



MOTIFSIM - MOTIF SIMilarity Detection Tool

Version 2.1

INPUT

Input Parameters

Number of files:	1
Number of top significant motifs:	10
Number of best matches:	5
Similarity cutoff >=	0.75
Matching motif database:	UniProbe Mus Musculus
Phylogenetic tree:	Yes
Combined similar motifs:	Yes
Output file type:	All
Output file format:	All

Input files and motif counts

File name	Count of motifs	Dataset number
CisFinder_DM721_Cluster.txt	153	1

RESULTS

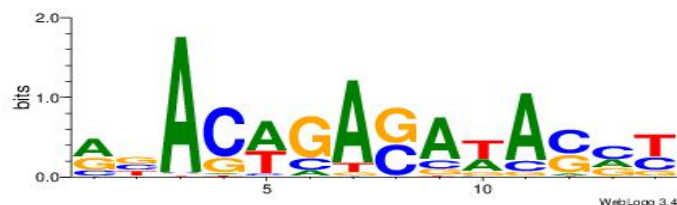
Top 10 Significant Motifs - Global Matching (Highest to Lowest)

There is no global matching for 1 motif file.

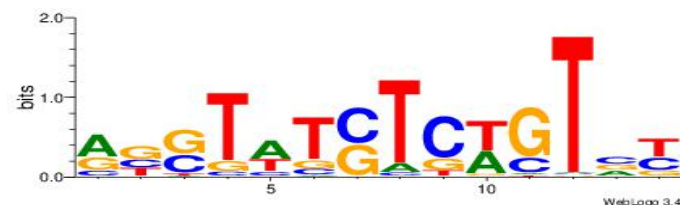
Significant Motifs - Global and Local Matching (Highest to Lowest)

Dataset #: 1 **Motif ID: 108** **Motif name: C108**

Original motif Consensus sequence: RBACWGASAWASVY



Reverse complement motif Consensus sequence: MVSTWTSTCWGTR



Best Matches for Significant Motif ID 108 (Highest to Lowest)

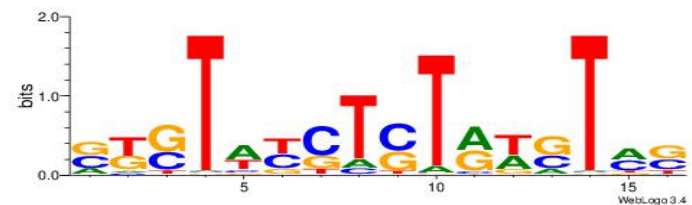
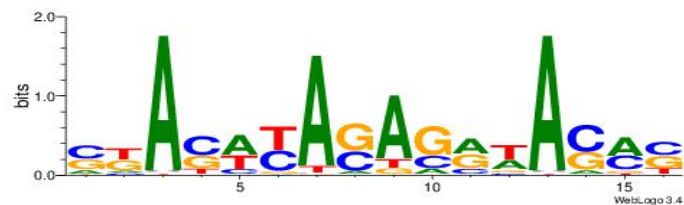
Dataset #:	1
Motif ID:	125
Motif name:	C125
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	14
Similarity score:	3.79502e-05

Alignment:

SKASWYASAGRWASMS
--RBACWGASAWASVY

Original motif Consensus sequence: SKASWYASAGRWASMS

Reverse complement motif Consensus sequence:
SYSTWKCTSTMWSTRS



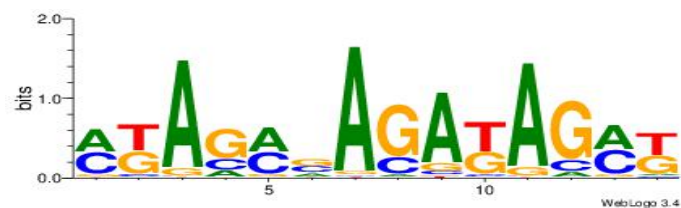
Dataset #: 1
 Motif ID: 21
 Motif name: C021
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0.00124361

Alignment:

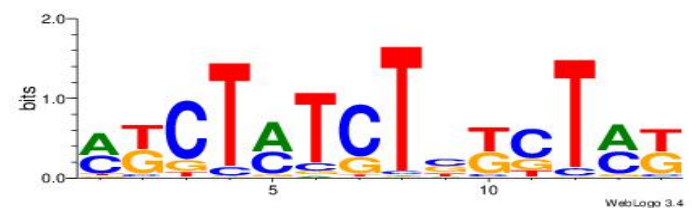
MKAGMVAGAKAGMK

RBACWGASAWASVY

Original motif Consensus sequence: MKAGMVAGAKAGMK



Reverse complement motif Consensus sequence: RYCTRTCTVYCTRY



Dataset #: 1
 Motif ID: 53

Motif name:	C053
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:	0.00887812

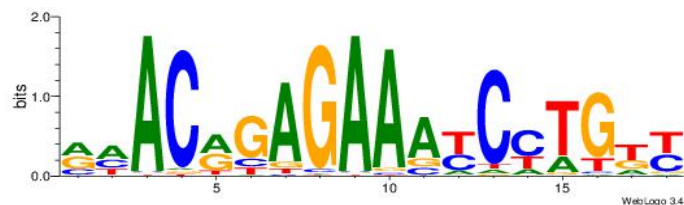
Alignment:

```

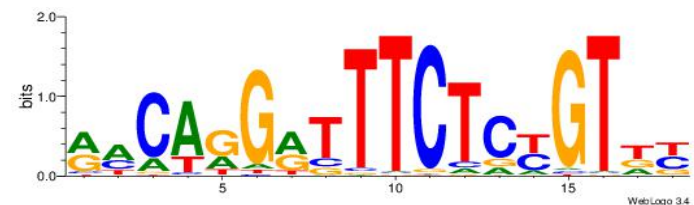
RMACRGAGAAAYCCTGKY
RBACWGASAWASVY----

```

Original motif Consensus sequence: RMACRGAGAAAYCCTGKY



Reverse complement motif Consensus sequence: MRCAGGMTTCTCKGTYK

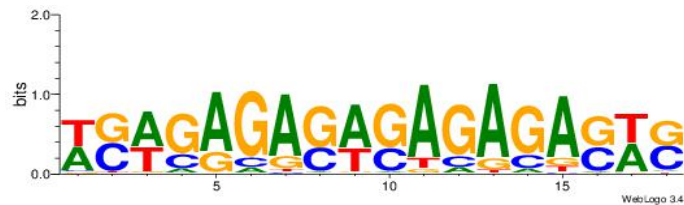


Dataset #:	1
Motif ID:	17
Motif name:	C017
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	5
Number of overlap:	14
Similarity score:	0.0104617

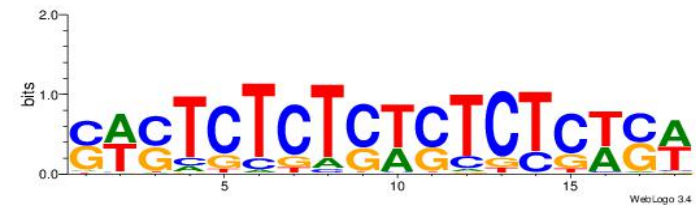
Alignment:

SWSTCTCTSWSTCTCWSW
MVSTWTSTCWGTBK----

Original motif Consensus sequence: WSWGAGASWSAGAGASWS



Reverse complement motif Consensus sequence:
SWSTCTCTSWSTCTCWSW



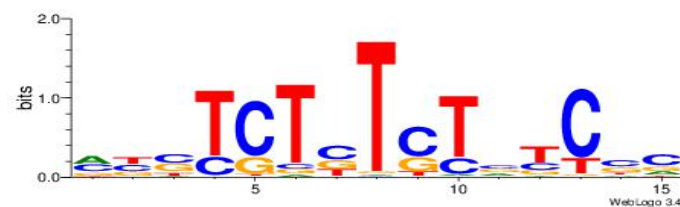
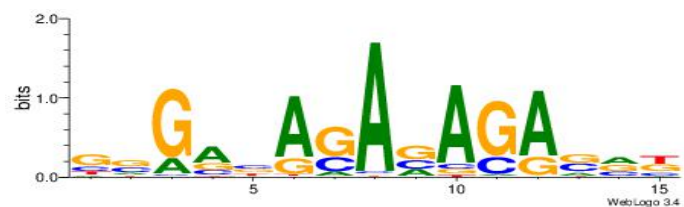
Dataset #:	1
Motif ID:	70
Motif name:	C070
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	14
Similarity score:	0.0119575

Alignment:

GVGABAGAVAGASVK
-RBACWGASAWASVY

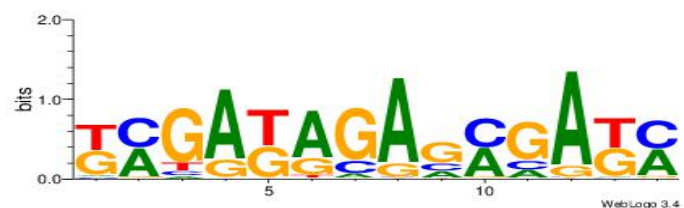
Original motif Consensus sequence: GVGABAGAVAGASVK

Reverse complement motif Consensus sequence: RBSTCTVTCTBTCV

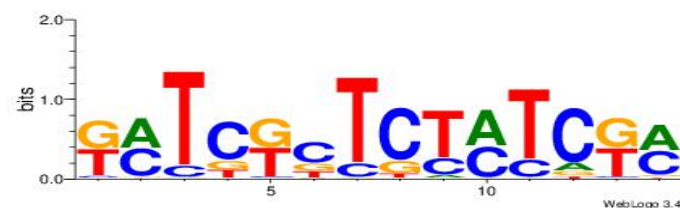


Dataset #: 1 Motif ID: 25 Motif name: C025

Original motif Consensus sequence: KMGAKAGAGMGAKM



Reverse complement motif Consensus sequence: RRTCRCCTCTCTCR

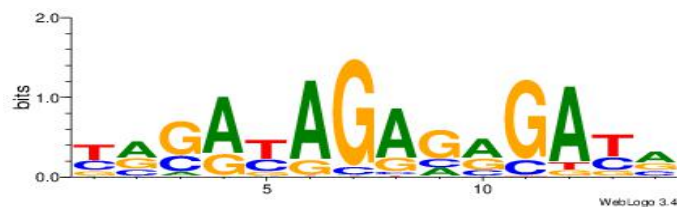


Best Matches for Significant Motif ID 25 (Highest to Lowest)

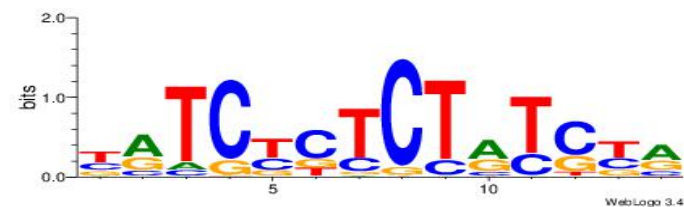
Dataset #:	1
Motif ID:	78
Motif name:	C078
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	14
Similarity score:	0.00248665

Alignment:
 YRGAYAGAGRGAYR
 KMGAKAGAGMGAKM

Original motif Consensus sequence: YRGAYAGAGRGAYR



Reverse complement motif Consensus sequence: KMTCKCTCTMTCK

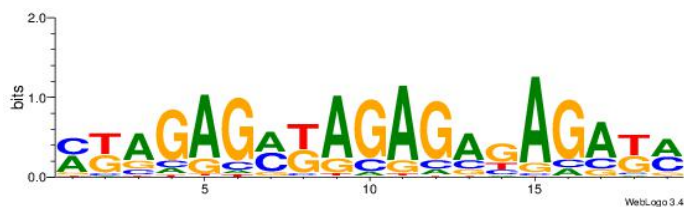


Dataset #: 1
 Motif ID: 12
 Motif name: C012
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0.00375955

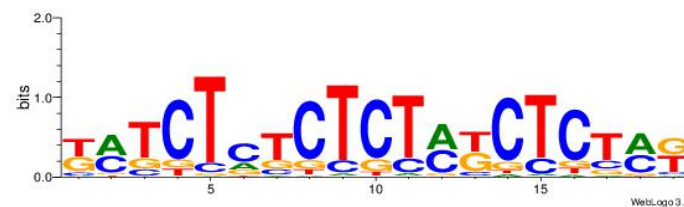
Alignment:

```
MKAGAGMKAGAGAGAGAKM
-----KMGAKAGAGMGAKM
```

Original motif Consensus sequence: MKAGAGMKAGAGAGAGAKM



Reverse complement motif Consensus sequence: YRTCTCTCTRYCTCTRR

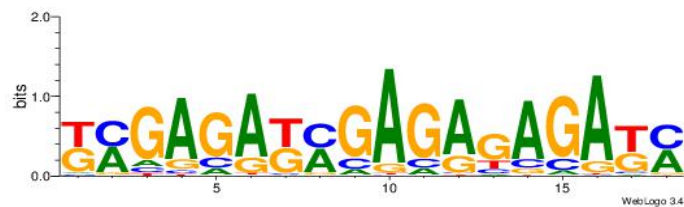


Dataset #: 1
 Motif ID: 11
 Motif name: C011
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 5
 Number of overlap: 14
 Similarity score: 0.00885823

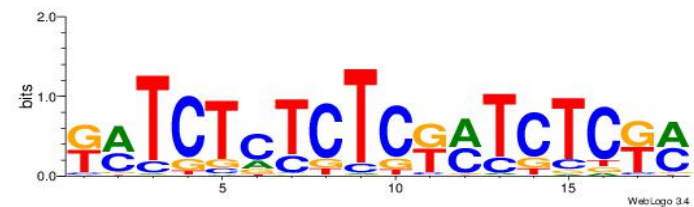
Alignment:

KMGAGAKMGAGAGAGAKM
 KMGAKAGAGMGAKM-----

Original motif Consensus sequence: KMGAGAKMGAGAGAGAKM



Reverse complement motif Consensus sequence: RRTCTCTCTCRRTCTCRR

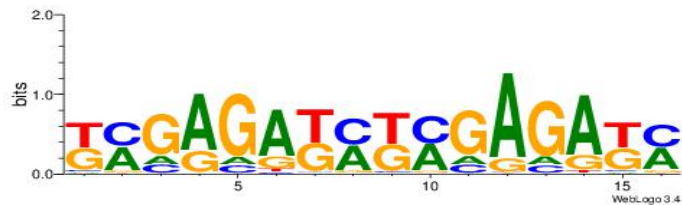


Dataset #: 1
 Motif ID: 26
 Motif name: C026
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3

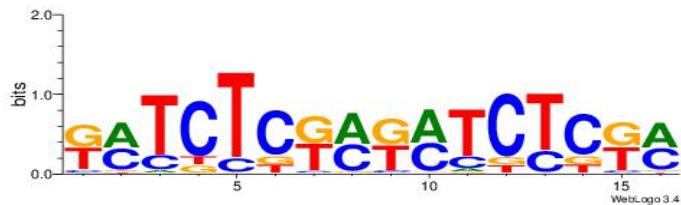
Number of overlap: 14
Similarity score: 0.0116747

Alignment:
KMGAGAKMKMGAGAKM
KMGAKAGAGMGAKM--

Original motif Consensus sequence: KMGAGAKMKMGAGAKM



Reverse complement motif Consensus sequence: RRTCTCRRRTCTCRR

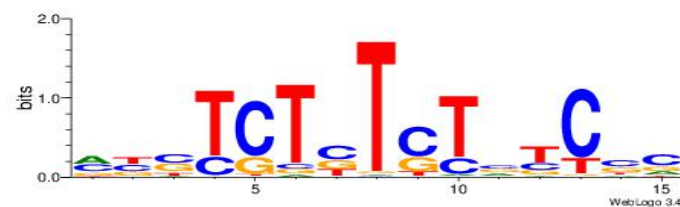
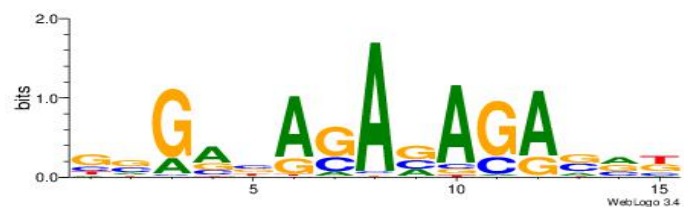


Dataset #: 1
Motif ID: 70
Motif name: C070
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2
Number of overlap: 14
Similarity score: 0.0139232

Alignment:
GVGABAGAVAGASVK
KMGAKAGAGMGAKM-

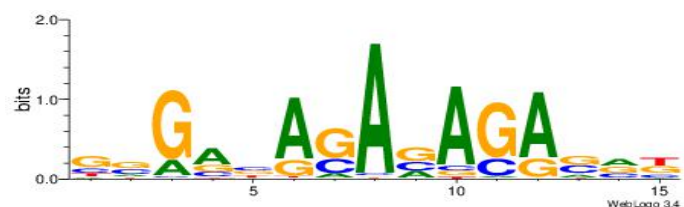
Original motif Consensus sequence: GVGABAGAVAGASVK

Reverse complement motif Consensus sequence: RBSTCTVTCTBTCV

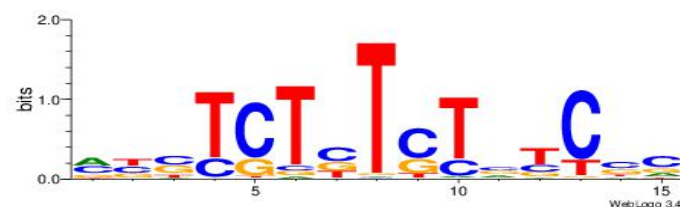


Dataset #: 1 **Motif ID: 70** **Motif name: C070**

Original motif Consensus sequence: GVGABAGAVAGASVK



Reverse complement motif Consensus sequence: RBSTCTVTCTBTCV



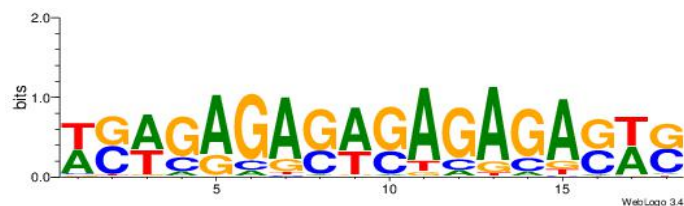
Best Matches for Significant Motif ID 70 (Highest to Lowest)

Dataset #:	1
Motif ID:	17
Motif name:	C017
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	4
Number of overlap:	15
Similarity score:	0.00174543

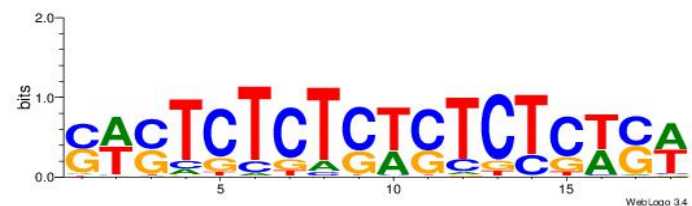
Alignment:

```
WSWGAGASWSAGAGASWS
---GVGABAGAVAGASVK
```

Original motif Consensus sequence: WSWGAGASWSAGAGASWS



Reverse complement motif Consensus sequence: SWSTCTCTSWSTCTCWSW

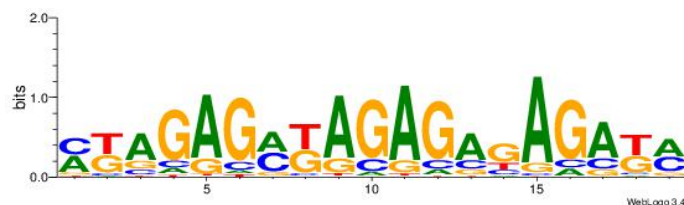


Dataset #: 1
 Motif ID: 12
 Motif name: C012
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 15
 Similarity score: 0.0027757

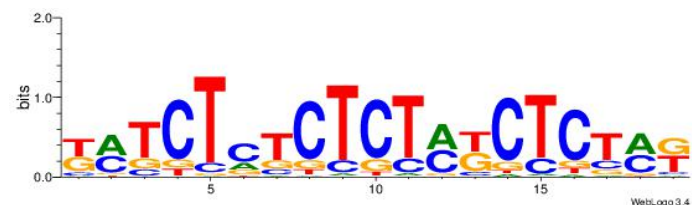
Alignment:

MKAGAGMKAGAGAGAGAKM
 ---GVGABAGAVAGASVK-

Original motif Consensus sequence: MKAGAGMKAGAGAGAGAKM



Reverse complement motif Consensus sequence: YRTCTCTCTRYCTCTRR

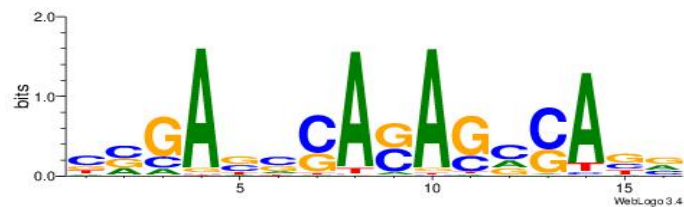


Dataset #: 1
 Motif ID: 28
 Motif name: C028
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 15
 Similarity score: 0.00931002

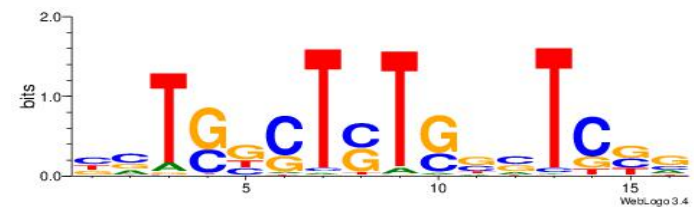
Alignment:

BVGASSCASAGVSABV
 GVGABAGAVAGASVK-

Original motif Consensus sequence: BVGASSCASAGVSABV



Reverse complement motif Consensus sequence: VBTSVCTSTGSSTCVB

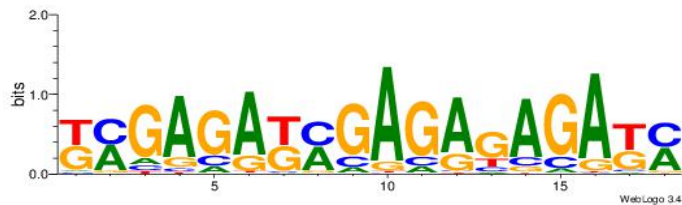


Dataset #: 1
 Motif ID: 11
 Motif name: C011
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3

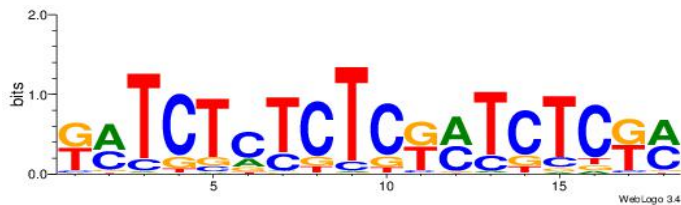
Number of overlap: 15
Similarity score: 0.0117141

Alignment:
KMGAGAKMGAGAGAGAKM
--GVGABAGAVAGASVK--

Original motif Consensus sequence: KMGAGAKMGAGAGAGAKM



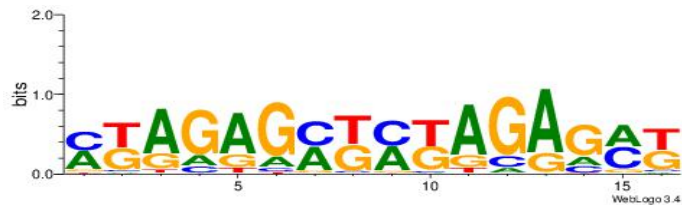
Reverse complement motif Consensus sequence: RRTCTCTCTCRRTCTCRR



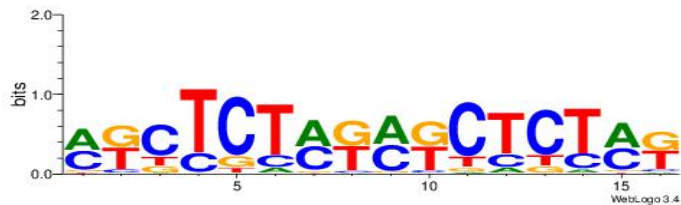
Dataset #: 1
Motif ID: 55
Motif name: C055
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 2
Number of overlap: 15
Similarity score: 0.0176331

Alignment:
MKAGAGMKMKAGAGMK
-GVGABAGAVAGASVK

Original motif Consensus sequence: MKAGAGMKMKAGAGMK



Reverse complement motif Consensus sequence: RYCTCTRRRRCTCTRR

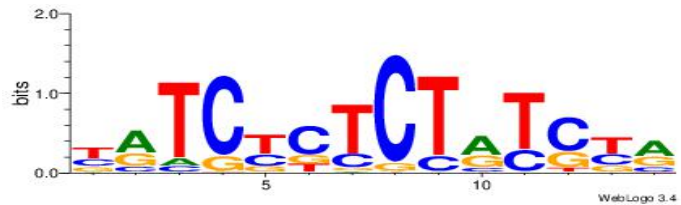


Dataset #: 1 Motif ID: 78 Motif name: C078

Original motif Consensus sequence: YRGAYAGAGRGAYR



Reverse complement motif Consensus sequence: KMTCKCTCTMTCK



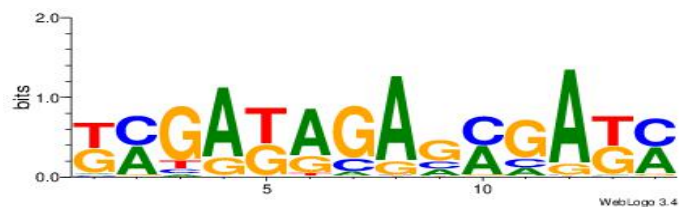
Best Matches for Significant Motif ID 78 (Highest to Lowest)

Dataset #:	1
Motif ID:	25
Motif name:	C025
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

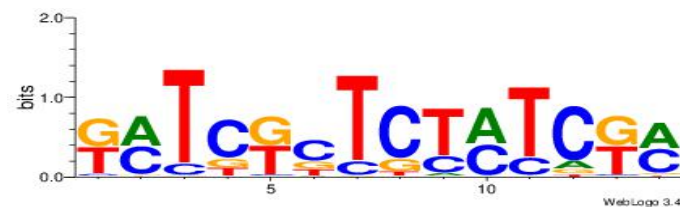
Alignment:

KMGAKAGAGMGAKM
YRGAYAGAGRGAYR

Original motif Consensus sequence: KMGAKAGAGMGAKM



Reverse complement motif Consensus sequence: RRTCRCCTCTCTCR



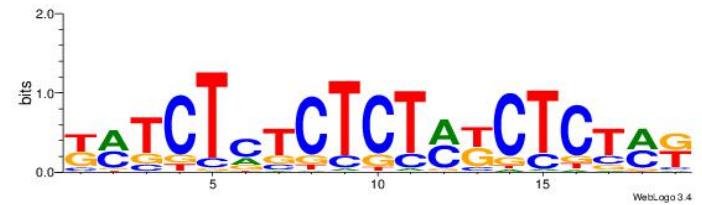
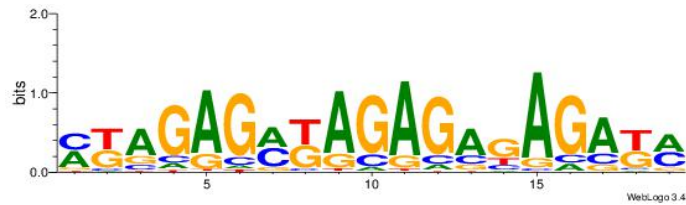
Dataset #:	1
Motif ID:	12
Motif name:	C012
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	3
Number of overlap:	14
Similarity score:	0.00828206

Alignment:

YRTCTCTCTCTRYCTCTRR
--KMTCKCTCTMTCKM---

Original motif Consensus sequence: MKAGAGMKAGAGAGAGAKM

Reverse complement motif Consensus sequence:
YRTCTCTCTCTRYCTCTRR



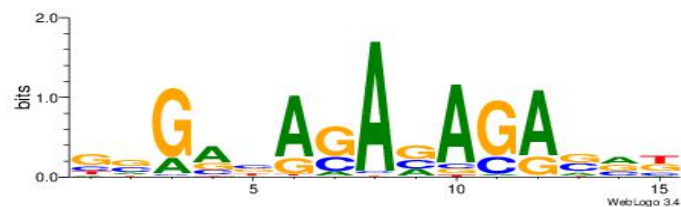
Dataset #: 1
 Motif ID: 70
 Motif name: C070
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 14
 Similarity score: 0.00930595

Alignment:

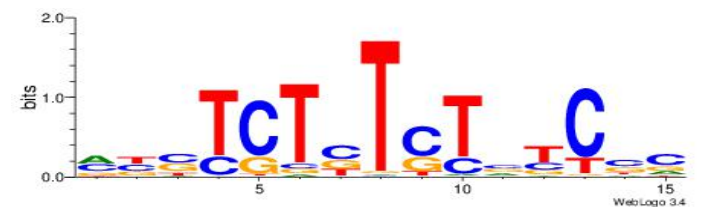
GVGABAGAVAGASVK

YRGAYAGAGRGAYR-

Original motif Consensus sequence: GVGABAGAVAGASVK



Reverse complement motif Consensus sequence: RBSTCTVTCTBTCV



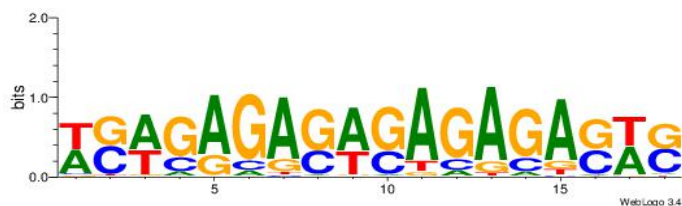
Dataset #: 1
 Motif ID: 17

Motif name:	C017
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	2
Number of overlap:	14
Similarity score:	0.0146835

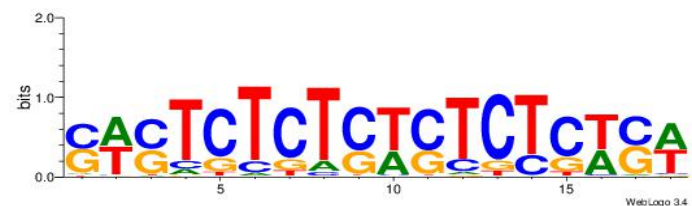
Alignment:

```
SWSTCTCTSWSTCTCWSW
---KMTCKCTCTMTCKM-
```

Original motif Consensus sequence: WSWGAGASWSAGAGASWS



Reverse complement motif Consensus sequence: SWSTCTCTSWSTCTCWSW



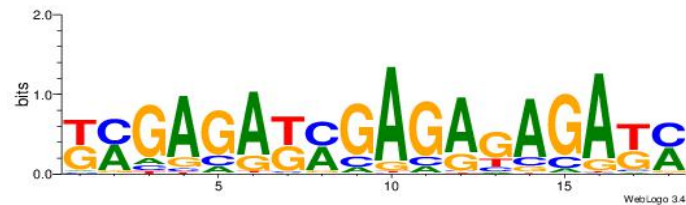
Dataset #:	1
Motif ID:	11
Motif name:	C011
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	5
Number of overlap:	14
Similarity score:	0.0193986

Alignment:

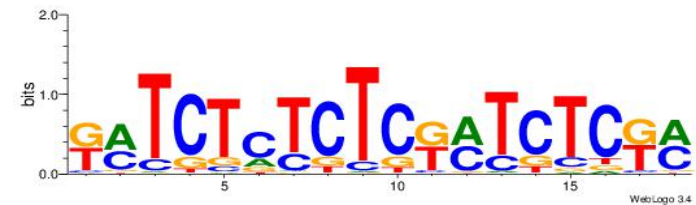
KMGAGAKMGAGAGAGAKM

----YRGAYAGAGRGAYR

Original motif Consensus sequence: KMGAGAKMGAGAGAGAKM

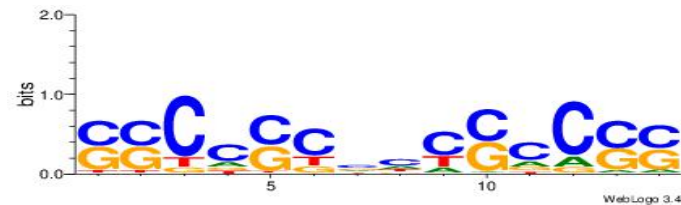


Reverse complement motif Consensus sequence: RRTCTCTCTCRRTCTCRR

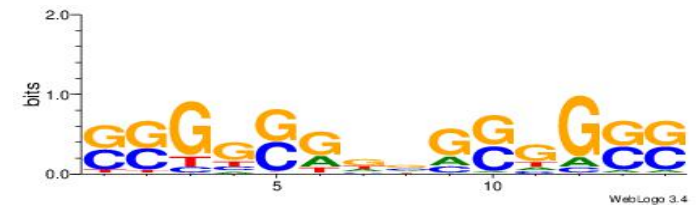


Dataset #: 1 Motif ID: 23 Motif name: C023

Original motif Consensus sequence: SSCCSCBHCSSCS



Reverse complement motif Consensus sequence: SSGSGDBGSGGS



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

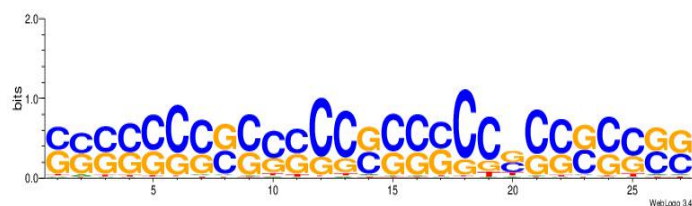
Dataset #:	1
Motif ID:	4
Motif name:	C004
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward

Position number: 2
 Number of overlap: 14
 Similarity score: 0.00461109

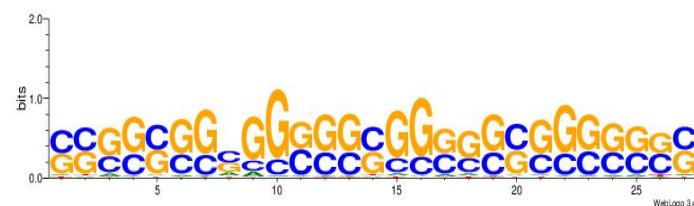
Alignment:

SSSSSSGSGGSSSSGSSSSGSSSSS
 -----SSGGSGBGSGGSS--

Original motif Consensus sequence:
 SSSSSCSSSSCCSSSSCCSCSSSSS



Reverse complement motif Consensus sequence:
 SSSSSGSGGSSSSGSSSSGSSSSS

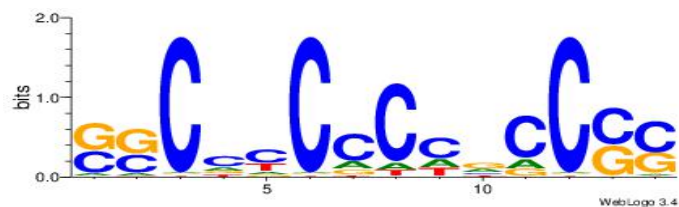


Dataset #: 1
 Motif ID: 104
 Motif name: C104
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0.00651203

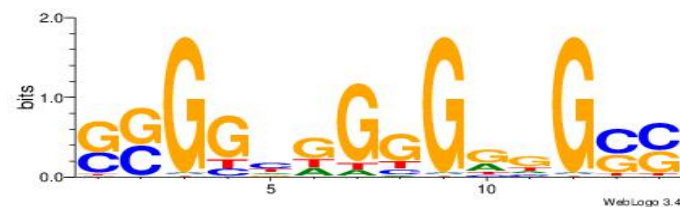
Alignment:

SSGGHGGGGKGGSS
 SSGGSGBGSGGSS

Original motif Consensus sequence: SSCCYCCCCDCCSS



Reverse complement motif Consensus sequence: SSGGHGGGGKGG



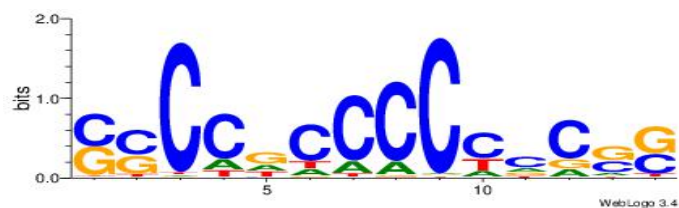
Dataset #: 1
Motif ID: 54
Motif name: C054
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 14
Similarity score: 0.0125092

Alignment:

SSGGGGGGGHGGSS

SSGGSGBGSGGSS

Original motif Consensus sequence: SSCDCCCCCCSCSS



Reverse complement motif Consensus sequence: SSGGGGGGGHGG

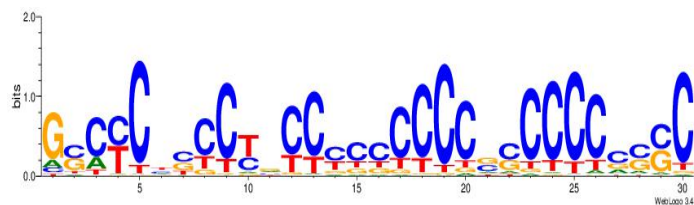


Dataset #: 1
 Motif ID: 3
 Motif name: C003
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 15
 Number of overlap: 14
 Similarity score: 0.0162482

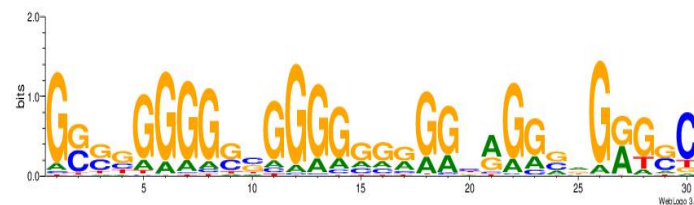
Alignment:

GSCYCHSCCYVCCYCCCCCSCCCCCSSC
 -----SSCCSCBHCSCCSS--

Original motif Consensus sequence:
 GSCYCHSCCYVCCYCCCCCSCCCCCSSC



Reverse complement motif Consensus sequence:
 GSSGGGGGSSGGGGGKGGVMGGSHGKGSC

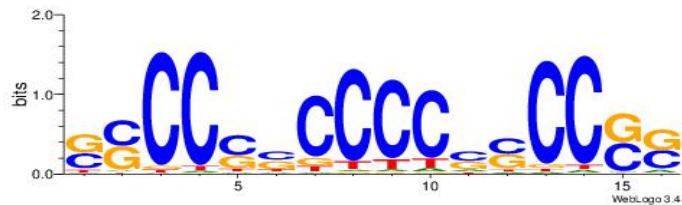


Dataset #: 1
 Motif ID: 8
 Motif name: C008
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2

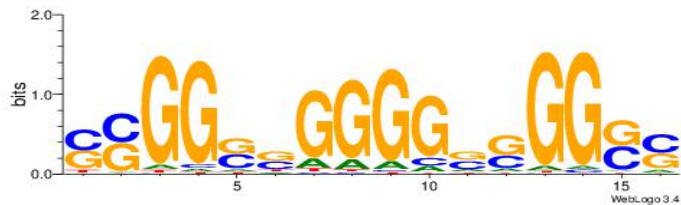
Number of overlap: 14
Similarity score: 0.0169024

Alignment:
SSCCSSCCCCSSCCSS
-SSCCSCBHCSSCCSS-

Original motif Consensus sequence: SSCCSSCCCCSSCCSS

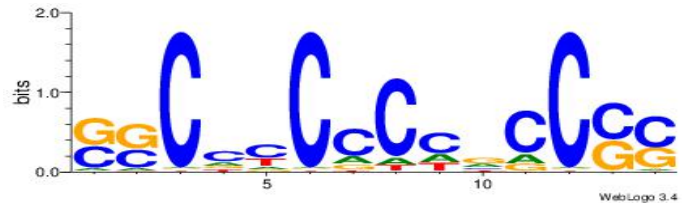


Reverse complement motif Consensus sequence: SSGGSSGGGGSSGGSS



Dataset #: 1 Motif ID: 104 Motif name: C104

Original motif Consensus sequence: SSCCYCCCCDCSS



Reverse complement motif Consensus sequence: SSGGHGGGGKGG



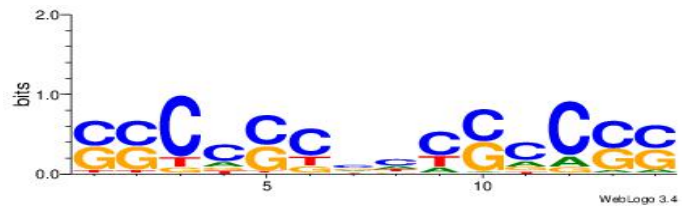
Best Matches for Significant Motif ID 104 (Highest to Lowest)

Dataset #: 1
Motif ID: 23
Motif name: C023
Matching format of first motif: Reverse Complement

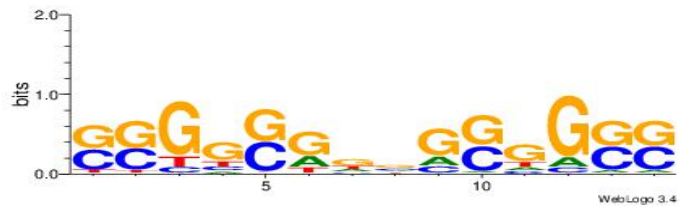
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 14
Similarity score: 0.00165547

Alignment:
SSGGSGDBGSGGSS
SSGGHGGGGKGGSS

Original motif Consensus sequence: SSCCSCBHCSCCSS



Reverse complement motif Consensus sequence: SSGGSGDBGSGGSS

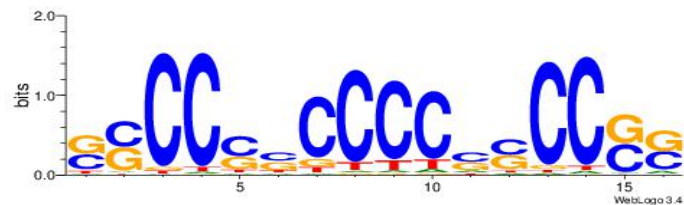


Dataset #: 1
Motif ID: 8
Motif name: C008
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 2
Number of overlap: 14
Similarity score: 0.00956764

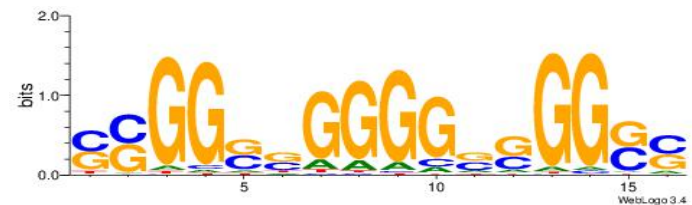
Alignment:

SSGGSSGGGGSSGGSS
 -SSGGHGGGGKGGSS-

Original motif Consensus sequence: SSCSSCCCCSSCCSS



Reverse complement motif Consensus sequence: SSGGSSGGGGSSGGSS

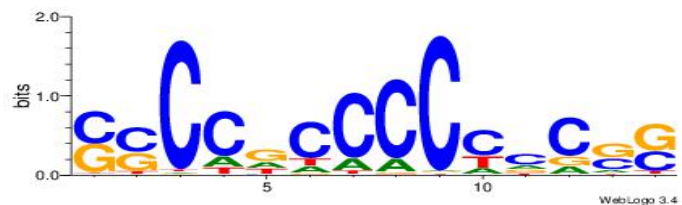


Dataset #:	1
Motif ID:	54
Motif name:	C054
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	14
Similarity score:	0.0123202

Alignment:
 SSCDCCCCCCCCSS
 SSCCYCCCCDCCSS

Original motif Consensus sequence: SSCDCCCCCCCCSS

Reverse complement motif Consensus sequence: SSGGGGGGGHGG

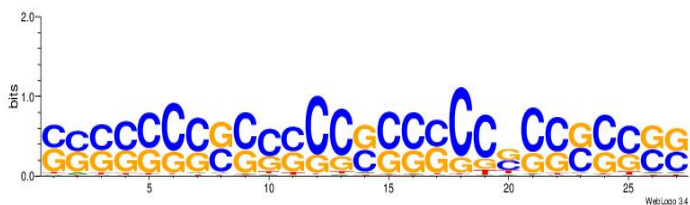


Dataset #: 1
 Motif ID: 4
 Motif name: C004
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 4
 Number of overlap: 14
 Similarity score: 0.0160908

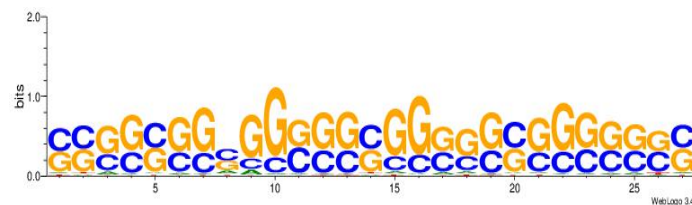
Alignment:

SSSSSSGSGGSSSSSGSSSSSGSSSSS
 ---SSGGHGGGGKGGSS-----

Original motif Consensus sequence:
 SSSSSCSSSSSCSSSSCCSCSSSSS



Reverse complement motif Consensus sequence:
 SSSSSSGSGGSSSSSGSSSSSGSSSSS



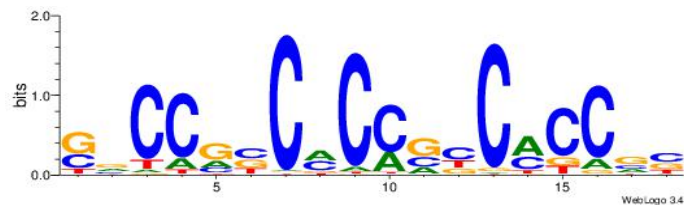
Dataset #: 1

Motif ID: 37
 Motif name: C037
 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: 0.0188565

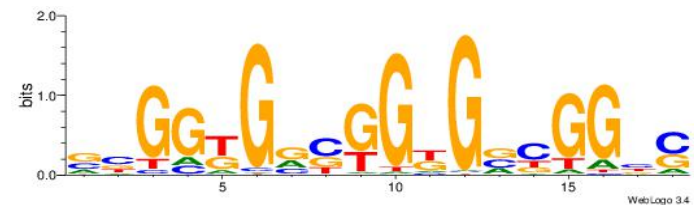
Alignment:

SVCCGBCMCCSYCMCCVB
 -SSCCYCCCCDCCSS---

Original motif Consensus sequence: SVCCGBCMCCSYCMCCVB

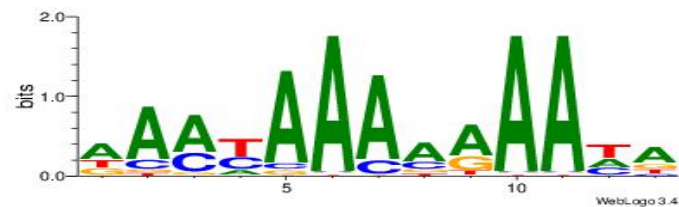


Reverse complement motif Consensus sequence: BVGGYGKSGGYGBCGGVS

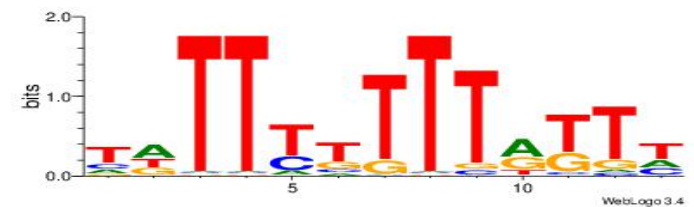


Dataset #: 1 Motif ID: 18 Motif name: C018

Original motif Consensus sequence: AAMYAAAAAAHA



Reverse complement motif Consensus sequence: THTTTTTTTMYTT



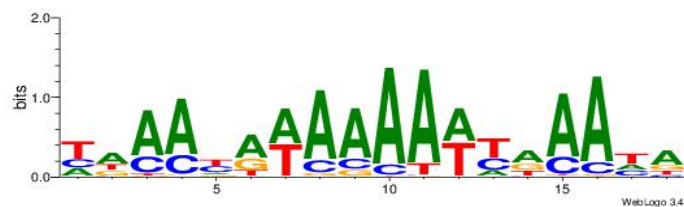
Best Matches for Significant Motif ID 18 (Highest to Lowest)

Dataset #: 1
Motif ID: 24
Motif name: C024
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: 0.00879109

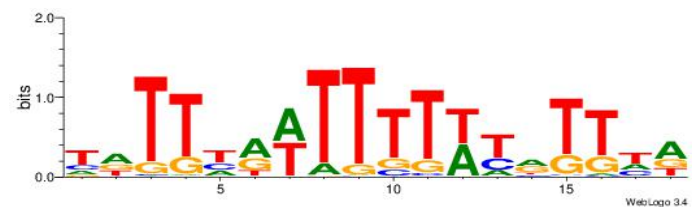
Alignment:

```
THTTDMWTTTTWKMTTDA  
-----THTTTTTTTTMYTT-
```

Original motif Consensus sequence: TDAAYRWAAAWYDAAHA



Reverse complement motif Consensus sequence:
THTTDMWTTTTWKMTTDA



Dataset #: 1
Motif ID: 33
Motif name: C033
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif

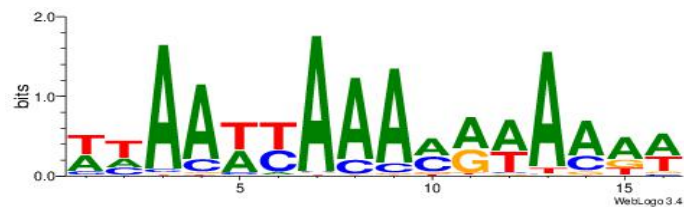
Direction: Backward
 Position number: 2
 Number of overlap: 13
 Similarity score: 0.0101683

Alignment:

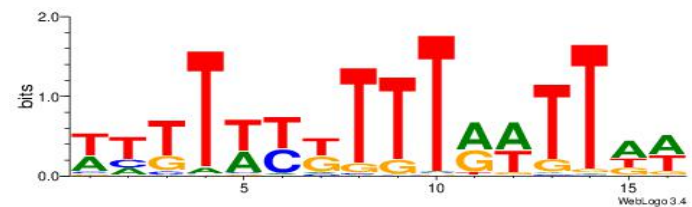
WWAAWYAAAMRWAAAW

--AAMYAAAAAAHA--

Original motif Consensus sequence: WWAAWYAAAMRWAAAW



Reverse complement motif Consensus sequence: WTTTWKYTTTMWTTWW



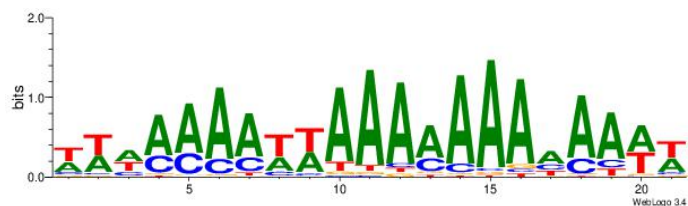
Dataset #: 1
 Motif ID: 10
 Motif name: C010
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 4
 Number of overlap: 13
 Similarity score: 0.0128694

Alignment:

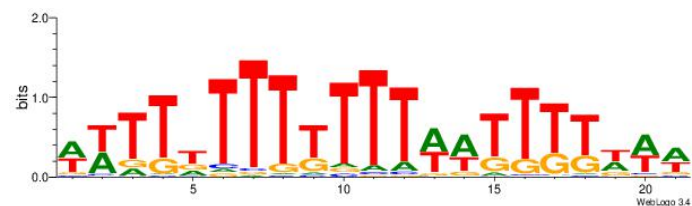
WWAAAAWWAAAAAAAAAAWW

-----AAMYAAAAAAHA---

Original motif Consensus sequence: WWWAAAWWAAAAAAAAAAWW



Reverse complement motif Consensus sequence: WWTTTTTTTTTTWWTTTTWW

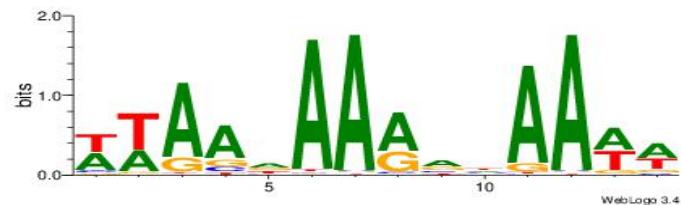


Dataset #: 1
Motif ID: 131
Motif name: C131
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 13
Similarity score: 0.0136352

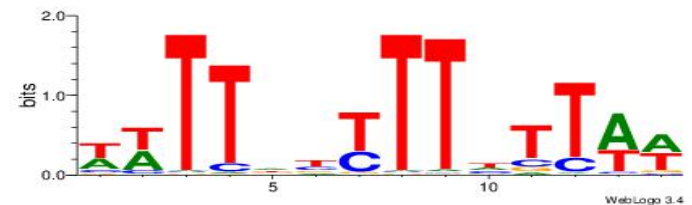
Alignment:

WWTTHBKTTDTTWW
THTTTTTTTMYTT-

Original motif Consensus sequence: WWAADAARVHAAWW



Reverse complement motif Consensus sequence: WWTTHBKTTDTTV

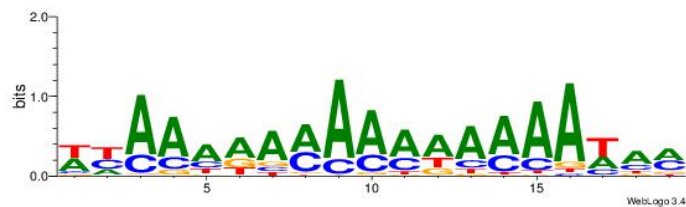


Dataset #: 1
 Motif ID: 30
 Motif name: C030
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 13
 Similarity score: 0.0161198

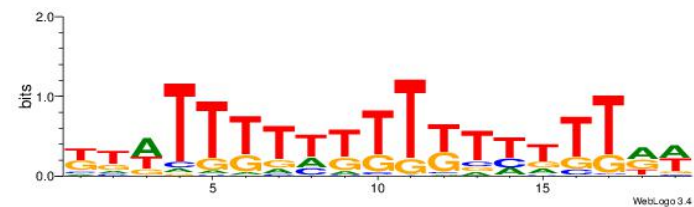
Alignment:

YTWTTTTTTTTYTTTTMW
 -THTTTTTTTMYTT-----

Original motif Consensus sequence: WYAAAAAIAAAAAAAWAM



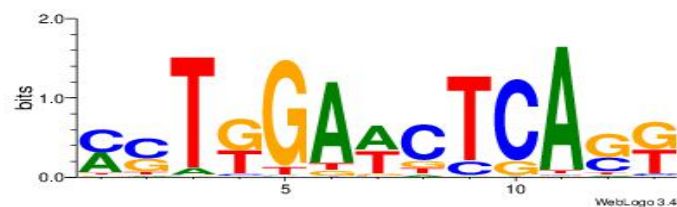
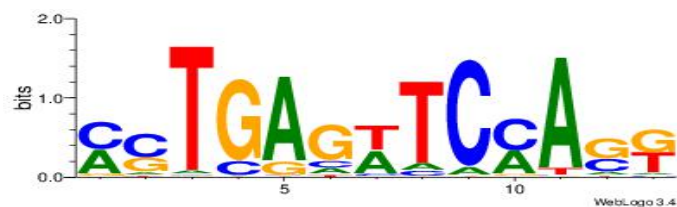
Reverse complement motif Consensus sequence: YTWTTTTTTTTYTTTTMW



Dataset #: 1 Motif ID: 65 Motif name: C065

Original motif Consensus sequence: MSTGAGWTCMASK

Reverse complement motif Consensus sequence: YSTRGAWCTCASR



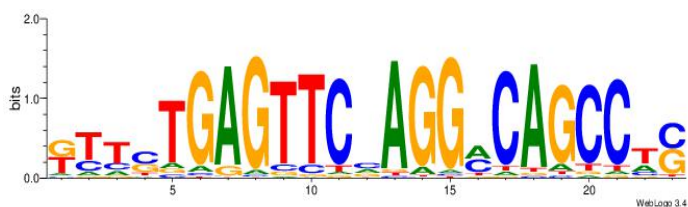
Best Matches for Significant Motif ID 65 (Highest to Lowest)

Dataset #: 1
 Motif ID: 7
 Motif name: C007
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 9
 Number of overlap: 13
 Similarity score: 0.00190829

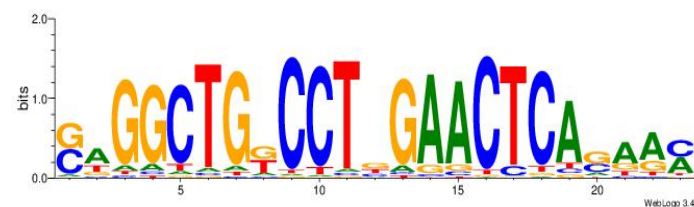
Alignment:

SAGGCTGYCCTVGAAGTCASAAY
 -----YSTRGAWCTCASR--

Original motif Consensus sequence: KTTSTGAGTTCVAGGMCAGCCTS



Reverse complement motif Consensus sequence: SAGGCTGYCCTVGAAGTCASAAY

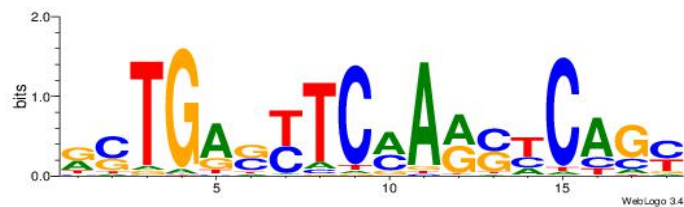


Dataset #: 1
 Motif ID: 40
 Motif name: C040
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 6
 Number of overlap: 13
 Similarity score: 0.0036319

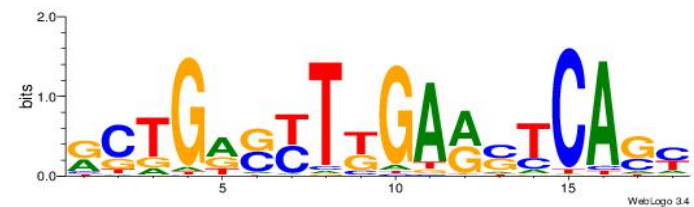
Alignment:

RSTGASYTCMARSYCAGY
 MSTGAGWTCMASK-----

Original motif Consensus sequence: RSTGASYTCMARSYCAGY



Reverse complement motif Consensus sequence: KCTGMSKTYGAMSTCASM



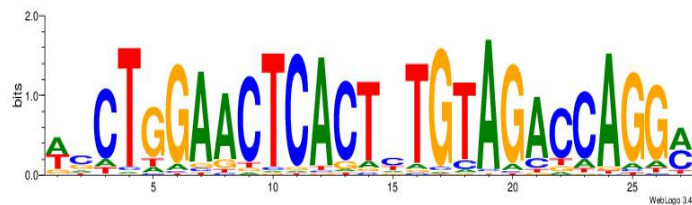
Dataset #: 1
 Motif ID: 13
 Motif name: C013
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 14

Number of overlap: 13
Similarity score: 0.0058849

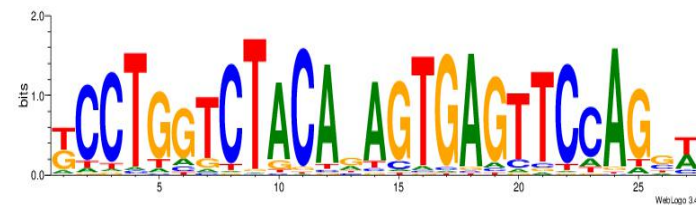
Alignment:

WVCTGGAAC TCACTHTGTAGACCAGGM
-----YSTRGAWCTCASR-

Original motif Consensus sequence:
WVCTGGAAC TCACTHTGTAGACCAGGM



Reverse complement motif Consensus sequence:
YCCTGGTCTACADAGTGAGTTCCAGVW

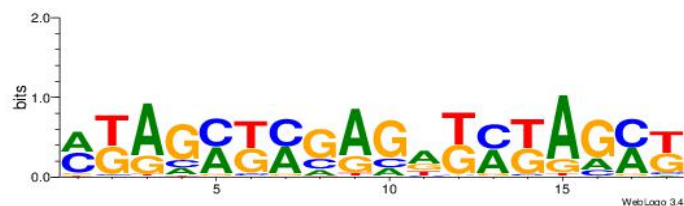


Dataset #: 1
Motif ID: 36
Motif name: C036
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 5
Number of overlap: 13
Similarity score: 0.0245754

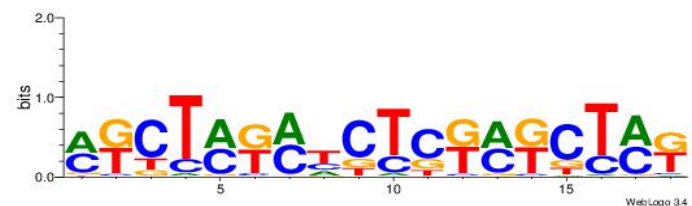
Alignment:

RRCTRRRTCTCRRRCTRY
-YSTRGAWCTCASR----

Original motif Consensus sequence: MKAGMKMGAGAKMKAGMK



Reverse complement motif Consensus sequence: RRCTRRRTCTCRRRCTRY

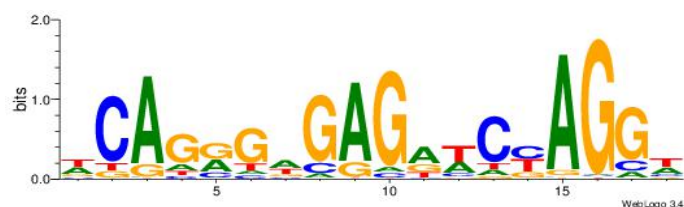


Dataset #: 1
Motif ID: 132
Motif name: C132
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 5
Number of overlap: 13
Similarity score: 0.0272182

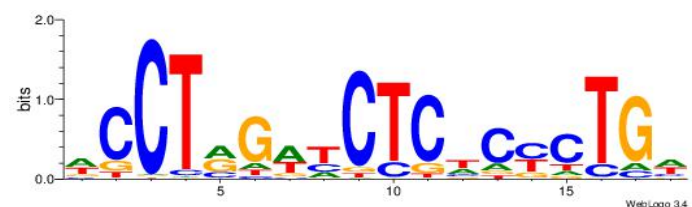
Alignment:

WCAGRGWGAGAWCYAGGW
----MSTGAGWTCMASK-

Original motif Consensus sequence: WCAGRGWGAGAWCYAGGW

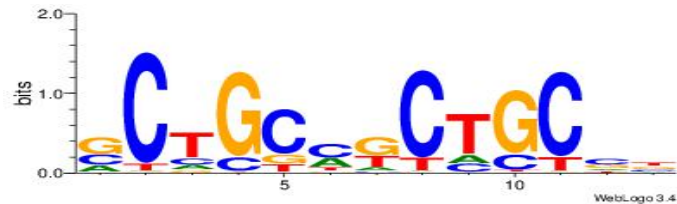


Reverse complement motif Consensus sequence: WCCTKGWTCWCMTGW



Dataset #: 1 **Motif ID: 84** **Motif name: C084**

Original motif Consensus sequence: SCTGCMKCTGCVB



Reverse complement motif Consensus sequence: VVGCAGYRGCAGS



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

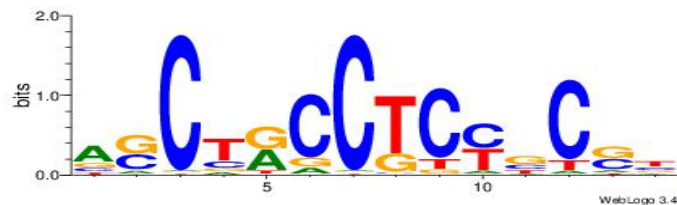
Dataset #:	1
Motif ID:	76
Motif name:	C076
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	13
Similarity score:	0.00787805

Alignment:

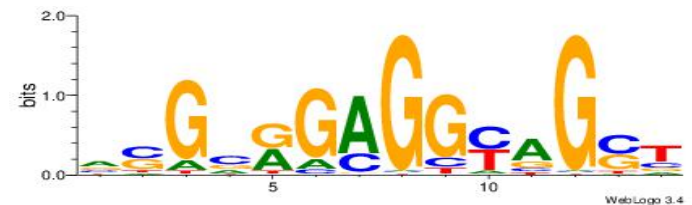
ASCTRCCTCYBCSB

–SCTGCMKCTGCVB

Original motif Consensus sequence: ASCTRCCTCYBCSB



Reverse complement motif Consensus sequence: VSGBKGAGGMAGS

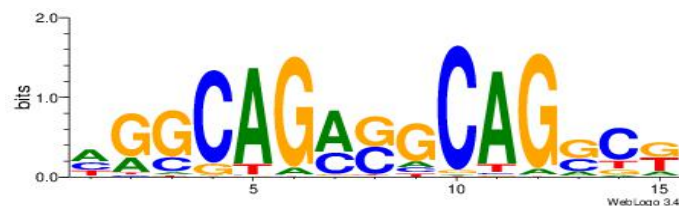


Dataset #: 1
 Motif ID: 75
 Motif name: C075
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 13
 Similarity score: 0.0120992

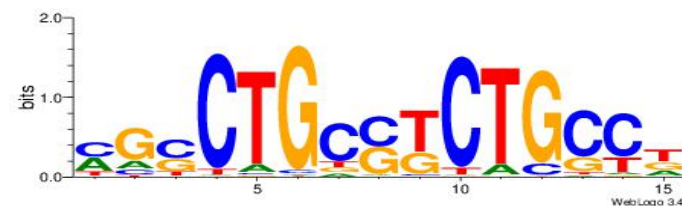
Alignment:

YGSCTGCSYCTGCCY
 SCTGCMKCTGCVB--

Original motif Consensus sequence: MGGCAGMSGCAGSCK



Reverse complement motif Consensus sequence: YGSCTGCSYCTGCC

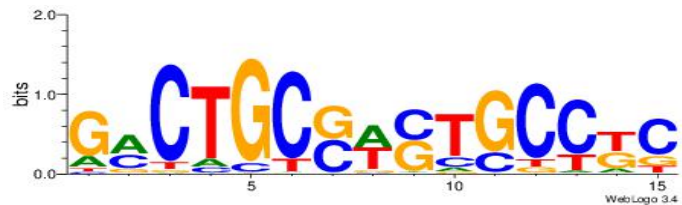


Dataset #: 1
 Motif ID: 118
 Motif name: C118
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2

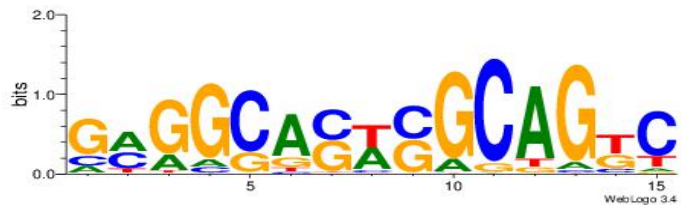
Number of overlap: 13
Similarity score: 0.0130639

Alignment:
GMCTGCSWSTGCCKC
-SCTGCMKCTGCVB-

Original motif Consensus sequence: GMCTGCSWSTGCCKC



Reverse complement motif Consensus sequence: GRGGCASWSGCAGYC

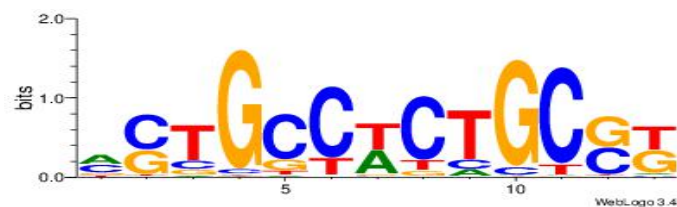
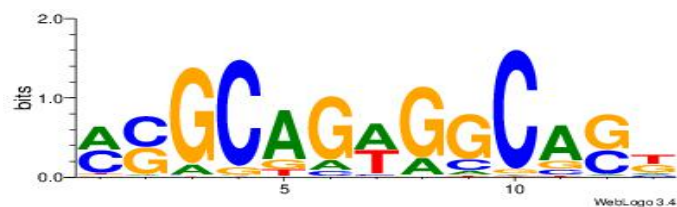


Dataset #: 1
Motif ID: 106
Motif name: C106
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 13
Similarity score: 0.0148962

Alignment:
RSTGCCWCTGCSY
SCTGCMKCTGCVB

Original motif Consensus sequence: MSGCAGWGGCASK

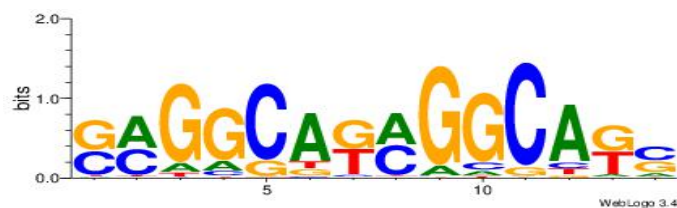
Reverse complement motif Consensus sequence: RSTGCCWCTGCSY



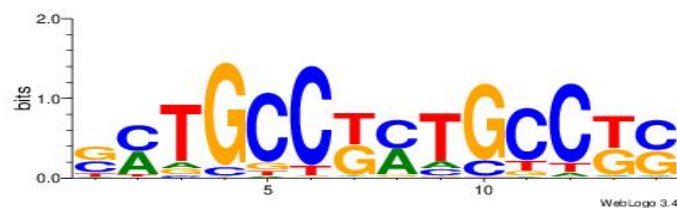
Dataset #: 1
 Motif ID: 60
 Motif name: C060
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 13
 Similarity score: 0.0166117

Alignment:
 SYTGCCYYTGCCYS
 -SCTGCMKCTGCVB

Original motif Consensus sequence: SMGGCAKMGGCAKS

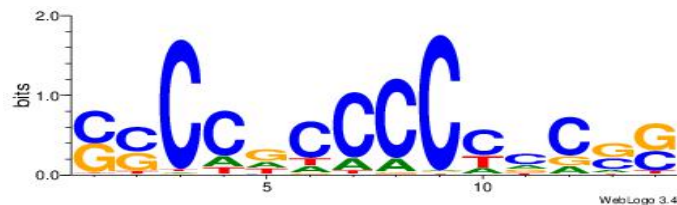


Reverse complement motif Consensus sequence: SYTGCCYYTGCCYS



Dataset #: 1 Motif ID: 54 Motif name: C054

Original motif Consensus sequence: SSCCDCCCCCCCSS



Reverse complement motif Consensus sequence: SSGGGGGGGHGG



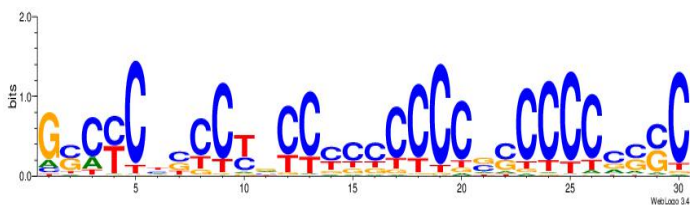
Best Matches for Significant Motif ID 54 (Highest to Lowest)

Dataset #:	1
Motif ID:	3
Motif name:	C003
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:	0.010752

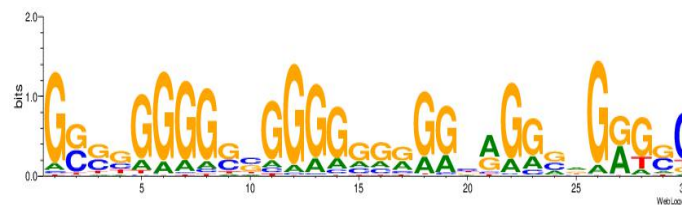
Alignment:

```
GSCYCHSCCYVCCYCCCCCSCCCCCSSC
-----SSCCDCCCCCCCSS
```

Original motif Consensus sequence:
GSCYCHSCCYVCCYCCCCCSCCCCCSSC



Reverse complement motif Consensus sequence:
GSSGGGGGSSGGGGGKGGVMGGSHGKGC



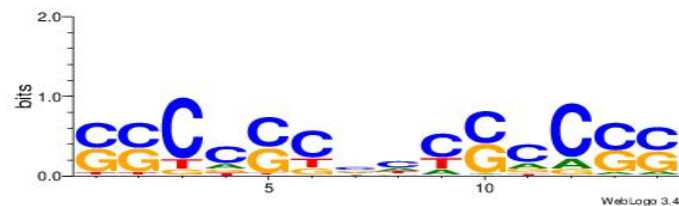
Dataset #: 1
 Motif ID: 23
 Motif name: C023
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0.0108829

Alignment:

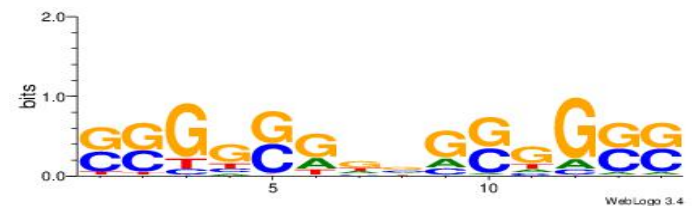
SSGGSGDBGSGGSS

SSGGGGGGGHGGSS

Original motif Consensus sequence: SSCCSCBHCSCCSS



Reverse complement motif Consensus sequence: SSGGSGDBGSGGSS

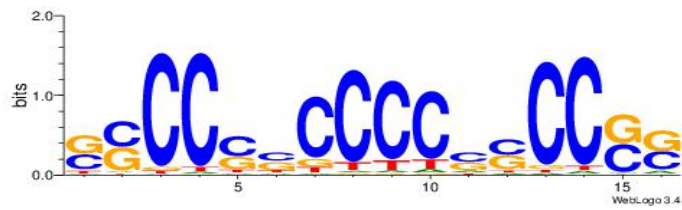


Dataset #: 1
 Motif ID: 8
 Motif name: C008
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 14

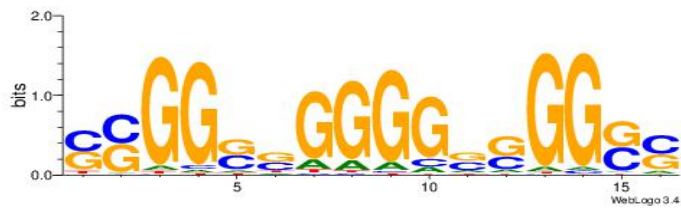
Similarity score: 0.0123397

Alignment:
SSCCSSCCCCSSCCSS
-SSCCDCCCCCCCCSS-

Original motif Consensus sequence: SSCCSSCCCCSSCCSS



Reverse complement motif Consensus sequence: SSGGSSGGGGSSGGSS

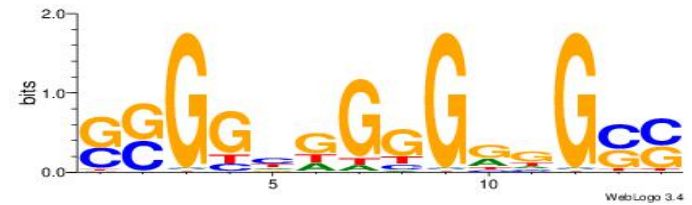


Dataset #: 1
Motif ID: 104
Motif name: C104
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 14
Similarity score: 0.0155505

Alignment:
SSCCYCCCCDCCSS
SSCCDCCCCCCCCSS

Original motif Consensus sequence: SSCCYCCCCDCCSS

Reverse complement motif Consensus sequence: SSGGHGGGGKGG



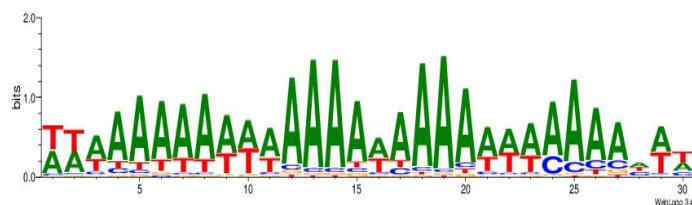
Alignment:

```
SSSSSSSGSGGSSSSSGGSSSSSSGSSSSS
----SSGGGGGGGGHGGSS-----
```

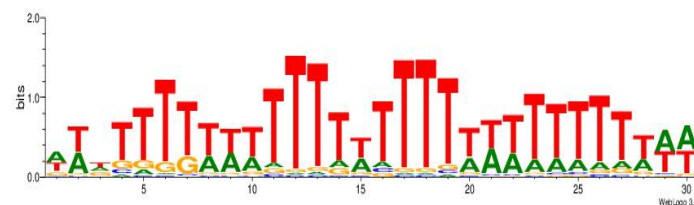
Best Matches for Each Motif (Highest to Lowest)

Dataset #: 1 Motif ID: 1 Motif name: C001

Original motif Consensus sequence:
WWWAAAAAWWAAAAWAAAAWWAAAAHWW



Reverse complement motif Consensus sequence:
WWHTTTTWWTTTTTWT TTTTWWTTTTTWWW



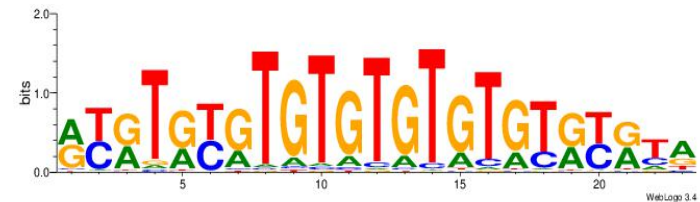
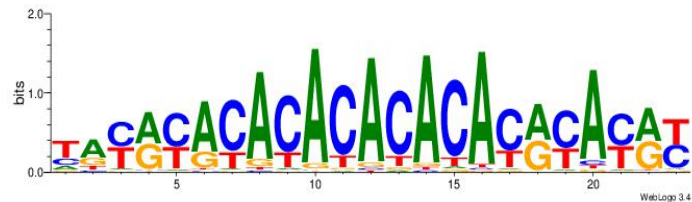
Best Matches for Motif ID 1 (Highest to Lowest)

Dataset #:	1
Motif ID:	2
Motif name:	C002
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	23
Similarity score:	0.0778495

Alignment:
-----MKKTKKGTGTGTGTGTGTTKKKTA
WWHTTTTWWTTTTTWT TTTTWWTTTTTWWW

Original motif Consensus sequence: TAYRYACACACACACRYAYRY

Reverse complement motif Consensus sequence:
MKKTKKGTGTGTGTGTGTTKKKTA



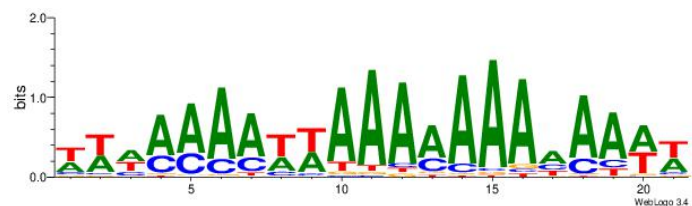
Dataset #: 1
 Motif ID: 10
 Motif name: C010
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 21
 Similarity score: 1.01726

Alignment:

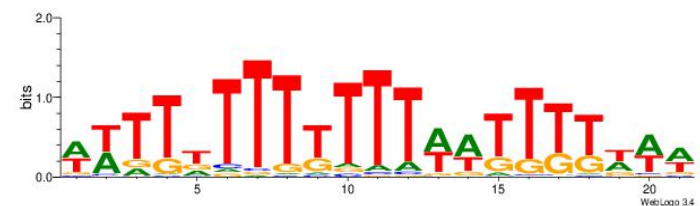
```

-----WWTTTTTTTTTWWTTTTWWW
WWHTTTTWTTTTTWWTTTTTWWTTTTWWW
  
```

Original motif Consensus sequence: WWAAAAWWAAAAAAAAAAWW



Reverse complement motif Consensus sequence: WWTTTTTTTTTTWWTTTTWWW

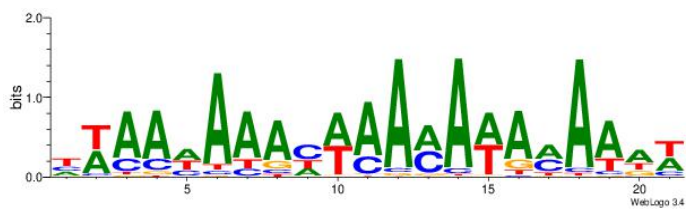


Dataset #: 1

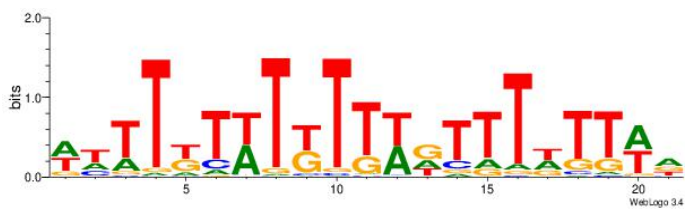
Motif ID: 16
Motif name: C016
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 21
Similarity score: 1.01956

Alignment:
-----WWTTYTWTYTTWDTTTWTTH
WWHTTTTWTTTTTWTTTTWWTTTTTWW

Original motif Consensus sequence: HWAAWAAHWAAMAWAMAAWW



Reverse complement motif Consensus sequence: WWTTYTWTYTTWDTTTWTTH

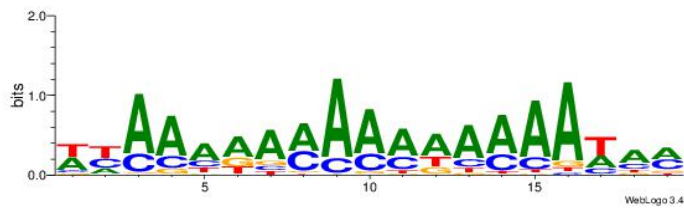


Dataset #: 1
Motif ID: 30
Motif name: C030
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 19

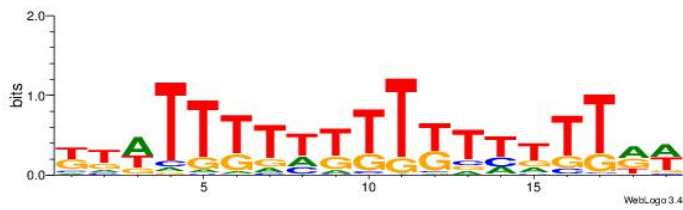
Similarity score: 2.02984

Alignment:
-----WYAAAAAMAAAAAAWAM
WWWAAAAAWWAAAAWAAAAWAAAAHWW

Original motif Consensus sequence: WYAAAAAMAAAAAAWAM



Reverse complement motif Consensus sequence:
YTWTTTTTTTTTTTTMW

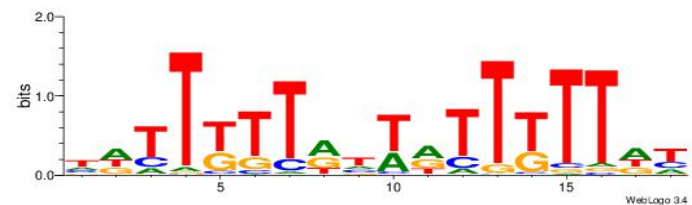
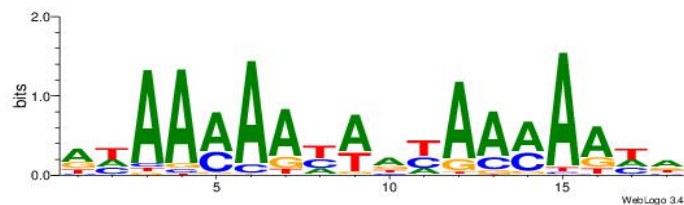


