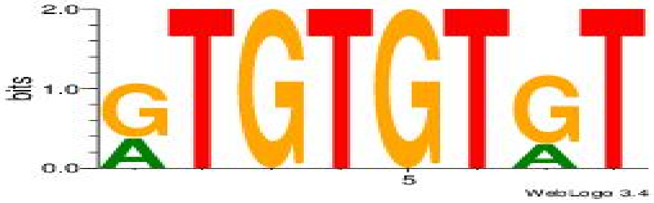
Alignment:

```
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

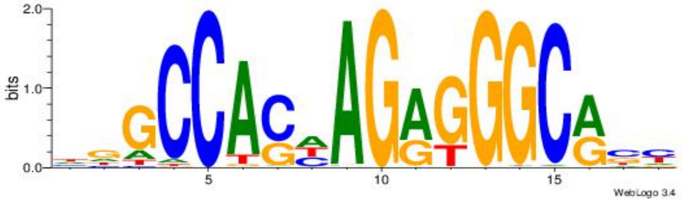
Best Matches for Top Significant Motif ID 101 (Highest to Lowest)

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

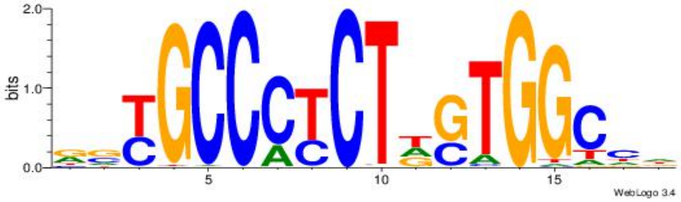
Alignment:

```
HDGCCACHAGRGGGCRBY
-DGCCAA-----------
```

Original motif Consensus sequence: HDGCCACHAGRGGGCRBY



Reverse complement motif Consensus sequence: KBKGCCCKCTHGTGGCHH

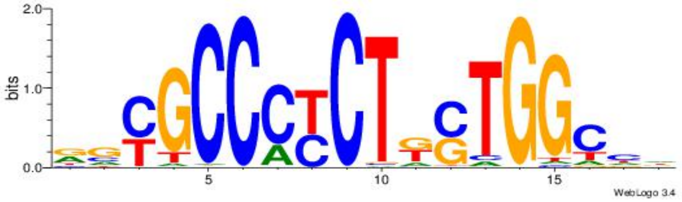


Dataset #:	4
Motif ID:	156
Motif name:	rgyGCCMyCTksTGGccd
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	12
Number of overlap:	6
Similarity score:	0.026631

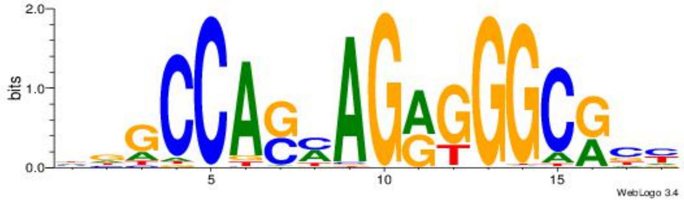
Alignment:

```
DDGCCASYAGMGGGCKVM
-DGCCAA-----------
```

Original motif   Consensus sequence: RVYGCCCYCTKSTGGCHD



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

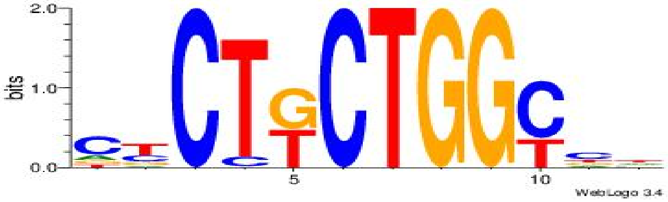
Number of overlap:	6
Similarity score:	0.0273632

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:	Forward
Position number:	2
Number of overlap:	6
Similarity score:	0.0280507

Alignment:

```
SWGCCACC
-DGCCAA-
```

Original motif Consensus sequence: GGTGGCWS

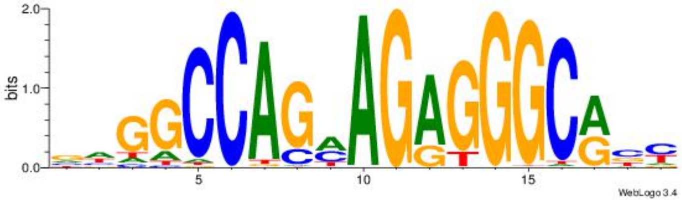
Reverse complement motif Consensus sequence: SWGCCACC

Dataset #:	4
Motif ID:	163
Motif name:	gwGGCCAGmAGAGGGCrby
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	12
Number of overlap:	6
Similarity score:	0.0280858

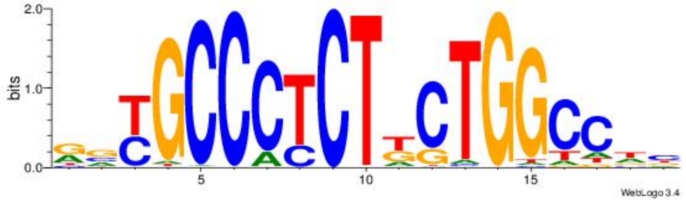
Alignment:

```
KBKGCCCTCTYCTGGCCHV
-----------TTGGCD--
```

Original motif Consensus sequence: VHGGCCAGMAGAGGGCRBY



Reverse complement motif Consensus sequence: KBKGCCCTCTYCTGGCCHV



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

Dataset #: 3 **Motif ID: 71** **Motif name: Arnt**

Original motif Consensus sequence: CACGTG

Reverse complement motif Consensus sequence: CACGTG

Best Matches for Significant Motif ID 71 (Highest to Lowest)

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

Alignment:

```
MACGTG
CACGTG
```

Original motif Consensus sequence: CACGTR

Reverse complement motif Consensus sequence: MACGTG

Dataset #:	3
Motif ID:	91
Motif name:	MAX
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:	0.00380329

Alignment:

```
BCACGTGDTD
-CACGTG---
```

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: Backward
Position number: 1
Number of overlap: 6
Similarity score: 0.00445689

Alignment:

```
MCACGTG
-CACGTG
```

Original motif Consensus sequence: CACGTGR

Reverse complement motif Consensus sequence: MCACGTG

Dataset #: 3
Motif ID: 95
Motif name: MYCMAX
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 3
Number of overlap: 6
Similarity score: 0.00495292

Alignment:

```
RASCACGTGGT
---CACGTG--
```

Original motif Consensus sequence: RASCACGTGGT

Reverse complement motif Consensus sequence: ACCACGTGSTM

Dataset #:	3
Motif ID:	94
Motif name:	Myc
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	3
Number of overlap:	6
Similarity score:	0.0173209

Alignment:

```
DCCACGTGCV
--CACGTG--
```

Original motif Consensus sequence: VGCACGTGGH

Reverse complement motif Consensus sequence: DCCACGTGCV

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

Original motif Consensus sequence: AGRKGGCR

Reverse complement motif Consensus sequence: KGCCYKCT

Best Matches for 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

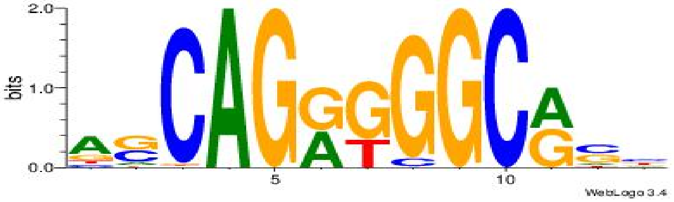
Reverse complement motif Consensus sequence: KGCCYKCT

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
---AGRKGGCR--
```

Original motif Consensus sequence: ASCAGRGGGCRSB



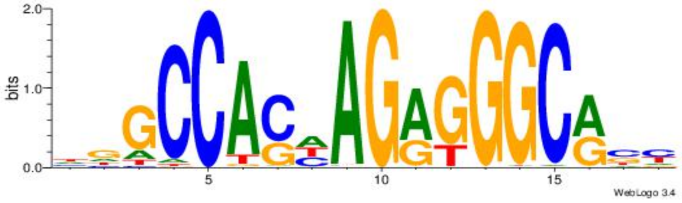
Reverse complement motif Consensus sequence: BSKGCCCMCTGST

Dataset #: 4
Motif ID: 165
Motif name: wgGCCAshAGrGGGCrsy
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 9
Number of overlap: 8
Similarity score: 0.0102443

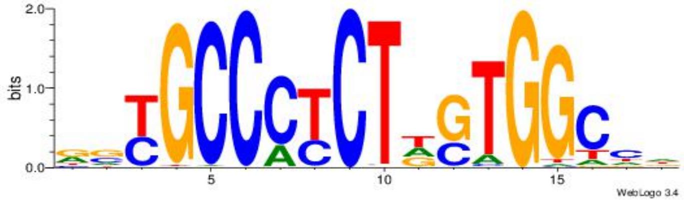
Alignment:

```
KBKGCCCKCTHGTGGCHH
--KGCCYKCT--------
```

Original motif Consensus sequence: HDGCCACHAGRGGGCRBY



Reverse complement motif Consensus sequence: KBKGCCCKCTHGTGGCHH



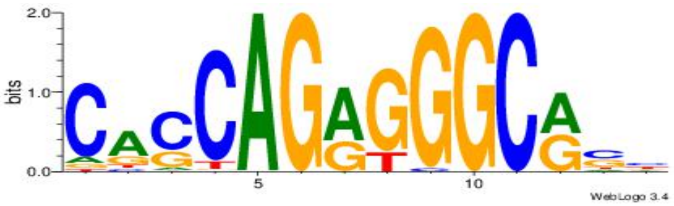
Dataset #: 4
Motif ID: 166
Motif name: CasCAGrGGGCrsy
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 5

Number of overlap: 8
Similarity score: 0.0104954

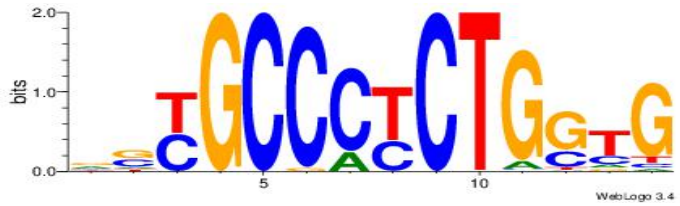
Alignment:

```
BSKGCCCKCTGGTG
--KGCCYKCT----
```

Original motif Consensus sequence: CACCAGRGGGCRSB



Reverse complement motif Consensus sequence: BSKGCCCKCTGGT



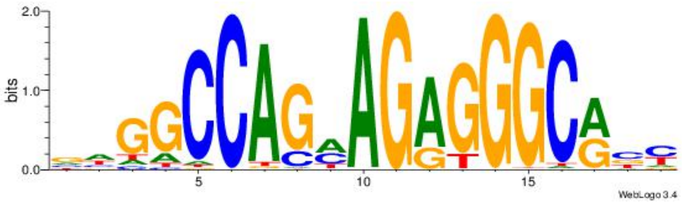
Dataset #: 4
Motif ID: 163
Motif name: gwGGCCAGmAGAGGGCrby
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 3
Number of overlap: 8
Similarity score: 0.0165822

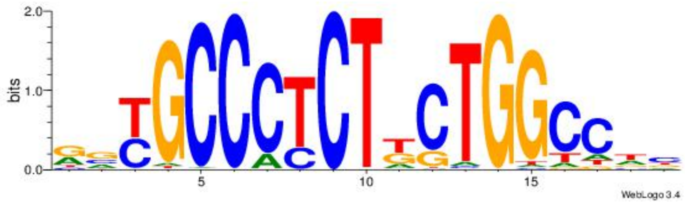
Alignment:

```
KBKGCCCTCTYCTGGCCHV
--KGCCYKCT---------
```

Original motif Consensus sequence: VHGGCCAGMAGAGGGCRBY

Reverse complement motif Consensus sequence: KBKGCCCTCTYCTGGCCHV





Dataset #: 4 **Motif ID: 133** **Motif name: shAGrGGGCAgy**

Original motif Consensus sequence: SHAGRGGGCABH

Reverse complement motif Consensus sequence: DBTGCCCKCTDS

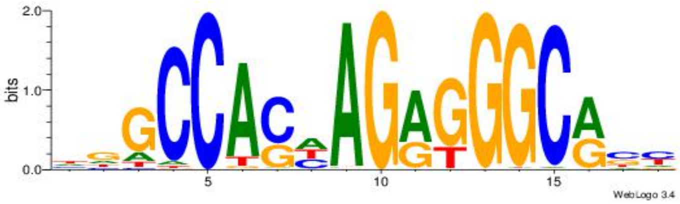
Best Matches for Significant Motif ID 133 (Highest to Lowest)

Dataset #:	4
Motif ID:	165
Motif name:	wgGCCAshAGrGGGCrsy
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	7
Number of overlap:	12
Similarity score:	0.00159897

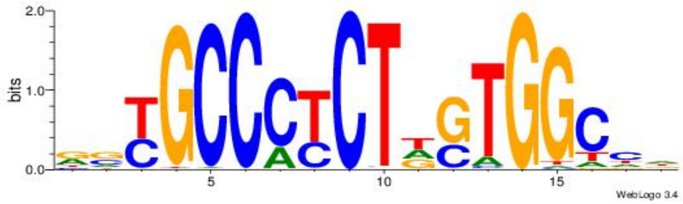
Alignment:

```
HDGCCACHAGRGGGCRBY
------SHAGRGGGCABH
```

Original motif Consensus sequence: HDGCCACHAGRGGGCRBY



Reverse complement motif Consensus sequence: KBKGCCCKCTHGTGGCHH

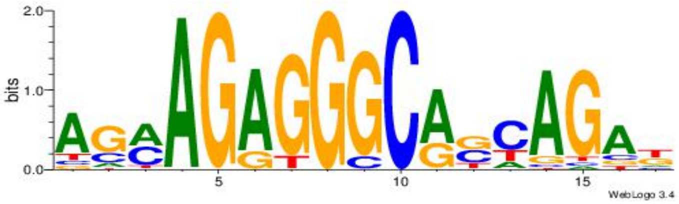


Dataset #:	4
Motif ID:	143
Motif name:	AgmAGAGGGCrscAGak
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	5
Number of overlap:	12
Similarity score:	0.00815796

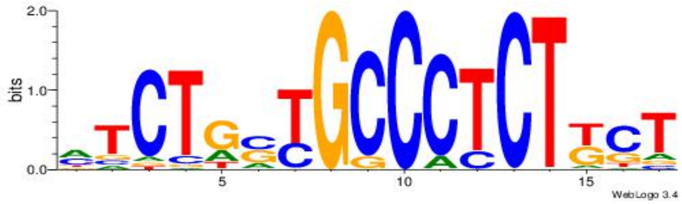
Alignment:

```
AGMAGAGGGCASCAGAK
-SHAGRGGGCABH----
```

Original motif Consensus sequence: AGMAGAGGGCASCAGAK



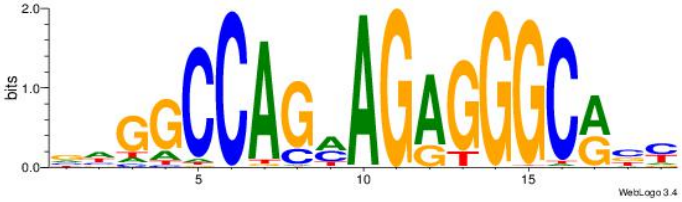
Reverse complement motif Consensus sequence: RTCTGSTGCCCTCTYCT



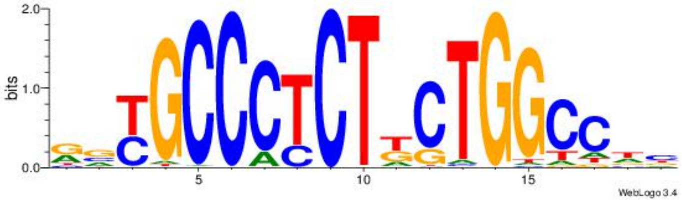
Dataset #:	4
Motif ID:	163
Motif name:	gwGGCCAGmAGAGGGCrby
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	8
Number of overlap:	12
Similarity score:	0.0109424

Alignment:
VHGGCCAGMAGAGGGCRBY
-------SHAGRGGGCABH

Original motif   Consensus sequence: VHGGCCAGMAGAGGGCRBY



Reverse complement motif   Consensus sequence: KBKGCCCTCTYCTGGCCHV



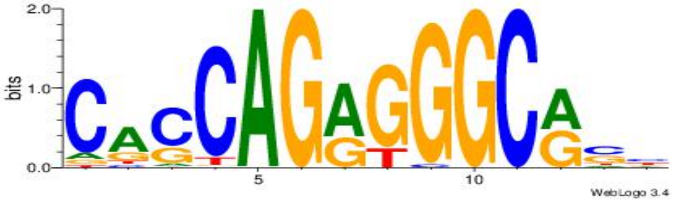
Dataset #:	4
Motif ID:	166
Motif name:	CasCAGrGGGCrsy
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1

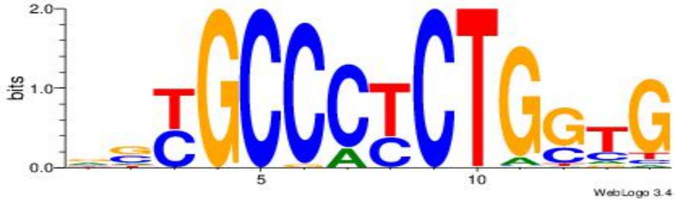
Number of overlap: 12
Similarity score: 0.0124424

Alignment:
CACCAGRGGGCRSB
--SHAGRGGGCABH

Original motif Consensus sequence: CACCAGRGGGCRSB

Reverse complement motif Consensus sequence: BSKGCCCKCTGGT



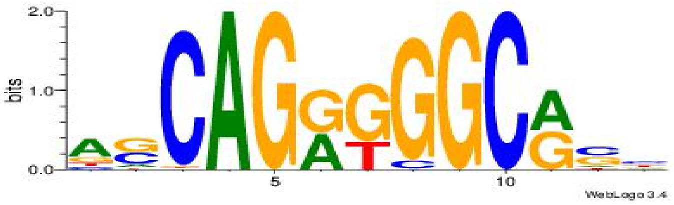


Dataset #: 4
Motif ID: 147
Motif name: asCAGrkGGCrsy
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 2
Number of overlap: 12
Similarity score: 0.0128393

Alignment:
ASCAGRGGGCRSB
-SHAGRGGGCABH

Original motif Consensus sequence: ASCAGRGGGCRSB

Reverse complement motif Consensus sequence: BSKGCCCMCTGST



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

Original motif Consensus sequence: AAATAH

Reverse complement motif Consensus sequence: DTATTT

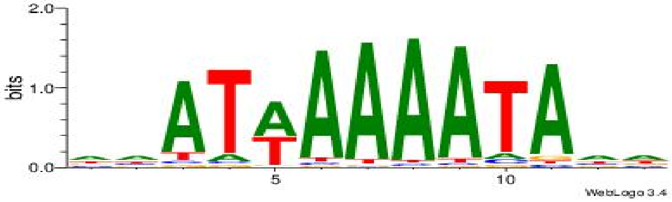
Best Matches for Significant Motif ID 8 (Highest to Lowest)

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

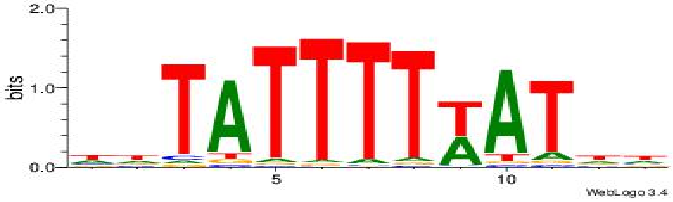
Alignment:

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

Original motif   Consensus sequence: DHATWAAAATAHD



Reverse complement motif   Consensus sequence: DHTATTTTWATHD

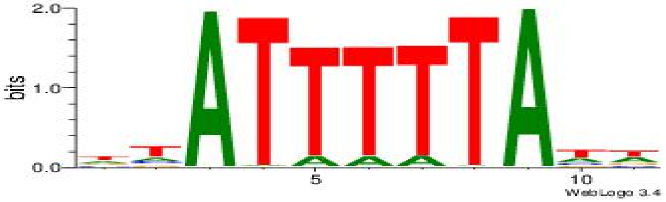


Dataset #:	4
Motif ID:	157
Motif name:	wtATTTTTAww
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	6
Number of overlap:	6
Similarity score:	0.00556446

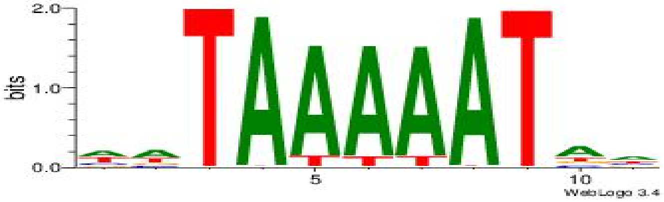
Alignment:

```
WWTAAAAATAD
-----AAATAH
```

Original motif   Consensus sequence: DTATTTTTAWW



Reverse complement motif   Consensus sequence: WWTAAAAATAD

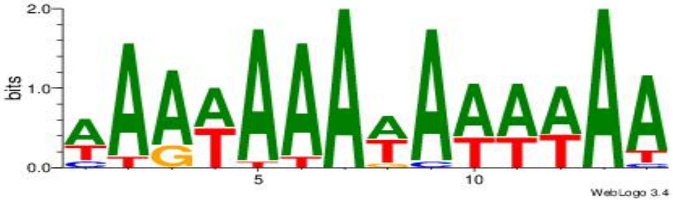


Dataset #:	2
Motif ID:	68
Motif name:	Motif 68
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	5
Number of overlap:	6
Similarity score:	0.0128826

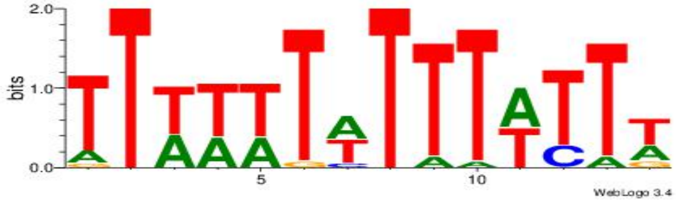
Alignment:

```
WAAWAAAWAWWWAA
----AAATAH----
```

Original motif Consensus sequence: WAAWAAAWAWWWAA



Reverse complement motif Consensus sequence: TTWWWTWTTTWTTW

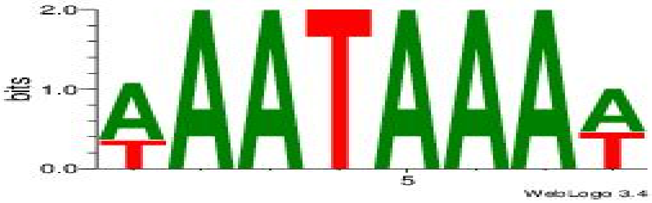


Dataset #:	2
Motif ID:	52
Motif name:	Motif 52
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1

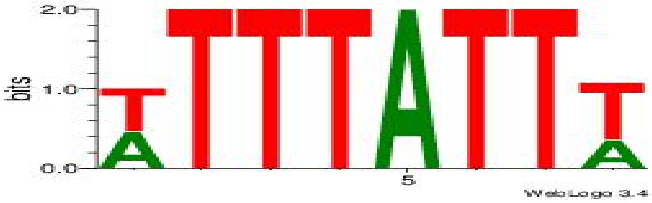
Number of overlap: 6
Similarity score: 0.0167304

Alignment:
```
AAATAAAW
AAATAH--
```

Original motif Consensus sequence: AAATAAAW



Reverse complement motif Consensus sequence: WTTTATTT

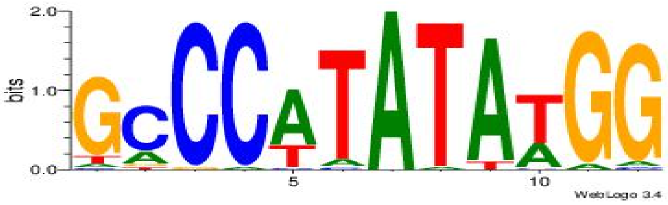


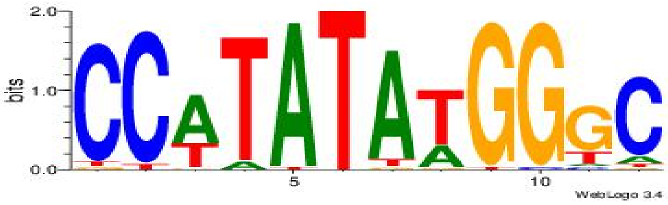
Dataset #: 3
Motif ID: 118
Motif name: SRF
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 3
Number of overlap: 6
Similarity score: 0.0210491

Alignment:
```
GCCCATATATGG
----AAATAH--
```

Original motif Consensus sequence: GCCCATATATGG

Reverse complement motif Consensus sequence: CCATATATGGGC

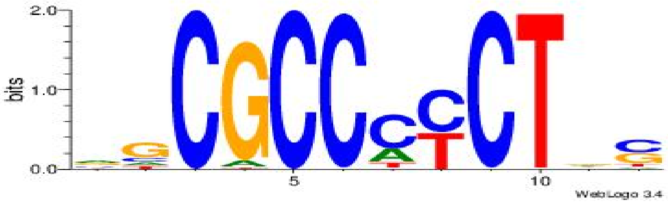




Dataset #: 4 **Motif ID: 153** **Motif name: scAGrkGGCGcy**

Original motif Consensus sequence: SHAGRGGGCGCB

Reverse complement motif Consensus sequence: VGCGCCCMCTDS



Best Matches for Significant Motif ID 153 (Highest to Lowest)

Dataset #:	4
Motif ID:	137
Motif name:	rgCGCCmyCTgs
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	12
Similarity score:	0

Alignment:

```
VGCGCCCYCTDS
VGCGCCCMCTDS
```

Original motif   Consensus sequence: VGCGCCCYCTDS

Reverse complement motif   Consensus sequence: SHAGKGGGCGCB

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:	2
Number of overlap:	12
Similarity score:	0.0112071

Alignment:

```
ASCAGRGGGCRSB
-SHAGRGGGCGCB
```

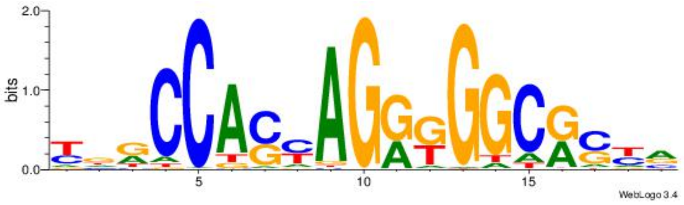
Original motif   Consensus sequence: ASCAGRGGGCRSB

Reverse complement motif   Consensus sequence: BSKGCCCMCTGST

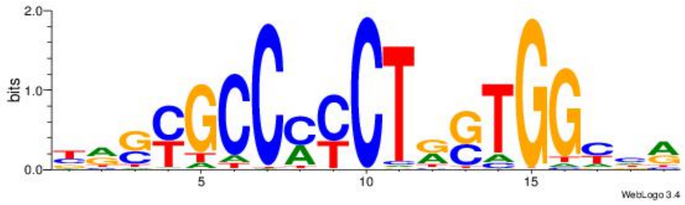
Dataset #: 3
Motif ID: 74
Motif name: CTCF
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 7
Number of overlap: 12
Similarity score: 0.0133899

Alignment:
BMSMGCCYMCTKSTGGMHM
-VGCGCCCMCTDS------

Original motif Consensus sequence: YDRCCASYAGRKGGCRSYV



Reverse complement motif Consensus sequence: BMSMGCCYMCTKSTGGMHM



Dataset #: 4
Motif ID: 165
Motif name: wgGCCAshAGrGGGCrsy
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1

Number of overlap: 12

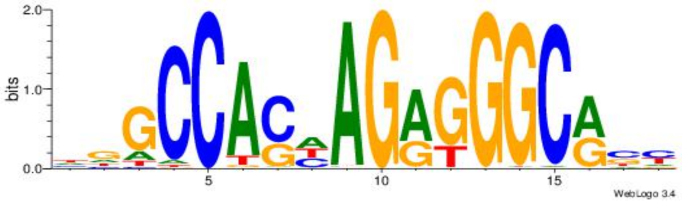
Similarity score: 0.0146442

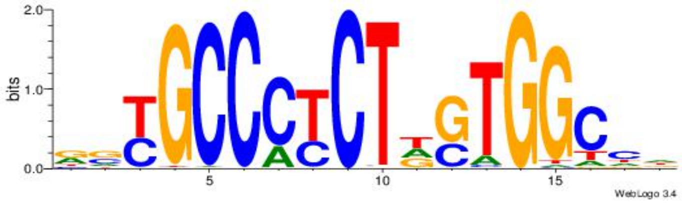
Alignment:

```
HDGCCACHAGRGGGCRBY
------SHAGRGGGCGCB
```

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: Forward

Position number: 3

Number of overlap: 12

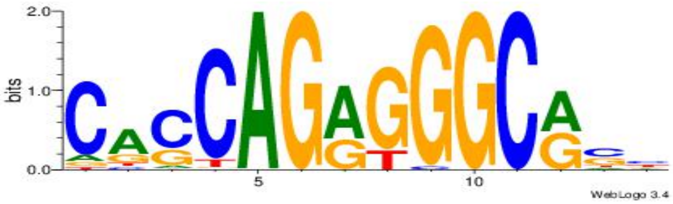
Similarity score: 0.0200811

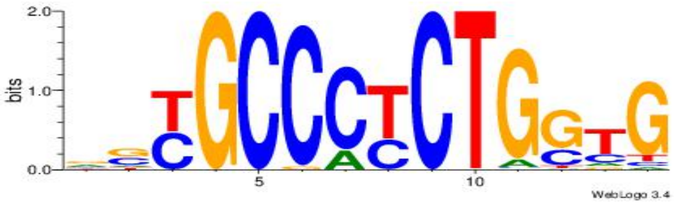
Alignment:

```
CACCAGRGGGCRSB
--SHAGRGGGCGCB
```

Original motif Consensus sequence: CACCAGRGGGCRSB

Reverse complement motif Consensus sequence: BSKGCCCKCTGGT





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

Original motif Consensus sequence: CACGTR

Reverse complement motif Consensus sequence: MACGTG

Best Matches for 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:	Forward
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:	Forward
Position number:	4
Number of overlap:	6
Similarity score:	0.0102183

Alignment:

```
RASCACGTGGT
---MACGTG--
```

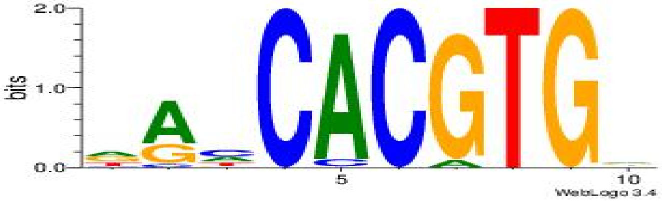
Original motif Consensus sequence: RASCACGTGGT

Reverse complement motif Consensus sequence: ACCACGTGSTM

Dataset #: 3
Motif ID: 91
Motif name: MAX
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2
Number of overlap: 6
Similarity score: 0.011152

Alignment:
DAHCACGTGD
---MACGTG-

Original motif Consensus sequence: DAHCACGTGD



Reverse complement motif Consensus sequence: BCACGTGDTD

Dataset #: 3
Motif ID: 126
Motif name: USF1
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: 0.0131944

Alignment:
CACGTGR
MACGTG-

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 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

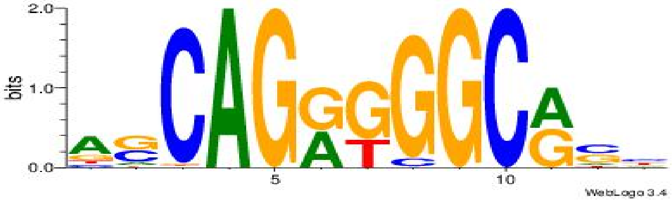
Reverse complement motif Consensus sequence: KGCCYKCT

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



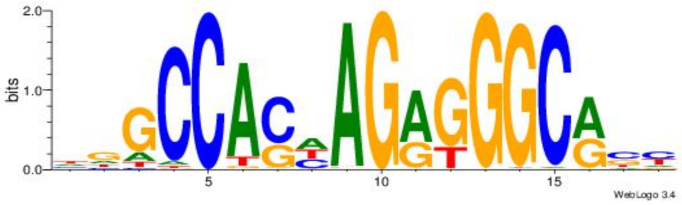
Reverse complement motif Consensus sequence: BSKGCCCMCTGST

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

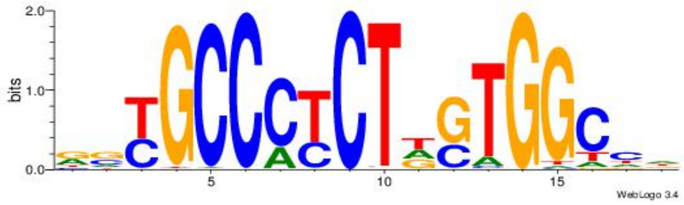
Alignment:

```
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: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 3

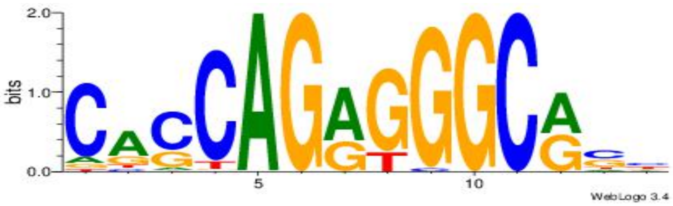
Number of overlap: 8

Similarity score: 0.0106761

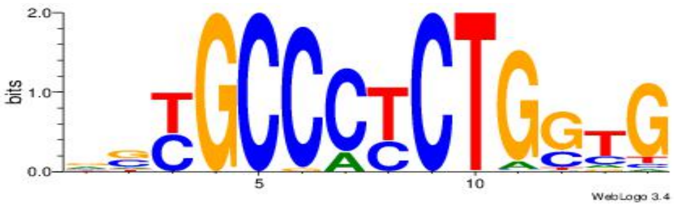
Alignment:

```
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

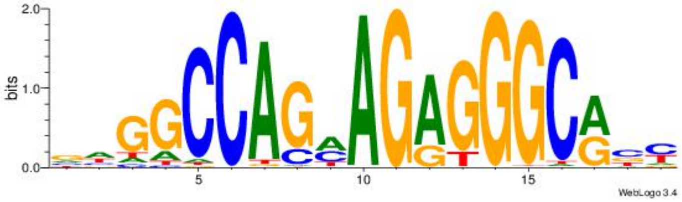
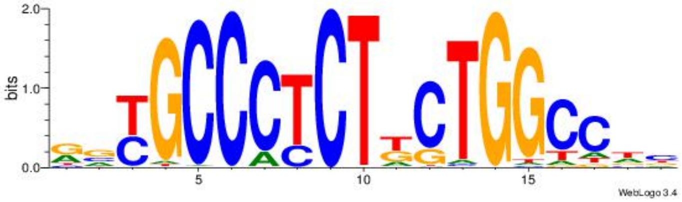
Similarity score: 0.016658

Alignment:

```
KBKGCCCTCTYCTGGCCHV
--KGCCYKCT---------
```

Original motif Consensus sequence: VHGGCCAGMAGAGGGCRBY

Reverse complement motif Consensus sequence: KBKGCCCTCTYCTGGCCHV

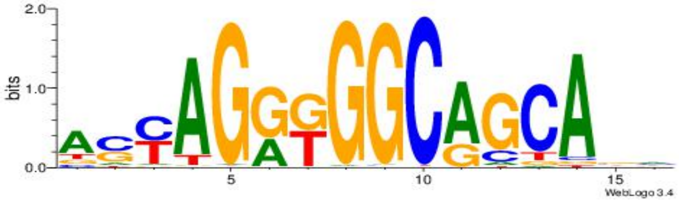



Dataset #:	4
Motif ID:	164
Motif name:	asyAGrkGGCRGCAga
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	4
Number of overlap:	8
Similarity score:	0.0201849

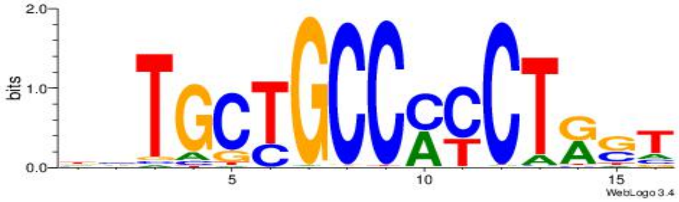
Alignment:

```
ASYAGRKGGCAGCABH
---AGRKGGCR-----
```

Original motif Consensus sequence: ASYAGRKGGCAGCABH



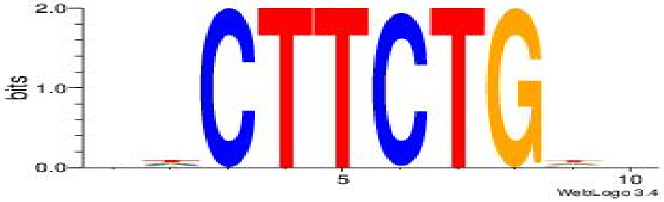
Reverse complement motif Consensus sequence: HBTGCTGCCYMCTKST



Dataset #: 4 Motif ID: 136 Motif name: dwCAGAAGwh

Original motif Consensus sequence: DHCAGAAGDH

Reverse complement motif Consensus sequence: HDCTTCTGHD



Best Matches for Significant Motif ID 136 (Highest to Lowest)

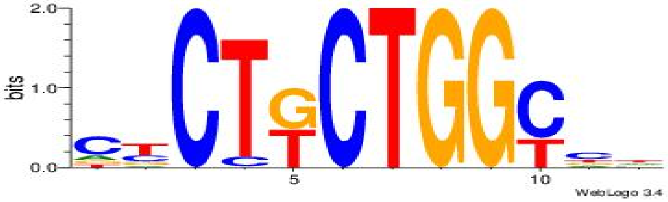
Dataset #:	4
Motif ID:	151
Motif name:	agrCCAGmAGrg
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	3
Number of overlap:	10
Similarity score:	0.00562474

Alignment:

```
HVGCCAGMAGRG
--DHCAGAAGDH
```

Original motif Consensus sequence: HVGCCAGMAGRG

Reverse complement motif Consensus sequence: CKCTRCTGGCVH



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: 1
Number of overlap: 10
Similarity score: 0.0107169

Alignment:
DACAAAACAH
DHCAGAAGDH

Original motif Consensus sequence: DACAAAACAH

Reverse complement motif Consensus sequence: HTGTTTTGTD

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: 1
Number of overlap: 10

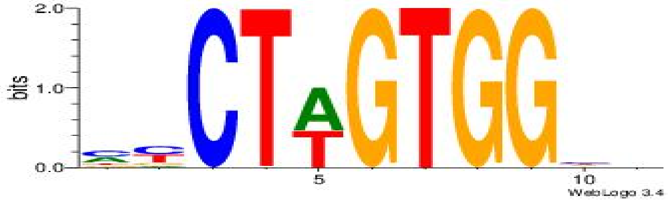
Similarity score: 0.0167426

Alignment:

```
DDCCACWAGRK
-DHCAGAAGDH
```

Original motif Consensus sequence: DDCCACWAGRK

Reverse complement motif Consensus sequence: YMCTWGTGGHH



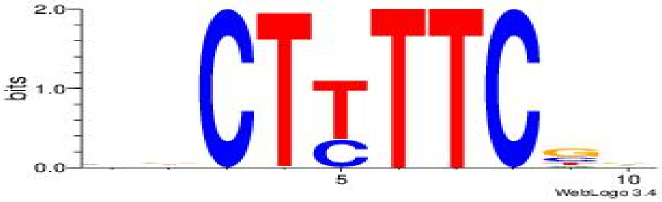
Dataset #:	4
Motif ID:	139
Motif name:	mkCTyTTCsg
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	10
Similarity score:	0.0207259

Alignment:

```
HBCTTTTCBD
HDCTTCTGHD
```

Original motif Consensus sequence: HBCTTTTCBD

Reverse complement motif Consensus sequence: HBGAAAAGBD

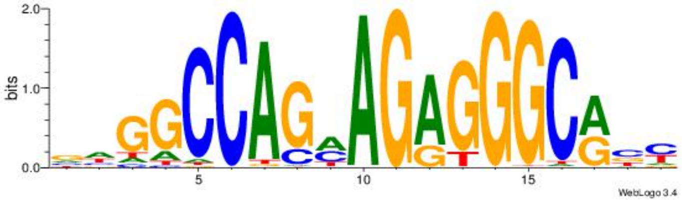


Dataset #:	4
Motif ID:	163
Motif name:	gwGGCCAGmAGAGGGCrby
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	4
Number of overlap:	10
Similarity score:	0.0212719

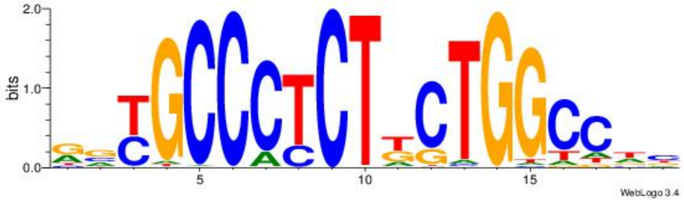
Alignment:

```
VHGGCCAGMAGAGGGCRBY
---DHCAGAAGDH------
```

Original motif Consensus sequence: VHGGCCAGMAGAGGGCRBY



Reverse complement motif Consensus sequence: KBKGCCCTCTYCTGGCCHV



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

Original motif Consensus sequence: RCCATB

Reverse complement motif Consensus sequence: BATGGM

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

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

Alignment:

```
KCCATCT
-RCCATB
```

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

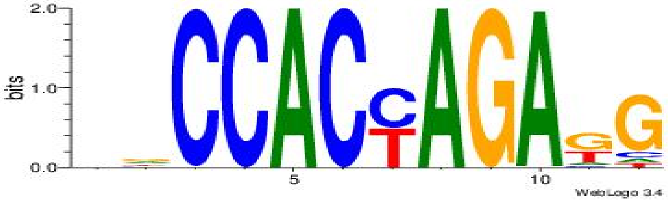
Dataset #:	4
Motif ID:	145
Motif name:	grCCACyAGAkG
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	2
Number of overlap:	6

Similarity score: 0.022036

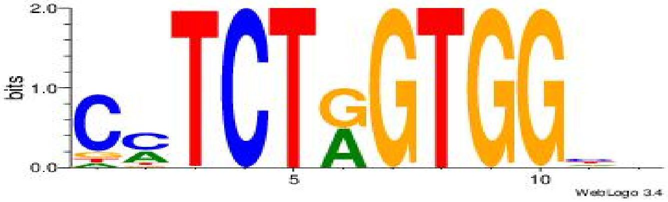
Alignment:

```
CYTCTKGTGGHH
-----BATGGM-
```

Original motif Consensus sequence: DDCCACYAGAKG



Reverse complement motif Consensus sequence: CYTCTKGTGGHH



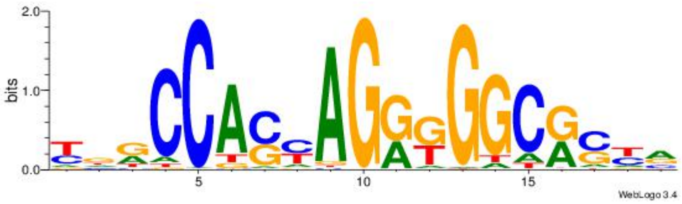
Dataset #:	3
Motif ID:	74
Motif name:	CTCF
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	3
Number of overlap:	6
Similarity score:	0.0220417

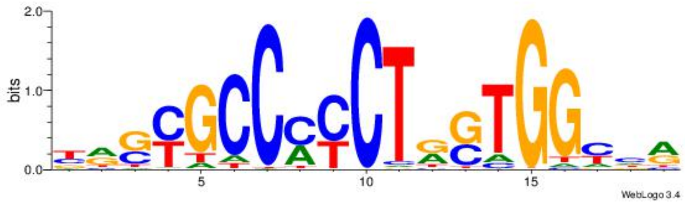
Alignment:

```
BMSMGCCYMCTKSTGGMHM
-----------BATGGM--
```

Original motif Consensus sequence: YDRCCASYAGRKGGCRSYV

Reverse complement motif Consensus sequence: BMSMGCCYMCTKSTGGMHM



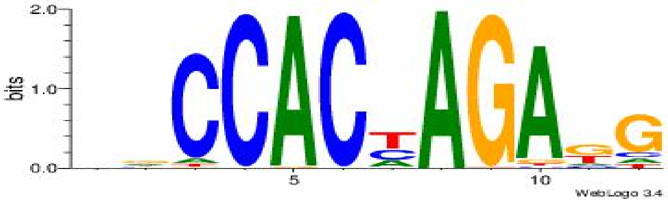


Dataset #:	4
Motif ID:	138
Motif name:	grCCACyAGAkG
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	6
Similarity score:	0.0223679

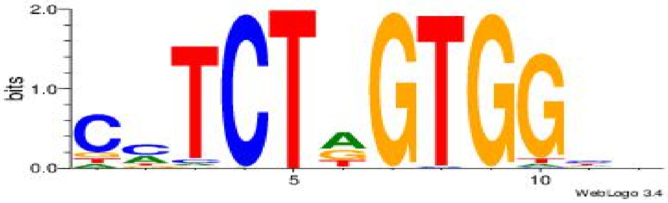
Alignment:

```
DDCCACYAGAKG
-RCCATB-----
```

Original motif Consensus sequence: DDCCACYAGAKG



Reverse complement motif Consensus sequence: CYTCTMGTGGHH



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

Original motif Consensus sequence: YGCGTG

Reverse complement motif Consensus sequence: CACGCM

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

Dataset #:	3
Motif ID:	86
Motif name:	HIF1AARNT
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2
Number of overlap:	6
Similarity score:	0

Alignment:

```
VBACGTGV
-YGCGTG-
```

Original motif Consensus sequence: VBACGTGV

Reverse complement motif Consensus sequence: VCACGTBV

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 #: 3
Motif ID: 71
Motif name: Arnt
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 6

Similarity score:	0.0203526

Alignment:
CACGTG
YGCGTG

Original motif Consensus sequence: CACGTG

Reverse complement motif Consensus sequence: CACGTG

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 #:	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:	0.0255609

Alignment:

```
MCACGTG
-YGCGTG
```

Original motif Consensus sequence: CACGTGR

Reverse complement motif Consensus sequence: MCACGTG

Best Matches for Each Motif (Highest to Lowest)

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

Original motif Consensus sequence: AGRKGGCR

Reverse complement motif Consensus sequence: KGCCYKCT

Best Matches for 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

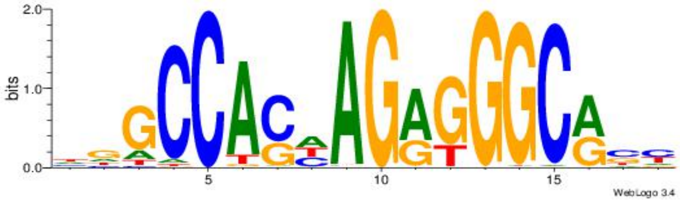
Dataset #:	4
Motif ID:	165

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

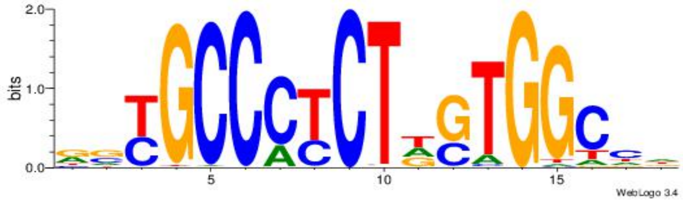
Alignment:

```
KBKGCCCKCTHGTGGCHH
--KGCCYKCT--------
```

Original motif Consensus sequence: HDGCCACHAGRGGGCRBY



Reverse complement motif Consensus sequence: KBKGCCCKCTHGTGGCHH

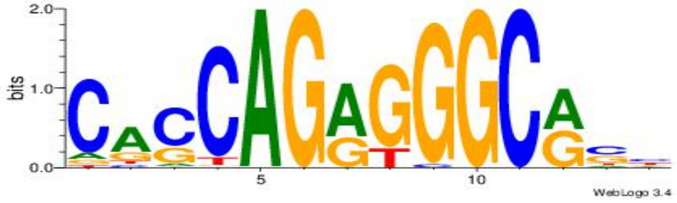


Dataset #: 4
Motif ID: 166
Motif name: CasCAGrGGGCrsy
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 3
Number of overlap: 8
Similarity score: 0.0106761

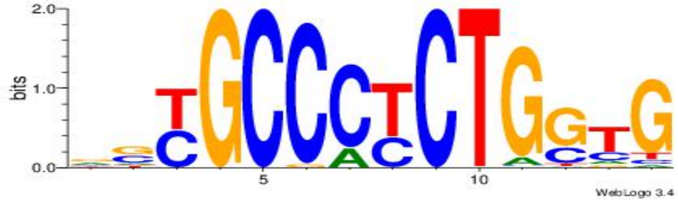
Alignment:

BSKGCCCKCTGGTG
--KGCCYKCT----

Original motif Consensus sequence: CACCAGRGGGCRSB



Reverse complement motif Consensus sequence: BSKGCCCKCTGGT



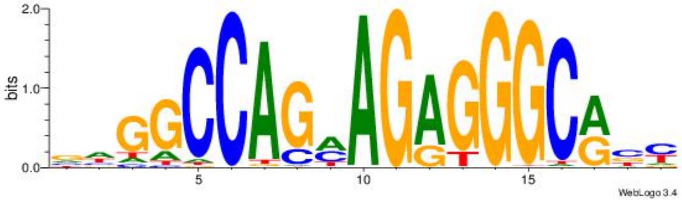
Dataset #:	4
Motif ID:	163
Motif name:	gwGGCCAGmAGAGGGCrby
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	3
Number of overlap:	8
Similarity score:	0.016658

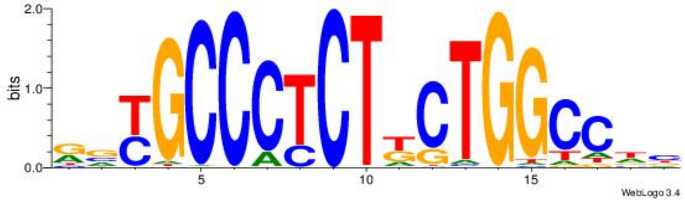
Alignment:

KBKGCCCTCTYCTGGCCHV
--KGCCYKCT---------

Original motif Consensus sequence: VHGGCCAGMAGAGGGCRBY

Reverse complement motif Consensus sequence: KBKGCCCTCTYCTGGCCHV



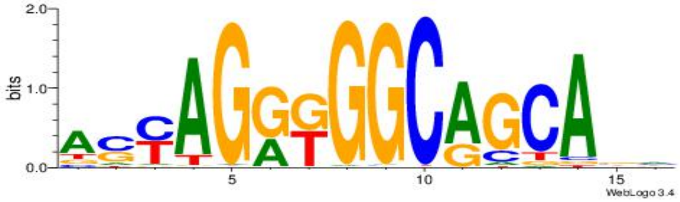


Dataset #:	4
Motif ID:	164
Motif name:	asyAGrkGGCRGCAga
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	4
Number of overlap:	8
Similarity score:	0.0201849

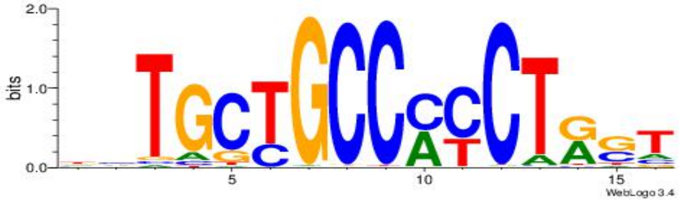
Alignment:

```
ASYAGRKGGCAGCABH
---AGRKGGCR-----
```

Original motif   Consensus sequence: ASYAGRKGGCAGCABH

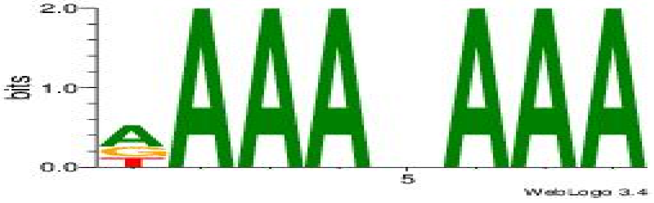


Reverse complement motif   Consensus sequence: HBTGCTGCCYMCTKST

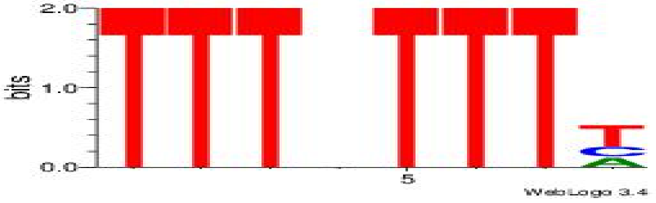


Dataset #: 1   Motif ID: 2   Motif name: Motif 2

Original motif Consensus sequence: AAAAHAAA



Reverse complement motif Consensus sequence: TTTDTTTT



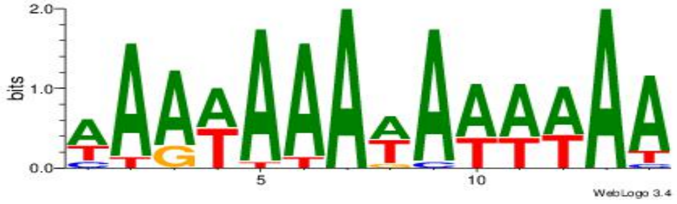
Best Matches for Motif ID 2 (Highest to Lowest)

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:	4
Number of overlap:	8
Similarity score:	0.034263

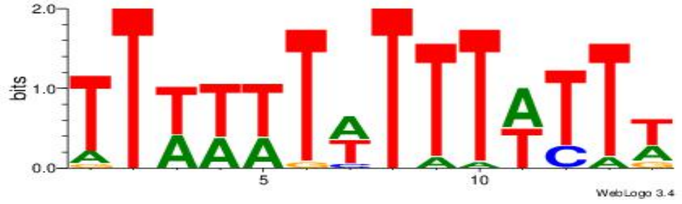
Alignment:

```
WAAWAAAWAWWWAA
---AAAAHAAA---
```

Original motif Consensus sequence: WAAWAAAWAWWWAA



Reverse complement motif Consensus sequence: TTWWWTWTTTWTTW

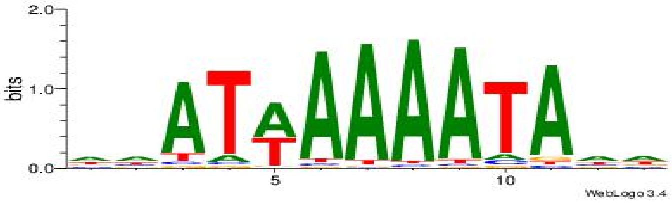


Dataset #:	4
Motif ID:	150
Motif name:	waATwAAAATAww
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	6
Number of overlap:	8
Similarity score:	0.061025

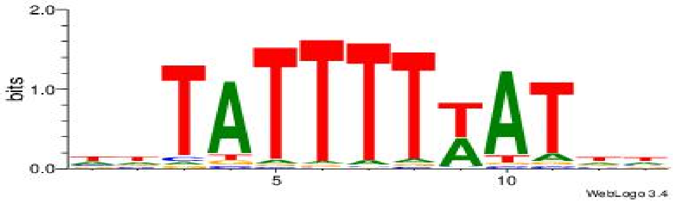
Alignment:

```
DHTATTTTWATHD
TTTDTTTT-----
```

Original motif   Consensus sequence: DHATWAAAATAHD



Reverse complement motif   Consensus sequence: DHTATTTTWATHD

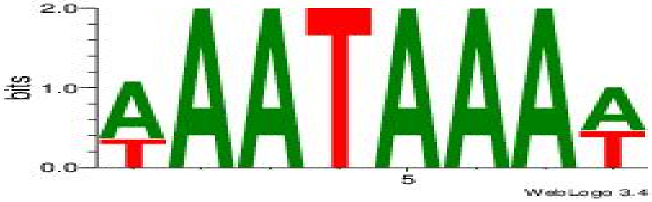


Dataset #:	2
Motif ID:	52
Motif name:	Motif 52
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	8

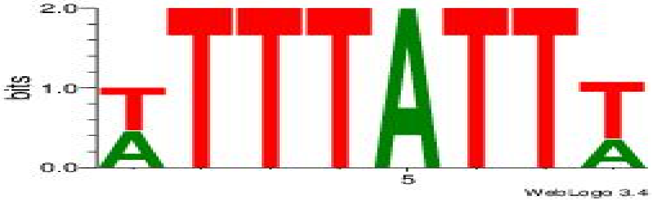
Similarity score: 0.0613251

Alignment:
AAATAAAW
AAAAHAAA

Original motif Consensus sequence: AAATAAAW



Reverse complement motif Consensus sequence: WTTTATTT

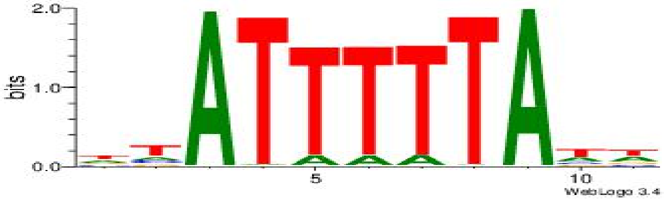


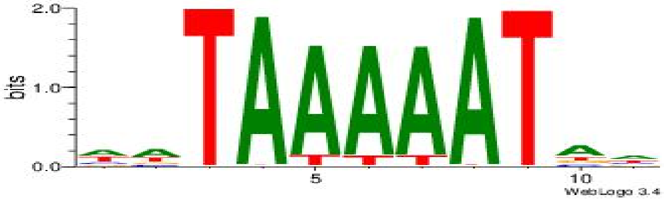
Dataset #:	4
Motif ID:	157
Motif name:	wtATTTTTAww
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	4
Number of overlap:	8
Similarity score:	0.0669479

Alignment:
WWTAAAAATAD
AAAAHAAA---

Original motif Consensus sequence: DTATTTTTAWW

Reverse complement motif Consensus sequence: WWTAAAAATAD





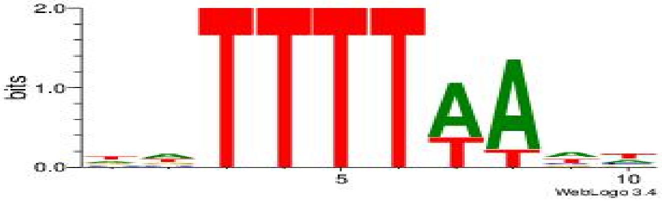
Dataset #:	4
Motif ID:	148
Motif name:	wwTwAAAAww
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	8
Similarity score:	0.0808845

Alignment:

```
DDTWAAAAHH
AAAAHAAA--
```

Original motif Consensus sequence: DDTWAAAAHH

Reverse complement motif Consensus sequence: HHTTTTWADD



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

Original motif   Consensus sequence: CACACACA

Reverse complement motif   Consensus sequence: TGTGTGTG

Best Matches for Motif ID 3 (Highest to Lowest)

Dataset #:	1
Motif ID:	24
Motif name:	Motif 24
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	8
Similarity score:	0.0443933

Alignment:

```
TGTGGGTG
TGTGTGTG
```

Original motif   Consensus sequence: TGTGGGTG

Reverse complement motif   Consensus sequence: CACCCACA

Dataset #:	1
Motif ID:	31
Motif name:	Motif 31
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:	0.0599548

Alignment:

```
CATGYACA
CACACACA
```

Original motif Consensus sequence: CATGYACA

Reverse complement motif Consensus sequence: TGTKCATG

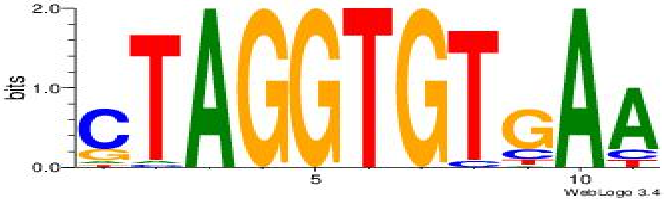
Dataset #:	3
Motif ID:	120
Motif name:	T
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	3
Number of overlap:	8

Similarity score: 0.065511

Alignment:

```
TTCACACCTAG
--CACACACA-
```

Original motif Consensus sequence: CTAGGTGTGAA



Reverse complement motif Consensus sequence: TTCACACCTAG

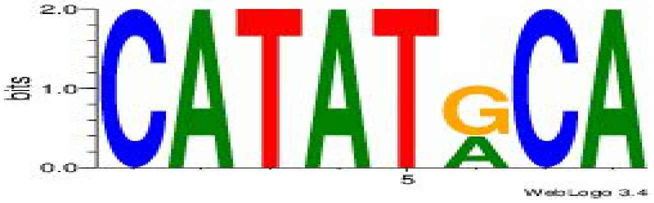
Dataset #: 2
Motif ID: 64
Motif name: Motif 64
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 8
Similarity score: 0.0681512

Alignment:

```
CATATRCA
CACACACA
```

Original motif Consensus sequence: CATATRCA

Reverse complement motif Consensus sequence: TGMATATG

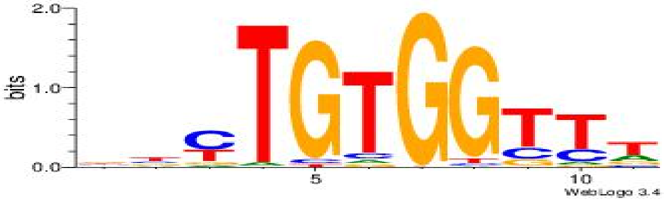


Dataset #:	3
Motif ID:	114
Motif name:	RUNX1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	4
Number of overlap:	8
Similarity score:	0.0795385

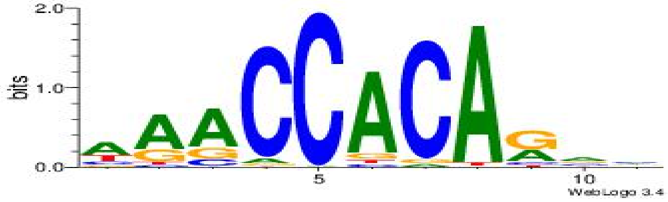
Alignment:

```
BBYTGTGGTTT
---TGTGTGTG
```

Original motif　　Consensus sequence: BBYTGTGGTTT



Reverse complement motif　　Consensus sequence: AAACCACAKVB



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

Original motif Consensus sequence: TTTWWAW

Reverse complement motif Consensus sequence: WTWWAAA

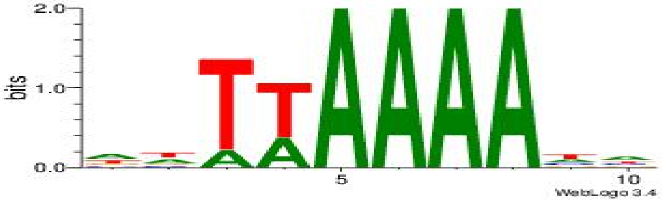
Best Matches for Motif ID 4 (Highest to Lowest)

Dataset #:	4
Motif ID:	148
Motif name:	wwTwAAAAww
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:	0.0204013

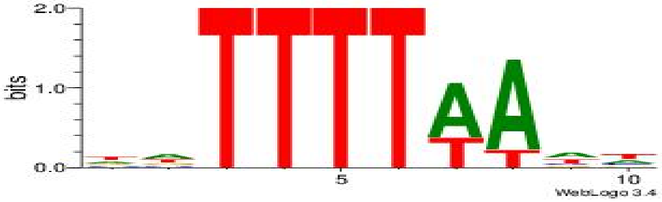
Alignment:

```
DDTWAAAAHH
-WTWWAAA--
```

Original motif Consensus sequence: DDTWAAAAHH



Reverse complement motif Consensus sequence: HHTTTTWADD

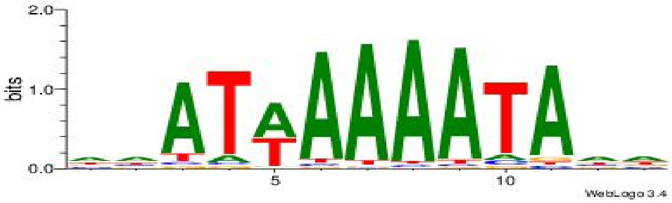


Dataset #: 4
Motif ID: 150
Motif name: waATwAAAATAww
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 3
Number of overlap: 7
Similarity score: 0.0245609

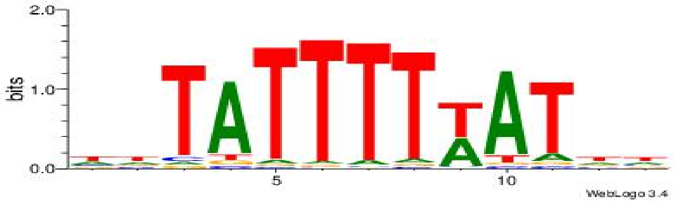
Alignment:

```
DHTATTTTWATHD
----TTTWWAW--
```

Original motif Consensus sequence: DHATWAAAATAHD



Reverse complement motif Consensus sequence: DHTATTTTWATHD

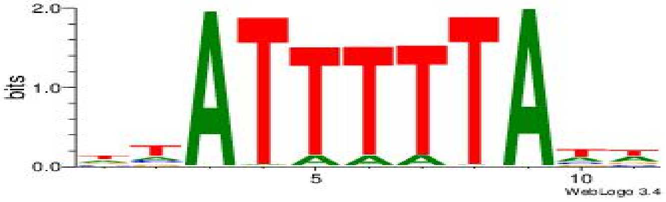


Dataset #: 4
Motif ID: 157
Motif name: wtATTTTTAww
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 4
Number of overlap: 7

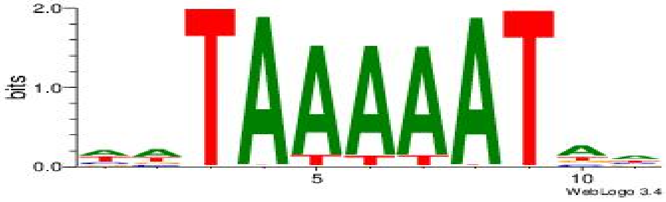
Similarity score: 0.028753

Alignment:
```
WWTAAAAATAD
-WTWWAAA---
```

Original motif Consensus sequence: DTATTTTTAWW



Reverse complement motif Consensus sequence: WWTAAAAATAD

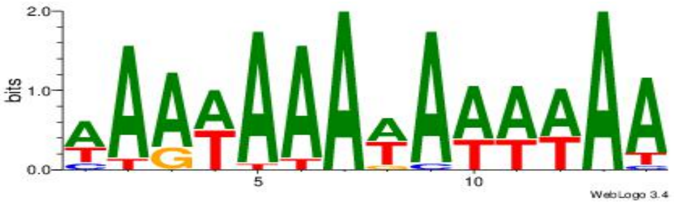


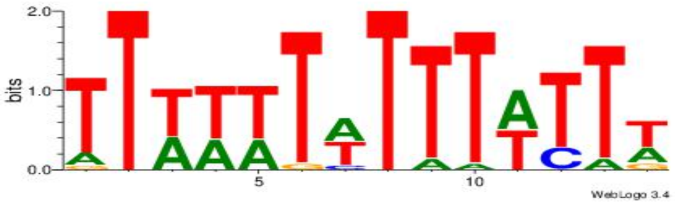
Dataset #: 2
Motif ID: 68
Motif name: Motif 68
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 7
Similarity score: 0.048084

Alignment:
```
WAAWAAAWAWWWAA
WTWWAAA-------
```

Original motif Consensus sequence: WAAWAAAWAWWWAA

Reverse complement motif Consensus sequence: TTWWWTWTTTWTTW



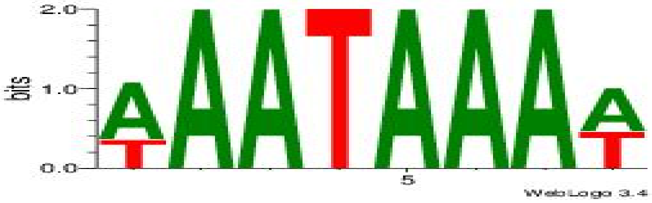


Dataset #:	2
Motif ID:	52
Motif name:	Motif 52
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	7
Similarity score:	0.0637767

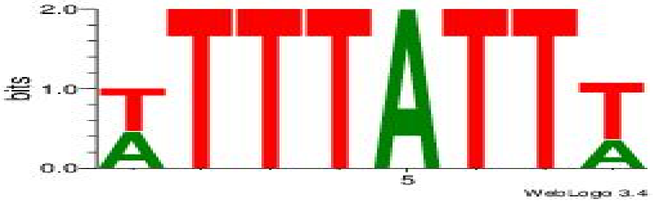
Alignment:

```
AAATAAAW
WTWWAAA-
```

Original motif   Consensus sequence: AAATAAAW



Reverse complement motif   Consensus sequence: WTTTATTT



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

Original motif Consensus sequence: CCCCDCCC

Reverse complement motif Consensus sequence: GGGDGGGG

Best Matches for 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:

```
CCCCRCCC
CCCCDCCC
```

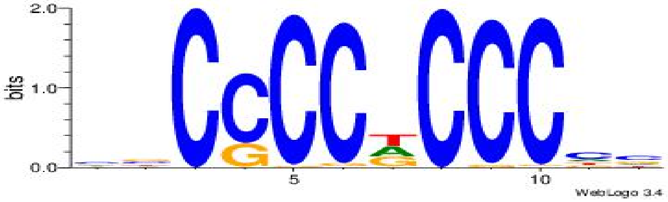
Original motif Consensus sequence: CCCCRCCC

Reverse complement motif Consensus sequence: GGGKGGGG

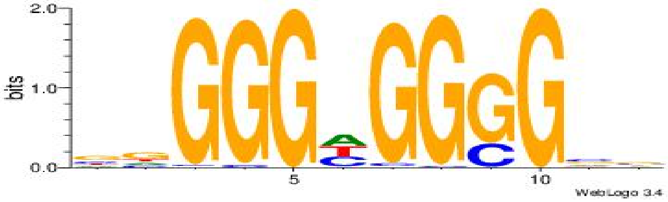
Dataset #: 4
Motif ID: 155
Motif name: csCSCCdCCCcs
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 3
Number of overlap: 8
Similarity score: 0.00464015

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

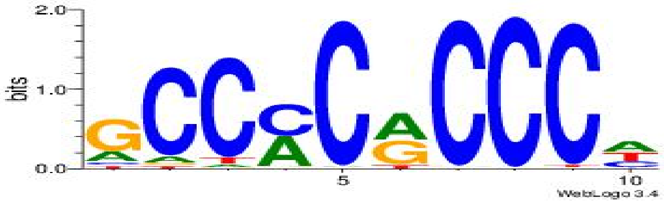
Similarity score: 0.0352587

Alignment:

```
GCCYCMCCCD
-CCCCDCCC-
```

Original motif Consensus sequence: DGGGYGKGGC

Reverse complement motif Consensus sequence: GCCYCMCCCD



Dataset #: 4

Motif ID: 154

Motif name: csCsCCTCCcc

Matching format of first motif: Reverse Complement

Matching format of second motif: Reverse Complement

Direction: Forward

Position number: 2

Number of overlap: 8

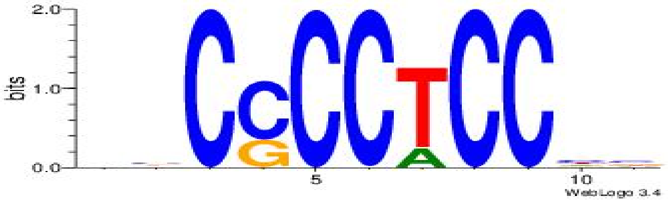
Similarity score: 0.0361349

Alignment:

```
BDGGAGGGGBV
-GGGDGGGG--
```

Original motif Consensus sequence: VBCCCCTCCHB

Reverse complement motif Consensus sequence: BDGGAGGGGBV

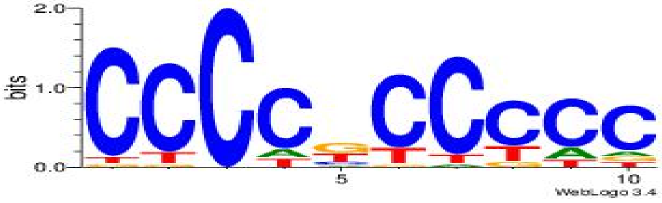


Dataset #:	3
Motif ID:	116
Motif name:	SP1
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	8
Similarity score:	0.0368066

Alignment:

```
CCCCKCCCCC
CCCCDCCC--
```

Original motif Consensus sequence: CCCCKCCCCC



Reverse complement motif Consensus sequence: GGGGGYGGGG

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

Original motif Consensus sequence: CTGGRRA

Reverse complement motif Consensus sequence: TMMCCAG

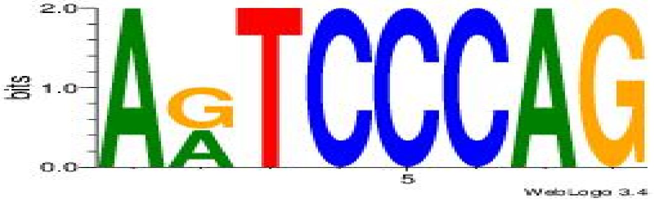
Best Matches for Motif ID 6 (Highest to Lowest)

Dataset #:	1
Motif ID:	40
Motif name:	Motif 40
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	7
Similarity score:	0.0326828

Alignment:

```
CTGGGAMT
CTGGRRA-
```

Original motif Consensus sequence: ARTCCCAG



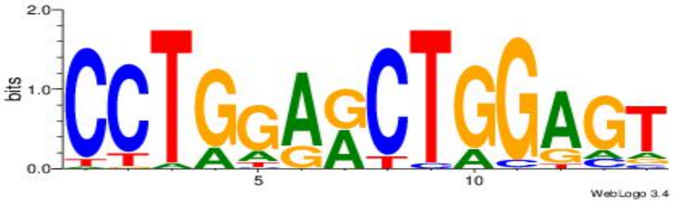
Reverse complement motif Consensus sequence: CTGGGAMT

Dataset #:	2
Motif ID:	69
Motif name:	Motif 69
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	7
Number of overlap:	7
Similarity score:	0.0472643

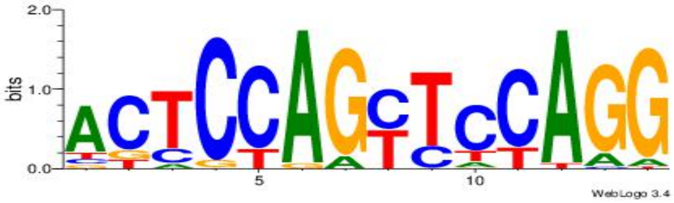
Alignment:

```
CCTGGARCTGGAGT
-CTGGRRA------
```

Original motif   Consensus sequence: CCTGGARCTGGAGT



Reverse complement motif   Consensus sequence: ACTCCAGMTCCAG



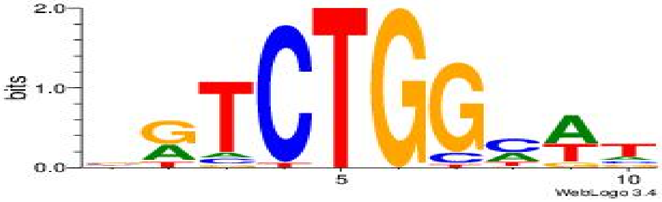
Dataset #:	3
Motif ID:	85
Motif name:	Hand1Tcfe2a
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	4
Number of overlap:	7

Similarity score:	0.0513687

Alignment:

```
BRTCTGGMWT
---CTGGRRA
```

Original motif Consensus sequence: BRTCTGGMWT



Reverse complement motif Consensus sequence: AWRCCAGAMB

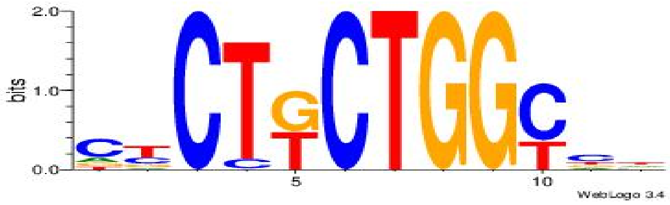
Dataset #:	4
Motif ID:	151
Motif name:	agrCCAGmAGrg
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	6
Number of overlap:	7
Similarity score:	0.0514331

Alignment:

```
HVGCCAGMAGRG
TMMCCAG-----
```

Original motif Consensus sequence: HVGCCAGMAGRG

Reverse complement motif Consensus sequence: CKCTRCTGGCVH



Dataset #:	1
Motif ID:	33
Motif name:	Motif 33
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:	0.0553656

Alignment:

```
GWAGCCAG
-TMMCCAG
```

Original motif Consensus sequence: CTGGCTWC

Reverse complement motif Consensus sequence: GWAGCCAG

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

Original motif   Consensus sequence: AGRAAA

Reverse complement motif   Consensus sequence: TTTMCT

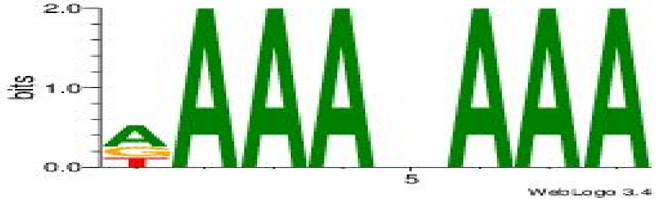
Best Matches for Motif ID 7 (Highest to Lowest)

Dataset #:	1
Motif ID:	2
Motif name:	Motif 2
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	6
Similarity score:	0.0617932

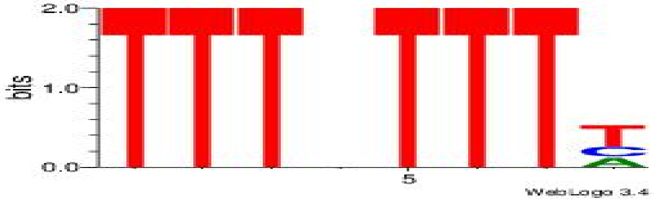
Alignment:

```
TTTDTTTT
TTTMCT--
```

Original motif   Consensus sequence: AAAAHAAA



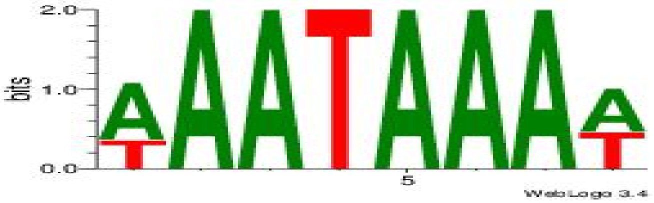
Reverse complement motif   Consensus sequence: TTTDTTTT



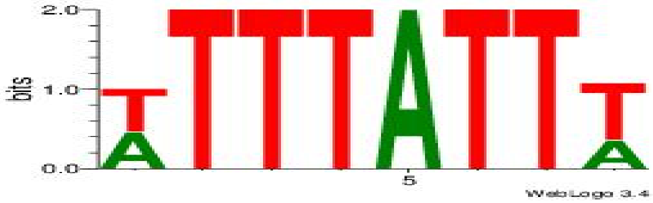
Dataset #: 2
Motif ID: 52
Motif name: Motif 52
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 2
Number of overlap: 6
Similarity score: 0.0627423

Alignment:
WTTTATTT
-TTTMCT-

Original motif Consensus sequence: AAATAAAW



Reverse complement motif Consensus sequence: WTTTATTT

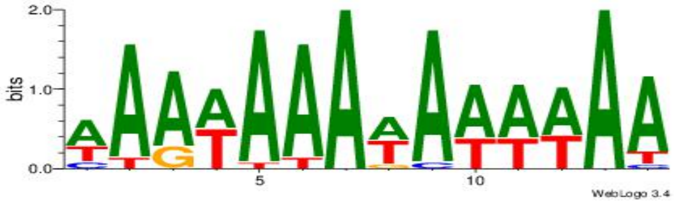


Dataset #: 2
Motif ID: 68
Motif name: Motif 68
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 2
Number of overlap: 6

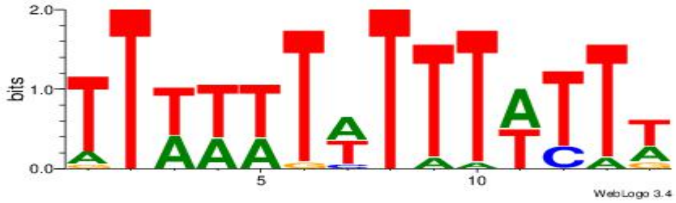
Similarity score: 0.0627423

Alignment:
WAAWAAAWAWWWAA
-AGRAAA-------

Original motif Consensus sequence: WAAWAAAWAWWWAA



Reverse complement motif Consensus sequence: TTWWWTWTTTWTTW



Dataset #: 1
Motif ID: 32
Motif name: Motif 32
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 6
Similarity score: 0.0627423

Alignment:
TTTATTY
TTTMCT-

Original motif Consensus sequence: KAATAAA

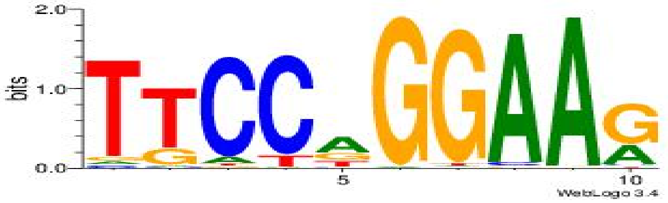
Reverse complement motif Consensus sequence: TTTATTY

Dataset #:	3
Motif ID:	119
Motif name:	Stat3
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:	0.069443

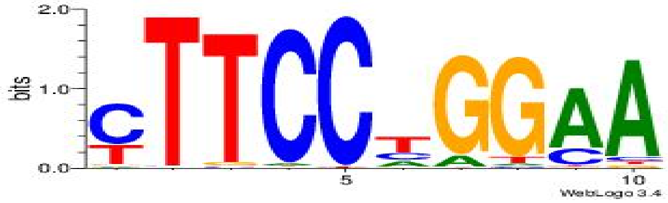
Alignment:

```
TTCCAGGAAG
----AGRAAA
```

Original motif Consensus sequence: TTCCAGGAAG



Reverse complement motif Consensus sequence: CTTCCTGGAA



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

Original motif Consensus sequence: AAATAH

Reverse complement motif Consensus sequence: DTATTT

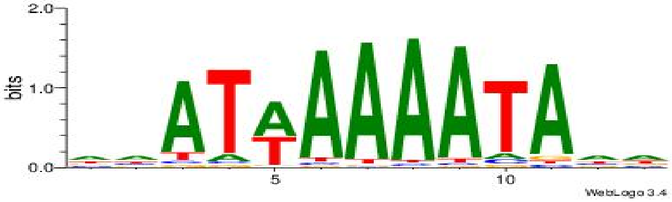
Best Matches for Motif ID 8 (Highest to Lowest)

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

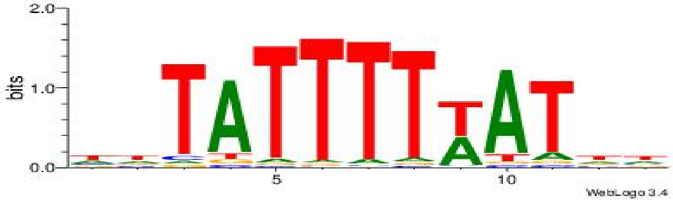
Alignment:

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

Original motif Consensus sequence: DHATWAAAATAHD



Reverse complement motif Consensus sequence: DHTATTTTWATHD

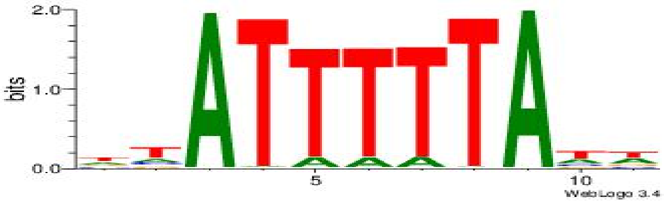


Dataset #:	4
Motif ID:	157
Motif name:	wtATTTTTAww
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	6
Number of overlap:	6
Similarity score:	0.00556446

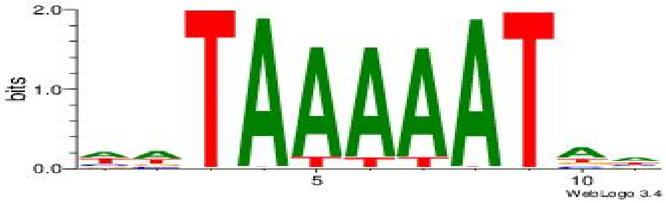
Alignment:

```
WWTAAAAATAD
-----AAATAH
```

Original motif Consensus sequence: DTATTTTTAWW



Reverse complement motif Consensus sequence: WWTAAAAATAD

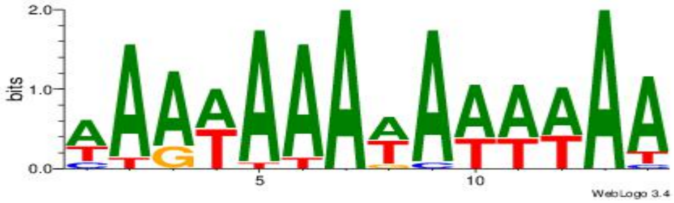


Dataset #:	2
Motif ID:	68
Motif name:	Motif 68
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	5
Number of overlap:	6

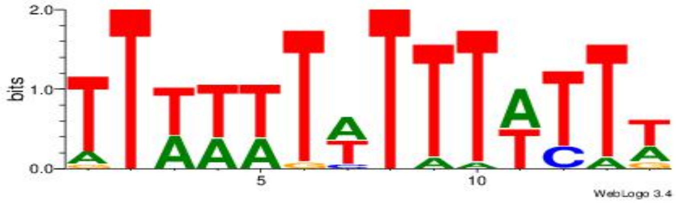
Similarity score: 0.0128826

Alignment:
WAAWAAAWAWWWAA
----AAATAH----

Original motif Consensus sequence: WAAWAAAWAWWWAA



Reverse complement motif Consensus sequence: TTWWWTWTTTWTTW

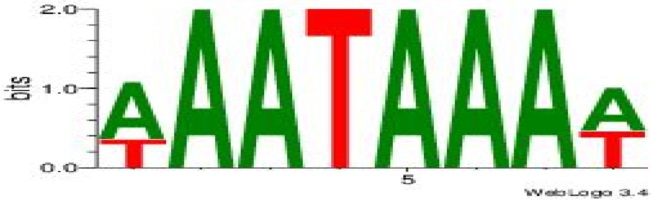


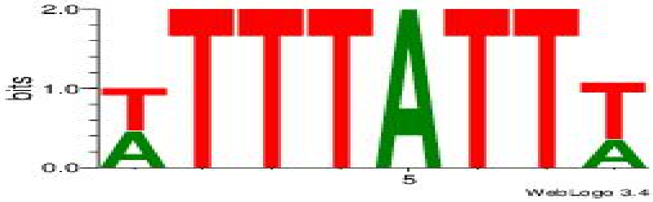
Dataset #: 2
Motif ID: 52
Motif name: Motif 52
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 6
Similarity score: 0.0167304

Alignment:
AAATAAAW
AAATAH--

Original motif Consensus sequence: AAATAAAW

Reverse complement motif Consensus sequence: WTTTATTT



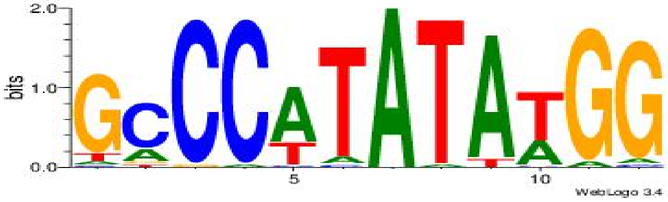


Dataset #:	3
Motif ID:	118
Motif name:	SRF
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	3
Number of overlap:	6
Similarity score:	0.0210491

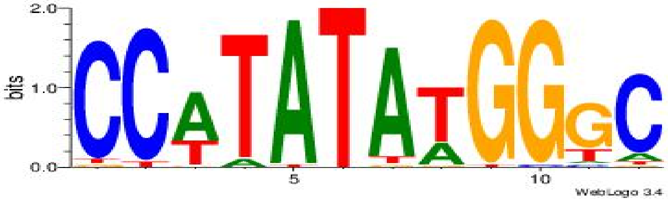
Alignment:

```
GCCCATATATGG
----AAATAH--
```

Original motif Consensus sequence: GCCCATATATGG



Reverse complement motif Consensus sequence: CCATATATGGGC



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

Original motif Consensus sequence: GGTGGCWS

Reverse complement motif Consensus sequence: SWGCCACC

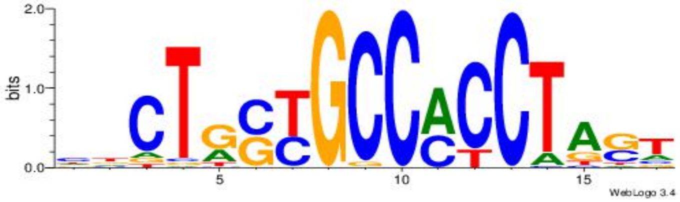
Best Matches for Motif ID 9 (Highest to Lowest)

Dataset #:	4
Motif ID:	144
Motif name:	ctCTrsyGCCmCCTast
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	5
Number of overlap:	8
Similarity score:	0.0240374

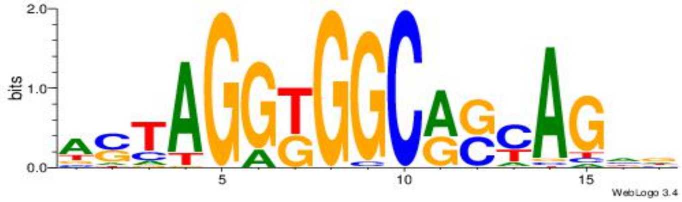
Alignment:

```
ASTAGGYGGCMSCAGDD
----GGTGGCWS-----
```

Original motif Consensus sequence: HDCTGSYGCCMCCTAST



Reverse complement motif Consensus sequence: ASTAGGYGGCMSCAGDD

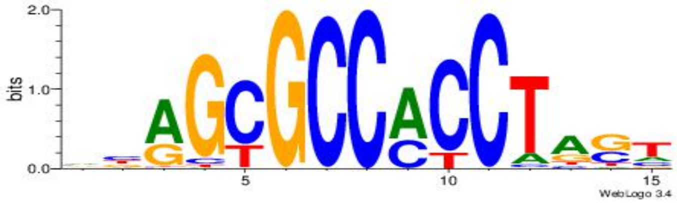


Dataset #: 4
Motif ID: 146
Motif name: myrGYGCCmCCTast
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 5
Number of overlap: 8
Similarity score: 0.0280157

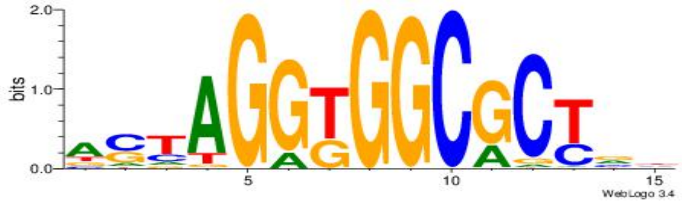
Alignment:

```
ASTAGGYGGCGCTBB
----GGTGGCWS---
```

Original motif Consensus sequence: VBAGCGCCMCCTAST



Reverse complement motif Consensus sequence: ASTAGGYGGCGCT

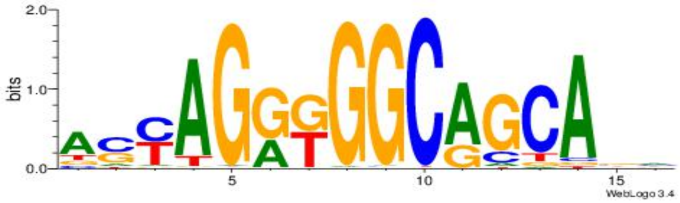


Dataset #: 4
Motif ID: 164
Motif name: asyAGrkGGCRGCAga
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 5
Number of overlap: 8

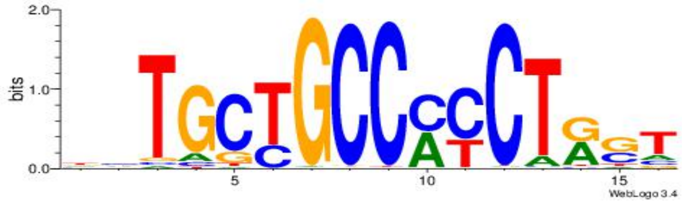
Similarity score: 0.0360935

Alignment:
```
ASYAGRKGGCAGCABH
----GGTGGCWS----
```

Original motif Consensus sequence: ASYAGRKGGCAGCABH



Reverse complement motif Consensus sequence: HBTGCTGCCYMCTKST



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: 5
Number of overlap: 8
Similarity score: 0.0392839

Alignment:
```
ASCAGRGGGCRSB
----GGTGGCWS-
```

Original motif Consensus sequence: ASCAGRGGGCRSB

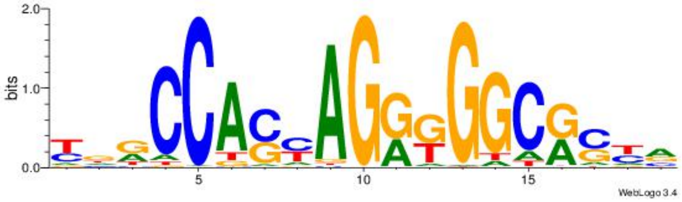
Reverse complement motif Consensus sequence: BSKGCCCMCTGST

Dataset #:	3
Motif ID:	74
Motif name:	CTCF
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:	0.0429881

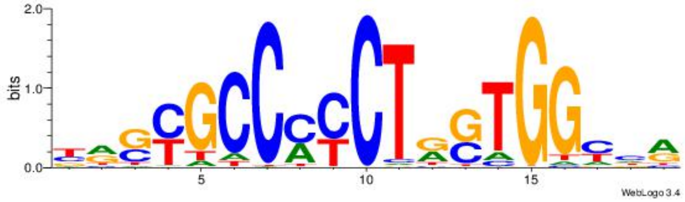
Alignment:

```
YDRCCASYAGRKGGCRSYV
---------GGTGGCWS--
```

Original motif Consensus sequence: YDRCCASYAGRKGGCRSYV



Reverse complement motif Consensus sequence: BMSMGCCYMCTKSTGGMHM



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

Original motif Consensus sequence: CTGGCCTC

Reverse complement motif Consensus sequence: GAGGCCAG

Best Matches for Motif ID 10 (Highest to Lowest)

Dataset #:	2
Motif ID:	49
Motif name:	Motif 49
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

Alignment:

```
GAGGCCAG
GAGGCCAG
```

Original motif Consensus sequence: CTGGCCTC

Reverse complement motif Consensus sequence: GAGGCCAG

Dataset #: 1
Motif ID: 33
Motif name: Motif 33
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: 0.0326888

Alignment:
```
CTGGCTWC
CTGGCCTC
```

Original motif Consensus sequence: CTGGCTWC

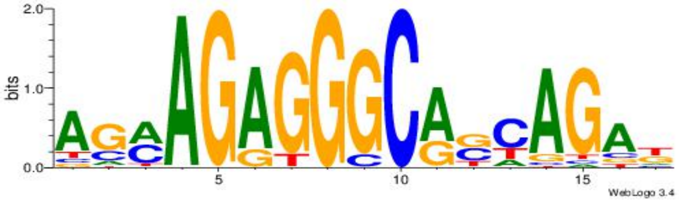
Reverse complement motif Consensus sequence: GWAGCCAG

Dataset #: 4
Motif ID: 143
Motif name: AgmAGAGGGCrscAGak
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 5
Number of overlap: 8

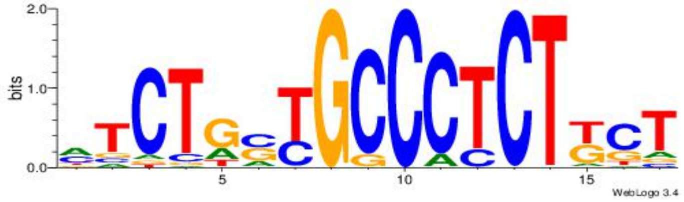
Similarity score: 0.047812

Alignment:
```
AGMAGAGGGCASCAGAK
----GAGGCCAG-----
```

Original motif Consensus sequence: AGMAGAGGGCASCAGAK



Reverse complement motif Consensus sequence: RTCTGSTGCCCTCTYCT

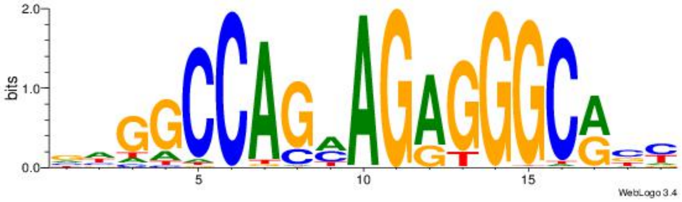


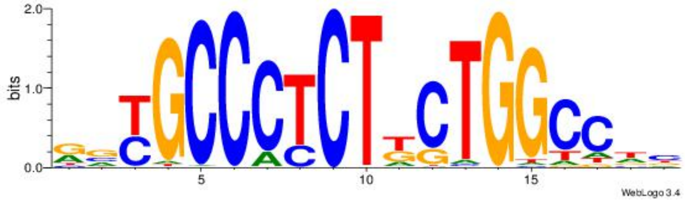
Dataset #:	4
Motif ID:	163
Motif name:	gwGGCCAGmAGAGGGCrby
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	8
Similarity score:	0.0506629

Alignment:
```
VHGGCCAGMAGAGGGCRBY
GAGGCCAG-----------
```

Original motif Consensus sequence: VHGGCCAGMAGAGGGCRBY

Reverse complement motif Consensus sequence: KBKGCCCTCTYCTGGCCHV





Dataset #: 4
Motif ID: 133
Motif name: shAGrGGGCAgy
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 4
Number of overlap: 8
Similarity score: 0.0509007

Alignment:

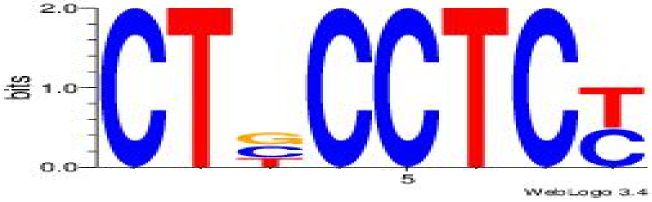
```
DBTGCCCKCTDS
-CTGGCCTC---
```

Original motif Consensus sequence: SHAGRGGGCABH

Reverse complement motif Consensus sequence: DBTGCCCKCTDS

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

Original motif Consensus sequence: CTBCCTCY



Reverse complement motif Consensus sequence: MGAGGBAG

Best Matches for Motif ID 11 (Highest to Lowest)

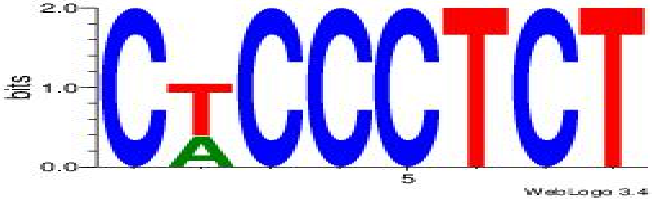
Dataset #:	2
Motif ID:	63
Motif name:	Motif 63
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	8
Similarity score:	0.0297241

Alignment:

```
CWCCCTCT
CTBCCTCY
```

Original motif Consensus sequence: AGAGGGWG

Reverse complement motif Consensus sequence: CWCCCTCT



Dataset #: 1
Motif ID: 17
Motif name: Motif 17
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: 0.0448422

Alignment:
CCDCCTCC
CTBCCTCY

Original motif Consensus sequence: CCDCCTCC

Reverse complement motif Consensus sequence: GGAGGDGG

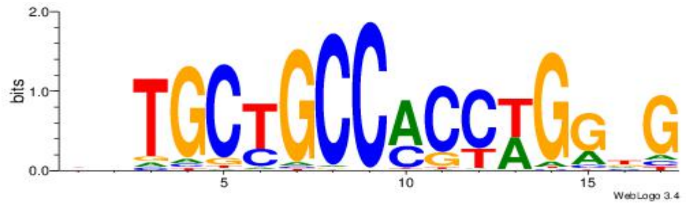
Dataset #: 4
Motif ID: 169
Motif name: yvTGCyGCCmCCwGgtG
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 5
Number of overlap: 8

Similarity score: 0.0620322

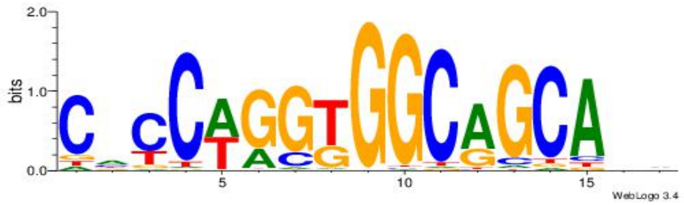
Alignment:

```
BVTGCTGCCACCWGGDG
----CTBCCTCY-----
```

Original motif Consensus sequence: BVTGCTGCCACCWGGDG



Reverse complement motif Consensus sequence: CDCCWGGTGGCAGCAVV



Dataset #: 4

Motif ID: 164

Motif name: asyAGrkGGCRGCAga

Matching format of first motif: Original Motif

Matching format of second motif: Reverse Complement

Direction: Forward

Position number: 5

Number of overlap: 8

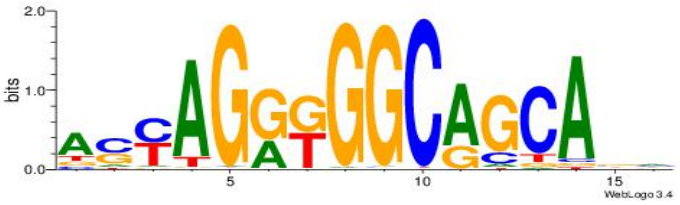
Similarity score: 0.0623054

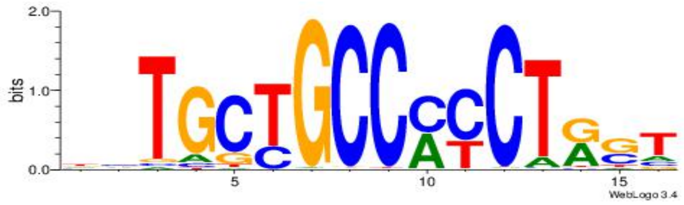
Alignment:

```
HBTGCTGCCYMCTKST
----CTBCCTCY----
```

Original motif Consensus sequence: ASYAGRKGGCAGCABH

Reverse complement motif Consensus sequence: HBTGCTGCCYMCTKST





Dataset #:	4
Motif ID:	154
Motif name:	csCsCCTCCcc
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:	0.067516

Alignment:

```
VBCCCCTCCHB
-CTBCCTCY--
```

Original motif Consensus sequence: VBCCCCTCCHB

Reverse complement motif Consensus sequence: BDGGAGGGGBV

Dataset #: 1 **Motif ID: 12** **Motif name: Motif 12**

Original motif Consensus sequence: GATGGCTC

Reverse complement motif Consensus sequence: GAGCCATC

Best Matches for Motif ID 12 (Highest to Lowest)

Dataset #:	1
Motif ID:	9
Motif name:	Motif 9
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	8
Similarity score:	0.0446318

Alignment:

```
GGTGGCWS
GATGGCTC
```

Original motif Consensus sequence: GGTGGCWS

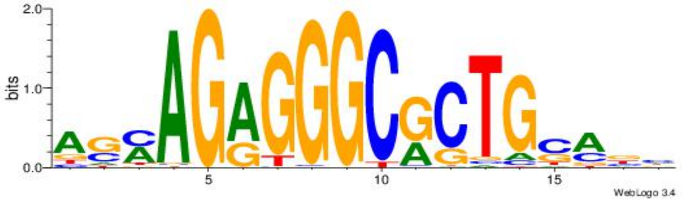
Reverse complement motif Consensus sequence: SWGCCACC

Dataset #: 4
Motif ID: 149
Motif name: asmAGRGGGCrCTGsmkc
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 5
Number of overlap: 8
Similarity score: 0.053856

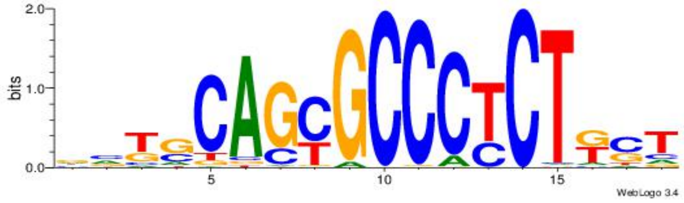
Alignment:

```
DBTSCAGMGCCCTCTRST
------GAGCCATC----
```

Original motif Consensus sequence: ASMAGAGGGCRCTGSABH



Reverse complement motif Consensus sequence: DBTSCAGMGCCCTCTRST



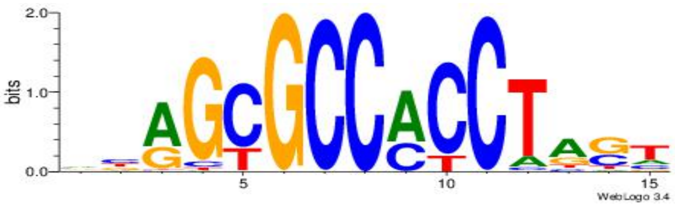
Dataset #: 4
Motif ID: 146
Motif name: myrGYGCCmCCTast
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 5

Number of overlap: 8
Similarity score: 0.0558657

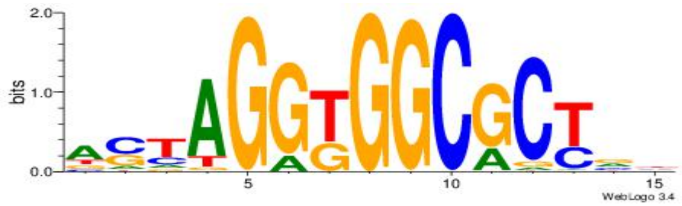
Alignment:

```
ASTAGGYGGCGCTBB
----GATGGCTC---
```

Original motif Consensus sequence: VBAGCGCCMCCTAST



Reverse complement motif Consensus sequence: ASTAGGYGGCGCT



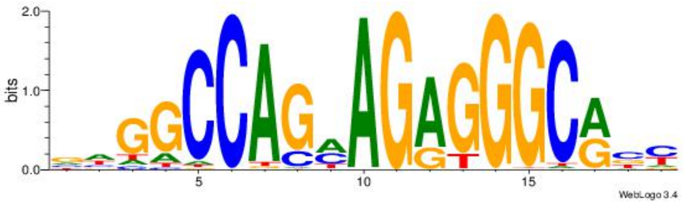
Dataset #: 4
Motif ID: 163
Motif name: gwGGCCAGmAGAGGGCrby
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 11
Number of overlap: 8
Similarity score: 0.0592323

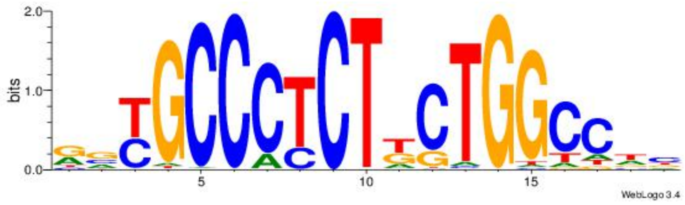
Alignment:

```
VHGGCCAGMAGAGGGCRBY
----------GATGGCTC-
```

Original motif Consensus sequence: VHGGCCAGMAGAGGGCRBY

Reverse complement motif Consensus sequence: KBKGCCCTCTYCTGGCCHV





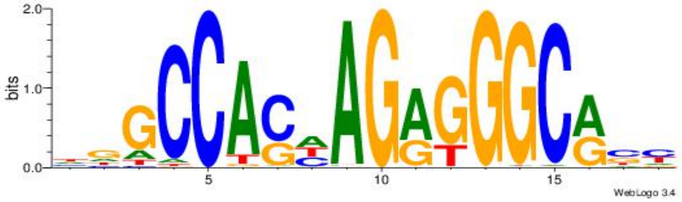
Dataset #:	4
Motif ID:	165
Motif name:	wgGCCAshAGrGGGCrsy
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2
Number of overlap:	8
Similarity score:	0.0607886

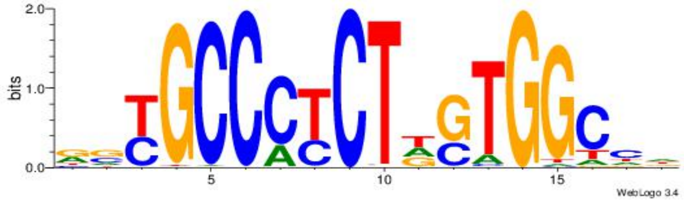
Alignment:

```
HDGCCACHAGRGGGCRBY
---------GATGGCTC-
```

Original motif Consensus sequence: HDGCCACHAGRGGGCRBY

Reverse complement motif Consensus sequence: KBKGCCCKCTHGTGGCHH





Dataset #: 1 Motif ID: 13 Motif name: Motif 13

Original motif Consensus sequence: CAGYDCC

Reverse complement motif Consensus sequence: GGDKCTG

Best Matches for Motif ID 13 (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:	1
Number of overlap:	7
Similarity score:	0

Alignment:

```
CAGYDCC
CAGYDCC
```

Original motif Consensus sequence: CAGYDCC

Reverse complement motif Consensus sequence: GGDKCTG

Dataset #:	2
Motif ID:	53
Motif name:	Motif 53
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:	0.0294104

Alignment:
GGGATCTG
-GGDKCTG

Original motif Consensus sequence: CAGATCCC

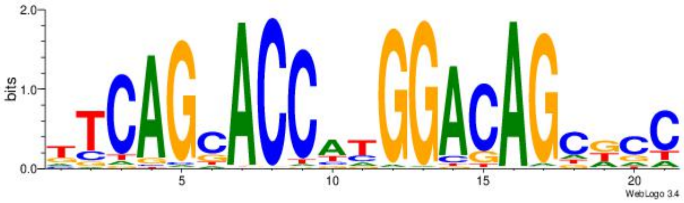
Reverse complement motif Consensus sequence: GGGATCTG

Dataset #:	3
Motif ID:	113
Motif name:	REST
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	13
Number of overlap:	7

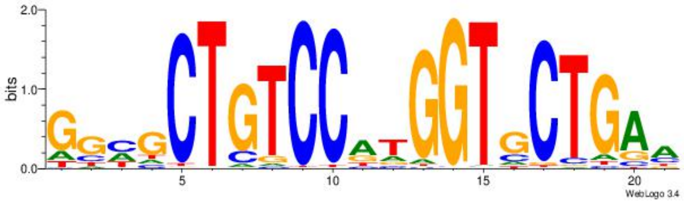
Similarity score: 0.0500473

Alignment:
TTCAGCACCATGGACAGCKCC
--CAGYDCC------------

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC



Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA



Dataset #:	1
Motif ID:	22
Motif name:	Motif 22
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	2
Number of overlap:	7
Similarity score:	0.0533516

Alignment:
GGKATCTG
-GGDKCTG

Original motif Consensus sequence: CAGATYCC

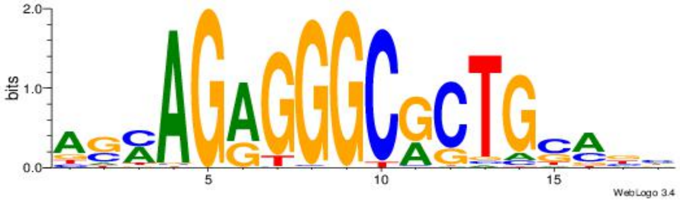
Reverse complement motif Consensus sequence: GGKATCTG

Dataset #:	4
Motif ID:	149
Motif name:	asmAGRGGGCrCTGsmkc
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	8
Number of overlap:	7
Similarity score:	0.0558573

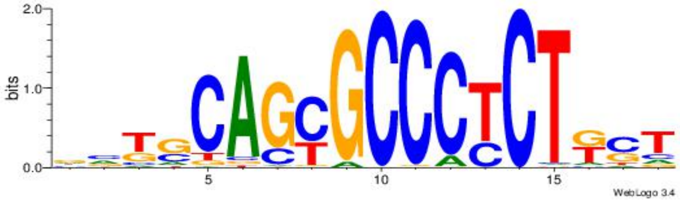
Alignment:

```
DBTSCAGMGCCCTCTRST
----CAGYDCC-------
```

Original motif   Consensus sequence: ASMAGAGGGCRCTGSABH



Reverse complement motif   Consensus sequence: DBTSCAGMGCCCTCTRST



Dataset #: 1   **Motif ID: 14**   **Motif name: Motif 14**

Original motif Consensus sequence: TSTGTR

Reverse complement motif Consensus sequence: MACASA

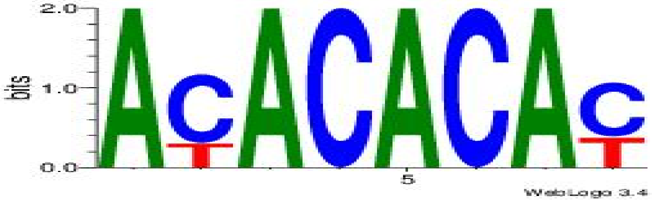
Best Matches for Motif ID 14 (Highest to Lowest)

Dataset #:	2
Motif ID:	57
Motif name:	Motif 57
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:	0.0165773

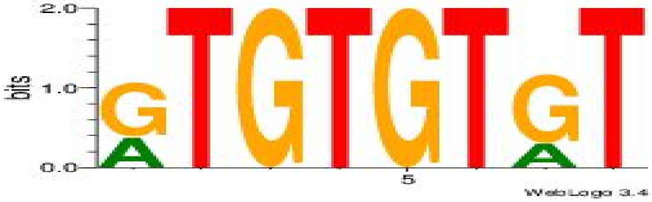
Alignment:

```
KTGTGTGT
-TSTGTR-
```

Original motif Consensus sequence: ACACACAY



Reverse complement motif Consensus sequence: KTGTGTGT



Dataset #:	1
Motif ID:	3
Motif name:	Motif 3
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:	0.0165773

Alignment:

```
CACACACA
MACASA--
```

Original motif Consensus sequence: CACACACA

Reverse complement motif Consensus sequence: TGTGTGTG

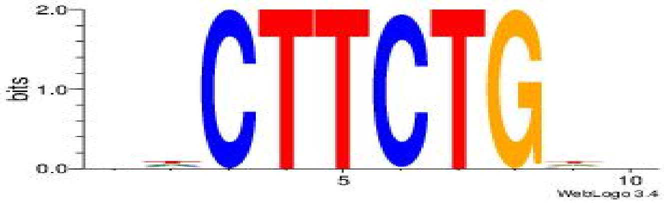
Dataset #:	4
Motif ID:	136
Motif name:	dwCAGAAGwh
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	6

Similarity score: 0.0401476

Alignment:
HDCTTCTGHD
----TSTGTR

Original motif Consensus sequence: DHCAGAAGDH

Reverse complement motif Consensus sequence: HDCTTCTGHD

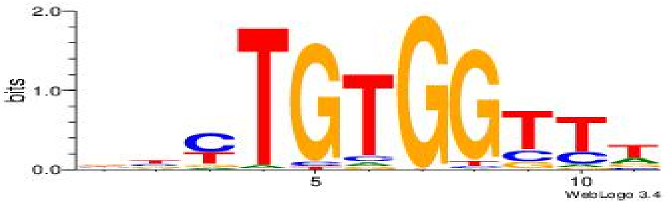


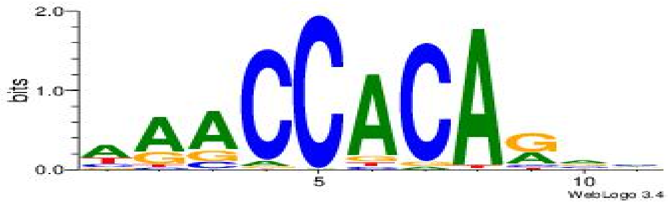
Dataset #: 3
Motif ID: 114
Motif name: RUNX1
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 2
Number of overlap: 6
Similarity score: 0.0445836

Alignment:
BBYTGTGGTTT
-TSTGTR----

Original motif Consensus sequence: BBYTGTGGTTT

Reverse complement motif Consensus sequence: AAACCACAKVB





Dataset #: 1
Motif ID: 24
Motif name: Motif 24
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: 0.0456841

Alignment:

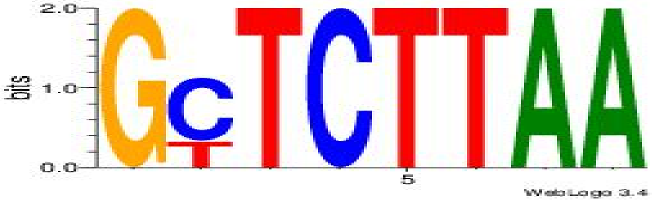
```
TGTGGGTG
--TSTGTR
```

Original motif Consensus sequence: TGTGGGTG

Reverse complement motif Consensus sequence: CACCCACA

Dataset #: 1 Motif ID: 15 Motif name: Motif 15

Original motif Consensus sequence: GCTCTTAA



Reverse complement motif Consensus sequence: TTAAGAGC

Best Matches for Motif ID 15 (Highest to Lowest)

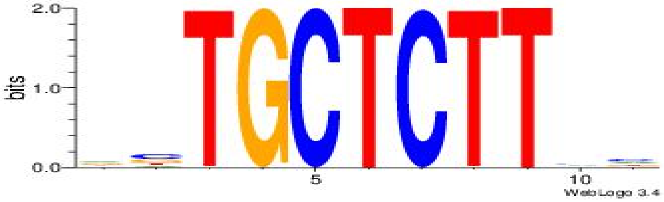
Dataset #:	4
Motif ID:	159
Motif name:	kkAAGAGCAsy
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	8
Similarity score:	0.0216416

Alignment:

```
DBAAGAGCAVH
TTAAGAGC---
```

Original motif Consensus sequence: DBAAGAGCAVH

Reverse complement motif Consensus sequence: HVTGCTCTTBH

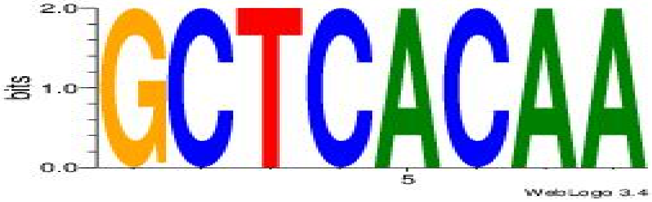


Dataset #:	2
Motif ID:	55
Motif name:	Motif 55
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	8
Similarity score:	0.0390835

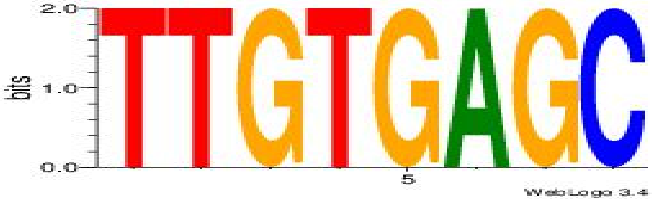
Alignment:

```
GCTCACAA
GCTCTTAA
```

Original motif Consensus sequence: GCTCACAA



Reverse complement motif Consensus sequence: TTGTGAGC

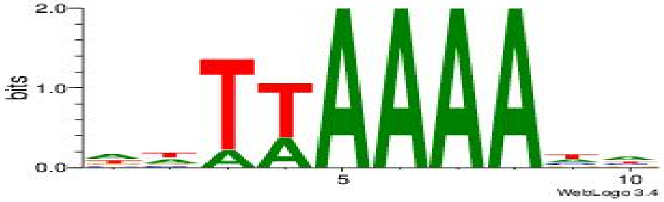


Dataset #:	4
Motif ID:	148
Motif name:	wwTwAAAAww
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	3
Number of overlap:	8

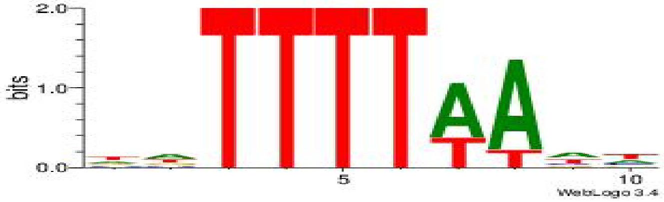
Similarity score: 0.0584188

Alignment:
HHTTTTWADD
GCTCTTAA--

Original motif Consensus sequence: DDTWAAAAHH



Reverse complement motif Consensus sequence: HHTTTTWADD



Dataset #:	3
Motif ID:	120
Motif name:	T
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:	0.0666592

Alignment:
CTAGGTGTGAA
---GCTCTTAA

Original motif Consensus sequence: CTAGGTGTGAA

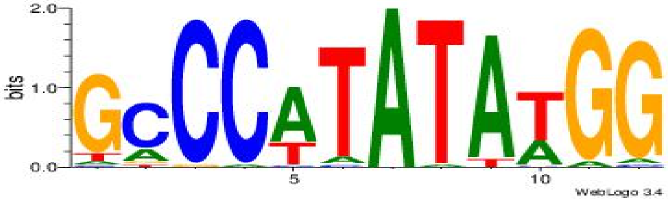
Reverse complement motif Consensus sequence: TTCACACCTAG

Dataset #:	3
Motif ID:	118
Motif name:	SRF
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	5
Number of overlap:	8
Similarity score:	0.0676161

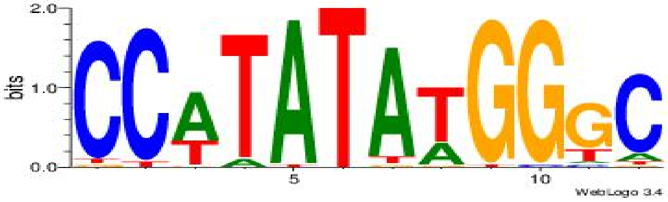
Alignment:

```
CCATATATGGGC
----TTAAGAGC
```

Original motif Consensus sequence: GCCCATATATGG



Reverse complement motif Consensus sequence: CCATATATGGGC



Dataset #: 1 Motif ID: 16 Motif name: Motif 16

Original motif Consensus sequence: GGAAGRR

Reverse complement motif Consensus sequence: MMCTTCC

Best Matches for Motif ID 16 (Highest to Lowest)

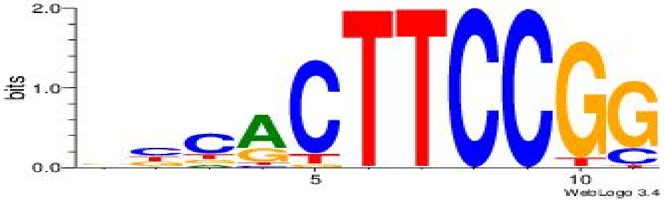
Dataset #:	3
Motif ID:	84
Motif name:	GABPA
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	3
Number of overlap:	7
Similarity score:	0.0238137

Alignment:

```
VVCACTTCCGG
--MMCTTCC--
```

Original motif Consensus sequence: CCGGAAGTGVV

Reverse complement motif Consensus sequence: VVCACTTCCGG



Dataset #: 1
Motif ID: 17
Motif name: Motif 17
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 7
Similarity score: 0.0632856

Alignment:
GGAGGDGG
GGAAGRR-

Original motif Consensus sequence: CCDCCTCC

Reverse complement motif Consensus sequence: GGAGGDGG

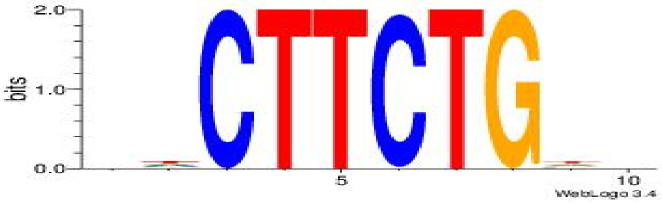
Dataset #: 4
Motif ID: 136
Motif name: dwCAGAAGwh
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 7

Similarity score:	0.0705782

Alignment:
HDCTTCTGHD
MMCTTCC---

Original motif Consensus sequence: DHCAGAAGDH

Reverse complement motif Consensus sequence: HDCTTCTGHD

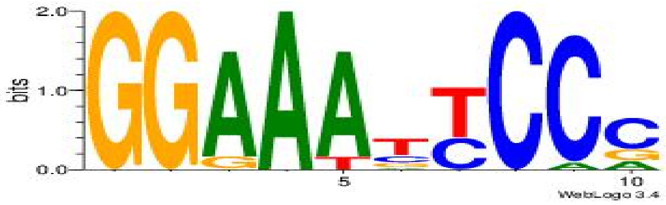


Dataset #:	3
Motif ID:	112
Motif name:	RELA
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	7
Similarity score:	0.0712379

Alignment:
GGGRATTTCC
---MMCTTCC

Original motif Consensus sequence: GGGRATTTCC

Reverse complement motif Consensus sequence: GGAAATKCCC



Dataset #:	4
Motif ID:	154
Motif name:	csCsCCTCCcc
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	3
Number of overlap:	7
Similarity score:	0.0768131

Alignment:

```
BDGGAGGGGBV
--GGAAGRR--
```

Original motif Consensus sequence: VBCCCCTCCHB

Reverse complement motif Consensus sequence: BDGGAGGGGBV

Dataset #: 1 Motif ID: 17 Motif name: Motif 17

Original motif Consensus sequence: CCDCCTCC

Reverse complement motif Consensus sequence: GGAGGDGG

Best Matches for Motif ID 17 (Highest to Lowest)

Dataset #:	4
Motif ID:	154
Motif name:	csCsCCTCCcc
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	2
Number of overlap:	8
Similarity score:	0.0325807

Alignment:

```
BDGGAGGGGBV
--GGAGGDGG-
```

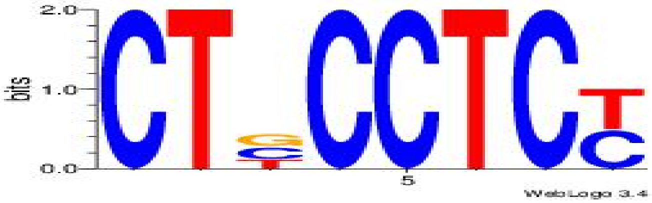
Original motif Consensus sequence: VBCCCCTCCHB

Reverse complement motif Consensus sequence: BDGGAGGGGBV

Dataset #: 1
Motif ID: 11
Motif name: Motif 11
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 8
Similarity score: 0.0441606

Alignment:
CTBCCTCY
CCDCCTCC

Original motif Consensus sequence: CTBCCTCY



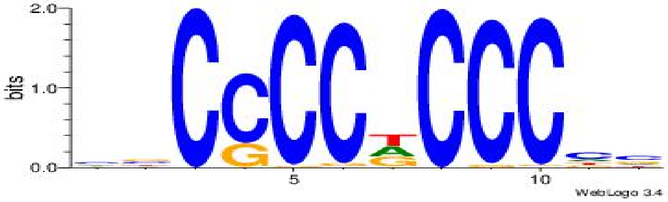
Reverse complement motif Consensus sequence: MGAGGBAG

Dataset #: 4
Motif ID: 155
Motif name: csCSCCdCCCcs
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 2
Number of overlap: 8

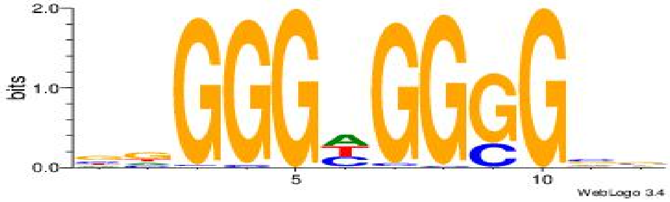
Similarity score: 0.0485525

Alignment:
VDGGGDGGGGBV
---GGAGGDGG-

Original motif   Consensus sequence: VBCCCCDCCCHV



Reverse complement motif   Consensus sequence: VDGGGDGGGGBV



Dataset #: 1
Motif ID: 27
Motif name: Motif 27
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: 0.0499486

Alignment:
CSGCCGCC
CCDCCTCC

Original motif   Consensus sequence: CSGCCGCC

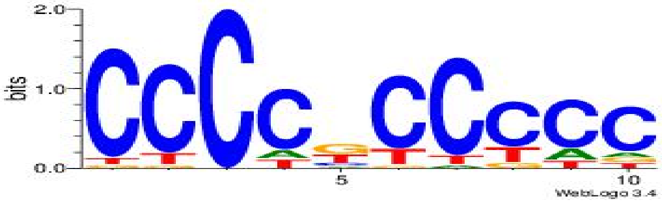
Reverse complement motif   Consensus sequence: GGCGGCSG

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:	1
Number of overlap:	8
Similarity score:	0.0500496

Alignment:

```
CCCCKCCCCC
--CCDCCTCC
```

Original motif   Consensus sequence: CCCCKCCCCC



Reverse complement motif   Consensus sequence: GGGGGYGGGG

Dataset #: 1   Motif ID: 18   Motif name: Motif 18

Original motif Consensus sequence: CATGYATG

Reverse complement motif Consensus sequence: CATKCATG

Best Matches for Motif ID 18 (Highest to Lowest)