Dataset #: 1
Motif ID: 69
Motif name: C069
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 18
Similarity score: 2.53311

Alignment:
-----DHTTYTTMDWMTTYTHT
WWHTTTTWTTTTTWTTTTWWTTTTWWW

Original motif Consensus sequence: AHAAMAAYWDYAAMAAHD

Reverse complement motif Consensus sequence:
DHTTYTTMDWMTTYTHT

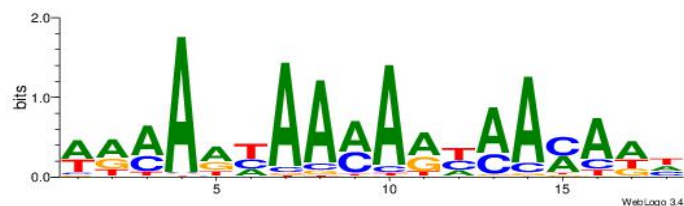


Dataset #: 1
 Motif ID: 57
 Motif name: C057
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 18
 Similarity score: 2.54092

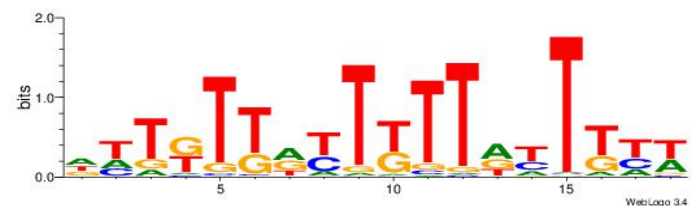
Alignment:

-----WRMARYAAMARYAAMAWH
 WWWAAAAWAAAAWAAAAWAAAAHWW

Original motif Consensus sequence: WRMARYAAMARYAAMAWH

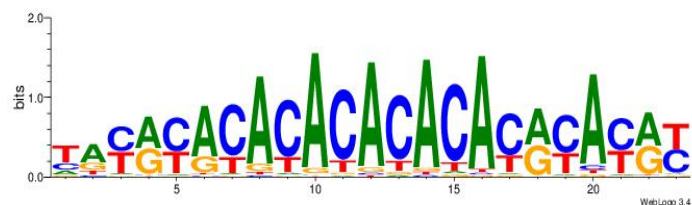


Reverse complement motif Consensus sequence: HWTRTTMKTYTTMKTYKW

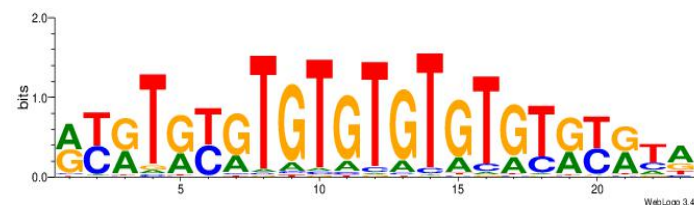


Dataset #: 1 Motif ID: 2 Motif name: C002

Original motif Consensus sequence: TAYRYACACACACACRYAYRY



Reverse complement motif Consensus sequence: MKKTKKGTGTGTGTGTGTTKKTA



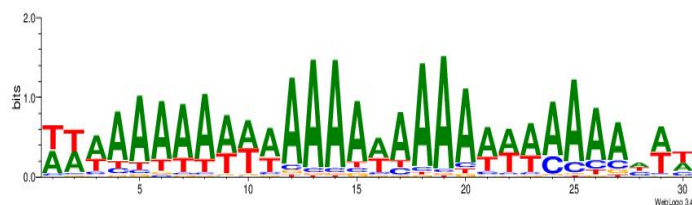
Best Matches for Motif ID 2 (Highest to Lowest)

Dataset #: 1
 Motif ID: 1
 Motif name: C001
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 6
 Number of overlap: 23
 Similarity score: 0.0750684

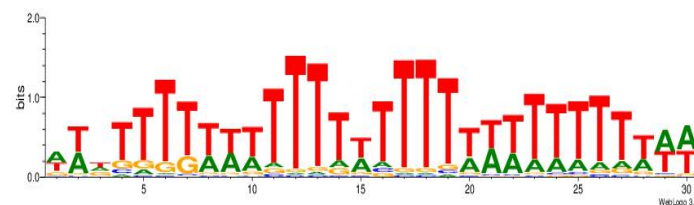
Alignment:

WWHTTTTWWTTTTTWWTTTTTWWTTTTTWW
 --MKKTKKGTGTGTGTGTGTTKKTA-----

Original motif Consensus sequence: WWWAAAAWWAAAAWAAAAWAAAAHWW



Reverse complement motif Consensus sequence: WWHTTTTWWTTTTTWWTTTTTWWTTTTTWW

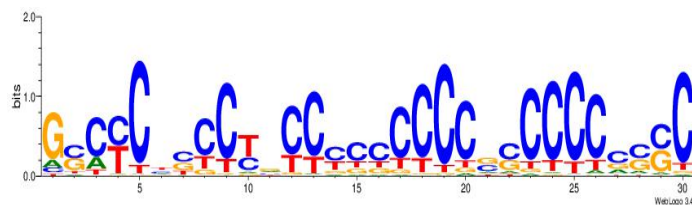


Dataset #: 1
 Motif ID: 3
 Motif name: C003
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 6
 Number of overlap: 23
 Similarity score: 0.076772

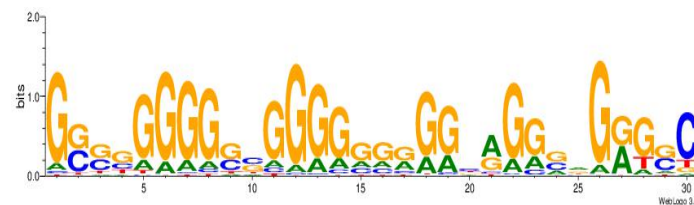
Alignment:

GSSGGGGGSSGGGGGKGGVMGGSHGKGC
 --MKKTKKGTGTGTGTGTGTTKKTA-----

Original motif Consensus sequence:
 GSCYCHSCCYVCCYCCCCCSCCCCCSSC



Reverse complement motif Consensus sequence:
 GSSGGGGGSSGGGGGKGGVMGGSHGKGC

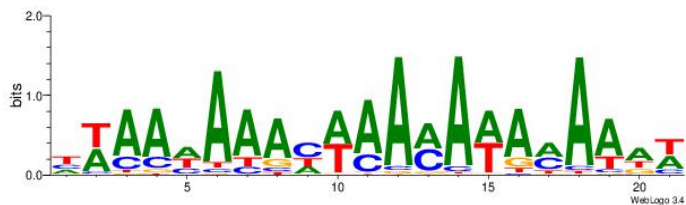


Dataset #: 1
 Motif ID: 16
 Motif name: C016
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward

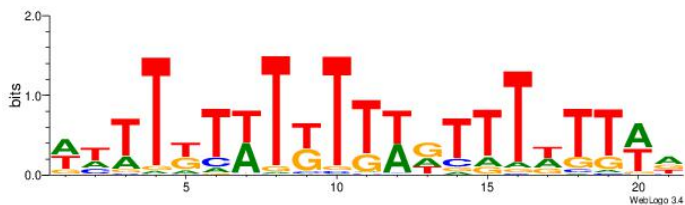
Position number: 1
Number of overlap: 21
Similarity score: 1.05891

Alignment:
--HWAAWAAAHWAAMAWAMAAWW
TAYRYACACACACACACRYAYRY

Original motif Consensus sequence: HWAAWAAAHWAAMAWAMAAWW



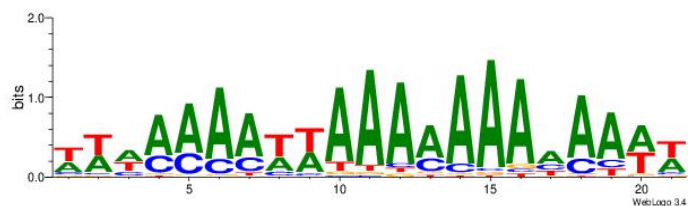
Reverse complement motif Consensus sequence: WWTYYTWYTTWDTTTWTTWH



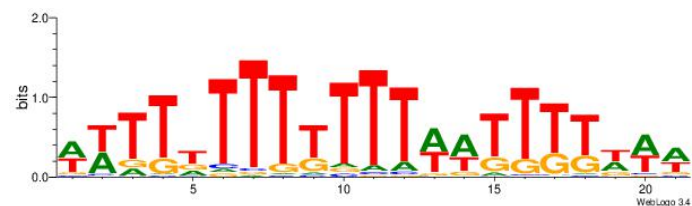
Dataset #: 1
Motif ID: 10
Motif name: C010
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 21
Similarity score: 1.07752

Alignment:
WWWAAAAWWAAAAAAAAAAWW--
TAYRYACACACACACACRYAYRY

Original motif Consensus sequence: WWWAAAWWAAAAAAAAAAWW



Reverse complement motif Consensus sequence: WWTTTTTTTTTTWWTTTTWWW

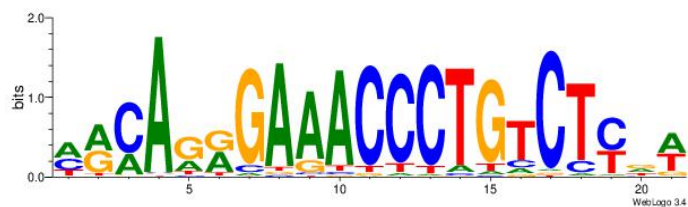


Dataset #: 1
 Motif ID: 27
 Motif name: C027
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 21
 Similarity score: 1.08199

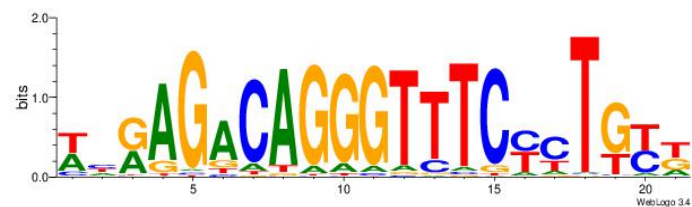
Alignment:

--MRCAGRGAAACCCTGTCTYDW
 TAYRYACACACACACRYAYRY

Original motif Consensus sequence: MRCAGRGAAACCCTGTCTYDW

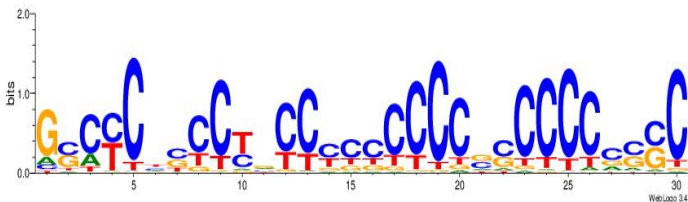


Reverse complement motif Consensus sequence: WHKAGACAGGGTTTCMCTGKY

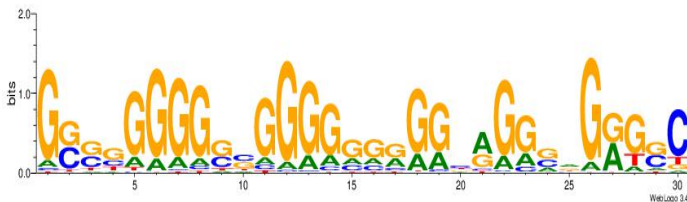


Dataset #: 1 Motif ID: 3 Motif name: C003

Original motif Consensus sequence:
GSCYCHSCCYVCCYCCCCCSCCCCCSSC



Reverse complement motif Consensus sequence:
GSSGGGGGSSGGGGGKGGVMGGSHGKGC



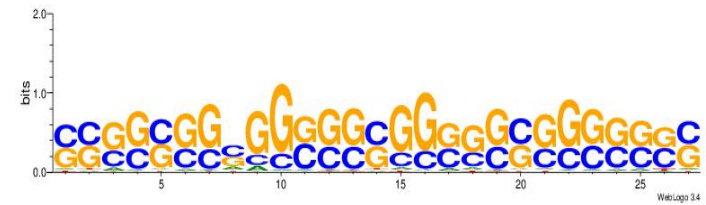
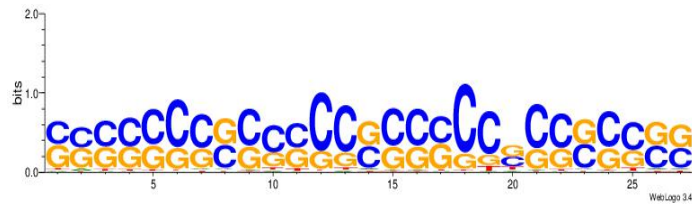
Best Matches for Motif ID 3 (Highest to Lowest)

Dataset #:	1
Motif ID:	4
Motif name:	C004
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	27
Similarity score:	0.0402886

Alignment:
SSSSSCSSSSSCCSSSSCCSCSSSSSS---
GSCYCHSCCYVCCYCCCCCSCCCCCSSC

Original motif Consensus sequence:
SSSSSCSSSSSCCSSSSCCSCSSSSSS

Reverse complement motif Consensus sequence:
SSSSSSGSGGSSSSGGSSSSSGSSSSS

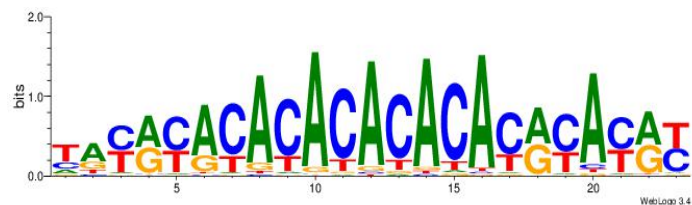


Dataset #: 1
 Motif ID: 2
 Motif name: C002
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 23
 Similarity score: 2.07737

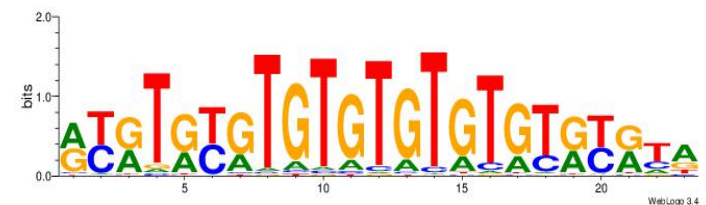
Alignment:

-----MKKTKKGTGTGTGTGTGTTKKTA
 GSSGGGGGSSGGGGGKGGVMGGSHGKGSC

Original motif Consensus sequence: TAYRYACACACACACRYAYRY



Reverse complement motif Consensus sequence: MKKTKKGTGTGTGTGTGTTKKTA



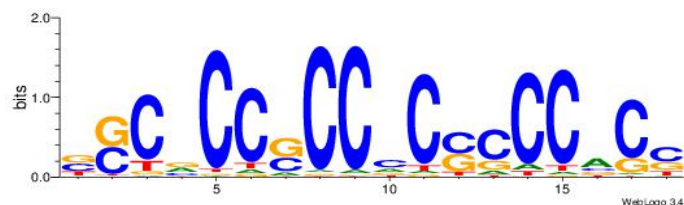
Dataset #: 1

Motif ID: 20
 Motif name: C020
 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: 4.53926

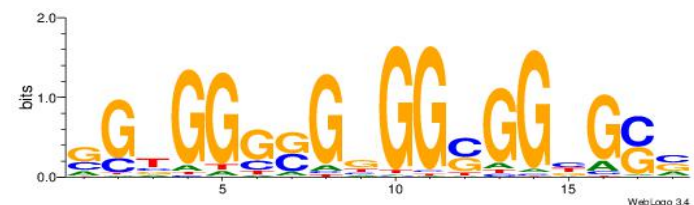
Alignment:

-----BSCVCCSCCVSCCCACS
 GSCYCHSCCYVCCYCCCCCSCCCCCSSC

Original motif Consensus sequence: BSCVCCSCCVSCCCACS



Reverse complement motif Consensus sequence: SGTGGGSGVGGSGGVGSB

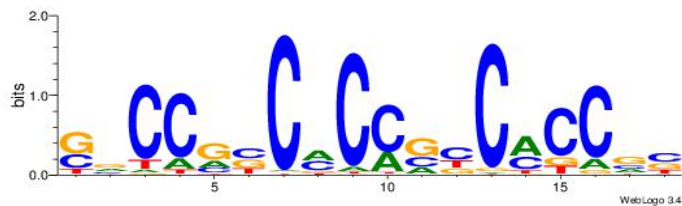


Dataset #: 1
 Motif ID: 37
 Motif name: C037
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 18

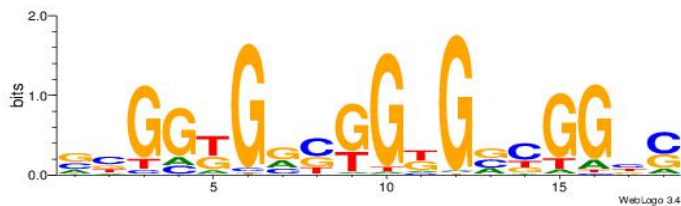
Similarity score: 4.54973

Alignment:
SVCCGBCMCCSYCMCCVB-----
GSCYCHSCCYVCCYCCCCCSCCCCCSSC

Original motif Consensus sequence: SVCCGBCMCCSYCMCCVB



Reverse complement motif Consensus sequence:
BVGGYGKSGGYBCGGVS

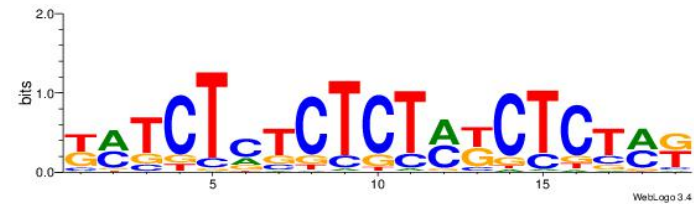
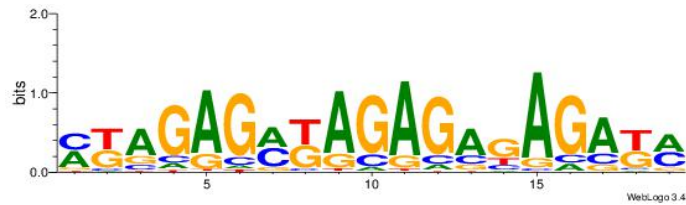


Dataset #: 1
Motif ID: 12
Motif name: C012
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 2
Number of overlap: 18
Similarity score: 4.56368

Alignment:
YRTCTCTCTCTRYCTCTRR-----
-GSCYCHSCCYVCCYCCCCCSCCCCCSSC

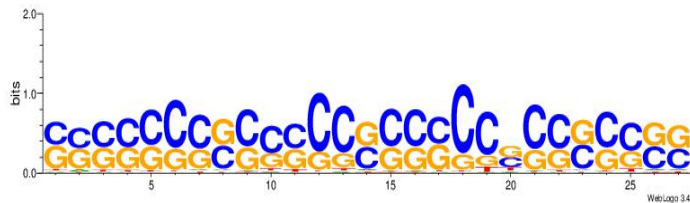
Original motif Consensus sequence: MKAGAGMKAGAGAGAGAKM

Reverse complement motif Consensus sequence:
YRTCTCTCTCTRYCTCTRR

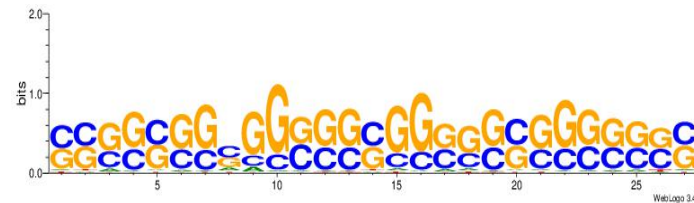


Dataset #: 1 Motif ID: 4 Motif name: C004

Original motif Consensus sequence:
SSSSSCSSSSSCSSSSCCSCSSSSS



Reverse complement motif Consensus sequence:
SSSSSGSGGSSSSGGSSSSSGSSSSS



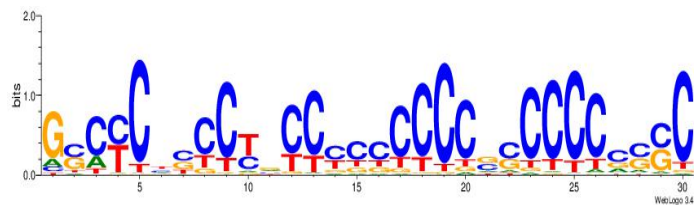
Best Matches for Motif ID 4 (Highest to Lowest)

Dataset #:	1
Motif ID:	3
Motif name:	C003
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	2
Number of overlap:	27
Similarity score:	0.0327958

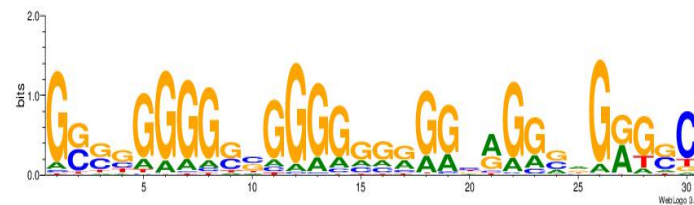
Alignment:

GSSGGGGSSGGGGGKGGVMGGSHGKGS
 --SSSSSSSGSGSSSSGGSSSSSGSSSSS--

Original motif Consensus sequence:
 GSCYCHSCCYVCCYCCCCSSCCCCSSC



Reverse complement motif Consensus sequence:
 GSSGGGGSSGGGGGKGGVMGGSHGKGS

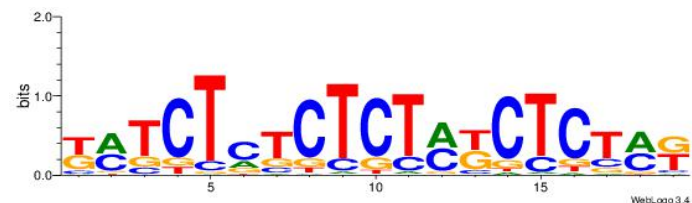
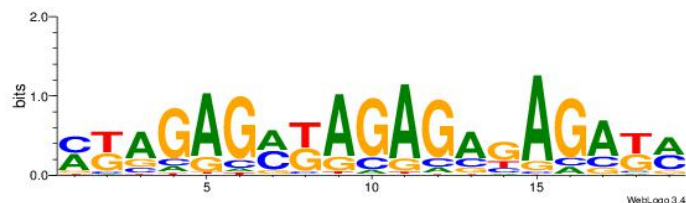


Dataset #:	1
Motif ID:	12
Motif name:	C012
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	19
Similarity score:	4.07247

Alignment:
 -----YRTCTCTCTCTRYCTCTRR
 SSSSSCSSSSSCSSSSCCSCSSSSSS

Original motif Consensus sequence: MKAGAGMKAGAGAGAGAKM

Reverse complement motif Consensus sequence:
 YRTCTCTCTCTRYCTCTRR

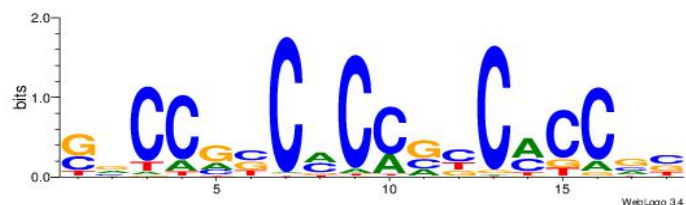


Dataset #: 1
 Motif ID: 37
 Motif name: C037
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 18
 Similarity score: 4.52829

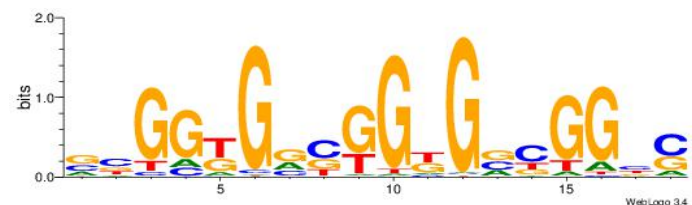
Alignment:

BVGGYGKSGGYGBCGGVS-----
 SSSSSSGSGGSSSSSGSSSSSGSSSS

Original motif Consensus sequence: SVCCGBCMCCSYCMCCVB



Reverse complement motif Consensus sequence: BVGGYGKSGGYGBCGGVS



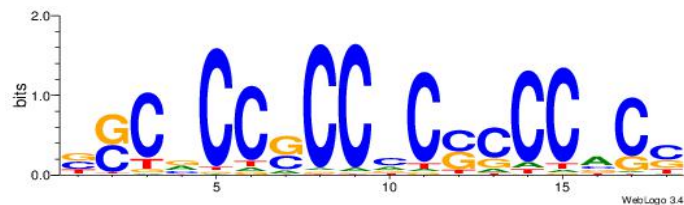
Dataset #: 1

Motif ID: 20
 Motif name: C020
 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: 4.5346

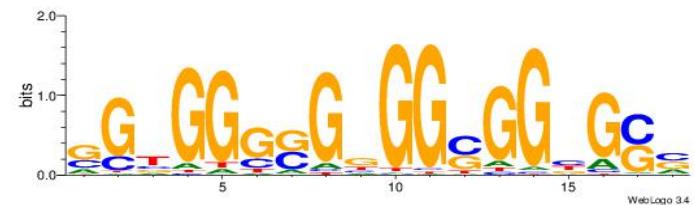
Alignment:

BSCVCCSCCVSCCCACS-----
 SSSSSCSSSSSCSSSSCCSCSSSSSS

Original motif Consensus sequence: BSCVCCSCCVSCCCACS



Reverse complement motif Consensus sequence: SGTGGGSGVGGSGGVGSB

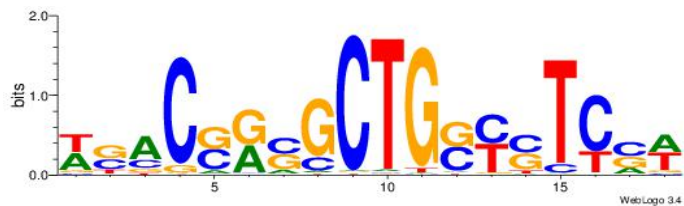


Dataset #: 1
 Motif ID: 124
 Motif name: C124
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 18

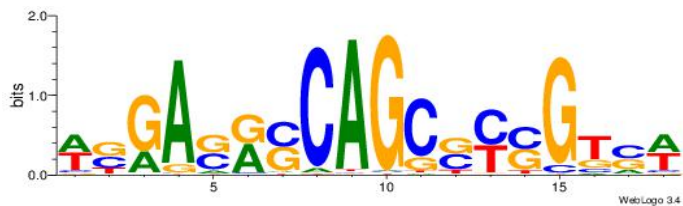
Similarity score: 4.55821

Alignment:
-----WSACSRSGCTGSYSTCSW
SSSSSCSSSSSCSSSSCCSCSSSSSS

Original motif Consensus sequence: WSACSRSGCTGSYSTCSW

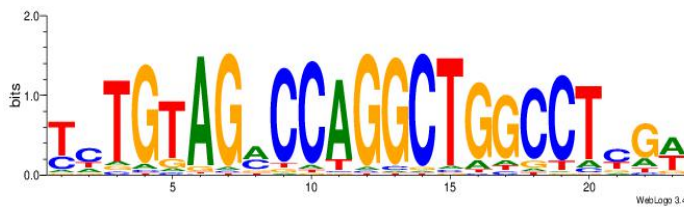


Reverse complement motif Consensus sequence: WSGASKSCAGCSMSGTSW

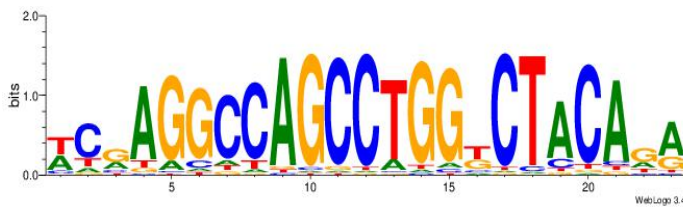


Dataset #: 1 Motif ID: 5 Motif name: C005

Original motif Consensus sequence: TCTGTAGMCCAGGCTGGCCTYGW



Reverse complement motif Consensus sequence: WCKAGGCCAGCCTGGYCTACAGA



Best Matches for Motif ID 5 (Highest to Lowest)

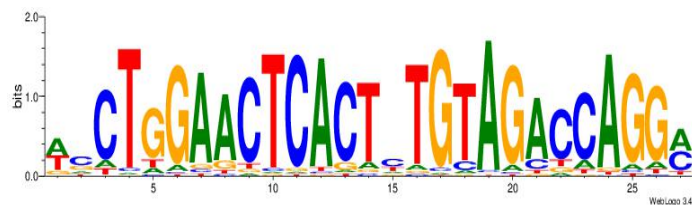
Dataset #:	1
Motif ID:	13
Motif name:	C013
Matching format of first motif:	Original Motif

Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	23
Similarity score:	0.0900989

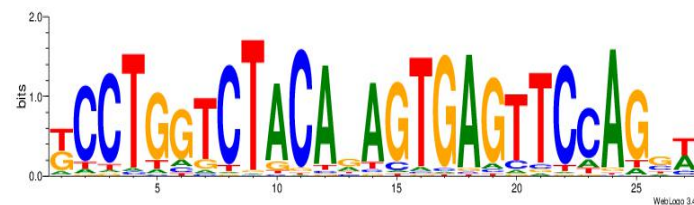
Alignment:

```
WVCTGGAAC TCACTHTGTAGACCAGGM
-TCTGTAGMCCAGGCTGGCCTYGW---
```

Original motif Consensus sequence:
WVCTGGAAC TCACTHTGTAGACCAGGM



Reverse complement motif Consensus sequence:
YCCTGGTCTACADAGTGAGTTCCAGVW

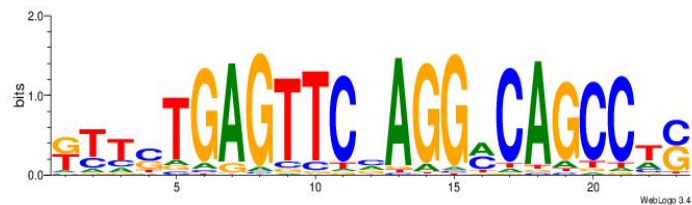


Dataset #:	1
Motif ID:	7
Motif name:	C007
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	3
Number of overlap:	21
Similarity score:	1.05522

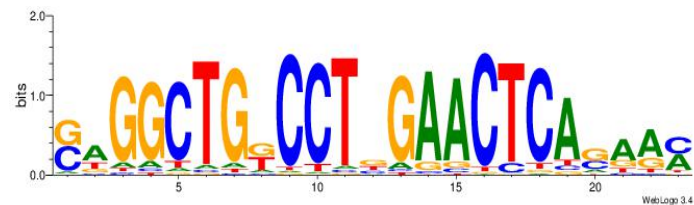
Alignment:

KTTSTGAGTTCVAGGMCAGCCTS--
 --TCTGTAGMCCAGGCTGGCCTYGW

Original motif Consensus sequence: KTTSTGAGTTCVAGGMCAGCCTS



Reverse complement motif Consensus sequence: SAGGCTGYCCTVGAAGTCASAAY



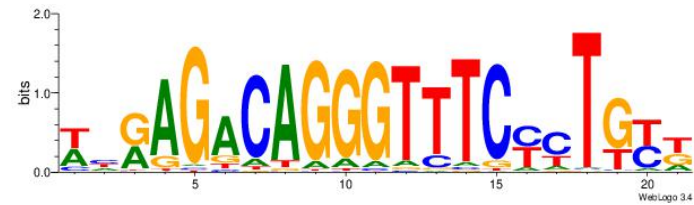
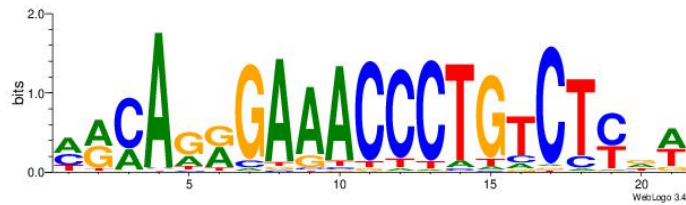
Dataset #:	1
Motif ID:	27
Motif name:	C027
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	21
Similarity score:	1.07502

Alignment:

--WHKAGACAGGGTTTCMCTGKY
 TCTGTAGMCCAGGCTGGCCTYGW

Original motif Consensus sequence: MRCAGRGAAACCCTGTCTYDW

Reverse complement motif Consensus sequence: WHKAGACAGGGTTTCMCTGKY

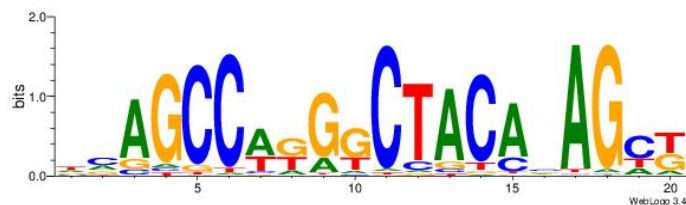


Dataset #: 1
 Motif ID: 15
 Motif name: C015
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 20
 Similarity score: 1.5897

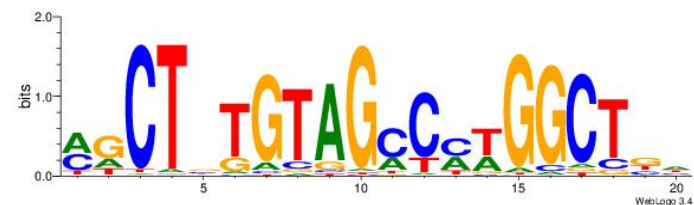
Alignment:

---DVAGCCWKGCTACAVAGCK
 TCTGTAGMCCAGGCTGGCCTYGW

Original motif Consensus sequence: DVAGCCWKGCTACAVAGCK



Reverse complement motif Consensus sequence: RGCTVTGTAGCCYWGCTVD



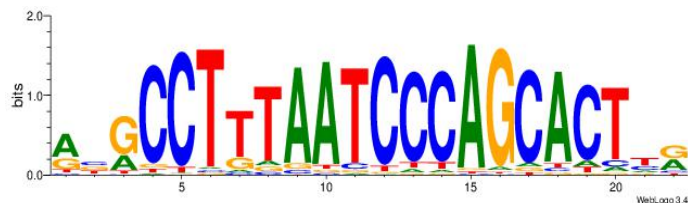
Dataset #: 1

Motif ID: 9
 Motif name: C009
 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: 2.09004

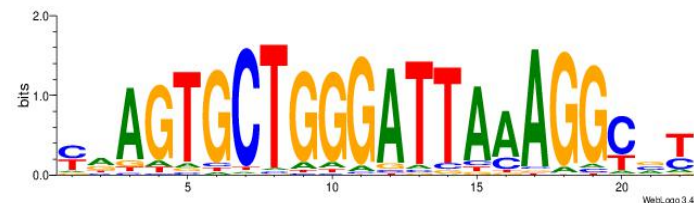
Alignment:

ABGCCTTTAATCCCAGCACTHR----
 ---TCTGTAGMCCAGGCTGGCCTYGW

Original motif Consensus sequence: ABGCCTTTAATCCCAGCACTHR

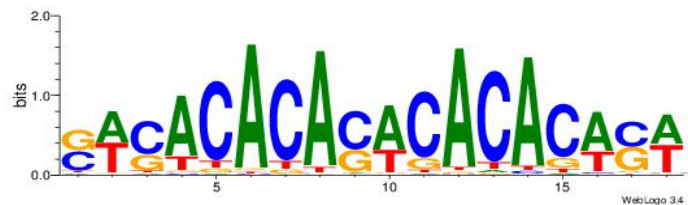


Reverse complement motif Consensus sequence: MHAGTGCTGGGATTAAAGGCBT

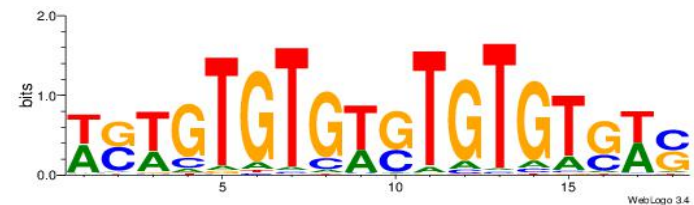


Dataset #: 1 Motif ID: 6 Motif name: C006

Original motif Consensus sequence: SWCACACASWCACACWSW



Reverse complement motif Consensus sequence: WSWGTTGTWSTGTGTGWS



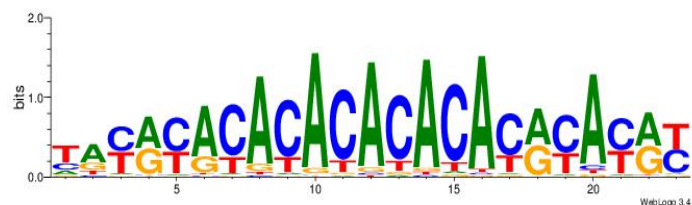
Best Matches for Motif ID 6 (Highest to Lowest)

Dataset #: 1
Motif ID: 2
Motif name: C002
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: 0.00644556

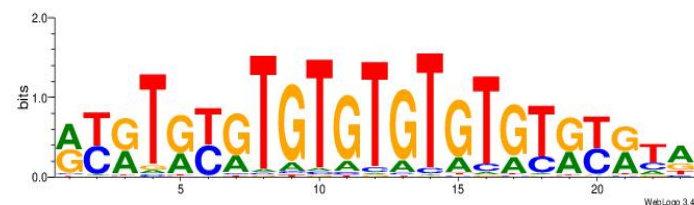
Alignment:

```
MKKTKKGTGTGTGTGTGTTKKKTA  
---WSWGTGTGWSTGTGTGWS---
```

Original motif Consensus sequence: TAYRYACACACACACRYAYRY



Reverse complement motif Consensus sequence: MKKTKKGTGTGTGTGTGTTKKKTA



Dataset #: 1
Motif ID: 17
Motif name: C017
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif

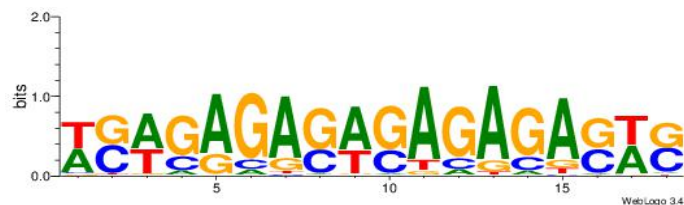
Direction: Backward
 Position number: 1
 Number of overlap: 18
 Similarity score: 0.0313003

Alignment:

WSWGAGASWSAGAGASWS

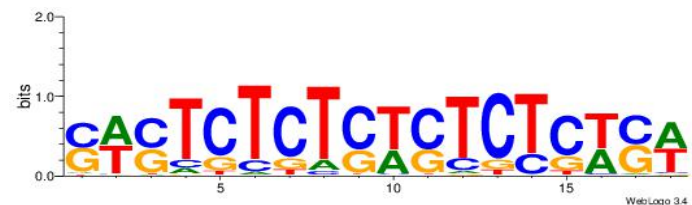
WSWGTGTGWSTGTGTGWS

Original motif Consensus sequence: WSWGAGASWSAGAGASWS



Reverse complement motif
 SWSTCTCTSWSTCTCWSW

Consensus sequence:



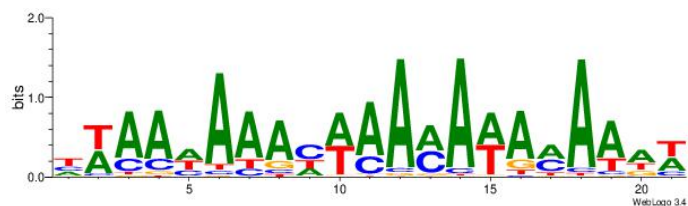
Dataset #: 1
 Motif ID: 16
 Motif name: C016
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 4
 Number of overlap: 18
 Similarity score: 0.0487405

Alignment:

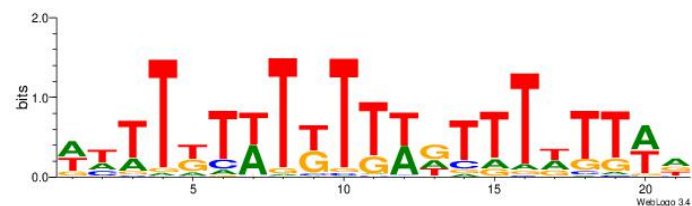
HWAAWAAAHWAAMAWAMAAWW

SWCACACASWCACACWSW---

Original motif Consensus sequence: HWAAWAAHWAAMAWAMAAWW



Reverse complement motif Consensus sequence: WWTYYTWYTTWDTTTWTTWH

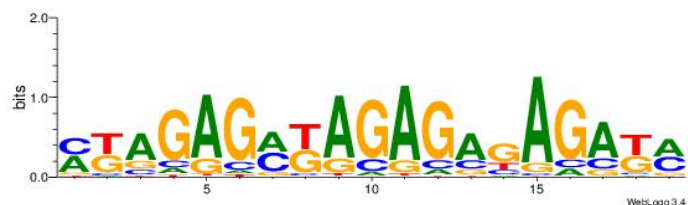


Dataset #: 1
 Motif ID: 12
 Motif name: C012
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 18
 Similarity score: 0.0606253

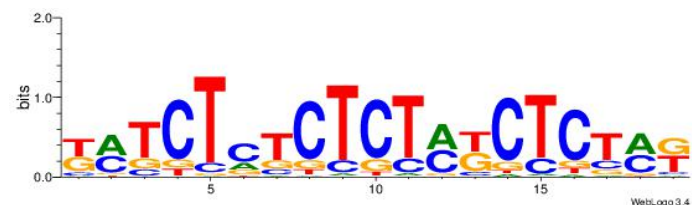
Alignment:

YRTCTCTCTCTRYCTCTRR
 WSWGTTGTGWSTGTGTGWS-

Original motif Consensus sequence: MKAGAGMKAGAGAGAGAKM



Reverse complement motif Consensus sequence: YRTCTCTCTCTRYCTCTRR



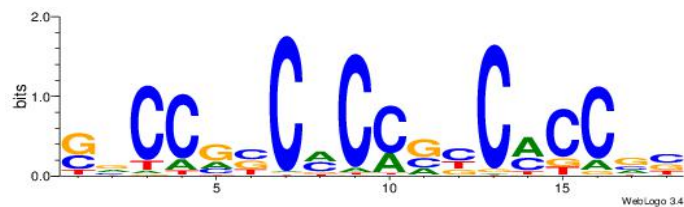
Dataset #: 1
 Motif ID: 37
 Motif name: C037
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 18
 Similarity score: 0.0644383

Alignment:

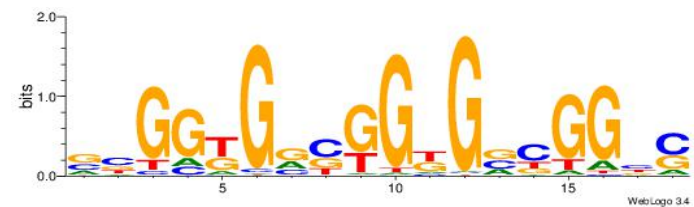
BVGGYGKSGGYGBCGGVS

WSWGTGTGWSTGTGTGWS

Original motif Consensus sequence: SVCCGBCMCCSYCMCCVB



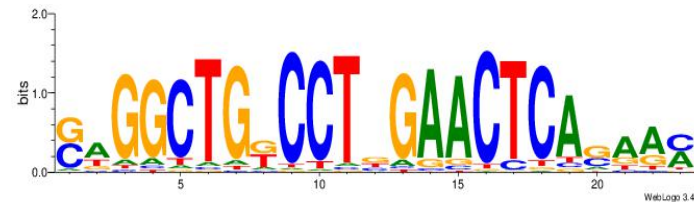
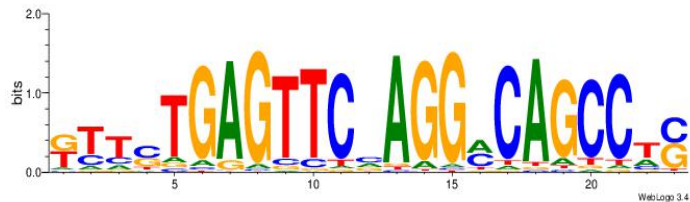
Reverse complement motif Consensus sequence: BVGGYGKSGGYGBCGGVS



Dataset #: 1 Motif ID: 7 Motif name: C007

Original motif Consensus sequence: KTTSTGAGTTCVAGGMCAGCCTS

Reverse complement motif Consensus sequence: SAGGCTGYCCTVGA ACTCASAAY



Best Matches for Motif ID 7 (Highest to Lowest)

Dataset #:	1
Motif ID:	19
Motif name:	C019
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	22
Similarity score:	0.0703515

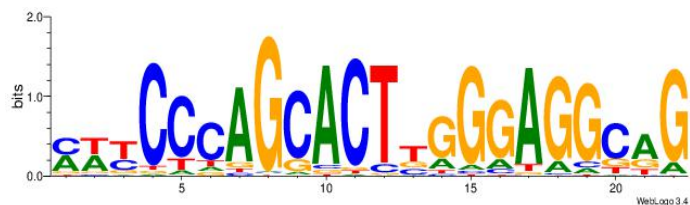
Alignment:

```

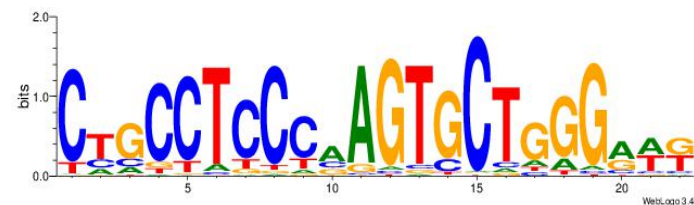
-CTGCCTCCCAAGTGCTGGGMWR
SAGGCTGYCCTVGAAGTCASAA

```

Original motif Consensus sequence: MWYCCCAGCACTTGGGAGGCAG



Reverse complement motif Consensus sequence: CTGCCTCCCAAGTGCTGGGMWR

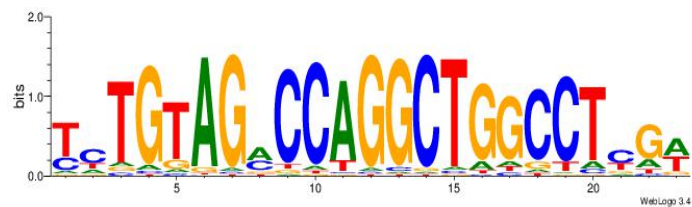


Dataset #: 1
 Motif ID: 5
 Motif name: C005
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 21
 Similarity score: 0.538292

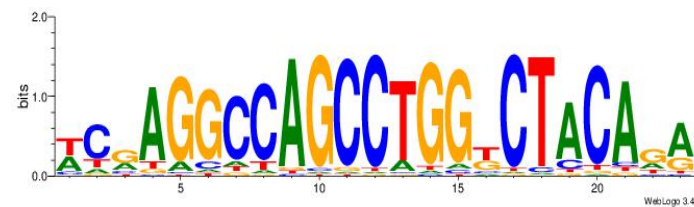
Alignment:

--TCTGTAGMCCAGGCTGGCCTYGW
 KTTSTGAGTTCVAGGMCAGCCTS--

Original motif Consensus sequence: TCTGTAGMCCAGGCTGGCCTYGW



Reverse complement motif Consensus sequence: WCKAGGCCAGCCTGGYCTACAGA



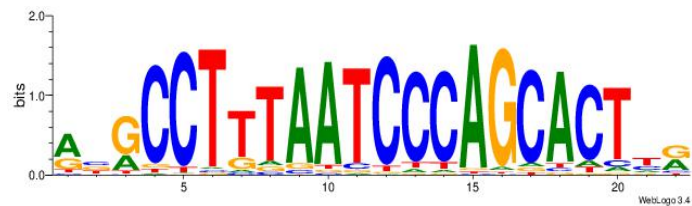
Dataset #: 1
 Motif ID: 9
 Motif name: C009
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3

Number of overlap: 20
Similarity score: 1.06978

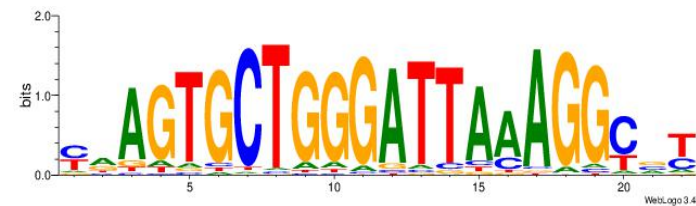
Alignment:

ABGCCTTTAATCCCAGCACTHR---
--KTTSTGAGTTCVAGGMCAGCCTS

Original motif Consensus sequence: ABGCCTTTAATCCCAGCACTHR



Reverse complement motif Consensus sequence: MHAGTGCTGGGATTAAAGGCBT

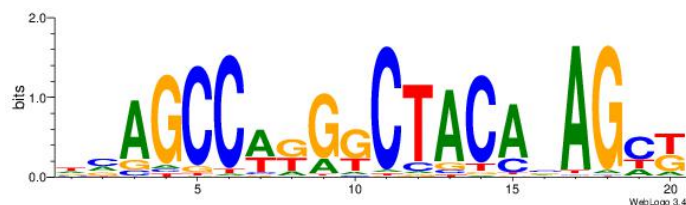


Dataset #: 1
Motif ID: 15
Motif name: C015
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 2
Number of overlap: 19
Similarity score: 1.564

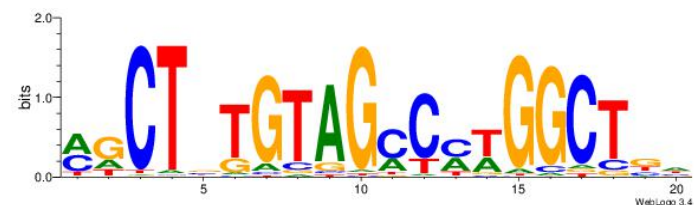
Alignment:

RGCTVTGTAGCCYWGCTVD----
-KTTSTGAGTTCVAGGMCAGCCTS

Original motif Consensus sequence: DVAGCCWKGCTACAVAGCK



Reverse complement motif Consensus sequence: RGCTVTGTAGCCYWGGCTVD

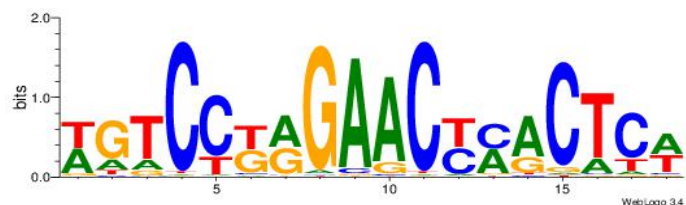


Dataset #: 1
 Motif ID: 42
 Motif name: C042
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 18
 Similarity score: 2.02563

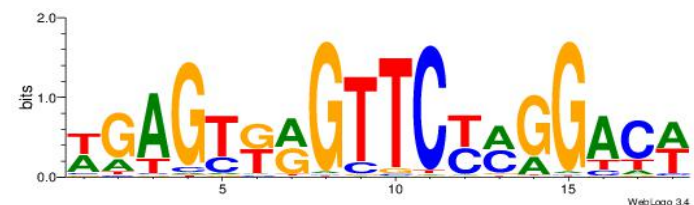
Alignment:

-----WGTCCCKRGAACYMACTCW
 SAGGCTGYCCTVGAACTCASAA

Original motif Consensus sequence: WGTCCCKRGAACYMACTCW

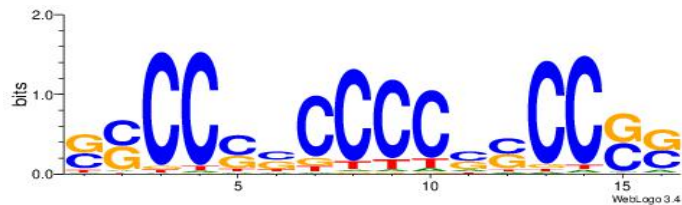


Reverse complement motif Consensus sequence: WGAGTRMGTTCKRGGACW

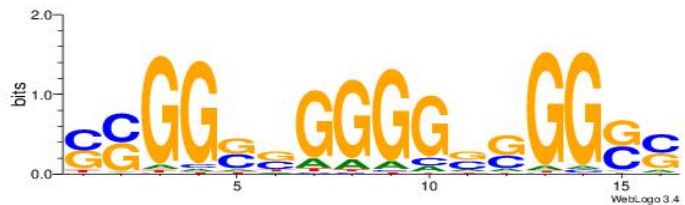


Dataset #: 1 Motif ID: 8 Motif name: C008

Original motif Consensus sequence: SSCCSSCCCCSSCCSS



Reverse complement motif Consensus sequence: SSGGSSGGGGSSGGSS



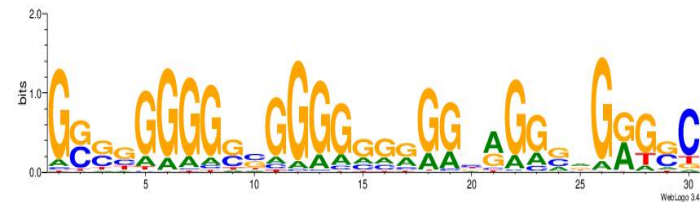
Best Matches for Motif ID 8 (Highest to Lowest)

Dataset #:	1
Motif ID:	3
Motif name:	C003
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:	0.0125829

Alignment:
GSCYCHSCCYVCCYCCCCCSCCCCCSSC
-----SSCCSSCCCCSSCCSS-----

Original motif Consensus sequence:
GSCYCHSCCYVCCYCCCCCSCCCCCSSC

Reverse complement motif Consensus sequence:
GSSGGGGGSSGGGGGGKGGVMGGSHGKGSC

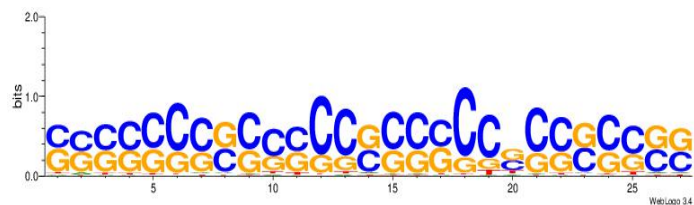


Dataset #:	1
Motif ID:	4
Motif name:	C004
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	3
Number of overlap:	16
Similarity score:	0.0162389

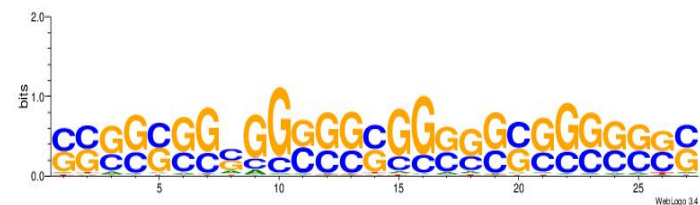
Alignment:

```
SSSSSCSSSSSCSSSSCCSCSSSSSS
-----SSCCSSCCCCSSCCSS--
```

Original motif Consensus sequence:
SSSSSCSSSSSCSSSSCCSCSSSSSS



Reverse complement motif Consensus sequence:
SSSSSSGSGSSSSGSSSSGSSSSS



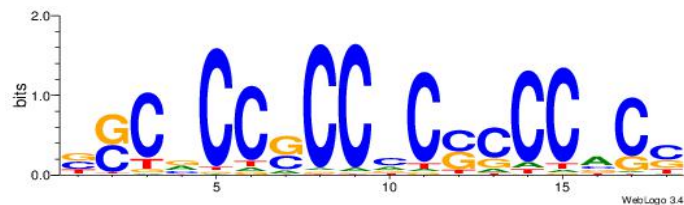
Dataset #: 1

Motif ID: 20
 Motif name: C020
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 16
 Similarity score: 0.0195292

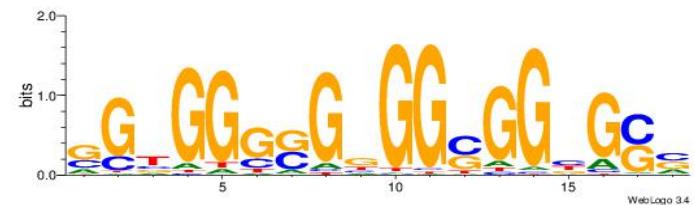
Alignment:

SGTGGGSGVGGSGGVGSB
 -SSGGSSGGGGSSGGSS-

Original motif Consensus sequence: BSCVCCSCCVSCCCACS



Reverse complement motif Consensus sequence: SGTGGGSGVGGSGGVGSB

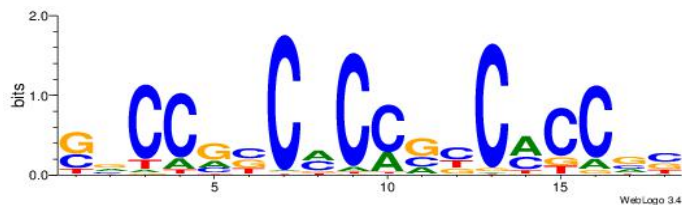


Dataset #: 1
 Motif ID: 37
 Motif name: C037
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 16

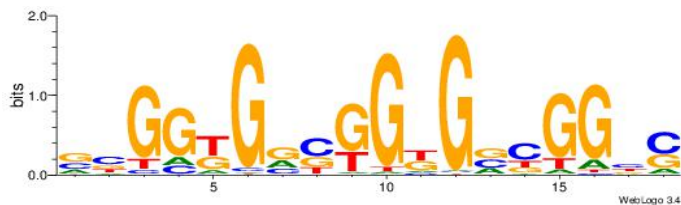
Similarity score: 0.0247991

Alignment:
SVCCGBCMCCSYCMCCVB
SSCCSSCCCCSSCCSS--

Original motif Consensus sequence: SVCCGBCMCCSYCMCCVB



Reverse complement motif Consensus sequence:
BVGGYGKSGGYGBCGGVS

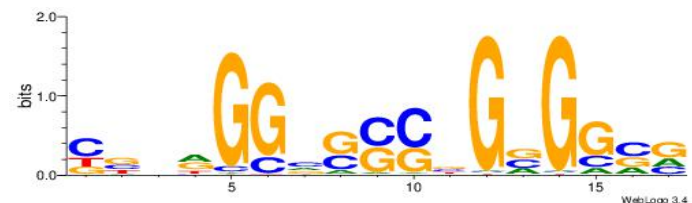
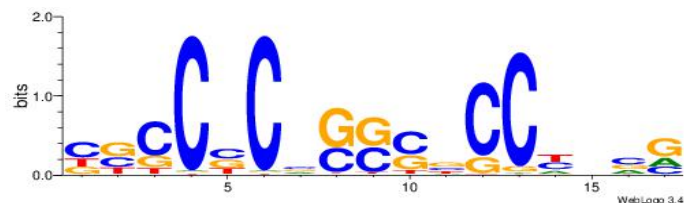


Dataset #: 1
Motif ID: 140
Motif name: C140
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 16
Similarity score: 0.041903

Alignment:
BSCCBVSSSBCCYHVG
SSCCSSCCCCSSCCSS-

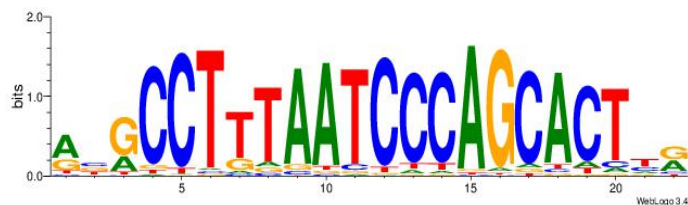
Original motif Consensus sequence: BSCCBVSSSBCCYHVG

Reverse complement motif Consensus sequence:
CVDMGGBSSSVGBGGSB

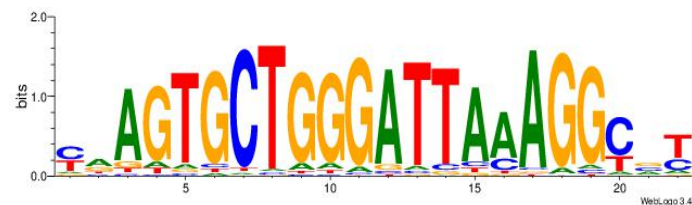


Dataset #: 1 Motif ID: 9 Motif name: C009

Original motif Consensus sequence: ABGCCTTTAATCCCAGCACTHR



Reverse complement motif Consensus sequence: MHAGTGCTGGGATTAAAGGCBT



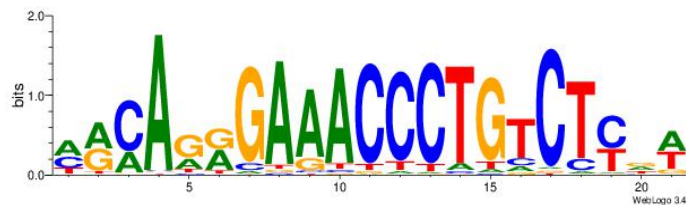
Best Matches for Motif ID 9 (Highest to Lowest)

Dataset #:	1
Motif ID:	27
Motif name:	C027
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	21
Similarity score:	0.0757308

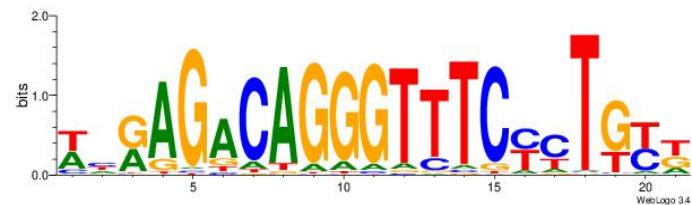
Alignment:

-MRCAGRGAAACCCTGTCTYDW
ABGCCTTTAATCCCAGCACTHR

Original motif Consensus sequence: MRCAGRGAAACCCTGTCTYDW



Reverse complement motif Consensus sequence:
WHKAGACAGGGTTTCMCTGKY



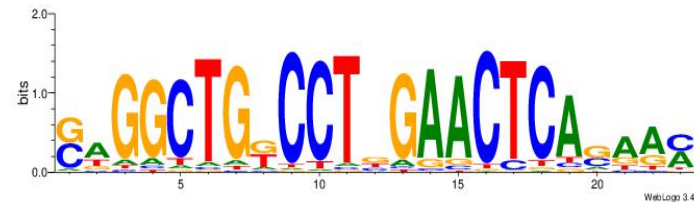
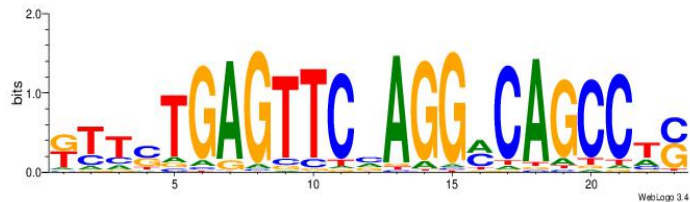
Dataset #:	1
Motif ID:	7
Motif name:	C007
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	4
Number of overlap:	20
Similarity score:	0.576852

Alignment:

--KTTSTGAGTTCVAGGMCAGCCTS
ABGCCTTTAATCCCAGCACTHR---

Original motif Consensus sequence: KTTSTGAGTTCVAGGMCAGCCTS

Reverse complement motif Consensus sequence:
SAGGCTGYCCTVGA ACTCASAAY

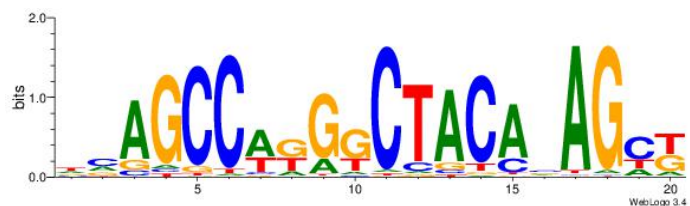


Dataset #: 1
 Motif ID: 15
 Motif name: C015
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.580317

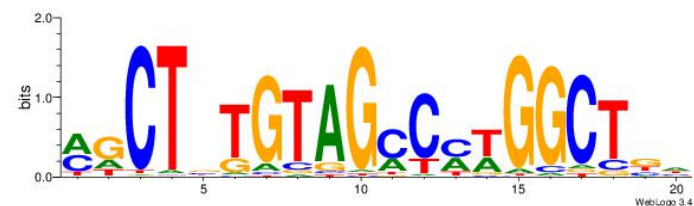
Alignment:

RGCTVTGTAGCCYWGGCTVD--
 ABGCCTTTAATCCCAGCACTHR

Original motif Consensus sequence: DVAGCCWKGCTACAVAGCK



Reverse complement motif Consensus sequence: RGCTVTGTAGCCYWGGCTVD



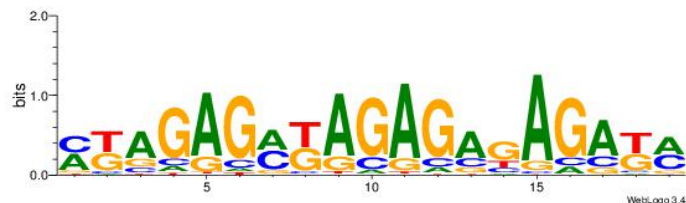
Dataset #: 1

Motif ID: 12
 Motif name: C012
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 19
 Similarity score: 1.07996

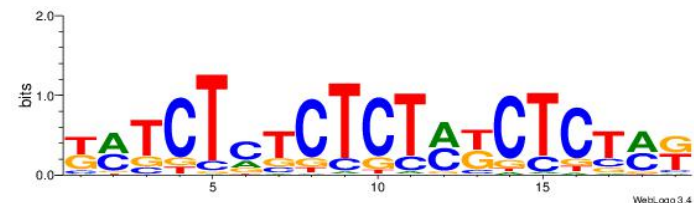
Alignment:

MKAGAGMKAGAGAGAGAKM---
 MHAGTGCTGGGATTAAAGGCBT

Original motif Consensus sequence: MKAGAGMKAGAGAGAGAKM



Reverse complement motif Consensus sequence: YRTCTCTCTRYCTCTRR

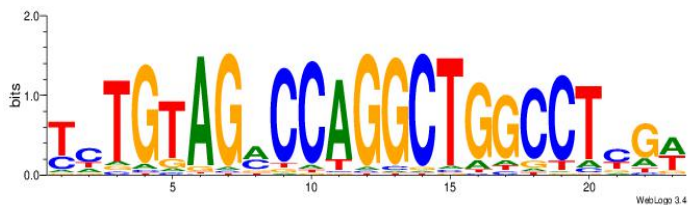


Dataset #: 1
 Motif ID: 5
 Motif name: C005
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 5
 Number of overlap: 19

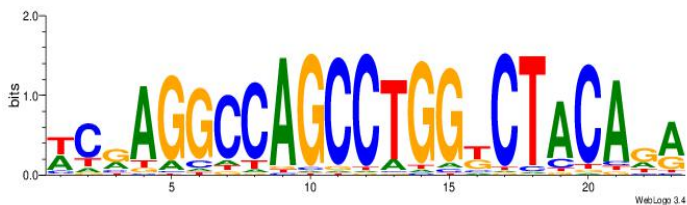
Similarity score: 1.08019

Alignment:
---TCTGTAGMCCAGGCTGGCCTYGW
ABGCCTTTAATCCCAGCACTHR----

Original motif Consensus sequence: TCTGTAGMCCAGGCTGGCCTYGW

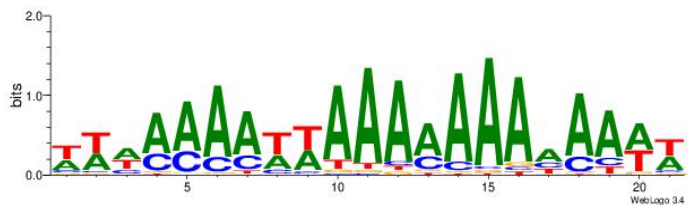


Reverse complement motif Consensus sequence: WCKAGGCCAGCCTGGYCTACAGA

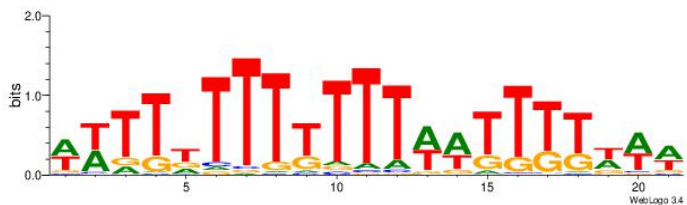


Dataset #: 1 Motif ID: 10 Motif name: C010

Original motif Consensus sequence: WWWAAAWWAAAAAAAAAAWW



Reverse complement motif Consensus sequence: WWTTTTTTTTTWWTTTTWWW



Best Matches for Motif ID 10 (Highest to Lowest)

Dataset #:	1
Motif ID:	1
Motif name:	C001
Matching format of first motif:	Reverse Complement

Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	9
Number of overlap:	21
Similarity score:	0.0115098

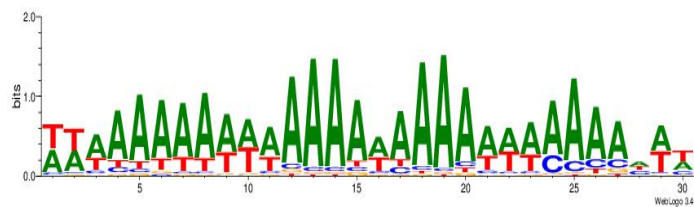
Alignment:

```

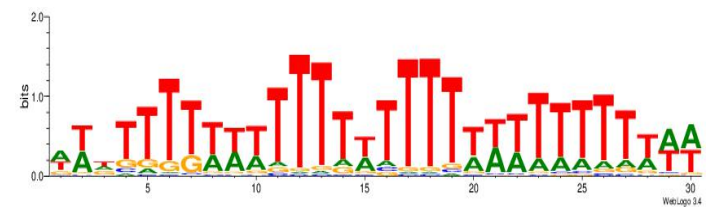
WWHTTTTWWTTTTTWWTTTTTWWTTTTTWWW
-----WWTTTTTTTTTTWWTTTTTWWW-

```

Original motif Consensus sequence:
WWWAAAAWWAAAAWAAAAWAAAAHWW



Reverse complement motif Consensus sequence:
WWHTTTTWWTTTTTWWTTTTTWWTTTTTWWW

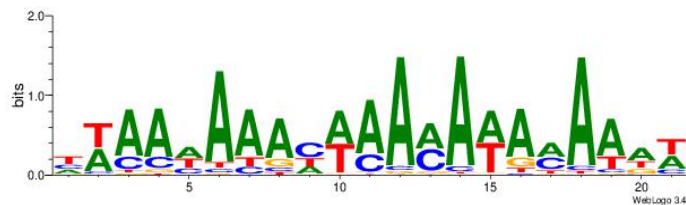


Dataset #:	1
Motif ID:	16
Motif name:	C016
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	21
Similarity score:	0.0128672

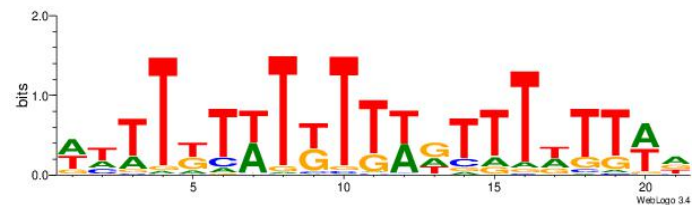
Alignment:

HWAAWAAAHWAAMAWAMAAWW
 WWWAAAAWWAAAAAAAAAAWW

Original motif Consensus sequence: HWAAWAAAHWAAMAWAMAAWW



Reverse complement motif Consensus sequence:
 WWTYYTWYTTWDTTTWTTWH



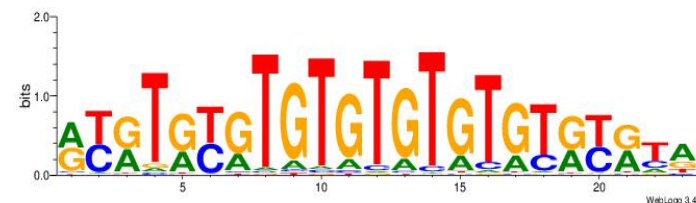
Dataset #:	1
Motif ID:	2
Motif name:	C002
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	21
Similarity score:	0.0748547

Alignment:

TAYRYACACACACACRYAYRY
 WWWAAAAWWAAAAAAAAAAWW--

Original motif Consensus sequence: TAYRYACACACACACRYAYRY

Reverse complement motif Consensus sequence:
 MKKTKKGTGTGTGTGTGKKT

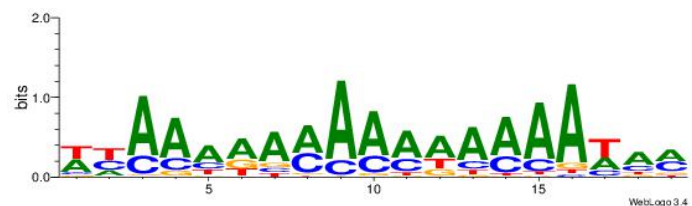


Dataset #:	1
Motif ID:	30
Motif name:	C030
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	19
Similarity score:	1.02629

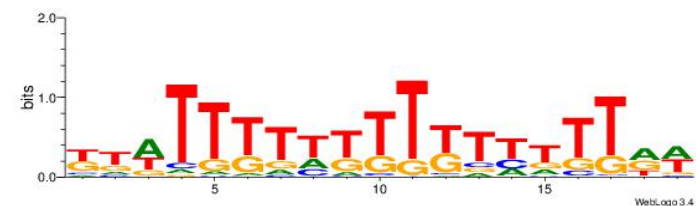
Alignment:

--YTWTTTTTTTYTTTTMW
WWTTTTTTTTTWWTTTWWW

Original motif Consensus sequence: WYAAAAAMAAAAAAAWAM



Reverse complement motif Consensus sequence:
YTWTTTTTTTTYTTTTMW



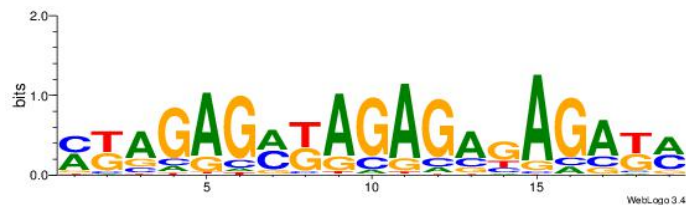
Dataset #: 1

Motif ID: 12
 Motif name: C012
 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: 1.0801

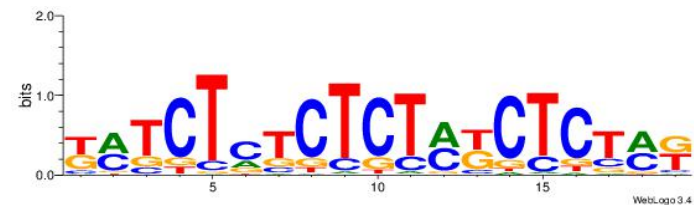
Alignment:

--YRTCTCTCTCTRYCTCTRR
 WTTTTTTTTTTTTWTTTTWWW

Original motif Consensus sequence: MKAGAGMKAGAGAGAGAKM

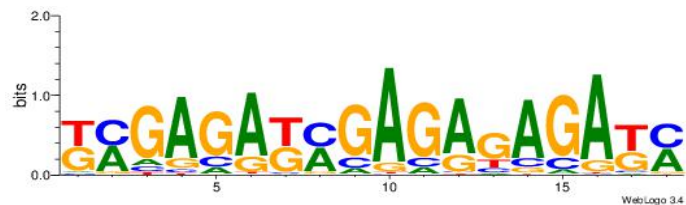


Reverse complement motif Consensus sequence: YRTCTCTCTCTRYCTCTRR

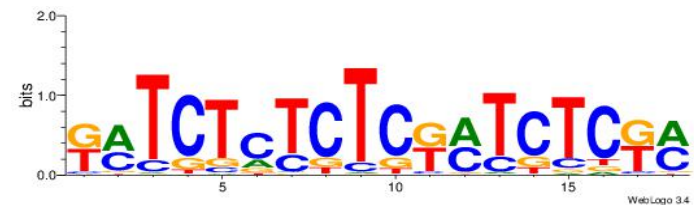


Dataset #: 1 Motif ID: 11 Motif name: C011

Original motif Consensus sequence: KMGAGAKMGAGAGAGAKM



Reverse complement motif Consensus sequence: RRTCTCTCTCRRTCTCRR



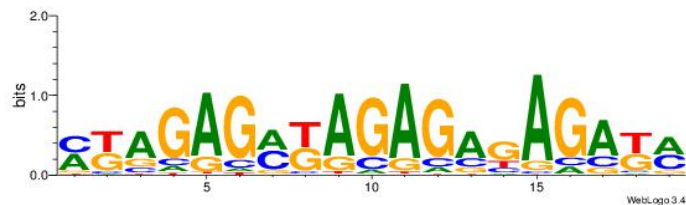
Best Matches for Motif ID 11 (Highest to Lowest)

Dataset #: 1
Motif ID: 12
Motif name: C012
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: 0.0233796

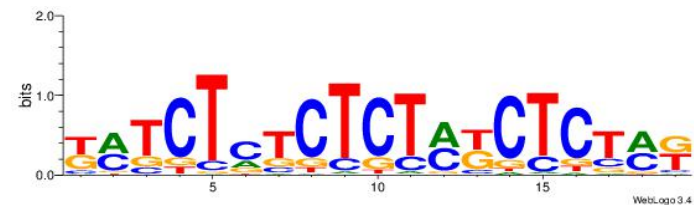
Alignment:

MKAGAGMKAGAGAGAGAKM
-KMGAGAKMGAGAGAGAKM

Original motif Consensus sequence: MKAGAGMKAGAGAGAGAKM



Reverse complement motif Consensus sequence: YRTCTCTCTRYCTCTRR



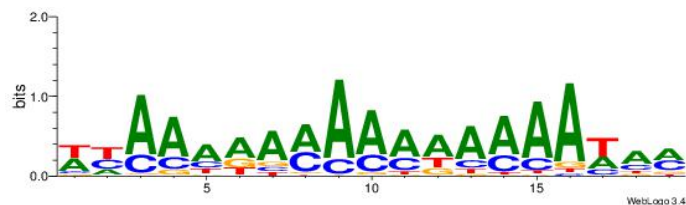
Dataset #: 1
Motif ID: 30
Motif name: C030
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif

Direction: Forward
 Position number: 1
 Number of overlap: 18
 Similarity score: 0.0993282

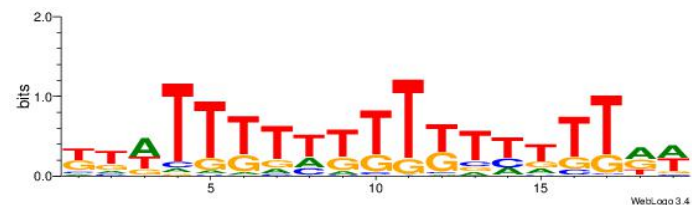
Alignment:

WYAAAAAMAAAAAAWAM
 KMGAGAKMGAGAGAGAKM-

Original motif Consensus sequence: WYAAAAAMAAAAAAWAM



Reverse complement motif Consensus sequence: YTWTTTTTTTTYTTTTMW

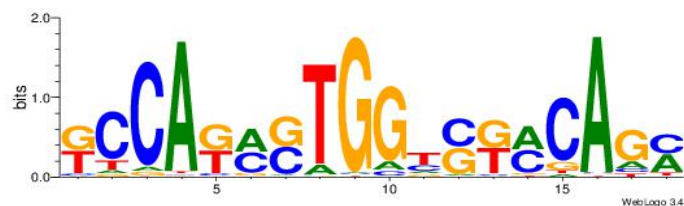


Dataset #: 1
 Motif ID: 95
 Motif name: C095
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 18
 Similarity score: 0.101588

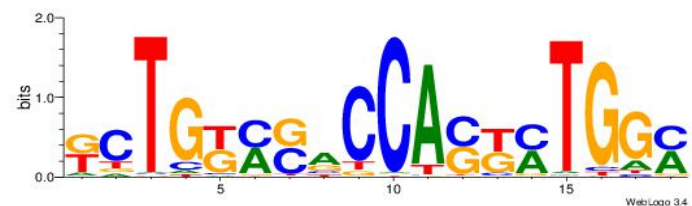
Alignment:

KCCAKMSTGGTSKMCAGM
 KMGAGAKMGAGAGAGAKM

Original motif Consensus sequence: KCCAKMSTGGTSKMCAGM



Reverse complement motif Consensus sequence: RCTGYYSACCASYYTGGY

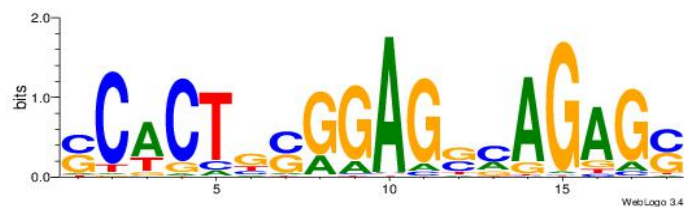


Dataset #: 1
 Motif ID: 34
 Motif name: C034
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 18
 Similarity score: 0.102501

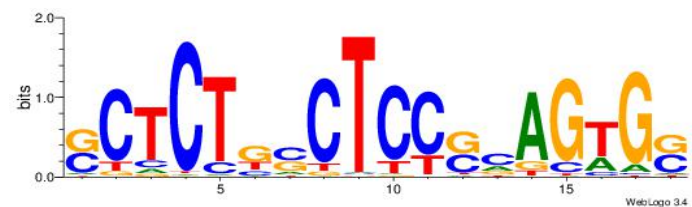
Alignment:

SCTCTRSCTCCSCAGTGS
 RRTCTCTCTCRRTCTCRR

Original motif Consensus sequence: SCACTGSGGAGSMAGAGS



Reverse complement motif Consensus sequence: SCTCTRSCTCCSCAGTGS

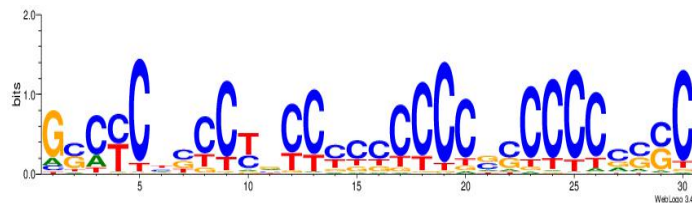


Dataset #: 1
 Motif ID: 3
 Motif name: C003
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 11
 Number of overlap: 18
 Similarity score: 0.103902