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:	8
Similarity score:	0.058327

Alignment:

```
BRCATGCABD
--CATKCATG
```

Original motif Consensus sequence: BRCATGCABD

Reverse complement motif Consensus sequence: HVTGCATGKV

Dataset #:	1
Motif ID:	31
Motif name:	Motif 31
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:	0.0666244

Alignment:

```
CATGYACA
CATGYATG
```

Original motif Consensus sequence: CATGYACA

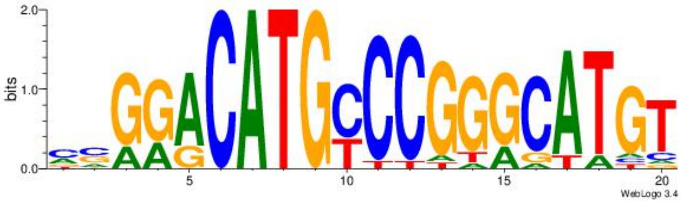
Reverse complement motif Consensus sequence: TGTKCATG

Dataset #:	3
Motif ID:	125
Motif name:	TP53
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	8
Number of overlap:	8

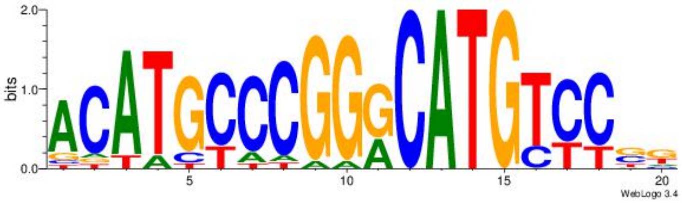
Similarity score: 0.068413

Alignment:
ACATGCCCGGKCATGTCCSR
-------CATKCATG-----

Original motif Consensus sequence: MSGGACATGYCCGGGCATGT



Reverse complement motif Consensus sequence: ACATGCCCGGKCATGTCCSR

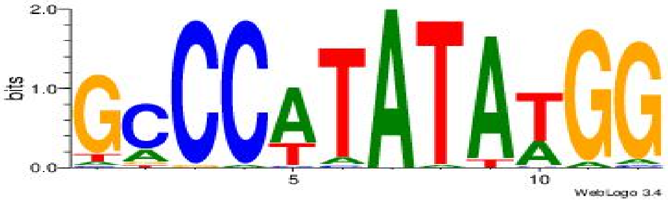


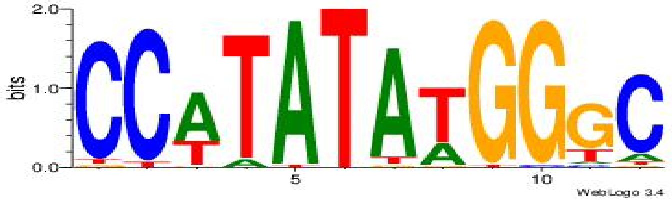
Dataset #: 3
Motif ID: 118
Motif name: SRF
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 2
Number of overlap: 8
Similarity score: 0.0745698

Alignment:
CCATATATGGGC
-CATGYATG---

Original motif Consensus sequence: GCCCATATATGG

Reverse complement motif Consensus sequence: CCATATATGGGC

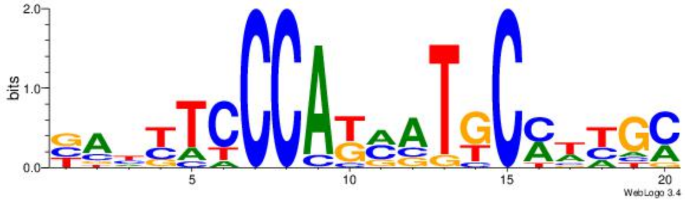




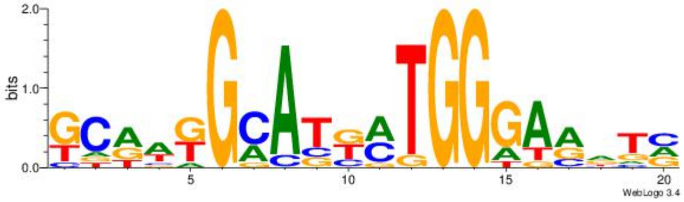
Dataset #: 3
Motif ID: 131
Motif name: znf143
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 3
Number of overlap: 8
Similarity score: 0.105729

Alignment:
```
BAHYTCCCAKMATGCMWYGC
----------CATKCATG--
```

Original motif Consensus sequence: BAHYTCCCAKMATGCMWYGC



Reverse complement motif Consensus sequence: GCMWRGCATYRTGGGAMHTB



Dataset #: 1 Motif ID: 19 Motif name: Motif 19

Original motif Consensus sequence: CAGSCAG

Reverse complement motif Consensus sequence: CTGSCTG

Best Matches for Motif ID 19 (Highest to Lowest)

Dataset #:	1
Motif ID:	33
Motif name:	Motif 33
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	7
Similarity score:	0.0196488

Alignment:

```
CTGGCTWC
CTGSCTG-
```

Original motif Consensus sequence: CTGGCTWC

Reverse complement motif Consensus sequence: GWAGCCAG

Dataset #: 1
Motif ID: 28
Motif name: Motif 28
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 7
Similarity score: 0.0338273

Alignment:

```
CTTCCTG
CTGSCTG
```

Original motif Consensus sequence: CTTCCTG

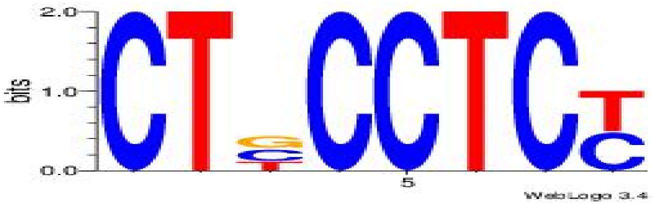
Reverse complement motif Consensus sequence: CAGGAAG

Dataset #: 1
Motif ID: 11
Motif name: Motif 11
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 2
Number of overlap: 7

Similarity score: 0.0430055

Alignment:
MGAGGBAG
CAGSCAG-

Original motif Consensus sequence: CTBCCTCY



Reverse complement motif Consensus sequence: MGAGGBAG

Dataset #: 1
Motif ID: 10
Motif name: Motif 10
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 7
Similarity score: 0.0473229

Alignment:
CTGGCCTC
-CTGSCTG

Original motif Consensus sequence: CTGGCCTC

Reverse complement motif Consensus sequence: GAGGCCAG

Dataset #:	1
Motif ID:	25
Motif name:	Motif 25
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	7
Similarity score:	0.0479304

Alignment:

```
CTGRGTTC
CTGSCTG-
```

Original motif Consensus sequence: CTGRGTTC

Reverse complement motif Consensus sequence: GAACKCAG

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

Original motif Consensus sequence: CACGTR

Reverse complement motif Consensus sequence: MACGTG

Best Matches for 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:	Forward
Position number:	1
Number of overlap:	6
Similarity score:	0

Alignment:

```
CACGTG
CACGTR
```

Original motif Consensus sequence: CACGTG

Reverse complement motif Consensus sequence: CACGTG

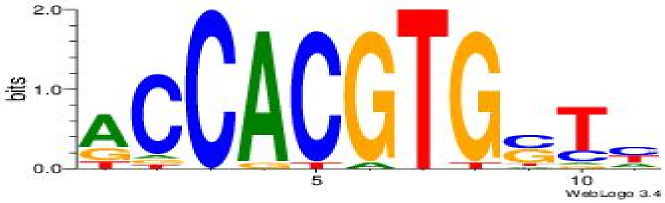
Dataset #:	3
Motif ID:	95
Motif name:	MYCMAX
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	4
Number of overlap:	6
Similarity score:	0.0102183

Alignment:

```
RASCACGTGGT
---MACGTG--
```

Original motif Consensus sequence: RASCACGTGGT

Reverse complement motif Consensus sequence: ACCACGTGSTM

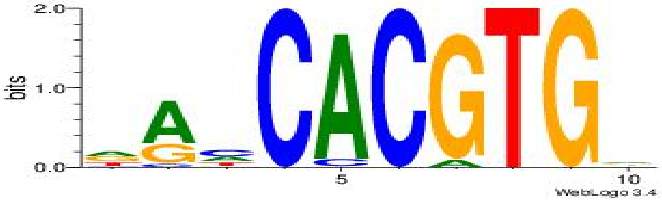


Dataset #:	3
Motif ID:	91
Motif name:	MAX
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2
Number of overlap:	6

Similarity score: 0.011152

Alignment:
DAHCACGTGD
---MACGTG-

Original motif Consensus sequence: DAHCACGTGD



Reverse complement motif Consensus sequence: BCACGTGDTD

Dataset #: 3
Motif ID: 126
Motif name: USF1
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: 0.0131944

Alignment:
CACGTGR
MACGTG-

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: 21 Motif name: Motif 21

Original motif Consensus sequence: CCACYAGG

Reverse complement motif Consensus sequence: CCTKGTGG

Best Matches for Motif ID 21 (Highest to Lowest)

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

```
CCACYAGR
CCACYAGG
```

Original motif Consensus sequence: CCACYAGR

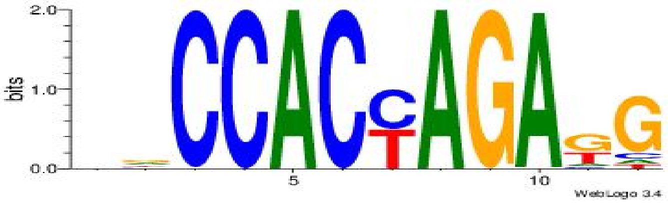
Reverse complement motif Consensus sequence: MCTKGTGG

Dataset #:	4
Motif ID:	145
Motif name:	grCCACyAGAkG
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:	0.028408

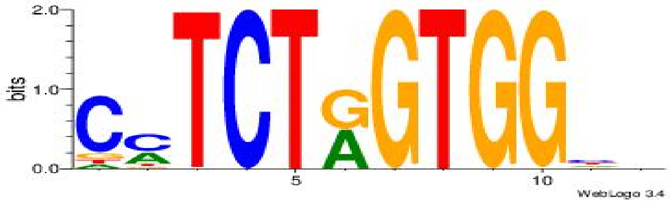
Alignment:

```
CYTCTKGTGGHH
--CCTKGTGG--
```

Original motif Consensus sequence: DDCCACYAGAKG



Reverse complement motif Consensus sequence: CYTCTKGTGGHH



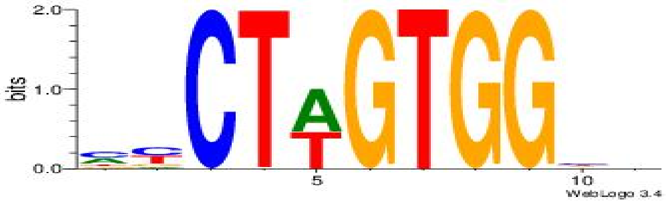
Dataset #:	4
Motif ID:	158
Motif name:	grCCACwAGrk
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2
Number of overlap:	8

Similarity score: 0.0314791

Alignment:
DDCCACWAGRK
--CCACYAGG-

Original motif Consensus sequence: DDCCACWAGRK

Reverse complement motif Consensus sequence: YMCTWGTGGHH

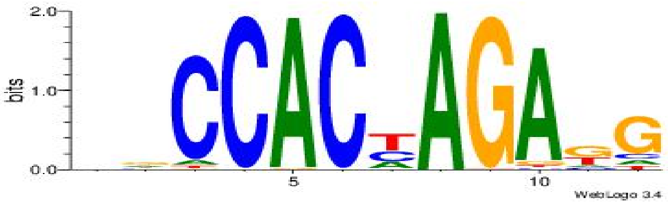
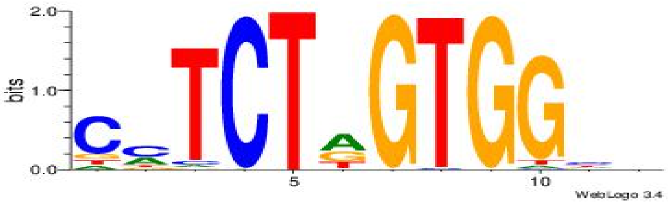


Dataset #: 4
Motif ID: 138
Motif name: grCCACyAGAkG
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 3
Number of overlap: 8
Similarity score: 0.0373754

Alignment:
DDCCACYAGAKG
--CCACYAGG--

Original motif Consensus sequence: DDCCACYAGAKG

Reverse complement motif Consensus sequence: CYTCTMGTGGHH

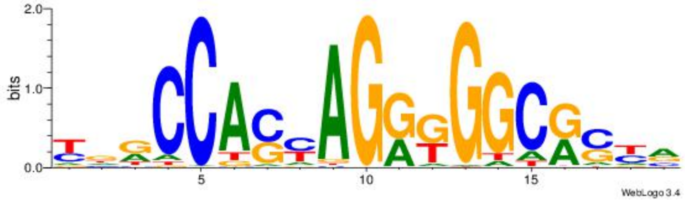



Dataset #:	3
Motif ID:	74
Motif name:	CTCF
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	9
Number of overlap:	8
Similarity score:	0.0387762

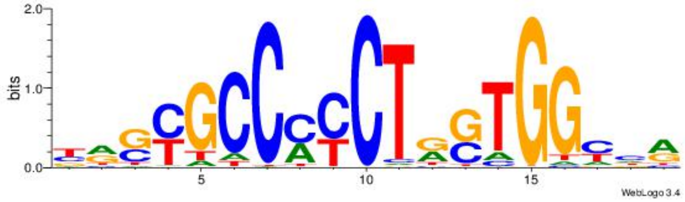
Alignment:

```
BMSMGCCYMCTKSTGGMHM
--------CCTKGTGG---
```

Original motif Consensus sequence: YDRCCASYAGRKGGCRSYV



Reverse complement motif Consensus sequence: BMSMGCCYMCTKSTGGMHM



Dataset #: 1 Motif ID: 22 Motif name: Motif 22

Original motif Consensus sequence: CAGATYCC

Reverse complement motif Consensus sequence: GGKATCTG

Best Matches for Motif ID 22 (Highest to Lowest)

Dataset #:	2
Motif ID:	53
Motif name:	Motif 53
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

Alignment:

```
GGGATCTG
GGKATCTG
```

Original motif Consensus sequence: CAGATCCC

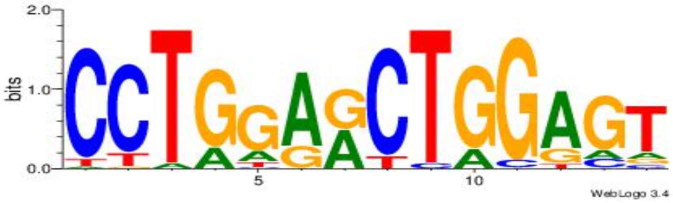
Reverse complement motif Consensus sequence: GGGATCTG

Dataset #: 2
Motif ID: 69
Motif name: Motif 69
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 5
Number of overlap: 8
Similarity score: 0.060058

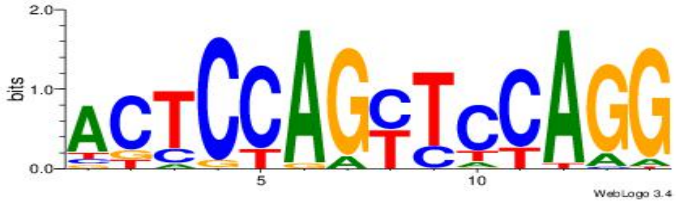
Alignment:

```
ACTCCAGMTCCAGG
----CAGATYCC--
```

Original motif Consensus sequence: CCTGGARCTGGAGT



Reverse complement motif Consensus sequence: ACTCCAGMTCCAG

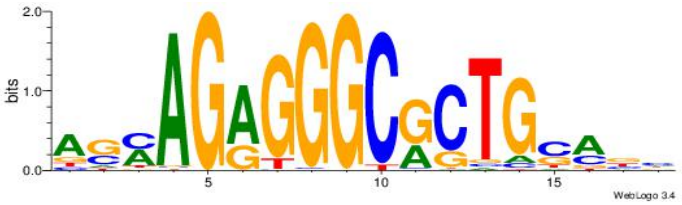


Dataset #: 4
Motif ID: 149
Motif name: asmAGRGGGCrCTGsmkc
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 7
Number of overlap: 8

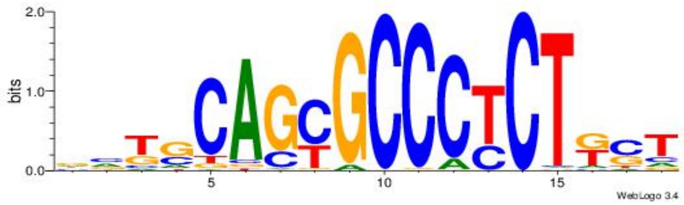
Similarity score: 0.0603056

Alignment:
DBTSCAGMGCCCTCTRST
----CAGATYCC------

Original motif Consensus sequence: ASMAGAGGGCRCTGSABH



Reverse complement motif Consensus sequence: DBTSCAGMGCCCTCTRST

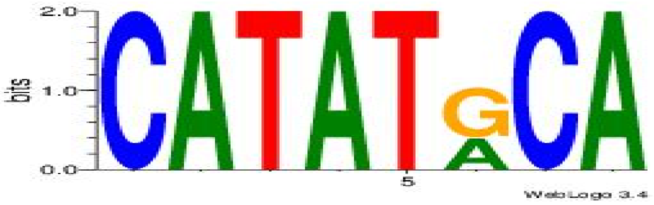


Dataset #: 2
Motif ID: 64
Motif name: Motif 64
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 8
Similarity score: 0.0721296

Alignment:
CATATRCA
CAGATYCC

Original motif Consensus sequence: CATATRCA

Reverse complement motif Consensus sequence: TGMATATG



Dataset #: 4
Motif ID: 160
Motif name: brCAGGGCCrs
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 3
Number of overlap: 8
Similarity score: 0.0730966

Alignment:

```
BBGGCCCTGBB
-GGKATCTG--
```

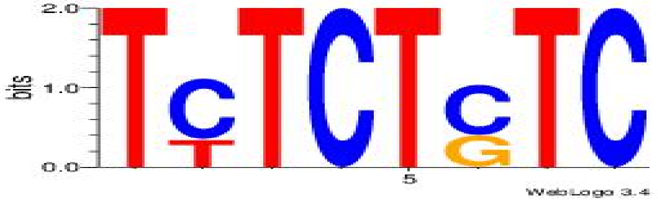
Original motif Consensus sequence: BVCAGGGCCVB

Reverse complement motif Consensus sequence: BBGGCCCTGBB

Dataset #: 1 **Motif ID: 23** **Motif name: Motif 23**

Original motif Consensus sequence: GASAGAGA

Reverse complement motif Consensus sequence: TCTCTSTC



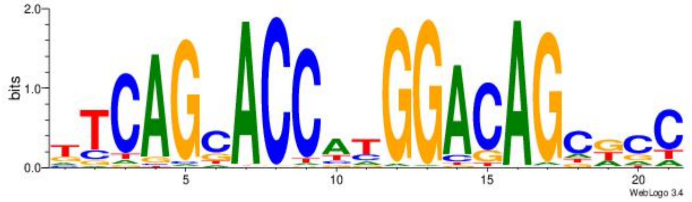
Best Matches for Motif ID 23 (Highest to Lowest)

Dataset #:	3
Motif ID:	113
Motif name:	REST
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	13
Number of overlap:	8
Similarity score:	0.0614501

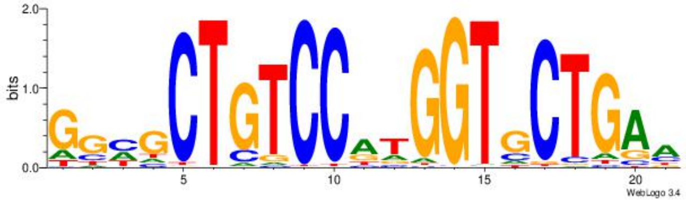
Alignment:

```
TTCAGCACCATGGACAGCKCC
------------GASAGAGA-
```

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC



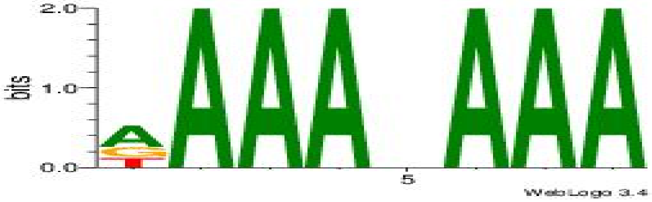
Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA



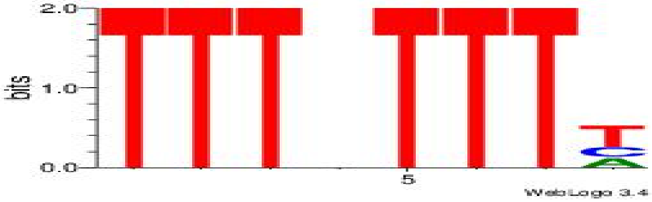
Dataset #:	1
Motif ID:	2
Motif name:	Motif 2
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	8
Similarity score:	0.0761109

Alignment:
AAAAHAAA
GASAGAGA

Original motif   Consensus sequence: AAAAHAAA



Reverse complement motif   Consensus sequence: TTTDTTTT



Dataset #:	1
Motif ID:	38
Motif name:	Motif 38
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: 0.081673

Alignment:
GAGTTACA
GASAGAGA

Original motif Consensus sequence: GAGTTACA

Reverse complement motif Consensus sequence: TGTAACTC

Dataset #:	2
Motif ID:	51
Motif name:	Motif 51
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:	0.081673

Alignment:
GAGTTACA
GASAGAGA

Original motif Consensus sequence: GAGTTACA

Reverse complement motif Consensus sequence: TGTAACTC

Dataset #: 1
Motif ID: 3
Motif name: Motif 3
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 8
Similarity score: 0.0826138

Alignment:
CACACACA
GASAGAGA

Original motif Consensus sequence: CACACACA

Reverse complement motif Consensus sequence: TGTGTGTG

Dataset #: 1 Motif ID: 24 Motif name: Motif 24

Original motif Consensus sequence: TGTGGGTG

Reverse complement motif Consensus sequence: CACCCACA

Best Matches for Motif ID 24 (Highest to Lowest)

Dataset #:	1
Motif ID:	3
Motif name:	Motif 3
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	8
Similarity score:	0.0589779

Alignment:

TGTGTGTG
TGTGGGTG

Original motif Consensus sequence: CACACACA

Reverse complement motif Consensus sequence: TGTGTGTG

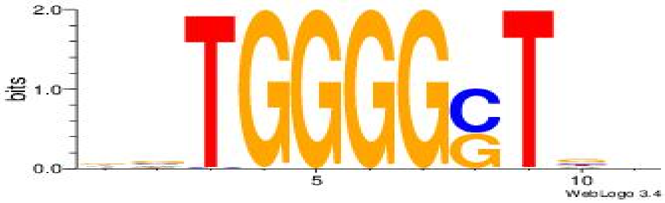
Dataset #: 4
Motif ID: 162
Motif name: ccAsCCCCAcc
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 3
Number of overlap: 8
Similarity score: 0.060611

Alignment:

```
DBTGGGGSTVD
--TGTGGGTG-
```

Original motif Consensus sequence: HVASCCCCABH

Reverse complement motif Consensus sequence: DBTGGGGSTVD

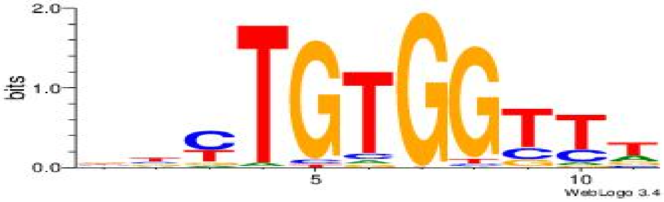


Dataset #: 3
Motif ID: 114
Motif name: RUNX1
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 4
Number of overlap: 8

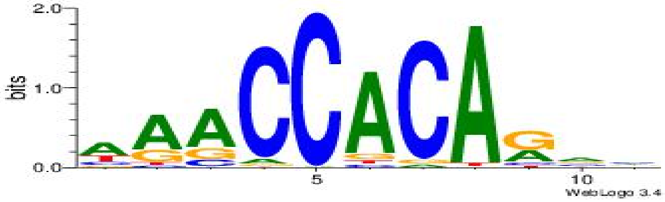
Similarity score: 0.0649239

Alignment:
AAACCACAKVB
CACCCACA---

Original motif Consensus sequence: BBYTGTGGTTT



Reverse complement motif Consensus sequence: AAACCACAKVB



Dataset #: 1
Motif ID: 31
Motif name: Motif 31
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: 0.0828996

Alignment:
CATGYACA
CACCCACA

Original motif Consensus sequence: CATGYACA

Reverse complement motif Consensus sequence: TGTKCATG

Dataset #:	1
Motif ID:	34
Motif name:	Motif 34
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	8
Similarity score:	0.0843302

Alignment:

```
TGTGGYCA
TGTGGGTG
```

Original motif Consensus sequence: TGKCCACA

Reverse complement motif Consensus sequence: TGTGGYCA

Dataset #: 1 Motif ID: 25 Motif name: Motif 25

Original motif Consensus sequence: CTGRGTTC

Reverse complement motif Consensus sequence: GAACKCAG

Best Matches for Motif ID 25 (Highest to Lowest)

Dataset #:	1
Motif ID:	33
Motif name:	Motif 33
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:	0.0224867

Alignment:

```
CTGGCTWC
CTGRGTTC
```

Original motif Consensus sequence: CTGGCTWC

Reverse complement motif Consensus sequence: GWAGCCAG

Dataset #: 1
Motif ID: 10
Motif name: Motif 10
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 8
Similarity score: 0.034485

Alignment:
CTGGCCTC
CTGRGTTC

Original motif Consensus sequence: CTGGCCTC

Reverse complement motif Consensus sequence: GAGGCCAG

Dataset #: 2
Motif ID: 49
Motif name: Motif 49
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: 0.052298

Alignment:

```
CTGGCCTC
CTGRGTTC
```

Original motif Consensus sequence: CTGGCCTC

Reverse complement motif Consensus sequence: GAGGCCAG

Dataset #: 3

Motif ID: 107

Motif name: NR2F1

Matching format of first motif: Reverse Complement

Matching format of second motif: Original Motif

Direction: Backward

Position number: 6

Number of overlap: 8

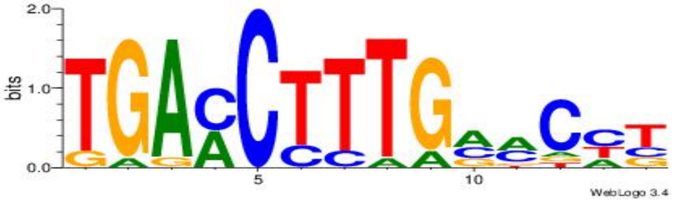
Similarity score: 0.0551569

Alignment:

```
TGAMCTTTGMMCYT
-GAACKCAG-----
```

Original motif Consensus sequence: TGAMCTTTGMMCYT

Reverse complement motif Consensus sequence: AKGYYCAAAGRTC




Dataset #: 1
Motif ID: 37
Motif name: Motif 37
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: 0.0560348

Alignment:
`CTGAGCYA`
`CTGRGTTC`

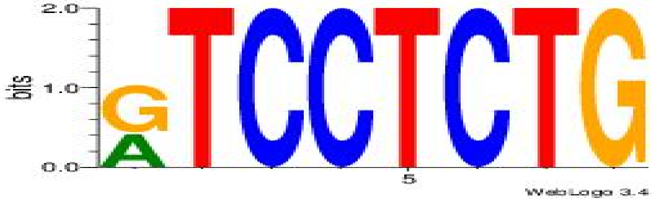
Original motif Consensus sequence: CTGAGCYA

Reverse complement motif Consensus sequence: TKGCTCAG

Dataset #: 1 **Motif ID: 26** **Motif name: Motif 26**

Original motif Consensus sequence: CAGAGGAY

Reverse complement motif Consensus sequence: KTCCTCTG



Best Matches for Motif ID 26 (Highest to Lowest)

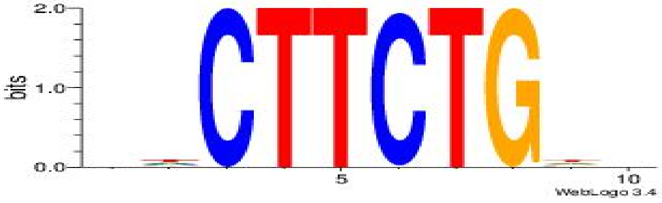
Dataset #:	4
Motif ID:	136
Motif name:	dwCAGAAGwh
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	3
Number of overlap:	8
Similarity score:	0.0359628

Alignment:

```
DHCAGAAGDH
--CAGAGGAY
```

Original motif Consensus sequence: DHCAGAAGDH

Reverse complement motif Consensus sequence: HDCTTCTGHD



Dataset #: 4

Motif ID: 166

Motif name: CasCAGrGGGCrsy

Matching format of first motif: Original Motif

Matching format of second motif: Original Motif

Direction: Forward

Position number: 4

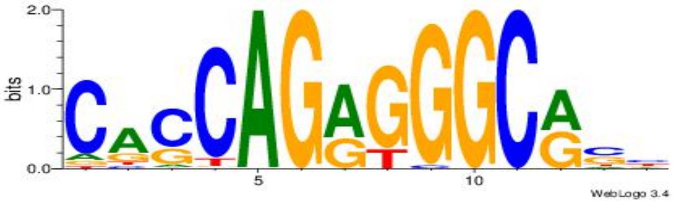
Number of overlap: 8

Similarity score: 0.036576

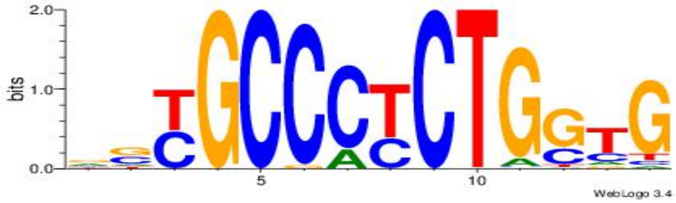
Alignment:

```
CACCAGRGGGCRSB
---CAGAGGAY---
```

Original motif   Consensus sequence: CACCAGRGGGCRSB



Reverse complement motif   Consensus sequence: BSKGCCCKCTGGT



Dataset #: 4

Motif ID: 143

Motif name: AgmAGAGGGCrscAGak

Matching format of first motif: Original Motif

Matching format of second motif: Original Motif

Direction: Backward

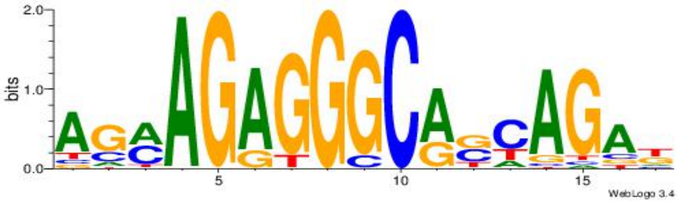
Position number: 8

Number of overlap: 8

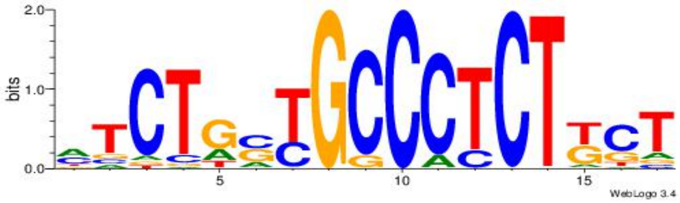
Similarity score: 0.0438271

Alignment:
AGMAGAGGGCASCAGAK
--CAGAGGAY-------

Original motif Consensus sequence: AGMAGAGGGCASCAGAK



Reverse complement motif Consensus sequence: RTCTGSTGCCCTCTYCT

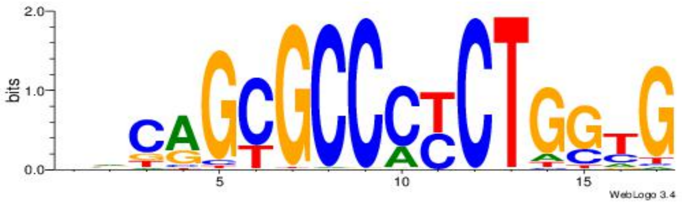


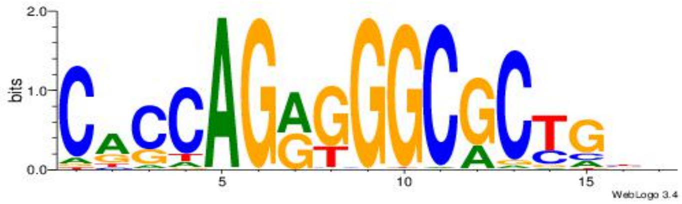
Dataset #: 4
Motif ID: 168
Motif name: yrcrGYGCCMyCTGGtG
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 7
Number of overlap: 8
Similarity score: 0.0450811

Alignment:
CACCAGMGGGCGCTGBD
---CAGAGGAY------

Original motif Consensus sequence: HVCAGCGCCCYCTGGTG

Reverse complement motif Consensus sequence: CACCAGMGGGCGCTGBD





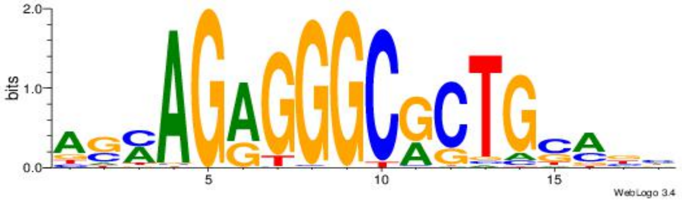
Dataset #: 4
Motif ID: 149
Motif name: asmAGRGGGCrCTGsmkc
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 9
Number of overlap: 8
Similarity score: 0.0460269

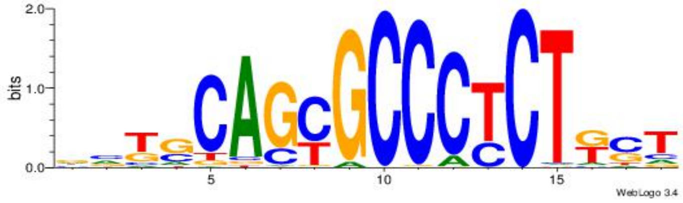
Alignment:

```
DBTSCAGMGCCCTCTRST
--------KTCCTCTG--
```

Original motif Consensus sequence: ASMAGAGGGCRCTGSABH

Reverse complement motif Consensus sequence: DBTSCAGMGCCCTCTRST





Dataset #: 1 Motif ID: 27 Motif name: Motif 27

Original motif Consensus sequence: CSGCCGCC

Reverse complement motif Consensus sequence: GGCGGCSG

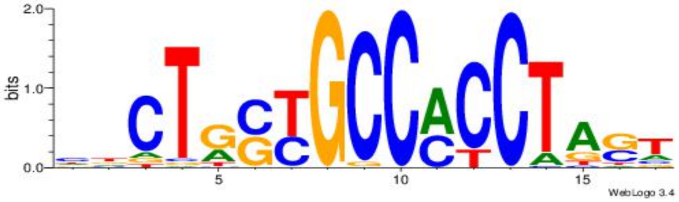
Best Matches for Motif ID 27 (Highest to Lowest)

Dataset #:	4
Motif ID:	144
Motif name:	ctCTrsyGCCmCCTast
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	5
Number of overlap:	8
Similarity score:	0.0594103

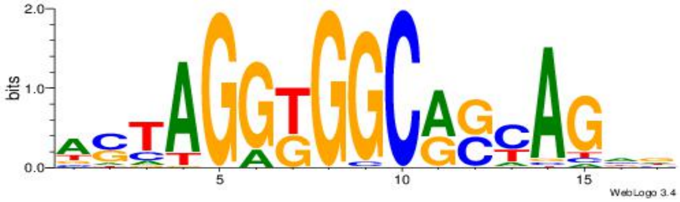
Alignment:

```
ASTAGGYGGCMSCAGDD
----GGCGGCSG-----
```

Original motif Consensus sequence: HDCTGSYGCCMCCTAST



Reverse complement motif Consensus sequence: ASTAGGYGGCMSCAGDD

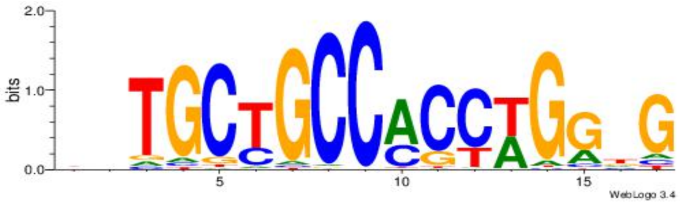


Dataset #: 4
Motif ID: 169
Motif name: yvTGCyGCCmCCwGgtG
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 5
Number of overlap: 8
Similarity score: 0.0661709

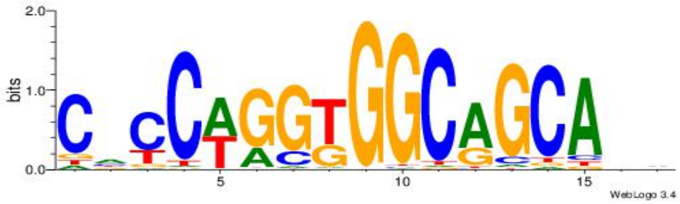
Alignment:

```
CDCCWGGTGGCAGCAVV
-----GGCGGCSG----
```

Original motif Consensus sequence: BVTGCTGCCACCWGGDG



Reverse complement motif Consensus sequence: CDCCWGGTGGCAGCAVV



Dataset #: 1
Motif ID: 17
Motif name: Motif 17
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: 0.0678225

Alignment:

```
CCDCCTCC
CSGCCGCC
```

Original motif Consensus sequence: CCDCCTCC

Reverse complement motif Consensus sequence: GGAGGDGG

Dataset #: 4

Motif ID: 146

Motif name: myrGYGCCmCCTast

Matching format of first motif: Reverse Complement

Matching format of second motif: Reverse Complement

Direction: Backward

Position number: 4

Number of overlap: 8

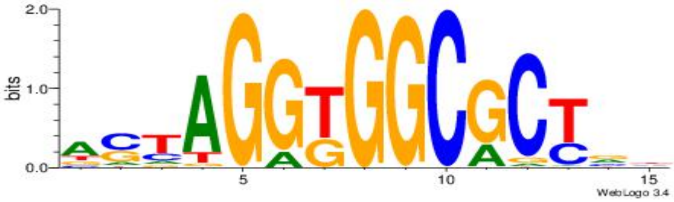
Similarity score: 0.0682918

Alignment:

```
ASTAGGYGGCGCTBB
----GGCGGCSG---
```

Original motif Consensus sequence: VBAGCGCCMCCTAST

Reverse complement motif Consensus sequence: ASTAGGYGGCGCT



Dataset #:	4
Motif ID:	135
Motif name:	ssCGGCCGss
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:	0.0688339

Alignment:

```
BSCGGCCGSV
GGCGGCSG--
```

Original motif Consensus sequence: BSCGGCCGSV

Reverse complement motif Consensus sequence: VSCGGCCGSB

Dataset #: 1 Motif ID: 28 Motif name: Motif 28

Original motif Consensus sequence: CTTCCTG

Reverse complement motif Consensus sequence: CAGGAAG

Best Matches for Motif ID 28 (Highest to Lowest)

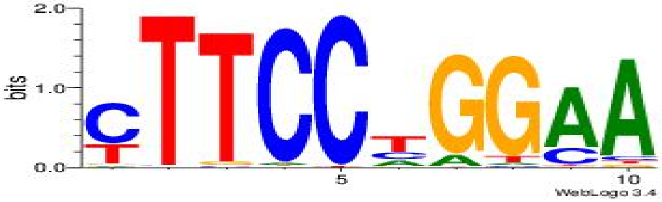
Dataset #:	3
Motif ID:	119
Motif name:	Stat3
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	4
Number of overlap:	7
Similarity score:	0.0301014

Alignment:

```
CTTCCTGGAA
CTTCCTG---
```

Original motif Consensus sequence: TTCCAGGAAG

Reverse complement motif Consensus sequence: CTTCCTGGAA



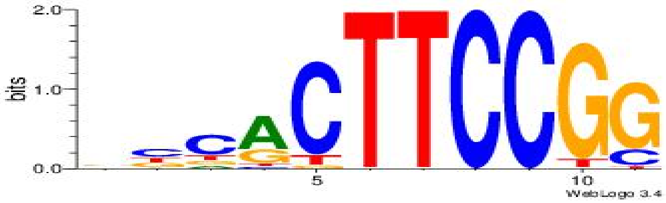
Dataset #: 3
Motif ID: 84
Motif name: GABPA
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 7
Similarity score: 0.0389741

Alignment:

```
CCGGAAGTGVV
CAGGAAG----
```

Original motif Consensus sequence: CCGGAAGTGVV

Reverse complement motif Consensus sequence: VVCACTTCCGG



Dataset #: 3
Motif ID: 80
Motif name: ELK4
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 2
Number of overlap: 7

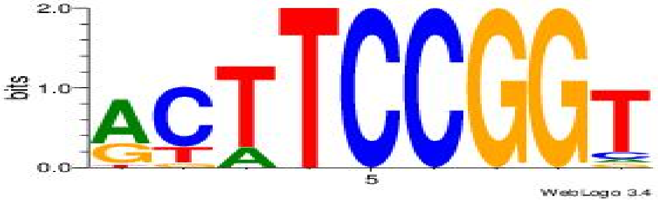
Similarity score: 0.044949

Alignment:

```
ACCGGAAGT
-CAGGAAG-
```

Original motif Consensus sequence: ACCGGAAGT

Reverse complement motif Consensus sequence: ACTTCCGGT



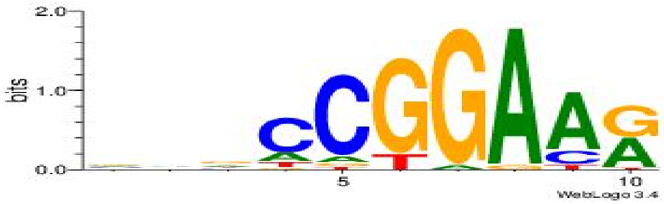
Dataset #: 3
Motif ID: 79
Motif name: ELK1
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 7
Similarity score: 0.0709694

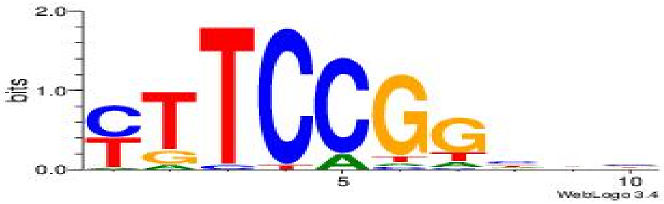
Alignment:

```
VDDCCGGAAR
---CAGGAAG
```

Original motif Consensus sequence: VDDCCGGAAR

Reverse complement motif Consensus sequence: MTTCCGGHBV





Dataset #: 1
Motif ID: 19
Motif name: Motif 19
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 7
Similarity score: 0.0713134

Alignment:
CAGSCAG
CAGGAAG

Original motif Consensus sequence: CAGSCAG

Reverse complement motif Consensus sequence: CTGSCTG

Dataset #: 1 Motif ID: 29 Motif name: Motif 29

Original motif   Consensus sequence: CATTTCY

Reverse complement motif   Consensus sequence: MGAAATG

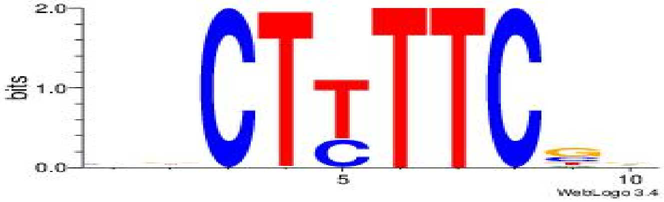
Best Matches for Motif ID 29 (Highest to Lowest)

Dataset #:	4
Motif ID:	139
Motif name:	mkCTyTTCsg
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	3
Number of overlap:	7
Similarity score:	0.0479916

Alignment:

```
HBGAAAAGBD
-MGAAATG--
```

Original motif   Consensus sequence: HBCTTTTCBD



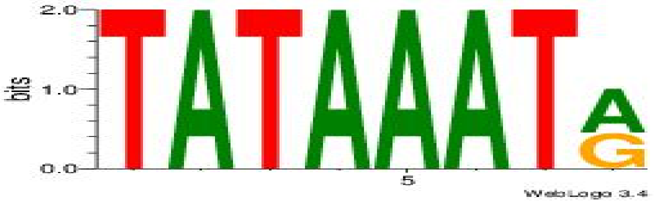
Reverse complement motif   Consensus sequence: HBGAAAAGBD

Dataset #:	2
Motif ID:	66
Motif name:	Motif 66
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	7
Similarity score:	0.050303

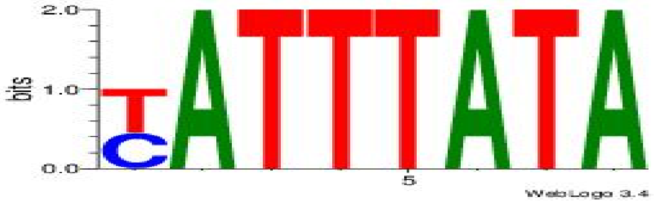
Alignment:

```
TATAAATR
-MGAAATG
```

Original motif   Consensus sequence: TATAAATR



Reverse complement motif   Consensus sequence: KATTTATA

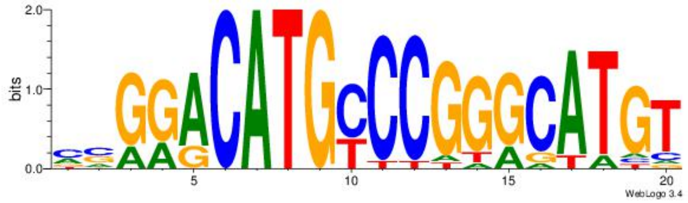


Dataset #:	3
Motif ID:	125
Motif name:	TP53
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	12
Number of overlap:	7

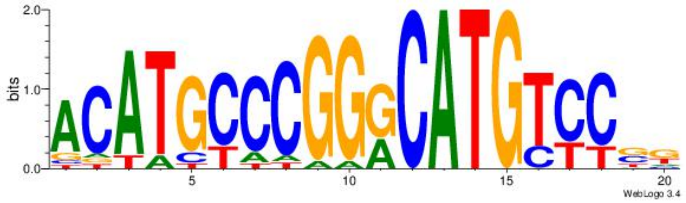
Similarity score: 0.058821

Alignment:
ACATGCCCGGKCATGTCCSR
-----------CATTTCY--

Original motif Consensus sequence: MSGGACATGYCCGGGCATGT



Reverse complement motif Consensus sequence: ACATGCCCGGKCATGTCCSR

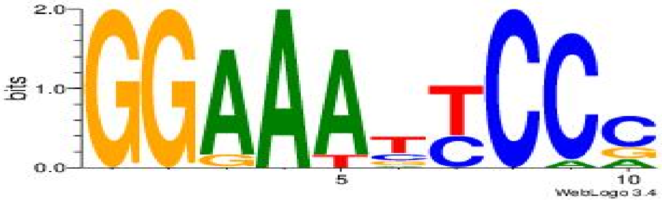


Dataset #: 3
Motif ID: 112
Motif name: RELA
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 7
Similarity score: 0.0629654

Alignment:
GGAAATKCCC
MGAAATG---

Original motif Consensus sequence: GGGRATTTCC

Reverse complement motif Consensus sequence: GGAAATKCCC



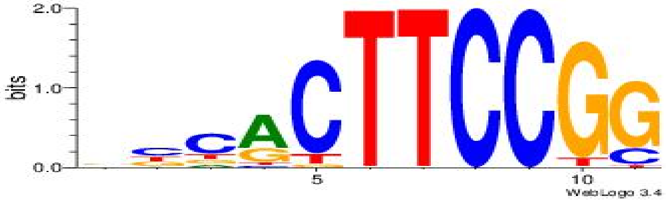
Dataset #: 3
Motif ID: 84
Motif name: GABPA
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 3
Number of overlap: 7
Similarity score: 0.0668119

Alignment:

```
VVCACTTCCGG
--CATTTCY--
```

Original motif Consensus sequence: CCGGAAGTGVV

Reverse complement motif Consensus sequence: VVCACTTCCGG



Dataset #: 1 Motif ID: 30 Motif name: Motif 30

Original motif Consensus sequence: CWGCAGC

Reverse complement motif Consensus sequence: GCTGCWG

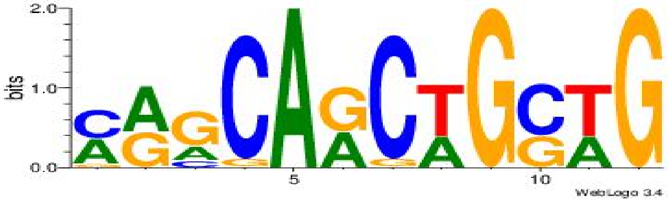
Best Matches for Motif ID 30 (Highest to Lowest)

Dataset #:	3
Motif ID:	97
Motif name:	Myf
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	7
Similarity score:	0.0232337

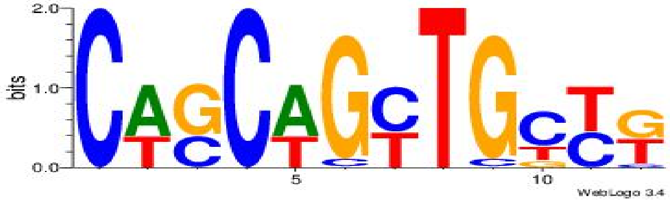
Alignment:

```
MRGCARCWGSWG
-----GCTGCWG
```

Original motif Consensus sequence: MRGCARCWGSWG



Reverse complement motif Consensus sequence: CWSCWGMTGCKR



Dataset #:	1
Motif ID:	41
Motif name:	Motif 41
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	2
Number of overlap:	7
Similarity score:	0.027698

Alignment:

```
YCAGCAGG
-CWGCAGC
```

Original motif Consensus sequence: CCTGCTGK

Reverse complement motif Consensus sequence: YCAGCAGG

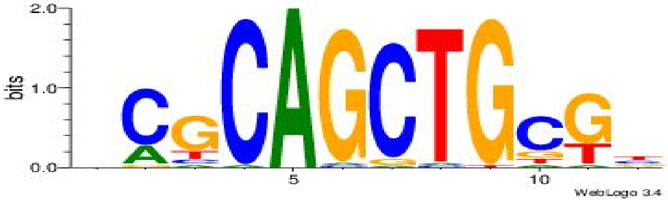
Dataset #:	3
Motif ID:	105
Motif name:	NHLH1
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	7

Similarity score:	0.032311

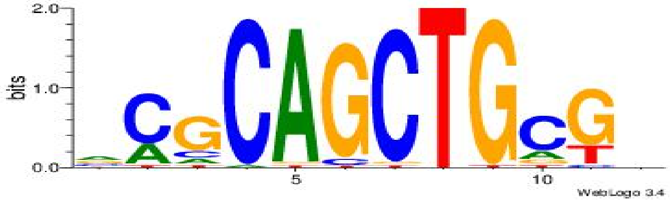
Alignment:

```
VCGCAGCTGCGV
CWGCAGC-----
```

Original motif Consensus sequence: VCGCAGCTGCGB



Reverse complement motif Consensus sequence: VCGCAGCTGCGV



Dataset #:	1
Motif ID:	27
Motif name:	Motif 27
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:	0.037602

Alignment:

```
GGCGGCSG
-GCTGCWG
```

Original motif Consensus sequence: CSGCCGCC

Reverse complement motif Consensus sequence: GGCGGCSG

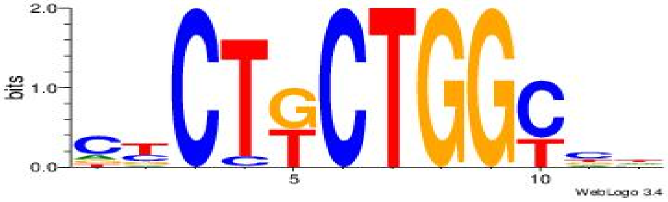
Dataset #:	4
Motif ID:	151
Motif name:	agrCCAGmAGrg
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	5
Number of overlap:	7
Similarity score:	0.0377961

Alignment:

```
CKCTRCTGGCVH
-GCTGCWG----
```

Original motif Consensus sequence: HVGCCAGMAGRG

Reverse complement motif Consensus sequence: CKCTRCTGGCVH



Dataset #: 1 Motif ID: 31 Motif name: Motif 31

Original motif Consensus sequence: CATGYACA

Reverse complement motif Consensus sequence: TGTKCATG

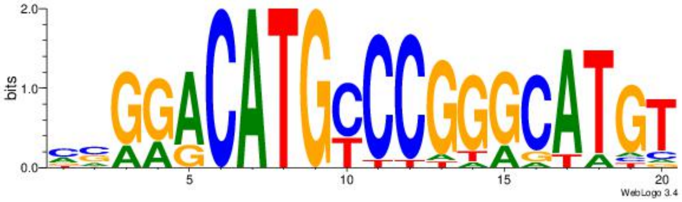
Best Matches for Motif ID 31 (Highest to Lowest)

Dataset #:	3
Motif ID:	125
Motif name:	TP53
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	8
Number of overlap:	8
Similarity score:	0.0607115

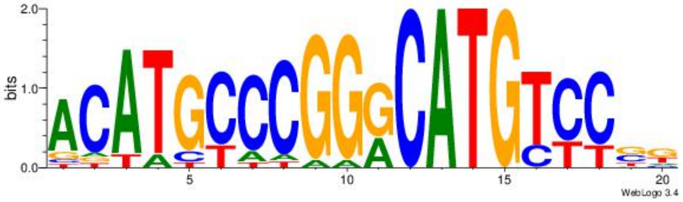
Alignment:

```
ACATGCCCGGKCATGTCCSR
-------TGTKCATG-----
```

Original motif Consensus sequence: MSGGACATGYCCGGGCATGT



Reverse complement motif Consensus sequence: ACATGCCCGGKCATGTCCSR



Dataset #: 4
Motif ID: 152
Motif name: yrCATGCAyr
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: 0.0609044

Alignment:
BRCATGCABD
--CATGYACA

Original motif Consensus sequence: BRCATGCABD

Reverse complement motif Consensus sequence: HVTGCATGKV

Dataset #: 1
Motif ID: 18
Motif name: Motif 18
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:	0.0666244

Alignment:
CATGYATG
CATGYACA

Original motif Consensus sequence: CATGYATG

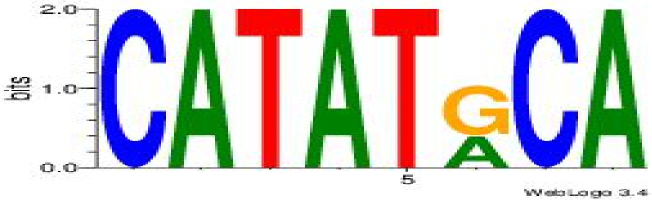
Reverse complement motif Consensus sequence: CATKCATG

Dataset #:	2
Motif ID:	64
Motif name:	Motif 64
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:	0.0706964

Alignment:
CATATRCA
CATGYACA

Original motif Consensus sequence: CATATRCA

Reverse complement motif Consensus sequence: TGMATATG

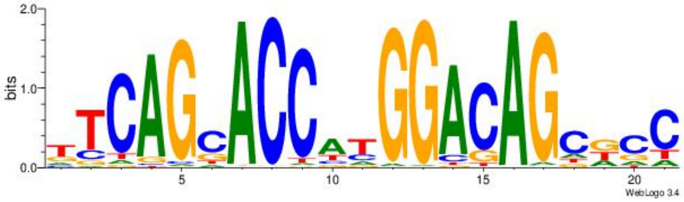


Dataset #:	3
Motif ID:	113
Motif name:	REST
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	6
Number of overlap:	8
Similarity score:	0.0726387

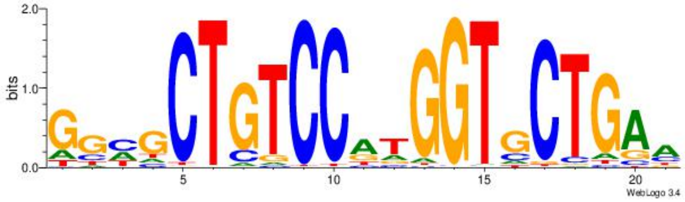
Alignment:

```
TTCAGCACCATGGACAGCKCC
--------CATGYACA-----
```

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC



Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA



Dataset #: 1 Motif ID: 32 Motif name: Motif 32

Original motif Consensus sequence: KAATAAA

Reverse complement motif Consensus sequence: TTTATTY

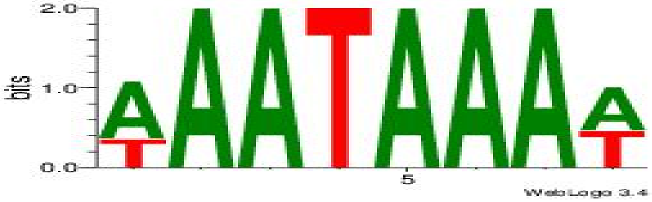
Best Matches for Motif ID 32 (Highest to Lowest)

Dataset #:	2
Motif ID:	52
Motif name:	Motif 52
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:	0.017829

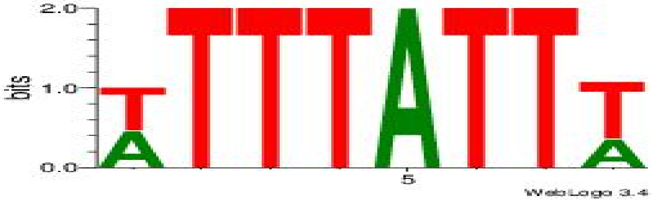
Alignment:

```
WTTTATTT
-TTTATTY
```

Original motif Consensus sequence: AAATAAAW



Reverse complement motif Consensus sequence: WTTTATTT

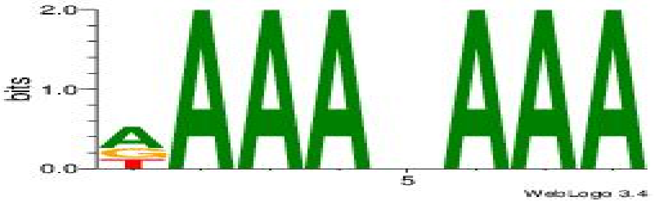


Dataset #:	1
Motif ID:	2
Motif name:	Motif 2
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	7
Similarity score:	0.0445453

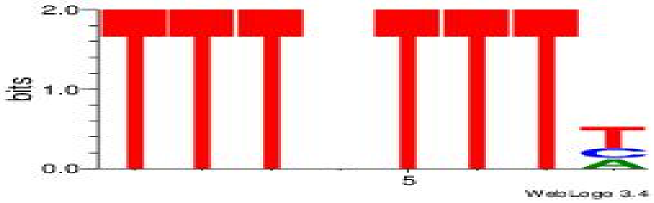
Alignment:

```
TTTDTTTT
TTTATTY-
```

Original motif   Consensus sequence: AAAAHAAA



Reverse complement motif   Consensus sequence: TTTDTTTT



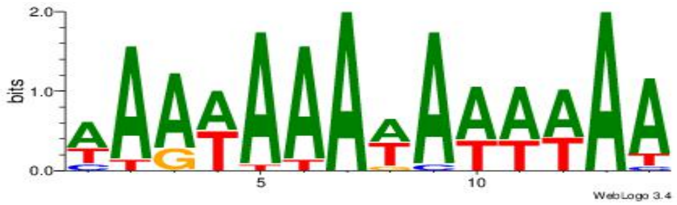
Dataset #:	2
Motif ID:	68
Motif name:	Motif 68
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	8
Number of overlap:	7

Similarity score:	0.0470498

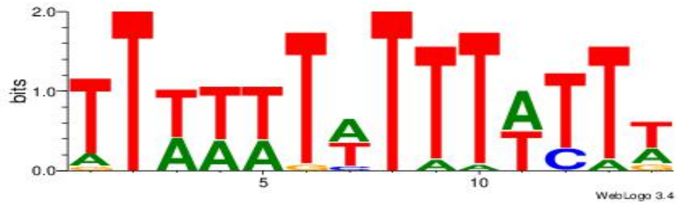
Alignment:

```
TTWWWTWTTTWTTW
-------TTTATTY
```

Original motif Consensus sequence: WAAWAAAWAWWWAA



Reverse complement motif Consensus sequence: TTWWWTWTTTWTTW



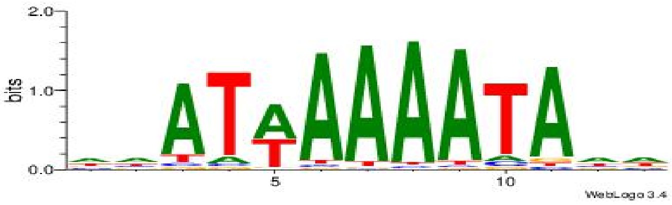
Dataset #:	4
Motif ID:	150
Motif name:	waATwAAAATAww
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	7
Similarity score:	0.0674341

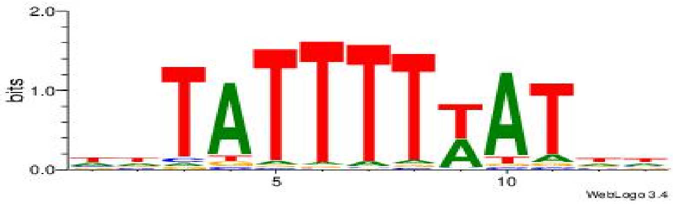
Alignment:

```
DHTATTTTWATHD
------TTTATTY
```

Original motif Consensus sequence: DHATWAAAATAHD

Reverse complement motif Consensus sequence: DHTATTTTWATHD





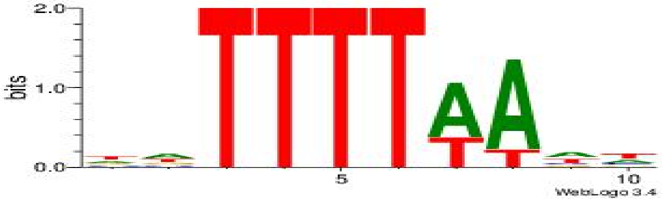
Dataset #:	4
Motif ID:	148
Motif name:	wwTwAAAAww
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	4
Number of overlap:	7
Similarity score:	0.0811175

Alignment:

```
HHTTTTWADD
---TTTATTY
```

Original motif   Consensus sequence: DDTWAAAAHH

Reverse complement motif   Consensus sequence: HHTTTTWADD



Dataset #: 1   Motif ID: 33   Motif name: Motif 33

Original motif Consensus sequence: CTGGCTWC

Reverse complement motif Consensus sequence: GWAGCCAG

Best Matches for Motif ID 33 (Highest to Lowest)

Dataset #:	2
Motif ID:	49
Motif name:	Motif 49
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:	0.011666

Alignment:

```
CTGGCCTC
CTGGCTWC
```

Original motif Consensus sequence: CTGGCCTC

Reverse complement motif Consensus sequence: GAGGCCAG

Dataset #: 1
Motif ID: 10
Motif name: Motif 10
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 8
Similarity score: 0.029479

Alignment:

```
CTGGCCTC
CTGGCTWC
```

Original motif Consensus sequence: CTGGCCTC

Reverse complement motif Consensus sequence: GAGGCCAG

Dataset #: 1
Motif ID: 25
Motif name: Motif 25
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 8

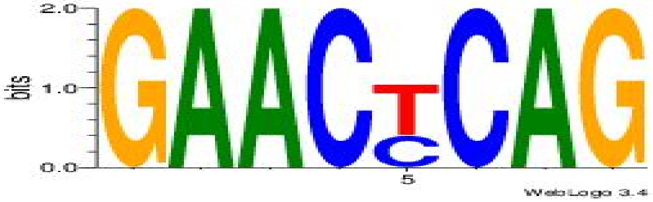
Similarity score: 0.0400133

Alignment:

```
CTGRGTTC
CTGGCTWC
```

Original motif Consensus sequence: CTGRGTTC

Reverse complement motif Consensus sequence: GAACKCAG



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: 1

Number of overlap: 8

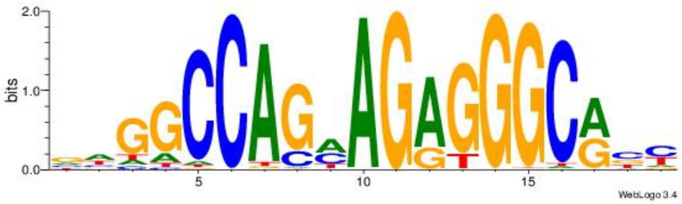
Similarity score: 0.050611

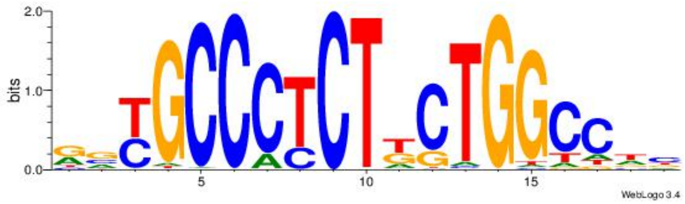
Alignment:

```
KBKGCCCTCTYCTGGCCHV
-----------CTGGCTWC
```

Original motif Consensus sequence: VHGGCCAGMAGAGGGCRBY

Reverse complement motif Consensus sequence: KBKGCCCTCTYCTGGCCHV





Dataset #:	4
Motif ID:	133
Motif name:	shAGrGGGCAgy
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	2
Number of overlap:	8
Similarity score:	0.0636793

Alignment:

```
DBTGCCCKCTDS
-CTGGCTWC---
```

Original motif Consensus sequence: SHAGRGGGCABH

Reverse complement motif Consensus sequence: DBTGCCCKCTDS

Dataset #: 1 Motif ID: 34 Motif name: Motif 34

Original motif   Consensus sequence: TGKCCACA

Reverse complement motif   Consensus sequence: TGTGGYCA

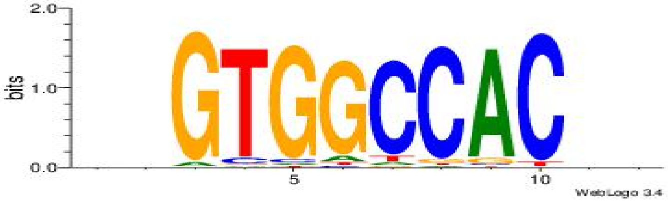
Best Matches for Motif ID 34 (Highest to Lowest)

Dataset #:	4
Motif ID:	171
Motif name:	ysGTGGCCACsr
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:	0.0504663

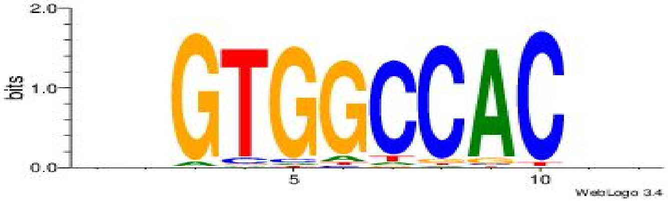
Alignment:

```
VBGTGGCCACVB
---TGKCCACA-
```

Original motif   Consensus sequence: BVGTGGCCACBV



Reverse complement motif   Consensus sequence: VBGTGGCCACVB

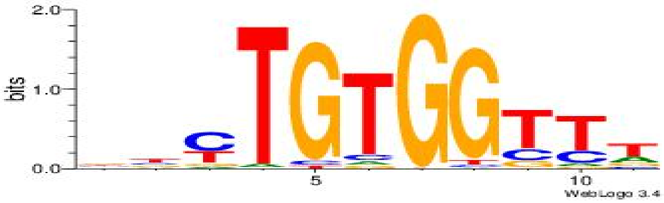


Dataset #: 3
Motif ID: 114
Motif name: RUNX1
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 4
Number of overlap: 8
Similarity score: 0.0690177

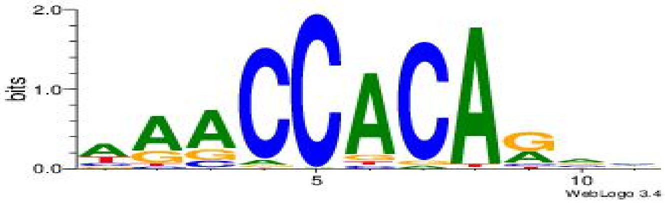
Alignment:

```
BBYTGTGGTTT
---TGTGGYCA
```

Original motif Consensus sequence: BBYTGTGGTTT



Reverse complement motif Consensus sequence: AAACCACAKVB

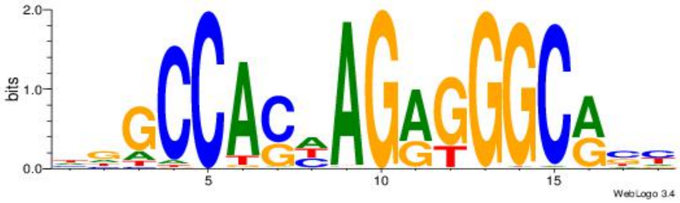


Dataset #: 4
Motif ID: 165
Motif name: wgGCCAshAGrGGGCrsy
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 11
Number of overlap: 8

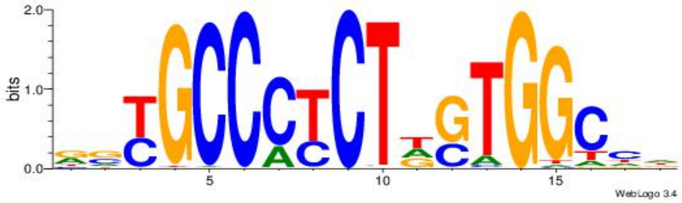
Similarity score: 0.083395

Alignment:
KBKGCCCKCTHGTGGCHH
----------TGTGGYCA

Original motif Consensus sequence: HDGCCACHAGRGGGCRBY



Reverse complement motif Consensus sequence: KBKGCCCKCTHGTGGCHH



Dataset #:	1
Motif ID:	24
Motif name:	Motif 24
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	8
Similarity score:	0.0843302

Alignment:
CACCCACA
TGKCCACA

Original motif Consensus sequence: TGTGGGTG

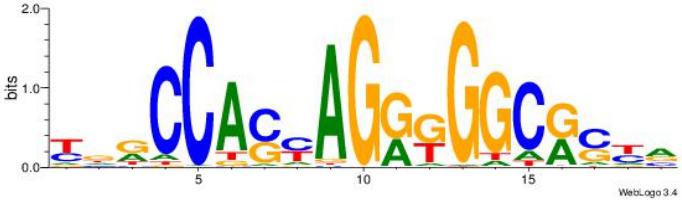
Reverse complement motif Consensus sequence: CACCCACA

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: 12
Number of overlap: 8
Similarity score: 0.0872346

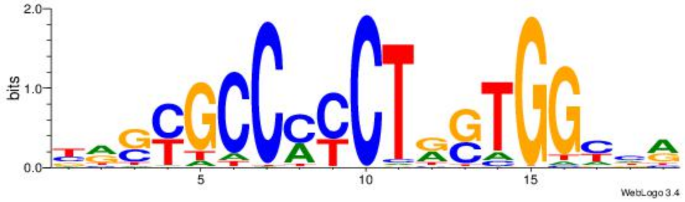
Alignment:

```
BMSMGCCYMCTKSTGGMHM
-----------TGTGGYCA
```

Original motif Consensus sequence: YDRCCASYAGRKGGCRSYV



Reverse complement motif Consensus sequence: BMSMGCCYMCTKSTGGMHM



Dataset #: 1 **Motif ID: 35** **Motif name: Motif 35**

Original motif Consensus sequence: ACAACCAY

Reverse complement motif Consensus sequence: KTGGTTGT

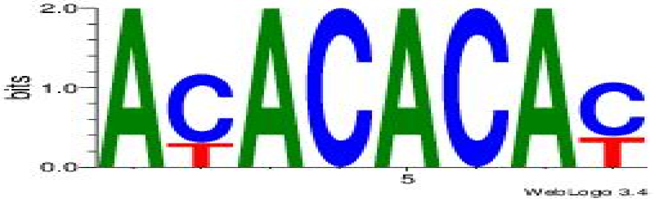
Best Matches for Motif ID 35 (Highest to Lowest)

Dataset #:	2
Motif ID:	57
Motif name:	Motif 57
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:	0.0737654

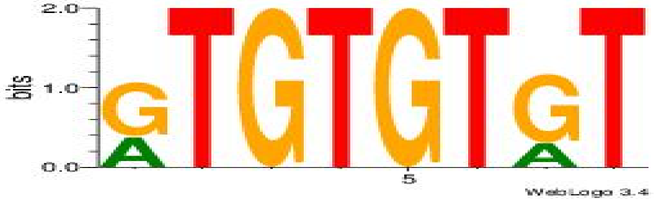
Alignment:

```
ACACACAY
ACAACCAY
```

Original motif Consensus sequence: ACACACAY



Reverse complement motif Consensus sequence: KTGTGTGT

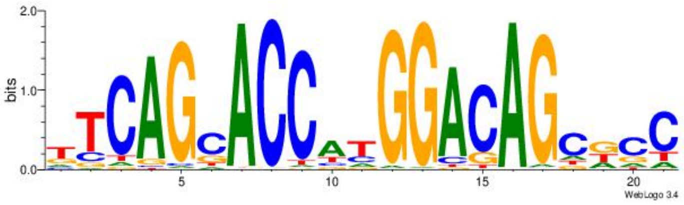


Dataset #: 3
Motif ID: 113
Motif name: REST
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 4
Number of overlap: 8
Similarity score: 0.0887654

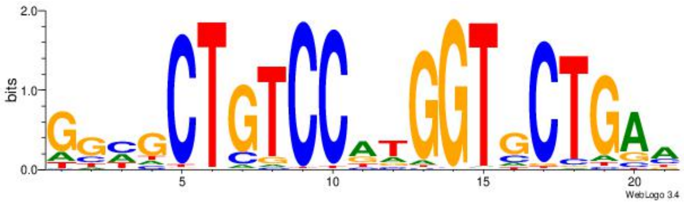
Alignment:

```
TTCAGCACCATGGACAGCKCC
---ACAACCAY----------
```

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC



Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA

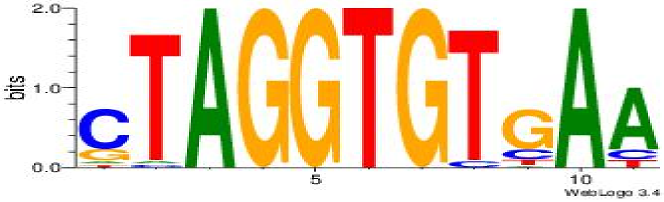


Dataset #: 3
Motif ID: 120
Motif name: T
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 4

Number of overlap: 8
Similarity score: 0.0890625

Alignment:
```
TTCACACCTAG
---ACAACCAY
```

Original motif Consensus sequence: CTAGGTGTGAA



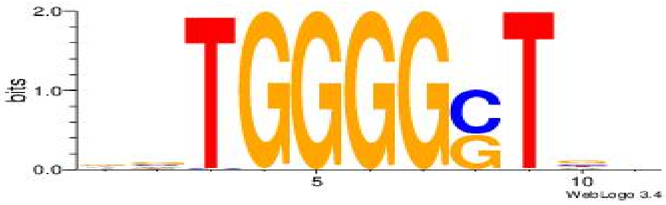
Reverse complement motif Consensus sequence: TTCACACCTAG

Dataset #: 4
Motif ID: 162
Motif name: ccAsCCCCAcc
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: 0.0921848

Alignment:
```
HVASCCCCABH
--ACAACCAY-
```

Original motif Consensus sequence: HVASCCCCABH

Reverse complement motif Consensus sequence: DBTGGGGSTVD



Dataset #:	4
Motif ID:	152
Motif name:	yrCATGCAyr
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:	0.0932982

Alignment:

```
BRCATGCABD
-ACAACCAY-
```

Original motif Consensus sequence: BRCATGCABD

Reverse complement motif Consensus sequence: HVTGCATGKV

Dataset #: 1 **Motif ID: 36** **Motif name: Motif 36**

Original motif Consensus sequence: TCCTGGRA

Reverse complement motif Consensus sequence: TMCCAGGA

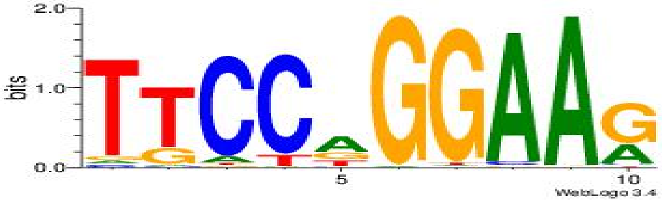
Best Matches for Motif ID 36 (Highest to Lowest)

Dataset #:	3
Motif ID:	119
Motif name:	Stat3
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:	0.0190833

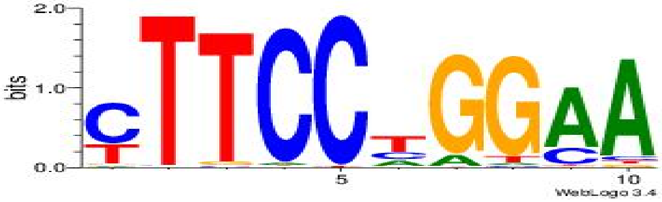
Alignment:

```
CTTCCTGGAA
--TCCTGGRA
```

Original motif Consensus sequence: TTCCAGGAAG



Reverse complement motif Consensus sequence: CTTCCTGGAA



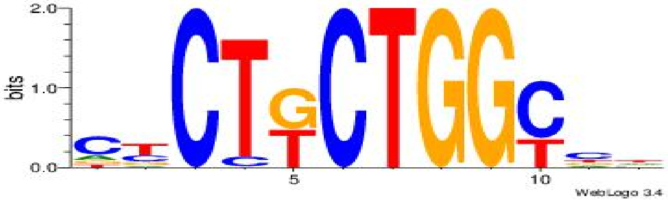
Dataset #: 4
Motif ID: 151
Motif name: agrCCAGmAGrg
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 2
Number of overlap: 8
Similarity score: 0.0609014

Alignment:

```
CKCTRCTGGCVH
---TCCTGGRA-
```

Original motif Consensus sequence: HVGCCAGMAGRG

Reverse complement motif Consensus sequence: CKCTRCTGGCVH

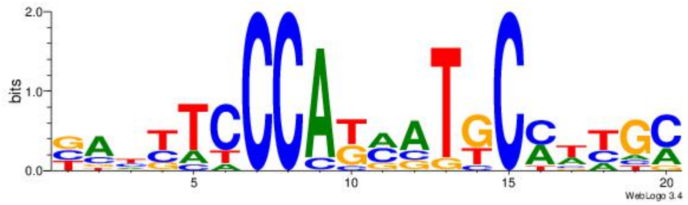


Dataset #: 3
Motif ID: 131
Motif name: znf143
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 5
Number of overlap: 8

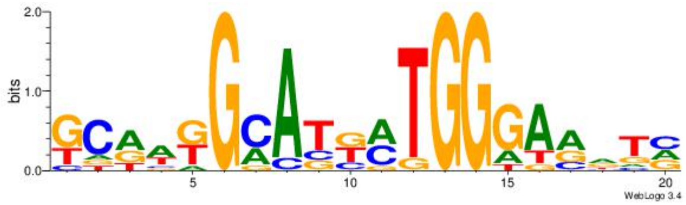
Similarity score:	0.061907

Alignment:
BAHYTCCCAKMATGCMWYGC
----TMCCAGGA--------

Original motif Consensus sequence: BAHYTCCCAKMATGCMWYGC



Reverse complement motif Consensus sequence: GCMWRGCATYRTGGGAMHTB

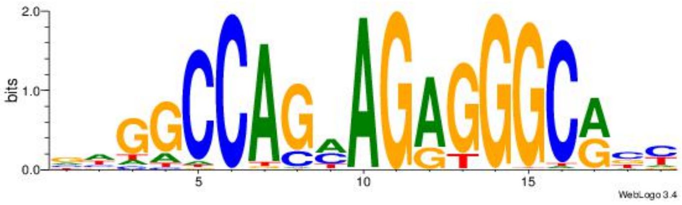


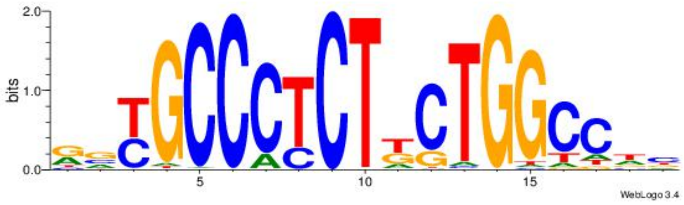
Dataset #:	4
Motif ID:	163
Motif name:	gwGGCCAGmAGAGGGCrby
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	3
Number of overlap:	8
Similarity score:	0.0667495

Alignment:
KBKGCCCTCTYCTGGCCHV
---------TCCTGGRA--

Original motif Consensus sequence: VHGGCCAGMAGAGGGCRBY

Reverse complement motif Consensus sequence: KBKGCCCTCTYCTGGCCHV



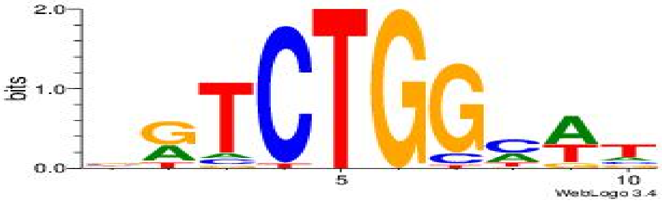


Dataset #:	3
Motif ID:	85
Motif name:	Hand1Tcfe2a
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	2
Number of overlap:	8
Similarity score:	0.0719458

Alignment:

```
AWRCCAGAMB
-TMCCAGGA-
```

Original motif Consensus sequence: BRTCTGGMWT



Reverse complement motif Consensus sequence: AWRCCAGAMB

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

Original motif Consensus sequence: CTGAGCYA

Reverse complement motif Consensus sequence: TKGCTCAG

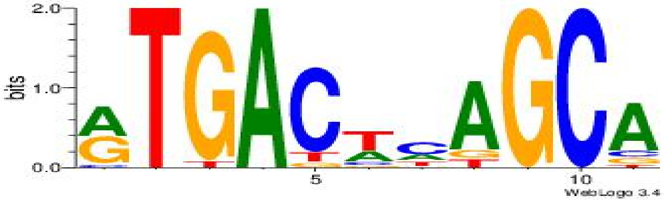
Best Matches for Motif ID 37 (Highest to Lowest)

Dataset #:	3
Motif ID:	100
Motif name:	NFE2L2
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:	0.0542114

Alignment:

```
TGCTDWGTCAK
--CTGAGCYA-
```

Original motif Consensus sequence: RTGACWHAGCA



Reverse complement motif Consensus sequence: TGCTDWGTCAK

Dataset #: 4

Motif ID: 160

Motif name: brCAGGGCCrs

Matching format of first motif: Reverse Complement

Matching format of second motif: Reverse Complement

Direction: Backward

Position number: 3

Number of overlap: 8

Similarity score: 0.0573364

Alignment:

```
BBGGCCCTGBB
-TKGCTCAG--
```

Original motif Consensus sequence: BVCAGGGCCVB

Reverse complement motif Consensus sequence: BBGGCCCTGBB

Dataset #: 4

Motif ID: 142

Motif name: ctCTTAACyw

Matching format of first motif: Reverse Complement

Matching format of second motif: Reverse Complement

Direction: Forward

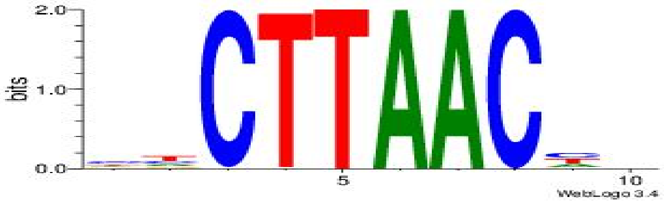
Position number: 1

Number of overlap: 8

Similarity score: 0.0660909

Alignment:
DDGTTAAGHD
TKGCTCAG--

Original motif Consensus sequence: HHCTTAACHD



Reverse complement motif Consensus sequence: DDGTTAAGHD

Dataset #:	1
Motif ID:	25
Motif name:	Motif 25
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:	0.0673416

Alignment:
CTGRGTTC
CTGAGCYA

Original motif Consensus sequence: CTGRGTTC

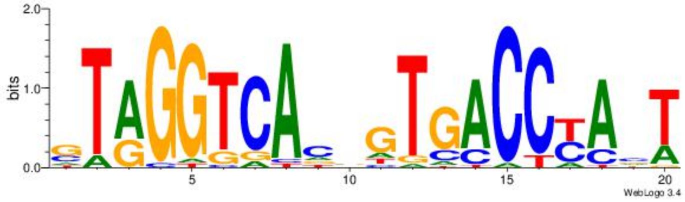
Reverse complement motif Consensus sequence: GAACKCAG

Dataset #: 3
Motif ID: 111
Motif name: PPARG
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: 0.0687591

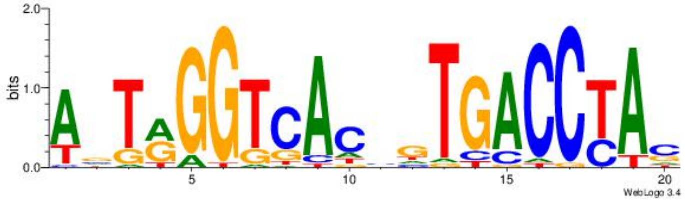
Alignment:

```
STAGGTCACBGTGACCYABT
----------CTGAGCYA--
```

Original motif Consensus sequence: STAGGTCACBGTGACCYABT



Reverse complement motif Consensus sequence: ABTMGGTCACBGTGACCTAS



Dataset #: 1 **Motif ID: 38** **Motif name: Motif 38**

Original motif Consensus sequence: GAGTTACA

Reverse complement motif Consensus sequence: TGTAACTC

Best Matches for Motif ID 38 (Highest to Lowest)

Dataset #:	2
Motif ID:	51
Motif name:	Motif 51
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:

```
GAGTTACA
GAGTTACA
```

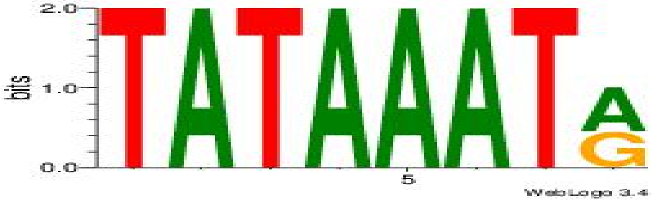
Original motif Consensus sequence: GAGTTACA

Reverse complement motif Consensus sequence: TGTAACTC

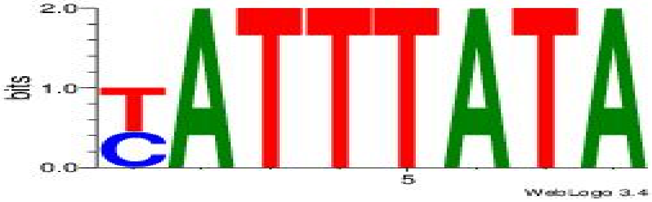
Dataset #: 2
Motif ID: 66
Motif name: Motif 66
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 8
Similarity score: 0.0742432

Alignment:
KATTTATA
GAGTTACA

Original motif Consensus sequence: TATAAATR



Reverse complement motif Consensus sequence: KATTTATA



Dataset #: 3
Motif ID: 117
Motif name: Spz1
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 3
Number of overlap: 8

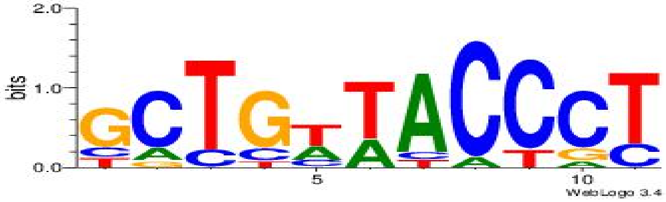
Similarity score:	0.0855279

Alignment:

```
AGGGTAWCAGC
-GAGTTACA--
```

Original motif Consensus sequence: AGGGTAWCAGC

Reverse complement motif Consensus sequence: GCTGWTACCCT



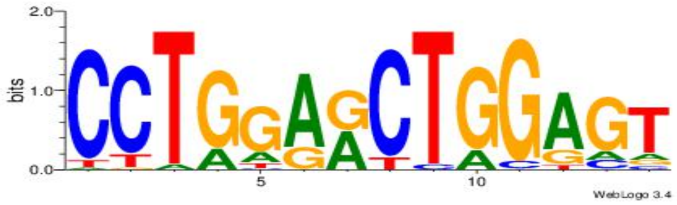
Dataset #:	2
Motif ID:	69
Motif name:	Motif 69
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	5
Number of overlap:	8
Similarity score:	0.0901267

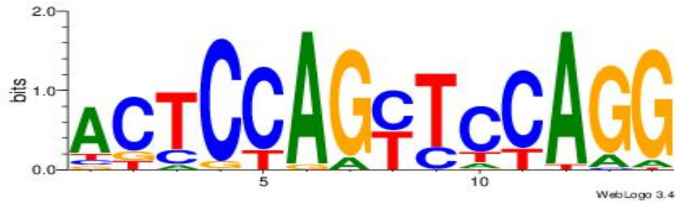
Alignment:

```
CCTGGARCTGGAGT
--TGTAACTC----
```

Original motif Consensus sequence: CCTGGARCTGGAGT

Reverse complement motif Consensus sequence: ACTCCAGMTCCAG



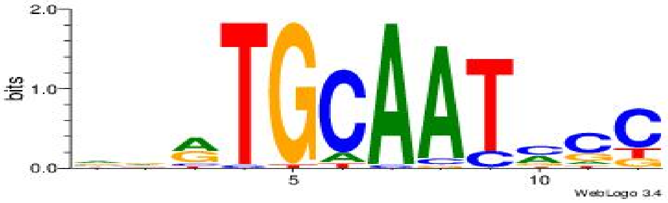


Dataset #:	3
Motif ID:	75
Motif name:	Ddit3Cebpa
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	4
Number of overlap:	8
Similarity score:	0.0913372

Alignment:

```
GGRATTGCAKHB
-GAGTTACA---
```

Original motif Consensus sequence: VDRTGCAATMCC



Reverse complement motif Consensus sequence: GGRATTGCAKHB

Dataset #: 1 Motif ID: 39 Motif name: Motif 39

Original motif   Consensus sequence: BAGAAA

Reverse complement motif   Consensus sequence: TTTCTB

Best Matches for Motif ID 39 (Highest to Lowest)

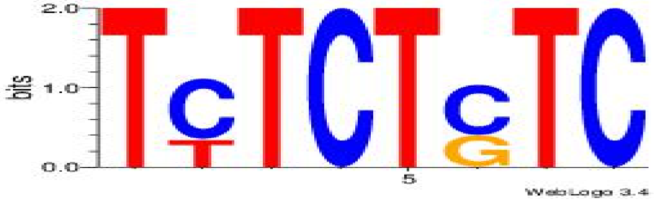
Dataset #:	1
Motif ID:	23
Motif name:	Motif 23
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	3
Number of overlap:	6
Similarity score:	0.0215381

Alignment:

```
GASAGAGA
--BAGAAA
```

Original motif   Consensus sequence: GASAGAGA

Reverse complement motif   Consensus sequence: TCTCTSTC



Dataset #: 1
Motif ID: 45
Motif name: Motif 45
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 2
Number of overlap: 6
Similarity score: 0.0344566

Alignment:

```
GSAGAGA
-BAGAAA
```

Original motif Consensus sequence: GSAGAGA

Reverse complement motif Consensus sequence: TCTCTSC

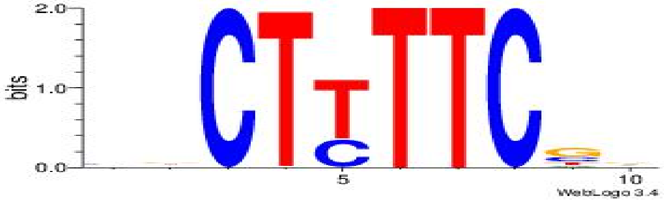
Dataset #: 4
Motif ID: 139
Motif name: mkCTyTTCsg
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 5
Number of overlap: 6

Similarity score: 0.0384118

Alignment:

```
HBCTTTTCBD
----TTTCTB
```

Original motif Consensus sequence: HBCTTTTCBD



Reverse complement motif Consensus sequence: HBGAAAAGBD

Dataset #: 1

Motif ID: 2

Motif name: Motif 2

Matching format of first motif: Reverse Complement

Matching format of second motif: Reverse Complement

Direction: Forward

Position number: 1

Number of overlap: 6

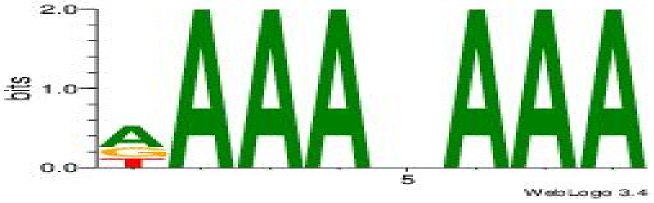
Similarity score: 0.0438306

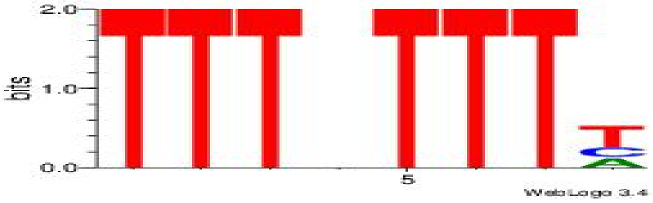
Alignment:

```
TTTDTTTT
TTTCTB--
```

Original motif Consensus sequence: AAAAHAAA

Reverse complement motif Consensus sequence: TTTDTTTT





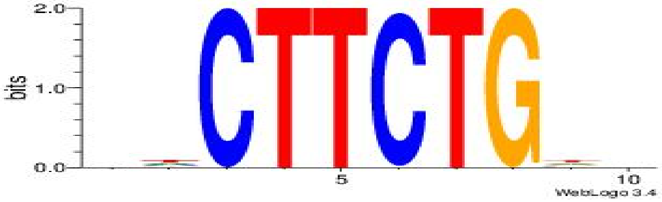
Dataset #:	4
Motif ID:	136
Motif name:	dwCAGAAGwh
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	3
Number of overlap:	6
Similarity score:	0.0496185

Alignment:

```
DHCAGAAGDH
--BAGAAA--
```

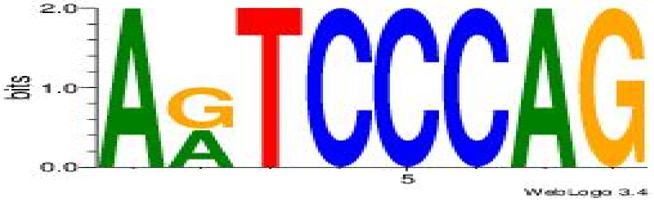
Original motif Consensus sequence: DHCAGAAGDH

Reverse complement motif Consensus sequence: HDCTTCTGHD



Dataset #: 1 Motif ID: 40 Motif name: Motif 40

Original motif Consensus sequence: ARTCCCAG



Reverse complement motif Consensus sequence: CTGGGAMT

Best Matches for Motif ID 40 (Highest to Lowest)

Dataset #:	4
Motif ID:	162
Motif name:	ccAsCCCCAcc
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:	0.0511488

Alignment:

```
HVASCCCCABH
--ARTCCCAG-
```

Original motif Consensus sequence: HVASCCCCABH

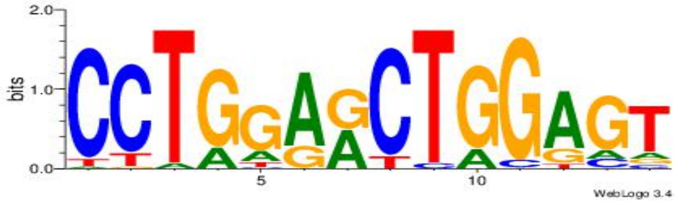
Reverse complement motif Consensus sequence: DBTGGGGSTVD

Dataset #:	2
Motif ID:	69
Motif name:	Motif 69
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:	0.0574096

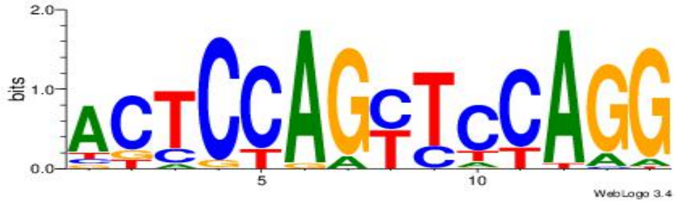
Alignment:

```
CCTGGARCTGGAGT
-CTGGGAMT-----
```

Original motif Consensus sequence: CCTGGARCTGGAGT



Reverse complement motif Consensus sequence: ACTCCAGMTCCAG



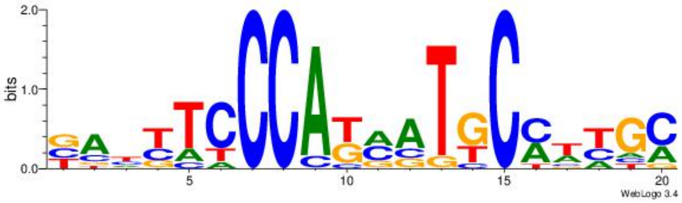
Dataset #:	3
Motif ID:	131
Motif name:	znf143
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	11
Number of overlap:	8

Similarity score: 0.0623563

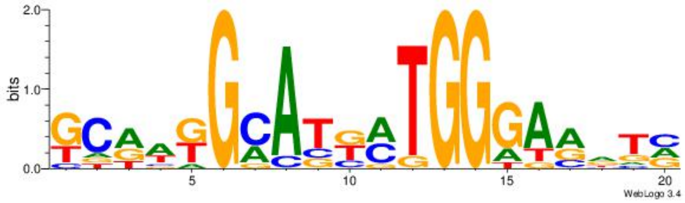
Alignment:

```
GCMWRGCATYRTGGGAMHTB
----------CTGGGAMT--
```

Original motif Consensus sequence: BAHYTCCCAKMATGCMWYGC



Reverse complement motif Consensus sequence: GCMWRGCATYRTGGGAMHTB



Dataset #: 3

Motif ID: 125

Motif name: TP53

Matching format of first motif: Reverse Complement

Matching format of second motif: Original Motif

Direction: Forward

Position number: 11

Number of overlap: 8

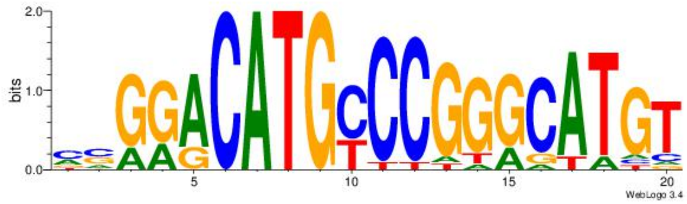
Similarity score: 0.0776137

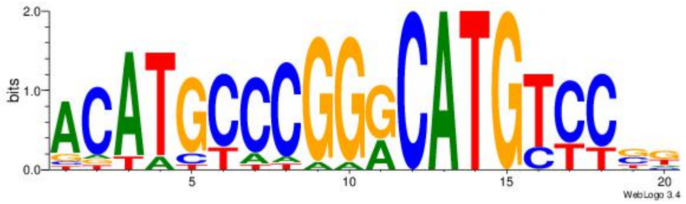
Alignment:

```
MSGGACATGYCCGGGCATGT
----------CTGGGAMT--
```

Original motif Consensus sequence: MSGGACATGYCCGGGCATGT

Reverse complement motif Consensus sequence: ACATGCCCGGKCATGTCCSR



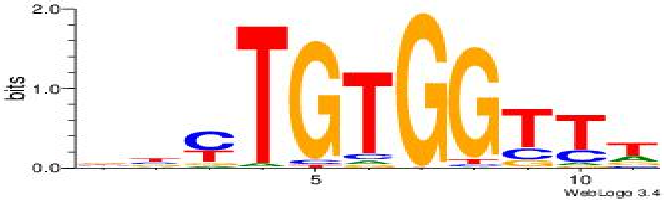


Dataset #: 3
Motif ID: 114
Motif name: RUNX1
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 2
Number of overlap: 8
Similarity score: 0.080122

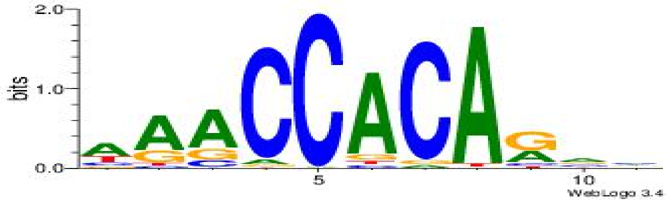
Alignment:

```
AAACCACAKVB
-ARTCCCAG--
```

Original motif Consensus sequence: BBYTGTGGTTT



Reverse complement motif Consensus sequence: AAACCACAKVB



Dataset #: 1 **Motif ID: 41** **Motif name: Motif 41**

Original motif Consensus sequence: CCTGCTGK

Reverse complement motif Consensus sequence: YCAGCAGG

Best Matches for Motif ID 41 (Highest to Lowest)

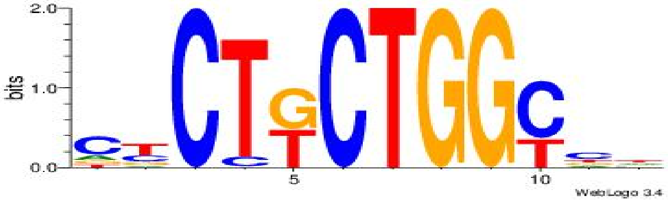
Dataset #:	4
Motif ID:	151
Motif name:	agrCCAGmAGrg
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	4
Number of overlap:	8
Similarity score:	0.028602

Alignment:

```
HVGCCAGMAGRG
---YCAGCAGG-
```

Original motif Consensus sequence: HVGCCAGMAGRG

Reverse complement motif Consensus sequence: CKCTRCTGGCVH

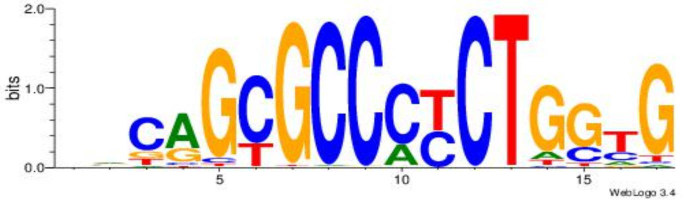


Dataset #:	4
Motif ID:	168
Motif name:	yrcrGYGCCMyCTGGtG
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	3
Number of overlap:	8
Similarity score:	0.0340048

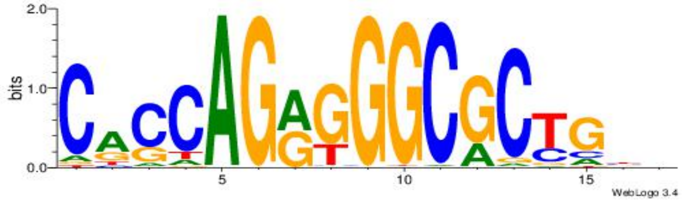
Alignment:

```
CACCAGMGGGCGCTGBD
--YCAGCAGG-------
```

Original motif Consensus sequence: HVCAGCGCCCYCTGGTG



Reverse complement motif Consensus sequence: CACCAGMGGGCGCTGBD



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

Number of overlap: 8
Similarity score: 0.0342298

Alignment:
CCTKGTGG
CCTGCTGK

Original motif Consensus sequence: CCACYAGG

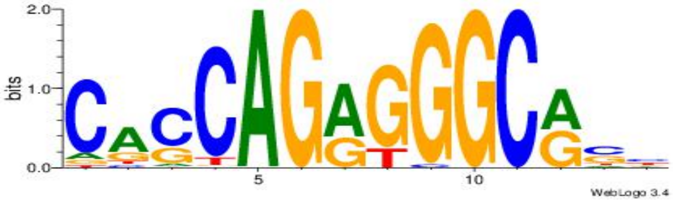
Reverse complement motif Consensus sequence: CCTKGTGG

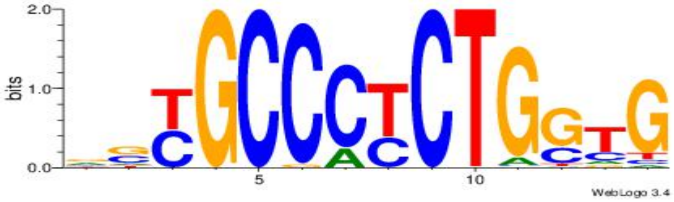
Dataset #: 4
Motif ID: 166
Motif name: CasCAGrGGGCrsy
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 5
Number of overlap: 8
Similarity score: 0.0366705

Alignment:
BSKGCCCKCTGGTG
----CCTGCTGK--

Original motif Consensus sequence: CACCAGRGGGCRSB

Reverse complement motif Consensus sequence: BSKGCCCKCTGGT



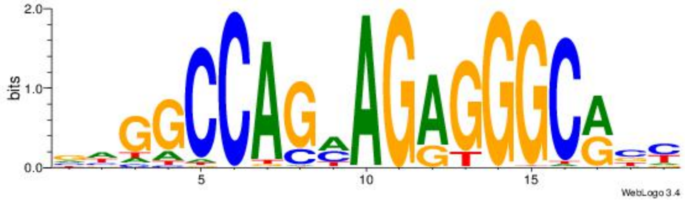


Dataset #:	4
Motif ID:	163
Motif name:	gwGGCCAGmAGAGGGCrby
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	5
Number of overlap:	8
Similarity score:	0.0407982

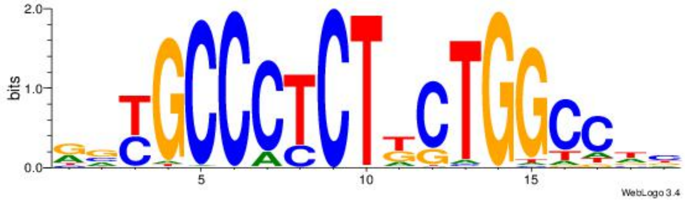
Alignment:

```
VHGGCCAGMAGAGGGCRBY
----YCAGCAGG-------
```

Original motif Consensus sequence: VHGGCCAGMAGAGGGCRBY



Reverse complement motif Consensus sequence: KBKGCCCTCTYCTGGCCHV



Dataset #: 1 **Motif ID: 42** **Motif name: Motif 42**

Original motif Consensus sequence: CGCGCSG

Reverse complement motif Consensus sequence: CSGCGCG

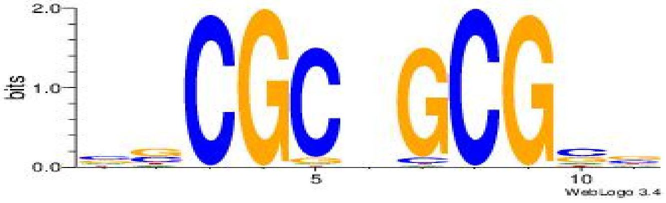
Best Matches for Motif ID 42 (Highest to Lowest)

Dataset #:	4
Motif ID:	161
Motif name:	ssCGCwGCGss
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	5
Number of overlap:	7
Similarity score:	0.0226692

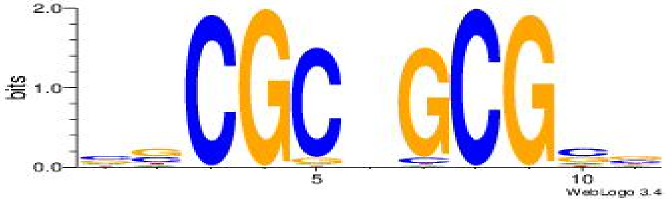
Alignment:

```
VSCGCDGCGSB
----CSGCGCG
```

Original motif Consensus sequence: VSCGCDGCGSB



Reverse complement motif Consensus sequence: BSCGCDGCGSV



Dataset #: 4
Motif ID: 134
Motif name: ssCGwGCGss
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 2
Number of overlap: 7
Similarity score: 0.0315768

Alignment:
BSCGWGCGBV
-CSGCGCG--

Original motif Consensus sequence: BSCGWGCGBV

Reverse complement motif Consensus sequence: VBCGCWCGSB

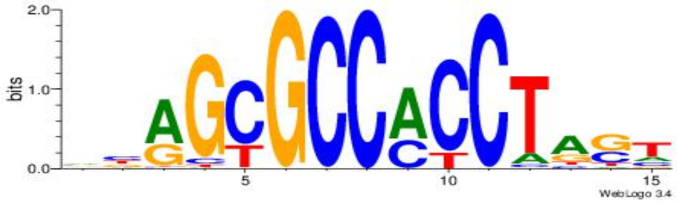
Dataset #: 4
Motif ID: 146
Motif name: myrGYGCCmCCTast
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 3
Number of overlap: 7

Similarity score:	0.0331622

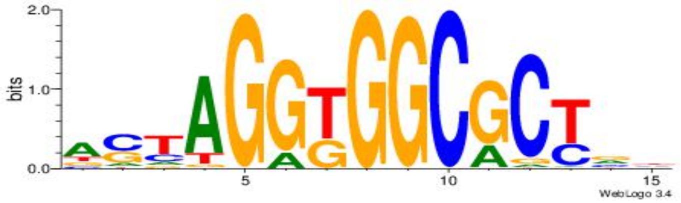
Alignment:

```
ASTAGGYGGCGCTBB
------CSGCGCG--
```

Original motif Consensus sequence: VBAGCGCCMCCTAST



Reverse complement motif Consensus sequence: ASTAGGYGGCGCT



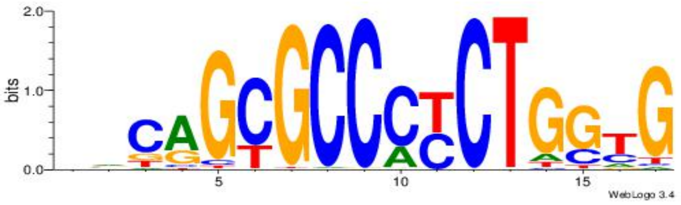
Dataset #:	4
Motif ID:	168
Motif name:	yrcrGYGCCMyCTGGtG
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	3
Number of overlap:	7
Similarity score:	0.0399606

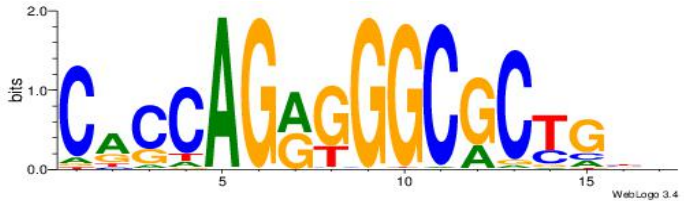
Alignment:

```
HVCAGCGCCCYCTGGTG
--CSGCGCG--------
```

Original motif Consensus sequence: HVCAGCGCCCYCTGGTG

Reverse complement motif Consensus sequence: CACCAGMGGGCGCTGBD



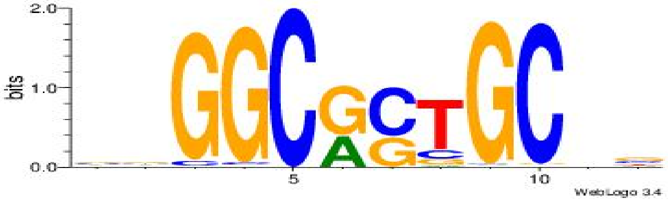


Dataset #: 4
Motif ID: 170
Motif name: ssGGCrsTGCrs
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 4
Number of overlap: 7
Similarity score: 0.0456255

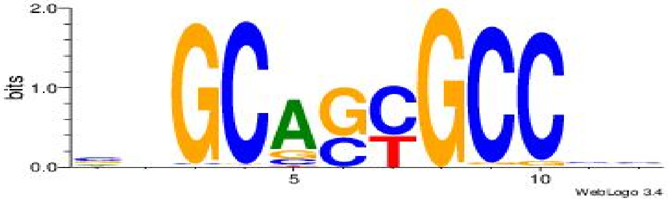
Alignment:

```
BVGCASMGCCVV
---CSGCGCG--
```

Original motif Consensus sequence: VVGGCRSTGCVB



Reverse complement motif Consensus sequence: BVGCASMGCCVV



Dataset #: 1 **Motif ID: 43** **Motif name: Motif 43**

Original motif Consensus sequence: ACATYTA

Reverse complement motif Consensus sequence: TAMATGT

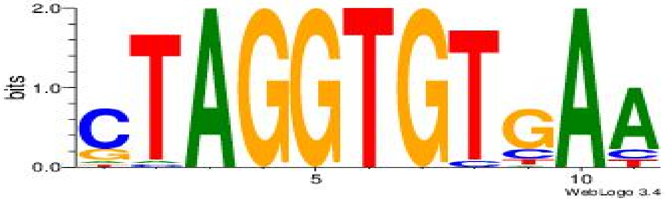
Best Matches for Motif ID 43 (Highest to Lowest)

Dataset #:	3
Motif ID:	120
Motif name:	T
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	4
Number of overlap:	7
Similarity score:	0.0260628

Alignment:

```
TTCACACCTAG
---ACATYTA-
```

Original motif Consensus sequence: CTAGGTGTGAA



Reverse complement motif Consensus sequence: TTCACACCTAG

Dataset #: 2
Motif ID: 58
Motif name: Motif 58
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2
Number of overlap: 7
Similarity score: 0.0342454

Alignment:
TACATGCA
TAMATGT-

Original motif Consensus sequence: TACATGCA

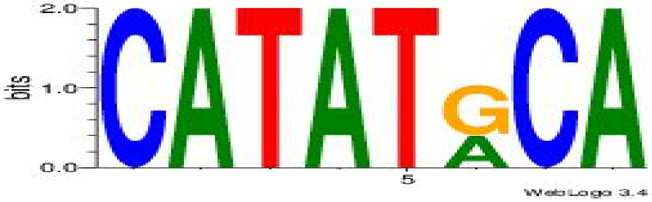
Reverse complement motif Consensus sequence: TGCATGTA

Dataset #: 2
Motif ID: 64
Motif name: Motif 64
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 7

Similarity score: 0.0444069

Alignment:
TGMATATG
TAMATGT-

Original motif Consensus sequence: CATATRCA



Reverse complement motif Consensus sequence: TGMATATG

Dataset #: 4
Motif ID: 152
Motif name: yrCATGCAyr
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 3
Number of overlap: 7
Similarity score: 0.0458993

Alignment:
HVTGCATGKV
--TAMATGT-

Original motif Consensus sequence: BRCATGCABD

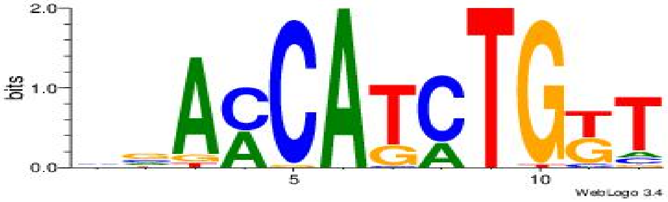
Reverse complement motif Consensus sequence: HVTGCATGKV

Dataset #: 3
Motif ID: 121
Motif name: TAL1TCF3
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: 0.0525238

Alignment:

```
HVAMCATCTGKT
---ACATYTA--
```

Original motif Consensus sequence: HVAMCATCTGKT



Reverse complement motif Consensus sequence: ARCAGATGRTVD

Dataset #: 1 Motif ID: 44 Motif name: Motif 44

Original motif Consensus sequence: GDAAACA

Reverse complement motif Consensus sequence: TGTTTDC

Best Matches for Motif ID 44 (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:	Backward
Position number:	2
Number of overlap:	7
Similarity score:	0.0588603

Alignment:

```
DACAAAACAH
--GDAAACA-
```

Original motif Consensus sequence: DACAAAACAH

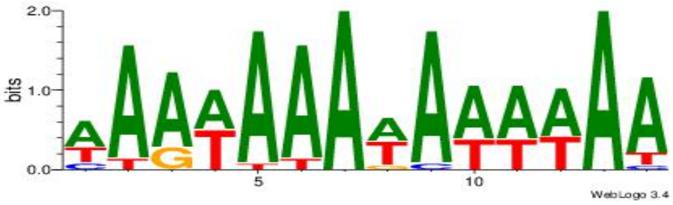
Reverse complement motif Consensus sequence: HTGTTTTGTD

Dataset #: 2
Motif ID: 68
Motif name: Motif 68
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 6
Number of overlap: 7
Similarity score: 0.0651624

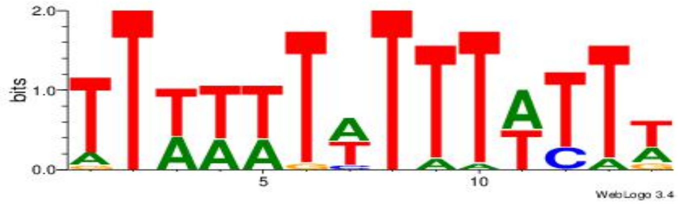
Alignment:

```
WAAWAAAWAWWWAA
--GDAAACA-----
```

Original motif Consensus sequence: WAAWAAAWAWWWAA



Reverse complement motif Consensus sequence: TTWWWTWTTTWTTW



Dataset #: 1
Motif ID: 33
Motif name: Motif 33
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2

Number of overlap:	7
Similarity score:	0.0667857

Alignment:

```
CTGGCTWC
TGTTTDC-
```

Original motif Consensus sequence: CTGGCTWC

Reverse complement motif Consensus sequence: GWAGCCAG

Dataset #:	1
Motif ID:	34
Motif name:	Motif 34
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:	0.066941

Alignment:

```
TGKCCACA
-GDAAACA
```

Original motif Consensus sequence: TGKCCACA

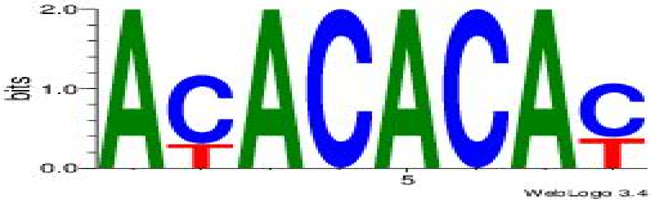
Reverse complement motif Consensus sequence: TGTGGYCA

Dataset #:	2
Motif ID:	57
Motif name:	Motif 57
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:	0.0694703

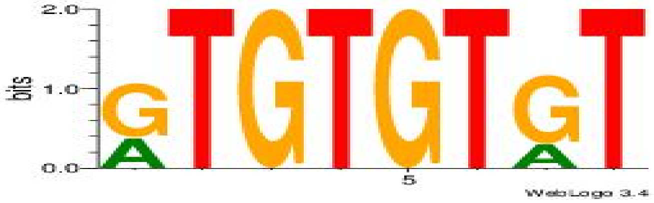
Alignment:

KTGTGTGT
-TGTTTDC

Original motif Consensus sequence: ACACACAY



Reverse complement motif Consensus sequence: KTGTGTGT



Dataset #: 1 Motif ID: 45 Motif name: Motif 45

Original motif Consensus sequence: GSAGAGA

Reverse complement motif Consensus sequence: TCTCTSC

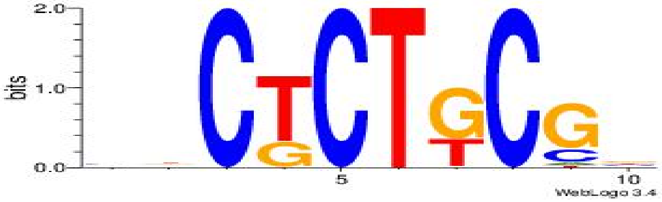
Best Matches for Motif ID 45 (Highest to Lowest)

Dataset #:	4
Motif ID:	140
Motif name:	vkCKCTkCGk
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	2
Number of overlap:	7
Similarity score:	0.0315852

Alignment:

```
BCGYAGAGDV
--GSAGAGA-
```

Original motif Consensus sequence: VDCTCTKCGB



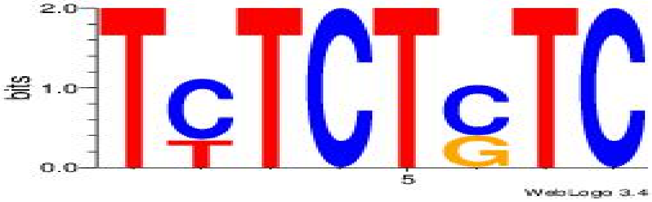
Reverse complement motif Consensus sequence: BCGYAGAGDV

Dataset #: 1
Motif ID: 23
Motif name: Motif 23
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 7
Similarity score: 0.0364931

Alignment:
TCTCTSTC
TCTCTSC-

Original motif Consensus sequence: GASAGAGA

Reverse complement motif Consensus sequence: TCTCTSTC

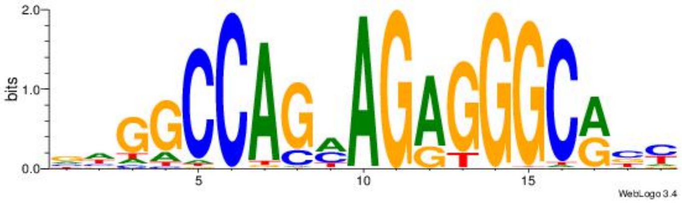


Dataset #: 4
Motif ID: 163
Motif name: gwGGCCAGmAGAGGGCrby
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 6
Number of overlap: 7

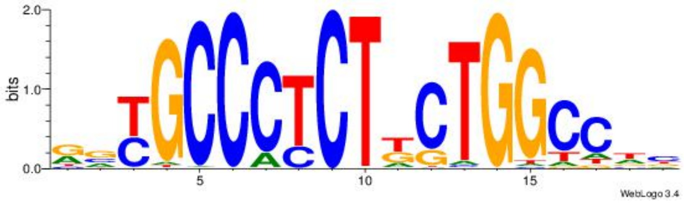
Similarity score: 0.0625376

Alignment:
VHGGCCAGMAGAGGGCRBY
-------GSAGAGA-----

Original motif Consensus sequence: VHGGCCAGMAGAGGGCRBY



Reverse complement motif Consensus sequence: KBKGCCCTCTYCTGGCCHV

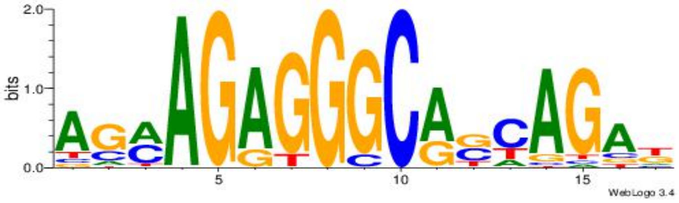


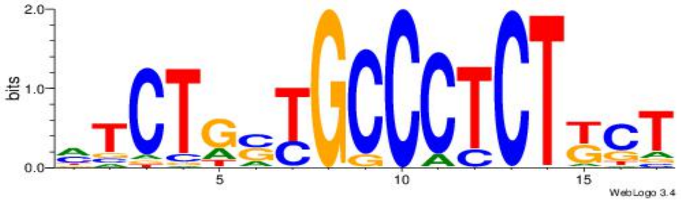
Dataset #: 4
Motif ID: 143
Motif name: AgmAGAGGGCrscAGak
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 10
Number of overlap: 7
Similarity score: 0.0633827

Alignment:
RTCTGSTGCCCTCTYCT
---------TCTCTSC-

Original motif Consensus sequence: AGMAGAGGGCASCAGAK

Reverse complement motif Consensus sequence: RTCTGSTGCCCTCTYCT



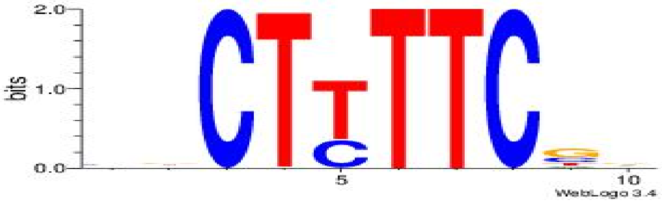


Dataset #:	4
Motif ID:	139
Motif name:	mkCTyTTCsg
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	7
Similarity score:	0.0693299

Alignment:

```
HBCTTTTCBD
-TCTCTSC--
```

Original motif   Consensus sequence: HBCTTTTCBD



Reverse complement motif   Consensus sequence: HBGAAAAGBD

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

Original motif Consensus sequence: AGRKGGCR

Reverse complement motif Consensus sequence: KGCCYKCT

Best Matches for 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
```

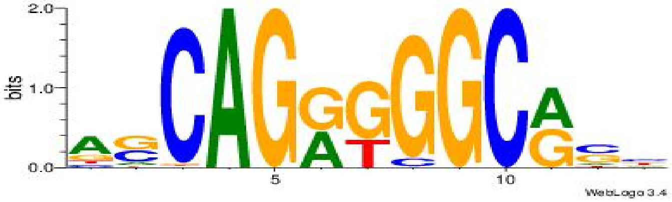
Original motif Consensus sequence: AGRKGGCR

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
---AGRKGGCR--

Original motif Consensus sequence: ASCAGRGGGCRSB



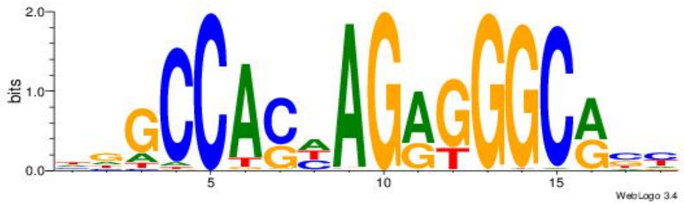
Reverse complement motif Consensus sequence: BSKGCCCMCTGST

Dataset #: 4
Motif ID: 165
Motif name: wgGCCAshAGrGGGCrsy
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 9
Number of overlap: 8

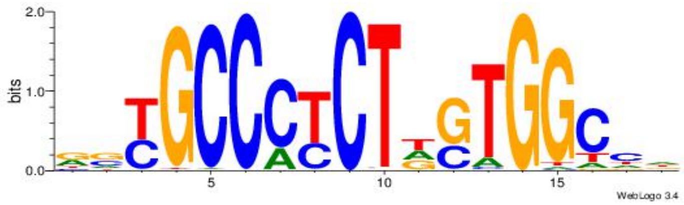
Similarity score: 0.0102443

Alignment:
KBKGCCCKCTHGTGGCHH
--KGCCYKCT--------

Original motif Consensus sequence: HDGCCACHAGRGGGCRBY



Reverse complement motif Consensus sequence: KBKGCCCKCTHGTGGCHH

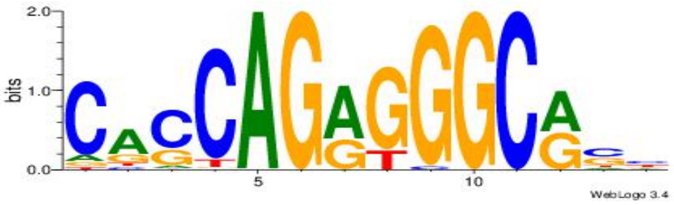


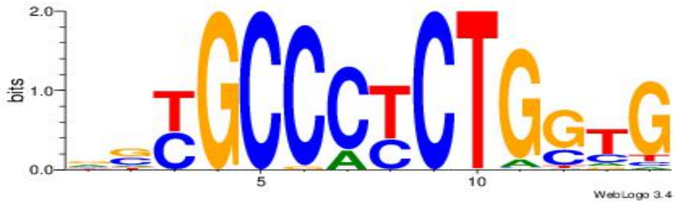
Dataset #:	4
Motif ID:	166
Motif name:	CasCAGrGGGCrsy
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	5
Number of overlap:	8
Similarity score:	0.0104954

Alignment:
BSKGCCCKCTGGTG
--KGCCYKCT----

Original motif Consensus sequence: CACCAGRGGGCRSB

Reverse complement motif Consensus sequence: BSKGCCCKCTGGT



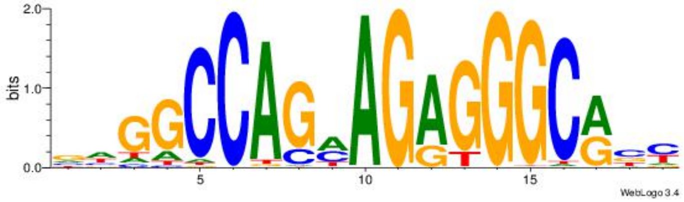


Dataset #:	4
Motif ID:	163
Motif name:	gwGGCCAGmAGAGGGCrby
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	3
Number of overlap:	8
Similarity score:	0.0165822

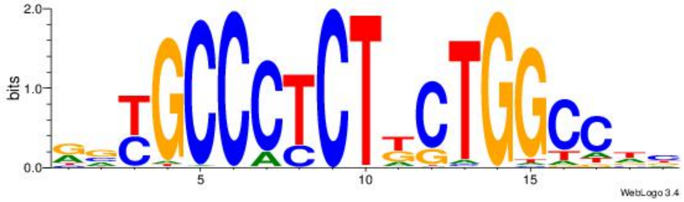
Alignment:

```
KBKGCCCTCTYCTGGCCHV
--KGCCYKCT---------
```

Original motif Consensus sequence: VHGGCCAGMAGAGGGCRBY



Reverse complement motif Consensus sequence: KBKGCCCTCTYCTGGCCHV



Dataset #: 2 Motif ID: 47 Motif name: Motif 47

Original motif Consensus sequence: CAGYDCC

Reverse complement motif Consensus sequence: GGDKCTG

Best Matches for Motif ID 47 (Highest to Lowest)

Dataset #:	1
Motif ID:	13
Motif name:	Motif 13
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	7
Similarity score:	0

Alignment:

```
GGDKCTG
GGDKCTG
```

Original motif Consensus sequence: CAGYDCC

Reverse complement motif Consensus sequence: GGDKCTG

Dataset #:	2
Motif ID:	53
Motif name:	Motif 53
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:	0.0288002

Alignment:

```
GGGATCTG
-GGDKCTG
```

Original motif Consensus sequence: CAGATCCC

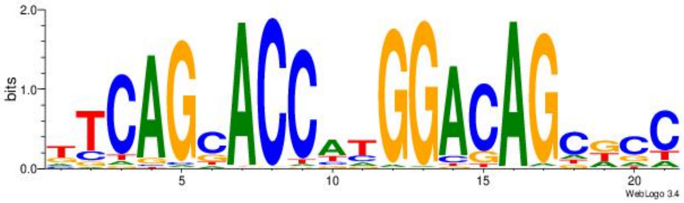
Reverse complement motif Consensus sequence: GGGATCTG

Dataset #:	3
Motif ID:	113
Motif name:	REST
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	13
Number of overlap:	7

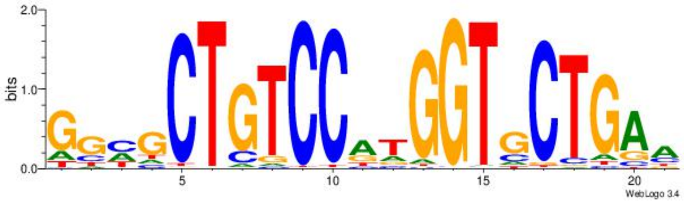
Similarity score: 0.0502666

Alignment:
GGYGCTGTCCATGGTGCTGAA
------------GGDKCTG--

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC



Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA



Dataset #: 1
Motif ID: 22
Motif name: Motif 22
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 2
Number of overlap: 7
Similarity score: 0.0531399

Alignment:
GGKATCTG
-GGDKCTG

Original motif Consensus sequence: CAGATYCC

Reverse complement motif Consensus sequence: GGKATCTG

Dataset #: 4
Motif ID: 160
Motif name: brCAGGGCCrs
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 3
Number of overlap: 7
Similarity score: 0.0559697

Alignment:

```
BVCAGGGCCVB
--CAGYDCC--
```

Original motif Consensus sequence: BVCAGGGCCVB

Reverse complement motif Consensus sequence: BBGGCCCTGBB

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

Original motif Consensus sequence: CCACYAGR

Reverse complement motif Consensus sequence: MCTKGTGG

Best Matches for 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
```

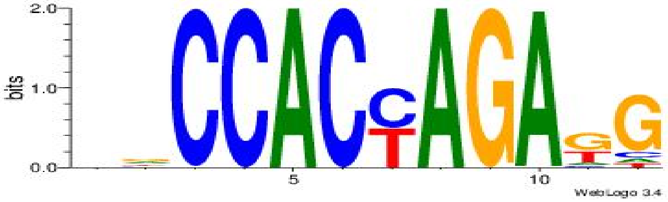
Original motif Consensus sequence: CCACYAGG

Reverse complement motif Consensus sequence: CCTKGTGG

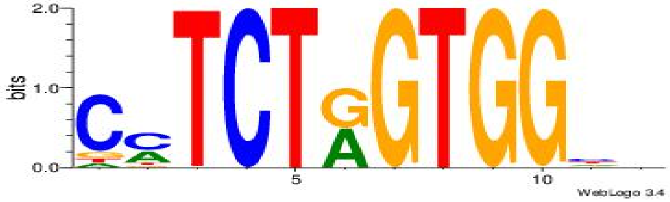
Dataset #: 4
Motif ID: 145
Motif name: grCCACyAGAkG
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 3
Number of overlap: 8
Similarity score: 0.0155354

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

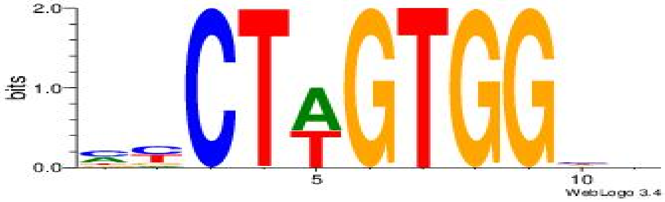
Similarity score: 0.0192652

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

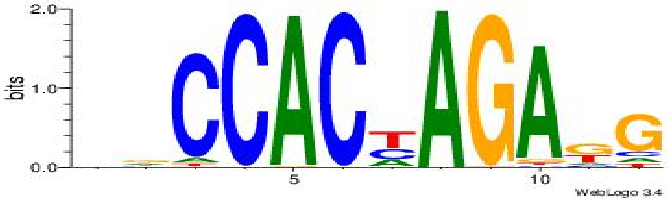
Similarity score: 0.0244381

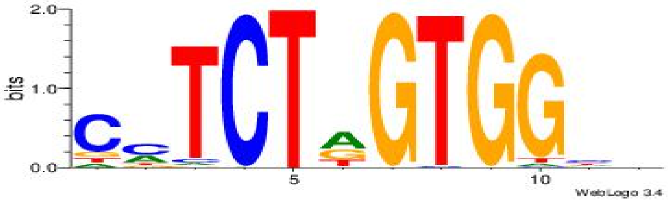
Alignment:

```
DDCCACYAGAKG
--CCACYAGR--
```

Original motif Consensus sequence: DDCCACYAGAKG

Reverse complement motif Consensus sequence: CYTCTMGTGGHH



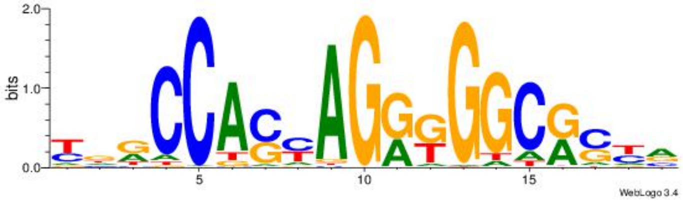


Dataset #:	3
Motif ID:	74
Motif name:	CTCF
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	9
Number of overlap:	8
Similarity score:	0.0284404

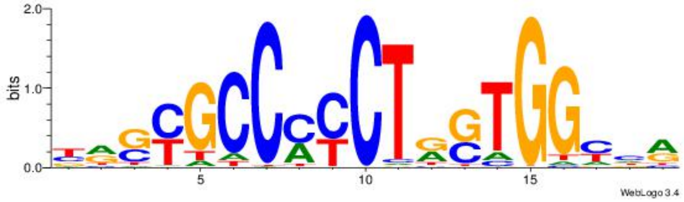
Alignment:

```
BMSMGCCYMCTKSTGGMHM
--------MCTKGTGG---
```

Original motif   Consensus sequence: YDRCCASYAGRKGGCRSYV



Reverse complement motif   Consensus sequence: BMSMGCCYMCTKSTGGMHM



Dataset #: 2   Motif ID: 49   Motif name: Motif 49

Original motif Consensus sequence: CTGGCCTC

Reverse complement motif Consensus sequence: GAGGCCAG

Best Matches for Motif ID 49 (Highest to Lowest)

Dataset #:	1
Motif ID:	10
Motif name:	Motif 10
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	8
Similarity score:	0

Alignment:

```
CTGGCCTC
CTGGCCTC
```

Original motif Consensus sequence: CTGGCCTC

Reverse complement motif Consensus sequence: GAGGCCAG

Dataset #:	1
Motif ID:	33
Motif name:	Motif 33
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:	0.0148758

Alignment:
CTGGCTWC
CTGGCCTC

Original motif Consensus sequence: CTGGCTWC

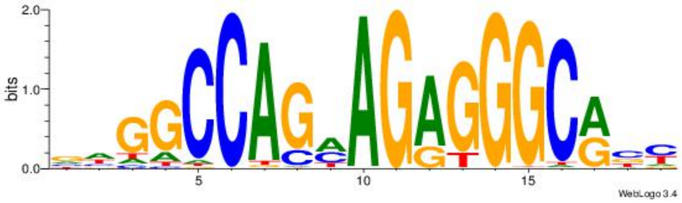
Reverse complement motif Consensus sequence: GWAGCCAG

Dataset #:	4
Motif ID:	163
Motif name:	gwGGCCAGmAGAGGGCrby
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	12
Number of overlap:	8

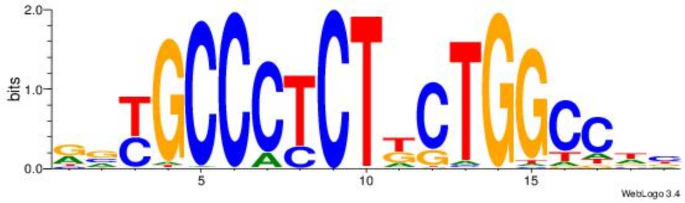
Similarity score:	0.0362649

Alignment:
VHGGCCAGMAGAGGGCRBY
GAGGCCAG-----------

Original motif Consensus sequence: VHGGCCAGMAGAGGGCRBY



Reverse complement motif Consensus sequence: KBKGCCCTCTYCTGGCCHV

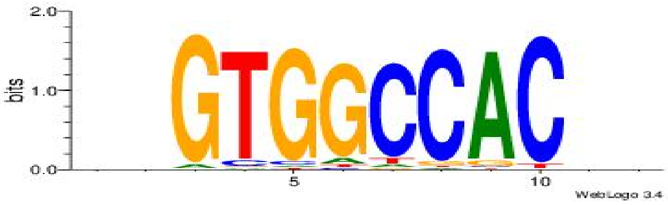


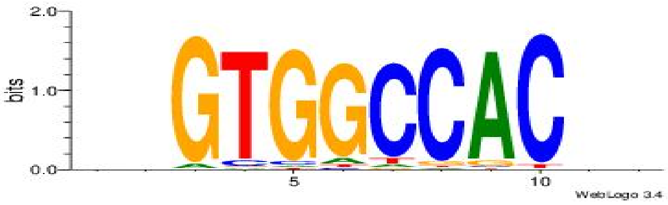
Dataset #:	4
Motif ID:	171
Motif name:	ysGTGGCCACsr
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	3
Number of overlap:	8
Similarity score:	0.0504205

Alignment:
VBGTGGCCACVB
--CTGGCCTC--

Original motif Consensus sequence: BVGTGGCCACBV

Reverse complement motif Consensus sequence: VBGTGGCCACVB





Dataset #:	4
Motif ID:	133
Motif name:	shAGrGGGCAgy
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	4
Number of overlap:	8
Similarity score:	0.0509007

Alignment:

```
SHAGRGGGCABH
---GAGGCCAG-
```

Original motif Consensus sequence: SHAGRGGGCABH

Reverse complement motif Consensus sequence: DBTGCCCKCTDS

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

Original motif Consensus sequence: AGRAA

Reverse complement motif Consensus sequence: TTMCT

Best Matches for Motif ID 50 (Highest to Lowest)

Dataset #:	1
Motif ID:	7
Motif name:	Motif 7
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2
Number of overlap:	5
Similarity score:	0

Alignment:

```
AGRAAA
AGRAA-
```

Original motif Consensus sequence: AGRAAA

Reverse complement motif Consensus sequence: TTTMCT

Dataset #: 1
Motif ID: 39
Motif name: Motif 39
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 2
Number of overlap: 5
Similarity score: 0.0244128

Alignment:

```
BAGAAA
-AGRAA
```

Original motif Consensus sequence: BAGAAA

Reverse complement motif Consensus sequence: TTTCTB

Dataset #: 1
Motif ID: 28
Motif name: Motif 28
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 2
Number of overlap: 5

Similarity score:	0.0419638

Alignment:

CAGGAAG
-AGRAA-

Original motif Consensus sequence: CTTCCTG

Reverse complement motif Consensus sequence: CAGGAAG

Dataset #:	1
Motif ID:	29
Motif name:	Motif 29
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	5
Similarity score:	0.0427966

Alignment:

CATTTCY
TTMCT--

Original motif Consensus sequence: CATTTCY

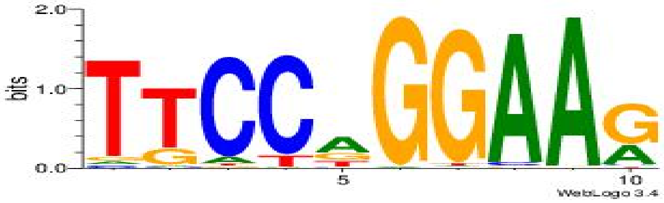
Reverse complement motif Consensus sequence: MGAAATG

Dataset #:	3
Motif ID:	119
Motif name:	Stat3
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2
Number of overlap:	5
Similarity score:	0.0502276

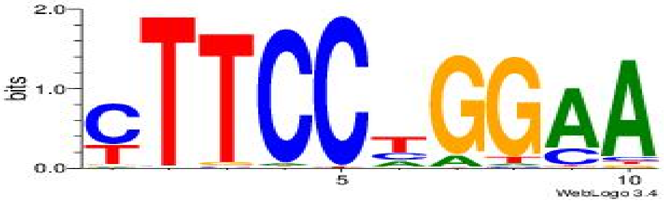
Alignment:

```
TTCCAGGAAG
----AGRAA-
```

Original motif   Consensus sequence: TTCCAGGAAG



Reverse complement motif   Consensus sequence: CTTCCTGGAA



Dataset #: 2   Motif ID: 51   Motif name: Motif 51

Original motif   Consensus sequence: GAGTTACA

Reverse complement motif   Consensus sequence: TGTAACTC

Best Matches for Motif ID 51 (Highest to Lowest)

Dataset #:	1
Motif ID:	38
Motif name:	Motif 38
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:

```
GAGTTACA
GAGTTACA
```

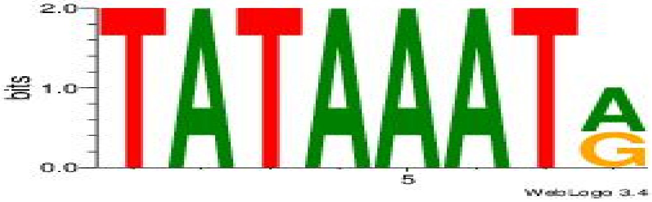
Original motif   Consensus sequence: GAGTTACA

Reverse complement motif   Consensus sequence: TGTAACTC

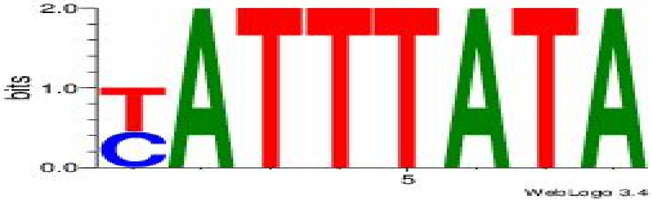
Dataset #:	2
Motif ID:	66
Motif name:	Motif 66
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	8
Similarity score:	0.0742432

Alignment:
KATTTATA
GAGTTACA

Original motif Consensus sequence: TATAAATR



Reverse complement motif Consensus sequence: KATTTATA

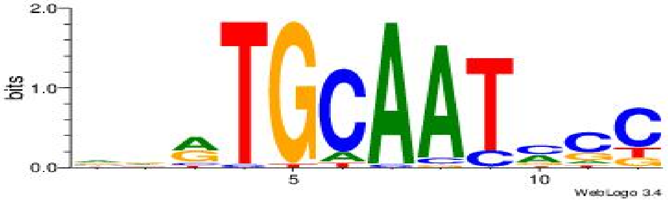


Dataset #:	3
Motif ID:	75
Motif name:	Ddit3Cebpa
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	4
Number of overlap:	8

Similarity score: 0.0857192

Alignment:
GGRATTGCAKHB
-GAGTTACA---

Original motif Consensus sequence: VDRTGCAATMCC



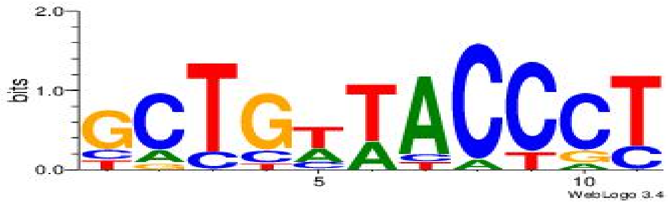
Reverse complement motif Consensus sequence: GGRATTGCAKHB

Dataset #:	3
Motif ID:	117
Motif name:	Spz1
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:	0.0885417

Alignment:
AGGGTAWCAGC
-GAGTTACA--

Original motif Consensus sequence: AGGGTAWCAGC

Reverse complement motif Consensus sequence: GCTGWTACCCT



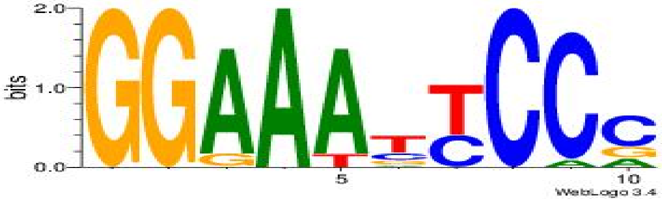
Dataset #:	3
Motif ID:	112
Motif name:	RELA
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	3
Number of overlap:	8
Similarity score:	0.0911946

Alignment:

```
GGGRATTTCC
--GAGTTACA
```

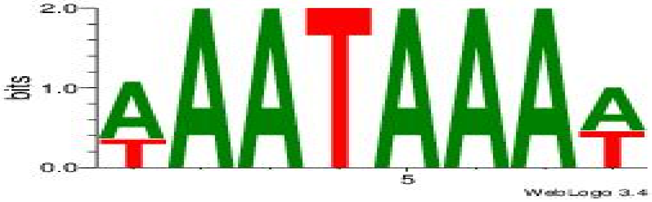
Original motif Consensus sequence: GGGRATTTCC

Reverse complement motif Consensus sequence: GGAAATKCCC

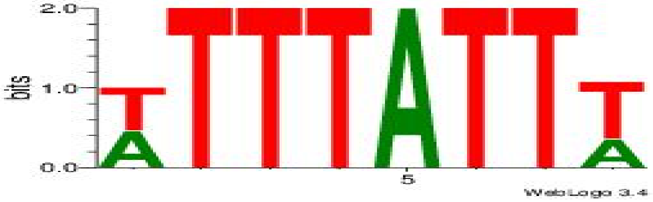


Dataset #: 2 Motif ID: 52 Motif name: Motif 52

Original motif Consensus sequence: AAATAAAW



Reverse complement motif Consensus sequence: WTTTATTT



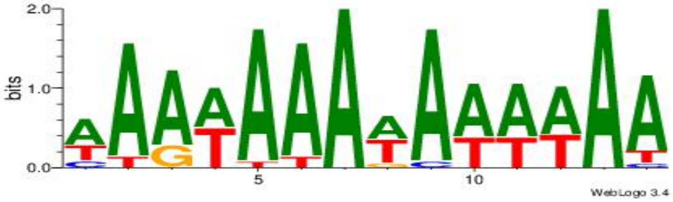
Best Matches for Motif ID 52 (Highest to Lowest)

Dataset #:	2
Motif ID:	68
Motif name:	Motif 68
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	8
Similarity score:	0.0178205

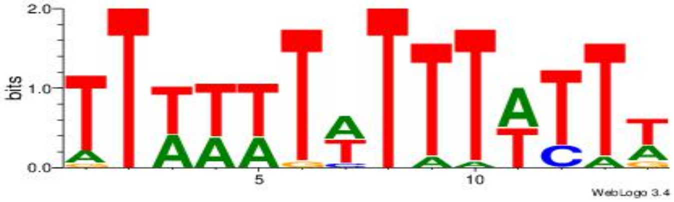
Alignment:

```
TTWWWTWTTTWTTW
------WTTTATTT
```

Original motif Consensus sequence: WAAWAAAWAWWWAA



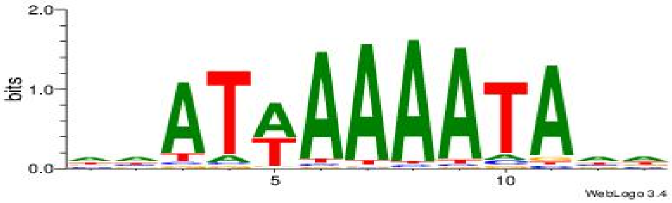
Reverse complement motif Consensus sequence: TTWWWTWTTTWTTW



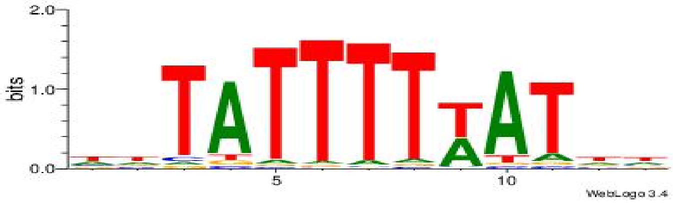
Dataset #: 4
Motif ID: 150
Motif name: waATwAAAATAww
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 8
Similarity score: 0.0502803

Alignment:
DHTATTTTWATHD
-----WTTTATTT

Original motif Consensus sequence: DHATWAAAATAHD



Reverse complement motif Consensus sequence: DHTATTTTWATHD

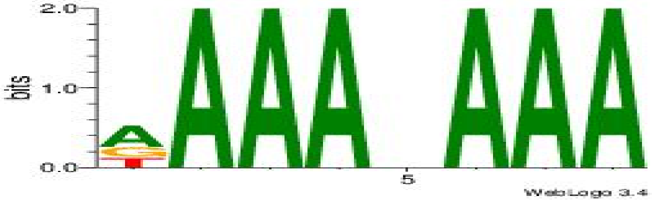


Dataset #: 1
Motif ID: 2
Motif name: Motif 2
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 8

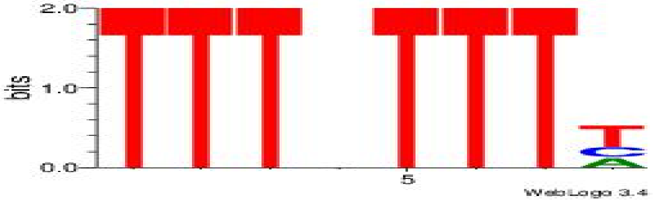
Similarity score: 0.0573886

Alignment:
AAAAHAAA
AAATAAAW

Original motif Consensus sequence: AAAAHAAA



Reverse complement motif Consensus sequence: TTTDTTTT

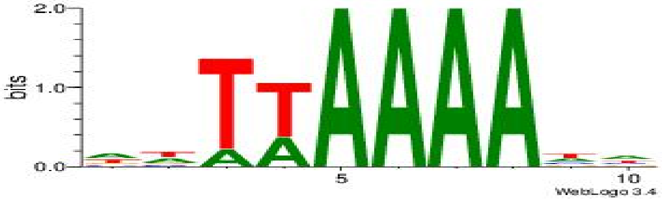


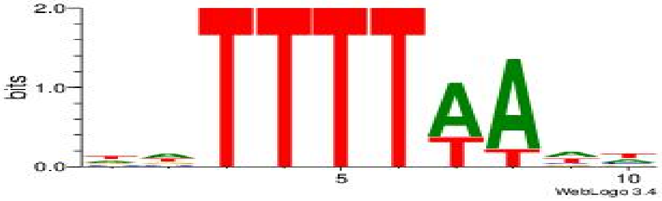
Dataset #: 4
Motif ID: 148
Motif name: wwTwAAAAww
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 8
Similarity score: 0.0617903

Alignment:
HHTTTTWADD
--WTTTATTT

Original motif Consensus sequence: DDTWAAAAHH

Reverse complement motif Consensus sequence: HHTTTTWADD



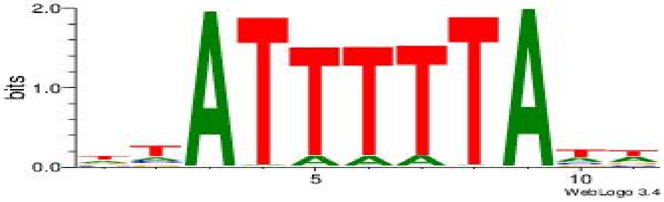


Dataset #: 4
Motif ID: 157
Motif name: wtATTTTTAww
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 3
Number of overlap: 8
Similarity score: 0.0718936

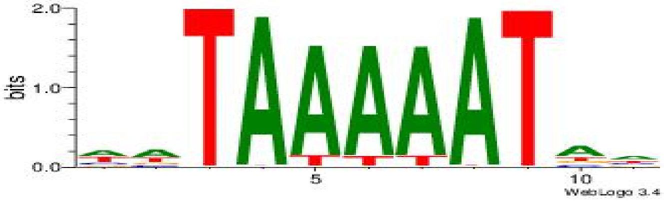
Alignment:

```
DTATTTTTAWW
--WTTTATTT-
```

Original motif Consensus sequence: DTATTTTTAWW



Reverse complement motif Consensus sequence: WWTAAAAATAD



Dataset #: 2 Motif ID: 53 Motif name: Motif 53

Original motif Consensus sequence: CAGATCCC

Reverse complement motif Consensus sequence: GGGATCTG

Best Matches for Motif ID 53 (Highest to Lowest)

Dataset #:	1
Motif ID:	22
Motif name:	Motif 22
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

Alignment:

```
CAGATYCC
CAGATCCC
```

Original motif Consensus sequence: CAGATYCC

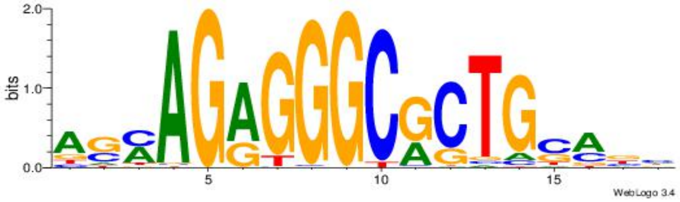
Reverse complement motif Consensus sequence: GGKATCTG

Dataset #: 4
Motif ID: 149
Motif name: asmAGRGGGCrCTGsmkc
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 7
Number of overlap: 8
Similarity score: 0.0479917

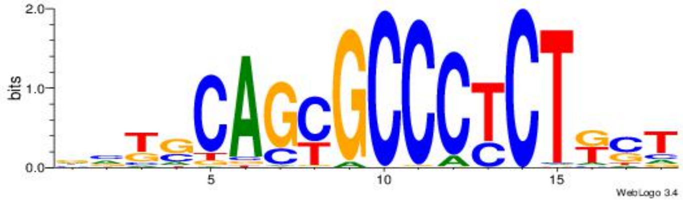
Alignment:

```
DBTSCAGMGCCCTCTRST
----CAGATCCC------
```

Original motif Consensus sequence: ASMAGAGGGCRCTGSABH



Reverse complement motif Consensus sequence: DBTSCAGMGCCCTCTRST



Dataset #: 4
Motif ID: 160
Motif name: brCAGGGCCrs
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 3

Number of overlap:	8
Similarity score:	0.0605671

Alignment:

```
BBGGCCCTGBB
-GGGATCTG--
```

Original motif Consensus sequence: BVCAGGGCCVB

Reverse complement motif Consensus sequence: BBGGCCCTGBB

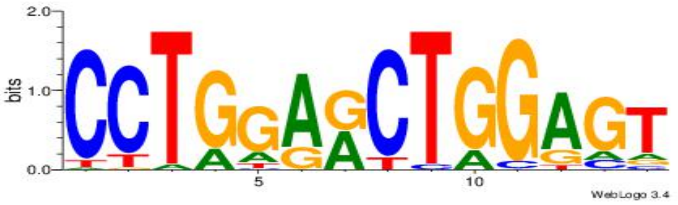
Dataset #:	2
Motif ID:	69
Motif name:	Motif 69
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	5
Number of overlap:	8
Similarity score:	0.0606088

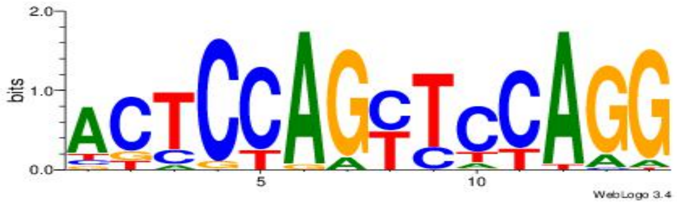
Alignment:

```
ACTCCAGMTCCAGG
----CAGATCCC--
```

Original motif Consensus sequence: CCTGGARCTGGAGT

Reverse complement motif Consensus sequence: ACTCCAGMTCCAG



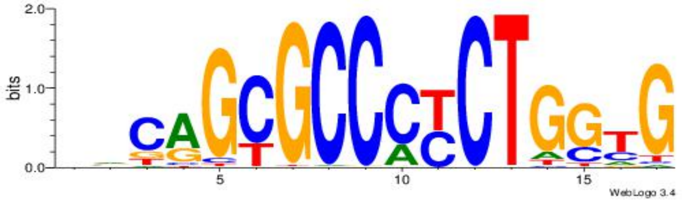


Dataset #: 4
Motif ID: 168
Motif name: yrcrGYGCCMyCTGGtG
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 3
Number of overlap: 8
Similarity score: 0.065385

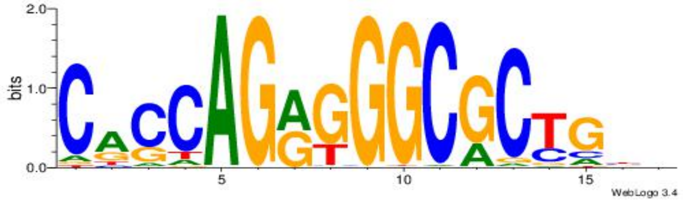
Alignment:

```
CACCAGMGGGCGCTGBD
-------GGGATCTG--
```

Original motif Consensus sequence: HVCAGCGCCCYCTGGTG

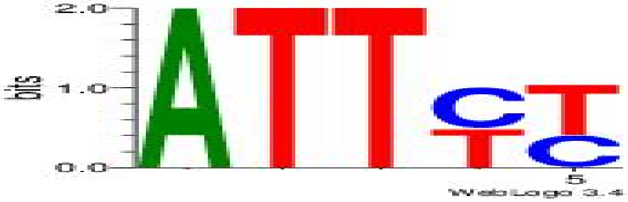


Reverse complement motif Consensus sequence: CACCAGMGGGCGCTGBD



Dataset #: 2 **Motif ID: 54** **Motif name: Motif 54**

Original motif Consensus sequence: ATTYY



Reverse complement motif Consensus sequence: MKAAT

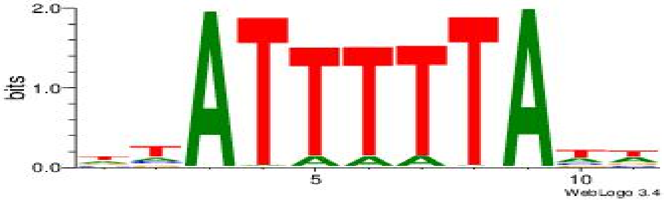
Best Matches for Motif ID 54 (Highest to Lowest)

Dataset #:	4
Motif ID:	157
Motif name:	wtATTTTTAww
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	3
Number of overlap:	5
Similarity score:	0.0491344

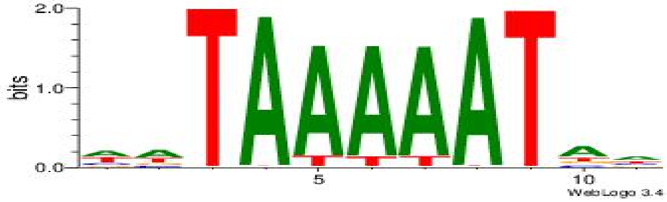
Alignment:

```
DTATTTTTAWW
--ATTYY----
```

Original motif Consensus sequence: DTATTTTTAWW



Reverse complement motif Consensus sequence: WWTAAAAATAD



Dataset #: 1
Motif ID: 29
Motif name: Motif 29
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 2
Number of overlap: 5
Similarity score: 0.0551561

Alignment:

```
CATTTCY
-ATTYY-
```

Original motif Consensus sequence: CATTTCY

Reverse complement motif Consensus sequence: MGAAATG

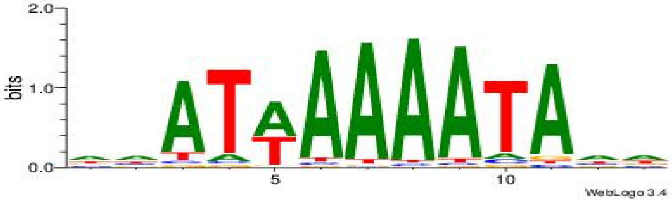
Dataset #: 4
Motif ID: 150
Motif name: waATwAAAATAww
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 6
Number of overlap: 5

Similarity score:	0.0567288

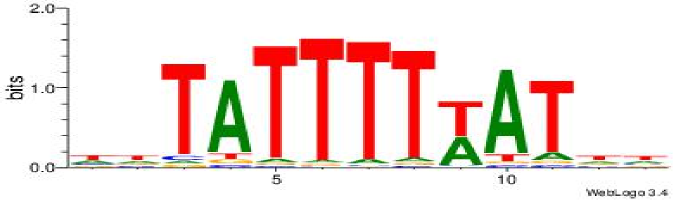
Alignment:

```
DHTATTTTWATHD
---ATTYY-----
```

Original motif Consensus sequence: DHATWAAAATAHD



Reverse complement motif Consensus sequence: DHTATTTTWATHD



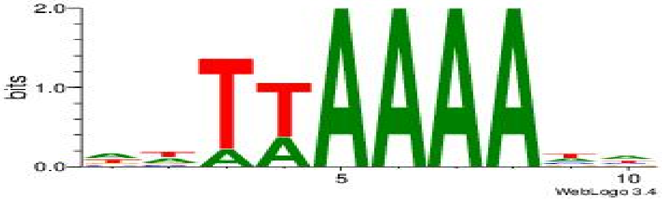
Dataset #:	4
Motif ID:	148
Motif name:	wwTwAAAAww
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	2
Number of overlap:	5
Similarity score:	0.0727457

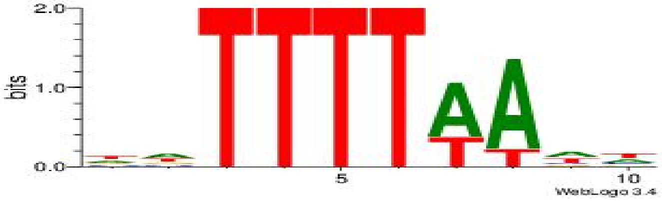
Alignment:

```
HHTTTTWADD
-ATTYY----
```

Original motif Consensus sequence: DDTWAAAAHH

Reverse complement motif Consensus sequence: HHTTTTWADD



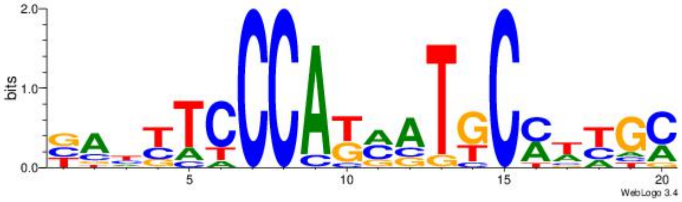


Dataset #:	3
Motif ID:	131
Motif name:	znf143
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	9
Number of overlap:	5
Similarity score:	0.0737392

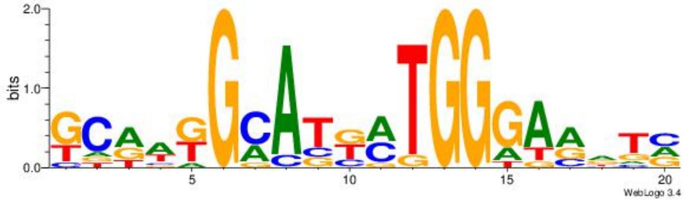
Alignment:

```
BAHYTCCCAKMATGCMWYGC
--------MKAAT-------
```

Original motif Consensus sequence: BAHYTCCCAKMATGCMWYGC

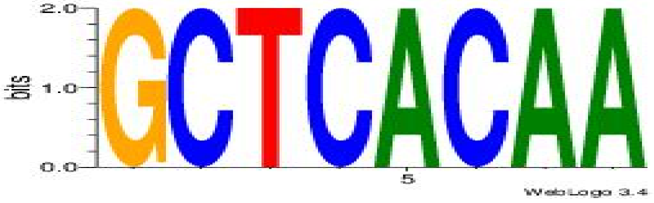


Reverse complement motif Consensus sequence: GCMWRGCATYRTGGGAMHTB



Dataset #: 2 **Motif ID: 55** **Motif name: Motif 55**

Original motif Consensus sequence: GCTCACAA



Reverse complement motif Consensus sequence: TTGTGAGC

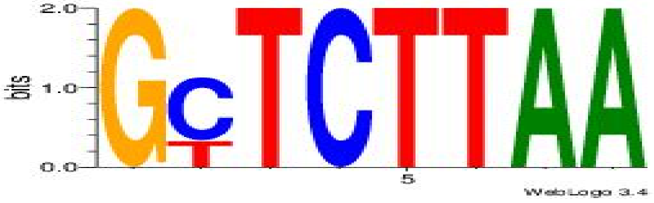
Best Matches for Motif ID 55 (Highest to Lowest)

Dataset #:	1
Motif ID:	15
Motif name:	Motif 15
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:	0.071643

Alignment:

```
GCTCTTAA
GCTCACAA
```

Original motif Consensus sequence: GCTCTTAA



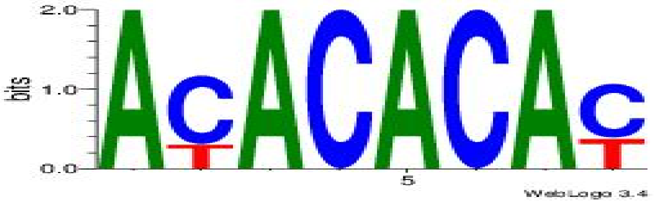
Reverse complement motif Consensus sequence: TTAAGAGC

Dataset #:	2
Motif ID:	57
Motif name:	Motif 57
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:	0.0907452

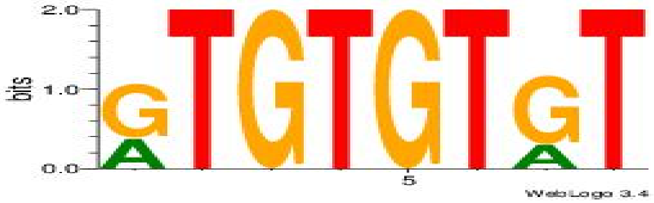
Alignment:

```
KTGTGTGT
TTGTGAGC
```

Original motif   Consensus sequence: ACACACAY



Reverse complement motif   Consensus sequence: KTGTGTGT



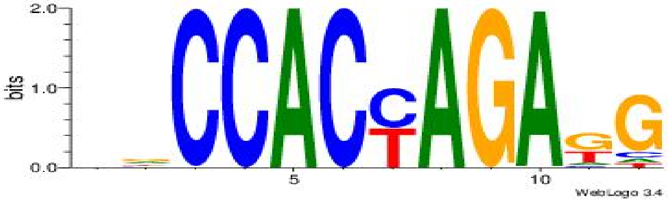
Dataset #:	4
Motif ID:	145
Motif name:	grCCACyAGAkG
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	5
Number of overlap:	8

Similarity score: 0.0949146

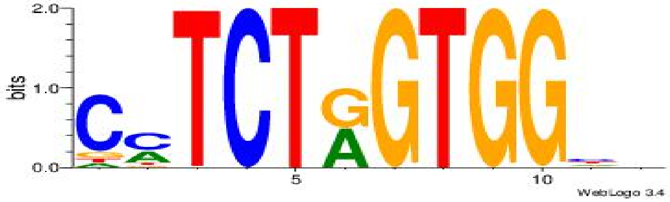
Alignment:

```
CYTCTKGTGGHH
----TTGTGAGC
```

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: 4

Number of overlap: 8

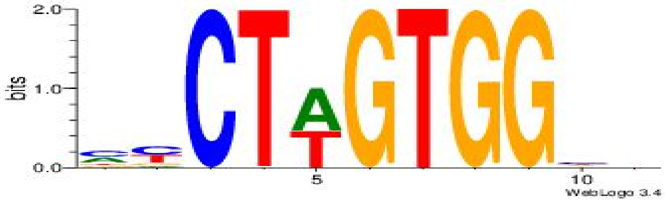
Similarity score: 0.0951691

Alignment:

```
DDCCACWAGRK
GCTCACAA---
```

Original motif Consensus sequence: DDCCACWAGRK

Reverse complement motif Consensus sequence: YMCTWGTGGHH



Dataset #: 3
Motif ID: 76
Motif name: E2F1
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 8
Similarity score: 0.103125

Alignment:
GCGCSAAA
GCTCACAA

Original motif Consensus sequence: TTTSGCGC

Reverse complement motif Consensus sequence: GCGCSAAA

Dataset #: 2 Motif ID: 56 Motif name: Motif 56

Original motif Consensus sequence: CCACATGG

Reverse complement motif Consensus sequence: CCATGTGG

Best Matches for Motif ID 56 (Highest to Lowest)

Dataset #:	1
Motif ID:	21
Motif name:	Motif 21
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	8
Similarity score:	0.0480363

Alignment:

```
CCTKGTGG
CCATGTGG
```

Original motif Consensus sequence: CCACYAGG

Reverse complement motif Consensus sequence: CCTKGTGG

Dataset #:	2
Motif ID:	48
Motif name:	Motif 48
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	8
Similarity score:	0.0609421

Alignment:

```
MCTKGTGG
CCATGTGG
```

Original motif Consensus sequence: CCACYAGR

Reverse complement motif Consensus sequence: MCTKGTGG

Dataset #:	3
Motif ID:	95
Motif name:	MYCMAX
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	3
Number of overlap:	8

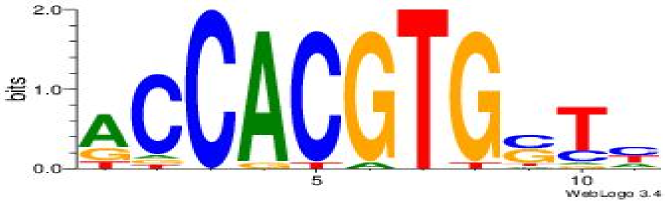
Similarity score: 0.0616071

Alignment:

```
RASCACGTGGT
--CCACATGG-
```

Original motif Consensus sequence: RASCACGTGGT

Reverse complement motif Consensus sequence: ACCACGTGSTM



Dataset #: 3

Motif ID: 96

Motif name: Mycn

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: 0.0634989

Alignment:

```
HSCACGTGGC
-CCACATGG-
```

Original motif Consensus sequence: HSCACGTGGC

Reverse complement motif Consensus sequence: GCCACGTGSD

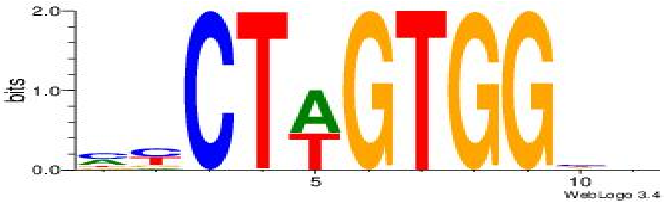
Dataset #:	4
Motif ID:	158
Motif name:	grCCACwAGrk
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2
Number of overlap:	8
Similarity score:	0.0666667

Alignment:

```
DDCCACWAGRK
--CCACATGG-
```

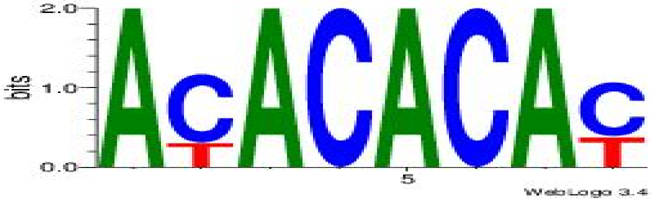
Original motif Consensus sequence: DDCCACWAGRK

Reverse complement motif Consensus sequence: YMCTWGTGGHH



Dataset #: 2 Motif ID: 57 Motif name: Motif 57

Original motif Consensus sequence: ACACACAY



Reverse complement motif Consensus sequence: KTGTGTGT

Best Matches for Motif ID 57 (Highest to Lowest)

Dataset #:	1
Motif ID:	35
Motif name:	Motif 35
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:	0.0591808

Alignment:

```
ACAACCAY
ACACACAY
```

Original motif Consensus sequence: ACAACCAY

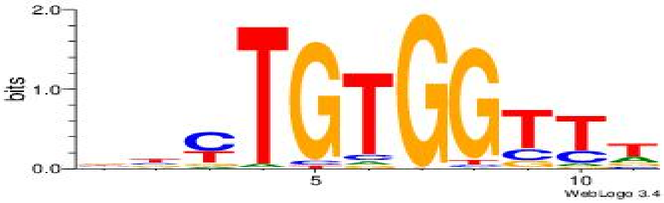
Reverse complement motif Consensus sequence: KTGGTTGT

Dataset #: 3
Motif ID: 114
Motif name: RUNX1
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 3
Number of overlap: 8
Similarity score: 0.0712868

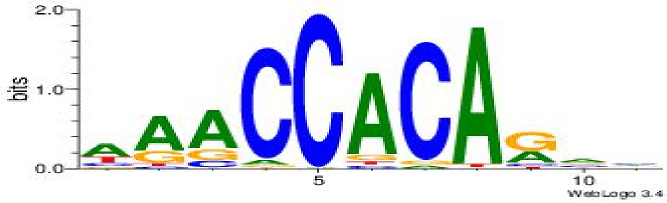
Alignment:

```
BBYTGTGGTTT
--KTGTGTGT-
```

Original motif Consensus sequence: BBYTGTGGTTT



Reverse complement motif Consensus sequence: AAACCACAKVB

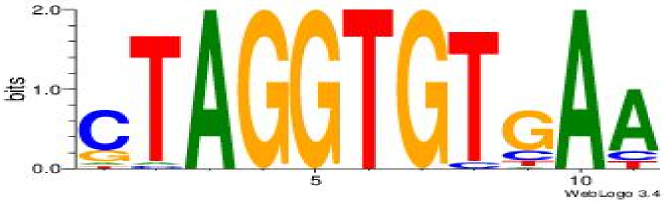


Dataset #: 3
Motif ID: 120
Motif name: T
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 3
Number of overlap: 8

Similarity score: 0.0758601

Alignment:
TTCACACCTAG
-ACACACAY--

Original motif Consensus sequence: CTAGGTGTGAA



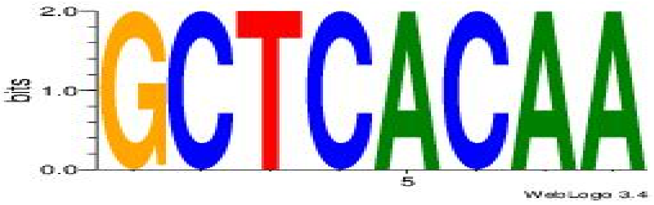
Reverse complement motif Consensus sequence: TTCACACCTAG

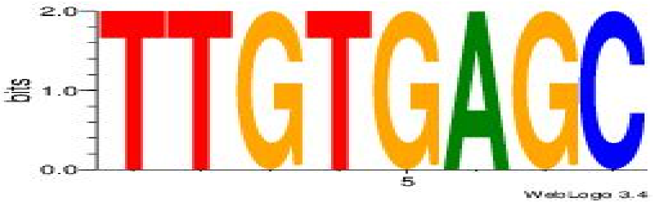
Dataset #: 2
Motif ID: 55
Motif name: Motif 55
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 8
Similarity score: 0.0761605

Alignment:
TTGTGAGC
KTGTGTGT

Original motif Consensus sequence: GCTCACAA

Reverse complement motif Consensus sequence: TTGTGAGC





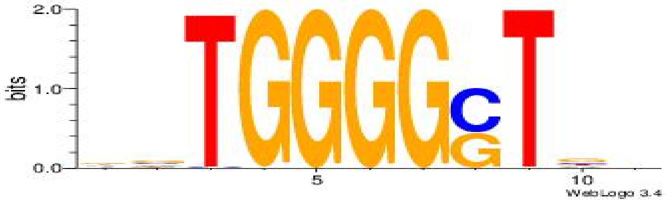
Dataset #:	4
Motif ID:	162
Motif name:	ccAsCCCCAcc
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2
Number of overlap:	8
Similarity score:	0.0776002

Alignment:

```
HVASCCCCABH
--ACACACAY-
```

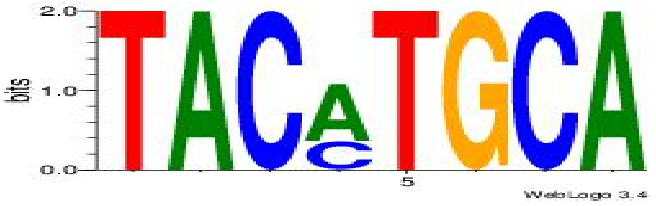
Original motif Consensus sequence: HVASCCCCABH

Reverse complement motif Consensus sequence: DBTGGGGSTVD



Dataset #: 2 **Motif ID: 58** **Motif name: Motif 58**

Original motif Consensus sequence: TACATGCA



Reverse complement motif Consensus sequence: TGCATGTA

Best Matches for Motif ID 58 (Highest to Lowest)

Dataset #:	4
Motif ID:	152
Motif name:	yrCATGCAyr
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:	0.0160706

Alignment:

```
HVTGCATGKV
--TGCATGTA
```

Original motif Consensus sequence: BRCATGCABD

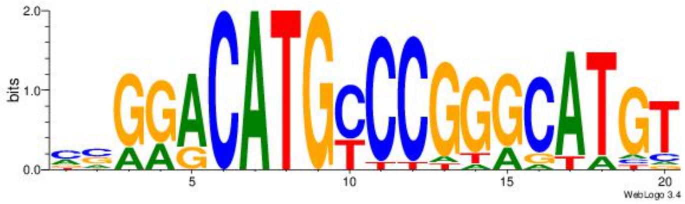
Reverse complement motif Consensus sequence: HVTGCATGKV

Dataset #: 3
Motif ID: 125
Motif name: TP53
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 4
Number of overlap: 8
Similarity score: 0.0595681

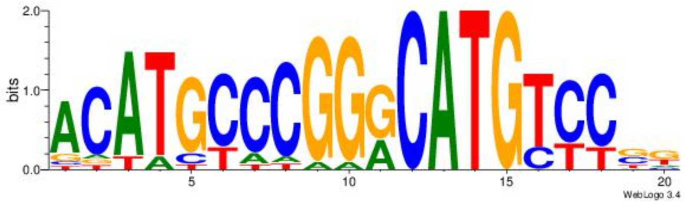
Alignment:

```
ACATGCCCGGKCATGTCCSR
---------TGCATGTA---
```

Original motif Consensus sequence: MSGGACATGYCCGGGCATGT



Reverse complement motif Consensus sequence: ACATGCCCGGKCATGTCCSR

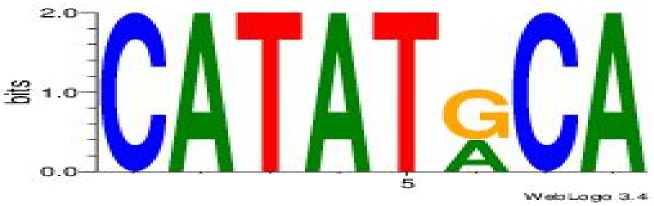


Dataset #: 2
Motif ID: 64
Motif name: Motif 64
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1

Number of overlap: 8
Similarity score: 0.0642891

Alignment:
CATATRCA
TACATGCA

Original motif Consensus sequence: CATATRCA



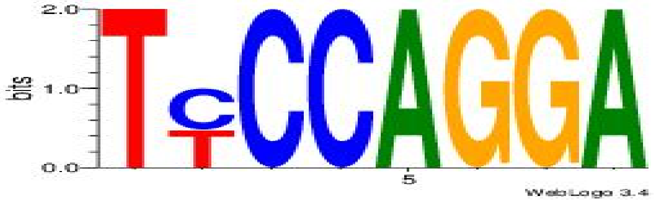
Reverse complement motif Consensus sequence: TGMATATG

Dataset #: 1
Motif ID: 36
Motif name: Motif 36
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: 0.0792922

Alignment:
TCCTGGRA
TGCATGTA

Original motif Consensus sequence: TCCTGGRA

Reverse complement motif Consensus sequence: TMCCAGGA



Dataset #:	3
Motif ID:	95
Motif name:	MYCMAX
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:	0.0822408

Alignment:

```
RASCACGTGGT
-TGCATGTA--
```

Original motif Consensus sequence: RASCACGTGGT

Reverse complement motif Consensus sequence: ACCACGTGSTM

Dataset #: 2 Motif ID: 59 Motif name: Motif 59

Original motif Consensus sequence: CCCCRCCC

Reverse complement motif Consensus sequence: GGGKGGGG

Best Matches for Motif ID 59 (Highest to Lowest)

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:	1
Number of overlap:	8
Similarity score:	0.00363191

Alignment:

```
CCCCDCCC
CCCCRCCC
```

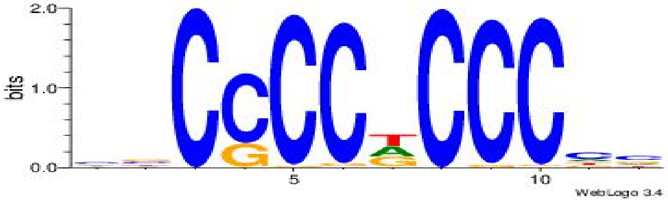
Original motif Consensus sequence: CCCCDCCC

Reverse complement motif Consensus sequence: GGGDGGGG

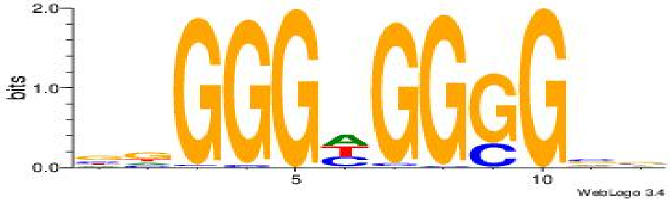
Dataset #: 4
Motif ID: 155
Motif name: csCSCCdCCCcs
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 3
Number of overlap: 8
Similarity score: 0.0143924

Alignment:
VDGGGDGGGGBV
--GGGKGGGG--

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: 0.0334874

Alignment:
GCCYCMCCCD
-CCCCRCCC-

Original motif Consensus sequence: DGGGYGKGGC

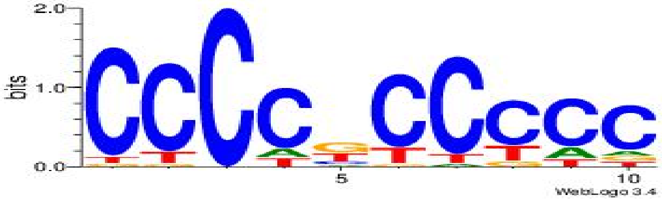
Reverse complement motif Consensus sequence: GCCYCMCCCD

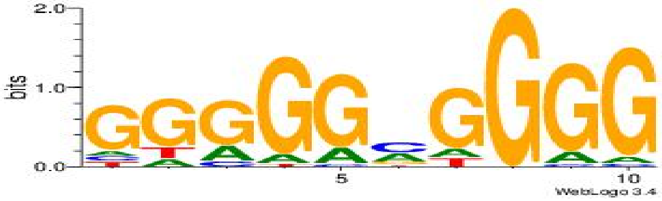
Dataset #: 3
Motif ID: 116
Motif name: SP1
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 8
Similarity score: 0.0421627

Alignment:
GGGGGYGGGG
--GGGKGGGG

Original motif Consensus sequence: CCCCKCCCCC

Reverse complement motif Consensus sequence: GGGGGYGGGG





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:	0.0467112

Alignment:

```
VBCCCCTCCHB
--CCCCRCCC-
```

Original motif Consensus sequence: VBCCCCTCCHB

Reverse complement motif Consensus sequence: BDGGAGGGGBV

Dataset #: 2 **Motif ID: 60** **Motif name: Motif 60**

Original motif Consensus sequence: CTGGAR

Reverse complement motif Consensus sequence: MTCCAG

Best Matches for Motif ID 60 (Highest to Lowest)

Dataset #:	1
Motif ID:	6
Motif name:	Motif 6
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:	0.00500479

Alignment:

```
CTGGRRA
CTGGAR-
```

Original motif Consensus sequence: CTGGRRA

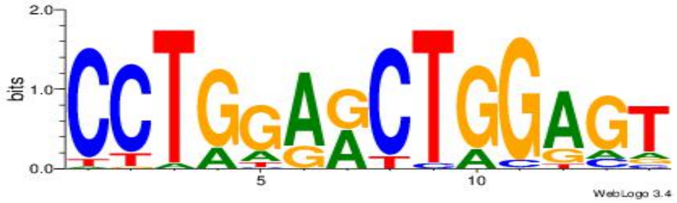
Reverse complement motif Consensus sequence: TMMCCAG

Dataset #: 2
Motif ID: 69
Motif name: Motif 69
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 8
Number of overlap: 6
Similarity score: 0.0149252

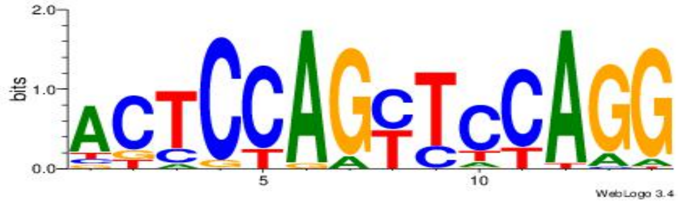
Alignment:

```
CCTGGARCTGGAGT
-------CTGGAR-
```

Original motif Consensus sequence: CCTGGARCTGGAGT



Reverse complement motif Consensus sequence: ACTCCAGMTCCAG



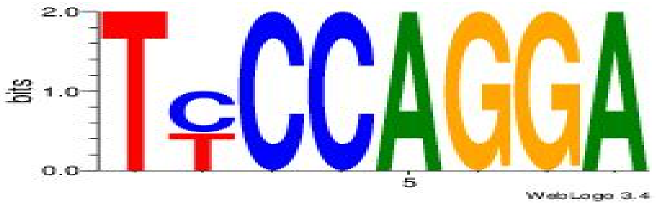
Dataset #: 1
Motif ID: 36
Motif name: Motif 36
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 6

Similarity score:	0.0273394

Alignment:
TCCTGGRA
--CTGGAR

Original motif Consensus sequence: TCCTGGRA

Reverse complement motif Consensus sequence: TMCCAGGA

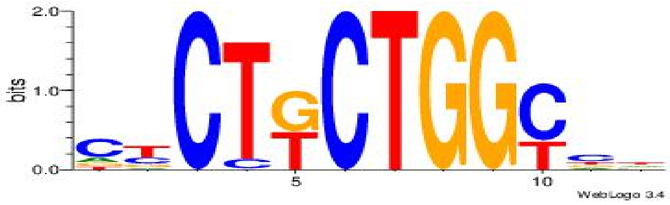


Dataset #:	4
Motif ID:	151
Motif name:	agrCCAGmAGrg
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	6
Number of overlap:	6
Similarity score:	0.0324331

Alignment:
CKCTRCTGGCVH
-----CTGGAR-

Original motif Consensus sequence: HVGCCAGMAGRG

Reverse complement motif Consensus sequence: CKCTRCTGGCVH

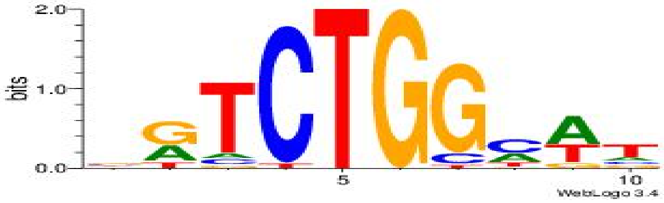


Dataset #:	3
Motif ID:	85
Motif name:	Hand1Tcfe2a
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	4
Number of overlap:	6
Similarity score:	0.0370865

Alignment:

```
BRTCTGGMWT
---CTGGAR-
```

Original motif Consensus sequence: BRTCTGGMWT



Reverse complement motif Consensus sequence: AWRCCAGAMB

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

Original motif   Consensus sequence: AGATGGY

Reverse complement motif   Consensus sequence: KCCATCT

Best Matches for Motif ID 61 (Highest to Lowest)

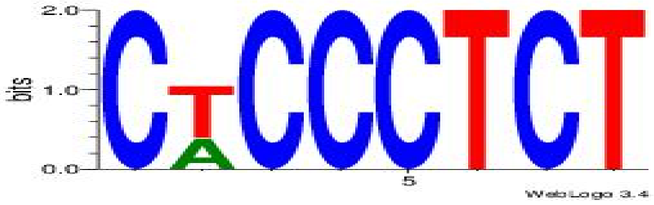
Dataset #:	2
Motif ID:	63
Motif name:	Motif 63
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	2
Number of overlap:	7
Similarity score:	0.0339703

Alignment:

```
CWCCCTCT
-KCCATCT
```

Original motif   Consensus sequence: AGAGGGWG

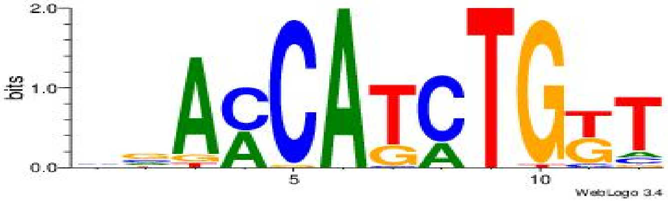
Reverse complement motif   Consensus sequence: CWCCCTCT



Dataset #: 3
Motif ID: 121
Motif name: TAL1TCF3
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 4
Number of overlap: 7
Similarity score: 0.034782

Alignment:
```
ARCAGATGRTVD
---AGATGGY--
```

Original motif Consensus sequence: HVAMCATCTGKT



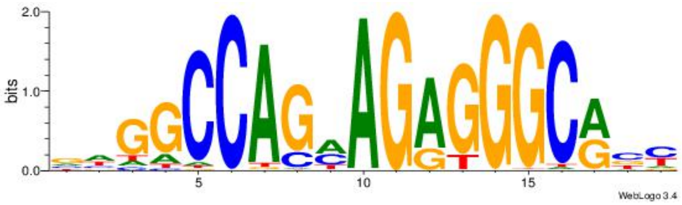
Reverse complement motif Consensus sequence: ARCAGATGRTVD

Dataset #: 4
Motif ID: 163
Motif name: gwGGCCAGmAGAGGGCrby
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 4
Number of overlap: 7

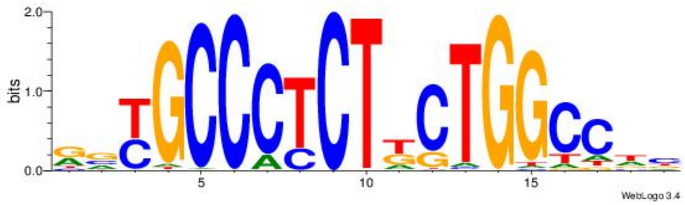
Similarity score:	0.0365189

Alignment:
VHGGCCAGMAGAGGGCRBY
---------AGATGGY---

Original motif Consensus sequence: VHGGCCAGMAGAGGGCRBY



Reverse complement motif Consensus sequence: KBKGCCCTCTYCTGGCCHV



Dataset #:	2
Motif ID:	46
Motif name:	Motif 46
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2
Number of overlap:	7
Similarity score:	0.0371728

Alignment:
AGRKGGCR
AGATGGY-

Original motif Consensus sequence: AGRKGGCR

Reverse complement motif Consensus sequence: KGCCYKCT

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:	7
Similarity score:	0.0375558

Alignment:

```
AGRKGGCR
AGATGGY-
```

Original motif Consensus sequence: AGRKGGCR

Reverse complement motif Consensus sequence: KGCCYKCT

Dataset #: 2 **Motif ID: 62** **Motif name: Motif 62**

Original motif   Consensus sequence: CGCCVCC

Reverse complement motif   Consensus sequence: GGVGGCG

Best Matches for Motif ID 62 (Highest to Lowest)

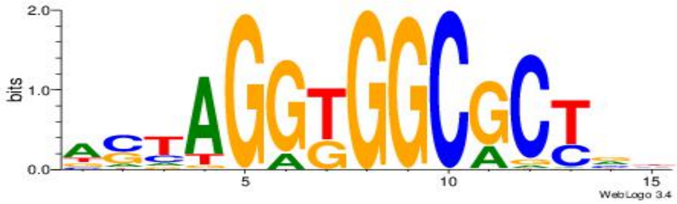
Dataset #:	4
Motif ID:	146
Motif name:	myrGYGCCmCCTast
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	5
Number of overlap:	7
Similarity score:	0.0315476

Alignment:

```
VBAGCGCCMCCTAST
----CGCCVCC----
```

Original motif   Consensus sequence: VBAGCGCCMCCTAST

Reverse complement motif   Consensus sequence: ASTAGGYGGCGCT



Dataset #:	1
Motif ID:	27
Motif name:	Motif 27
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:	0.0348335

Alignment:

```
CSGCCGCC
-CGCCVCC
```

Original motif Consensus sequence: CSGCCGCC

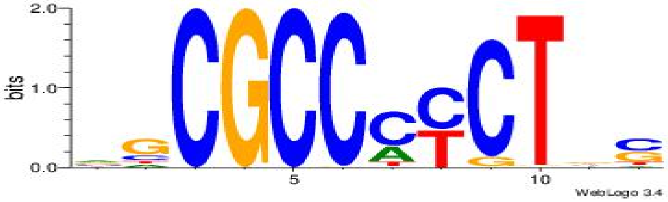
Reverse complement motif Consensus sequence: GGCGGCSG

Dataset #:	4
Motif ID:	137
Motif name:	rgCGCCmyCTgs
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	4
Number of overlap:	7

Similarity score: 0.0357527

Alignment:
SHAGKGGGCGCB
---GGVGGCG--

Original motif Consensus sequence: VGCGCCCYCTDS



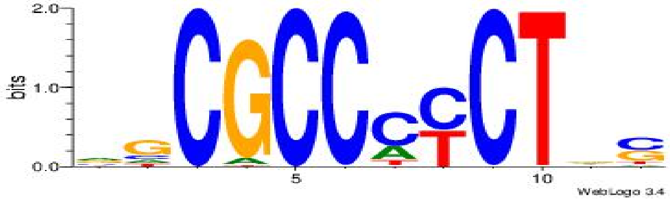
Reverse complement motif Consensus sequence: SHAGKGGGCGCB

Dataset #:	4
Motif ID:	153
Motif name:	scAGrkGGCGcy
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	3
Number of overlap:	7
Similarity score:	0.0403279

Alignment:
VGCGCCCMCTDS
--CGCCVCC---

Original motif Consensus sequence: SHAGRGGGCGCB

Reverse complement motif Consensus sequence: VGCGCCCMCTDS

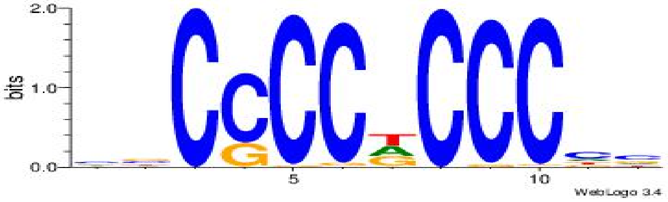


Dataset #:	4
Motif ID:	155
Motif name:	csCSCCdCCCcs
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	3
Number of overlap:	7
Similarity score:	0.0439081

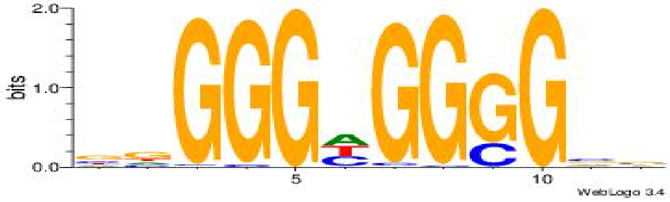
Alignment:

```
VBCCCCDCCCHV
--CGCCVCC---
```

Original motif   Consensus sequence: VBCCCCDCCCHV



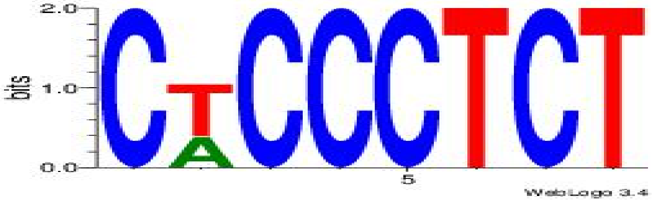
Reverse complement motif   Consensus sequence: VDGGGDGGGGBV



Dataset #: 2   Motif ID: 63   Motif name: Motif 63

Original motif Consensus sequence: AGAGGGWG

Reverse complement motif Consensus sequence: CWCCCTCT



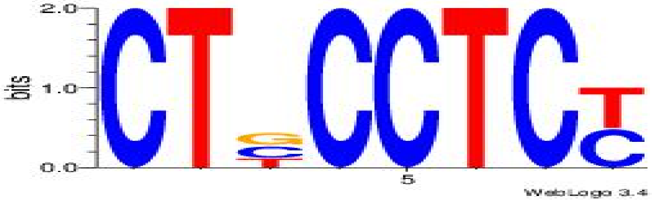
Best Matches for Motif ID 63 (Highest to Lowest)

Dataset #:	1
Motif ID:	11
Motif name:	Motif 11
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	8
Similarity score:	0.0323316

Alignment:

```
MGAGGBAG
AGAGGGWG
```

Original motif Consensus sequence: CTBCCTCY



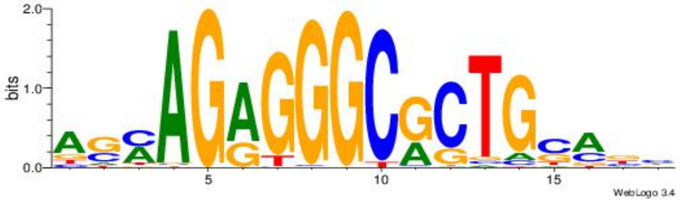
Reverse complement motif Consensus sequence: MGAGGBAG

Dataset #: 4
Motif ID: 149
Motif name: asmAGRGGGCrCTGsmkc
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 8
Number of overlap: 8
Similarity score: 0.040911

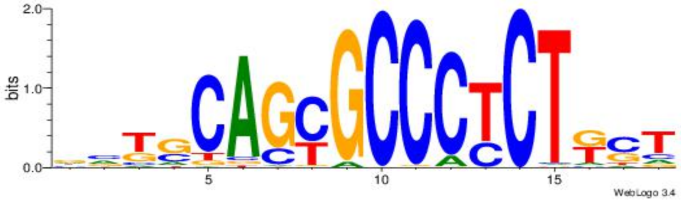
Alignment:

```
DBTSCAGMGCCCTCTRST
-------CWCCCTCT---
```

Original motif Consensus sequence: ASMAGAGGGCRCTGSABH



Reverse complement motif Consensus sequence: DBTSCAGMGCCCTCTRST



Dataset #: 4
Motif ID: 153
Motif name: scAGrkGGCGcy
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 3

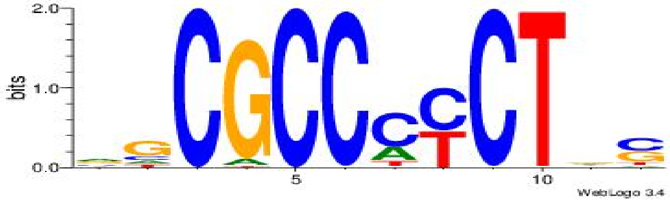
Number of overlap:	8
Similarity score:	0.0435349

Alignment:

```
SHAGRGGGCGCB
--AGAGGGWG--
```

Original motif Consensus sequence: SHAGRGGGCGCB

Reverse complement motif Consensus sequence: VGCGCCCMCTDS



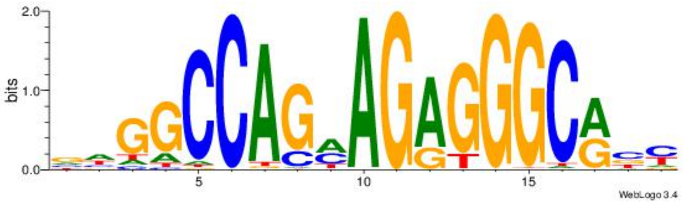
Dataset #:	4
Motif ID:	163
Motif name:	gwGGCCAGmAGAGGGCrby
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	3
Number of overlap:	8
Similarity score:	0.0462891

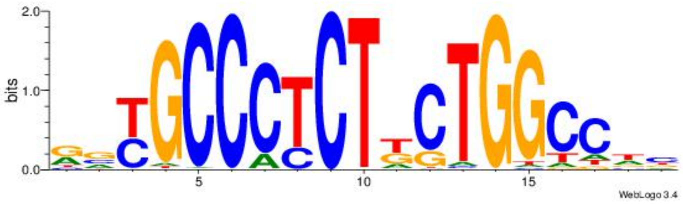
Alignment:

```
VHGGCCAGMAGAGGGCRBY
---------AGAGGGWG--
```

Original motif Consensus sequence: VHGGCCAGMAGAGGGCRBY

Reverse complement motif Consensus sequence: KBKGCCCTCTYCTGGCCHV





Dataset #:	4
Motif ID:	137
Motif name:	rgCGCCmyCTgs
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	3
Number of overlap:	8
Similarity score:	0.0481673

Alignment:

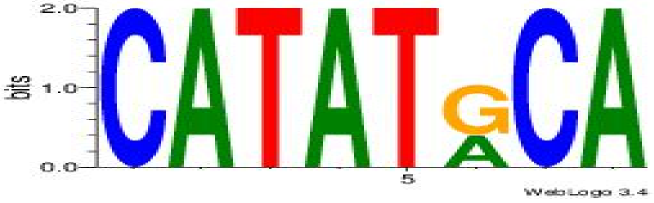
```
VGCGCCCYCTDS
--CWCCCTCT--
```

Original motif Consensus sequence: VGCGCCCYCTDS

Reverse complement motif Consensus sequence: SHAGKGGGCGCB

Dataset #: 2 Motif ID: 64 Motif name: Motif 64

Original motif Consensus sequence: CATATRCA



Reverse complement motif Consensus sequence: TGMATATG

Best Matches for Motif ID 64 (Highest to Lowest)

Dataset #:	1
Motif ID:	31
Motif name:	Motif 31
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:	0.0465487

Alignment:

```
CATGYACA
CATATRCA
```

Original motif Consensus sequence: CATGYACA

Reverse complement motif Consensus sequence: TGTKCATG

Dataset #: 1
Motif ID: 3
Motif name: Motif 3
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 8
Similarity score: 0.0585881

Alignment:

```
CACACACA
CATATRCA
```

Original motif Consensus sequence: CACACACA

Reverse complement motif Consensus sequence: TGTGTGTG

Dataset #: 2
Motif ID: 58
Motif name: Motif 58
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:	0.0607109

Alignment:

```
TACATGCA
CATATRCA
```

Original motif Consensus sequence: TACATGCA

Reverse complement motif Consensus sequence: TGCATGTA

Dataset #:	4
Motif ID:	152
Motif name:	yrCATGCAyr
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:	0.0626249

Alignment:

```
BRCATGCABD
CATATRCA--
```

Original motif Consensus sequence: BRCATGCABD

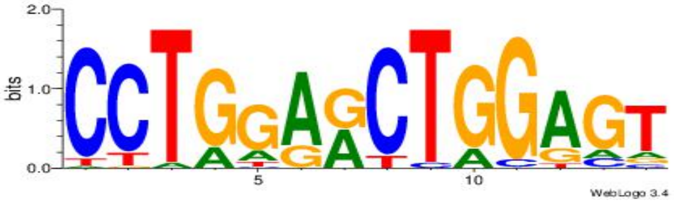
Reverse complement motif Consensus sequence: HVTGCATGKV

Dataset #:	2
Motif ID:	69
Motif name:	Motif 69
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	5
Number of overlap:	8
Similarity score:	0.0676075

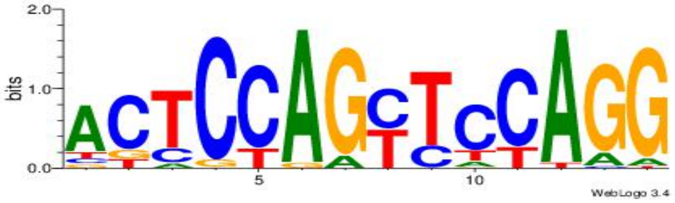
Alignment:

```
ACTCCAGMTCCAGG
----CATATRCA--
```

Original motif Consensus sequence: CCTGGARCTGGAGT



Reverse complement motif Consensus sequence: ACTCCAGMTCCAG



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

Original motif Consensus sequence: ARAACA

Reverse complement motif Consensus sequence: TGTTMT

Best Matches for 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

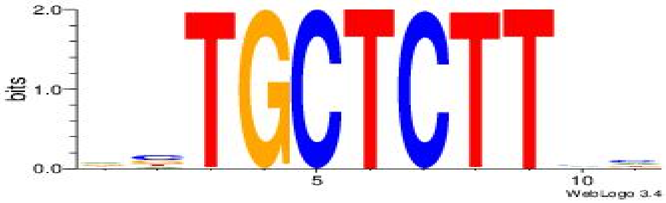
Similarity score: 0.0232212

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

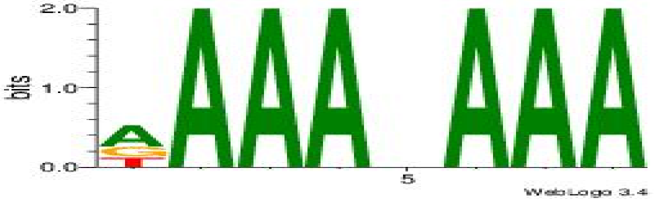
Reverse complement motif Consensus sequence: ARCAGATGRTVD

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

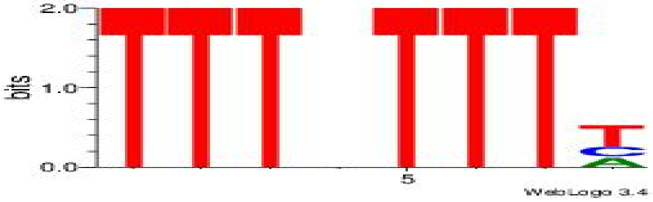
Alignment:

```
AAAAHAAA
ARAACA--
```

Original motif Consensus sequence: AAAAHAAA

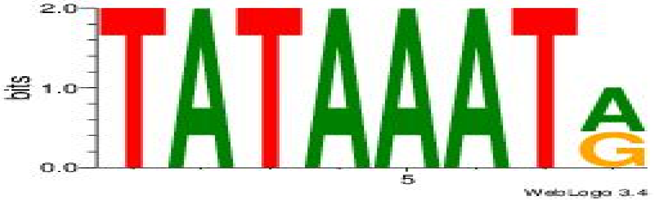


Reverse complement motif Consensus sequence: TTTDTTTT

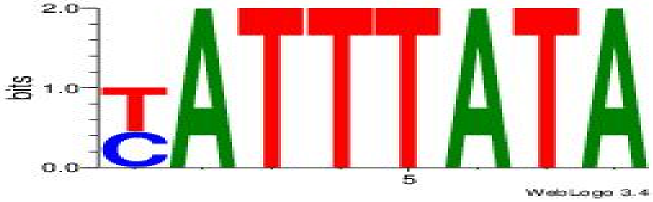


Dataset #: 2 **Motif ID: 66** **Motif name: Motif 66**

Original motif Consensus sequence: TATAAATR



Reverse complement motif Consensus sequence: KATTTATA



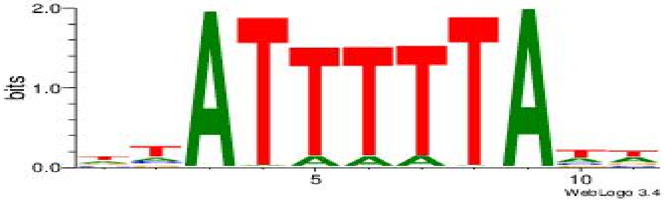
Best Matches for Motif ID 66 (Highest to Lowest)

Dataset #:	4
Motif ID:	157
Motif name:	wtATTTTTAww
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:	0.00950221

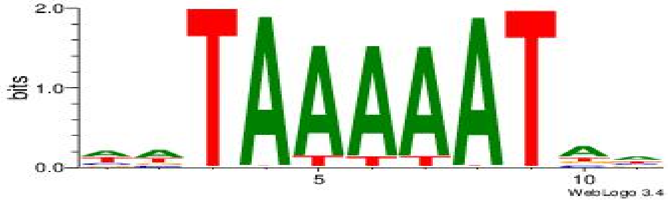
Alignment:

```
WWTAAAAATAD
--TATAAATR-
```

Original motif Consensus sequence: DTATTTTTAWW



Reverse complement motif Consensus sequence: WWTAAAAATAD

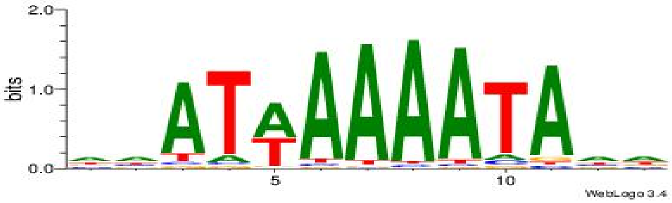


Dataset #:	4
Motif ID:	150
Motif name:	waATwAAAATAww
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	4
Number of overlap:	8
Similarity score:	0.0358566

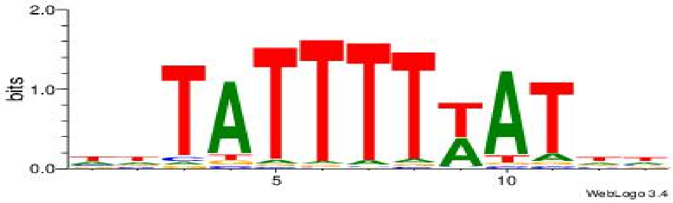
Alignment:

```
DHATWAAAATAHD
---TATAAATR--
```

Original motif Consensus sequence: DHATWAAAATAHD



Reverse complement motif Consensus sequence: DHTATTTTWATHD



Dataset #:	1
Motif ID:	38
Motif name:	Motif 38
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: 0.0432007

Alignment:
TGTAACTC
TATAAATR

Original motif Consensus sequence: GAGTTACA

Reverse complement motif Consensus sequence: TGTAACTC

Dataset #: 2
Motif ID: 51
Motif name: Motif 51
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: 0.0432007

Alignment:
TGTAACTC
TATAAATR

Original motif Consensus sequence: GAGTTACA

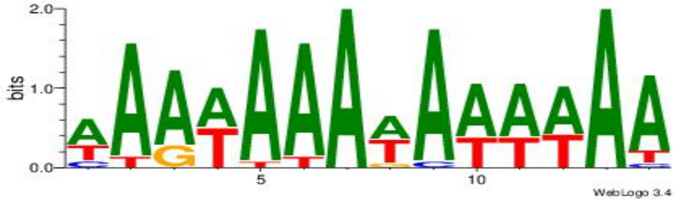
Reverse complement motif Consensus sequence: TGTAACTC

Dataset #:	2
Motif ID:	68
Motif name:	Motif 68
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	6
Number of overlap:	8
Similarity score:	0.0496717

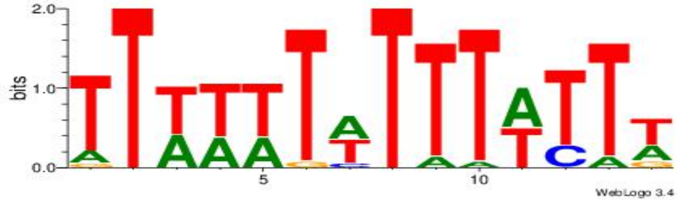
Alignment:

```
WAAWAAAWAWWWAA
-TATAAATR-----
```

Original motif Consensus sequence: WAAWAAAWAWWWAA

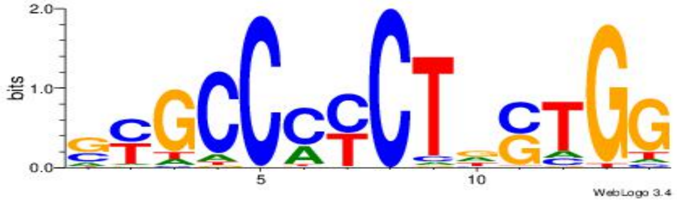


Reverse complement motif Consensus sequence: TTWWWTWTTTWTTW

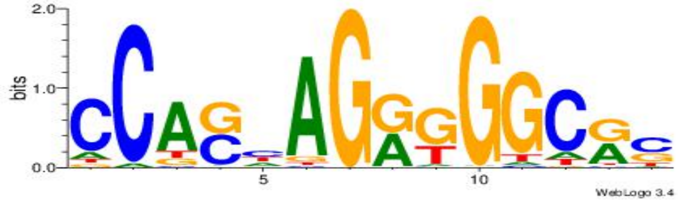


Dataset #: 2 **Motif ID: 67** **Motif name: Motif 67**

Original motif Consensus sequence: SYGCCCYCTDSTGG



Reverse complement motif Consensus sequence: CCASHAGKGGGC



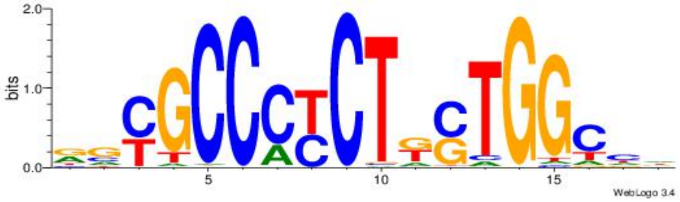
Best Matches for Motif ID 67 (Highest to Lowest)

Dataset #:	4
Motif ID:	156
Motif name:	rgyGCCMyCTksTGGccd
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	4
Number of overlap:	14
Similarity score:	0

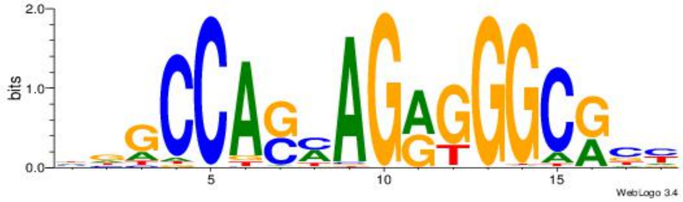
Alignment:

```
RVYGCCCYCTKSTGGCHD
-SYGCCCYCTDSTGG---
```

Original motif Consensus sequence: RVYGCCCYCTKSTGGCHD



Reverse complement motif Consensus sequence: DDGCCASYAGMGGGCKVM

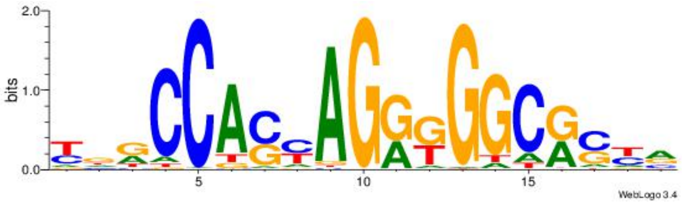


Dataset #:	3
Motif ID:	74
Motif name:	CTCF
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	3
Number of overlap:	14
Similarity score:	0.0137353

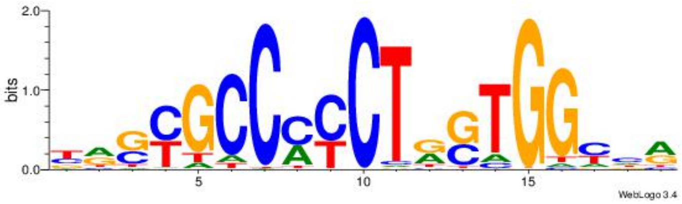
Alignment:

```
BMSMGCCYMCTKSTGGMHM
--SYGCCCYCTDSTGG---
```

Original motif Consensus sequence: YDRCCASYAGRKGGCRSYV



Reverse complement motif Consensus sequence: BMSMGCCYMCTKSTGGMHM



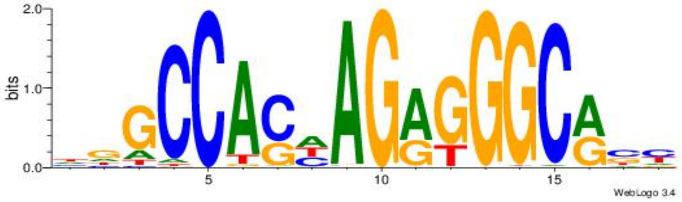
Dataset #:	4
Motif ID:	165
Motif name:	wgGCCAshAGrGGGCrsy
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	4

Number of overlap:	14
Similarity score:	0.0259772

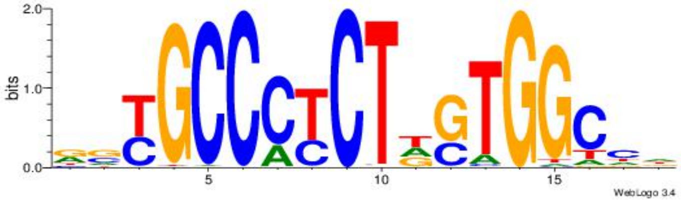
Alignment:

```
HDGCCACHAGRGGGCRBY
---CCASHAGKGGGCKS-
```

Original motif Consensus sequence: HDGCCACHAGRGGGCRBY



Reverse complement motif Consensus sequence: KBKGCCCKCTHGTGGCHH

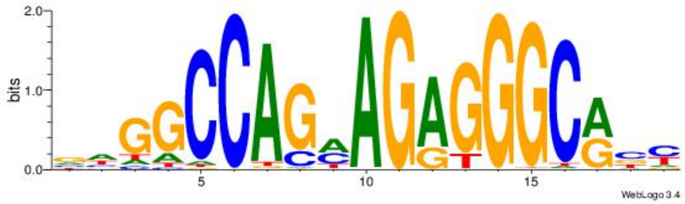


Dataset #:	4
Motif ID:	163
Motif name:	gwGGCCAGmAGAGGGCrby
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2
Number of overlap:	14
Similarity score:	0.0316372

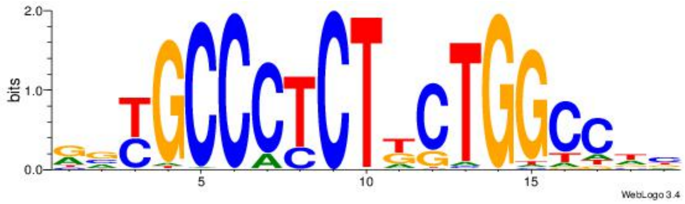
Alignment:

```
VHGGCCAGMAGAGGGCRBY
----CCASHAGKGGGCKS-
```

Original motif Consensus sequence: VHGGCCAGMAGAGGGCRBY



Reverse complement motif Consensus sequence: KBKGCCCTCTYCTGGCCHV

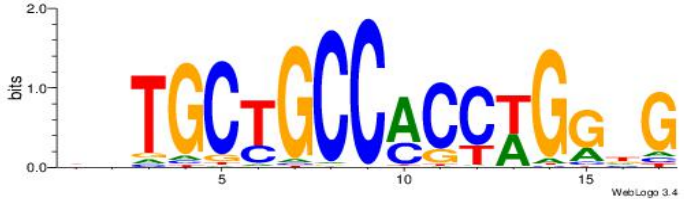


Dataset #:	4
Motif ID:	169
Motif name:	yvTGCyGCCmCCwGgtG
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	3
Number of overlap:	14
Similarity score:	0.0786902

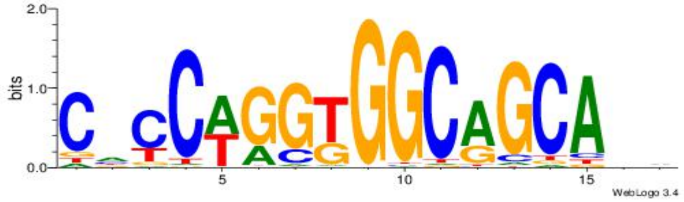
Alignment:

```
BVTGCTGCCACCWGGDG
-SYGCCCYCTDSTGG--
```

Original motif Consensus sequence: BVTGCTGCCACCWGGDG

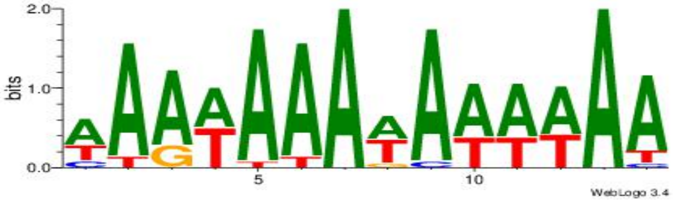


Reverse complement motif Consensus sequence: CDCCWGGTGGCAGCAVV

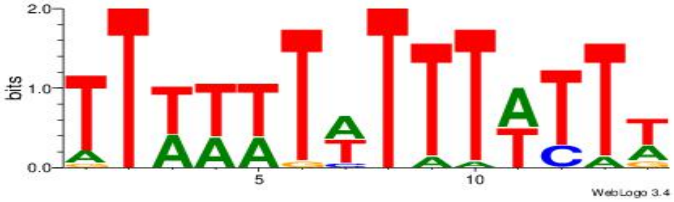


Dataset #: 2 Motif ID: 68 Motif name: Motif 68

Original motif Consensus sequence: WAAWAAAWAWWWAA



Reverse complement motif Consensus sequence: TTWWWTWTTTWTTW



Best Matches for Motif ID 68 (Highest to Lowest)

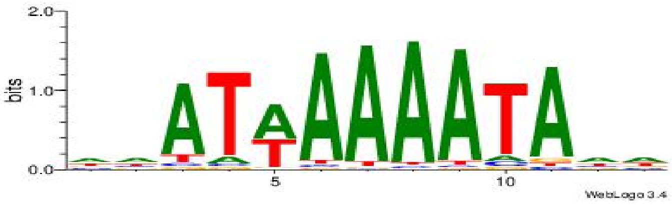
Dataset #:	4
Motif ID:	150
Motif name:	waATwAAAATAww
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	13
Similarity score:	0.0423083

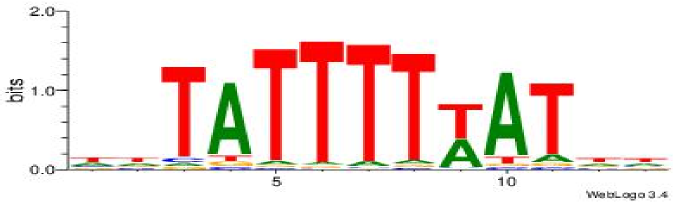
Alignment:

```
-DHTATTTTWATHD
TTWWWTWTTTWTTW
```

Original motif Consensus sequence: DHATWAAAATAHD

Reverse complement motif Consensus sequence: DHTATTTTWATHD



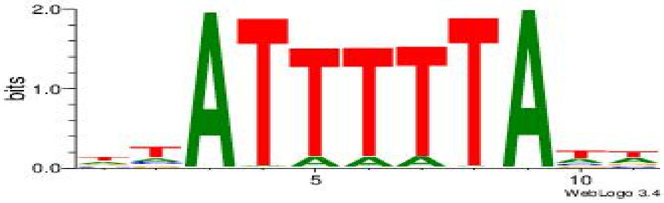


Dataset #:	4
Motif ID:	157
Motif name:	wtATTTTTAww
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	11
Similarity score:	1.06057

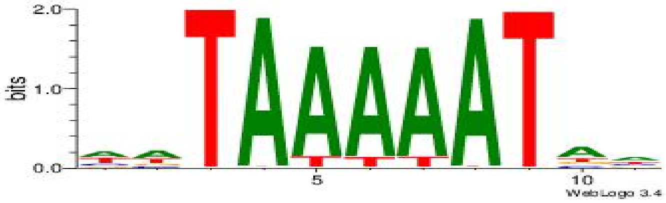
Alignment:

```
DTATTTTTAWW---
TTWWWTWTTTWTTW
```

Original motif Consensus sequence: DTATTTTTAWW



Reverse complement motif Consensus sequence: WWTAAAAATAD

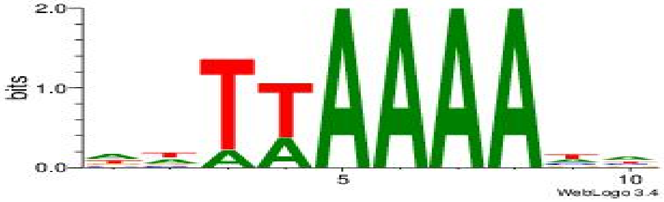


Dataset #:	4
Motif ID:	148

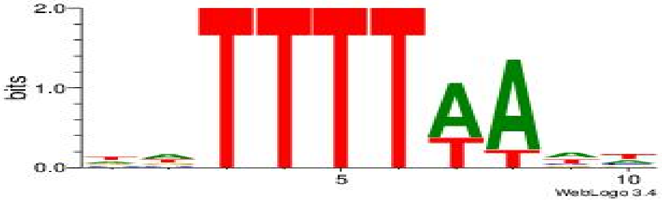
Motif name: wwTwAAAAww
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 10
Similarity score: 1.54726

Alignment:
DDTWAAAAHH----
WAAWAAAWAWWWAA

Original motif Consensus sequence: DDTWAAAAHH



Reverse complement motif Consensus sequence: HHTTTTWADD



Dataset #: 4
Motif ID: 141
Motif name: raCAAAACam
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 10
Similarity score: 1.55678

Alignment:

```
----HTGTTTTGTD
TTWWWTWTTTWTTW
```

Original motif Consensus sequence: DACAAAACAH

Reverse complement motif Consensus sequence: HTGTTTTGTD

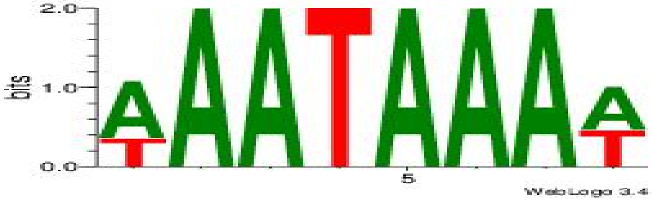
Dataset #:	2
Motif ID:	52
Motif name:	Motif 52
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	8
Similarity score:	2.5

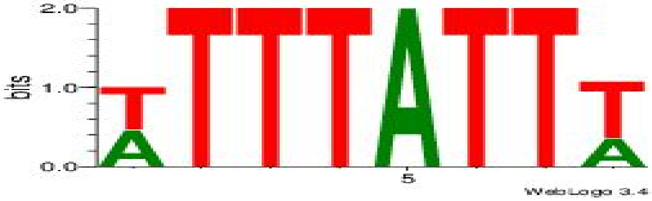
Alignment:

```
------WTTTATTT
TTWWWTWTTTWTTW
```

Original motif Consensus sequence: AAATAAAW

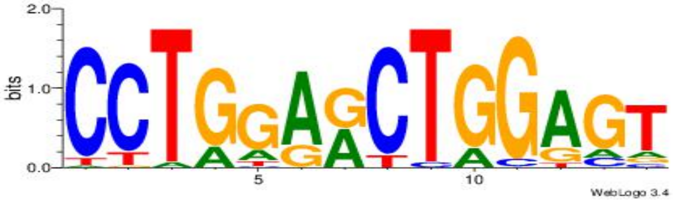
Reverse complement motif Consensus sequence: WTTTATTT



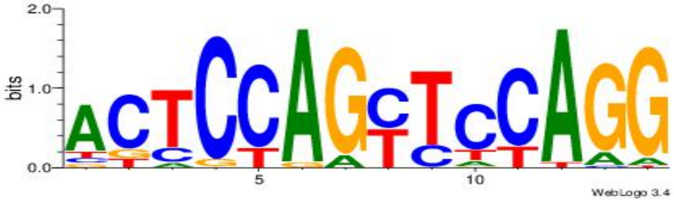


Dataset #: 2 **Motif ID: 69** **Motif name: Motif 69**

Original motif Consensus sequence: CCTGGARCTGGAGT



Reverse complement motif Consensus sequence: ACTCCAGMTCCAG



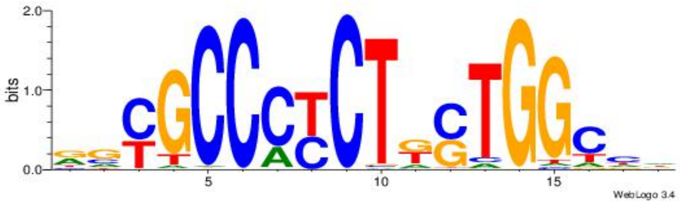
Best Matches for Motif ID 69 (Highest to Lowest)

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:	1
Number of overlap:	14
Similarity score:	0.070946

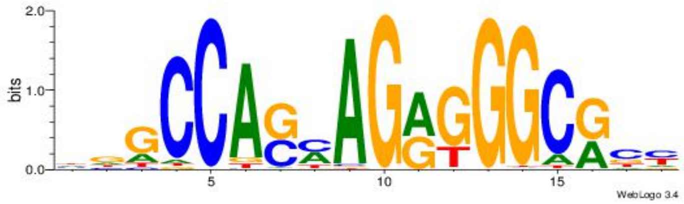
Alignment:

```
DDGCCASYAGMGGGCKVM
ACTCCAGMTCCAGG----
```

Original motif Consensus sequence: RVYGCCCYCTKSTGGCHD



Reverse complement motif Consensus sequence: DDGCCASYAGMGGGCKVM

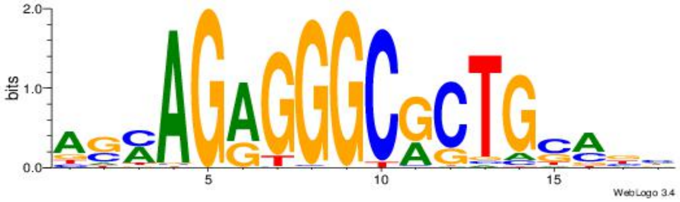


Dataset #:	4
Motif ID:	149
Motif name:	asmAGRGGGCrCTGsmkc
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	5
Number of overlap:	14
Similarity score:	0.073647

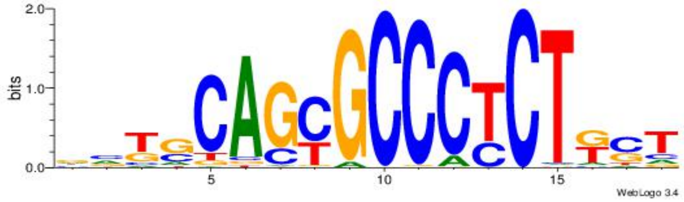
Alignment:

```
DBTSCAGMGCCCTCTRST
ACTCCAGMTCCAGG----
```

Original motif Consensus sequence: ASMAGAGGGCRCTGSABH



Reverse complement motif Consensus sequence: DBTSCAGMGCCCTCTRST

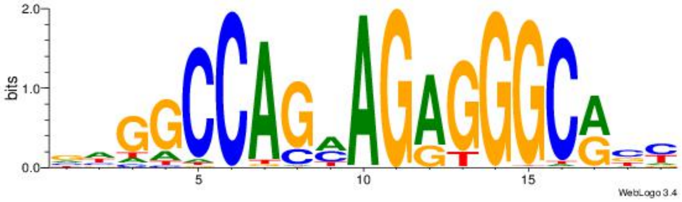


Dataset #: 4
Motif ID: 163
Motif name: gwGGCCAGmAGAGGGCrby
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 2
Number of overlap: 14
Similarity score: 0.0761843

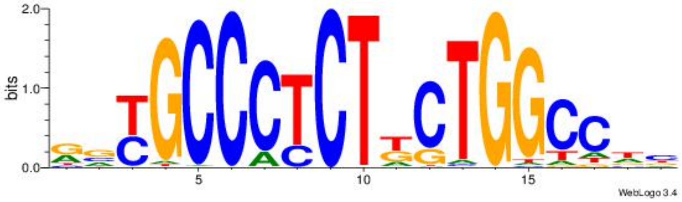
Alignment:

```
VHGGCCAGMAGAGGGCRBY
-ACTCCAGMTCCAGG----
```

Original motif Consensus sequence: VHGGCCAGMAGAGGGCRBY



Reverse complement motif Consensus sequence: KBKGCCCTCTYCTGGCCHV



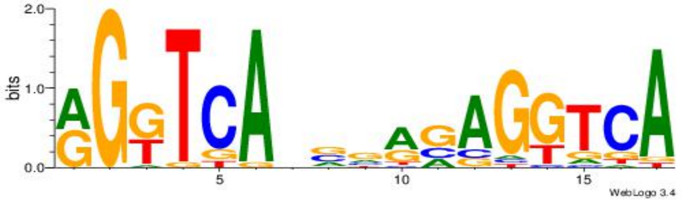
Dataset #: 3
Motif ID: 115
Motif name: RXRRAR_DR5
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1

Number of overlap:	14
Similarity score:	0.0775577

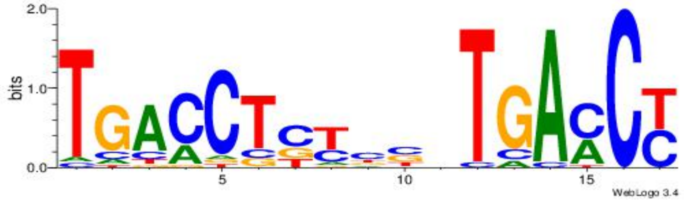
Alignment:

```
RGKTCABVVRGAGGTCA
ACTCCAGMTCCAGG---
```

Original motif Consensus sequence: RGKTCABVVRGAGGTCA



Reverse complement motif Consensus sequence: TGACCTCKVVBTGAYCK



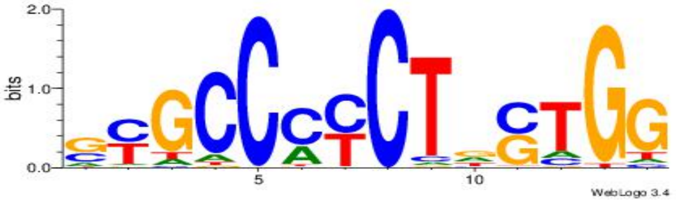
Dataset #:	2
Motif ID:	67
Motif name:	Motif 67
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	14
Similarity score:	0.0806144

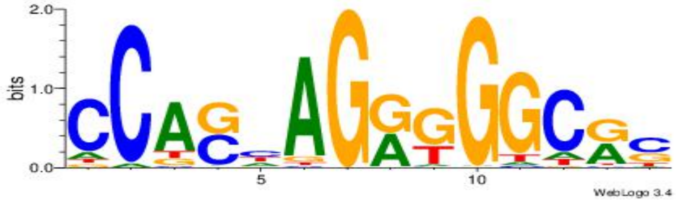
Alignment:

```
CCASHAGKGGGCKS
CCTGGARCTGGAGT
```

Original motif Consensus sequence: SYGCCCYCTDSTGG

Reverse complement motif Consensus sequence: CCASHAGKGGGCK

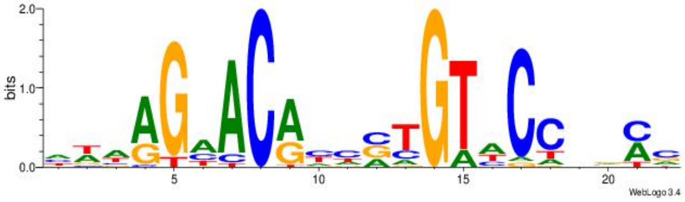


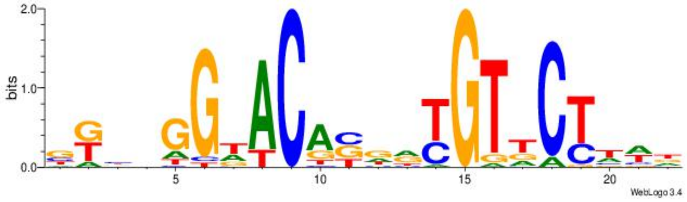


Dataset #: 3 **Motif ID: 70** **Motif name: Ar**

Original motif Consensus sequence: HWDAGHACRHHVTGTHCCHVMV

Reverse complement motif Consensus sequence: VRVDGGHACAVDDKGTHCTDWH





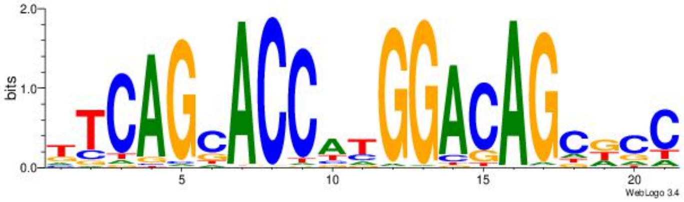
Best Matches for Motif ID 70 (Highest to Lowest)

Dataset #:	3
Motif ID:	113
Motif name:	REST
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	21
Similarity score:	0.0696331

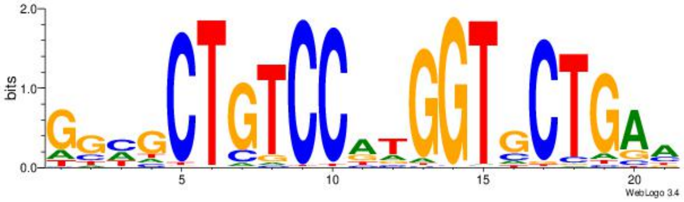
Alignment:

```
-GGYGCTGTCCATGGTGCTGAA
VRVDGGHACAVDDKGTHCTDWH
```

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC



Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA



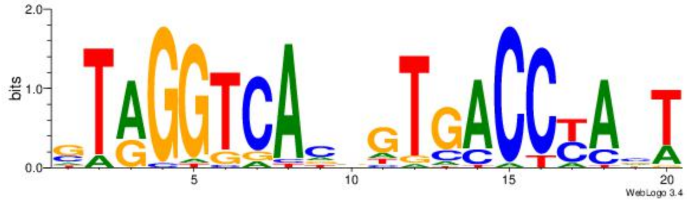
Dataset #:	3
Motif ID:	111
Motif name:	PPARG
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	20
Similarity score:	0.55978

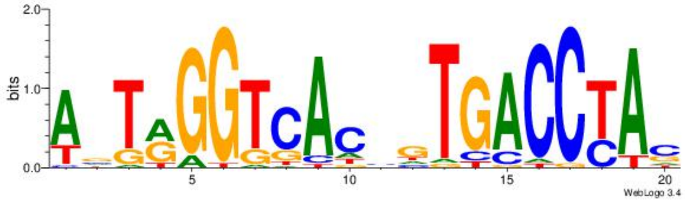
Alignment:

```
--STAGGTCACBGTGACCYABT
VRVDGGHACAVDDKGTHCTDWH
```

Original motif Consensus sequence: STAGGTCACBGTGACCYABT

Reverse complement motif Consensus sequence: ABTMGGTCACBGTGACCTAS



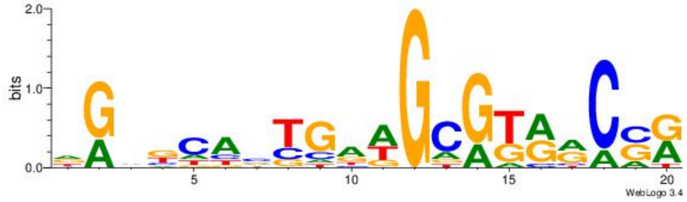


Dataset #: 3
Motif ID: 109
Motif name: Pax5
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 20
Similarity score: 0.564914

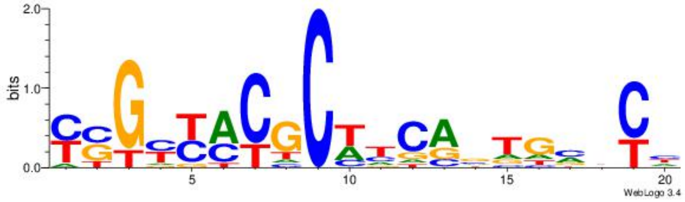
Alignment:

```
--MSGKKRCGCWDCABTGBBCD
VRVDGGHACAVDDKGTHCTDWH
```

Original motif Consensus sequence: DGVBCABTGDWGCGKRRCSR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD



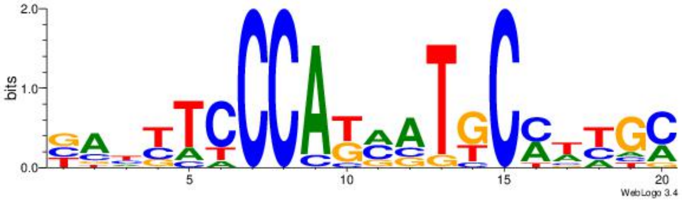
Dataset #: 3

Motif ID:	131
Motif name:	znf143
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	20
Similarity score:	0.566373

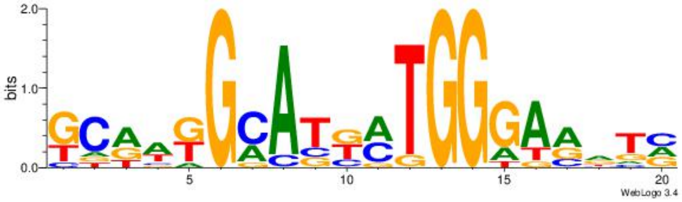
Alignment:

```
GCMWRGCATYRTGGGAMHTB--
VRVDGGHACAVDDKGTHCTDWH
```

Original motif Consensus sequence: BAHYTCCCAKMATGCMWYGC



Reverse complement motif Consensus sequence: GCMWRGCATYRTGGGAMHTB



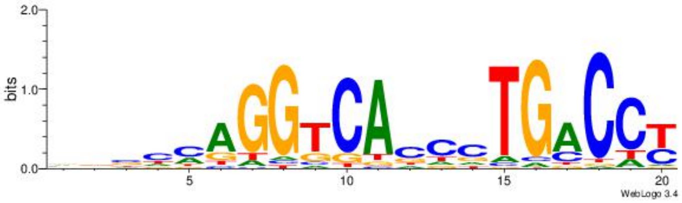
Dataset #:	3
Motif ID:	81
Motif name:	ESR1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	19

Similarity score:	1.05195

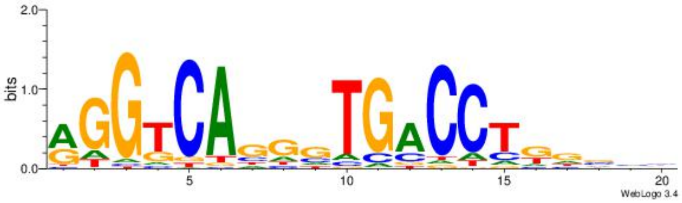
Alignment:

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

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV



Dataset #: 3 Motif ID: 71 Motif name: Arnt

Original motif Consensus sequence: CACGTG

Reverse complement motif Consensus sequence: CACGTG

Best Matches for Motif ID 71 (Highest to Lowest)

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

Alignment:

MACGTG
CACGTG

Original motif Consensus sequence: CACGTR

Reverse complement motif Consensus sequence: MACGTG

Dataset #:	3
Motif ID:	91
Motif name:	MAX
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:	0.00380329

Alignment:

BCACGTGDTD
-CACGTG---

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:	Backward
Position number:	1
Number of overlap:	6
Similarity score:	0.00445689

Alignment:

```
MCACGTG
-CACGTG
```

Original motif Consensus sequence: CACGTGR

Reverse complement motif Consensus sequence: MCACGTG

Dataset #: 3
Motif ID: 95
Motif name: MYCMAX
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 3
Number of overlap: 6
Similarity score: 0.00495292

Alignment:

```
RASCACGTGGT
---CACGTG--
```

Original motif Consensus sequence: RASCACGTGGT

Reverse complement motif Consensus sequence: ACCACGTGSTM

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

Similarity score:	0.0173209

Alignment:
DCCACGTGCV
--CACGTG--

Original motif Consensus sequence: VGCACGTGGH

Reverse complement motif Consensus sequence: DCCACGTGCV

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

Original motif Consensus sequence: YGCGTG

Reverse complement motif Consensus sequence: CACGCM

Best Matches for Motif ID 72 (Highest to Lowest)

Dataset #:	3
Motif ID:	86
Motif name:	HIF1AARNT
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward

Position number: 2
Number of overlap: 6
Similarity score: 0

Alignment:
```
VBACGTGV
-YGCGTG-
```

Original motif Consensus sequence: VBACGTGV

Reverse complement motif Consensus sequence: VCACGTBV

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 #:	3
Motif ID:	71
Motif name:	Arnt
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	6
Similarity score:	0.0203526

Alignment:

```
CACGTG
YGCGTG
```

Original motif Consensus sequence: CACGTG

Reverse complement motif Consensus sequence: CACGTG

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 #: 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: 0.0255609

Alignment:

```
MCACGTG
-YGCGTG
```

Original motif Consensus sequence: CACGTGR

Reverse complement motif Consensus sequence: MCACGTG

Dataset #: 3 **Motif ID: 73** **Motif name: CREB1**

Original motif Consensus sequence: TGACGTCA

Reverse complement motif Consensus sequence: TGACGTCA

Best Matches for Motif ID 73 (Highest to Lowest)

Dataset #:	3
Motif ID:	92
Motif name:	MIZF
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: 0.00956439

Alignment:

```
GCGGACGTTV
--TGACGTCA
```

Original motif Consensus sequence: BAACGTCCGC

Reverse complement motif Consensus sequence: GCGGACGTTV

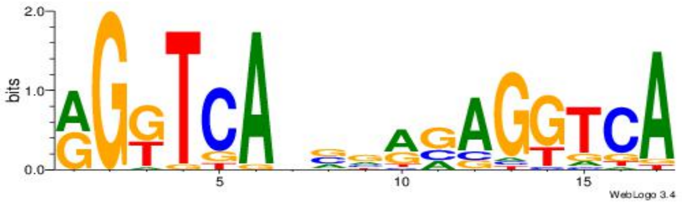
Dataset #: 3
Motif ID: 115
Motif name: RXRRAR_DR5
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 10
Number of overlap: 8
Similarity score: 0.0133811

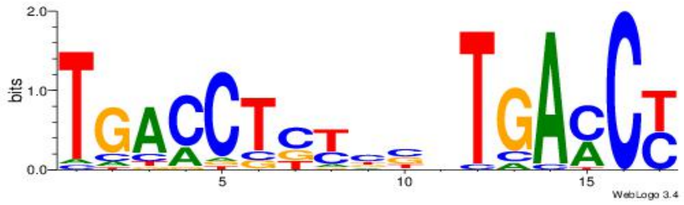
Alignment:

```
TGACCTCKVVBTGAYCK
TGACGTCA---------
```

Original motif Consensus sequence: RGKTCABVVRGAGGTCA

Reverse complement motif Consensus sequence: TGACCTCKVVBTGAYCK



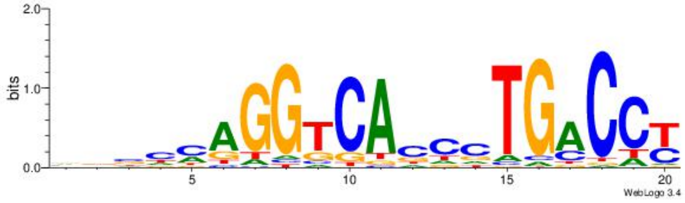


Dataset #:	3
Motif ID:	81
Motif name:	ESR1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	4
Number of overlap:	8
Similarity score:	0.0197902

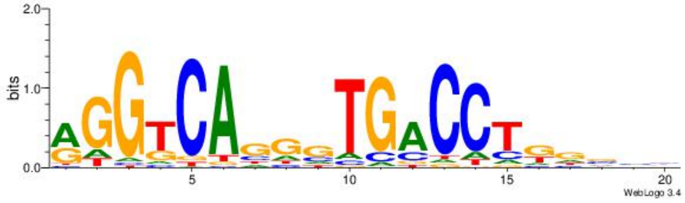
Alignment:

```
VDBHMAGGTCACCCTGACCY
---TGACGTCA---------
```

Original motif   Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif   Consensus sequence: MGGTCAGGGTGACCTRDBHV



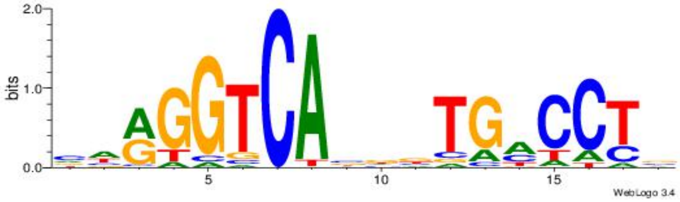
Dataset #:	3

Motif ID:	82
Motif name:	ESR2
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:	0.0208174

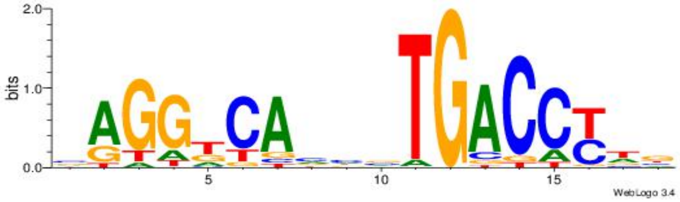
Alignment:

```
BAGGYCABHBTGACCKHV
----------TGACGTCA
```

Original motif Consensus sequence: VHRGGTCABDBTGMCCTB



Reverse complement motif Consensus sequence: BAGGYCABHBTGACCKHV



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:	1
Number of overlap:	8

Similarity score: 0.0253747

Alignment:

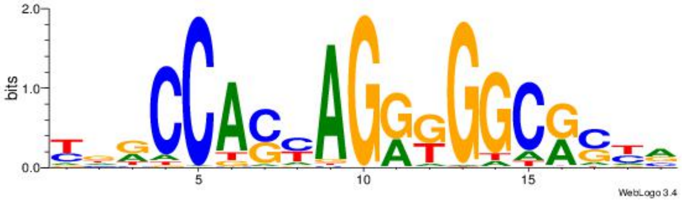
```
TGKCCACA
TGACGTCA
```

Original motif Consensus sequence: TGKCCACA

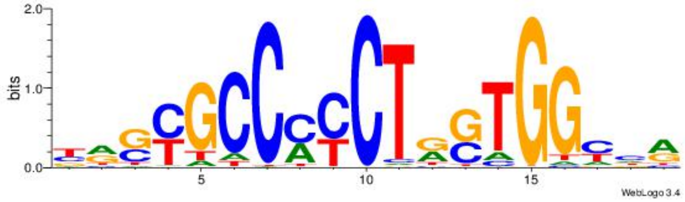
Reverse complement motif Consensus sequence: TGTGGYCA

Dataset #: 3 Motif ID: 74 Motif name: CTCF

Original motif Consensus sequence: YDRCCASYAGRKGGCRSYV



Reverse complement motif Consensus sequence: BMSMGCCYMCTKSTGGMHM



Best Matches for Motif ID 74 (Highest to Lowest)

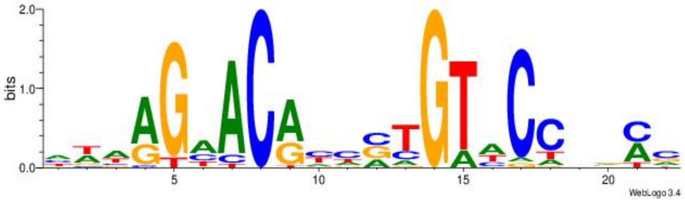
Dataset #:	3
Motif ID:	70
Motif name:	Ar
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif

Direction:	Forward
Position number:	3
Number of overlap:	19
Similarity score:	0.0903626

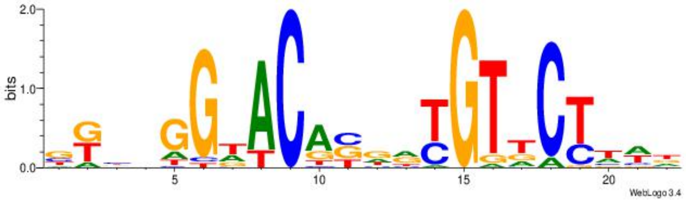
Alignment:

HWDAGHACRHHVTGTHCCHVMV
--BMSMGCCYMCTKSTGGMHM-

Original motif   Consensus sequence: HWDAGHACRHHVTGTHCCHVMV



Reverse complement motif   Consensus sequence: VRVDGGHACAVDDKGTHCTDWH

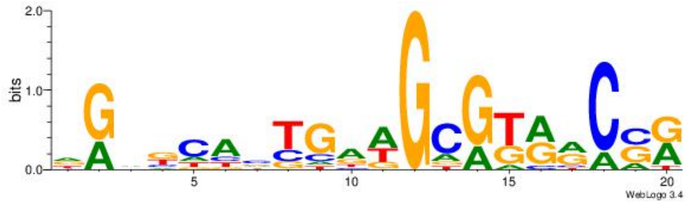


Dataset #:	3
Motif ID:	109
Motif name:	Pax5
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	19
Similarity score:	0.0909586

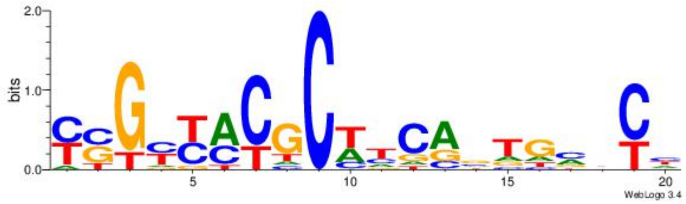
Alignment:

DGVBCABTGDWGCGKRRCSR
YDRCCASYAGRKGGCRSYV-

Original motif Consensus sequence: DGVBCABTGDWGCGKRRCSR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD

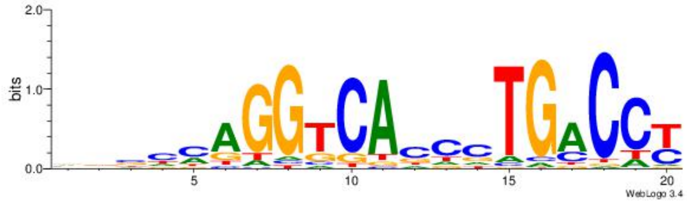


Dataset #:	3
Motif ID:	81
Motif name:	ESR1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	19
Similarity score:	0.0943322

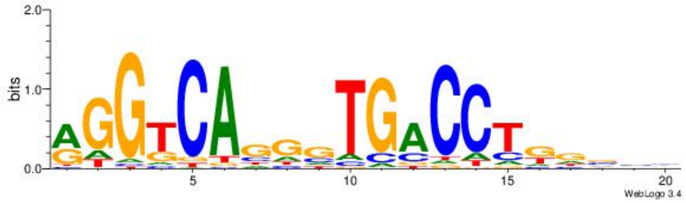
Alignment:

```
VDBHMAGGTCACCCTGACCY
-BMSMGCCYMCTKSTGGMHM
```

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



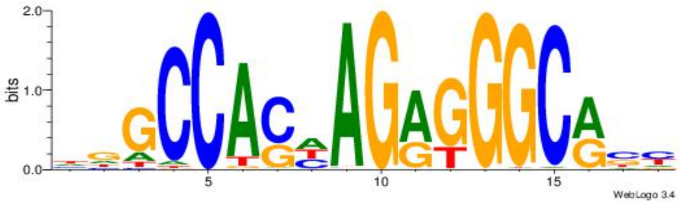
Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV



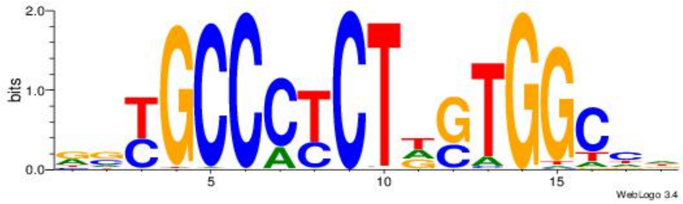
Dataset #: 4
Motif ID: 165
Motif name: wgGCCAshAGrGGGCrsy
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 18
Similarity score: 0.504548

Alignment:
```
HDGCCACHAGRGGGCRBY-
YDRCCASYAGRKGGCRSYV
```

Original motif Consensus sequence: HDGCCACHAGRGGGCRBY



Reverse complement motif Consensus sequence: KBKGCCCKCTHGTGGCHH



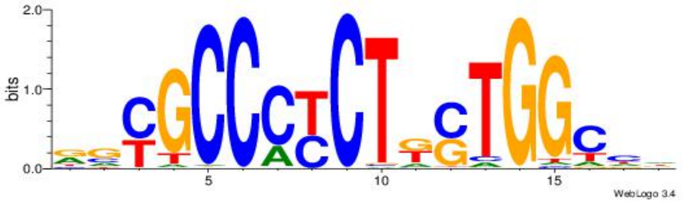
Dataset #: 4
Motif ID: 156
Motif name: rgyGCCMyCTksTGGccd
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1

Number of overlap:	18
Similarity score:	0.515938

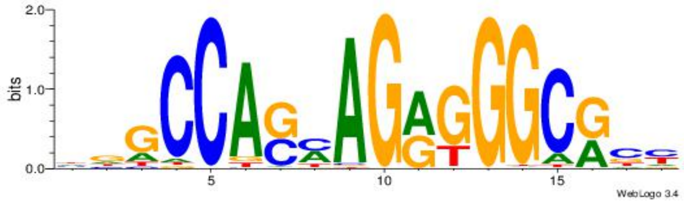
Alignment:

```
-RVYGCCCYCTKSTGGCHD
BMSMGCCYMCTKSTGGMHM
```