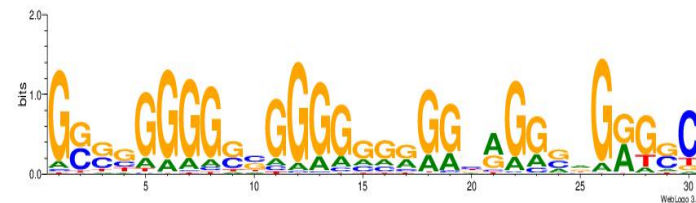
Alignment:

GSCYCHSCCYVCCYCCCCCSCCCCCSSC
 --RRTCTCTCTCRRCTCTCRR-----

Original motif Consensus sequence:
 GSCYCHSCCYVCCYCCCCCSCCCCCSSC



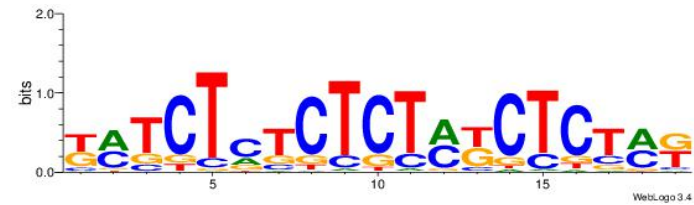
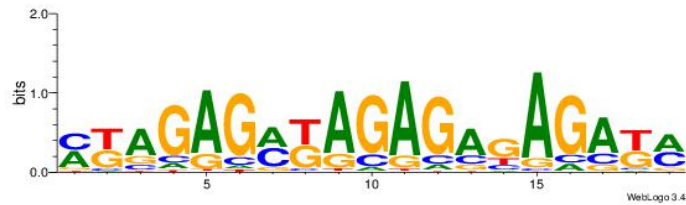
Reverse complement motif Consensus sequence:
 GSSGGGGGSSGGGGGKGGVMGGSHGKGSC



Dataset #: 1 Motif ID: 12 Motif name: C012

Original motif Consensus sequence: MKAGAGMKAGAGAGAGAKM

Reverse complement motif Consensus sequence:
 YRTCTCTCTCTRYCTCTRR



Best Matches for Motif ID 12 (Highest to Lowest)

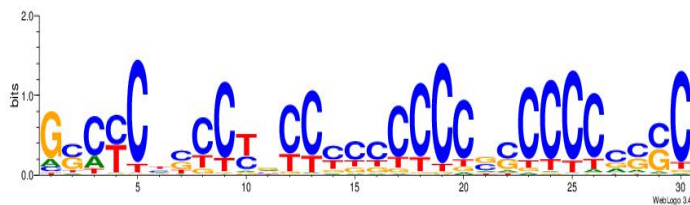
Dataset #: 1
 Motif ID: 3
 Motif name: C003
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 19
 Similarity score: 0.0795922

Alignment:

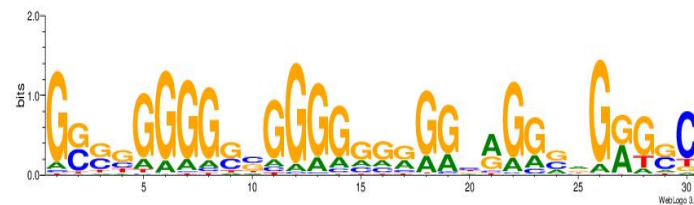
```

GSSGGGGGSSGGGGGKGGVMGGSHGKGSC
-----MKAGAGMKAGAGAGAGAKM--
  
```

Original motif Consensus sequence:
 GSCYCHSCCYVCCYCCCCSSCCCCSSC



Reverse complement motif Consensus sequence:
 GSSGGGGGSSGGGGGKGGVMGGSHGKGSC

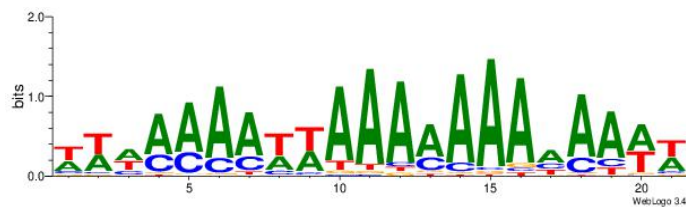


Dataset #: 1
 Motif ID: 10
 Motif name: C010
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 19
 Similarity score: 0.090302

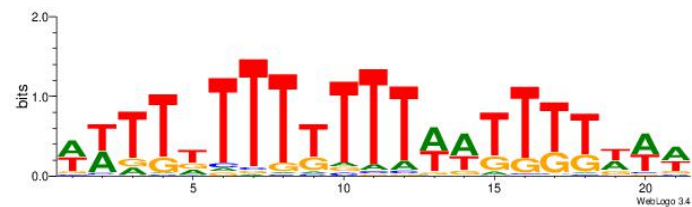
Alignment:

WWTTTTTTTTTTWWTTTTWWW
 -YRTCTCTCTCTRYCTCTRR-

Original motif Consensus sequence: WWWAAAWWAAAAAAAAAAWW



Reverse complement motif Consensus sequence: WWTTTTTTTTTTWWTTTTWWW



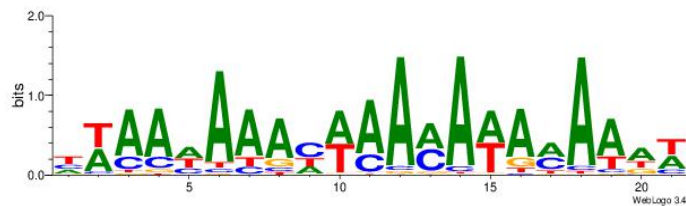
Dataset #: 1
 Motif ID: 16
 Motif name: C016
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2

Number of overlap: 19
Similarity score: 0.0908644

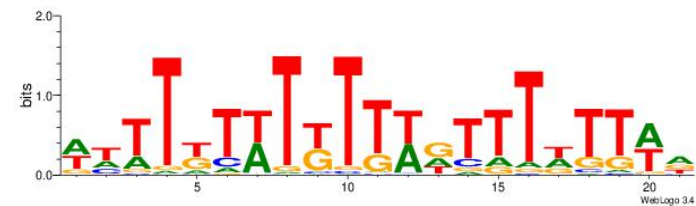
Alignment:

WTTYTWYTTWDTTTWTWH
-YRTCTCTCTRYCTCTRR-

Original motif Consensus sequence: HWAAWAAAHWAAMAWAMAAWW



Reverse complement motif Consensus sequence: WTTYTWYTTWDTTTWTWH

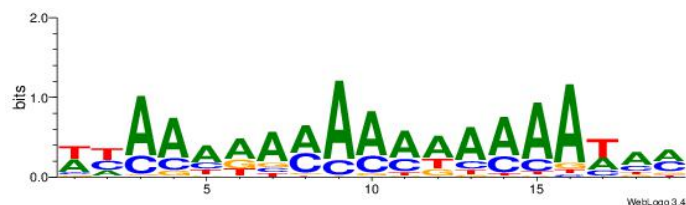


Dataset #: 1
Motif ID: 30
Motif name: C030
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 19
Similarity score: 0.0978175

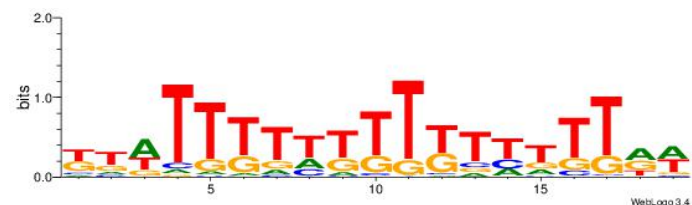
Alignment:

YTWTTTTTTTTYTTTTMW
YRTCTCTCTRYCTCTRR

Original motif Consensus sequence: WYAAAAAMAAAAAAAWAM



Reverse complement motif Consensus sequence: YTWTTTTTTTTTMTTMW

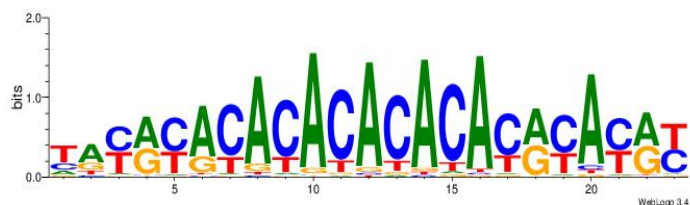


Dataset #: 1
 Motif ID: 2
 Motif name: C002
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 4
 Number of overlap: 19
 Similarity score: 0.0979442

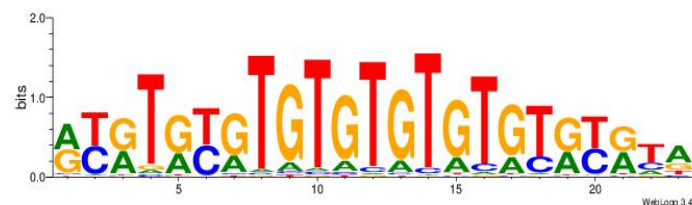
Alignment:

MKKTKKGTGTGTGTGTGTTKKKTA
 ---YRTCTCTCTCTRYCTCTRR-

Original motif Consensus sequence: TAYRYACACACACACRYAYRY

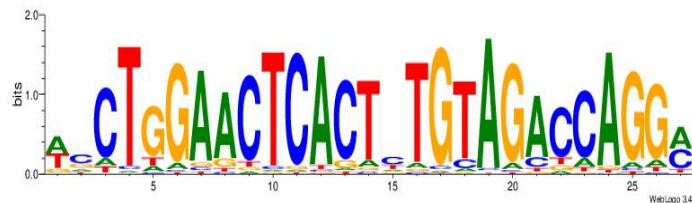


Reverse complement motif Consensus sequence: MKKTKKGTGTGTGTGTGTTKKKTA

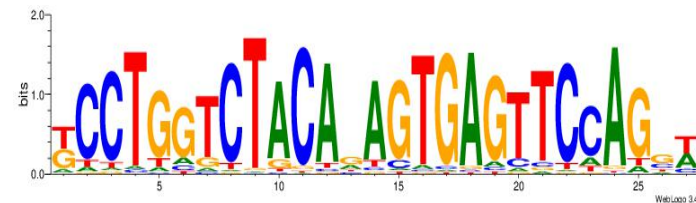


Dataset #: 1 Motif ID: 13 Motif name: C013

Original motif Consensus sequence:
WVCTGGAAC TCACTHTGTAGACCAGGM



Reverse complement motif Consensus sequence:
YCCTGGTCTACADAGTGAGTTCCAGVW



Best Matches for Motif ID 13 (Highest to Lowest)

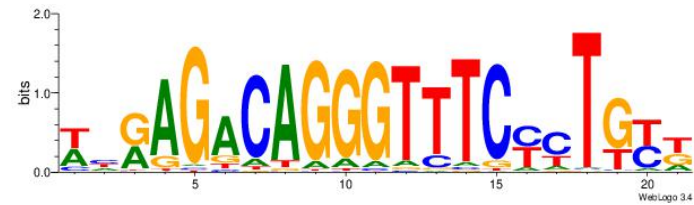
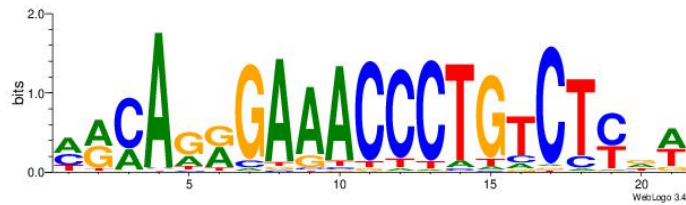
Dataset #:	1
Motif ID:	27
Motif name:	C027
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	21
Similarity score:	1.07948

Alignment:

```
-----WHKAGACAGGGTTTCMCTGKY
YCCTGGTCTACADAGTGAGTTCCAGVW
```

Original motif Consensus sequence: MRCAGRGAAACCCTGTCTYDW

Reverse complement motif Consensus sequence:
WHKAGACAGGGTTTCMCTGKY

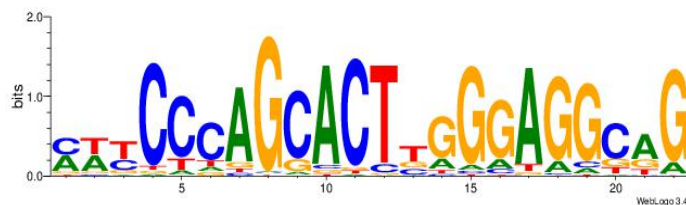


Dataset #: 1
 Motif ID: 19
 Motif name: C019
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 20
 Similarity score: 1.58576

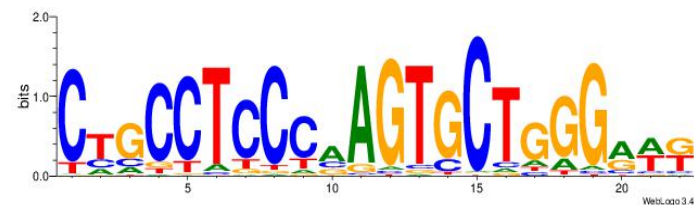
Alignment:

-----CTGCCTCCCAAGTGCTGGGMWR
 YCCTGGTCTACADAGTGAGTTCCAGVW--

Original motif Consensus sequence: MWYCCCAGCACTTGGGAGGCAG



Reverse complement motif Consensus sequence: CTGCCTCCCAAGTGCTGGGMWR



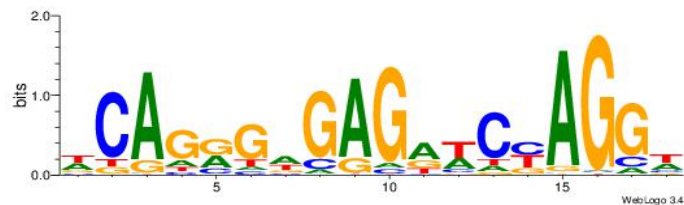
Dataset #: 1

Motif ID: 132
 Motif name: C132
 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: 2.53219

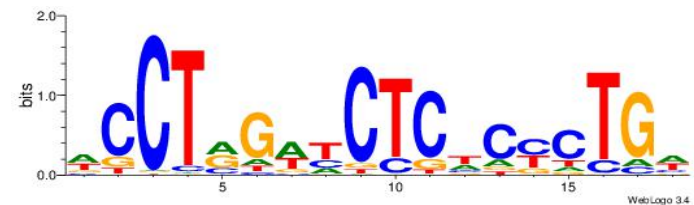
Alignment:

-----WCAGRGWGAGAWCYAGGW
 YCCTGGTCTACADAGTGAGTTCCAGVW

Original motif Consensus sequence: WCAGRGWGAGAWCYAGGW



Reverse complement motif Consensus sequence: WCCTKGWTCTCWCMTGW

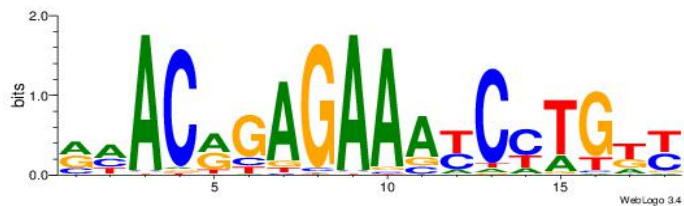


Dataset #: 1
 Motif ID: 53
 Motif name: C053
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 18

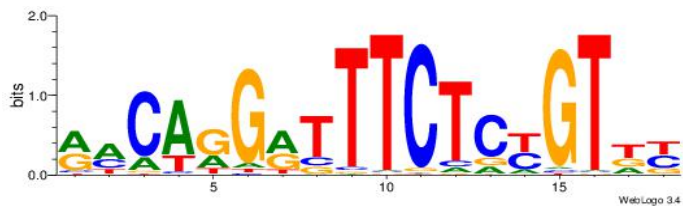
Similarity score: 2.56997

Alignment:
-----RMACRGAGAAAYCCTGKY
YCCTGGTCTACADAGTGAGTTCCAGVW

Original motif Consensus sequence: RMACRGAGAAAYCCTGKY



Reverse complement motif Consensus sequence: MRCAGGMTTCTCKGTYK

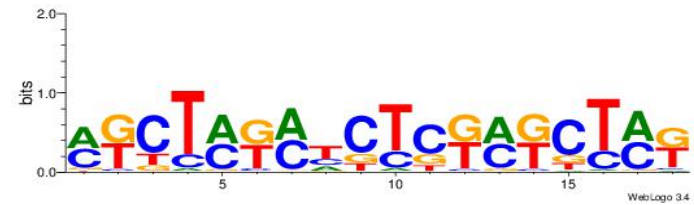
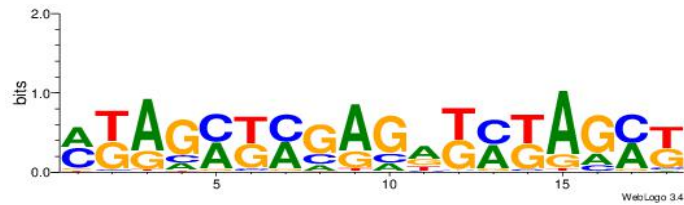


Dataset #: 1
Motif ID: 36
Motif name: C036
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 18
Similarity score: 2.57014

Alignment:
RRCTRRRTCTCRRRCTRY-----
WVCTGGAAC TCACTHTGTAGACCAGGM

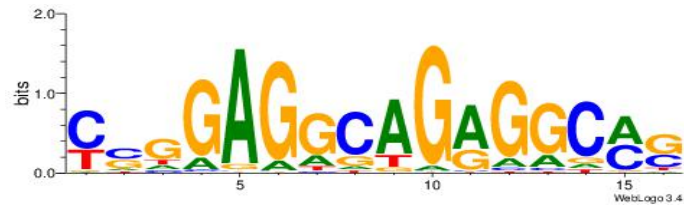
Original motif Consensus sequence: MKAGMKMGAGAKMKAGMK

Reverse complement motif Consensus sequence: RRCTRRRTCTCRRRCTRY

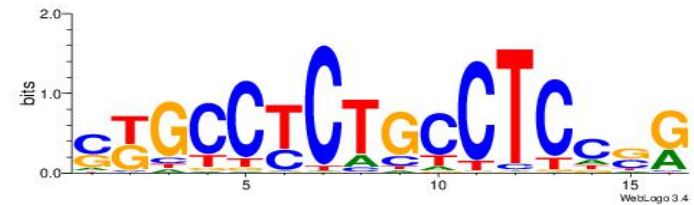


Dataset #: 1 Motif ID: 14 Motif name: C014

Original motif Consensus sequence: YSGGAGGCAGAGGCMS



Reverse complement motif Consensus sequence: SYGCCTCTGCCTCCSK



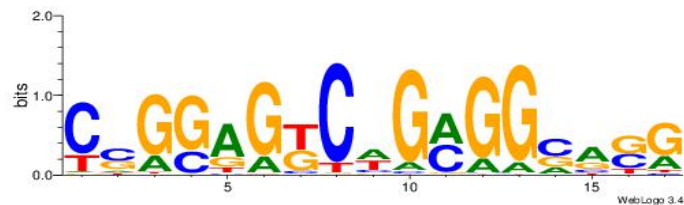
Best Matches for Motif ID 14 (Highest to Lowest)

Dataset #:	1
Motif ID:	86
Motif name:	C086
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:	0.0100715

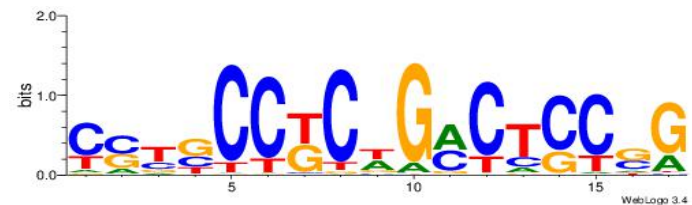
Alignment:

CSGGAGKCWGMGGSASG
YSGGAGGCAGAGGCMS-

Original motif Consensus sequence: CSGGAGKCWGMGGSASG



Reverse complement motif Consensus sequence: CSTSCCYCWGRCTCCSG

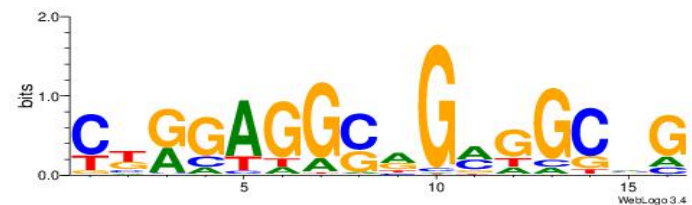
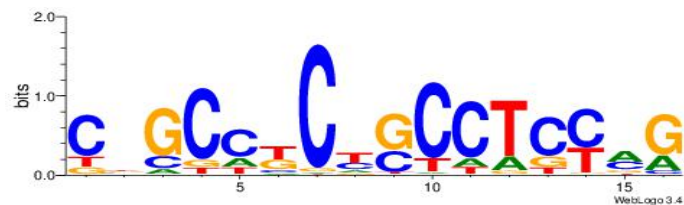


Dataset #: 1
Motif ID: 50
Motif name: C050
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 16
Similarity score: 0.0116342

Alignment:
CBGCCCKYSCCTCYMG
SYGCCTCTGCCTCCSK

Original motif Consensus sequence: CBGCCCKYSCCTCYMG

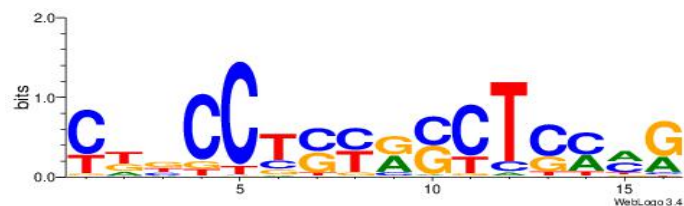
Reverse complement motif Consensus sequence: CYKGAGGSMGRGGCVG



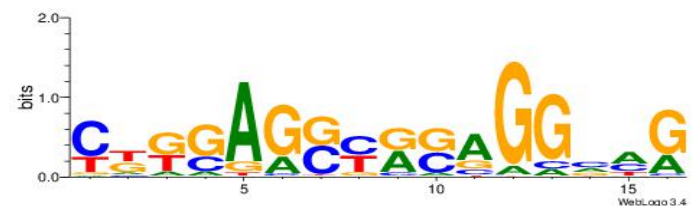
Dataset #: 1
 Motif ID: 83
 Motif name: C083
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 16
 Similarity score: 0.0348886

Alignment:
 CKBCCTSYRSCTCMMG
 SYGCCTCTGCCTCCSK

Original motif Consensus sequence: CKBCCTSYRSCTCMMG



Reverse complement motif Consensus sequence: CYRGAGSMKSAGGBRG



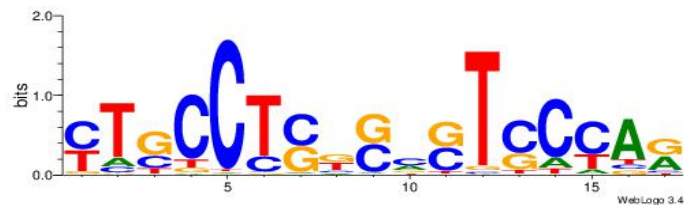
Dataset #: 1

Motif ID:	101
Motif name:	C101
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:	0.0376801

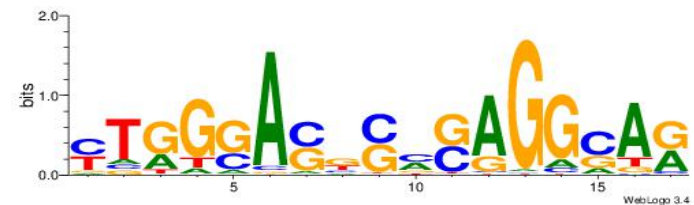
Alignment:

MTGGGASVSY SAGGSAK
 -YSGGAGGCAGAGGCMS

Original motif Consensus sequence: YTSCCTSKSVSTCCCAR



Reverse complement motif Consensus sequence: MTGGGASVSY SAGGSAK

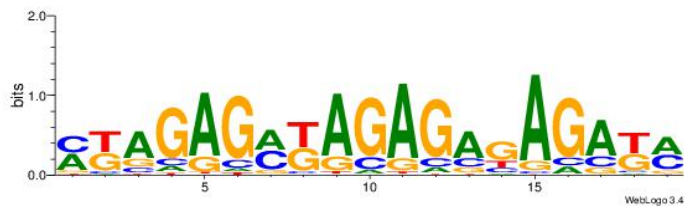


Dataset #:	1
Motif ID:	12
Motif name:	C012
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	16

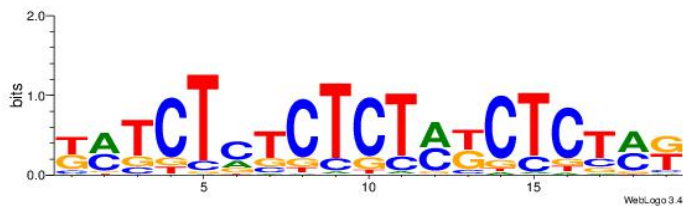
Similarity score: 0.0398723

Alignment:
YRTCTCTCTCTRYCTCTRR
---SYGCCTCTGCCTCCSK

Original motif Consensus sequence: MKAGAGMKAGAGAGAGAKM

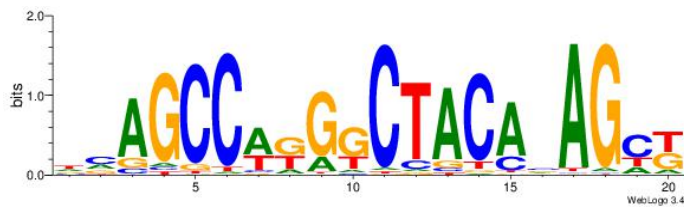


Reverse complement motif Consensus sequence: YRTCTCTCTCTRYCTCTRR

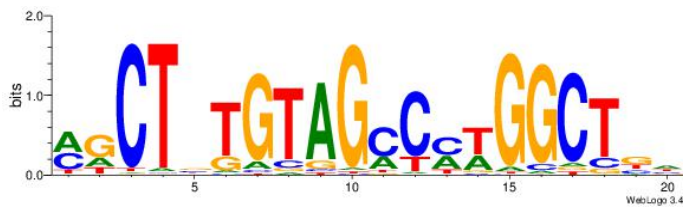


Dataset #: 1 Motif ID: 15 Motif name: C015

Original motif Consensus sequence: DVAGCCWKGCTACAVAGCK



Reverse complement motif Consensus sequence: RGCTVTGTAGCCYWGCTVD



Best Matches for Motif ID 15 (Highest to Lowest)

Dataset #:	1
Motif ID:	27
Motif name:	C027
Matching format of first motif:	Original Motif

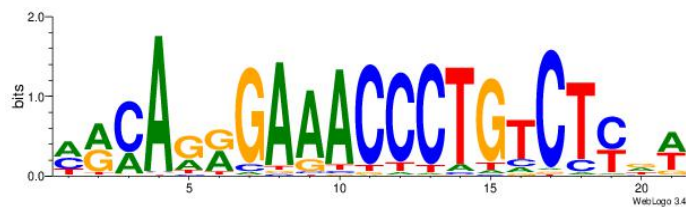
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	2
Number of overlap:	20
Similarity score:	0.0455946

Alignment:

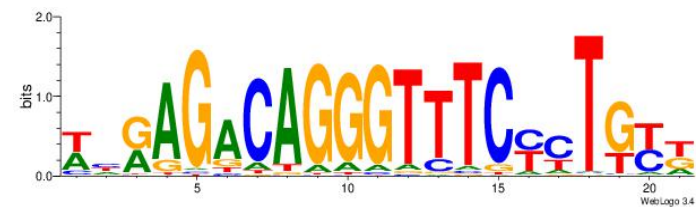
```

WHKAGACAGGGTTTCMCTGKY
-DVAGCCWKG GCTACAVAGCK
  
```

Original motif Consensus sequence: MRCAGRGAAACCCTGTCTYDW



Reverse complement motif Consensus sequence: WHKAGACAGGGTTTCMCTGKY

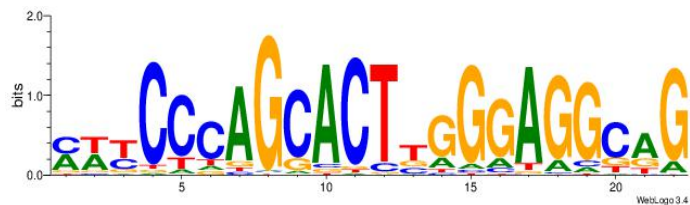


Dataset #:	1
Motif ID:	19
Motif name:	C019
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	20
Similarity score:	0.0624466

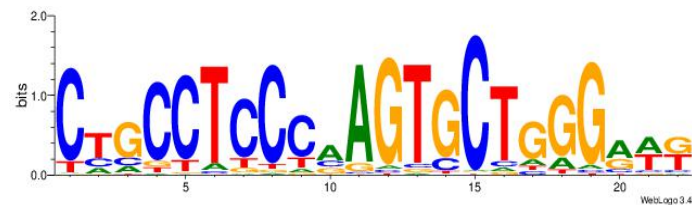
Alignment:

CTGCCTCCCAAGTGCTGGGMWR
 --RGCTVTGTAGCCYWGGCTVD

Original motif Consensus sequence: MWYCCCAGCACTTGGGAGGCAG



Reverse complement motif Consensus sequence:
 CTGCCTCCCAAGTGCTGGGMWR

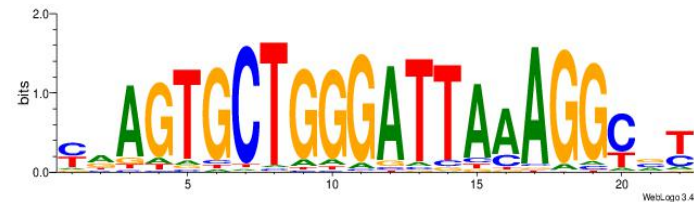
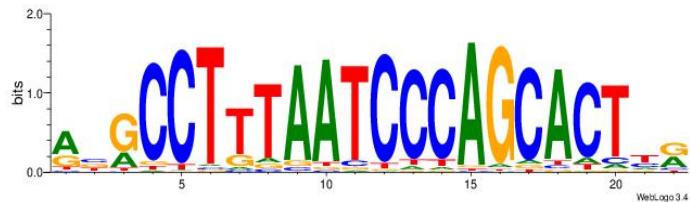


Dataset #:	1
Motif ID:	9
Motif name:	C009
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2
Number of overlap:	20
Similarity score:	0.0690755

Alignment:
 ABGCCTTTAATCCCAGCACTHR
 -RGCTVTGTAGCCYWGGCTVD-

Original motif Consensus sequence: ABGCCTTTAATCCCAGCACTHR

Reverse complement motif Consensus sequence:
 MHAGTGCTGGGATTAAAGGCBT

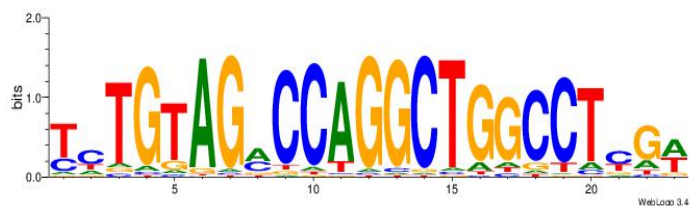


Dataset #: 1
 Motif ID: 5
 Motif name: C005
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 20
 Similarity score: 0.0692469

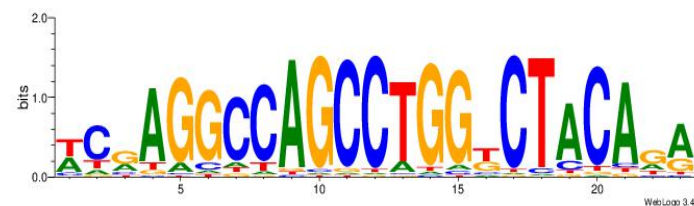
Alignment:

TCTGTAGMCCAGGCTGGCCTYGW
 ---DVAGCCWKGCTACAVAGCK

Original motif Consensus sequence: TCTGTAGMCCAGGCTGGCCTYGW



Reverse complement motif Consensus sequence: WCKAGGCCAGCCTGGYCTACAGA



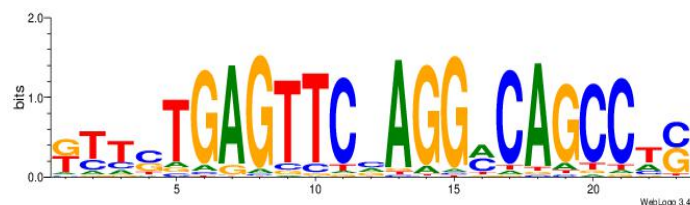
Dataset #: 1

Motif ID: 7
 Motif name: C007
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 5
 Number of overlap: 19
 Similarity score: 0.560476

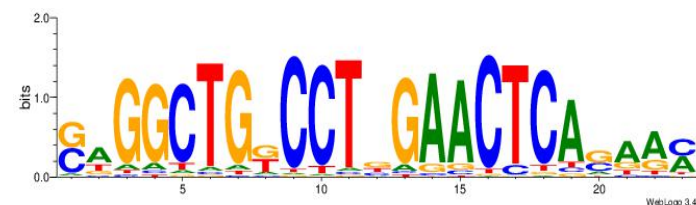
Alignment:

-SAGGCTGYCCTVGAAGTCASAAY
 DVAGCCWKGCTACAVAGCK----

Original motif Consensus sequence: KTTSTGAGTTCVAGGMCAGCCTS

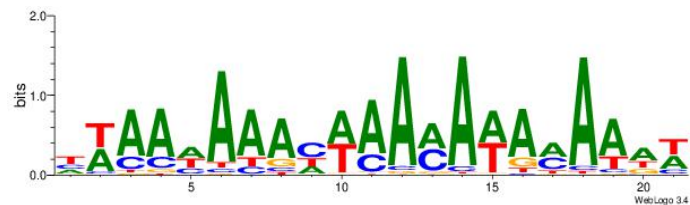


Reverse complement motif Consensus sequence: SAGGCTGYCCTVGAAGTCASAAY

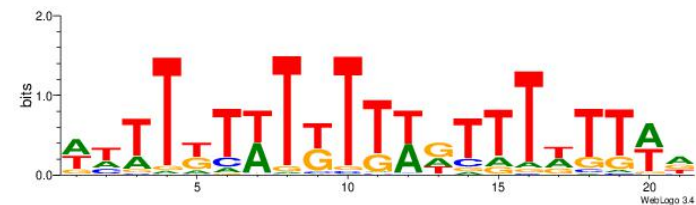


Dataset #: 1 Motif ID: 16 Motif name: C016

Original motif Consensus sequence: HWAAWAAAHWAAMAWAMAAWW



Reverse complement motif Consensus sequence: WWTYYTWYTTWDTTTWTWH



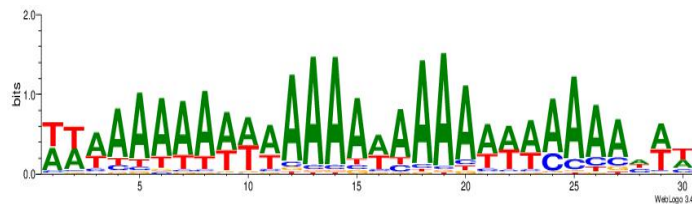
Best Matches for Motif ID 16 (Highest to Lowest)

Dataset #: 1
Motif ID: 1
Motif name: C001
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 9
Number of overlap: 21
Similarity score: 0.00714978

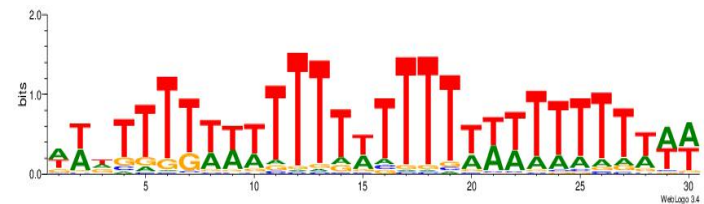
Alignment:

```
WWHTTTTWWTTTTTWWTTTTTWWTTTTTWW  
-----WWTTYTWTYTTWDTTTWTTH--
```

Original motif Consensus sequence:
WWWAAAAAWWAAAAWAAAAWWAAAAHWW



Reverse complement motif Consensus sequence:
WWHTTTTWWTTTTTWWTTTTTWWTTTTTWW



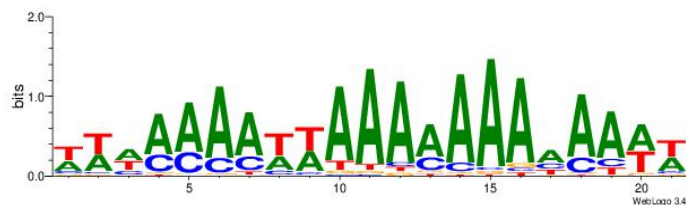
Dataset #: 1
Motif ID: 10
Motif name: C010
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif

Direction: Backward
 Position number: 1
 Number of overlap: 21
 Similarity score: 0.00880991

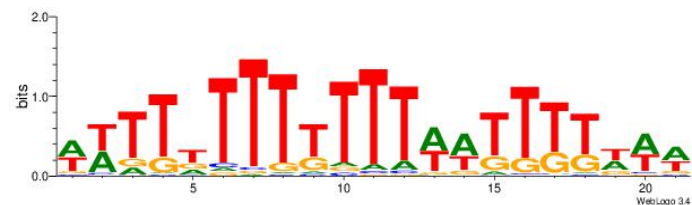
Alignment:

WWWAAAAWWAAAAAAAAAAWW
 HWAAWAAAHWAAMAWAMAAWW

Original motif Consensus sequence: WWWAAAAWWAAAAAAAAAAWW



Reverse complement motif Consensus sequence: WWTTTTTTTTTTWWTTTTWWW

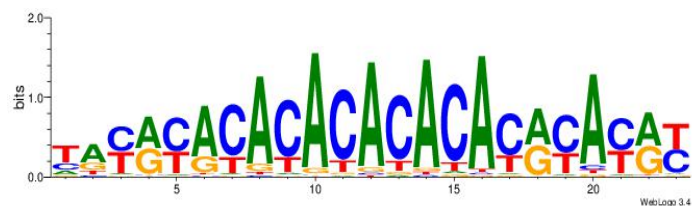


Dataset #: 1
 Motif ID: 2
 Motif name: C002
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 21
 Similarity score: 0.0521896

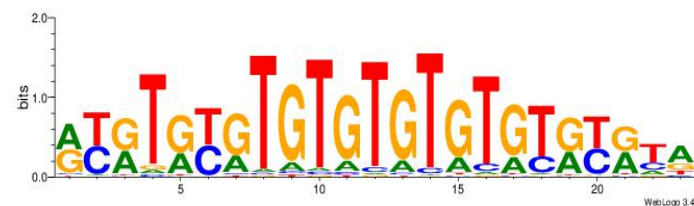
Alignment:

TAYRYACACACACACRYAYRY
 --HWAAWAAAHWAAMAWAMAAWW

Original motif Consensus sequence: TAYRYACACACACACRYAYRY



Reverse complement motif Consensus sequence: MKKTKKGTGTGTGTGTGTTKKTA

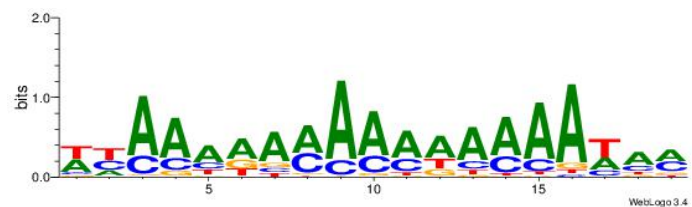


Dataset #: 1
 Motif ID: 30
 Motif name: C030
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 19
 Similarity score: 1.02826

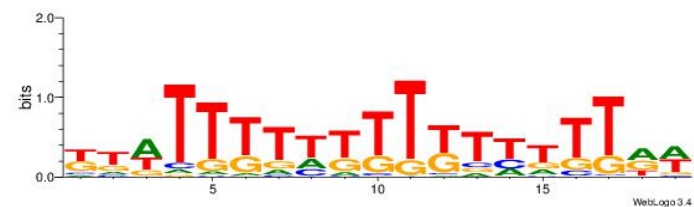
Alignment:

WYAAAAAAMAAAAAAAWAM--
 HWAAWAAAHWAAMAWAMAAWW

Original motif Consensus sequence: WYAAAAAAMAAAAAAAWAM



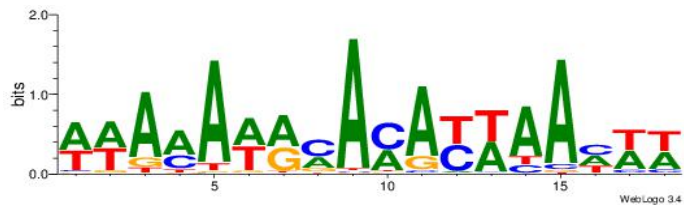
Reverse complement motif Consensus sequence: YTWTTTTTTTTYTTTTTMW



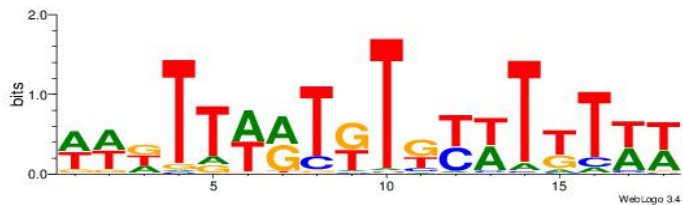
Dataset #: 1
Motif ID: 62
Motif name: C062
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 18
Similarity score: 1.52114

Alignment:
---WWAMAWRMAMAYWAAHWW
HWAAWAAAHWAAMAWAMAAWW

Original motif Consensus sequence: WWAMAWRMAMAYWAAHWW



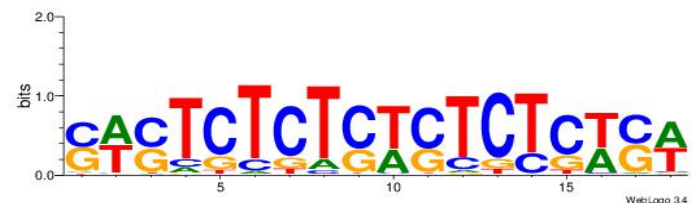
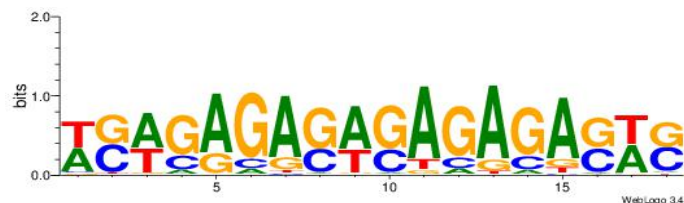
Reverse complement motif Consensus sequence: WWDTTWMTRTRKWTYTW



Dataset #: 1 Motif ID: 17 Motif name: C017

Original motif Consensus sequence: WSWGAGASWSAGAGASWS

Reverse complement motif Consensus sequence: SWSTCTCTSWSTCTCWSW

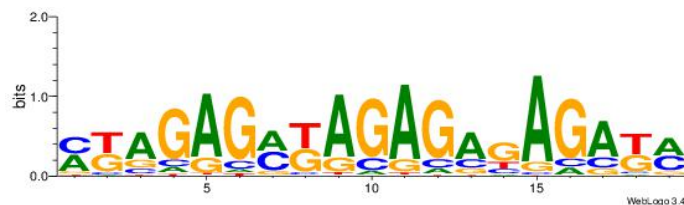


Best Matches for Motif ID 17 (Highest to Lowest)

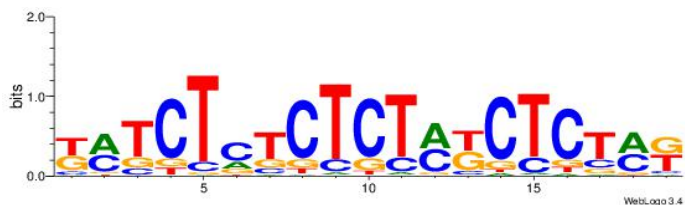
Dataset #: 1
 Motif ID: 12
 Motif name: C012
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 18
 Similarity score: 0.0157523

Alignment:
 MKAGAGMKAGAGAGAGAKM
 WSWGAGASWSAGAGASWS-

Original motif Consensus sequence: MKAGAGMKAGAGAGAGAKM



Reverse complement motif Consensus sequence: YRTCTCTCTCTRYCTCTRR

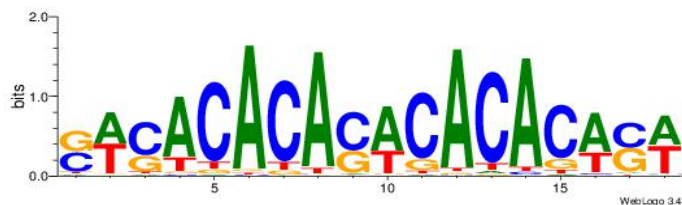


Dataset #: 1
 Motif ID: 6
 Motif name: C006
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 18
 Similarity score: 0.0313003

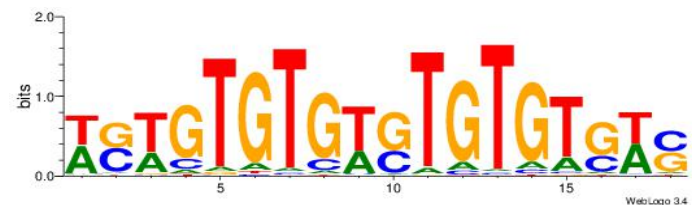
Alignment:

SWCACACASWCACACWSW
 SWSTCTCTSWSTCTCWSW

Original motif Consensus sequence: SWCACACASWCACACWSW



Reverse complement motif Consensus sequence: WSWGTTGTGWSTGTGTGWS

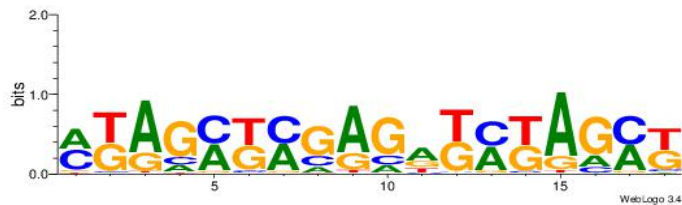


Dataset #: 1
 Motif ID: 36
 Motif name: C036
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1

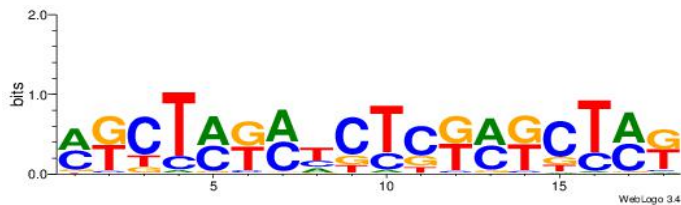
Number of overlap: 18
Similarity score: 0.0395256

Alignment:
MKAGMKMGAGAKMKAGMK
WSWGAGASWSAGAGASWS

Original motif Consensus sequence: MKAGMKMGAGAKMKAGMK



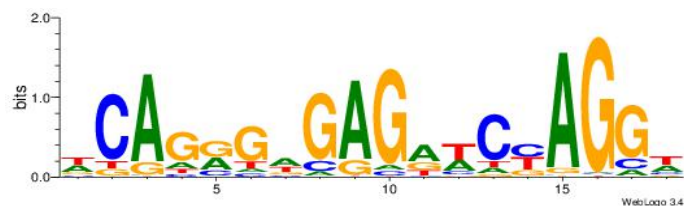
Reverse complement motif Consensus sequence: RRCTRRRTCTCRRRCTRY



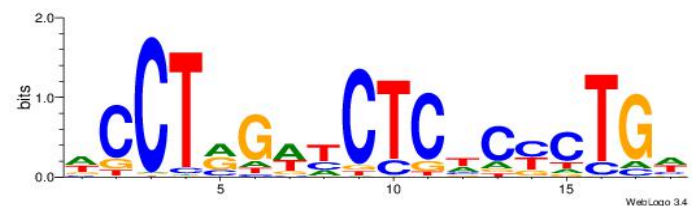
Dataset #: 1
Motif ID: 132
Motif name: C132
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 18
Similarity score: 0.0518509

Alignment:
WCAGRGWGAGAWCYAGGW
WSWGAGASWSAGAGASWS

Original motif Consensus sequence: WCAGRGWGAGAWCYAGGW



Reverse complement motif Consensus sequence: WCCTKGWTCTCWCMTCTGW

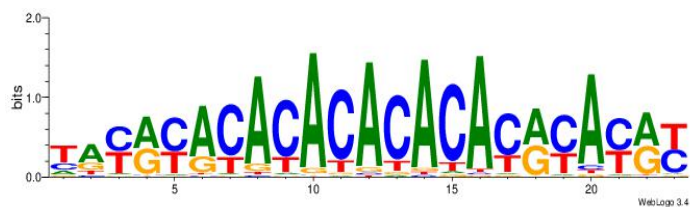


Dataset #: 1
 Motif ID: 2
 Motif name: C002
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 18
 Similarity score: 0.0559963

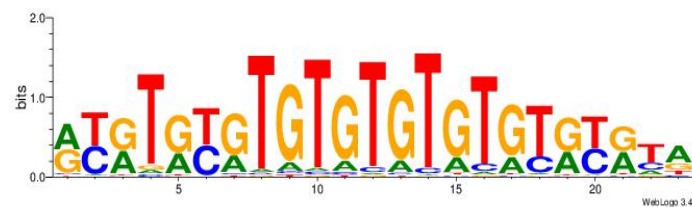
Alignment:

MKKTKKGTGTGTGTGTGTTKKTA
 ----SWSTCTCTSWSTCTCWSW-

Original motif Consensus sequence: TAYRYACACACACACACRYAYRY

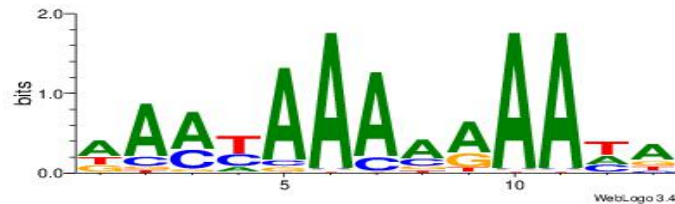


Reverse complement motif Consensus sequence: MKKTKKGTGTGTGTGTGTTKKTA

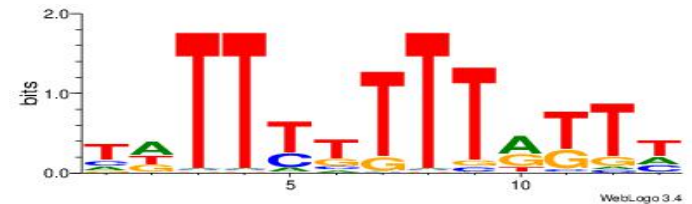


Dataset #: 1 Motif ID: 18 Motif name: C018

Original motif Consensus sequence: AAMYAAAAAHA



Reverse complement motif Consensus sequence: THTTTTTTMYTT



Best Matches for Motif ID 18 (Highest to Lowest)

Dataset #:	1
Motif ID:	24
Motif name:	C024
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:	0.00879109

Alignment:

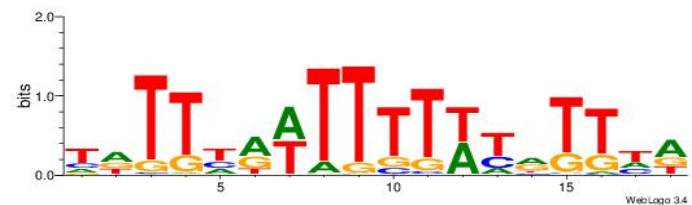
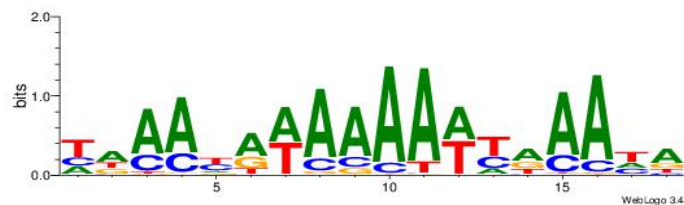
```

THTTDMWTTTTWKMTTDA
----THTTTTTTTMYTT-

```

Original motif Consensus sequence: TDAAYRWAAAAYDAAHA

Reverse complement motif Consensus sequence:
THTTDMWTTTTWKMTTDA

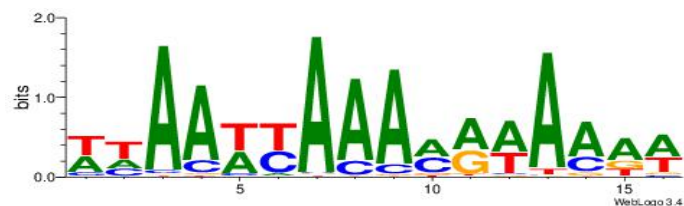


Dataset #: 1
 Motif ID: 33
 Motif name: C033
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 13
 Similarity score: 0.0101683

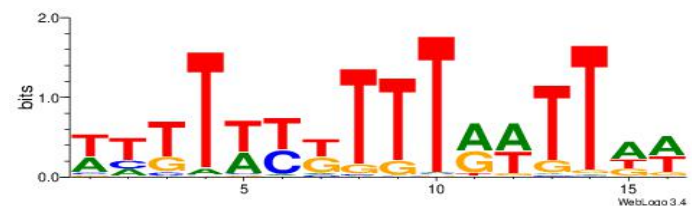
Alignment:

WWAAWYAAAMRWAAAW
 --AAMYAAAAAAHA--

Original motif Consensus sequence: WWAAWYAAAMRWAAAW



Reverse complement motif Consensus sequence: WTTTWKYTTTMTTWW



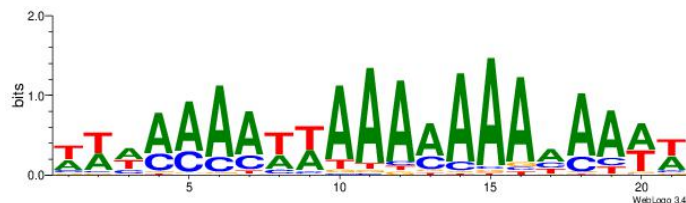
Dataset #: 1

Motif ID: 10
 Motif name: C010
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 4
 Number of overlap: 13
 Similarity score: 0.0128694

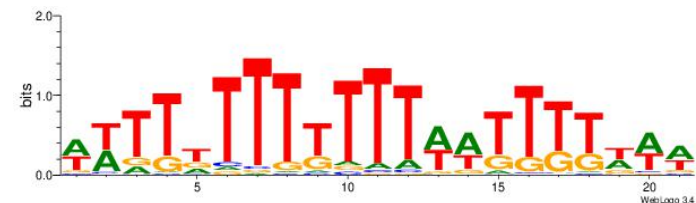
Alignment:

WWWAAAAWWAAAAAAAAAAWW
 -----AAMYAAAAAAAAHA----

Original motif Consensus sequence: WWWAAAAWWAAAAAAAAAAWW



Reverse complement motif Consensus sequence: WWTTTTTTTTTTWWTTTTWWW



Dataset #: 1
 Motif ID: 131
 Motif name: C131
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 13

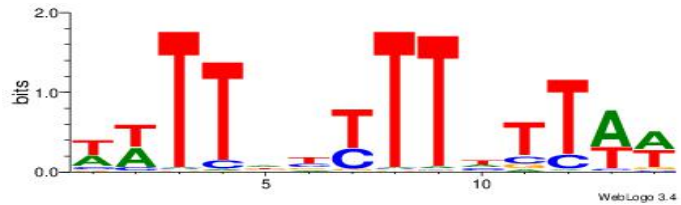
Similarity score: 0.0136352

Alignment:
WWTTHBKTTD TTWW
THTTTTTTTMYTT-

Original motif Consensus sequence: WWAADAARVHAAWW



Reverse complement motif Consensus sequence: WWTTHBKTTD TTW

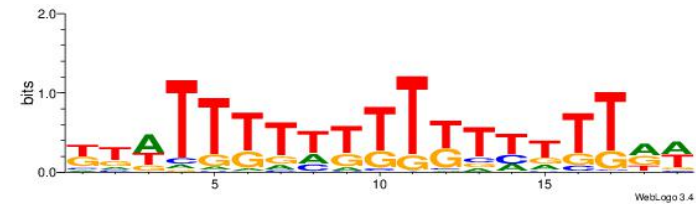


Dataset #: 1
Motif ID: 30
Motif name: C030
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 2
Number of overlap: 13
Similarity score: 0.0161198

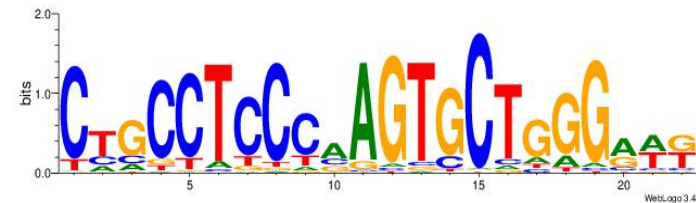
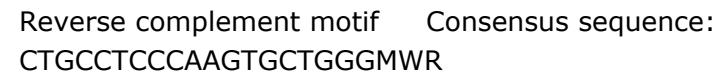
Alignment:
YTWTTTTTTTTYTTTTMW
-THTTTTTTTMYTT-----

Original motif Consensus sequence: WYAAAAA MA AAAAAA WAM

Reverse complement motif Consensus sequence:
YTWTTTTTTTTYTTTTMW



Original motif Consensus sequence: MWYCCAGCACTTGGGAGGCAG



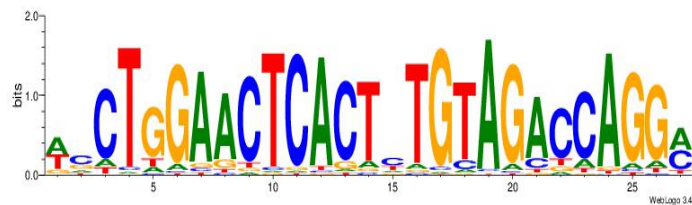
Best Matches for Motif ID 19 (Highest to Lowest)

Dataset #:	1
Motif ID:	13
Motif name:	C013
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	4
Number of overlap:	22
Similarity score:	0.0741117

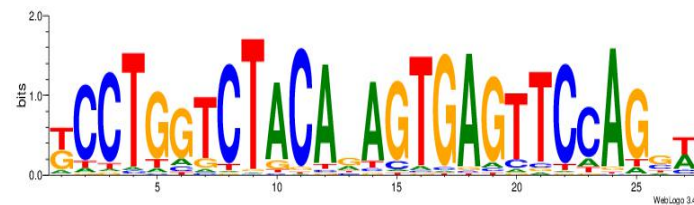
Alignment:

YCCTGGTCTACADAGTGAGTTCCAGVW
 ---CTGCCTCCCAAGTGCTGGGMWR---

Original motif Consensus sequence:
 WVCTGGAAC TCACTHTGTAGACCAGGM



Reverse complement motif Consensus sequence:
 YCCTGGTCTACADAGTGAGTTCCAGVW

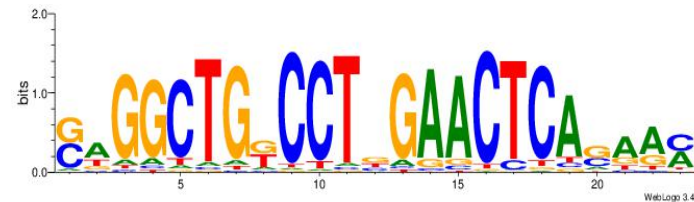
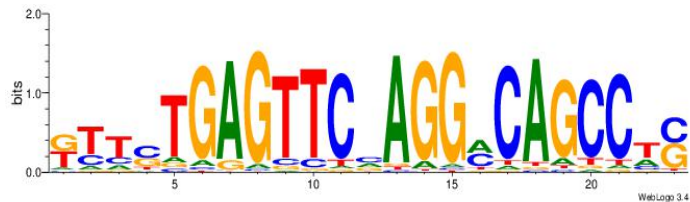


Dataset #:	1
Motif ID:	7
Motif name:	C007
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	22
Similarity score:	0.0774233

Alignment:
 SAGGCTGYCCTVGAAC TCASAA Y
 -CTGCCTCCCAAGTGCTGGGMWR

Original motif Consensus sequence: KTTSTGAGTTCVAGGMCAGCCTS

Reverse complement motif Consensus sequence:
 SAGGCTGYCCTVGAAC TCASAA Y

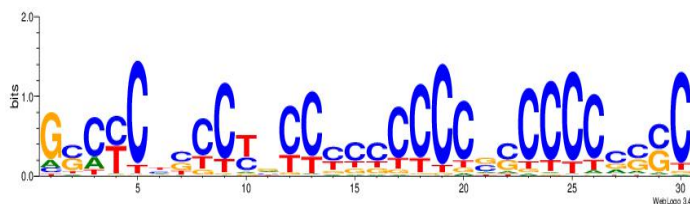


Dataset #: 1
 Motif ID: 3
 Motif name: C003
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 5
 Number of overlap: 22
 Similarity score: 0.0793936

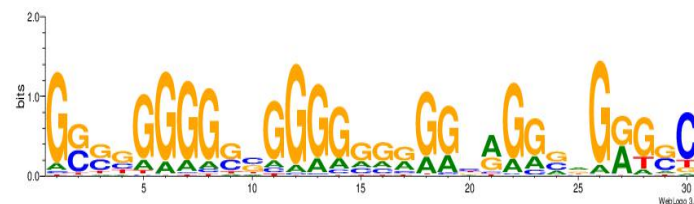
Alignment:

GSCYCHSCCYVCCYCCCCCSCCCCCSSC
 ----CTGCCTCCCAAGTGCTGGGMWR----

Original motif Consensus sequence:
 GSCYCHSCCYVCCYCCCCCSCCCCCSSC



Reverse complement motif Consensus sequence:
 GSSGGGGGSSGGGGGGKGGVMGGSHGKGC



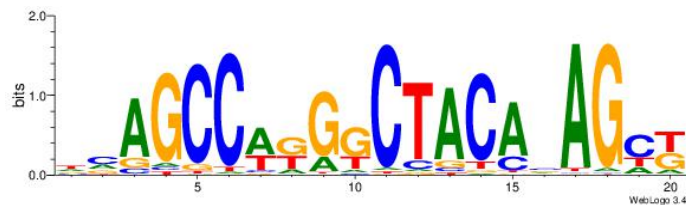
Dataset #: 1

Motif ID: 15
 Motif name: C015
 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: 1.07305

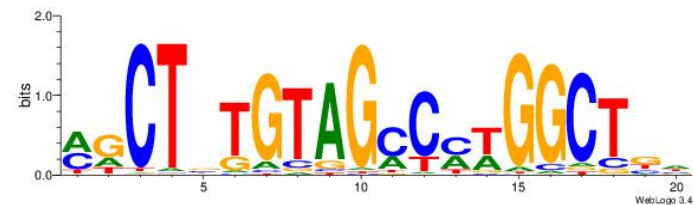
Alignment:

--RGCTVTGTAGCCYWGGCTVD
 CTGCCTCCCAAGTGCTGGGMWR

Original motif Consensus sequence: DVAGCCWKGCTACAVAGCK



Reverse complement motif Consensus sequence: RGCTVTGTAGCCYWGGCTVD

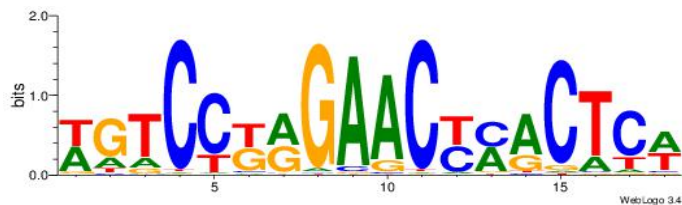


Dataset #: 1
 Motif ID: 42
 Motif name: C042
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 18

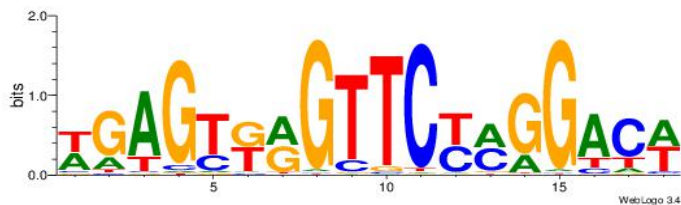
Similarity score: 2.06763

Alignment:
----WGAGTRMGTTCKRGGACW
CTGCCTCCCAAGTGCTGGGMWR

Original motif Consensus sequence: WGTCKRGAACYMACTCW

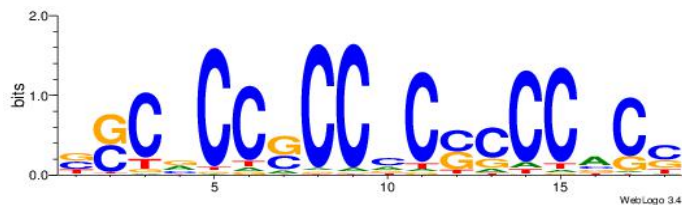


Reverse complement motif Consensus sequence: WGAGTRMGTTCKRGGACW

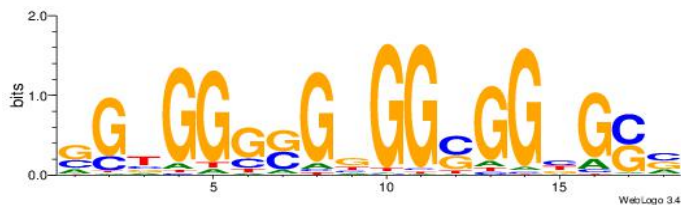


Dataset #: 1 Motif ID: 20 Motif name: C020

Original motif Consensus sequence: BSCVCCSCCVSCCCACS



Reverse complement motif Consensus sequence: SGTGGGSGVGGSGGVGSB



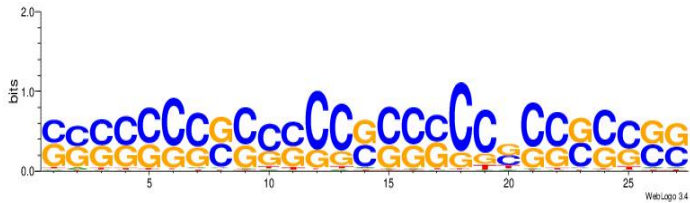
Best Matches for Motif ID 20 (Highest to Lowest)

Dataset #:	1
Motif ID:	4
Motif name:	C004
Matching format of first motif:	Reverse Complement

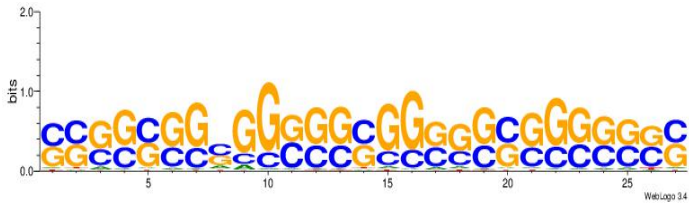
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 5
Number of overlap: 18
Similarity score: 0.0217831

Alignment:
SSSSSSGSGGSSSSGSGSSSSGSSSSS
-----SGTGGGSGVGGSGGVGSB-----

Original motif Consensus sequence:
SSSSSCSSSSSCSSSSCCSCSSSSSS



Reverse complement motif Consensus sequence:
SSSSSSGSGGSSSSGSGSSSSGSSSSS

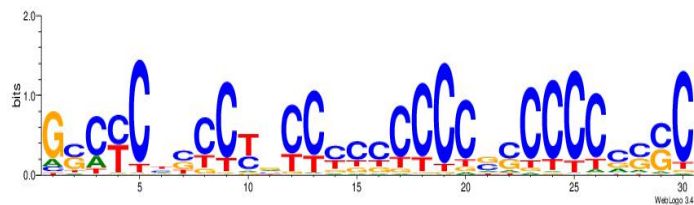


Dataset #: 1
Motif ID: 3
Motif name: C003
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 4
Number of overlap: 18
Similarity score: 0.0273212

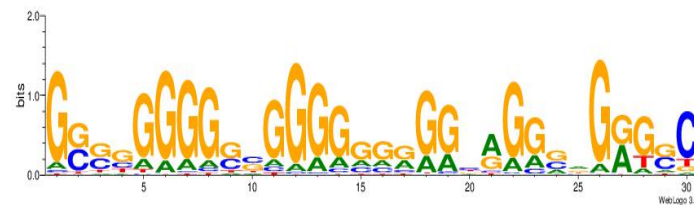
Alignment:

GSCYCHSCCYVCCYCCCCCSCCCCCSSC
 -----BSCVCCSCCVCSCCCACS----

Original motif Consensus sequence:
 GSCYCHSCCYVCCYCCCCCSCCCCCSSC



Reverse complement motif Consensus sequence:
 GSSGGGGGSSGGGGGKGGVMGGSHGKGSC

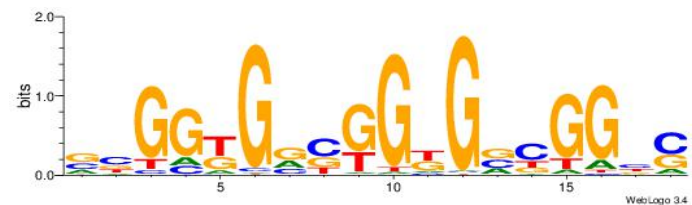
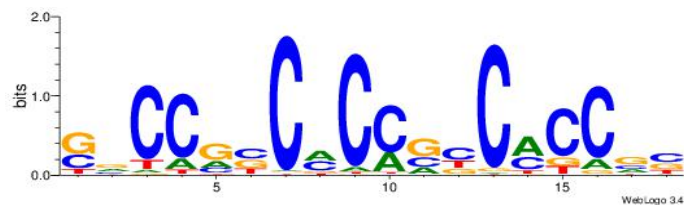


Dataset #:	1
Motif ID:	37
Motif name:	C037
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	18
Similarity score:	0.0555507

Alignment:
 SVCCGBCMCCSYCMCCVB
 BSCVCCSCCVCSCCCACS

Original motif Consensus sequence: SVCCGBCMCCSYCMCCVB

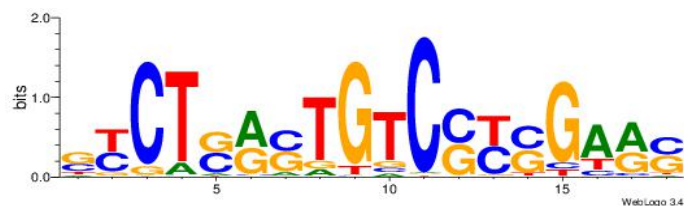
Reverse complement motif Consensus sequence:
 BVGGYGKSGGYGBCGGVS



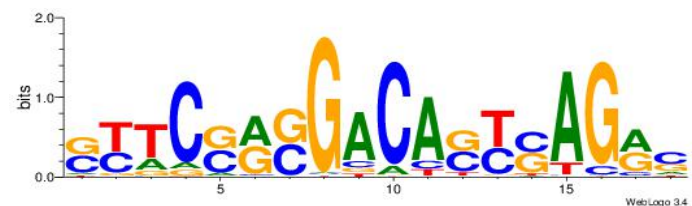
Dataset #: 1
 Motif ID: 128
 Motif name: C128
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 18
 Similarity score: 0.0687296

Alignment:
 SKTCSMSGACASKSAGMS
 SGTGGGSGVGGSGGVGSB

Original motif Consensus sequence: SYCTSRSTGTCSYSGARS



Reverse complement motif Consensus sequence: SKTCSMSGACASKSAGMS



Dataset #: 1

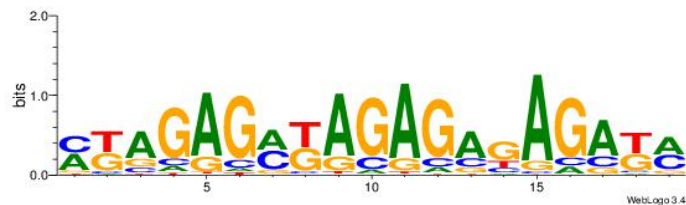
Motif ID:	12
Motif name:	C012
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	2
Number of overlap:	18
Similarity score:	0.0738675

Alignment:

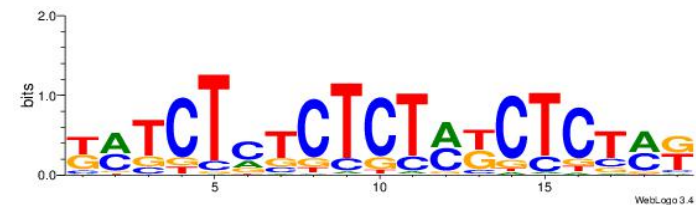
YRTCTCTCTRYCTCTR

BSCVCCSCCVCSCCCACS-

Original motif Consensus sequence: MKAGAGMKAGAGAGAGAKM

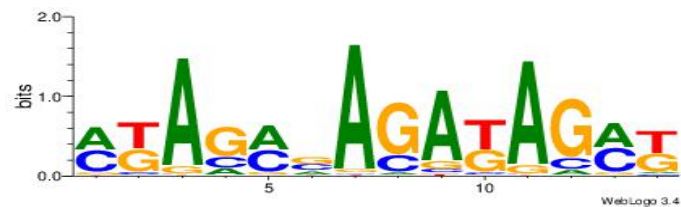


Reverse complement motif Consensus sequence:
YRTCTCTCTRYCTCTRR

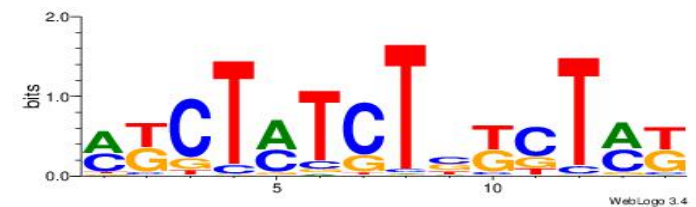


Dataset #: 1 Motif ID: 21 Motif name: C021

Original motif Consensus sequence: MKAGMVAGAKAGMK



Reverse complement motif Consensus sequence: RYCTR|CTVYCTRY



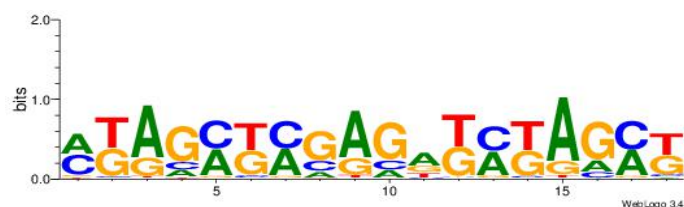
Best Matches for Motif ID 21 (Highest to Lowest)

Dataset #: 1
Motif ID: 36
Motif name: C036
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: 0.0195753

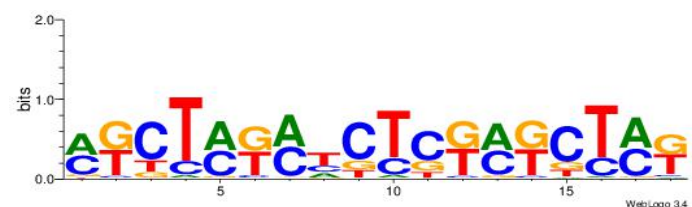
Alignment:

MKAGMKMGAGAKMKAGMK
-----MKAGMVAGAKAGMK

Original motif Consensus sequence: MKAGMKMGAGAKMKAGMK



Reverse complement motif Consensus sequence: RRCTRRRTCTCRRRCTRY



Dataset #: 1
Motif ID: 11
Motif name: C011
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif

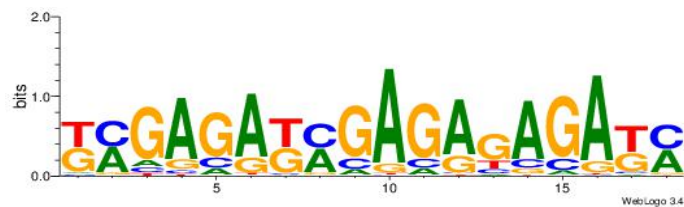
Direction: Forward
 Position number: 4
 Number of overlap: 14
 Similarity score: 0.0223902

Alignment:

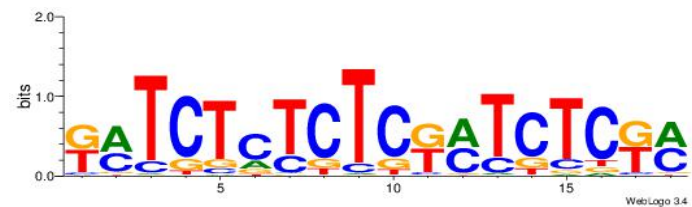
KMGAGAKMGAGAGAGAKM

---MKAGMVAGAKAGMK--

Original motif Consensus sequence: KMGAGAKMGAGAGAGAKM



Reverse complement motif Consensus sequence: RRTCTCTCTCRRTCTCRR



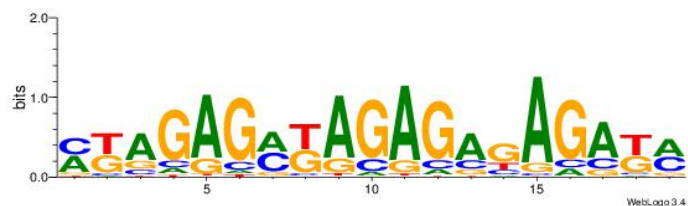
Dataset #: 1
 Motif ID: 12
 Motif name: C012
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0.0297307

Alignment:

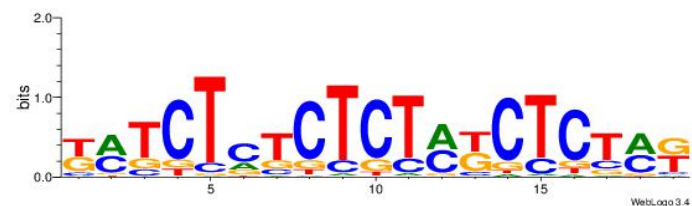
MKAGAGMKAGAGAGAGAKM

MKAGMVAGAKAGMK-----

Original motif Consensus sequence: MKAGAGMKAGAGAGAGAKM



Reverse complement motif Consensus sequence: YRTCTCTCTCTRYCTCTRR

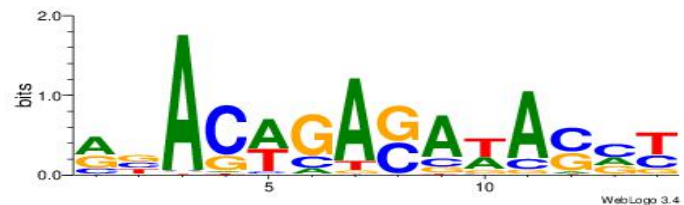


Dataset #: 1
Motif ID: 108
Motif name: C108
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 14
Similarity score: 0.031488

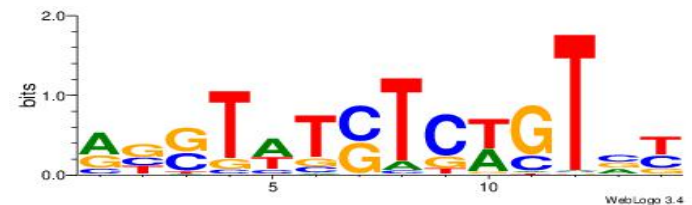
Alignment:

RBACWGASAWASVY
MKAGMVAGAKAGMK

Original motif Consensus sequence: RBACWGASAWASVY



Reverse complement motif Consensus sequence: MVSTWTSTCWGTR

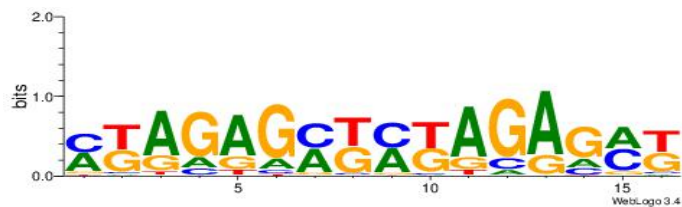


Dataset #: 1
 Motif ID: 55
 Motif name: C055
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 14
 Similarity score: 0.0327219

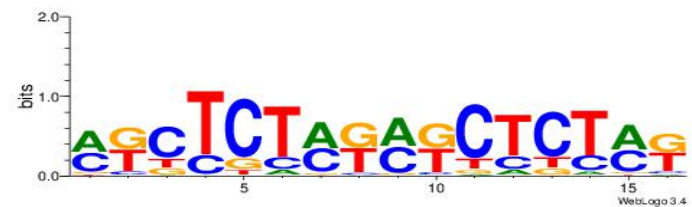
Alignment:

MKAGAGMKMKAGAGMK
 MKAGMVAGAKAGMK--

Original motif Consensus sequence: MKAGAGMKMKAGAGMK



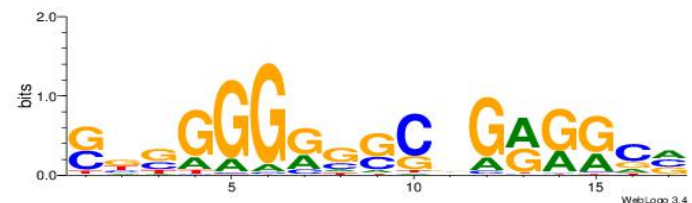
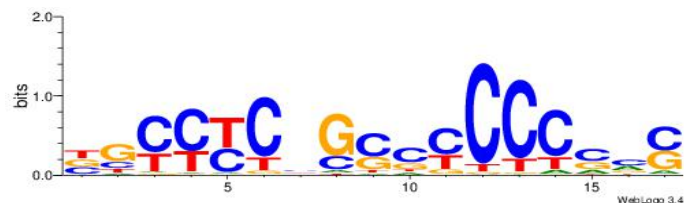
Reverse complement motif Consensus sequence: RYCTCTRRRRCTCTRR



Dataset #: 1 Motif ID: 22 Motif name: C022

Original motif Consensus sequence: BGCCYCBGSCYCCCSVS

Reverse complement motif Consensus sequence: SVSGGGKGGSCBGMGGCV



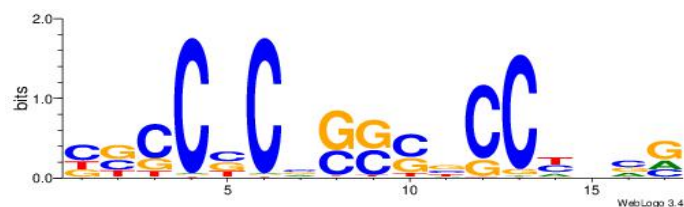
Best Matches for Motif ID 22 (Highest to Lowest)

Dataset #: 1
 Motif ID: 140
 Motif name: C140
 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: 0.0048476