Original motif Consensus sequence: RVYGCCCYCTKSTGGCHD

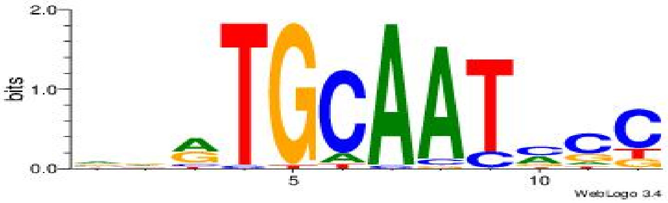


Reverse complement motif Consensus sequence: DDGCCASYAGMGGGCKVM



Dataset #: 3 Motif ID: 75 Motif name: Ddit3Cebpa

Original motif Consensus sequence: VDRTGCAATMCC



Reverse complement motif Consensus sequence: GGRATTGCAKHB

Best Matches for Motif ID 75 (Highest to Lowest)

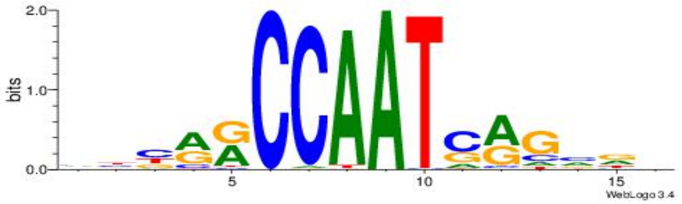
Dataset #:	3
Motif ID:	104
Motif name:	NFYA
Matching format of first motif:	Reverse Complement

Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 2
Number of overlap: 12
Similarity score: 0.018401

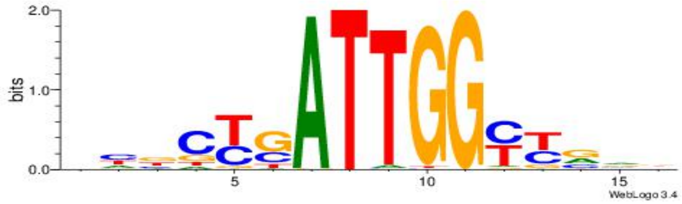
Alignment:

```
BHVCKSATTGGMKBVV
---GGRATTGCAKHB-
```

Original motif Consensus sequence: VBBRRCCAATSRGVDB



Reverse complement motif Consensus sequence: BHVCKSATTGGMKBVV

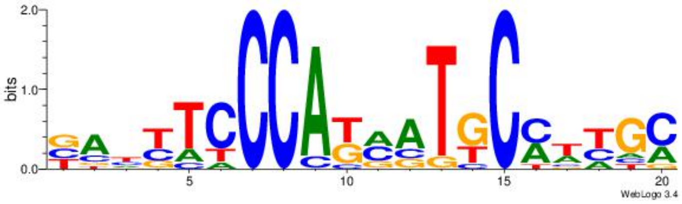


Dataset #: 3
Motif ID: 131
Motif name: znf143
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 9
Number of overlap: 12
Similarity score: 0.037862

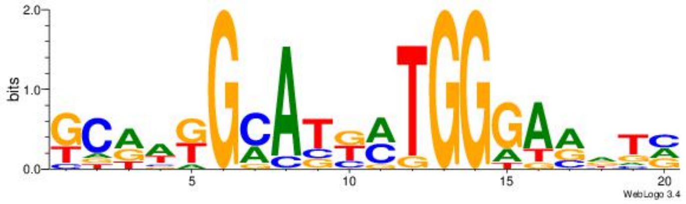
Alignment:

BAHYTCCCAKMATGCMWYGC
GGRATTGCAKHB--------

Original motif Consensus sequence: BAHYTCCCAKMATGCMWYGC



Reverse complement motif Consensus sequence: GCMWRGCATYRTGGGAMHTB

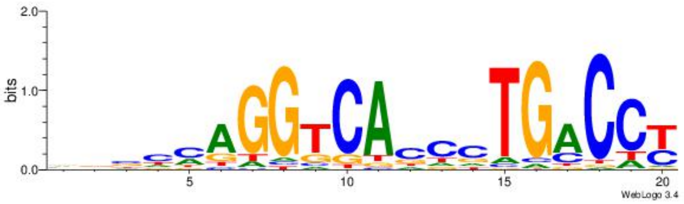


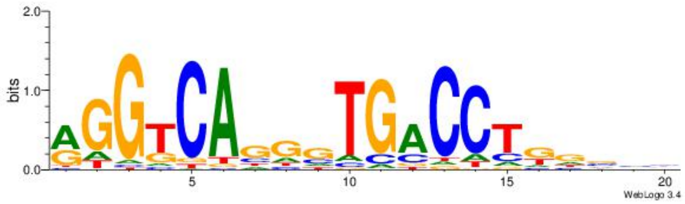
Dataset #:	3
Motif ID:	81
Motif name:	ESR1
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	3
Number of overlap:	12
Similarity score:	0.0416577

Alignment:
MGGTCAGGGTGACCTRDBHV
------VDRTGCAATMCC--

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY

Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV



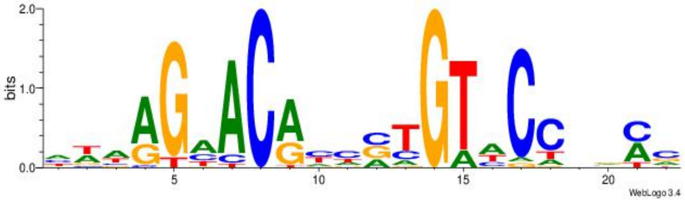


Dataset #:	3
Motif ID:	70
Motif name:	Ar
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	12
Similarity score:	0.0468764

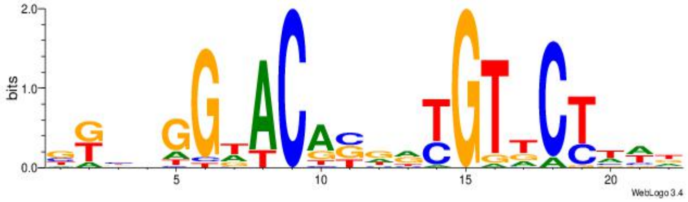
Alignment:

```
HWDAGHACRHHVTGTHCCHVMV
----------GGRATTGCAKHB
```

Original motif Consensus sequence: HWDAGHACRHHVTGTHCCHVMV



Reverse complement motif Consensus sequence: VRVDGGHACAVDDKGTHCTDWH



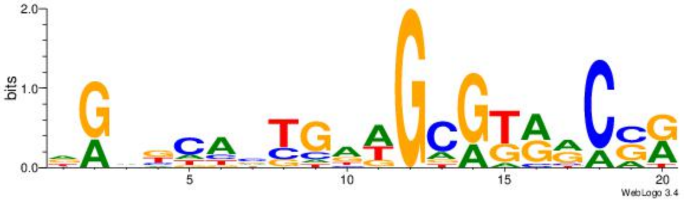
Dataset #:	3

Motif ID:	109
Motif name:	Pax5
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	8
Number of overlap:	12
Similarity score:	0.0480116

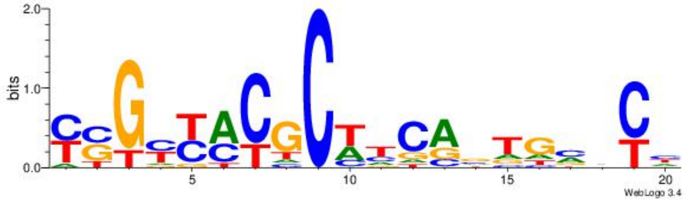
Alignment:

```
DGVBCABTGDWGCGKRRCSR
-------VDRTGCAATMCC-
```

Original motif Consensus sequence: DGVBCABTGDWGCGKRRCSR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD



Dataset #: 3 **Motif ID: 76** **Motif name: E2F1**

Original motif Consensus sequence: TTTSGCGC

Reverse complement motif Consensus sequence: GCGCSAAA

Best Matches for Motif ID 76 (Highest to Lowest)

Dataset #:	3
Motif ID:	78
Motif name:	Egr1
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	8
Similarity score:	0

Alignment:

```
TTTSGCGC
TTTSGCGC
```

Original motif Consensus sequence: TTTSGCGC

Reverse complement motif Consensus sequence: GCGCSAAA

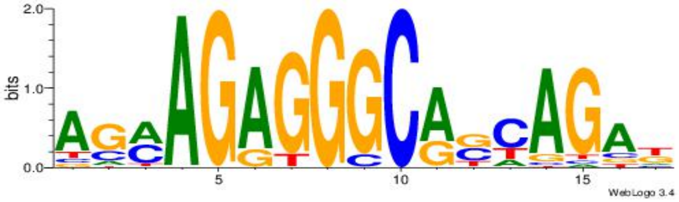
Dataset #:	4
Motif ID:	143
Motif name:	AgmAGAGGGCrscAGak
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif

Direction:	Backward
Position number:	2
Number of overlap:	8
Similarity score:	0.0915396

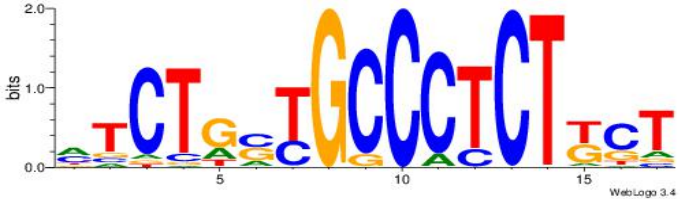
Alignment:

```
AGMAGAGGGCASCAGAK
--------GCGCSAAA-
```

Original motif   Consensus sequence: AGMAGAGGGCASCAGAK



Reverse complement motif   Consensus sequence: RTCTGSTGCCCTCTYCT

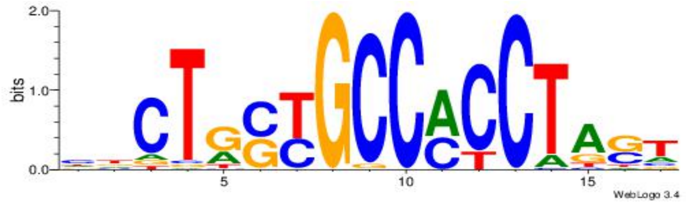


Dataset #:	4
Motif ID:	144
Motif name:	ctCTrsyGCCmCCTast
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	8
Similarity score:	0.0943326

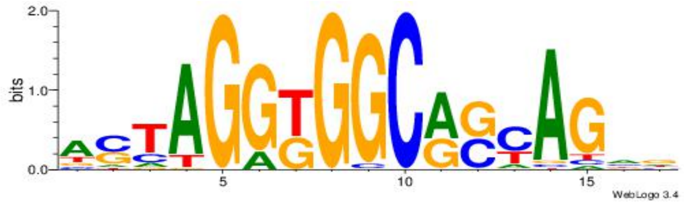
Alignment:

```
HDCTGSYGCCMCCTAST
-TTTSGCGC--------
```

Original motif Consensus sequence: HDCTGSYGCCMCCTAST



Reverse complement motif Consensus sequence: ASTAGGYGGCMSCAGDD

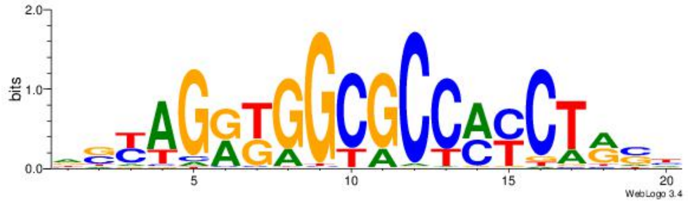


Dataset #:	4
Motif ID:	167
Motif name:	rsyAGrkGGCGCCmyCTrsy
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	9
Number of overlap:	8
Similarity score:	0.0955357

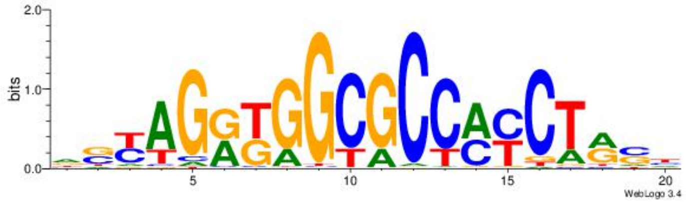
Alignment:

```
HSKAGKYGGCGCCRMCTMSD
--------GCGCSAAA----
```

Original motif Consensus sequence: DSYAGRKGGCGCCMYCTRSH



Reverse complement motif Consensus sequence: HSKAGKYGGCGCCRMCTMSD



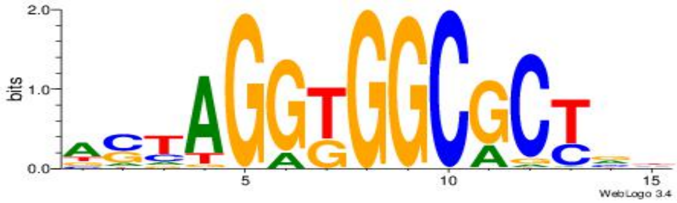
Dataset #:	4
Motif ID:	146
Motif name:	myrGYGCCmCCTast
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	4
Number of overlap:	8
Similarity score:	0.0975521

Alignment:

```
ASTAGGYGGCGCTBB
----TTTSGCGC---
```

Original motif Consensus sequence: VBAGCGCCMCCTAST

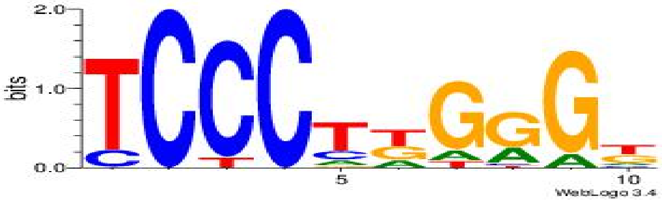
Reverse complement motif Consensus sequence: ASTAGGYGGCGCT



Dataset #: 3 **Motif ID: 77** **Motif name: EBF1**

Original motif Consensus sequence: MCCCMAGGGA

Reverse complement motif Consensus sequence: TCCCTYGGGY



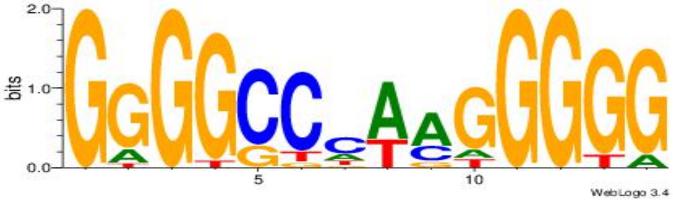
Best Matches for Motif ID 77 (Highest to Lowest)

Dataset #:	3
Motif ID:	110
Motif name:	PLAG1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	4
Number of overlap:	10
Similarity score:	0.0581959

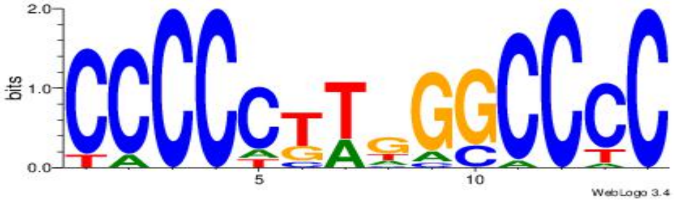
Alignment:

```
CCCCCTTGGGCCCC
-TCCCTYGGGY---
```

Original motif Consensus sequence: GGGGCCCAAGGGGG



Reverse complement motif Consensus sequence: CCCCCTTGGGCCC



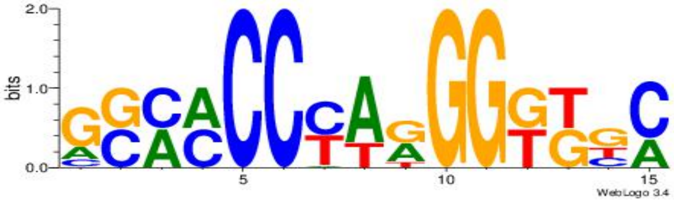
Dataset #:	3
Motif ID:	129
Motif name:	Zfp423
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif

Direction:	Backward
Position number:	3
Number of overlap:	10
Similarity score:	0.05861

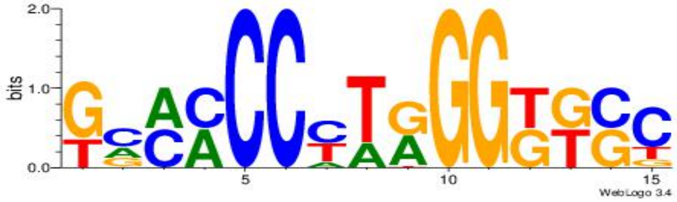
Alignment:

```
GSMMCCYARGGKKKC
---MCCCMAGGGA--
```

Original motif   Consensus sequence: GSMMCCYARGGKKKC



Reverse complement motif   Consensus sequence: GYRYCCMTKGGYR



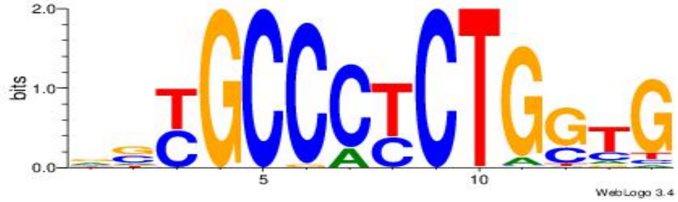
Dataset #:	4
Motif ID:	166
Motif name:	CasCAGrGGGCrsy
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	4
Number of overlap:	10
Similarity score:	0.0747791

Alignment:

```
BSKGCCCKCTGGTG
---TCCCTYGGGY-
```

Original motif Consensus sequence: CACCAGRGGGCRSB

Reverse complement motif Consensus sequence: BSKGCCCKCTGGT

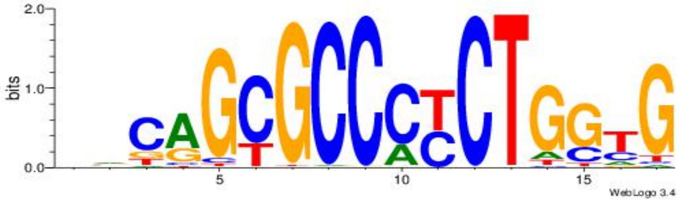


Dataset #:	4
Motif ID:	168
Motif name:	yrcrGYGCCMyCTGGtG
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	7
Number of overlap:	10
Similarity score:	0.076024

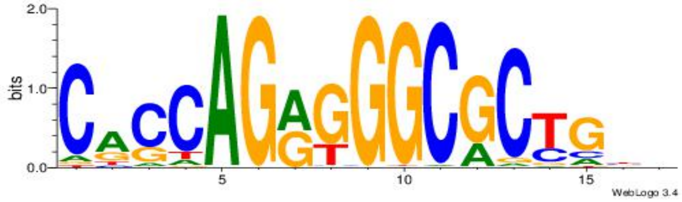
Alignment:

```
HVCAGCGCCCYCTGGTG
------TCCCTYGGGY-
```

Original motif Consensus sequence: HVCAGCGCCCYCTGGTG



Reverse complement motif Consensus sequence: CACCAGMGGGCGCTGBD

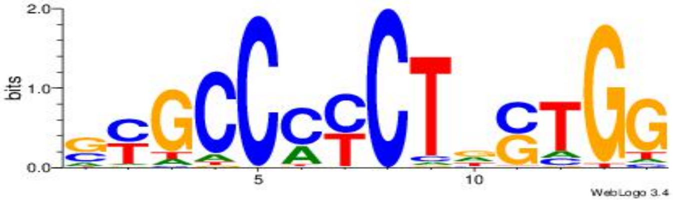


Dataset #: 2
Motif ID: 67
Motif name: Motif 67
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 10
Similarity score: 0.076343

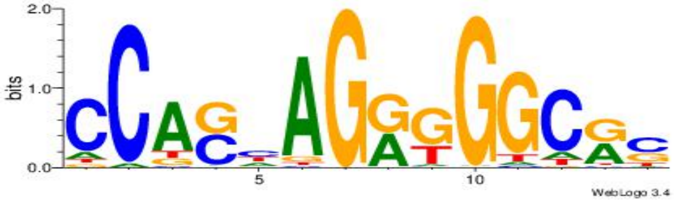
Alignment:

```
SYGCCCYCTDSTGG
TCCCTYGGGY----
```

Original motif Consensus sequence: SYGCCCYCTDSTGG



Reverse complement motif Consensus sequence: CCASHAGKGGGCK



Dataset #: 3 Motif ID: 78 Motif name: Egr1

Original motif Consensus sequence: TTTSGCGC

Reverse complement motif Consensus sequence: GCGCSAAA

Best Matches for Motif ID 78 (Highest to Lowest)

Dataset #:	3
Motif ID:	76
Motif name:	E2F1
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:

```
TTTSGCGC
TTTSGCGC
```

Original motif Consensus sequence: TTTSGCGC

Reverse complement motif Consensus sequence: GCGCSAAA

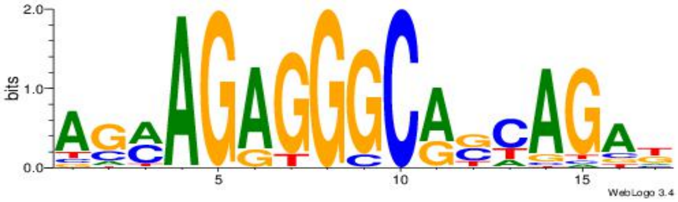
Dataset #:	4
Motif ID:	143
Motif name:	AgmAGAGGGCrscAGak
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif

Direction:	Backward
Position number:	2
Number of overlap:	8
Similarity score:	0.0915396

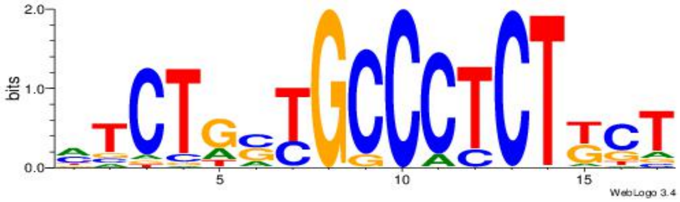
Alignment:

```
AGMAGAGGGCASCAGAK
--------GCGCSAAA-
```

Original motif   Consensus sequence: AGMAGAGGGCASCAGAK



Reverse complement motif   Consensus sequence: RTCTGSTGCCCTCTYCT

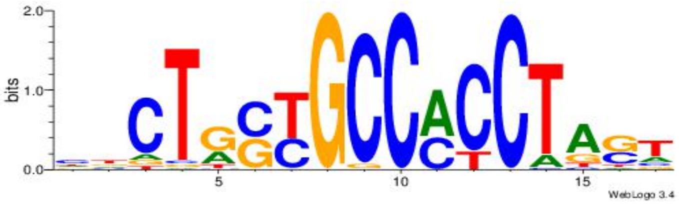


Dataset #:	4
Motif ID:	144
Motif name:	ctCTrsyGCCmCCTast
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	8
Similarity score:	0.0943326

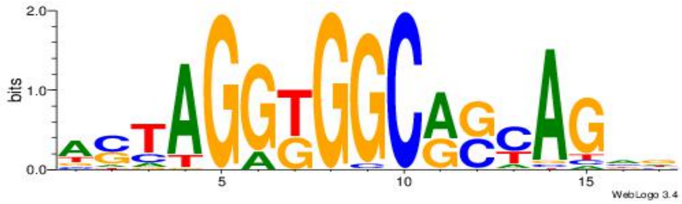
Alignment:

```
HDCTGSYGCCMCCTAST
-TTTSGCGC--------
```

Original motif Consensus sequence: HDCTGSYGCCMCCTAST



Reverse complement motif Consensus sequence: ASTAGGYGGCMSCAGDD

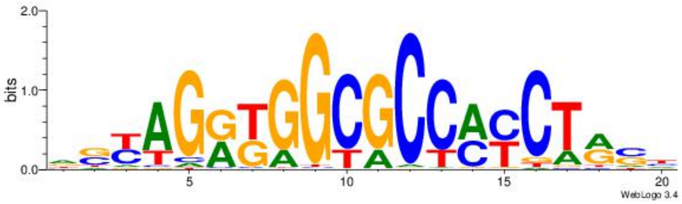


Dataset #:	4
Motif ID:	167
Motif name:	rsyAGrkGGCGCCmyCTrsy
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	9
Number of overlap:	8
Similarity score:	0.0955357

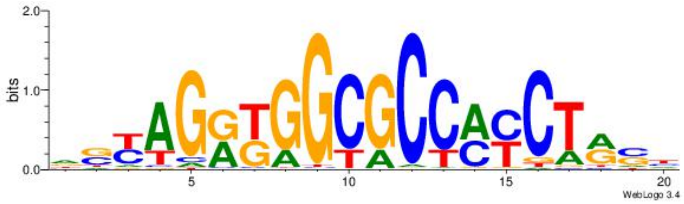
Alignment:

```
HSKAGKYGGCGCCRMCTMSD
--------GCGCSAAA----
```

Original motif Consensus sequence: DSYAGRKGGCGCCMYCTRSH



Reverse complement motif Consensus sequence: HSKAGKYGGCGCCRMCTMSD



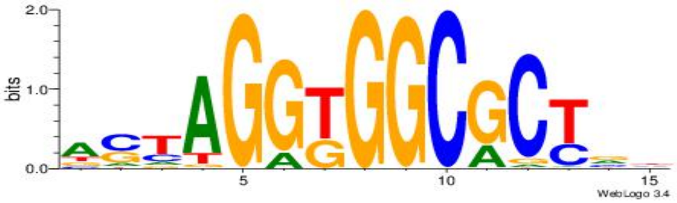
Dataset #: 4
Motif ID: 146
Motif name: myrGYGCCmCCTast
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 4
Number of overlap: 8
Similarity score: 0.0975521

Alignment:

```
ASTAGGYGGCGCTBB
----TTTSGCGC---
```

Original motif Consensus sequence: VBAGCGCCMCCTAST

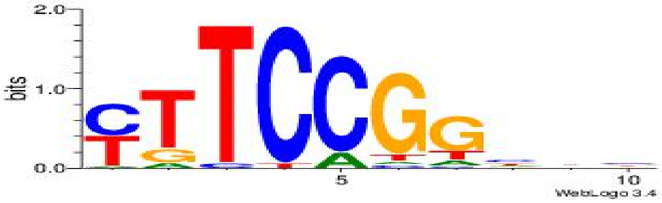
Reverse complement motif Consensus sequence: ASTAGGYGGCGCT



Dataset #: 3 Motif ID: 79 Motif name: ELK1

Original motif Consensus sequence: VDDCCGGAAR

Reverse complement motif Consensus sequence: MTTCCGGHBV



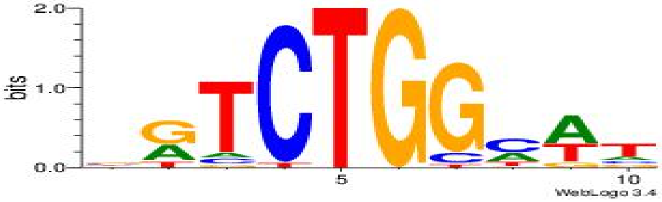
Best Matches for Motif ID 79 (Highest to Lowest)

Dataset #:	3
Motif ID:	85
Motif name:	Hand1Tcfe2a
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	10
Similarity score:	0.0406986

Alignment:

```
AWRCCAGAMB
VDDCCGGAAR
```

Original motif Consensus sequence: BRTCTGGMWT



Reverse complement motif Consensus sequence: AWRCCAGAMB

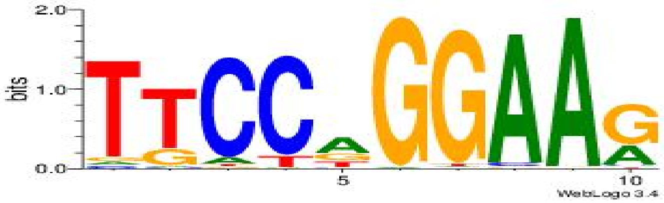
Dataset #:	3
Motif ID:	119
Motif name:	Stat3
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement

Direction:	Backward
Position number:	1
Number of overlap:	10
Similarity score:	0.0421921

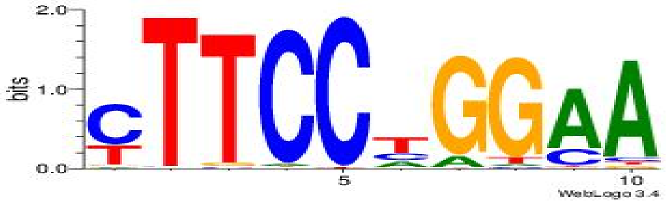
Alignment:

CTTCCTGGAA
MTTCCGGHBV

Original motif Consensus sequence: TTCCAGGAAG



Reverse complement motif Consensus sequence: CTTCCTGGAA



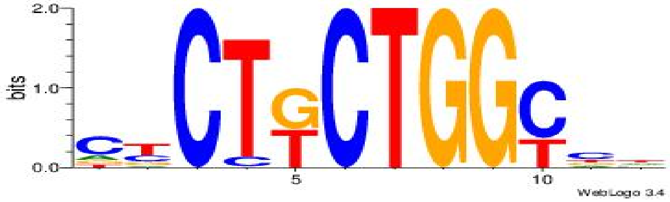
Dataset #:	4
Motif ID:	151
Motif name:	agrCCAGmAGrg
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	10
Similarity score:	0.0478168

Alignment:

HVGCCAGMAGRG
VDDCCGGAAR--

Original motif   Consensus sequence: HVGCCAGMAGRG

Reverse complement motif   Consensus sequence: CKCTRCTGGCVH

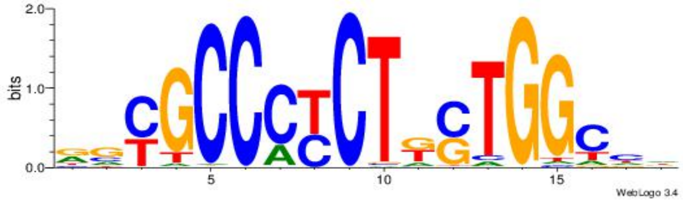


Dataset #:	4
Motif ID:	156
Motif name:	rgyGCCMyCTksTGGccd
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	10
Similarity score:	0.0493569

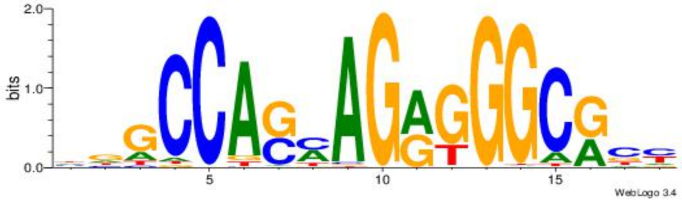
Alignment:

```
RVYGCCCYCTKSTGGCHD
--------MTTCCGGHBV
```

Original motif   Consensus sequence: RVYGCCCYCTKSTGGCHD



Reverse complement motif   Consensus sequence: DDGCCASYAGMGGGCKVM

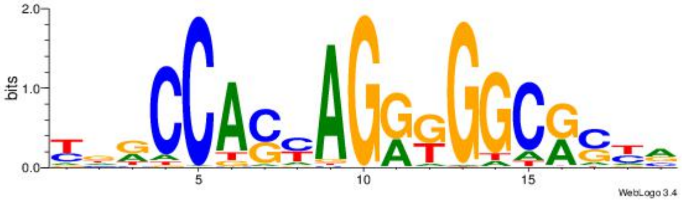


Dataset #: 3
Motif ID: 74
Motif name: CTCF
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 10
Number of overlap: 10
Similarity score: 0.0506531

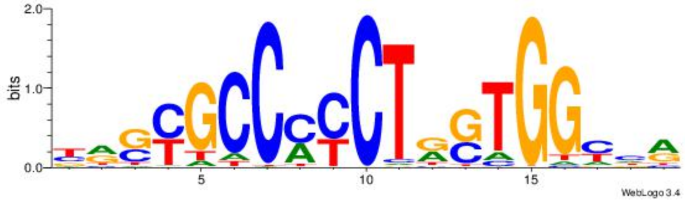
Alignment:

```
BMSMGCCYMCTKSTGGMHM
---------MTTCCGGHBV
```

Original motif Consensus sequence: YDRCCASYAGRKGGCRSYV



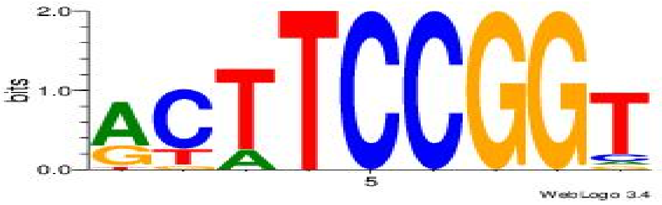
Reverse complement motif Consensus sequence: BMSMGCCYMCTKSTGGMHM



Dataset #: 3 **Motif ID: 80** **Motif name: ELK4**

Original motif Consensus sequence: ACCGGAAGT

Reverse complement motif Consensus sequence: ACTTCCGGT

Best Matches for Motif ID 80 (Highest to Lowest)

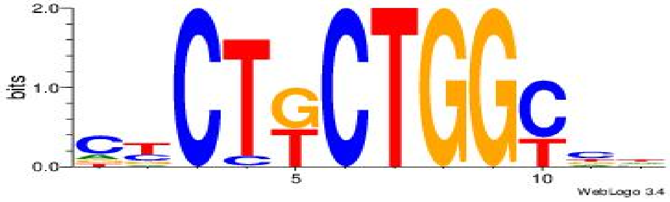
Dataset #:	4
Motif ID:	151
Motif name:	agrCCAGmAGrg
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	3
Number of overlap:	9
Similarity score:	0.0699758

Alignment:

```
HVGCCAGMAGRG
--ACCGGAAGT-
```

Original motif Consensus sequence: HVGCCAGMAGRG

Reverse complement motif Consensus sequence: CKCTRCTGGCVH



Dataset #:	4

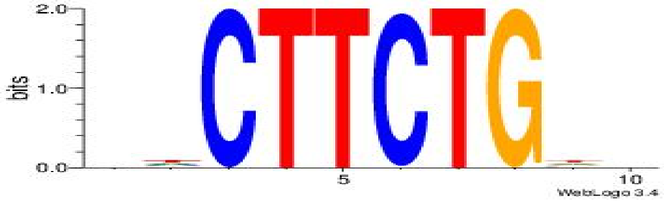
Motif ID:	136
Motif name:	dwCAGAAGwh
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	9
Similarity score:	0.0710473

Alignment:

```
DHCAGAAGDH
ACCGGAAGT-
```

Original motif Consensus sequence: DHCAGAAGDH

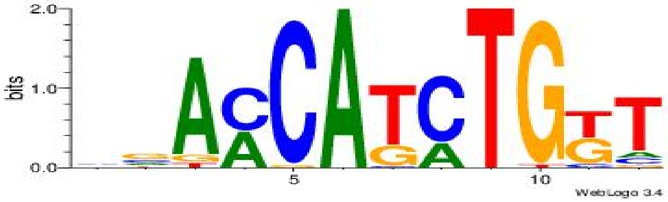
Reverse complement motif Consensus sequence: HDCTTCTGHD



Dataset #:	3
Motif ID:	121
Motif name:	TAL1TCF3
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	4
Number of overlap:	9
Similarity score:	0.0754906

Alignment:
HVAMCATCTGKT
---ACTTCCGGT

Original motif Consensus sequence: HVAMCATCTGKT



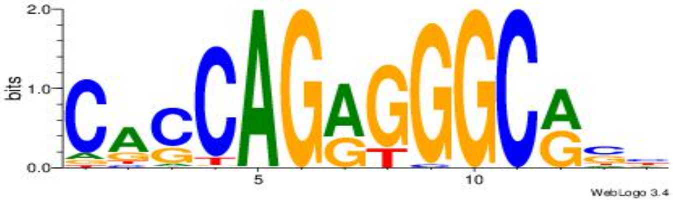
Reverse complement motif Consensus sequence: ARCAGATGRTVD

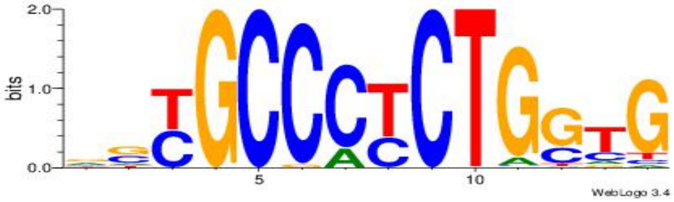
Dataset #:	4
Motif ID:	166
Motif name:	CasCAGrGGGCrsy
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	2
Number of overlap:	9
Similarity score:	0.0818647

Alignment:
BSKGCCCKCTGGTG
----ACTTCCGGT-

Original motif Consensus sequence: CACCAGRGGGCRSB

Reverse complement motif Consensus sequence: BSKGCCCKCTGGT



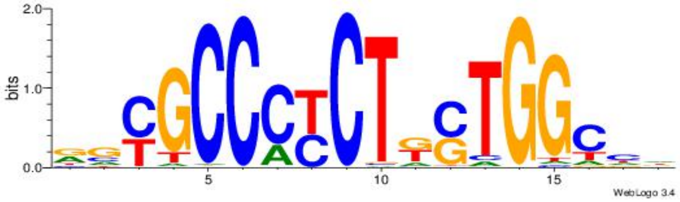


Dataset #:	4
Motif ID:	156
Motif name:	rgyGCCMyCTksTGGccd
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	8
Number of overlap:	9
Similarity score:	0.0852431

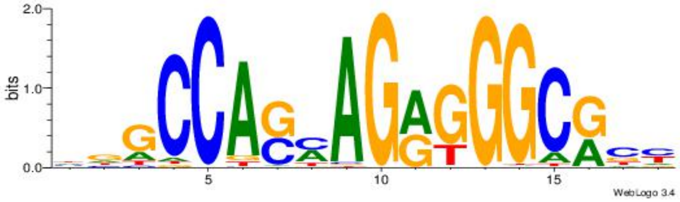
Alignment:

```
RVYGCCCYCTKSTGGCHD
-------ACTTCCGGT--
```

Original motif Consensus sequence: RVYGCCCYCTKSTGGCHD

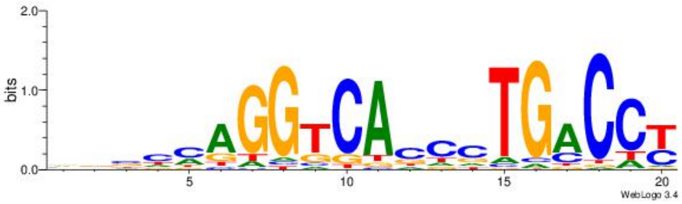


Reverse complement motif Consensus sequence: DDGCCASYAGMGGGCKVM

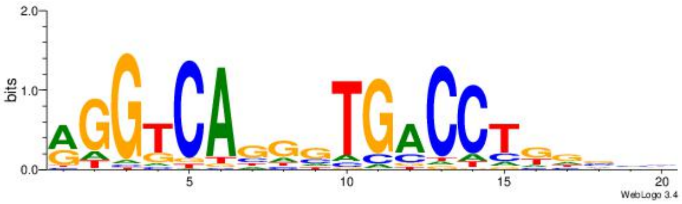


Dataset #: 3 **Motif ID: 81** **Motif name: ESR1**

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV



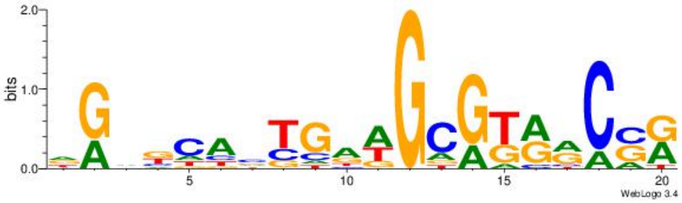
Best Matches for Motif ID 81 (Highest to Lowest)

Dataset #:	3
Motif ID:	109
Motif name:	Pax5
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	20
Similarity score:	0.0624908

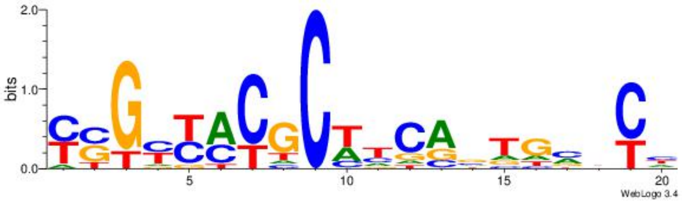
Alignment:

```
MSGKKRCGCWDCABTGBBCD
MGGTCAGGGTGACCTRDBHV
```

Original motif Consensus sequence: DGVBCABTGDWGCGKRRCSR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD

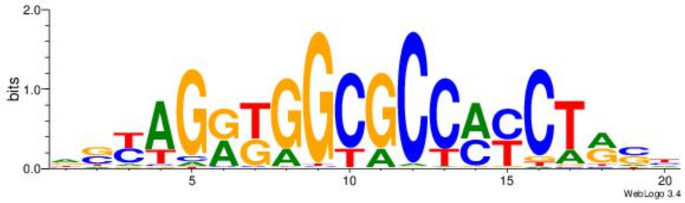


Dataset #:	4
Motif ID:	167
Motif name:	rsyAGrkGGCGCCmyCTrsy
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	20
Similarity score:	0.0752066

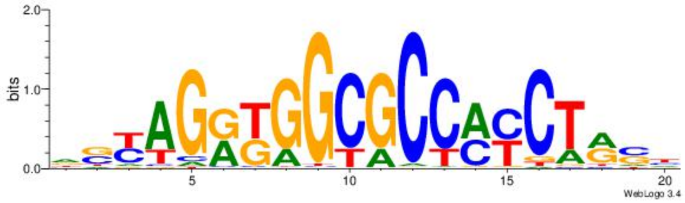
Alignment:

```
DSYAGRKGGCGCCMYCTRSH
VDBHMAGGTCACCCTGACCY
```

Original motif Consensus sequence: DSYAGRKGGCGCCMYCTRSH



Reverse complement motif Consensus sequence: HSKAGKYGGCGCCRMCTMSD



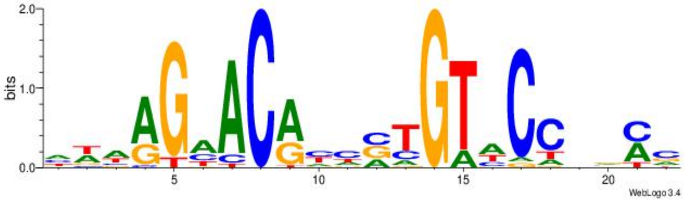
Dataset #:	3
Motif ID:	70
Motif name:	Ar
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward

Position number:	4
Number of overlap:	19
Similarity score:	0.556363

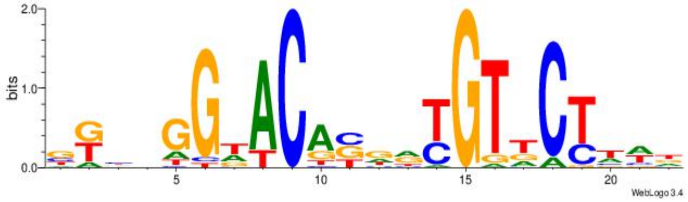
Alignment:

```
-HWDAGHACRHHVTGTHCCHVMV
MGGTCAGGGTGACCTRDBHV---
```

Original motif Consensus sequence: HWDAGHACRHHVTGTHCCHVMV



Reverse complement motif Consensus sequence: VRVDGGHACAVDDKGTHCTDWH

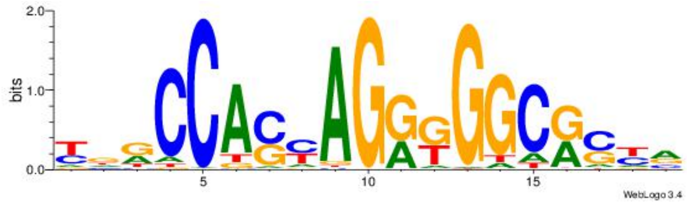


Dataset #:	3
Motif ID:	74
Motif name:	CTCF
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	19
Similarity score:	0.579928

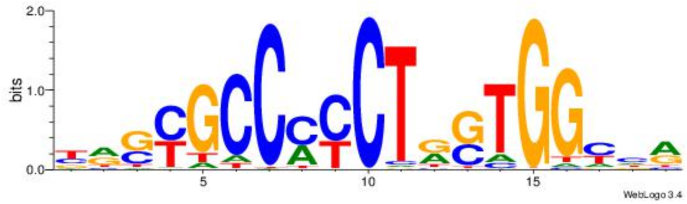
Alignment:

```
-YDRCCASYAGRKGGCRSYV
MGGTCAGGGTGACCTRDBHV
```

Original motif Consensus sequence: YDRCCASYAGRKGGCRSYV



Reverse complement motif Consensus sequence: BMSMGCCYMCTKSTGGMHM

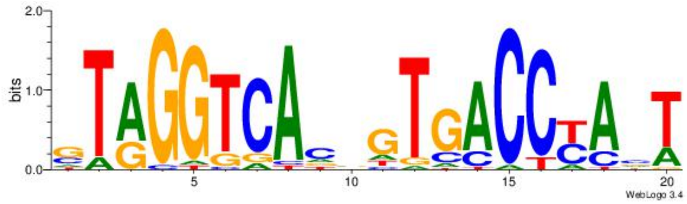


Dataset #:	3
Motif ID:	111
Motif name:	PPARG
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	3
Number of overlap:	18
Similarity score:	1.01936

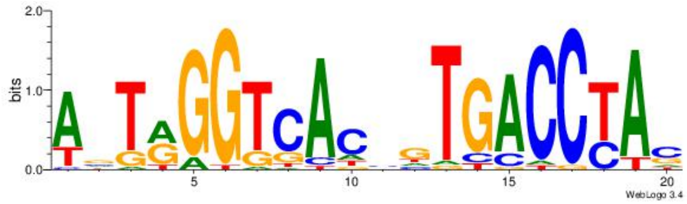
Alignment:

```
STAGGTCACBGTGACCYABT--
--MGGTCAGGGTGACCTRDBHV
```

Original motif Consensus sequence: STAGGTCACBGTGACCYABT

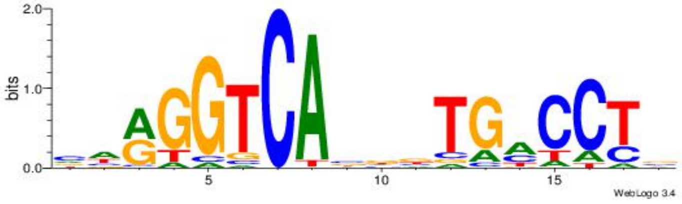


Reverse complement motif Consensus sequence: ABTMGGTCACBGTGACCTAS

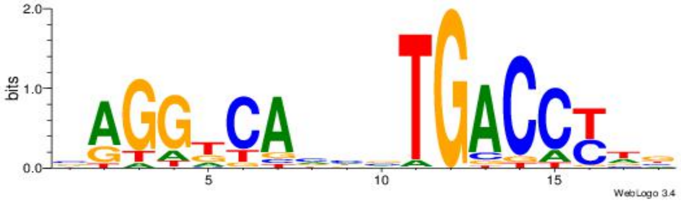


Dataset #: 3 Motif ID: 82 Motif name: ESR2

Original motif Consensus sequence: VHRGGTCABDBTGMCCTB



Reverse complement motif Consensus sequence: BAGGYCABHBTGACCKHV



Best Matches for Motif ID 82 (Highest to Lowest)

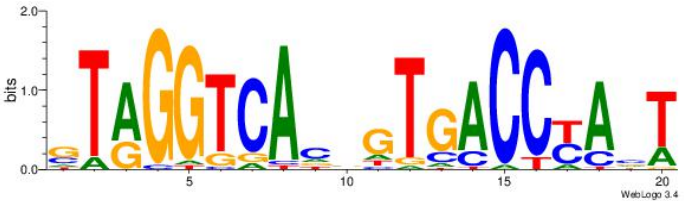
Dataset #:	3
Motif ID:	111
Motif name:	PPARG
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	18
Similarity score:	0.0125377

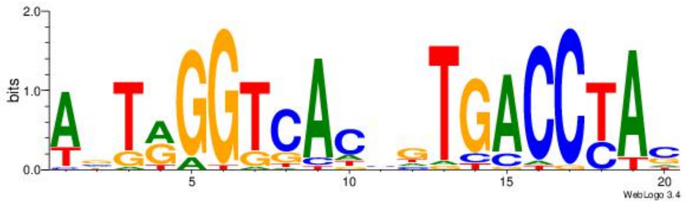
Alignment:

```
ABTMGGTCACBGTGACCTAS
--BAGGYCABHBTGACCKHV
```

Original motif Consensus sequence: STAGGTCACBGTGACCYABT

Reverse complement motif Consensus sequence: ABTMGGTCACBGTGACCTAS





Dataset #: 3

Motif ID: 70

Motif name: Ar

Matching format of first motif: Reverse Complement

Matching format of second motif: Original Motif

Direction: Forward

Position number: 3

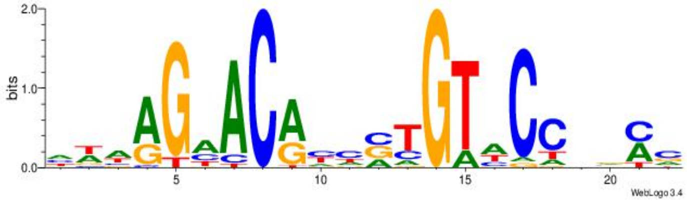
Number of overlap: 18

Similarity score: 0.0399216

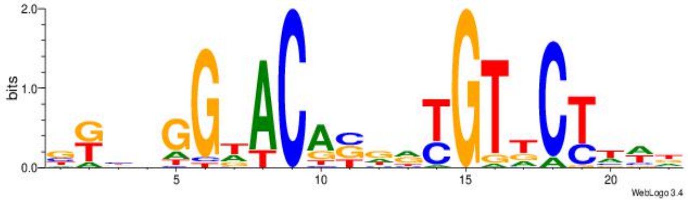
Alignment:

```
HWDAGHACRHHVTGTHCCHVMV
--BAGGYCABHBTGACCKHV--
```

Original motif Consensus sequence: HWDAGHACRHHVTGTHCCHVMV



Reverse complement motif Consensus sequence: VRVDGGHACAVDDKGTHCTDWH



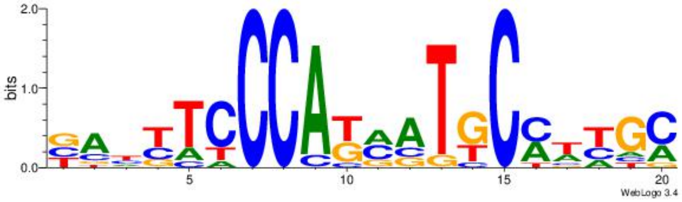
Dataset #: 3

Motif ID: 131
Motif name: znf143
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 2
Number of overlap: 18
Similarity score: 0.0692215

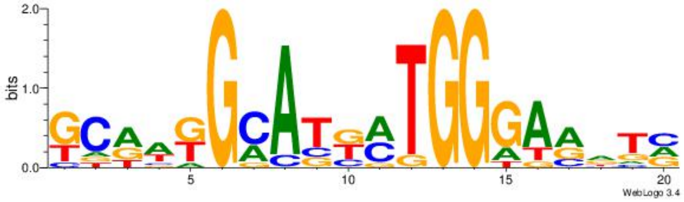
Alignment:

```
GCMWRGCATYRTGGGAMHTB
-BAGGYCABHBTGACCKHV-
```

Original motif Consensus sequence: BAHYTCCCAKMATGCMWYGC



Reverse complement motif Consensus sequence: GCMWRGCATYRTGGGAMHTB



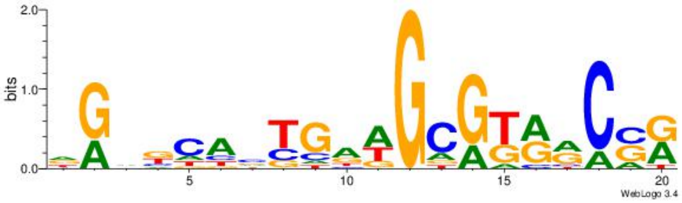
Dataset #: 3
Motif ID: 109
Motif name: Pax5
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 3
Number of overlap: 18

Similarity score:	0.0761757

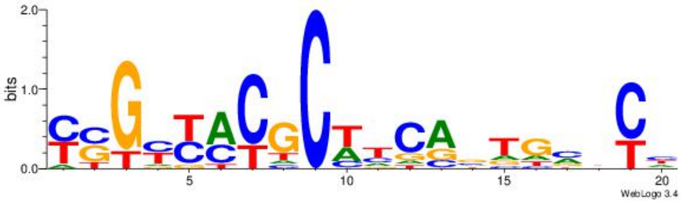
Alignment:

MSGKKRCGCWDCABTGBBCD
BAGGYCABHBTGACCKHV--

Original motif Consensus sequence: DGVBCABTGDWGCGKRRCSR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD



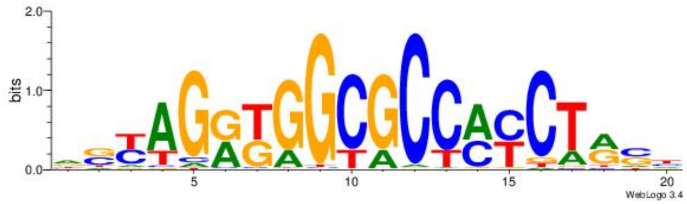
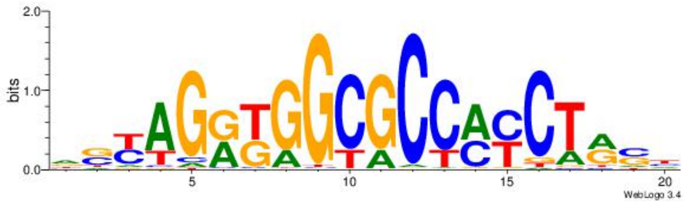
Dataset #:	4
Motif ID:	167
Motif name:	rsyAGrkGGCGCCmyCTrsy
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	18
Similarity score:	0.0808384

Alignment:

HSKAGKYGGCGCCRMCTMSD
VHRGGTCABDBTGMCCTB--

Original motif Consensus sequence: DSYAGRKGGCGCCMYCTRSH

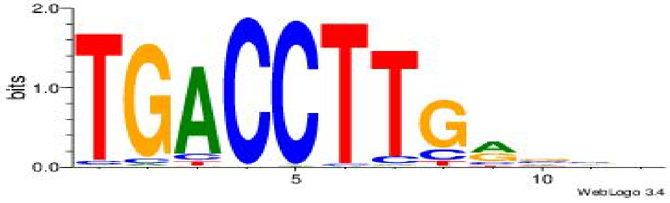
Reverse complement motif Consensus sequence: HSKAGKYGGCGCCRMCTMSD

Dataset #: 3 Motif ID: 83 Motif name: Esrrb

Original motif Consensus sequence: VBBYCAAGGTCA

Reverse complement motif Consensus sequence: TGACCTTGMBBB



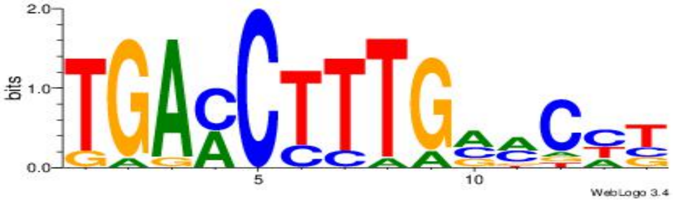
Best Matches for Motif ID 83 (Highest to Lowest)

Dataset #:	3
Motif ID:	107
Motif name:	NR2F1
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	12
Similarity score:	0.0442611

Alignment:

```
AKGYYCAAAGRTCA
--VBBYCAAGGTCA
```

Original motif Consensus sequence: TGAMCTTTGMMCYT



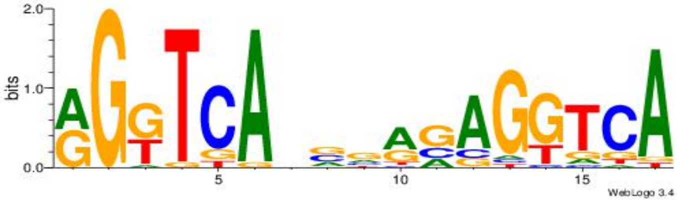
Reverse complement motif Consensus sequence: AKGYYCAAAGRTC

Dataset #: 3
Motif ID: 115
Motif name: RXRRAR_DR5
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 12
Similarity score: 0.0442659

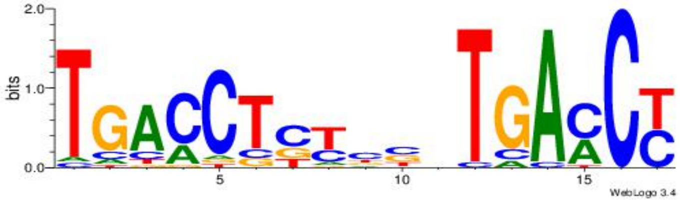
Alignment:

```
TGACCTCKVVBTGAYCK
TGACCTTGMBBB-----
```

Original motif Consensus sequence: RGKTCABVVRGAGGTCA



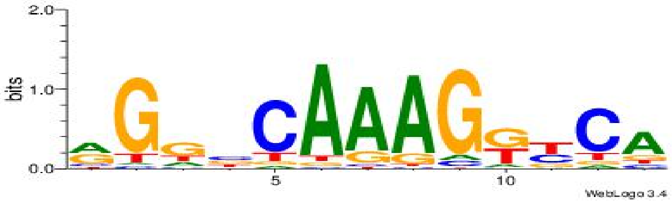
Reverse complement motif Consensus sequence: TGACCTCKVVBTGAYCK



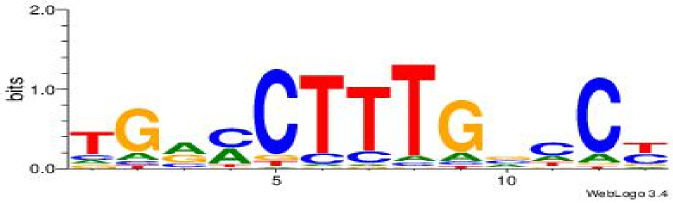
Dataset #: 3
Motif ID: 87
Motif name: HNF4A
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 12
Similarity score: 0.0470808

Alignment:
```
RGGBCAAAGKYCA
-VBBYCAAGGTCA
```

Original motif Consensus sequence: RGGBCAAAGKYCA



Reverse complement motif Consensus sequence: TGMYCTTTGBCCK

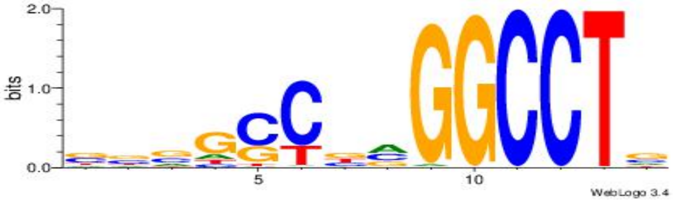


Dataset #: 3
Motif ID: 130
Motif name: Zfx
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 2
Number of overlap: 12

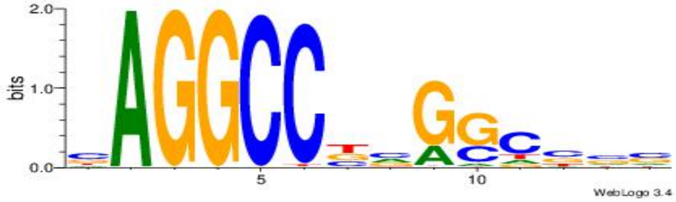
Similarity score: 0.0625961

Alignment:
`VAGGCCBBGGCVBB`
`-TGACCTTGMBBB-`

Original motif Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif Consensus sequence: VAGGCCBBGGCV

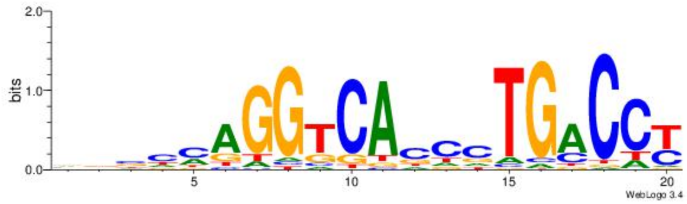


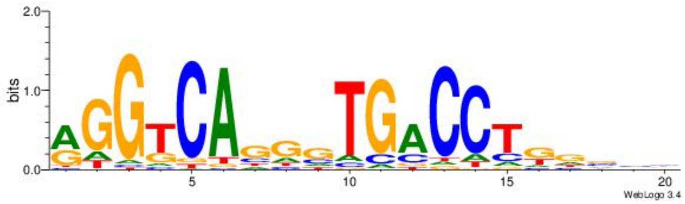
Dataset #: 3
Motif ID: 81
Motif name: ESR1
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 9
Number of overlap: 12
Similarity score: 0.0628484

Alignment:
`VDBHMAGGTCACCCTGACCY`
`TGACCTTGMBBB--------`

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY

Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV

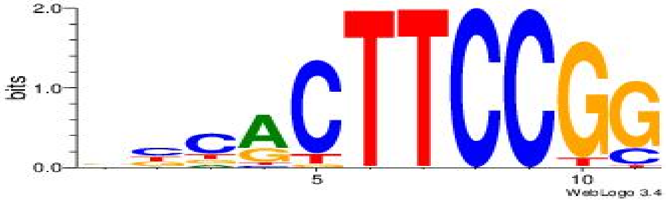




Dataset #: 3 **Motif ID: 84** **Motif name: GABPA**

Original motif Consensus sequence: CCGGAAGTGVV

Reverse complement motif Consensus sequence: VVCACTTCCGG



Best Matches for Motif ID 84 (Highest to Lowest)

Dataset #:	4
Motif ID:	154
Motif name:	csCsCCTCCcc
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:	0.0708637

Alignment:

```
VBCCCCTCCHB
VVCACTTCCGG
```

Original motif Consensus sequence: VBCCCCTCCHB

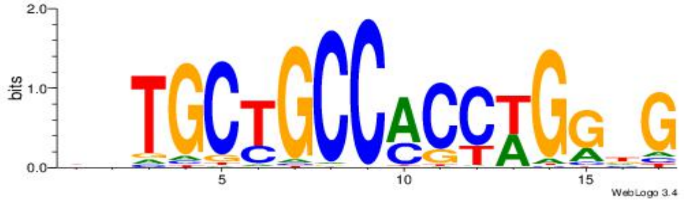
Reverse complement motif Consensus sequence: BDGGAGGGGBV

Dataset #:	4
Motif ID:	169
Motif name:	yvTGCyGCCmCCwGgtG
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	7
Number of overlap:	11
Similarity score:	0.0756694

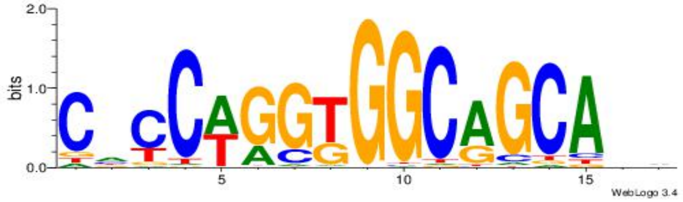
Alignment:

```
CDCCWGGTGGCAGCAVV
------CCGGAAGTGVV
```

Original motif Consensus sequence: BVTGCTGCCACCWGGDG



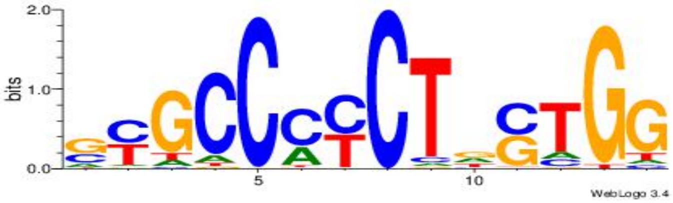
Reverse complement motif Consensus sequence: CDCCWGGTGGCAGCAVV



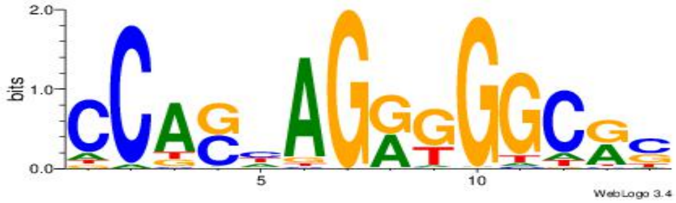
Dataset #: 2
Motif ID: 67
Motif name: Motif 67
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 4
Number of overlap: 11
Similarity score: 0.0810917

Alignment:
```
SYGCCCYCTDSTGG
VVCACTTCCGG---
```

Original motif Consensus sequence: SYGCCCYCTDSTGG



Reverse complement motif Consensus sequence: CCASHAGKGGGCK



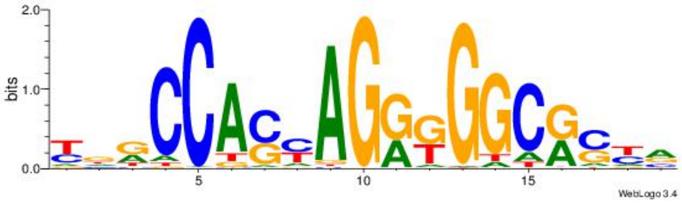
Dataset #: 3
Motif ID: 74
Motif name: CTCF
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 4
Number of overlap: 11

Similarity score: 0.0813947

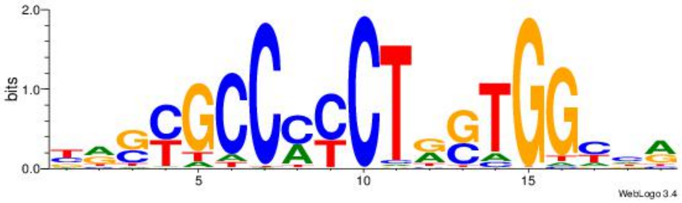
Alignment:

```
BMSMGCCYMCTKSTGGMHM
-----VVCACTTCCGG---
```

Original motif Consensus sequence: YDRCCASYAGRKGGCRSYV



Reverse complement motif Consensus sequence: BMSMGCCYMCTKSTGGMHM



Dataset #: 4

Motif ID: 156

Motif name: rgyGCCMyCTksTGGccd

Matching format of first motif: Reverse Complement

Matching format of second motif: Original Motif

Direction: Forward

Position number: 5

Number of overlap: 11

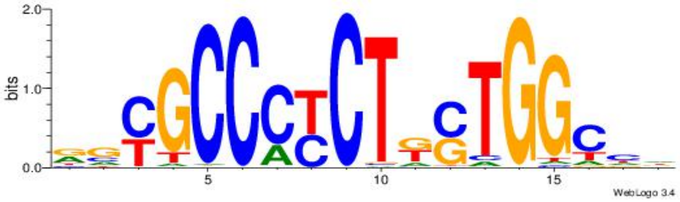
Similarity score: 0.0837237

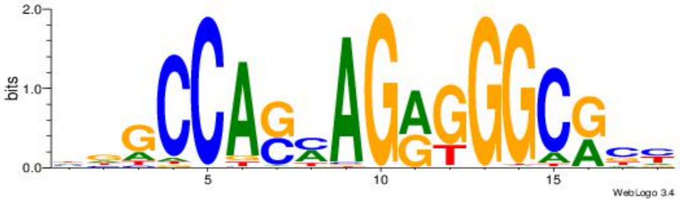
Alignment:

```
RVYGCCCYCTKSTGGCHD
----VVCACTTCCGG---
```

Original motif Consensus sequence: RVYGCCCYCTKSTGGCHD

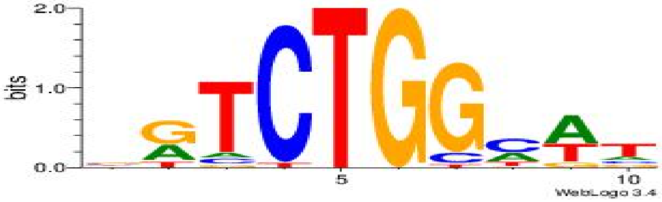
Reverse complement motif Consensus sequence: DDGCCASYAGMGGGCKVM





Dataset #: 3 **Motif ID: 85** **Motif name: Hand1Tcfe2a**

Original motif Consensus sequence: BRTCTGGMWT



Reverse complement motif Consensus sequence: AWRCCAGAMB

Best Matches for Motif ID 85 (Highest to Lowest)

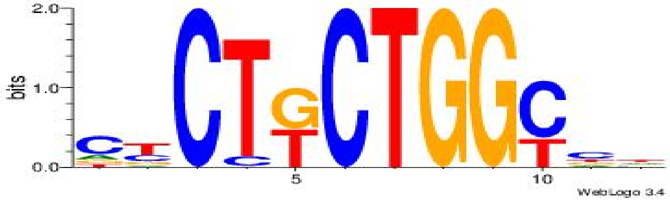
Dataset #:	4
Motif ID:	151
Motif name:	agrCCAGmAGrg
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	3
Number of overlap:	10
Similarity score:	0.0194367

Alignment:

```
HVGCCAGMAGRG
AWRCCAGAMB--
```

Original motif Consensus sequence: HVGCCAGMAGRG

Reverse complement motif Consensus sequence: CKCTRCTGGCVH

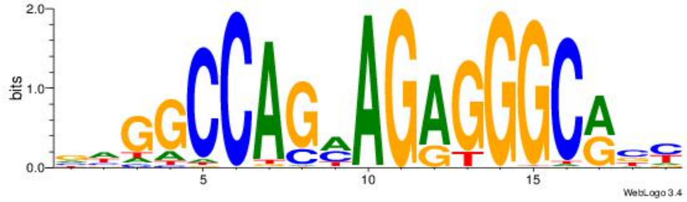


Dataset #:	4
Motif ID:	163
Motif name:	gwGGCCAGmAGAGGGCrby
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	10
Similarity score:	0.027647

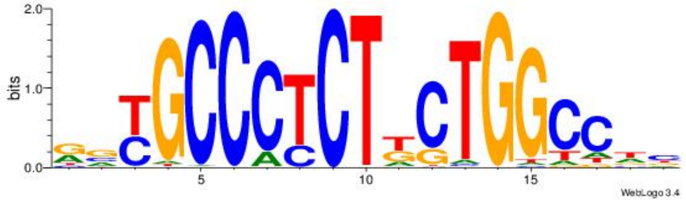
Alignment:

```
VHGGCCAGMAGAGGGCRBY
-AWRCCAGAMB--------
```

Original motif Consensus sequence: VHGGCCAGMAGAGGGCRBY



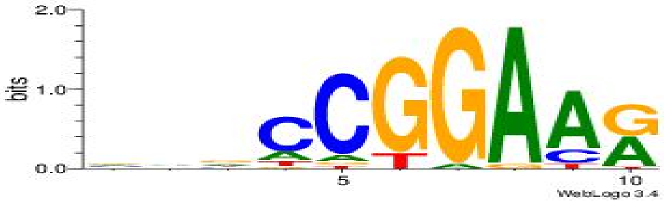
Reverse complement motif Consensus sequence: KBKGCCCTCTYCTGGCCHV



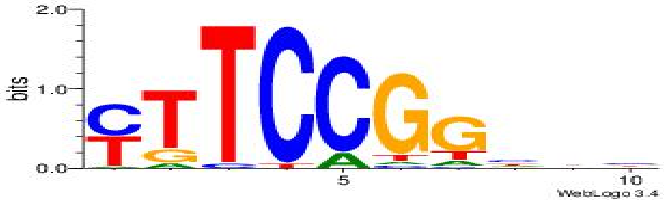
Dataset #: 3
Motif ID: 79
Motif name: ELK1
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 10
Similarity score: 0.0297824

Alignment:
MTTCCGGHBV
BRTCTGGMWT

Original motif Consensus sequence: VDDCCGGAAR



Reverse complement motif Consensus sequence: MTTCCGGHBV



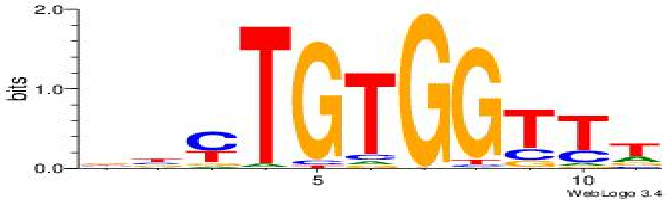
Dataset #: 3
Motif ID: 114
Motif name: RUNX1
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 2
Number of overlap: 10

Similarity score: 0.0323511

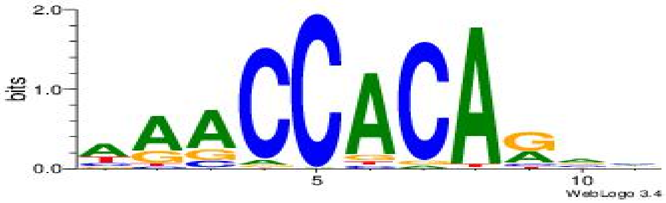
Alignment:

```
BBYTGTGGTTT
-BRTCTGGMWT
```

Original motif Consensus sequence: BBYTGTGGTTT



Reverse complement motif Consensus sequence: AAACCACAKVB



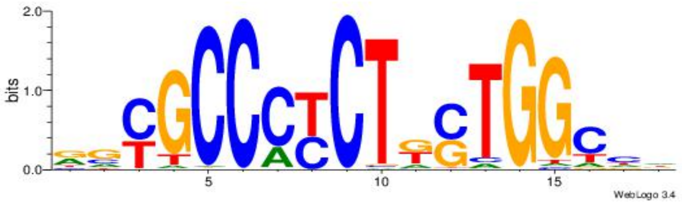
Dataset #:	4
Motif ID:	156
Motif name:	rgyGCCMyCTksTGGccd
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	9
Number of overlap:	10
Similarity score:	0.0371584

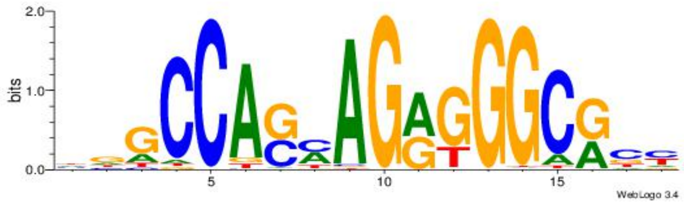
Alignment:

```
RVYGCCCYCTKSTGGCHD
--------BRTCTGGMWT
```

Original motif Consensus sequence: RVYGCCCYCTKSTGGCHD

Reverse complement motif Consensus sequence: DDGCCASYAGMGGGCKVM





Dataset #: 3 **Motif ID: 86** **Motif name: HIF1AARNT**

Original motif Consensus sequence: VBACGTGV

Reverse complement motif Consensus sequence: VCACGTBV

Best Matches for Motif ID 86 (Highest to Lowest)

Dataset #:	3
Motif ID:	91
Motif name:	MAX
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	3
Number of overlap:	8
Similarity score:	0.0166242

Alignment:

```
BCACGTGDTD
VCACGTBV--
```

Original motif Consensus sequence: DAHCACGTGD

Reverse complement motif Consensus sequence: BCACGTGDTD

Dataset #:	3
Motif ID:	96
Motif name:	Mycn
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:	0.0228069

Alignment:

```
GCCACGTGSD
-VBACGTGV-
```

Original motif Consensus sequence: HSCACGTGGC

Reverse complement motif Consensus sequence: GCCACGTGSD

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: 2
Number of overlap: 8
Similarity score: 0.0249459

Alignment:

```
DCCACGTGCV
-VBACGTGV-
```

Original motif Consensus sequence: VGCACGTGGH

Reverse complement motif Consensus sequence: DCCACGTGCV

Dataset #: 3
Motif ID: 95
Motif name: MYCMAX
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 2
Number of overlap: 8

Similarity score: 0.0254922

Alignment:

```
ACCACGTGSTM
-VCACGTBV--
```

Original motif Consensus sequence: RASCACGTGGT

Reverse complement motif Consensus sequence: ACCACGTGSTM

Dataset #: 3

Motif ID: 125

Motif name: TP53

Matching format of first motif: Original Motif

Matching format of second motif: Original Motif

Direction: Backward

Position number: 11

Number of overlap: 8

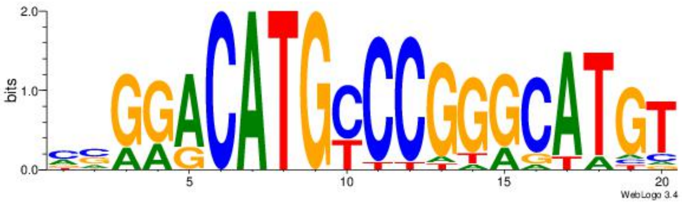
Similarity score: 0.0362969

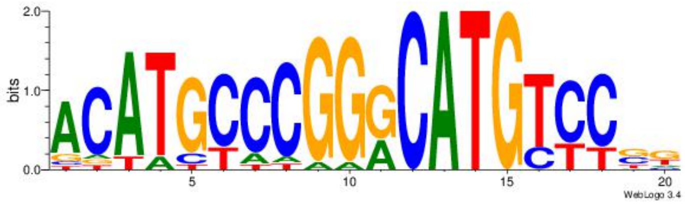
Alignment:

```
MSGGACATGYCCGGGCATGT
--VBACGTGV----------
```

Original motif Consensus sequence: MSGGACATGYCCGGGCATGT

Reverse complement motif Consensus sequence: ACATGCCCGGKCATGTCCSR

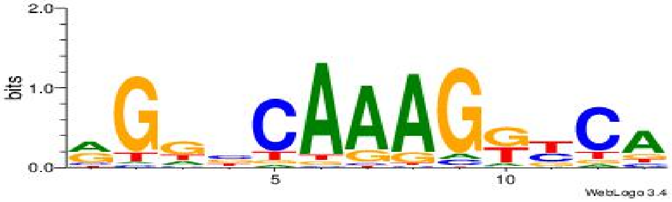


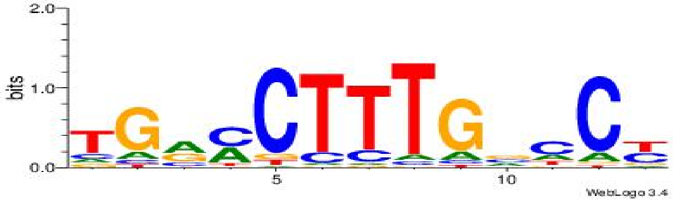


Dataset #: 3 **Motif ID: 87** **Motif name: HNF4A**

Original motif Consensus sequence: RGGBCAAAGKYCA

Reverse complement motif Consensus sequence: TGMYCTTTGBCCK





Best Matches for Motif ID 87 (Highest to Lowest)

Dataset #:	3
Motif ID:	107
Motif name:	NR2F1
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	2
Number of overlap:	13
Similarity score:	0.0127044

Alignment:

```
AKGYYCAAAGRTCA
-RGGBCAAAGKYCA
```

Original motif Consensus sequence: TGAMCTTTGMMCYT

Reverse complement motif Consensus sequence: AKGYYCAAAGRTC

Dataset #: 3

Motif ID: 115

Motif name: RXRRAR_DR5

Matching format of first motif: Reverse Complement

Matching format of second motif: Reverse Complement

Direction: Forward

Position number: 1

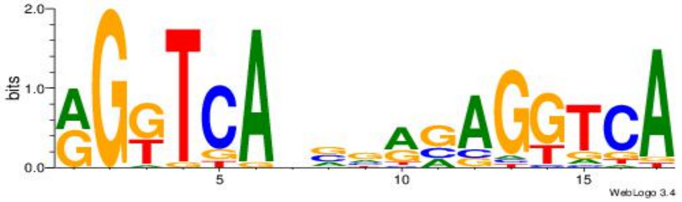
Number of overlap: 13

Similarity score: 0.0388151

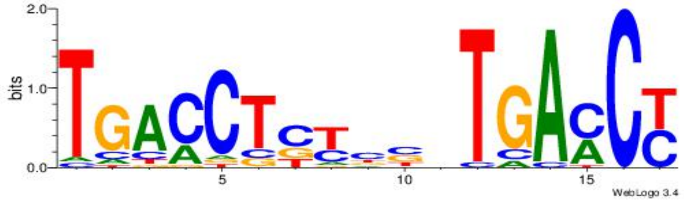
Alignment:

```
TGACCTCKVVBTGAYCK
TGMYCTTTGBCCK----
```

Original motif Consensus sequence: RGKTCABVVRGAGGTCA



Reverse complement motif Consensus sequence: TGACCTCKVVBTGAYCK

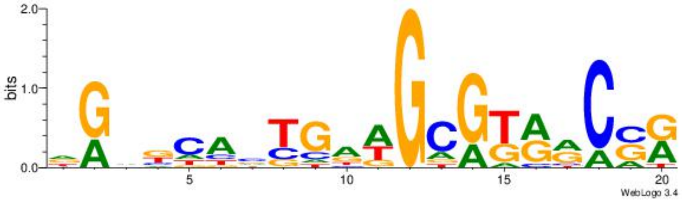


Dataset #:	3
Motif ID:	109
Motif name:	Pax5
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	8
Number of overlap:	13
Similarity score:	0.0538871

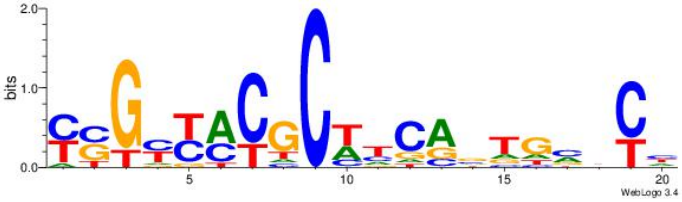
Alignment:

```
MSGKKRCGCWDCABTGBBCD
-------RGGBCAAAGKYCA
```

Original motif Consensus sequence: DGVBCABTGDWGCGKRRCSR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD



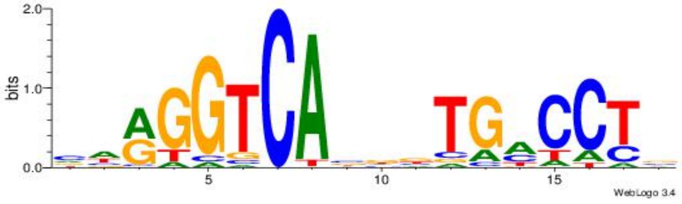
Dataset #:	3
Motif ID:	82
Motif name:	ESR2
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	3

Number of overlap:	13
Similarity score:	0.0571246

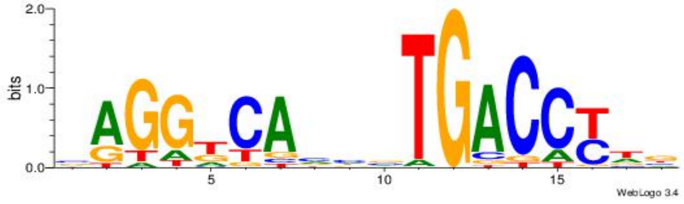
Alignment:

```
VHRGGTCABDBTGMCCTB
--RGGBCAAAGKYCA---
```

Original motif   Consensus sequence: VHRGGTCABDBTGMCCTB



Reverse complement motif   Consensus sequence:
BAGGYCABHBTGACCKHV

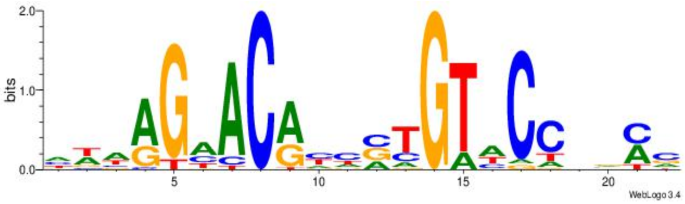


Dataset #:	3
Motif ID:	70
Motif name:	Ar
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	4
Number of overlap:	13
Similarity score:	0.0577381

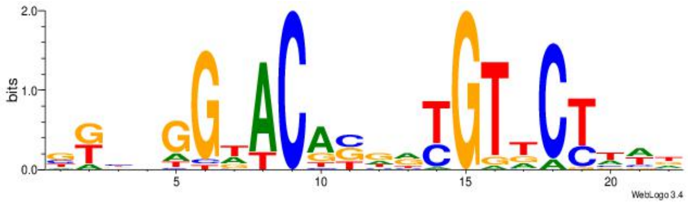
Alignment:

```
VRVDGGHACAVDDKGTHCTDWH
------TGMYCTTTGBCCK---
```

Original motif Consensus sequence: HWDAGHACRHHVTGTHCCHVMV



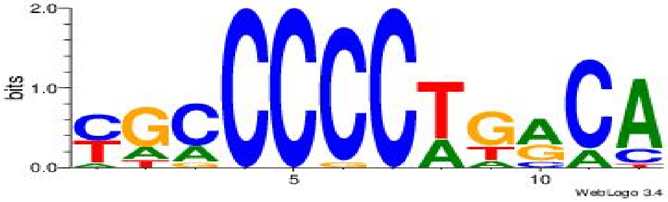
Reverse complement motif Consensus sequence: VRVDGGHACAVDDKGTHCTDWH



Dataset #: 3 Motif ID: 88 Motif name: INSM1

Original motif Consensus sequence: TGYCAGGGGGCR

Reverse complement motif Consensus sequence: MGCCCCCTGMCA



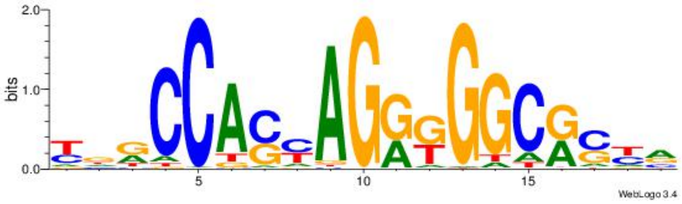
Best Matches for Motif ID 88 (Highest to Lowest)

Dataset #:	3
Motif ID:	74
Motif name:	CTCF
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	5
Number of overlap:	12
Similarity score:	0.0323447

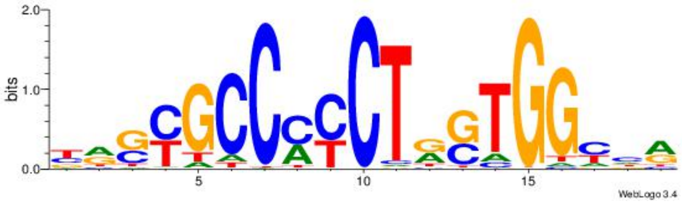
Alignment:

BMSMGCCYMCTKSTGGMHM
---MGCCCCCTGMCA----

Original motif Consensus sequence: YDRCCASYAGRKGGCRSYV



Reverse complement motif Consensus sequence: BMSMGCCYMCTKSTGGMHM

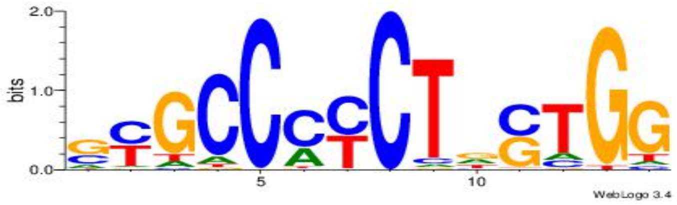


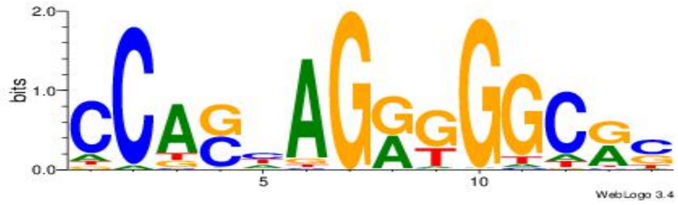
Dataset #:	2
Motif ID:	67
Motif name:	Motif 67
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	2
Number of overlap:	12
Similarity score:	0.0361443

Alignment:
CCASHAGKGGGCKS
-TGYCAGGGGGCR-

Original motif Consensus sequence: SYGCCCYCTDSTGG

Reverse complement motif Consensus sequence: CCASHAGKGGGC





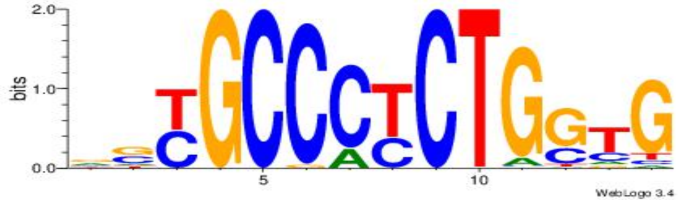
Dataset #:	4
Motif ID:	166
Motif name:	CasCAGrGGGCrsy
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	3
Number of overlap:	12
Similarity score:	0.0386733

Alignment:

```
CACCAGRGGGCRSB
TGYCAGGGGGCR--
```

Original motif Consensus sequence: CACCAGRGGGCRSB

Reverse complement motif Consensus sequence: BSKGCCCKCTGGT



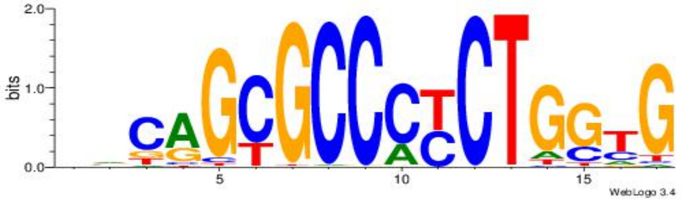
Dataset #:	4
Motif ID:	168

Motif name:	yrcrGYGCCMyCTGGtG
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	12
Similarity score:	0.0393748

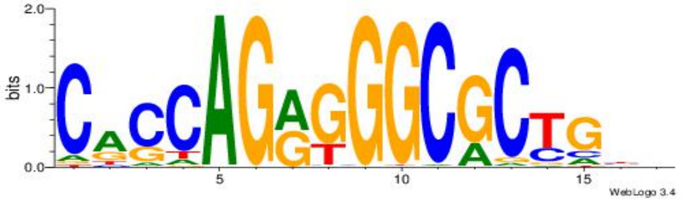
Alignment:

```
HVCAGCGCCCYCTGGTG
-----MGCCCCCTGMCA
```

Original motif Consensus sequence: HVCAGCGCCCYCTGGTG



Reverse complement motif Consensus sequence: CACCAGMGGGCGCTGBD

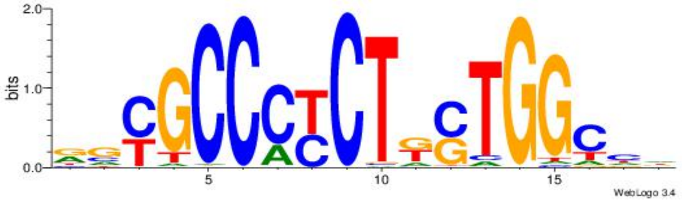


Dataset #:	4
Motif ID:	156
Motif name:	rgyGCCMyCTksTGGccd
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	3
Number of overlap:	12
Similarity score:	0.0427424

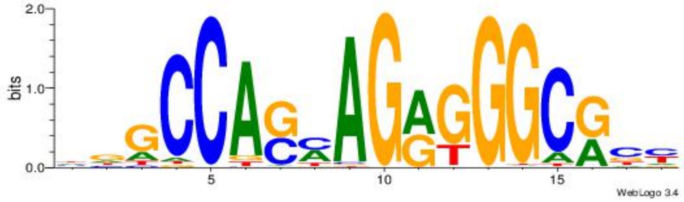
Alignment:

```
RVYGCCCYCTKSTGGCHD
--MGCCCCCTGMCA----
```

Original motif Consensus sequence: RVYGCCCYCTKSTGGCHD



Reverse complement motif Consensus sequence: DDGCCASYAGMGGGCKVM



Dataset #: 3 **Motif ID: 89** **Motif name: Klf4**

Original motif Consensus sequence: DGGGYGKGGC

Reverse complement motif Consensus sequence: GCCYCMCCCD

Best Matches for Motif ID 89 (Highest to Lowest)

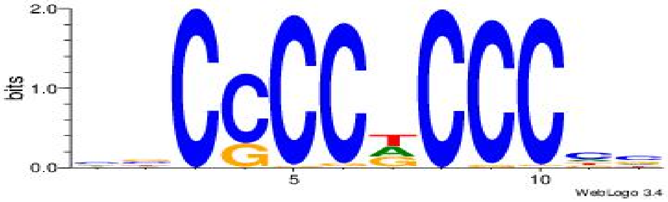
Dataset #:	4
Motif ID:	155
Motif name:	csCSCCdCCCcs
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward

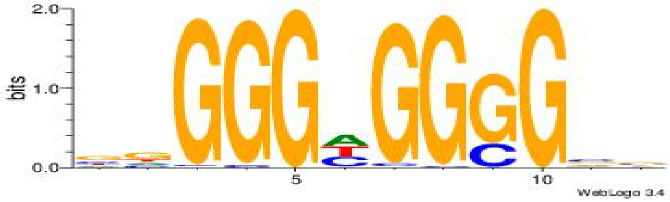
Position number:	2
Number of overlap:	10
Similarity score:	0.0234217

Alignment:

```
VDGGGDGGGGBV
-DGGGYGKGGC-
```

Original motif Consensus sequence: VBCCCCDCCCHV Reverse complement motif Consensus sequence: VDGGGDGGGGBV





Dataset #:	4
Motif ID:	154
Motif name:	csCsCCTCCcc
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	10
Similarity score:	0.0429499

Alignment:

```
VBCCCCTCCHB
-GCCYCMCCCD
```

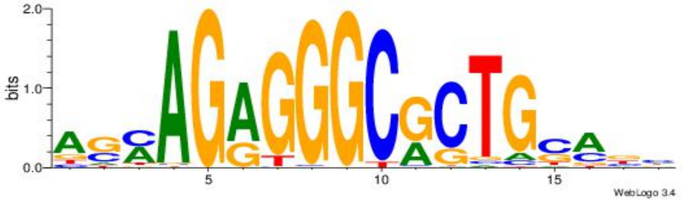
Original motif Consensus sequence: VBCCCCTCCHB Reverse complement motif Consensus sequence: BDGGAGGGGBV

Dataset #: 4
Motif ID: 149
Motif name: asmAGRGGGCrCTGsmkc
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 4
Number of overlap: 10
Similarity score: 0.0512984

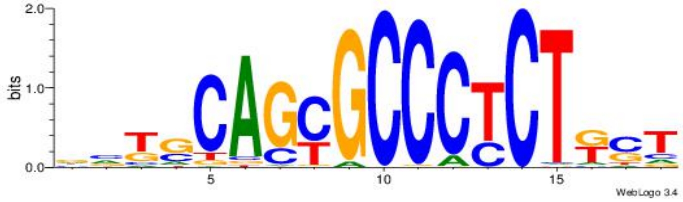
Alignment:

```
ASMAGAGGGCRCTGSABH
-----DGGGYGKGGC---
```

Original motif Consensus sequence: ASMAGAGGGCRCTGSABH



Reverse complement motif Consensus sequence: DBTSCAGMGCCCTCTRST



Dataset #: 4

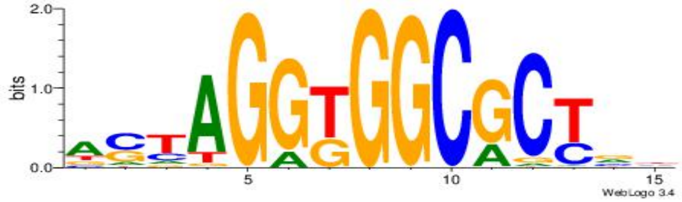
Motif ID:	146
Motif name:	myrGYGCCmCCTast
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	3
Number of overlap:	10
Similarity score:	0.0522764

Alignment:

```
VBAGCGCCMCCTAST
---GCCYCMCCCD--
```

Original motif Consensus sequence: VBAGCGCCMCCTAST

Reverse complement motif Consensus sequence: ASTAGGYGGCGCT

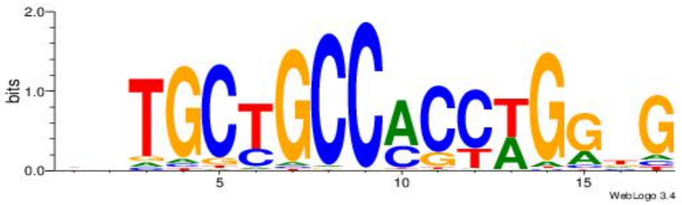


Dataset #:	4
Motif ID:	169
Motif name:	yvTGCyGCCmCCwGgtG
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	4
Number of overlap:	10
Similarity score:	0.0619219

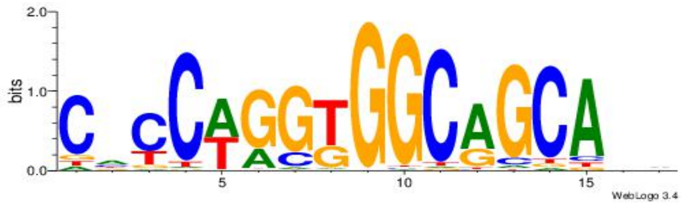
Alignment:

```
BVTGCTGCCACCWGGDG
---GCCYCMCCCD----
```

Original motif Consensus sequence: BVTGCTGCCACCWGGDG



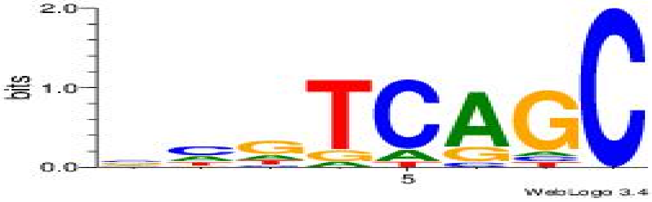
Reverse complement motif Consensus sequence: CDCCWGGTGGCAGCAVV



Dataset #: 3 Motif ID: 90 Motif name: Mafb

Original motif Consensus sequence: GCTGACDB

Reverse complement motif Consensus sequence: BHGTCAGC



Best Matches for Motif ID 90 (Highest to Lowest)

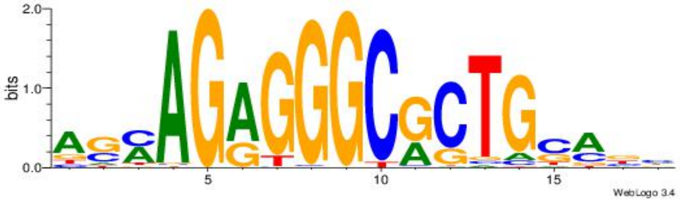
Dataset #:	4
Motif ID:	149
Motif name:	asmAGRGGGCrCTGsmkc
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward

Position number: 1
Number of overlap: 8
Similarity score: 0.0232655

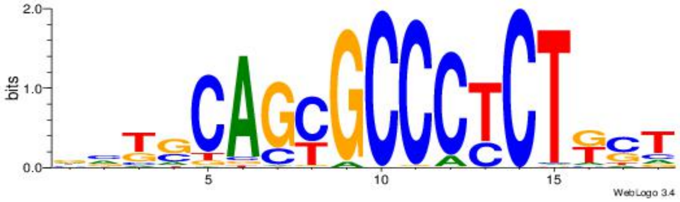
Alignment:

```
ASMAGAGGGCRCTGSABH
----------GCTGACDB
```

Original motif Consensus sequence: ASMAGAGGGCRCTGSABH



Reverse complement motif Consensus sequence: DBTSCAGMGCCCTCTRST

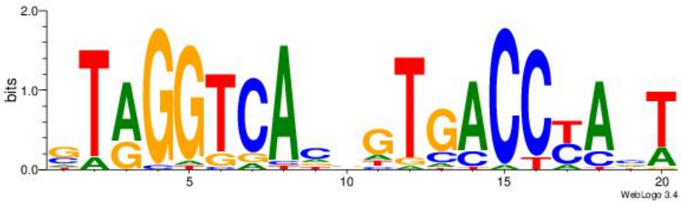


Dataset #: 3
Motif ID: 111
Motif name: PPARG
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 10
Number of overlap: 8
Similarity score: 0.0322069

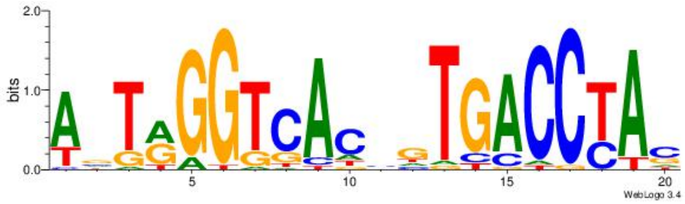
Alignment:

```
STAGGTCACBGTGACCYABT
---GCTGACDB---------
```

Original motif Consensus sequence: STAGGTCACBGTGACCYABT



Reverse complement motif Consensus sequence: ABTMGGTCACBGTGACCTAS

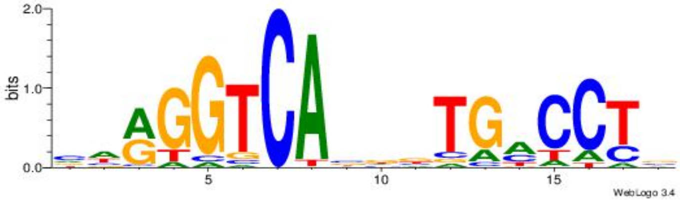


Dataset #:	3
Motif ID:	82
Motif name:	ESR2
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	3
Number of overlap:	8
Similarity score:	0.035275

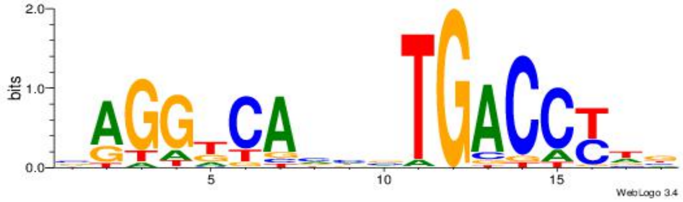
Alignment:

```
BAGGYCABHBTGACCKHV
--------GCTGACDB--
```

Original motif Consensus sequence: VHRGGTCABDBTGMCCTB



Reverse complement motif Consensus sequence: BAGGYCABHBTGACCKHV



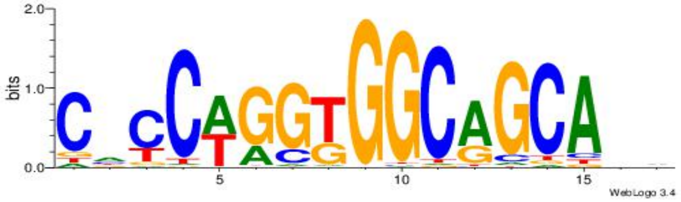
Dataset #: 4
Motif ID: 169
Motif name: yvTGCyGCCmCCwGgtG
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 7
Number of overlap: 8
Similarity score: 0.0358393

Alignment:

```
CDCCWGGTGGCAGCAVV
------BHGTCAGC---
```

Original motif Consensus sequence: BVTGCTGCCACCWGGDG

Reverse complement motif Consensus sequence: CDCCWGGTGGCAGCAVV



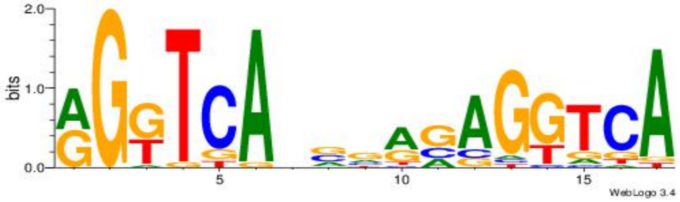
Dataset #: 3
Motif ID: 115
Motif name: RXRRAR_DR5
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 2

Number of overlap:	8
Similarity score:	0.0388936

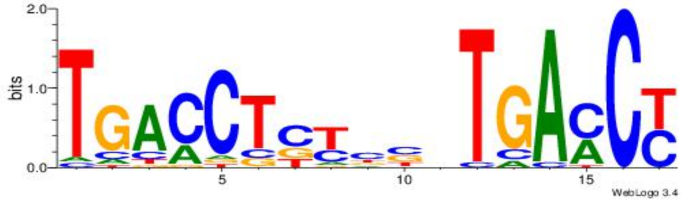
Alignment:

```
RGKTCABVVRGAGGTCA
-GCTGACDB--------
```

Original motif Consensus sequence: RGKTCABVVRGAGGTCA

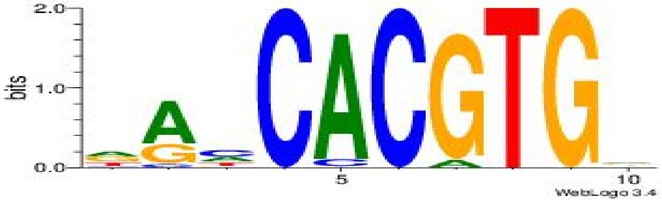


Reverse complement motif Consensus sequence: TGACCTCKVVBTGAYCK



Dataset #: 3 Motif ID: 91 Motif name: MAX

Original motif Consensus sequence: DAHCACGTGD



Reverse complement motif Consensus sequence: BCACGTGDTD

Best Matches for Motif ID 91 (Highest to Lowest)

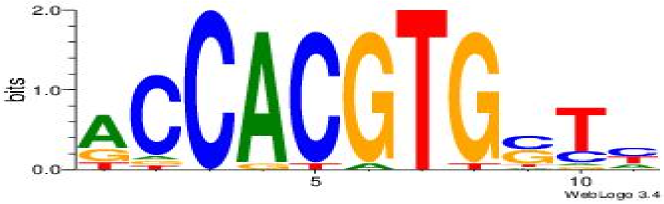
Dataset #:	3
Motif ID:	95
Motif name:	MYCMAX
Matching format of first motif:	Original Motif

Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 10
Similarity score: 0.0266106

Alignment:
```
RASCACGTGGT
DAHCACGTGD-
```

Original motif Consensus sequence: RASCACGTGGT

Reverse complement motif Consensus sequence: ACCACGTGSTM

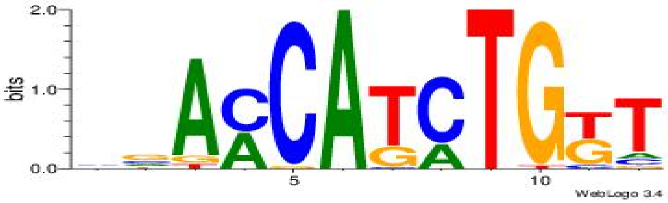


Dataset #: 3
Motif ID: 121
Motif name: TAL1TCF3
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 2
Number of overlap: 10
Similarity score: 0.0735692

Alignment:

ARCAGATGRTVD
-BCACGTGDTD-

Original motif Consensus sequence: HVAMCATCTGKT



Reverse complement motif Consensus sequence: ARCAGATGRTVD

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:	10
Similarity score:	0.0740659

Alignment:
DDCCACWAGRK
DAHCACGTGD-

Original motif Consensus sequence: DDCCACWAGRK

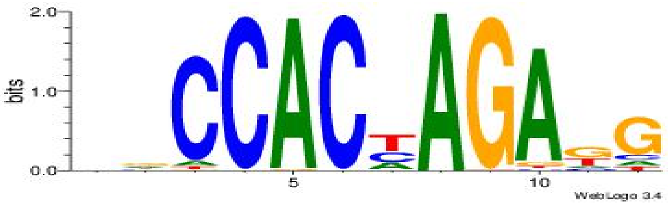
Reverse complement motif Consensus sequence: YMCTWGTGGHH

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:	1
Number of overlap:	10
Similarity score:	0.0824309

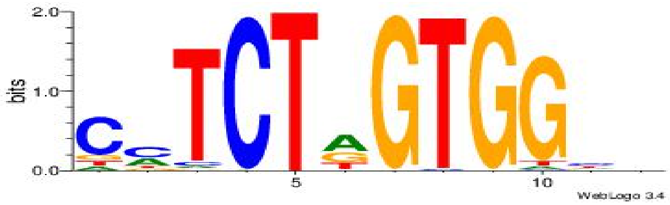
Alignment:

```
DDCCACYAGAKG
DAHCACGTGD--
```

Original motif Consensus sequence: DDCCACYAGAKG



Reverse complement motif Consensus sequence: CYTCTMGTGGHH



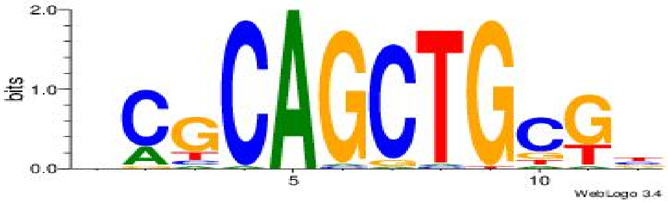
Dataset #:	3
Motif ID:	105
Motif name:	NHLH1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1

Number of overlap:	10
Similarity score:	0.0853797

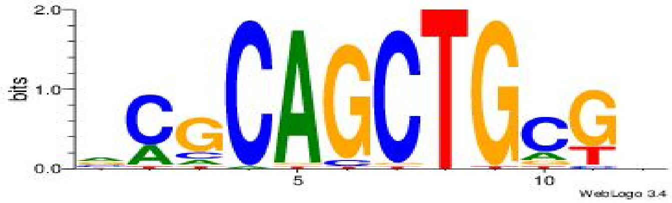
Alignment:

```
VCGCAGCTGCGB
--BCACGTGDTD
```

Original motif Consensus sequence: VCGCAGCTGCGB



Reverse complement motif Consensus sequence: VCGCAGCTGCGV



Dataset #: 3 Motif ID: 92 Motif name: MIZF

Original motif Consensus sequence: BAACGTCCGC

Reverse complement motif Consensus sequence: GCGGACGTTV

Best Matches for Motif ID 92 (Highest to Lowest)

Dataset #:	3
Motif ID:	84
Motif name:	GABPA
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement

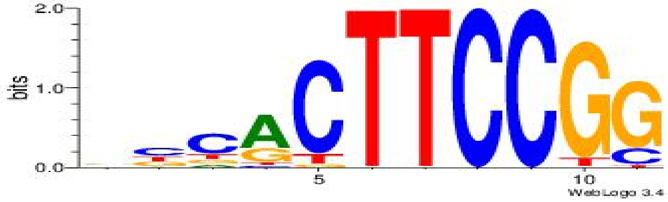
Direction: Forward
Position number: 1
Number of overlap: 10
Similarity score: 0.0326212

Alignment:

```
VVCACTTCCGG
BAACGTCCGC-
```

Original motif Consensus sequence: CCGGAAGTGVV

Reverse complement motif Consensus sequence: VVCACTTCCGG

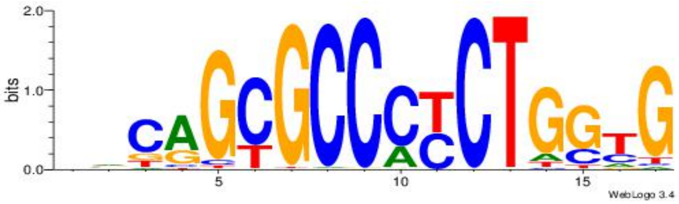


Dataset #: 4
Motif ID: 168
Motif name: yrcrGYGCCMyCTGGtG
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 6
Number of overlap: 10
Similarity score: 0.0553693

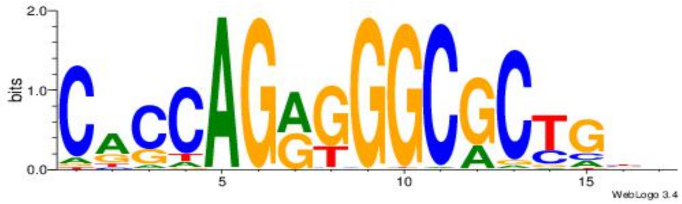
Alignment:

```
CACCAGMGGGCGCTGBD
-----GCGGACGTTV--
```

Original motif Consensus sequence: HVCAGCGCCCYCTGGTG



Reverse complement motif Consensus sequence: CACCAGMGGGCGCTGBD

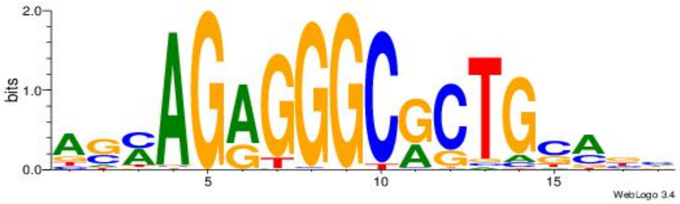


Dataset #:	4
Motif ID:	149
Motif name:	asmAGRGGGCrCTGsmkc
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	5
Number of overlap:	10
Similarity score:	0.0554206

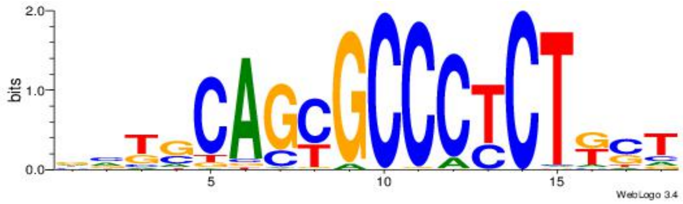
Alignment:

```
DBTSCAGMGCCCTCTRST
----BAACGTCCGC----
```

Original motif Consensus sequence: ASMAGAGGGCRCTGSABH



Reverse complement motif Consensus sequence: DBTSCAGMGCCCTCTRST



Dataset #: 3
Motif ID: 95
Motif name: MYCMAX
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 2
Number of overlap: 10
Similarity score: 0.0558866

Alignment:
ACCACGTGSTM
-BAACGTCCGC

Original motif Consensus sequence: RASCACGTGGT

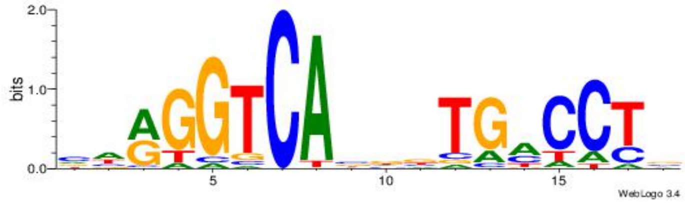
Reverse complement motif Consensus sequence: ACCACGTGSTM

Dataset #: 3
Motif ID: 82
Motif name: ESR2
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 10

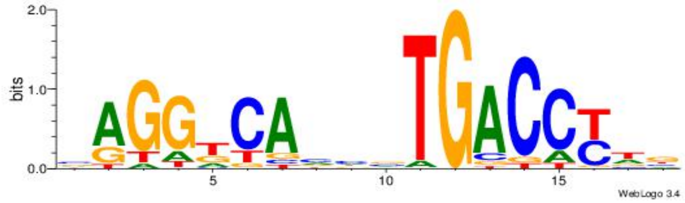
Similarity score: 0.0567619

Alignment:
BAGGYCABHBTGACCKHV
--------GCGGACGTTV

Original motif Consensus sequence: VHRGGTCABDBTGMCCTB



Reverse complement motif Consensus sequence: BAGGYCABHBTGACCKHV



Dataset #: 3 Motif ID: 93 Motif name: Myb

Original motif Consensus sequence: GRCVGTTG

Reverse complement motif Consensus sequence: CAACVGMC

Best Matches for Motif ID 93 (Highest to Lowest)

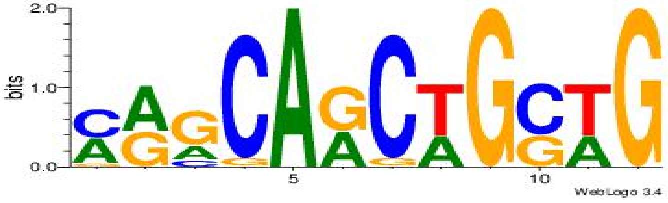
Dataset #:	3
Motif ID:	97
Motif name:	Myf
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif

Direction: Backward
Position number: 2
Number of overlap: 8
Similarity score: 0.0229626

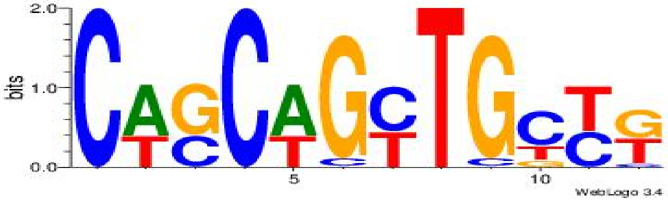
Alignment:

```
MRGCARCWGSWG
---CAACVGMC-
```

Original motif Consensus sequence: MRGCARCWGSWG



Reverse complement motif Consensus sequence: CWSCWGMTGCKR

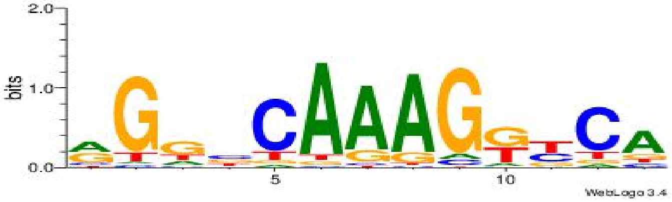


Dataset #: 3
Motif ID: 87
Motif name: HNF4A
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 5
Number of overlap: 8
Similarity score: 0.0239903

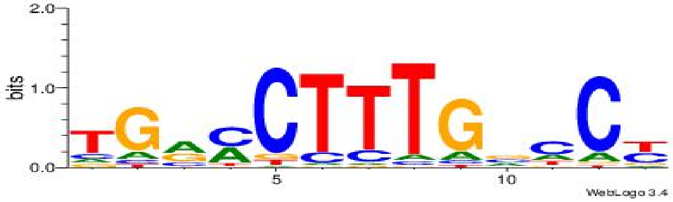
Alignment:

```
RGGBCAAAGKYCA
-CAACVGMC----
```

Original motif Consensus sequence: RGGBCAAAGKYCA



Reverse complement motif Consensus sequence: TGMYCTTTGBCCK

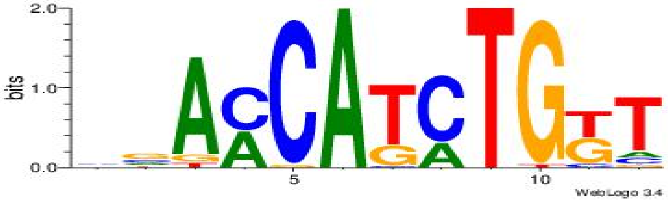


Dataset #:	3
Motif ID:	121
Motif name:	TAL1TCF3
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	8
Similarity score:	0.0259637

Alignment:

```
ARCAGATGRTVD
GRCVGTTG----
```

Original motif Consensus sequence: HVAMCATCTGKT



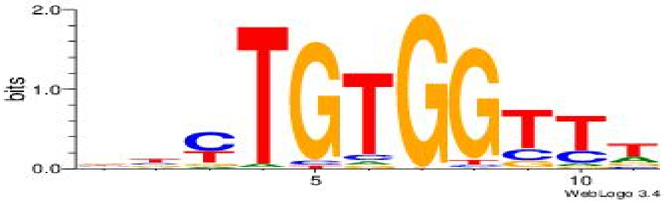
Reverse complement motif Consensus sequence: ARCAGATGRTVD

Dataset #: 3
Motif ID: 114
Motif name: RUNX1
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: 0.0297264

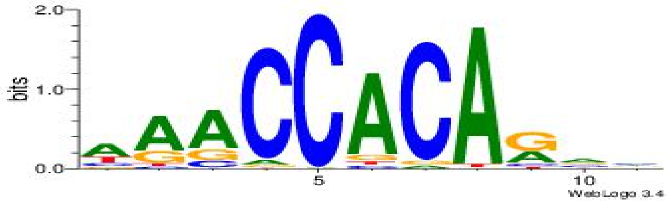
Alignment:

```
AAACCACAKVB
---CAACVGMC
```

Original motif Consensus sequence: BBYTGTGGTTT



Reverse complement motif Consensus sequence: AAACCACAKVB



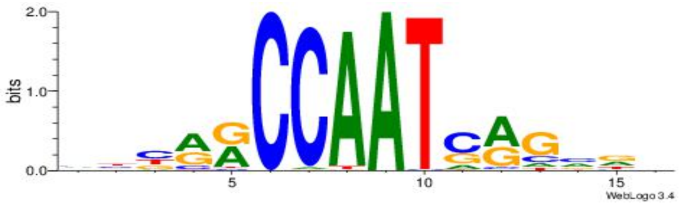
Dataset #: 3
Motif ID: 104
Motif name: NFYA
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 3
Number of overlap: 8

Similarity score:	0.0310894

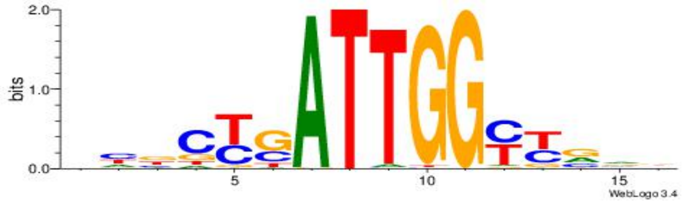
Alignment:

```
VBBRRCCAATSRGVDB
------CAACVGMC--
```

Original motif   Consensus sequence: VBBRRCCAATSRGVDB



Reverse complement motif   Consensus sequence: BHVCKSATTGGMKBVV



Dataset #: 3   Motif ID: 94   Motif name: Myc

Original motif   Consensus sequence: VGCACGTGGH

Reverse complement motif   Consensus sequence: DCCACGTGCV

Best Matches for Motif ID 94 (Highest to Lowest)

Dataset #:	3
Motif ID:	96
Motif name:	Mycn
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif

Direction:	Backward
Position number:	1
Number of overlap:	10
Similarity score:	0

Alignment:

```
HSCACGTGGC
VGCACGTGGH
```

Original motif   Consensus sequence: HSCACGTGGC

Reverse complement motif   Consensus sequence: GCCACGTGSD

Dataset #:	3
Motif ID:	95
Motif name:	MYCMAX
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	10
Similarity score:	0.0209359

Alignment:

```
RASCACGTGGT
-VGCACGTGGH
```

Original motif Consensus sequence: RASCACGTGGT

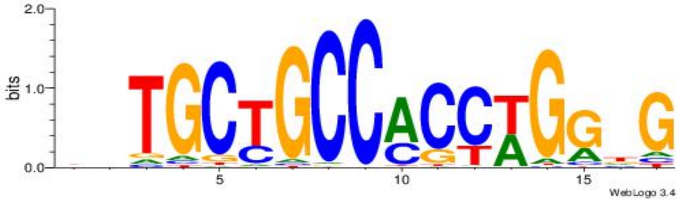
Reverse complement motif Consensus sequence: ACCACGTGSTM

Dataset #:	4
Motif ID:	169
Motif name:	yvTGCyGCCmCCwGgtG
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	7
Number of overlap:	10
Similarity score:	0.0628757

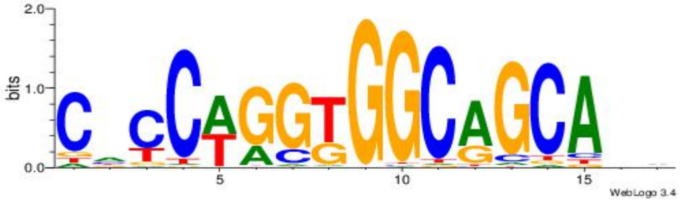
Alignment:

```
CDCCWGGTGGCAGCAVV
-VGCACGTGGH------
```

Original motif Consensus sequence: BVTGCTGCCACCWGGDG



Reverse complement motif Consensus sequence: CDCCWGGTGGCAGCAVV

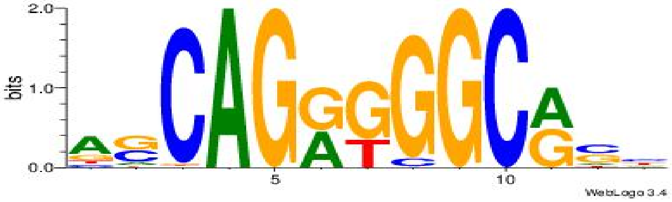


Dataset #: 4
Motif ID: 147
Motif name: asCAGrkGGCrsy
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 10
Similarity score: 0.0675017

Alignment:

```
ASCAGRGGGCRSB
VGCACGTGGH---
```

Original motif Consensus sequence: ASCAGRGGGCRSB



Reverse complement motif Consensus sequence: BSKGCCCMCTGST

Dataset #: 4
Motif ID: 158
Motif name: grCCACwAGrk
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 2
Number of overlap: 10

Similarity score: 0.0682475

Alignment:

```
DDCCACWAGRK
-DCCACGTGCV
```

Original motif Consensus sequence: DDCCACWAGRK

Reverse complement motif Consensus sequence: YMCTWGTGGHH

Dataset #: 3 Motif ID: 95 Motif name: MYCMAX

Original motif Consensus sequence: RASCACGTGGT

Reverse complement motif Consensus sequence: ACCACGTGSTM

Best Matches for Motif ID 95 (Highest to Lowest)

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: 1

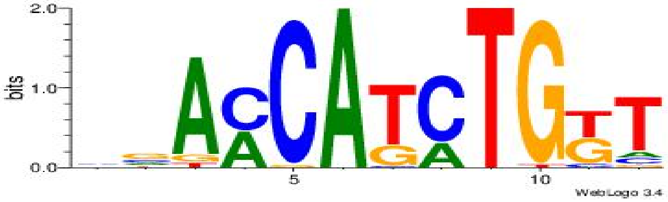
Number of overlap: 11

Similarity score: 0.0652343

Alignment:

```
HVAMCATCTGKT
-RASCACGTGGT
```

Original motif Consensus sequence: HVAMCATCTGKT



Reverse complement motif Consensus sequence: ARCAGATGRTVD

Dataset #: 4

Motif ID: 158

Motif name: grCCACwAGrk

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: 0.0786918

Alignment:

```
DDCCACWAGRK
RASCACGTGGT
```

Original motif Consensus sequence: DDCCACWAGRK

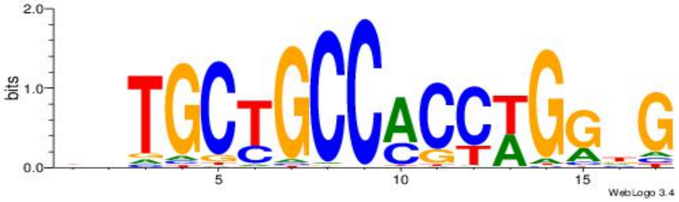
Reverse complement motif Consensus sequence: YMCTWGTGGHH

Dataset #:	4
Motif ID:	169
Motif name:	yvTGCyGCCmCCwGgtG
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	7
Number of overlap:	11
Similarity score:	0.0804522

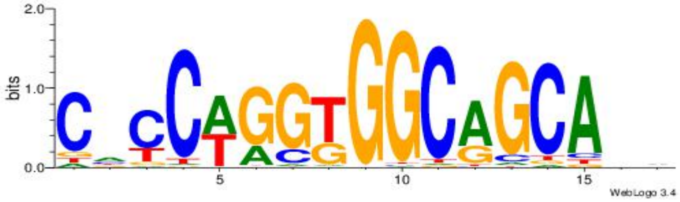
Alignment:

```
CDCCWGGTGGCAGCAVV
RASCACGTGGT------
```

Original motif Consensus sequence: BVTGCTGCCACCWGGDG



Reverse complement motif Consensus sequence: CDCCWGGTGGCAGCAVV



Dataset #: 3

Motif ID: 97

Motif name: Myf

Matching format of first motif: Reverse Complement

Matching format of second motif: Reverse Complement

Direction: Forward

Position number: 2

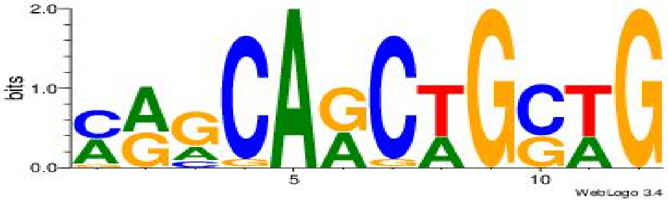
Number of overlap: 11

Similarity score: 0.0843705

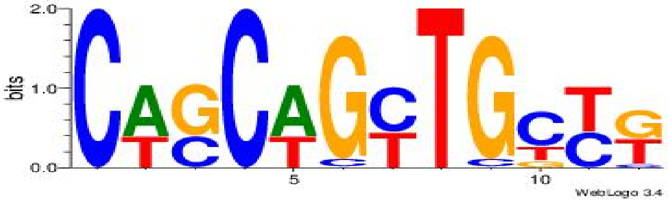
Alignment:

```
CWSCWGMTGCKR
-ACCACGTGSTM
```

Original motif Consensus sequence: MRGCARCWGSWG



Reverse complement motif Consensus sequence: CWSCWGMTGCKR



Dataset #: 3

Motif ID: 74

Motif name: CTCF

Matching format of first motif: Original Motif

Matching format of second motif: Original Motif

Direction: Forward

Position number: 5

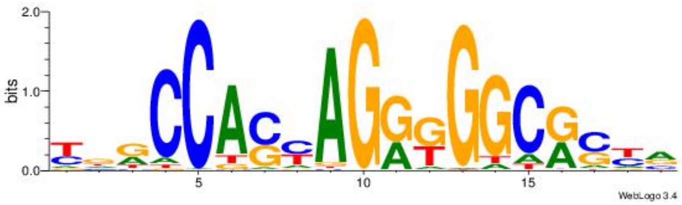
Number of overlap: 11

Similarity score: 0.084904

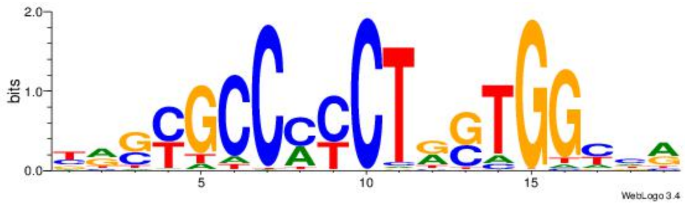
Alignment:

```
YDRCCASYAGRKGGCRSYV
----RASCACGTGGT----
```