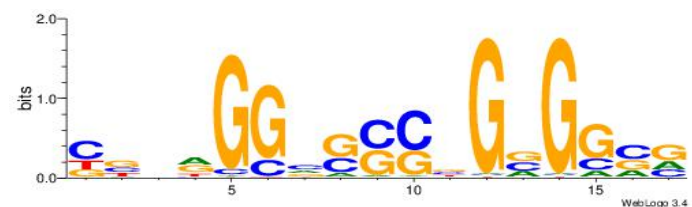
Alignment:

BSCCBVSSSBCCYHVG
 BGCCYCBGSCYCCCSVS

Original motif Consensus sequence: BSCCBVSSSBCCYHVG



Reverse complement motif Consensus sequence: CVDMGGBSSSVGBGGSB

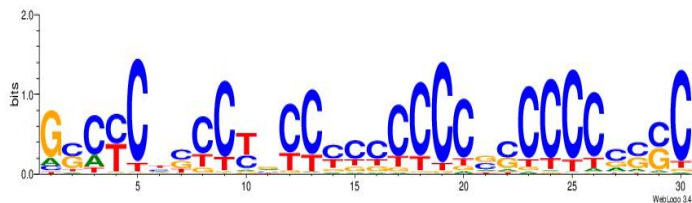


Dataset #: 1
 Motif ID: 3
 Motif name: C003
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 17
 Similarity score: 0.00796864

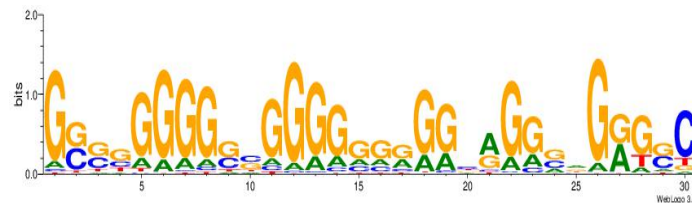
Alignment:

GSCYCHSCCYVCCYCCCCCSCCCCCSSC
 -----BGCCYCBGSCYCCCSVS-

Original motif Consensus sequence:
 GSCYCHSCCYVCCYCCCCCSCCCCCSSC



Reverse complement motif Consensus sequence:
 GSSGGGGGSSGGGGGKGGVMGGSHGKGC

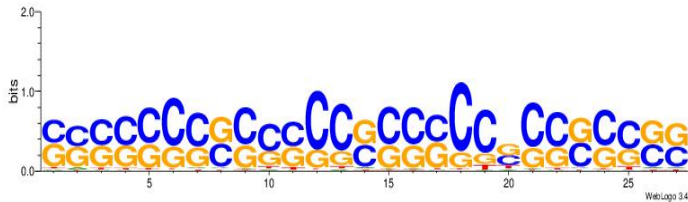


Dataset #: 1
 Motif ID: 4
 Motif name: C004
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 7

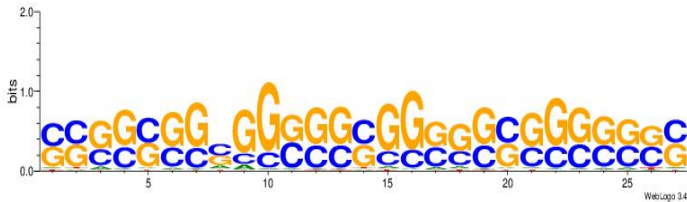
Number of overlap: 17
Similarity score: 0.0148301

Alignment:
SSSSSCSSSSSCSSSSCCSCSSSSSS
-----BGCCYCBGSCYCCCSVS-----

Original motif Consensus sequence:
SSSSSCSSSSSCSSSSCCSCSSSSSS



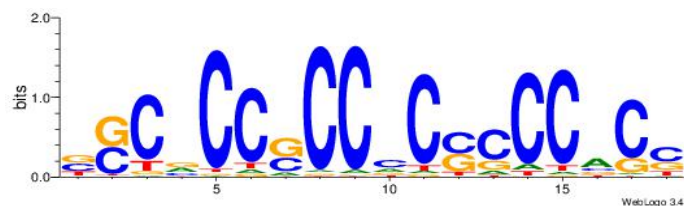
Reverse complement motif Consensus sequence:
SSSSSSGSGGSSSSGGSSSSSGSSSSS



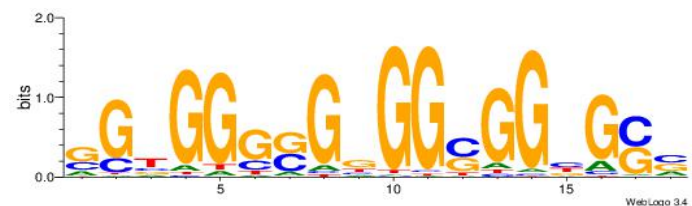
Dataset #: 1
Motif ID: 20
Motif name: C020
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 17
Similarity score: 0.0301912

Alignment:
BSCVCCSCCVCSCCCACS
BGCCYCBGSCYCCCSVS-

Original motif Consensus sequence: BSCVCCSCCVSCCCACS



Reverse complement motif Consensus sequence: SGTGGGSGVGGSGGVGSB

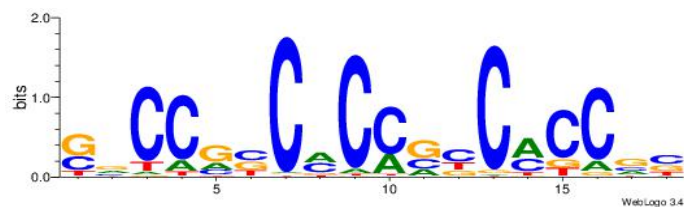


Dataset #: 1
 Motif ID: 37
 Motif name: C037
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 17
 Similarity score: 0.0352503

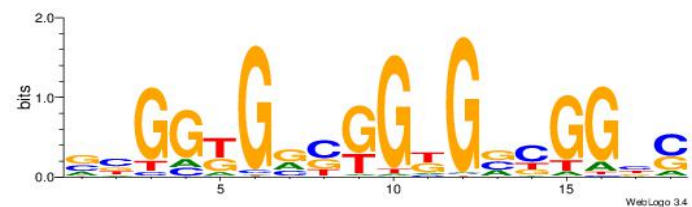
Alignment:

SVCCGBCMCCSYCMCCVB
 -BGCCYCBGSCYCCCSVS

Original motif Consensus sequence: SVCCGBCMCCSYCMCCVB

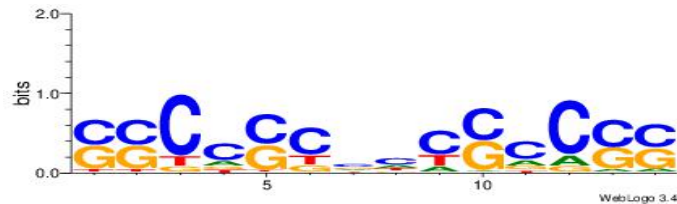


Reverse complement motif Consensus sequence: BVGGYGKSGGYGBCGGVS

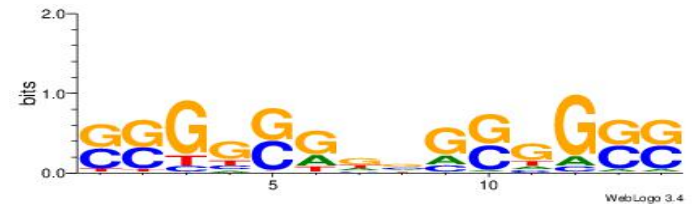


Dataset #: 1 Motif ID: 23 Motif name: C023

Original motif Consensus sequence: SSCCSCBHCSCCSS



Reverse complement motif Consensus sequence: SSGGSGDBGSGGSS



Best Matches for Motif ID 23 (Highest to Lowest)

Dataset #:	1
Motif ID:	4
Motif name:	C004
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	2
Number of overlap:	14
Similarity score:	0.00461109

Alignment:

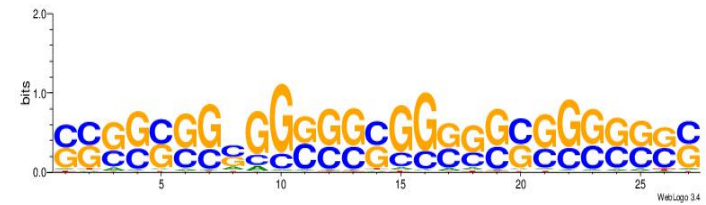
```

SSSSSSGSGGSSSSSGGSSSSSSGSSSSS
-----SSGGSGDBGSGGSS-

```

Original motif Consensus sequence:
SSSSSCSSSSCCSSSSCCSCSSSSSS

Reverse complement motif Consensus sequence:
SSSSSSGSGGSSSSSGGSSSSSSGSSSSS



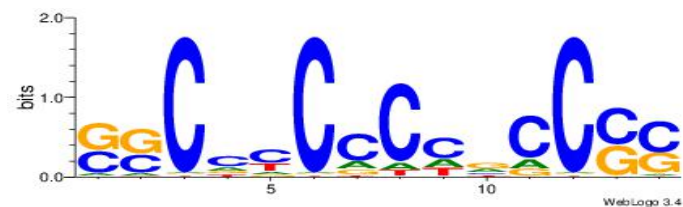
Dataset #:	1
Motif ID:	104
Motif name:	C104
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	14
Similarity score:	0.00651203

Alignment:

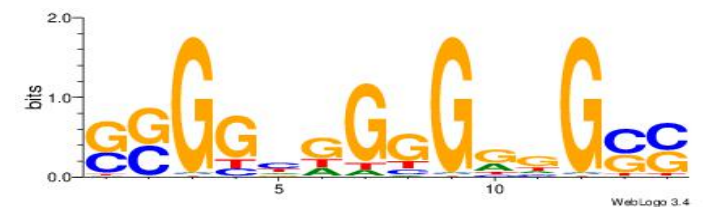
SSGGHGGGGKGGSS

SSGGSGDBSGGSS

Original motif Consensus sequence: SSCCYCCCCDCCSS



Reverse complement motif Consensus sequence: SSGGHGGGGKGG



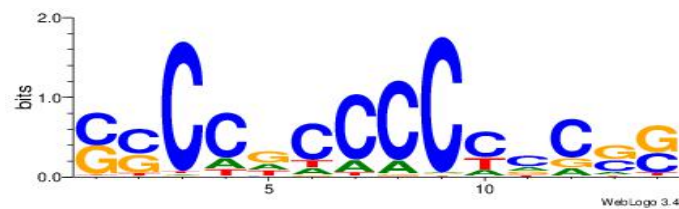
Dataset #: 1
Motif ID: 54

Motif name:	C054
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:	0.0125092

Alignment:

SSGGGGGGGHGGSS
SSGGSGBGSGGSS

Original motif Consensus sequence: SSCCDCCCCCSCSS



Reverse complement motif Consensus sequence: SSGGGGGGHGGSS

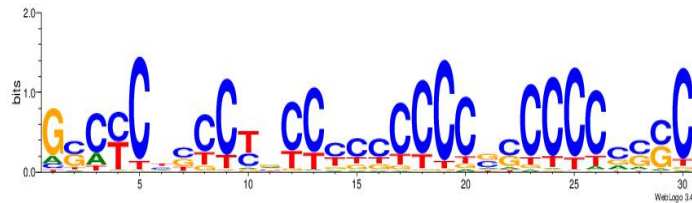


Dataset #:	1
Motif ID:	3
Motif name:	C003
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	15
Number of overlap:	14
Similarity score:	0.0162482

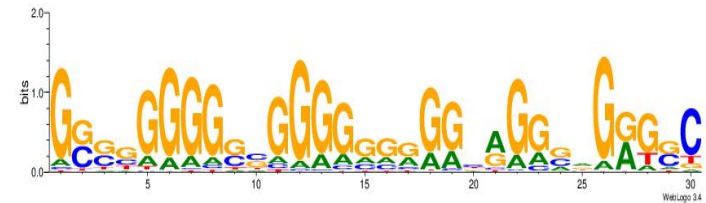
Alignment:

GSCYCHSCCYVCCYCCCCCSCCCCCSSC
-----SSCCSCBHCSCCSS--

Original motif Consensus sequence:
GSCYCHSCCYVCCYCCCCCSCCCCCSSC



Reverse complement motif Consensus sequence:
GSSGGGGGSSGGGGGGKGGVMGGSHGKGSC



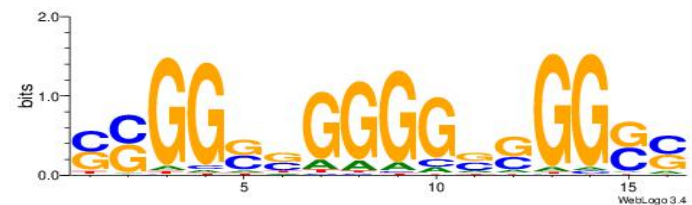
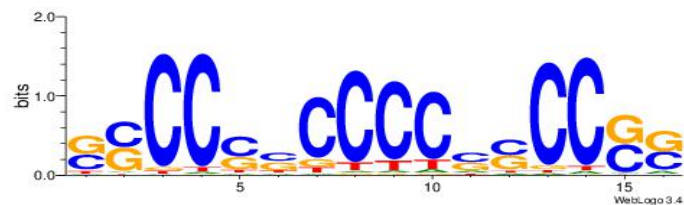
Dataset #:	1
Motif ID:	8
Motif name:	C008
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2
Number of overlap:	14
Similarity score:	0.0169024

Alignment:

SSCCSSCCCCSSCCSS
-SSCCSCBHCSCCSS-

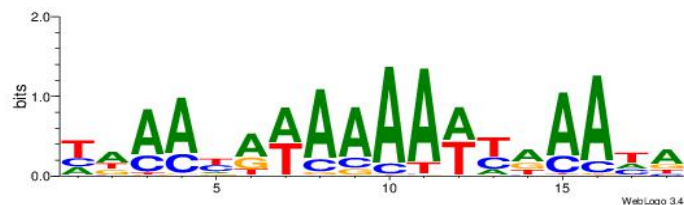
Original motif Consensus sequence: SSCCSSCCCCSSCCSS

Reverse complement motif Consensus sequence:
SSGSSGGGGSSGGSS

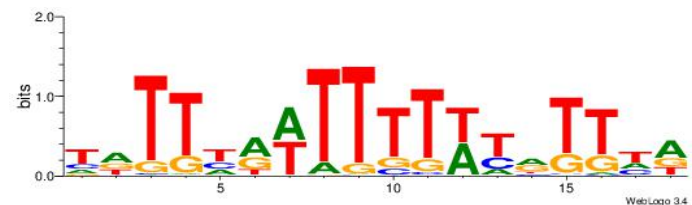


Dataset #: 1 Motif ID: 24 Motif name: C024

Original motif Consensus sequence: TDAAYRWAAAAYDAAHA



Reverse complement motif Consensus sequence: THTTDMWTTTTWKMTTDA



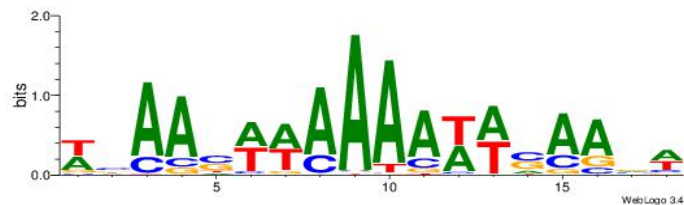
Best Matches for Motif ID 24 (Highest to Lowest)

Dataset #:	1
Motif ID:	97
Motif name:	C097
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:	0.0138646

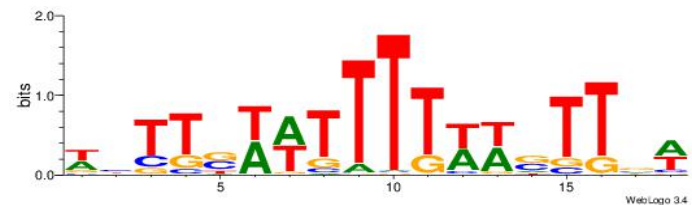
Alignment:

WVTTSWWTTTTWWSTTBW
 THTTDMWTTTTWKMTTDA

Original motif Consensus sequence: WBAASWWAAAAWWSAAVW



Reverse complement motif Consensus sequence:
 WVTTSWWTTTTWWSTTBW



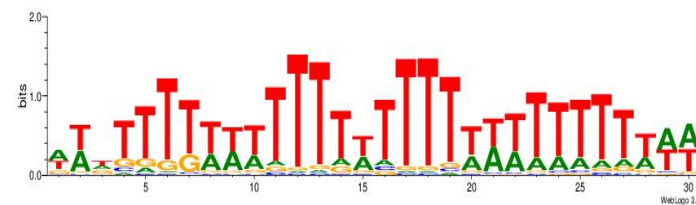
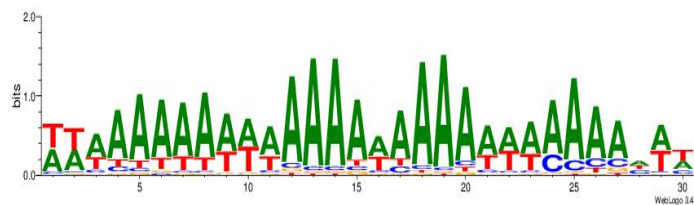
Dataset #:	1
Motif ID:	1
Motif name:	C001
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	10
Number of overlap:	18
Similarity score:	0.0165298

Alignment:

WWHTTTTWWTTTTTWTTTTWWTTTTTWW
 ---THTTDMWTTTTWKMTTDA-----

Original motif Consensus sequence:
 WWWAAAAWWAAAAWAAAAWAAAAHWW

Reverse complement motif Consensus sequence:
 WWHTTTTWWTTTTTWTTTTWWTTTTTWW

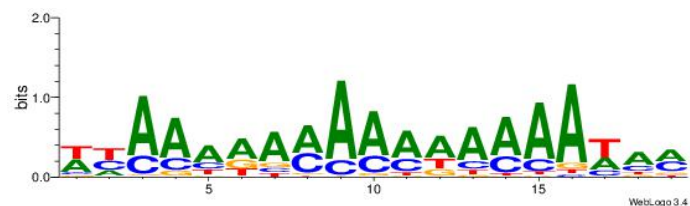


Dataset #: 1
 Motif ID: 30
 Motif name: C030
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 18
 Similarity score: 0.0167795

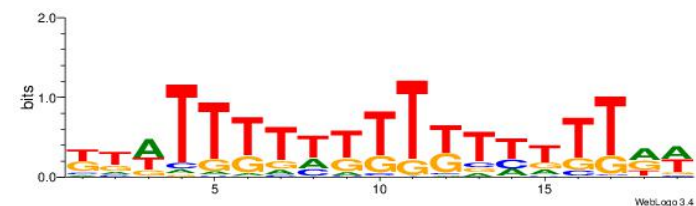
Alignment:

WYAAAAAMAAAAAAWAM
 TDAAYRWAAAWYDAAHA-

Original motif Consensus sequence: WYAAAAAMAAAAAAWAM



Reverse complement motif Consensus sequence: YTWTTTTTTTTYTTTTMW



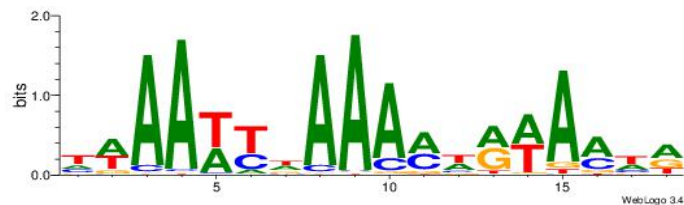
Dataset #: 1

Motif ID: 32
 Motif name: C032
 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: 0.0276297

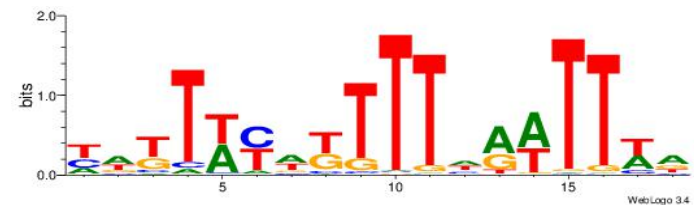
Alignment:

KWTWKWYTTTDMWTTWH
 TTTTDMWTTTTWKMTTDA

Original motif Consensus sequence: HWAAWYDAAAMWRWAMWR



Reverse complement motif Consensus sequence: KWTWKWYTTTDMWTTWH

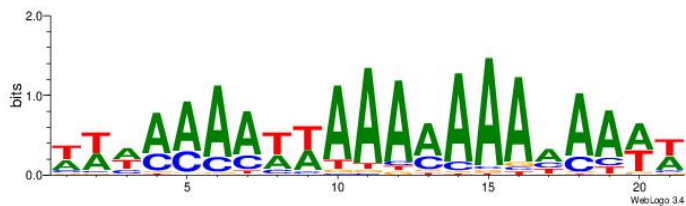


Dataset #: 1
 Motif ID: 10
 Motif name: C010
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 4
 Number of overlap: 18

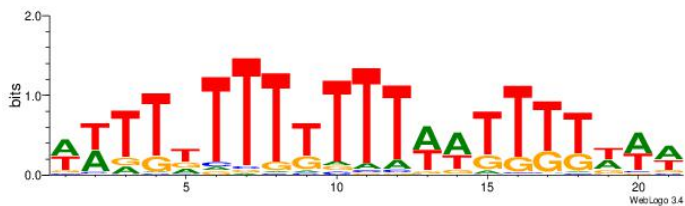
Similarity score: 0.0288095

Alignment:
WWTTTTTTTTTTWWTTTTWWW
THTTDMWTTTTWKMTTDA---

Original motif Consensus sequence: WWWAAAWWAAAAAAAAAAWW



Reverse complement motif Consensus sequence: WWTTTTTTTTTTWWTTTTWWW

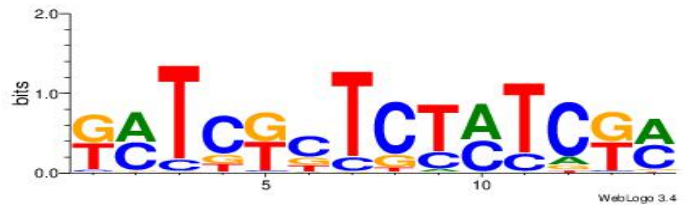


Dataset #: 1 Motif ID: 25 Motif name: C025

Original motif Consensus sequence: KMGAKAGAGMGAKM



Reverse complement motif Consensus sequence: RRTCRCCTCTRCR



Best Matches for Motif ID 25 (Highest to Lowest)

Dataset #:	1
Motif ID:	78
Motif name:	C078
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif

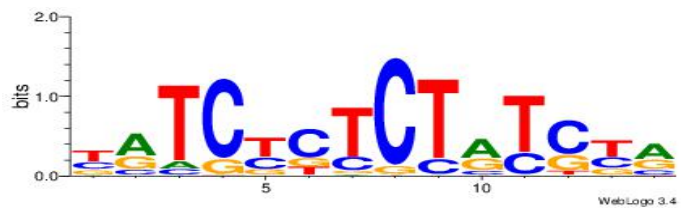
Direction: Backward
Position number: 1
Number of overlap: 14
Similarity score: 0.00248665

Alignment:
YRGAYAGAGRGAYR
KMGAKAGAGMGAKM

Original motif Consensus sequence: YRGAYAGAGRGAYR



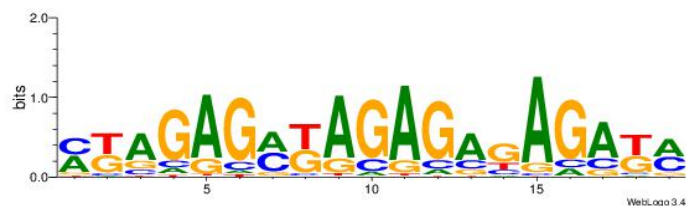
Reverse complement motif Consensus sequence: KMTCKCTCTMTCK



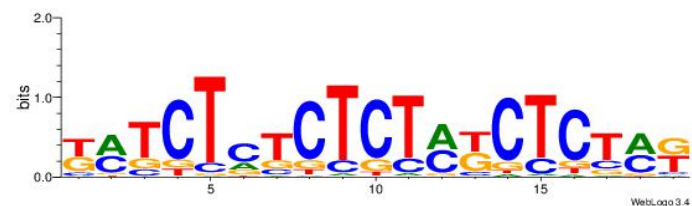
Dataset #: 1
Motif ID: 12
Motif name: C012
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 14
Similarity score: 0.00375955

Alignment:
MKAGAGMKAGAGAGAGAKM
-----KMGAKAGAGMGAKM

Original motif Consensus sequence: MKAGAGMKAGAGAGAGAKM



Reverse complement motif Consensus sequence: YRTCTCTCTCTRYCTCTRR



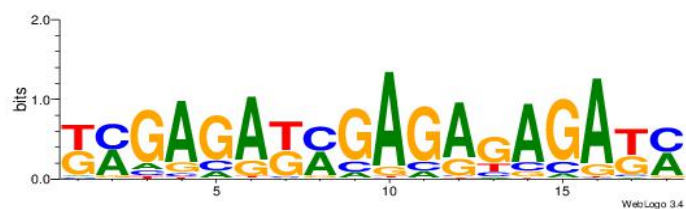
Dataset #: 1
Motif ID: 11
Motif name: C011
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 5
Number of overlap: 14
Similarity score: 0.00885823

Alignment:

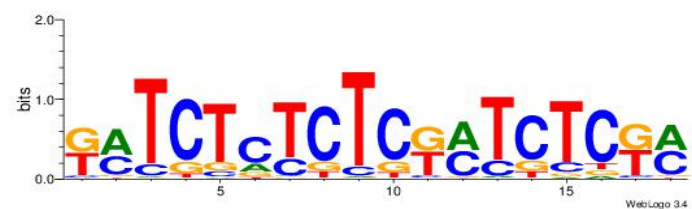
KMGAGAKMGAGAGAGAKM

KMGAKAGAGMGAKM-----

Original motif Consensus sequence: KMGAGAKMGAGAGAGAKM



Reverse complement motif Consensus sequence: RRTCTCTCTCRRTCTCRR

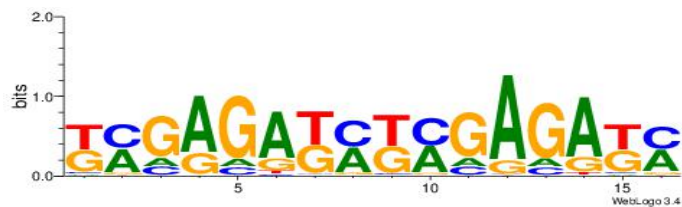


Dataset #: 1
 Motif ID: 26
 Motif name: C026
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 14
 Similarity score: 0.0116747

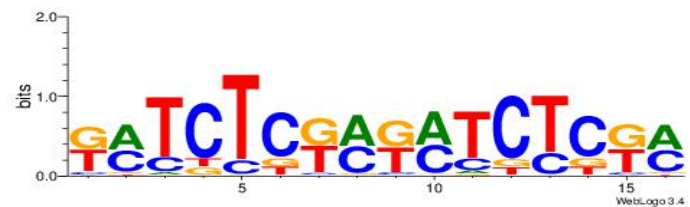
Alignment:

KMGAGAKMKMGAGAKM
 KMGAKAGAGMGAKM--

Original motif Consensus sequence: KMGAGAKMKMGAGAKM



Reverse complement motif Consensus sequence: RRTCTCRRRTCTCRR



Dataset #: 1
 Motif ID: 70
 Motif name: C070
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2

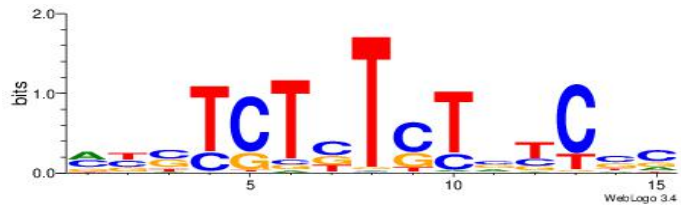
Number of overlap: 14
Similarity score: 0.0139232

Alignment:
GVGABAGAVAGASVK
KMGAKAGAGMGAKM-

Original motif Consensus sequence: GVGABAGAVAGASVK

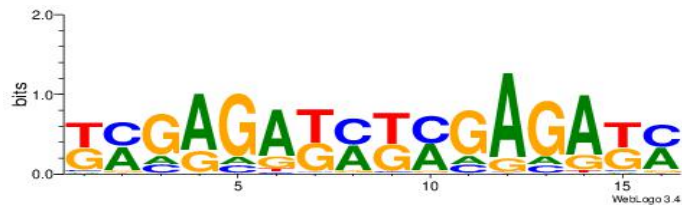


Reverse complement motif Consensus sequence: RBSTCTVTCTBTCV

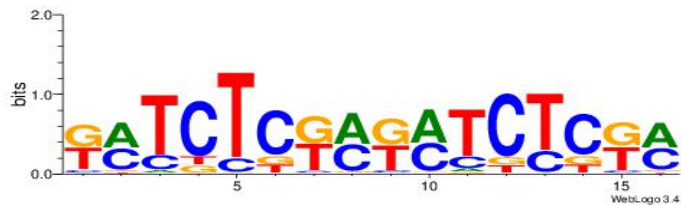


Dataset #: 1 Motif ID: 26 Motif name: C026

Original motif Consensus sequence: KMGAGAKMKMGAGAKM



Reverse complement motif Consensus sequence:
RRTCTCRRRTCTCRR



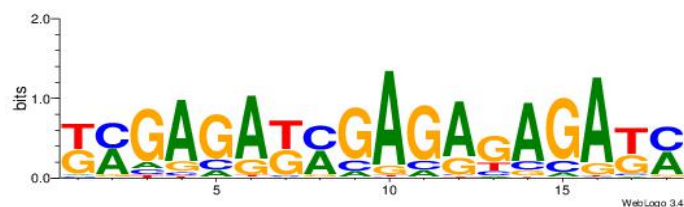
Best Matches for Motif ID 26 (Highest to Lowest)

Dataset #: 1
Motif ID: 11
Motif name: C011
Matching format of first motif: Original Motif

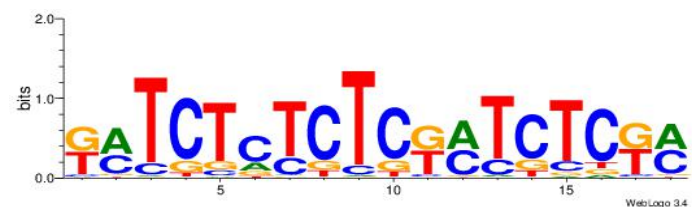
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	16
Similarity score:	0.0355709

Alignment:
KMGAGAKMGAGAGAGAKM
KMGAGAKMKMGAGAKM--

Original motif Consensus sequence: KMGAGAKMGAGAGAGAKM



Reverse complement motif Consensus sequence:
RRTCTCTCTCRRTCTCRR

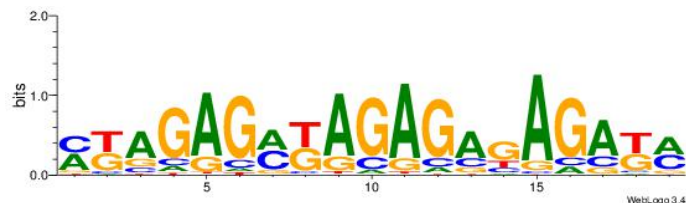


Dataset #:	1
Motif ID:	12
Motif name:	C012
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	16
Similarity score:	0.0522586

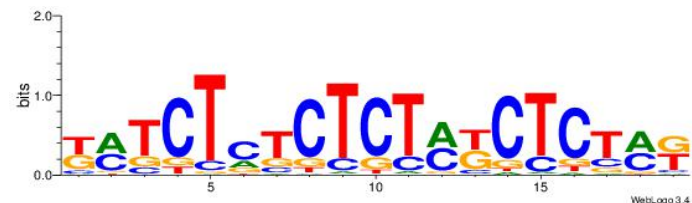
Alignment:

MKAGAGMKAGAGAGAGAKM
-KMGAGAKMKMGAGAKM--

Original motif Consensus sequence: MKAGAGMKAGAGAGAGAKM



Reverse complement motif Consensus sequence: YRTCTCTCTRYCTCTRR

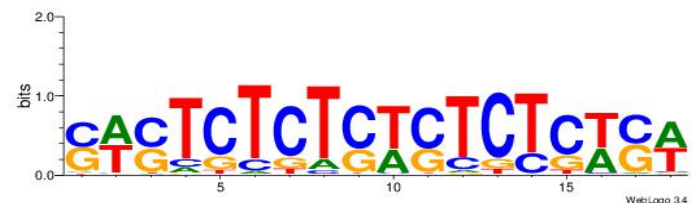
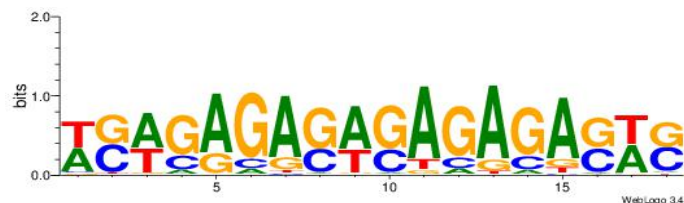


Dataset #:	1
Motif ID:	17
Motif name:	C017
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2
Number of overlap:	16
Similarity score:	0.0591037

Alignment:
WSWGAGASWSAGAGASWS
-KMGAGAKMKMGAGAKM-

Original motif Consensus sequence: WSWGAGASWSAGAGASWS

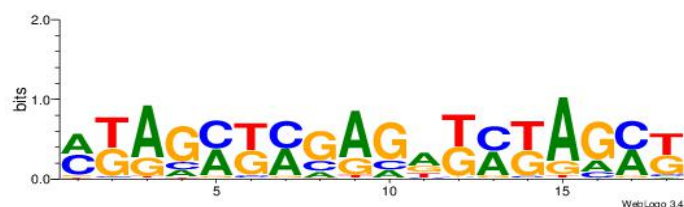
Reverse complement motif Consensus sequence: SWSTCTCTSWSTCTCWSW



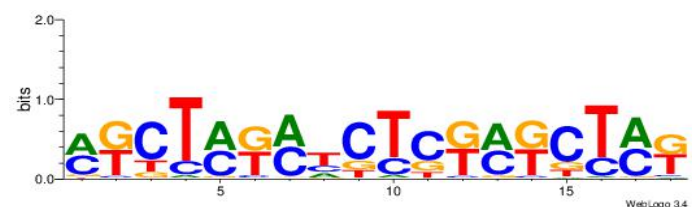
Dataset #: 1
 Motif ID: 36
 Motif name: C036
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 16
 Similarity score: 0.0805523

Alignment:
 MKAGMKMGAGAKMKAGMK
 -RRCTCTCRRRTCTCRR-

Original motif Consensus sequence: MKAGMKMGAGAKMKAGMK



Reverse complement motif Consensus sequence: RRCTRRRTCTCRRRCTRY



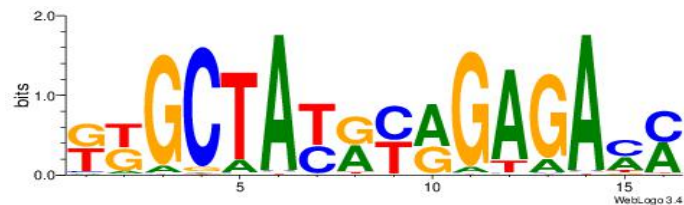
Dataset #: 1

Motif ID: 129
 Motif name: C129
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 16
 Similarity score: 0.0816986

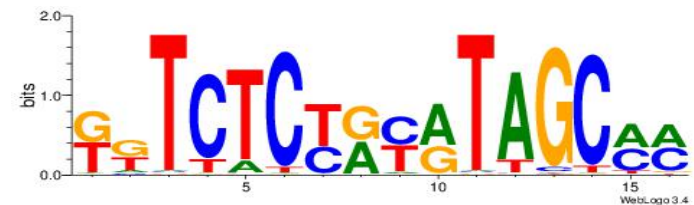
Alignment:

RRTCTCKKMMTAGCRY
 RRTCTCRRRTCTCRR

Original motif Consensus sequence: KKGCTAYRYRGAGAMM

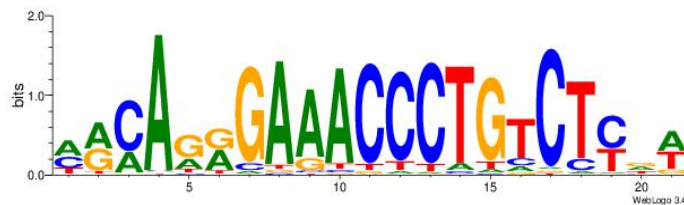


Reverse complement motif Consensus sequence: RRTCTCKKMMTAGCRY

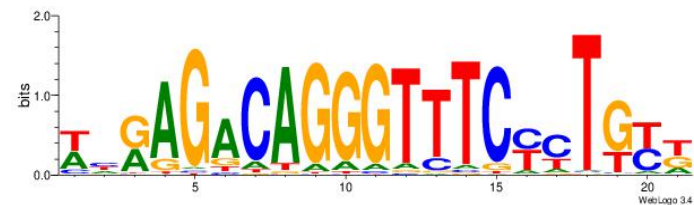


Dataset #: 1 Motif ID: 27 Motif name: C027

Original motif Consensus sequence: MRCAGRGAAACCCTGTCTYDW



Reverse complement motif Consensus sequence: WHKAGACAGGGTTTCMCTGKY



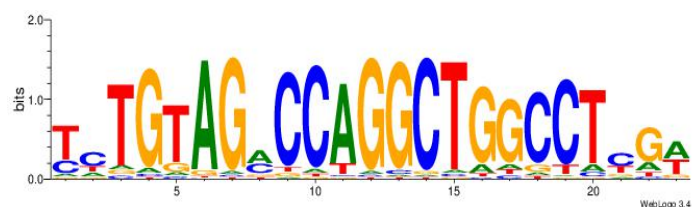
Best Matches for Motif ID 27 (Highest to Lowest)

Dataset #: 1
Motif ID: 5
Motif name: C005
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 3
Number of overlap: 21
Similarity score: 0.0518564

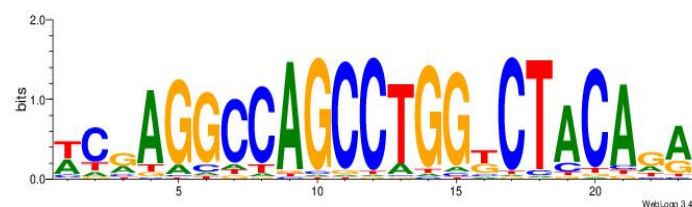
Alignment:

WCKAGGCCAGCCTGGYCTACAGA
--MRCAGRGAAACCCTGTCTYDW

Original motif Consensus sequence: TCTGTAGMCCAGGCTGGCCTYGW



Reverse complement motif Consensus sequence: WCKAGGCCAGCCTGGYCTACAGA



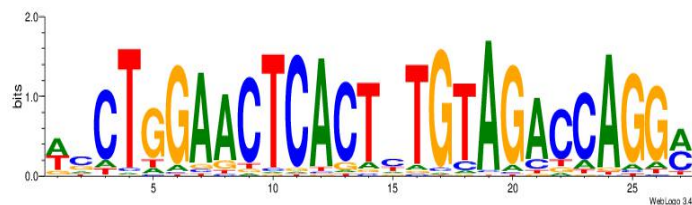
Dataset #: 1
Motif ID: 13
Motif name: C013
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement

Direction: Backward
 Position number: 1
 Number of overlap: 21
 Similarity score: 0.0563181

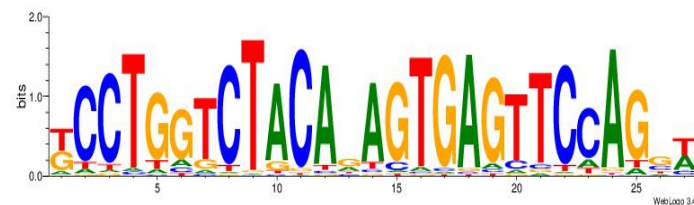
Alignment:

YCCTGGTCTACADAGTGAGTTCCAGVW
 -----WHKAGACAGGGTTTCMCTGKY

Original motif Consensus sequence:
 WVCTGGAAC TCACTHTGTAGACCAGGM



Reverse complement motif Consensus sequence:
 YCCTGGTCTACADAGTGAGTTCCAGVW

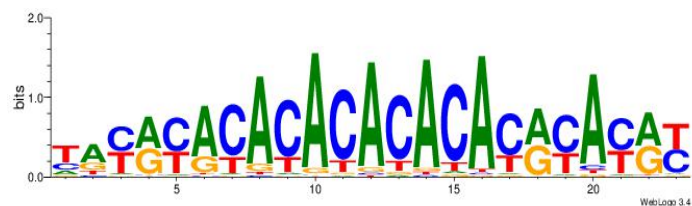


Dataset #: 1
 Motif ID: 2
 Motif name: C002
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 21
 Similarity score: 0.0592534

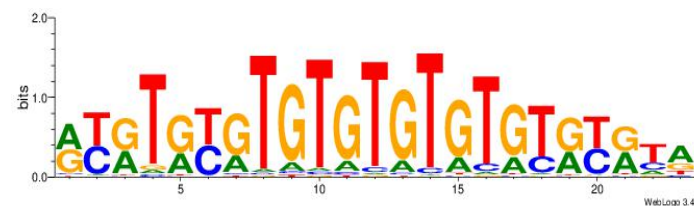
Alignment:

TAYRYACACACACACRYAYRY
 --MRCAGRGAAACCCTGTCTYDW

Original motif Consensus sequence: TAYRYACACACACACRYAYRY



Reverse complement motif Consensus sequence: MKKTKKGTGTGTGTGTGTTKKTA

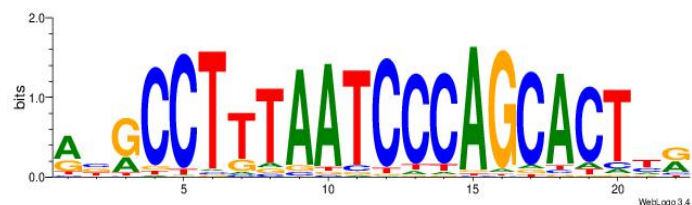


Dataset #: 1
 Motif ID: 9
 Motif name: C009
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 21
 Similarity score: 0.0624213

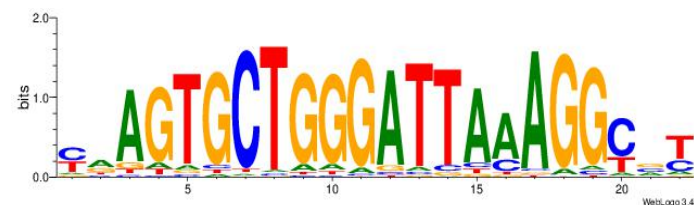
Alignment:

ABGCCTTTAATCCCAGCACTHR
 -MRCAGRGAACCCCTGTCTYDW

Original motif Consensus sequence: ABGCCTTTAATCCCAGCACTHR



Reverse complement motif Consensus sequence: MHAGTGCTGGGATTAAAGGCBT

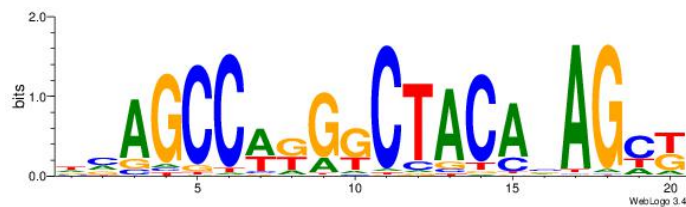


Dataset #: 1
 Motif ID: 15
 Motif name: C015
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 20
 Similarity score: 0.542884

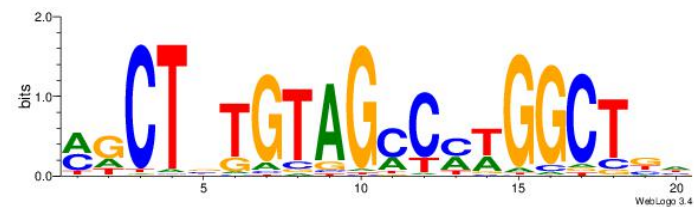
Alignment:

-RGCTVTGTAGCCYWGGCTVD
 MRCAGRGAAACCCTGTCTYDW

Original motif Consensus sequence: DVAGCCWKGCTACAVAGCK



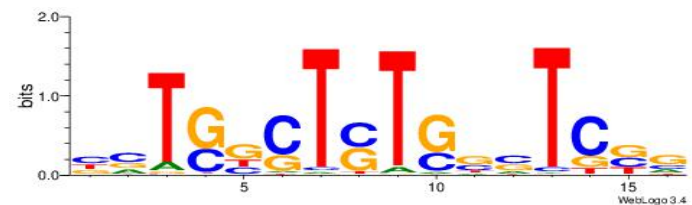
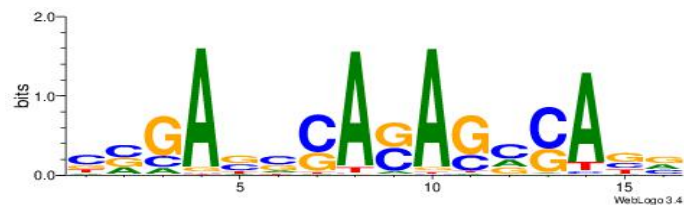
Reverse complement motif Consensus sequence: RGCTVTGTAGCCYWGGCTVD



Dataset #: 1 Motif ID: 28 Motif name: C028

Original motif Consensus sequence: BVGASSCASAGVSABV

Reverse complement motif Consensus sequence: VBTSVCTSTGSSTCVB



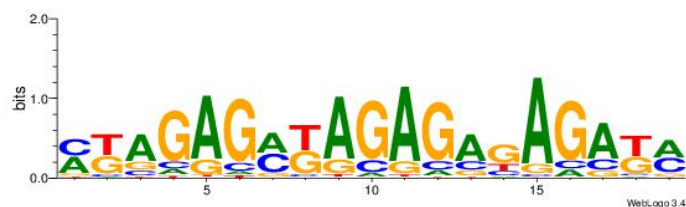
Best Matches for Motif ID 28 (Highest to Lowest)

Dataset #: 1
 Motif ID: 12
 Motif name: C012
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 16
 Similarity score: 0.0221234

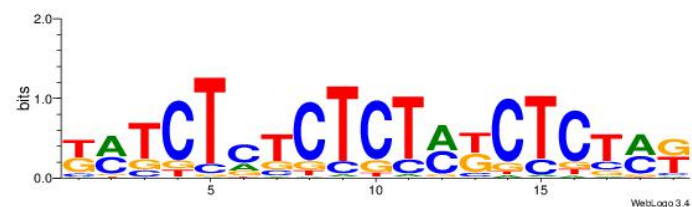
Alignment:

MKAGAGMKAGAGAGAGAKM
 -BVGASSCASAGVSABV--

Original motif Consensus sequence: MKAGAGMKAGAGAGAGAKM



Reverse complement motif Consensus sequence: YRTCTCTCTRYCTCTRR

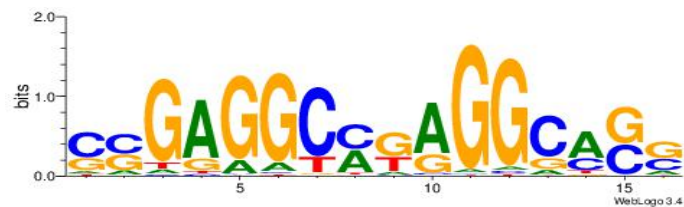


Dataset #: 1
 Motif ID: 41
 Motif name: C041
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 16
 Similarity score: 0.0252792

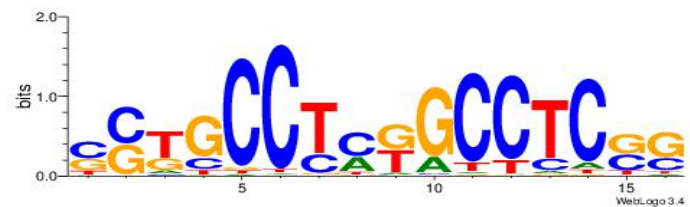
Alignment:

CSGAGGCMKAGGCASS
 BVGASSCASAGVSABV

Original motif Consensus sequence: CSGAGGCMKAGGCASS



Reverse complement motif Consensus sequence: SSTGCCTYRGCTCSG

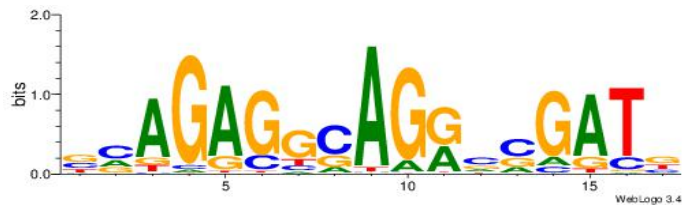


Dataset #: 1
 Motif ID: 44
 Motif name: C044
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2

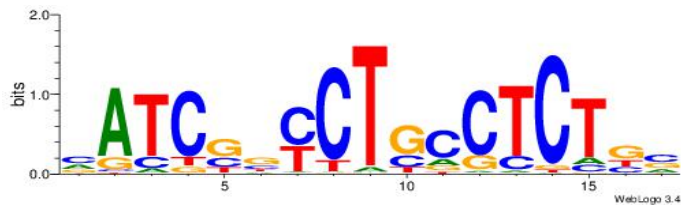
Number of overlap: 16
Similarity score: 0.0258827

Alignment:
BVAGAGGCAGRVSGATB
-BVGASSCASAGVSABV

Original motif Consensus sequence: BVAGAGGCAGRVSGATB



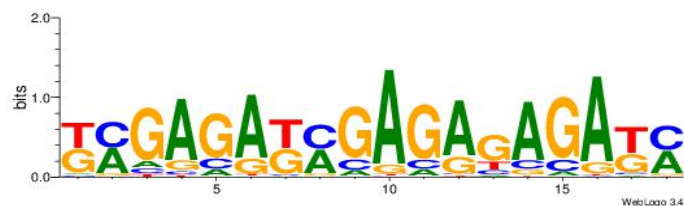
Reverse complement motif Consensus sequence: BATCSVMCTGCCTCTVB



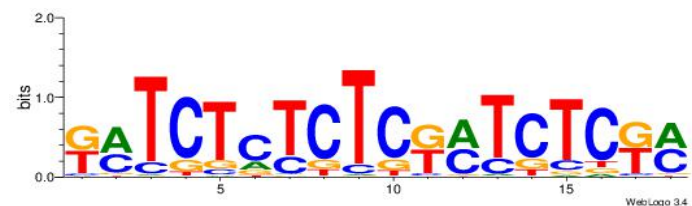
Dataset #: 1
Motif ID: 11
Motif name: C011
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 3
Number of overlap: 16
Similarity score: 0.0260543

Alignment:
KMGAGAKMGAGAGAGAKM
--BVGASSCASAGVSABV

Original motif Consensus sequence: KMGAGAKMGAGAGAGAKM



Reverse complement motif Consensus sequence: RRTCTCTCTCRRTCTCRR

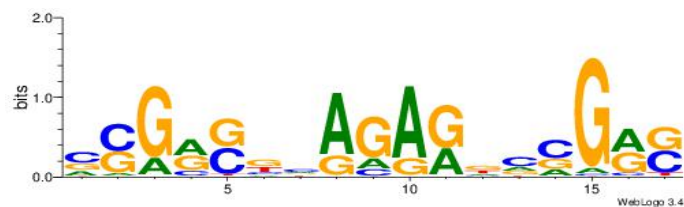


Dataset #: 1
Motif ID: 85
Motif name: C085
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2
Number of overlap: 16
Similarity score: 0.0271866

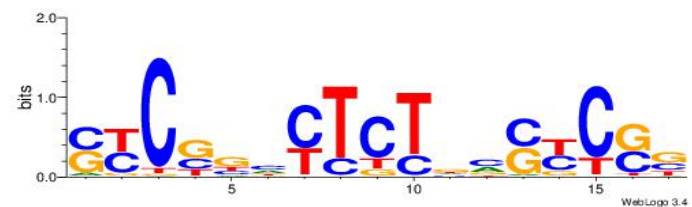
Alignment:

VSGRSBHAGARDVSGRS
BVGASSCASAGVSABV-

Original motif Consensus sequence: VSGRSBHAGARDVSGRS

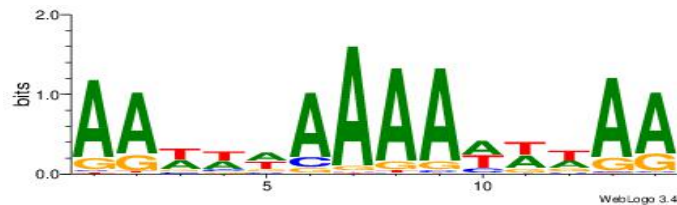


Reverse complement motif Consensus sequence: SKCSVHMTCTDBSKCSV

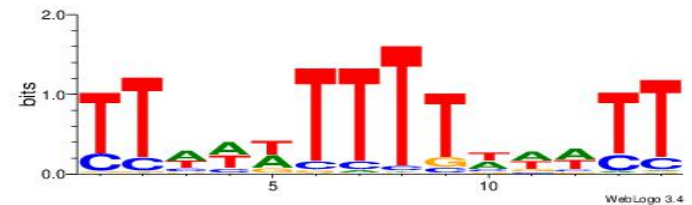


Dataset #: 1 Motif ID: 29 Motif name: C029

Original motif Consensus sequence: AAWWWAAA AWWAA



Reverse complement motif Consensus sequence: TTWWTTTTTWWTT



Best Matches for Motif ID 29 (Highest to Lowest)

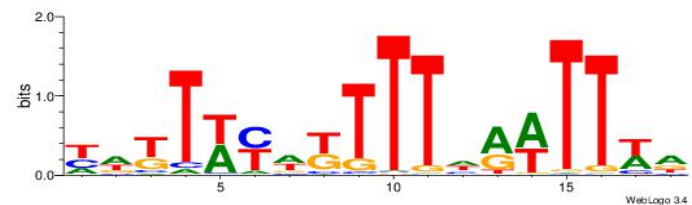
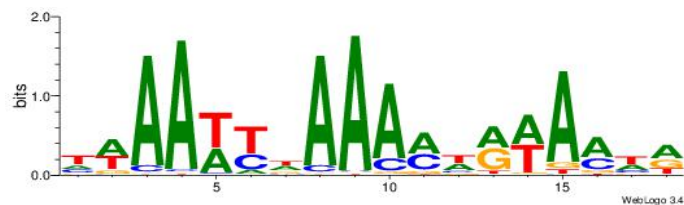
Dataset #:	1
Motif ID:	32
Motif name:	C032
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	3
Number of overlap:	14
Similarity score:	0.0196644

Alignment:

```
KWYTWKWYTTTDMWTTWH
--TTWWTTTWWTT--
```

Original motif Consensus sequence: HWAAWYDAAAMWRWAMWR

Reverse complement motif Consensus sequence: KWYTWKWYTTTDMWTTWH

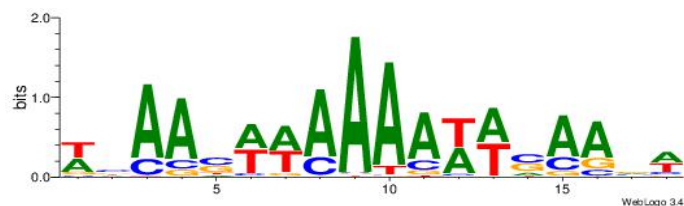


Dataset #: 1
 Motif ID: 97
 Motif name: C097
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 14
 Similarity score: 0.0201332

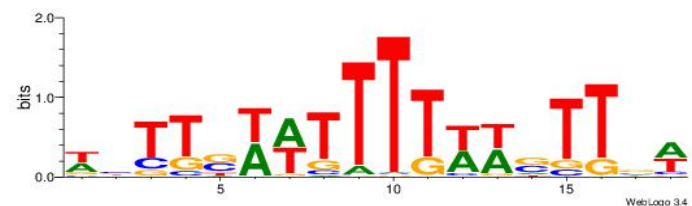
Alignment:

WTTTSWWTTTTWWSTTBW
 --TTWWWTTTTWWWT--

Original motif Consensus sequence: WBAASWWAAAWWSAAVW



Reverse complement motif Consensus sequence: WTTTSWWTTTTWWSTTBW



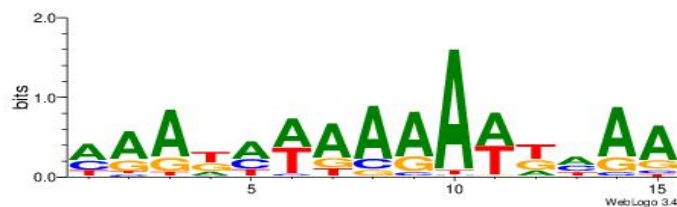
Dataset #: 1

Motif ID: 63
 Motif name: C063
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 14
 Similarity score: 0.0201809

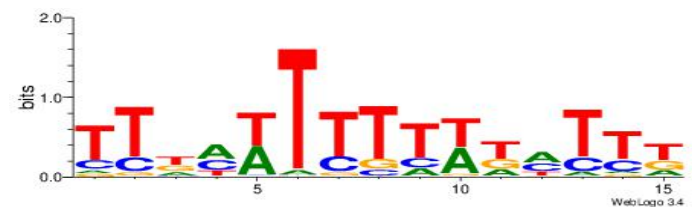
Alignment:

MAAKMWAAAANKHAA
 -AAWWWAAAANKWAA

Original motif Consensus sequence: MAAKMWAAAANKHAA



Reverse complement motif Consensus sequence: TTHRWTATTTWYRT

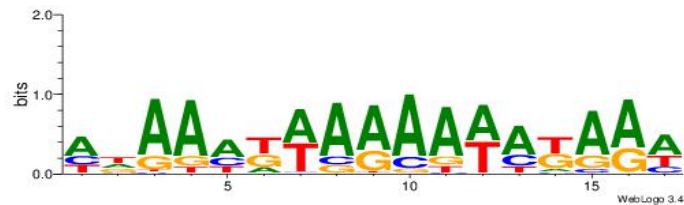


Dataset #: 1
 Motif ID: 79
 Motif name: C079
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 14
 Similarity score: 0.020478

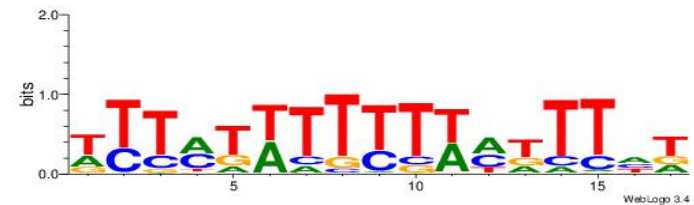
Alignment:

WKTRTWTTTTWRTTTDT
-TTWWTTTTTWWTT--

Original motif Consensus sequence: ADAAKWAAAAWAKARW



Reverse complement motif Consensus sequence:
WKTRTWTTTTWRTTTDT



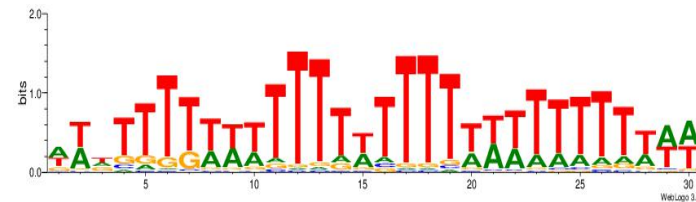
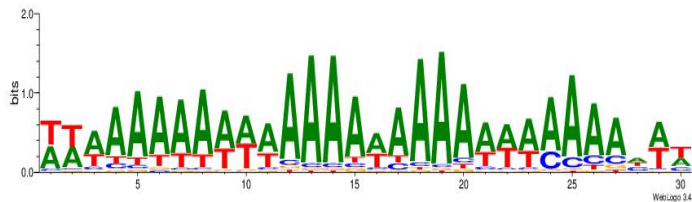
Dataset #:	1
Motif ID:	1
Motif name:	C001
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	6
Number of overlap:	14
Similarity score:	0.0204858

Alignment:

WWWAAAAAWWAAAAWAAAAWWAAAAHWW
-----AAWWAAAAWWWAA-----

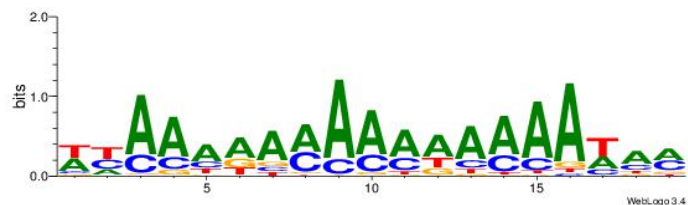
Original motif Consensus sequence:
WWWAAAAAWWAAAAWAAAAWWAAAAHWW

Reverse complement motif Consensus sequence:
WWHTTTTWWTTTTTWWTTTTTWWTTTTTWW

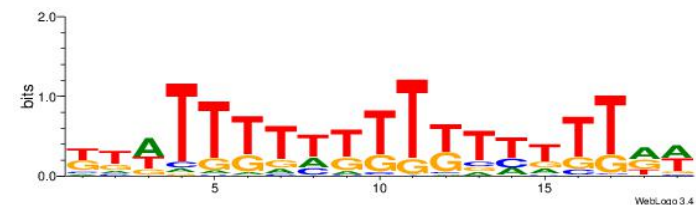


Dataset #: 1 Motif ID: 30 Motif name: C030

Original motif Consensus sequence: WYAAAAAMAAAAAAWAM



Reverse complement motif Consensus sequence: YTWTTTTTTTTTTTTTMW



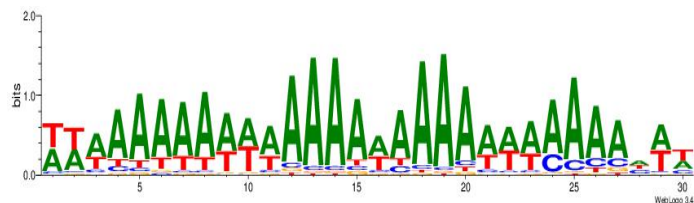
Best Matches for Motif ID 30 (Highest to Lowest)

Dataset #:	1
Motif ID:	1
Motif name:	C001
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	10
Number of overlap:	19
Similarity score:	0.0117121

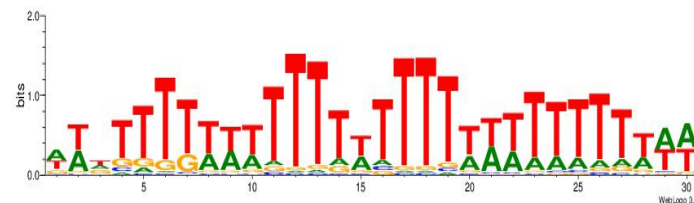
Alignment:

WWWAAAAWAAAAWAAAAWAAAAHWW
 -----WYAAAAMAAAAAAAWAM--

Original motif Consensus sequence:
 WWWAAAAWAAAAWAAAAWAAAAHWW



Reverse complement motif Consensus sequence:
 WWHTTTTWWTTTTWTTTTWTTTTWWW

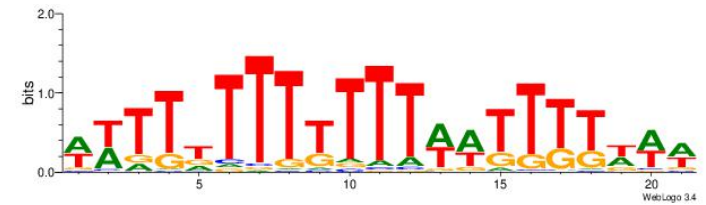


Dataset #: 1
 Motif ID: 10
 Motif name: C010
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 19
 Similarity score: 0.0158814

Alignment:
 WWWAAAAWAAAAAAAAAAW
 WYAAAAAIAAAAAAAWAM--

Original motif Consensus sequence: WWWAAAAWAAAAAAAAAAW

Reverse complement motif Consensus sequence:
 WWTTTTTTTTTWWTTTTWWW

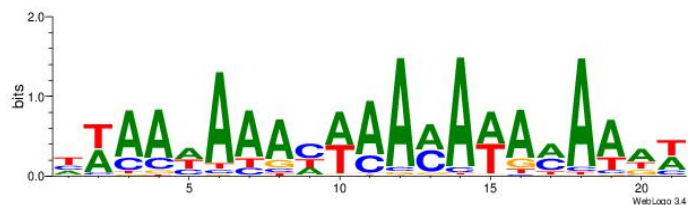


Dataset #:	1
Motif ID:	16
Motif name:	C016
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	3
Number of overlap:	19
Similarity score:	0.0219024

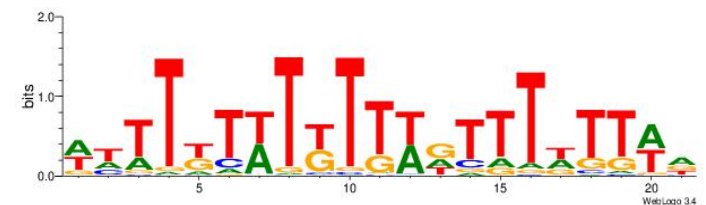
Alignment:

HWAAWAAAHWAAMAWAMAAWW
WYAAAAAMAAAAAAAWAM--

Original motif Consensus sequence: HWAAWAAHWAAMAWAMAAWW



Reverse complement motif Consensus sequence:
WWTTYTWYTTWDTTWTWH



Dataset #: 1

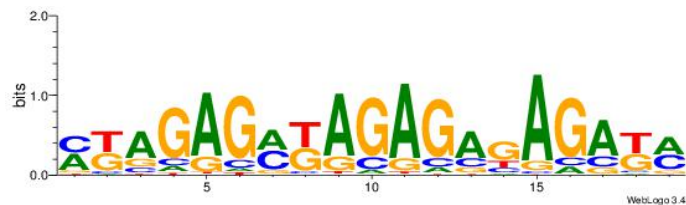
Motif ID:	12
Motif name:	C012
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	19
Similarity score:	0.0679227

Alignment:

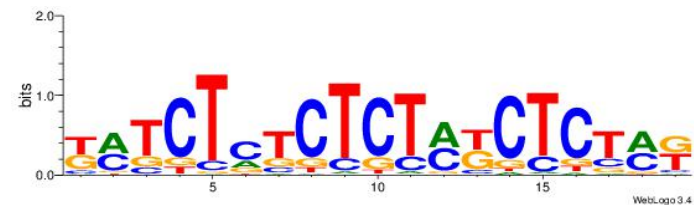
YRTCTCTCTCTRYCTCTR

YTWTTTTTTTTTYTTTTMW

Original motif Consensus sequence: MKAGAGMKAGAGAGAGAKM



Reverse complement motif Consensus sequence:
YRTCTCTCTRYCTCTRR

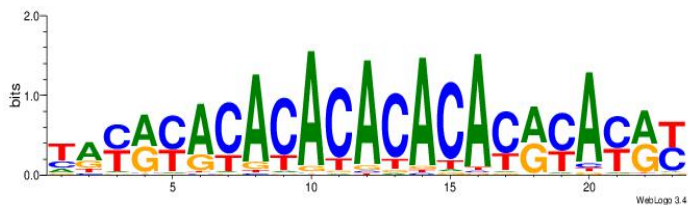


Dataset #:	1
Motif ID:	2
Motif name:	C002
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	19

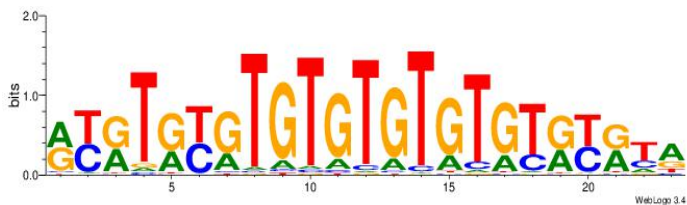
Similarity score: 0.0690814

Alignment:
TAYRYACACACACACRYAYRY
WYAAAAAMAAAAAAWAM----

Original motif Consensus sequence: TAYRYACACACACACRYAYRY

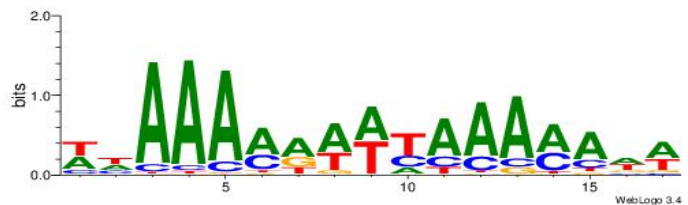


Reverse complement motif Consensus sequence: MKKTKKGTGTGTGTGTGKKKTA

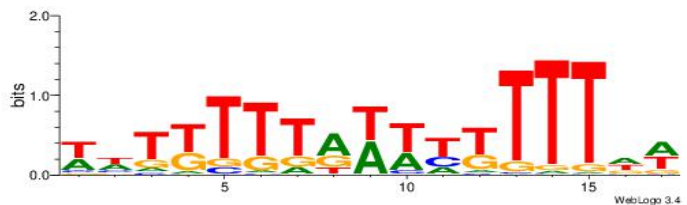


Dataset #: 1 Motif ID: 31 Motif name: C031

Original motif Consensus sequence: WHAAAMRWWYAAAMAWW



Reverse complement motif Consensus sequence: WWTYTTTMMWWKYTTTHW



Best Matches for Motif ID 31 (Highest to Lowest)

Dataset #: 1
Motif ID: 139
Motif name: C139
Matching format of first motif: Original Motif

Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	17
Similarity score:	0.0108942

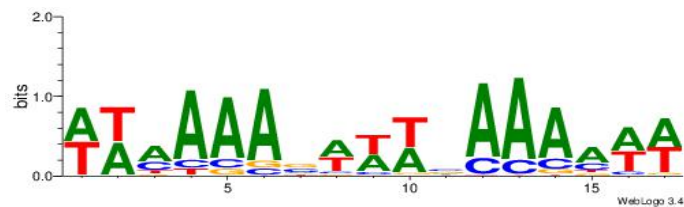
Alignment:

```

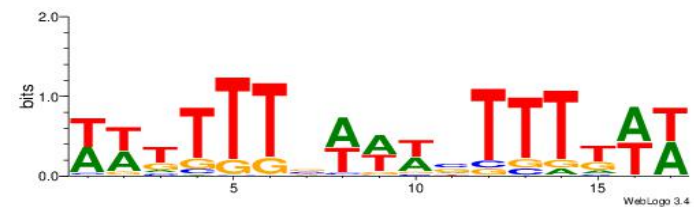
WWMAAABWWWVAAAAWW
WHAAAMRWYAAAMAWW

```

Original motif Consensus sequence: WWMAAABWWWVAAAAWW



Reverse complement motif Consensus sequence: WWTTTTVWWBTTTYWW

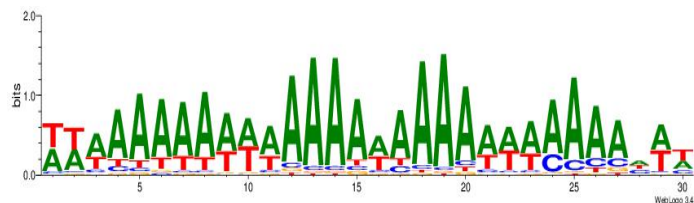


Dataset #:	1
Motif ID:	1
Motif name:	C001
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	14
Number of overlap:	17
Similarity score:	0.0139635

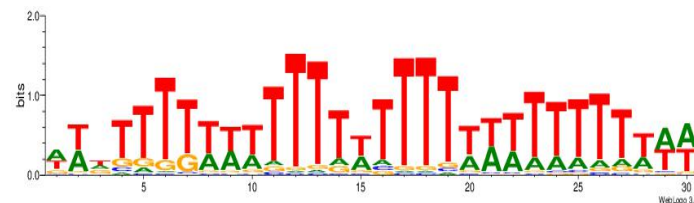
Alignment:

WWHTTTTWWTTTTTTWTTTTTWWTTTTTWW
 -----WWTYTTTMWWKYTTTHW

Original motif Consensus sequence:
 WWWAAAAWWAAAAWAAAAWWAAAHWW



Reverse complement motif Consensus sequence:
 WWHTTTTWWTTTTTTWTTTTTWWTTTTTWW

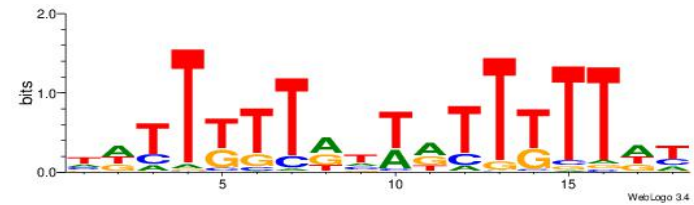


Dataset #:	1
Motif ID:	69
Motif name:	C069
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	17
Similarity score:	0.0179323

Alignment:
 AHAAMAA YWDYAAMAAHD
 -WHAAAMRWWYAAAMAWW

Original motif Consensus sequence: AHAAMAA YWDYAAMAAHD

Reverse complement motif Consensus sequence:
 DHTTYTTMDWMTTYTTHT

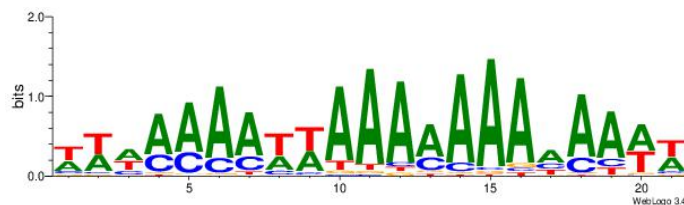


Dataset #:	1
Motif ID:	10
Motif name:	C010
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	4
Number of overlap:	17
Similarity score:	0.0242721

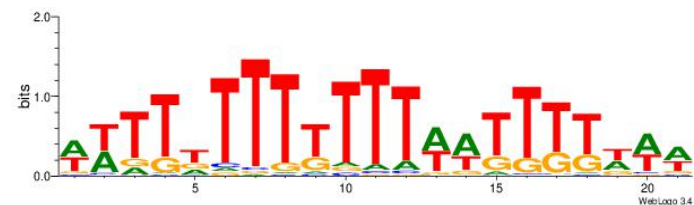
Alignment:

WWWAAA W WAAAAAA W W
-W HAA M R W Y A A M A W W - - -

Original motif Consensus sequence: WWWAAAWWAAAAAAAAAAWW



Reverse complement motif Consensus sequence:
WWTTTTTTTTTWWTTTWWW



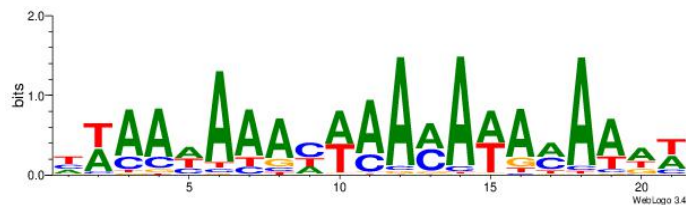
Dataset #: 1

Motif ID: 16
 Motif name: C016
 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: 0.0270447

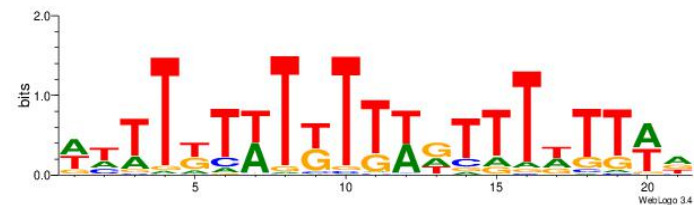
Alignment:

HWAAWAAAHWAAMAWAMAAWW
 ---WHAAAMRWYAAAMAWW-

Original motif Consensus sequence: HWAAWAAAHWAAMAWAMAAWW

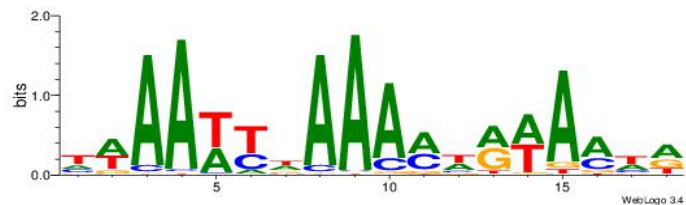


Reverse complement motif Consensus sequence: WWTYYTWYTTWDTTWTWH

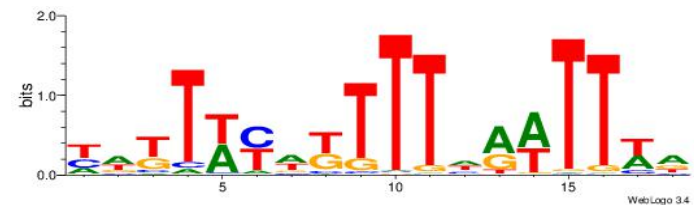


Dataset #: 1 Motif ID: 32 Motif name: C032

Original motif Consensus sequence: HWAAWYDAAAMWRWAMWR



Reverse complement motif Consensus sequence: KWTWKWYTTTDMWTTWH



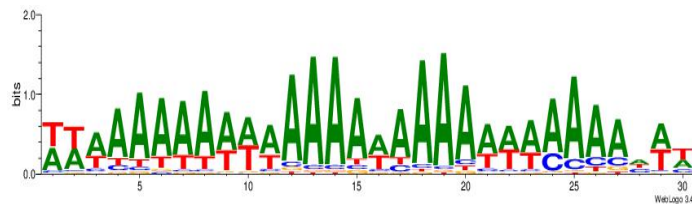
Best Matches for Motif ID 32 (Highest to Lowest)

Dataset #: 1
Motif ID: 1
Motif name: C001
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 9
Number of overlap: 18
Similarity score: 0.0271766

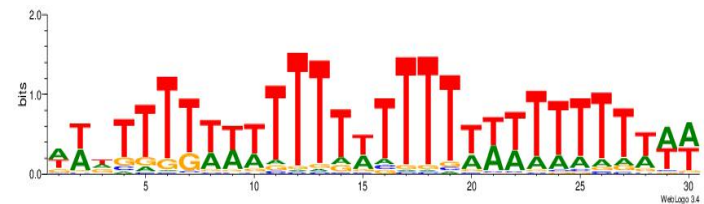
Alignment:

```
WWHTTTTWWTTTTTWWTTTTTWWTTTTTWW  
-----KWYTWKWYTTTDMWTTWH-----
```

Original motif Consensus sequence:
WWWAAAAAWWAAAAWAAAAWWAAAAHWW



Reverse complement motif Consensus sequence:
WWHTTTTWWTTTTTWWTTTTTWWTTTTTWW



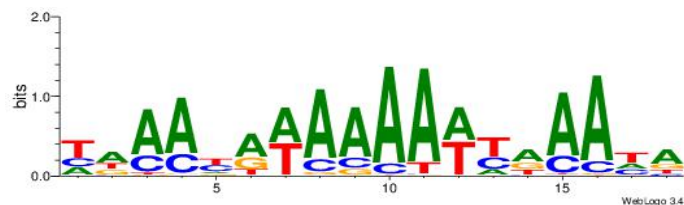
Dataset #: 1
Motif ID: 24
Motif name: C024
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif

Direction: Forward
Position number: 1
Number of overlap: 18
Similarity score: 0.0299469

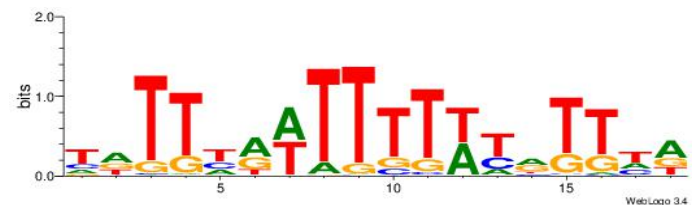
Alignment:

TDAAYRWAAAAYDAAHA
HWAAYDAAAMWRWAMWR

Original motif Consensus sequence: TDAAYRWAAAAYDAAHA



Reverse complement motif Consensus sequence: THTTDMWTTTTWKMTTDA

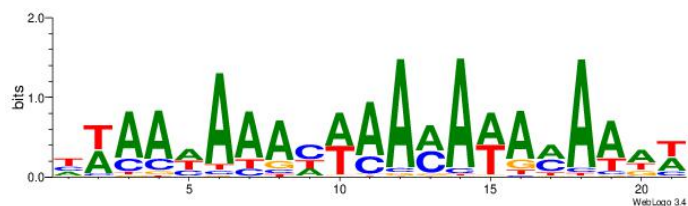


Dataset #: 1
Motif ID: 16
Motif name: C016
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 4
Number of overlap: 18
Similarity score: 0.0305692

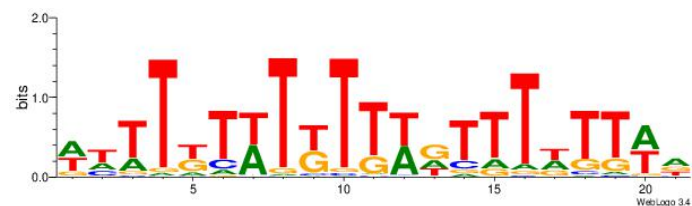
Alignment:

HWAAWAAAHWAAMAWAMAAWW
---HWAAYDAAAMWRWAMWR

Original motif Consensus sequence: HWAAWAAHWAAMAWAMAAWW



Reverse complement motif Consensus sequence: WWTYYTWYTTWDTTTWTTWH

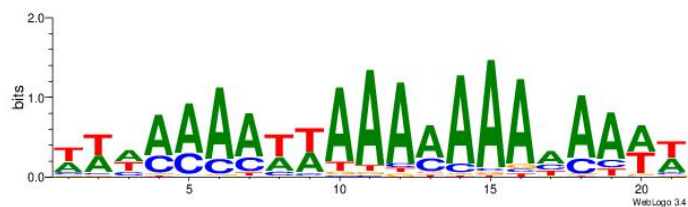


Dataset #: 1
 Motif ID: 10
 Motif name: C010
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 18
 Similarity score: 0.0334855

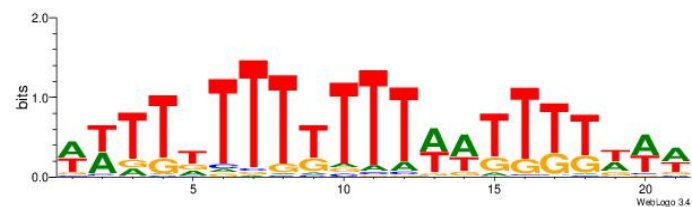
Alignment:

WWWAAAAWWAAAAAAAAAAWW
 --HWAAWYDAAAMWRWAMWR--

Original motif Consensus sequence: WWWAAAWWAAAAAAAAAAWW



Reverse complement motif Consensus sequence: WWTYYYYTTTTTWWTTTTWWW

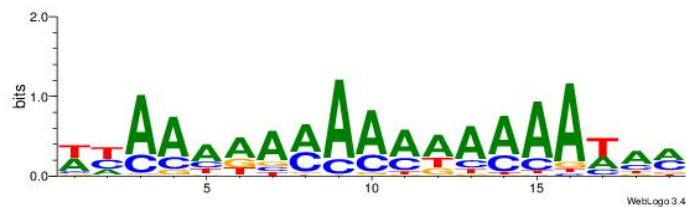


Dataset #: 1
 Motif ID: 30
 Motif name: C030
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 18
 Similarity score: 0.033959

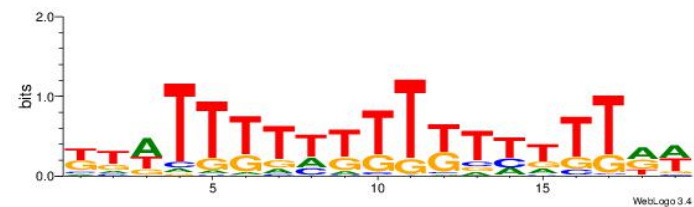
Alignment:

YTWTTTTTTTTYTTTTMW
 -KWYTWKWYTTTDMWTTWH

Original motif Consensus sequence: WYAAAAAIAAAAAAAWAM



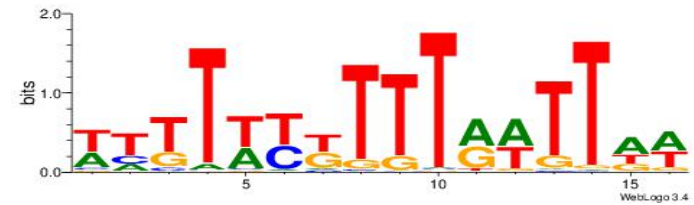
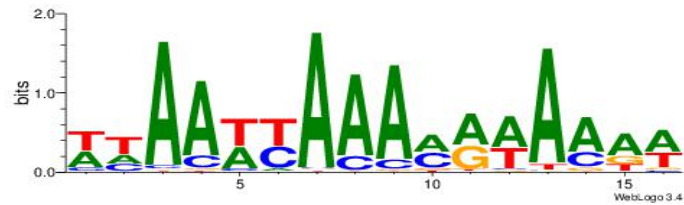
Reverse complement motif Consensus sequence: YTWTTTTTTTTYTTTTMW



Dataset #: 1 Motif ID: 33 Motif name: C033

Original motif Consensus sequence: WWAAYAAAMRWAAW

Reverse complement motif Consensus sequence: WTTTWKYTTTMMWTTWW



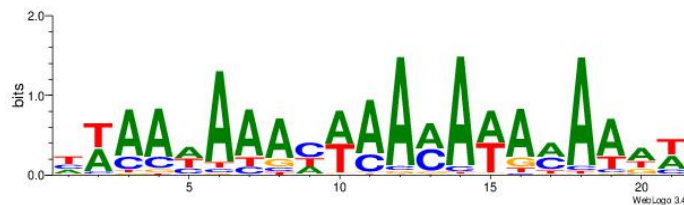
Best Matches for Motif ID 33 (Highest to Lowest)

Dataset #: 1
 Motif ID: 16
 Motif name: C016
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 16
 Similarity score: 0.0145744

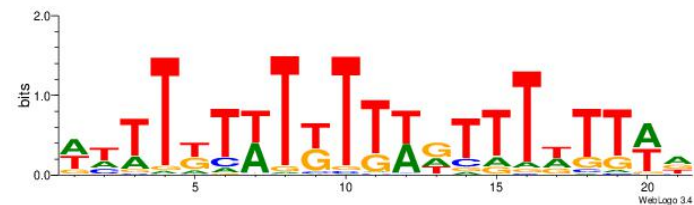
Alignment:

HWAAWAAAHWAAMAWAMAAWW
 ---WWAAWYAAAMRWAAAW---

Original motif Consensus sequence: HWAAWAAAHWAAMAWAMAAWW



Reverse complement motif Consensus sequence: WWTTYTWYTTWDTTTWTTWH

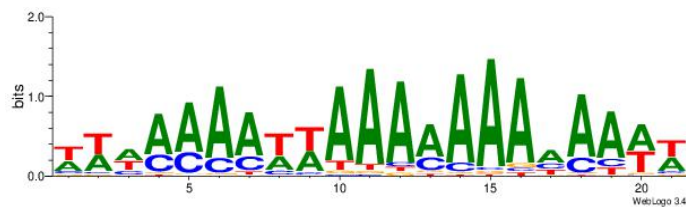


Dataset #: 1
 Motif ID: 10
 Motif name: C010
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 16
 Similarity score: 0.0181127

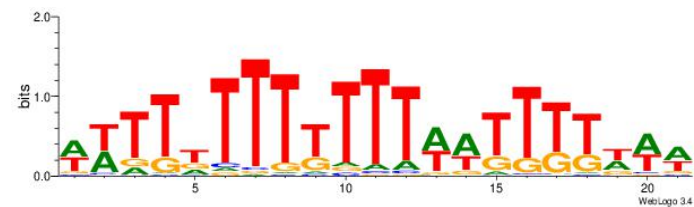
Alignment:

WWWAAAWWAAAAAAAAAAWW
 ---WWAAWYAAAMRWAAW---

Original motif Consensus sequence: WWWAAAWWAAAAAAAAAAWW



Reverse complement motif Consensus sequence: WWTTTTTTTTTTWWTTTTWWW



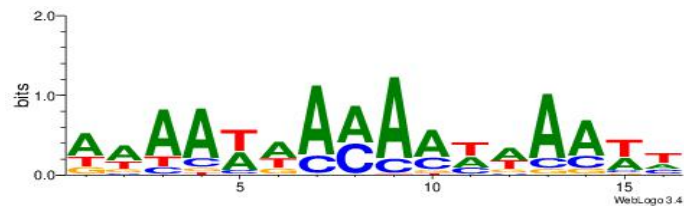
Dataset #: 1
 Motif ID: 98
 Motif name: C098
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1

Number of overlap: 16
Similarity score: 0.0203419

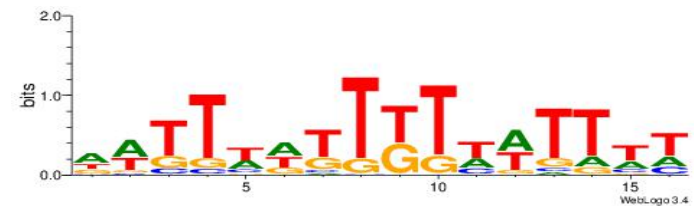
Alignment:

AAAAWWAMAAWWAAWH
WWAAWYAAAMRWAAAW

Original motif Consensus sequence: AAAAWWAMAAWWAAWH



Reverse complement motif Consensus sequence: HWTTWWTTYTWTTTTT

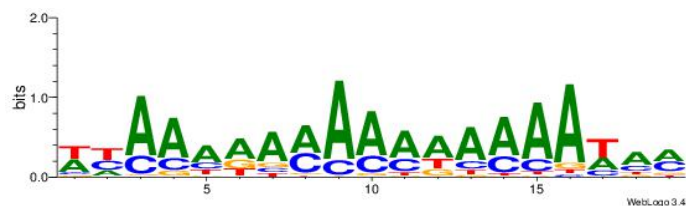


Dataset #: 1
Motif ID: 30
Motif name: C030
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 16
Similarity score: 0.0203703

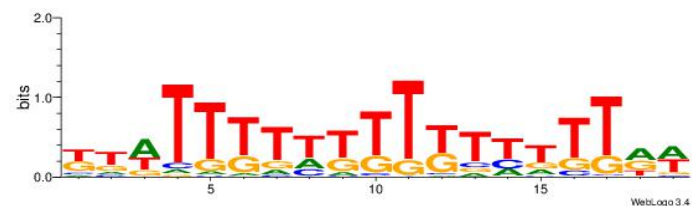
Alignment:

YTWTTTTTTTTYTTTTMW
---WTTTWKYTTTMWTTWW

Original motif Consensus sequence: WYAAAAAMAAAAAAAWAM



Reverse complement motif Consensus sequence: YTWTTTTTTTTYTTTTMW



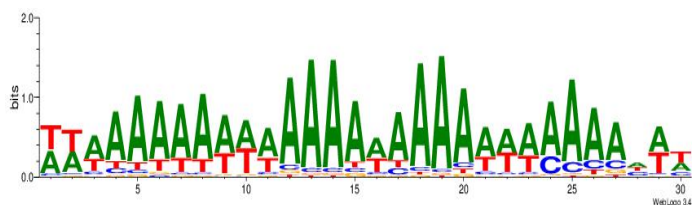
Dataset #: 1
 Motif ID: 1
 Motif name: C001
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 10
 Number of overlap: 16
 Similarity score: 0.0209377

Alignment:

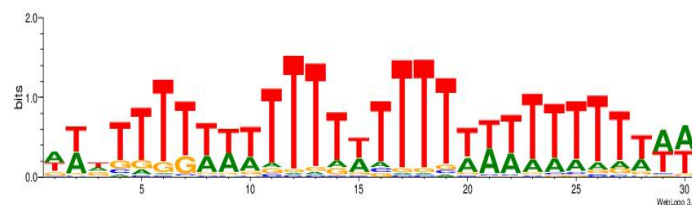
```

WWWAAAAAWWAAAAAWAAAAWWAAAAHWW
-----WWAAWYAAAMRWAAW-----
  
```

Original motif Consensus sequence:
 WWWAAAAAWWAAAAAWAAAAWWAAAAHWW

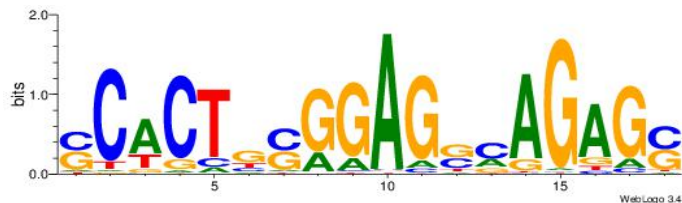


Reverse complement motif Consensus sequence:
 WWHTTTTWWTTTTTWT TTTTWWTTTTTWW

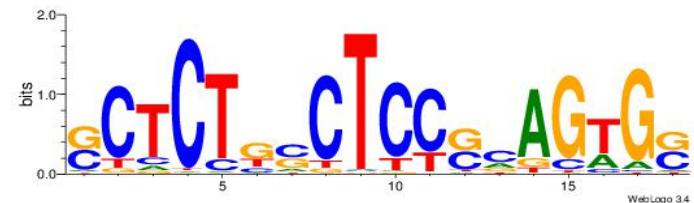


Dataset #: 1 Motif ID: 34 Motif name: C034

Original motif Consensus sequence: SCACTGSGGAGSMAGAGS



Reverse complement motif Consensus sequence: SCTCTRSCTCCSCAGTGS



Best Matches for Motif ID 34 (Highest to Lowest)

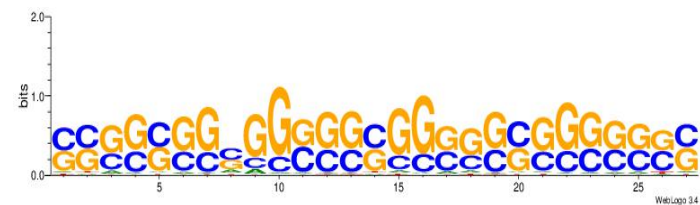
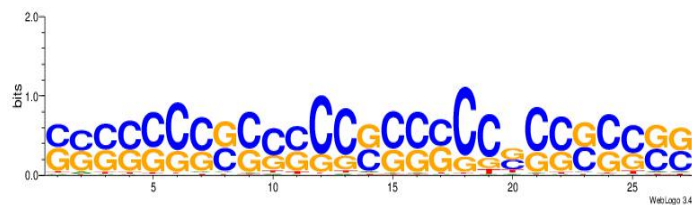
Dataset #:	1
Motif ID:	4
Motif name:	C004
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	2
Number of overlap:	18
Similarity score:	0.0701833

Alignment:

```
SSSSSSGSGGSSSSGSGSSSSGSSSSS
-----SCACTGSGGAGSMAGAGS-
```

Original motif Consensus sequence:
SSSSCSSSSSCSSSSCCSCSSSSS

Reverse complement motif Consensus sequence:
SSSSSSGSGGSSSSGSGSSSSGSSSSS

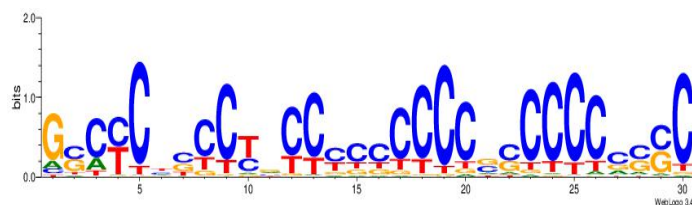


Dataset #: 1
 Motif ID: 3
 Motif name: C003
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 18
 Similarity score: 0.0741737

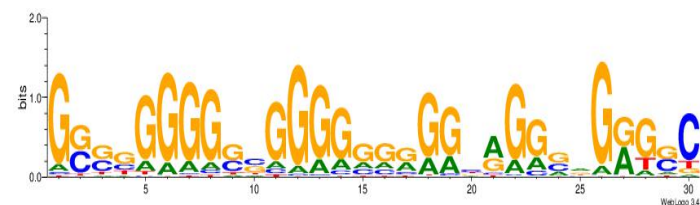
Alignment:

GSSGGGGSSGGGGGKGGVMGGSHGKGC
 -SCACTGSGGAGSMAGAGS-----

Original motif Consensus sequence:
 GSCYCHSCCYVCCYCCCCSSCCCCSSC



Reverse complement motif Consensus sequence:
 GSSGGGGSSGGGGGKGGVMGGSHGKGC



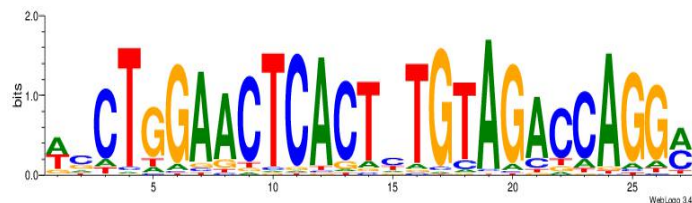
Dataset #: 1

Motif ID: 13
 Motif name: C013
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 10
 Number of overlap: 18
 Similarity score: 0.0750158

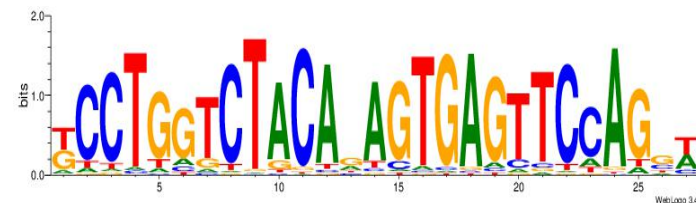
Alignment:

YCCTGGTCTACADAGTGAGTTCCAGVW
 SCTCTRSCTCCSCAGTGS-----

Original motif Consensus sequence:
 WVCTGGAAC TCACTHTGTAGACCAGGM



Reverse complement motif Consensus sequence:
 YCCTGGTCTACADAGTGAGTTCCAGVW

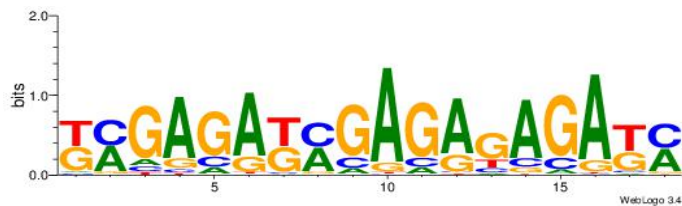


Dataset #: 1
 Motif ID: 11
 Motif name: C011
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 18

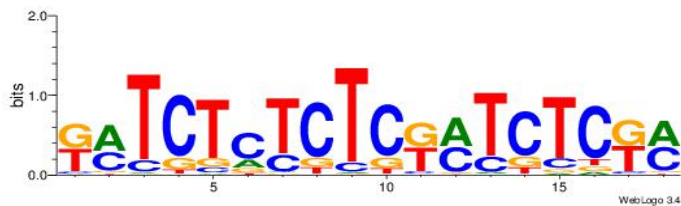
Similarity score: 0.0801719

Alignment:
RRTCTCTCTCRRTCTCRR
SCTCTRSCTCCSCAGTGS

Original motif Consensus sequence: KMGAGAKMGAGAGAGAKM



Reverse complement motif Consensus sequence:
RRTCTCTCTCRRTCTCRR

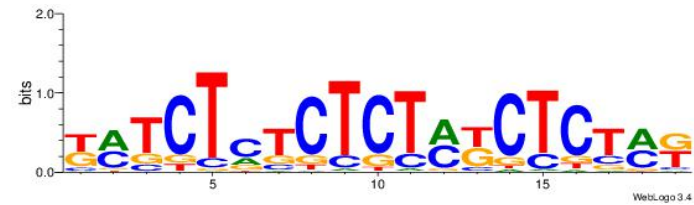
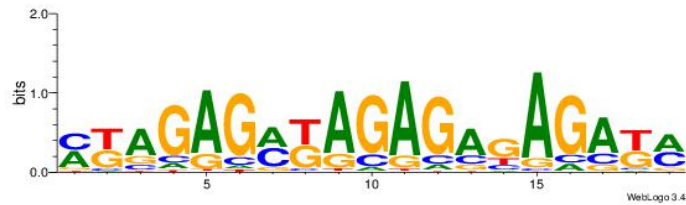


Dataset #: 1
Motif ID: 12
Motif name: C012
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 2
Number of overlap: 18
Similarity score: 0.0806452

Alignment:
YRTCTCTCTCTRYCTCTRR
SCTCTRSCTCCSCAGTGS-

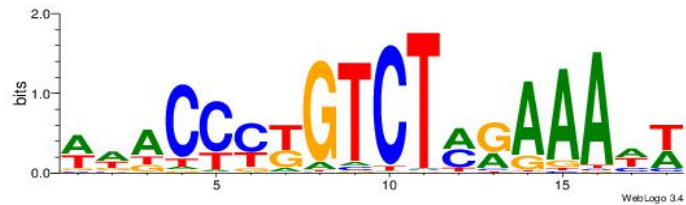
Original motif Consensus sequence: MKAGAGMKAGAGAGAGAKM

Reverse complement motif Consensus sequence:
YRTCTCTCTCTRYCTCTRR

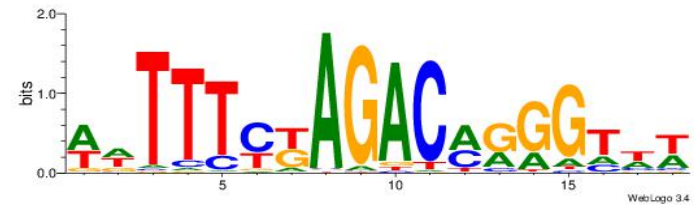


Dataset #: 1 Motif ID: 35 Motif name: C035

Original motif Consensus sequence: WWACCYKGTCTMRAAAWW



Reverse complement motif Consensus sequence: WWTTTYAGACRKGGTWW



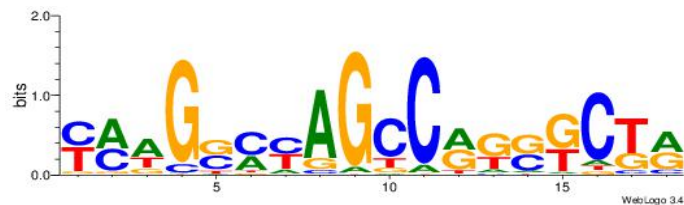
Best Matches for Motif ID 35 (Highest to Lowest)

Dataset #:	1
Motif ID:	73
Motif name:	C073
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:	0.0646565

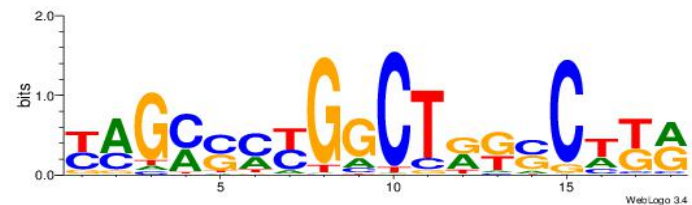
Alignment:

YMWGSMYAGCCRKSKCTR
WTTTMYAGACRKGGTWW

Original motif Consensus sequence: YMWGSMYAGCCRKSKCTR



Reverse complement motif Consensus sequence:
KAGYSYKGGCTKRSCWYK



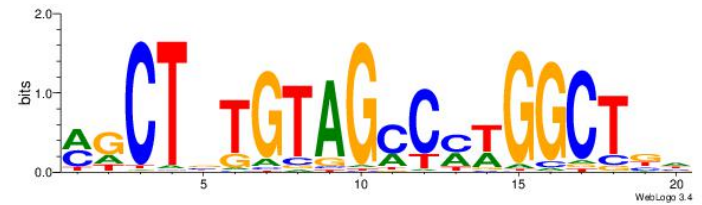
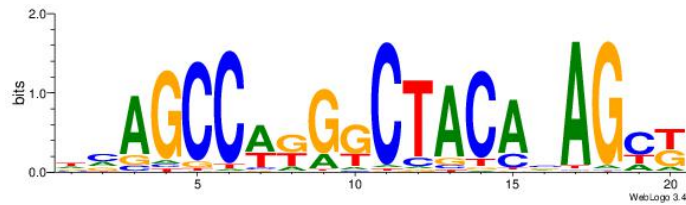
Dataset #:	1
Motif ID:	15
Motif name:	C015
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2
Number of overlap:	18
Similarity score:	0.0694959

Alignment:

DVAGCCWKGCTACAVAGCK
-WWACCYKGTCTMRAAWW-

Original motif Consensus sequence: DVAGCCWKGCTACAVAGCK

Reverse complement motif Consensus sequence:
RGCTVTGTAGCCYWGGCTVD

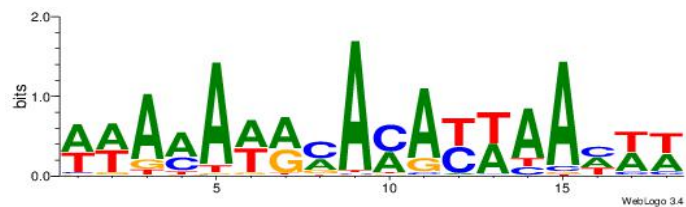


Dataset #: 1
 Motif ID: 62
 Motif name: C062
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 18
 Similarity score: 0.0825414

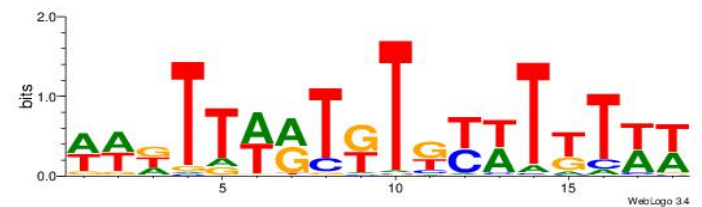
Alignment:

WWAMAWRMAMAYWAAHWW
 WWACCYKGTCTMRAAAWW

Original motif Consensus sequence: WWAMAWRMAMAYWAAHWW



Reverse complement motif Consensus sequence: WWDTTWMTRTRKWTYTW



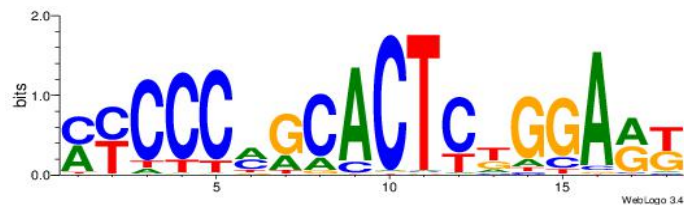
Dataset #: 1

Motif ID: 99
 Motif name: C099
 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: 0.0841277

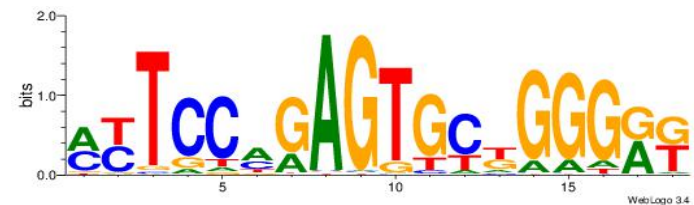
Alignment:

MYCCCMGCACTCKGGARK
 WWACCYKGTCTMRAAAWW

Original motif Consensus sequence: MYCCCMGCACTCKGGARK



Reverse complement motif Consensus sequence: RKTCCRGAGTGCYGGGKR

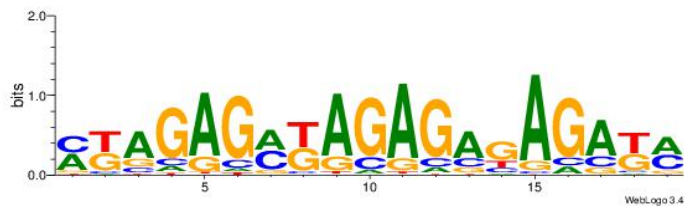


Dataset #: 1
 Motif ID: 12
 Motif name: C012
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 18

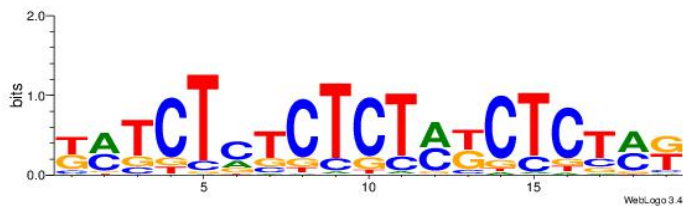
Similarity score: 0.0841589

Alignment:
YRTCTCTCTCTRYCTCTRR
-WWACCYKGTCTMRAAAWW

Original motif Consensus sequence: MKAGAGMKAGAGAGAGAKM

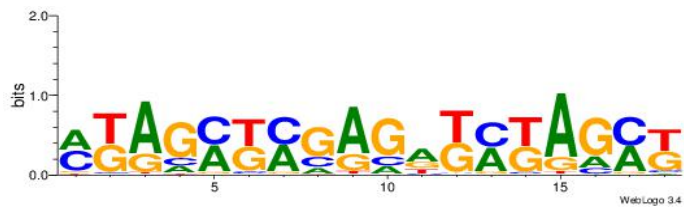


Reverse complement motif Consensus sequence: YRTCTCTCTCTRYCTCTRR

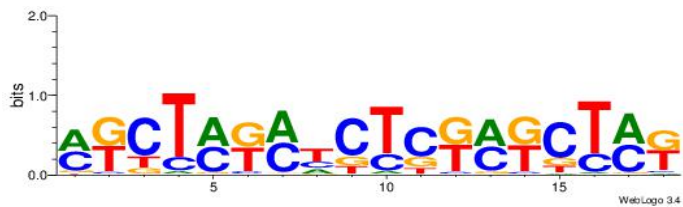


Dataset #: 1 Motif ID: 36 Motif name: C036

Original motif Consensus sequence: MKAGMKMGAGAKMKAGMK



Reverse complement motif Consensus sequence: RRCTRRRTCTCRRRCTRY



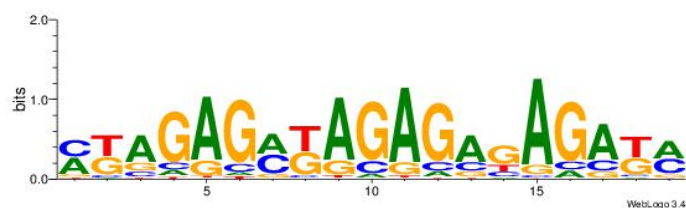
Best Matches for Motif ID 36 (Highest to Lowest)

Dataset #:	1
Motif ID:	12
Motif name:	C012
Matching format of first motif:	Original Motif

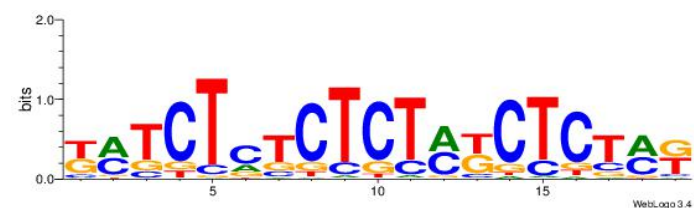
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2
Number of overlap:	18
Similarity score:	0.0191946

Alignment:
 MKAGAGMKAGAGAGAGAKM
 MKAGMKMGAGAKMKAGMK-

Original motif Consensus sequence: MKAGAGMKAGAGAGAGAKM



Reverse complement motif Consensus sequence: YRTCTCTCTCTRYCTCTRR

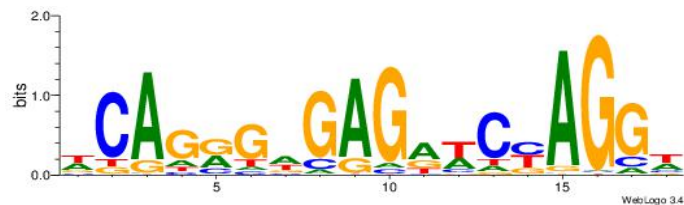


Dataset #:	1
Motif ID:	132
Motif name:	C132
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	18
Similarity score:	0.0475695

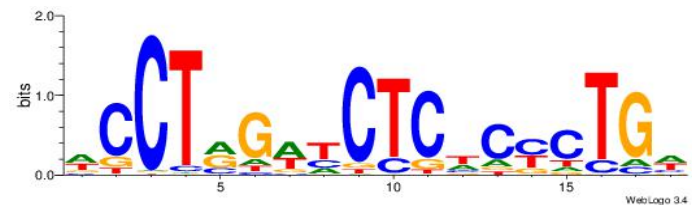
Alignment:

WCAGRGWGAGAWCYAGGW
MKAGMKMGAGAKMKAGMK

Original motif Consensus sequence: WCAGRGWGAGAWCYAGGW



Reverse complement motif Consensus sequence: WCCTKGWTCTCWCMTCTGW

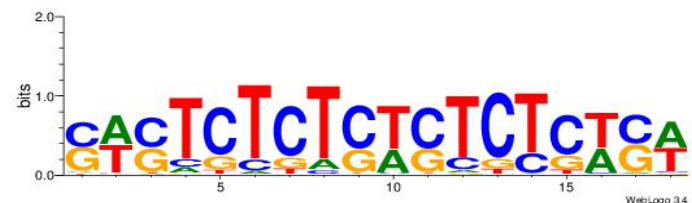
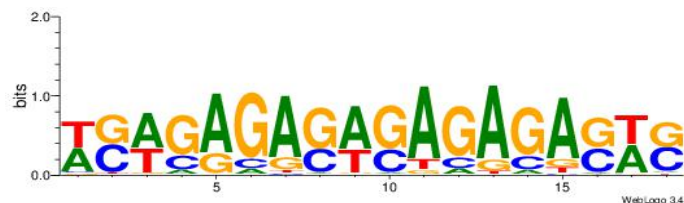


Dataset #:	1
Motif ID:	17
Motif name:	C017
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	18
Similarity score:	0.056317

Alignment:
WSWGAGASWSAGAGASWS
MKAGMKMGAGAKMKAGMK

Original motif Consensus sequence: WSWGAGASWSAGAGASWS

Reverse complement motif Consensus sequence: SWSTCTCTSWSTCTCWSW

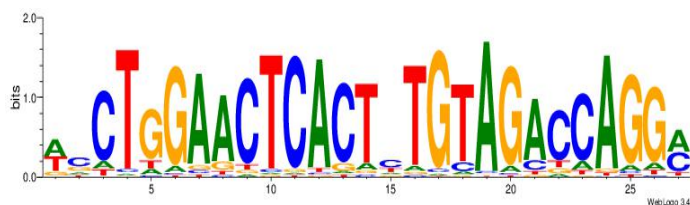


Dataset #: 1
 Motif ID: 13
 Motif name: C013
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 18
 Similarity score: 0.070064

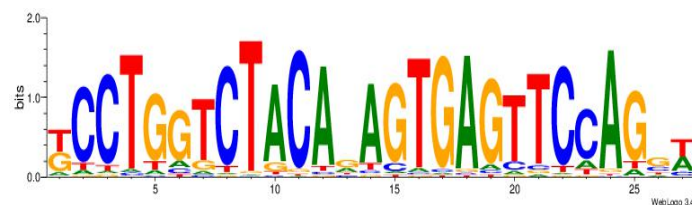
Alignment:

YCCTGGTCTACADAGTGAGTTCCAGVW
 MKAGMKMGAGAKMKAGMK-----

Original motif Consensus sequence:
 WVCTGGAAC TCACTHTGTAGACCAGGM



Reverse complement motif Consensus sequence:
 YCCTGGTCTACADAGTGAGTTCCAGVW

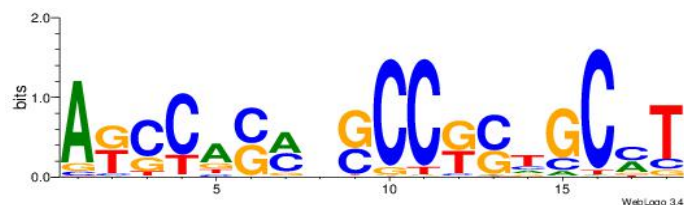


Dataset #: 1

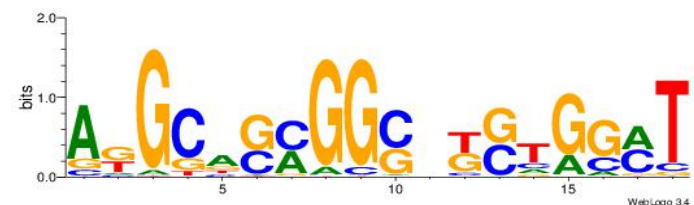
Motif ID: 93
 Motif name: C093
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 18
 Similarity score: 0.0760646

Alignment:
 ARGCASYGGSVYSTGGYT
 MKAGMKMGAGAKMKAGMK

Original motif Consensus sequence: AKCCASMBSCCKSTGCMT

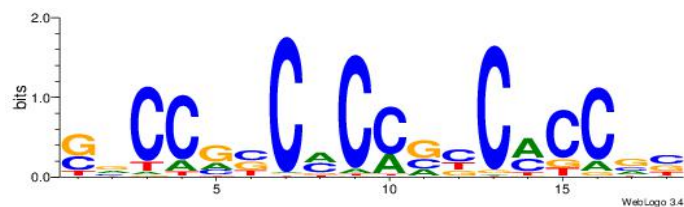


Reverse complement motif Consensus sequence: ARGCASYGGSVYSTGGYT

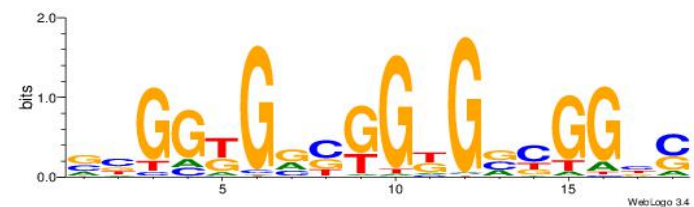


Dataset #: 1 Motif ID: 37 Motif name: C037

Original motif Consensus sequence: SVCCGBCMCCSYCMCCVB



Reverse complement motif Consensus sequence: BVGGYGKSGGYBCGGVS



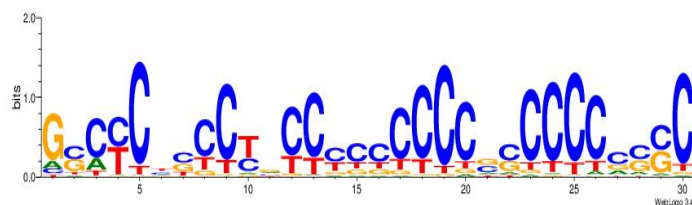
Best Matches for Motif ID 37 (Highest to Lowest)

Dataset #: 1
 Motif ID: 3
 Motif name: C003
 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: 0.0262566

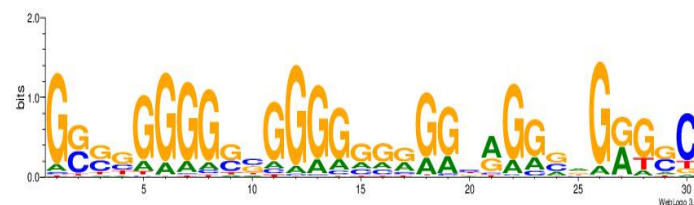
Alignment:

GSCYCHSCCYVCCYCCCCCSCCCCCSSC
 -----SVCCGBCMCCSYCMCCVB--

Original motif Consensus sequence:
 GSCYCHSCCYVCCYCCCCCSCCCCCSSC



Reverse complement motif Consensus sequence:
 GSSGGGGGSSGGGGGGKGGVMGGSHGKGSC

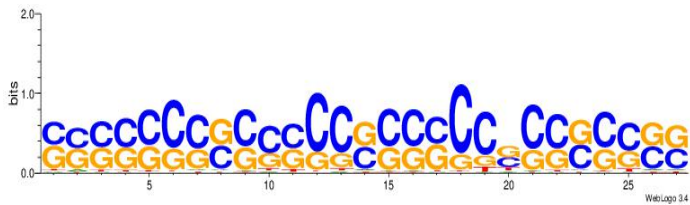


Dataset #: 1
 Motif ID: 4
 Motif name: C004
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement

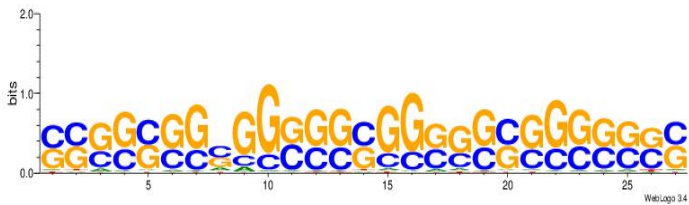
Direction: Forward
Position number: 7
Number of overlap: 18
Similarity score: 0.0296812

Alignment:
SSSSSSGSGGSSSSGSGSSSSGSSSSS
-----BVGGYGKSGGYGBCGGVS---

Original motif Consensus sequence:
SSSSSCSSSSCCSSSSCCSCSSSSSS



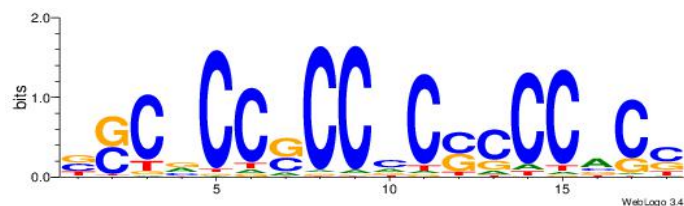
Reverse complement motif Consensus sequence:
SSSSSSGSGGSSSSGSGSSSSGSSSSS



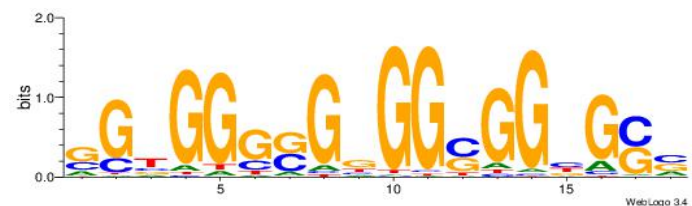
Dataset #: 1
Motif ID: 20
Motif name: C020
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 18
Similarity score: 0.054777

Alignment:
BSCVCCSCCVCSCCCACS
SVCCGBCMCCSYCMCCVB

Original motif Consensus sequence: BSCVCCSCCVSCCCACS



Reverse complement motif Consensus sequence: SGTGGGSGVGGSGGVGSB

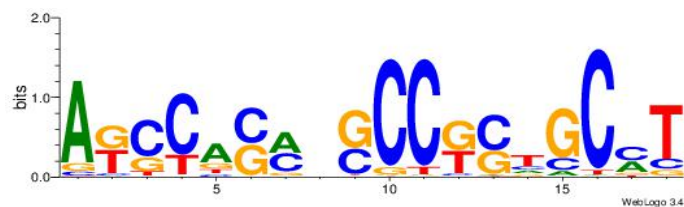


Dataset #: 1
Motif ID: 93
Motif name: C093
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 18
Similarity score: 0.0696791

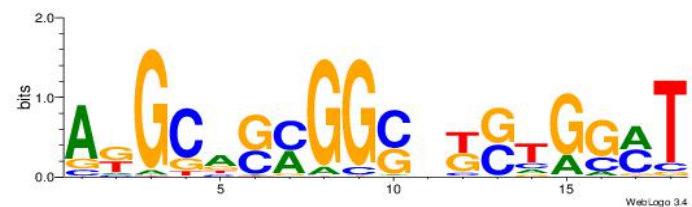
Alignment:

AKCCASMBSCCKSTGCMT
SVCCGBCMCCSYCMCCVB

Original motif Consensus sequence: AKCCASMBSCCKSTGCMT



Reverse complement motif Consensus sequence: ARGCASVGGSVYSTGGYT

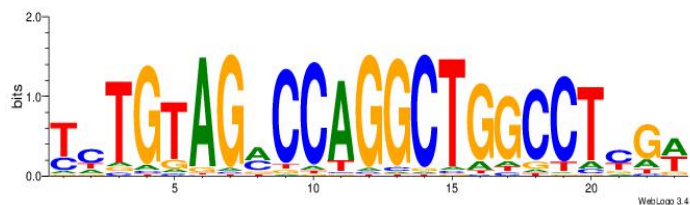


Dataset #: 1
 Motif ID: 5
 Motif name: C005
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 18
 Similarity score: 0.0697843

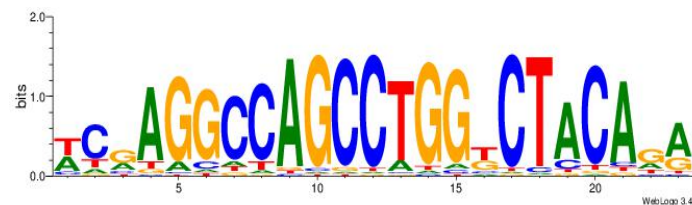
Alignment:

TCTGTAGMCCAGGCTGGCCTYGW
 ----BVGGYGKSGGYGBCGGVS-

Original motif Consensus sequence: TCTGTAGMCCAGGCTGGCCTYGW



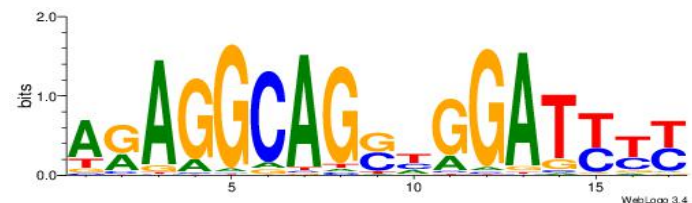
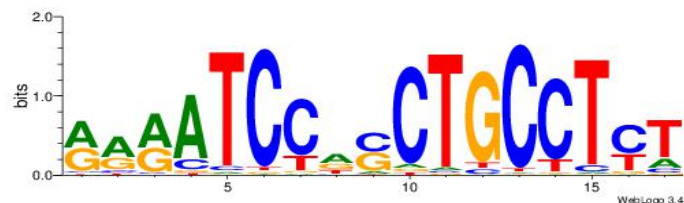
Reverse complement motif Consensus sequence: WCKAGGCCAGCCTGGYCTACAGA



Dataset #: 1 Motif ID: 38 Motif name: C038

Original motif Consensus sequence: RRRATCCDSCTGCCTYT

Reverse complement motif Consensus sequence: AKAGGCAGSDGGATKKK



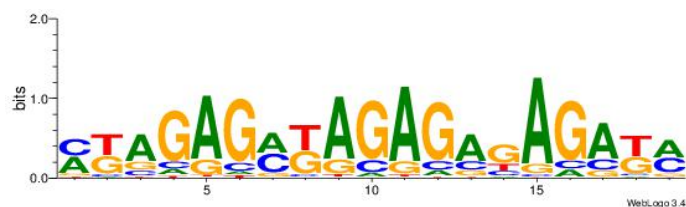
Best Matches for Motif ID 38 (Highest to Lowest)

Dataset #: 1
 Motif ID: 12
 Motif name: C012
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 17
 Similarity score: 0.0591022

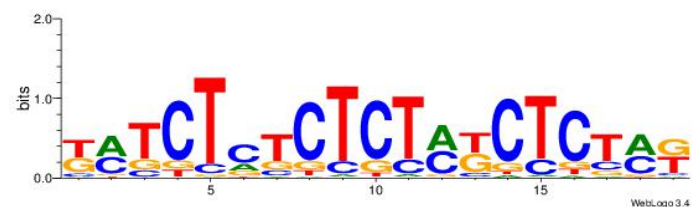
Alignment:

MKAGAGMKAGAGAGAGAKM
 AKAGGCAGSDGGATKKK--

Original motif Consensus sequence: MKAGAGMKAGAGAGAGAKM



Reverse complement motif Consensus sequence: YRTCTCTCTRYCTCTRR

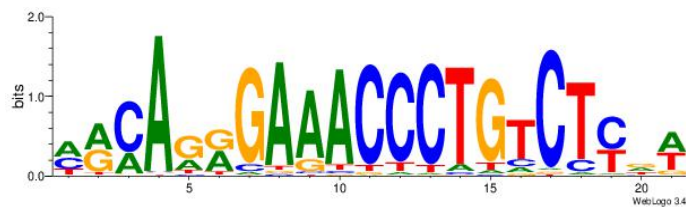


Dataset #: 1
 Motif ID: 27
 Motif name: C027
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 17
 Similarity score: 0.064359

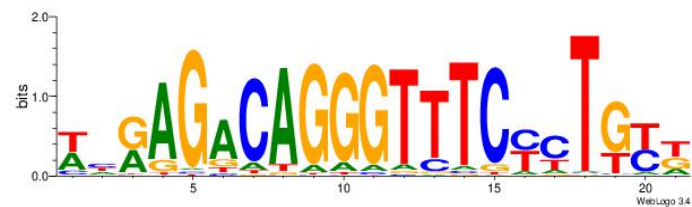
Alignment:

MRCAGRGAAACCCTGTCTYDW
 ---RRRATCCDSCTGCCTYT-

Original motif Consensus sequence: MRCAGRGAAACCCTGTCTYDW



Reverse complement motif Consensus sequence: WHKAGACAGGGTTTCMCTGKY

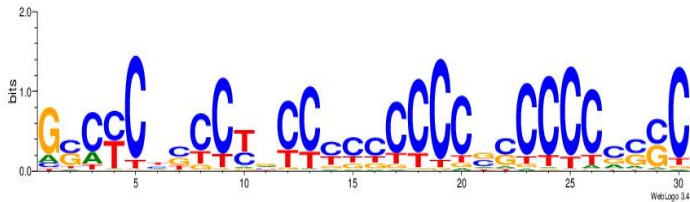


Dataset #: 1
 Motif ID: 3
 Motif name: C003
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 7

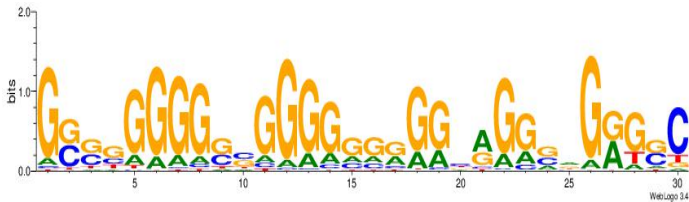
Number of overlap: 17
Similarity score: 0.0650972

Alignment:
GSSGGGGGSSGGGGGKGGVMGGSHGKGSC
-----AKAGGCAGSDGGATKKK-----

Original motif Consensus sequence:
GSCYCHSCCYVCCYCCCCSSCCCCSSC



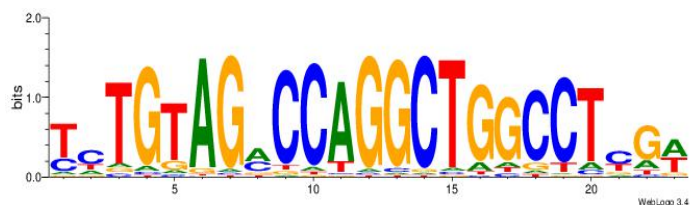
Reverse complement motif Consensus sequence:
GSSGGGGGSSGGGGGKGGVMGGSHGKGSC



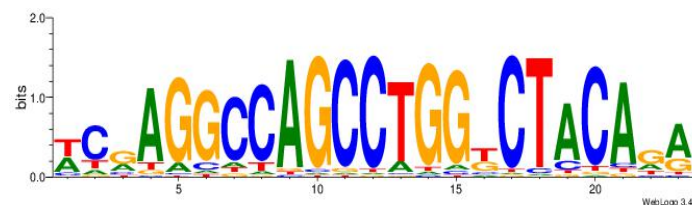
Dataset #: 1
Motif ID: 5
Motif name: C005
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 3
Number of overlap: 17
Similarity score: 0.0704235

Alignment:
TCTGTAGMCCAGGCTGGCCTYGW
----RRRATCCDSCTGCCTYT--

Original motif Consensus sequence: TCTGTAGMCCAGGCTGGCCTYGW



Reverse complement motif Consensus sequence: WCKAGGCCAGCCTGGYCTACAGA



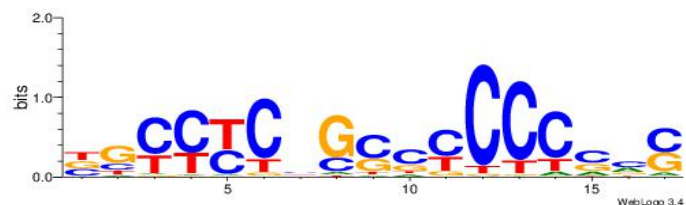
Dataset #: 1
Motif ID: 22
Motif name: C022
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 17
Similarity score: 0.072572

Alignment:

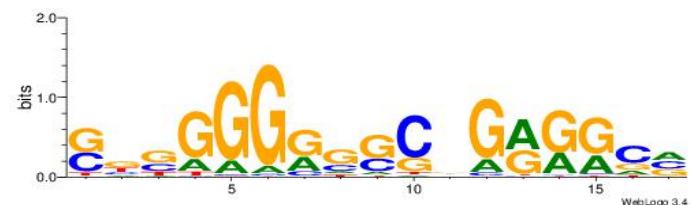
SVSGGGKGSBCBGMGGCV

AKAGGCAGSDGGATKKK

Original motif Consensus sequence: BGCCYCBGSCYCCCSVS

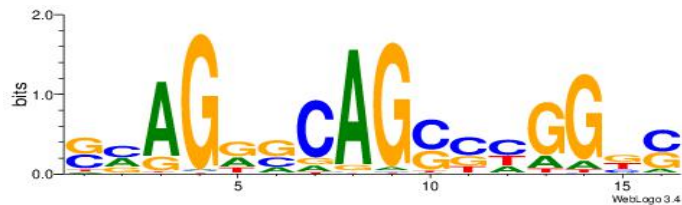


Reverse complement motif Consensus sequence: SVSGGGKGSBCBGMGGCV

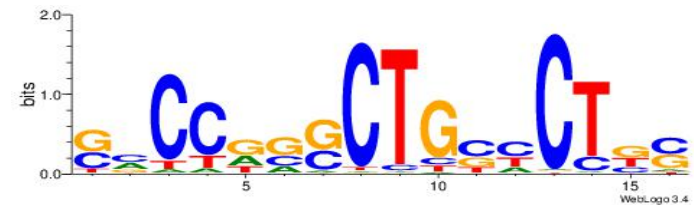


Dataset #: 1 Motif ID: 39 Motif name: C039

Original motif Consensus sequence: SMAGRSCAGSSYGGBS



Reverse complement motif Consensus sequence: SBCKSSCTGSMCTRS



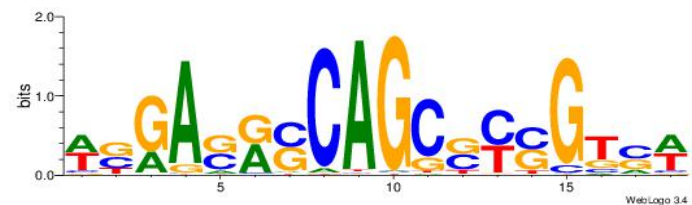
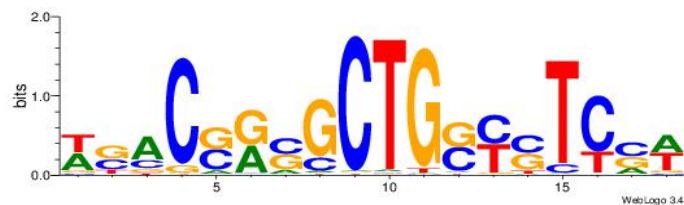
Best Matches for Motif ID 39 (Highest to Lowest)

Dataset #:	1
Motif ID:	124
Motif name:	C124
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:	0.0146199

Alignment:
 WSGASKSCAGCSMSGTSW
 -SMAGRSCAGSSYGGBS-

Original motif Consensus sequence: WSACSRSGCTGSYSTCSW

Reverse complement motif Consensus sequence:
 WSGASKSCAGCSMSGTSW

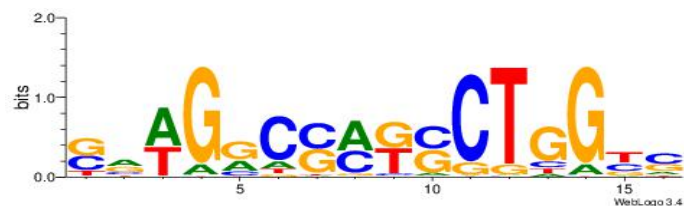


Dataset #: 1
 Motif ID: 126
 Motif name: C126
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 16
 Similarity score: 0.0197777

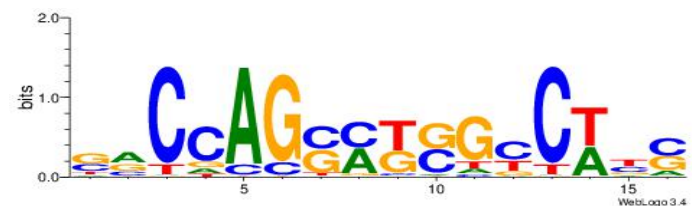
Alignment:

SVWGRCSMKSTGGYS
 SMAGRSCAGSSYGGBS

Original motif Consensus sequence: SVWGRCSMKSTGGYS



Reverse complement motif Consensus sequence: SMCCAGSYYSGMCWBS



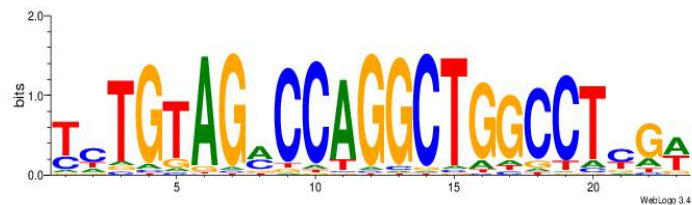
Dataset #: 1

Motif ID: 5
 Motif name: C005
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 16
 Similarity score: 0.0245094

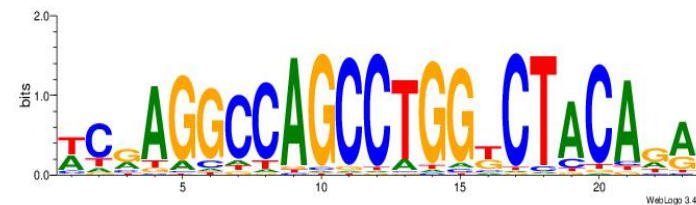
Alignment:

TCTGTAGMCCAGGCTGGCCTYGW
 -SBCKSSCTGSMCTRS-----

Original motif Consensus sequence: TCTGTAGMCCAGGCTGGCCTYGW



Reverse complement motif Consensus sequence: WCKAGGCCAGCCTGGYCTACAGA

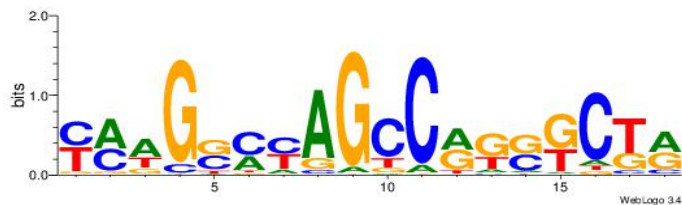


Dataset #: 1
 Motif ID: 73
 Motif name: C073
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 16

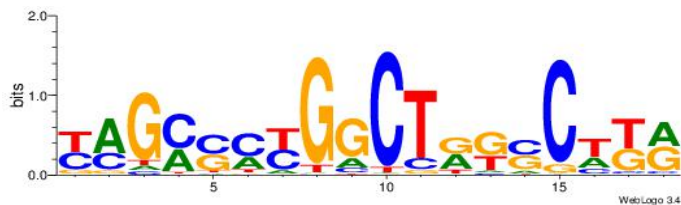
Similarity score: 0.0296818

Alignment:
KAGYSYKGGCTKRSCWYK
--SBCKSSCTGSMCTRS

Original motif Consensus sequence: YMWGSMYAGCCRKSKCTR



Reverse complement motif Consensus sequence: KAGYSYKGGCTKRSCWYK

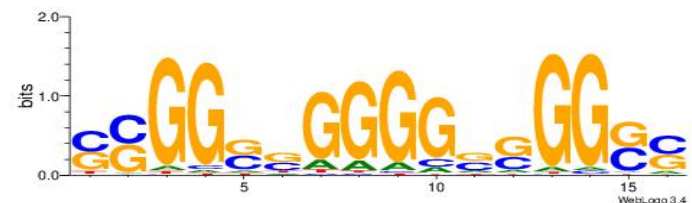
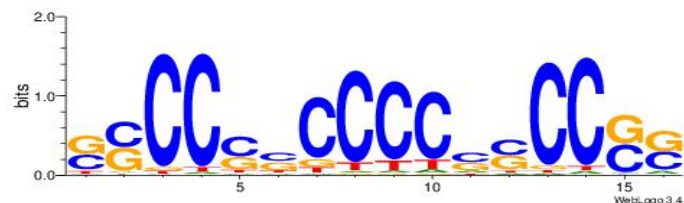


Dataset #: 1
Motif ID: 8
Motif name: C008
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 16
Similarity score: 0.0361944

Alignment:
SSCCSSCCCCSSCCSS
SBCKSSCTGSMCTRS

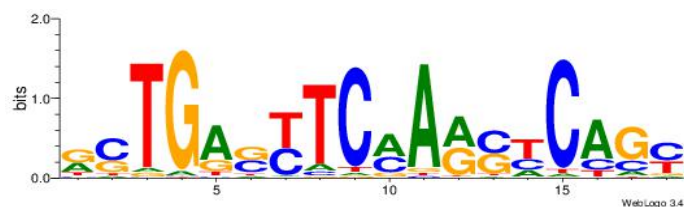
Original motif Consensus sequence: SSCSSCCCCSSCCSS

Reverse complement motif Consensus sequence: SSGSSGGGGSSGGSS

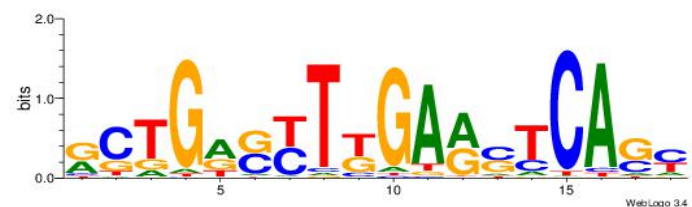


Dataset #: 1 Motif ID: 40 Motif name: C040

Original motif Consensus sequence: RSTGASYTCMARSYCAGY



Reverse complement motif Consensus sequence: KCTGMSKTYGAMSTCASM



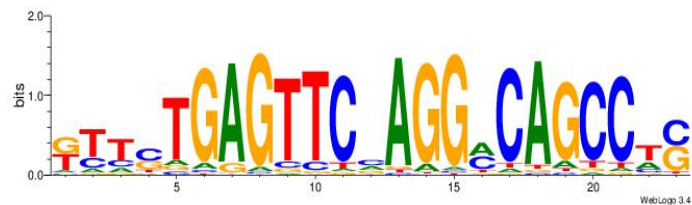
Best Matches for Motif ID 40 (Highest to Lowest)

Dataset #:	1
Motif ID:	7
Motif name:	C007
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:	0.00837268

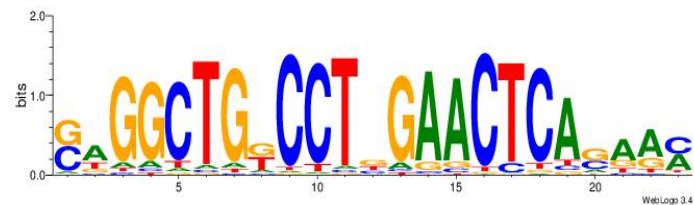
Alignment:

KTTSTGAGTTCVAGGMCAGCCTS
--RSTGASYTCMARSYCAGY---

Original motif Consensus sequence: KTTSTGAGTTCVAGGMCAGCCTS



Reverse complement motif Consensus sequence:
SAGGCTGYCCTVGAAGTCASAAY



Dataset #:	1
Motif ID:	95
Motif name:	C095
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:	0.0459628

Alignment:

RCTGYYSACCAASYTGGY
RSTGASYTCMARSYCAGY

Original motif Consensus sequence: KCCAKMSTGGTSKMCAGM

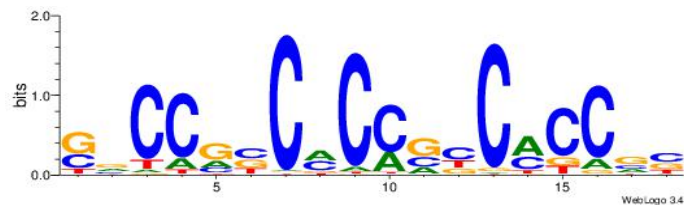
Reverse complement motif Consensus sequence:
RCTGYYSACCAASYTGGY

Motif ID: 37
 Motif name: C037
 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: 0.0631815

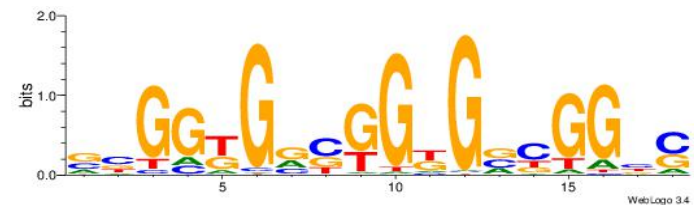
Alignment:

SVCCGBCMCCSYCMCCVB
 RSTGASYTCMARSYCAGY

Original motif Consensus sequence: SVCCGBCMCCSYCMCCVB



Reverse complement motif Consensus sequence: BVGGYGKSGGYGBCGGVS

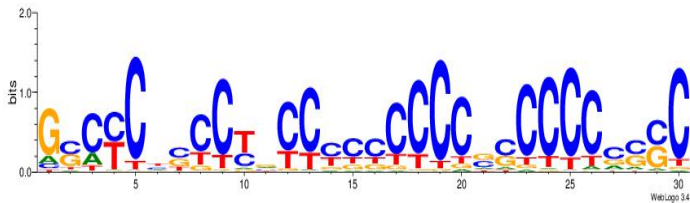


Dataset #: 1
 Motif ID: 3
 Motif name: C003
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 11
 Number of overlap: 18

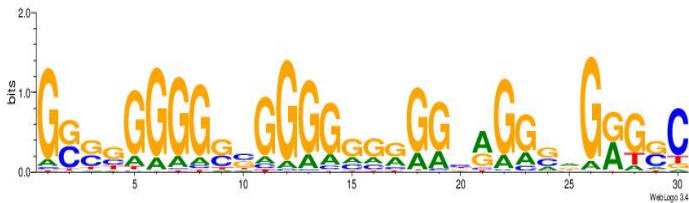
Similarity score: 0.0639062

Alignment:
GSCYCHSCCYVCCYCCCCCSCCCCCSSC
-----RSTGASYTCMARSYCAGY--

Original motif Consensus sequence:
GSCYCHSCCYVCCYCCCCCSCCCCCSSC

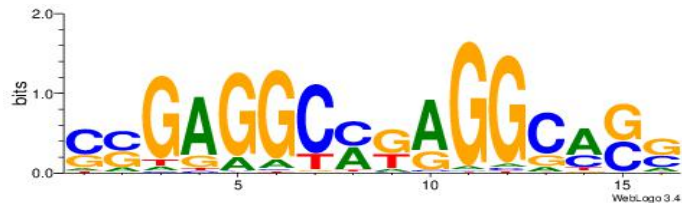


Reverse complement motif Consensus sequence:
GSSGGGGGSSGGGGGGKGGVMGGSHGKGC

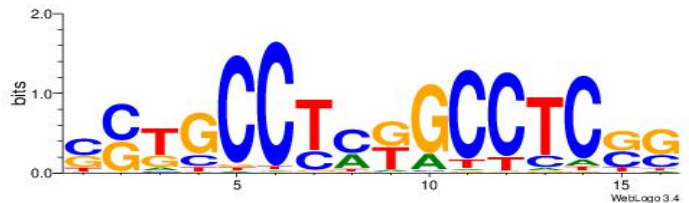


Dataset #: 1 Motif ID: 41 Motif name: C041

Original motif Consensus sequence: CSGAGGCMKAGGCASS



Reverse complement motif Consensus sequence:
SSTGCCTYRGCTCSG



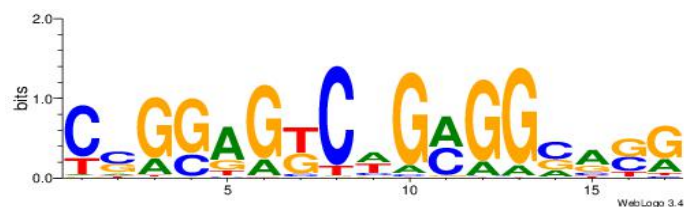
Best Matches for Motif ID 41 (Highest to Lowest)

Dataset #: 1
Motif ID: 86
Motif name: C086
Matching format of first motif: Original Motif

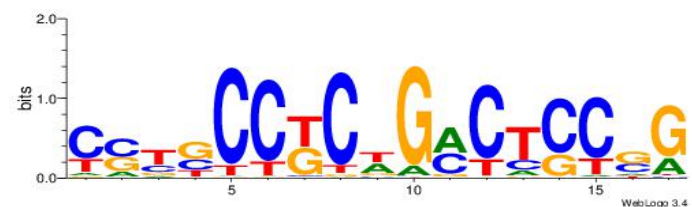
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	16
Similarity score:	0.0124428

Alignment:
 CSGGAGKWCWGMGGSASG
 -CSGAGGCMKAGGCASS

Original motif Consensus sequence: CSGGAGKWCWGMGGSASG



Reverse complement motif Consensus sequence: CSTSCCYCWGRCTCCSG

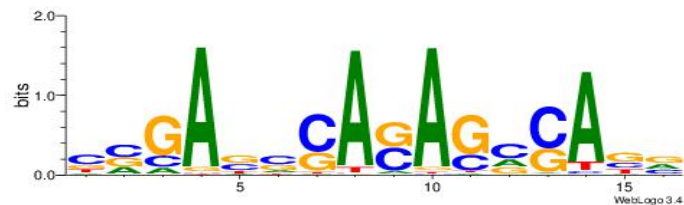


Dataset #:	1
Motif ID:	28
Motif name:	C028
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	16
Similarity score:	0.0322593

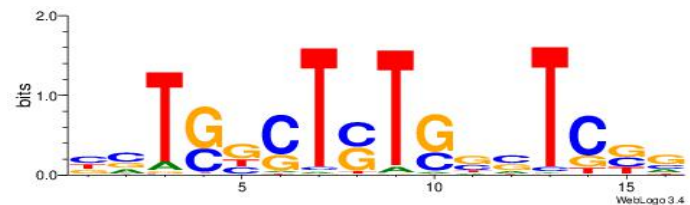
Alignment:

BVGASSCASAGVSABV
CSGAGGCMKAGGCASS

Original motif Consensus sequence: BVGASSCASAGVSABV



Reverse complement motif Consensus sequence: VBTSVCTSTGSSTCVB

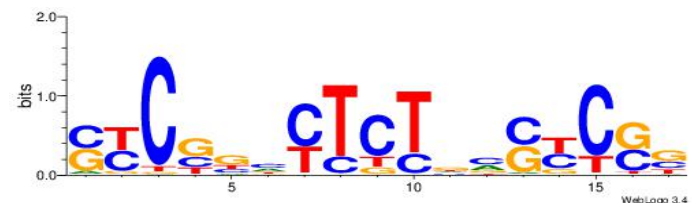
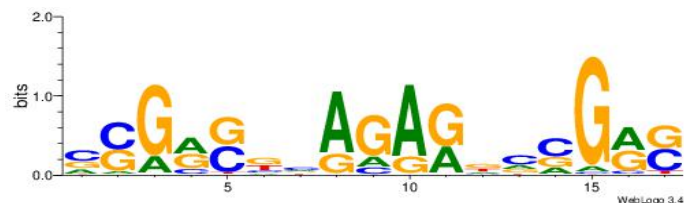


Dataset #:	1
Motif ID:	85
Motif name:	C085
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2
Number of overlap:	16
Similarity score:	0.0352485

Alignment:
VSGRSBHAGARDVSGRS
CSGAGGCMKAGGCASS-

Original motif Consensus sequence: VSGRSBHAGARDVSGRS

Reverse complement motif Consensus sequence: SKCSVHMTCTDBSKCSV

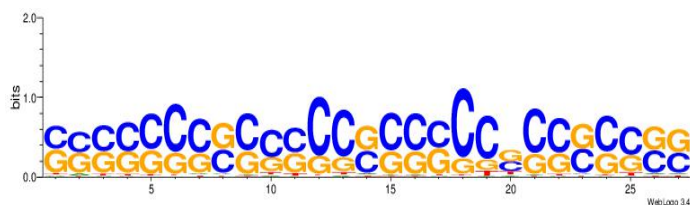


Dataset #: 1
 Motif ID: 4
 Motif name: C004
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 8
 Number of overlap: 16
 Similarity score: 0.0383703

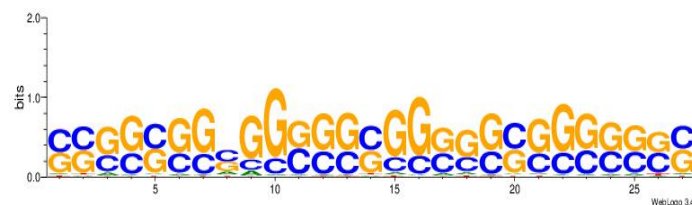
Alignment:

SSSSSSGSGGSSSSSGSSSSSGSSSSS
 -----CSGAGGCMKAGGCASS-----

Original motif Consensus sequence:
 SSSSSCSSSSSCSSSSCCSCSSSSS



Reverse complement motif Consensus sequence:
 SSSSSSGSGGSSSSSGSSSSSGSSSSS



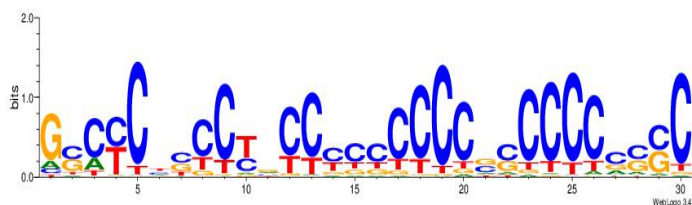
Dataset #: 1

Motif ID: 3
 Motif name: C003
 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: 0.0441523

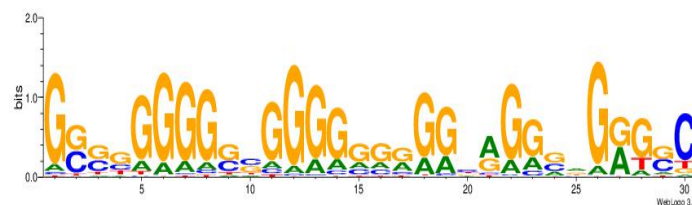
Alignment:

GSSGGGGSSGGGGGKGGVMGGSHGKGC
 -----CSGAGGCMKAGGCASS--

Original motif Consensus sequence:
 GSCYCHSCCYVCCYCCCCSSCCCCSSC

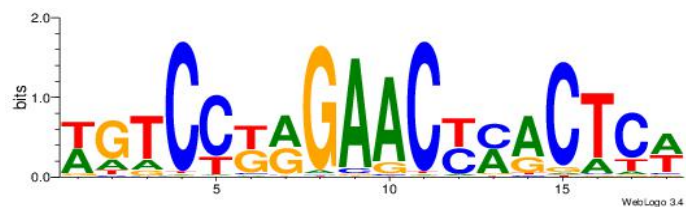


Reverse complement motif Consensus sequence:
 GSSGGGGSSGGGGGKGGVMGGSHGKGC

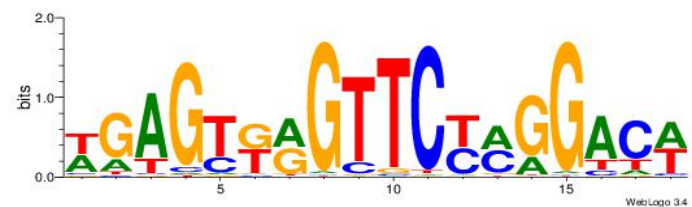


Dataset #: 1 Motif ID: 42 Motif name: C042

Original motif Consensus sequence: WGTCKRGAACYMACTCW



Reverse complement motif Consensus sequence: WGAGTRMGTTCKRGGACW



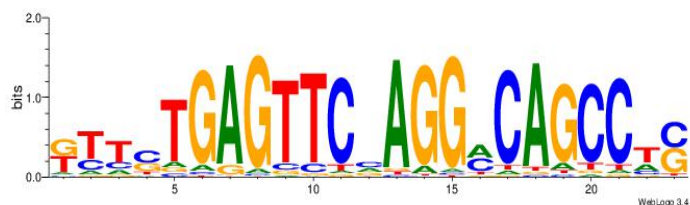
Best Matches for Motif ID 42 (Highest to Lowest)

Dataset #: 1
Motif ID: 7
Motif name: C007
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: 0.0228216

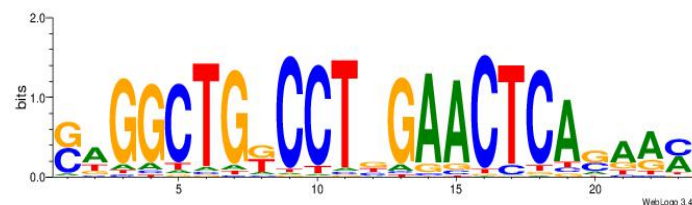
Alignment:

KTTSTGAGTTCVAGGMCAGCCTS
-----WGAGTRMGTTCRGGACW

Original motif Consensus sequence: KTTSTGAGTTCVAGGMCAGCCTS



Reverse complement motif Consensus sequence: SAGGCTGYCCTVGAAGTCASAAY

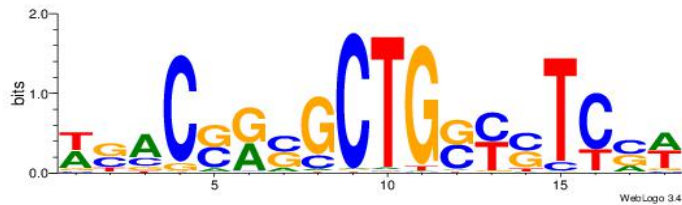


Dataset #: 1
Motif ID: 124
Motif name: C124
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement

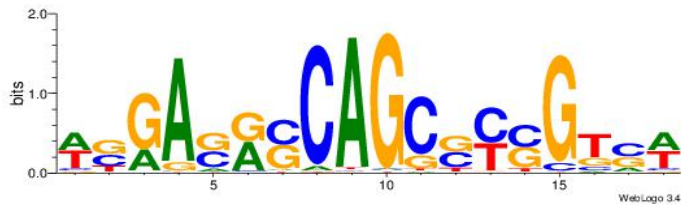
Direction: Forward
Position number: 1
Number of overlap: 18
Similarity score: 0.0523737

Alignment:
WSGASKSCAGCSMSGTSW
WGTCKKRGAACTCTCW

Original motif Consensus sequence: WSACSRSGCTGTSYSTCSW



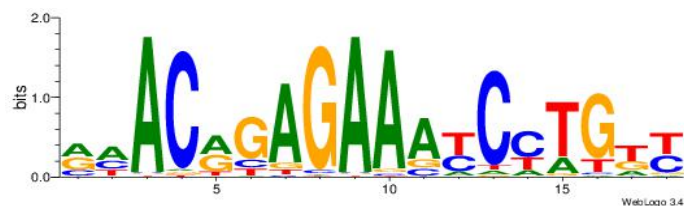
Reverse complement motif Consensus sequence: WSGASKSCAGCSMSGTSW



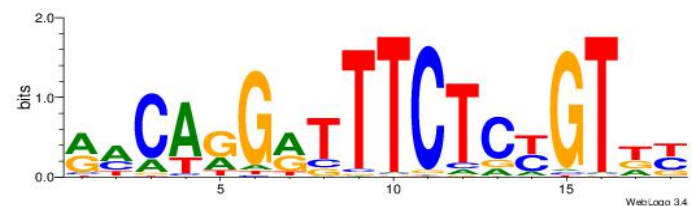
Dataset #: 1
Motif ID: 53
Motif name: C053
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 18
Similarity score: 0.0536019

Alignment:
MRCAGGTTTTCTCKGTYK
WGAGTRMGTTCKRGGACW

Original motif Consensus sequence: RMACRGAGAAAYCCTGKY



Reverse complement motif Consensus sequence: MRCAGGMTTCTCKGTYK

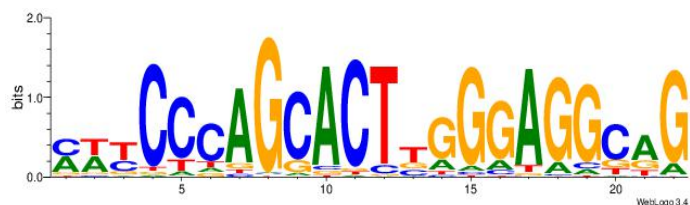


Dataset #: 1
Motif ID: 19
Motif name: C019
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 18
Similarity score: 0.0577538

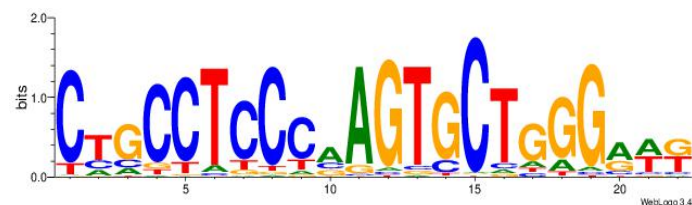
Alignment:

```
CTGCCTCCCAAGTGCTGGGMWR  
----WGAGTRMGTTCKRGGACW
```

Original motif Consensus sequence: MWYCCCAGCACTTGGGAGGCAG



Reverse complement motif Consensus sequence: CTGCCTCCCAAGTGCTGGGMWR

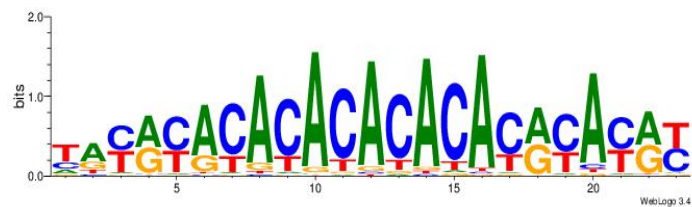


Dataset #: 1
 Motif ID: 2
 Motif name: C002
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 18
 Similarity score: 0.0602971

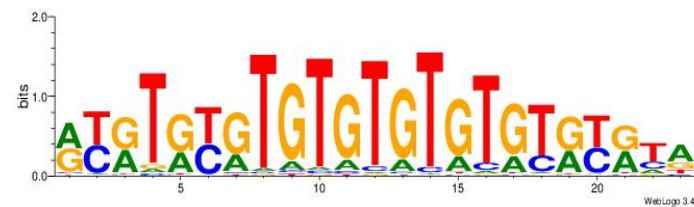
Alignment:

MKKTKKGTGTGTGTGTGTTKKKTA
 -----WGAGTRMGTTCRGGACW

Original motif Consensus sequence: TAYRYACACACACACRYAYRY



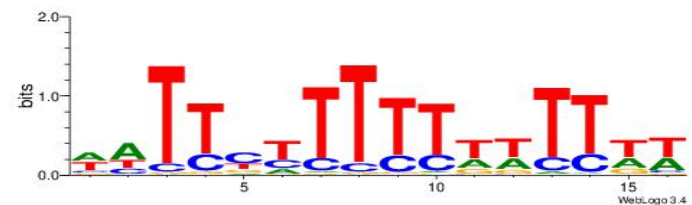
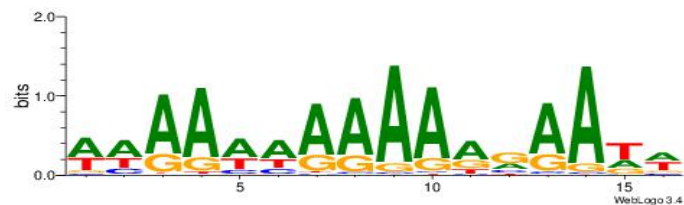
Reverse complement motif Consensus sequence: MKKTKKGTGTGTGTGTGTTKKKTA



Dataset #: 1 Motif ID: 43 Motif name: C043

Original motif Consensus sequence: WWAAWAAAAAARAATW

Reverse complement motif Consensus sequence: WATTMTTTTTTWTWW



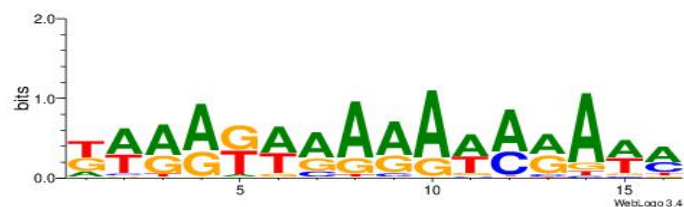
Best Matches for Motif ID 43 (Highest to Lowest)

Dataset #: 1
 Motif ID: 152
 Motif name: C152
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 16
 Similarity score: 0.0263401

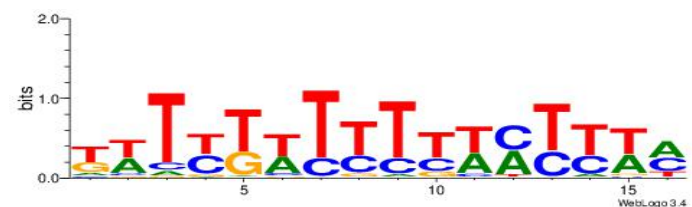
Alignment:

YWTKYWTKTKWYKKWR
 WATTMTTTTTTWTWW

Original motif Consensus sequence: KWRRKWRARAWMRAWM



Reverse complement motif Consensus sequence: YWTKYWTKTKWYKKWR

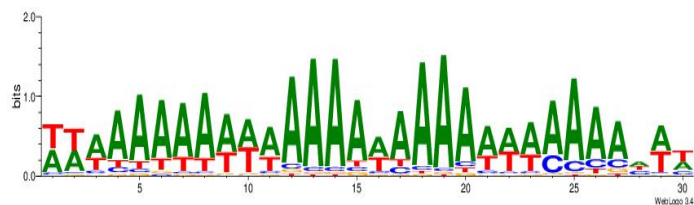


Dataset #: 1
 Motif ID: 1
 Motif name: C001
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 6
 Number of overlap: 16
 Similarity score: 0.0268347