Original motif Consensus sequence: YDRCCASYAGRKGGCRSYV



Reverse complement motif Consensus sequence: BMSMGCCYMCTKSTGGMHM



Dataset #: 3 Motif ID: 96 Motif name: Mycn

Original motif Consensus sequence: HSCACGTGGC

Reverse complement motif Consensus sequence: GCCACGTGSD

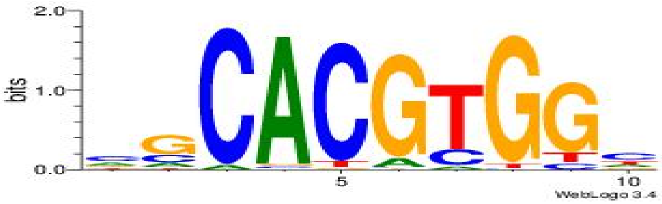
Best Matches for Motif ID 96 (Highest to Lowest)

Dataset #:	3
Motif ID:	94
Motif name:	Myc
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward

Position number: 1
Number of overlap: 10
Similarity score: 0

Alignment:
DCCACGTGCV
GCCACGTGSD

Original motif Consensus sequence: VGCACGTGGH



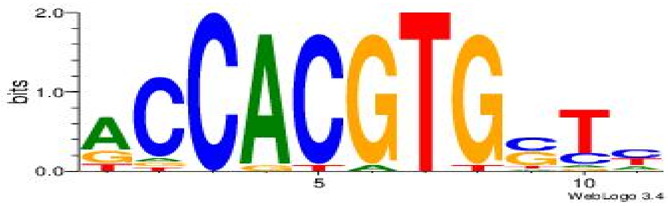
Reverse complement motif Consensus sequence: DCCACGTGCV

Dataset #: 3
Motif ID: 95
Motif name: MYCMAX
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 2
Number of overlap: 10
Similarity score: 0.0200467

Alignment:
RASCACGTGGT
-HSCACGTGGC

Original motif Consensus sequence: RASCACGTGGT

Reverse complement motif Consensus sequence: ACCACGTGSTM

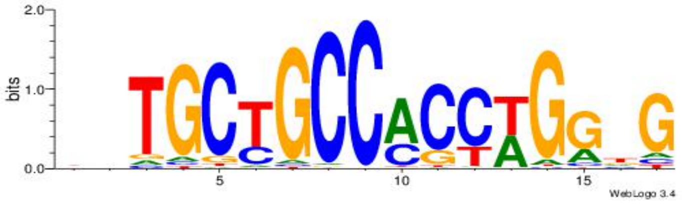


Dataset #:	4
Motif ID:	169
Motif name:	yvTGCyGCCmCCwGgtG
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	2
Number of overlap:	10
Similarity score:	0.0581322

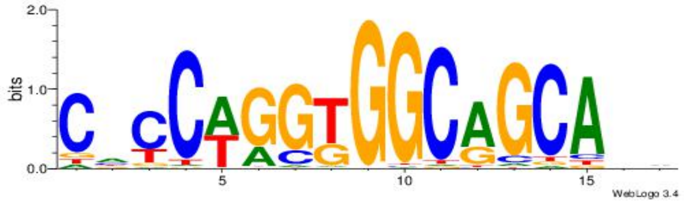
Alignment:

```
CDCCWGGTGGCAGCAVV
-HSCACGTGGC------
```

Original motif Consensus sequence: BVTGCTGCCACCWGGDG



Reverse complement motif Consensus sequence: CDCCWGGTGGCAGCAVV



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: 1
Number of overlap: 10
Similarity score: 0.0621075

Alignment:

```
ASCAGRGGGCRSB
HSCACGTGGC---
```

Original motif Consensus sequence: ASCAGRGGGCRSB

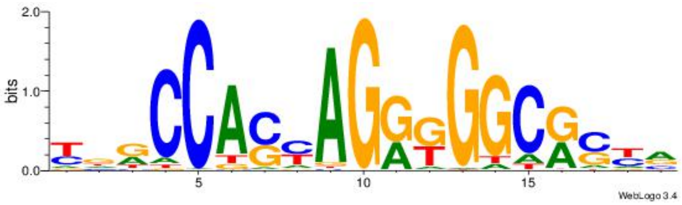
Reverse complement motif Consensus sequence: BSKGCCCMCTGST

Dataset #: 3
Motif ID: 74
Motif name: CTCF
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 6
Number of overlap: 10
Similarity score: 0.0679017

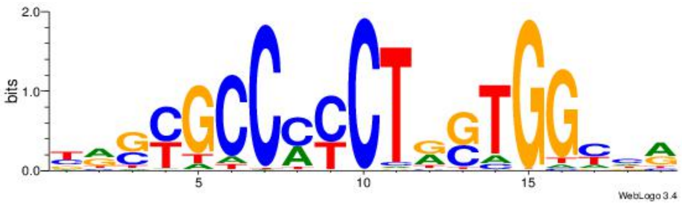
Alignment:

```
YDRCCASYAGRKGGCRSYV
-----HSCACGTGGC----
```

Original motif Consensus sequence: YDRCCASYAGRKGGCRSYV

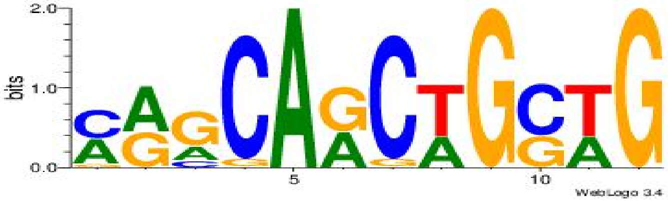


Reverse complement motif Consensus sequence: BMSMGCCYMCTKSTGGMHM

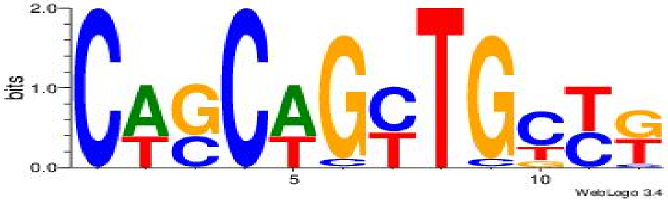


Dataset #: 3 Motif ID: 97 Motif name: Myf

Original motif Consensus sequence: MRGCARCWGSWG



Reverse complement motif Consensus sequence: CWSCWGMTGCKR



Best Matches for Motif ID 97 (Highest to Lowest)

Dataset #:	3
Motif ID:	105
Motif name:	NHLH1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward

Position number: 1

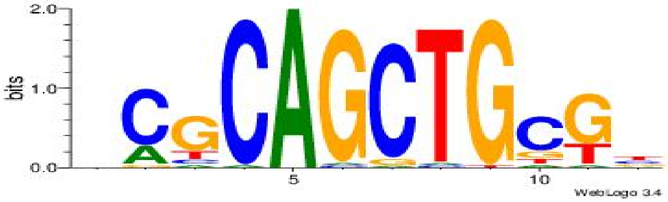
Number of overlap: 12

Similarity score: 0.0355504

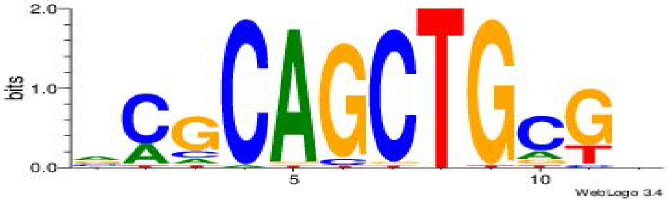
Alignment:

```
VCGCAGCTGCGV
CWSCWGMTGCKR
```

Original motif Consensus sequence: VCGCAGCTGCGB



Reverse complement motif Consensus sequence: VCGCAGCTGCGV



Dataset #: 3

Motif ID: 74

Motif name: CTCF

Matching format of first motif: Reverse Complement

Matching format of second motif: Original Motif

Direction: Backward

Position number: 5

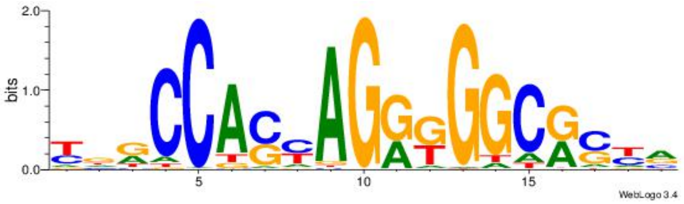
Number of overlap: 12

Similarity score: 0.0508517

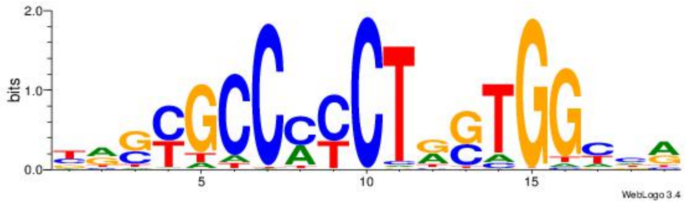
Alignment:

```
YDRCCASYAGRKGGCRSYV
---CWSCWGMTGCKR----
```

Original motif   Consensus sequence: YDRCCASYAGRKGGCRSYV



Reverse complement motif   Consensus sequence: BMSMGCCYMCTKSTGGMHM

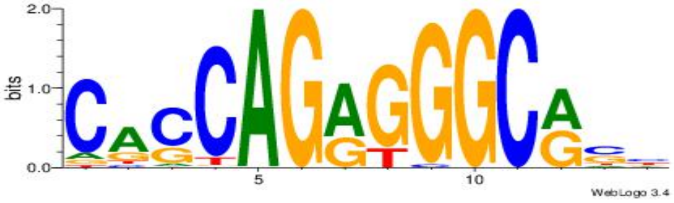


Dataset #:	4
Motif ID:	166
Motif name:	CasCAGrGGGCrsy
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	12
Similarity score:	0.055783

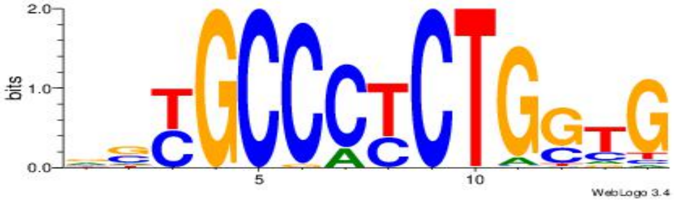
Alignment:

```
CACCAGRGGGCRSB
CWSCWGMTGCKR--
```

Original motif   Consensus sequence: CACCAGRGGGCRSB



Reverse complement motif   Consensus sequence: BSKGCCCKCTGGT

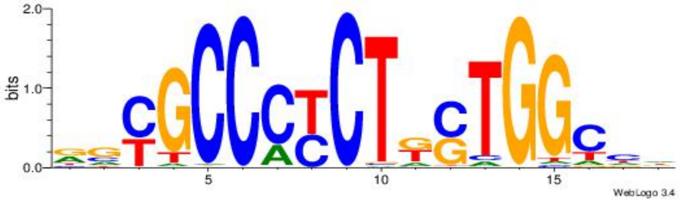


Dataset #: 4
Motif ID: 156
Motif name: rgyGCCMyCTksTGGccd
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 3
Number of overlap: 12
Similarity score: 0.058463

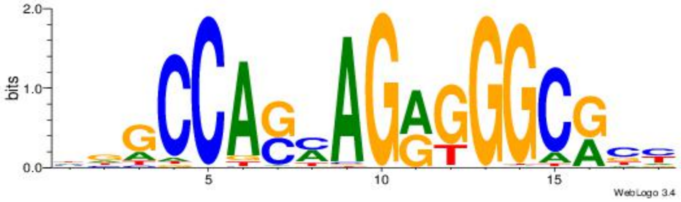
Alignment:

```
DDGCCASYAGMGGGCKVM
----CWSCWGMTGCKR--
```

Original motif Consensus sequence: RVYGCCCYCTKSTGGCHD



Reverse complement motif Consensus sequence: DDGCCASYAGMGGGCKVM



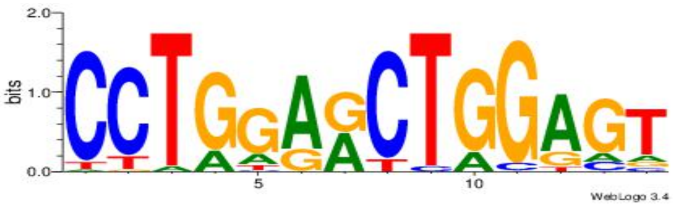
Dataset #: 2
Motif ID: 69
Motif name: Motif 69
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 2

Number of overlap:	12
Similarity score:	0.0591644

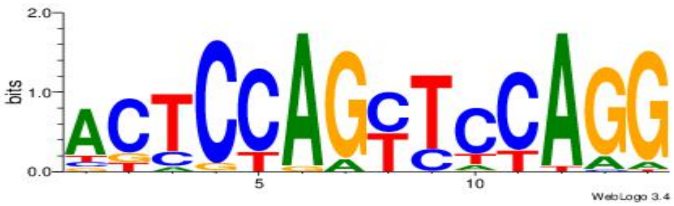
Alignment:

```
CCTGGARCTGGAGT
-MRGCARCWGSWG-
```

Original motif Consensus sequence: CCTGGARCTGGAGT



Reverse complement motif Consensus sequence: ACTCCAGMTCCAG



Dataset #: 3 Motif ID: 98 Motif name: MZF1_1-4

Original motif Consensus sequence: BGGGGA

Reverse complement motif Consensus sequence: TCCCCV

Best Matches for Motif ID 98 (Highest to Lowest)

Dataset #:	3
Motif ID:	88
Motif name:	INSM1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement

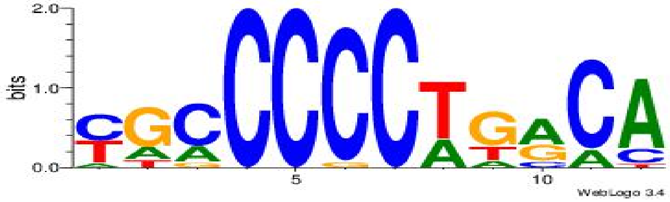
Direction: Backward
Position number: 5
Number of overlap: 6
Similarity score: 0.033712

Alignment:

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

Original motif Consensus sequence: TGYCAGGGGGCR

Reverse complement motif Consensus sequence: MGCCCCCTGMCA



Dataset #: 3
Motif ID: 77
Motif name: EBF1
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: 0.0339898

Alignment:

```
MCCCMAGGGA
----BGGGGA
```

Original motif Consensus sequence: MCCCMAGGGA

Reverse complement motif Consensus sequence: TCCCTYGGGY

Dataset #: 4

Motif ID: 155

Motif name: csCSCCdCCCcs

Matching format of first motif: Reverse Complement

Matching format of second motif: Original Motif

Direction: Backward

Position number: 1

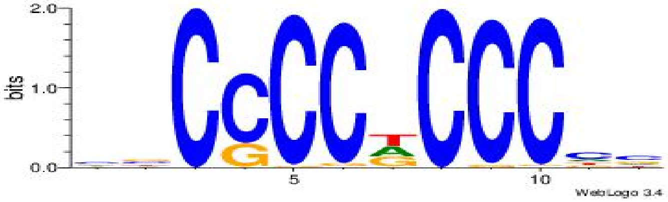
Number of overlap: 6

Similarity score: 0.0344568

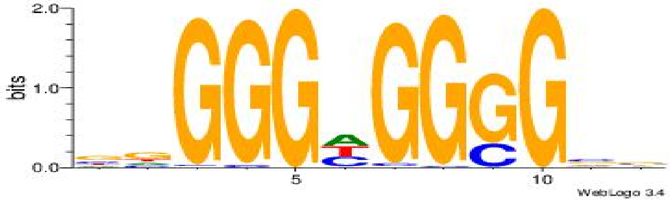
Alignment:

```
VBCCCCDCCCHV
------TCCCCV
```

Original motif Consensus sequence: VBCCCCDCCCHV



Reverse complement motif Consensus sequence: VDGGGDGGGGBV



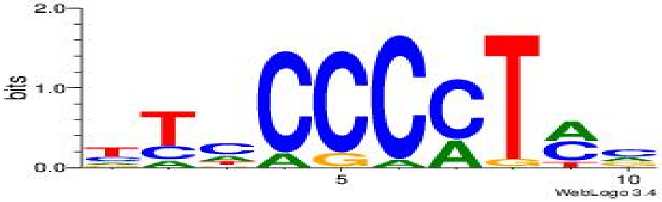
Dataset #:	3
Motif ID:	99
Motif name:	MZF1_5-13
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	4
Number of overlap:	6
Similarity score:	0.0375315

Alignment:

```
BKAGGGGDAD
---BGGGGA-
```

Original motif Consensus sequence: BKAGGGGDAD

Reverse complement motif Consensus sequence: BTHCCCCTYB



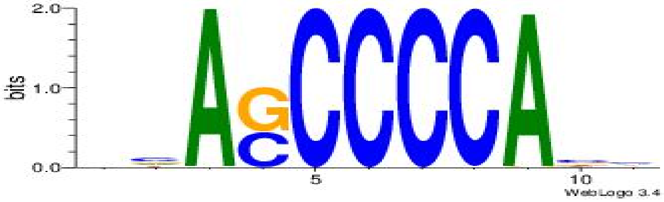
Dataset #:	4
Motif ID:	162
Motif name:	ccAsCCCCAcc
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	4
Number of overlap:	6

Similarity score:	0.0465466

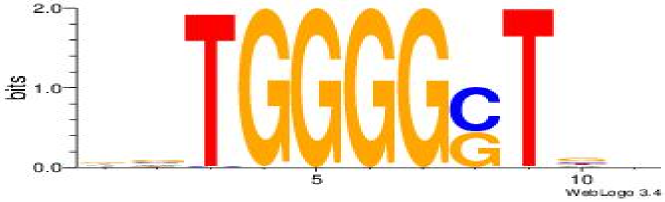
Alignment:

```
HVASCCCCABH
---TCCCCV--
```

Original motif Consensus sequence: HVASCCCCABH



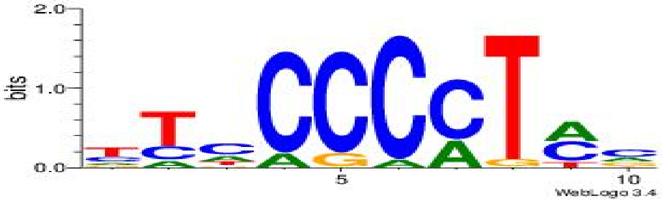
Reverse complement motif Consensus sequence: DBTGGGGSTVD



Dataset #: 3 **Motif ID: 99** **Motif name: MZF1_5-13**

Original motif Consensus sequence: BKAGGGGDAD

Reverse complement motif Consensus sequence: BTHCCCCTYB



Best Matches for Motif ID 99 (Highest to Lowest)

Dataset #:	3
Motif ID:	88
Motif name:	INSM1
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward

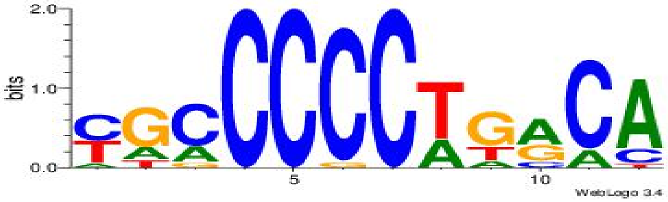
Position number:	3
Number of overlap:	10
Similarity score:	0.0360532

Alignment:

```
TGYCAGGGGGCR
--BKAGGGGDAD
```

Original motif   Consensus sequence: TGYCAGGGGGCR

Reverse complement motif   Consensus sequence: MGCCCCCTGMCA

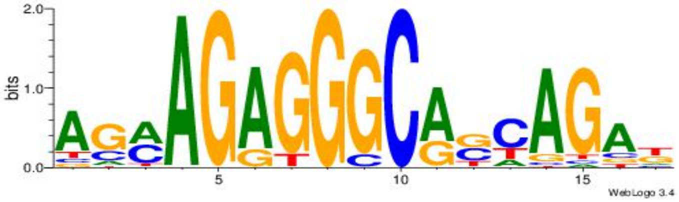


Dataset #:	4
Motif ID:	143
Motif name:	AgmAGAGGGCrscAGak
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	2
Number of overlap:	10
Similarity score:	0.0361803

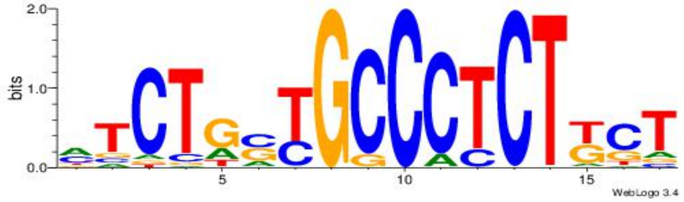
Alignment:

```
RTCTGSTGCCCTCTYCT
------BTHCCCCTYB-
```

Original motif Consensus sequence: AGMAGAGGGCASCAGAK



Reverse complement motif Consensus sequence: RTCTGSTGCCCTCTYCT

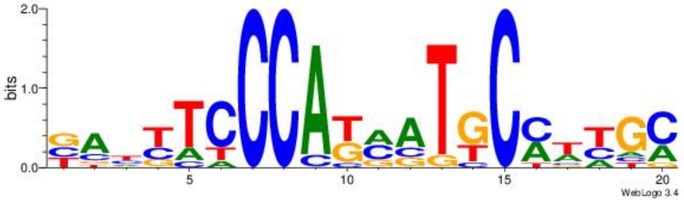


Dataset #:	3
Motif ID:	131
Motif name:	znf143
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	3
Number of overlap:	10
Similarity score:	0.0377199

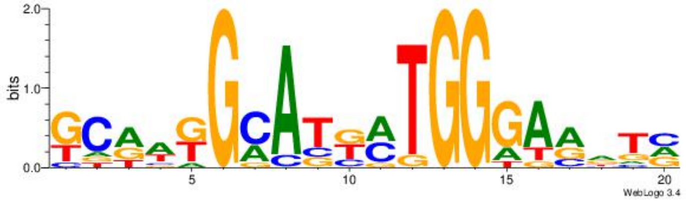
Alignment:

```
GCMWRGCATYRTGGGAMHTB
--------BKAGGGGDAD--
```

Original motif Consensus sequence: BAHYTCCCAKMATGCMWYGC



Reverse complement motif Consensus sequence: GCMWRGCATYRTGGGAMHTB

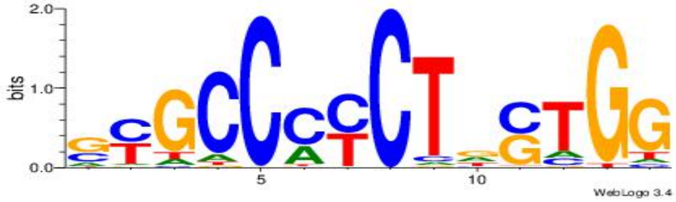


Dataset #:	2
Motif ID:	67
Motif name:	Motif 67
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	2
Number of overlap:	10
Similarity score:	0.0386182

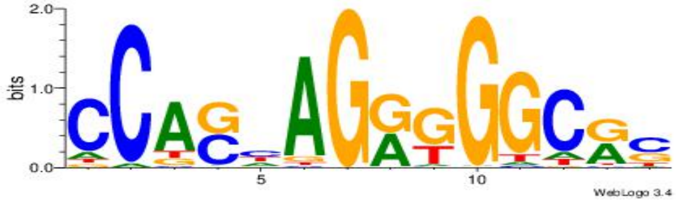
Alignment:

```
CCASHAGKGGGCKS
-BKAGGGGDAD---
```

Original motif Consensus sequence: SYGCCCYCTDSTGG



Reverse complement motif Consensus sequence: CCASHAGKGGGCK



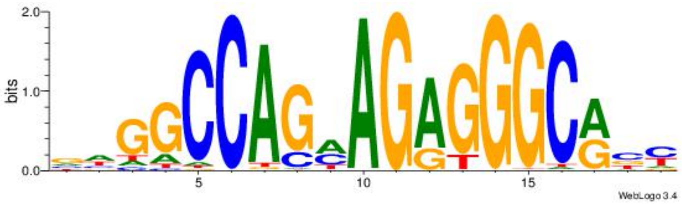
Dataset #:	4
Motif ID:	163
Motif name:	gwGGCCAGmAGAGGGCrby
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	3
Number of overlap:	10

Similarity score:	0.0397537

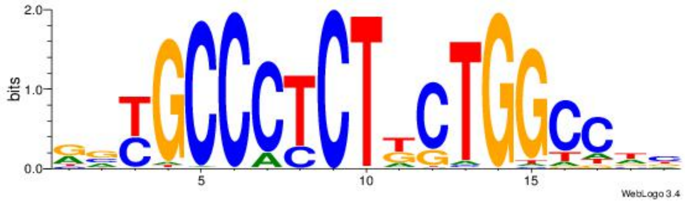
Alignment:

```
KBKGCCCTCTYCTGGCCHV
--BTHCCCCTYB-------
```

Original motif Consensus sequence: VHGGCCAGMAGAGGGCRBY

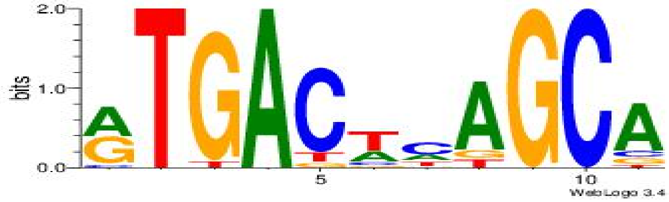


Reverse complement motif Consensus sequence: KBKGCCCTCTYCTGGCCHV



Dataset #: 3 **Motif ID: 100** **Motif name: NFE2L2**

Original motif Consensus sequence: RTGACWHAGCA



Reverse complement motif Consensus sequence: TGCTDWGTCAK

Best Matches for Motif ID 100 (Highest to Lowest)

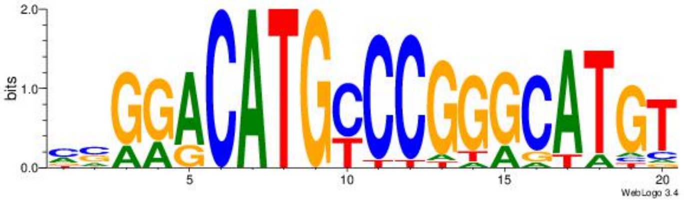
Dataset #:	3
Motif ID:	125
Motif name:	TP53
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement

Direction: Forward
Position number: 4
Number of overlap: 11
Similarity score: 0.0588881

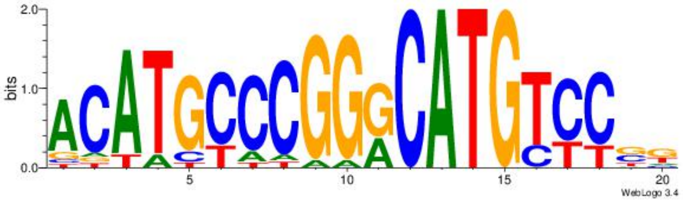
Alignment:

```
ACATGCCCGGKCATGTCCSR
---TGCTDWGTCAK------
```

Original motif Consensus sequence: MSGGACATGYCCGGGCATGT



Reverse complement motif Consensus sequence:
ACATGCCCGGKCATGTCCSR

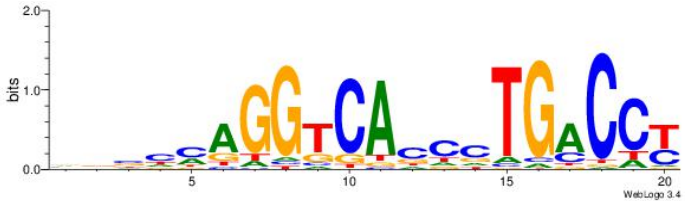


Dataset #: 3
Motif ID: 81
Motif name: ESR1
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2
Number of overlap: 11
Similarity score: 0.0627853

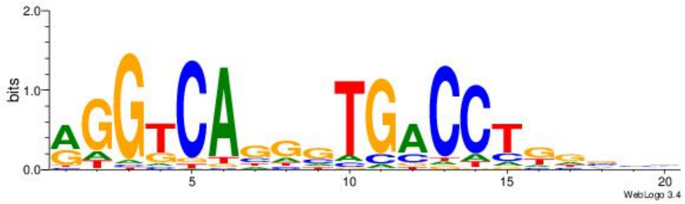
Alignment:

```
VDBHMAGGTCACCCTGACCY
--------TGCTDWGTCAK-
```

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV

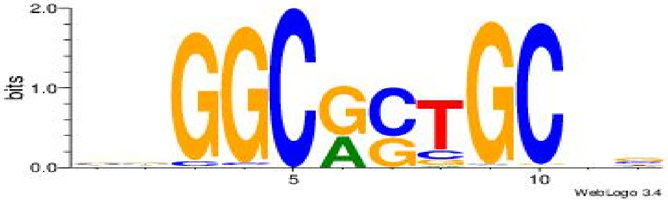


Dataset #:	4
Motif ID:	170
Motif name:	ssGGCrsTGCrs
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	11
Similarity score:	0.0672435

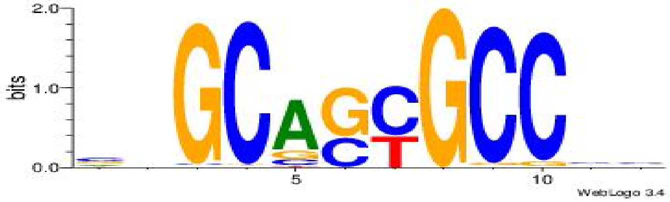
Alignment:

```
VVGGCRSTGCVB
RTGACWHAGCA-
```

Original motif Consensus sequence: VVGGCRSTGCVB



Reverse complement motif Consensus sequence: BVGCASMGCCVV

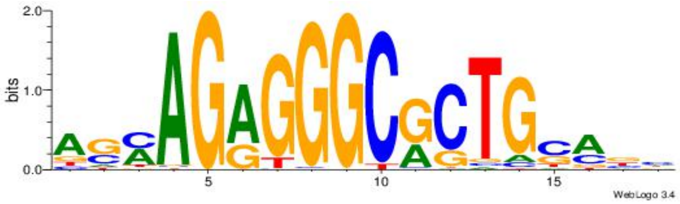


Dataset #:	4
Motif ID:	149
Motif name:	asmAGRGGGCrCTGsmkc
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	6
Number of overlap:	11
Similarity score:	0.070397

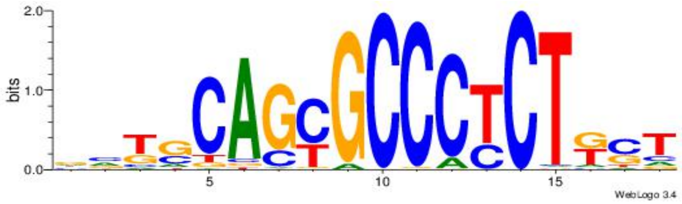
Alignment:

```
ASMAGAGGGCRCTGSABH
-----RTGACWHAGCA--
```

Original motif Consensus sequence: ASMAGAGGGCRCTGSABH



Reverse complement motif Consensus sequence: DBTSCAGMGCCCTCTRST



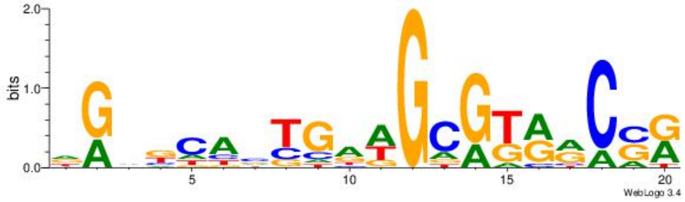
Dataset #:	3
Motif ID:	109
Motif name:	Pax5
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	3

Number of overlap:	11
Similarity score:	0.0725913

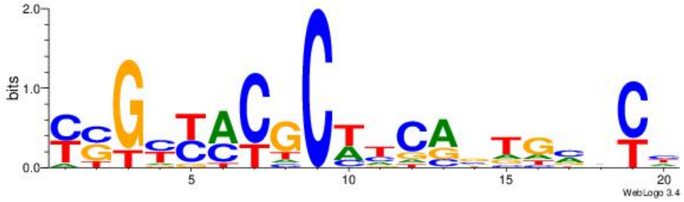
Alignment:

```
MSGKKRCGCWDCABTGBBCD
--RTGACWHAGCA-------
```

Original motif Consensus sequence: DGVBCABTGDWGCGKRRCSR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD



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

Original motif Consensus sequence: TTGGCD

Reverse complement motif Consensus sequence: DGCCAA

Best Matches for Motif ID 101 (Highest to Lowest)

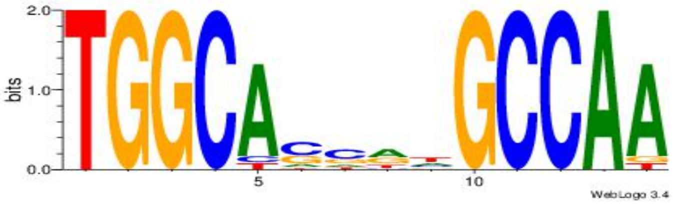
Dataset #:	3
Motif ID:	124
Motif name:	TLX1NFIC
Matching format of first motif:	Original Motif

Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 6
Similarity score: 0

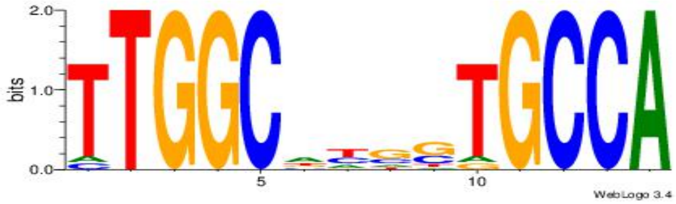
Alignment:

```
TTGGCHDBSTGCCA
TTGGCD--------
```

Original motif Consensus sequence: TGGCASBDHGCCAA



Reverse complement motif Consensus sequence: TTGGCHDBSTGCC

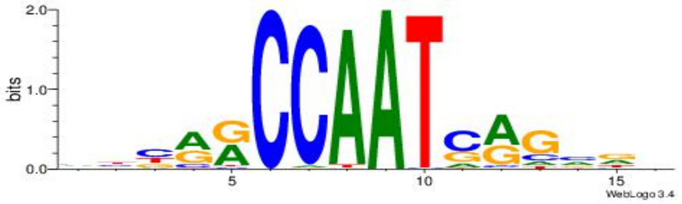


Dataset #: 3
Motif ID: 104
Motif name: NFYA
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 4
Number of overlap: 6
Similarity score: 0.020508

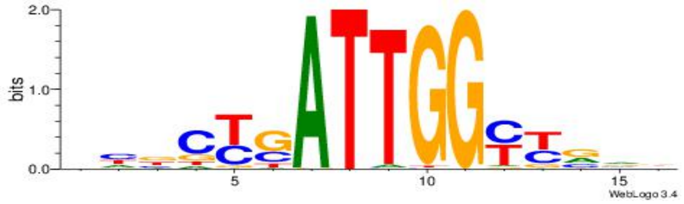
Alignment:

```
VBBRRCCAATSRGVDB
---DGCCAA-------
```

Original motif Consensus sequence: VBBRRCCAATSRGVDB



Reverse complement motif Consensus sequence: BHVCKSATTGGMKBVV



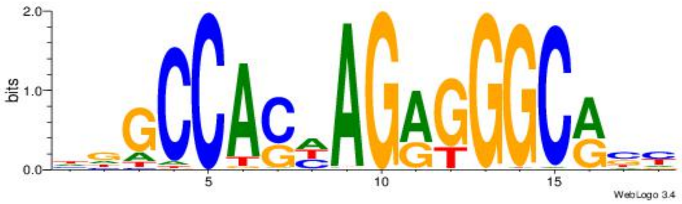
Dataset #:	4
Motif ID:	165
Motif name:	wgGCCAshAGrGGGCrsy
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	12
Number of overlap:	6
Similarity score:	0.0215379

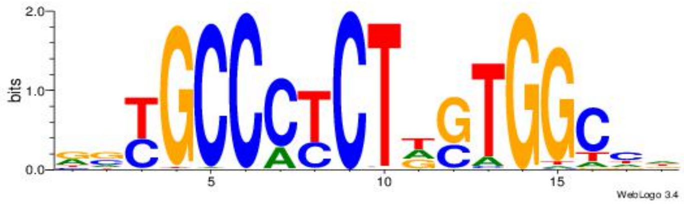
Alignment:

```
HDGCCACHAGRGGGCRBY
-DGCCAA-----------
```

Original motif Consensus sequence: HDGCCACHAGRGGGCRBY

Reverse complement motif Consensus sequence: KBKGCCCKCTHGTGGCHH





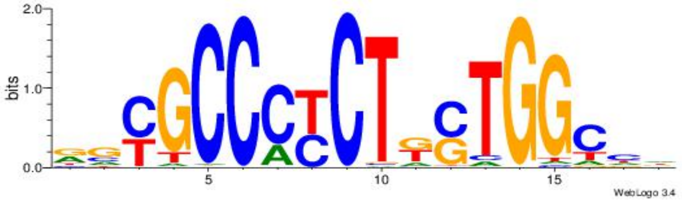
Dataset #:	4
Motif ID:	156
Motif name:	rgyGCCMyCTksTGGccd
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	2
Number of overlap:	6
Similarity score:	0.026631

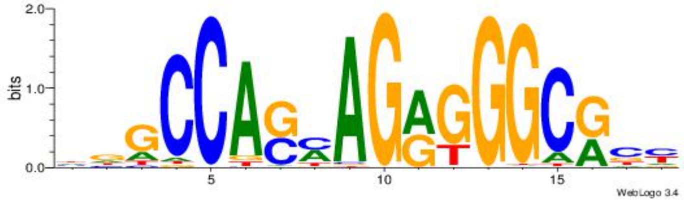
Alignment:

```
DDGCCASYAGMGGGCKVM
-DGCCAA-----------
```

Original motif   Consensus sequence: RVYGCCCYCTKSTGGCHD

Reverse complement motif   Consensus sequence: DDGCCASYAGMGGGCKVM





Dataset #:	4

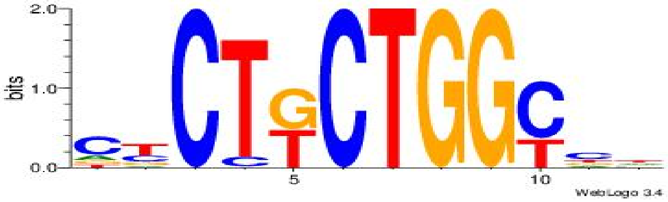
Motif ID:	151
Motif name:	agrCCAGmAGrg
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	2
Number of overlap:	6
Similarity score:	0.0273632

Alignment:

```
CKCTRCTGGCVH
-----TTGGCD-
```

Original motif Consensus sequence: HVGCCAGMAGRG

Reverse complement motif Consensus sequence: CKCTRCTGGCVH



Dataset #: 3 Motif ID: 102 Motif name: NF-kappaB

Original motif Consensus sequence: GGGRMTTYCC

Reverse complement motif Consensus sequence: GGMAAYKCCC

Best Matches for Motif ID 102 (Highest to Lowest)

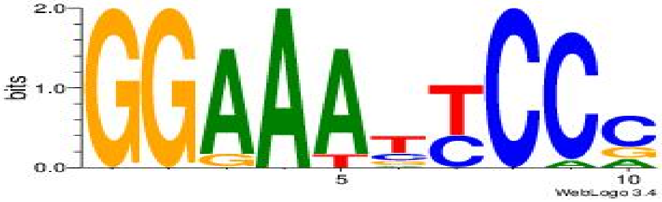
Dataset #:	3
Motif ID:	112
Motif name:	RELA
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	10
Similarity score:	0.0219591

Alignment:

```
GGGRATTTCC
GGGRMTTYCC
```

Original motif Consensus sequence: GGGRATTTCC

Reverse complement motif Consensus sequence: GGAAATKCCC



Dataset #:	3
Motif ID:	103
Motif name:	NFKB1
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif

Direction:	Forward
Position number:	1
Number of overlap:	10
Similarity score:	0.0264912

Alignment:

```
GGGGRTTCCCC
GGGRMTTYCC-
```

Original motif Consensus sequence: GGGGRTTCCCC

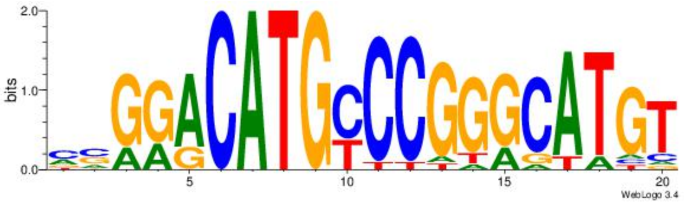
Reverse complement motif Consensus sequence: GGGGAAKCCCC

Dataset #:	3
Motif ID:	125
Motif name:	TP53
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	9
Number of overlap:	10
Similarity score:	0.0780263

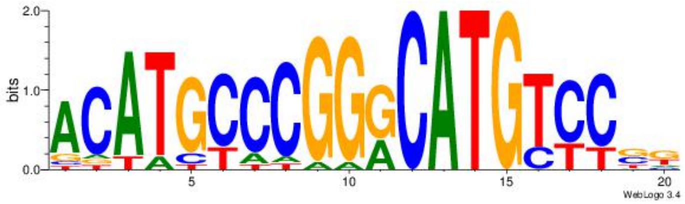
Alignment:

```
MSGGACATGYCCGGGCATGT
--GGMAAYKCCC--------
```

Original motif Consensus sequence: MSGGACATGYCCGGGCATGT



Reverse complement motif Consensus sequence: ACATGCCCGGKCATGTCCSR

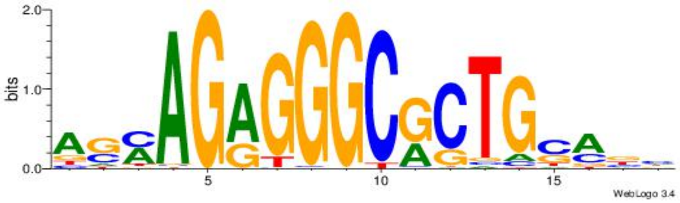


Dataset #:	4
Motif ID:	149
Motif name:	asmAGRGGGCrCTGsmkc
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	7
Number of overlap:	10
Similarity score:	0.078539

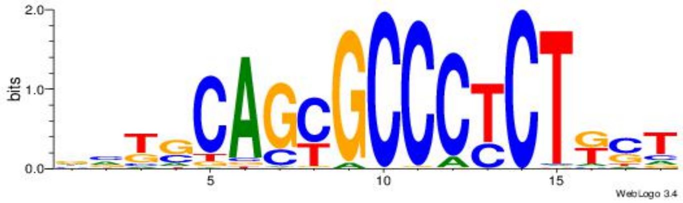
Alignment:

```
DBTSCAGMGCCCTCTRST
--GGMAAYKCCC------
```

Original motif Consensus sequence: ASMAGAGGGCRCTGSABH



Reverse complement motif Consensus sequence: DBTSCAGMGCCCTCTRST

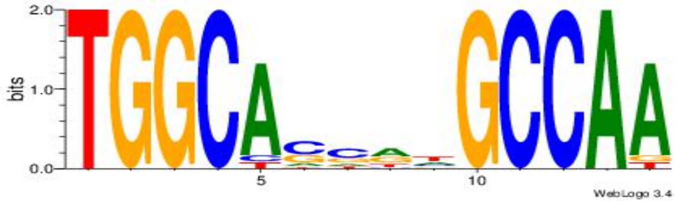


Dataset #: 3
Motif ID: 124
Motif name: TLX1NFIC
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 2
Number of overlap: 10
Similarity score: 0.0847697

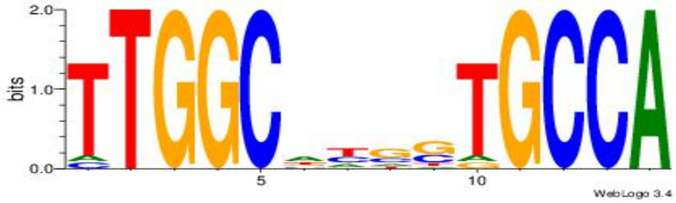
Alignment:

```
TGGCASBDHGCCAA
-GGMAAYKCCC---
```

Original motif Consensus sequence: TGGCASBDHGCCAA



Reverse complement motif Consensus sequence: TTGGCHDBSTGCC



Dataset #: 3 Motif ID: 103 Motif name: NFKB1

Original motif Consensus sequence: GGGGRTTCCCC

Reverse complement motif Consensus sequence: GGGGAAKCCCC

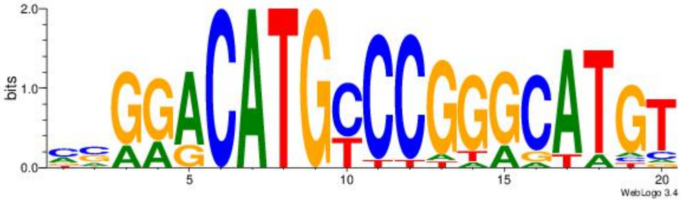
Best Matches for Motif ID 103 (Highest to Lowest)

Dataset #:	3
Motif ID:	125
Motif name:	TP53
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	11
Similarity score:	0.100899

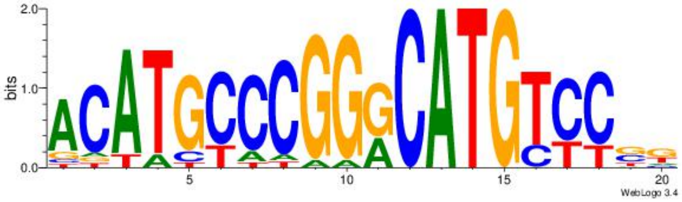
Alignment:

```
MSGGACATGYCCGGGCATGT
-GGGGAAKCCCC--------
```

Original motif Consensus sequence: MSGGACATGYCCGGGCATGT



Reverse complement motif Consensus sequence: ACATGCCCGGKCATGTCCSR



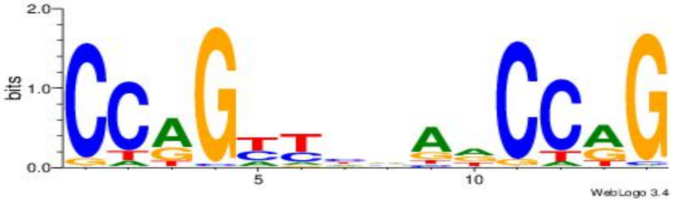
Dataset #:	3
Motif ID:	122
Motif name:	Tcfcp2l1
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement

Direction: Backward
Position number: 4
Number of overlap: 11
Similarity score: 0.103405

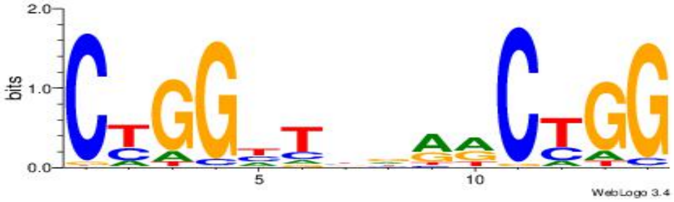
Alignment:

```
CKGGDTBDMMCTGG
GGGGRTTCCCC---
```

Original motif Consensus sequence: CCAGYYHVADCCRG



Reverse complement motif Consensus sequence: CKGGDTBDMMCT

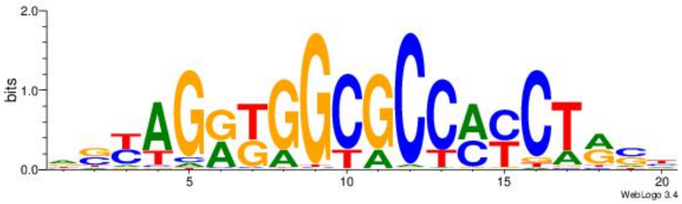


Dataset #: 4
Motif ID: 167
Motif name: rsyAGrkGGCGCCmyCTrsy
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 5
Number of overlap: 11
Similarity score: 0.104275

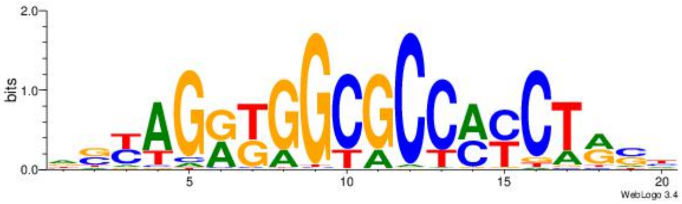
Alignment:

```
DSYAGRKGGCGCCMYCTRSH
-----GGGGRTTCCCC----
```

Original motif Consensus sequence: DSYAGRKGGCGCCMYCTRSH



Reverse complement motif Consensus sequence: HSKAGKYGGCGCCRMCTMSD

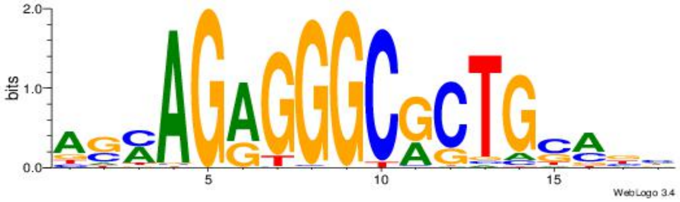


Dataset #:	4
Motif ID:	149
Motif name:	asmAGRGGGCrCTGsmkc
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	11
Similarity score:	0.109809

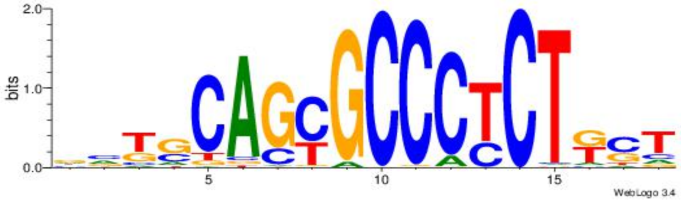
Alignment:

```
DBTSCAGMGCCCTCTRST
GGGGAAKCCCC-------
```

Original motif Consensus sequence: ASMAGAGGGCRCTGSABH



Reverse complement motif Consensus sequence: DBTSCAGMGCCCTCTRST



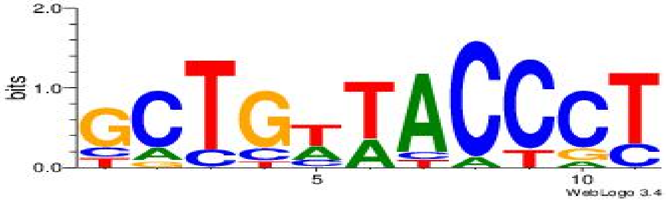
Dataset #:	3
Motif ID:	117
Motif name:	Spz1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	11
Similarity score:	0.11048

Alignment:

```
AGGGTAWCAGC
GGGGAAKCCCC
```

Original motif Consensus sequence: AGGGTAWCAGC

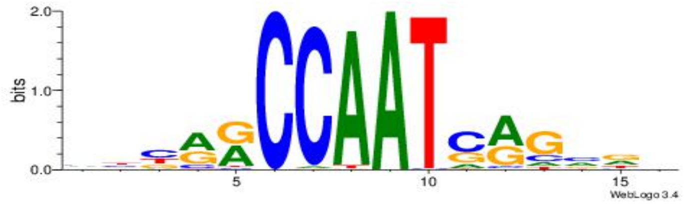
Reverse complement motif Consensus sequence: GCTGWTACCCT

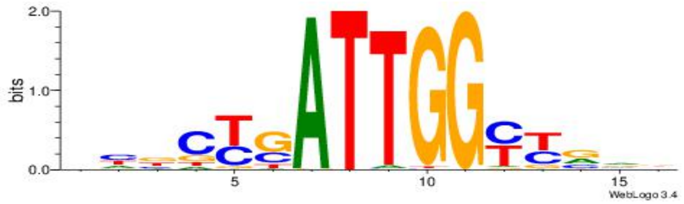


Dataset #: 3 **Motif ID: 104** **Motif name: NFYA**

Original motif Consensus sequence: VBBRRCCAATSRGVDB

Reverse complement motif Consensus sequence: BHVCKSATTGGMKBVV





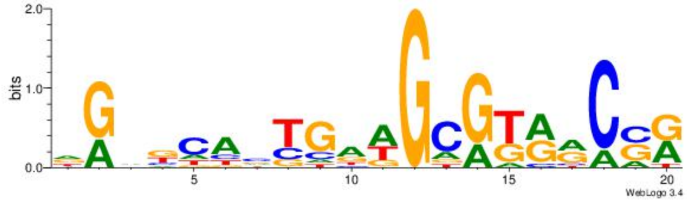
Best Matches for Motif ID 104 (Highest to Lowest)

Dataset #:	3
Motif ID:	109
Motif name:	Pax5
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	2
Number of overlap:	16
Similarity score:	0.0555608

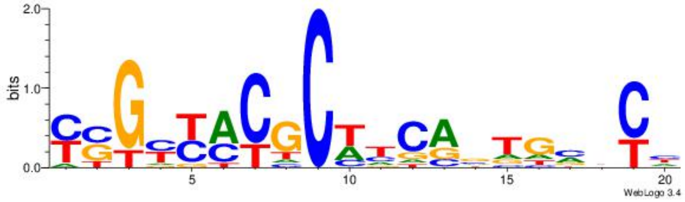
Alignment:

```
MSGKKRCGCWDCABTGBBCD
-VBBRRCCAATSRGVDB---
```

Original motif Consensus sequence: DGVBCABTGDWGCGKRRCSR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD

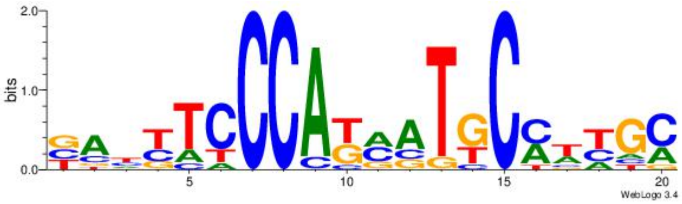


Dataset #:	3
Motif ID:	131
Motif name:	znf143
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	16
Similarity score:	0.0645227

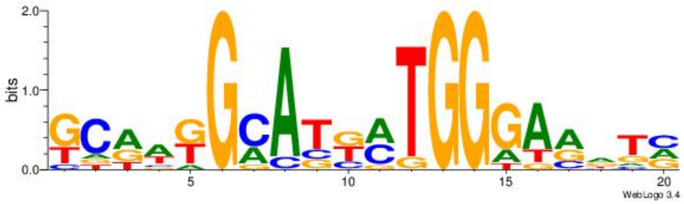
Alignment:

```
BAHYTCCCAKMATGCMWYGC
-VBBRRCCAATSRGVDB---
```

Original motif Consensus sequence: BAHYTCCCAKMATGCMWYGC



Reverse complement motif Consensus sequence: GCMWRGCATYRTGGGAMHTB



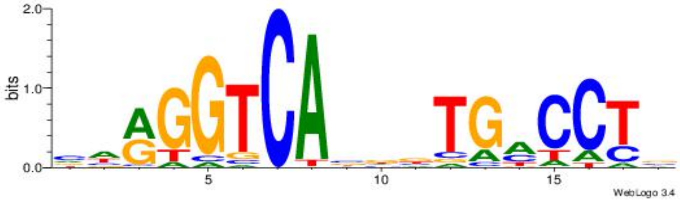
Dataset #:	3
Motif ID:	82
Motif name:	ESR2
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	3

Number of overlap: 16
Similarity score: 0.0658537

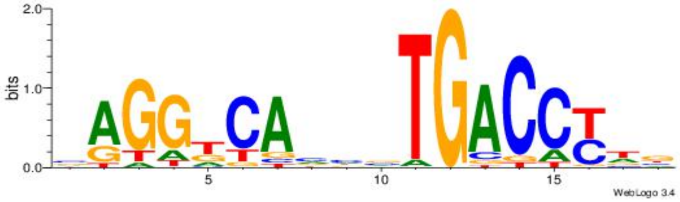
Alignment:

```
BAGGYCABHBTGACCKHV
--BHVCKSATTGGMKBVV
```

Original motif Consensus sequence: VHRGGTCABDBTGMCCTB



Reverse complement motif Consensus sequence: BAGGYCABHBTGACCKHV

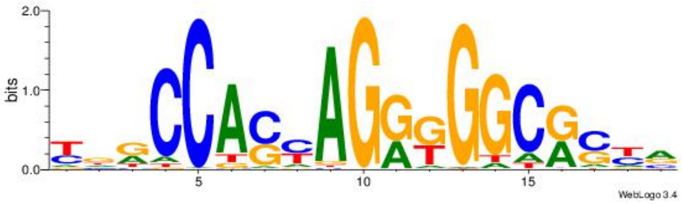


Dataset #: 3
Motif ID: 74
Motif name: CTCF
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 2
Number of overlap: 16
Similarity score: 0.0705004

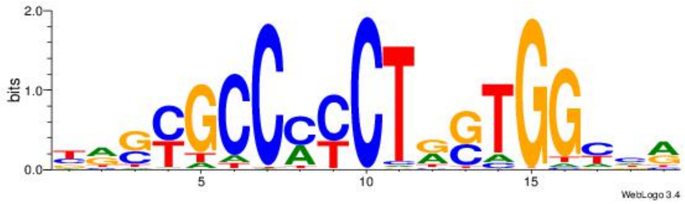
Alignment:

```
BMSMGCCYMCTKSTGGMHM
--BHVCKSATTGGMKBVV-
```

Original motif Consensus sequence: YDRCCASYAGRKGGCRSYV



Reverse complement motif Consensus sequence: BMSMGCCYMCTKSTGGMHM

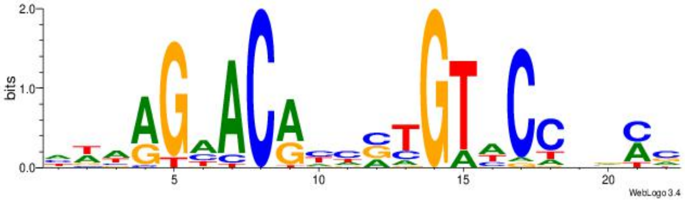


Dataset #:	3
Motif ID:	70
Motif name:	Ar
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	3
Number of overlap:	16
Similarity score:	0.0709164

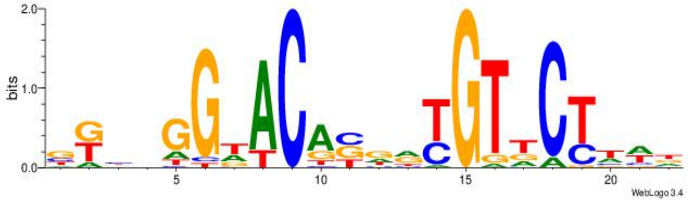
Alignment:

```
VRVDGGHACAVDDKGTHCTDWH
----VBBRRCCAATSRGVDB--
```

Original motif Consensus sequence: HWDAGHACRHHVTGTHCCHVMV

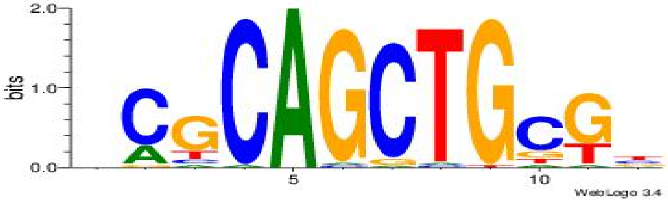


Reverse complement motif Consensus sequence: VRVDGGHACAVDDKGTHCTDWH

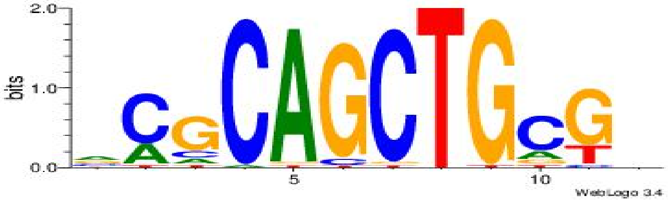


Dataset #: 3 Motif ID: 105 Motif name: NHLH1

Original motif Consensus sequence: VCGCAGCTGCGB



Reverse complement motif Consensus sequence: VCGCAGCTGCGV



Best Matches for Motif ID 105 (Highest to Lowest)

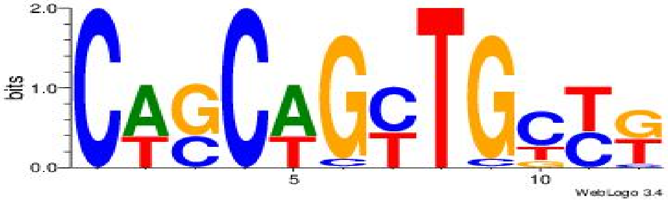
Dataset #:	3
Motif ID:	97
Motif name:	Myf
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	12
Similarity score:	0.0173692

Alignment:

```
CWSCWGMTGCKR
VCGCAGCTGCGV
```

Original motif Consensus sequence: MRGCARCWGSWG

Reverse complement motif Consensus sequence: CWSCWGMTGCKR

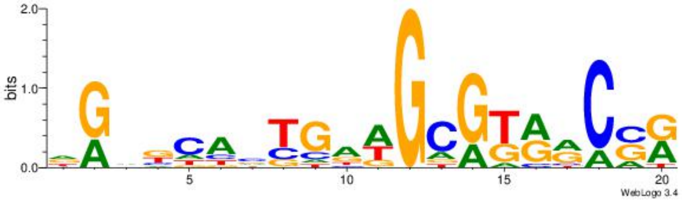


Dataset #: 3
Motif ID: 109
Motif name: Pax5
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 4
Number of overlap: 12
Similarity score: 0.0355984

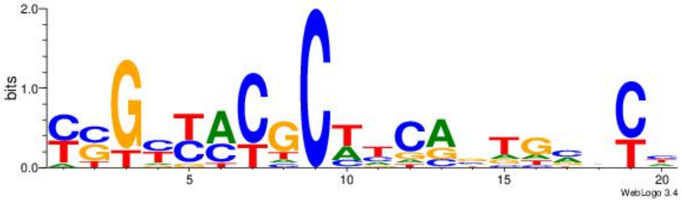
Alignment:

```
MSGKKRCGCWDCABTGBBCD
-----VCGCAGCTGCGB---
```

Original motif Consensus sequence: DGVBCABTGDWGCGKRRCSR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD



Dataset #: 4
Motif ID: 170
Motif name: ssGGCrsTGCrs
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward

Position number: 1

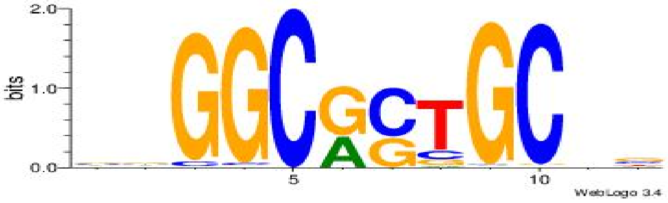
Number of overlap: 12

Similarity score: 0.0376107

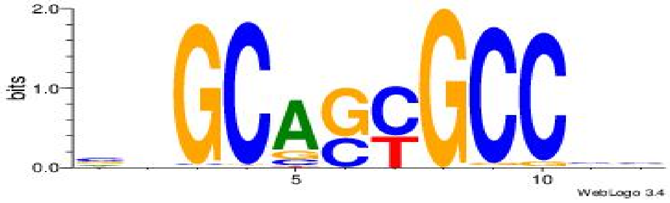
Alignment:

```
VVGGCRSTGCVB
VCGCAGCTGCGB
```

Original motif Consensus sequence: VVGGCRSTGCVB



Reverse complement motif Consensus sequence: BVGCASMGCCVV



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

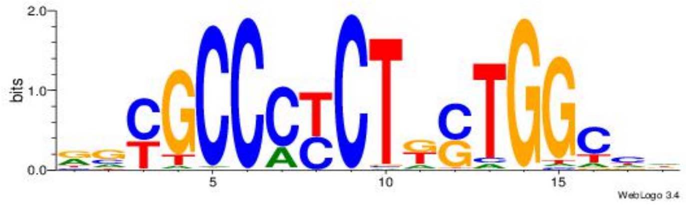
Number of overlap: 12

Similarity score: 0.0465866

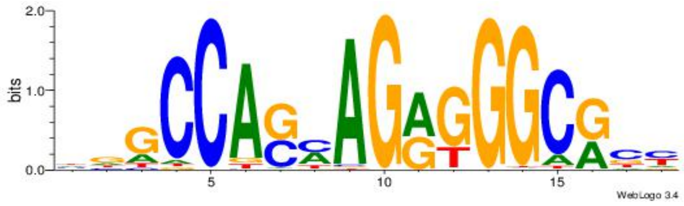
Alignment:

```
DDGCCASYAGMGGGCKVM
-VCGCAGCTGCGV-----
```

Original motif Consensus sequence: RVYGCCCYCTKSTGGCHD



Reverse complement motif Consensus sequence: DDGCCASYAGMGGGCKVM

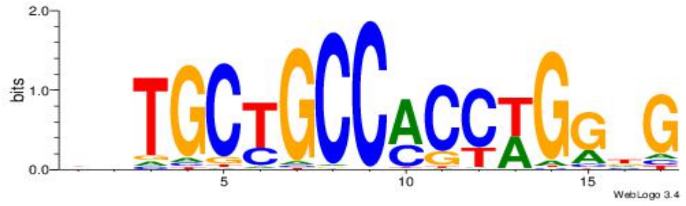


Dataset #:	4
Motif ID:	169
Motif name:	yvTGCyGCCmCCwGgtG
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	2
Number of overlap:	12
Similarity score:	0.0468076

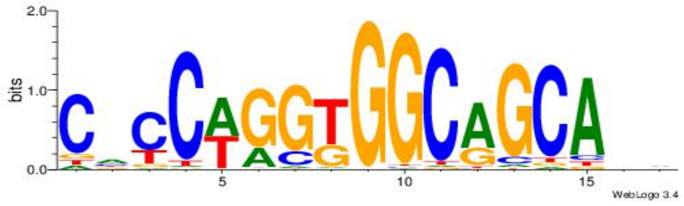
Alignment:

```
CDCCWGGTGGCAGCAVV
----VCGCAGCTGCGV-
```

Original motif Consensus sequence: BVTGCTGCCACCWGGDG



Reverse complement motif Consensus sequence: CDCCWGGTGGCAGCAVV



Dataset #: 3 **Motif ID: 106** **Motif name: Nkx3-2**

Original motif Consensus sequence: BTRAGTGVV

Reverse complement motif Consensus sequence: BVCACTKAH

Best Matches for Motif ID 106 (Highest to Lowest)

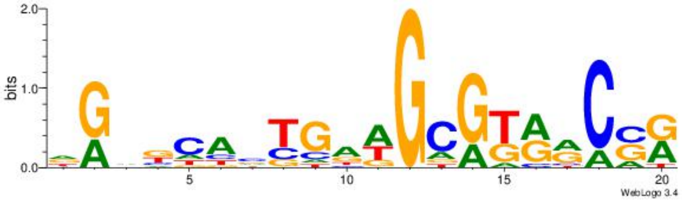
Dataset #:	3
Motif ID:	109
Motif name:	Pax5
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	8
Number of overlap:	9
Similarity score:	0.0239583

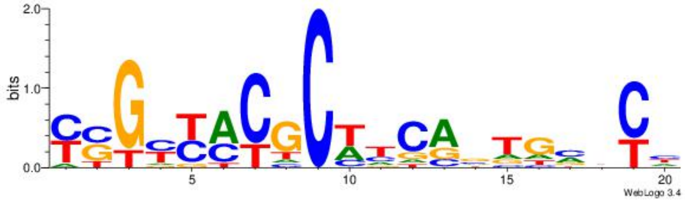
Alignment:

```
MSGKKRCGCWDCABTGBBCD
----BVCACTKAH-------
```

Original motif Consensus sequence: DGVBCABTGDWGCGKRRCSR

Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD





Dataset #: 3

Motif ID: 104

Motif name: NFYA

Matching format of first motif: Reverse Complement

Matching format of second motif: Original Motif

Direction: Backward

Position number: 5

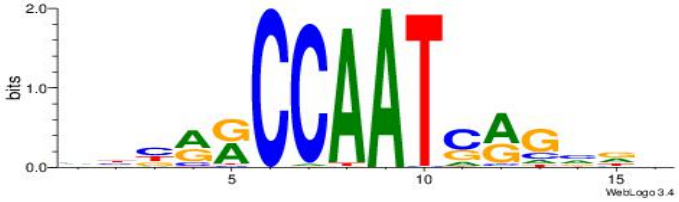
Number of overlap: 9

Similarity score: 0.0250758

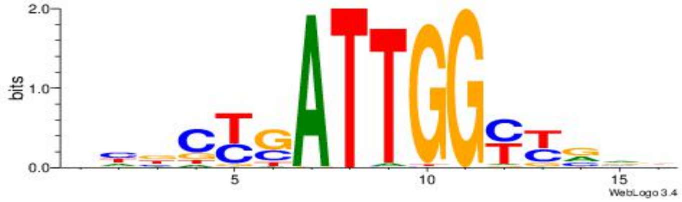
Alignment:

```
VBBRRCCAATSRGVDB
---BVCACTKAH----
```

Original motif Consensus sequence: VBBRRCCAATSRGVDB



Reverse complement motif Consensus sequence: BHVCKSATTGGMKBVV



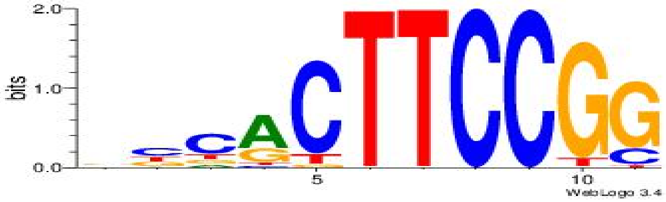
Dataset #: 3

Motif ID: 84
Motif name: GABPA
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 3
Number of overlap: 9
Similarity score: 0.0255754

Alignment:
CCGGAAGTGVV
--BTRAGTGVV

Original motif Consensus sequence: CCGGAAGTGVV

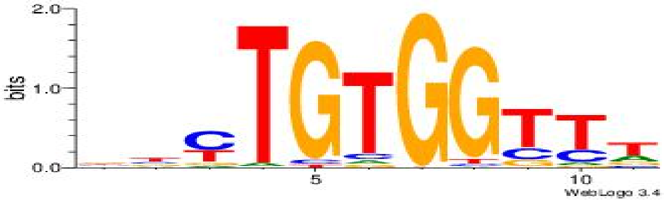
Reverse complement motif Consensus sequence: VVCACTTCCGG



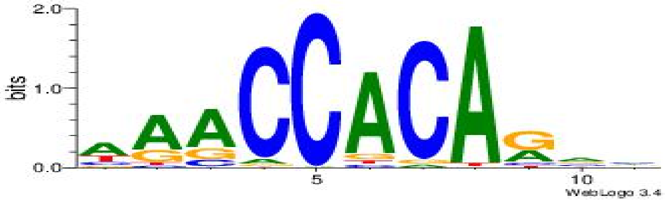
Dataset #: 3
Motif ID: 114
Motif name: RUNX1
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 9
Similarity score: 0.0262083

Alignment:
AAACCACAKVB
--BVCACTKAH

Original motif Consensus sequence: BBYTGTGGTTT



Reverse complement motif Consensus sequence: AAACCACAKVB



Dataset #:	3
Motif ID:	96
Motif name:	Mycn
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	9
Similarity score:	0.0296502

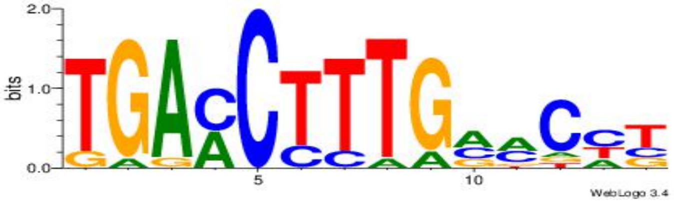
Alignment:
HSCACGTGGC
-BVCACTKAH

Original motif Consensus sequence: HSCACGTGGC

Reverse complement motif Consensus sequence: GCCACGTGSD

Dataset #: 3 **Motif ID: 107** **Motif name: NR2F1**

Original motif Consensus sequence: TGAMCTTTGMMCYT



Reverse complement motif Consensus sequence: AKGYYCAAAGRTC

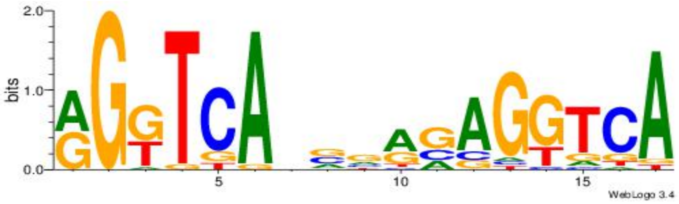
Best Matches for Motif ID 107 (Highest to Lowest)

Dataset #:	3
Motif ID:	115
Motif name:	RXRRAR_DR5
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	4
Number of overlap:	14
Similarity score:	0.0610709

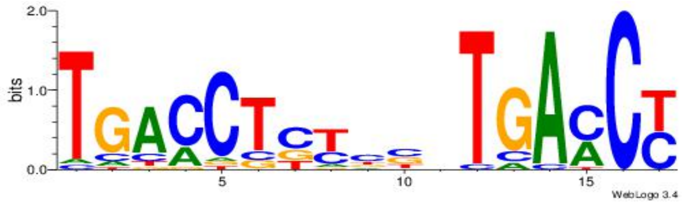
Alignment:

```
RGKTCABVVRGAGGTCA
---AKGYYCAAAGRTCA
```

Original motif Consensus sequence: RGKTCABVVRGAGGTCA



Reverse complement motif Consensus sequence: TGACCTCKVVBTGAYCK

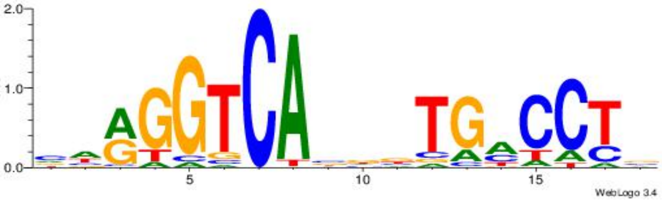


Dataset #:	3
Motif ID:	82
Motif name:	ESR2
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2
Number of overlap:	14
Similarity score:	0.0695855

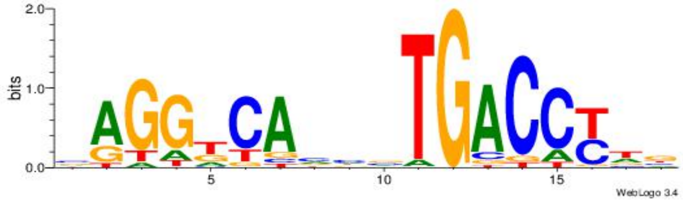
Alignment:

VHRGGTCABDBTGMCCTB
---AKGYYCAAAGRTCA-

Original motif Consensus sequence: VHRGGTCABDBTGMCCTB



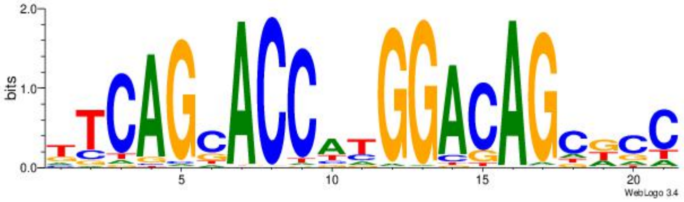
Reverse complement motif Consensus sequence: BAGGYCABHBTGACCKHV



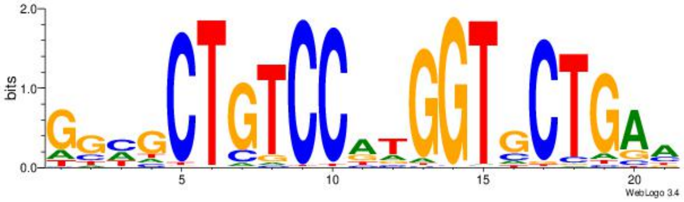
Dataset #: 3
Motif ID: 113
Motif name: REST
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 6
Number of overlap: 14
Similarity score: 0.0703341

Alignment:
TTCAGCACCATGGACAGCKCC
--AKGYYCAAAGRTCA-----

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC



Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA



Dataset #: 3
Motif ID: 104
Motif name: NFYA
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 3

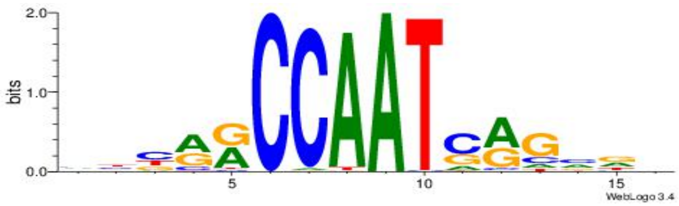
Number of overlap:	14
Similarity score:	0.0715605

Alignment:

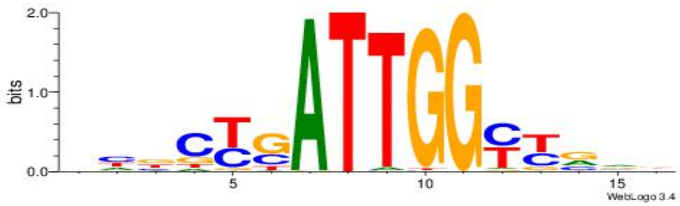
VBBRRCCAATSRGVDB

--TGAMCTTTGMMCYT

Original motif   Consensus sequence: VBBRRCCAATSRGVDB



Reverse complement motif   Consensus sequence: BHVCKSATTGGMKBVV



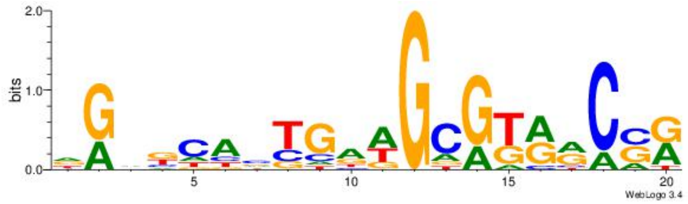
Dataset #:	3
Motif ID:	109
Motif name:	Pax5
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	5
Number of overlap:	14
Similarity score:	0.0727368

Alignment:

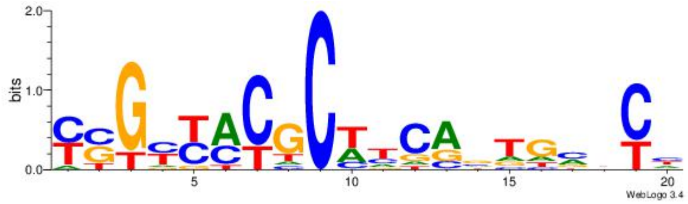
MSGKKRCGCWDCABTGBBCD

----TGAMCTTTGMMCYT--

Original motif Consensus sequence: DGVBCABTGDWGCGKRRCSR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD



Dataset #: 3 **Motif ID: 108** **Motif name: NR4A2**

Original motif Consensus sequence: AAGGTCAC

Reverse complement motif Consensus sequence: GTGACCTT

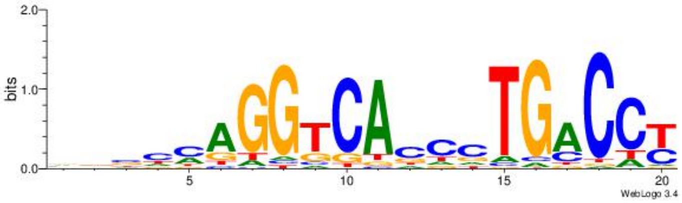
Best Matches for Motif ID 108 (Highest to Lowest)

Dataset #:	3
Motif ID:	81
Motif name:	ESR1
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	5
Number of overlap:	8
Similarity score:	0.0193781

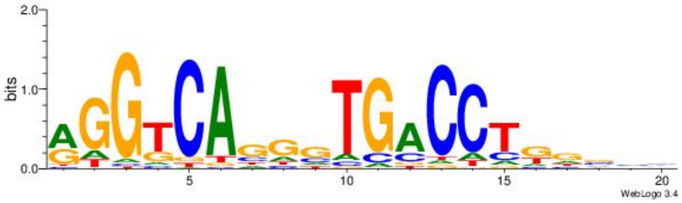
Alignment:

VDBHMAGGTCACCCTGACCY
----AAGGTCAC--------

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV

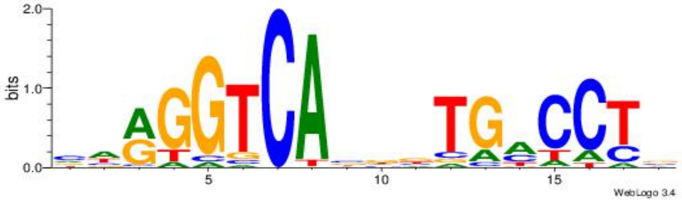


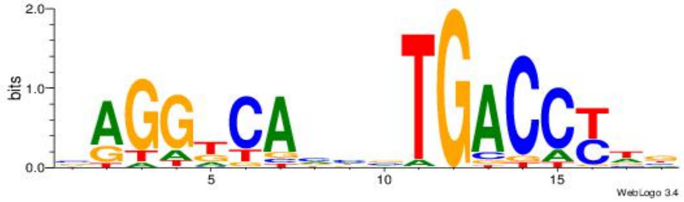
Dataset #:	3
Motif ID:	82
Motif name:	ESR2
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	10
Number of overlap:	8
Similarity score:	0.0196918

Alignment:
BAGGYCABHBTGACCKHV
---------GTGACCTT-

Original motif Consensus sequence: VHRGGTCABDBTGMCCTB

Reverse complement motif Consensus sequence: BAGGYCABHBTGACCKHV





Dataset #: 3

Motif ID: 111

Motif name: PPARG

Matching format of first motif: Reverse Complement

Matching format of second motif: Reverse Complement

Direction: Forward

Position number: 12

Number of overlap: 8

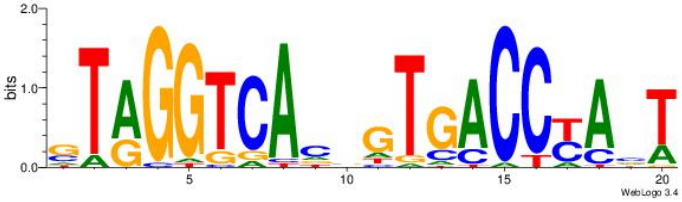
Similarity score: 0.0275817

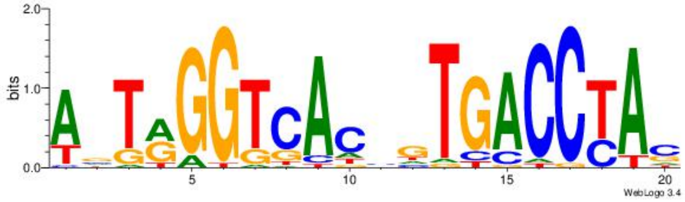
Alignment:

```
ABTMGGTCACBGTGACCTAS
-----------GTGACCTT-
```

Original motif Consensus sequence: STAGGTCACBGTGACCYABT

Reverse complement motif Consensus sequence: ABTMGGTCACBGTGACCTAS





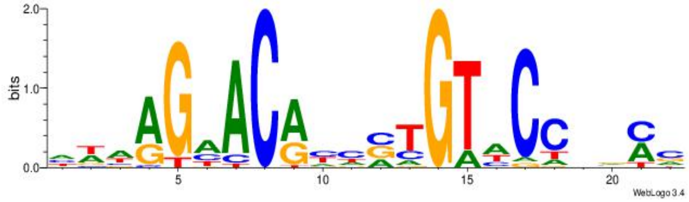
Dataset #: 3

Motif ID: 70
Motif name: Ar
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 13
Number of overlap: 8
Similarity score: 0.0486154

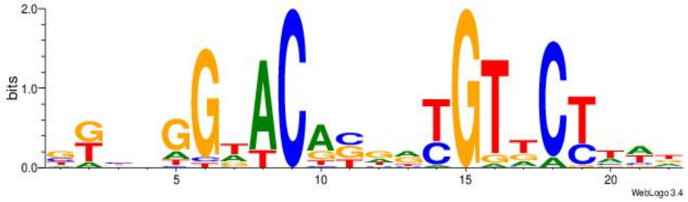
Alignment:

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

Original motif Consensus sequence: HWDAGHACRHHVTGTHCCHVMV



Reverse complement motif Consensus sequence: VRVDGGHACAVDDKGTHCTDWH



Dataset #: 1
Motif ID: 10
Motif name: Motif 10
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 8

Similarity score:	0.0525645

Alignment:

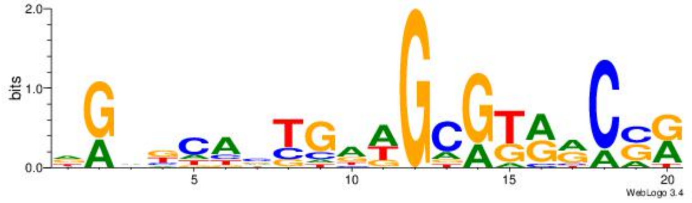
```
CTGGCCTC
GTGACCTT
```

Original motif Consensus sequence: CTGGCCTC

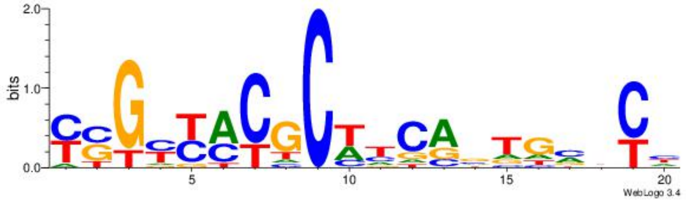
Reverse complement motif Consensus sequence: GAGGCCAG

Dataset #: 3 Motif ID: 109 Motif name: Pax5

Original motif Consensus sequence: DGVBCABTGDWGCGKRRCSR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD



Best Matches for Motif ID 109 (Highest to Lowest)

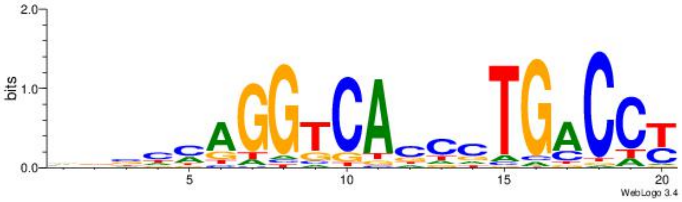
Dataset #:	3
Motif ID:	81
Motif name:	ESR1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement

Direction:	Backward
Position number:	1
Number of overlap:	20
Similarity score:	0.0458242

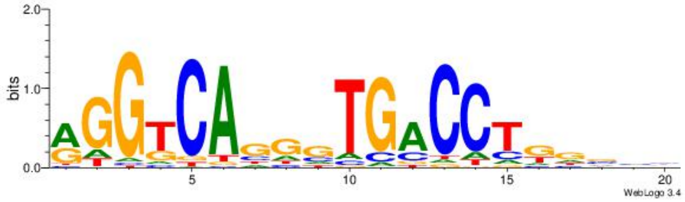
Alignment:

```
MGGTCAGGGTGACCTRDBHV
MSGKKRCGCWDCABTGBBCD
```

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV

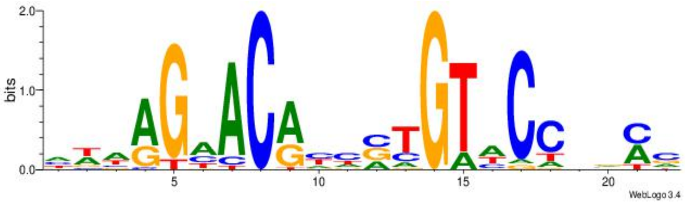


Dataset #:	3
Motif ID:	70
Motif name:	Ar
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	20
Similarity score:	0.052658

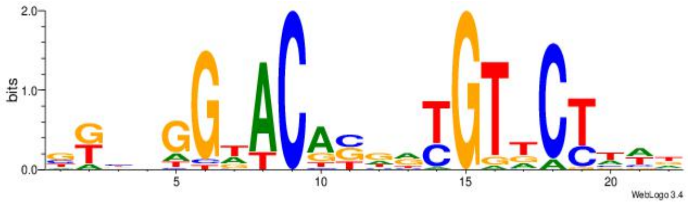
Alignment:

```
VRVDGGHACAVDDKGTHCTDWH
--MSGKKRCGCWDCABTGBBCD
```

Original motif Consensus sequence: HWDAGHACRHHVTGTHCCHVMV



Reverse complement motif Consensus sequence: VRVDGGHACAVDDKGTHCTDWH

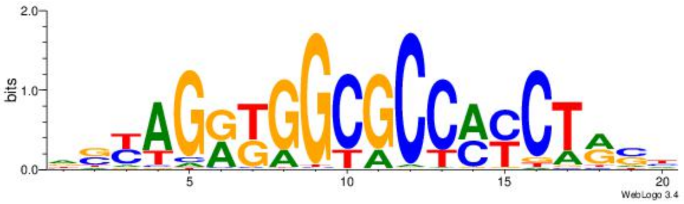


Dataset #:	4
Motif ID:	167
Motif name:	rsyAGrkGGCGCCmyCTrsy
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	20
Similarity score:	0.0660509

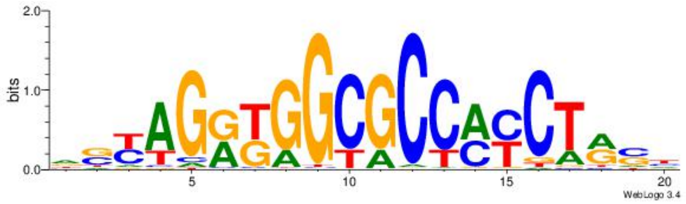
Alignment:

```
HSKAGKYGGCGCCRMCTMSD
MSGKKRCGCWDCABTGBBCD
```

Original motif Consensus sequence: DSYAGRKGGCGCCMYCTRSH



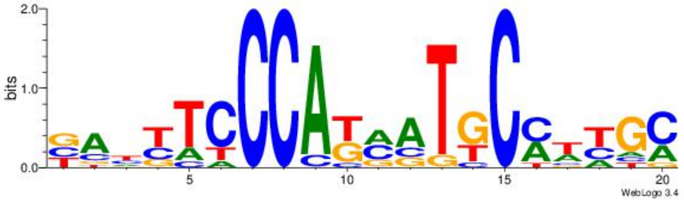
Reverse complement motif Consensus sequence: HSKAGKYGGCGCCRMCTMSD



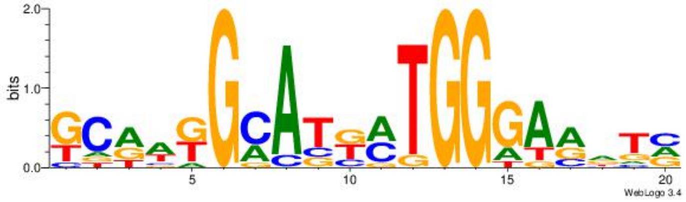
Dataset #: 3
Motif ID: 131
Motif name: znf143
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2
Number of overlap: 19
Similarity score: 0.552768

Alignment:
```
-BAHYTCCCAKMATGCMWYGC
MSGKKRCGCWDCABTGBBCD-
```

Original motif Consensus sequence: BAHYTCCCAKMATGCMWYGC



Reverse complement motif Consensus sequence: GCMWRGCATYRTGGGAMHTB



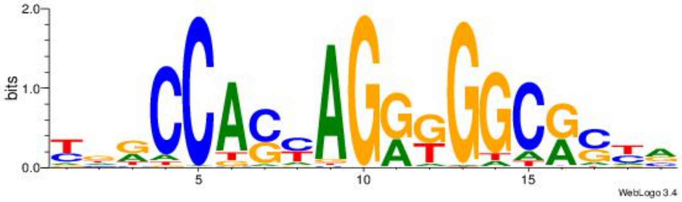
Dataset #: 3
Motif ID: 74
Motif name: CTCF
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1

Number of overlap:	19
Similarity score:	0.559888

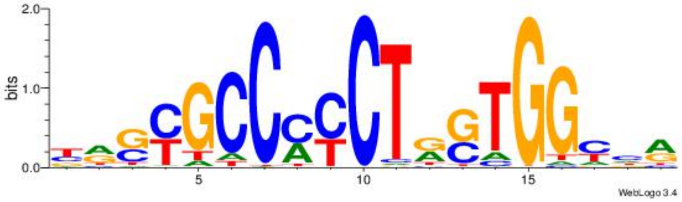
Alignment:

```
YDRCCASYAGRKGGCRSYV-
DGVBCABTGDWGCGKRRCSR
```

Original motif Consensus sequence: YDRCCASYAGRKGGCRSYV

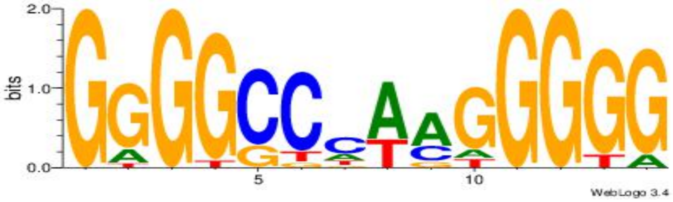


Reverse complement motif Consensus sequence: BMSMGCCYMCTKSTGGMHM

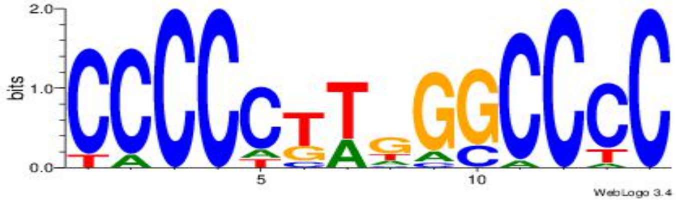


Dataset #: 3 Motif ID: 110 Motif name: PLAG1

Original motif Consensus sequence: GGGGCCCAAGGGGG



Reverse complement motif Consensus sequence: CCCCCTTGGGCCC



Best Matches for Motif ID 110 (Highest to Lowest)

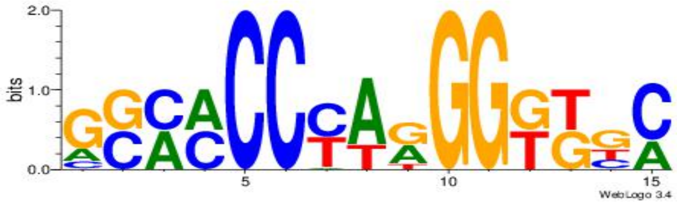
Dataset #:	3
Motif ID:	129
Motif name:	Zfp423
Matching format of first motif:	Original Motif

Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	14
Similarity score:	0.0944264

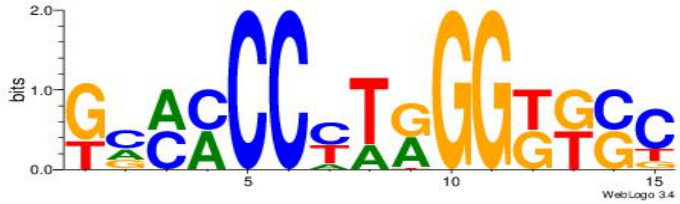
Alignment:

```
GSMMCCYARGGKKKC
GGGGCCCAAGGGGG-
```

Original motif Consensus sequence: GSMMCCYARGGKKKC



Reverse complement motif Consensus sequence: GYRYCCMTKGGYR

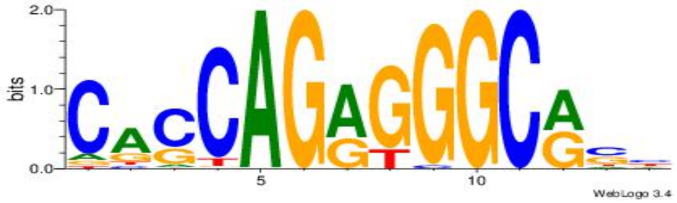


Dataset #:	4
Motif ID:	166
Motif name:	CasCAGrGGGCrsy
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	14
Similarity score:	0.0955683

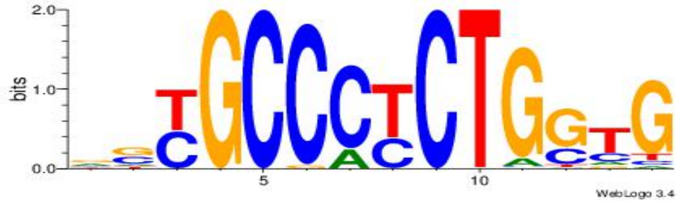
Alignment:

BSKGCCCKCTGGTG
GGGGCCCAAGGGGG

Original motif Consensus sequence: CACCAGRGGGCRSB



Reverse complement motif Consensus sequence: BSKGCCCKCTGGT



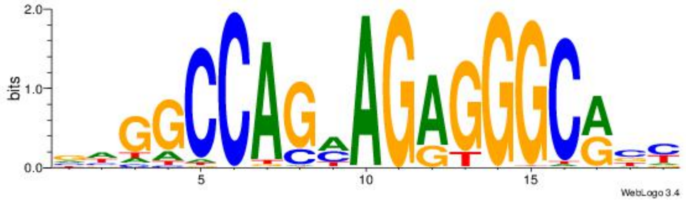
Dataset #:	4
Motif ID:	163
Motif name:	gwGGCCAGmAGAGGGCrby
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	6
Number of overlap:	14
Similarity score:	0.0963962

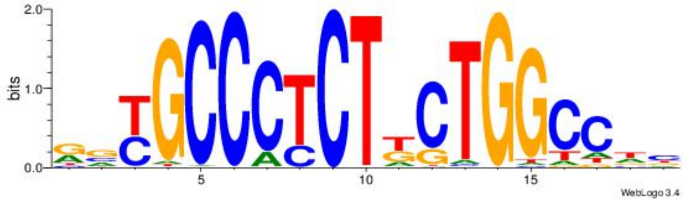
Alignment:

VHGGCCAGMAGAGGGCRBY
GGGGCCCAAGGGGG-----

Original motif Consensus sequence: VHGGCCAGMAGAGGGCRBY

Reverse complement motif Consensus sequence: KBKGCCCTCTYCTGGCCHV



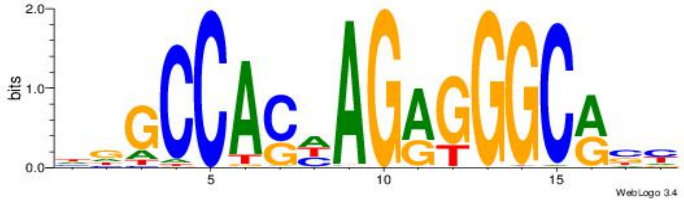


Dataset #:	4
Motif ID:	165
Motif name:	wgGCCAshAGrGGGCrsy
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	14
Similarity score:	0.0984905

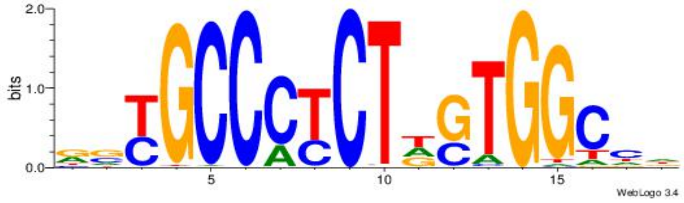
Alignment:

```
HDGCCACHAGRGGGCRBY
GGGGCCCAAGGGGG----
```

Original motif Consensus sequence: HDGCCACHAGRGGGCRBY



Reverse complement motif Consensus sequence: KBKGCCCKCTHGTGGCHH



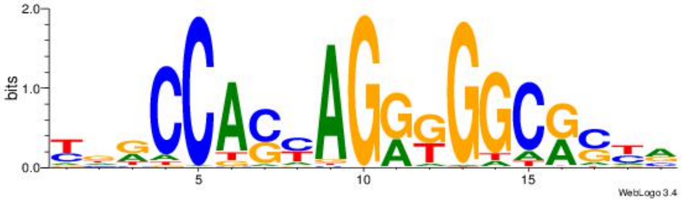
Dataset #:	3

Motif ID:	74
Motif name:	CTCF
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	14
Similarity score:	0.0985427

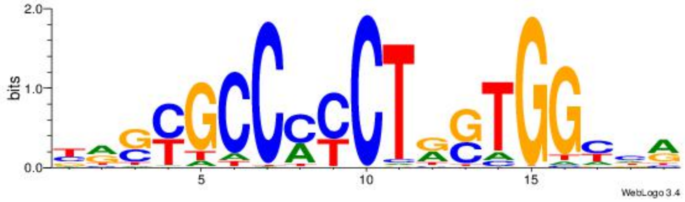
Alignment:

```
BMSMGCCYMCTKSTGGMHM
-----CCCCCTTGGGCCCC
```

Original motif   Consensus sequence: YDRCCASYAGRKGGCRSYV

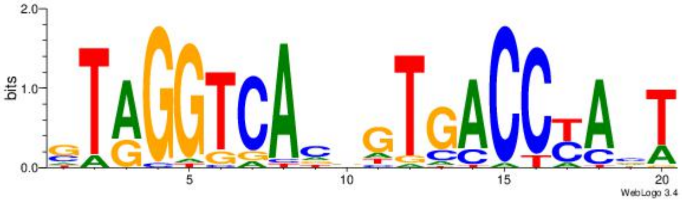


Reverse complement motif   Consensus sequence: BMSMGCCYMCTKSTGGMHM

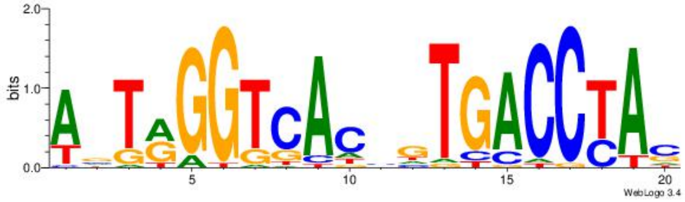


Dataset #: 3   Motif ID: 111   Motif name: PPARG

Original motif   Consensus sequence: STAGGTCACBGTGACCYABT



Reverse complement motif   Consensus sequence: ABTMGGTCACBGTGACCTAS



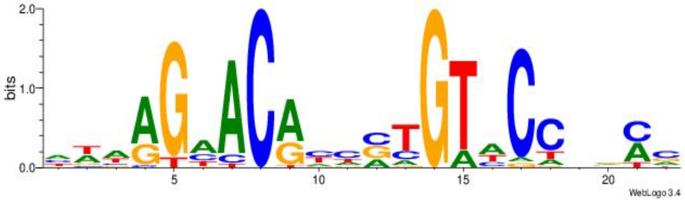
Best Matches for Motif ID 111 (Highest to Lowest)

Dataset #:	3
Motif ID:	70
Motif name:	Ar
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	3
Number of overlap:	20
Similarity score:	0.0567628

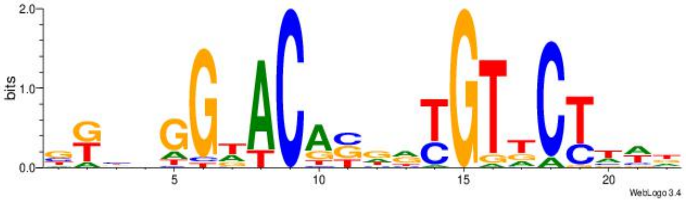
Alignment:

```
HWDAGHACRHHVTGTHCCHVMV
--ABTMGGTCACBGTGACCTAS
```

Original motif Consensus sequence: HWDAGHACRHHVTGTHCCHVMV



Reverse complement motif Consensus sequence: VRVDGGHACAVDDKGTHCTDWH



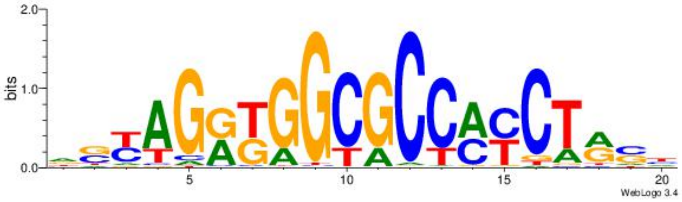
Dataset #:	4
Motif ID:	167
Motif name:	rsyAGrkGGCGCCmyCTrsy
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement

Direction:	Forward
Position number:	2
Number of overlap:	19
Similarity score:	0.574193

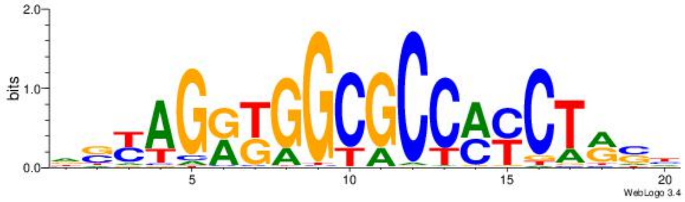
Alignment:

```
HSKAGKYGGCGCCRMCTMSD-
-STAGGTCACBGTGACCYABT
```

Original motif Consensus sequence: DSYAGRKGGCGCCMYCTRSH



Reverse complement motif Consensus sequence: HSKAGKYGGCGCCRMCTMSD

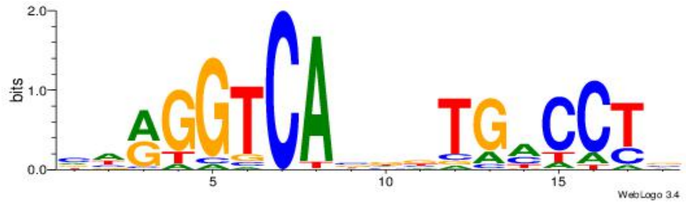


Dataset #:	3
Motif ID:	82
Motif name:	ESR2
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	18
Similarity score:	1.00511

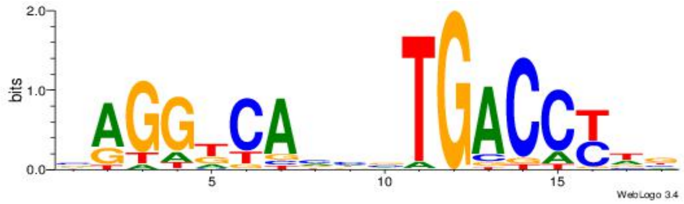
Alignment:

```
--BAGGYCABHBTGACCKHV
ABTMGGTCACBGTGACCTAS
```

Original motif Consensus sequence: VHRGGTCABDBTGMCCTB



Reverse complement motif Consensus sequence: BAGGYCABHBTGACCKHV

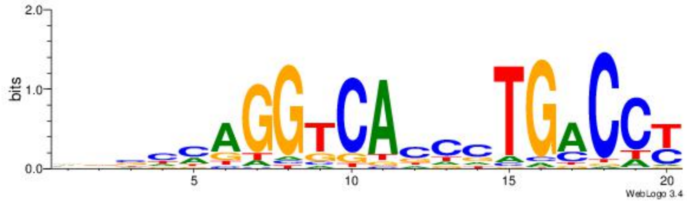


Dataset #:	3
Motif ID:	81
Motif name:	ESR1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	3
Number of overlap:	18
Similarity score:	1.01193

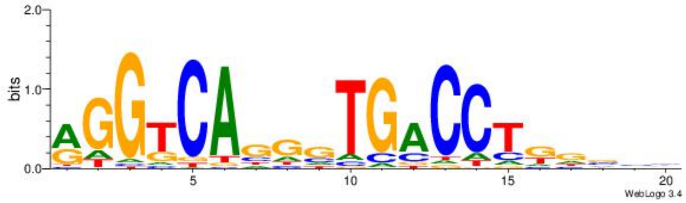
Alignment:

```
--VDBHMAGGTCACCCTGACCY
ABTMGGTCACBGTGACCTAS--
```

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV

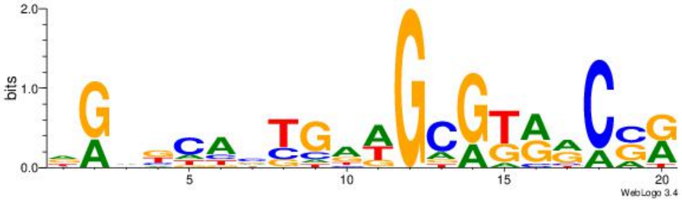


Dataset #:	3
Motif ID:	109
Motif name:	Pax5
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	3
Number of overlap:	18
Similarity score:	1.07268

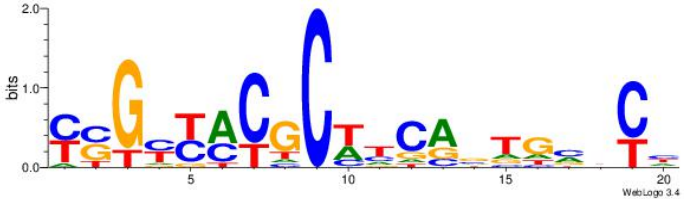
Alignment:

```
MSGKKRCGCWDCABTGBBCD--
--STAGGTCACBGTGACCYABT
```

Original motif Consensus sequence: DGVBCABTGDWGCGKRRCSR



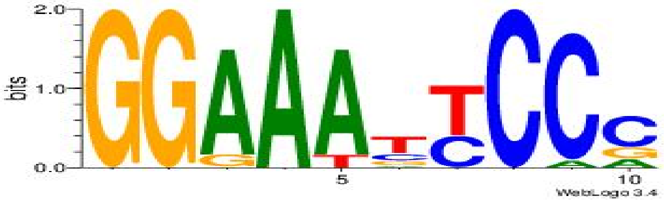
Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD



Dataset #: 3 Motif ID: 112 Motif name: RELA

Original motif Consensus sequence: GGGRATTTCC

Reverse complement motif Consensus sequence: GGAAATKCCC



Best Matches for Motif ID 112 (Highest to Lowest)

Dataset #:	3
Motif ID:	102
Motif name:	NF-kappaB
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	10
Similarity score:	0.00719219

Alignment:

```
GGMAAYKCCC
GGAAATKCCC
```

Original motif Consensus sequence: GGGRMTTYCC

Reverse complement motif Consensus sequence: GGMAAYKCCC

Dataset #:	3

Motif ID: 103
Motif name: NFKB1
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2
Number of overlap: 10
Similarity score: 0.0283179

Alignment:

```
GGGGRTTCCCC
GGGRATTTCC-
```

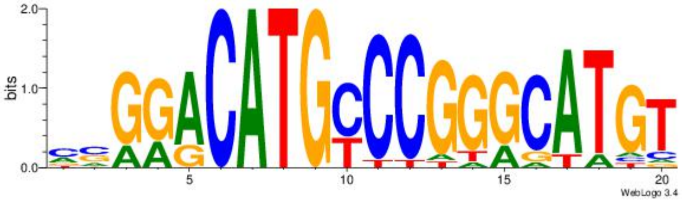
Original motif Consensus sequence: GGGGRTTCCCC

Reverse complement motif Consensus sequence: GGGGAAKCCCC

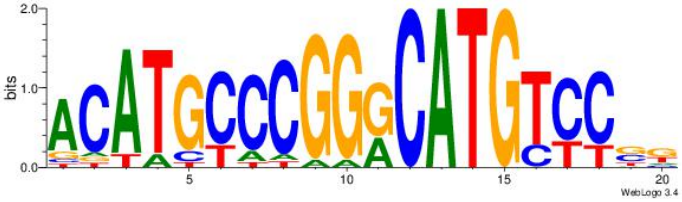
Dataset #: 3
Motif ID: 125
Motif name: TP53
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 9
Number of overlap: 10
Similarity score: 0.057648

Alignment:
MSGGACATGYCCGGGCATGT
--GGAAATKCCC--------

Original motif Consensus sequence: MSGGACATGYCCGGGCATGT



Reverse complement motif Consensus sequence: ACATGCCCGGKCATGTCCSR

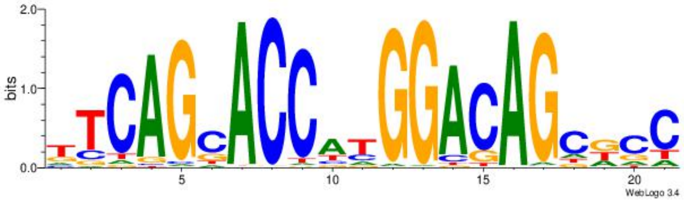


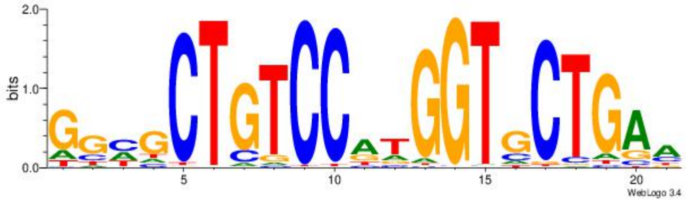
Dataset #:	3
Motif ID:	113
Motif name:	REST
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	10
Similarity score:	0.0666417

Alignment:
GGYGCTGTCCATGGTGCTGAA
GGGRATTTCC-----------

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC

Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA



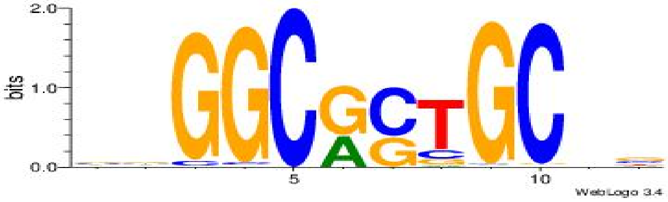


Dataset #:	4
Motif ID:	170
Motif name:	ssGGCrsTGCrs
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	10
Similarity score:	0.0784221

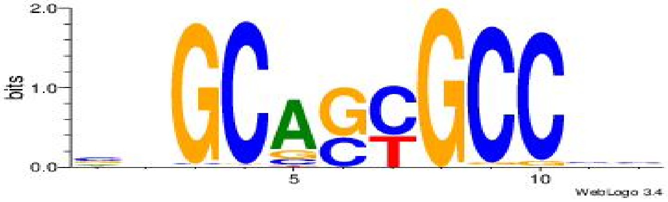
Alignment:

```
VVGGCRSTGCVB
--GGAAATKCCC
```

Original motif Consensus sequence: VVGGCRSTGCVB

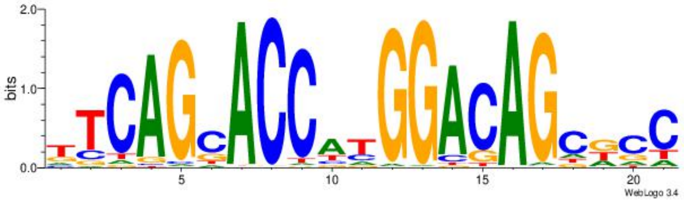


Reverse complement motif Consensus sequence: BVGCASMGCCVV

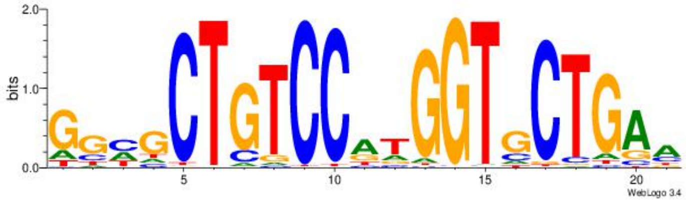


Dataset #: 3 Motif ID: 113 Motif name: REST

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC



Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA



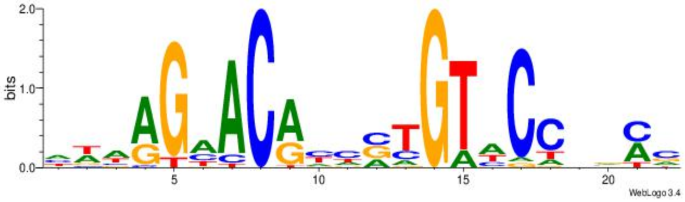
Best Matches for Motif ID 113 (Highest to Lowest)

Dataset #:	3
Motif ID:	70
Motif name:	Ar
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	21
Similarity score:	0.0685835

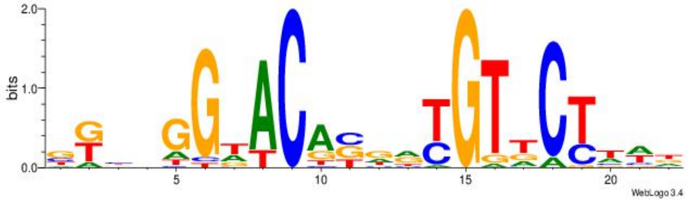
Alignment:

```
VRVDGGHACAVDDKGTHCTDWH
-GGYGCTGTCCATGGTGCTGAA
```

Original motif Consensus sequence: HWDAGHACRHHVTGTHCCHVMV



Reverse complement motif Consensus sequence: VRVDGGHACAVDDKGTHCTDWH

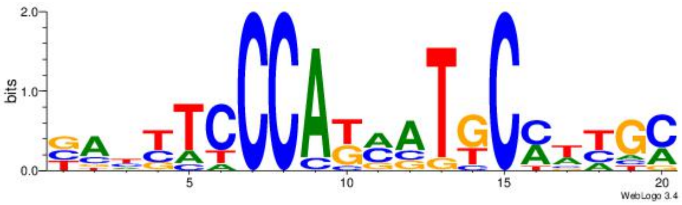


Dataset #:	3
Motif ID:	131
Motif name:	znf143
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	2
Number of overlap:	19
Similarity score:	1.0683

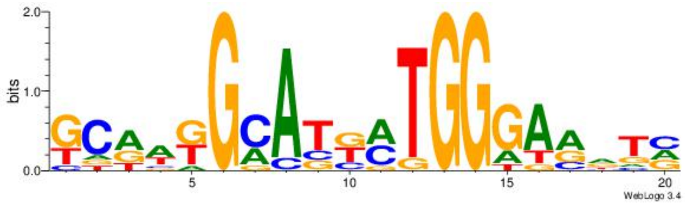
Alignment:

```
GCMWRGCATYRTGGGAMHTB--
-TTCAGCACCATGGACAGCKCC
```

Original motif Consensus sequence: BAHYTCCCAKMATGCMWYGC



Reverse complement motif Consensus sequence: GCMWRGCATYRTGGGAMHTB



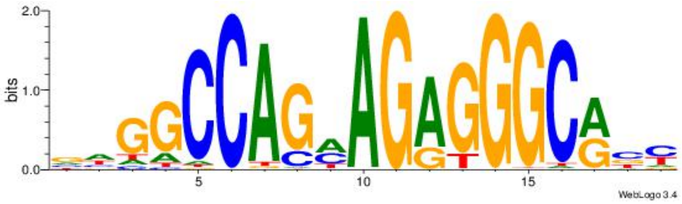
Dataset #:	4
Motif ID:	163
Motif name:	gwGGCCAGmAGAGGGCrby
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward

Position number: 1
Number of overlap: 19
Similarity score: 1.07477

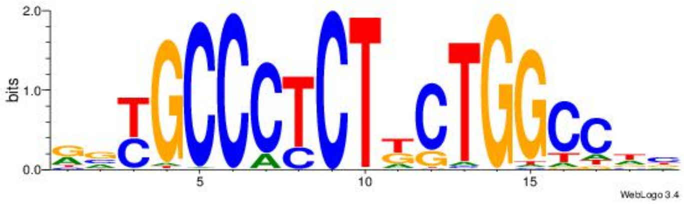
Alignment:

```
--VHGGCCAGMAGAGGGCRBY
TTCAGCACCATGGACAGCKCC
```

Original motif Consensus sequence: VHGGCCAGMAGAGGGCRBY



Reverse complement motif Consensus sequence: KBKGCCCTCTYCTGGCCHV

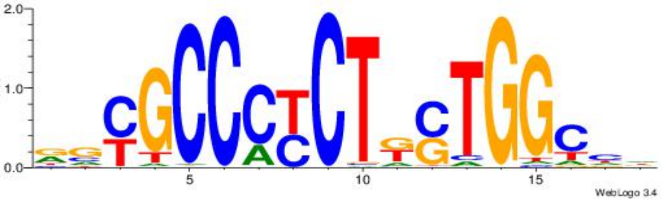


Dataset #: 4
Motif ID: 156
Motif name: rgyGCCMyCTksTGGccd
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 18
Similarity score: 1.57039

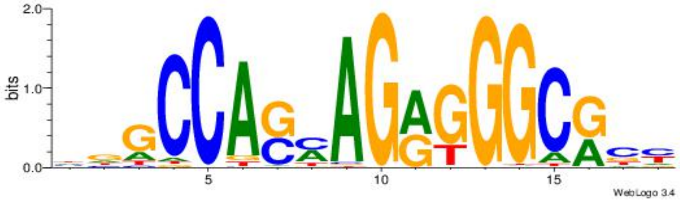
Alignment:

```
---DDGCCASYAGMGGGCKVM
TTCAGCACCATGGACAGCKCC
```

Original motif Consensus sequence: RVYGCCCYCTKSTGGCHD



Reverse complement motif Consensus sequence: DDGCCASYAGMGGGCKVM

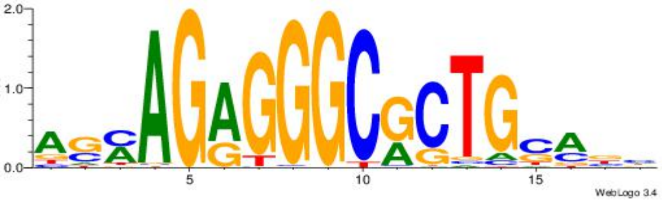


Dataset #:	4
Motif ID:	149
Motif name:	asmAGRGGGCrCTGsmkc
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	18
Similarity score:	1.57097

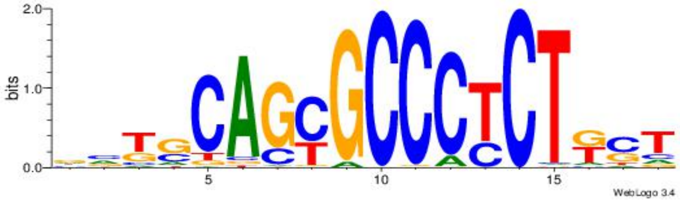
Alignment:

```
DBTSCAGMGCCCTCTRST---
GGYGCTGTCCATGGTGCTGAA
```

Original motif Consensus sequence: ASMAGAGGGCRCTGSABH

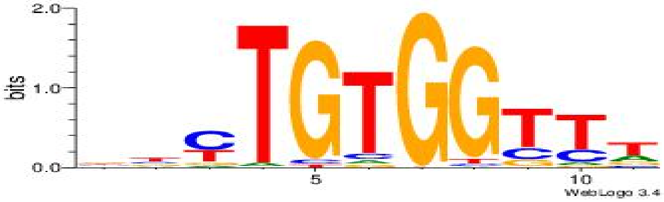


Reverse complement motif Consensus sequence: DBTSCAGMGCCCTCTRST

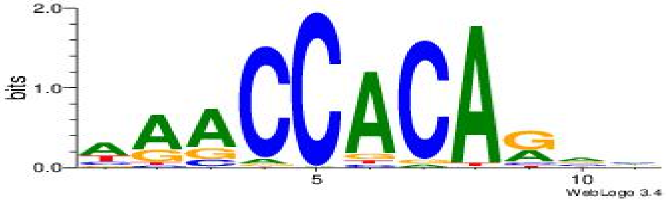


Dataset #: 3 **Motif ID: 114** **Motif name: RUNX1**

Original motif Consensus sequence: BBYTGTGGTTT



Reverse complement motif Consensus sequence: AAACCACAKVB



Best Matches for Motif ID 114 (Highest to Lowest)

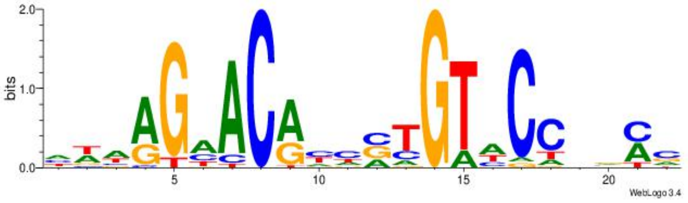
Dataset #:	3
Motif ID:	70
Motif name:	Ar
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	2
Number of overlap:	11
Similarity score:	0.0360379

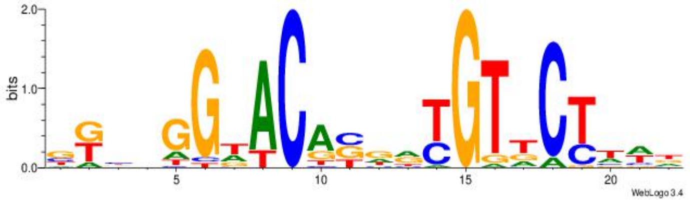
Alignment:

```
VRVDGGHACAVDDKGTHCTDWH
-BBYTGTGGTTT----------
```

Original motif Consensus sequence: HWDAGHACRHHVTGTHCCHVMV

Reverse complement motif Consensus sequence: VRVDGGHACAVDDKGTHCTDWH



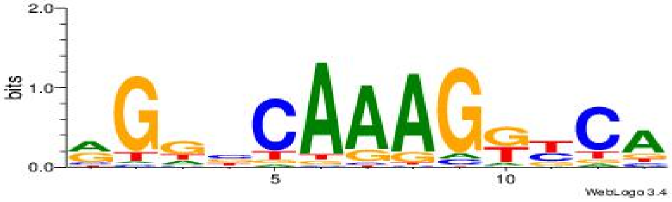


Dataset #:	3
Motif ID:	87
Motif name:	HNF4A
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	11
Similarity score:	0.0433682

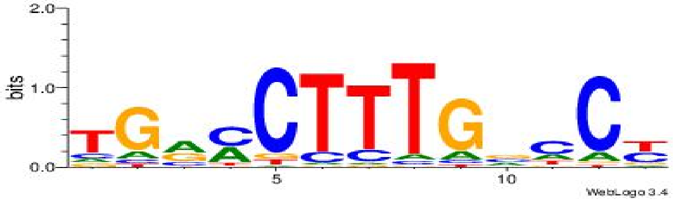
Alignment:

```
RGGBCAAAGKYCA
--AAACCACAKVB
```

Original motif Consensus sequence: RGGBCAAAGKYCA



Reverse complement motif Consensus sequence: TGMYCTTTGBCCK



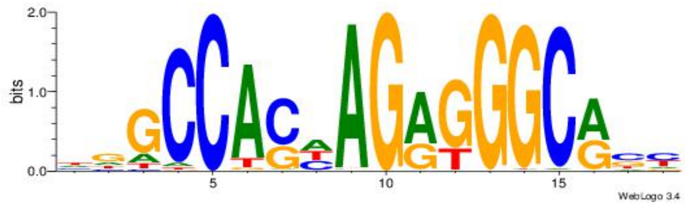
Dataset #:	4
Motif ID:	165

Motif name: wgGCCAshAGrGGGCrsy
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 8
Number of overlap: 11
Similarity score: 0.0447401

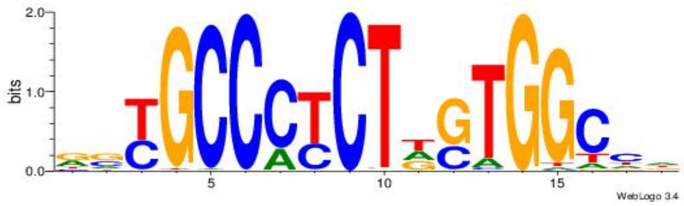
Alignment:

```
KBKGCCCKCTHGTGGCHH
-------BBYTGTGGTTT
```

Original motif Consensus sequence: HDGCCACHAGRGGGCRBY



Reverse complement motif Consensus sequence: KBKGCCCKCTHGTGGCHH



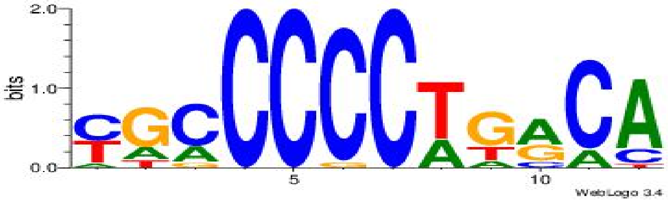
Dataset #: 3
Motif ID: 88
Motif name: INSM1
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 2
Number of overlap: 11
Similarity score: 0.0456894

Alignment:

```
TGYCAGGGGGCR
-BBYTGTGGTTT
```

Original motif Consensus sequence: TGYCAGGGGGCR

Reverse complement motif Consensus sequence: MGCCCCCTGMCA



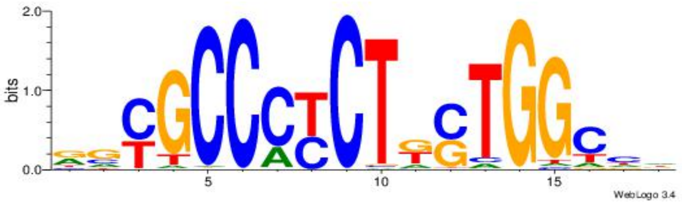
Dataset #:	4
Motif ID:	156
Motif name:	rgyGCCMyCTksTGGccd
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	8
Number of overlap:	11
Similarity score:	0.0459745

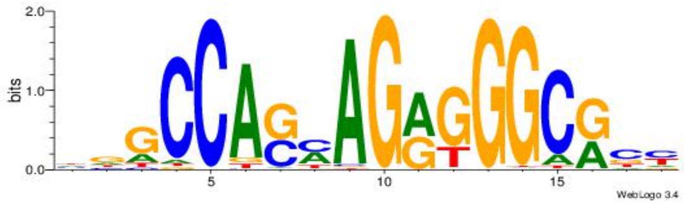
Alignment:

```
RVYGCCCYCTKSTGGCHD
-------BBYTGTGGTTT
```

Original motif Consensus sequence: RVYGCCCYCTKSTGGCHD

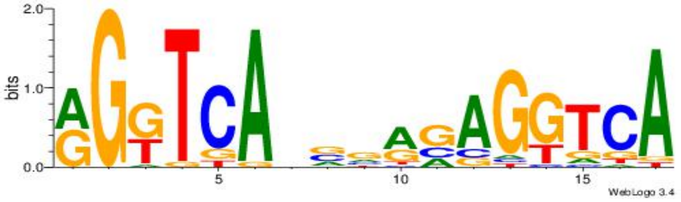
Reverse complement motif Consensus sequence: DDGCCASYAGMGGGCKVM



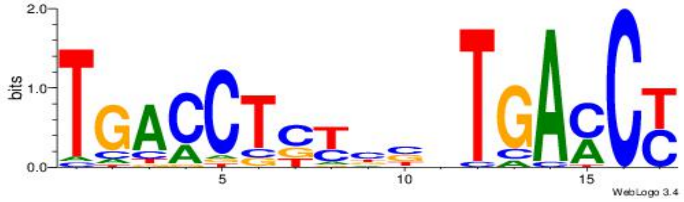


Dataset #: 3 Motif ID: 115 Motif name: RXRRAR_DR5

Original motif Consensus sequence: RGKTCABVVRGAGGTCA



Reverse complement motif Consensus sequence: TGACCTCKVVBTGAYCK



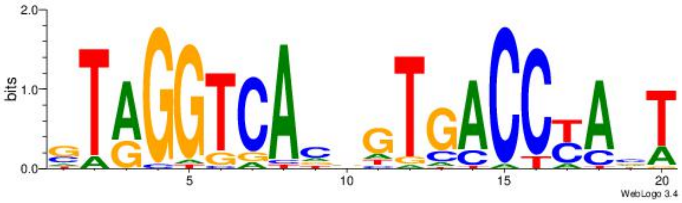
Best Matches for Motif ID 115 (Highest to Lowest)

Dataset #:	3
Motif ID:	111
Motif name:	PPARG
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	3
Number of overlap:	17
Similarity score:	0.0471437

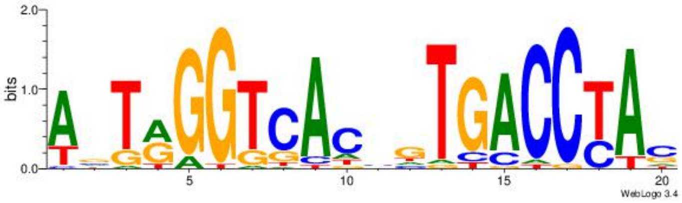
Alignment:

STAGGTCACBGTGACCYABT
--RGKTCABVVRGAGGTCA-

Original motif Consensus sequence: STAGGTCACBGTGACCYABT



Reverse complement motif Consensus sequence: ABTMGGTCACBGTGACCTAS

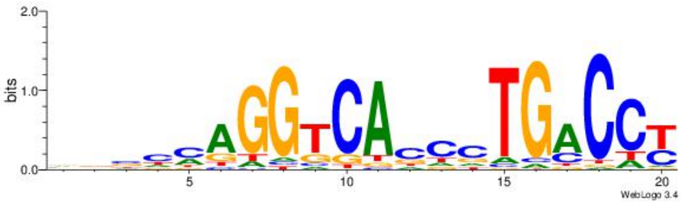


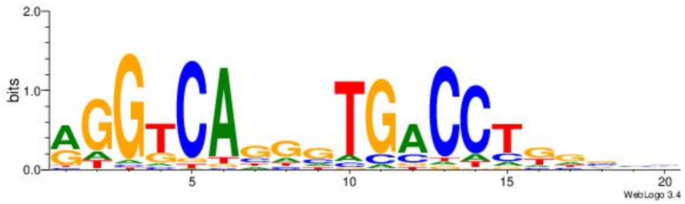
Dataset #:	3
Motif ID:	81
Motif name:	ESR1
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	17
Similarity score:	0.0543729

Alignment:
MGGTCAGGGTGACCTRDBHV
---RGKTCABVVRGAGGTCA

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY

Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV



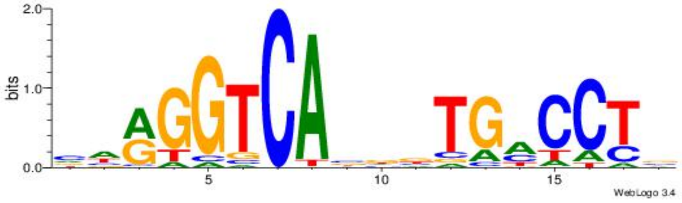


Dataset #:	3
Motif ID:	82
Motif name:	ESR2
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	17
Similarity score:	0.058015

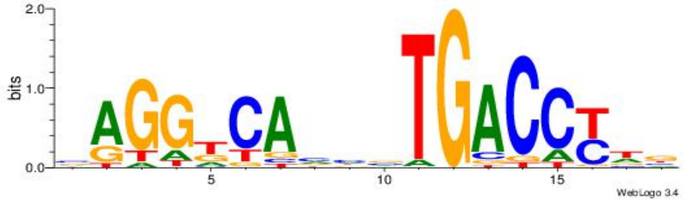
Alignment:

```
VHRGGTCABDBTGMCCTB
-TGACCTCKVVBTGAYCK
```

Original motif   Consensus sequence: VHRGGTCABDBTGMCCTB



Reverse complement motif   Consensus sequence: BAGGYCABHBTGACCKHV



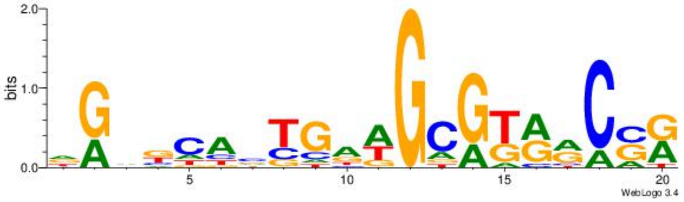
Dataset #:   3

Motif ID:	109
Motif name:	Pax5
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	17
Similarity score:	0.0584167

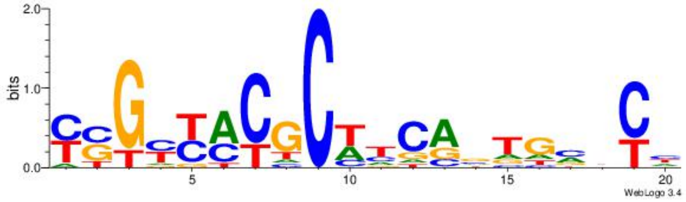
Alignment:

```
MSGKKRCGCWDCABTGBBCD
---TGACCTCKVVBTGAYCK
```

Original motif Consensus sequence: DGVBCABTGDWGCGKRRCSR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD



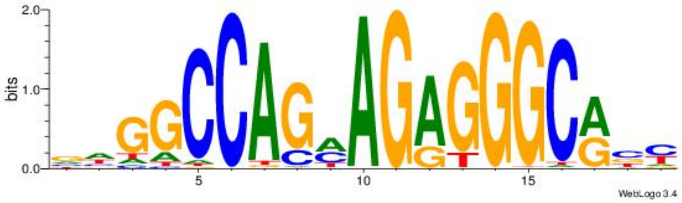
Dataset #:	4
Motif ID:	163
Motif name:	gwGGCCAGmAGAGGGCrby
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	3
Number of overlap:	17

Similarity score:	0.0732845

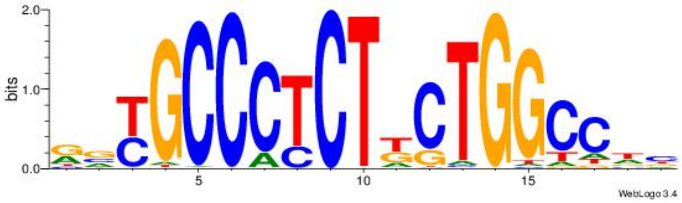
Alignment:

```
KBKGCCCTCTYCTGGCCHV
--TGACCTCKVVBTGAYCK
```

Original motif Consensus sequence: VHGGCCAGMAGAGGGCRBY

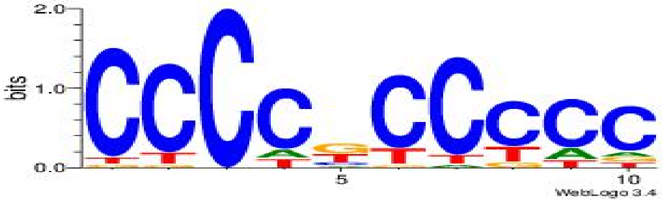


Reverse complement motif Consensus sequence: KBKGCCCTCTYCTGGCCHV



Dataset #: 3 Motif ID: 116 Motif name: SP1

Original motif Consensus sequence: CCCCKCCCCC



Reverse complement motif Consensus sequence: GGGGGYGGGG

Best Matches for Motif ID 116 (Highest to Lowest)

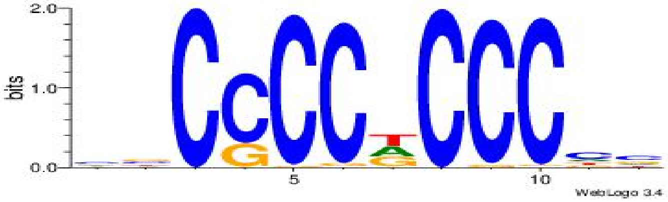
Dataset #:	4
Motif ID:	155
Motif name:	csCSCCdCCCcs
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif

Direction:	Forward
Position number:	3
Number of overlap:	10
Similarity score:	0.0226218

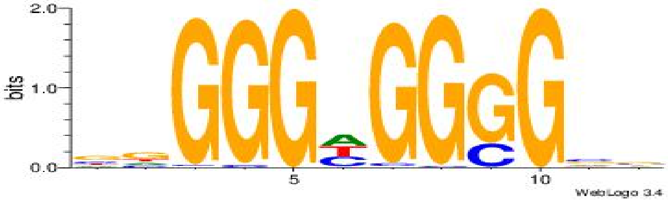
Alignment:

```
VBCCCCDCCCHV
--CCCCKCCCCC
```

Original motif Consensus sequence: VBCCCCDCCCHV



Reverse complement motif Consensus sequence: VDGGGDGGGGBV

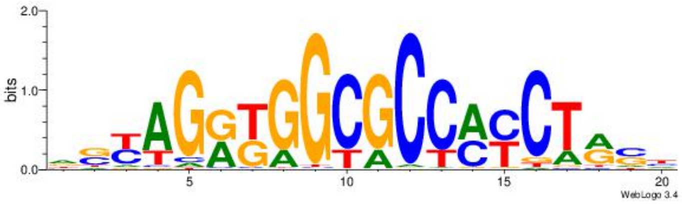


Dataset #:	4
Motif ID:	167
Motif name:	rsyAGrkGGCGCCmyCTrsy
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	10
Number of overlap:	10
Similarity score:	0.0535317

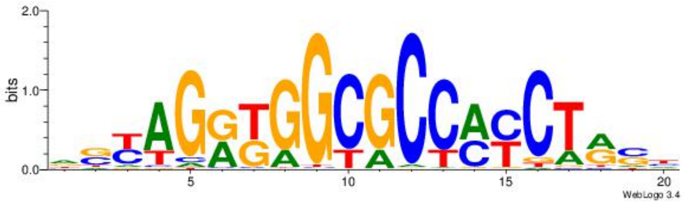
Alignment:

```
HSKAGKYGGCGCCRMCTMSD
-GGGGGYGGGG---------
```

Original motif Consensus sequence: DSYAGRKGGCGCCMYCTRSH



Reverse complement motif Consensus sequence: HSKAGKYGGCGCCRMCTMSD

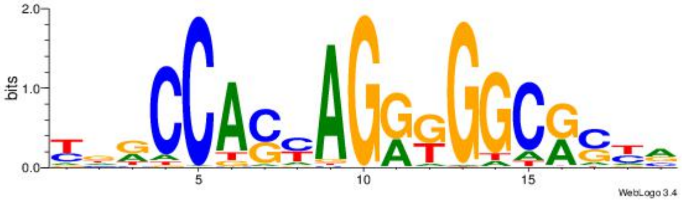


Dataset #:	3
Motif ID:	74
Motif name:	CTCF
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	10
Number of overlap:	10
Similarity score:	0.0604118

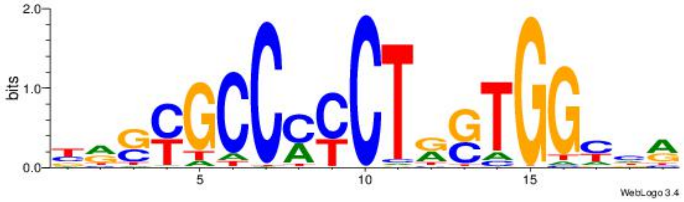
Alignment:

```
YDRCCASYAGRKGGCRSYV
GGGGGYGGGG---------
```

Original motif Consensus sequence: YDRCCASYAGRKGGCRSYV



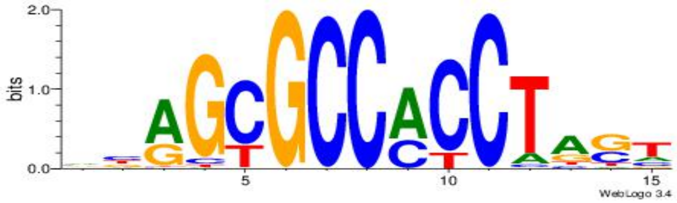
Reverse complement motif Consensus sequence: BMSMGCCYMCTKSTGGMHM



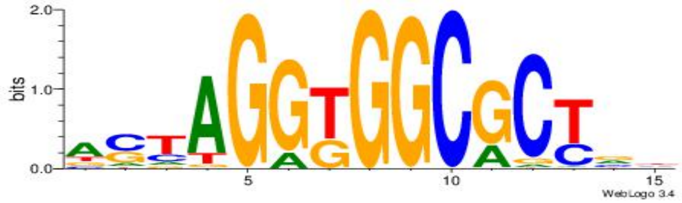
Dataset #:	4
Motif ID:	146
Motif name:	myrGYGCCmCCTast
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	5
Number of overlap:	10
Similarity score:	0.0650794

Alignment:
ASTAGGYGGCGCTBB
-GGGGGYGGGG----

Original motif Consensus sequence: VBAGCGCCMCCTAST



Reverse complement motif Consensus sequence: ASTAGGYGGCGCT

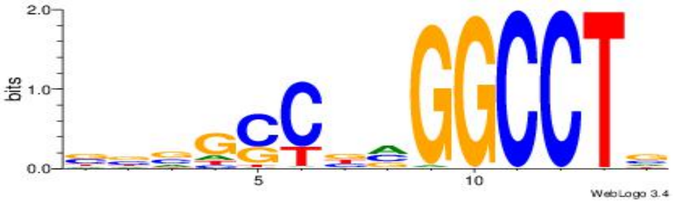


Dataset #:	3
Motif ID:	130
Motif name:	Zfx
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	10

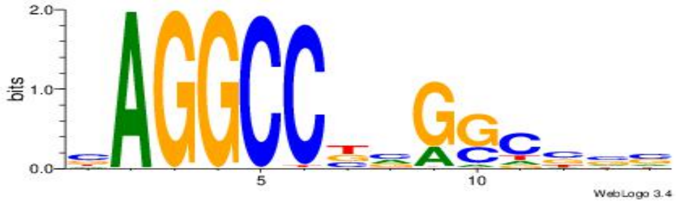
Similarity score:	0.0664832

Alignment:
VAGGCCBBGGCVBB
----CCCCKCCCCC

Original motif Consensus sequence: BBVGCCBVGGCCTV



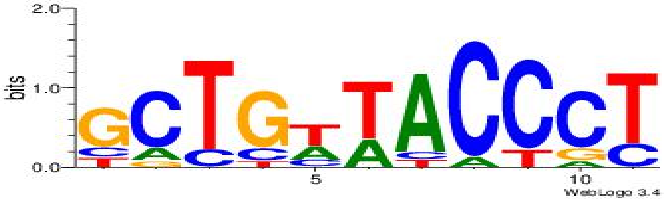
Reverse complement motif Consensus sequence: VAGGCCBBGGCV



Dataset #: 3 Motif ID: 117 Motif name: Spz1

Original motif Consensus sequence: AGGGTAWCAGC

Reverse complement motif Consensus sequence: GCTGWTACCCT



Best Matches for Motif ID 117 (Highest to Lowest)

Dataset #:	4
Motif ID:	143
Motif name:	AgmAGAGGGCrscAGak
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward

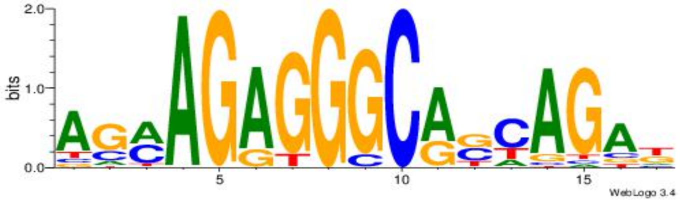
Position number:	6
Number of overlap:	11
Similarity score:	0.0235542

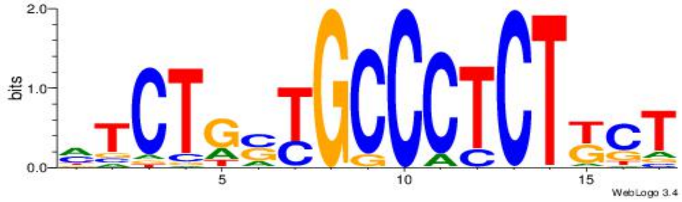
Alignment:

```
RTCTGSTGCCCTCTYCT
-GCTGWTACCCT-----
```

Original motif Consensus sequence: AGMAGAGGGCASCAGAK

Reverse complement motif Consensus sequence: RTCTGSTGCCCTCTYCT



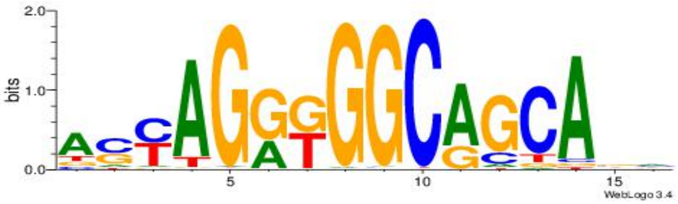


Dataset #:	4
Motif ID:	164
Motif name:	asyAGrkGGCRGCAga
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	6
Number of overlap:	11
Similarity score:	0.0381204

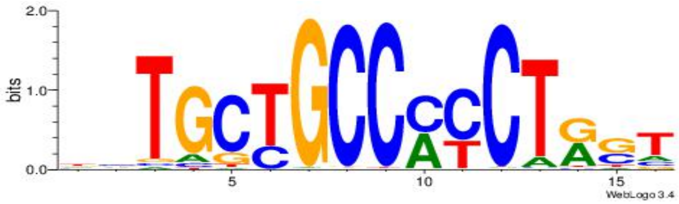
Alignment:

```
ASYAGRKGGCAGCABH
-----AGGGTAWCAGC
```

Original motif Consensus sequence: ASYAGRKGGCAGCABH



Reverse complement motif Consensus sequence: HBTGCTGCCYMCTKST

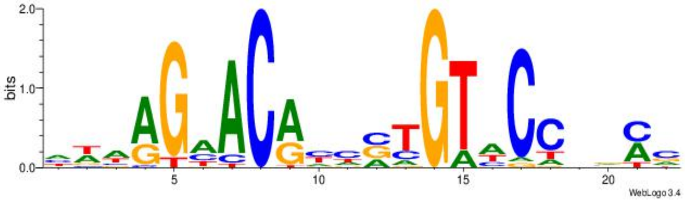


Dataset #:	3
Motif ID:	70
Motif name:	Ar
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	2
Number of overlap:	11
Similarity score:	0.0401654

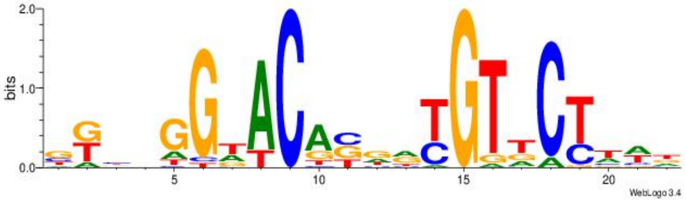
Alignment:

```
VRVDGGHACAVDDKGTHCTDWH
-GCTGWTACCCT----------
```

Original motif Consensus sequence: HWDAGHACRHHVTGTHCCHVMV



Reverse complement motif Consensus sequence: VRVDGGHACAVDDKGTHCTDWH



Dataset #: 3

Motif ID: 81

Motif name: ESR1

Matching format of first motif: Reverse Complement

Matching format of second motif: Original Motif

Direction: Backward

Position number: 5

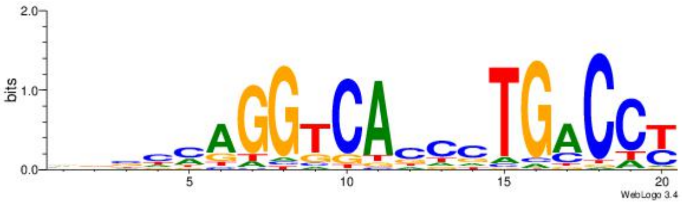
Number of overlap: 11

Similarity score: 0.0458949

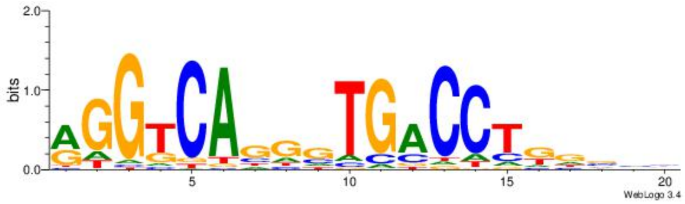
Alignment:

```
VDBHMAGGTCACCCTGACCY
-----GCTGWTACCCT----
```

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV



Dataset #: 3

Motif ID: 122

Motif name: Tcfcp2l1

Matching format of first motif: Reverse Complement

Matching format of second motif: Original Motif

Direction: Forward

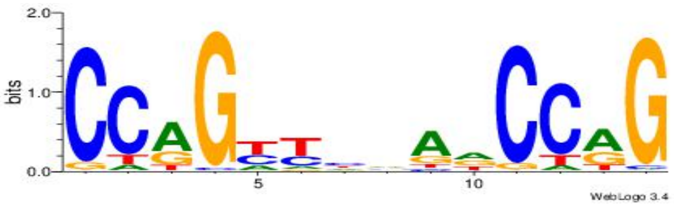
Position number: 4

Number of overlap:	11
Similarity score:	0.0503934

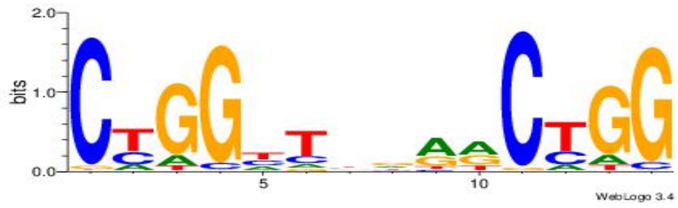
Alignment:

```
CCAGYYHVADCCRG
---GCTGWTACCCT
```

Original motif Consensus sequence: CCAGYYHVADCCRG

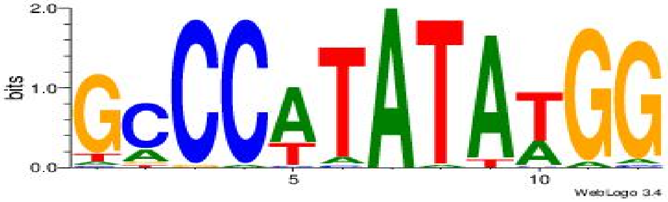


Reverse complement motif Consensus sequence: CKGGDTBDMMCT

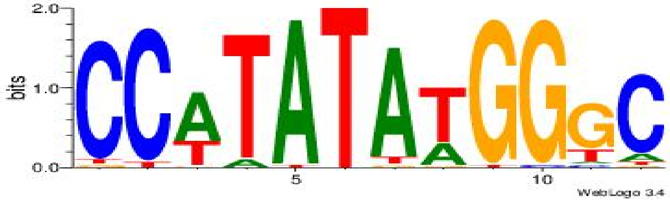


Dataset #: 3 Motif ID: 118 Motif name: SRF

Original motif Consensus sequence: GCCCATATATGG



Reverse complement motif Consensus sequence: CCATATATGGGC



Best Matches for Motif ID 118 (Highest to Lowest)

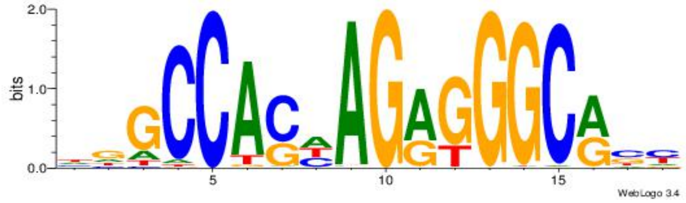
Dataset #:	4
Motif ID:	165
Motif name:	wgGCCAshAGrGGGCrsy
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement

Direction:	Forward
Position number:	5
Number of overlap:	12
Similarity score:	0.0548555

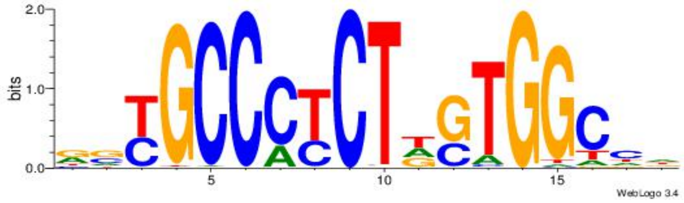
Alignment:

```
KBKGCCCKCTHGTGGCHH
----CCATATATGGGC--
```

Original motif Consensus sequence: HDGCCACHAGRGGGCRBY



Reverse complement motif Consensus sequence: KBKGCCCKCTHGTGGCHH

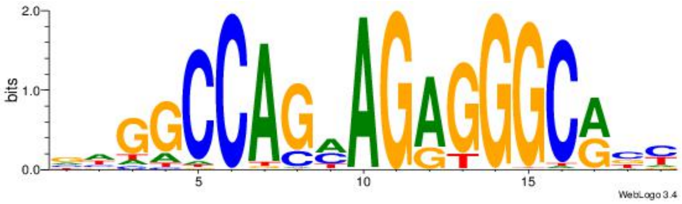


Dataset #:	4
Motif ID:	163
Motif name:	gwGGCCAGmAGAGGGCrby
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	5
Number of overlap:	12
Similarity score:	0.0556649

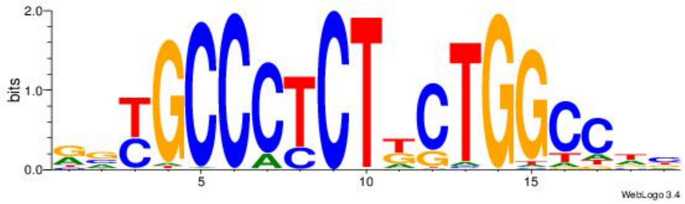
Alignment:

```
KBKGCCCTCTYCTGGCCHV
---GCCCATATATGG----
```

Original motif   Consensus sequence: VHGGCCAGMAGAGGGCRBY



Reverse complement motif   Consensus sequence: KBKGCCCTCTYCTGGCCHV

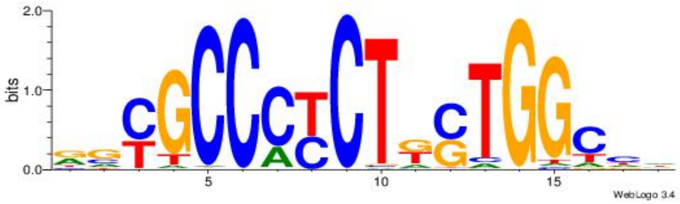


Dataset #:	4
Motif ID:	156
Motif name:	rgyGCCMyCTksTGGccd
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	3
Number of overlap:	12
Similarity score:	0.0558448

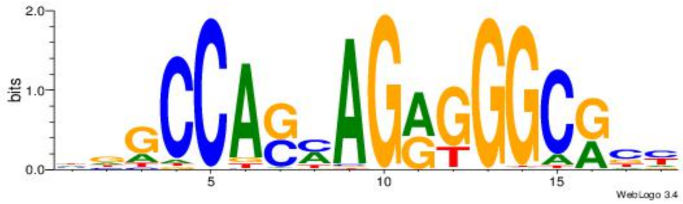
Alignment:

```
DDGCCASYAGMGGGCKVM
--GCCCATATATGG----
```

Original motif   Consensus sequence: RVYGCCCYCTKSTGGCHD



Reverse complement motif   Consensus sequence: DDGCCASYAGMGGGCKVM



Dataset #: 3

Motif ID: 74

Motif name: CTCF

Matching format of first motif: Reverse Complement

Matching format of second motif: Original Motif

Direction: Backward

Position number: 4

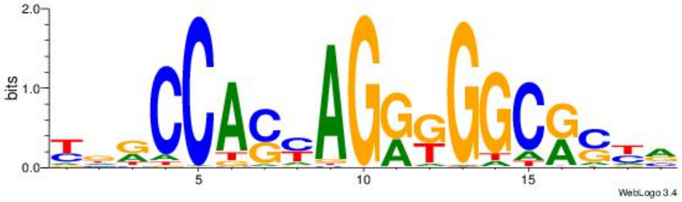
Number of overlap: 12

Similarity score: 0.0566321

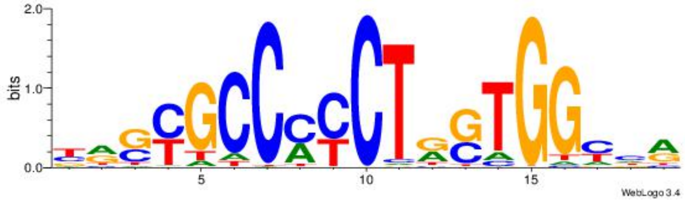
Alignment:

```
YDRCCASYAGRKGGCRSYV
----CCATATATGGGC---
```

Original motif Consensus sequence: YDRCCASYAGRKGGCRSYV



Reverse complement motif Consensus sequence: BMSMGCCYMCTKSTGGMHM



Dataset #: 2

Motif ID: 67

Motif name: Motif 67

Matching format of first motif: Reverse Complement

Matching format of second motif: Reverse Complement

Direction: Backward

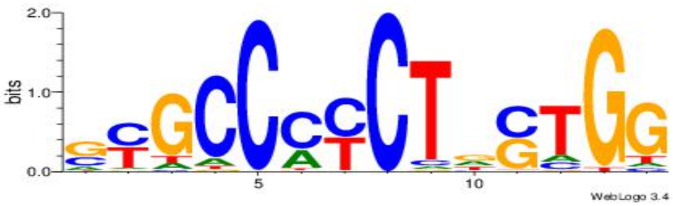
Position number: 3

Number of overlap:	12
Similarity score:	0.0566949

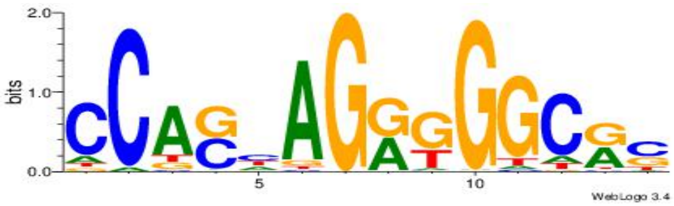
Alignment:

```
CCASHAGKGGGCKS
CCATATATGGGC--
```

Original motif   Consensus sequence: SYGCCCYCTDSTGG

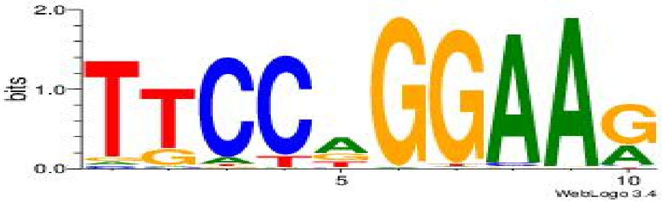


Reverse complement motif   Consensus sequence: CCASHAGKGGGCK

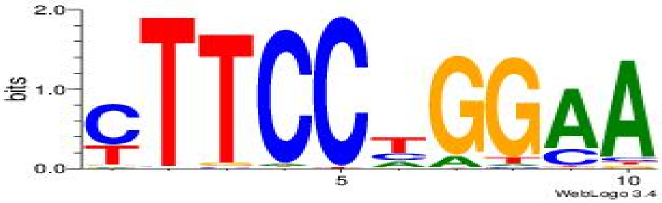


Dataset #: 3   Motif ID: 119   Motif name: Stat3

Original motif   Consensus sequence: TTCCAGGAAG



Reverse complement motif   Consensus sequence: CTTCCTGGAA



Best Matches for Motif ID 119 (Highest to Lowest)

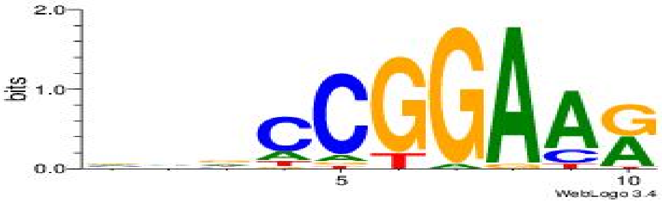
Dataset #:	3
Motif ID:	79
Motif name:	ELK1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement

Direction:	Backward
Position number:	1
Number of overlap:	10
Similarity score:	0.0612721

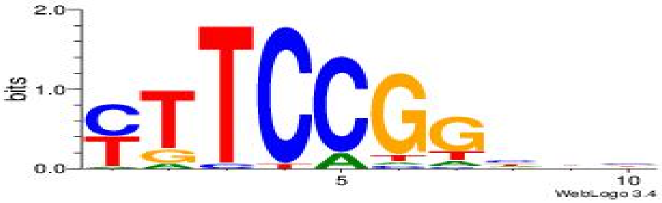
Alignment:

MTTCCGGHBV
CTTCCTGGAA

Original motif Consensus sequence: VDDCCGGAAR



Reverse complement motif Consensus sequence: MTTCCGGHBV



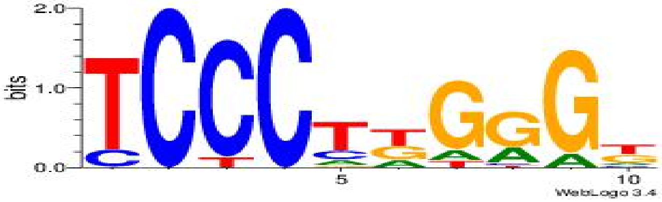
Dataset #:	3
Motif ID:	77
Motif name:	EBF1
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	10
Similarity score:	0.0803002

Alignment:

TCCCTYGGGY
TTCCAGGAAG

Original motif Consensus sequence: MCCCMAGGGA

Reverse complement motif Consensus sequence: TCCCTYGGGY



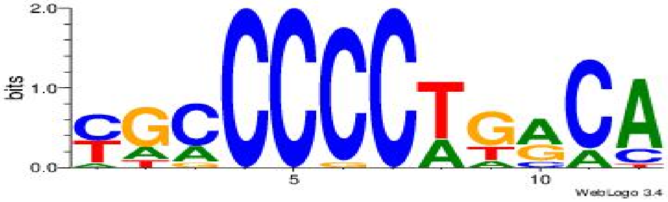
Dataset #:	3
Motif ID:	88
Motif name:	INSM1
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	10
Similarity score:	0.0834676

Alignment:

```
TGYCAGGGGGCR
TTCCAGGAAG--
```

Original motif Consensus sequence: TGYCAGGGGGCR

Reverse complement motif Consensus sequence: MGCCCCCTGMCA

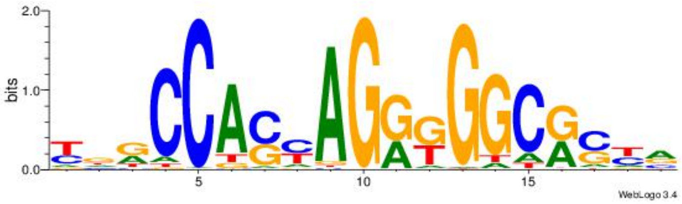


Dataset #: 3
Motif ID: 74
Motif name: CTCF
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 2
Number of overlap: 10
Similarity score: 0.0852106

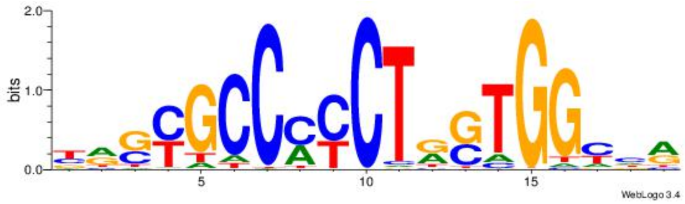
Alignment:

```
YDRCCASYAGRKGGCRSYV
-TTCCAGGAAG--------
```

Original motif Consensus sequence: YDRCCASYAGRKGGCRSYV



Reverse complement motif Consensus sequence: BMSMGCCYMCTKSTGGMHM



Dataset #: 3
Motif ID: 125
Motif name: TP53
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 8

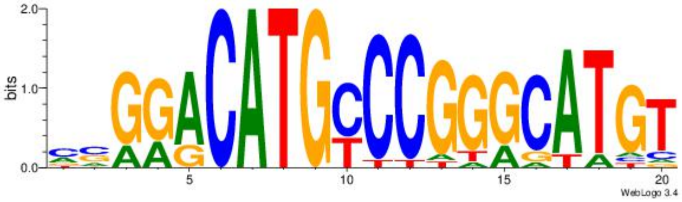
Number of overlap: 10

Similarity score: 0.087969

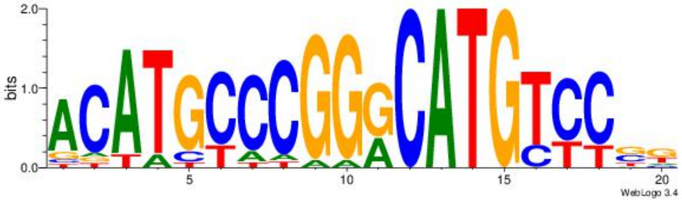
Alignment:

```
MSGGACATGYCCGGGCATGT
-------CTTCCTGGAA---
```

Original motif Consensus sequence: MSGGACATGYCCGGGCATGT

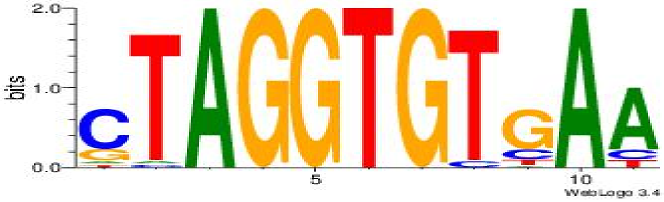


Reverse complement motif Consensus sequence: ACATGCCCGGKCATGTCCSR



Dataset #: 3 Motif ID: 120 Motif name: T

Original motif Consensus sequence: CTAGGTGTGAA



Reverse complement motif Consensus sequence: TTCACACCTAG

Best Matches for Motif ID 120 (Highest to Lowest)

Dataset #: 4

Motif ID: 144

Motif name: ctCTrsyGCCmCCTast

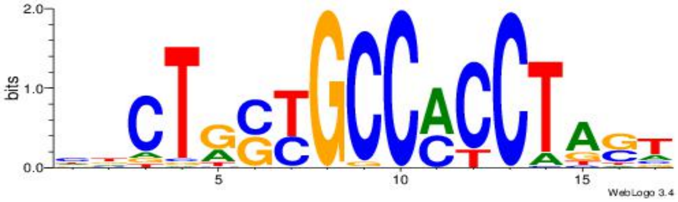
Matching format of first motif: Reverse Complement

Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2
Number of overlap:	11
Similarity score:	0.0559721

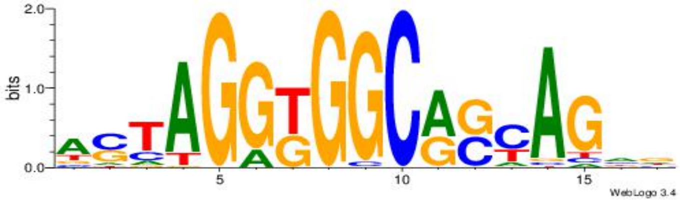
Alignment:

```
HDCTGSYGCCMCCTAST
-----TTCACACCTAG-
```

Original motif Consensus sequence: HDCTGSYGCCMCCTAST



Reverse complement motif Consensus sequence: ASTAGGYGGCMSCAGDD

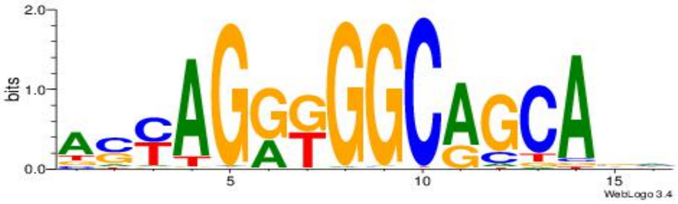


Dataset #:	4
Motif ID:	164
Motif name:	asyAGrkGGCRGCAga
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	11
Similarity score:	0.0641201

Alignment:

```
ASYAGRKGGCAGCABH
-CTAGGTGTGAA----
```

Original motif   Consensus sequence: ASYAGRKGGCAGCABH



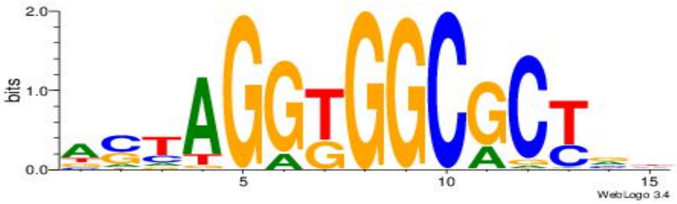
Reverse complement motif   Consensus sequence: HBTGCTGCCYMCTKST

Dataset #:	4
Motif ID:	146
Motif name:	myrGYGCCmCCTast
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	4
Number of overlap:	11
Similarity score:	0.0654989

Alignment:

```
VBAGCGCCMCCTAST
---TTCACACCTAG-
```

Original motif   Consensus sequence: VBAGCGCCMCCTAST   Reverse complement motif   Consensus sequence: ASTAGGYGGCGCT

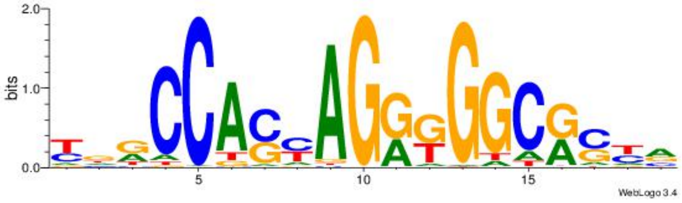


Dataset #:	3
Motif ID:	74
Motif name:	CTCF
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	7
Number of overlap:	11
Similarity score:	0.0692022

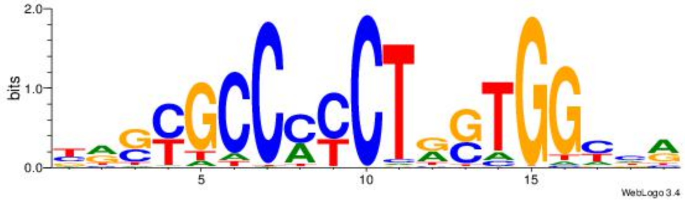
Alignment:

```
YDRCCASYAGRKGGCRSYV
------CTAGGTGTGAA--
```

Original motif Consensus sequence: YDRCCASYAGRKGGCRSYV



Reverse complement motif Consensus sequence: BMSMGCCYMCTKSTGGMHM



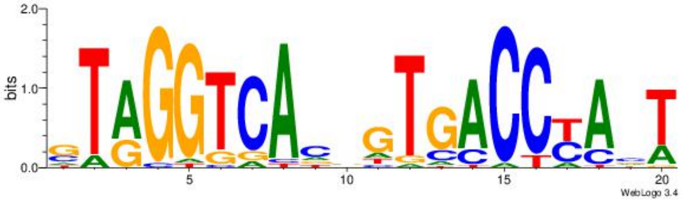
Dataset #:	3

Motif ID:	111
Motif name:	PPARG
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	10
Number of overlap:	11
Similarity score:	0.070764

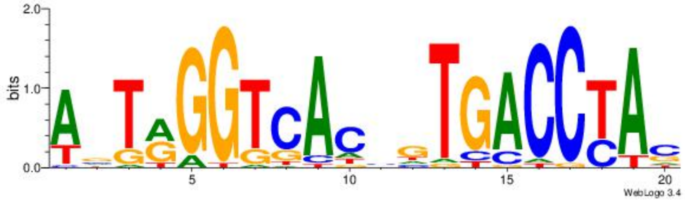
Alignment:

```
ABTMGGTCACBGTGACCTAS
---------TTCACACCTAG
```

Original motif Consensus sequence: STAGGTCACBGTGACCYABT

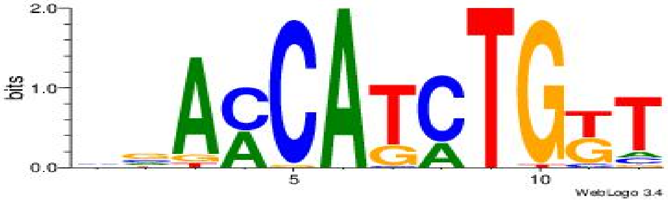


Reverse complement motif Consensus sequence: ABTMGGTCACBGTGACCTAS



Dataset #: 3 Motif ID: 121 Motif name: TAL1TCF3

Original motif Consensus sequence: HVAMCATCTGKT



Reverse complement motif Consensus sequence: ARCAGATGRTVD

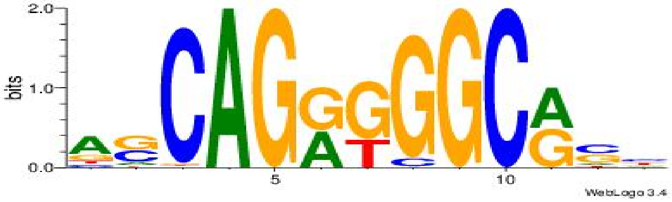
Best Matches for Motif ID 121 (Highest to Lowest)

Dataset #:	4
Motif ID:	147
Motif name:	asCAGrkGGCrsy
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	12
Similarity score:	0.0388867

Alignment:

```
ASCAGRGGGCRSB
ARCAGATGRTVD-
```

Original motif Consensus sequence: ASCAGRGGGCRSB



Reverse complement motif Consensus sequence: BSKGCCCMCTGST

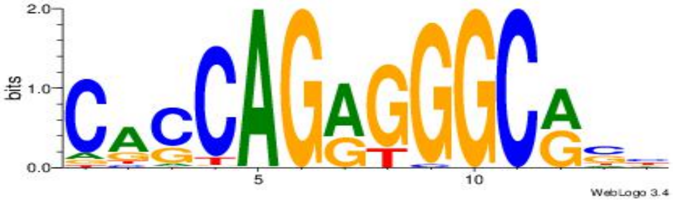
Dataset #:	4
Motif ID:	166
Motif name:	CasCAGrGGGCrsy
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement

Direction:	Forward
Position number:	2
Number of overlap:	12
Similarity score:	0.0389554

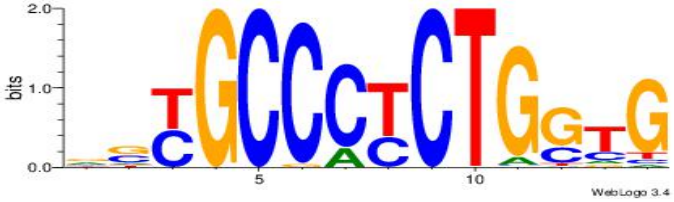
Alignment:

```
BSKGCCCKCTGGTG
-HVAMCATCTGKT-
```

Original motif Consensus sequence: CACCAGRGGGCRSB



Reverse complement motif Consensus sequence: BSKGCCCKCTGGT

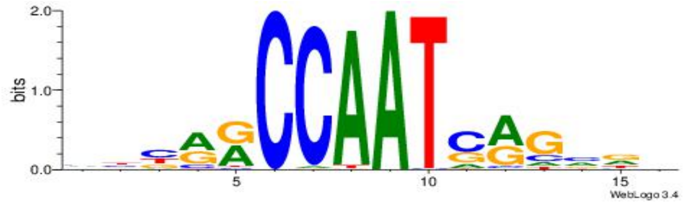


Dataset #:	3
Motif ID:	104
Motif name:	NFYA
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	4
Number of overlap:	12
Similarity score:	0.0418463

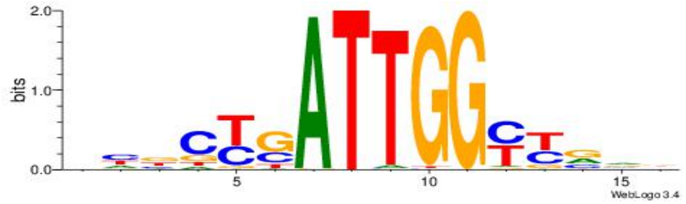
Alignment:

```
BHVCKSATTGGMKBVV
---HVAMCATCTGKT-
```

Original motif Consensus sequence: VBBRRCCAATSRGVDB



Reverse complement motif Consensus sequence: BHVCKSATTGGMKBVV



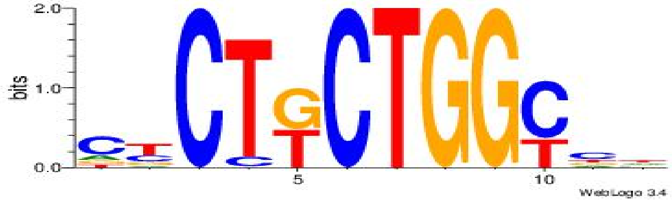
Dataset #: 4
Motif ID: 151
Motif name: agrCCAGmAGrg
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 12
Similarity score: 0.0439721

Alignment:

```
HVGCCAGMAGRG
HVAMCATCTGKT
```

Original motif Consensus sequence: HVGCCAGMAGRG

Reverse complement motif Consensus sequence: CKCTRCTGGCVH

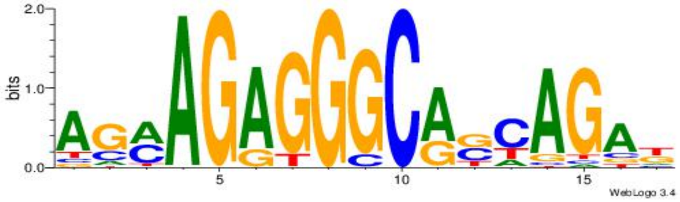


Dataset #:	4
Motif ID:	143
Motif name:	AgmAGAGGGCrscAGak
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	6
Number of overlap:	12
Similarity score:	0.0474478

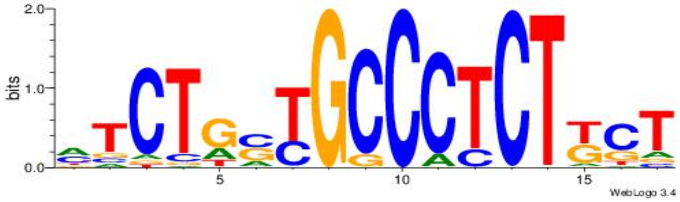
Alignment:

```
AGMAGAGGGCASCAGAK
ARCAGATGRTVD-----
```

Original motif Consensus sequence: AGMAGAGGGCASCAGAK



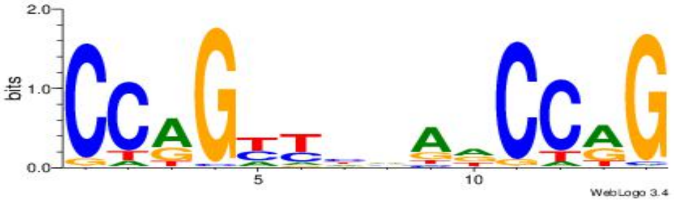
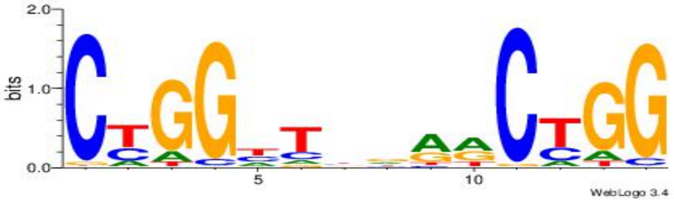
Reverse complement motif Consensus sequence: RTCTGSTGCCCTCTYCT



Dataset #: 3 Motif ID: 122 Motif name: Tcfcp2l1

Original motif Consensus sequence: CCAGYYHVADCCRG

Reverse complement motif Consensus sequence: CKGGDTBDMMCT

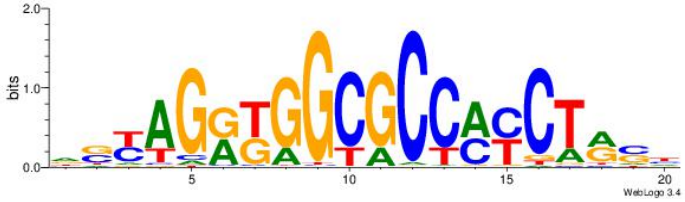
Best Matches for Motif ID 122 (Highest to Lowest)

Dataset #:	4
Motif ID:	167
Motif name:	rsyAGrkGGCGCCmyCTrsy
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	6
Number of overlap:	14
Similarity score:	0.0620246

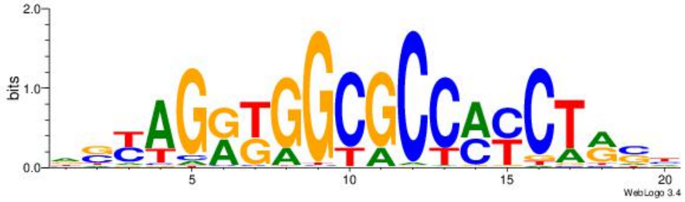
Alignment:

```
DSYAGRKGGCGCCMYCTRSH
-----CKGGDTBDMMCTGG-
```

Original motif   Consensus sequence: DSYAGRKGGCGCCMYCTRSH



Reverse complement motif   Consensus sequence: HSKAGKYGGCGCCRMCTMSD

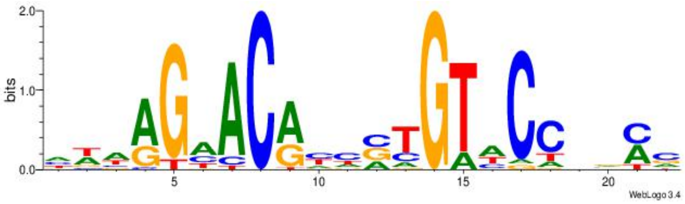


Dataset #: 3
Motif ID: 70
Motif name: Ar
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 7
Number of overlap: 14
Similarity score: 0.0642855

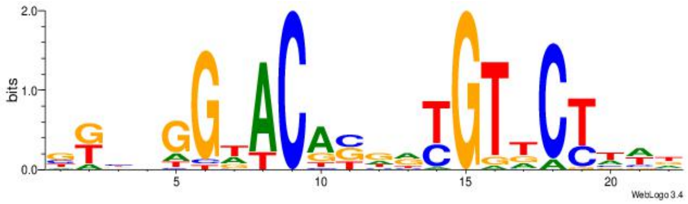
Alignment:

```
HWDAGHACRHHVTGTHCCHVMV
------CCAGYYHVADCCRG--
```

Original motif Consensus sequence: HWDAGHACRHHVTGTHCCHVMV



Reverse complement motif Consensus sequence: VRVDGGHACAVDDKGTHCTDWH



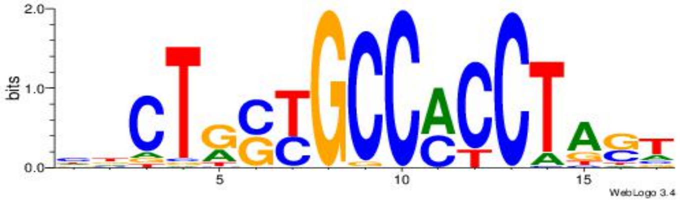
Dataset #: 4
Motif ID: 144
Motif name: ctCTrsyGCCmCCTast
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2

Number of overlap:	14
Similarity score:	0.0675705

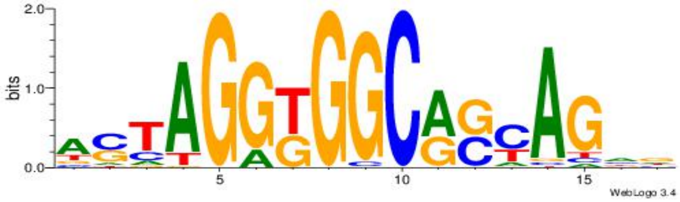
Alignment:

```
HDCTGSYGCCMCCTAST
--CKGGDTBDMMCTGG-
```

Original motif Consensus sequence: HDCTGSYGCCMCCTAST



Reverse complement motif Consensus sequence: ASTAGGYGGCMSCAGDD

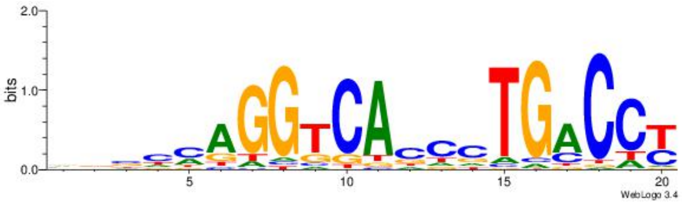


Dataset #:	3
Motif ID:	81
Motif name:	ESR1
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	4
Number of overlap:	14
Similarity score:	0.0676841

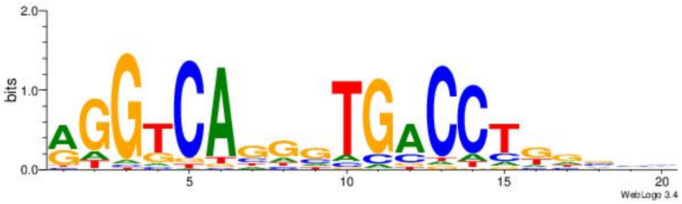
Alignment:

```
MGGTCAGGGTGACCTRDBHV
---CCAGYYHVADCCRG---
```

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV

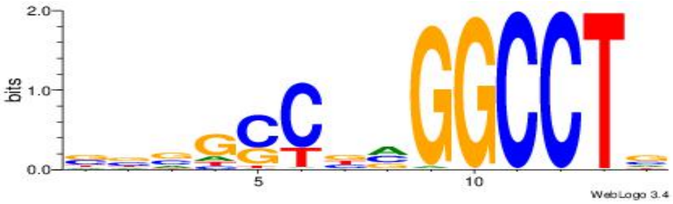


Dataset #:	3
Motif ID:	130
Motif name:	Zfx
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	14
Similarity score:	0.0677766

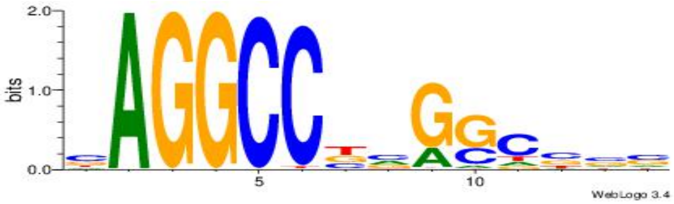
Alignment:

```
BBVGCCBVGGCCTV
CCAGYYHVADCCRG
```

Original motif Consensus sequence: BBVGCCBVGGCCTV

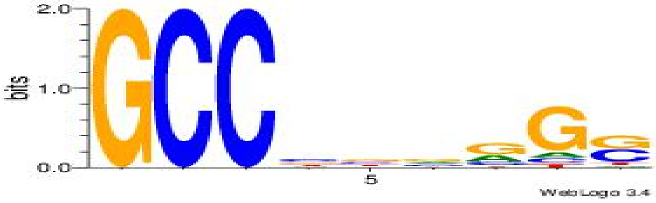


Reverse complement motif Consensus sequence: VAGGCCBBGGCV

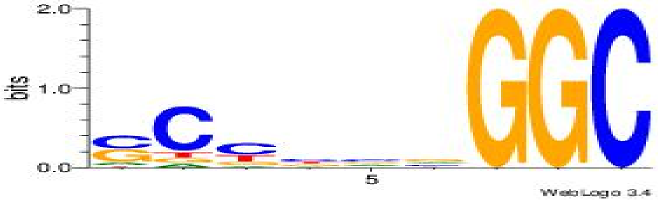


Dataset #: 3 **Motif ID: 123** **Motif name: TFAP2A**

Original motif Consensus sequence: GCCBBVRGS



Reverse complement motif Consensus sequence: SCMVBBGGC



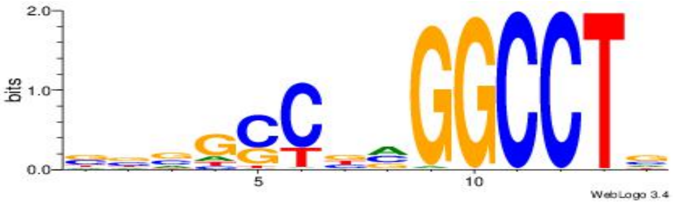
Best Matches for Motif ID 123 (Highest to Lowest)

Dataset #:	3
Motif ID:	130
Motif name:	Zfx
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	3
Number of overlap:	9
Similarity score:	0.0365038

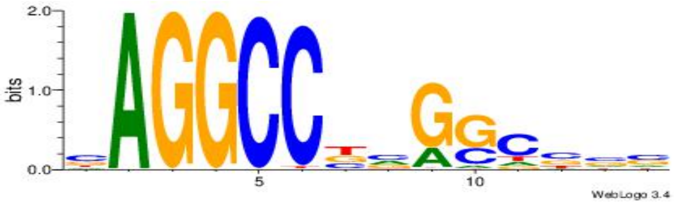
Alignment:

```
VAGGCCBBGGCVBB
---GCCBBVRGS--
```

Original motif Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif Consensus sequence: VAGGCCBBGGCV

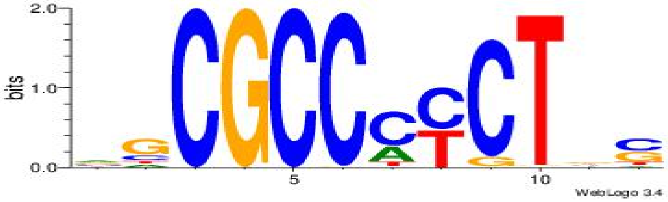


Dataset #:	4
Motif ID:	137
Motif name:	rgCGCCmyCTgs
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	4
Number of overlap:	9
Similarity score:	0.0578475

Alignment:

```
SHAGKGGGCGCB
SCMVBBGGC---
```

Original motif Consensus sequence: VGCGCCCYCTDS



Reverse complement motif Consensus sequence: SHAGKGGGCGCB

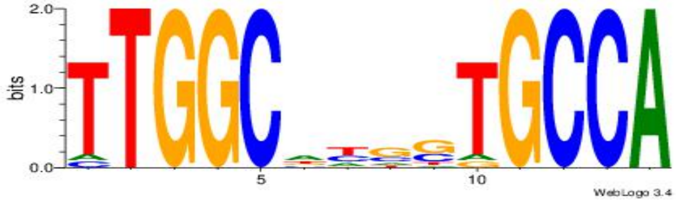
Dataset #:	3
Motif ID:	124
Motif name:	TLX1NFIC
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	3

Number of overlap: 9
Similarity score: 0.0626983

Alignment:
TGGCASBDHGCCAA
--GCCBBVRGS---

Original motif Consensus sequence: TGGCASBDHGCCAA

Reverse complement motif Consensus sequence: TTGGCHDBSTGCC



Dataset #: 4
Motif ID: 147
Motif name: asCAGrkGGCrsy
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 2
Number of overlap: 9
Similarity score: 0.0631625

Alignment:
ASCAGRGGGCRSB
-SCMVBBGGC---

Original motif Consensus sequence: ASCAGRGGGCRSB

Reverse complement motif Consensus sequence: BSKGCCCMCTGST

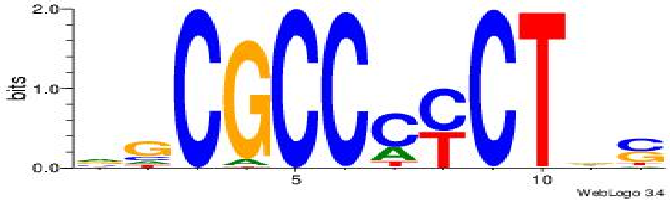
Dataset #: 4
Motif ID: 153
Motif name: scAGrkGGCGcy
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 4
Number of overlap: 9
Similarity score: 0.0640748

Alignment:

```
SHAGRGGGCGCB
SCMVBBGGC---
```

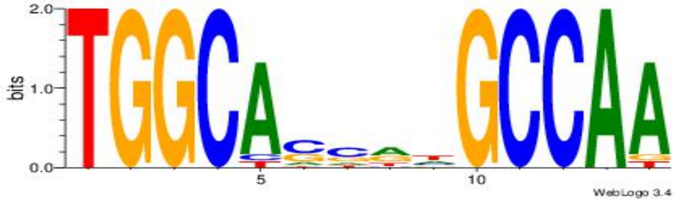
Original motif Consensus sequence: SHAGRGGGCGCB

Reverse complement motif Consensus sequence: VGCGCCCMCTDS

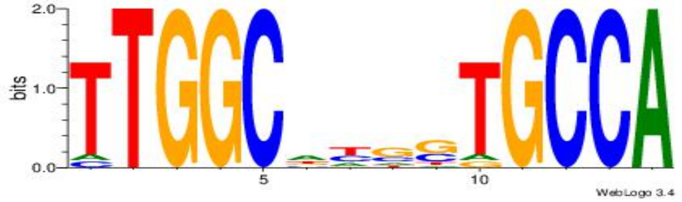


Dataset #: 3 Motif ID: 124 Motif name: TLX1NFIC

Original motif Consensus sequence: TGGCASBDHGCCAA



Reverse complement motif Consensus sequence: TTGGCHDBSTGCC



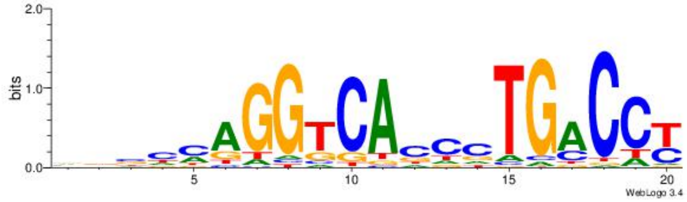
Best Matches for Motif ID 124 (Highest to Lowest)

Dataset #:	3
Motif ID:	81
Motif name:	ESR1
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	7
Number of overlap:	14
Similarity score:	0.0758334

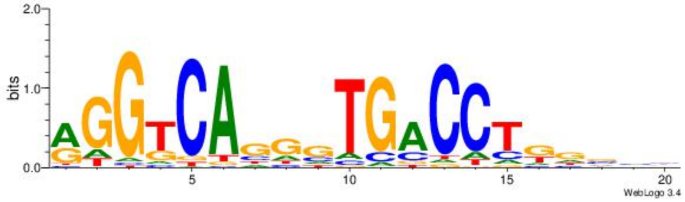
Alignment:

```
VDBHMAGGTCACCCTGACCY
------TGGCASBDHGCCAA
```

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV

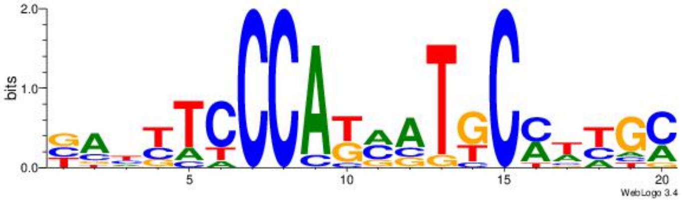


Dataset #:	3
Motif ID:	131
Motif name:	znf143
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	4
Number of overlap:	14
Similarity score:	0.0763138

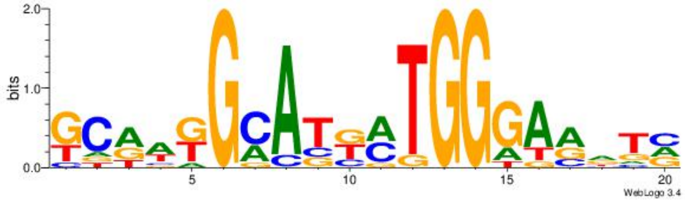
Alignment:

```
GCMWRGCATYRTGGGAMHTB
---TGGCASBDHGCCAA---
```

Original motif   Consensus sequence: BAHYTCCCAKMATGCMWYGC



Reverse complement motif   Consensus sequence: GCMWRGCATYRTGGGAMHTB



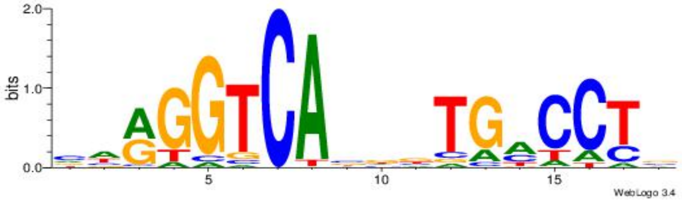
Dataset #:	3
Motif ID:	82
Motif name:	ESR2
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2

Number of overlap: 14
Similarity score: 0.0777688

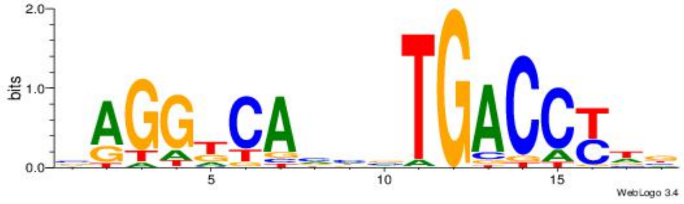
Alignment:

```
VHRGGTCABDBTGMCCTB
---TGGCASBDHGCCAA-
```

Original motif Consensus sequence: VHRGGTCABDBTGMCCTB



Reverse complement motif Consensus sequence: BAGGYCABHBTGACCKHV

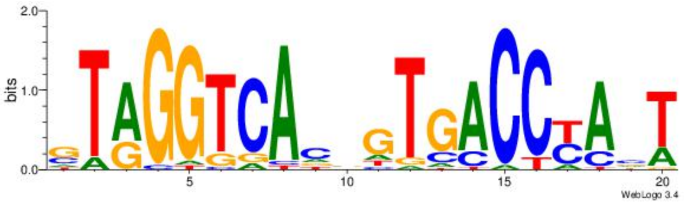


Dataset #: 3
Motif ID: 111
Motif name: PPARG
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 4
Number of overlap: 14
Similarity score: 0.0838712

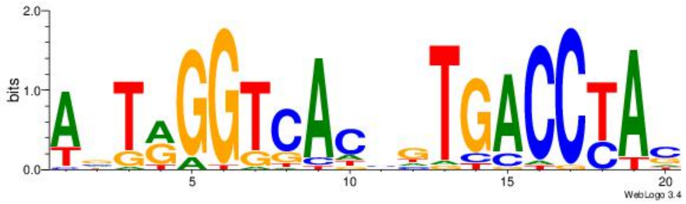
Alignment:

```
STAGGTCACBGTGACCYABT
---TGGCASBDHGCCAA---
```

Original motif Consensus sequence: STAGGTCACBGTGACCYABT



Reverse complement motif Consensus sequence: ABTMGGTCACBGTGACCTAS

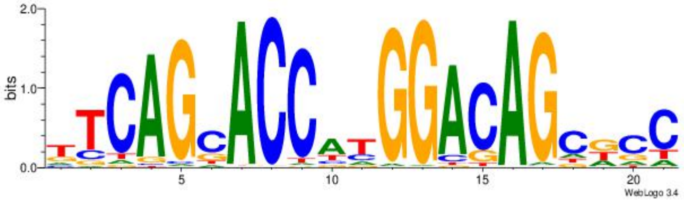


Dataset #:	3
Motif ID:	113
Motif name:	REST
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	3
Number of overlap:	14
Similarity score:	0.0916353

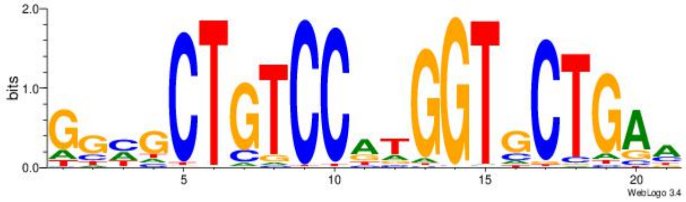
Alignment:

```
TTCAGCACCATGGACAGCKCC
--TGGCASBDHGCCAA-----
```

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC

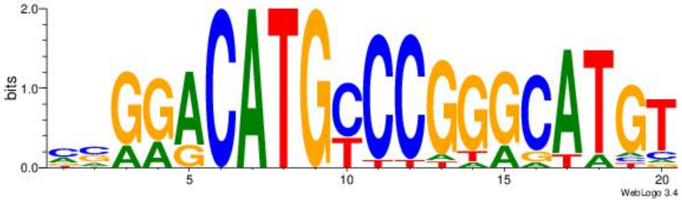


Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA

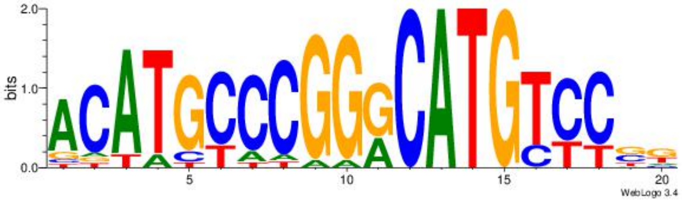


Dataset #: 3 Motif ID: 125 Motif name: TP53

Original motif Consensus sequence: MSGGACATGYCCGGGCATGT



Reverse complement motif Consensus sequence: ACATGCCCGGKCATGTCCSR



Best Matches for Motif ID 125 (Highest to Lowest)

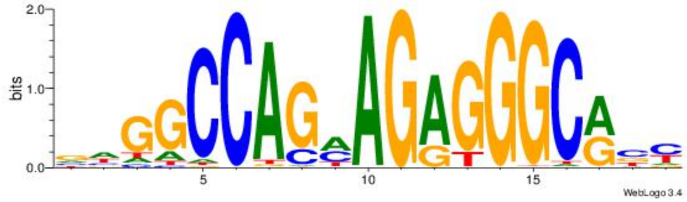
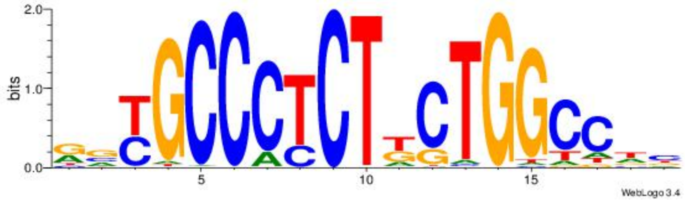
Dataset #:	4
Motif ID:	163
Motif name:	gwGGCCAGmAGAGGGCrby
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	19
Similarity score:	0.0641029

Alignment:

```
-KBKGCCCTCTYCTGGCCHV
ACATGCCCGGKCATGTCCSR
```

Original motif Consensus sequence: VHGGCCAGMAGAGGGCRBY

Reverse complement motif Consensus sequence: KBKGCCCTCTYCTGGCCHV

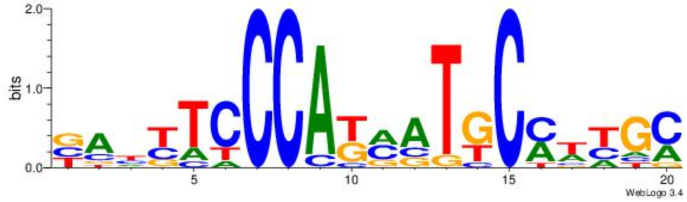



Dataset #:	3
Motif ID:	131
Motif name:	znf143
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2
Number of overlap:	19
Similarity score:	0.0730057

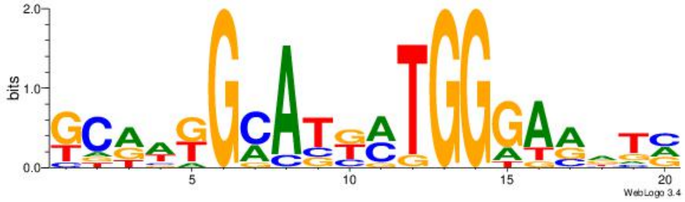
Alignment:

```
-BAHYTCCCAKMATGCMWYGC
ACATGCCCGGKCATGTCCSR-
```

Original motif Consensus sequence: BAHYTCCCAKMATGCMWYGC



Reverse complement motif Consensus sequence: GCMWRGCATYRTGGGAMHTB



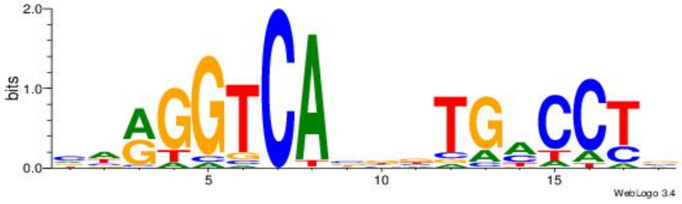
Dataset #:	3

Motif ID: 82
Motif name: ESR2
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 4
Number of overlap: 15
Similarity score: 2.07342

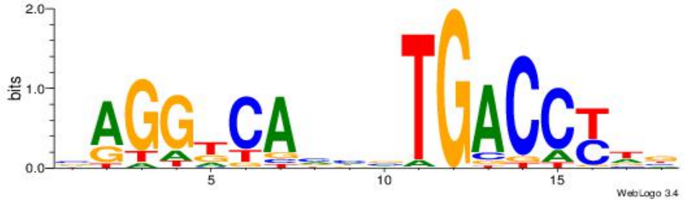
Alignment:

```
-----BAGGYCABHBTGACCKHV
MSGGACATGYCCGGGCATGT---
```

Original motif Consensus sequence: VHRGGTCABDBTGMCCTB



Reverse complement motif Consensus sequence: BAGGYCABHBTGACCKHV



Dataset #: 3
Motif ID: 130
Motif name: Zfx
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 14

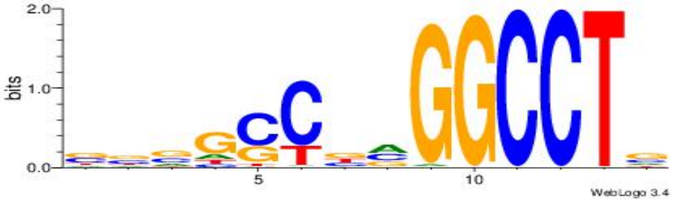
Similarity score: 2.55908

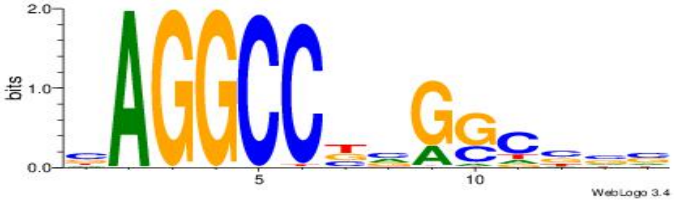
Alignment:

```
------VAGGCCBBGGCVBB
ACATGCCCGGKCATGTCCSR
```

Original motif Consensus sequence: BBVGCCBVGGCCTV

Reverse complement motif Consensus sequence: VAGGCCBBGGCV





Dataset #: 3

Motif ID: 122

Motif name: Tcfcp2l1

Matching format of first motif: Original Motif

Matching format of second motif: Reverse Complement

Direction: Backward

Position number: 1

Number of overlap: 14

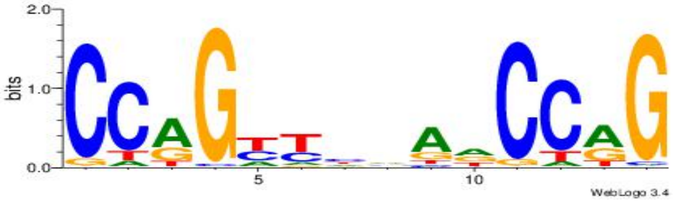
Similarity score: 2.56997

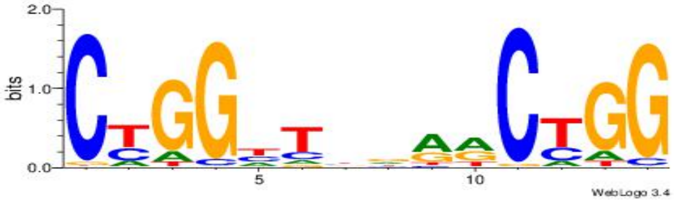
Alignment:

```
------CKGGDTBDMMCTGG
MSGGACATGYCCGGGCATGT
```

Original motif Consensus sequence: CCAGYYHVADCCRG

Reverse complement motif Consensus sequence: CKGGDTBDMMCT





Dataset #: 3 **Motif ID: 126** **Motif name: USF1**

Original motif Consensus sequence: CACGTGR

Reverse complement motif Consensus sequence: MCACGTG

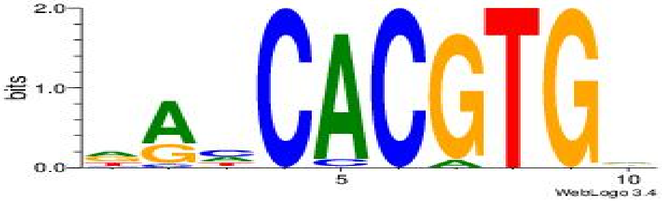
Best Matches for Motif ID 126 (Highest to Lowest)

Dataset #:	3
Motif ID:	91
Motif name:	MAX
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

Alignment:

```
DAHCACGTGD
-MCACGTG--
```

Original motif Consensus sequence: DAHCACGTGD



Reverse complement motif Consensus sequence: BCACGTGDTD

Dataset #:	3
Motif ID:	95
Motif name:	MYCMAX
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	2
Number of overlap:	7
Similarity score:	0.0108143

Alignment:

```
ACCACGTGSTM
-MCACGTG---
```

Original motif Consensus sequence: RASCACGTGGT

Reverse complement motif Consensus sequence: ACCACGTGSTM

Dataset #: 3
Motif ID: 94
Motif name: Myc
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2
Number of overlap: 7
Similarity score: 0.0198377

Alignment:

```
VGCACGTGGH
--CACGTGR-
```

Original motif Consensus sequence: VGCACGTGGH

Reverse complement motif Consensus sequence: DCCACGTGCV

Dataset #: 3
Motif ID: 96
Motif name: Mycn
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2
Number of overlap: 7

Similarity score: 0.0207062

Alignment:

```
HSCACGTGGC
--CACGTGR-
```

Original motif Consensus sequence: HSCACGTGGC

Reverse complement motif Consensus sequence: GCCACGTGSD

Dataset #:	3
Motif ID:	86
Motif name:	HIF1AARNT
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	7
Similarity score:	0.0436113

Alignment:

```
VBACGTGV
-MCACGTG
```

Original motif Consensus sequence: VBACGTGV

Reverse complement motif Consensus sequence: VCACGTBV

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

Original motif Consensus sequence: RCCATB

Reverse complement motif Consensus sequence: BATGGM

Best Matches for Motif ID 127 (Highest to Lowest)

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

Alignment:

```
KCCATCT
-RCCATB
```

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

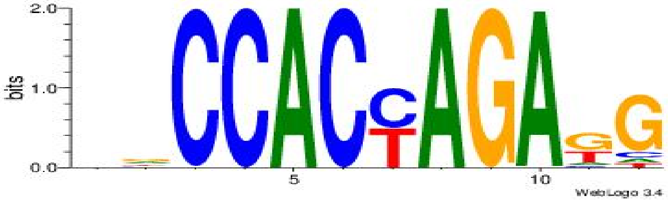
Reverse complement motif   Consensus sequence: GAGCCATC

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

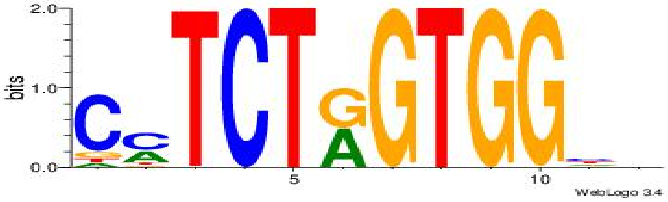
Alignment:

```
CYTCTKGTGGHH
-----BATGGM-
```

Original motif Consensus sequence: DDCCACYAGAKG



Reverse complement motif Consensus sequence: CYTCTKGTGGHH



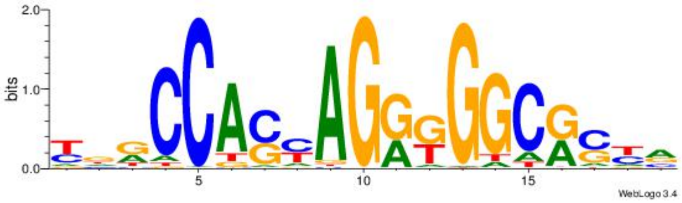
Dataset #:	3
Motif ID:	74
Motif name:	CTCF
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	3
Number of overlap:	6

Similarity score: 0.0220417

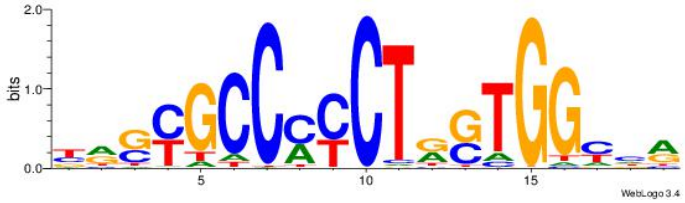
Alignment:

```
BMSMGCCYMCTKSTGGMHM
-----------BATGGM--
```

Original motif Consensus sequence: YDRCCASYAGRKGGCRSYV



Reverse complement motif Consensus sequence: BMSMGCCYMCTKSTGGMHM



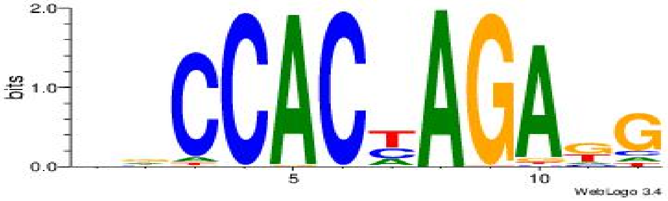
Dataset #:	4
Motif ID:	138
Motif name:	grCCACyAGAkG
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	6
Similarity score:	0.0223679

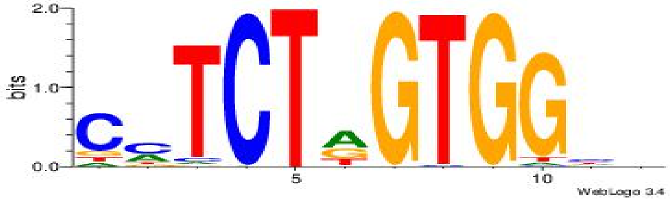
Alignment:

```
DDCCACYAGAKG
-RCCATB-----
```

Original motif Consensus sequence: DDCCACYAGAKG

Reverse complement motif Consensus sequence: CYTCTMGTGGHH





Dataset #: 3 **Motif ID: 128** **Motif name: ZEB1**

Original motif Consensus sequence: CACCTD

Reverse complement motif Consensus sequence: HAGGTG

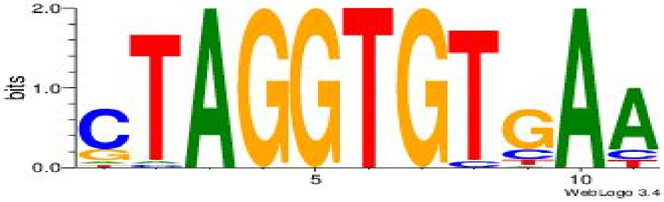
Best Matches for Motif ID 128 (Highest to Lowest)

Dataset #:	3
Motif ID:	120
Motif name:	T
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:	0.0192581

Alignment:

```
TTCACACCTAG
-CACCTD----
```

Original motif Consensus sequence: CTAGGTGTGAA



Reverse complement motif Consensus sequence: TTCACACCTAG

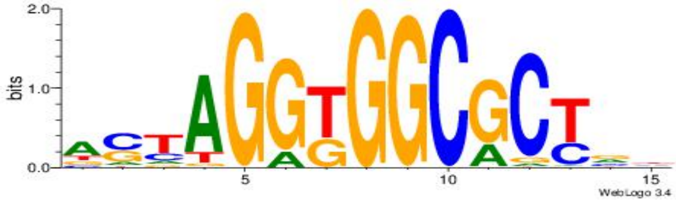
Dataset #:	4
Motif ID:	146
Motif name:	myrGYGCCmCCTast
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	3
Number of overlap:	6
Similarity score:	0.0325288

Alignment:

```
VBAGCGCCMCCTAST
-------CACCTD--
```

Original motif Consensus sequence: VBAGCGCCMCCTAST

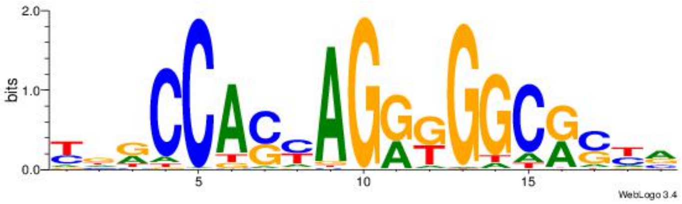
Reverse complement motif Consensus sequence: ASTAGGYGGCGCT



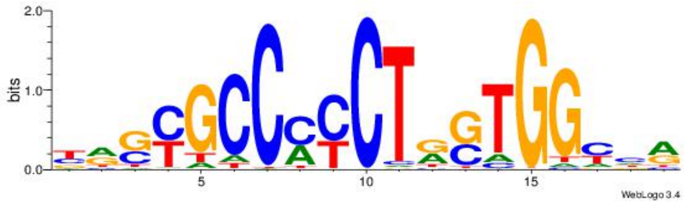
Dataset #: 3
Motif ID: 74
Motif name: CTCF
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 8
Number of overlap: 6
Similarity score: 0.0341274

Alignment:
BMSMGCCYMCTKSTGGMHM
-------CACCTD------

Original motif Consensus sequence: YDRCCASYAGRKGGCRSYV



Reverse complement motif Consensus sequence: BMSMGCCYMCTKSTGGMHM



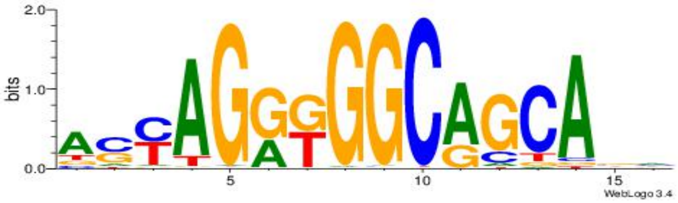
Dataset #: 4
Motif ID: 164
Motif name: asyAGrkGGCRGCAga
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 9

Number of overlap: 6
Similarity score: 0.0351031

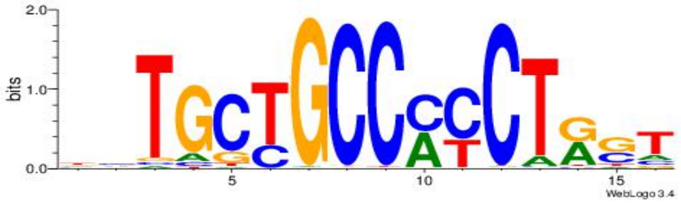
Alignment:

```
ASYAGRKGGCAGCABH
--HAGGTG--------
```

Original motif Consensus sequence: ASYAGRKGGCAGCABH



Reverse complement motif Consensus sequence: HBTGCTGCCYMCTKST

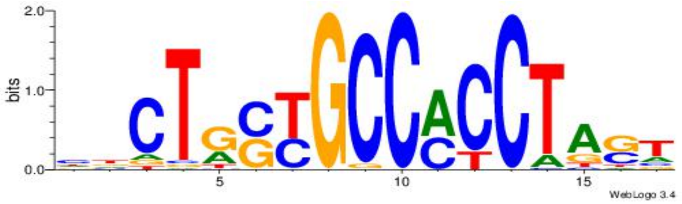


Dataset #: 4
Motif ID: 144
Motif name: ctCTrsyGCCmCCTast
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 3
Number of overlap: 6
Similarity score: 0.0356696

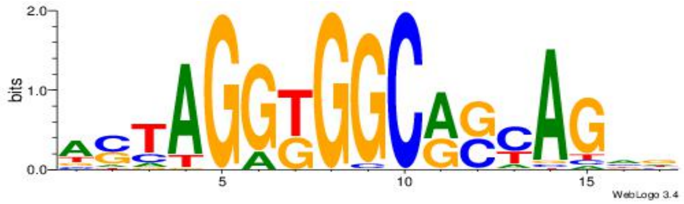
Alignment:

```
HDCTGSYGCCMCCTAST
---------CACCTD--
```

Original motif Consensus sequence: HDCTGSYGCCMCCTAST

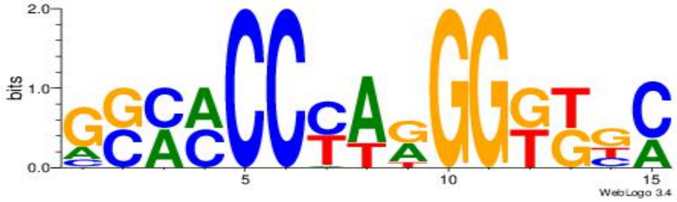


Reverse complement motif Consensus sequence: ASTAGGYGGCMSCAGDD

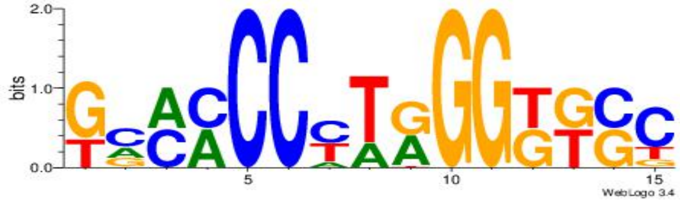


Dataset #: 3 Motif ID: 129 Motif name: Zfp423

Original motif Consensus sequence: GSMMCCYARGGKKKC



Reverse complement motif Consensus sequence: GYRYCCMTKGGYR



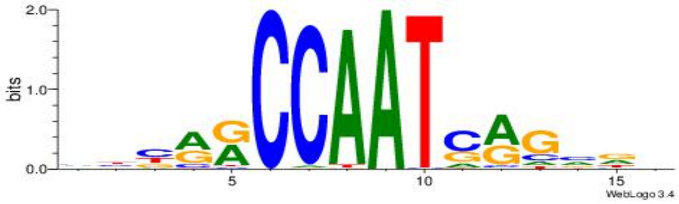
Best Matches for Motif ID 129 (Highest to Lowest)

Dataset #:	3
Motif ID:	104
Motif name:	NFYA
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	15
Similarity score:	0.0358106

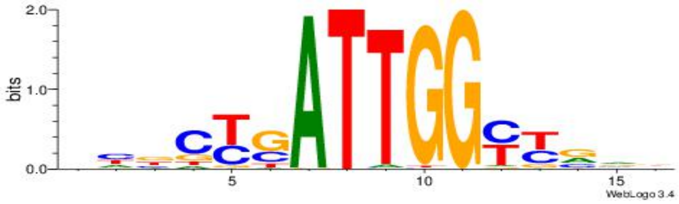
Alignment:

```
BHVCKSATTGGMKBVV
GYRYCCMTKGGYRSC-
```

Original motif Consensus sequence: VBBRRCCAATSRGVDB



Reverse complement motif Consensus sequence: BHVCKSATTGGMKBVV



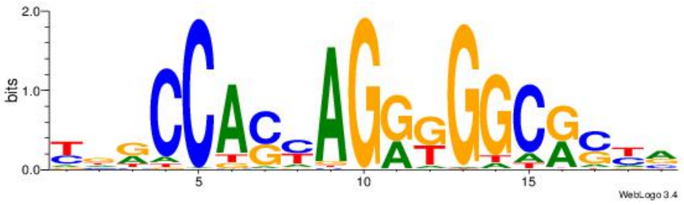
Dataset #:	3
Motif ID:	74
Motif name:	CTCF
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	3
Number of overlap:	15
Similarity score:	0.0359705

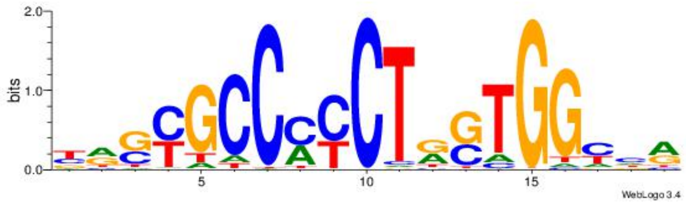
Alignment:

```
BMSMGCCYMCTKSTGGMHM
--GYRYCCMTKGGYRSC--
```

Original motif Consensus sequence: YDRCCASYAGRKGGCRSYV

Reverse complement motif Consensus sequence: BMSMGCCYMCTKSTGGMHM



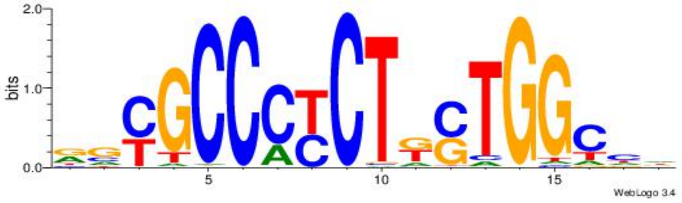


Dataset #:	4
Motif ID:	156
Motif name:	rgyGCCMyCTksTGGccd
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	3
Number of overlap:	15
Similarity score:	0.0382225

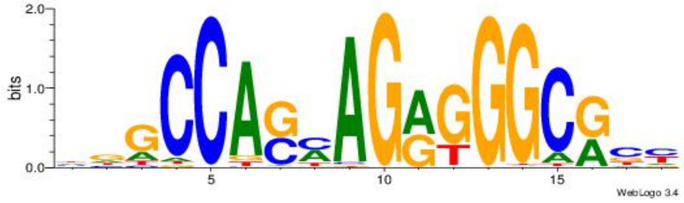
Alignment:

```
RVYGCCCYCTKSTGGCHD
-GYRYCCMTKGGYRSC--
```

Original motif Consensus sequence: RVYGCCCYCTKSTGGCHD



Reverse complement motif Consensus sequence: DDGCCASYAGMGGGCKVM



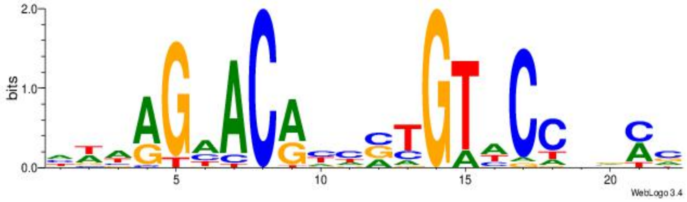
Dataset #:	3

Motif ID: 70
Motif name: Ar
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 5
Number of overlap: 15
Similarity score: 0.0429662

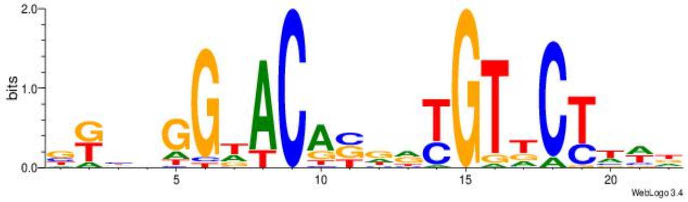
Alignment:

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

Original motif Consensus sequence: HWDAGHACRHHVTGTHCCHVMV



Reverse complement motif Consensus sequence: VRVDGGHACAVDDKGTHCTDWH



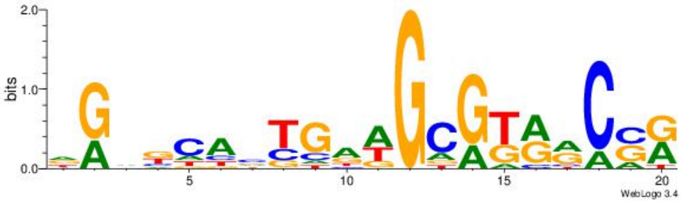
Dataset #: 3
Motif ID: 109
Motif name: Pax5
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 3
Number of overlap: 15

Similarity score:	0.0430294

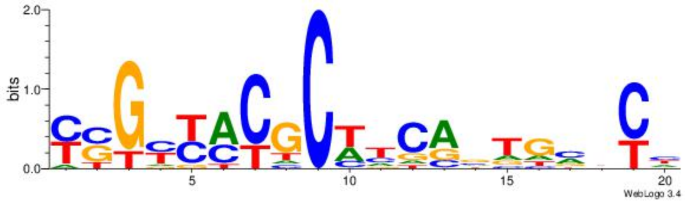
Alignment:

```
DGVBCABTGDWGCGKRRCSR
--GSMMCCYARGGKKKC---
```

Original motif Consensus sequence: DGVBCABTGDWGCGKRRCSR

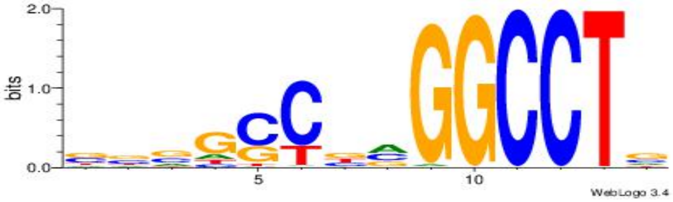


Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD

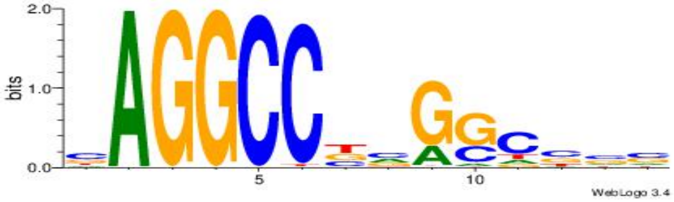


Dataset #: 3 Motif ID: 130 Motif name: Zfx

Original motif Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif Consensus sequence: VAGGCCBBGGCV



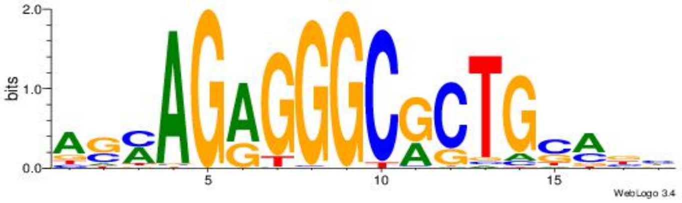
Best Matches for Motif ID 130 (Highest to Lowest)

Dataset #:	4
Motif ID:	149
Motif name:	asmAGRGGGCrCTGsmkc
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement

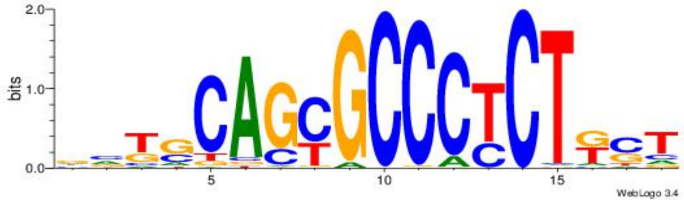
Direction: Forward
Position number: 1
Number of overlap: 14
Similarity score: 0.0651255

Alignment:
DBTSCAGMGCCCTCTRST
BBVGCCBVGGCCTV----

Original motif Consensus sequence: ASMAGAGGGCRCTGSABH



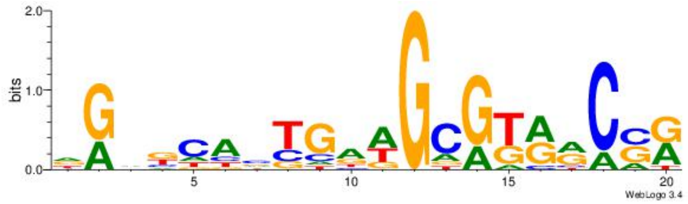
Reverse complement motif Consensus sequence: DBTSCAGMGCCCTCTRST



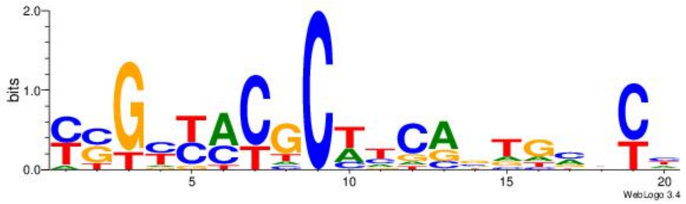
Dataset #: 3
Motif ID: 109
Motif name: Pax5
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 5
Number of overlap: 14
Similarity score: 0.0724025

Alignment:
DGVBCABTGDWGCGKRRCSR
--BBVGCCBVGGCCTV----

Original motif Consensus sequence: DGVBCABTGDWGCGKRRCSR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD



Dataset #: 3

Motif ID: 82

Motif name: ESR2

Matching format of first motif: Reverse Complement

Matching format of second motif: Original Motif

Direction: Backward

Position number: 2

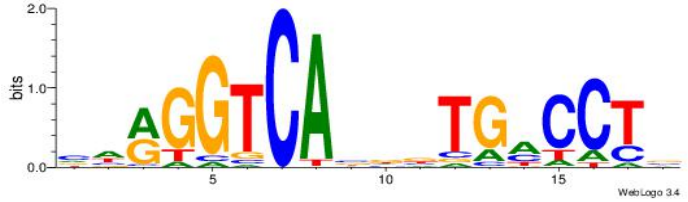
Number of overlap: 14

Similarity score: 0.0748557

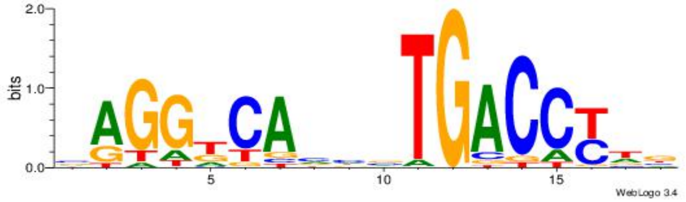
Alignment:

```
VHRGGTCABDBTGMCCTB
---VAGGCCBBGGCVBB-
```

Original motif Consensus sequence: VHRGGTCABDBTGMCCTB



Reverse complement motif Consensus sequence: BAGGYCABHBTGACCKHV

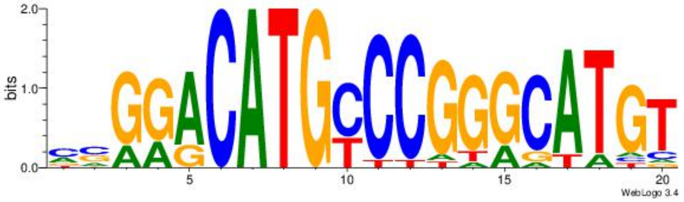


Dataset #: 3
Motif ID: 125
Motif name: TP53
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 6
Number of overlap: 14
Similarity score: 0.0763693

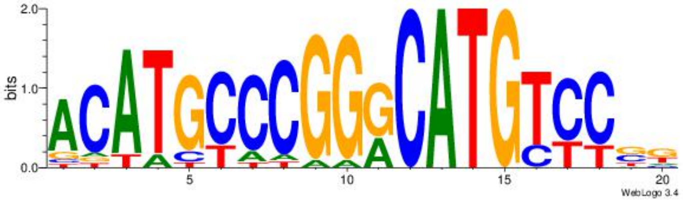
Alignment:

```
ACATGCCCGGKCATGTCCSR
-----BBVGCCBVGGCCTV-
```

Original motif Consensus sequence: MSGGACATGYCCGGGCATGT



Reverse complement motif Consensus sequence: ACATGCCCGGKCATGTCCSR



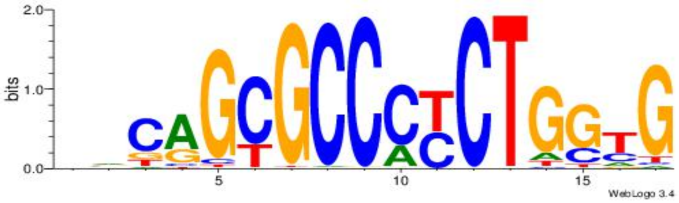
Dataset #: 4
Motif ID: 168
Motif name: yrcrGYGCCMyCTGGtG
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1

Number of overlap:	14
Similarity score:	0.0830122

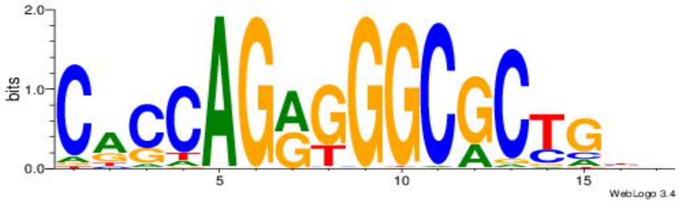
Alignment:

```
HVCAGCGCCCYCTGGTG
BBVGCCBVGGCCTV---
```

Original motif   Consensus sequence: HVCAGCGCCCYCTGGTG

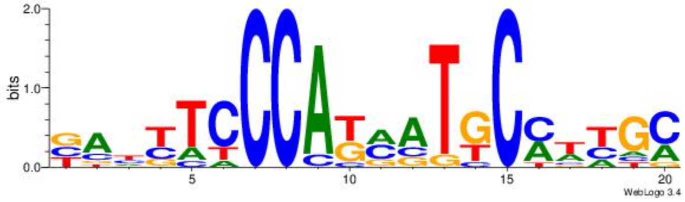


Reverse complement motif   Consensus sequence: CACCAGMGGGCGCTGBD

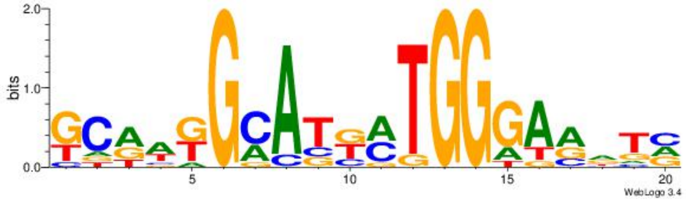


Dataset #: 3   Motif ID: 131   Motif name: znf143

Original motif   Consensus sequence: BAHYTCCCAKMATGCMWYGC



Reverse complement motif   Consensus sequence: GCMWRGCATYRTGGGAMHTB



Best Matches for Motif ID 131 (Highest to Lowest)

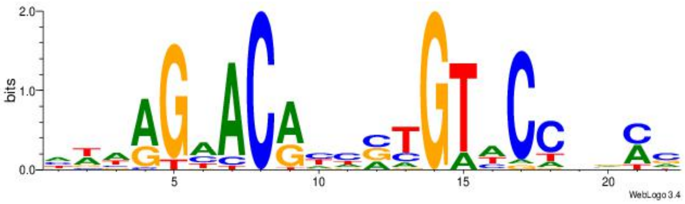
Dataset #:	3
Motif ID:	70
Motif name:	Ar

Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 20
Similarity score: 0.0555912

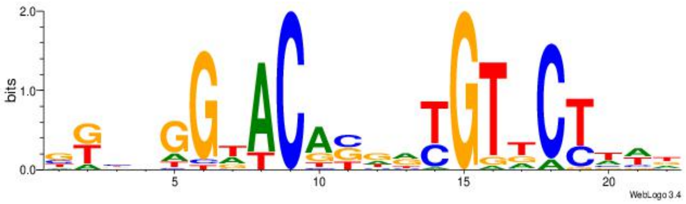
Alignment:

```
VRVDGGHACAVDDKGTHCTDWH
GCMWRGCATYRTGGGAMHTB--
```

Original motif Consensus sequence: HWDAGHACRHHVTGTHCCHVMV



Reverse complement motif Consensus sequence: VRVDGGHACAVDDKGTHCTDWH

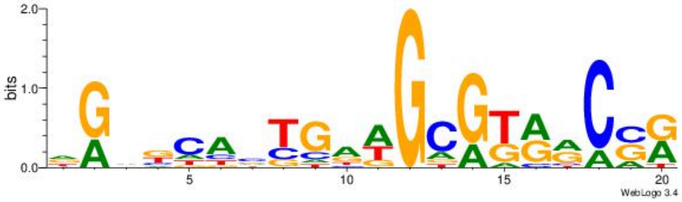


Dataset #: 3
Motif ID: 109
Motif name: Pax5
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 2
Number of overlap: 19
Similarity score: 0.554242

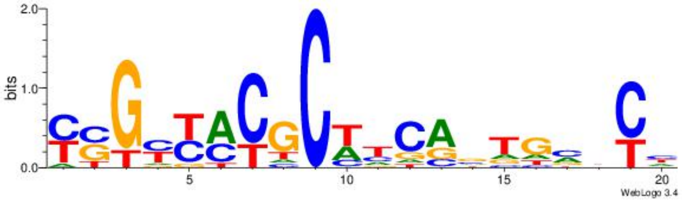
Alignment:

```
DGVBCABTGDWGCGKRRCSR-
-GCMWRGCATYRTGGGAMHTB
```

Original motif Consensus sequence: DGVBCABTGDWGCGKRRCSR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD



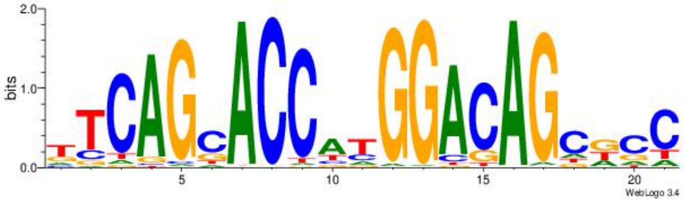
Dataset #:	3
Motif ID:	113
Motif name:	REST
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	3
Number of overlap:	19
Similarity score:	0.558571

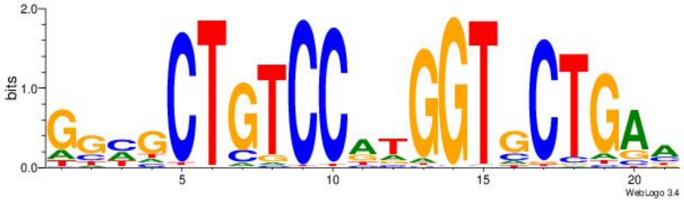
Alignment:

```
-GGYGCTGTCCATGGTGCTGAA
BAHYTCCCAKMATGCMWYGC--
```

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC

Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA



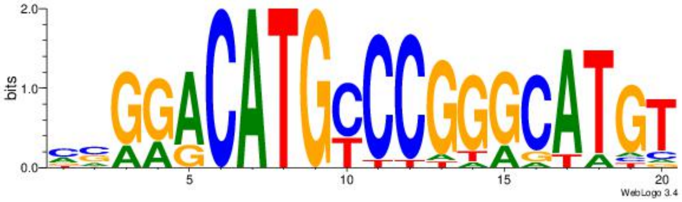


Dataset #:	3
Motif ID:	125
Motif name:	TP53
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	19
Similarity score:	0.566085

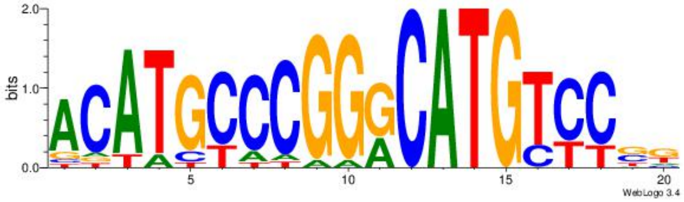
Alignment:

```
MSGGACATGYCCGGGCATGT-
-GCMWRGCATYRTGGGAMHTB
```

Original motif Consensus sequence: MSGGACATGYCCGGGCATGT



Reverse complement motif Consensus sequence: ACATGCCCGGKCATGTCCSR



Dataset #:	3

Motif ID: 81

Motif name: ESR1

Matching format of first motif: Original Motif

Matching format of second motif: Original Motif

Direction: Forward

Position number: 3

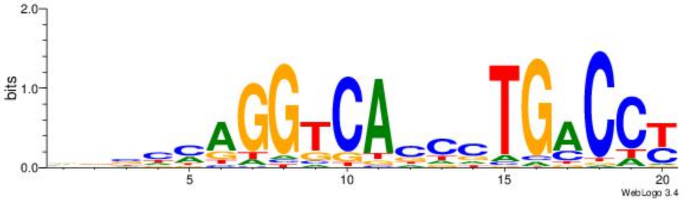
Number of overlap: 18

Similarity score: 1.05907

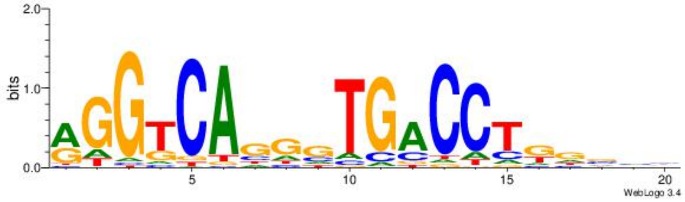
Alignment:

```
VDBHMAGGTCACCCTGACCY--
--BAHYTCCCAKMATGCMWYGC
```

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV



Dataset #: 3 Motif ID: 132 Motif name: ZNF354C

Original motif Consensus sequence: MTCCAC

Reverse complement motif Consensus sequence: GTGGAY

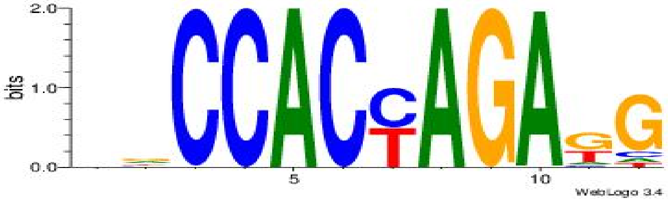
Best Matches for Motif ID 132 (Highest to Lowest)

Dataset #:	4
Motif ID:	145
Motif name:	grCCACyAGAkG
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	7
Number of overlap:	6
Similarity score:	0.0253111

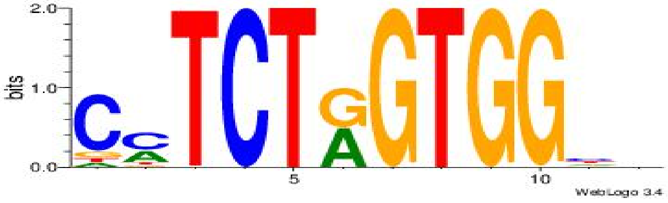
Alignment:

```
CYTCTKGTGGHH
------GTGGAY
```

Original motif Consensus sequence: DDCCACYAGAKG



Reverse complement motif Consensus sequence: CYTCTKGTGGHH



Dataset #:	4
Motif ID:	158
Motif name:	grCCACwAGrk
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement

Direction: Backward
Position number: 1
Number of overlap: 6
Similarity score: 0.0266594

Alignment:

```
YMCTWGTGGHH
-----GTGGAY
```

Original motif Consensus sequence: DDCCACWAGRK

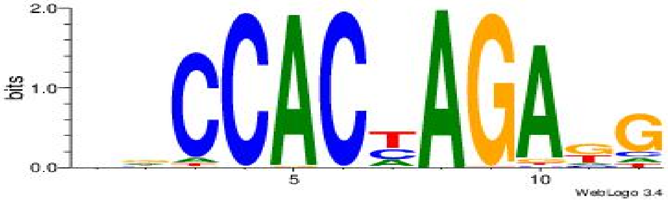
Reverse complement motif Consensus sequence: YMCTWGTGGHH

Dataset #: 4
Motif ID: 138
Motif name: grCCACyAGAkG
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 7
Number of overlap: 6
Similarity score: 0.0292621

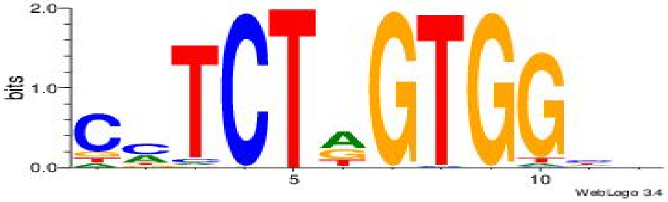
Alignment:

```
CYTCTMGTGGHH
------GTGGAY
```

Original motif Consensus sequence: DDCCACYAGAKG



Reverse complement motif Consensus sequence: CYTCTMGTGGHH

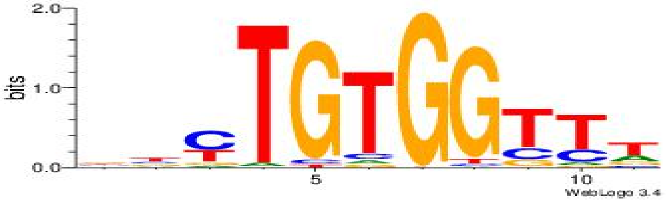


Dataset #:	3
Motif ID:	114
Motif name:	RUNX1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	5
Number of overlap:	6
Similarity score:	0.0470937

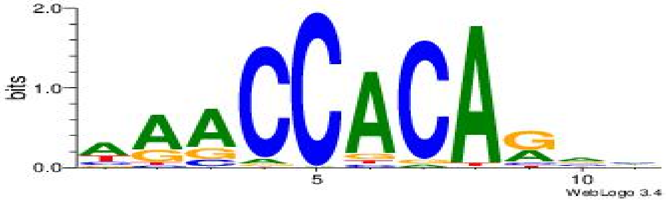
Alignment:

```
BBYTGTGGTTT
-GTGGAY----
```

Original motif Consensus sequence: BBYTGTGGTTT



Reverse complement motif Consensus sequence: AAACCACAKVB



Dataset #:	1
Motif ID:	9
Motif name:	Motif 9
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	2
Number of overlap:	6
Similarity score:	0.0507812

Alignment:

```
SWGCCACC
-MTCCAC-
```

Original motif Consensus sequence: GGTGGCWS

Reverse complement motif Consensus sequence: SWGCCACC

Dataset #: 4 Motif ID: 133 Motif name: shAGrGGGCAgy

Original motif Consensus sequence: SHAGRGGGCABH

Reverse complement motif Consensus sequence: DBTGCCCKCTDS

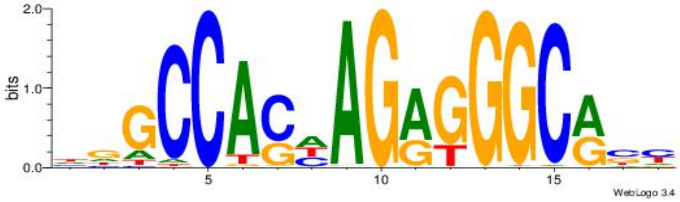
Best Matches for Motif ID 133 (Highest to Lowest)

Dataset #:	4
Motif ID:	165
Motif name:	wgGCCAshAGrGGGCrsy
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	7
Number of overlap:	12
Similarity score:	0.00159897

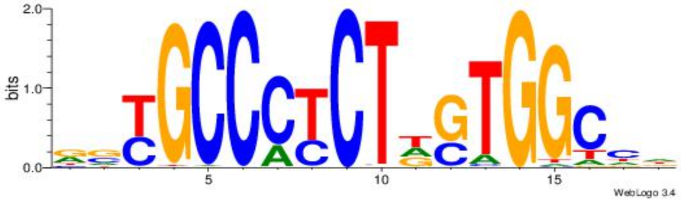
Alignment:

```
HDGCCACHAGRGGGCRBY
------SHAGRGGGCABH
```

Original motif Consensus sequence: HDGCCACHAGRGGGCRBY



Reverse complement motif Consensus sequence: KBKGCCCKCTHGTGGCHH



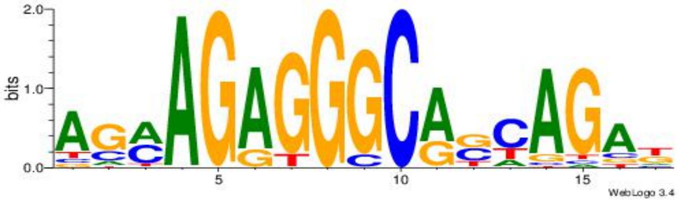
Dataset #:	4
Motif ID:	143
Motif name:	AgmAGAGGGCrscAGak
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif

Direction:	Backward
Position number:	5
Number of overlap:	12
Similarity score:	0.00815796

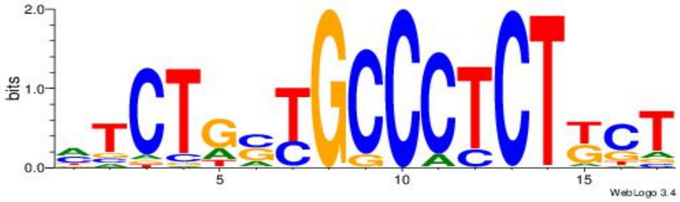
Alignment:

```
AGMAGAGGGCASCAGAK
-SHAGRGGGCABH----
```

Original motif Consensus sequence: AGMAGAGGGCASCAGAK



Reverse complement motif Consensus sequence: RTCTGSTGCCCTCTYCT

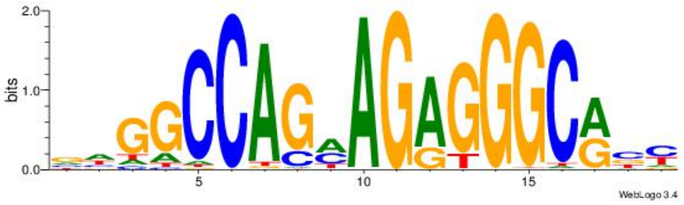


Dataset #:	4
Motif ID:	163
Motif name:	gwGGCCAGmAGAGGGCrby
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	8
Number of overlap:	12
Similarity score:	0.0109424

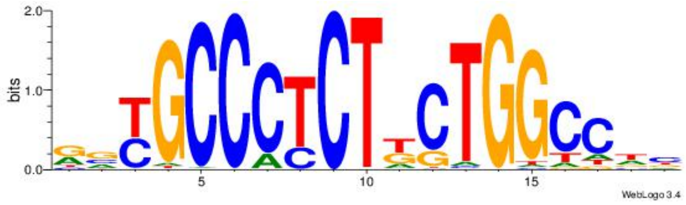
Alignment:

```
VHGGCCAGMAGAGGGCRBY
-------SHAGRGGGCABH
```

Original motif Consensus sequence: VHGGCCAGMAGAGGGCRBY



Reverse complement motif Consensus sequence: KBKGCCCTCTYCTGGCCHV



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: 1

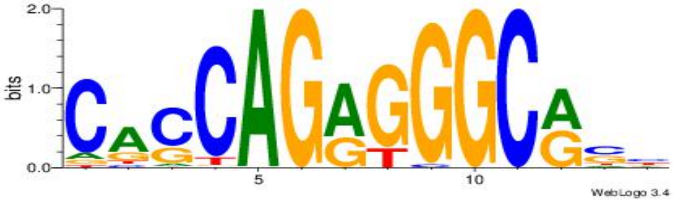
Number of overlap: 12

Similarity score: 0.0124424

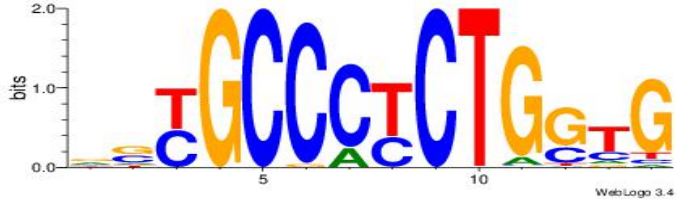
Alignment:

```
CACCAGRGGGCRSB
--SHAGRGGGCABH
```

Original motif Consensus sequence: CACCAGRGGGCRSB



Reverse complement motif Consensus sequence: BSKGCCCKCTGGT



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: 2
Number of overlap: 12
Similarity score: 0.0128393

Alignment:

```
ASCAGRGGGCRSB
-SHAGRGGGCABH
```

Original motif Consensus sequence: ASCAGRGGGCRSB

Reverse complement motif Consensus sequence: BSKGCCCMCTGST

Dataset #: 4 Motif ID: 134 Motif name: ssCGwGCGss

Original motif Consensus sequence: BSCGWGCGBV

Reverse complement motif Consensus sequence: VBCGCWCGSB

Best Matches for Motif ID 134 (Highest to Lowest)

Dataset #:	4
Motif ID:	135
Motif name:	ssCGGCCGss
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	10
Similarity score:	0.0113669

Alignment:

```
BSCGGCCGSV
VBCGCWCGSB
```

Original motif Consensus sequence: BSCGGCCGSV

Reverse complement motif Consensus sequence: VSCGGCCGSB

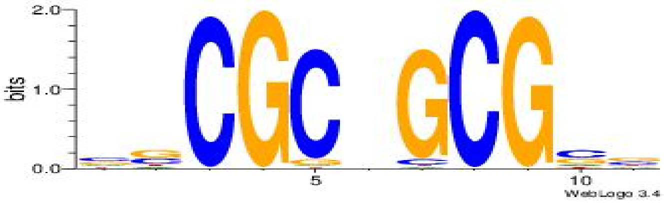
Dataset #:	4
Motif ID:	161
Motif name:	ssCGCwGCGss
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement

Direction:	Forward
Position number:	2
Number of overlap:	10
Similarity score:	0.0473417