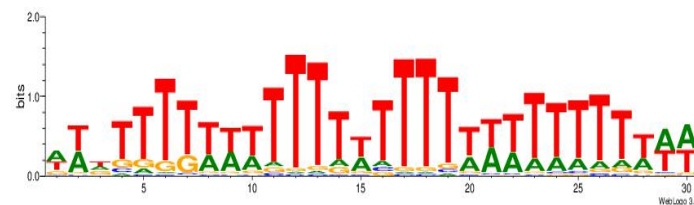
Alignment:

WWWAAAAWWAAAAWAAAAWWAAAAHWW
 -----WWAAWAAAAAARAATW-----

Original motif Consensus sequence:
 WWWAAAAWWAAAAWAAAAWWAAAAHWW



Reverse complement motif Consensus sequence:
 WWHTTTTWWTTTTWTTTTWTTTTWWW



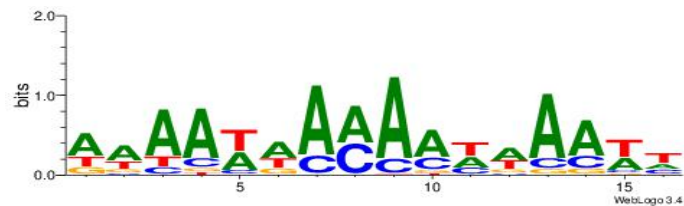
Dataset #: 1
 Motif ID: 98
 Motif name: C098
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1

Number of overlap: 16
Similarity score: 0.0286206

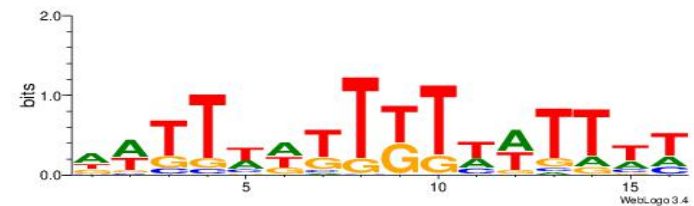
Alignment:

AAAAWWAMAAWWAAWH
WWAAWAAAAARAATW

Original motif Consensus sequence: AAAAWWAMAAWWAAWH



Reverse complement motif Consensus sequence: HWTTWWTTYTWTTTT

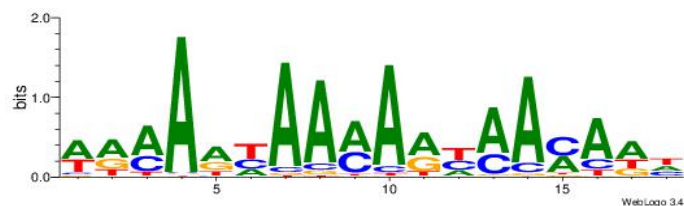


Dataset #: 1
Motif ID: 57
Motif name: C057
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 3
Number of overlap: 16
Similarity score: 0.0288669

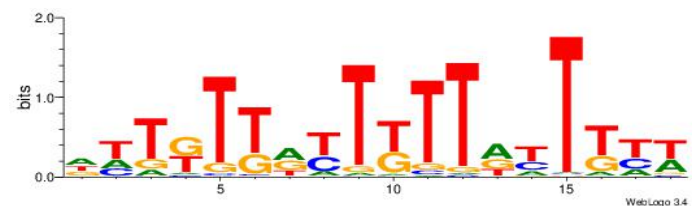
Alignment:

HWTRTTMKTYTTMKTYKW
--WATTMTTTTTTWTWW

Original motif Consensus sequence: WRMARYAAMARYAAMAWH



Reverse complement motif Consensus sequence: HWTRTTMKTYTTMKTYKW

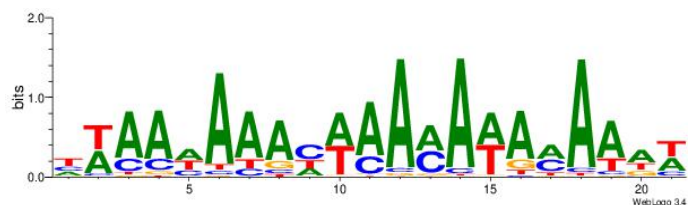


Dataset #: 1
Motif ID: 16
Motif name: C016
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 6
Number of overlap: 16
Similarity score: 0.0348696

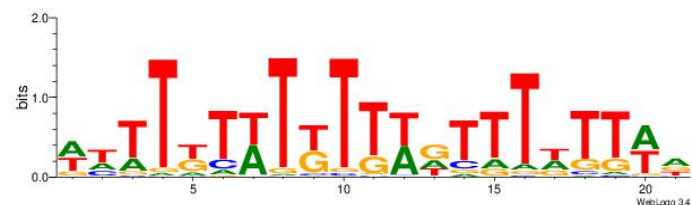
Alignment:

WWTYYTWYTTWDTTTWTTWH
WATMTTTTTTTWTTWW-----

Original motif Consensus sequence: HWAAWAAAHWAAMAWAMAAWW

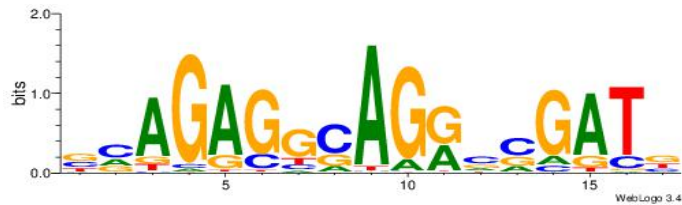


Reverse complement motif Consensus sequence: WWTYYTWYTTWDTTTWTTWH

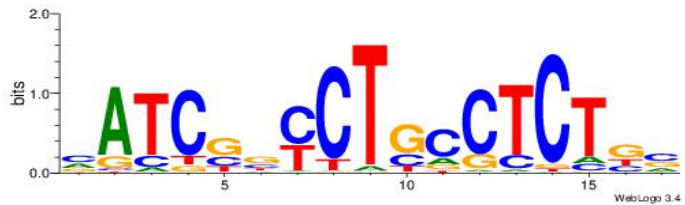


Dataset #: 1 Motif ID: 44 Motif name: C044

Original motif Consensus sequence: BVAGAGGCAGRVSGATB



Reverse complement motif Consensus sequence:
BATCSVMCTGCCTCTVB



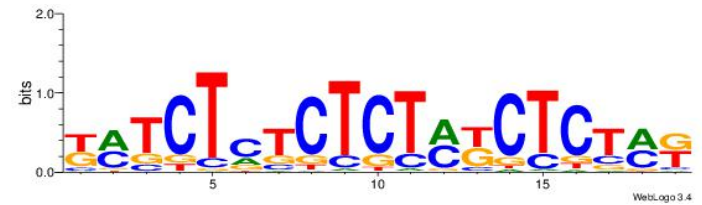
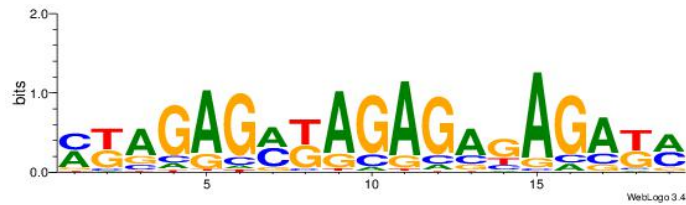
Best Matches for Motif ID 44 (Highest to Lowest)

Dataset #:	1
Motif ID:	12
Motif name:	C012
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:	0.0528812

Alignment:
YRTCTCTCTCTRYCTCTRR
--BATCSVMCTGCCTCTVB

Original motif Consensus sequence: MKAGAGMKAGAGAGAGAKM

Reverse complement motif Consensus sequence:
YRTCTCTCTCTRYCTCTRR

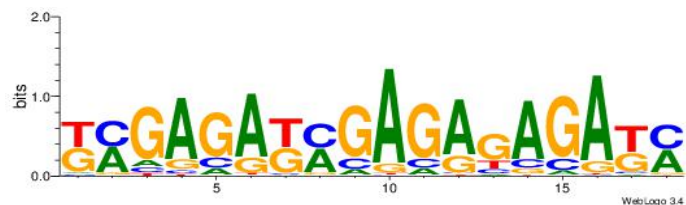


Dataset #: 1
 Motif ID: 11
 Motif name: C011
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 17
 Similarity score: 0.0560283

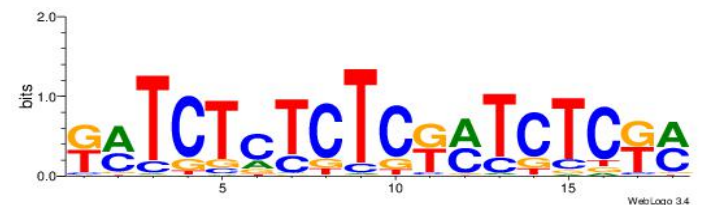
Alignment:

KMGAGAKMGAGAGAGAKM
 -BVAGAGGCAGRVSGATB

Original motif Consensus sequence: KMGAGAKMGAGAGAGAKM



Reverse complement motif Consensus sequence: RRTCTCTCTCRRTCTCRR

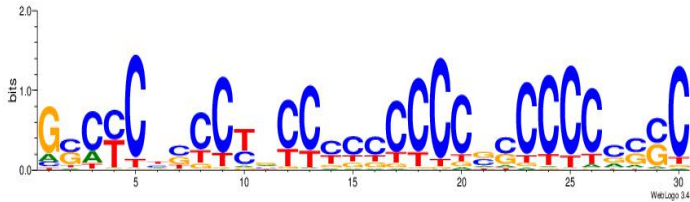


Dataset #: 1

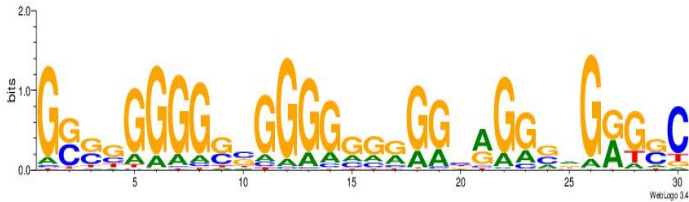
Motif ID: 3
Motif name: C003
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 2
Number of overlap: 17
Similarity score: 0.0593342

Alignment:
GSSGGGGSSGGGGGKGGVMGGSHGKGC
-BVAGAGGCAGRVSGATB-----

Original motif Consensus sequence:
GSCYCHSCCYVCCYCCCCSSCCCCSSC



Reverse complement motif Consensus sequence:
GSSGGGGSSGGGGGKGGVMGGSHGKGC



Dataset #: 1
Motif ID: 132
Motif name: C132
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2
Number of overlap: 17

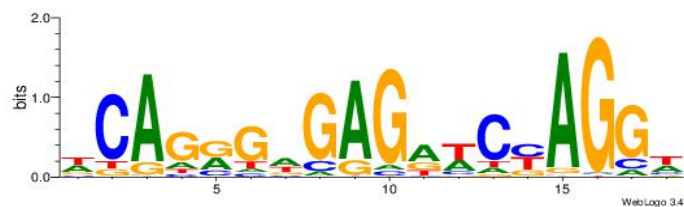
Similarity score: 0.0642688

Alignment:

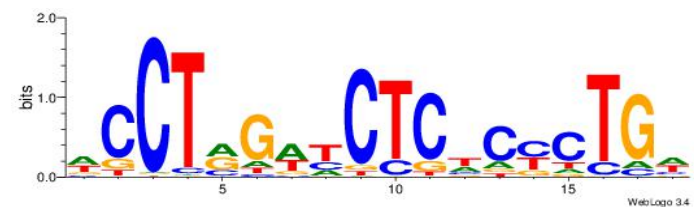
WCAGRGWGAGAWCYAGGW

BVAGAGGCAGRVSGATB-

Original motif Consensus sequence: WCAGRGWGAGAWCYAGGW



Reverse complement motif Consensus sequence: WCCTKGWTCTCWCMTGW



Dataset #: 1
Motif ID: 17
Motif name: C017
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: 0.0653649

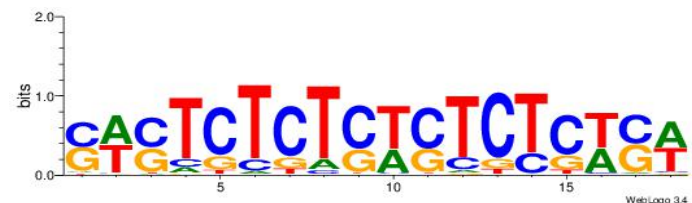
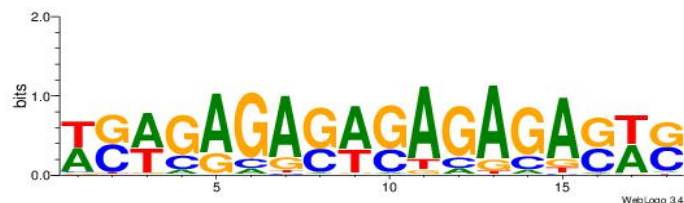
Alignment:

WSWGAGASWSAGAGASWS

BVAGAGGCAGRVSGATB-

Original motif Consensus sequence: WSWGAGASWSAGAGASWS

Reverse complement motif Consensus sequence: SWSTCTCTSWSTCTCWSW

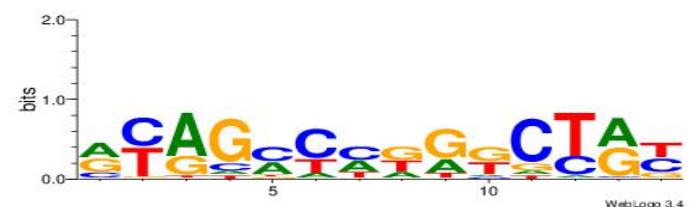


Dataset #: 1 Motif ID: 45 Motif name: C045

Original motif Consensus sequence: RYAGMCMKGKCTRY



Reverse complement motif Consensus sequence: MKAGYCYRGRCTK



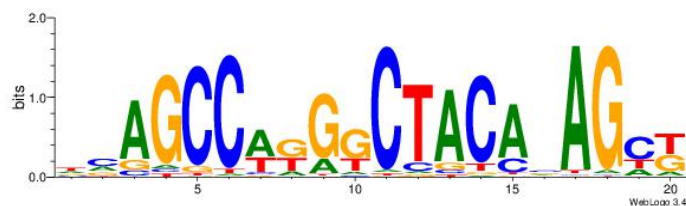
Best Matches for Motif ID 45 (Highest to Lowest)

Dataset #:	1
Motif ID:	15
Motif name:	C015
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	7
Number of overlap:	14
Similarity score:	0.0138521

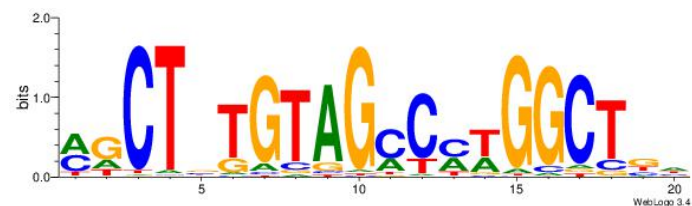
Alignment:

```
DVAGCCWKG GCTACAVAGCK
RYAGMCMKGKCTRY-----
```

Original motif Consensus sequence: DVAGCCWKGCTACAVAGCK



Reverse complement motif Consensus sequence: RGCTVTGTAGCCYWGGCTVD

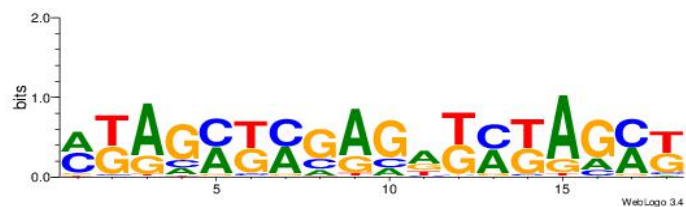


Dataset #: 1
Motif ID: 36
Motif name: C036
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 5
Number of overlap: 14
Similarity score: 0.0258669

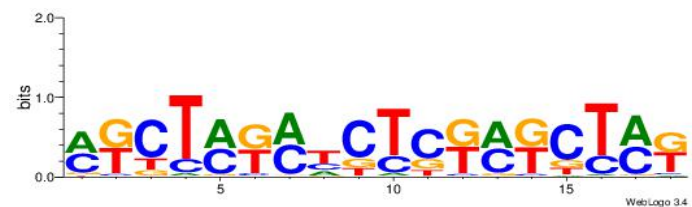
Alignment:

MKAGMKMGAGAKMKAGMK
----MKAGCYRGRCTKK

Original motif Consensus sequence: MKAGMKMGAGAKMKAGMK



Reverse complement motif Consensus sequence: RRCTRRRTCTCRRRCTRY

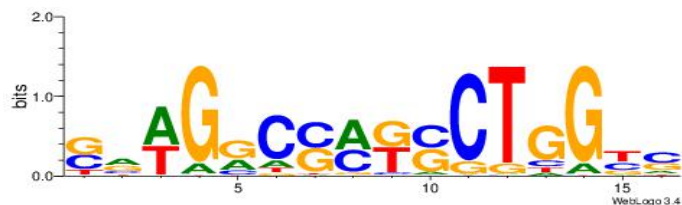


Dataset #: 1
 Motif ID: 126
 Motif name: C126
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0.0290459

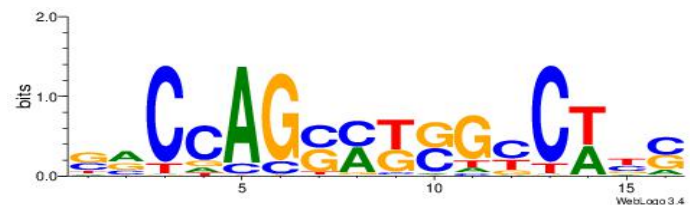
Alignment:

SMCCAGSYYSGM CWBS
 --MKAGYCYRGRCTKK

Original motif Consensus sequence: SVWGRCSMK SCTGGYS



Reverse complement motif Consensus sequence: SMCCAGSYYSGM CWBS

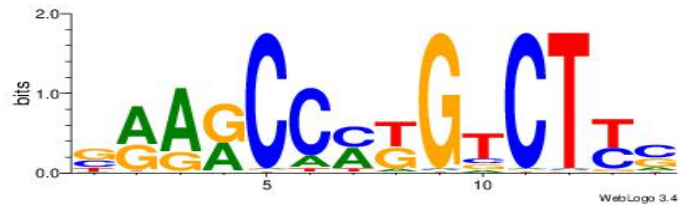


Dataset #: 1
 Motif ID: 114
 Motif name: C114
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1

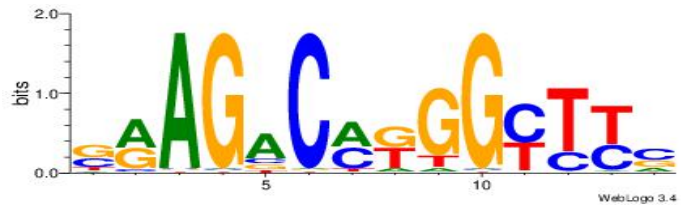
Number of overlap: 14
Similarity score: 0.0329285

Alignment:
SMAGACRRGGMTKS
RYAGMCMKGKCTRY

Original motif Consensus sequence: SRARCCMKGCTCTYS



Reverse complement motif Consensus sequence: SMAGACRRGGMTKS

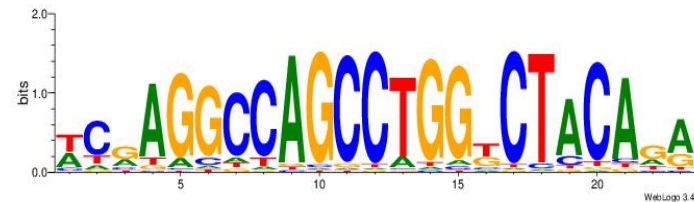
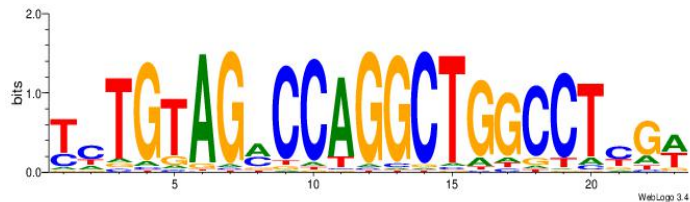


Dataset #: 1
Motif ID: 5
Motif name: C005
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 4
Number of overlap: 14
Similarity score: 0.0377209

Alignment:
TCTGTAGMCCAGGCTGGCCTYGW
---RYAGMCMKGKCTRY-----

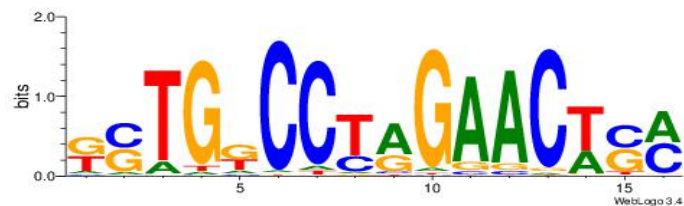
Original motif Consensus sequence: TCTGTAGMCCAGGCTGGCCTYGW

Reverse complement motif Consensus sequence:
WCKAGGCCAGCCTGGYCTACAGA

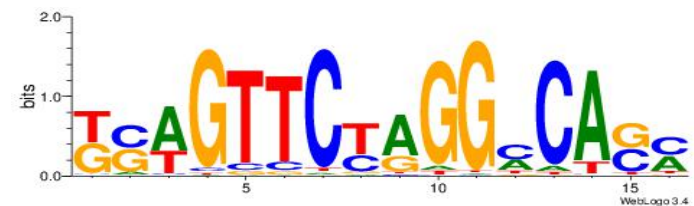


Dataset #: 1 Motif ID: 46 Motif name: C046

Original motif Consensus sequence: KSTGKCCTRGAACWSM



Reverse complement motif Consensus sequence: YSWGTTCKAGGYCASY



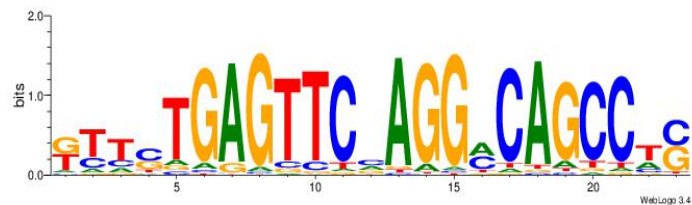
Best Matches for Motif ID 46 (Highest to Lowest)

Dataset #:	1
Motif ID:	7
Motif name:	C007
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	5
Number of overlap:	16
Similarity score:	0

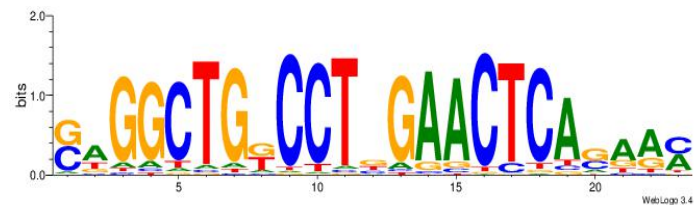
Alignment:

KTTSTGAGTTCVAGGMCAGCCTS
 ---YSWGTTCKAGGYCASY----

Original motif Consensus sequence: KTTSTGAGTTCVAGGMCAGCCTS



Reverse complement motif Consensus sequence:
 SAGGCTGYCCTVGAAGTCASAAY

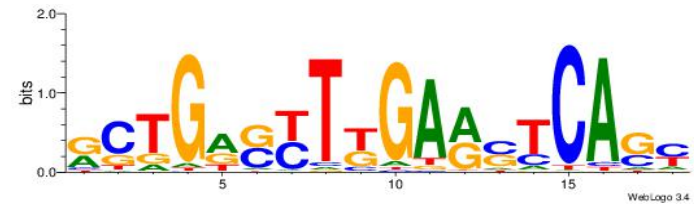
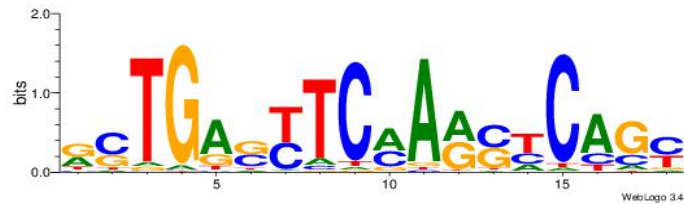


Dataset #:	1
Motif ID:	40
Motif name:	C040
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	3
Number of overlap:	16
Similarity score:	0.0254973

Alignment:
 KCTGMSKTYGAMSTCASM
 --KSTGKCCTRGAAACWSM

Original motif Consensus sequence: RSTGASYTCMARSYCAGY

Reverse complement motif Consensus sequence:
 KCTGMSKTYGAMSTCASM

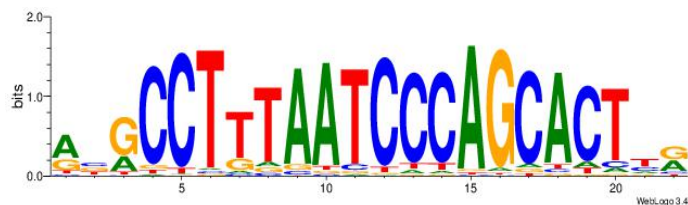


Dataset #: 1
 Motif ID: 9
 Motif name: C009
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 7
 Number of overlap: 16
 Similarity score: 0.0542082

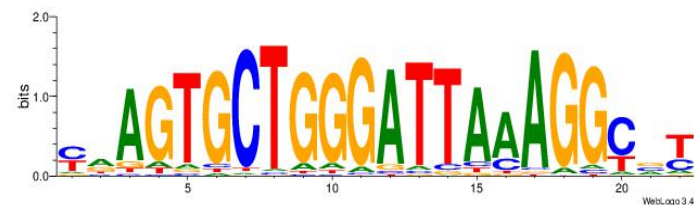
Alignment:

ABGCCTTTAATCCCAGCACTHR
 -----KSTGKCCTRGAACWSM

Original motif Consensus sequence: ABGCCTTTAATCCCAGCACTHR



Reverse complement motif Consensus sequence: MHAGTGCTGGGATTAAAGGCBT



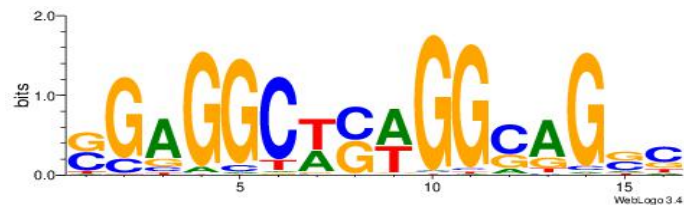
Dataset #: 1

Motif ID: 48
 Motif name: C048
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 16
 Similarity score: 0.0603648

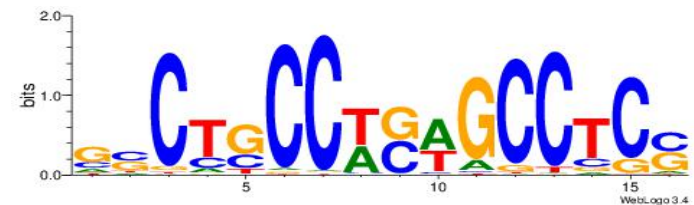
Alignment:

GSCTGCCWSWGCCTCS
 KSTGKCCTRGAACWSM

Original motif Consensus sequence: SGAGGCWSWGGCAGSC



Reverse complement motif Consensus sequence: GSCTGCCWSWGCCTCS

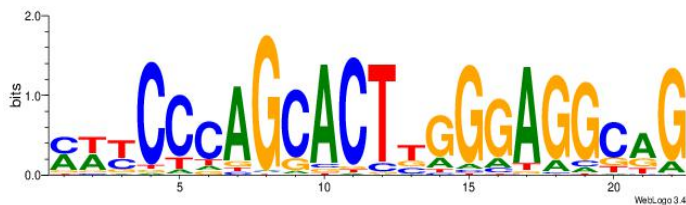


Dataset #: 1
 Motif ID: 19
 Motif name: C019
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 16

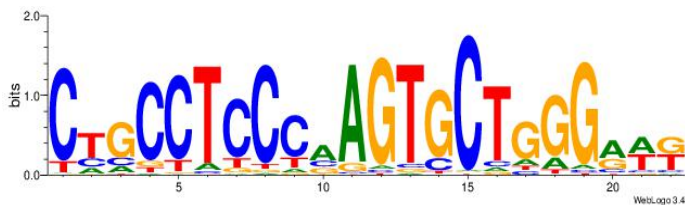
Similarity score: 0.0612865

Alignment:
CTGCCTCCCAAGTGCTGGGMWR
----KSTGKCCTRGAAACWSM--

Original motif Consensus sequence: MWYCCCAGCACTTGGGAGGCAG

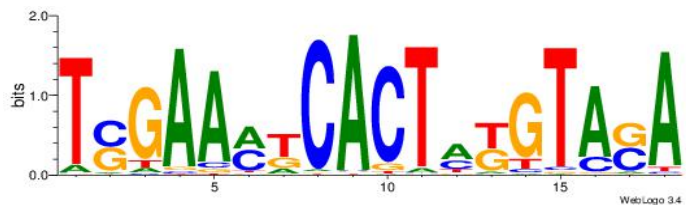


Reverse complement motif Consensus sequence: CTGCCTCCCAAGTGCTGGGMWR

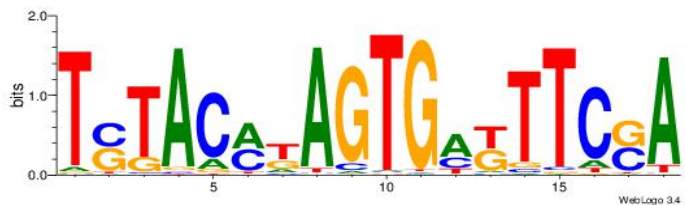


Dataset #: 1 Motif ID: 47 Motif name: C047

Original motif Consensus sequence: TSGAAMTCACTMKGTASA



Reverse complement motif Consensus sequence: TSTACRYAGTGAYTTCSA



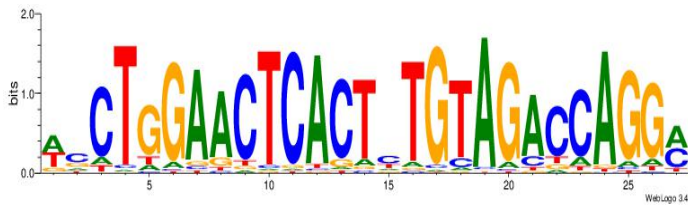
Best Matches for Motif ID 47 (Highest to Lowest)

Dataset #:	1
Motif ID:	13
Motif name:	C013
Matching format of first motif:	Original Motif

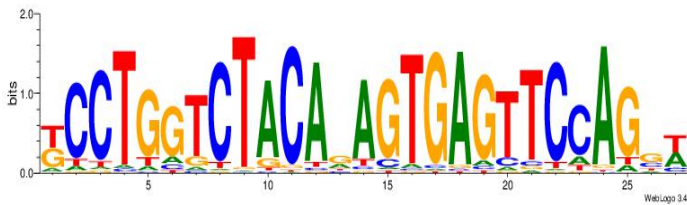
Matching format of second motif: Original Motif
Direction: Backward
Position number: 7
Number of overlap: 18
Similarity score: 0

Alignment:
WVCTGGAAC TCACTHTGTAGACCAGGM
---TSGAAMTCACTMKGTASA-----

Original motif Consensus sequence:
WVCTGGAAC TCACTHTGTAGACCAGGM



Reverse complement motif Consensus sequence:
YCCTGGTCTACADAGTGAGTTCCAGVW

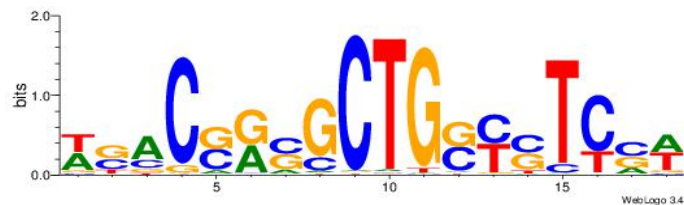


Dataset #: 1
Motif ID: 124
Motif name: C124
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 18
Similarity score: 0.0566388

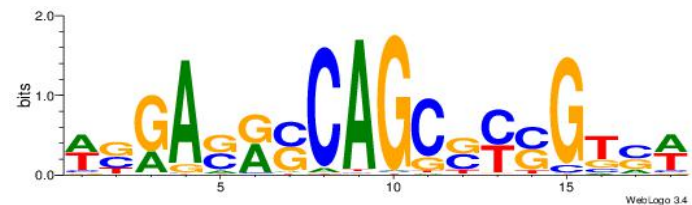
Alignment:

WSACSRSGCTGSYSTCSW
TSTACRYAGTGAYTTCSA

Original motif Consensus sequence: WSACSRSGCTGSYSTCSW



Reverse complement motif Consensus sequence: WSGASKSCAGCSMSGTSW



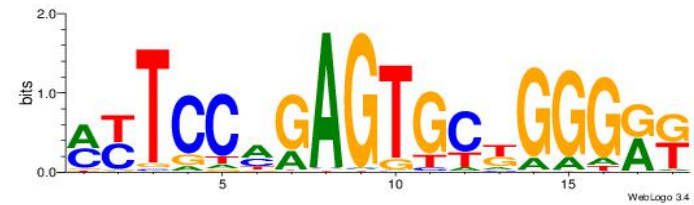
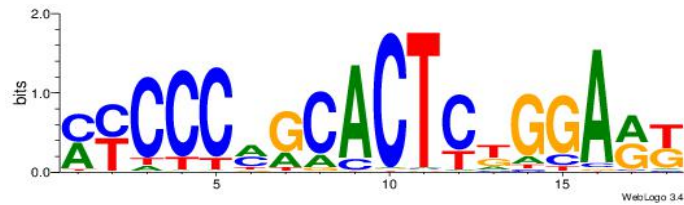
Dataset #:	1
Motif ID:	99
Motif name:	C099
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	18
Similarity score:	0.0603351

Alignment:

RKTCCRGAGTGCYGGGKR
TSTACRYAGTGAYTTCSA

Original motif Consensus sequence: MYCCCMGCACTCKGGARK

Reverse complement motif Consensus sequence:
RKTCCRGAGTGCYGGGKR

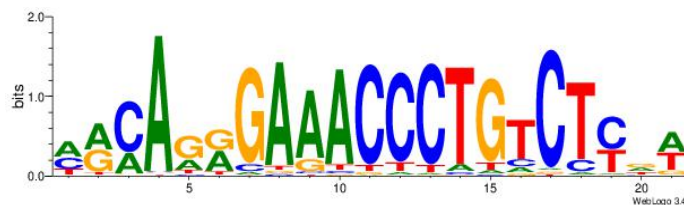


Dataset #: 1
 Motif ID: 27
 Motif name: C027
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 18
 Similarity score: 0.0686391

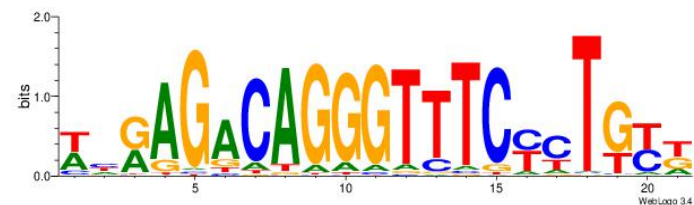
Alignment:

WHKAGACAGGGTTTCMCTGKY
 TSTACRYAGTGAYTTCSA---

Original motif Consensus sequence: MRCAGRGAAACCCTGTCTYDW



Reverse complement motif Consensus sequence: WHKAGACAGGGTTTCMCTGKY



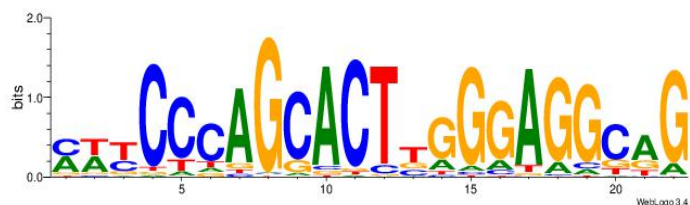
Dataset #: 1

Motif ID: 19
 Motif name: C019
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 4
 Number of overlap: 18
 Similarity score: 0.0699568

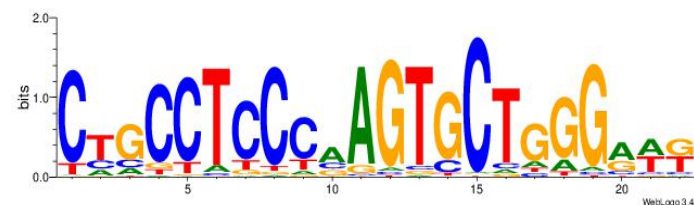
Alignment:

MWYCCCAGCACTTGGGAGGCAG
 -TSGAAMTCACTMKGTASA---

Original motif Consensus sequence: MWYCCCAGCACTTGGGAGGCAG

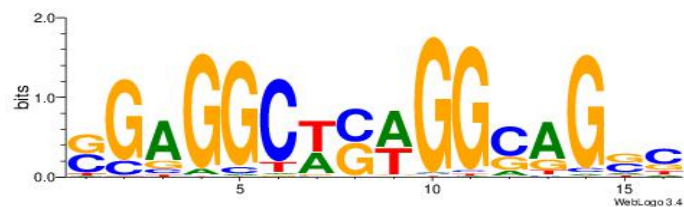


Reverse complement motif Consensus sequence: CTGCCTCCCAAGTGCTGGGMWR

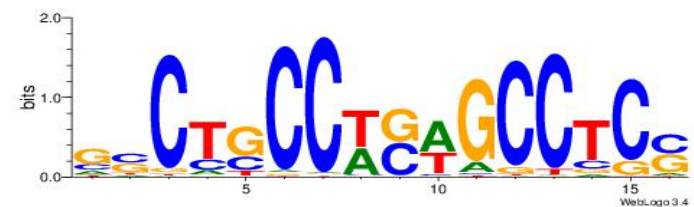


Dataset #: 1 Motif ID: 48 Motif name: C048

Original motif Consensus sequence: SGAGGCWSWGGCAGSC



Reverse complement motif Consensus sequence: GSCTGCCWSWGCTCS



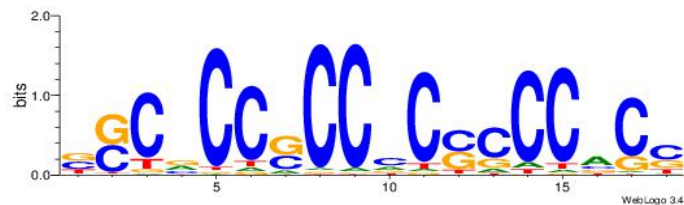
Best Matches for Motif ID 48 (Highest to Lowest)

Dataset #: 1
Motif ID: 20
Motif name: C020
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: 0.0377625

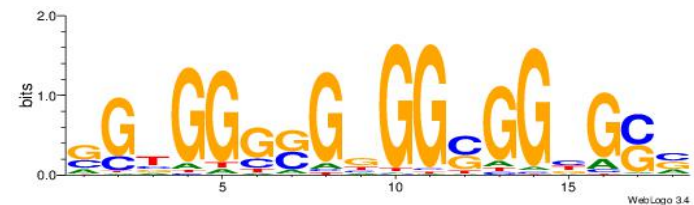
Alignment:

BSCVCCSCCVCSCCCACS
GSCTGCCWSWGCCTCS--

Original motif Consensus sequence: BSCVCCSCCVCSCCCACS



Reverse complement motif Consensus sequence: SGTGGGSGVGGSGGVGSB

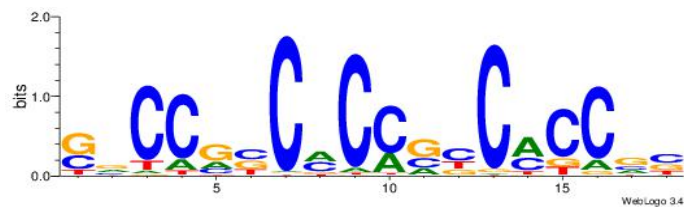


Dataset #: 1
Motif ID: 37
Motif name: C037
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif

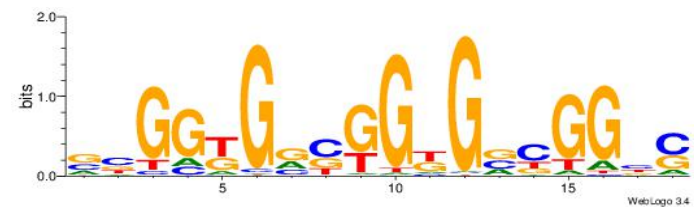
Direction: Forward
 Position number: 3
 Number of overlap: 16
 Similarity score: 0.0430637

Alignment:
 SVCCGBCMCCSYCMCCVB
 --GSCTGCCWSWGCCTCS

Original motif Consensus sequence: SVCCGBCMCCSYCMCCVB



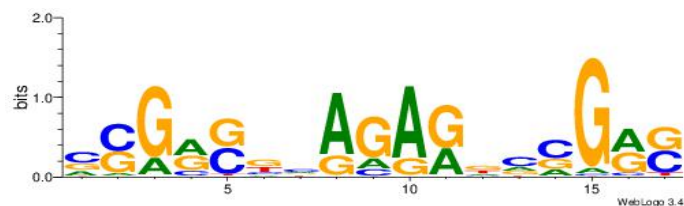
Reverse complement motif Consensus sequence: BVGGYGKSGGYGBCGGVS



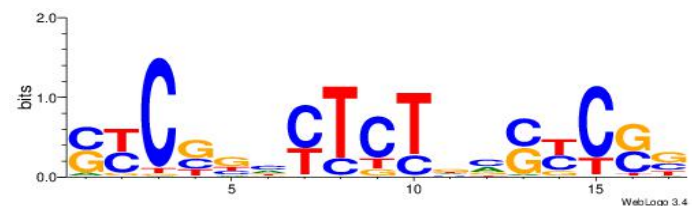
Dataset #: 1
 Motif ID: 85
 Motif name: C085
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 16
 Similarity score: 0.0452719

Alignment:
 VSGRSBHAGARDVSGRS
 -SGAGGCWSWGGCAGSC

Original motif Consensus sequence: VSGRSBHAGARDVSGRS



Reverse complement motif Consensus sequence: SKCSVHMTCTDBSKCSV

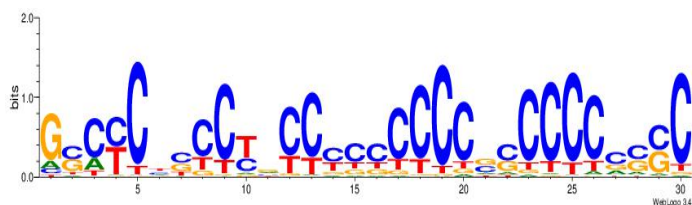


Dataset #: 1
 Motif ID: 3
 Motif name: C003
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 7
 Number of overlap: 16
 Similarity score: 0.0453102

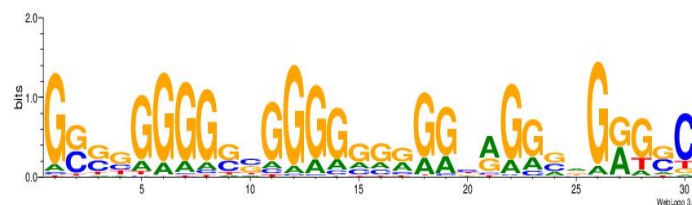
Alignment:

GSCYCHSCCYVCCYCCCCCSCCCCCSSC
 -----GSCTGCCWSWGCTCS-----

Original motif Consensus sequence:
 GSCYCHSCCYVCCYCCCCCSCCCCCSSC



Reverse complement motif Consensus sequence:
 GSSGGGGGSSGGGGGKGGVMGGSHGKGSC

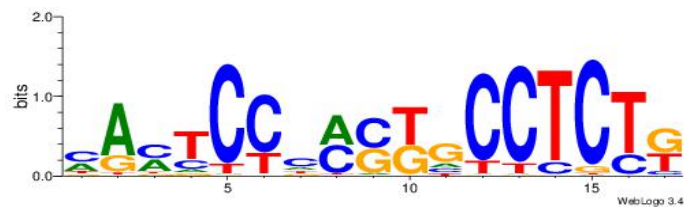


Dataset #: 1
 Motif ID: 66
 Motif name: C066
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 16
 Similarity score: 0.0464071

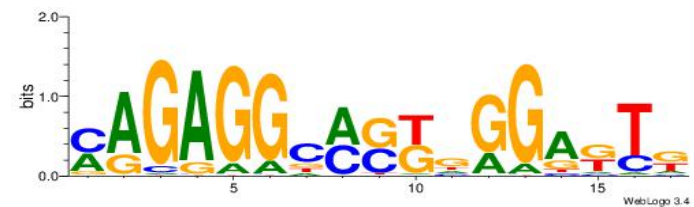
Alignment:

MAMTCCCMSKGCCTCTK
 GSCTGCCWSWGCCTCS-

Original motif Consensus sequence: MAMTCCCMSKGCCTCTK



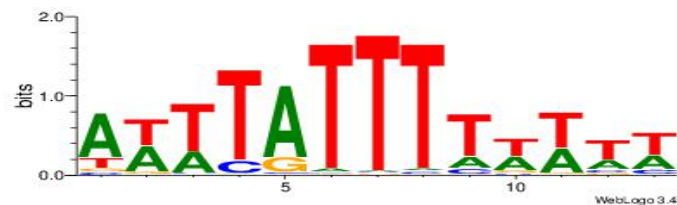
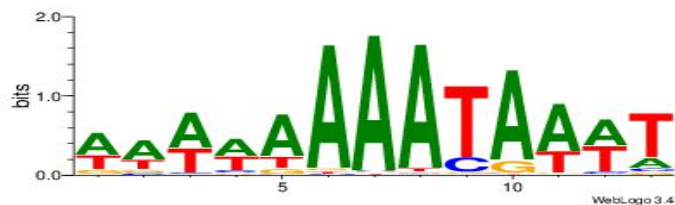
Reverse complement motif Consensus sequence: YAGAGGCRSYGGGARTR



Dataset #: 1 Motif ID: 49 Motif name: C049

Original motif Consensus sequence: WAWWAAAATAAWT

Reverse complement motif Consensus sequence: AWTTATTTTWWTV



Best Matches for Motif ID 49 (Highest to Lowest)

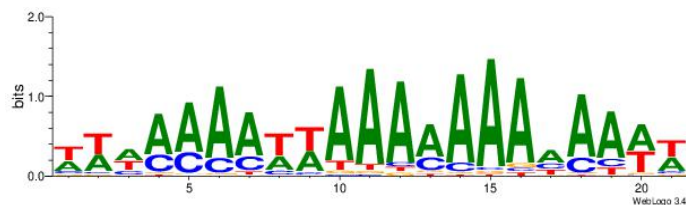
Dataset #: 1
 Motif ID: 10
 Motif name: C010
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 13
 Similarity score: 0.0183622

Alignment:

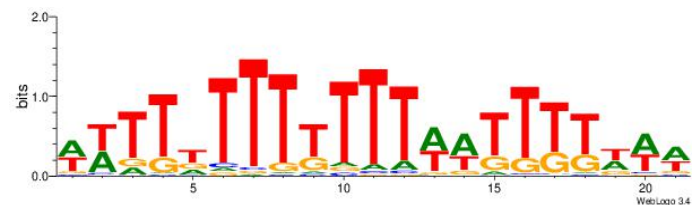
```

WWTTTTTTTTTTWWTTTTWWW
AWTTATTTTWWTW-----
  
```

Original motif Consensus sequence: WWAAAAWWAAAAAAAAAAWW



Reverse complement motif Consensus sequence: WWTTTTTTTTTTWWTTTTWWW

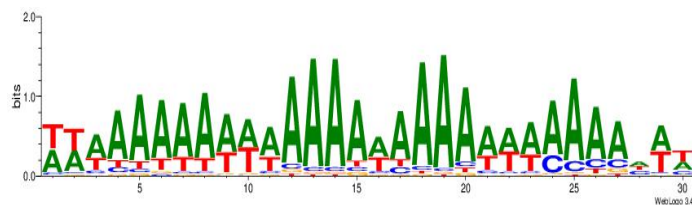


Dataset #: 1
 Motif ID: 1
 Motif name: C001
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 8
 Number of overlap: 13
 Similarity score: 0.0229227

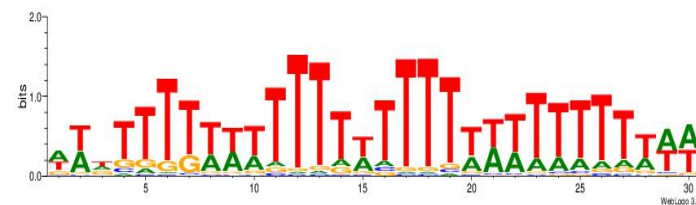
Alignment:

WWHTTTTWWTTTTTWWTTTTTWWTTTTTWW
 -----AWTTATTTTWWTW-----

Original motif Consensus sequence:
 WWWAAAAWWAAAAWAAAAWAAAAHWW



Reverse complement motif Consensus sequence:
 WWHTTTTWWTTTTTWWTTTTTWWTTTTTWW



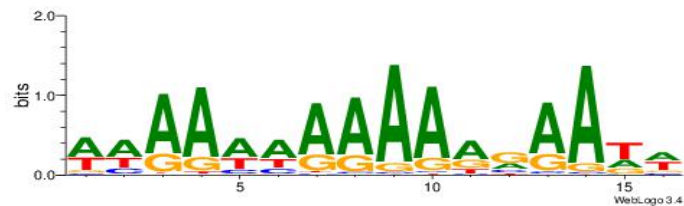
Dataset #: 1
 Motif ID: 43
 Motif name: C043
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 4

Number of overlap: 13
Similarity score: 0.0257709

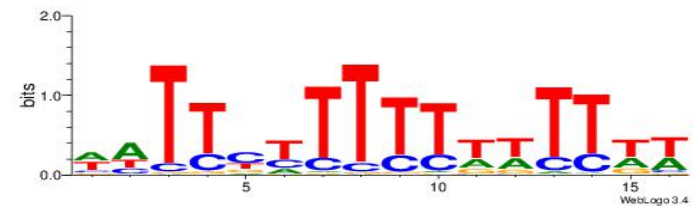
Alignment:

WATTMTTTTTTWTWW
AWTTATTTTWWTW---

Original motif Consensus sequence: WWAAWAAAAARAATW



Reverse complement motif Consensus sequence: WATTMTTTTTTWTWW

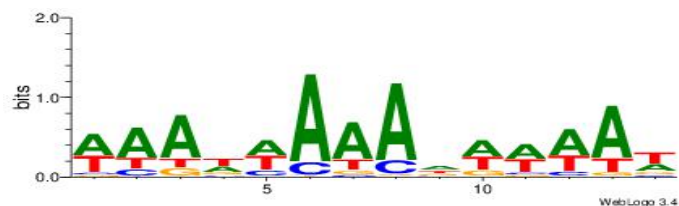


Dataset #: 1
Motif ID: 90
Motif name: C090
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 2
Number of overlap: 13
Similarity score: 0.0285191

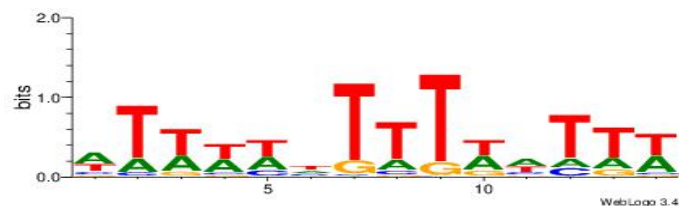
Alignment:

WTWWWDTTTWWTTW
-AWTTATTTTWWTW

Original motif Consensus sequence: WAAWWAAADWWAW



Reverse complement motif Consensus sequence: WTWWWDTTTWTTW



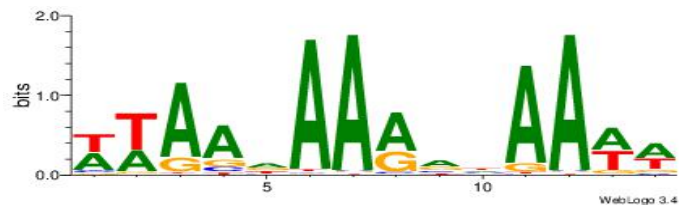
Dataset #: 1
Motif ID: 131
Motif name: C131
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 13
Similarity score: 0.0290134

Alignment:

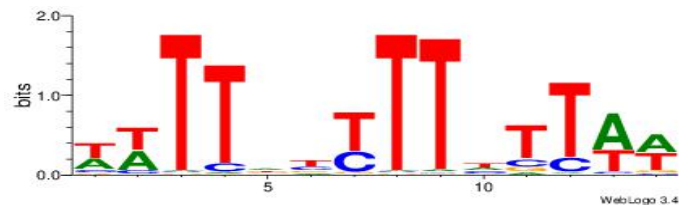
WTTTHBKTTDTTWW

AWTTATTTTWWTW-

Original motif Consensus sequence: WWAADAARVHAAWW

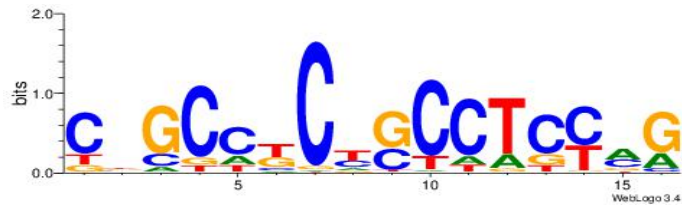


Reverse complement motif Consensus sequence: WTTTHBKTTDTTWW

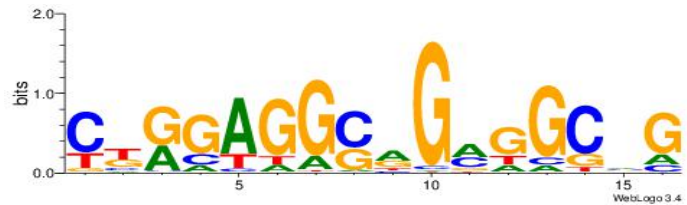


Dataset #: 1 Motif ID: 50 Motif name: C050

Original motif Consensus sequence: CBGCCCKCYSCCTCYMG



Reverse complement motif Consensus sequence: CYKGAGGSMGRGGCVG



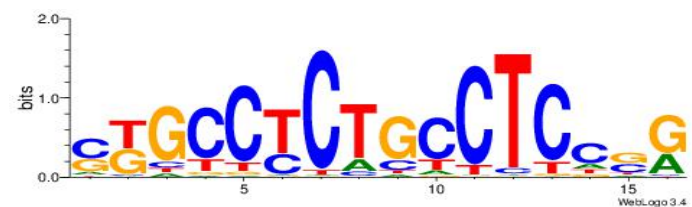
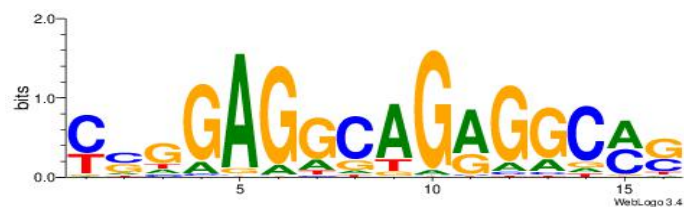
Best Matches for Motif ID 50 (Highest to Lowest)

Dataset #:	1
Motif ID:	14
Motif name:	C014
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:	0.0103992

Alignment:
YSGGAGGCAGAGGCMS
CYKGAGGSMGRGGCVG

Original motif Consensus sequence: YSGGAGGCAGAGGCMS

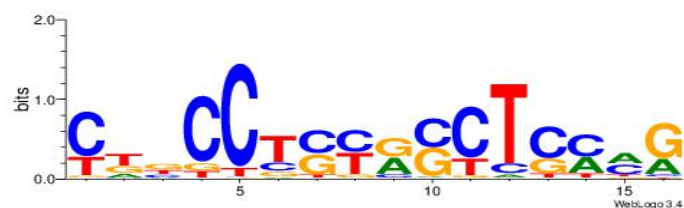
Reverse complement motif Consensus sequence: SYGCCTCTGCCTCCSK



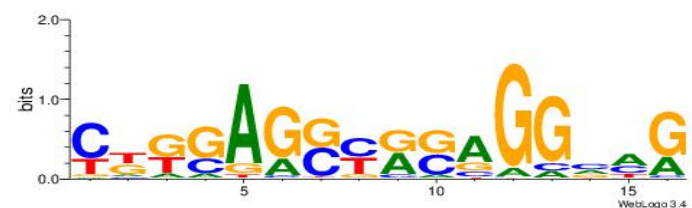
Dataset #: 1
 Motif ID: 83
 Motif name: C083
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 16
 Similarity score: 0.0119507

Alignment:
 CKBCCTSYRSCTCMMG
 CBGCKCYSCCTCYMG

Original motif Consensus sequence: CKBCCTSYRSCTCMMG



Reverse complement motif Consensus sequence: CYRGAGSMKSAGGBRG

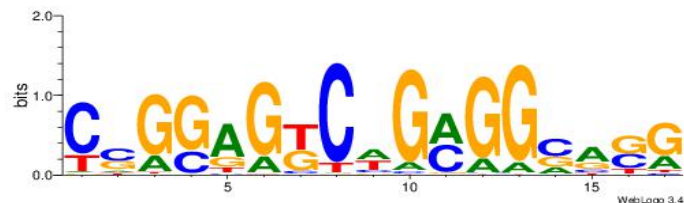


Dataset #: 1

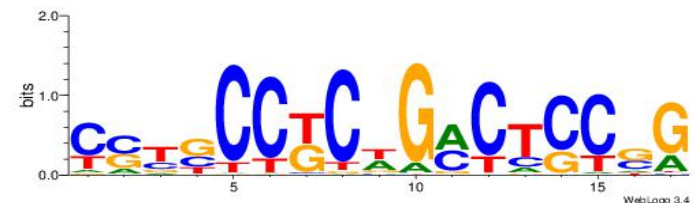
Motif ID: 86
 Motif name: C086
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 16
 Similarity score: 0.0161878

Alignment:
 CSGGAGKWCWGMGGSASG
 CYKGAGGSMGRGGCVG-

Original motif Consensus sequence: CSGGAGKWCWGMGGSASG



Reverse complement motif Consensus sequence: CSTSCCYCWGRCTCCSG



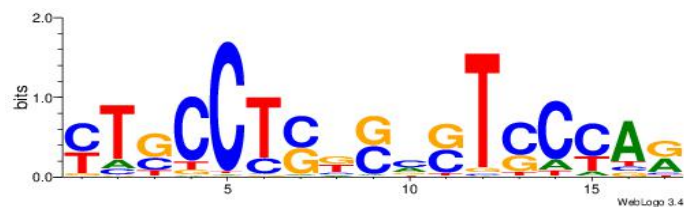
Dataset #: 1
 Motif ID: 101
 Motif name: C101
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 16

Similarity score: 0.0346088

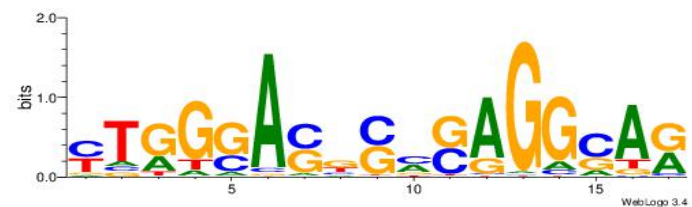
Alignment:

YTSCCTSKSVSTCCCAR
CBGCCCKYSCCTCYMG-

Original motif Consensus sequence: YTSCCTSKSVSTCCCAR



Reverse complement motif Consensus sequence:
MTGGGASVSYSAGGSAK



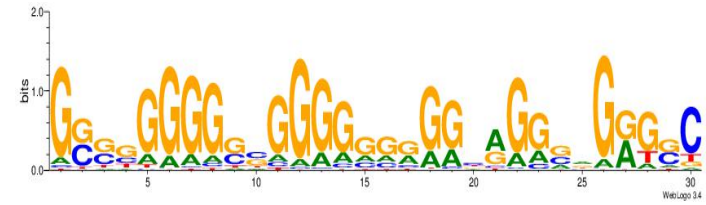
Dataset #: 1
Motif ID: 3
Motif name: C003
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 2
Number of overlap: 16
Similarity score: 0.0359906

Alignment:

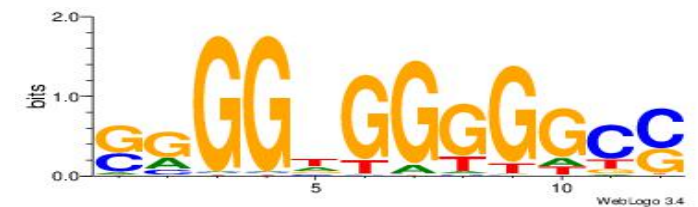
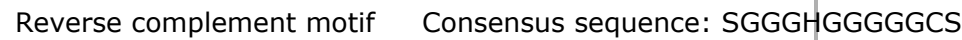
GSSGGGGGSSGGGGGKGGVMGGSHGKGC
-CYKGAGGSMGRGGCVG-----

Original motif Consensus sequence:
GSCYCHSCCYVCCYCCCCSSCCCCSSC

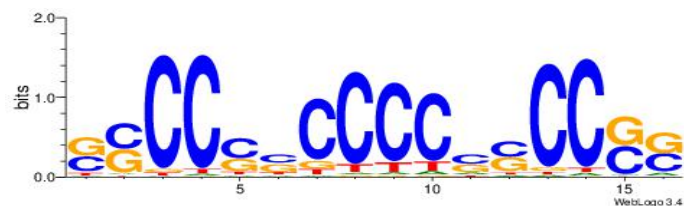
Reverse complement motif Consensus sequence:
GSSGGGGGSSGGGGGKGGVMGGSHGKGC



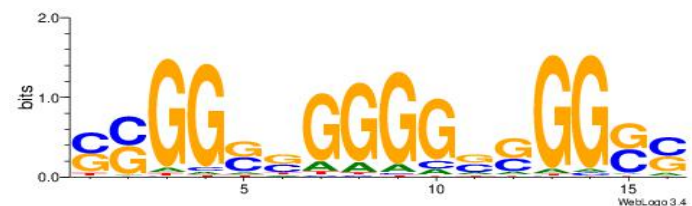
Original motif Consensus sequence: SGCCCCCHCCCS



Original motif Consensus sequence: SSCCSSCCCCSSCCSS



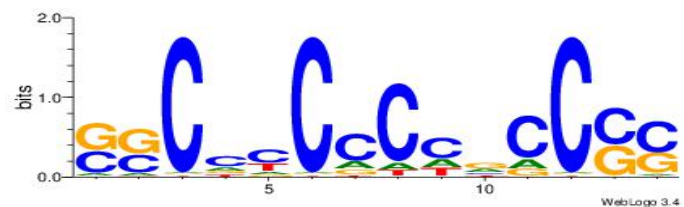
Reverse complement motif Consensus sequence: SSGGSSGGGGSSGGSS



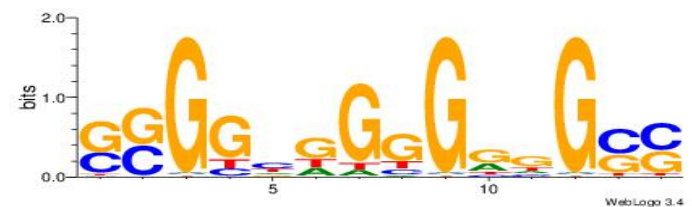
Dataset #: 1
Motif ID: 104
Motif name: C104
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 12
Similarity score: 0.0155693

Alignment:
SSCCYCCCCDCCSS
--SGCCCCCHCCCS

Original motif Consensus sequence: SSCCYCCCCDCCSS



Reverse complement motif Consensus sequence: SSGGHGGGGKGG

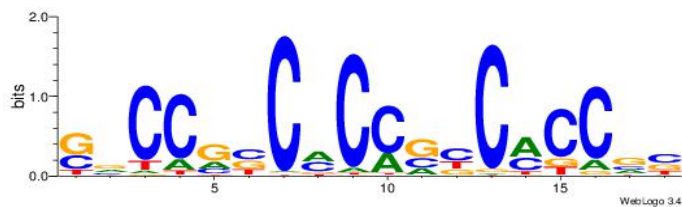


Dataset #: 1
 Motif ID: 37
 Motif name: C037
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 12
 Similarity score: 0.0205815

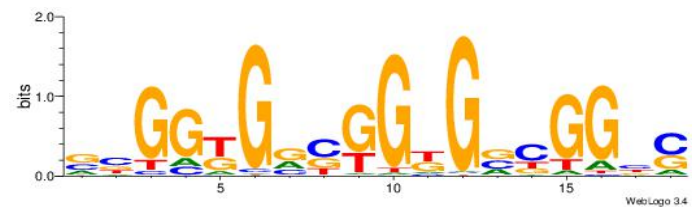
Alignment:

SVCCGBCMCCSYCMCCVB
 SGCCCCCHCCCS-----

Original motif Consensus sequence: SVCCGBCMCCSYCMCCVB



Reverse complement motif Consensus sequence: BVGGYGKSGGYGBCGGVS

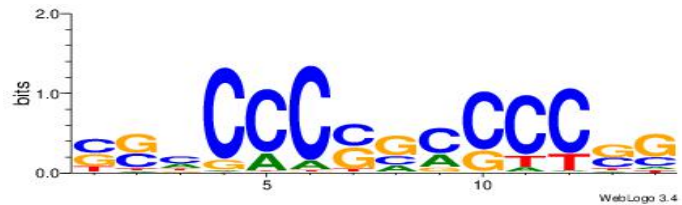


Dataset #: 1
 Motif ID: 94
 Motif name: C094
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 3

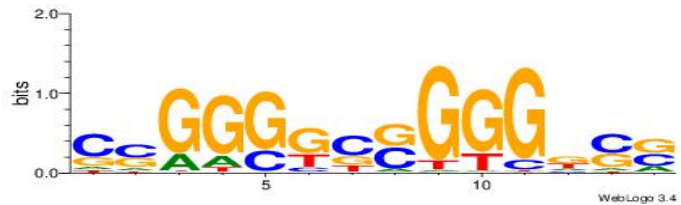
Number of overlap: 12
Similarity score: 0.0236035

Alignment:
CSGGGGCSGGGDSS
--SGGGHGGGGGCS

Original motif Consensus sequence: SSHCCCSGCCCCSG



Reverse complement motif Consensus sequence: CSGGGGCSGGGD

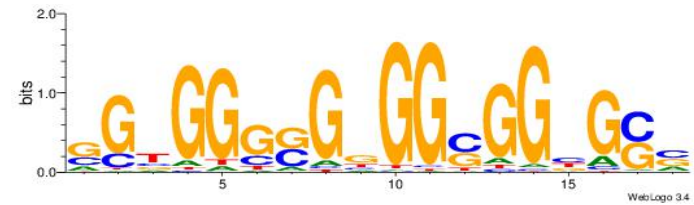


Dataset #: 1
Motif ID: 20
Motif name: C020
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 6
Number of overlap: 12
Similarity score: 0.0237251

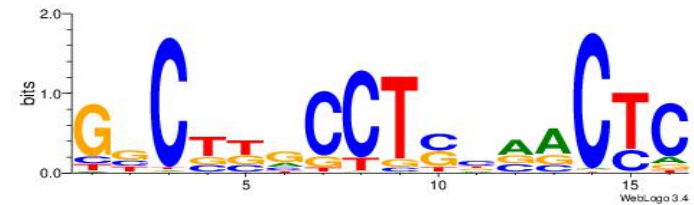
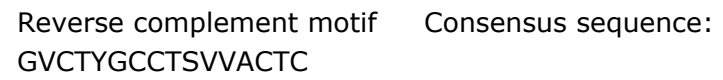
Alignment:
SGTGGGSGVGGSGGVGSB
-SGGGHGGGGGCS-----

Original motif Consensus sequence: BSCVCCSCCVCSCCCACS

Reverse complement motif Consensus sequence:
SGTGGGSGVGGSGGVGSB

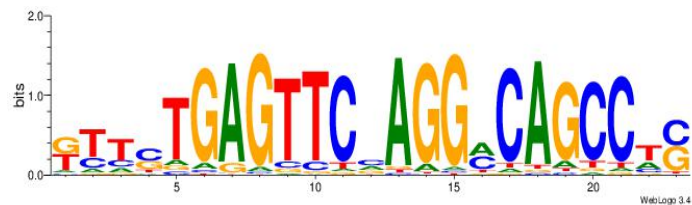


Original motif Consensus sequence: GAGTBVSAGGCMAGVC

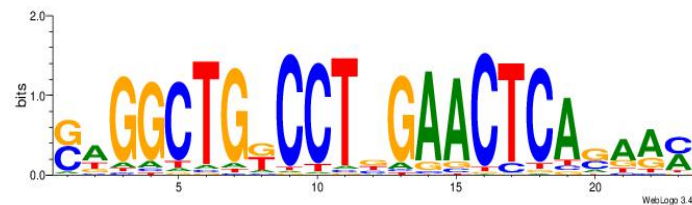


KTTSTGAGTTCVAGGMCAGCCTS
 -----GAGTBVSAGGCMAGVC--

Original motif Consensus sequence: KTTSTGAGTTCVAGGMCAGCCTS



Reverse complement motif Consensus sequence:
 SAGGCTGYCCTVGAAGTCASAAY

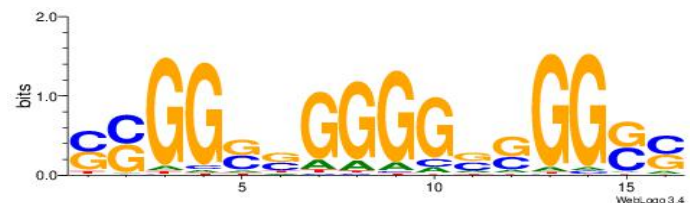
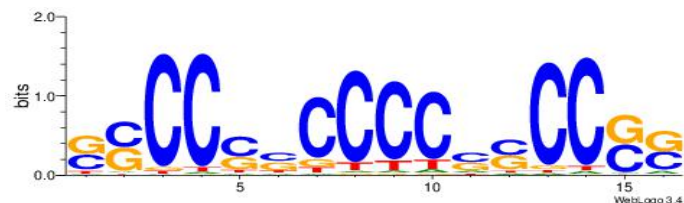


Dataset #:	1
Motif ID:	8
Motif name:	C008
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	16
Similarity score:	0.0404907

Alignment:
 SSGGSSGGGGSSGGSS
 GAGTBVSAGGCMAGVC

Original motif Consensus sequence: SSCCSCCCCCSSCCSS

Reverse complement motif Consensus sequence:
 SSGGSSGGGGSSGGSS

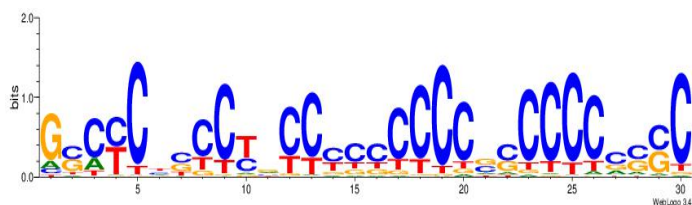


Dataset #: 1
 Motif ID: 3
 Motif name: C003
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 16
 Similarity score: 0.0415476

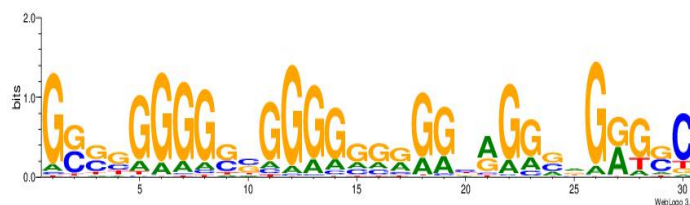
Alignment:

GSCYCHSCCYVCCYCCCCCSCCCCCSSC
 -----GVCTYGCCTSVVACTC-

Original motif Consensus sequence:
 GSCYCHSCCYVCCYCCCCCSCCCCCSSC



Reverse complement motif Consensus sequence:
 GSSGGGGGSSGGGGGKGGVMGGSHGKGC



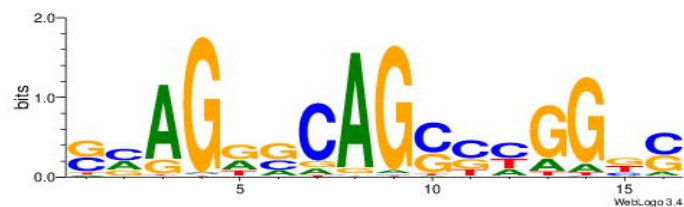
Dataset #: 1

Motif ID: 39
 Motif name: C039
 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: 0.0450105

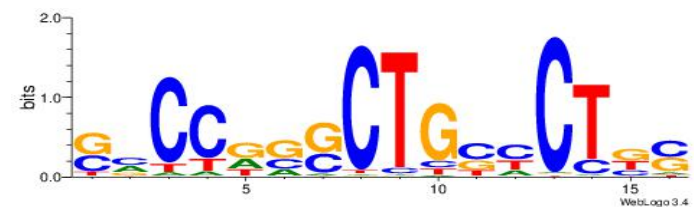
Alignment:

SMAGRSCAGSSYGGBS
 GAGTBVSAGGCMAGVC

Original motif Consensus sequence: SMAGRSCAGSSYGGBS



Reverse complement motif Consensus sequence: SBCKSSCTGSMCTRS

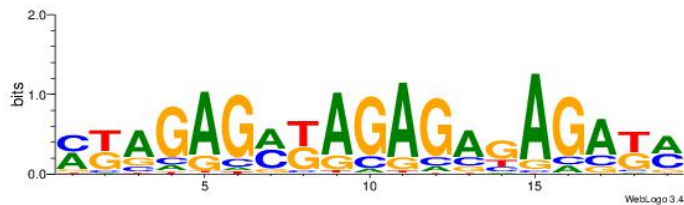


Dataset #: 1
 Motif ID: 12
 Motif name: C012
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 16

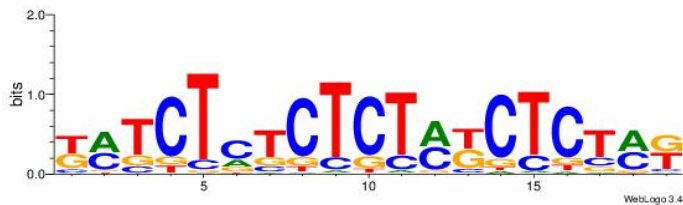
Similarity score: 0.0456684

Alignment:
MKAGAGMKAGAGAGAGAKM
---GAGTBVSAGGCMAGVC

Original motif Consensus sequence: MKAGAGMKAGAGAGAGAKM

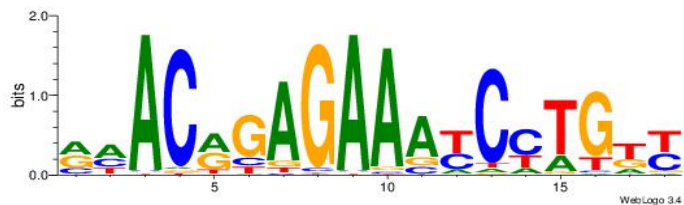


Reverse complement motif Consensus sequence: YRTCTCTCTRYCTCTRR

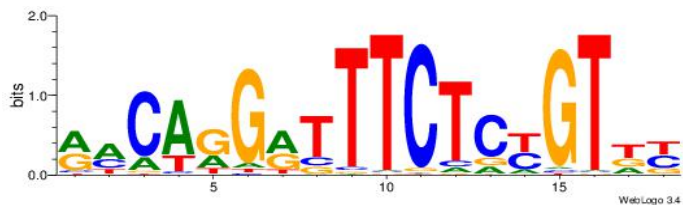


Dataset #: 1 Motif ID: 53 Motif name: C053

Original motif Consensus sequence: RMACRGAGAAAYCCTGKY



Reverse complement motif Consensus sequence: MRCAGGMTTCTCKGTYK



Best Matches for Motif ID 53 (Highest to Lowest)

Dataset #:	1
Motif ID:	132
Motif name:	C132
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:	0.0360527

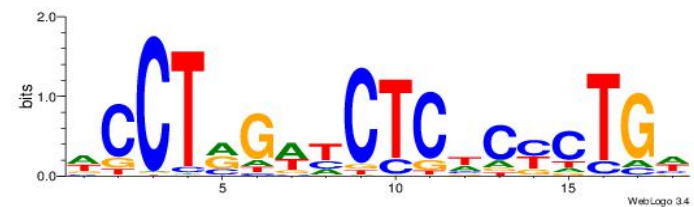
Alignment:

```
WCAGRGWGAGAWCYAGGW
RMACRGAGAAAYCCTGKY
```

Original motif Consensus sequence: WCAGRGWGAGAWCYAGGW



Reverse complement motif Consensus sequence: WCCTKGWTCTCWCMTGW

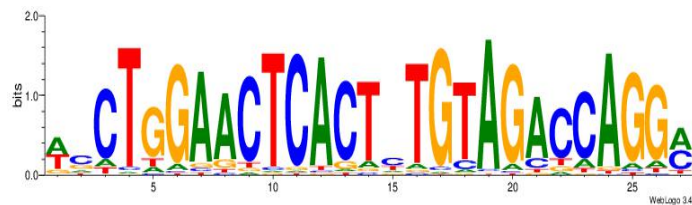


Dataset #:	1
Motif ID:	13
Motif name:	C013
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	18
Similarity score:	0.0481145

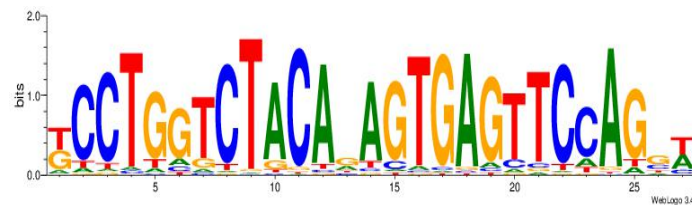
Alignment:

WVCTGGAACTCACTHTGTAGACCAGGM
 -----MRCAGGMTTTCTCKGTYK

Original motif Consensus sequence:
 WVCTGGAACTCACTHTGTAGACCAGGM



Reverse complement motif Consensus sequence:
 YCCTGGTCTACADAGTGAGTTCCAGVW



Dataset #:	1
Motif ID:	42
Motif name:	C042
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:	0.0514739

Alignment:
 WGAGTRMGTTCKRGGACW
 MRCAGGMTTTCTCKGTYK

Original motif Consensus sequence: WGTCCKRGAACTMACTCW

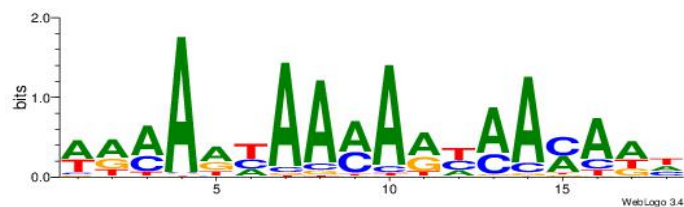
Reverse complement motif Consensus sequence:
 WGAGTRMGTTCKRGGACW

Motif ID: 57
 Motif name: C057
 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: 0.0535024

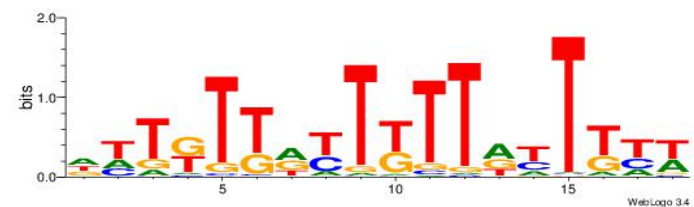
Alignment:

HWTRTTMKTYTTMKTYKW
 MRCAGGMTTCTCTCKGTYK

Original motif Consensus sequence: WRMARYAAMARYAAMAWH

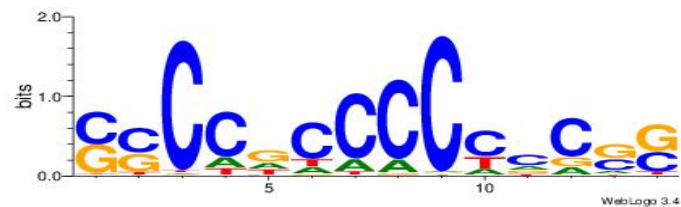


Reverse complement motif Consensus sequence: HWTRTTMKTYTTMKTYKW



Dataset #: 1 Motif ID: 54 Motif name: C054

Original motif Consensus sequence: SSCDCCCCCCCCSS



Reverse complement motif Consensus sequence: SSGGGGGGGHGG



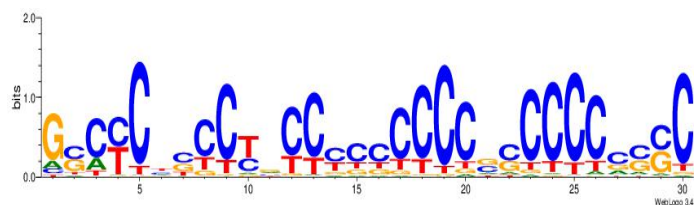
Best Matches for Motif ID 54 (Highest to Lowest)

Dataset #: 1
Motif ID: 3
Motif name: C003
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: 0.010752

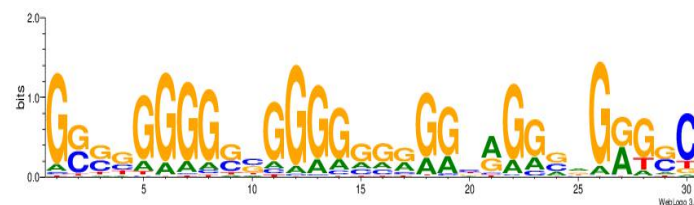
Alignment:

```
GSCYCHSCCYVCCYCCCCCSCCCCCSSC  
-----SSCCDCCCCCCCSS
```

Original motif Consensus sequence:
GSCYCHSCCYVCCYCCCCCSCCCCCSSC



Reverse complement motif Consensus sequence:
GSSGGGGGSSGGGGGGKGGVMGGSHGKGSC

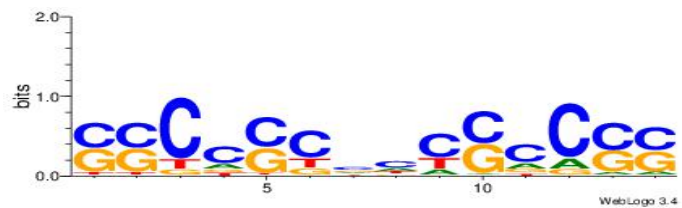


Dataset #: 1
Motif ID: 23
Motif name: C023
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement

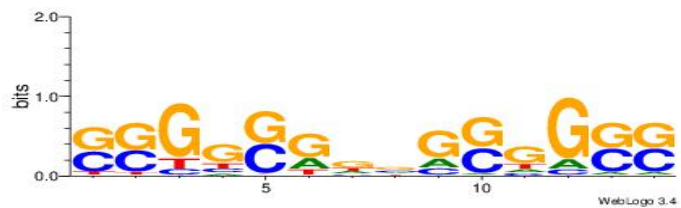
Direction: Backward
Position number: 1
Number of overlap: 14
Similarity score: 0.0108829

Alignment:
SSGGSGDBGSGGSS
SSGGGGGGGHGGSS

Original motif Consensus sequence: SSCCSCBHCSS



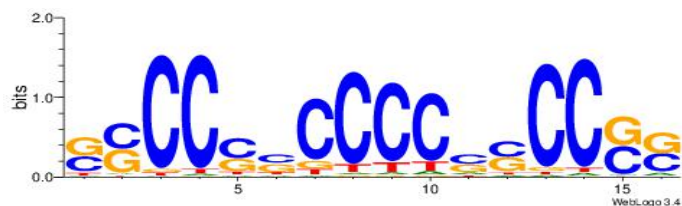
Reverse complement motif Consensus sequence: SSGSGDBGSGG



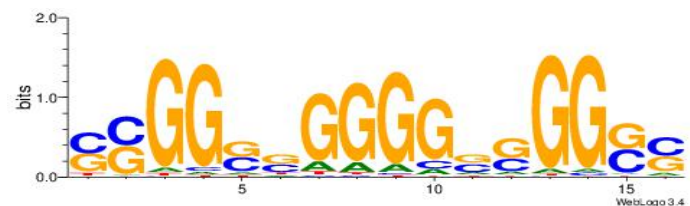
Dataset #: 1
Motif ID: 8
Motif name: C008
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2
Number of overlap: 14
Similarity score: 0.0123397

Alignment:
SSCCSSCCCCSSCCSS
-SSCCDCCCCCCCCSS-

Original motif Consensus sequence: SSCCSSCCCCSSCCSS



Reverse complement motif Consensus sequence: SSGGSSGGGGSSGGSS



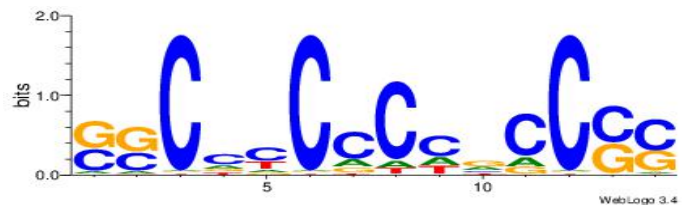
Dataset #: 1
Motif ID: 104
Motif name: C104
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 14
Similarity score: 0.0155505

Alignment:

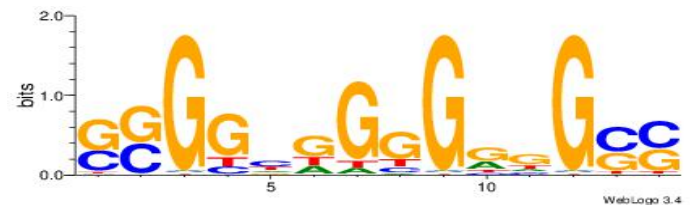
SSCCYCCCCDCCSS

SSCCDCCCCCCCSS

Original motif Consensus sequence: SSCCYCCCCDCCSS



Reverse complement motif Consensus sequence: SSGGHGGGGKGG

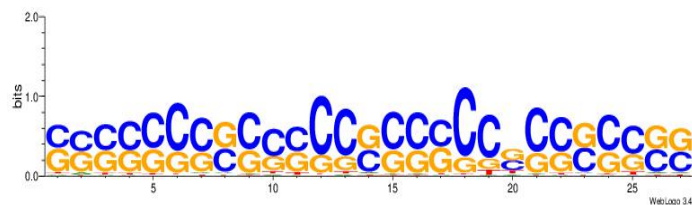


Dataset #: 1
 Motif ID: 4
 Motif name: C004
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 5
 Number of overlap: 14
 Similarity score: 0.0155642

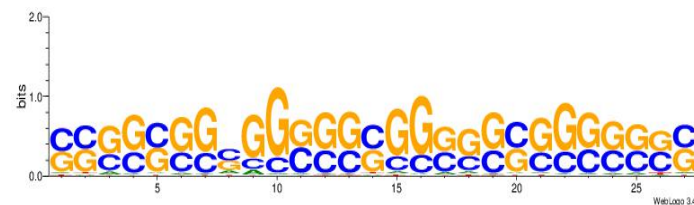
Alignment:

SSSSSSGSGGSSSSSGSSSSSGSSSSS
 ----SSGGGGGGHGGSS-----

Original motif Consensus sequence:
 SSSSSCSSSSCCSSSSCCSCSSSSSS



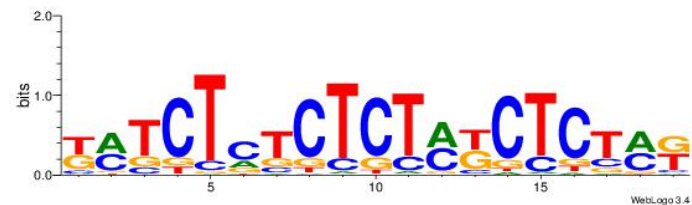
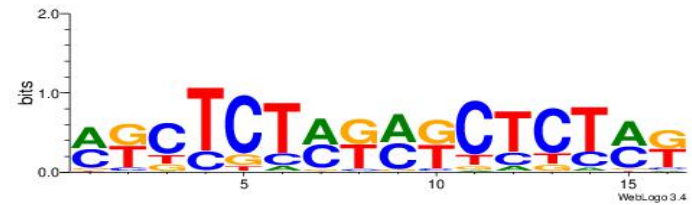
Reverse complement motif Consensus sequence:
 SSSSSSGSGGSSSSSGSSSSSGSSSSS



Dataset #: 1 Motif ID: 55 Motif name: C055

Original motif Consensus sequence: MKAGAGMKMKAGAGMK

Reverse complement motif Consensus sequence:
 RYCTCTRRRRCTCTRR

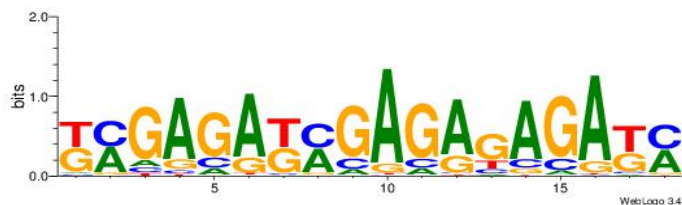


Dataset #: 1
 Motif ID: 11
 Motif name: C011
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 16
 Similarity score: 0.0407596

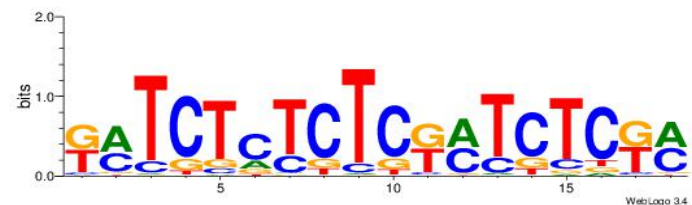
Alignment:

KMGAGAKMGAGAGAGAKM
 -MKAGAGMKMKAGAGMK-

Original motif Consensus sequence: KMGAGAKMGAGAGAGAKM



Reverse complement motif Consensus sequence: RRTCTCTCTCRRTCTCRR



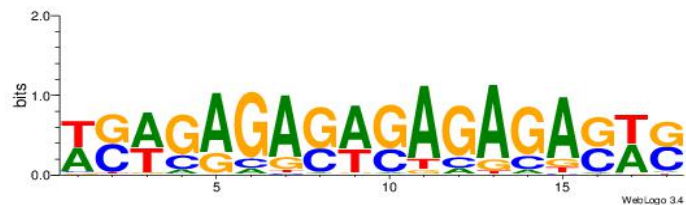
Dataset #: 1
 Motif ID: 17
 Motif name: C017
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1

Number of overlap: 16
Similarity score: 0.0572526

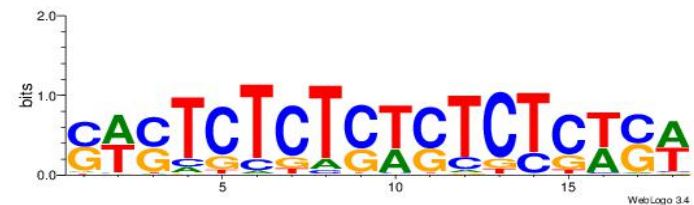
Alignment:

WSWGAGASWSAGAGASWS
MKAGAGMKMKAGAGMK--

Original motif Consensus sequence: WSWGAGASWSAGAGASWS



Reverse complement motif Consensus sequence: SWSTCTCTSWSTCTCWSW

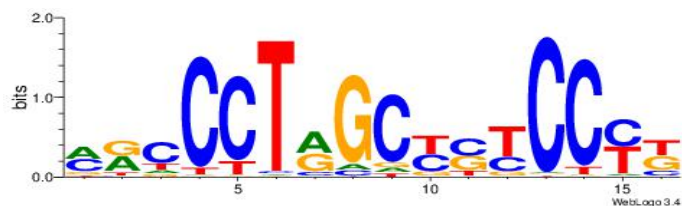


Dataset #: 1
Motif ID: 121
Motif name: C121
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 16
Similarity score: 0.0582287

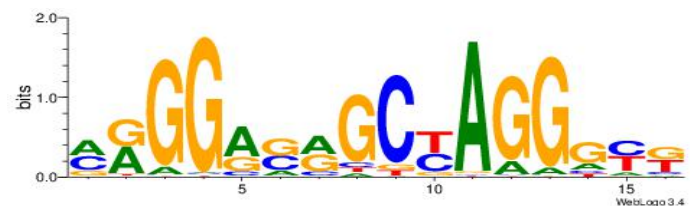
Alignment:

RKGGASMGCKAGGGMY
MKAGAGMKMKAGAGMK

Original motif Consensus sequence: MRCCCTRGCYSTCCYK



Reverse complement motif Consensus sequence: RKGGASMGCKAGGGMV

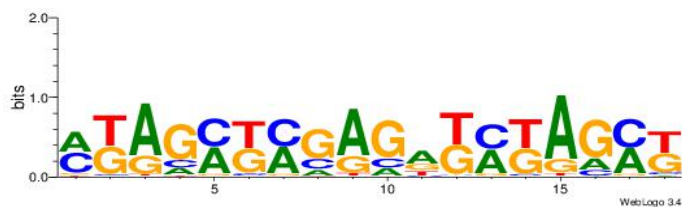


Dataset #: 1
Motif ID: 36
Motif name: C036
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 3
Number of overlap: 16
Similarity score: 0.0615114

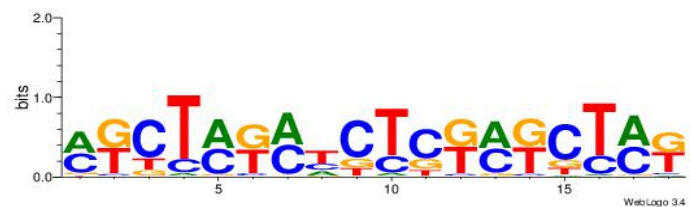
Alignment:

MKAGMKMGAGAKMKAGMK
--MKAGAGMKMKAGAGMK

Original motif Consensus sequence: MKAGMKMGAGAKMKAGMK

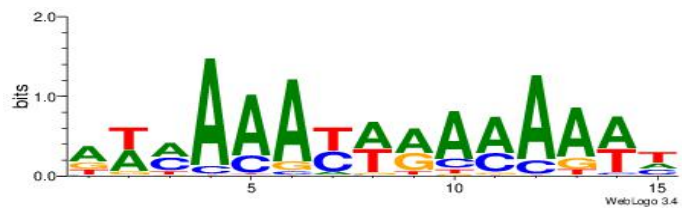


Reverse complement motif Consensus sequence: RRCTRRRTCTCRRRCTRY

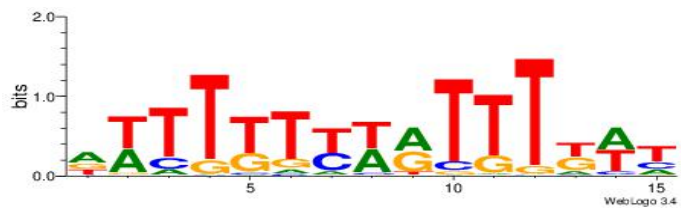


Dataset #: 1 Motif ID: 56 Motif name: C056

Original motif Consensus sequence: AWMAAAYWRAMAAWH



Reverse complement motif Consensus sequence: HWTTYTKWMTTTYWT



Best Matches for Motif ID 56 (Highest to Lowest)

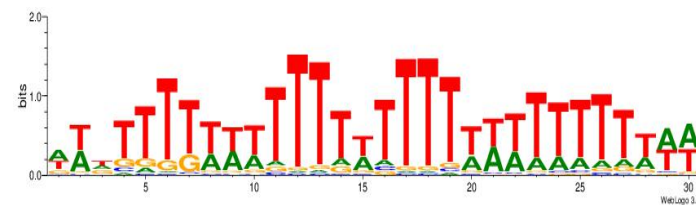
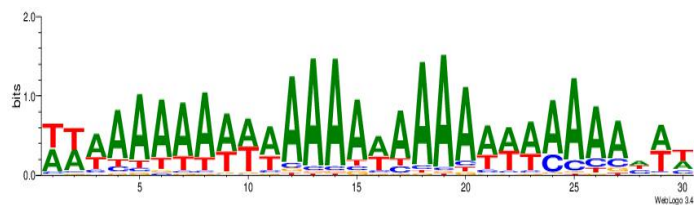
Dataset #:	1
Motif ID:	1
Motif name:	C001
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	15
Number of overlap:	15
Similarity score:	0.0174059

Alignment:

```
WWWAAAAAWWAAAAWAAAAWAAAAHWW
-----AWMAAAYWRAMAAWH-----
```

Original motif Consensus sequence:
WWWAAAAAWWAAAAWAAAAWAAAAHWW

Reverse complement motif Consensus sequence:
WWHTTTTWWTTTTWTTTTWTTTTWWW

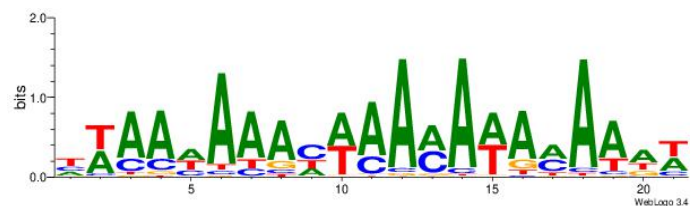


Dataset #: 1
 Motif ID: 16
 Motif name: C016
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 5
 Number of overlap: 15
 Similarity score: 0.0238582

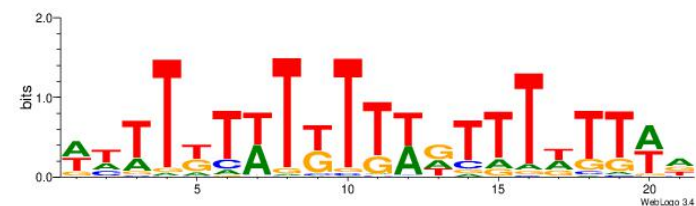
Alignment:

HWAAWAAAHWAAMAWAMAAWW
 --AWMAAAYWRAMAAWH----

Original motif Consensus sequence: HWAAWAAAHWAAMAWAMAAWW



Reverse complement motif Consensus sequence: WWTYYTWYTTWDTTTWTTWH



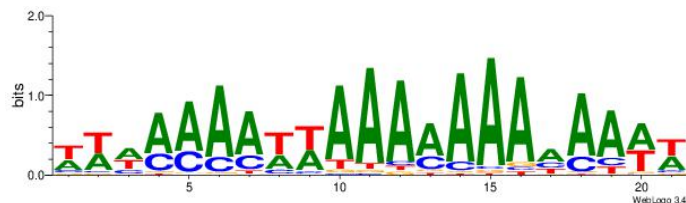
Dataset #: 1

Motif ID: 10
 Motif name: C010
 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: 0.0247988

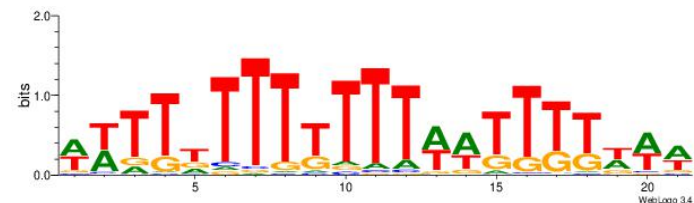
Alignment:

WWTTTTTTTTTTWWTTTTWWW
 HWTTYTKWMTTTYWT-----

Original motif Consensus sequence: WWWAAAWWAAAAAAAAAAWW



Reverse complement motif Consensus sequence: WWTTTTTTTTTTWWTTTTWWW

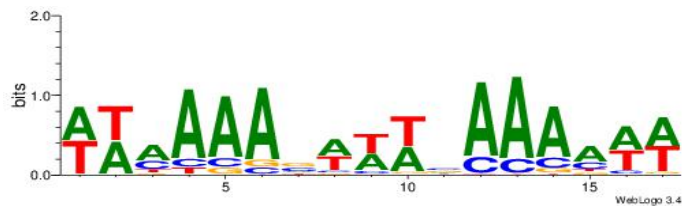


Dataset #: 1
 Motif ID: 139
 Motif name: C139
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 15

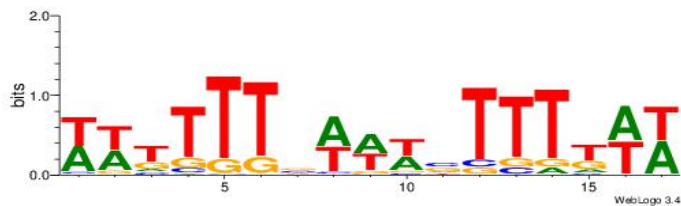
Similarity score: 0.0262578

Alignment:
WWMAAABWWWVAAA
AWMAAAYWRAMA--

Original motif Consensus sequence: WWMAAABWWWVAAA



Reverse complement motif Consensus sequence: WWTTTTVWWBTTTYWW

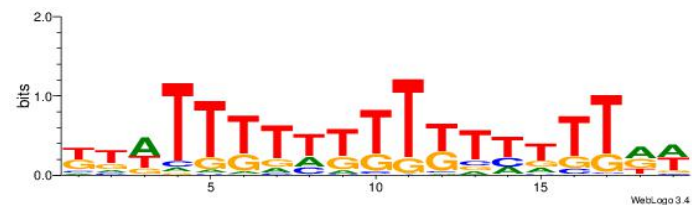
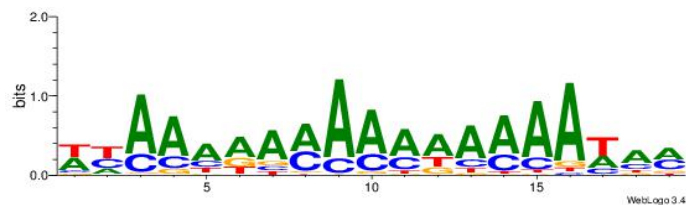


Dataset #: 1
Motif ID: 30
Motif name: C030
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 4
Number of overlap: 15
Similarity score: 0.0280412

Alignment:
WYAAAAAMAAAAAAWAM
---AWMAAAYWRAMA--

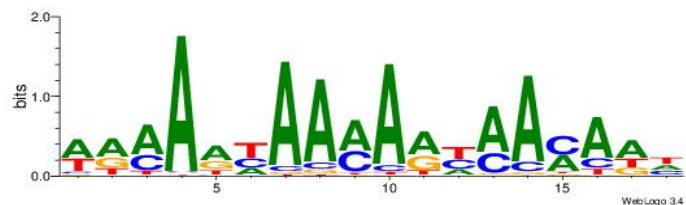
Original motif Consensus sequence: WYAAAAAMAAAAAAWAM

Reverse complement motif Consensus sequence: YTWTTTTTTTTYTTTTMW

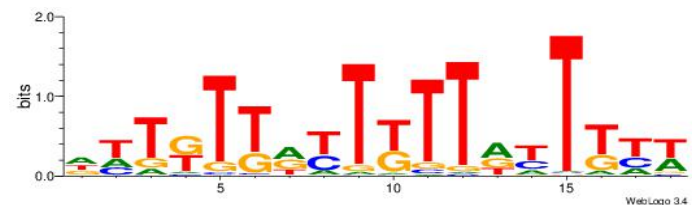


Dataset #: 1 Motif ID: 57 Motif name: C057

Original motif Consensus sequence: WRMARYAAMARYAAMAWH



Reverse complement motif Consensus sequence: HWTRTTMKTYTTMKTYKW



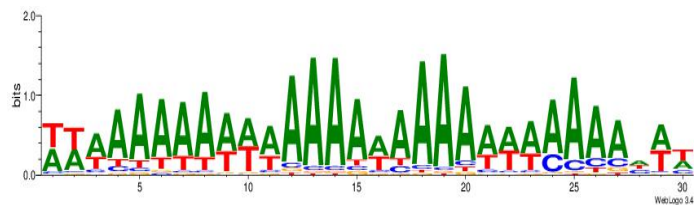
Best Matches for Motif ID 57 (Highest to Lowest)

Dataset #:	1
Motif ID:	1
Motif name:	C001
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:	0.0188081

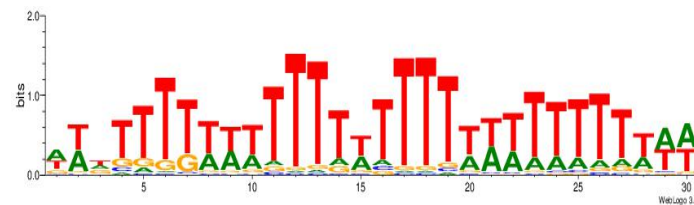
Alignment:

WWWAAAAAWWAAAAAWAAAAWWAAAAHWW
 -----WRMARYAAMARYAAMAWH--

Original motif Consensus sequence:
 WWWAAAAAWWAAAAAWAAAAWWAAAAHWW



Reverse complement motif Consensus sequence:
 WWHTTTTTWWTTTTWTTTTWTTTTTWWW

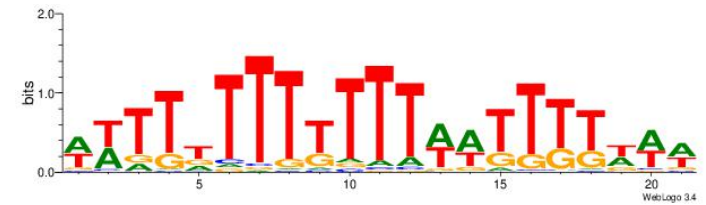


Dataset #:	1
Motif ID:	10
Motif name:	C010
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2
Number of overlap:	18
Similarity score:	0.0244335

Alignment:
 WWWAAAAWWAAAAAAAAAAWW
 --WRMARYAAMARYAAMAWH--

Original motif Consensus sequence: WWWAAAAWWAAAAAAAAAAWW

Reverse complement motif Consensus sequence:
 WWTTTTTTTTTTWWTTTTWWW

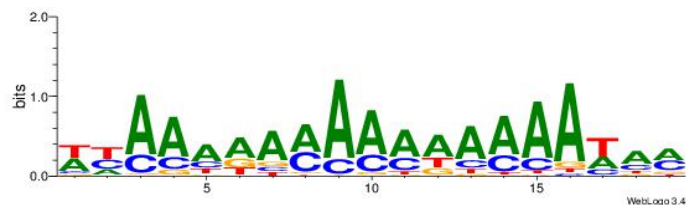


Dataset #:	1
Motif ID:	30
Motif name:	C030
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	18
Similarity score:	0.032013

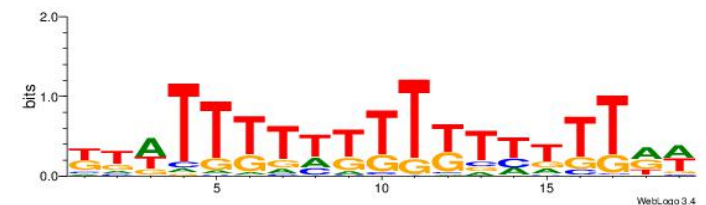
Alignment:

WYAAAAAMAAAAAAWAM
-WRMARYAAMARYAAMAWH

Original motif Consensus sequence: WYAAAAAMAAAAAAAWAM



Reverse complement motif Consensus sequence:
YTWTTTTTTTTYTTTTMW



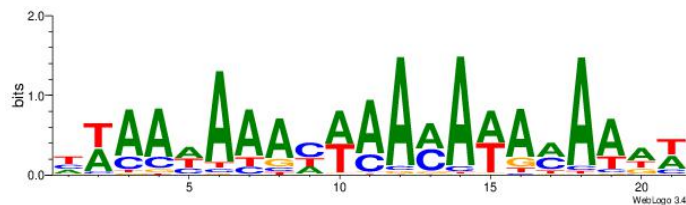
Dataset #: 1

Motif ID: 16
 Motif name: C016
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 18
 Similarity score: 0.0342459

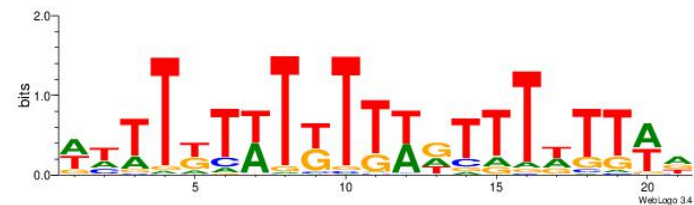
Alignment:

HWAAWAAAHWAAMAWAMAAWW
 ---WRMARYAAMARYAAMAWH

Original motif Consensus sequence: HWAAWAAAHWAAMAWAMAAWW



Reverse complement motif Consensus sequence: WWTYYTWYTTWDTTWTTH

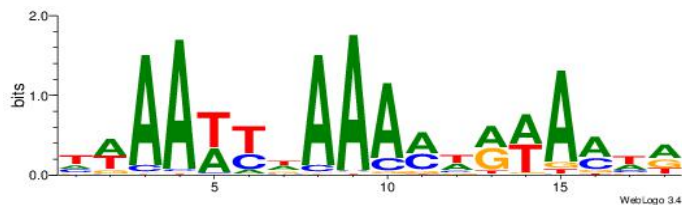


Dataset #: 1
 Motif ID: 32
 Motif name: C032
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 18

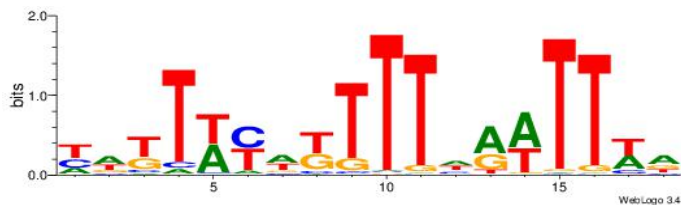
Similarity score: 0.0370038

Alignment:
HWAAWYDAAAMWRWAMWR
WRMARYAAMARYAAMAWH

Original motif Consensus sequence: HWAAWYDAAAMWRWAMWR

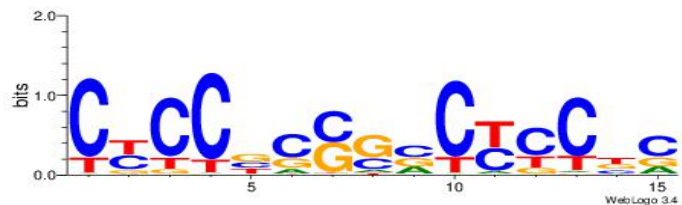


Reverse complement motif Consensus sequence: KWYTWKWYTTTDMWTTWH

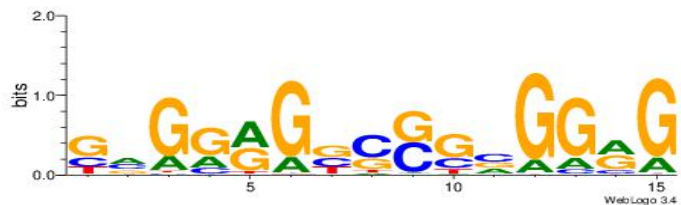


Dataset #: 1 Motif ID: 58 Motif name: C058

Original motif Consensus sequence: CYCCBCSGVCYCCBC



Reverse complement motif Consensus sequence: GVGGMGVCSGBGGMG



Best Matches for Motif ID 58 (Highest to Lowest)

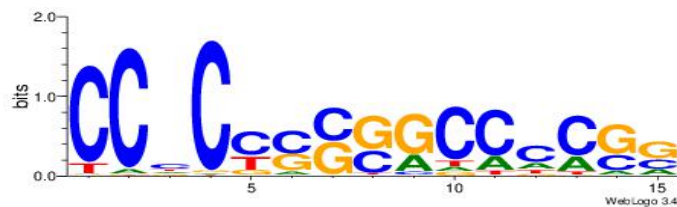
Dataset #:	1
Motif ID:	112
Motif name:	C112
Matching format of first motif:	Original Motif

Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	15
Similarity score:	0.0133513

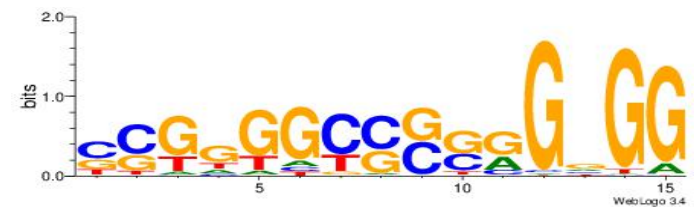
Alignment:

```
CCBCYSSSGCCCCSS
CYCCBCSGVCYCCBC
```

Original motif Consensus sequence: CCBCYSSSGCCCCSS



Reverse complement motif Consensus sequence: SSGGGGCSSSKGBGG

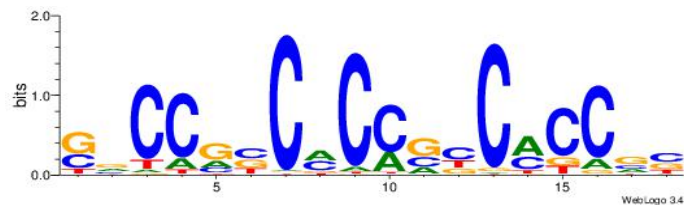


Dataset #:	1
Motif ID:	37
Motif name:	C037
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	4
Number of overlap:	15
Similarity score:	0.0170428

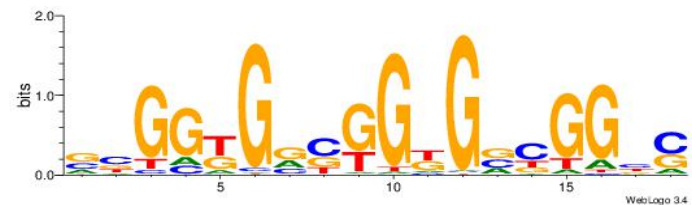
Alignment:

BVGGYGKSGGYGBCGGVS
GVGGMGVCSGBGGMG---

Original motif Consensus sequence: SVCCGBCMCCSYCMCCVB



Reverse complement motif Consensus sequence:
BVGGYGKSGGYGBCGGVS

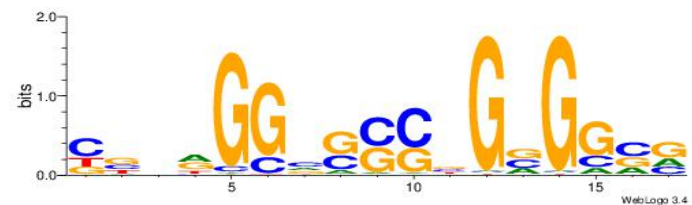
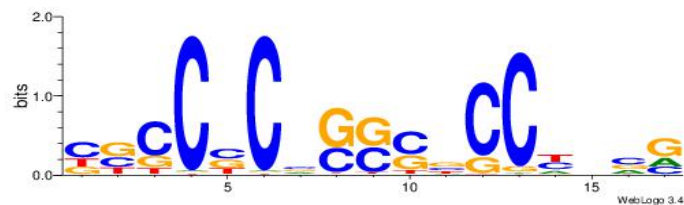


Dataset #: 1
Motif ID: 140
Motif name: C140
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 15
Similarity score: 0.0187263

Alignment:
BSCCBVSSSBCCYHVG
CYCCBCSGVCYCCBC--

Original motif Consensus sequence: BSCCBVSSSBCCYHVG

Reverse complement motif Consensus sequence:
CVDMGGBSSSVGBGGSB

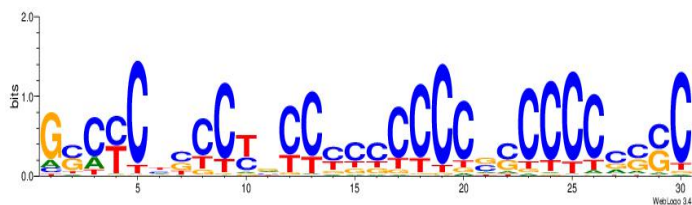


Dataset #: 1
 Motif ID: 3
 Motif name: C003
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 14
 Number of overlap: 15
 Similarity score: 0.0189191

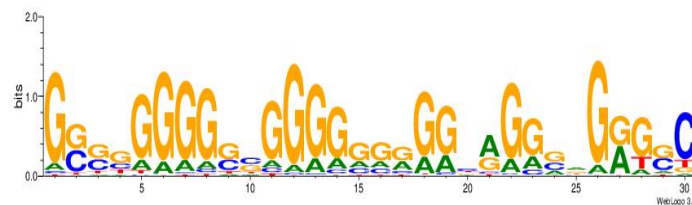
Alignment:

GSCYCHSCCYVCCYCCCCCSCCCCCSSC
 -----CYCCBCSGVCYCCBC--

Original motif Consensus sequence:
 GSCYCHSCCYVCCYCCCCCSCCCCCSSC



Reverse complement motif Consensus sequence:
 GSSGGGGGSSGGGGGKGGVMGGSHGKGC



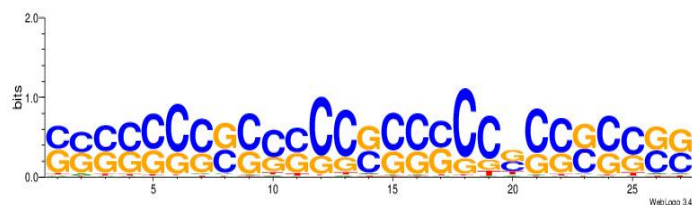
Dataset #: 1

Motif ID: 4
 Motif name: C004
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 4
 Number of overlap: 15
 Similarity score: 0.0189308

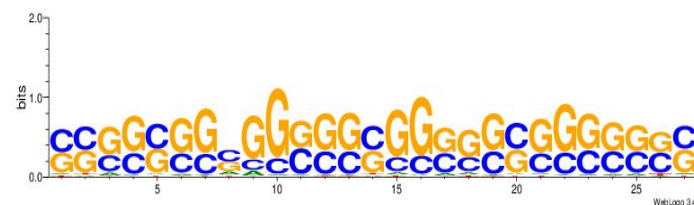
Alignment:

SSSSSCSSSSSCSSSSCCSCSSSSSS
 -----CYCCBCSGVCYCCBC---

Original motif Consensus sequence:
 SSSSSCSSSSSCSSSSCCSCSSSSSS

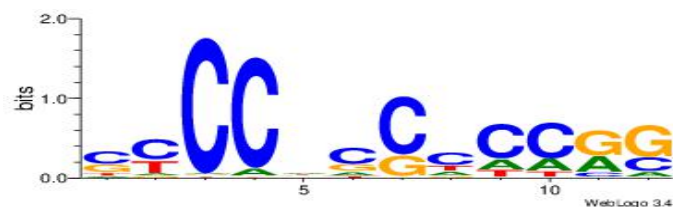


Reverse complement motif Consensus sequence:
 SSSSSSGSGGSSSSSGSSSSSGSSSSS

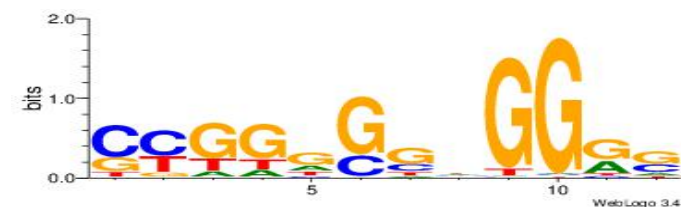


Dataset #: 1 Motif ID: 59 Motif name: C059

Original motif Consensus sequence: SYCCDCCCCCRG



Reverse complement motif Consensus sequence: CMGGGGGDGGKS



Best Matches for Motif ID 59 (Highest to Lowest)

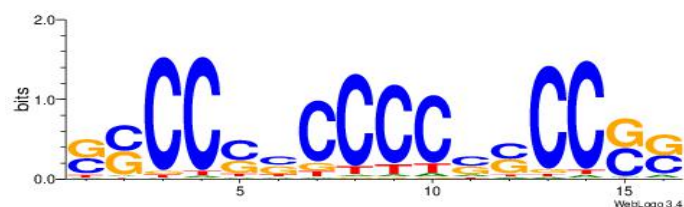
Dataset #: 1
Motif ID: 8
Motif name: C008
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 12
Similarity score: 0.0187581

Alignment:

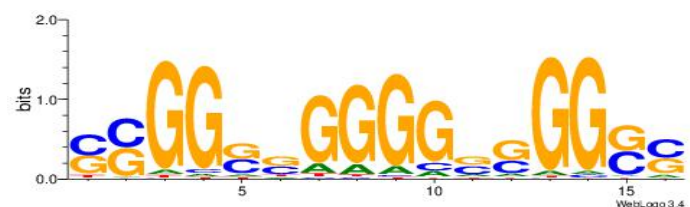
SSCCSSCCCCSSCCSS

SYCCDCCCCCRG----

Original motif Consensus sequence: SSCCSSCCCCSSCCSS



Reverse complement motif Consensus sequence: SSGGSSGGGGSSGGSS

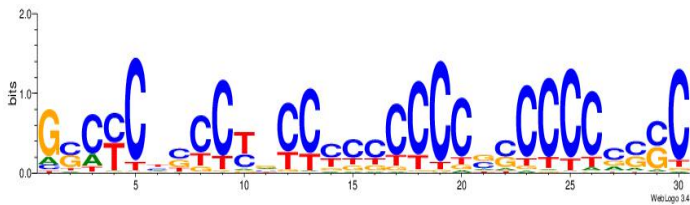


Dataset #: 1
Motif ID: 3
Motif name: C003
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif

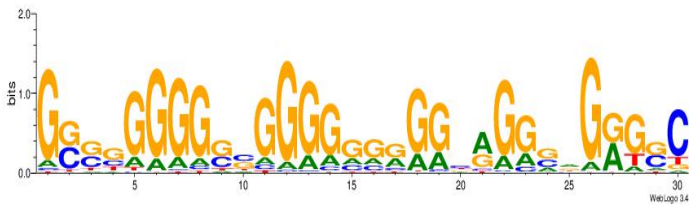
Direction: Backward
Position number: 3
Number of overlap: 12
Similarity score: 0.0189659

Alignment:
GSCYCHSCCYVCCYCCCCCSCCCCCSSC
-----SYCCDCCCCCRG--

Original motif Consensus sequence:
GSCYCHSCCYVCCYCCCCCSCCCCCSSC



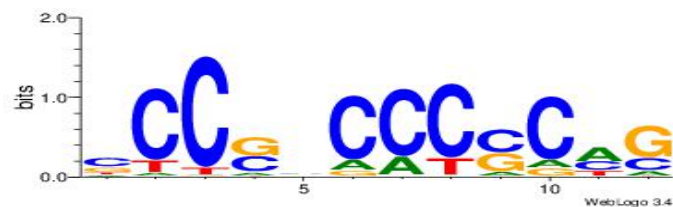
Reverse complement motif Consensus sequence:
GSSGGGGSSGGGGGKGGVMGGSHGKGSC



Dataset #: 1
Motif ID: 81
Motif name: C081
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: 0.0197846

Alignment:
CYGSGGGHSGGB
CMGGGGGDGGKS

Original motif Consensus sequence: BCCSHCCCSCMG



Reverse complement motif Consensus sequence: CYGSGGGHSGGB

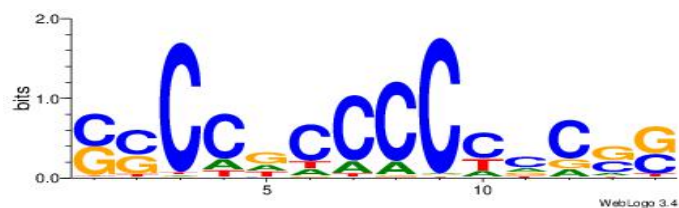


Dataset #: 1
Motif ID: 54
Motif name: C054
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 3
Number of overlap: 12
Similarity score: 0.0243956

Alignment:

SSCCDCCCCCCCSS
SYCCDCCCCCRG--

Original motif Consensus sequence: SSCCDCCCCCCCSS



Reverse complement motif Consensus sequence: SSGGGGGGGHGG

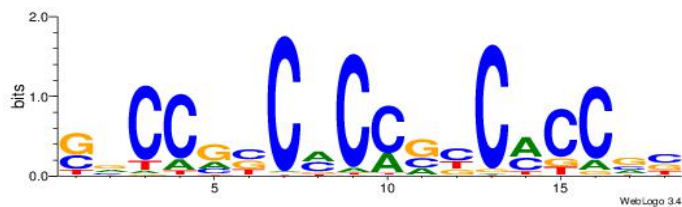


Dataset #: 1
 Motif ID: 37
 Motif name: C037
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 7
 Number of overlap: 12
 Similarity score: 0.025237

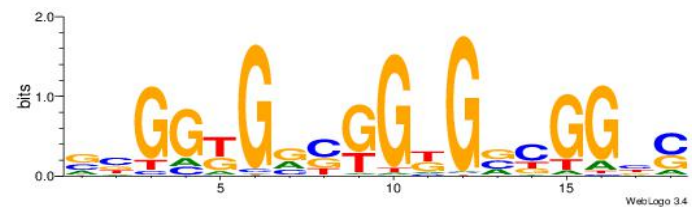
Alignment:

SVCCGBCMCCSYCMCCVB
 SYCCDCCCCCRG-----

Original motif Consensus sequence: SVCCGBCMCCSYCMCCVB



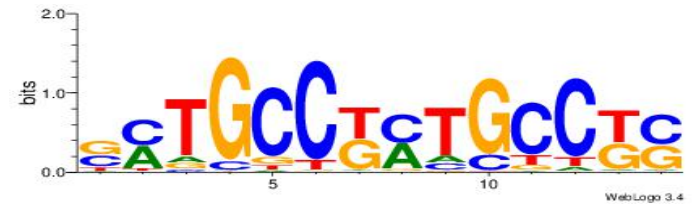
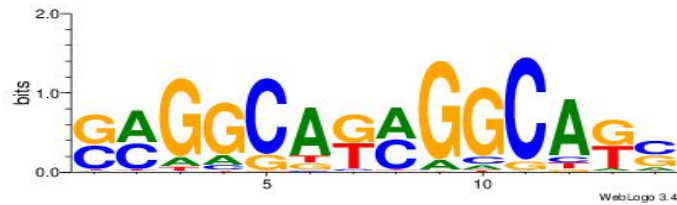
Reverse complement motif Consensus sequence: BVGGYGKSGGYGBCGGVS



Dataset #: 1 Motif ID: 60 Motif name: C060

Original motif Consensus sequence: SMGGCAKMGGCAKS

Reverse complement motif Consensus sequence: SYTGCCYYTGCCYS



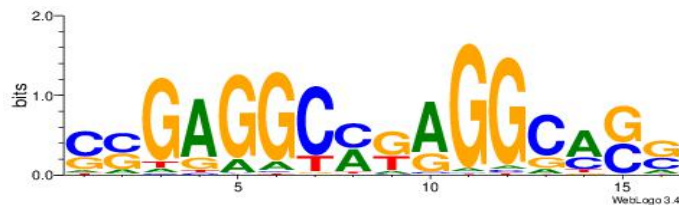
Best Matches for Motif ID 60 (Highest to Lowest)

Dataset #: 1
 Motif ID: 41
 Motif name: C041
 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: 0.0270843

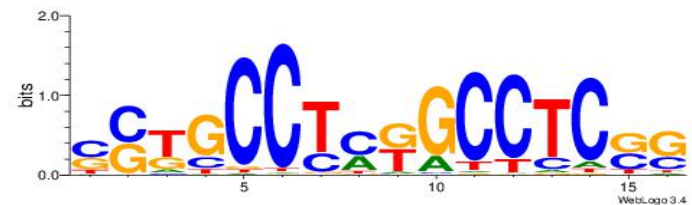
Alignment:

CSGAGGCMKAGGCASS
 --SMGGCAKMGGCAKS

Original motif Consensus sequence: CSGAGGCMKAGGCASS



Reverse complement motif Consensus sequence: SSTGCCTYRGCTCSG

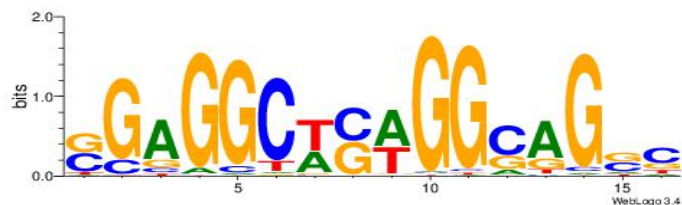


Dataset #: 1
 Motif ID: 48
 Motif name: C048
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 14
 Similarity score: 0.0323426

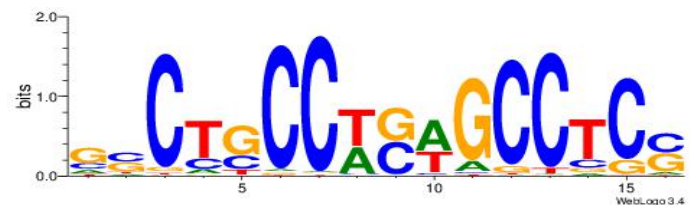
Alignment:

GSCTGCCWSWGCCTCS
 -SYTGCCYYTGCCYS-

Original motif Consensus sequence: SGAGGCWSWGGCAGSC



Reverse complement motif Consensus sequence: GSCTGCCWSWGCCTCS

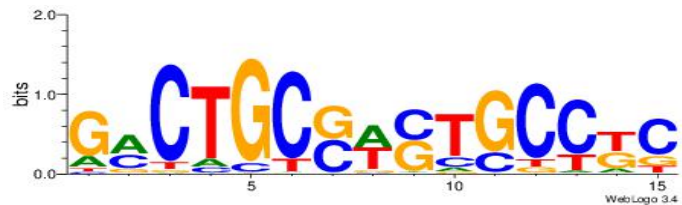


Dataset #: 1
 Motif ID: 118
 Motif name: C118
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1

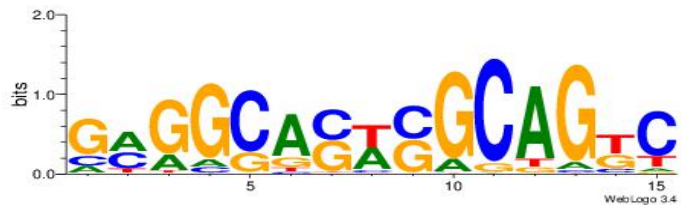
Number of overlap: 14
Similarity score: 0.0327086

Alignment:
GMCTGCSWSTGCCCKC
-SYTGCCYYTGCCYS

Original motif Consensus sequence: GMCTGCSWSTGCCCKC



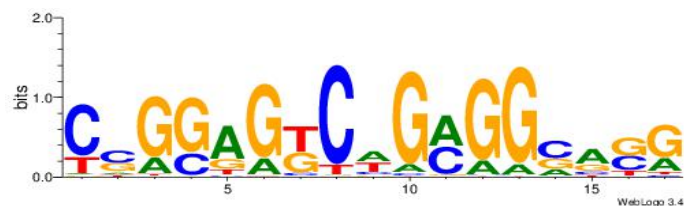
Reverse complement motif Consensus sequence: GRGGCASWSGCAGYC



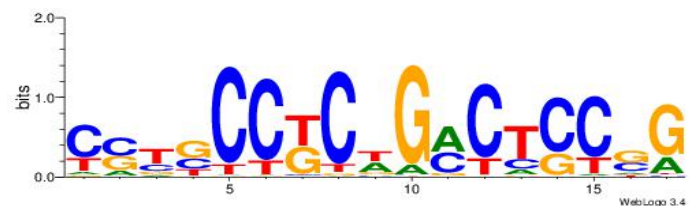
Dataset #: 1
Motif ID: 86
Motif name: C086
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 4
Number of overlap: 14
Similarity score: 0.0345156

Alignment:
CSGGAGK CWGMGGSASG
---SMGGCAKMGGCAKS

Original motif Consensus sequence: CSGGAGKCWGMGGSASG



Reverse complement motif Consensus sequence: CSTSCCYCWGRCTCCSG

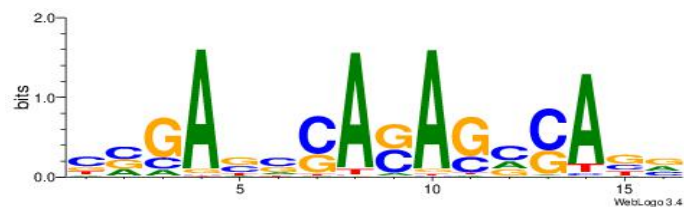


Dataset #: 1
Motif ID: 28
Motif name: C028
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 14
Similarity score: 0.0496439

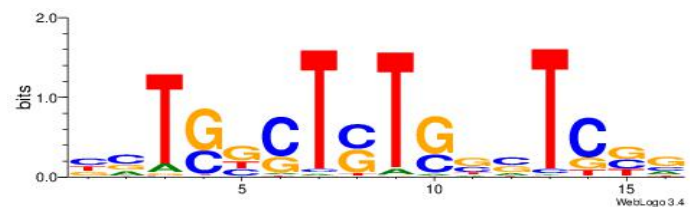
Alignment:

VBTSVCTSTGSSTCVB
SYTGCCYYTGCCYS--

Original motif Consensus sequence: BVGASSCASAGVSABV

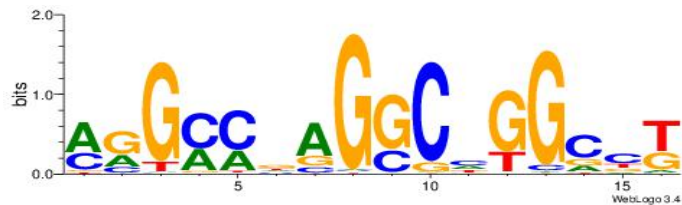


Reverse complement motif Consensus sequence: VBTSVCTSTGSSTCVB

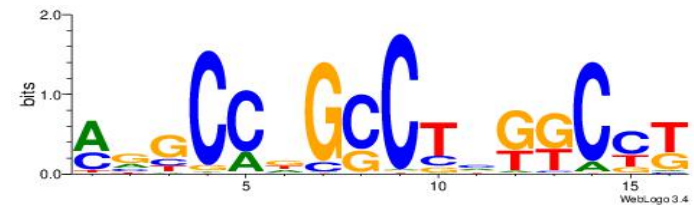


Dataset #: 1 Motif ID: 61 Motif name: C061

Original motif Consensus sequence: MRGMMBAGGCHGGCCK



Reverse complement motif Consensus sequence: RGGCCDGCCTBRRCMY



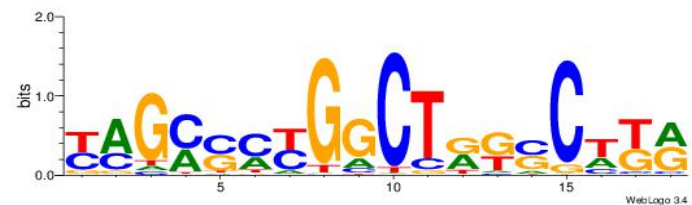
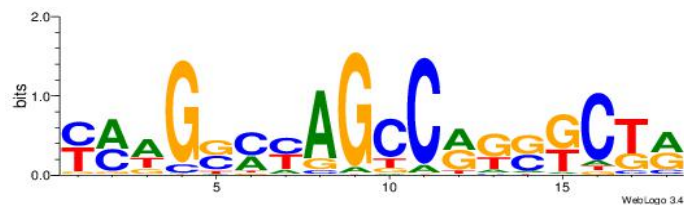
Best Matches for Motif ID 61 (Highest to Lowest)

Dataset #:	1
Motif ID:	73
Motif name:	C073
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	2
Number of overlap:	16
Similarity score:	0.0275681

Alignment:
KAGYSYKGGCTKRSCWYK
-RGGCCDGCCTBRRCMY-

Original motif Consensus sequence: YMWGSMYAGCCRKSKCTR

Reverse complement motif Consensus sequence: KAGYSYKGGCTKRSCWYK



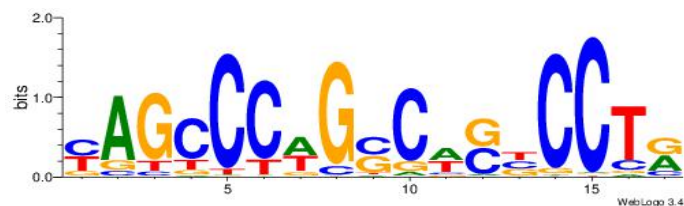
Dataset #: 1
 Motif ID: 122
 Motif name: C122
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 16
 Similarity score: 0.033106

Alignment:

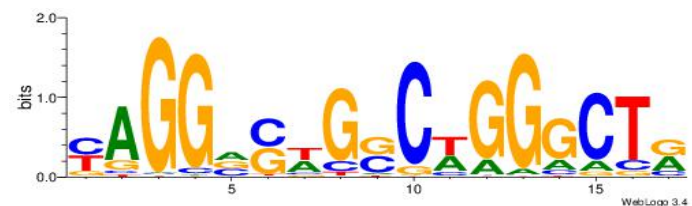
MAGGVSWGSCWGGGCTK

MRGMMBAGGCHGGCCK-

Original motif Consensus sequence: YAGCCCWGSCWSBCCTR



Reverse complement motif Consensus sequence: MAGGVSWGSCWGGGCTK



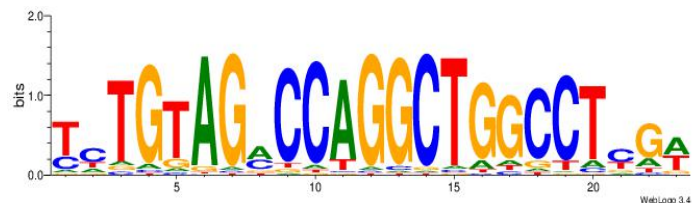
Dataset #: 1

Motif ID: 5
 Motif name: C005
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 4
 Number of overlap: 16
 Similarity score: 0.0398636

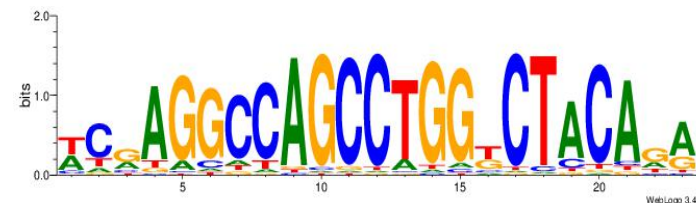
Alignment:

TCTGTAGMCCAGGCTGGCCTYGW
 ----MRGMMBAGGCHGGCCK----

Original motif Consensus sequence: TCTGTAGMCCAGGCTGGCCTYGW



Reverse complement motif Consensus sequence: WCKAGGCCAGCCTGGYCTACAGA

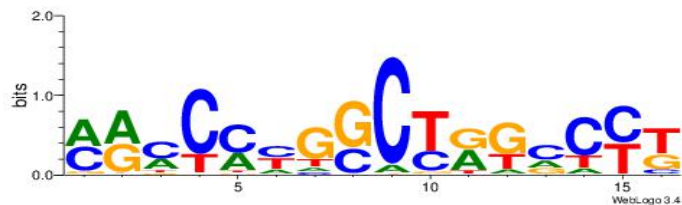


Dataset #: 1
 Motif ID: 96
 Motif name: C096
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 16

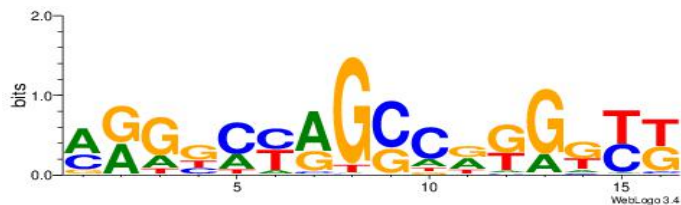
Similarity score: 0.0431269

Alignment:
MRMCMYGSCYRGCCYK
RGGCCDGCCTBRRCMY

Original motif Consensus sequence: MRMCMYGSCYRGCCYK



Reverse complement motif Consensus sequence: RKGGCMMGSCCKRGRKY

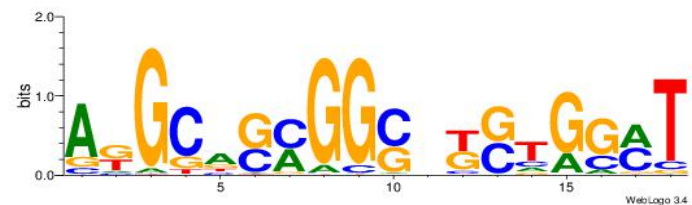
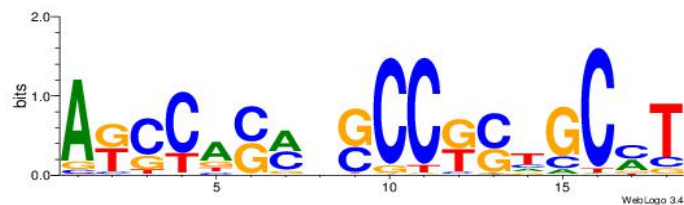


Dataset #: 1
Motif ID: 93
Motif name: C093
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 3
Number of overlap: 16
Similarity score: 0.0437797

Alignment:
AKCCASMBSCCKSTGCMT
--RGGCCDGCCTBRRCMY

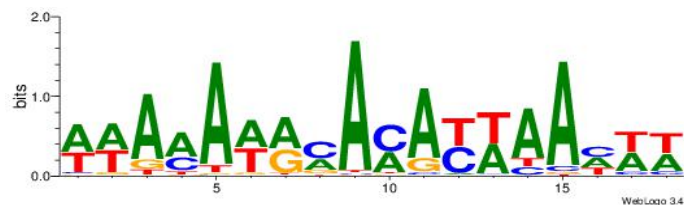
Original motif Consensus sequence: AKCCASMBSCCKSTGCMT

Reverse complement motif Consensus sequence: ARGCASYGGSVYSTGGYT

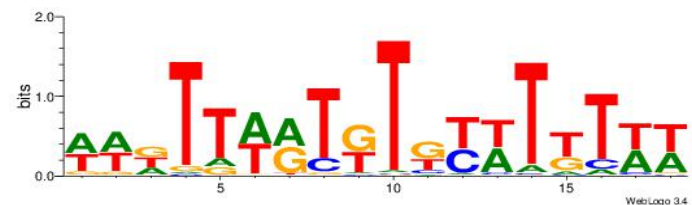


Dataset #: 1 Motif ID: 62 Motif name: C062

Original motif Consensus sequence: WWAMAWRMAMAYWAAHWW



Reverse complement motif Consensus sequence: WWDTTWMTRTRKWTYTTWW



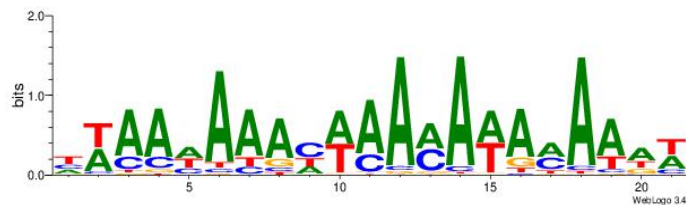
Best Matches for Motif ID 62 (Highest to Lowest)

Dataset #:	1
Motif ID:	16
Motif name:	C016
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:	0.0181545

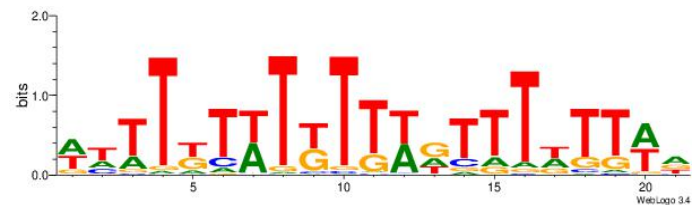
Alignment:

HWAAWAAAHWAAMAWAMAAWW
 ---WWAMAWRMAMAYWAAHWW

Original motif Consensus sequence: HWAAWAAAHWAAMAWAMAAWW



Reverse complement motif Consensus sequence: WWTYYTWYTTWDTTTWTTWH



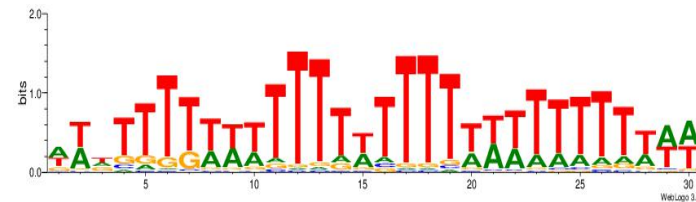
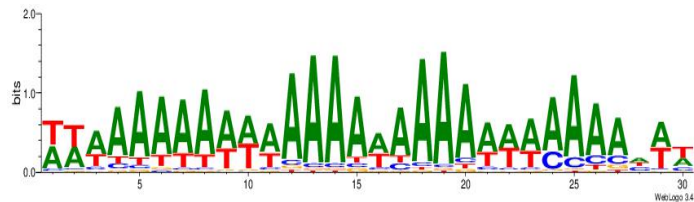
Dataset #:	1
Motif ID:	1
Motif name:	C001
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	9
Number of overlap:	18
Similarity score:	0.022296

Alignment:

WWAAAAAWWAAAAWAAAAWWAAAAHWW
 ----WWAMAWRMAMAYWAAHWW-----

Original motif Consensus sequence:
 WWWAAAAWWAAAAWAAAAWWAAAAHWW

Reverse complement motif Consensus sequence:
 WWHTTTTWWTTTTTWWTTTTTWWTTTTTWW

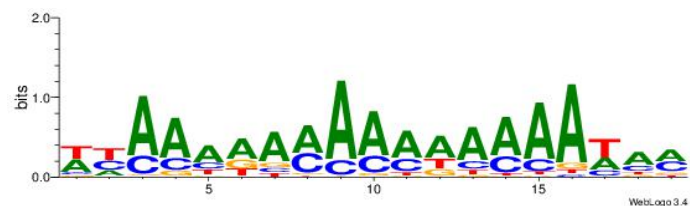


Dataset #: 1
 Motif ID: 30
 Motif name: C030
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 18
 Similarity score: 0.0268461

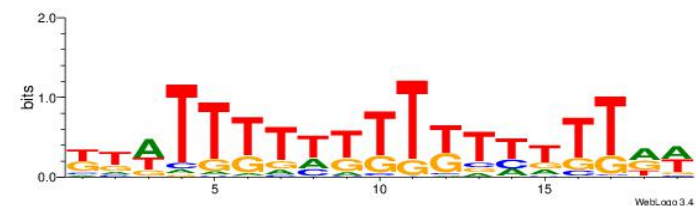
Alignment:

WYAAAAAMAAAAAAWAM
 WWAMAWRMAMAYWAAHWW-

Original motif Consensus sequence: WYAAAAAMAAAAAAWAM



Reverse complement motif Consensus sequence: YTWTTTTTTTTYTTTTMW



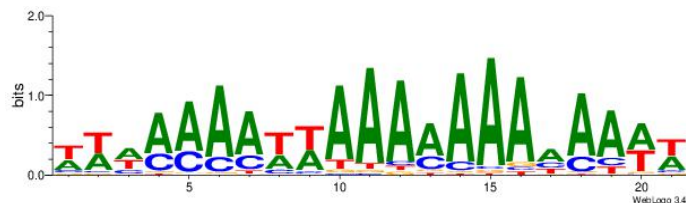
Dataset #: 1

Motif ID: 10
 Motif name: C010
 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: 0.0319895

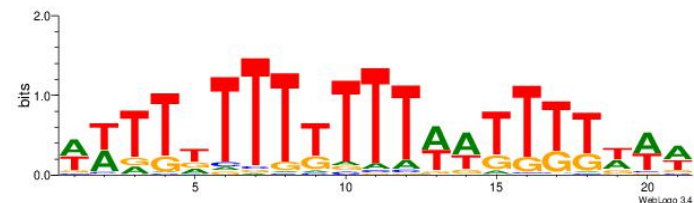
Alignment:

WWWAAAAWWAAAAAAAAAAWW
 ---WWAMAWRMAMAYWAAHWW

Original motif Consensus sequence: WWWAAAAWWAAAAAAAAAAWW



Reverse complement motif Consensus sequence: WWTTTTTTTTTTWWTTTTWWW

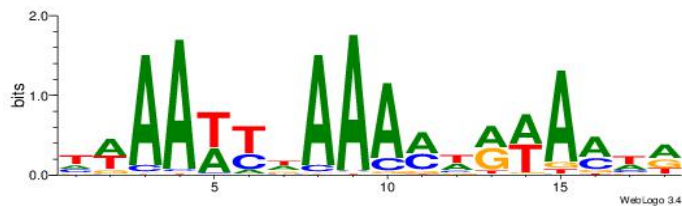


Dataset #: 1
 Motif ID: 32
 Motif name: C032
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 18

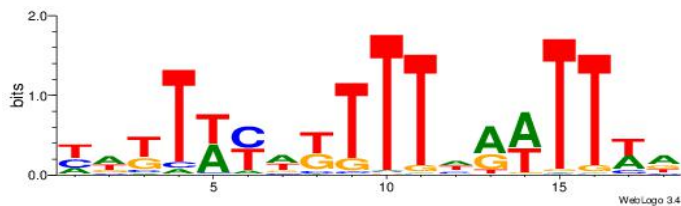
Similarity score: 0.0355184

Alignment:
HWAAWYDAAAMWRWAMWR
WWAMAWRMAMAYWAAHWW

Original motif Consensus sequence: HWAAWYDAAAMWRWAMWR

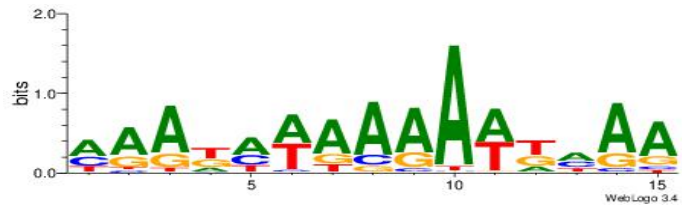


Reverse complement motif Consensus sequence: KWYTWKWYTTTDMWTTWH

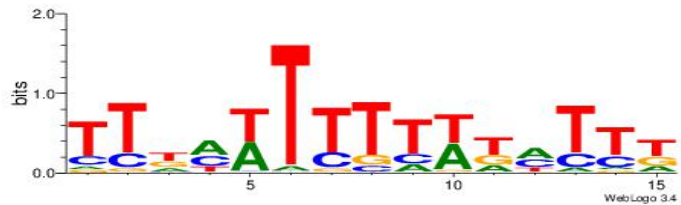


Dataset #: 1 Motif ID: 63 Motif name: C063

Original motif Consensus sequence: MAAKMWAAA WKHAA



Reverse complement motif Consensus sequence: TTHRWT TTTTWYRT



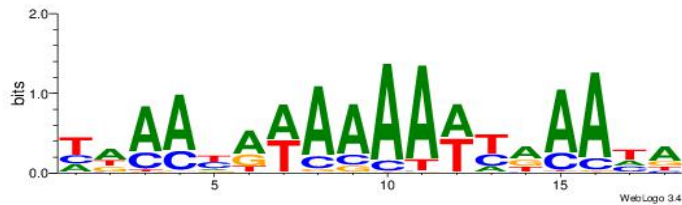
Best Matches for Motif ID 63 (Highest to Lowest)

Dataset #:	1
Motif ID:	24
Motif name:	C024
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement

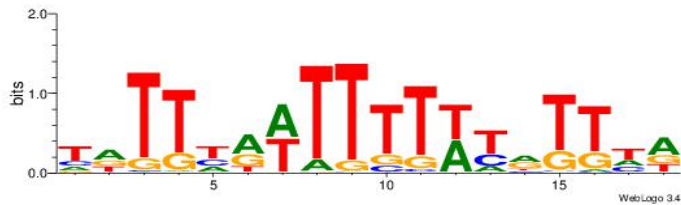
Direction: Forward
Position number: 3
Number of overlap: 15
Similarity score: 0.0248724

Alignment:
THTTDMWTTTTWKMTTDA
--TTHRWTTTTTWYRTTY-

Original motif Consensus sequence: TDAAYRWAAAAYDAAHA



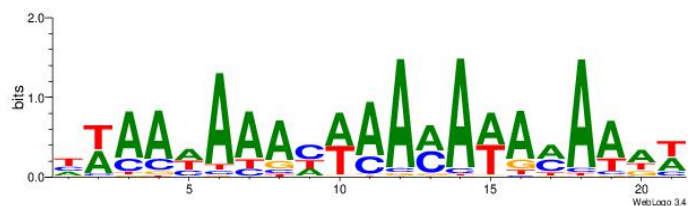
Reverse complement motif Consensus sequence: THTTDMWTTTTWKMTTDA



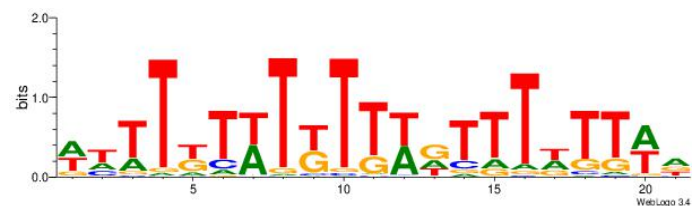
Dataset #: 1
Motif ID: 16
Motif name: C016
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 3
Number of overlap: 15
Similarity score: 0.0290274

Alignment:
HWAAWAAAHWAAMAWAMAAWW
----MAAKMWAAAANKHAA--

Original motif Consensus sequence: HWAAWAAHWAAMAWAMAAWW



Reverse complement motif Consensus sequence: WWTYYTWYTTWDTTTWTTWH

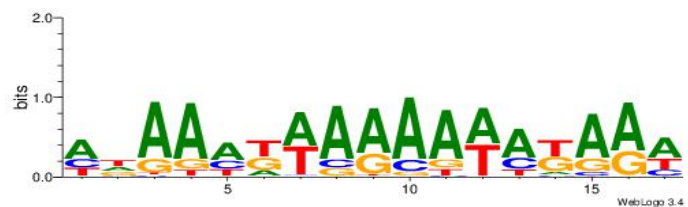


Dataset #: 1
Motif ID: 79
Motif name: C079
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 3
Number of overlap: 15
Similarity score: 0.0322494

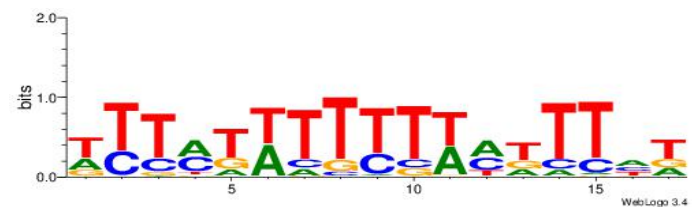
Alignment:

WKTRTWTTTTWRTTTDT
--TTHRWTWWWYRTTY

Original motif Consensus sequence: ADAAKWAAAAWAKARW



Reverse complement motif Consensus sequence: WKTRTWTTTTWRTTTDT

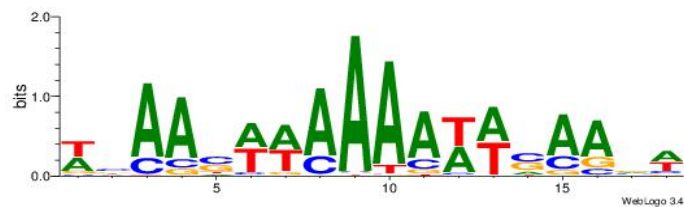


Dataset #: 1
 Motif ID: 97
 Motif name: C097
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 15
 Similarity score: 0.0331992

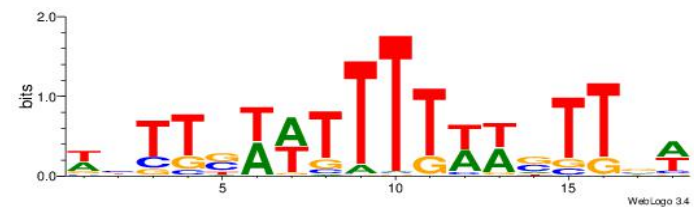
Alignment:

WBAASWWAAA WWSAAVW
 -MAAKMWAAA WKHAA--

Original motif Consensus sequence: WBAASWWAAA WWSAAVW



Reverse complement motif Consensus sequence: WTTTSWTTT TWWSTTBW

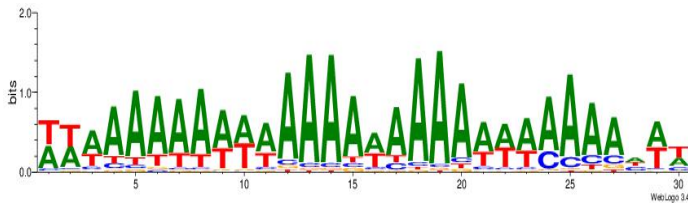


Dataset #: 1
 Motif ID: 1
 Motif name: C001
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 5

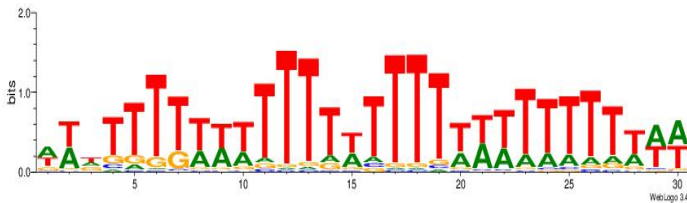
Number of overlap: 15
Similarity score: 0.0352734

Alignment:
WWAAAAAWAAAAWAAAAWAAAAHWW
----MAAKMWAAAAWKHAA-----

Original motif Consensus sequence:
WWAAAAAWAAAAWAAAAWAAAAHWW

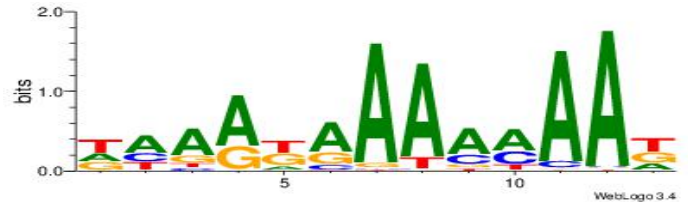


Reverse complement motif Consensus sequence:
WWHTTTTWTTTWTTTTWWTTTWW

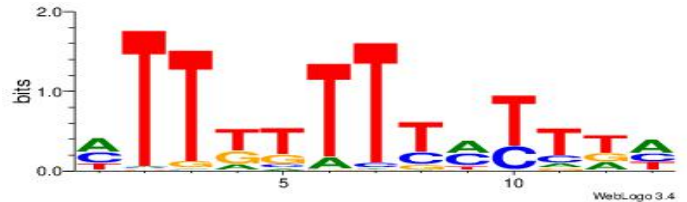


Dataset #: 1 Motif ID: 64 Motif name: C064

Original motif Consensus sequence: DAAKAAAAMAAK



Reverse complement motif Consensus sequence: RTTYTTTTRTTD



Best Matches for Motif ID 64 (Highest to Lowest)

Dataset #: 1
Motif ID: 131
Motif name: C131
Matching format of first motif: Original Motif

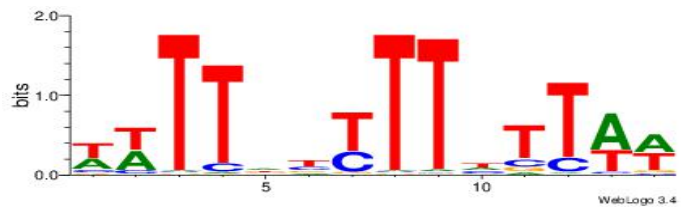
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2
Number of overlap: 13
Similarity score: 0.029048

Alignment:
WWAADAARVHAAWW
DAAAKAAAAMAAK-

Original motif Consensus sequence: WWAADAARVHAAWW



Reverse complement motif Consensus sequence: WWTTHBKTTDTTV

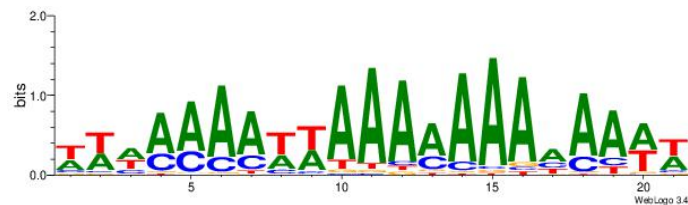


Dataset #: 1
Motif ID: 10
Motif name: C010
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 8
Number of overlap: 13
Similarity score: 0.0335106

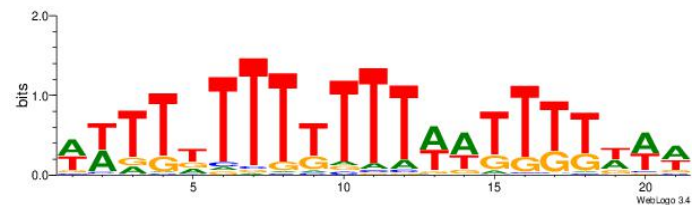
Alignment:

WWWAAAWWAAAAAAAAAAWW
 -----DAAAKAAAAMAAK-

Original motif Consensus sequence: WWWAAAWWAAAAAAAAAAWW



Reverse complement motif Consensus sequence: WWTTTTTTTTTTWWTTTTWWW



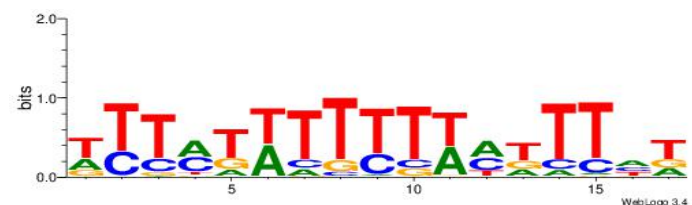
Dataset #:	1
Motif ID:	79
Motif name:	C079
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	4
Number of overlap:	13
Similarity score:	0.037939

Alignment:

WKTRTWTTTTWRTTTDT
 ---RTTYTTTTTRTTTD-

Original motif Consensus sequence: ADAAKWAAAAWAKARW

Reverse complement motif Consensus sequence:
 WKTRTWTTTTWRTTTDT



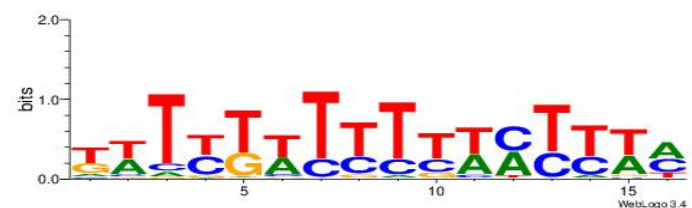
Dataset #:	1
Motif ID:	152
Motif name:	C152
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	4
Number of overlap:	13
Similarity score:	0.0379551

Alignment:

```
KWRRKWRARAWMRAWM
DAAAKAAAAMAAK---
```

Original motif Consensus sequence: KWRRKWRARAWMRAWM

Reverse complement motif Consensus sequence:
YWTKYWTKTKWYKKWR



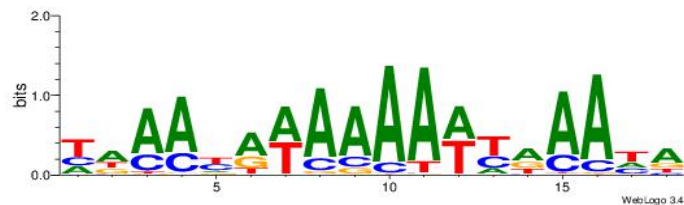
Dataset #: 1

Motif ID: 24
 Motif name: C024
 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: 0.0419927

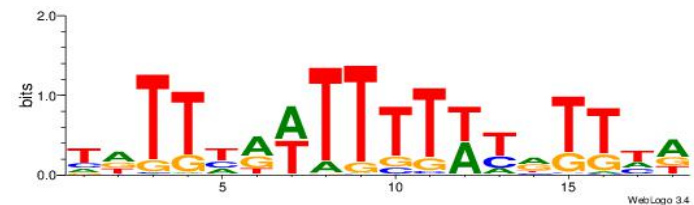
Alignment:

TDAAYRWAAAAYDAAHA
 DAAAKAAAAMAAK-----

Original motif Consensus sequence: TDAAYRWAAAAYDAAHA



Reverse complement motif Consensus sequence: THTTDMWTTTTWKMTTDA



Dataset #: 1 Motif ID: 65 Motif name: C065

Original motif Consensus sequence: MSTGAGWTCMASK



Reverse complement motif Consensus sequence: YSTRGAWCTCASR



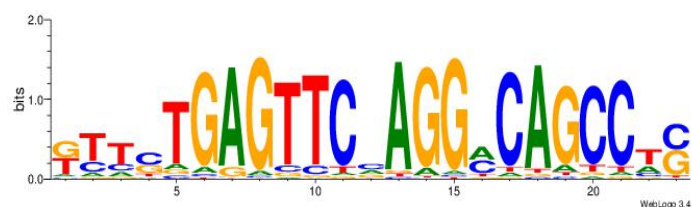
Best Matches for Motif ID 65 (Highest to Lowest)

Dataset #: 1
Motif ID: 7
Motif name: C007
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 9
Number of overlap: 13
Similarity score: 0.00190829

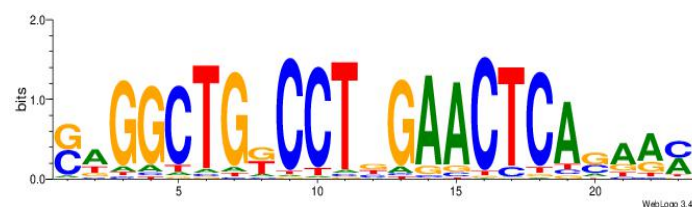
Alignment:

```
SAGGCTGYCCTVGAAGTCASAAY  
-----YSTRGAWCTCASR--
```