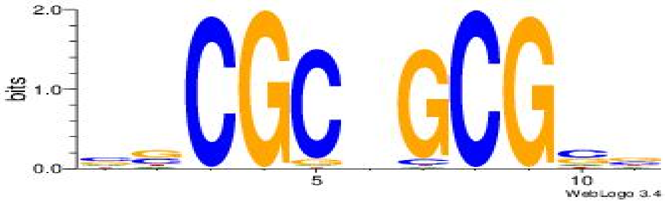
Alignment:

```
BSCGCDGCGSV
-BSCGWGCGBV
```

Original motif Consensus sequence: VSCGCDGCGSB



Reverse complement motif Consensus sequence: BSCGCDGCGSV



Dataset #:	4
Motif ID:	152
Motif name:	yrCATGCAyr
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	10
Similarity score:	0.0541916

Alignment:

```
BRCATGCABD
BSCGWGCGBV
```

Original motif Consensus sequence: BRCATGCABD

Reverse complement motif Consensus sequence: HVTGCATGKV

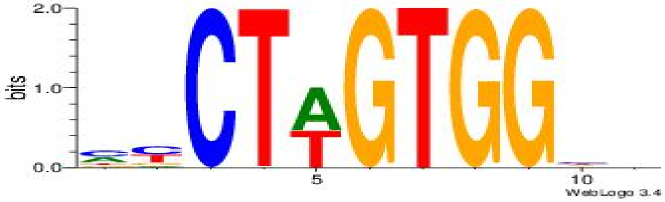
Dataset #:	4
Motif ID:	158
Motif name:	grCCACwAGrk
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	10
Similarity score:	0.0546634

Alignment:

```
DDCCACWAGRK
-VBCGCWCGSB
```

Original motif Consensus sequence: DDCCACWAGRK

Reverse complement motif Consensus sequence: YMCTWGTGGHH

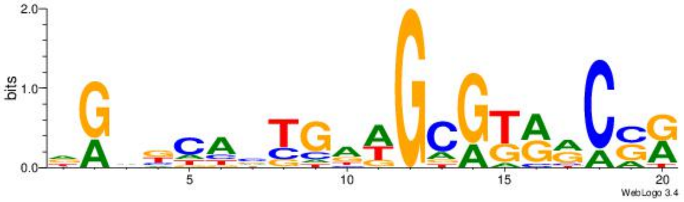


Dataset #:	3
Motif ID:	109
Motif name:	Pax5
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	7
Number of overlap:	10
Similarity score:	0.0551638

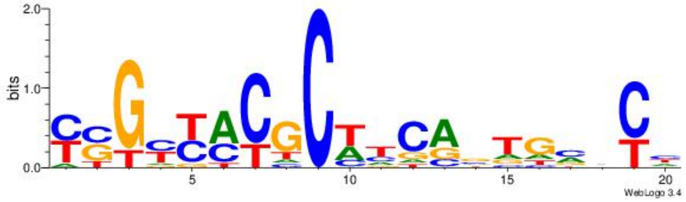
Alignment:

```
DGVBCABTGDWGCGKRRCSR
------BSCGWGCGBV----
```

Original motif Consensus sequence: DGVBCABTGDWGCGKRRCSR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD



Dataset #: 4 Motif ID: 135 Motif name: ssCGGCCGss

Original motif Consensus sequence: BSCGGCCGSV

Reverse complement motif Consensus sequence: VSCGGCCGSB

Best Matches for Motif ID 135 (Highest to Lowest)

Dataset #:	4
Motif ID:	134
Motif name:	ssCGwGCGss
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	10
Similarity score:	0

Alignment:

```
BSCGWGCGBV
VSCGGCCGSB
```

Original motif   Consensus sequence: BSCGWGCGBV

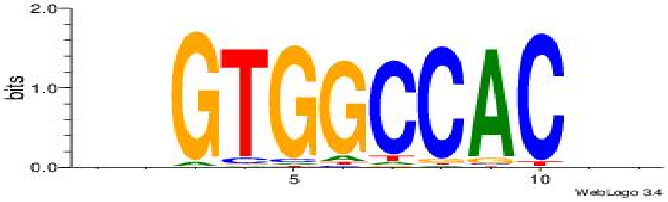
Reverse complement motif   Consensus sequence: VBCGCWCGSB

Dataset #:	4

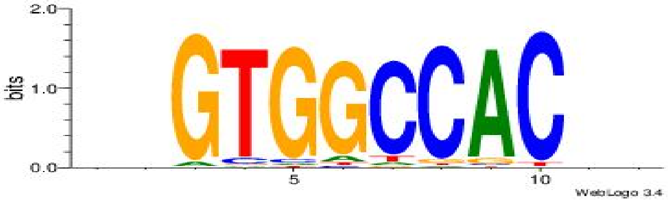
Motif ID: 171
Motif name: ysGTGGCCACsr
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 2
Number of overlap: 10
Similarity score: 0.0413265

Alignment:
BVGTGGCCACBV
-VSCGGCCGSB-

Original motif Consensus sequence: BVGTGGCCACBV



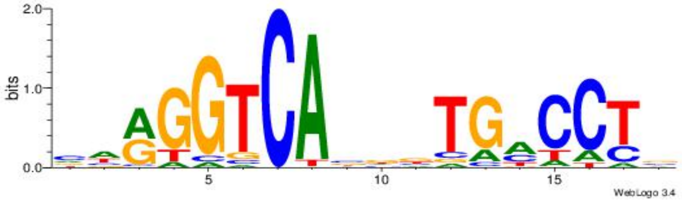
Reverse complement motif Consensus sequence: VBGTGGCCACVB



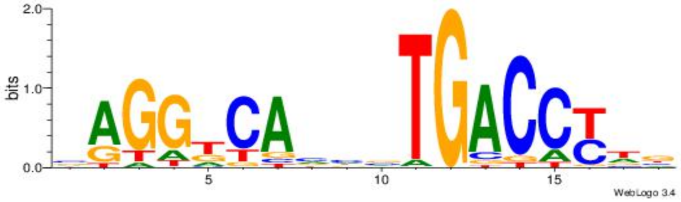
Dataset #: 3
Motif ID: 82
Motif name: ESR2
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 10
Similarity score: 0.0424008

Alignment:
BAGGYCABHBTGACCKHV
--------VSCGGCCGSB

Original motif Consensus sequence: VHRGGTCABDBTGMCCTB



Reverse complement motif Consensus sequence: BAGGYCABHBTGACCKHV

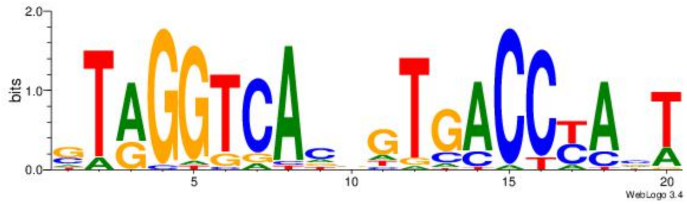
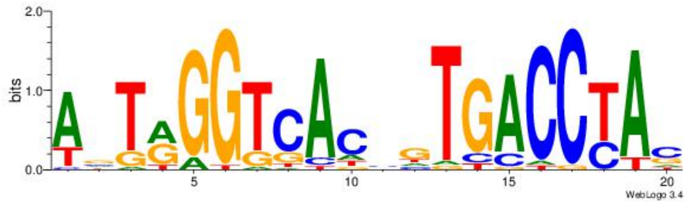


Dataset #: 3
Motif ID: 111
Motif name: PPARG
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 2
Number of overlap: 10
Similarity score: 0.046338

Alignment:
ABTMGGTCACBGTGACCTAS
-VSCGGCCGSB---------

Original motif Consensus sequence: STAGGTCACBGTGACCYABT

Reverse complement motif Consensus sequence: ABTMGGTCACBGTGACCTAS

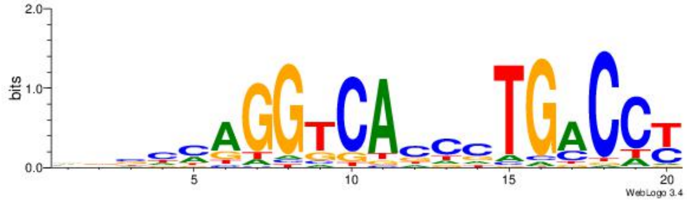



Dataset #:	3
Motif ID:	81
Motif name:	ESR1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	8
Number of overlap:	10
Similarity score:	0.0468951

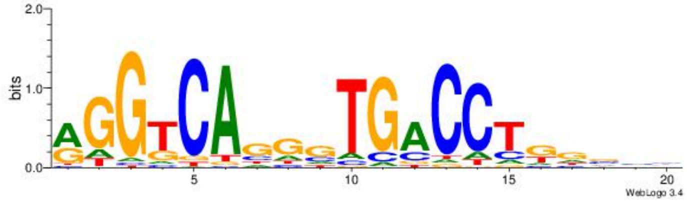
Alignment:

```
MGGTCAGGGTGACCTRDBHV
-------VSCGGCCGSB---
```

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



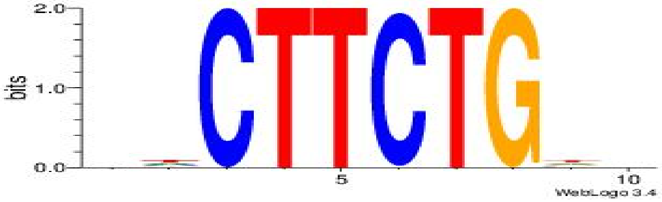
Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV



Dataset #: 4 Motif ID: 136 Motif name: dwCAGAAGwh

Original motif Consensus sequence: DHCAGAAGDH

Reverse complement motif Consensus sequence: HDCTTCTGHD



Best Matches for Motif ID 136 (Highest to Lowest)

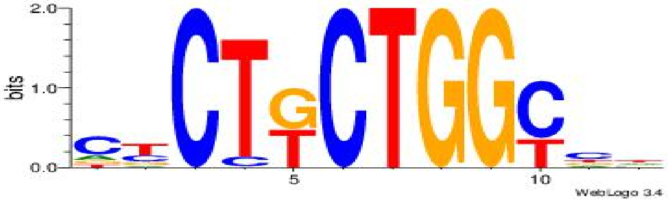
Dataset #:	4
Motif ID:	151
Motif name:	agrCCAGmAGrg
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	3
Number of overlap:	10
Similarity score:	0.00562474

Alignment:

```
HVGCCAGMAGRG
--DHCAGAAGDH
```

Original motif Consensus sequence: HVGCCAGMAGRG

Reverse complement motif Consensus sequence: CKCTRCTGGCVH



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: 1
Number of overlap: 10
Similarity score: 0.0107169

Alignment:
DACAAAACAH
DHCAGAAGDH

Original motif Consensus sequence: DACAAAACAH

Reverse complement motif Consensus sequence: HTGTTTTGTD

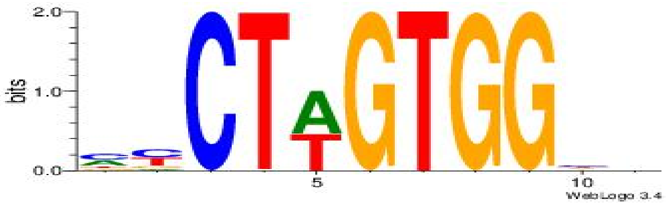
Dataset #: 4
Motif ID: 158
Motif name: grCCACwAGrk
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 10

Similarity score: 0.0167426

Alignment:
DDCCACWAGRK
-DHCAGAAGDH

Original motif Consensus sequence: DDCCACWAGRK

Reverse complement motif Consensus sequence: YMCTWGTGGHH

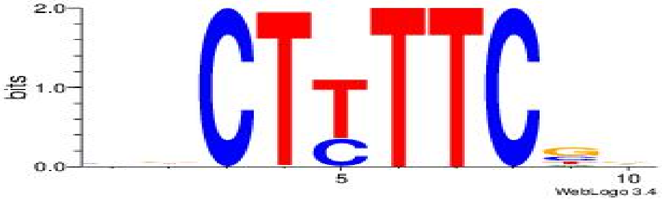


Dataset #: 4
Motif ID: 139
Motif name: mkCTyTTCsg
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 10
Similarity score: 0.0207259

Alignment:
HBCTTTTCBD
HDCTTCTGHD

Original motif Consensus sequence: HBCTTTTCBD

Reverse complement motif Consensus sequence: HBGAAAAGBD

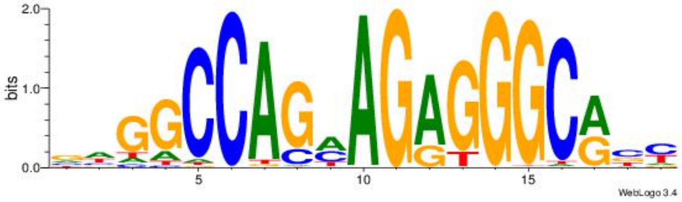


Dataset #:	4
Motif ID:	163
Motif name:	gwGGCCAGmAGAGGGCrby
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	4
Number of overlap:	10
Similarity score:	0.0212719

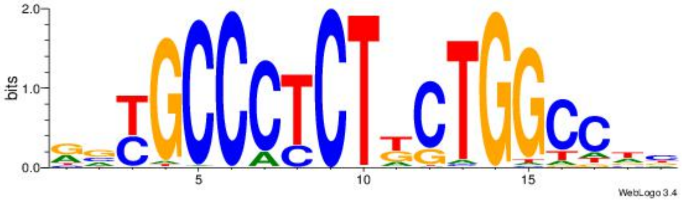
Alignment:

```
VHGGCCAGMAGAGGGCRBY
---DHCAGAAGDH------
```

Original motif Consensus sequence: VHGGCCAGMAGAGGGCRBY



Reverse complement motif Consensus sequence: KBKGCCCTCTYCTGGCCHV



Dataset #: 4 Motif ID: 137 Motif name: rgCGCCmyCTgs

Original motif Consensus sequence: VGCGCCCYCTDS

Reverse complement motif Consensus sequence: SHAGKGGGCGCB

Best Matches for Motif ID 137 (Highest to Lowest)

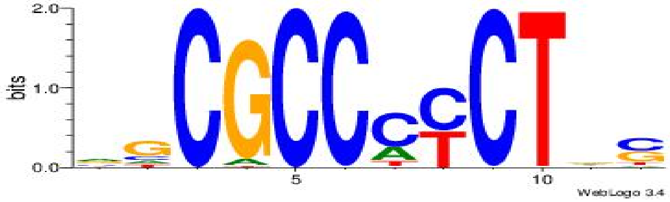
Dataset #:	4
Motif ID:	153
Motif name:	scAGrkGGCGcy
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	12
Similarity score:	0

Alignment:

VGCGCCCMCTDS
VGCGCCCYCTDS

Original motif Consensus sequence: SHAGRGGGCGCB

Reverse complement motif Consensus sequence: VGCGCCCMCTDS

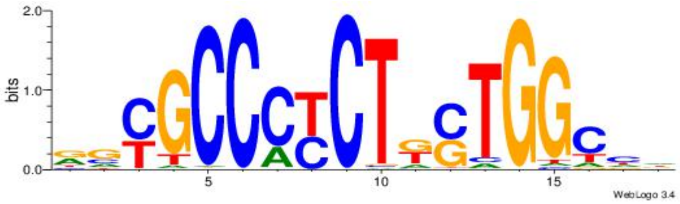


Dataset #:	4
Motif ID:	156
Motif name:	rgyGCCMyCTksTGGccd
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	7
Number of overlap:	12
Similarity score:	0.00894839

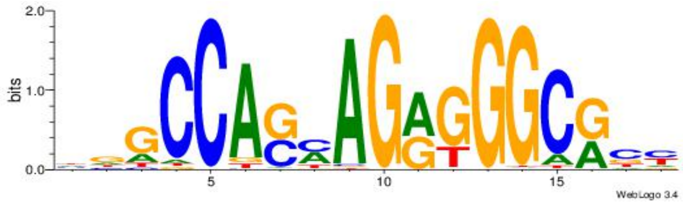
Alignment:

```
RVYGCCCYCTKSTGGCHD
VGCGCCCYCTDS------
```

Original motif Consensus sequence: RVYGCCCYCTKSTGGCHD



Reverse complement motif Consensus sequence: DDGCCASYAGMGGGCKVM

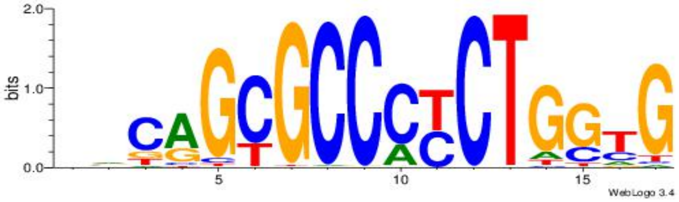


Dataset #:	4
Motif ID:	168
Motif name:	yrcrGYGCCMyCTGGtG
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	3

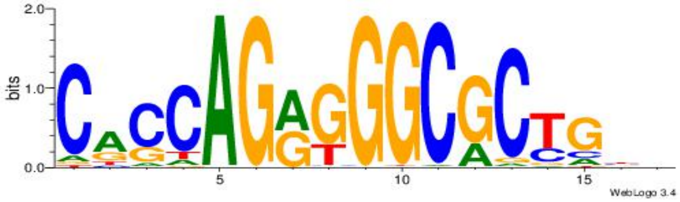
Number of overlap: 12
Similarity score: 0.0183868

Alignment:
```
HVCAGCGCCCYCTGGTG
---VGCGCCCYCTDS--
```

Original motif Consensus sequence: HVCAGCGCCCYCTGGTG



Reverse complement motif Consensus sequence: CACCAGMGGGCGCTGBD

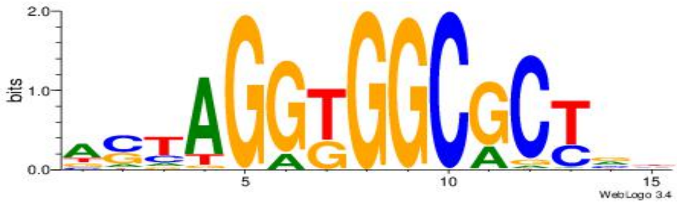


Dataset #: 4
Motif ID: 146
Motif name: myrGYGCCmCCTast
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 3
Number of overlap: 12
Similarity score: 0.0261893

Alignment:
```
VBAGCGCCMCCTAST
--VGCGCCCYCTDS-
```

Original motif Consensus sequence: VBAGCGCCMCCTAST

Reverse complement motif Consensus sequence: ASTAGGYGGCGCT



Dataset #:	4
Motif ID:	147
Motif name:	asCAGrkGGCrsy
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	12
Similarity score:	0.0284224

Alignment:

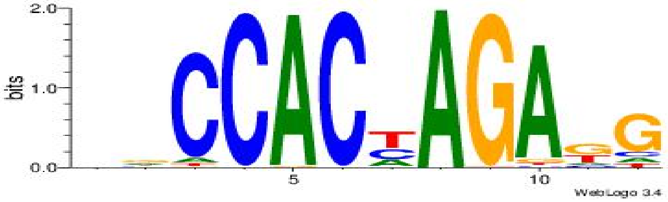
```
ASCAGRGGGCRSB
-SHAGKGGGCGCB
```

Original motif Consensus sequence: ASCAGRGGGCRSB

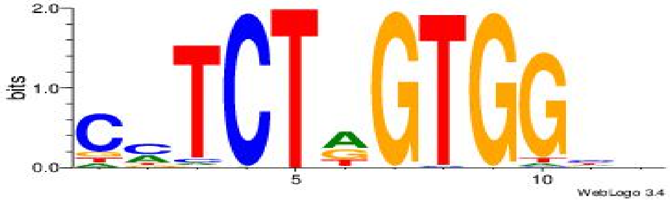
Reverse complement motif Consensus sequence: BSKGCCCMCTGST

Dataset #: 4 Motif ID: 138 Motif name: grCCACyAGAkG

Original motif Consensus sequence: DDCCACYAGAKG



Reverse complement motif Consensus sequence: CYTCTMGTGGHH



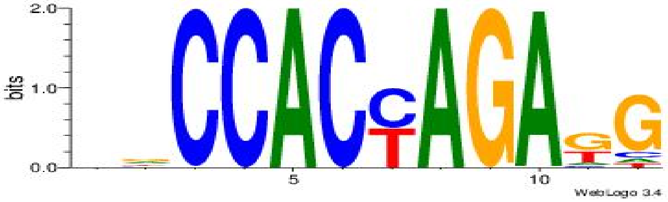
Best Matches for Motif ID 138 (Highest to Lowest)

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:	1
Number of overlap:	12
Similarity score:	0

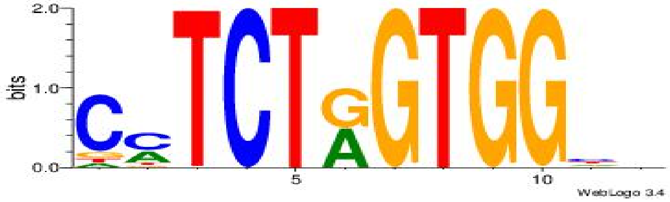
Alignment:

```
DDCCACYAGAKG
DDCCACYAGAKG
```

Original motif Consensus sequence: DDCCACYAGAKG



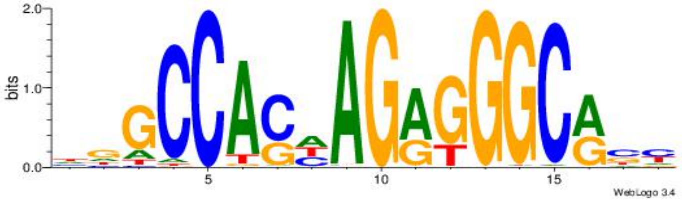
Reverse complement motif Consensus sequence: CYTCTKGTGGHH



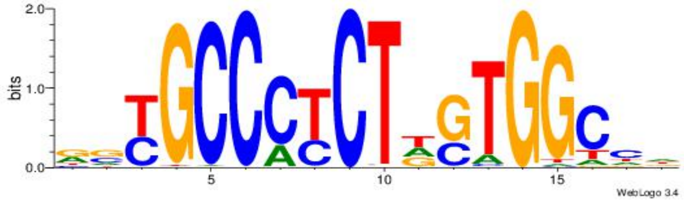
Dataset #: 4
Motif ID: 165
Motif name: wgGCCAshAGrGGGCrsy
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 2
Number of overlap: 12
Similarity score: 0.0317718

Alignment:
```
HDGCCACHAGRGGGCRBY
-DDCCACYAGAKG-----
```

Original motif Consensus sequence: HDGCCACHAGRGGGCRBY



Reverse complement motif Consensus sequence: KBKGCCCKCTHGTGGCHH



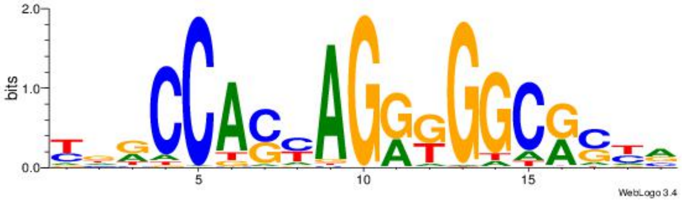
Dataset #: 3
Motif ID: 74
Motif name: CTCF
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 7

Number of overlap:	12
Similarity score:	0.0332329

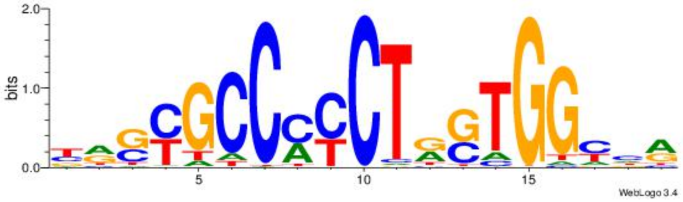
Alignment:

```
YDRCCASYAGRKGGCRSYV
-DDCCACYAGAKG------
```

Original motif Consensus sequence: YDRCCASYAGRKGGCRSYV



Reverse complement motif Consensus sequence: BMSMGCCYMCTKSTGGMHM

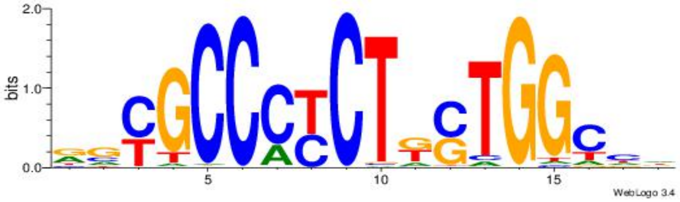


Dataset #:	4
Motif ID:	156
Motif name:	rgyGCCMyCTksTGGccd
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	6
Number of overlap:	12
Similarity score:	0.0390921

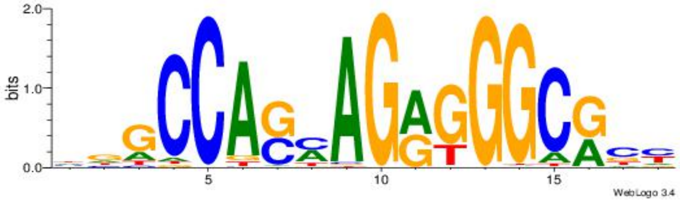
Alignment:

```
DDGCCASYAGMGGGCKVM
-DDCCACYAGAKG-----
```

Original motif Consensus sequence: RVYGCCCYCTKSTGGCHD



Reverse complement motif Consensus sequence: DDGCCASYAGMGGGCKVM



Dataset #: 4

Motif ID: 163

Motif name: gwGGCCAGmAGAGGGCrby

Matching format of first motif: Reverse Complement

Matching format of second motif: Reverse Complement

Direction: Backward

Position number: 3

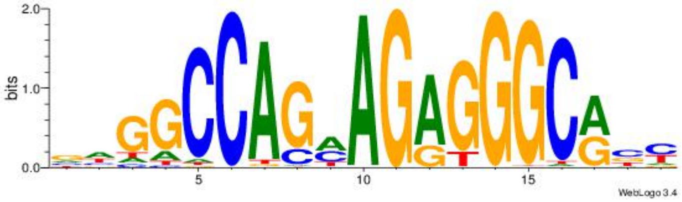
Number of overlap: 12

Similarity score: 0.0478776

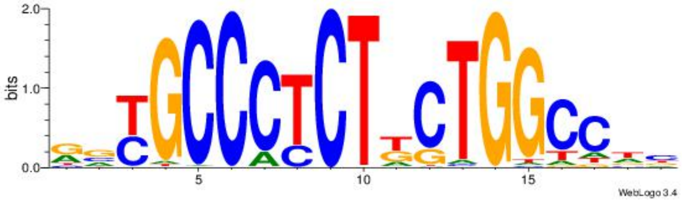
Alignment:

```
KBKGCCCTCTYCTGGCCHV
-----CYTCTMGTGGHH--
```

Original motif Consensus sequence: VHGGCCAGMAGAGGGCRBY

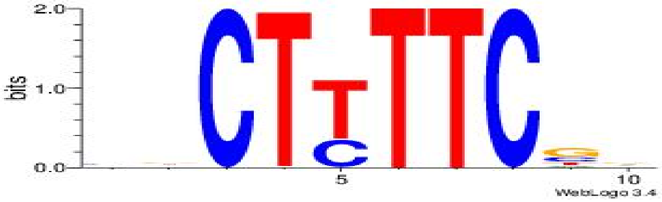


Reverse complement motif Consensus sequence: KBKGCCCTCTYCTGGCCHV



Dataset #: 4 Motif ID: 139 Motif name: mkCTyTTCsg

Original motif Consensus sequence: HBCTTTTCBD



Reverse complement motif Consensus sequence: HBGAAAAGBD

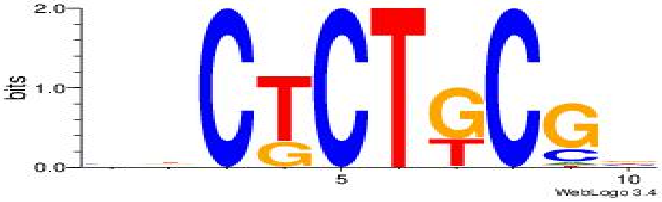
Best Matches for Motif ID 139 (Highest to Lowest)

Dataset #:	4
Motif ID:	140
Motif name:	vkCKCTkCGk
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	10
Similarity score:	0.000582108

Alignment:

```
VDCTCTKCGB
HBCTTTTCBD
```

Original motif Consensus sequence: VDCTCTKCGB



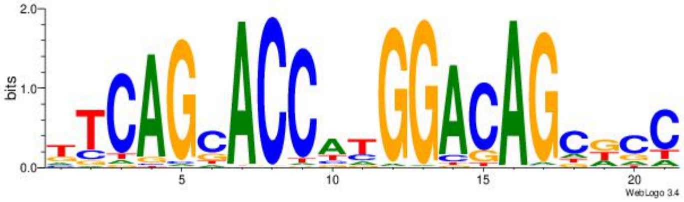
Reverse complement motif Consensus sequence: BCGYAGAGDV

Dataset #:	3
Motif ID:	113
Motif name:	REST
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	10
Number of overlap:	10
Similarity score:	0.0260893

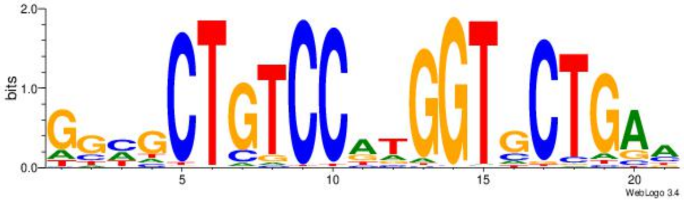
Alignment:

```
GGYGCTGTCCATGGTGCTGAA
---------HBCTTTTCBD--
```

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC



Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA

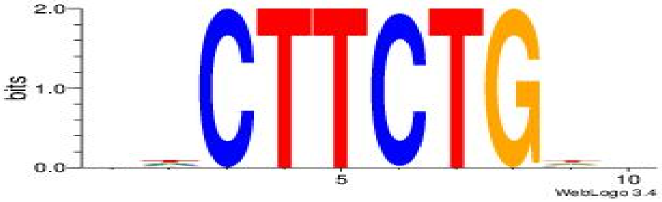


Dataset #:	4
Motif ID:	136
Motif name:	dwCAGAAGwh
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward

Position number:	1
Number of overlap:	10
Similarity score:	0.0271307

Alignment:
DHCAGAAGDH
HBGAAAAGBD

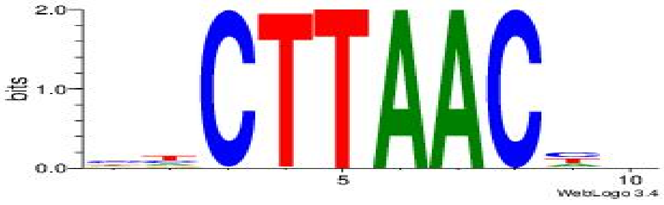
Original motif   Consensus sequence: DHCAGAAGDH   Reverse complement motif   Consensus sequence: HDCTTCTGHD



Dataset #:	4
Motif ID:	142
Motif name:	ctCTTAACyw
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	10
Similarity score:	0.0279851

Alignment:
HHCTTAACHD
HBCTTTTCBD

Original motif   Consensus sequence: HHCTTAACHD   Reverse complement motif   Consensus sequence: DDGTTAAGHD



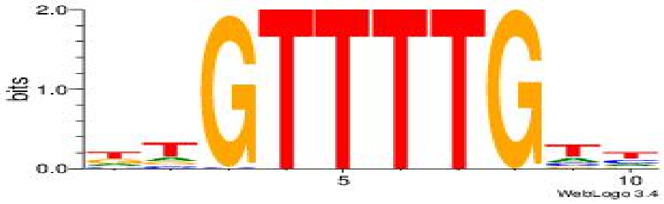
Dataset #: 4
Motif ID: 141
Motif name: raCAAAACam
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 10
Similarity score: 0.0368067

Alignment:

```
HTGTTTTGTD
HBCTTTTCBD
```

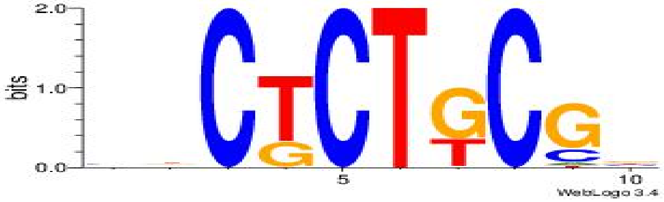
Original motif Consensus sequence: DACAAAACAH

Reverse complement motif Consensus sequence: HTGTTTTGTD



Dataset #: 4 Motif ID: 140 Motif name: vkCKCTkCGk

Original motif Consensus sequence: VDCTCTKCGB



Reverse complement motif Consensus sequence: BCGYAGAGDV

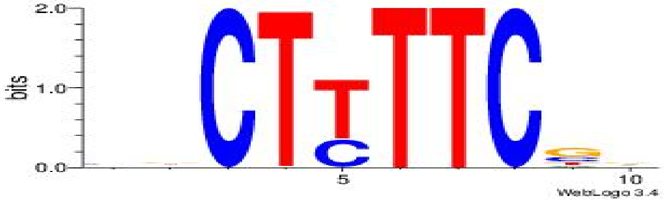
Best Matches for Motif ID 140 (Highest to Lowest)

Dataset #:	4
Motif ID:	139
Motif name:	mkCTyTTCsg
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	10
Similarity score:	0.00351595

Alignment:

```
HBCTTTTCBD
VDCTCTKCGB
```

Original motif Consensus sequence: HBCTTTTCBD



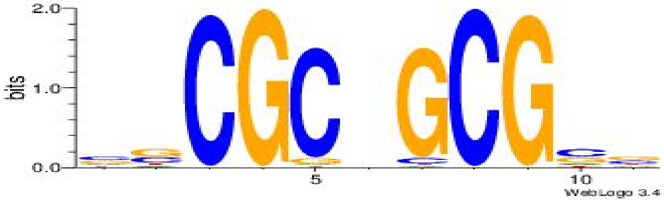
Reverse complement motif Consensus sequence: HBGAAAAGBD

Dataset #: 4
Motif ID: 161
Motif name: ssCGCwGCGss
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2
Number of overlap: 10
Similarity score: 0.0202536

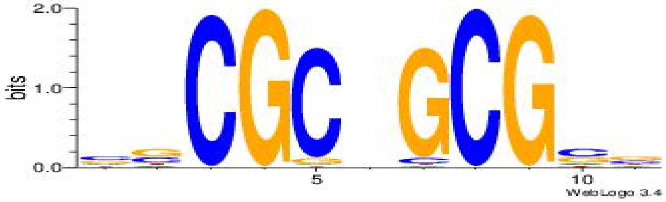
Alignment:

```
VSCGCDGCGSB
VDCTCTKCGB-
```

Original motif Consensus sequence: VSCGCDGCGSB



Reverse complement motif Consensus sequence: BSCGCDGCGSV



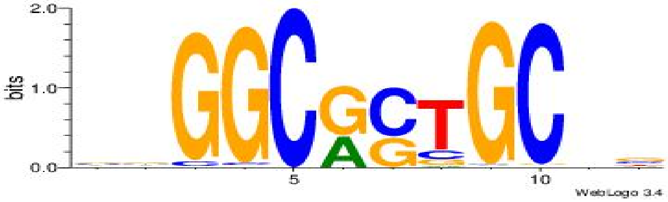
Dataset #: 4
Motif ID: 170
Motif name: ssGGCrsTGCrs
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 10

Similarity score: 0.0403601

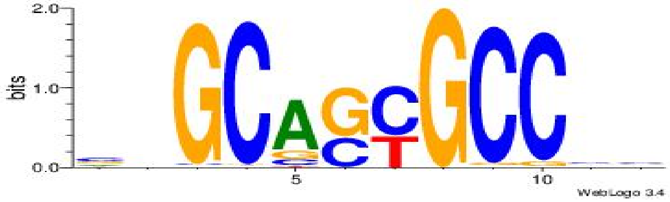
Alignment:

VVGGCRSTGCVB
--VDCTCTKCGB

Original motif Consensus sequence: VVGGCRSTGCVB



Reverse complement motif Consensus sequence: BVGCASMGCCVV



Dataset #: 4
Motif ID: 154
Motif name: csCsCCTCCcc
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2
Number of overlap: 10
Similarity score: 0.0407996

Alignment:

VBCCCCTCCHB
VDCTCTKCGB-

Original motif Consensus sequence: VBCCCCTCCHB

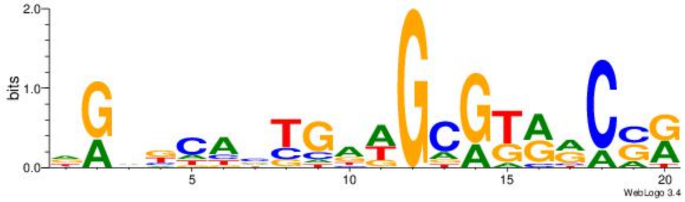
Reverse complement motif Consensus sequence: BDGGAGGGGBV

Dataset #:	3
Motif ID:	109
Motif name:	Pax5
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	7
Number of overlap:	10
Similarity score:	0.0447624

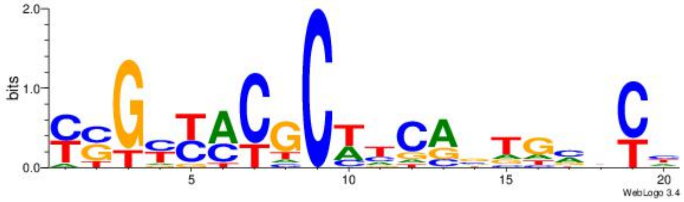
Alignment:

```
DGVBCABTGDWGCGKRRCSR
----BCGYAGAGDV------
```

Original motif Consensus sequence: DGVBCABTGDWGCGKRRCSR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD



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

Original motif Consensus sequence: DACAAAACAH

Reverse complement motif Consensus sequence: HTGTTTTGTD

Best Matches for Motif ID 141 (Highest to Lowest)

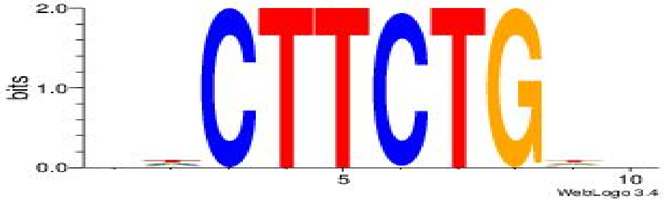
Dataset #:	4
Motif ID:	136
Motif name:	dwCAGAAGwh
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	10
Similarity score:	0.0286451

Alignment:

```
DHCAGAAGDH
DACAAAACAH
```

Original motif Consensus sequence: DHCAGAAGDH

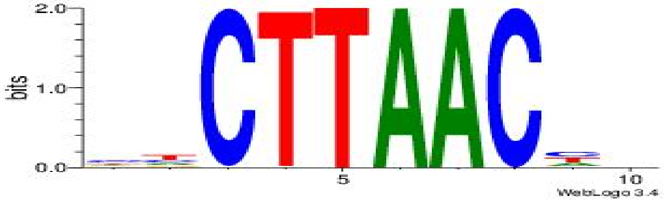
Reverse complement motif Consensus sequence: HDCTTCTGHD



Dataset #: 4
Motif ID: 142
Motif name: ctCTTAACyw
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 10
Similarity score: 0.0383253

Alignment:
DDGTTAAGHD
HTGTTTTGTD

Original motif Consensus sequence: HHCTTAACHD



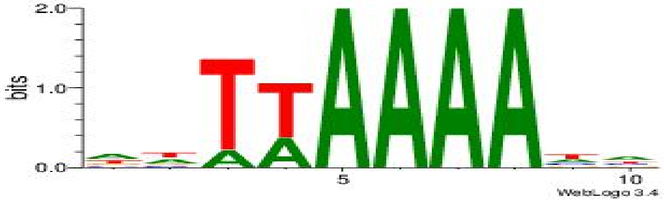
Reverse complement motif Consensus sequence: DDGTTAAGHD

Dataset #: 4
Motif ID: 148
Motif name: wwTwAAAAww
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 10

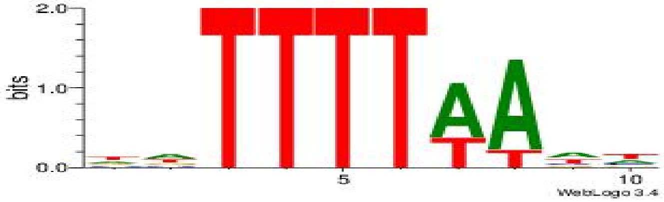
Similarity score: 0.0458158

Alignment:
DDTWAAAAHH
DACAAAACAH

Original motif Consensus sequence: DDTWAAAAHH



Reverse complement motif Consensus sequence: HHTTTTWADD

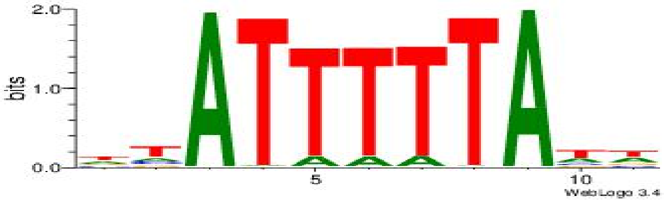


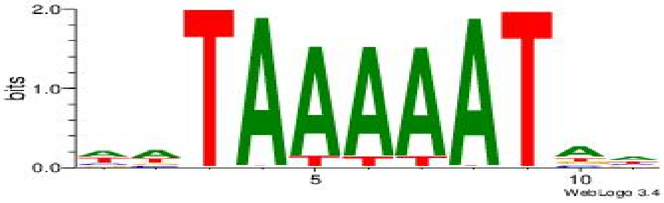
Dataset #: 4
Motif ID: 157
Motif name: wtATTTTTAww
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 2
Number of overlap: 10
Similarity score: 0.0464408

Alignment:
WWTAAAAATAD
-DACAAAACAH

Original motif Consensus sequence: DTATTTTTAWW

Reverse complement motif Consensus sequence: WWTAAAAATAD



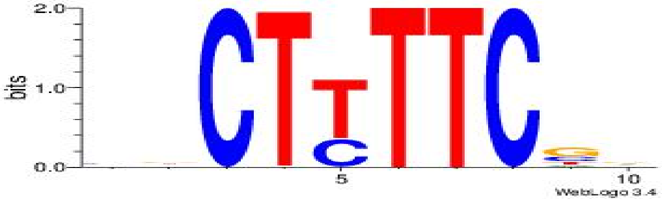


Dataset #:	4
Motif ID:	139
Motif name:	mkCTyTTCsg
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	10
Similarity score:	0.0483302

Alignment:

```
HBGAAAAGBD
DACAAAACAH
```

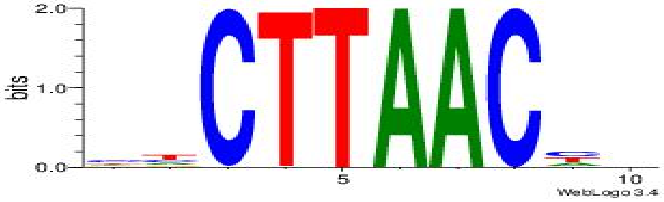
Original motif Consensus sequence: HBCTTTTCBD



Reverse complement motif Consensus sequence: HBGAAAAGBD

Dataset #: 4 Motif ID: 142 Motif name: ctCTTAACyw

Original motif Consensus sequence: HHCTTAACHD



Reverse complement motif Consensus sequence: DDGTTAAGHD

Best Matches for Motif ID 142 (Highest to Lowest)

Dataset #:	4
Motif ID:	141
Motif name:	raCAAAACam
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	10
Similarity score:	0.0459536

Alignment:

```
HTGTTTTGTD
DDGTTAAGHD
```

Original motif Consensus sequence: DACAAAACAH

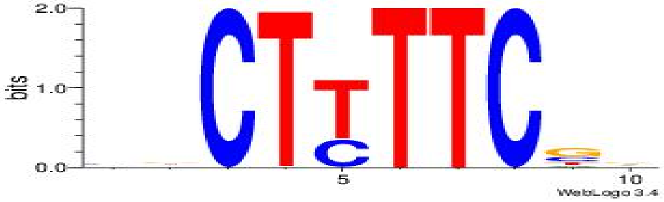
Reverse complement motif Consensus sequence: HTGTTTTGTD

Dataset #:	4
Motif ID:	139
Motif name:	mkCTyTTCsg
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	10
Similarity score:	0.0471369

Alignment:

```
HBCTTTTCBD
HHCTTAACHD
```

Original motif Consensus sequence: HBCTTTTCBD



Reverse complement motif Consensus sequence: HBGAAAAGBD

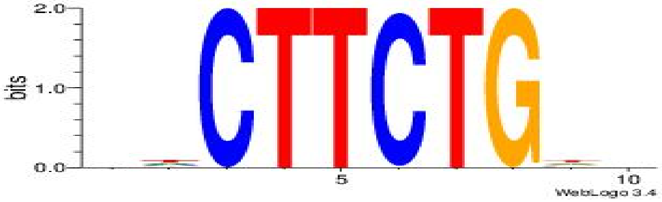
Dataset #:	4
Motif ID:	136
Motif name:	dwCAGAAGwh
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	10

Similarity score: 0.0550541

Alignment:
DHCAGAAGDH
DDGTTAAGHD

Original motif Consensus sequence: DHCAGAAGDH

Reverse complement motif Consensus sequence: HDCTTCTGHD

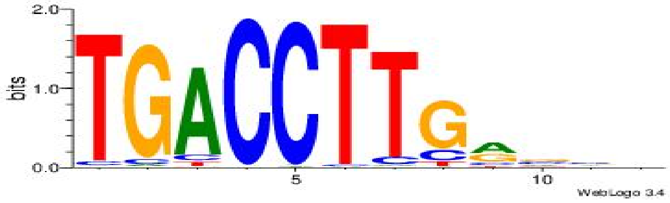


Dataset #: 3
Motif ID: 83
Motif name: Esrrb
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 10
Similarity score: 0.0663739

Alignment:
VBBYCAAGGTCA
--DDGTTAAGHD

Original motif Consensus sequence: VBBYCAAGGTCA

Reverse complement motif Consensus sequence: TGACCTTGMBBB

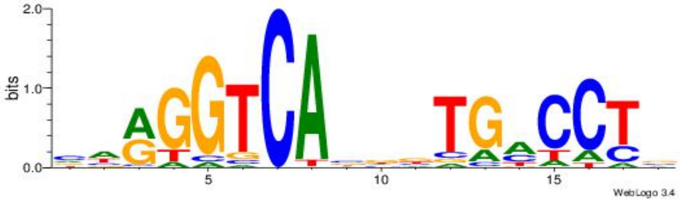


Dataset #:	3
Motif ID:	82
Motif name:	ESR2
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	2
Number of overlap:	10
Similarity score:	0.0691225

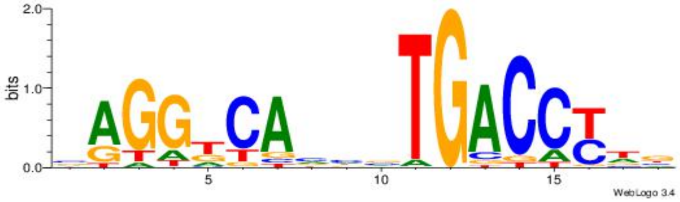
Alignment:

```
BAGGYCABHBTGACCKHV
-HHCTTAACHD-------
```

Original motif Consensus sequence: VHRGGTCABDBTGMCCTB

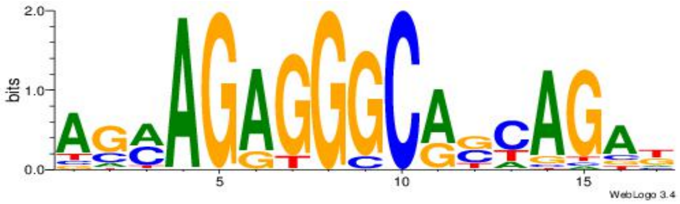


Reverse complement motif Consensus sequence: BAGGYCABHBTGACCKHV

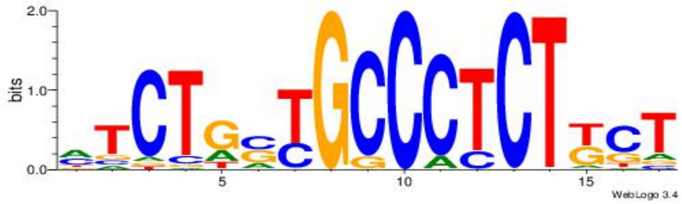


Dataset #: 4 Motif ID: 143 Motif name: AgmAGAGGGCrscAGak

Original motif Consensus sequence: AGMAGAGGGCASCAGAK



Reverse complement motif Consensus sequence: RTCTGSTGCCCTCTYCT



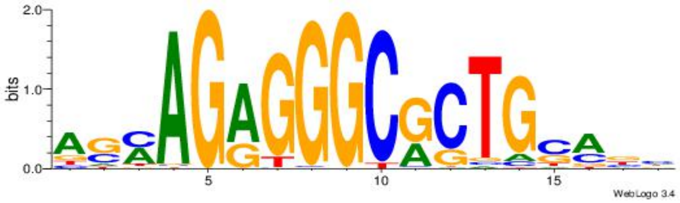
Best Matches for Motif ID 143 (Highest to Lowest)

Dataset #:	4
Motif ID:	149
Motif name:	asmAGRGGGCrCTGsmkc
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2
Number of overlap:	17
Similarity score:	0.0311468

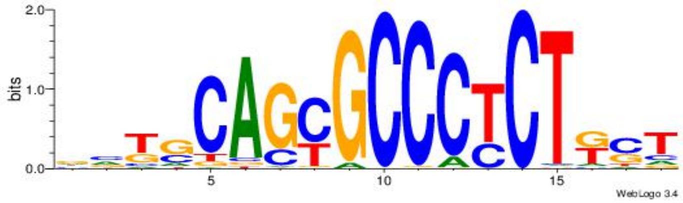
Alignment:

```
ASMAGAGGGCRCTGSABH
AGMAGAGGGCASCAGAK-
```

Original motif Consensus sequence: ASMAGAGGGCRCTGSABH



Reverse complement motif Consensus sequence: DBTSCAGMGCCCTCTRST

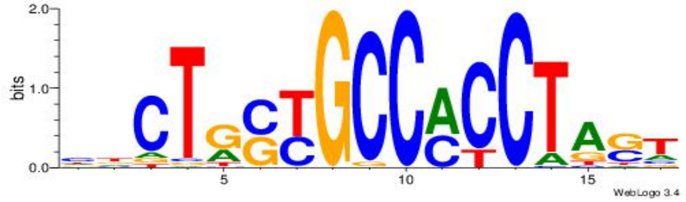


Dataset #: 4
Motif ID: 144
Motif name: ctCTrsyGCCmCCTast
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 17
Similarity score: 0.0415124

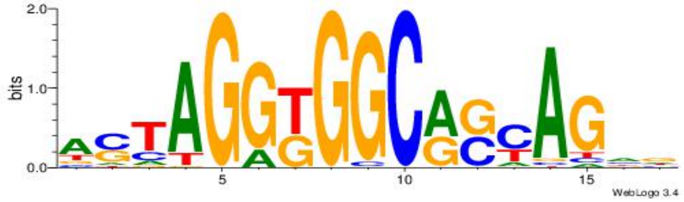
Alignment:

```
HDCTGSYGCCMCCTAST
RTCTGSTGCCCTCTYCT
```

Original motif   Consensus sequence: HDCTGSYGCCMCCTAST



Reverse complement motif   Consensus sequence: ASTAGGYGGCMSCAGDD

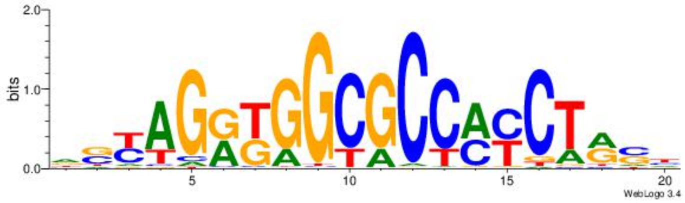


Dataset #: 4
Motif ID: 167
Motif name: rsyAGrkGGCGCCmyCTrsy
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward

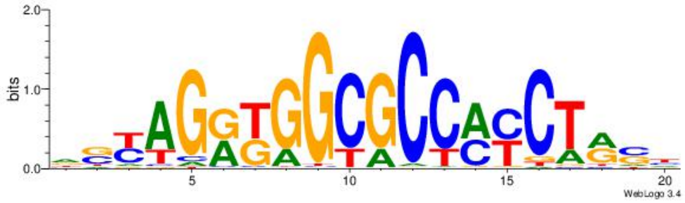
Position number: 1
Number of overlap: 17
Similarity score: 0.0702327

Alignment:
```
DSYAGRKGGCGCCMYCTRSH
AGMAGAGGGCASCAGAK---
```

Original motif Consensus sequence: DSYAGRKGGCGCCMYCTRSH



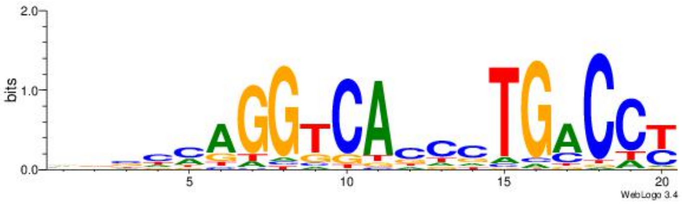
Reverse complement motif Consensus sequence: HSKAGKYGGCGCCRMCTMSD



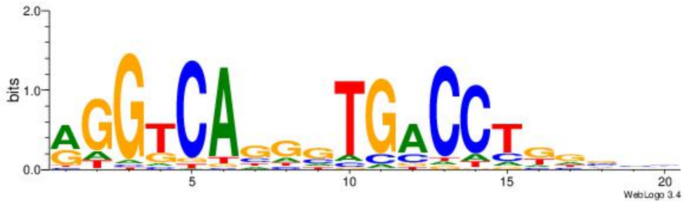
Dataset #: 3
Motif ID: 81
Motif name: ESR1
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 4
Number of overlap: 17
Similarity score: 0.0915393

Alignment:
```
VDBHMAGGTCACCCTGACCY
AGMAGAGGGCASCAGAK---
```

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV

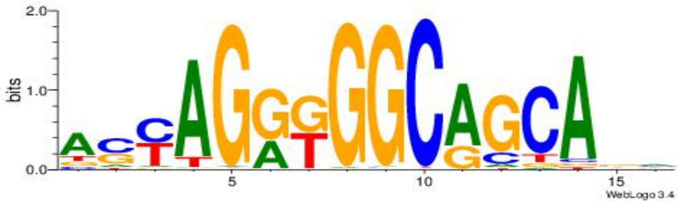


Dataset #:	4
Motif ID:	164
Motif name:	asyAGrkGGCRGCAga
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	16
Similarity score:	0.531077

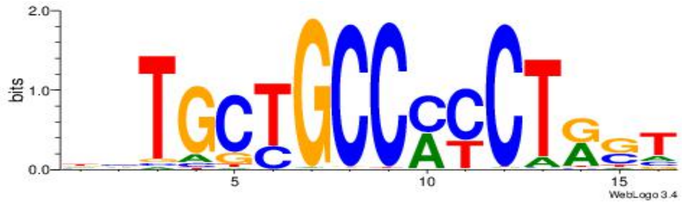
Alignment:

ASYAGRKGGCAGCABH-
AGMAGAGGGCASCAGAK

Original motif Consensus sequence: ASYAGRKGGCAGCABH

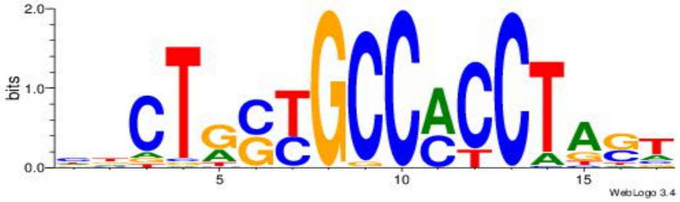


Reverse complement motif Consensus sequence: HBTGCTGCCYMCTKST

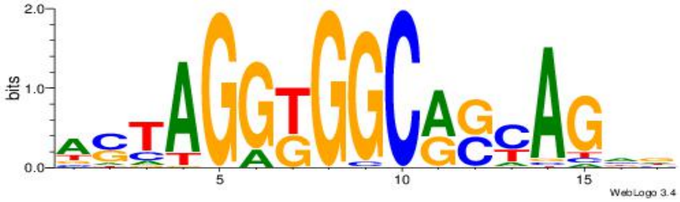


Dataset #: 4 Motif ID: 144 Motif name: ctCTrsyGCCmCCTast

Original motif Consensus sequence: HDCTGSYGCCMCCTAST



Reverse complement motif Consensus sequence: ASTAGGYGGCMSCAGDD



Best Matches for Motif ID 144 (Highest to Lowest)

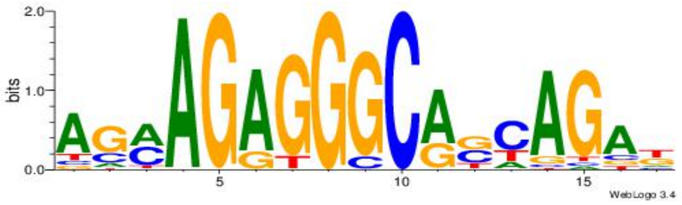
Dataset #:	4
Motif ID:	143
Motif name:	AgmAGAGGGCrscAGak
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	17
Similarity score:	0.0216483

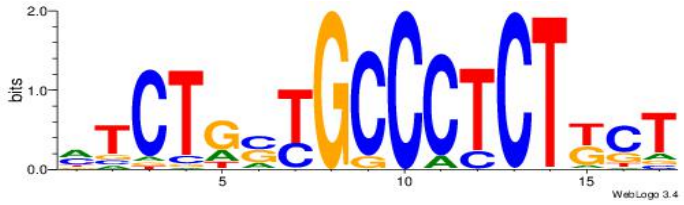
Alignment:

```
AGMAGAGGGCASCAGAK
ASTAGGYGGCMSCAGDD
```

Original motif Consensus sequence: AGMAGAGGGCASCAGAK

Reverse complement motif Consensus sequence: RTCTGSTGCCCTCTYCT



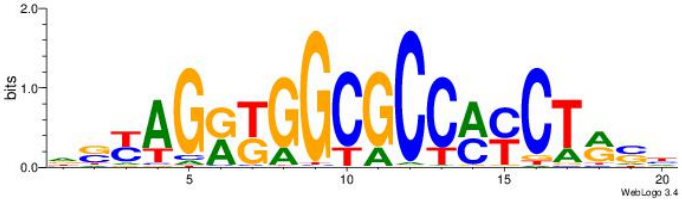


Dataset #:	4
Motif ID:	167
Motif name:	rsyAGrkGGCGCCmyCTrsy
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	4
Number of overlap:	17
Similarity score:	0.0316423

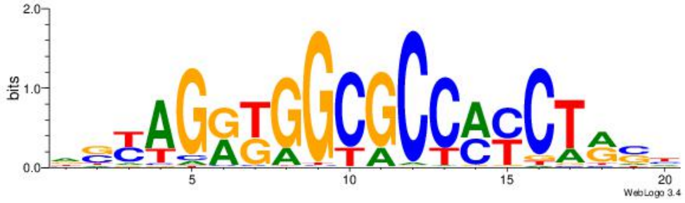
Alignment:

```
DSYAGRKGGCGCCMYCTRSH
---HDCTGSYGCCMCCTAST
```

Original motif Consensus sequence: DSYAGRKGGCGCCMYCTRSH



Reverse complement motif Consensus sequence: HSKAGKYGGCGCCRMCTMSD



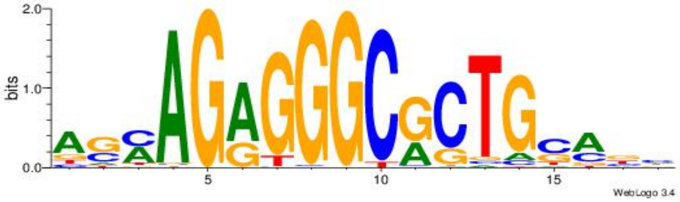
Dataset #:	4

Motif ID: 149
Motif name: asmAGRGGGCrCTGsmkc
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 2
Number of overlap: 17
Similarity score: 0.040379

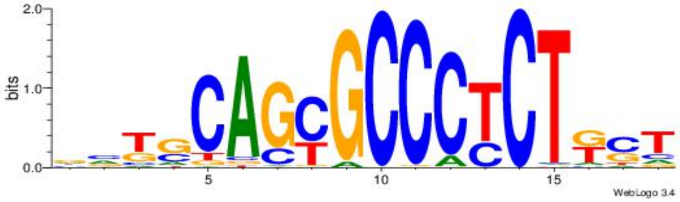
Alignment:

```
DBTSCAGMGCCCTCTRST
-HDCTGSYGCCMCCTAST
```

Original motif Consensus sequence: ASMAGAGGGCRCTGSABH



Reverse complement motif Consensus sequence: DBTSCAGMGCCCTCTRST

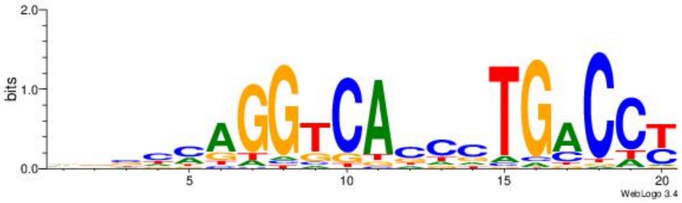


Dataset #: 3
Motif ID: 81
Motif name: ESR1
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 4
Number of overlap: 17

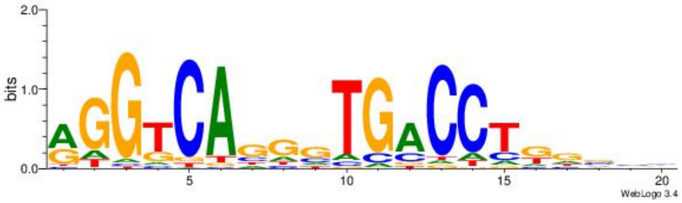
Similarity score: 0.0748345

Alignment:
MGGTCAGGGTGACCTRDBHV
---ASTAGGYGGCMSCAGDD

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV

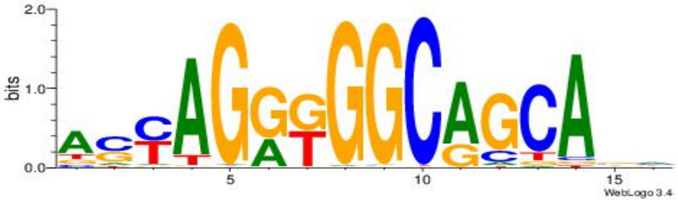


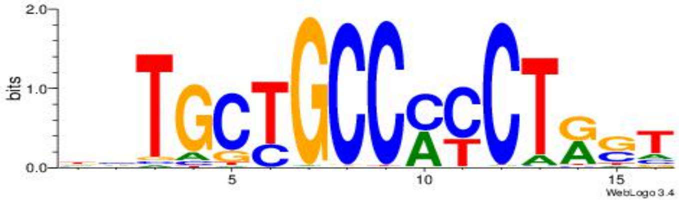
Dataset #: 4
Motif ID: 164
Motif name: asyAGrkGGCRGCAga
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 16
Similarity score: 0.503247

Alignment:
ASYAGRKGGCAGCABH-
ASTAGGYGGCMSCAGDD

Original motif Consensus sequence: ASYAGRKGGCAGCABH

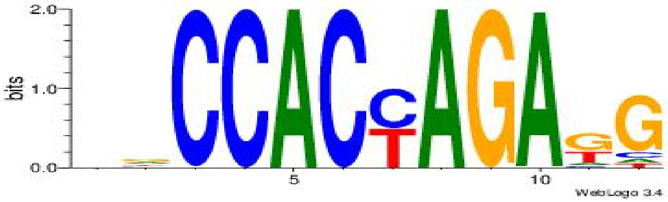
Reverse complement motif Consensus sequence: HBTGCTGCCYMCTKST



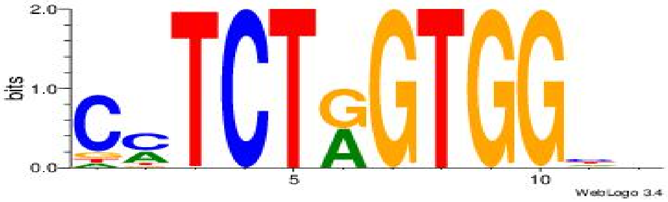


Dataset #: 4 **Motif ID: 145** **Motif name: grCCACyAGAkG**

Original motif Consensus sequence: DDCCACYAGAKG



Reverse complement motif Consensus sequence: CYTCTKGTGGHH



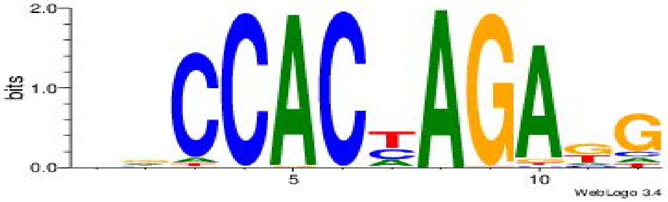
Best Matches for Motif ID 145 (Highest to Lowest)

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:	1
Number of overlap:	12
Similarity score:	0

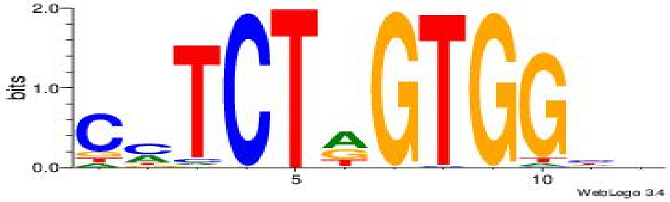
Alignment:

```
DDCCACYAGAKG
DDCCACYAGAKG
```

Original motif Consensus sequence: DDCCACYAGAKG



Reverse complement motif Consensus sequence: CYTCTMGTGGHH

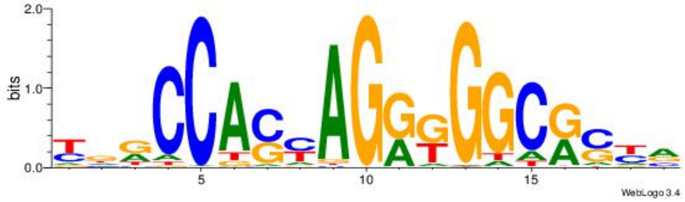


Dataset #:	3
Motif ID:	74
Motif name:	CTCF
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	12
Similarity score:	0.0323771

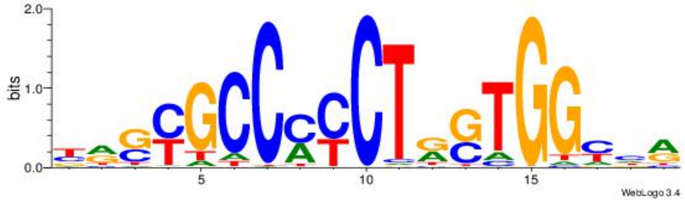
Alignment:

```
YDRCCASYAGRKGGCRSYV
-DDCCACYAGAKG------
```

Original motif Consensus sequence: YDRCCASYAGRKGGCRSYV



Reverse complement motif Consensus sequence: BMSMGCCYMCTKSTGGMHM

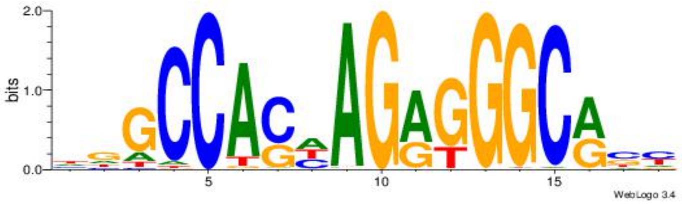


Dataset #:	4
Motif ID:	165
Motif name:	wgGCCAshAGrGGGCrsy
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	6
Number of overlap:	12
Similarity score:	0.0347955

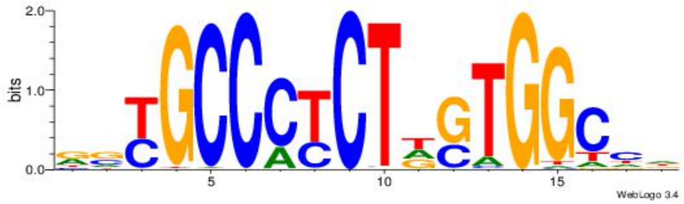
Alignment:

```
HDGCCACHAGRGGGCRBY
-DDCCACYAGAKG-----
```

Original motif Consensus sequence: HDGCCACHAGRGGGCRBY



Reverse complement motif Consensus sequence: KBKGCCCKCTHGTGGCHH



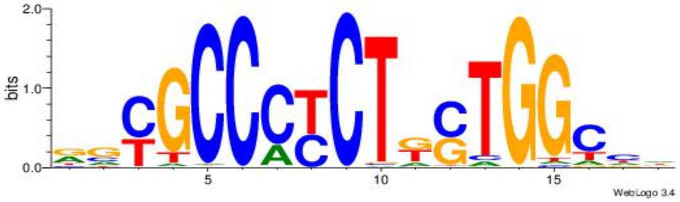
Dataset #:	4
Motif ID:	156
Motif name:	rgyGCCMyCTksTGGccd
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	6

Number of overlap: 12
Similarity score: 0.0388427

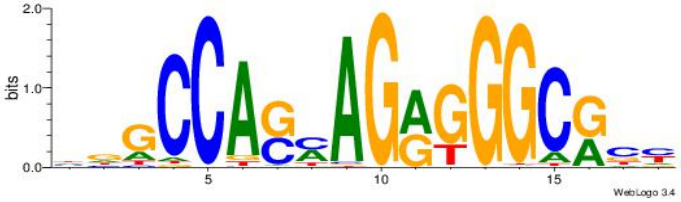
Alignment:

```
DDGCCASYAGMGGGCKVM
-DDCCACYAGAKG-----
```

Original motif Consensus sequence: RVYGCCCYCTKSTGGCHD



Reverse complement motif Consensus sequence: DDGCCASYAGMGGGCKVM

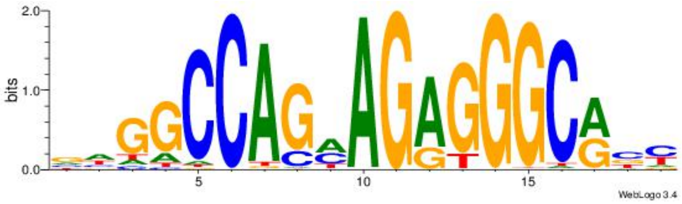


Dataset #: 4
Motif ID: 163
Motif name: gwGGCCAGmAGAGGGCrby
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 3
Number of overlap: 12
Similarity score: 0.0502736

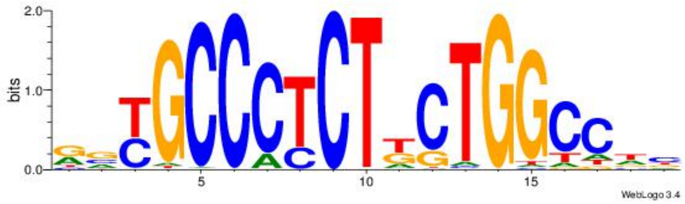
Alignment:

```
VHGGCCAGMAGAGGGCRBY
--DDCCACYAGAKG-----
```

Original motif Consensus sequence: VHGGCCAGMAGAGGGCRBY

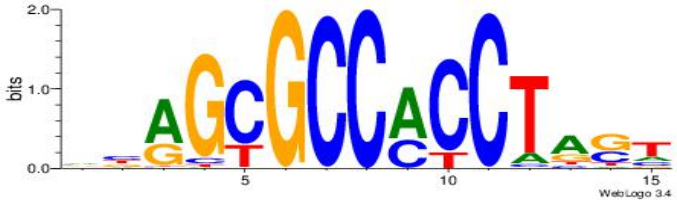


Reverse complement motif Consensus sequence: KBKGCCCTCTYCTGGCCHV

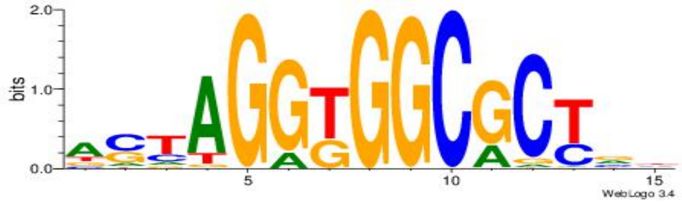


Dataset #: 4 Motif ID: 146 Motif name: myrGYGCCmCCTast

Original motif Consensus sequence: VBAGCGCCMCCTAST



Reverse complement motif Consensus sequence: ASTAGGYGGCGCT



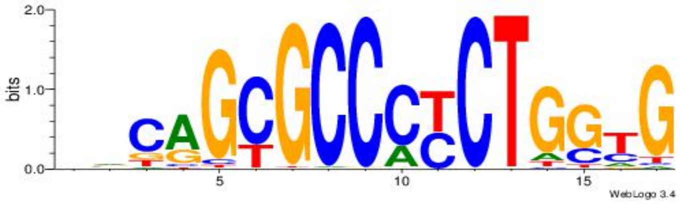
Best Matches for Motif ID 146 (Highest to Lowest)

Dataset #:	4
Motif ID:	168
Motif name:	yrcrGYGCCMyCTGGtG
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	15
Similarity score:	0.00670638

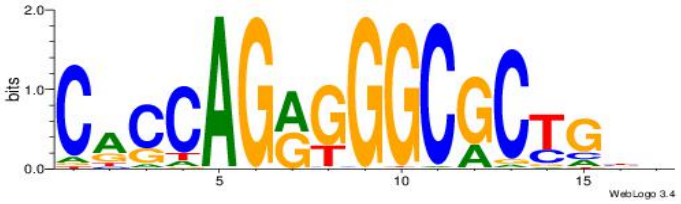
Alignment:

```
HVCAGCGCCCYCTGGTG
-VBAGCGCCMCCTAST-
```

Original motif Consensus sequence: HVCAGCGCCCYCTGGTG



Reverse complement motif Consensus sequence: CACCAGMGGGCGCTGBD



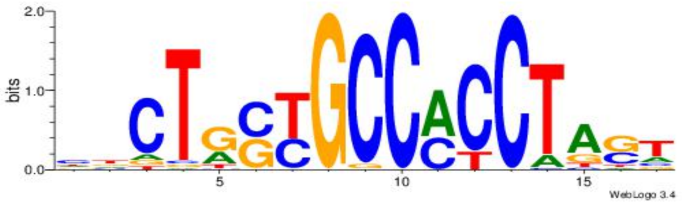
Dataset #:	4
Motif ID:	144
Motif name:	ctCTrsyGCCmCCTast
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	3
Number of overlap:	15
Similarity score:	0.0118351

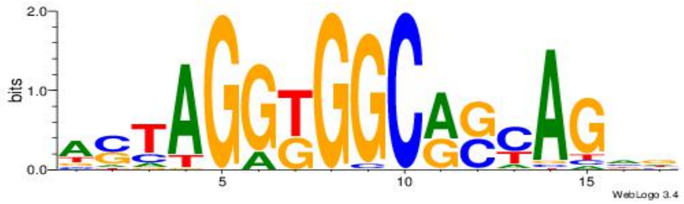
Alignment:

```
HDCTGSYGCCMCCTAST
--VBAGCGCCMCCTAST
```

Original motif Consensus sequence: HDCTGSYGCCMCCTAST

Reverse complement motif Consensus sequence: ASTAGGYGGCMSCAGDD



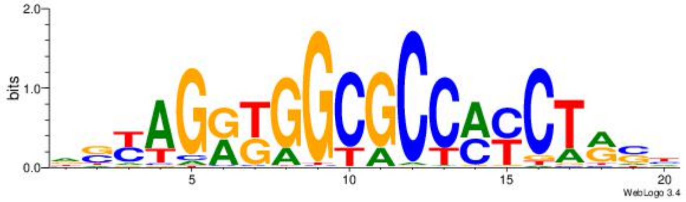


Dataset #:	4
Motif ID:	167
Motif name:	rsyAGrkGGCGCCmyCTrsy
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	6
Number of overlap:	15
Similarity score:	0.0178333

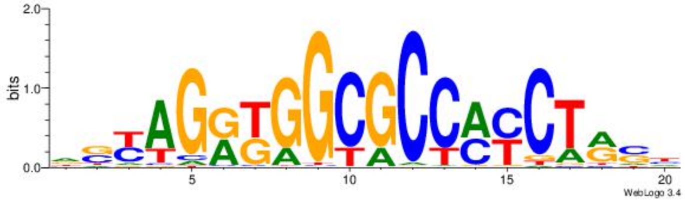
Alignment:

```
DSYAGRKGGCGCCMYCTRSH
-----VBAGCGCCMCCTAST
```

Original motif Consensus sequence: DSYAGRKGGCGCCMYCTRSH



Reverse complement motif Consensus sequence: HSKAGKYGGCGCCRMCTMSD



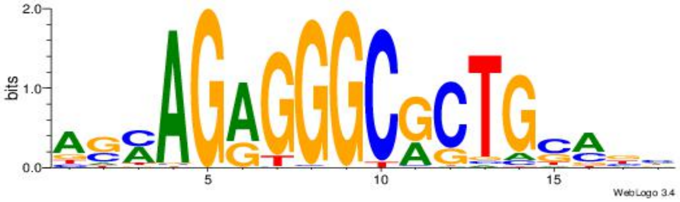
Dataset #:	4

Motif ID:	149
Motif name:	asmAGRGGGCrCTGsmkc
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	15
Similarity score:	0.0324399

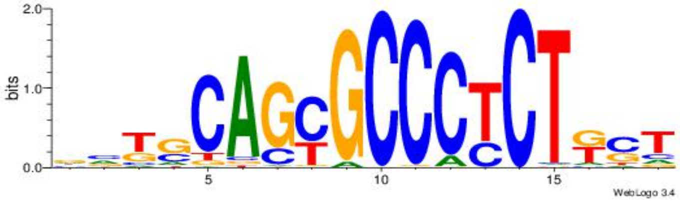
Alignment:

```
DBTSCAGMGCCCTCTRST
---VBAGCGCCMCCTAST
```

Original motif Consensus sequence: ASMAGAGGGCRCTGSABH



Reverse complement motif Consensus sequence: DBTSCAGMGCCCTCTRST



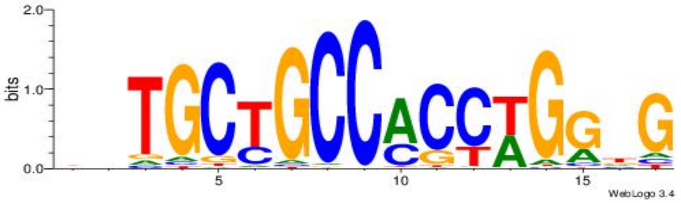
Dataset #:	4
Motif ID:	169
Motif name:	yvTGCyGCCmCCwGgtG
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	15

Similarity score:	0.0457506

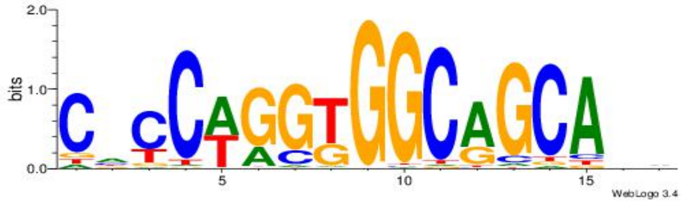
Alignment:

```
BVTGCTGCCACCWGGDG
-VBAGCGCCMCCTAST-
```

Original motif Consensus sequence: BVTGCTGCCACCWGGDG

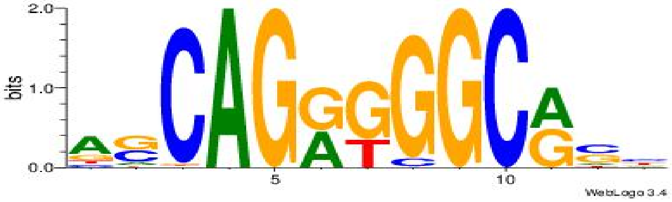


Reverse complement motif Consensus sequence: CDCCWGGTGGCAGCAVV



Dataset #: 4 Motif ID: 147 Motif name: asCAGrkGGCrsy

Original motif Consensus sequence: ASCAGRGGGCRSB



Reverse complement motif Consensus sequence: BSKGCCCMCTGST

Best Matches for Motif ID 147 (Highest to Lowest)

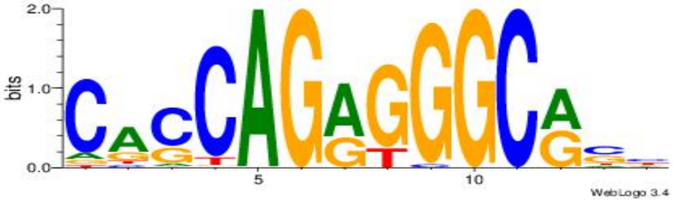
Dataset #:	4
Motif ID:	166
Motif name:	CasCAGrGGGCrsy
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif

Direction:	Backward
Position number:	1
Number of overlap:	13
Similarity score:	0.00871755

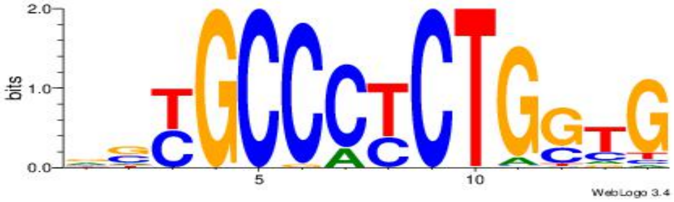
Alignment:

```
CACCAGRGGGCRSB
-ASCAGRGGGCRSB
```

Original motif Consensus sequence: CACCAGRGGGCRSB



Reverse complement motif Consensus sequence: BSKGCCCKCTGGT

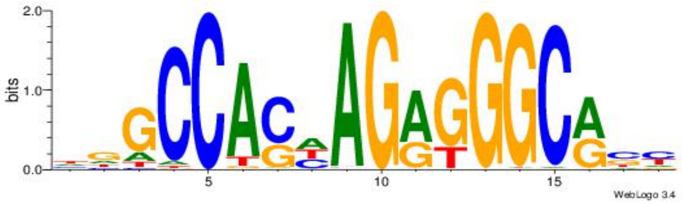


Dataset #:	4
Motif ID:	165
Motif name:	wgGCCAshAGrGGGCrsy
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	13
Similarity score:	0.0301924

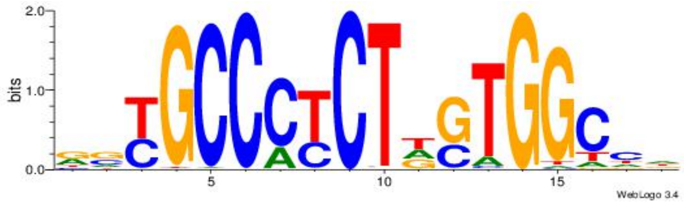
Alignment:

```
HDGCCACHAGRGGGCRBY
-----ASCAGRGGGCRSB
```

Original motif Consensus sequence: HDGCCACHAGRGGGCRBY



Reverse complement motif Consensus sequence: KBKGCCCKCTHGTGGCHH

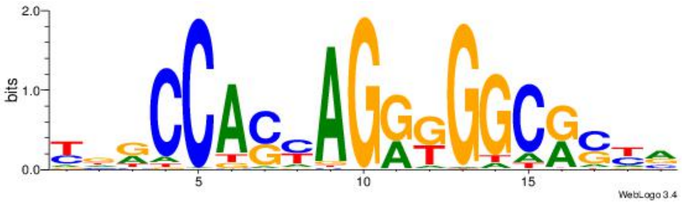


Dataset #:	3
Motif ID:	74
Motif name:	CTCF
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	6
Number of overlap:	13
Similarity score:	0.0305318

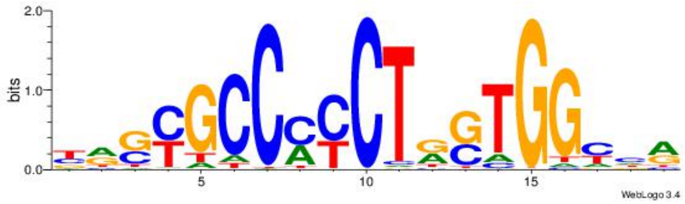
Alignment:

```
YDRCCASYAGRKGGCRSYV
-----ASCAGRGGGCRSB-
```

Original motif Consensus sequence: YDRCCASYAGRKGGCRSYV



Reverse complement motif Consensus sequence: BMSMGCCYMCTKSTGGMHM

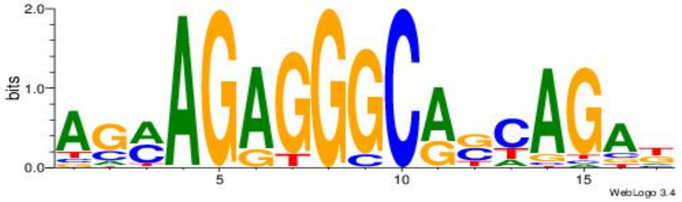


Dataset #:	4
Motif ID:	143
Motif name:	AgmAGAGGGCrscAGak
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	5
Number of overlap:	13
Similarity score:	0.0348963

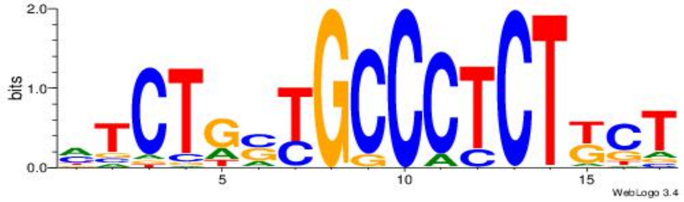
Alignment:

```
AGMAGAGGGCASCAGAK
ASCAGRGGGCRSB----
```

Original motif Consensus sequence: AGMAGAGGGCASCAGAK



Reverse complement motif Consensus sequence: RTCTGSTGCCCTCTYCT



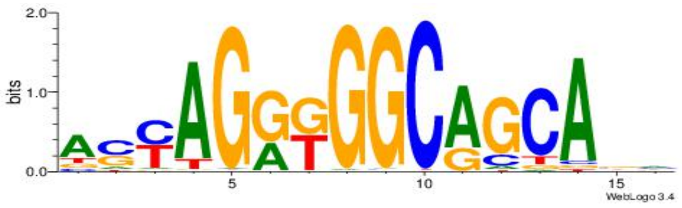
Dataset #:	4
Motif ID:	164
Motif name:	asyAGrkGGCRGCAga
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1

Number of overlap:	13
Similarity score:	0.0366623

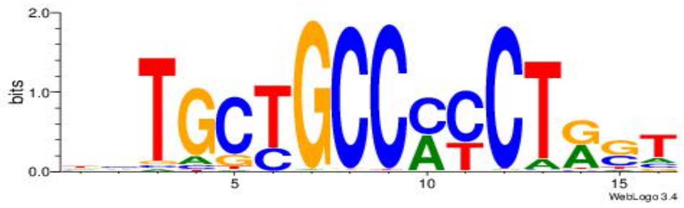
Alignment:

```
HBTGCTGCCYMCTKST
---BSKGCCCMCTGST
```

Original motif Consensus sequence: ASYAGRKGGCAGCABH

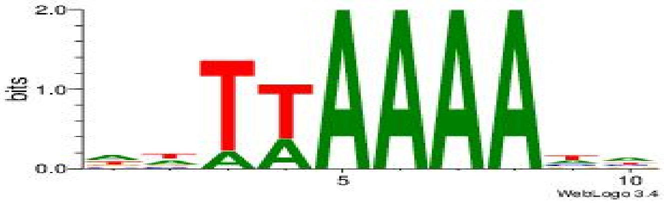


Reverse complement motif Consensus sequence: HBTGCTGCCYMCTKST

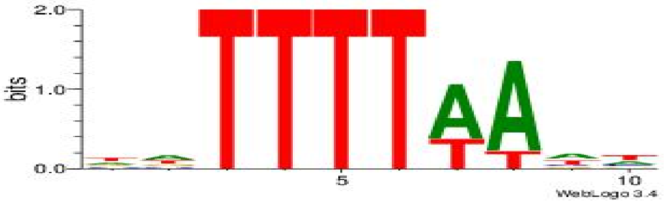


Dataset #: 4 Motif ID: 148 Motif name: wwTwAAAAww

Original motif Consensus sequence: DDTWAAAAHH



Reverse complement motif Consensus sequence: HHTTTTWADD



Best Matches for Motif ID 148 (Highest to Lowest)

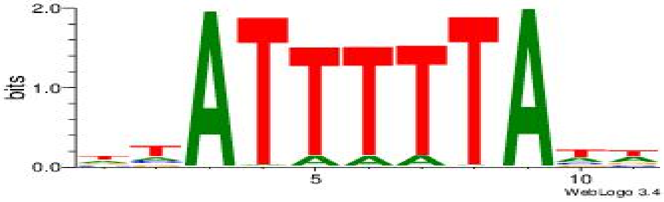
Dataset #:	4
Motif ID:	157
Motif name:	wtATTTTTAww
Matching format of first motif:	Original Motif

Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 2
Number of overlap: 10
Similarity score: 0.0143677

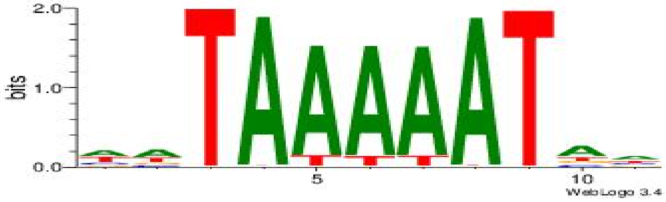
Alignment:

```
WWTAAAAATAD
DDTWAAAAHH-
```

Original motif Consensus sequence: DTATTTTAWW



Reverse complement motif Consensus sequence: WWTAAAAATAD

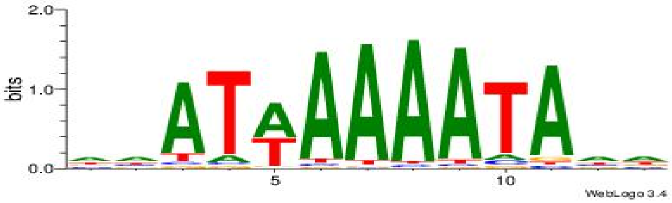


Dataset #: 4
Motif ID: 150
Motif name: waATwAAAATAww
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 3
Number of overlap: 10
Similarity score: 0.0146704

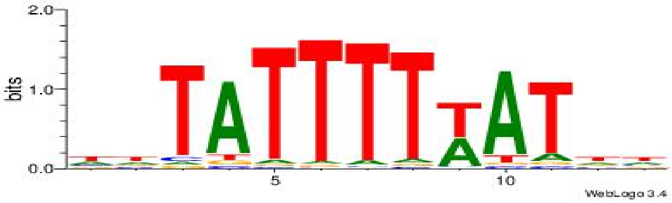
Alignment:

```
DHATWAAAATAHD
-DDTWAAAAHH--
```

Original motif   Consensus sequence: DHATWAAAATAHD



Reverse complement motif   Consensus sequence: DHTATTTTWATHD



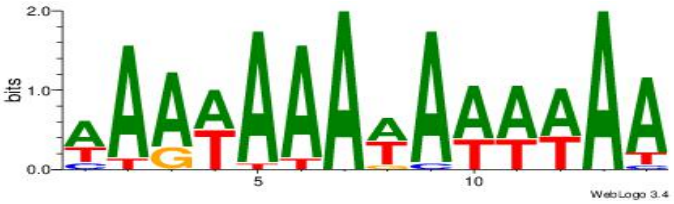
Dataset #:	2
Motif ID:	68
Motif name:	Motif 68
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	4
Number of overlap:	10
Similarity score:	0.0466767

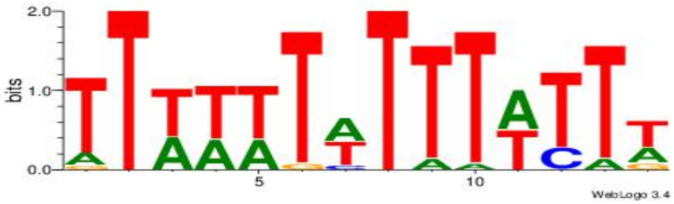
Alignment:

```
WAAWAAAWAWWWAA
-DDTWAAAAHH---
```

Original motif   Consensus sequence: WAAWAAAWAWWWAA

Reverse complement motif   Consensus sequence: TTWWWTWTTTWTTW





Dataset #:	4
Motif ID:	141
Motif name:	raCAAAACam
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	10
Similarity score:	0.0504274

Alignment:

DACAAAACAH
DDTWAAAAHH

Original motif Consensus sequence: DACAAAACAH

Reverse complement motif Consensus sequence: HTGTTTTGTD

Dataset #:	4
Motif ID:	142

Motif name: ctCTTAACyw

Matching format of first motif: Original Motif

Matching format of second motif: Original Motif

Direction: Forward

Position number: 1

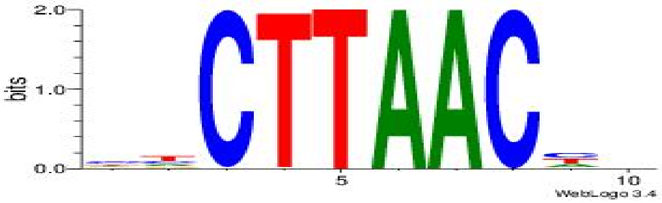
Number of overlap: 10

Similarity score: 0.0669752

Alignment:

```
HHCTTAACHD
DDTWAAAAHH
```

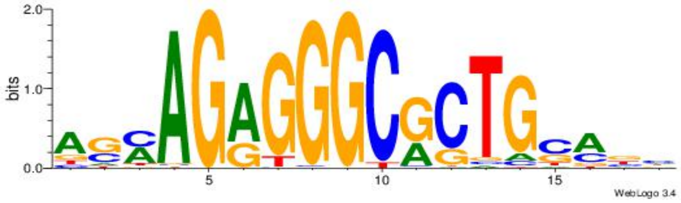
Original motif Consensus sequence: HHCTTAACHD



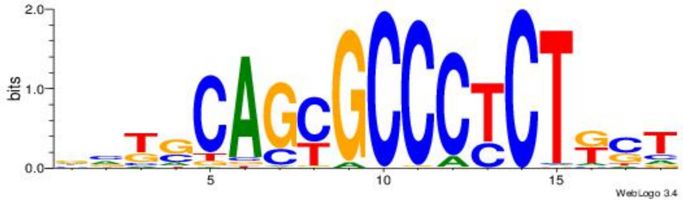
Reverse complement motif Consensus sequence: DDGTTAAGHD

Dataset #: 4 Motif ID: 149 Motif name: asmAGRGGGCrCTGsmkc

Original motif Consensus sequence: ASMAGAGGGCRCTGSABH



Reverse complement motif Consensus sequence: DBTSCAGMGCCCTCTRST



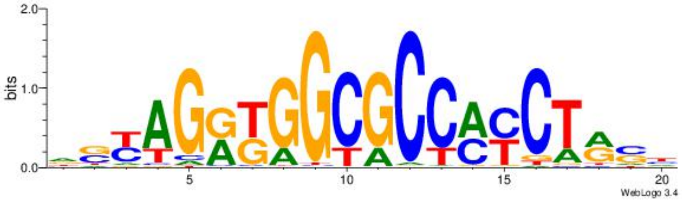
Best Matches for Motif ID 149 (Highest to Lowest)

Dataset #:	4
Motif ID:	167
Motif name:	rsyAGrkGGCGCCmyCTrsy
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	3
Number of overlap:	18
Similarity score:	0.0599593

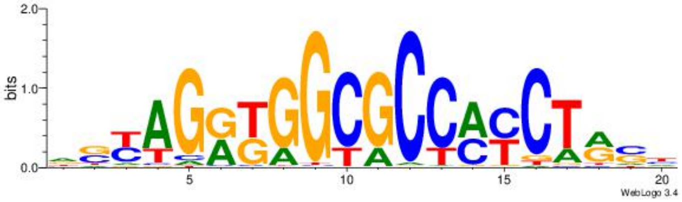
Alignment:

```
DSYAGRKGGCGCCMYCTRSH
ASMAGAGGGCRCTGSABH--
```

Original motif Consensus sequence: DSYAGRKGGCGCCMYCTRSH



Reverse complement motif Consensus sequence: HSKAGKYGGCGCCRMCTMSD



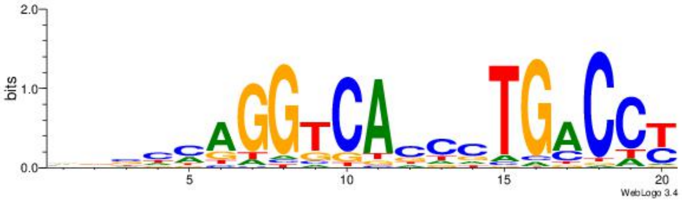
Dataset #:	3
Motif ID:	81
Motif name:	ESR1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif

Direction:	Backward
Position number:	1
Number of overlap:	18
Similarity score:	0.0884279

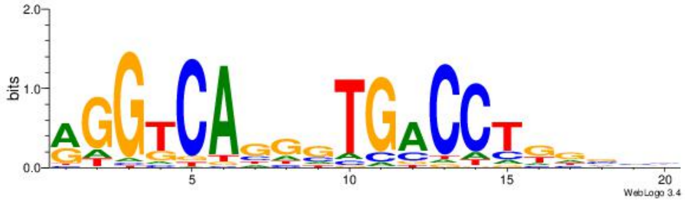
Alignment:

VDBHMAGGTCACCCTGACCY
--DBTSCAGMGCCCTCTRST

Original motif   Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif   Consensus sequence: MGGTCAGGGTGACCTRDBHV

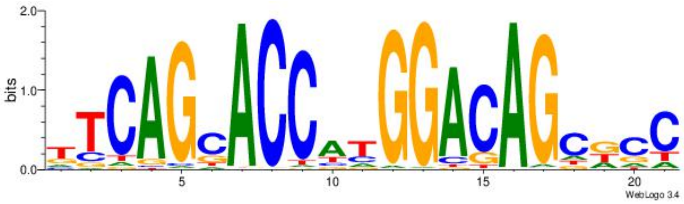


Dataset #:	3
Motif ID:	113
Motif name:	REST
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	4
Number of overlap:	18
Similarity score:	0.0932033

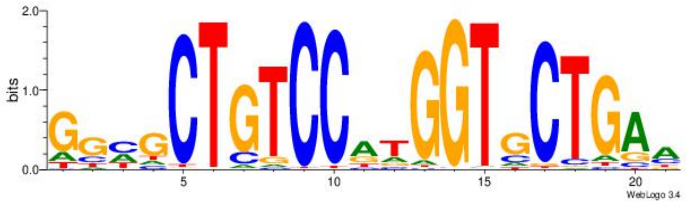
Alignment:

GGYGCTGTCCATGGTGCTGAA
DBTSCAGMGCCCTCTRST---

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC



Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA

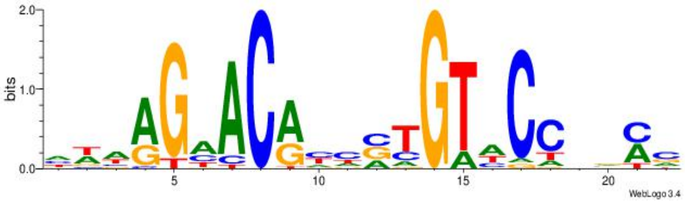


Dataset #:	3
Motif ID:	70
Motif name:	Ar
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	5
Number of overlap:	18
Similarity score:	0.0976041

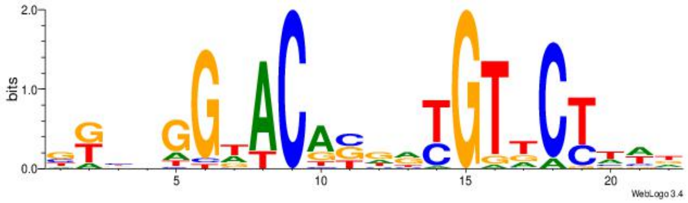
Alignment:

```
HWDAGHACRHHVTGTHCCHVMV
ASMAGAGGGCRCTGSABH----
```

Original motif Consensus sequence: HWDAGHACRHHVTGTHCCHVMV



Reverse complement motif Consensus sequence: VRVDGGHACAVDDKGTHCTDWH

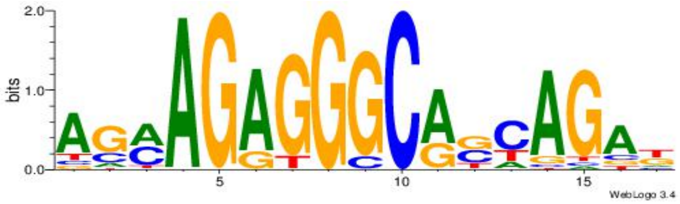


Dataset #:	4
Motif ID:	143
Motif name:	AgmAGAGGGCrscAGak
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	17
Similarity score:	0.529694

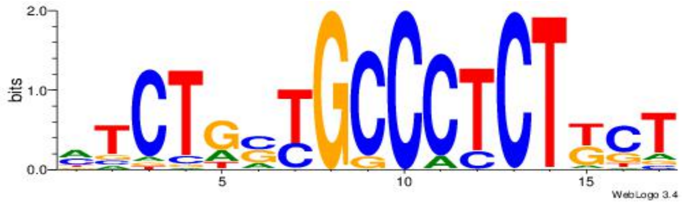
Alignment:

```
AGMAGAGGGCASCAGAK-
ASMAGAGGGCRCTGSABH
```

Original motif Consensus sequence: AGMAGAGGGCASCAGAK



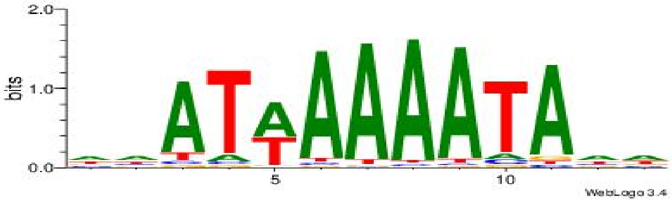
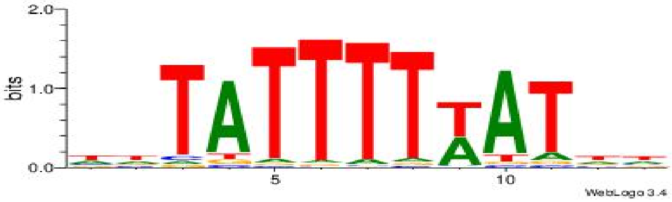
Reverse complement motif Consensus sequence: RTCTGSTGCCCTCTYCT



Dataset #: 4 **Motif ID: 150** **Motif name: waATwAAAATAww**

Original motif Consensus sequence: DHATWAAAATAHD

Reverse complement motif Consensus sequence: DHTATTTTWATHD

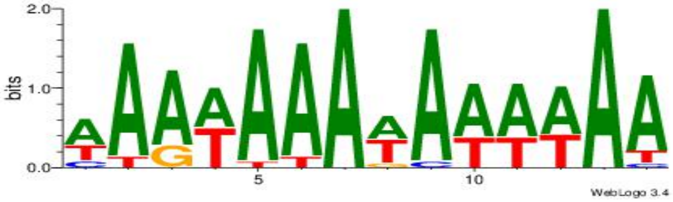
Best Matches for Motif ID 150 (Highest to Lowest)

Dataset #:	2
Motif ID:	68
Motif name:	Motif 68
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	13
Similarity score:	0.0403377

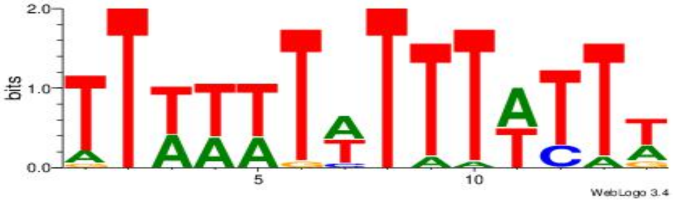
Alignment:

```
TTWWWTWTTTWTTW
-DHTATTTTWATHD
```

Original motif Consensus sequence: WAAWAAAWAWWWAA



Reverse complement motif Consensus sequence: TTWWWTWTTTWTTW

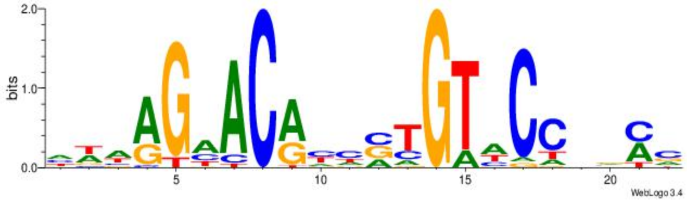


Dataset #:	3
Motif ID:	70
Motif name:	Ar
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	10
Number of overlap:	13
Similarity score:	0.0805462

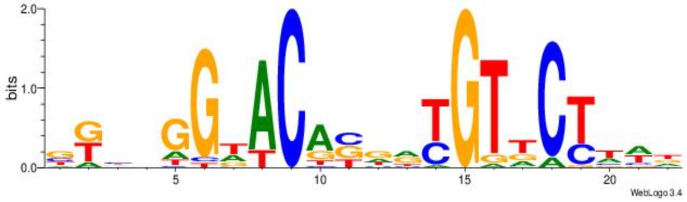
Alignment:

```
HWDAGHACRHHVTGTHCCHVMV
DHATWAAAATAHD---------
```

Original motif Consensus sequence: HWDAGHACRHHVTGTHCCHVMV



Reverse complement motif Consensus sequence: VRVDGGHACAVDDKGTHCTDWH



Dataset #:	3
Motif ID:	87
Motif name:	HNF4A
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1

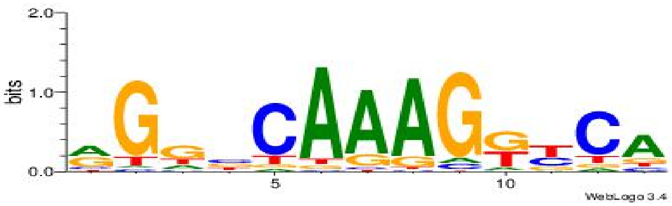
Number of overlap: 13

Similarity score: 0.081608

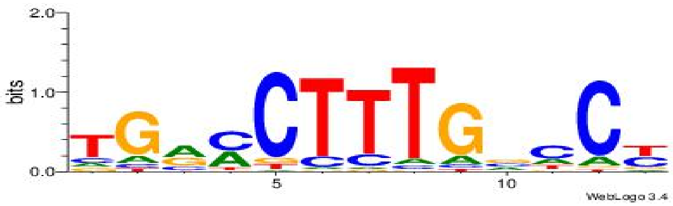
Alignment:

```
RGGBCAAAGKYCA
DHATWAAAATAHD
```

Original motif Consensus sequence: RGGBCAAAGKYCA



Reverse complement motif Consensus sequence: TGMYCTTTGBCCK



Dataset #: 3

Motif ID: 104

Motif name: NFYA

Matching format of first motif: Reverse Complement

Matching format of second motif: Reverse Complement

Direction: Backward

Position number: 2

Number of overlap: 13

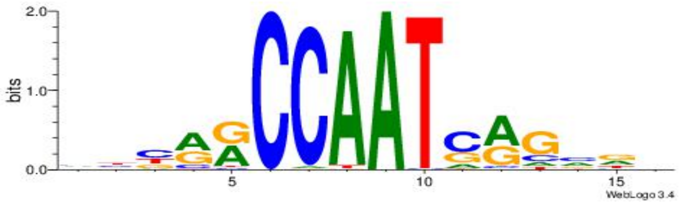
Similarity score: 0.0831397

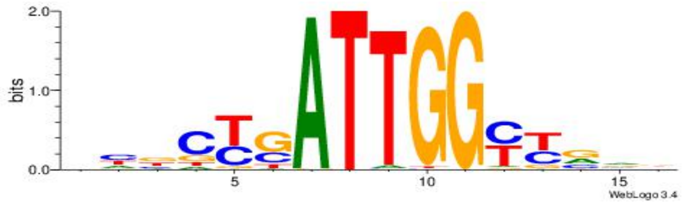
Alignment:

```
BHVCKSATTGGMKBVV
--DHTATTTTWATHD-
```

Original motif Consensus sequence: VBBRRCCAATSRGVDB

Reverse complement motif Consensus sequence: BHVCKSATTGGMKBVV



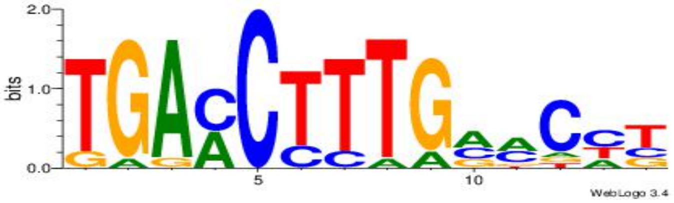


Dataset #:	3
Motif ID:	107
Motif name:	NR2F1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2
Number of overlap:	13
Similarity score:	0.0856949

Alignment:

```
TGAMCTTTGMMCYT
DHTATTTTWATHD-
```

Original motif Consensus sequence: TGAMCTTTGMMCYT

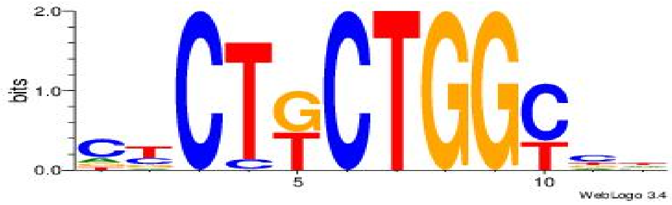


Reverse complement motif Consensus sequence: AKGYYCAAAGRTC

Dataset #: 4 Motif ID: 151 Motif name: agrCCAGmAGrg

Original motif Consensus sequence: HVGCCAGMAGRG

Reverse complement motif Consensus sequence: CKCTRCTGGCVH



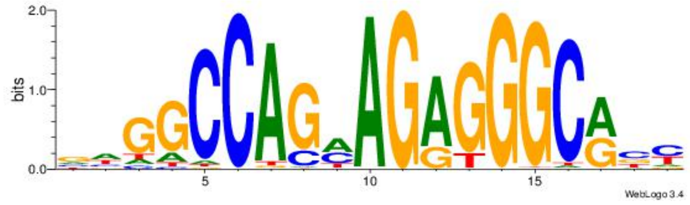
Best Matches for Motif ID 151 (Highest to Lowest)

Dataset #:	4
Motif ID:	163
Motif name:	gwGGCCAGmAGAGGGCrby
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	12
Similarity score:	0.00116274

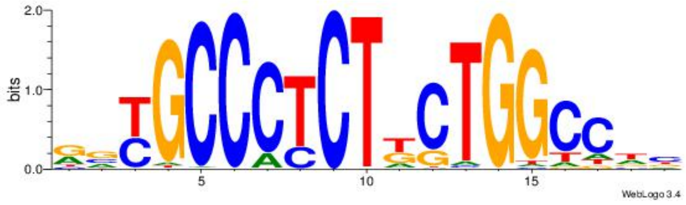
Alignment:

```
VHGGCCAGMAGAGGGCRBY
-HVGCCAGMAGRG------
```

Original motif Consensus sequence: VHGGCCAGMAGAGGGCRBY



Reverse complement motif Consensus sequence: KBKGCCCTCTYCTGGCCHV

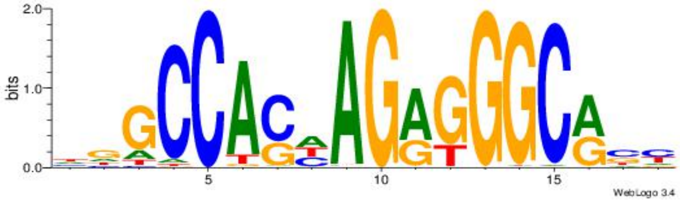


Dataset #:	4
Motif ID:	165
Motif name:	wgGCCAshAGrGGGCrsy
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	12
Similarity score:	0.0104581

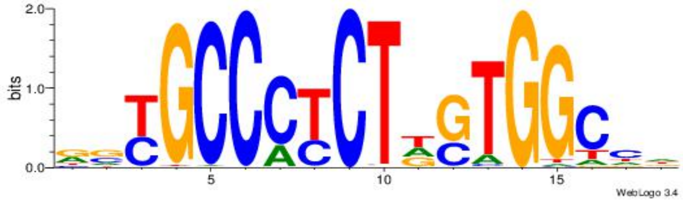
Alignment:

```
HDGCCACHAGRGGGCRBY
HVGCCAGMAGRG------
```

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:	Original Motif
Direction:	Backward
Position number:	1

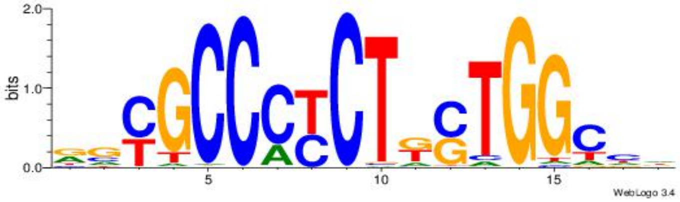
Number of overlap: 12

Similarity score: 0.0140707

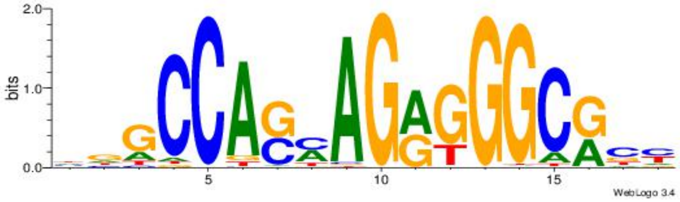
Alignment:

```
RVYGCCCYCTKSTGGCHD
------CKCTRCTGGCVH
```

Original motif Consensus sequence: RVYGCCCYCTKSTGGCHD



Reverse complement motif Consensus sequence: DDGCCASYAGMGGGCKVM



Dataset #: 3

Motif ID: 74

Motif name: CTCF

Matching format of first motif: Original Motif

Matching format of second motif: Original Motif

Direction: Forward

Position number: 1

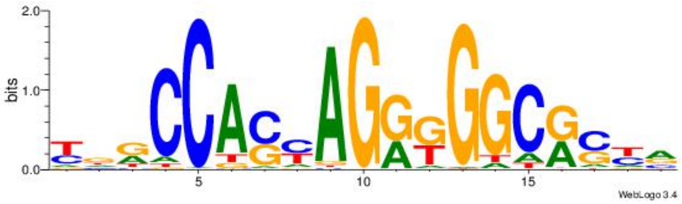
Number of overlap: 12

Similarity score: 0.0214576

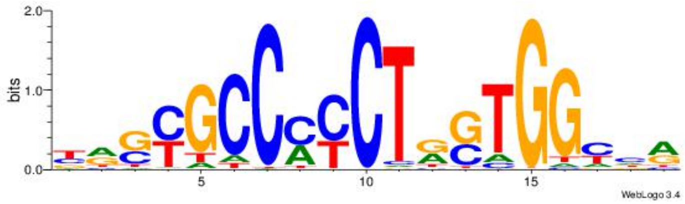
Alignment:

```
YDRCCASYAGRKGGCRSYV
HVGCCAGMAGRG-------
```

Original motif Consensus sequence: YDRCCASYAGRKGGCRSYV



Reverse complement motif Consensus sequence: BMSMGCCYMCTKSTGGMHM

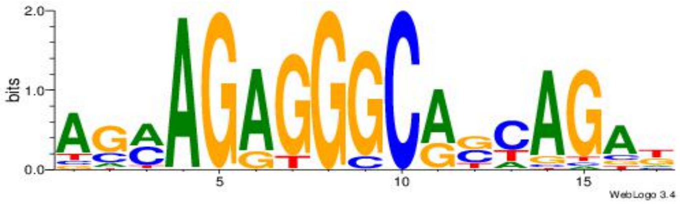


Dataset #:	4
Motif ID:	143
Motif name:	AgmAGAGGGCrscAGak
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	6
Number of overlap:	12
Similarity score:	0.0481806

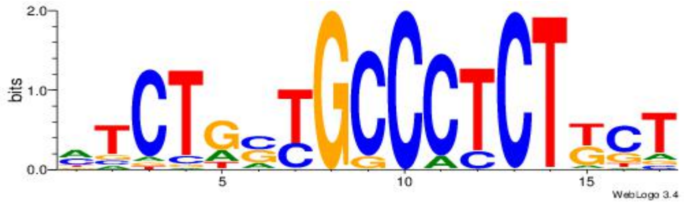
Alignment:

```
AGMAGAGGGCASCAGAK
-----HVGCCAGMAGRG
```

Original motif Consensus sequence: AGMAGAGGGCASCAGAK



Reverse complement motif Consensus sequence: RTCTGSTGCCCTCTYCT



Dataset #: 4 Motif ID: 152 Motif name: yrCATGCAyr

Original motif Consensus sequence: BRCATGCABD

Reverse complement motif Consensus sequence: HVTGCATGKV

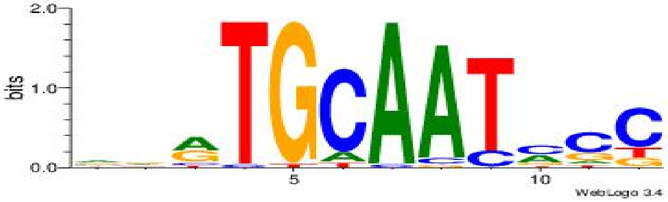
Best Matches for Motif ID 152 (Highest to Lowest)

Dataset #:	3
Motif ID:	75
Motif name:	Ddit3Cebpa
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2
Number of overlap:	10
Similarity score:	0.0420406

Alignment:

```
VDRTGCAATMCC
-HVTGCATGKV-
```

Original motif Consensus sequence: VDRTGCAATMCC



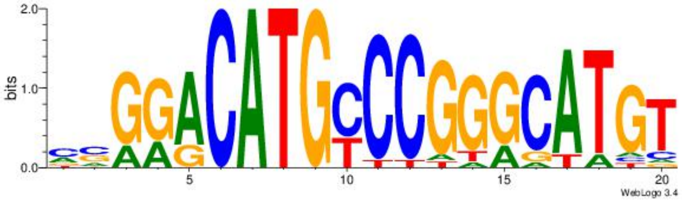
Reverse complement motif Consensus sequence: GGRATTGCAKHB

Dataset #: 3
Motif ID: 125
Motif name: TP53
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 4
Number of overlap: 10
Similarity score: 0.0472223

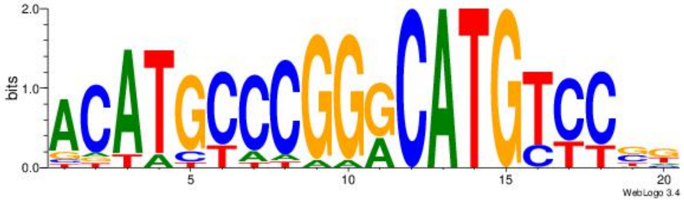
Alignment:

```
ACATGCCCGGKCATGTCCSR
-------HVTGCATGKV---
```

Original motif Consensus sequence: MSGGACATGYCCGGGCATGT



Reverse complement motif Consensus sequence: ACATGCCCGGKCATGTCCSR



Dataset #: 4
Motif ID: 134
Motif name: ssCGwGCGss
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward

Position number: 1
Number of overlap: 10
Similarity score: 0.055087

Alignment:
BSCGWGCGBV
BRCATGCABD

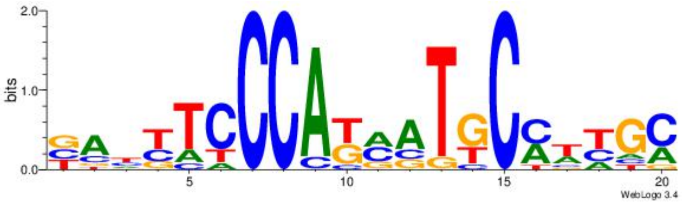
Original motif Consensus sequence: BSCGWGCGBV

Reverse complement motif Consensus sequence: VBCGCWCGSB

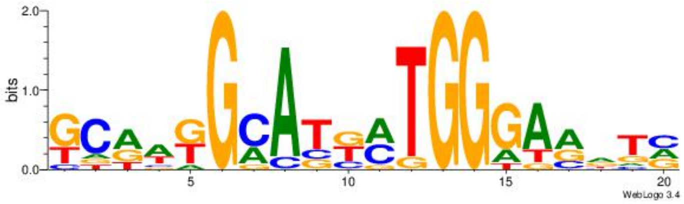
Dataset #: 3
Motif ID: 131
Motif name: znf143
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 10
Similarity score: 0.0551971

Alignment:
GCMWRGCATYRTGGGAMHTB
----------BRCATGCABD

Original motif Consensus sequence: BAHYTCCCAKMATGCMWYGC



Reverse complement motif Consensus sequence: GCMWRGCATYRTGGGAMHTB



Dataset #: 4

Motif ID: 159

Motif name: kkAAGAGCAsy

Matching format of first motif: Reverse Complement

Matching format of second motif: Reverse Complement

Direction: Forward

Position number: 1

Number of overlap: 10

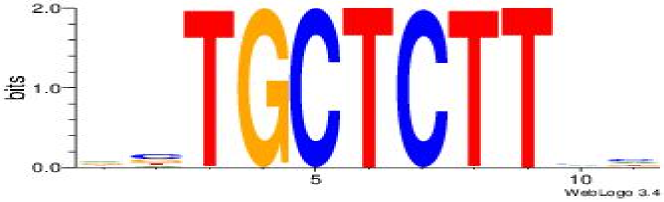
Similarity score: 0.0606344

Alignment:

```
HVTGCTCTTBH
HVTGCATGKV-
```

Original motif Consensus sequence: DBAAGAGCAVH

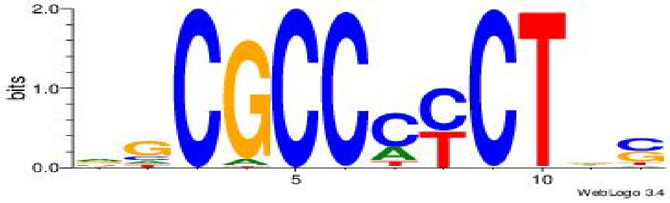
Reverse complement motif Consensus sequence: HVTGCTCTTBH



Dataset #: 4 Motif ID: 153 Motif name: scAGrkGGCGcy

Original motif Consensus sequence: SHAGRGGGCGCB

Reverse complement motif Consensus sequence: VGCGCCCMCTDS



Best Matches for Motif ID 153 (Highest to Lowest)

Dataset #:	4
Motif ID:	137
Motif name:	rgCGCCmyCTgs
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	12
Similarity score:	0

Alignment:

```
VGCGCCCYCTDS
VGCGCCCMCTDS
```

Original motif Consensus sequence: VGCGCCCYCTDS

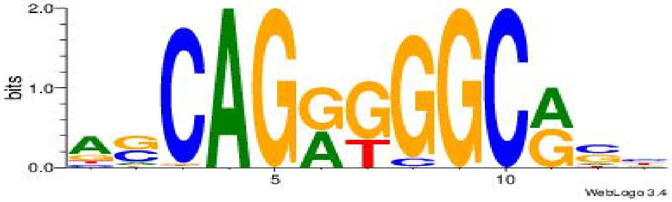
Reverse complement motif Consensus sequence: SHAGKGGGCGCB

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: 2
Number of overlap: 12
Similarity score: 0.0112071

Alignment:

```
ASCAGRGGGCRSB
-SHAGRGGGCGCB
```

Original motif Consensus sequence: ASCAGRGGGCRSB



Reverse complement motif Consensus sequence: BSKGCCCMCTGST

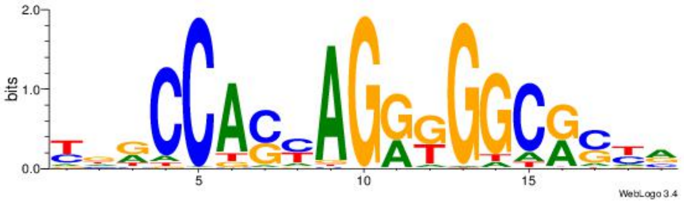
Dataset #: 3
Motif ID: 74
Motif name: CTCF
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 7

Number of overlap: 12
Similarity score: 0.0133899

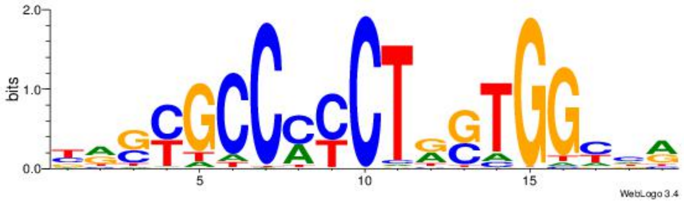
Alignment:

```
BMSMGCCYMCTKSTGGMHM
-VGCGCCCMCTDS------
```

Original motif Consensus sequence: YDRCCASYAGRKGGCRSYV



Reverse complement motif Consensus sequence: BMSMGCCYMCTKSTGGMHM

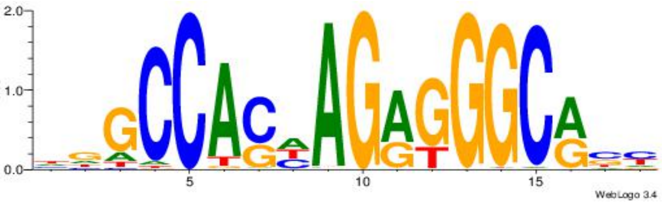


Dataset #: 4
Motif ID: 165
Motif name: wgGCCAshAGrGGGCrsy
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 12
Similarity score: 0.0146442

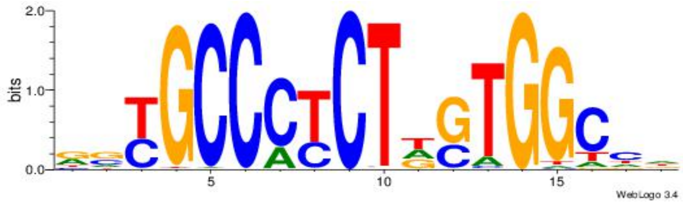
Alignment:

```
HDGCCACHAGRGGGCRBY
------SHAGRGGGCGCB
```

Original motif Consensus sequence: HDGCCACHAGRGGGCRBY



Reverse complement motif Consensus sequence: KBKGCCCKCTHGTGGCHH

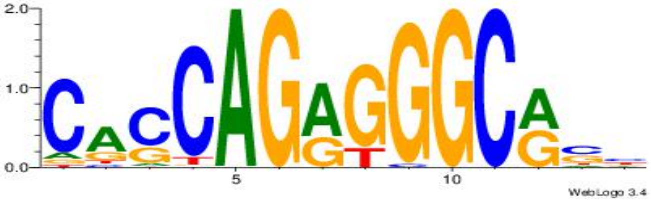


Dataset #:	4
Motif ID:	166
Motif name:	CasCAGrGGGCrsy
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	3
Number of overlap:	12
Similarity score:	0.0200811

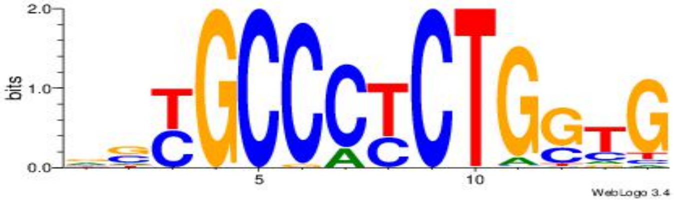
Alignment:

```
CACCAGRGGGCRSB
--SHAGRGGGCGCB
```

Original motif Consensus sequence: CACCAGRGGGCRSB



Reverse complement motif Consensus sequence: BSKGCCCKCTGGT



Dataset #: 4 Motif ID: 154 Motif name: csCsCCTCCcc

Original motif Consensus sequence: VBCCCCTCCHB

Reverse complement motif Consensus sequence: BDGGAGGGGBV

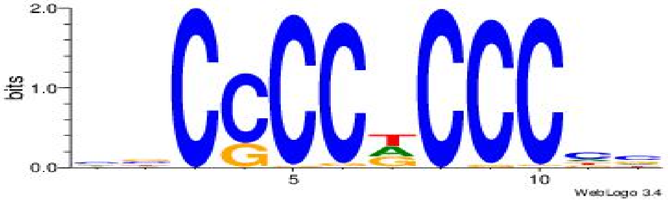
Best Matches for Motif ID 154 (Highest to Lowest)

Dataset #:	4
Motif ID:	155
Motif name:	csCSCCdCCCcs
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

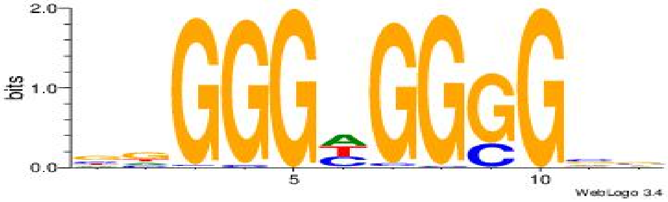
Alignment:

```
VBCCCCDCCCHV
VBCCCCTCCHB-
```

Original motif Consensus sequence: VBCCCCDCCCHV



Reverse complement motif Consensus sequence: VDGGGDGGGGBV



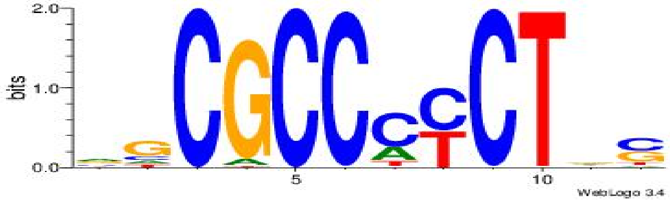
Dataset #: 4
Motif ID: 153
Motif name: scAGrkGGCGcy
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 11
Similarity score: 0.0415573

Alignment:

```
SHAGRGGGCGCB
BDGGAGGGGBV-
```

Original motif Consensus sequence: SHAGRGGGCGCB

Reverse complement motif Consensus sequence: VGCGCCCMCTDS



Dataset #: 4
Motif ID: 137
Motif name: rgCGCCmyCTgs
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1

Number of overlap: 11

Similarity score: 0.0446252

Alignment:

```
SHAGKGGGCGCB
-BDGGAGGGGBV
```

Original motif Consensus sequence: VGCGCCCYCTDS

Reverse complement motif Consensus sequence: SHAGKGGGCGCB

Dataset #: 4

Motif ID: 162

Motif name: ccAsCCCCAcc

Matching format of first motif: Reverse Complement

Matching format of second motif: Reverse Complement

Direction: Forward

Position number: 1

Number of overlap: 11

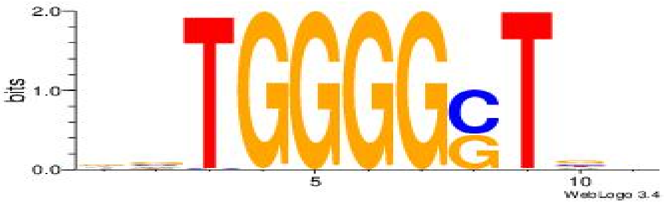
Similarity score: 0.049712

Alignment:

```
DBTGGGGSTVD
BDGGAGGGGBV
```

Original motif Consensus sequence: HVASCCCCABH

Reverse complement motif Consensus sequence: DBTGGGGSTVD

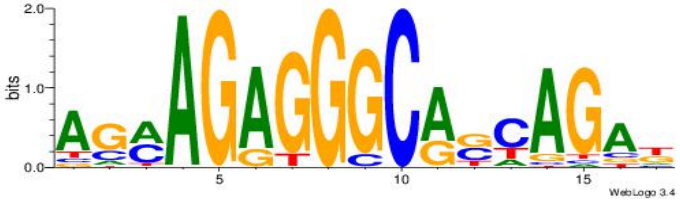


Dataset #:	4
Motif ID:	143
Motif name:	AgmAGAGGGCrscAGak
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2
Number of overlap:	11
Similarity score:	0.0533559

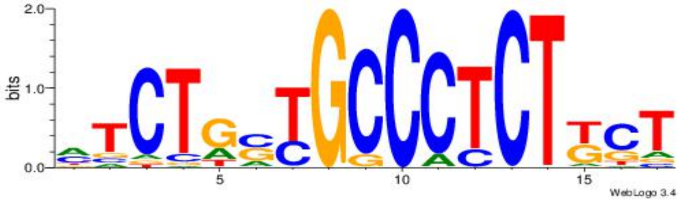
Alignment:

```
AGMAGAGGGCASCAGAK
-----BDGGAGGGGBV-
```

Original motif   Consensus sequence: AGMAGAGGGCASCAGAK

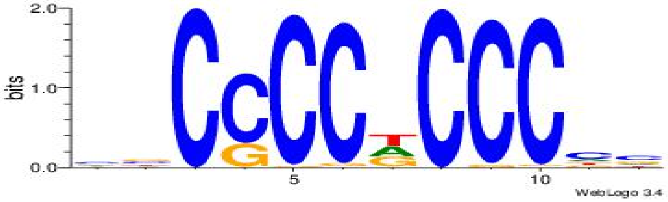


Reverse complement motif   Consensus sequence: RTCTGSTGCCCTCTYCT

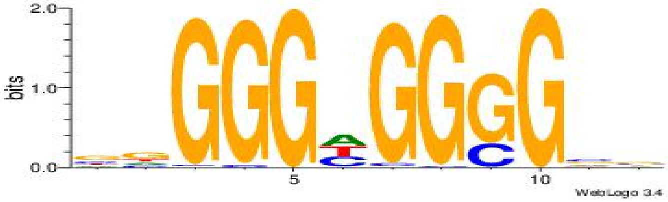


Dataset #: 4   Motif ID: 155   Motif name: csCSCCdCCCcs

Original motif Consensus sequence: VBCCCCDCCCHV



Reverse complement motif Consensus sequence: VDGGGDGGGGBV



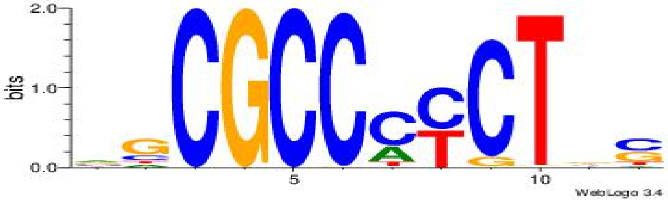
Best Matches for Motif ID 155 (Highest to Lowest)

Dataset #:	4
Motif ID:	137
Motif name:	rgCGCCmyCTgs
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	12
Similarity score:	0.0604731

Alignment:

```
SHAGKGGGCGCB
VDGGGDGGGGBV
```

Original motif Consensus sequence: VGCGCCCYCTDS



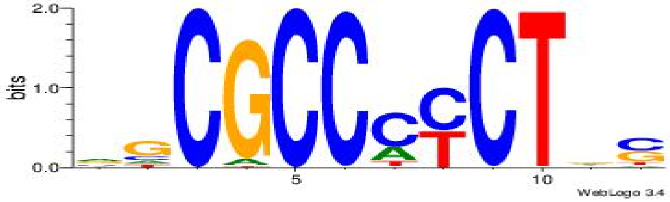
Reverse complement motif Consensus sequence: SHAGKGGGCGCB

Dataset #:	4
Motif ID:	153
Motif name:	scAGrkGGCGcy
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	12
Similarity score:	0.0624586

Alignment:
VGCGCCCMCTDS
VBCCCCDCCCHV

Original motif   Consensus sequence: SHAGRGGGCGCB

Reverse complement motif   Consensus sequence: VGCGCCCMCTDS



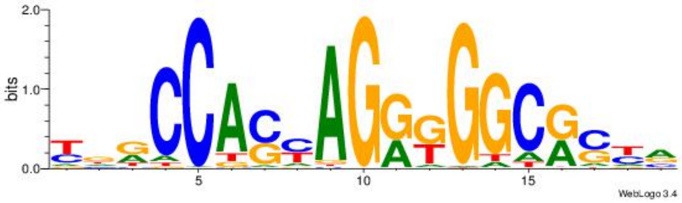
Dataset #:	3
Motif ID:	74
Motif name:	CTCF
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	2
Number of overlap:	12

Similarity score: 0.0800509

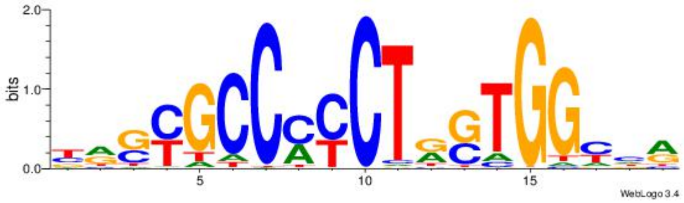
Alignment:

```
BMSMGCCYMCTKSTGGMHM
------VBCCCCDCCCHV-
```

Original motif Consensus sequence: YDRCCASYAGRKGGCRSYV



Reverse complement motif Consensus sequence: BMSMGCCYMCTKSTGGMHM



Dataset #: 4

Motif ID: 168

Motif name: yrcrGYGCCMyCTGGtG

Matching format of first motif: Original Motif

Matching format of second motif: Original Motif

Direction: Backward

Position number: 6

Number of overlap: 12

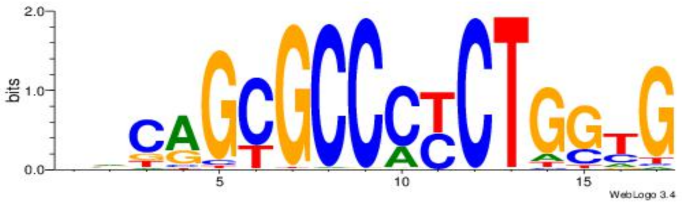
Similarity score: 0.0810683

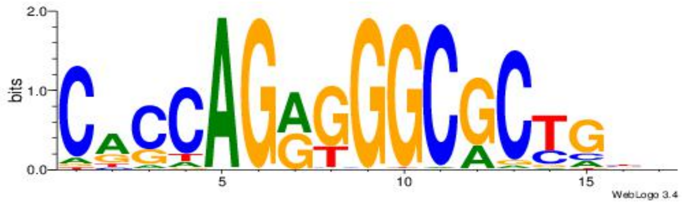
Alignment:

```
HVCAGCGCCCYCTGGTG
VBCCCCDCCCHV-----
```

Original motif Consensus sequence: HVCAGCGCCCYCTGGTG

Reverse complement motif Consensus sequence: CACCAGMGGGCGCTGBD





Dataset #:	4
Motif ID:	147
Motif name:	asCAGrkGGCrsy
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	12
Similarity score:	0.0823049

Alignment:

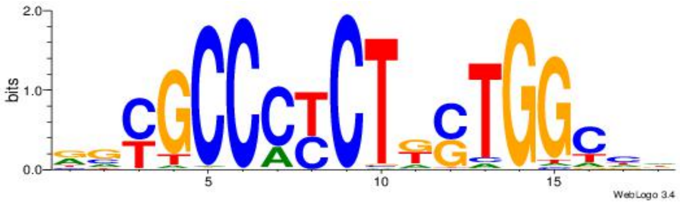
```
BSKGCCCMCTGST
-VBCCCCDCCCHV
```

Original motif Consensus sequence: ASCAGRGGGCRSB

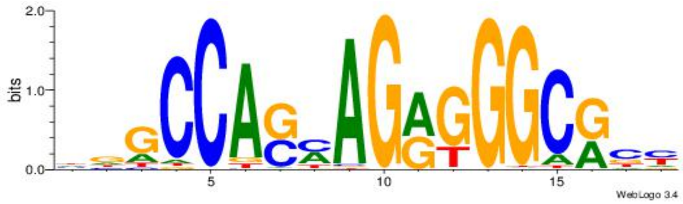
Reverse complement motif Consensus sequence: BSKGCCCMCTGST

Dataset #: 4 Motif ID: 156 Motif name: rgyGCCMyCTksTGGccd

Original motif Consensus sequence: RVYGCCCYCTKSTGGCHD



Reverse complement motif Consensus sequence: DDGCCASYAGMGGGCKVM



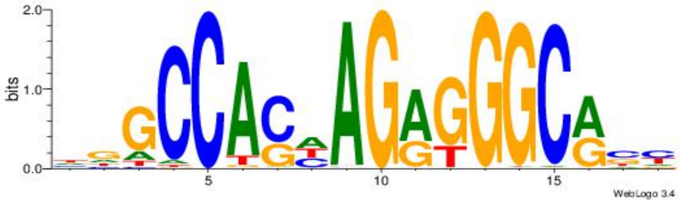
Best Matches for Motif ID 156 (Highest to Lowest)

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:	1
Number of overlap:	18
Similarity score:	0.0156448

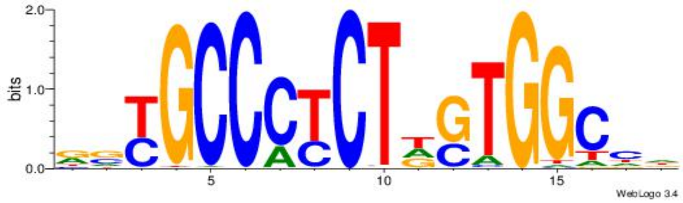
Alignment:

```
HDGCCACHAGRGGGCRBY
DDGCCASYAGMGGGCKVM
```

Original motif Consensus sequence: HDGCCACHAGRGGGCRBY



Reverse complement motif Consensus sequence: KBKGCCCKCTHGTGGCHH

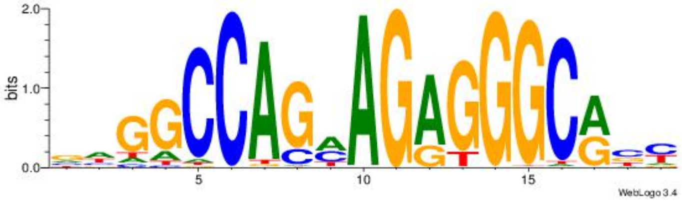


Dataset #:	4
Motif ID:	163
Motif name:	gwGGCCAGmAGAGGGCrby
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	18
Similarity score:	0.0201276

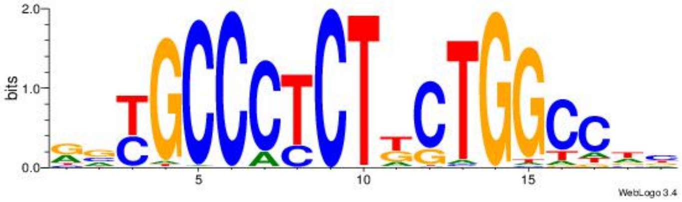
Alignment:

```
VHGGCCAGMAGAGGGCRBY
-DDGCCASYAGMGGGCKVM
```

Original motif Consensus sequence: VHGGCCAGMAGAGGGCRBY



Reverse complement motif Consensus sequence: KBKGCCCTCTYCTGGCCHV



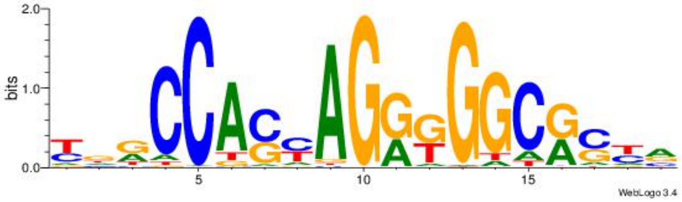
Dataset #:	3
Motif ID:	74
Motif name:	CTCF
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward

Position number:	1
Number of overlap:	18
Similarity score:	0.0207204

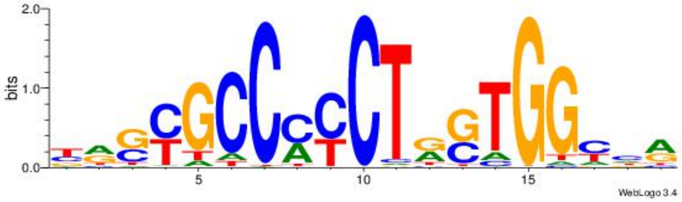
Alignment:

```
YDRCCASYAGRKGGCRSYV
-DDGCCASYAGMGGGCKVM
```

Original motif Consensus sequence: YDRCCASYAGRKGGCRSYV



Reverse complement motif Consensus sequence: BMSMGCCYMCTKSTGGMHM

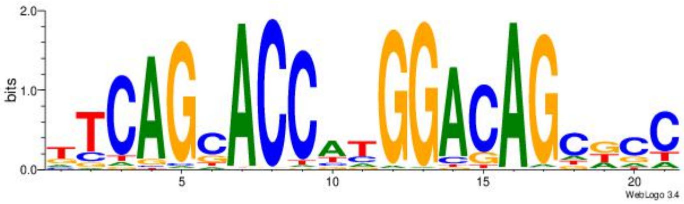


Dataset #:	3
Motif ID:	113
Motif name:	REST
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	18
Similarity score:	0.0950319

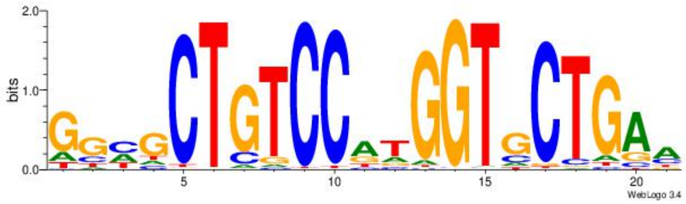
Alignment:

```
GGYGCTGTCCATGGTGCTGAA
---RVYGCCCYCTKSTGGCHD
```

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC



Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA

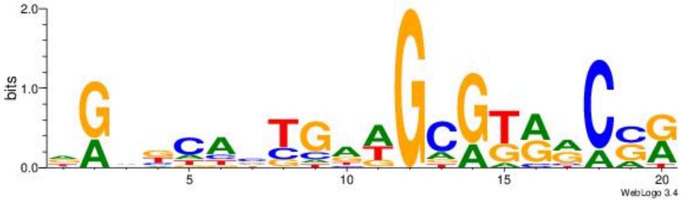


Dataset #:	3
Motif ID:	109
Motif name:	Pax5
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	18
Similarity score:	0.09559

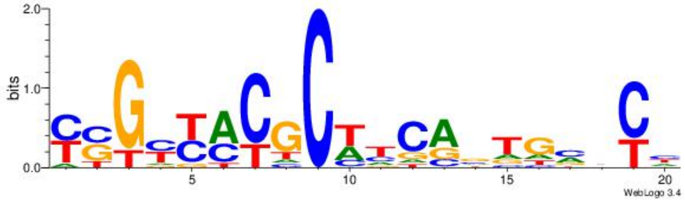
Alignment:

```
MSGKKRCGCWDCABTGBBCD
--RVYGCCCYCTKSTGGCHD
```

Original motif Consensus sequence: DGVBCABTGDWGCGKRRCSR

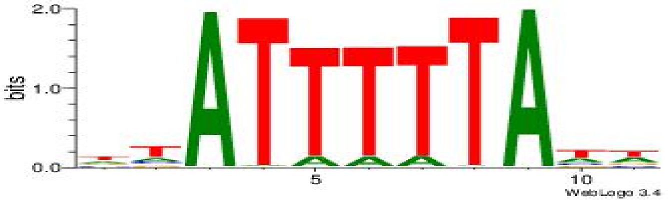


Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD

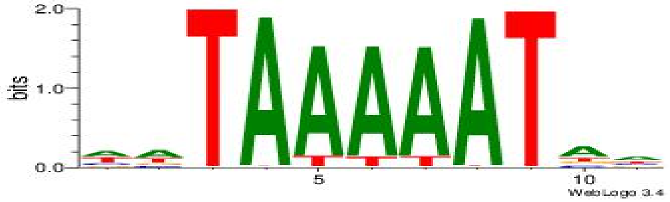


Dataset #: 4 **Motif ID: 157** **Motif name: wtATTTTTAww**

Original motif Consensus sequence: DTATTTTTAWW



Reverse complement motif Consensus sequence: WWTAAAAATAD



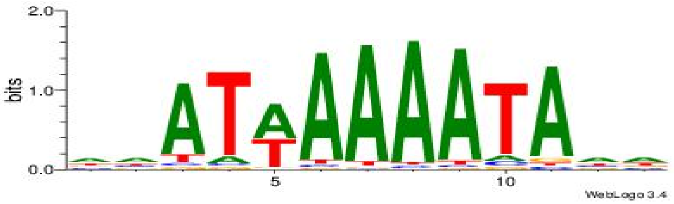
Best Matches for Motif ID 157 (Highest to Lowest)

Dataset #:	4
Motif ID:	150
Motif name:	waATwAAAATAww
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	2
Number of overlap:	11
Similarity score:	0

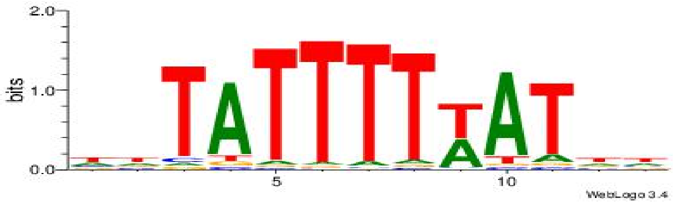
Alignment:

```
DHTATTTTWATHD
-DTATTTTTAWW-
```

Original motif Consensus sequence: DHATWAAAATAHD



Reverse complement motif Consensus sequence: DHTATTTTWATHD

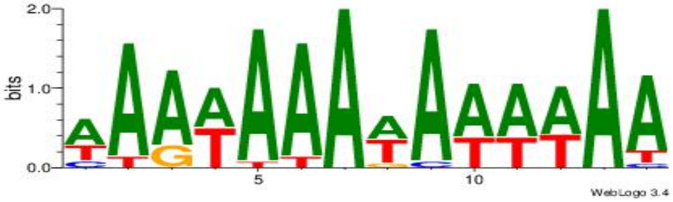


Dataset #: 2
Motif ID: 68
Motif name: Motif 68
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2
Number of overlap: 11
Similarity score: 0.0323073

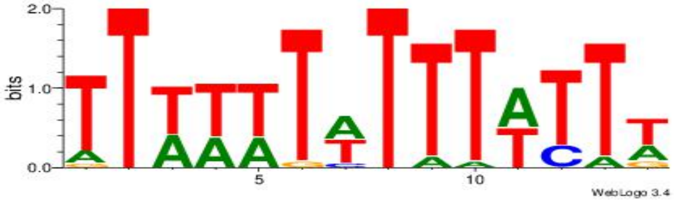
Alignment:

```
WAAWAAAWAWWWAA
--WWTAAAAATAD-
```

Original motif Consensus sequence: WAAWAAAWAWWWAA



Reverse complement motif Consensus sequence: TTWWWTWTTTWTTW



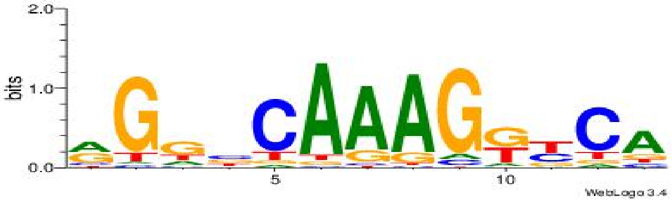
Dataset #: 3
Motif ID: 87
Motif name: HNF4A
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward

Position number: 1
Number of overlap: 11
Similarity score: 0.0727314

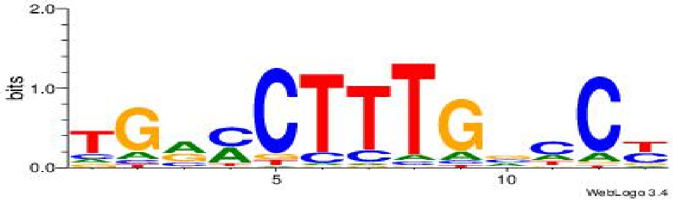
Alignment:

```
RGGBCAAAGKYCA
WWTAAAAATAD--
```

Original motif Consensus sequence: RGGBCAAAGKYCA



Reverse complement motif Consensus sequence: TGMYCTTTGBCCK



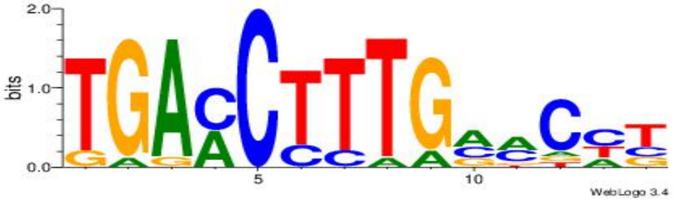
Dataset #: 3
Motif ID: 107
Motif name: NR2F1
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 11
Similarity score: 0.0739182

Alignment:

```
AKGYYCAAAGRTCA
---WWTAAAAATAD
```

Original motif Consensus sequence: TGAMCTTTGMMCYT

Reverse complement motif Consensus sequence: AKGYYCAAAGRTC

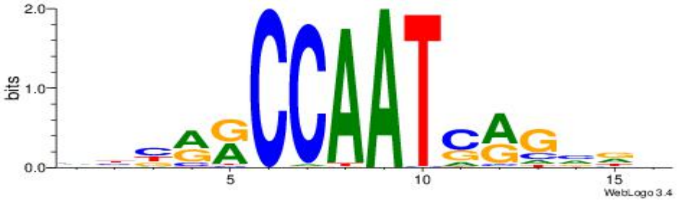


Dataset #: 3
Motif ID: 104
Motif name: NFYA
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 5
Number of overlap: 11
Similarity score: 0.0755742

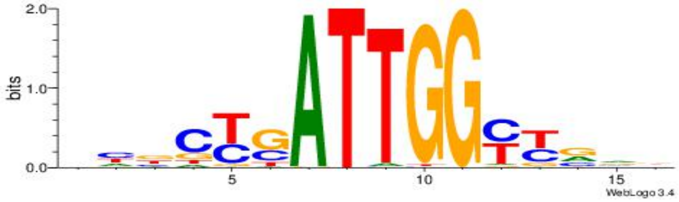
Alignment:

```
BHVCKSATTGGMKBVV
-DTATTTTTAWW----
```

Original motif Consensus sequence: VBBRRCCAATSRGVDB



Reverse complement motif Consensus sequence: BHVCKSATTGGMKBVV



Dataset #: 4 Motif ID: 158 Motif name: grCCACwAGrk

Original motif Consensus sequence: DDCCACWAGRK

Reverse complement motif Consensus sequence: YMCTWGTGGHH

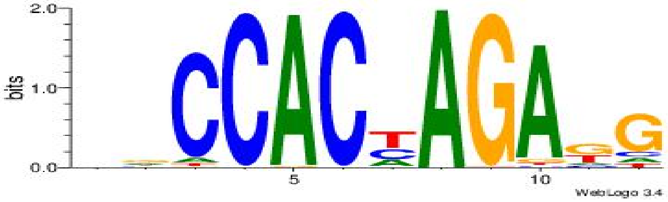
Best Matches for Motif ID 158 (Highest to Lowest)

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:	1
Number of overlap:	11
Similarity score:	0.0013909

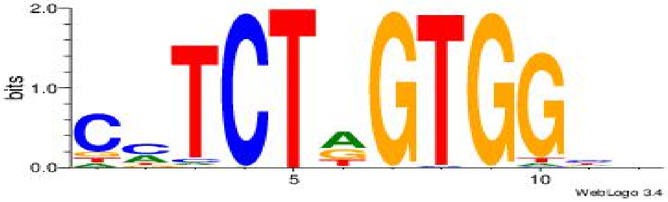
Alignment:

```
DDCCACYAGAKG
DDCCACWAGRK-
```

Original motif Consensus sequence: DDCCACYAGAKG



Reverse complement motif Consensus sequence: CYTCTMGTGGHH

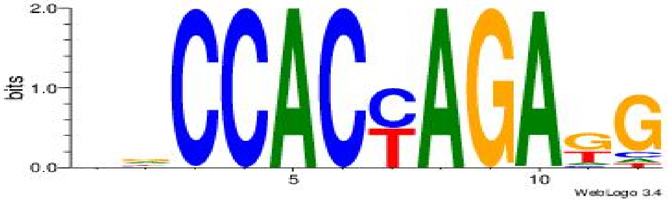


Dataset #: 4
Motif ID: 145
Motif name: grCCACyAGAkG
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2
Number of overlap: 11
Similarity score: 0.00619044

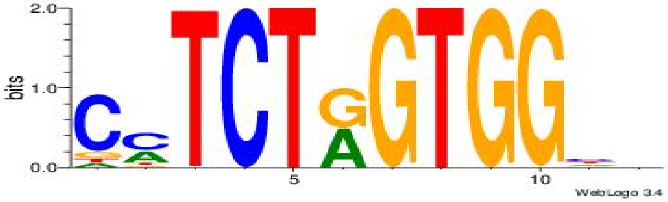
Alignment:

```
DDCCACYAGAKG
DDCCACWAGRK-
```

Original motif   Consensus sequence: DDCCACYAGAKG



Reverse complement motif   Consensus sequence: CYTCTKGTGGHH

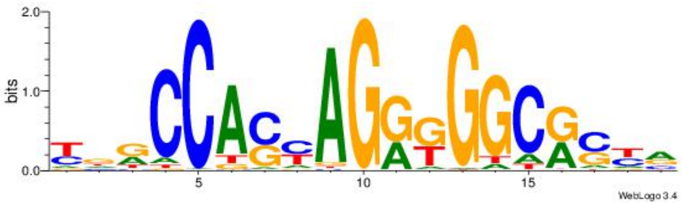


Dataset #: 3
Motif ID: 74
Motif name: CTCF
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 8
Number of overlap: 11

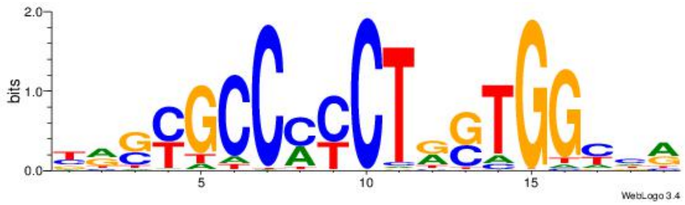
Similarity score:	0.0223616

Alignment:
BMSMGCCYMCTKSTGGMHM
-------YMCTWGTGGHH-

Original motif Consensus sequence: YDRCCASYAGRKGGCRSYV



Reverse complement motif Consensus sequence: BMSMGCCYMCTKSTGGMHM

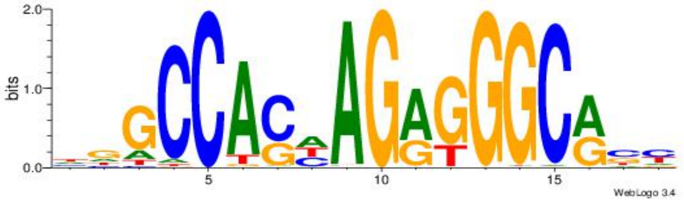


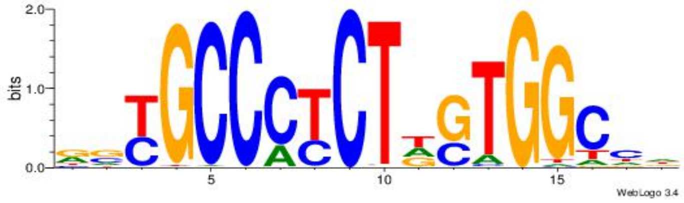
Dataset #:	4
Motif ID:	165
Motif name:	wgGCCAshAGrGGGCrsy
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	7
Number of overlap:	11
Similarity score:	0.0228739

Alignment:
HDGCCACHAGRGGGCRBY
-DDCCACWAGRK------

Original motif Consensus sequence: HDGCCACHAGRGGGCRBY

Reverse complement motif Consensus sequence: KBKGCCCKCTHGTGGCHH





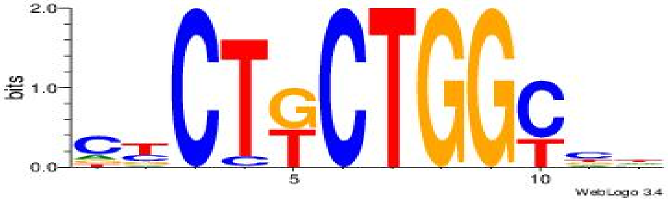
Dataset #:	4
Motif ID:	151
Motif name:	agrCCAGmAGrg
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	11
Similarity score:	0.0330864

Alignment:

```
HVGCCAGMAGRG
-DDCCACWAGRK
```

Original motif Consensus sequence: HVGCCAGMAGRG

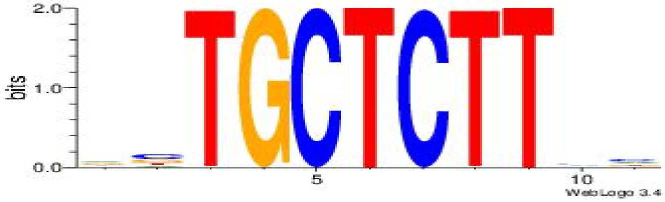
Reverse complement motif Consensus sequence: CKCTRCTGGCVH



Dataset #: 4 Motif ID: 159 Motif name: kkAAGAGCAsy

Original motif Consensus sequence: DBAAGAGCAVH

Reverse complement motif Consensus sequence: HVTGCTCTTBH



Best Matches for Motif ID 159 (Highest to Lowest)

Dataset #:	4
Motif ID:	160
Motif name:	brCAGGGCCrs
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	11
Similarity score:	0.0212428

Alignment:

```
BBGGCCCTGBB
HVTGCTCTTBH
```

Original motif Consensus sequence: BVCAGGGCCVB

Reverse complement motif Consensus sequence: BBGGCCCTGBB

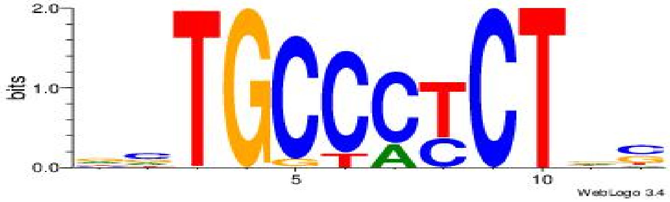
Dataset #:	4
Motif ID:	133
Motif name:	shAGrGGGCAgy
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	11
Similarity score:	0.0322726

Alignment:

```
SHAGRGGGCABH
-DBAAGAGCAVH
```

Original motif   Consensus sequence: SHAGRGGGCABH

Reverse complement motif   Consensus sequence: DBTGCCCKCTDS



Dataset #:	3
Motif ID:	70
Motif name:	Ar
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	12
Number of overlap:	11

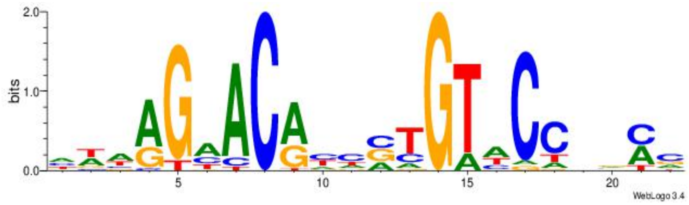
Similarity score:	0.0353029

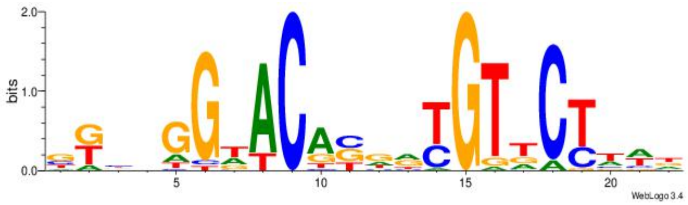
Alignment:

```
VRVDGGHACAVDDKGTHCTDWH
-----------HVTGCTCTTBH
```

Original motif Consensus sequence: HWDAGHACRHHVTGTHCCHVMV

Reverse complement motif Consensus sequence: VRVDGGHACAVDDKGTHCTDWH





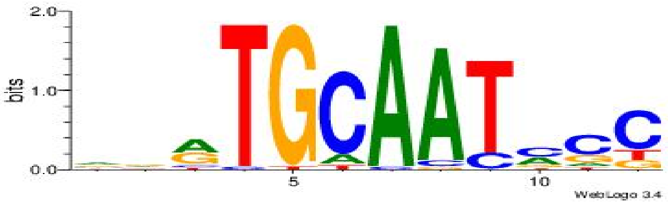
Dataset #:	3
Motif ID:	75
Motif name:	Ddit3Cebpa
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	11
Similarity score:	0.0380063

Alignment:

```
VDRTGCAATMCC
HVTGCTCTTBH-
```

Original motif Consensus sequence: VDRTGCAATMCC

Reverse complement motif Consensus sequence: GGRATTGCAKHB

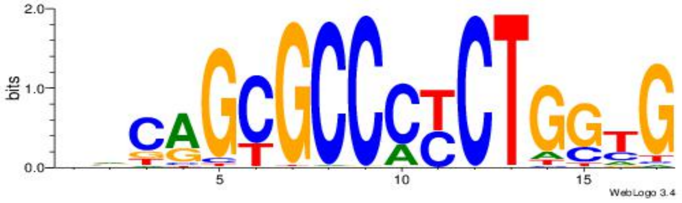


Dataset #:	4
Motif ID:	168
Motif name:	yrcrGYGCCMyCTGGtG
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	11
Similarity score:	0.0432631

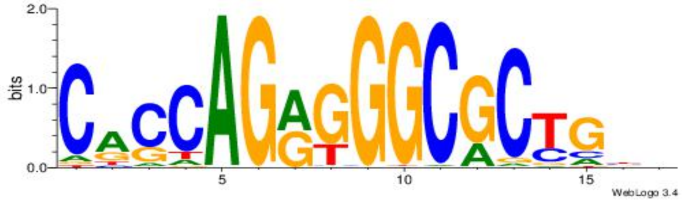
Alignment:

```
CACCAGMGGGCGCTGBD
------HVTGCTCTTBH
```

Original motif Consensus sequence: HVCAGCGCCCYCTGGTG



Reverse complement motif Consensus sequence: CACCAGMGGGCGCTGBD



Dataset #: 4 Motif ID: 160 Motif name: brCAGGGCCrs

Original motif   Consensus sequence: BVCAGGGCCVB

Reverse complement motif   Consensus sequence: BBGGCCCTGBB

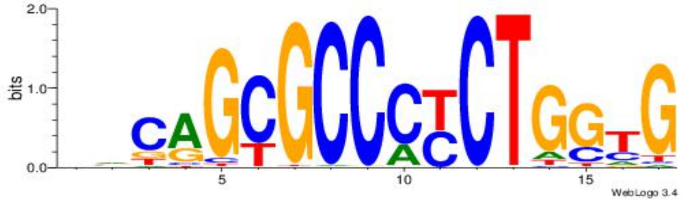
Best Matches for Motif ID 160 (Highest to Lowest)

Dataset #:	4
Motif ID:	168
Motif name:	yrcrGYGCCMyCTGGtG
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:	0.0430085

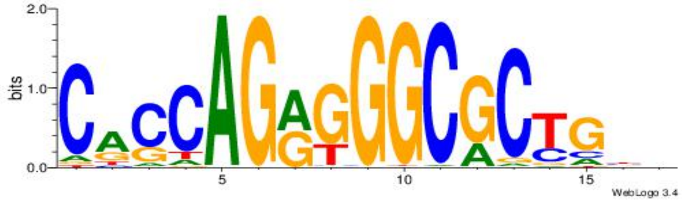
Alignment:

```
HVCAGCGCCCYCTGGTG
BVCAGGGCCVB------
```

Original motif   Consensus sequence: HVCAGCGCCCYCTGGTG



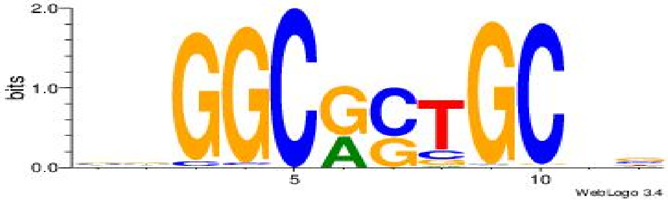
Reverse complement motif   Consensus sequence: CACCAGMGGGCGCTGBD



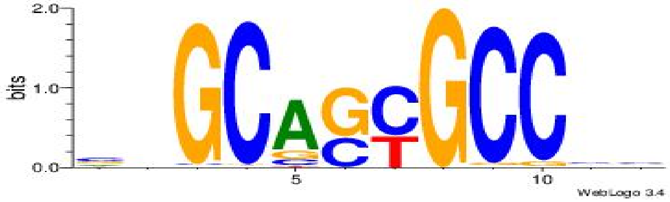
Dataset #: 4
Motif ID: 170
Motif name: ssGGCrsTGCrs
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 2
Number of overlap: 11
Similarity score: 0.0438378

Alignment:
BVGCASMGCCVV
-BVCAGGGCCVB

Original motif Consensus sequence: VVGGCRSTGCVB



Reverse complement motif Consensus sequence: BVGCASMGCCVV



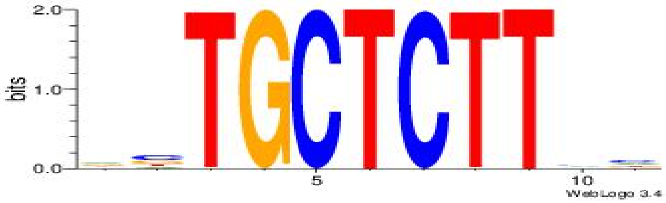
Dataset #: 4
Motif ID: 159
Motif name: kkAAGAGCAsy
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 11

Similarity score: 0.0567379

Alignment:
HVTGCTCTTBH
BBGGCCCTGBB

Original motif Consensus sequence: DBAAGAGCAVH

Reverse complement motif Consensus sequence: HVTGCTCTTBH

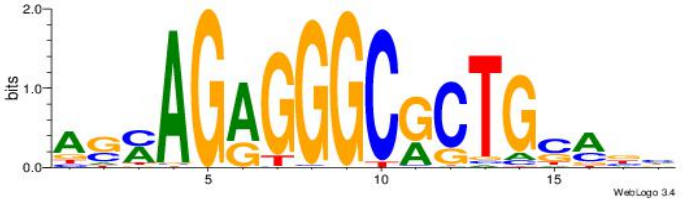


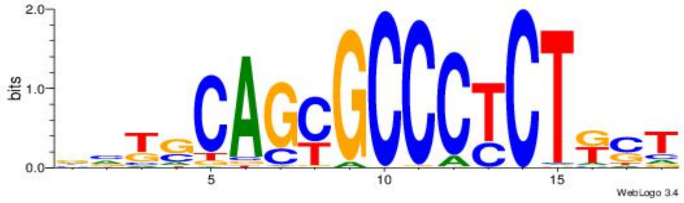
Dataset #: 4
Motif ID: 149
Motif name: asmAGRGGGCrCTGsmkc
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 6
Number of overlap: 11
Similarity score: 0.0583002

Alignment:
ASMAGAGGGCRCTGSABH
--BBGGCCCTGBB-----

Original motif Consensus sequence: ASMAGAGGGCRCTGSABH

Reverse complement motif Consensus sequence:
DBTSCAGMGCCCTCTRST



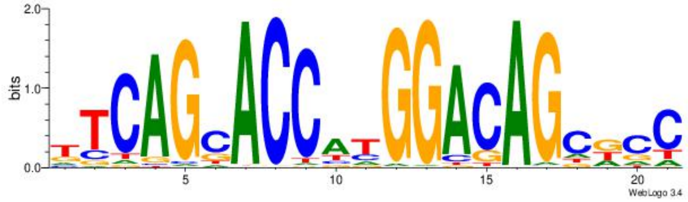


Dataset #:	3
Motif ID:	113
Motif name:	REST
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	11
Number of overlap:	11
Similarity score:	0.0603368

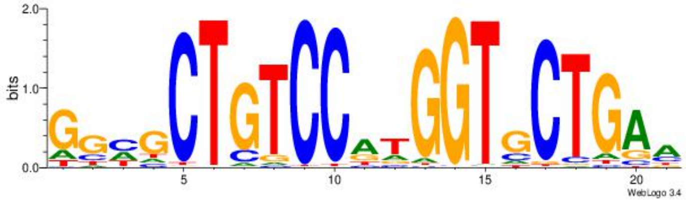
Alignment:

```
TTCAGCACCATGGACAGCKCC
BVCAGGGCCVB----------
```

Original motif Consensus sequence: TTCAGCACCATGGACAGCKCC

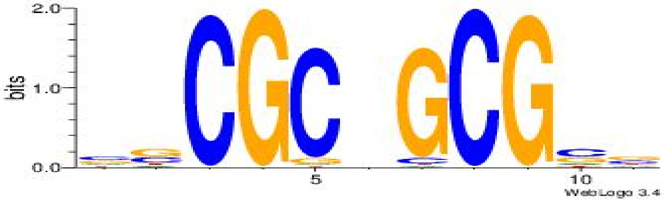


Reverse complement motif Consensus sequence: GGYGCTGTCCATGGTGCTGAA

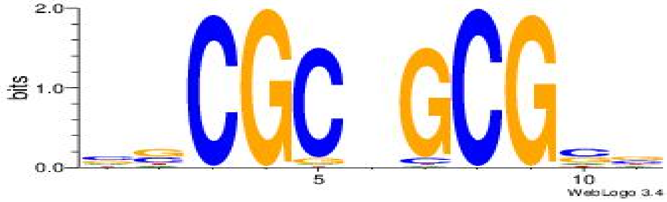


Dataset #: 4 Motif ID: 161 Motif name: ssCGCwGCGss

Original motif Consensus sequence: VSCGCDGCGSB



Reverse complement motif Consensus sequence: BSCGCDGCGSV



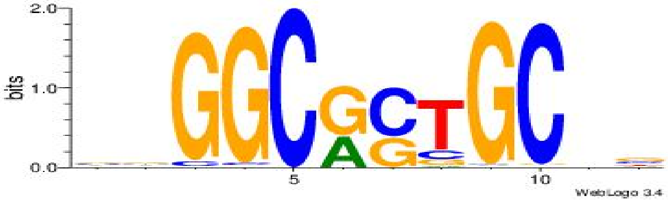
Best Matches for Motif ID 161 (Highest to Lowest)

Dataset #:	4
Motif ID:	170
Motif name:	ssGGCrsTGCrs
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2
Number of overlap:	11
Similarity score:	0.0546471

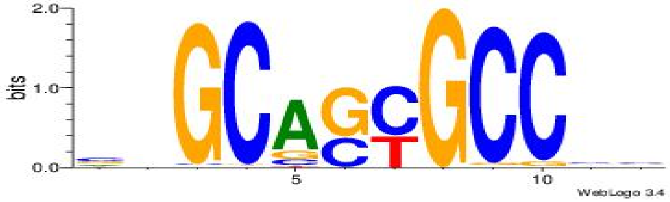
Alignment:

```
VVGGCRSTGCVB
BSCGCDGCGSV-
```

Original motif Consensus sequence: VVGGCRSTGCVB



Reverse complement motif Consensus sequence: BVGCASMGCCVV

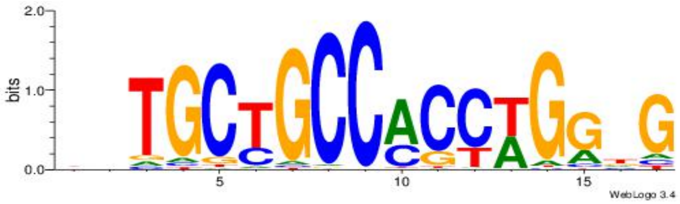


Dataset #:	4
Motif ID:	169
Motif name:	yvTGCyGCCmCCwGgtG
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	11
Similarity score:	0.0565318

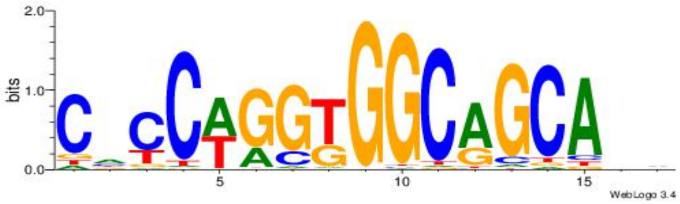
Alignment:

```
CDCCWGGTGGCAGCAVV
------BSCGCDGCGSV
```

Original motif Consensus sequence: BVTGCTGCCACCWGGDG



Reverse complement motif Consensus sequence: CDCCWGGTGGCAGCAVV



Dataset #:	4
Motif ID:	149
Motif name:	asmAGRGGGCrCTGsmkc
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1

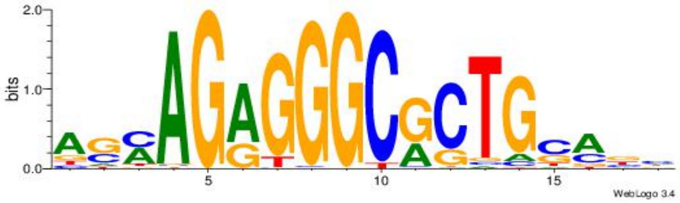
Number of overlap: 11

Similarity score: 0.0580603

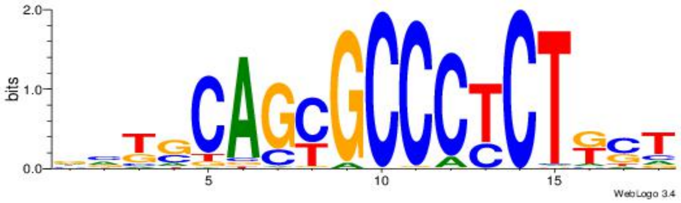
Alignment:

```
DBTSCAGMGCCCTCTRST
BSCGCDGCGSV-------
```

Original motif Consensus sequence: ASMAGAGGGCRCTGSABH



Reverse complement motif Consensus sequence: DBTSCAGMGCCCTCTRST



Dataset #: 4

Motif ID: 154

Motif name: csCsCCTCCcc

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: 0.0592711

Alignment:

```
VBCCCCTCCHB
BSCGCDGCGSV
```

Original motif Consensus sequence: VBCCCCTCCHB

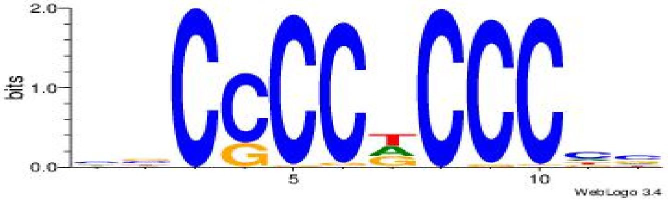
Reverse complement motif Consensus sequence: BDGGAGGGGBV

Dataset #:	4
Motif ID:	155
Motif name:	csCSCCdCCCcs
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	2
Number of overlap:	11
Similarity score:	0.0599572

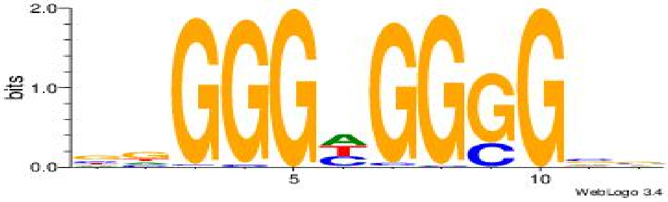
Alignment:

```
VDGGGDGGGGBV
VSCGCDGCGSB-
```

Original motif Consensus sequence: VBCCCCDCCCHV

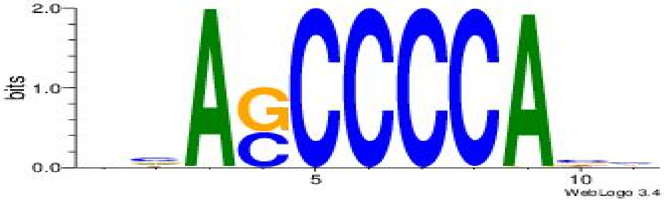


Reverse complement motif Consensus sequence: VDGGGDGGGGBV

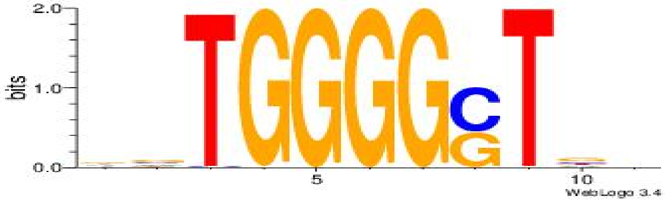


Dataset #: 4 Motif ID: 162 Motif name: ccAsCCCCAcc

Original motif Consensus sequence: HVASCCCCABH



Reverse complement motif Consensus sequence: DBTGGGGSTVD



Best Matches for Motif ID 162 (Highest to Lowest)

Dataset #:	4
Motif ID:	154
Motif name:	csCsCCTCCcc
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	11
Similarity score:	0.0318935

Alignment:

```
BDGGAGGGGBV
DBTGGGGSTVD
```

Original motif Consensus sequence: VBCCCCTCCHB

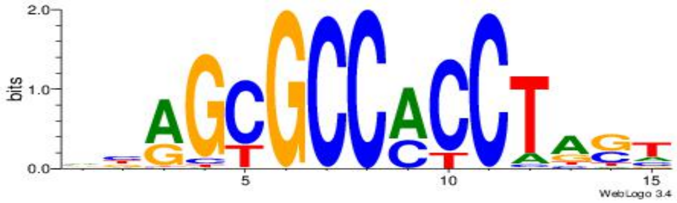
Reverse complement motif Consensus sequence: BDGGAGGGGBV

Dataset #:	4
Motif ID:	146
Motif name:	myrGYGCCmCCTast
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:	0.0360618

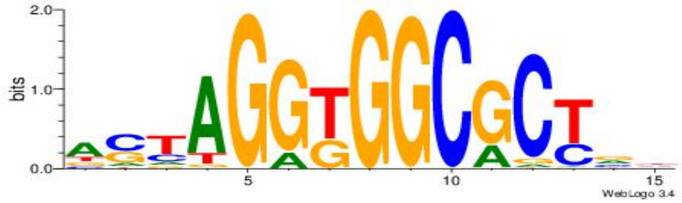
Alignment:

```
VBAGCGCCMCCTAST
HVASCCCCABH----
```

Original motif   Consensus sequence: VBAGCGCCMCCTAST



Reverse complement motif   Consensus sequence: ASTAGGYGGCGCT

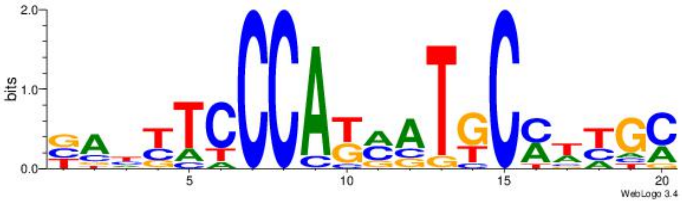


Dataset #:	3
Motif ID:	131
Motif name:	znf143
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	10
Number of overlap:	11

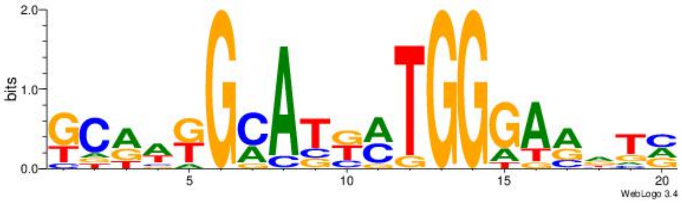
Similarity score: 0.0409371

Alignment:
BAHYTCCCAKMATGCMWYGC
HVASCCCCABH---------

Original motif Consensus sequence: BAHYTCCCAKMATGCMWYGC



Reverse complement motif Consensus sequence: GCMWRGCATYRTGGGAMHTB

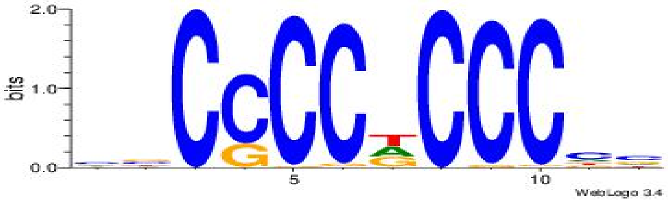


Dataset #: 4
Motif ID: 155
Motif name: csCSCCdCCCcs
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 2
Number of overlap: 11
Similarity score: 0.0412348

Alignment:
VDGGGDGGGGBV
-DBTGGGGSTVD

Original motif Consensus sequence: VBCCCCDCCCHV

Reverse complement motif Consensus sequence: VDGGGDGGGGBV

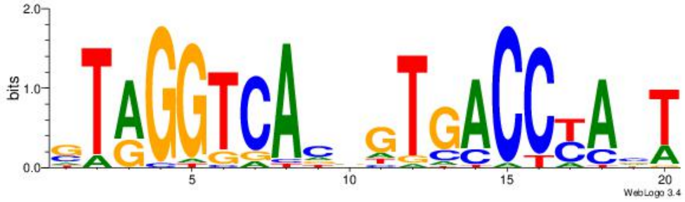



Dataset #: 3
Motif ID: 111
Motif name: PPARG
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 11
Similarity score: 0.0446625

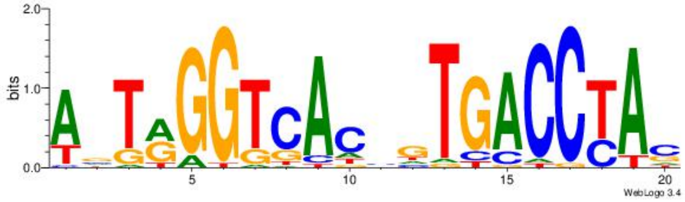
Alignment:

```
STAGGTCACBGTGACCYABT
---------HVASCCCCABH
```

Original motif Consensus sequence: STAGGTCACBGTGACCYABT

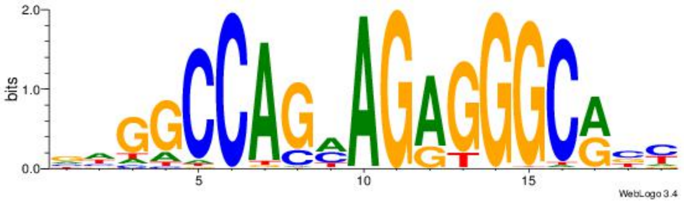


Reverse complement motif Consensus sequence: ABTMGGTCACBGTGACCTAS

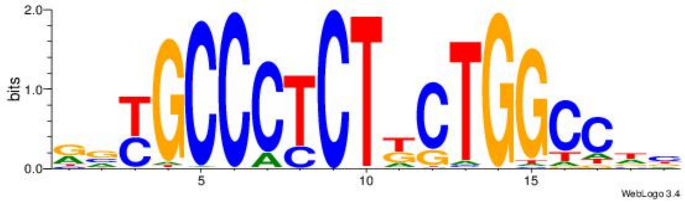


Dataset #: 4 Motif ID: 163 Motif name: gwGGCCAGmAGAGGGCrby

Original motif   Consensus sequence: VHGGCCAGMAGAGGGCRBY



Reverse complement motif   Consensus sequence: KBKGCCCTCTYCTGGCCHV



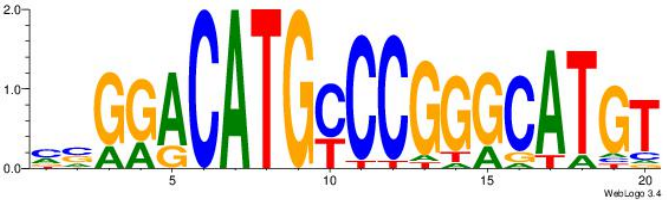
Best Matches for Motif ID 163 (Highest to Lowest)

Dataset #:	3
Motif ID:	125
Motif name:	TP53
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	19
Similarity score:	0.0964434

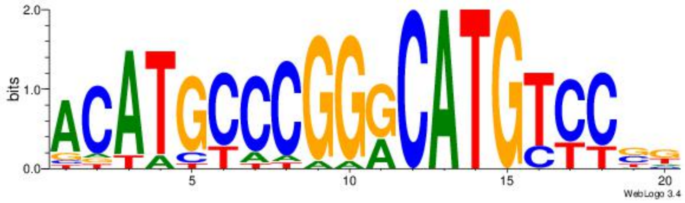
Alignment:

```
ACATGCCCGGKCATGTCCSR
-KBKGCCCTCTYCTGGCCHV
```

Original motif   Consensus sequence: MSGGACATGYCCGGGCATGT



Reverse complement motif   Consensus sequence: ACATGCCCGGKCATGTCCSR

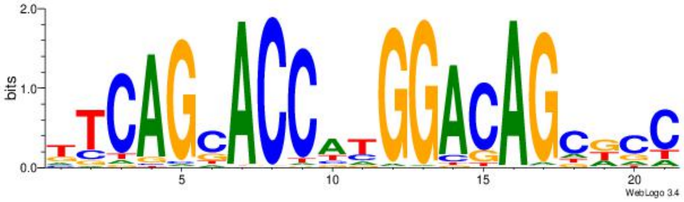


Dataset #:	3
Motif ID:	113
Motif name:	REST
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	19
Similarity score:	0.104301

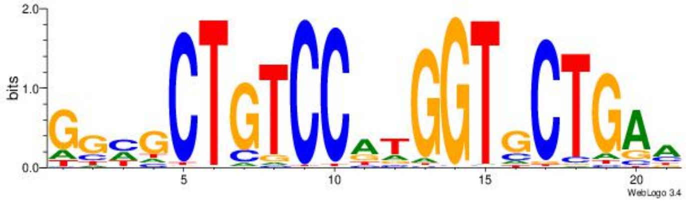
Alignment:

```
TTCAGCACCATGGACAGCKCC
--VHGGCCAGMAGAGGGCRBY
```

Original motif   Consensus sequence: TTCAGCACCATGGACAGCKCC



Reverse complement motif   Consensus sequence: GGYGCTGTCCATGGTGCTGAA

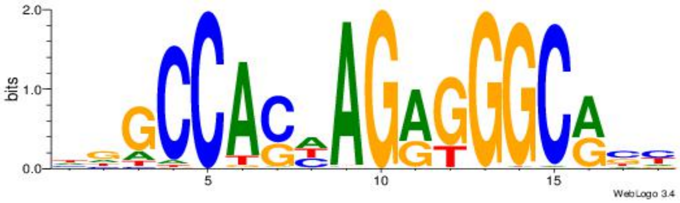


Dataset #:	4
Motif ID:	165
Motif name:	wgGCCAshAGrGGGCrsy
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward

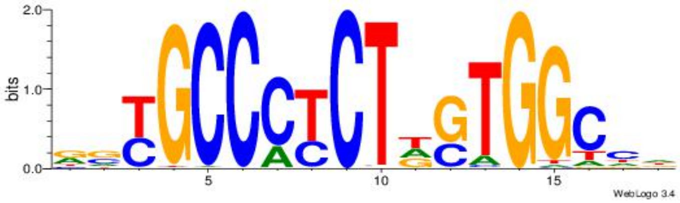
Position number: 1
Number of overlap: 18
Similarity score: 0.502859

Alignment:
```
-HDGCCACHAGRGGGCRBY
VHGGCCAGMAGAGGGCRBY
```

Original motif Consensus sequence: HDGCCACHAGRGGGCRBY



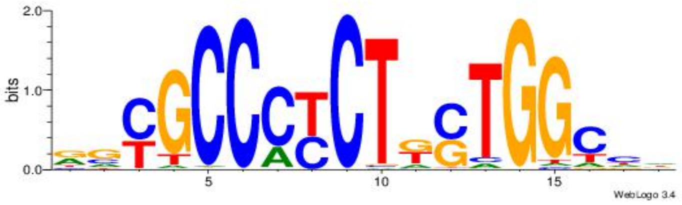
Reverse complement motif Consensus sequence: KBKGCCCKCTHGTGGCHH



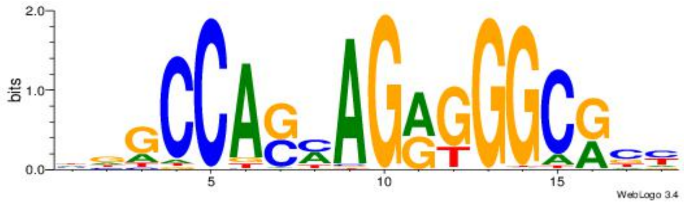
Dataset #: 4
Motif ID: 156
Motif name: rgyGCCMyCTksTGGccd
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 18
Similarity score: 0.525011

Alignment:
```
-RVYGCCCYCTKSTGGCHD
KBKGCCCTCTYCTGGCCHV
```

Original motif Consensus sequence: RVYGCCCYCTKSTGGCHD



Reverse complement motif Consensus sequence: DDGCCASYAGMGGGCKVM

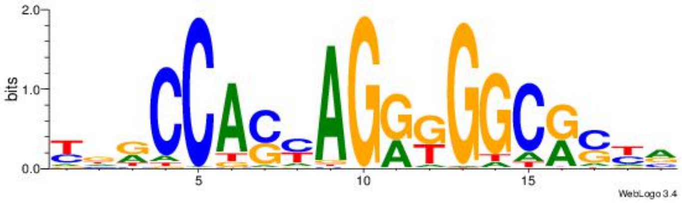


Dataset #:	3
Motif ID:	74
Motif name:	CTCF
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2
Number of overlap:	18
Similarity score:	0.529309

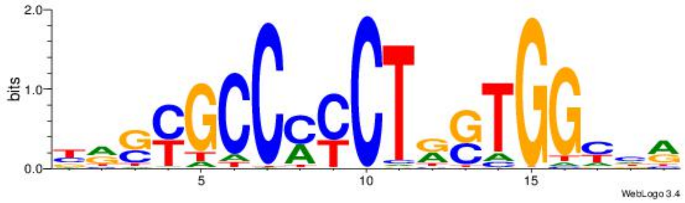
Alignment:

-YDRCCASYAGRKGGCRSYV
VHGGCCAGMAGAGGGCRBY-

Original motif Consensus sequence: YDRCCASYAGRKGGCRSYV

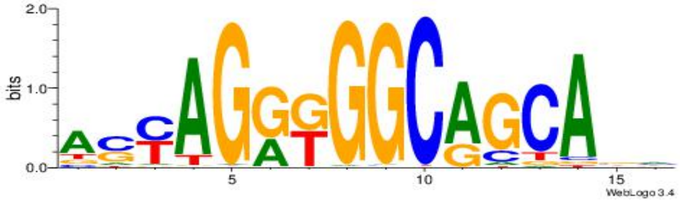


Reverse complement motif Consensus sequence: BMSMGCCYMCTKSTGGMHM

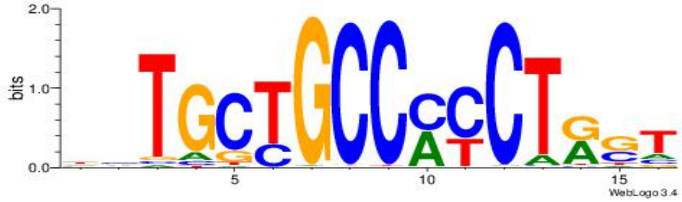


Dataset #: 4 Motif ID: 164 Motif name: asyAGrkGGCRGCAga

Original motif Consensus sequence: ASYAGRKGGCAGCABH



Reverse complement motif Consensus sequence: HBTGCTGCCYMCTKST



Best Matches for Motif ID 164 (Highest to Lowest)

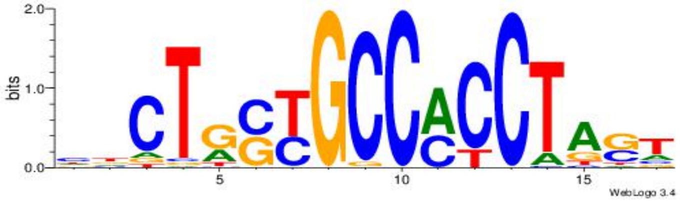
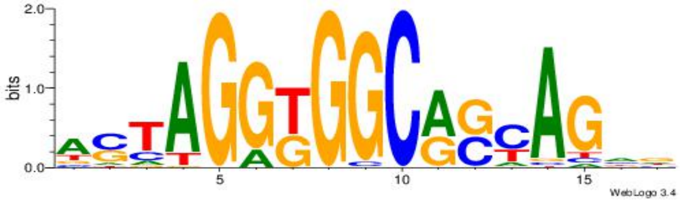
Dataset #:	4
Motif ID:	144
Motif name:	ctCTrsyGCCmCCTast
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2
Number of overlap:	16
Similarity score:	0.0253571

Alignment:

```
HDCTGSYGCCMCCTAST
HBTGCTGCCYMCTKST-
```

Original motif Consensus sequence: HDCTGSYGCCMCCTAST

Reverse complement motif Consensus sequence: ASTAGGYGGCMSCAGDD

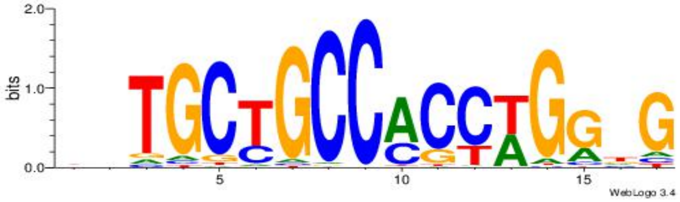



Dataset #: 4
Motif ID: 169
Motif name: yvTGCyGCCmCCwGgtG
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 2
Number of overlap: 16
Similarity score: 0.0299559

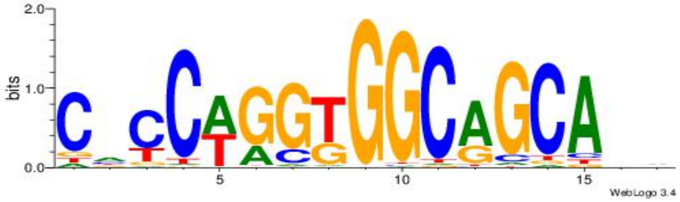
Alignment:

```
CDCCWGGTGGCAGCAVV
-ASYAGRKGGCAGCABH
```

Original motif Consensus sequence: BVTGCTGCCACCWGGDG



Reverse complement motif Consensus sequence: CDCCWGGTGGCAGCAVV



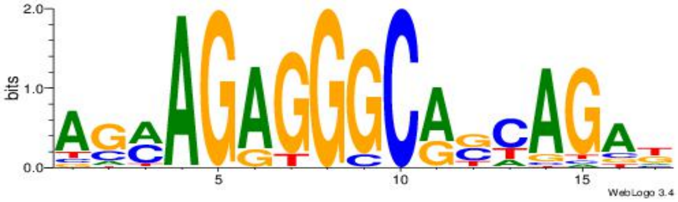
Dataset #: 4

Motif ID: 143
Motif name: AgmAGAGGGCrscAGak
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2
Number of overlap: 16
Similarity score: 0.0333221

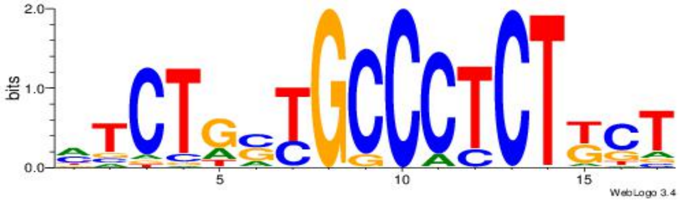
Alignment:

```
AGMAGAGGGCASCAGAK
ASYAGRKGGCAGCABH-
```

Original motif Consensus sequence: AGMAGAGGGCASCAGAK



Reverse complement motif Consensus sequence: RTCTGSTGCCCTCTYCT



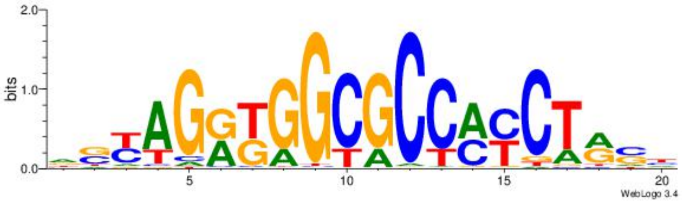
Dataset #: 4
Motif ID: 167
Motif name: rsyAGrkGGCGCCmyCTrsy
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 5
Number of overlap: 16

Similarity score: 0.0458621

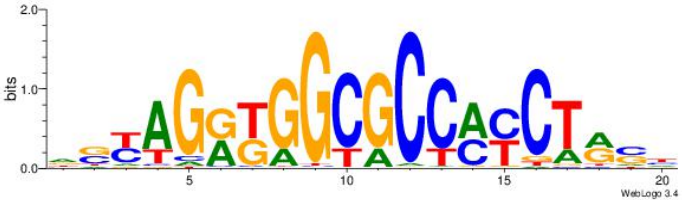
Alignment:

DSYAGRKGGCGCCMYCTRSH
ASYAGRKGGCAGCABH----

Original motif Consensus sequence: DSYAGRKGGCGCCMYCTRSH



Reverse complement motif Consensus sequence: HSKAGKYGGCGCCRMCTMSD



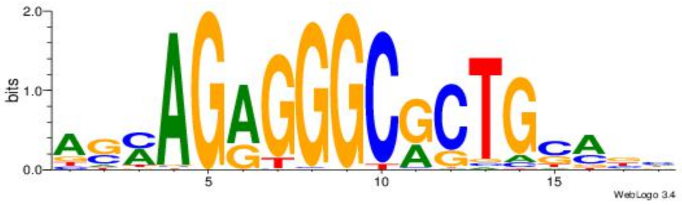
Dataset #:	4
Motif ID:	149
Motif name:	asmAGRGGGCrCTGsmkc
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	16
Similarity score:	0.0529808

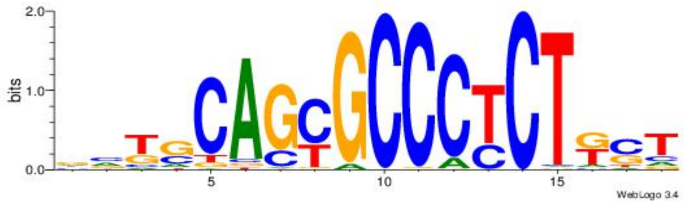
Alignment:

ASMAGAGGGCRCTGSABH
ASYAGRKGGCAGCABH--

Original motif Consensus sequence: ASMAGAGGGCRCTGSABH

Reverse complement motif Consensus sequence: DBTSCAGMGCCCTCTRST

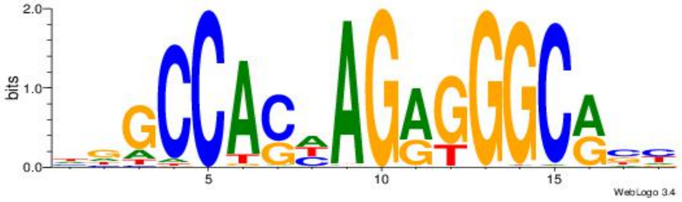


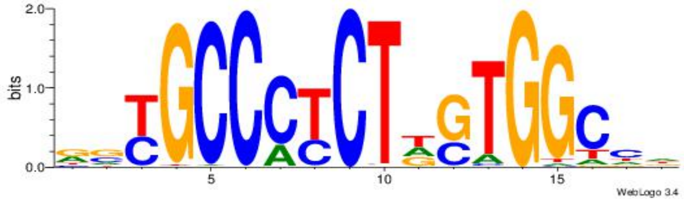


Dataset #: 4 Motif ID: 165 Motif name: wgGCCAshAGrGGGCrsy

Original motif Consensus sequence: HDGCCACHAGRGGGCRBY

Reverse complement motif Consensus sequence: KBKGCCCKCTHGTGGCHH





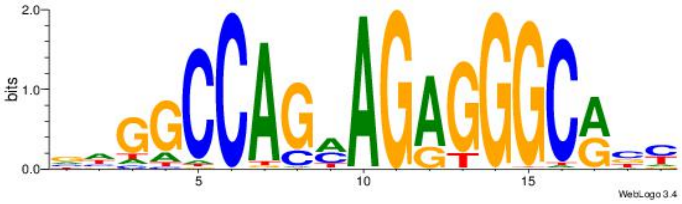
Best Matches for Motif ID 165 (Highest to Lowest)

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:	1
Number of overlap:	18
Similarity score:	0.00922625

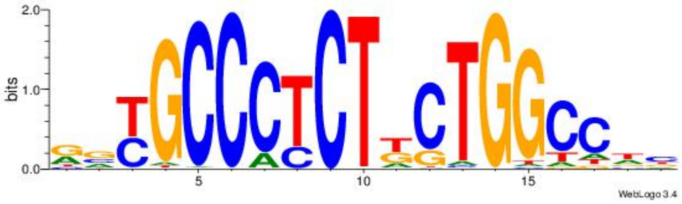
Alignment:

```
KBKGCCCTCTYCTGGCCHV
KBKGCCCKCTHGTGGCHH-
```

Original motif Consensus sequence: VHGGCCAGMAGAGGGCRBY



Reverse complement motif Consensus sequence: KBKGCCCTCTYCTGGCCHV



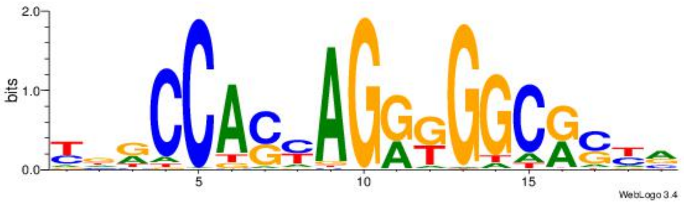
Dataset #:	3
Motif ID:	74
Motif name:	CTCF
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2
Number of overlap:	18
Similarity score:	0.0205802

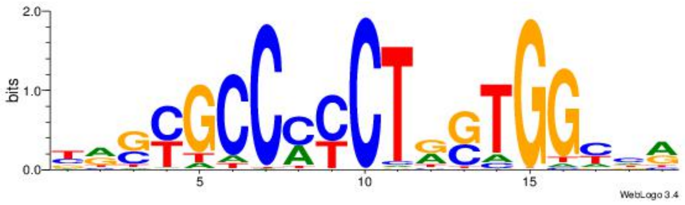
Alignment:

```
YDRCCASYAGRKGGCRSYV
HDGCCACHAGRGGGCRBY-
```

Original motif Consensus sequence: YDRCCASYAGRKGGCRSYV

Reverse complement motif Consensus sequence: BMSMGCCYMCTKSTGGMHM



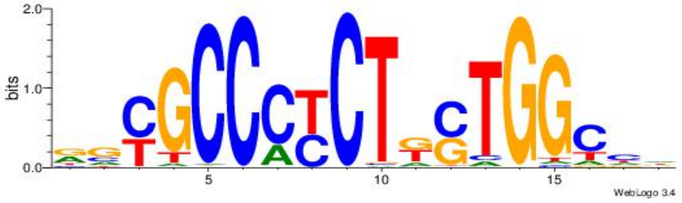


Dataset #: 4
Motif ID: 156
Motif name: rgyGCCMyCTksTGGccd
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 18
Similarity score: 0.0268949

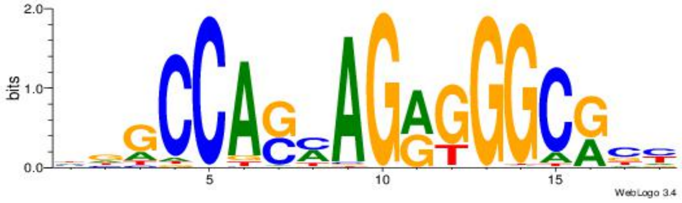
Alignment:

```
RVYGCCCYCTKSTGGCHD
KBKGCCCKCTHGTGGCHH
```

Original motif Consensus sequence: RVYGCCCYCTKSTGGCHD



Reverse complement motif Consensus sequence: DDGCCASYAGMGGGCKVM

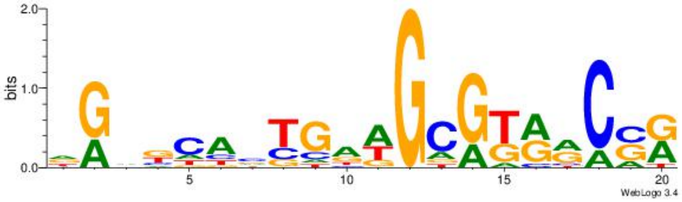


Dataset #: 3

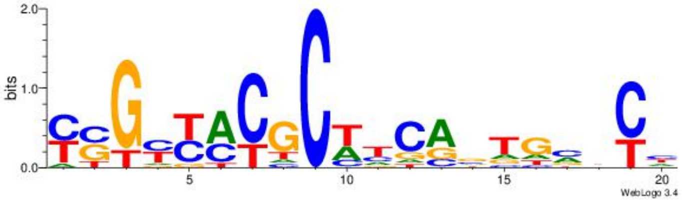
Motif ID: 109
Motif name: Pax5
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 3
Number of overlap: 18
Similarity score: 0.103512

Alignment:
MSGKKRCGCWDCABTGBBCD
--KBKGCCCKCTHGTGGCHH

Original motif Consensus sequence: DGVBCABTGDWGCGKRRCSR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD



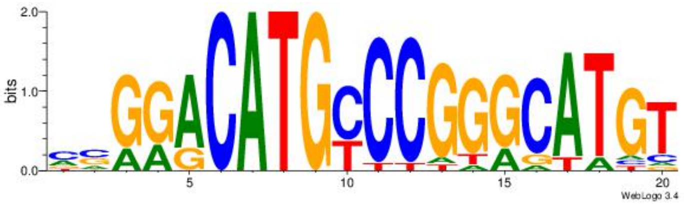
Dataset #: 3
Motif ID: 125
Motif name: TP53
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 2
Number of overlap: 18

Similarity score: 0.105007

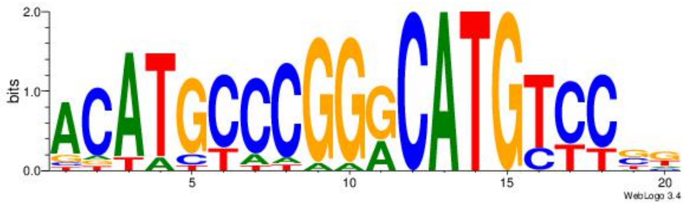
Alignment:

```
ACATGCCCGGKCATGTCCSR
-KBKGCCCKCTHGTGGCHH-
```

Original motif Consensus sequence: MSGGACATGYCCGGGCATGT

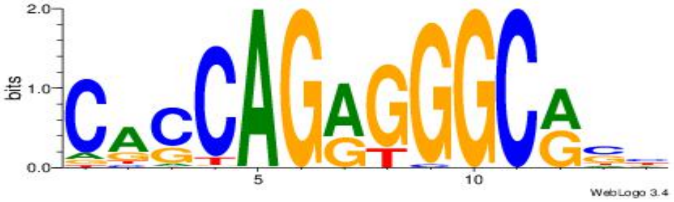


Reverse complement motif Consensus sequence: ACATGCCCGGKCATGTCCSR

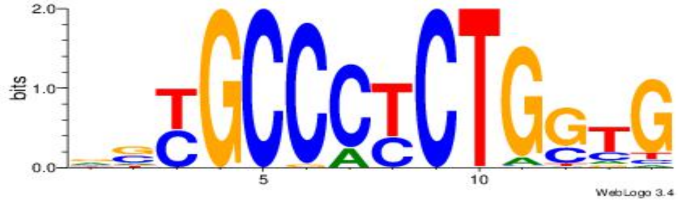


Dataset #: 4 Motif ID: 166 Motif name: CasCAGrGGGCrsy

Original motif Consensus sequence: CACCAGRGGGCRSB



Reverse complement motif Consensus sequence: BSKGCCCKCTGGT



Best Matches for Motif ID 166 (Highest to Lowest)

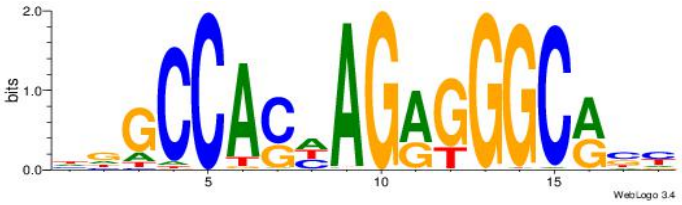
Dataset #:	4
Motif ID:	165
Motif name:	wgGCCAshAGrGGGCrsy
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif

Direction:	Forward
Position number:	5
Number of overlap:	14
Similarity score:	0.015353

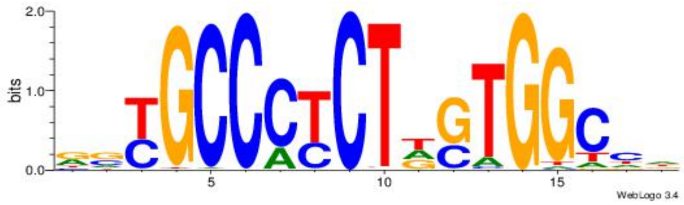
Alignment:

```
HDGCCACHAGRGGGCRBY
----CACCAGRGGGCRSB
```

Original motif Consensus sequence: HDGCCACHAGRGGGCRBY



Reverse complement motif Consensus sequence: KBKGCCCKCTHGTGGCHH

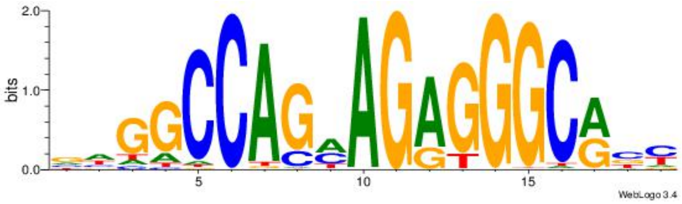


Dataset #:	4
Motif ID:	163
Motif name:	gwGGCCAGmAGAGGGCrby
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	6
Number of overlap:	14
Similarity score:	0.0273616

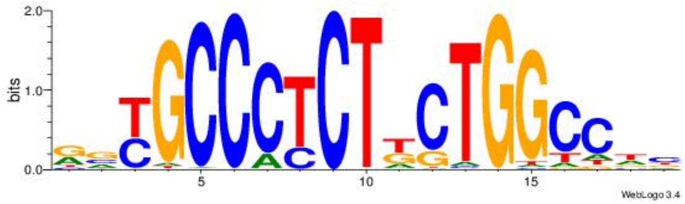
Alignment:

```
VHGGCCAGMAGAGGGCRBY
-----CACCAGRGGGCRSB
```

Original motif Consensus sequence: VHGGCCAGMAGAGGGCRBY



Reverse complement motif Consensus sequence: KBKGCCCTCTYCTGGCCHV

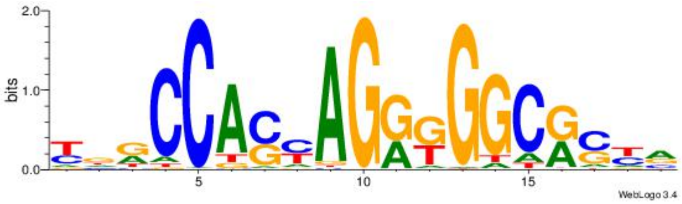


Dataset #:	3
Motif ID:	74
Motif name:	CTCF
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	5
Number of overlap:	14
Similarity score:	0.0281629

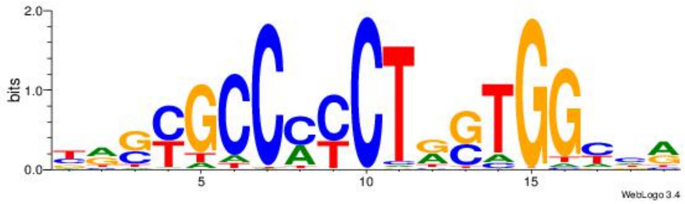
Alignment:

```
YDRCCASYAGRKGGCRSYV
----CACCAGRGGGCRSB-
```

Original motif Consensus sequence: YDRCCASYAGRKGGCRSYV



Reverse complement motif Consensus sequence: BMSMGCCYMCTKSTGGMHM

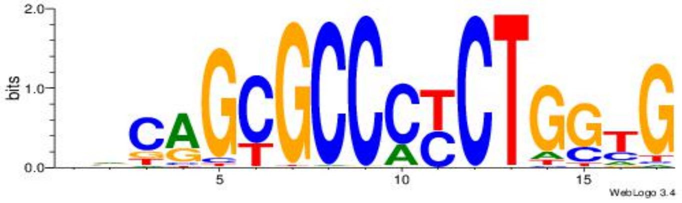


Dataset #:	4
Motif ID:	168
Motif name:	yrcrGYGCCMyCTGGtG
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	14
Similarity score:	0.03743

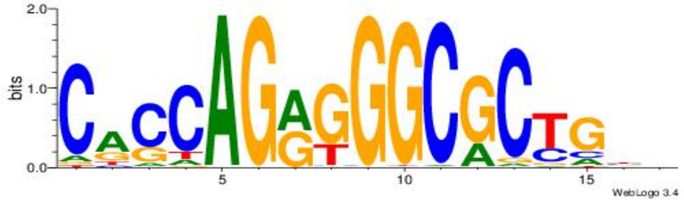
Alignment:

```
CACCAGMGGGCGCTGBD
CACCAGRGGGCRSB---
```

Original motif Consensus sequence: HVCAGCGCCCYCTGGTG



Reverse complement motif Consensus sequence: CACCAGMGGGCGCTGBD



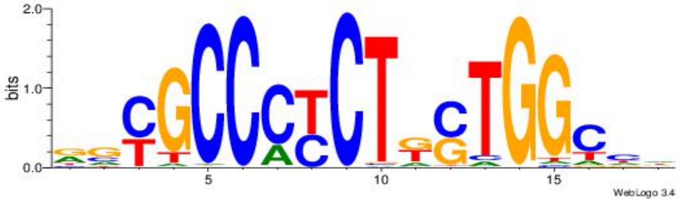
Dataset #:	4
Motif ID:	156
Motif name:	rgyGCCMyCTksTGGccd
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	5

Number of overlap: 14
Similarity score: 0.043415

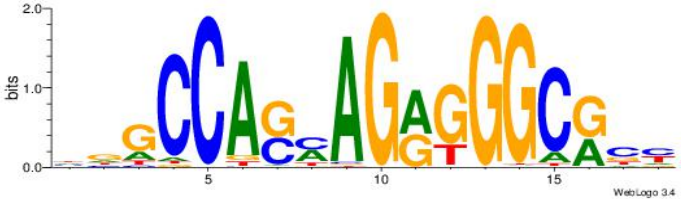
Alignment:

```
RVYGCCCYCTKSTGGCHD
----BSKGCCCKCTGGTG
```

Original motif Consensus sequence: RVYGCCCYCTKSTGGCHD

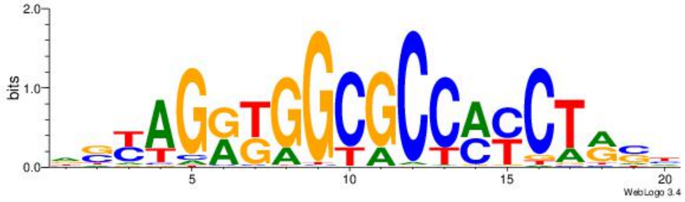


Reverse complement motif Consensus sequence: DDGCCASYAGMGGGCKVM

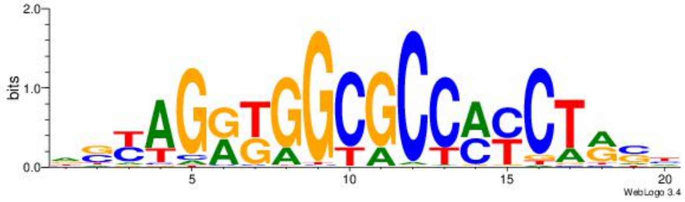


Dataset #: 4 Motif ID: 167 Motif name: rsyAGrkGGCGCCmyCTrsy

Original motif Consensus sequence: DSYAGRKGGCGCCMYCTRSH



Reverse complement motif Consensus sequence: HSKAGKYGGCGCCRMCTMSD



Best Matches for Motif ID 167 (Highest to Lowest)

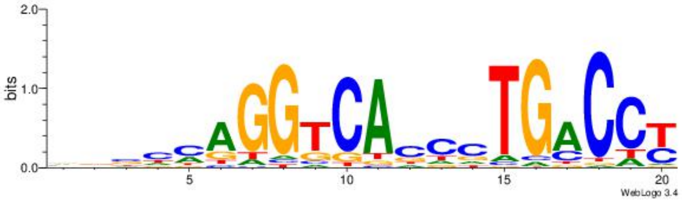
Dataset #: 3
Motif ID: 81
Motif name: ESR1

Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	20
Similarity score:	0.0672057

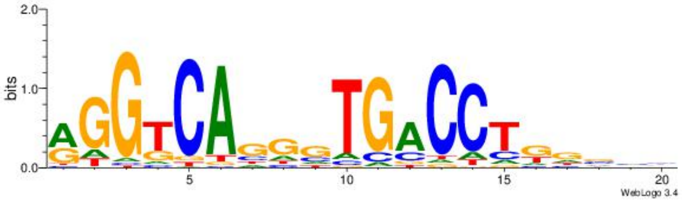
Alignment:

```
VDBHMAGGTCACCCTGACCY
DSYAGRKGGCGCCMYCTRSH
```

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV

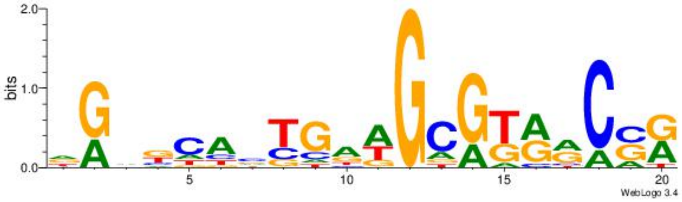


Dataset #:	3
Motif ID:	109
Motif name:	Pax5
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	20
Similarity score:	0.0747165

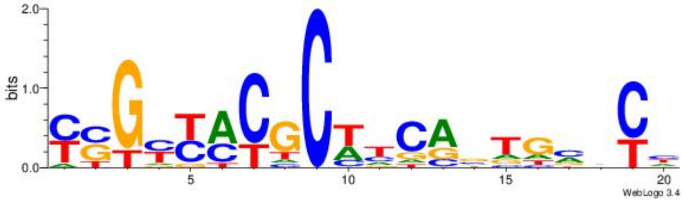
Alignment:

MSGKKRCGCWDCABTGBBCD
HSKAGKYGGCGCCRMCTMSD

Original motif Consensus sequence: DGVBCABTGDWGCGKRRCSR



Reverse complement motif Consensus sequence: MSGKKRCGCWDCABTGBBCD



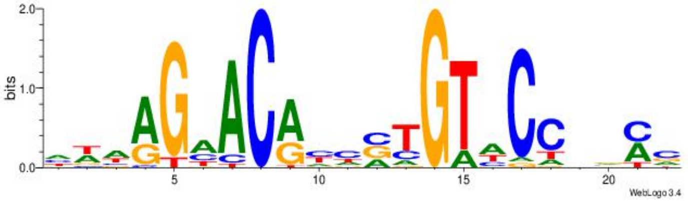
Dataset #:	3
Motif ID:	70
Motif name:	Ar
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	4
Number of overlap:	19
Similarity score:	0.57268

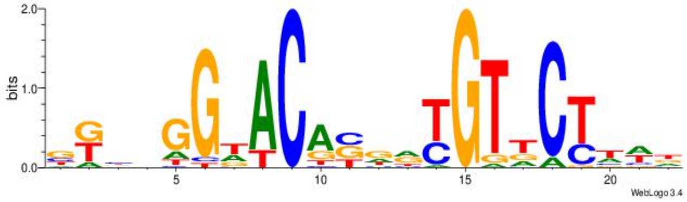
Alignment:

HWDAGHACRHHVTGTHCCHVMV-
---DSYAGRKGGCGCCMYCTRSH

Original motif Consensus sequence: HWDAGHACRHHVTGTHCCHVMV

Reverse complement motif Consensus sequence: VRVDGGHACAVDDKGTHCTDWH



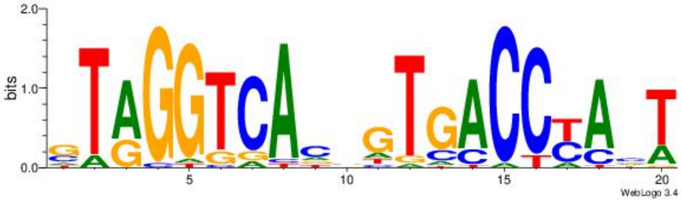


Dataset #:	3
Motif ID:	111
Motif name:	PPARG
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	2
Number of overlap:	19
Similarity score:	0.57362

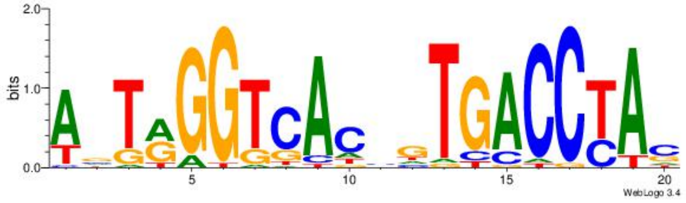
Alignment:

```
-ABTMGGTCACBGTGACCTAS
DSYAGRKGGCGCCMYCTRSH-
```

Original motif Consensus sequence: STAGGTCACBGTGACCYABT



Reverse complement motif Consensus sequence: ABTMGGTCACBGTGACCTAS



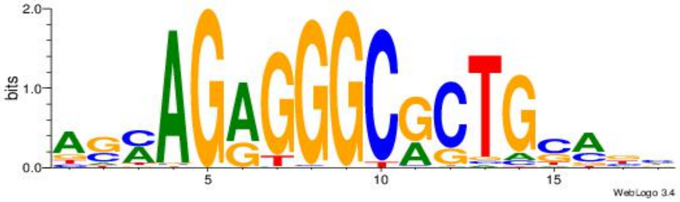
Dataset #:	4

Motif ID:	149
Motif name:	asmAGRGGGCrCTGsmkc
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	18
Similarity score:	1.03519

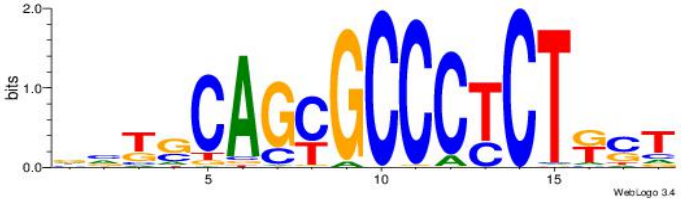
Alignment:

```
ASMAGAGGGCRCTGSABH--
DSYAGRKGGCGCCMYCTRSH
```

Original motif Consensus sequence: ASMAGAGGGCRCTGSABH

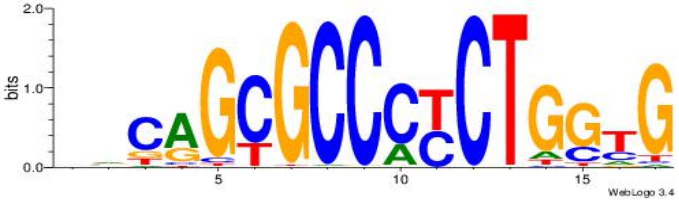


Reverse complement motif Consensus sequence: DBTSCAGMGCCCTCTRST

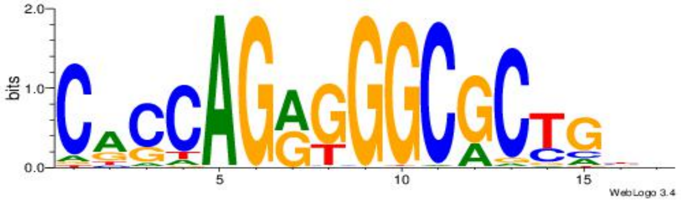


Dataset #: 4 Motif ID: 168 Motif name: yrcrGYGCCMyCTGGtG

Original motif Consensus sequence: HVCAGCGCCCYCTGGTG



Reverse complement motif Consensus sequence: CACCAGMGGGCGCTGBD



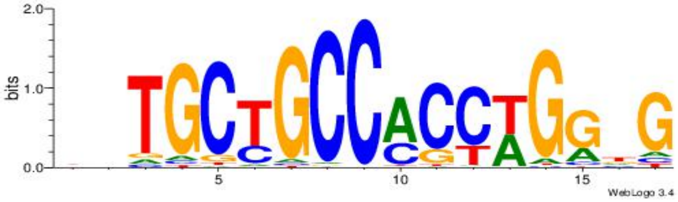
Best Matches for Motif ID 168 (Highest to Lowest)

Dataset #:	4
Motif ID:	169
Motif name:	yvTGCyGCCmCCwGgtG
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	17
Similarity score:	0.0386724

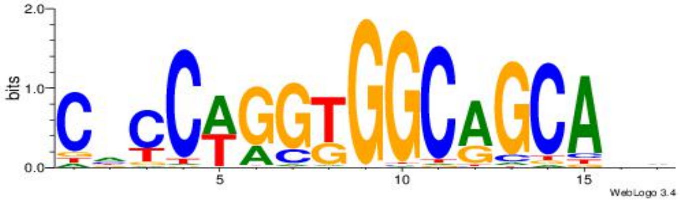
Alignment:

```
BVTGCTGCCACCWGGDG
HVCAGCGCCCYCTGGTG
```

Original motif Consensus sequence: BVTGCTGCCACCWGGDG



Reverse complement motif Consensus sequence: CDCCWGGTGGCAGCAVV



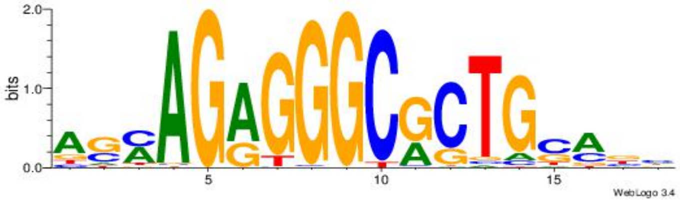
Dataset #:	4
Motif ID:	149
Motif name:	asmAGRGGGCrCTGsmkc
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement

Direction: Forward
Position number: 2
Number of overlap: 17
Similarity score: 0.0542719

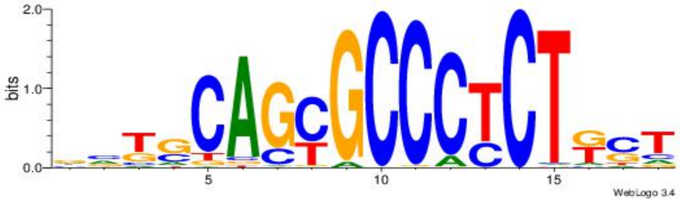
Alignment:

```
DBTSCAGMGCCCTCTRST
-CACCAGMGGGCGCTGBD
```

Original motif   Consensus sequence: ASMAGAGGGCRCTGSABH



Reverse complement motif   Consensus sequence: DBTSCAGMGCCCTCTRST

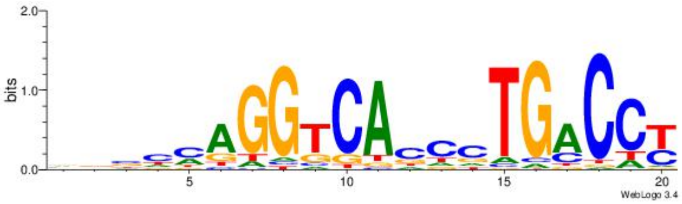


Dataset #: 3
Motif ID: 81
Motif name: ESR1
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2
Number of overlap: 17
Similarity score: 0.0695994

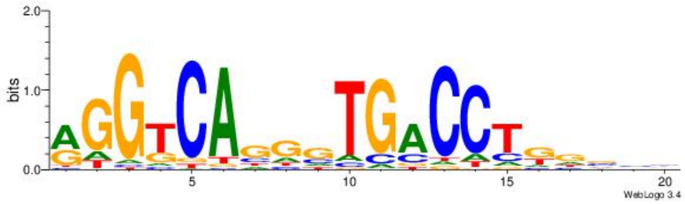
Alignment:

```
VDBHMAGGTCACCCTGACCY
--HVCAGCGCCCYCTGGTG-
```

Original motif   Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif   Consensus sequence: MGGTCAGGGTGACCTRDBHV

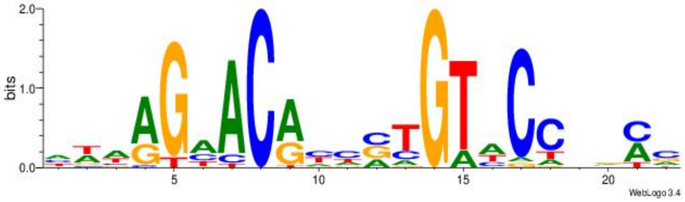


Dataset #:	3
Motif ID:	70
Motif name:	Ar
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	17
Similarity score:	0.074879

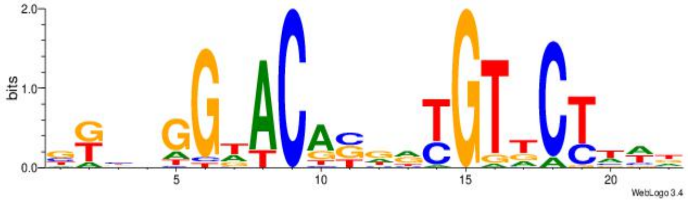
Alignment:

```
HWDAGHACRHHVTGTHCCHVMV
HVCAGCGCCCYCTGGTG-----
```

Original motif   Consensus sequence: HWDAGHACRHHVTGTHCCHVMV



Reverse complement motif   Consensus sequence: VRVDGGHACAVDDKGTHCTDWH

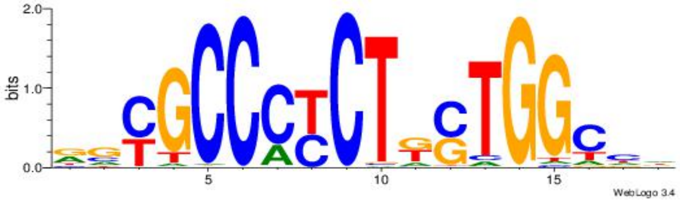


Dataset #: 4
Motif ID: 156
Motif name: rgyGCCMyCTksTGGccd
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2
Number of overlap: 17
Similarity score: 0.076934

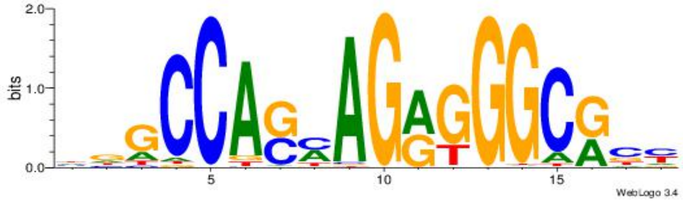
Alignment:

```
RVYGCCCYCTKSTGGCHD
HVCAGCGCCCYCTGGTG-
```

Original motif Consensus sequence: RVYGCCCYCTKSTGGCHD



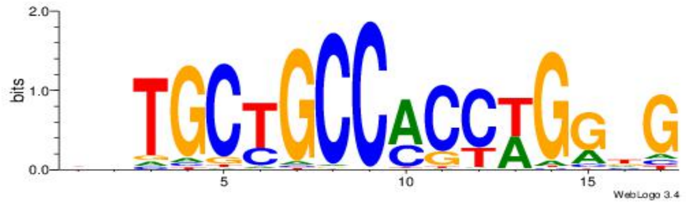
Reverse complement motif Consensus sequence: DDGCCASYAGMGGGCKVM

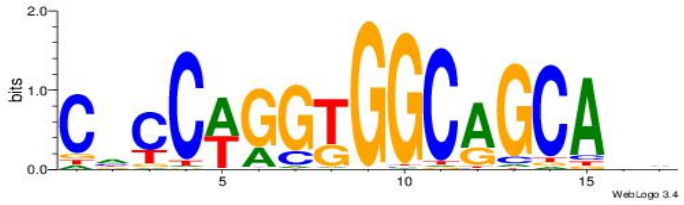


Dataset #: 4 Motif ID: 169 Motif name: yvTGCyGCCmCCwGgtG

Original motif Consensus sequence: BVTGCTGCCACCWGGDG

Reverse complement motif Consensus sequence: CDCCWGGTGGCAGCAVV





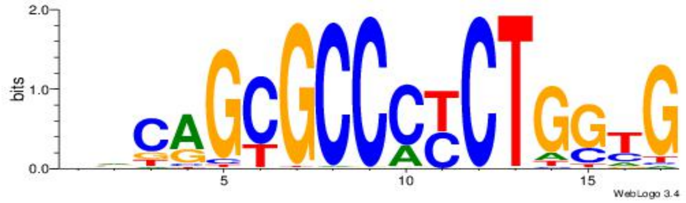
Best Matches for Motif ID 169 (Highest to Lowest)

Dataset #:	4
Motif ID:	168
Motif name:	yrcrGYGCCMyCTGGtG
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	17
Similarity score:	0.0263455

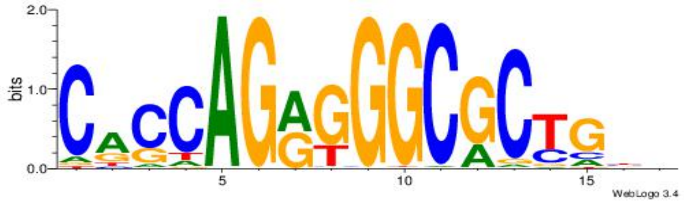
Alignment:

```
HVCAGCGCCCYCTGGTG
BVTGCTGCCACCWGGDG
```

Original motif   Consensus sequence: HVCAGCGCCCYCTGGTG



Reverse complement motif   Consensus sequence: CACCAGMGGGCGCTGBD



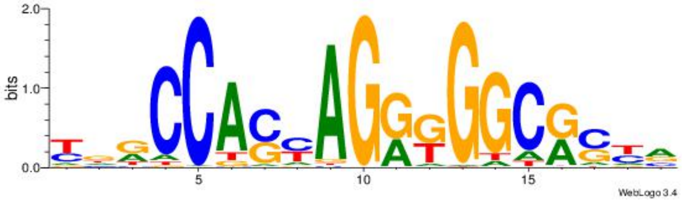
Dataset #:	3
Motif ID:	74
Motif name:	CTCF
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	2
Number of overlap:	17
Similarity score:	0.0578732

Alignment:

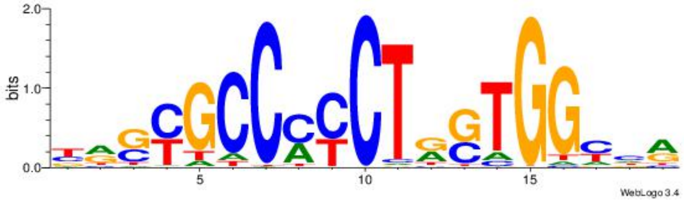
`BMSMGCCYMCTKSTGGMHM`

`-BVTGCTGCCACCWGGDG-`

Original motif Consensus sequence: YDRCCASYAGRKGGCRSYV



Reverse complement motif Consensus sequence: BMSMGCCYMCTKSTGGMHM



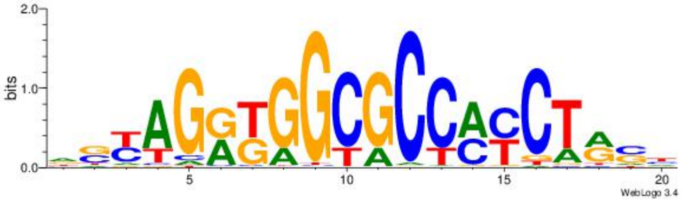
Dataset #:	4
Motif ID:	167
Motif name:	rsyAGrkGGCGCCmyCTrsy
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	3

Number of overlap: 17
Similarity score: 0.0596753

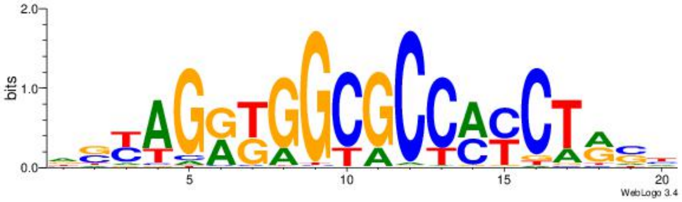
Alignment:

```
HSKAGKYGGCGCCRMCTMSD
--BVTGCTGCCACCWGGDG-
```

Original motif Consensus sequence: DSYAGRKGGCGCCMYCTRSH



Reverse complement motif Consensus sequence: HSKAGKYGGCGCCRMCTMSD

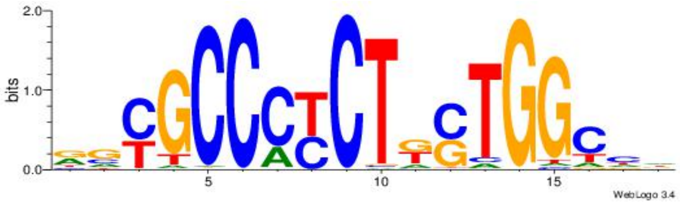


Dataset #: 4
Motif ID: 156
Motif name: rgyGCCMyCTksTGGccd
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 17
Similarity score: 0.0597938

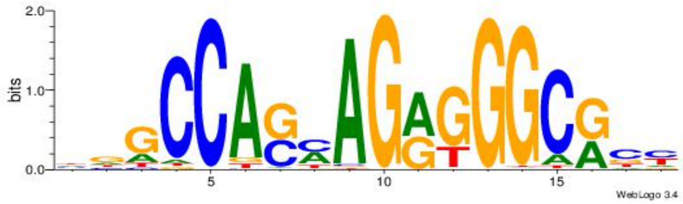
Alignment:

```
RVYGCCCYCTKSTGGCHD
BVTGCTGCCACCWGGDG-
```

Original motif   Consensus sequence: RVYGCCCYCTKSTGGCHD



Reverse complement motif   Consensus sequence:
DDGCCASYAGMGGGCKVM

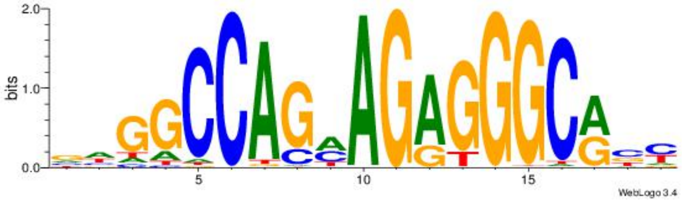


Dataset #:	4
Motif ID:	163
Motif name:	gwGGCCAGmAGAGGGCrby
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	17
Similarity score:	0.0605716

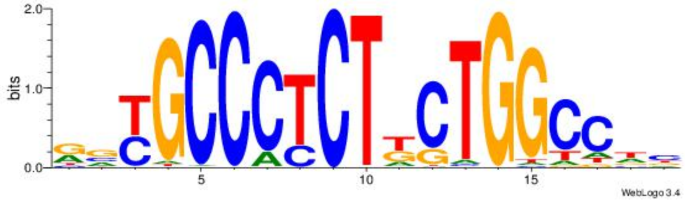
Alignment:

```
VHGGCCAGMAGAGGGCRBY
CDCCWGGTGGCAGCAVV--
```

Original motif   Consensus sequence: VHGGCCAGMAGAGGGCRBY

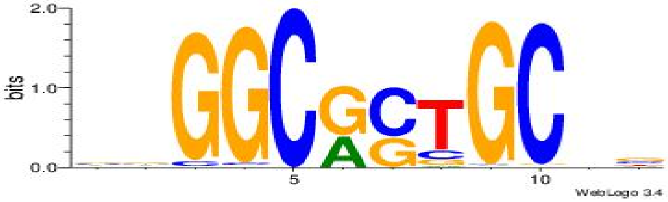


Reverse complement motif   Consensus sequence:
KBKGCCCTCTYCTGGCCHV

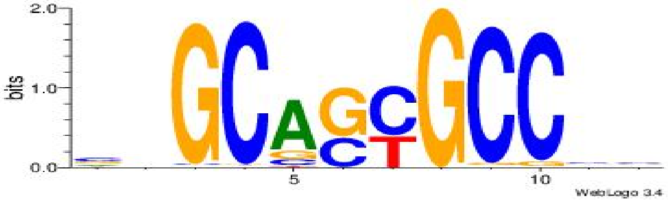


Dataset #: 4 **Motif ID: 170** **Motif name: ssGGCrsTGCrs**

Original motif Consensus sequence: VVGGCRSTGCVB



Reverse complement motif Consensus sequence: BVGCASMGCCVV



Best Matches for Motif ID 170 (Highest to Lowest)

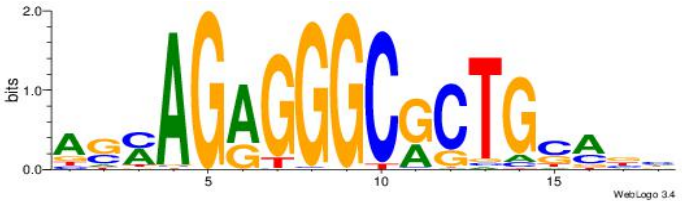
Dataset #:	4
Motif ID:	149
Motif name:	asmAGRGGGCrCTGsmkc
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2
Number of overlap:	12
Similarity score:	0.038906

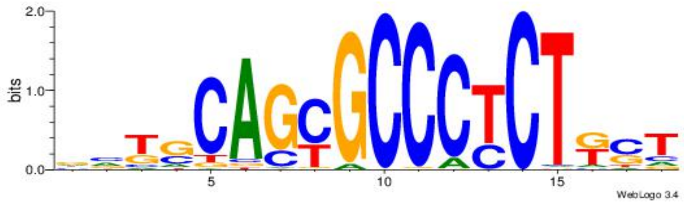
Alignment:

```
ASMAGAGGGCRCTGSABH
-----VVGGCRSTGCVB-
```

Original motif Consensus sequence: ASMAGAGGGCRCTGSABH

Reverse complement motif Consensus sequence: DBTSCAGMGCCCTCTRST



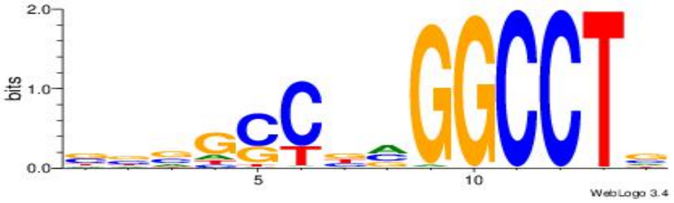


Dataset #:	3
Motif ID:	130
Motif name:	Zfx
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	12
Similarity score:	0.0768177

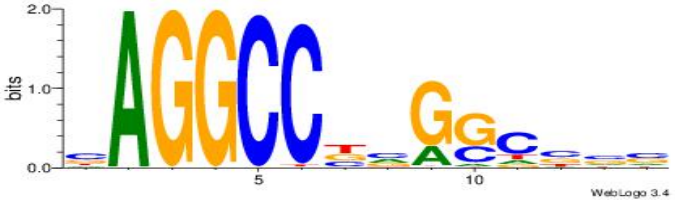
Alignment:

```
BBVGCCBVGGCCTV
BVGCASMGCCVV--
```

Original motif Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif Consensus sequence: VAGGCCBBGGCV



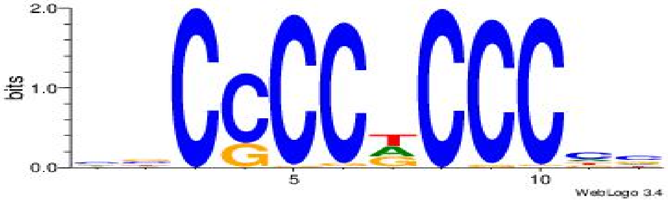
Dataset #:	4
Motif ID:	155

Motif name:	csCSCCdCCCcs
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	12
Similarity score:	0.0798188

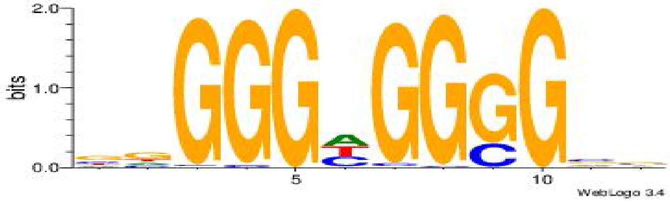
Alignment:

```
VBCCCCDCCCHV
BVGCASMGCCVV
```

Original motif Consensus sequence: VBCCCCDCCCHV



Reverse complement motif Consensus sequence: VDGGGDGGGGBV

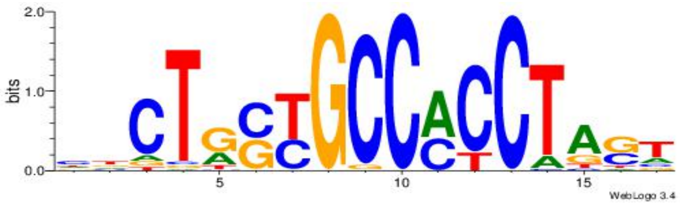


Dataset #:	4
Motif ID:	144
Motif name:	ctCTrsyGCCmCCTast
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	6
Number of overlap:	12
Similarity score:	0.0800293

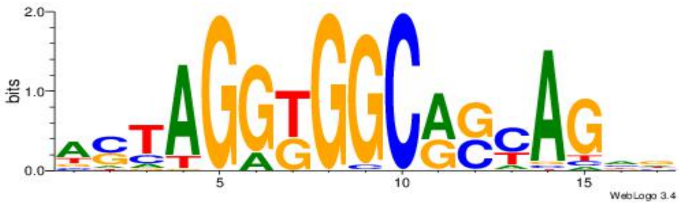
Alignment:

```
ASTAGGYGGCMSCAGDD
VVGGCRSTGCVB-----
```

Original motif Consensus sequence: HDCTGSYGCCMCCTAST



Reverse complement motif Consensus sequence: ASTAGGYGGCMSCAGDD



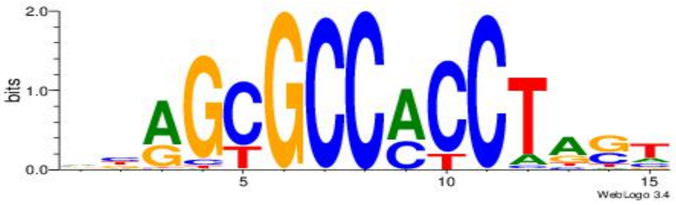
Dataset #:	4
Motif ID:	146
Motif name:	myrGYGCCmCCTast
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2
Number of overlap:	12
Similarity score:	0.0817044

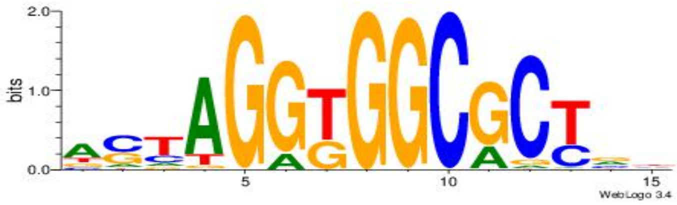
Alignment:

```
VBAGCGCCMCCTAST
--BVGCASMGCCVV-
```

Original motif Consensus sequence: VBAGCGCCMCCTAST

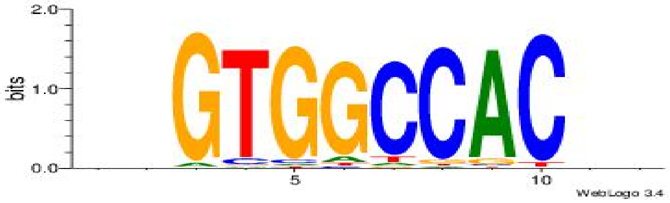
Reverse complement motif Consensus sequence: ASTAGGYGGCGCT



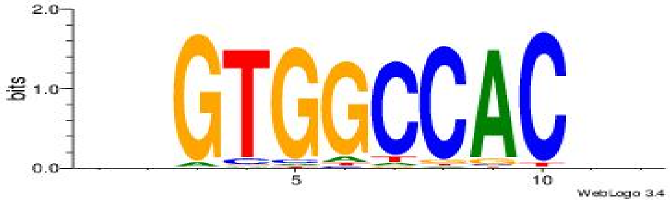


Dataset #: 4 **Motif ID: 171** **Motif name: ysGTGGCCACsr**

Original motif Consensus sequence: BVGTGGCCACBV



Reverse complement motif Consensus sequence: VBGTGGCCACVB



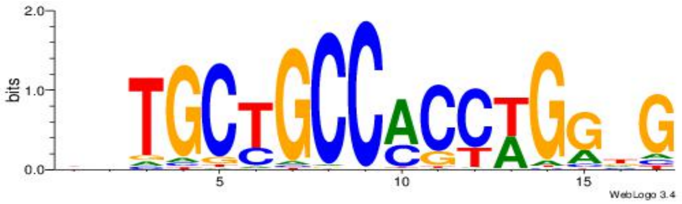
Best Matches for Motif ID 171 (Highest to Lowest)

Dataset #:	4
Motif ID:	169
Motif name:	yvTGCyGCCmCCwGgtG
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2
Number of overlap:	12
Similarity score:	0.0325062

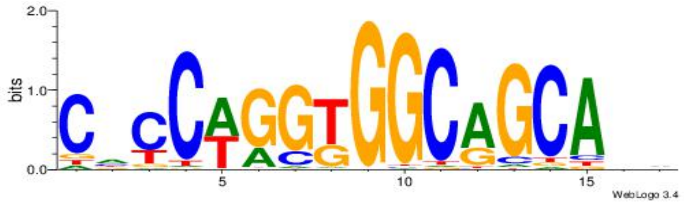
Alignment:

```
BVTGCTGCCACCWGGDG
----VBGTGGCCACVB-
```

Original motif Consensus sequence: BVTGCTGCCACCWGGDG



Reverse complement motif Consensus sequence: CDCCWGGTGGCAGCAVV

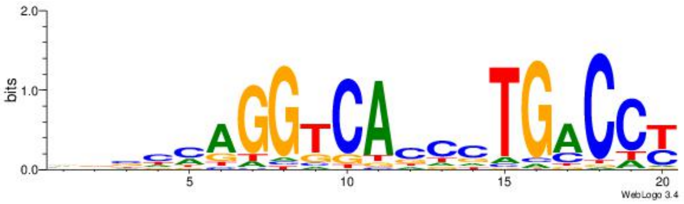


Dataset #:	3
Motif ID:	81
Motif name:	ESR1
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	3
Number of overlap:	12
Similarity score:	0.0344223

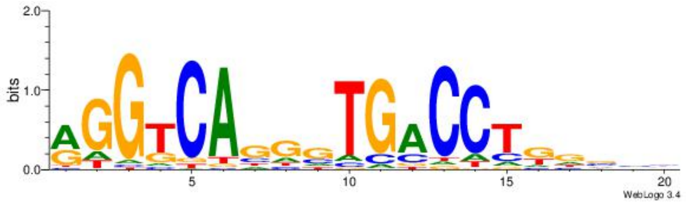
Alignment:

```
MGGTCAGGGTGACCTRDBHV
------VBGTGGCCACVB--
```

Original motif Consensus sequence: VDBHMAGGTCACCCTGACCY



Reverse complement motif Consensus sequence: MGGTCAGGGTGACCTRDBHV

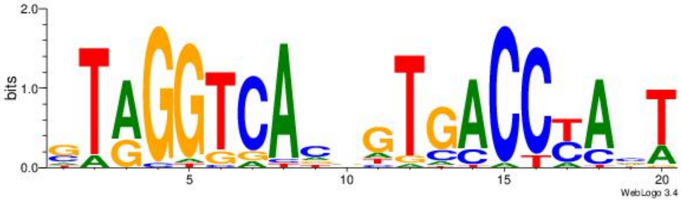


Dataset #:	3
Motif ID:	111
Motif name:	PPARG
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	12
Similarity score:	0.0381861

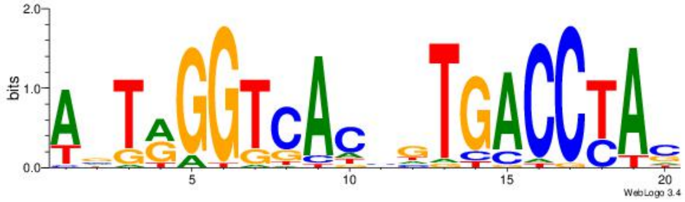
Alignment:

```
ABTMGGTCACBGTGACCTAS
--------BVGTGGCCACBV
```

Original motif Consensus sequence: STAGGTCACBGTGACCYABT



Reverse complement motif Consensus sequence: ABTMGGTCACBGTGACCTAS

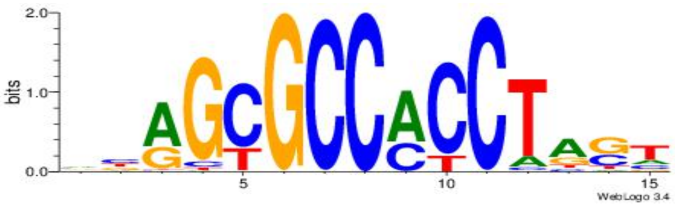


Dataset #:	4
Motif ID:	146
Motif name:	myrGYGCCmCCTast
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1

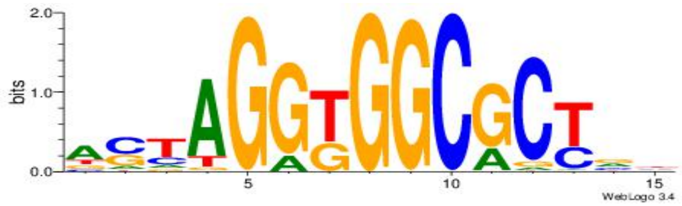
Number of overlap: 12
Similarity score: 0.0484805

Alignment:
ASTAGGYGGCGCTBB
BVGTGGCCACBV---

Original motif Consensus sequence: VBAGCGCCMCCTAST



Reverse complement motif Consensus sequence: ASTAGGYGGCGCT

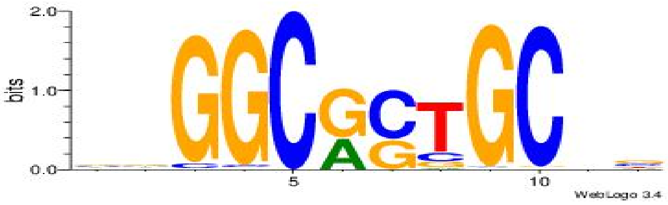


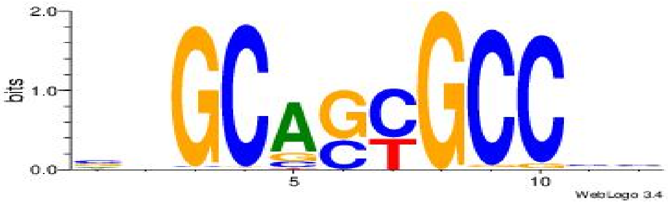
Dataset #: 4
Motif ID: 170
Motif name: ssGGCrsTGCrs
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 12
Similarity score: 0.0498451

Alignment:
BVGCASMGCCVV
BVGTGGCCACBV

Original motif Consensus sequence: VVGGCRSTGCVB

Reverse complement motif Consensus sequence: BVGCASMGCCVV





Results created by MOTIFSIM on 06-18-2018 16:50:38
Runtime: 1017.73 seconds

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