Original motif Consensus sequence: KTTSTGAGTTCVAGGMCAGCCTS



Reverse complement motif Consensus sequence: SAGGCTGYCCTVGAAGTCASAAY

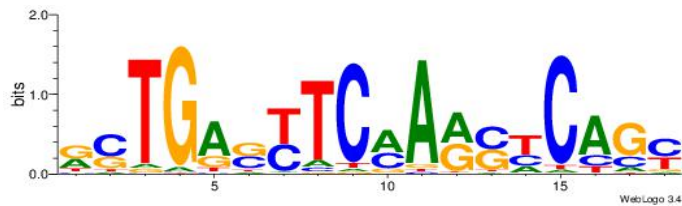


Dataset #: 1
Motif ID: 40
Motif name: C040
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif

Direction: Backward
Position number: 6
Number of overlap: 13
Similarity score: 0.0036319

Alignment:
RSTGASYTCMARSYCAGY
MSTGAGWTCMASK-----

Original motif Consensus sequence: RSTGASYTCMARSYCAGY



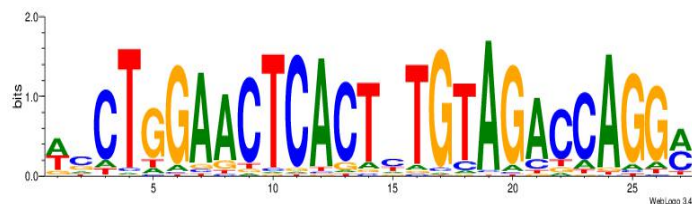
Reverse complement motif Consensus sequence: KCTGMSKTYGAMSTCASM



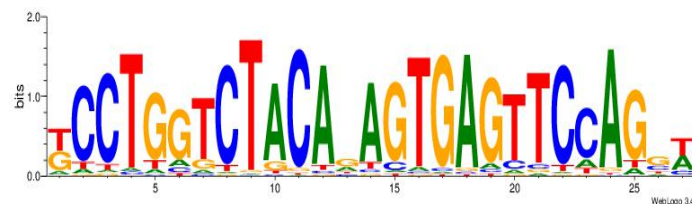
Dataset #: 1
Motif ID: 13
Motif name: C013
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 14
Number of overlap: 13
Similarity score: 0.0058849

Alignment:
WVCTGGAAC TCACTHTGTAGACCAGGM
-----YSTRGAWCTCASR-

Original motif Consensus sequence:
WVCTGGAAC TCACTHTGTAGACCAGGM



Reverse complement motif Consensus sequence:
YCCTGGTCTACADAGTGAGTTCCAGVW

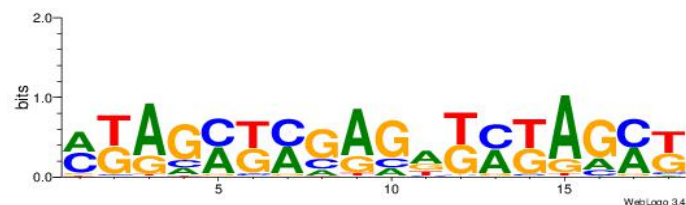


Dataset #: 1
Motif ID: 36
Motif name: C036
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 5
Number of overlap: 13
Similarity score: 0.0245754

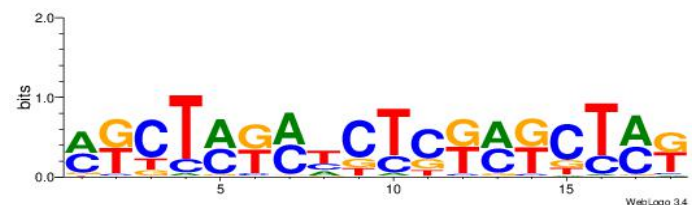
Alignment:

RRCTRRRTCTCRRRCTRY
-YSTRGAWCTCASR-----

Original motif Consensus sequence: MKAGMKMGAGAKMKAGMK



Reverse complement motif Consensus sequence:
RRCTRRRTCTCRRRCTRY

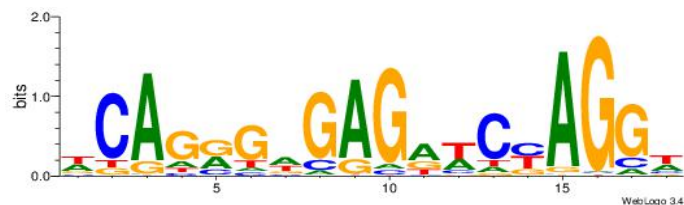


Dataset #: 1
 Motif ID: 132
 Motif name: C132
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 5
 Number of overlap: 13
 Similarity score: 0.0272182

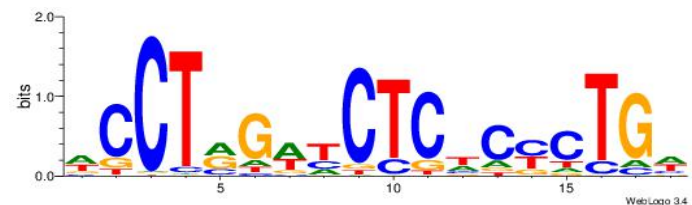
Alignment:

WCAGRGWGAGAWCYAGGW
 ----MSTGAGWTCMASK-

Original motif Consensus sequence: WCAGRGWGAGAWCYAGGW



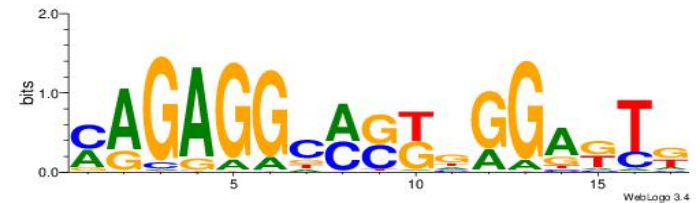
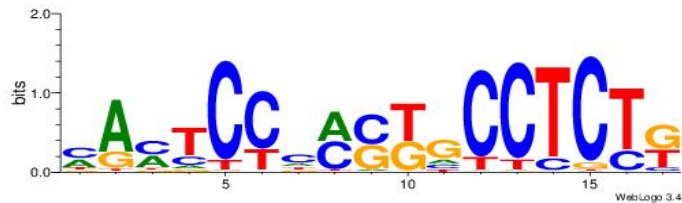
Reverse complement motif Consensus sequence: WCCTKGWTCTCWCMTGW



Dataset #: 1 Motif ID: 66 Motif name: C066

Original motif Consensus sequence: MAMTCCCMSKGCCTCTK

Reverse complement motif Consensus sequence: YAGAGGCRSYGGGARTR



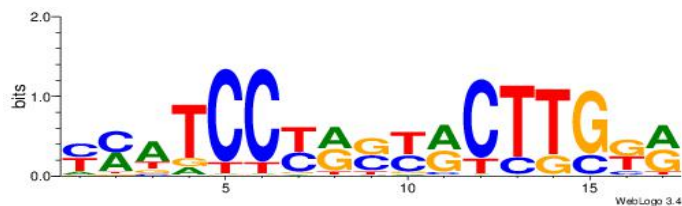
Best Matches for Motif ID 66 (Highest to Lowest)

Dataset #: 1
 Motif ID: 141
 Motif name: C141
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 17
 Similarity score: 0.0307474

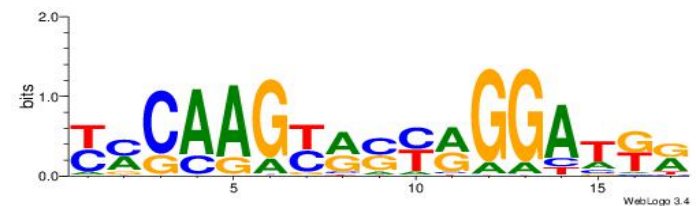
Alignment:

YMATCCYRSYRCTTGKR
 MAMTCCCMSKGCCTCTK

Original motif Consensus sequence: YMATCCYRSYRCTTGKR



Reverse complement motif Consensus sequence: KYCAAGKMSKMGGATRK

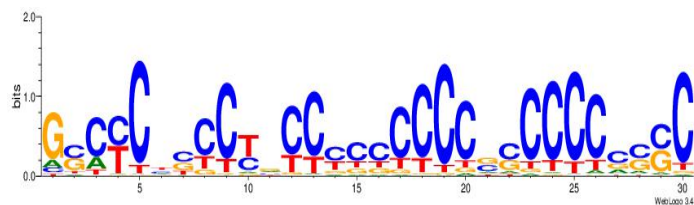


Dataset #: 1
 Motif ID: 3
 Motif name: C003
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 14
 Number of overlap: 17
 Similarity score: 0.0380115

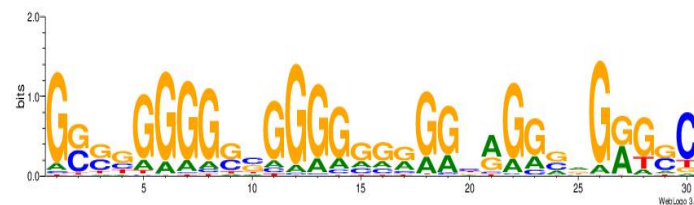
Alignment:

GSCYCHSCCYVCCYCCCCCSCCCCCSSC
 MAMTCCCMSKGCCTCTK-----

Original motif Consensus sequence:
 GSCYCHSCCYVCCYCCCCCSCCCCCSSC



Reverse complement motif Consensus sequence:
 GSSGGGGGSSGGGGGKGGVMGGSHGKGSC



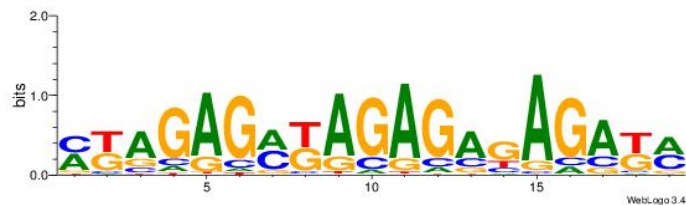
Dataset #: 1
 Motif ID: 12
 Motif name: C012
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2

Number of overlap: 17
Similarity score: 0.0393707

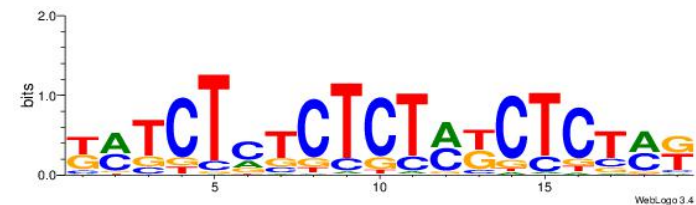
Alignment:

MKAGAGMKAGAGAGAGAKM
-YAGAGGCRSYGGGARTR-

Original motif Consensus sequence: MKAGAGMKAGAGAGAGAKM



Reverse complement motif Consensus sequence: YRTCTCTCTRYCTCTRR

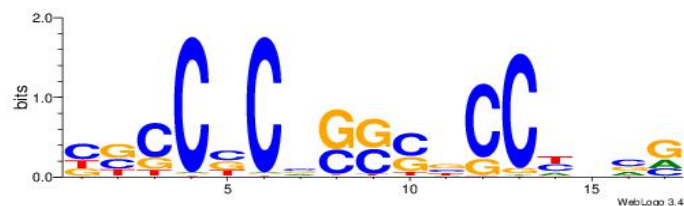


Dataset #: 1
Motif ID: 140
Motif name: C140
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 17
Similarity score: 0.04398

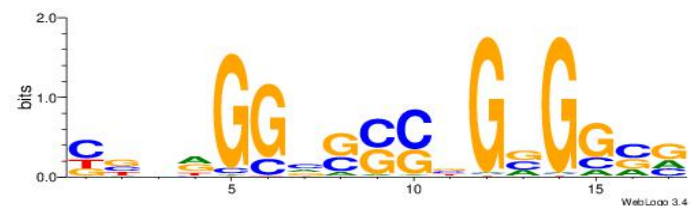
Alignment:

CVDMGGBSSSVGBGGSB
YAGAGGCRSYGGGARTR

Original motif Consensus sequence: BSCCBVCVSSSBCCYHVG



Reverse complement motif Consensus sequence: CVDMGGBSSSVGBGGSB

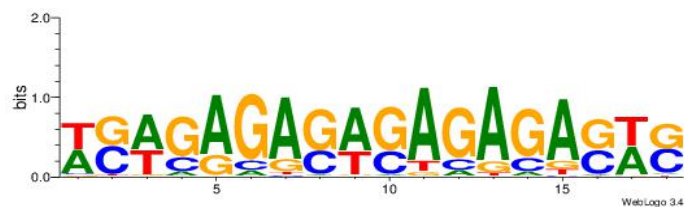


Dataset #: 1
 Motif ID: 17
 Motif name: C017
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 17
 Similarity score: 0.045244

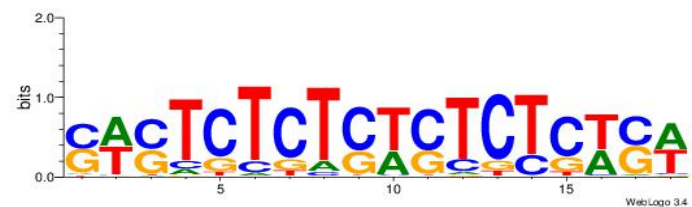
Alignment:

WSWGAGASWSAGAGASWS
 YAGAGGCRSYGGGARTR-

Original motif Consensus sequence: WSWGAGASWSAGAGASWS

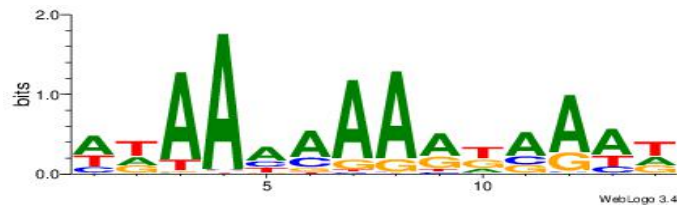


Reverse complement motif Consensus sequence: SWSTCTCTSWSTCTCWSW

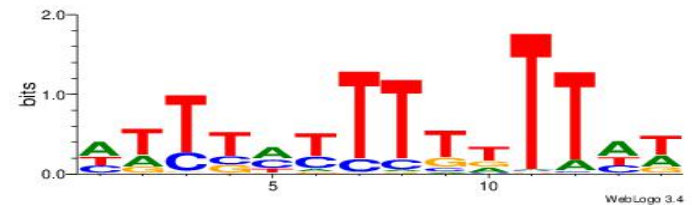


Dataset #: 1 **Motif ID: 67** **Motif name: C067**

Original motif Consensus sequence: WDAAAAARKAAAD



Reverse complement motif Consensus sequence: DTTTRKTTTTTTD



Best Matches for Motif ID 67 (Highest to Lowest)

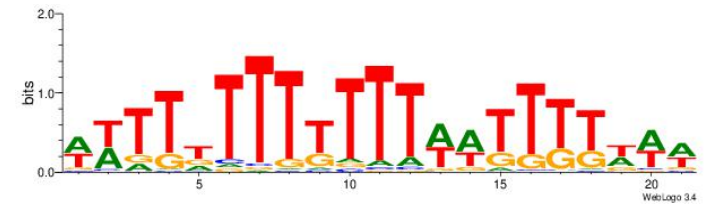
Dataset #:	1
Motif ID:	10
Motif name:	C010
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	8
Number of overlap:	14
Similarity score:	0.00893335

Alignment:

```
WWWAAAAWWAAAAAAAAAAWW
-----WDAAAAARKAAAD
```

Original motif Consensus sequence: WWWAAAAWWAAAAAAAAAAWW

Reverse complement motif Consensus sequence:
WWTTTTTTTTTTWWTTTTWWW



Alignment:

```
WWAAWAAAAAARAATW
-WDAAAAAARKAAAD-
```

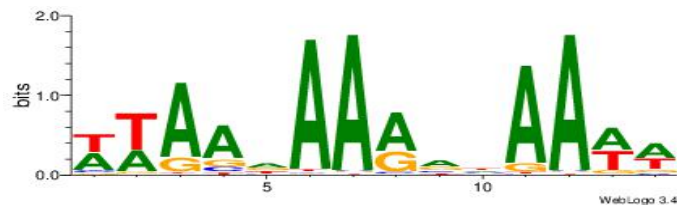
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Motif ID: 131
 Motif name: C131
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0.0175601

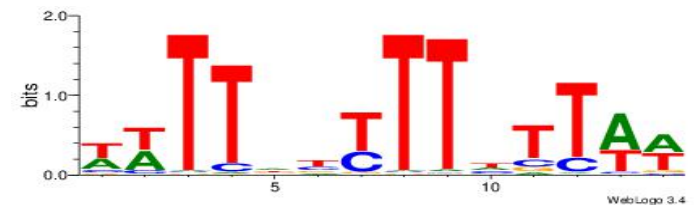
Alignment:

WWAADAARVHAAWW
 WDAAAAAARKAAAD

Original motif Consensus sequence: WWAADAARVHAAWW



Reverse complement motif Consensus sequence: WWTTHBKTTDTTV

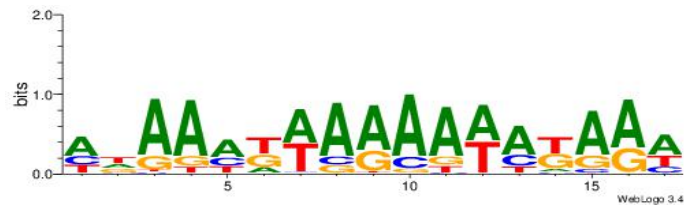


Dataset #: 1
 Motif ID: 79
 Motif name: C079
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0.0230592

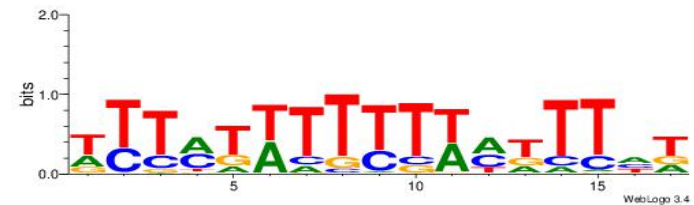
Alignment:

ADAAAKWAAAAWAKARW
WDAAAAAARKAAAD---

Original motif Consensus sequence: ADAAAKWAAAAWAKARW



Reverse complement motif Consensus sequence:
WKTRTWTTTTWRTTDT



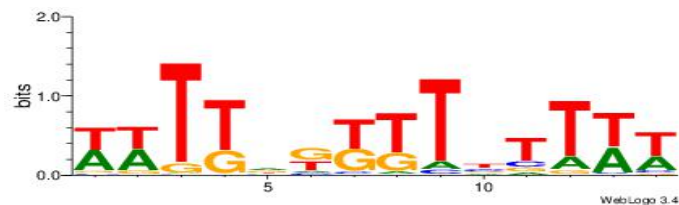
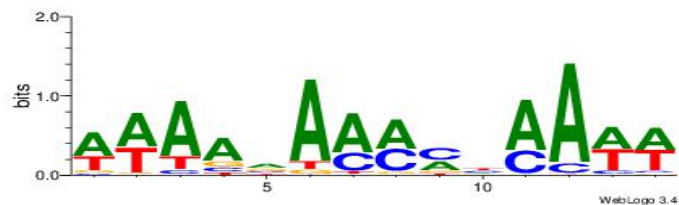
Dataset #:	1
Motif ID:	80
Motif name:	C080
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	14
Similarity score:	0.023743

Alignment:

WWAAVAAMMHAAWW
WDAAAAAARKAAAD

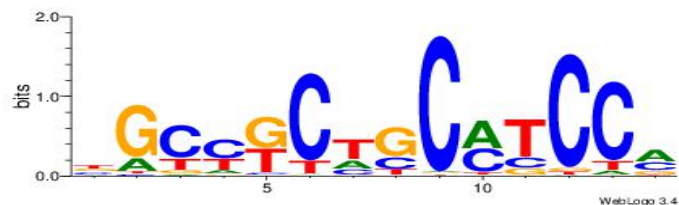
Original motif Consensus sequence: WWAAVAAMMHAAWW

Reverse complement motif Consensus sequence: WWTTHRYTTBTTW

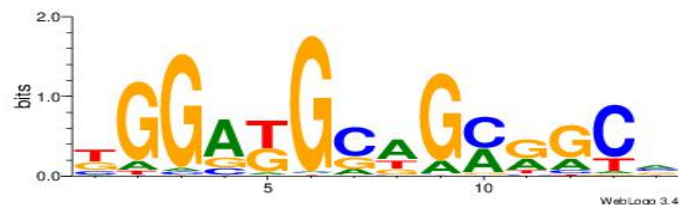


Dataset #: 1 Motif ID: 68 Motif name: C068

Original motif Consensus sequence: BGCYKCTGCMTCCM



Reverse complement motif Consensus sequence: YGGAYGCAGYKGC

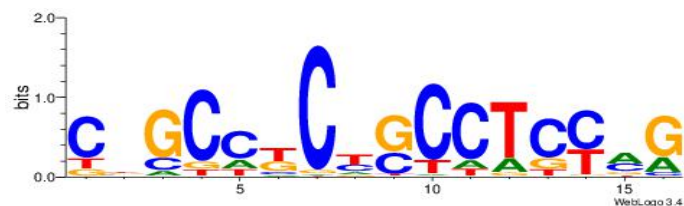


Best Matches for Motif ID 68 (Highest to Lowest)

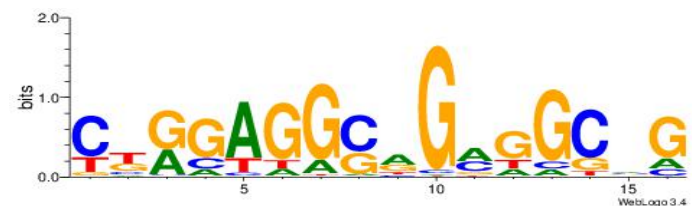
Dataset #:	1
Motif ID:	50
Motif name:	C050
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2
Number of overlap:	14
Similarity score:	0

Alignment:
 CBGCCCKCYSCCTCYMG
 -BGCYKCTGCMTCCM-

Original motif Consensus sequence: CBGCCCKCYSCCTCYMG



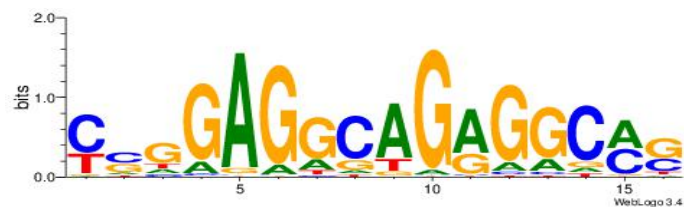
Reverse complement motif Consensus sequence: CYKGAGGSMGRGGCVG



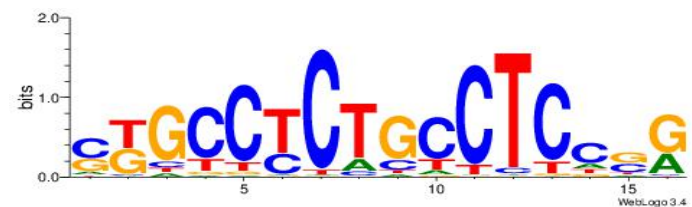
Dataset #: 1
 Motif ID: 14
 Motif name: C014
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 14
 Similarity score: 0.0156792

Alignment:
 YSGGAGGCAGAGGCMS
 -YGGAYGCAGYKGCV-

Original motif Consensus sequence: YSGGAGGCAGAGGCMS



Reverse complement motif Consensus sequence: SYGCCTCTGCCTCCSK

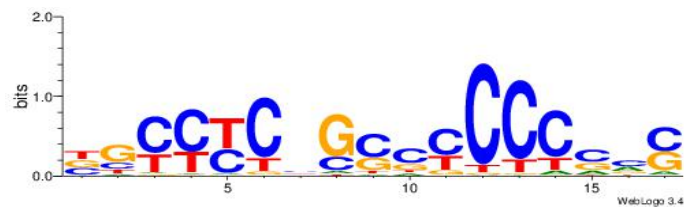


Dataset #: 1
 Motif ID: 22
 Motif name: C022
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0.0171497

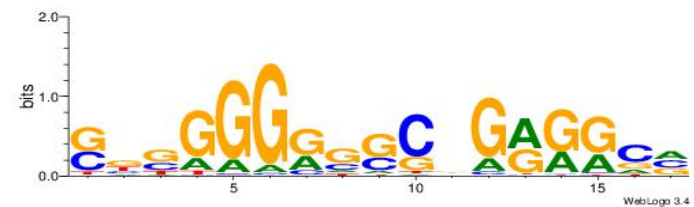
Alignment:

BGCCYCBGSCYCCCSVS
 BGCYKCTGCMTCM---

Original motif Consensus sequence: BGCCYCBGSCYCCCSVS



Reverse complement motif Consensus sequence: SVSGGGKGSGBMGGCV



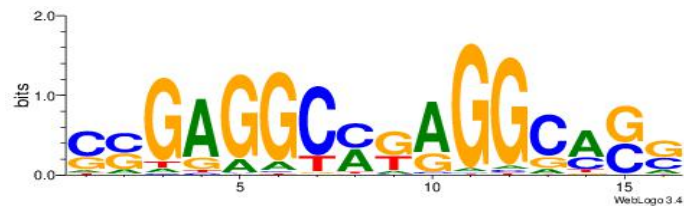
Dataset #: 1
 Motif ID: 41
 Motif name: C041
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3

Number of overlap: 14
Similarity score: 0.0309487

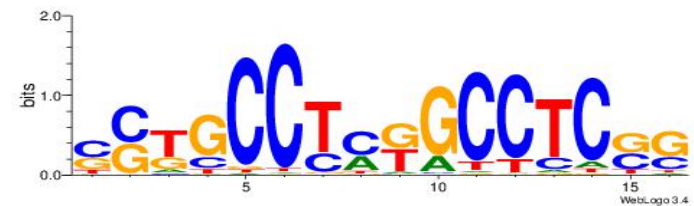
Alignment:

CSGAGGCMKAGGCASS
--YGGAYGCAGYKGCV

Original motif Consensus sequence: CSGAGGCMKAGGCASS



Reverse complement motif Consensus sequence: SSTGCCTYRGCTCSG

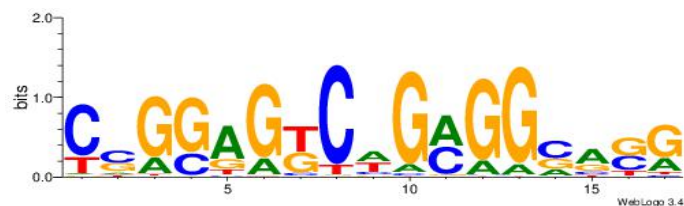


Dataset #: 1
Motif ID: 86
Motif name: C086
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 3
Number of overlap: 14
Similarity score: 0.0324714

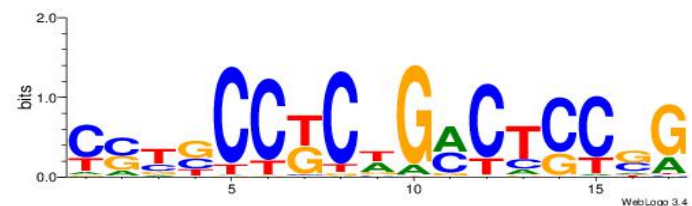
Alignment:

CSTSCCYCWGRCTCCSG
--BGCYKCTGCMTCM-

Original motif Consensus sequence: CSGGAGKCWGMGGSASG

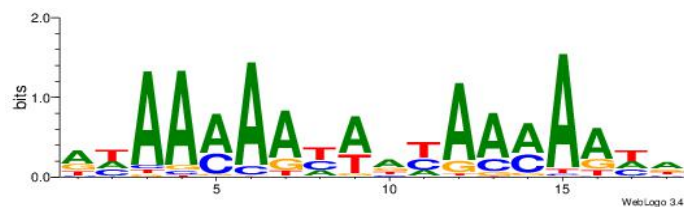


Reverse complement motif Consensus sequence: CSTSCCYCWGRCTCCSG

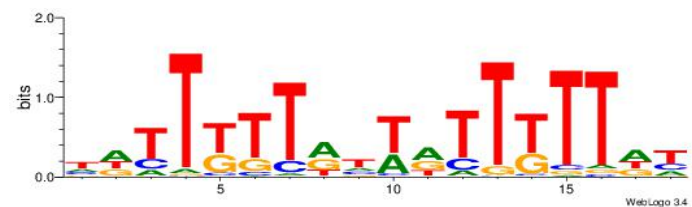


Dataset #: 1 Motif ID: 69 Motif name: C069

Original motif Consensus sequence: AHAAMAAYWDYAAMAAHD



Reverse complement motif Consensus sequence: DHTTYTTMDWMTTYTTHT



Best Matches for Motif ID 69 (Highest to Lowest)

Dataset #:	1
Motif ID:	30
Motif name:	C030
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	2
Number of overlap:	18
Similarity score:	0.0195386

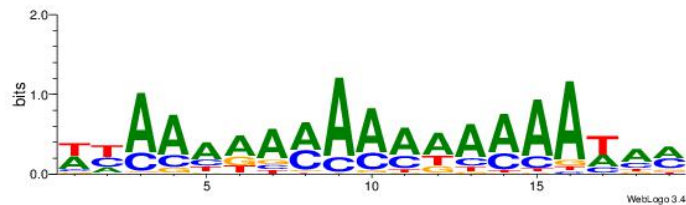
Alignment:

```

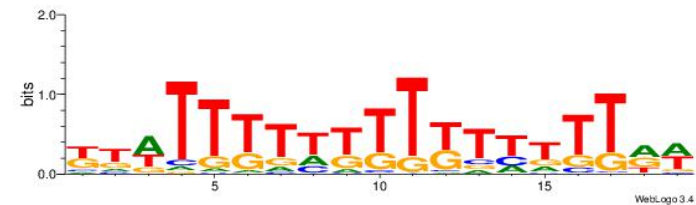
YTWTYYYYYYYYTTTTTMMW
-DHTTYTTMDWMTTYTHT

```

Original motif Consensus sequence: WYAAAAAAMAAAAAAAWAM



Reverse complement motif Consensus sequence:
YTWTYYYYYYYYTTTTTMMW



Dataset #:	1
Motif ID:	10
Motif name:	C010
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	4
Number of overlap:	18
Similarity score:	0.0236525

Alignment:

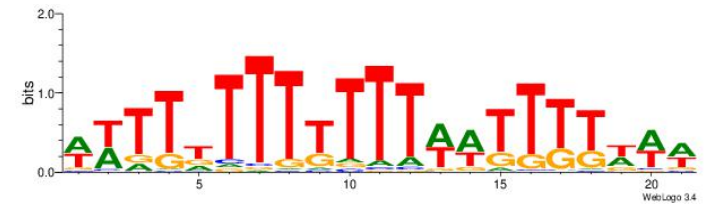
```

WWWAAAAWWAAAAAAAAAAWW
AHAAMAAWWDYAAMAAHD---

```

Original motif Consensus sequence: WWWAAAAWWAAAAAAAAAAWW

Reverse complement motif Consensus sequence:
WWTTTTTTTTTTWWTTTTWWW

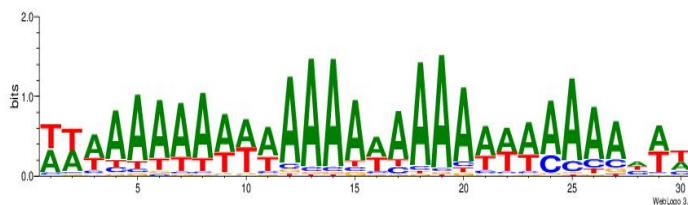


Dataset #:	1
Motif ID:	1
Motif name:	C001
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	2
Number of overlap:	18
Similarity score:	0.027345

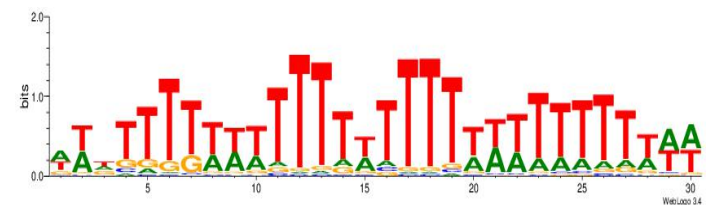
Alignment:

WWHTTTTWTTTTWTTTTWWTTTTWWW
-DHTTYTTMDWMTTYTHT-----

Original motif Consensus sequence:
 WWWAAAAWWAAAAWAAAAWAAAAHWW



Reverse complement motif Consensus sequence:
WWHTTTTWWTTTTTWTTTTWWTTTTWWW

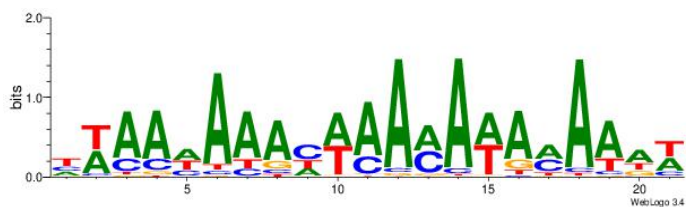


Dataset #: 1

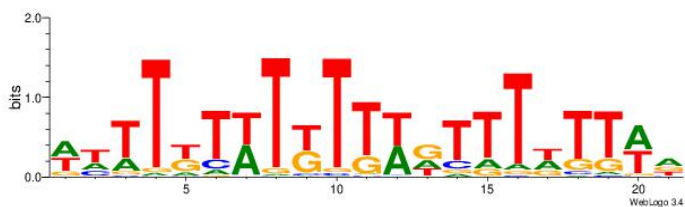
Motif ID: 16
Motif name: C016
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 18
Similarity score: 0.0364164

Alignment:
WWTTYTWTYTTWDTTTWTTWH
---DHTTYTTMDWMTTYTHT

Original motif Consensus sequence: HWAAWAAAHWAAMAWAMAAWW



Reverse complement motif Consensus sequence: WWTTYTWTYTTWDTTTWTTWH

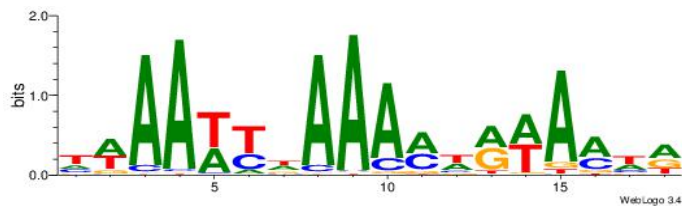


Dataset #: 1
Motif ID: 32
Motif name: C032
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 18

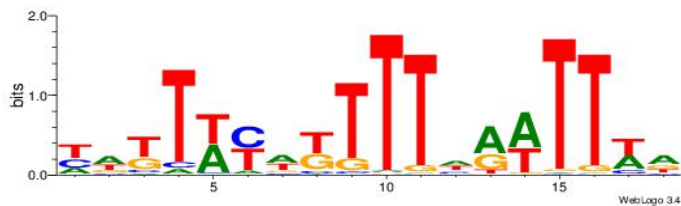
Similarity score: 0.0498109

Alignment:
HWAAWYDAAAMWRWAMWR
AHAAMAA YWDYAAMAAHD

Original motif Consensus sequence: HWAAWYDAAAMWRWAMWR



Reverse complement motif Consensus sequence: KWYTWKWYTTTDMWTTWH

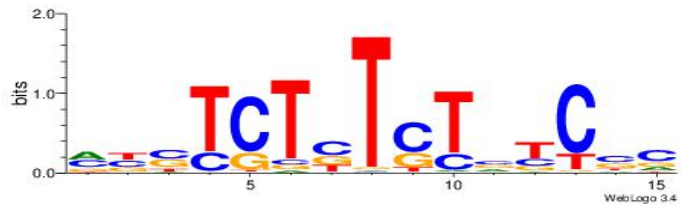


Dataset #: 1 Motif ID: 70 Motif name: C070

Original motif Consensus sequence: GVGABAGAVAGASVK



Reverse complement motif Consensus sequence: RBSTCTVTCTBTCV



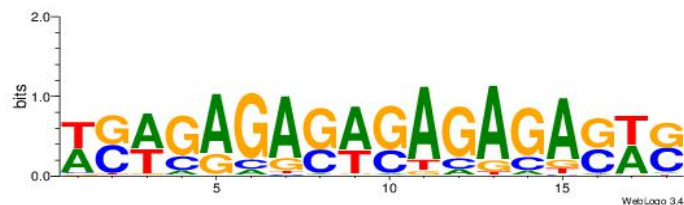
Best Matches for Motif ID 70 (Highest to Lowest)

Dataset #:	1
Motif ID:	17
Motif name:	C017
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif

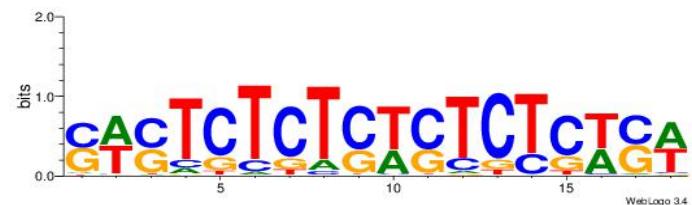
Direction: Forward
 Position number: 4
 Number of overlap: 15
 Similarity score: 0.00174543

Alignment:
 WSWGAGASWSAGAGASWS
 ---GVGABAGAVAGASVK

Original motif Consensus sequence: WSWGAGASWSAGAGASWS



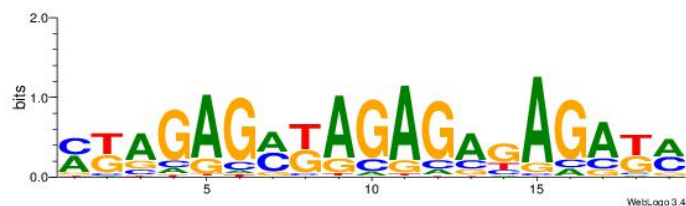
Reverse complement motif Consensus sequence: SWSTCTCTSWSTCTCWSW



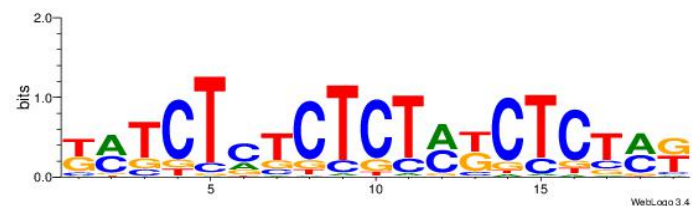
Dataset #: 1
 Motif ID: 12
 Motif name: C012
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 15
 Similarity score: 0.0027757

Alignment:
 MKAGAGMKAGAGAGAGAKM
 ---GVGABAGAVAGASVK-

Original motif Consensus sequence: MKAGAGMKAGAGAGAGAKM



Reverse complement motif Consensus sequence: YRTCTCTCTCTRYCTCTRR



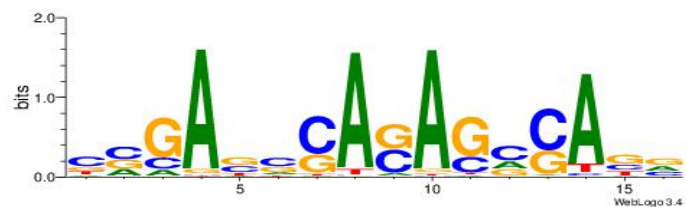
Dataset #: 1
Motif ID: 28
Motif name: C028
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 15
Similarity score: 0.00931002

Alignment:

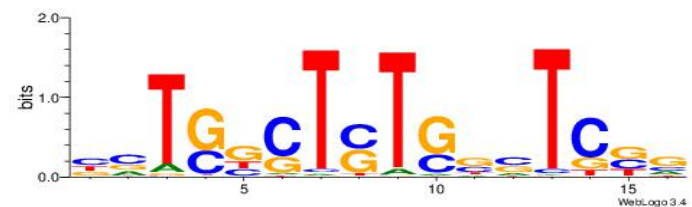
BVGASSCASAGVSABV

GVGABAGAVAGASVK-

Original motif Consensus sequence: BVGASSCASAGVSABV



Reverse complement motif Consensus sequence: VBTSVCTSTGSSTCVB

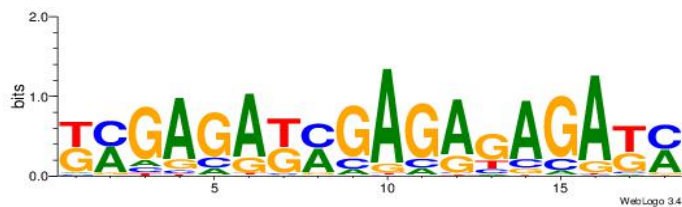


Dataset #: 1
 Motif ID: 11
 Motif name: C011
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 15
 Similarity score: 0.0117141

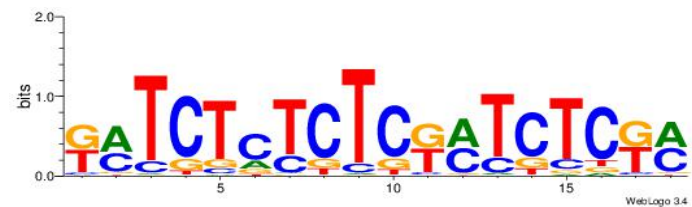
Alignment:

KMGAGAKMGAGAGAGAKM
 --GVGABAGAVAGASVK--

Original motif Consensus sequence: KMGAGAKMGAGAGAGAKM



Reverse complement motif Consensus sequence: RRTCTCTCTCRRTCTCRR

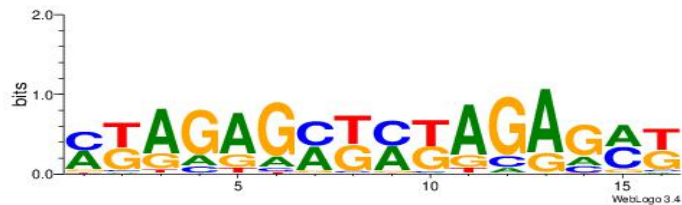


Dataset #: 1
 Motif ID: 55
 Motif name: C055
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2

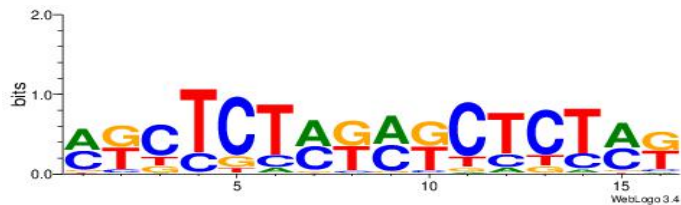
Number of overlap: 15
Similarity score: 0.0176331

Alignment:
MKAGAGMKMKAGAGMK
-GVGABAGAVAGASVK

Original motif Consensus sequence: MKAGAGMKMKAGAGMK

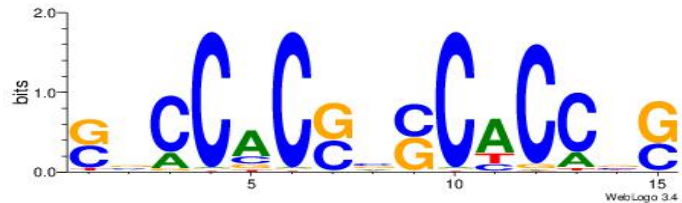


Reverse complement motif Consensus sequence: RYCTCTRRRRCTCTRR

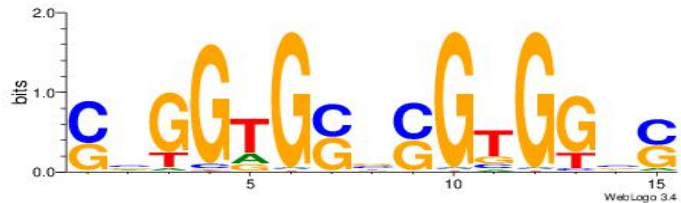


Dataset #: 1 Motif ID: 71 Motif name: C071

Original motif Consensus sequence: SVCCACSVSCACCBS



Reverse complement motif Consensus sequence: SBGGTGSVSGTGCG



Best Matches for Motif ID 71 (Highest to Lowest)

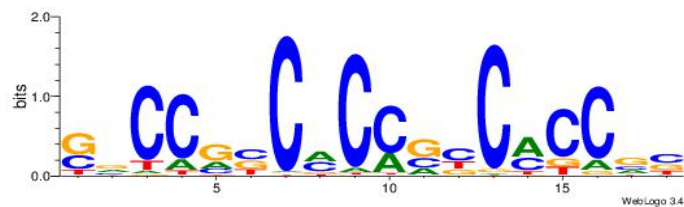
Dataset #: 1
Motif ID: 37
Motif name: C037
Matching format of first motif: Original Motif

Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	4
Number of overlap:	15
Similarity score:	0.0255433

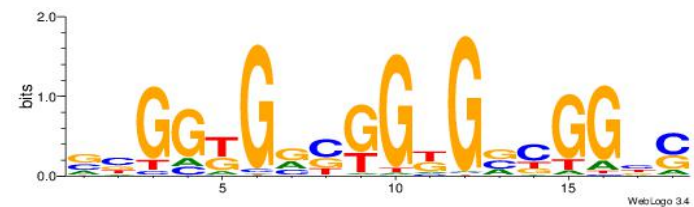
Alignment:

```
SVCCGBCMCCSYCMCCVB
---SVCCACSVSCACCBS
```

Original motif Consensus sequence: SVCCGBCMCCSYCMCCVB



Reverse complement motif Consensus sequence: BVGGYGKSGGYGBCGGVS

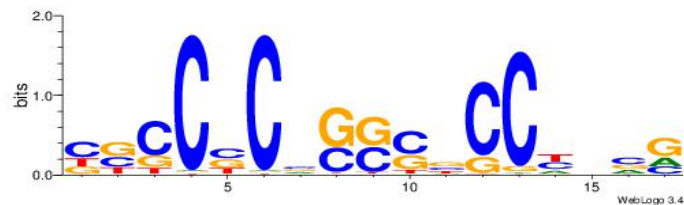


Dataset #:	1
Motif ID:	140
Motif name:	C140
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	15
Similarity score:	0.0303823

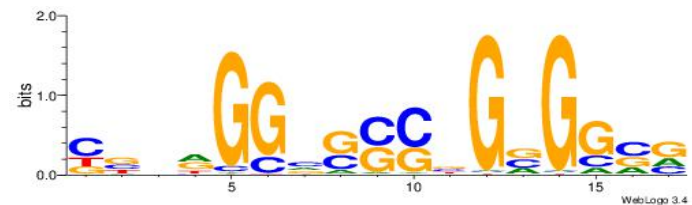
Alignment:

CVDMGGBSSSVGBGGSB
 --SBGGTGSVSGTGGVS

Original motif Consensus sequence: BSCCBCVSSSBCCYHVG



Reverse complement motif Consensus sequence:
 CVDMGGBSSSVGBGGSB

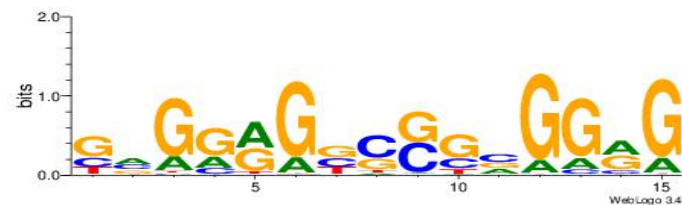
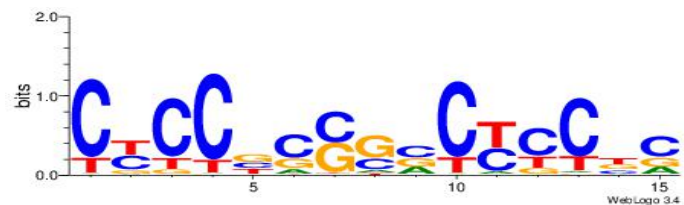


Dataset #:	1
Motif ID:	58
Motif name:	C058
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	15
Similarity score:	0.0375954

Alignment:
 GVGGMGVCSGBGGMG
 SBGGTGSVSGTGGVS

Original motif Consensus sequence: CYCCBCSGVCYCCBC

Reverse complement motif Consensus sequence:
 GVGGMGVCSGBGGMG

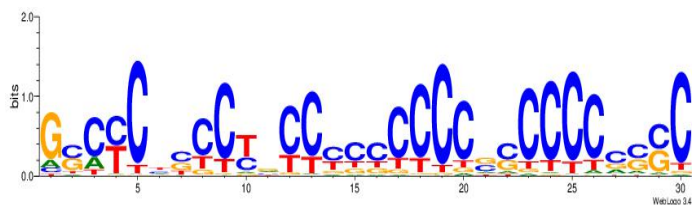


Dataset #: 1
 Motif ID: 3
 Motif name: C003
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 15
 Number of overlap: 15
 Similarity score: 0.0381134

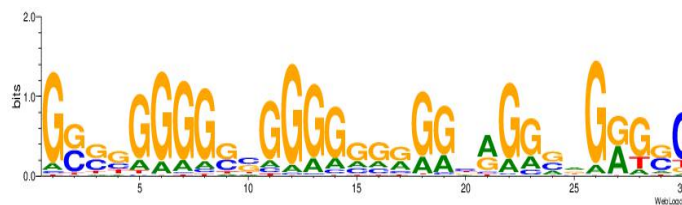
Alignment:

GSCYCHSCCYVCCYCCCCCSCCCCCSSC
 -----SVCCACSVSCACCBS-

Original motif Consensus sequence:
 GSCYCHSCCYVCCYCCCCCSCCCCCSSC



Reverse complement motif Consensus sequence:
 GSSGGGGGSSGGGGGKGGVMGGSHGKGC



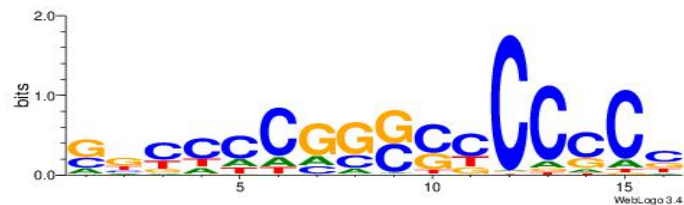
Dataset #: 1

Motif ID: 77
 Motif name: C077
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 15
 Similarity score: 0.0419016

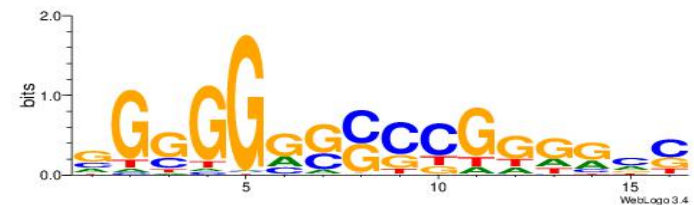
Alignment:

SBCCCCGGSSCCCCCB
 SVCCACSVSCACCBS-

Original motif Consensus sequence: SBCCCCGGSSCCCCCB

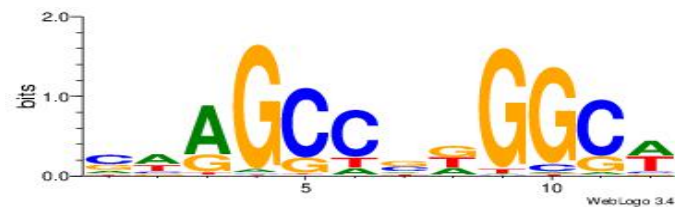


Reverse complement motif Consensus sequence: BGGGGGSSCCGGGGBS



Dataset #: 1 Motif ID: 72 Motif name: C072

Original motif Consensus sequence: SWAGCCVDGGCW



Reverse complement motif Consensus sequence: WGCCHVGGCTWS



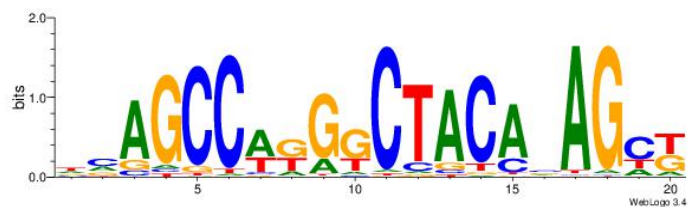
Best Matches for Motif ID 72 (Highest to Lowest)

Dataset #: 1
Motif ID: 15
Motif name: C015
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 3
Number of overlap: 12
Similarity score: 0.0223323

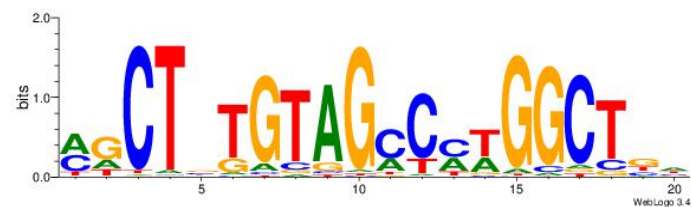
Alignment:

DVAGCCWKGCTACAVAGCK
-----WGCCHVGGCTWS--

Original motif Consensus sequence: DVAGCCWKGCTACAVAGCK



Reverse complement motif Consensus sequence: RGCTVTGTAGCCYWGGCTVD

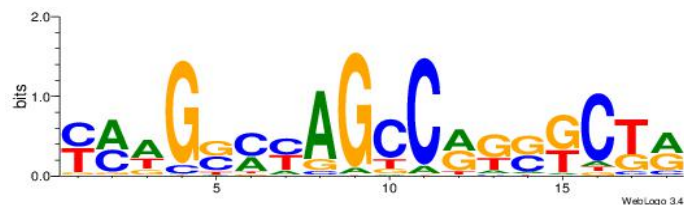


Dataset #: 1
Motif ID: 73
Motif name: C073
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement

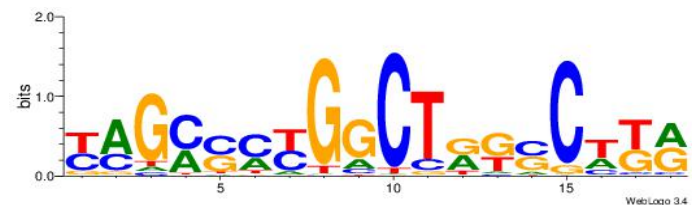
Direction: Forward
 Position number: 2
 Number of overlap: 12
 Similarity score: 0.0235561

Alignment:
 KAGYSYKGGCTKRSCWYK
 -WGCCHVGGCTWS-----

Original motif Consensus sequence: YMWGSMYAGCCRKSKCTR



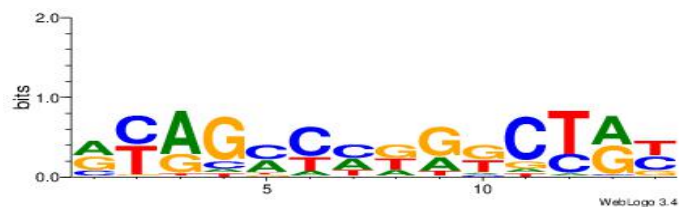
Reverse complement motif Consensus sequence: KAGYSYKGGCTKRSCWYK



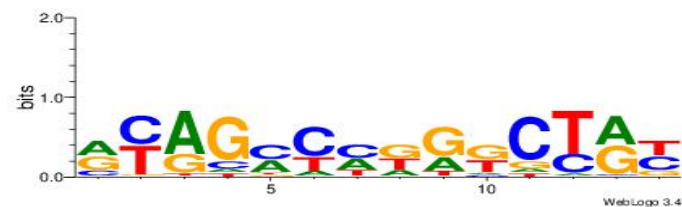
Dataset #: 1
 Motif ID: 45
 Motif name: C045
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 12
 Similarity score: 0.0249484

Alignment:
 MKAGYCYRGRCTKK
 --WGCCHVGGCTWS

Original motif Consensus sequence: RYAGMCMKGKCTRY



Reverse complement motif Consensus sequence: MKAGYCYRGRCTK



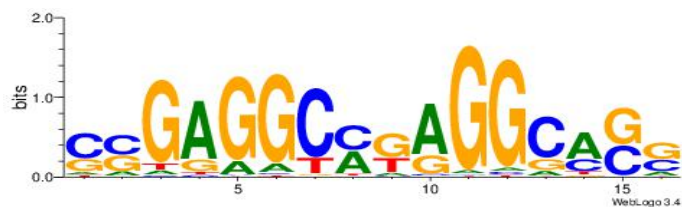
Dataset #: 1
Motif ID: 41
Motif name: C041
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 3
Number of overlap: 12
Similarity score: 0.0280879

Alignment:

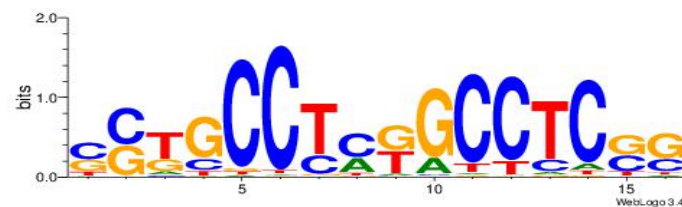
CSGAGGCMKAGGCASS

--SWAGCCVDGGCW--

Original motif Consensus sequence: CSGAGGCMKAGGCASS



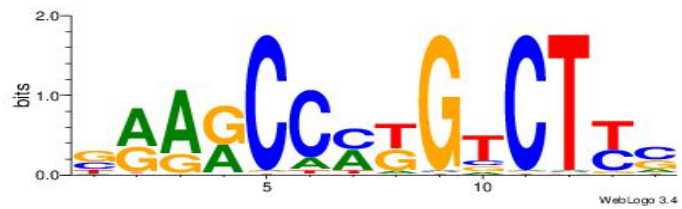
Reverse complement motif Consensus sequence: SSTGCCTYRGCTCSG



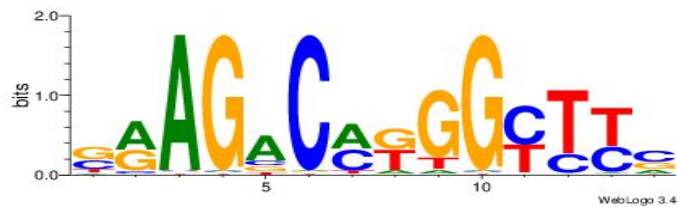
Dataset #: 1
Motif ID: 114
Motif name: C114
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 3
Number of overlap: 12
Similarity score: 0.0292595

Alignment:
SMAGACRRGGMTKS
SWAGCCVDGGCW--

Original motif Consensus sequence: SRARCCMKGCTCTYS



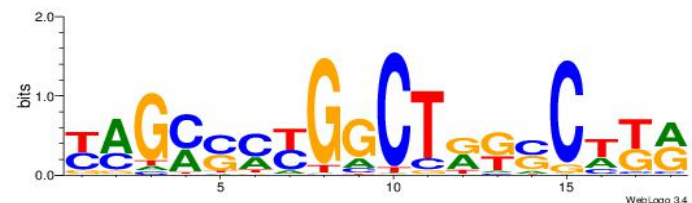
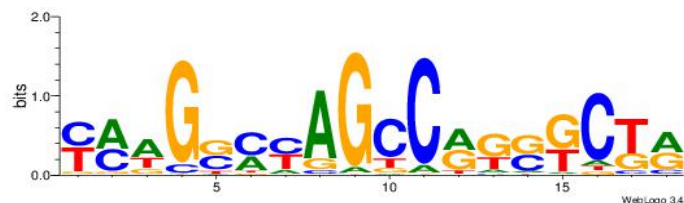
Reverse complement motif Consensus sequence: SMAGACRRGGMTKS



Dataset #: 1 Motif ID: 73 Motif name: C073

Original motif Consensus sequence: YMWGSMYAGCCRKSKCTR

Reverse complement motif Consensus sequence:
KAGYSYKGGCTKRSCWYK



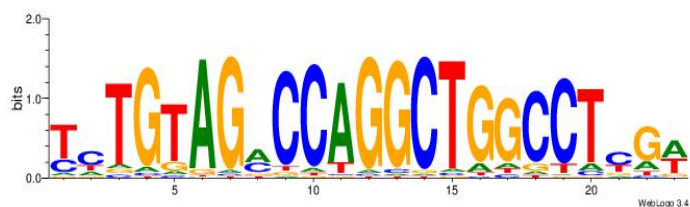
Best Matches for Motif ID 73 (Highest to Lowest)

Dataset #: 1
 Motif ID: 5
 Motif name: C005
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 18
 Similarity score: 0.0198254

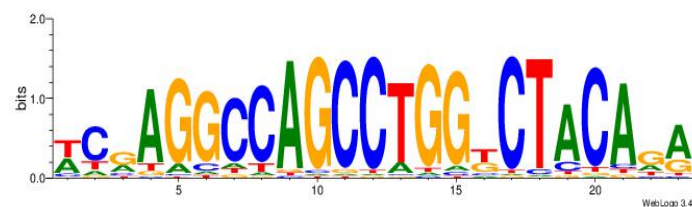
Alignment:

WCKAGGCCAGCCTGGYCTACAGA
 ----YMWGSMYAGCCRKSKCTR-

Original motif Consensus sequence: TCTGTAGMCCAGGCTGGCCTYGW



Reverse complement motif Consensus sequence: WCKAGGCCAGCCTGGYCTACAGA

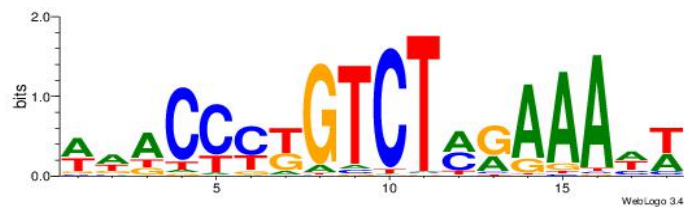


Dataset #: 1
 Motif ID: 35
 Motif name: C035
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 18
 Similarity score: 0.0398689

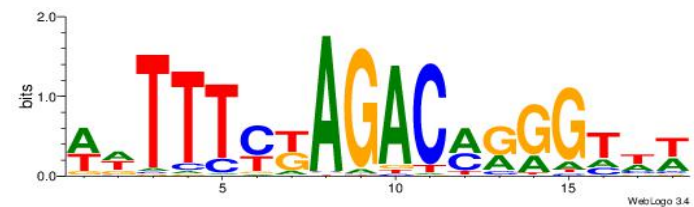
Alignment:

WWACCYKGTCTMRAAAWW
 KAGYSYKGGCTKRSCWYK

Original motif Consensus sequence: WWACCYKGTCTMRAAAWW



Reverse complement motif Consensus sequence: WWTTTMYAGACRKGGTWW



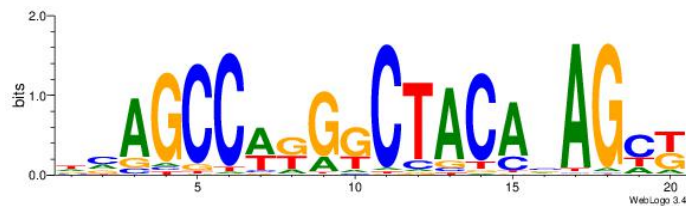
Dataset #: 1
 Motif ID: 15
 Motif name: C015
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2

Number of overlap: 18
Similarity score: 0.0475642

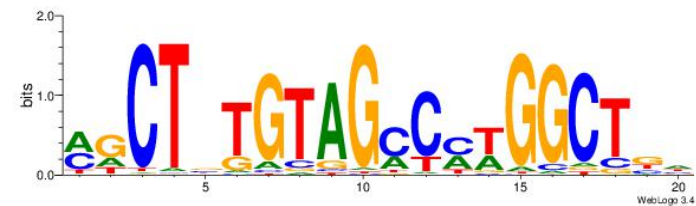
Alignment:

DVAGCCWKGCTACAVAGCK
-KAGYSYKGGCTKRSCWYK-

Original motif Consensus sequence: DVAGCCWKGCTACAVAGCK



Reverse complement motif Consensus sequence: RGCTVTGTAGCCYWGGCTVD

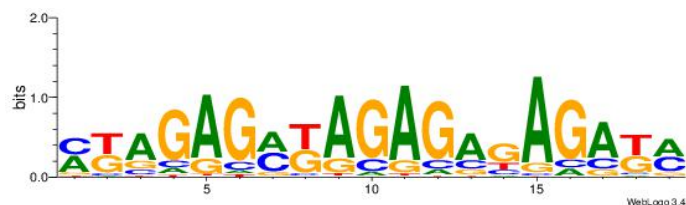


Dataset #: 1
Motif ID: 12
Motif name: C012
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 18
Similarity score: 0.0491912

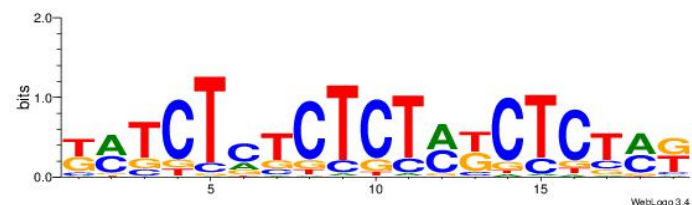
Alignment:

MKAGAGMKAGAGAGAGAKM
KAGYSYKGGCTKRSCWYK-

Original motif Consensus sequence: MKAGAGMKAGAGAGAGAKM



Reverse complement motif Consensus sequence: YRTCTCTCTCTRYCTCTRR

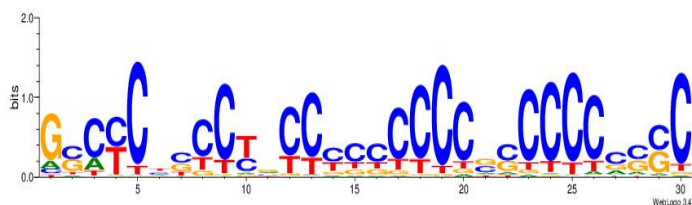


Dataset #: 1
 Motif ID: 3
 Motif name: C003
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 18
 Similarity score: 0.0508027

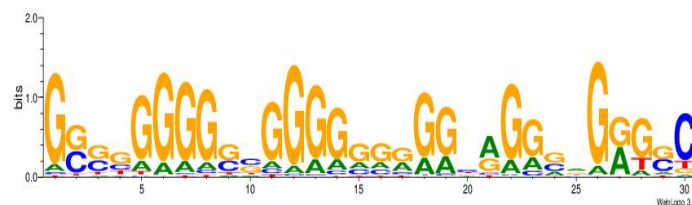
Alignment:

GSSGGGGGSSGGGGGKGGVMGGSHGKGSC
 -----KAGYSYKGGCTKRSCWYK--

Original motif Consensus sequence:
 GSCYCHSCCYVCCYCCCCCSCCCCCSSC

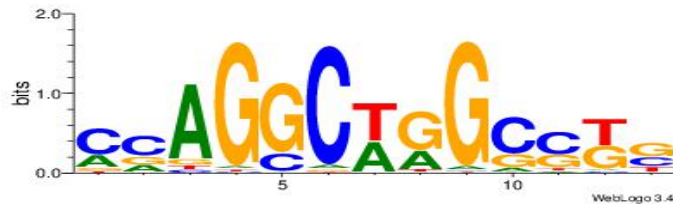


Reverse complement motif Consensus sequence:
 GSSGGGGGSSGGGGGKGGVMGGSHGKGSC

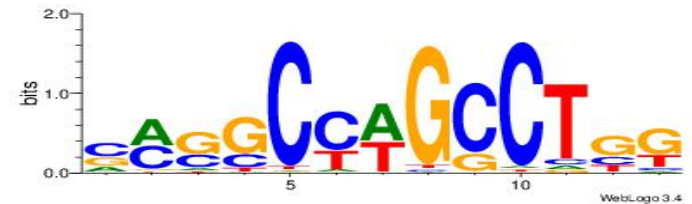


Dataset #: 1 Motif ID: 74 Motif name: C074

Original motif Consensus sequence: CCAGGCWGGCSKS



Reverse complement motif Consensus sequence: SRSGCCWGCCTGG



Best Matches for Motif ID 74 (Highest to Lowest)

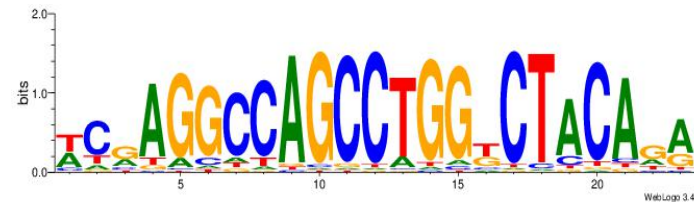
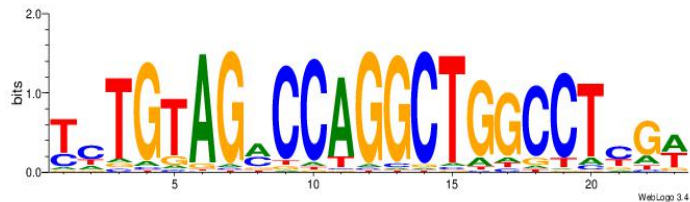
Dataset #:	1
Motif ID:	5
Motif name:	C005
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	9
Number of overlap:	13
Similarity score:	0.0135877

Alignment:

```
TCTGTAGMCCAGGCTGGCCTYGW
-----CCAGGCWGGCSKS--
```

Original motif Consensus sequence: TCTGTAGMCCAGGCTGGCCTYGW

Reverse complement motif Consensus sequence:
WCKAGGCCAGCCTGGYCTACAGA

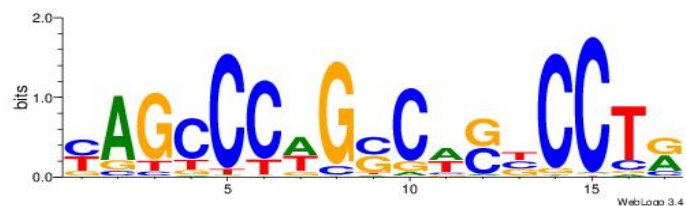


Dataset #: 1
 Motif ID: 122
 Motif name: C122
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 5
 Number of overlap: 13
 Similarity score: 0.0216217

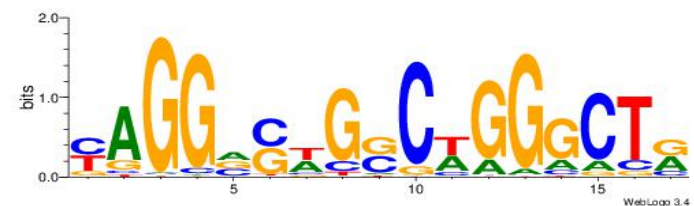
Alignment:

MAGGVSWGSCWGGGCTK
 ----CCAGGCWGGCSKS

Original motif Consensus sequence: YAGCCCWGSCWSBCCTR



Reverse complement motif Consensus sequence: MAGGVSWGSCWGGGCTK

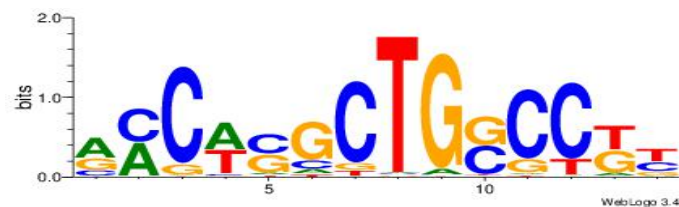


Dataset #: 1

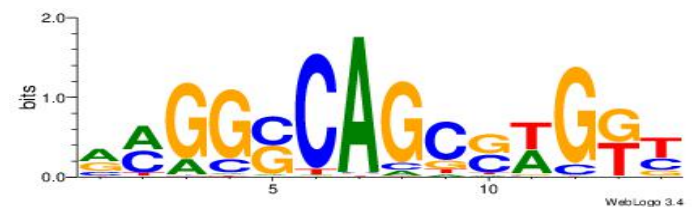
Motif ID: 109
 Motif name: C109
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 13
 Similarity score: 0.0278174

Alignment:
 RMCWSGCTGSCCKY
 -CCAGGCWGGCSKS

Original motif Consensus sequence: RMCWSGCTGSCCKY



Reverse complement motif Consensus sequence: MRGGSCAGCSWG



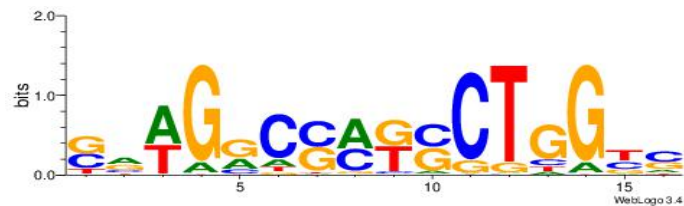
Dataset #: 1
 Motif ID: 126
 Motif name: C126
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 13
 Similarity score: 0.0314484

Alignment:

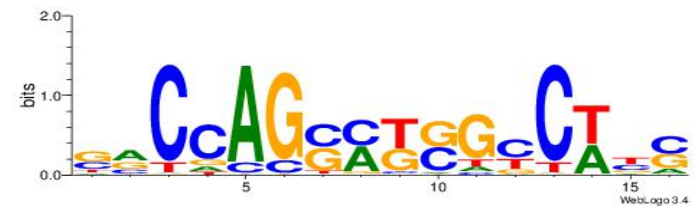
SMCCAGSYYSGMCWBS

--CCAGGCWGGCSKS--

Original motif Consensus sequence: SVWGRCSMKSTGGYS



Reverse complement motif Consensus sequence:
SMCCAGSYYSGMCWBS



Dataset #:	1
Motif ID:	96
Motif name:	C096
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:	0.031654

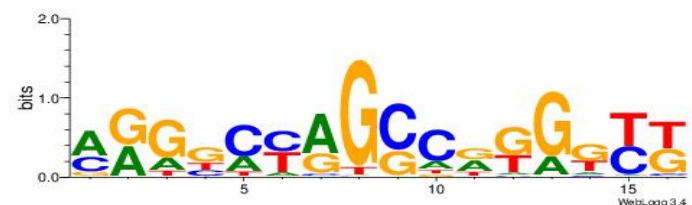
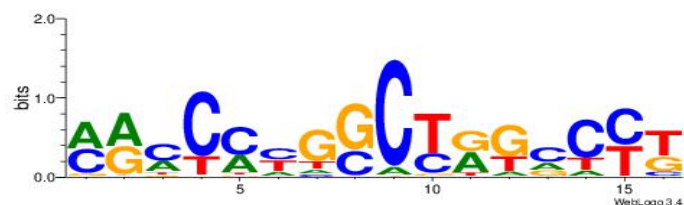
Alignment:

RKGGCMMGSCKRGRKY

SRSGCCWGCCTGG---

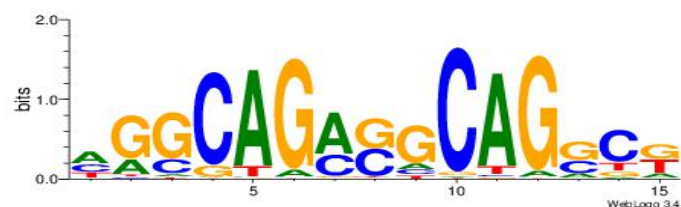
Original motif Consensus sequence: MRMCMYGSCYRGCCYK

Reverse complement motif Consensus sequence:
RKGGCMMGSCKRGRKY

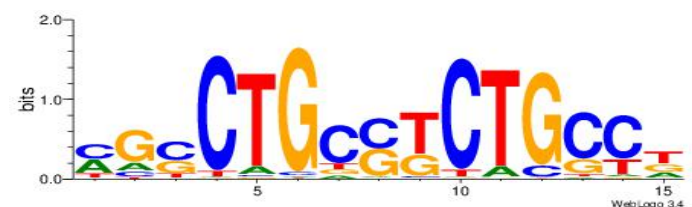


Dataset #: 1 Motif ID: 75 Motif name: C075

Original motif Consensus sequence: MGGCAGMSGCAGSCK



Reverse complement motif Consensus sequence: YGSCTGCSYCTGC

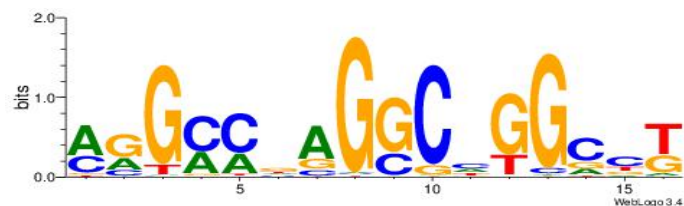


Best Matches for Motif ID 75 (Highest to Lowest)

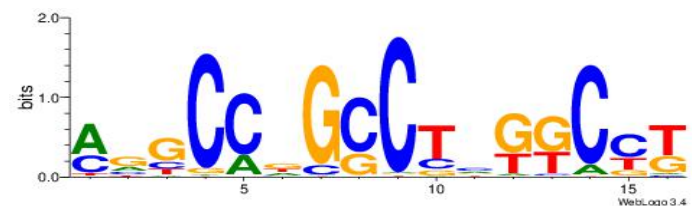
Dataset #:	1
Motif ID:	61
Motif name:	C061
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	15
Similarity score:	0.0391975

Alignment:
 MRGMMBAGGCHGGCCK
 MGGCAGMSGCAGSCK-

Original motif Consensus sequence: MRGMMBAGGCHGGCCK



Reverse complement motif Consensus sequence: RGGCCDGCCTBRRCMY

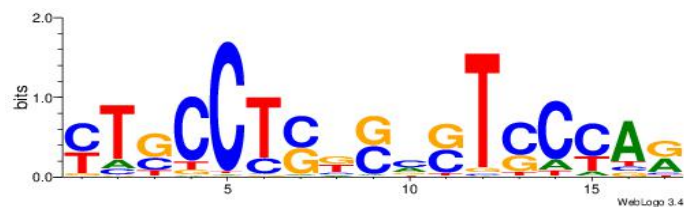


Dataset #: 1
Motif ID: 101
Motif name: C101
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2
Number of overlap: 15
Similarity score: 0.0421955

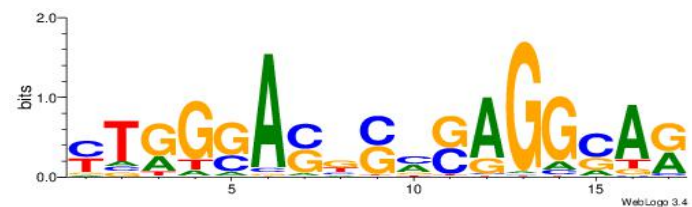
Alignment:

YTSCCTSKSVSTCCCAR
-YGSCTGCSYCTGCCY-

Original motif Consensus sequence: YTSCCTSKSVSTCCCAR



Reverse complement motif Consensus sequence: MTGGGASVSYSAGGSAK

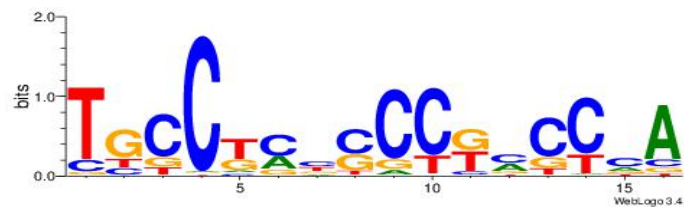


Dataset #: 1
 Motif ID: 105
 Motif name: C105
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 15
 Similarity score: 0.0441642

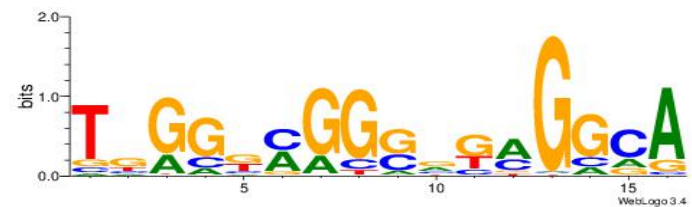
Alignment:

TGCKMBSCCKMCCVA
 YGCTGCSYCTGCCY-

Original motif Consensus sequence: TGCKMBSCCKMCCVA



Reverse complement motif Consensus sequence: TVGGRYGGSBRRGGCA



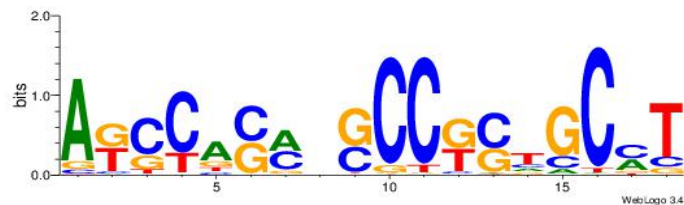
Dataset #: 1
 Motif ID: 93
 Motif name: C093
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1

Number of overlap: 15
Similarity score: 0.0450077

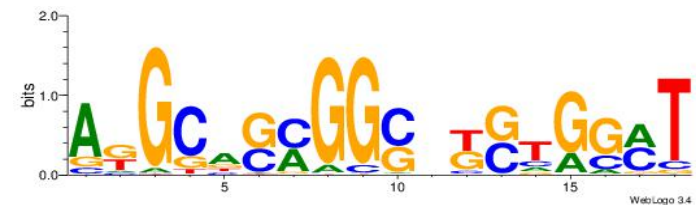
Alignment:

AKCCASMBSCCKSTGCMT
---YG SCTGCSYCTGCCY

Original motif Consensus sequence: AKCCASMBSCCKSTGCMT



Reverse complement motif Consensus sequence: ARGCAS YGGSVYSTGGYT

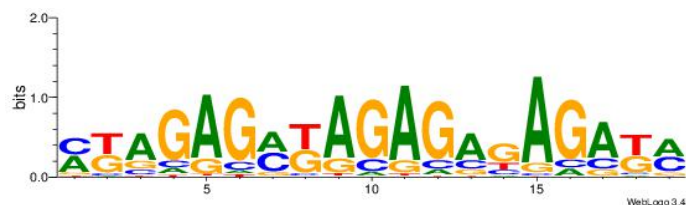


Dataset #: 1
Motif ID: 12
Motif name: C012
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 5
Number of overlap: 15
Similarity score: 0.0478052

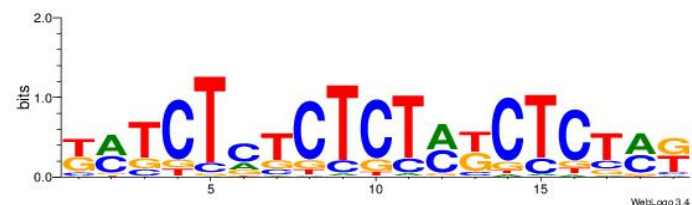
Alignment:

YRTCTCTCTCTRYCTCTRR
YG SCTGCSYCTGCCY----

Original motif Consensus sequence: MKAGAGMKAGAGAGAGAKM

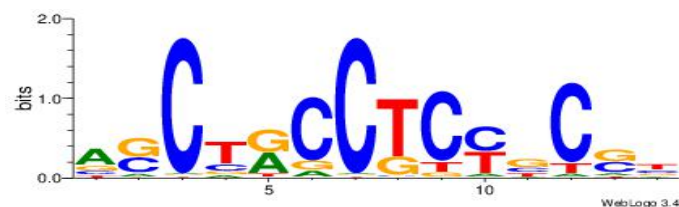


Reverse complement motif Consensus sequence: YRTCTCTCTCTRYCTCTRR

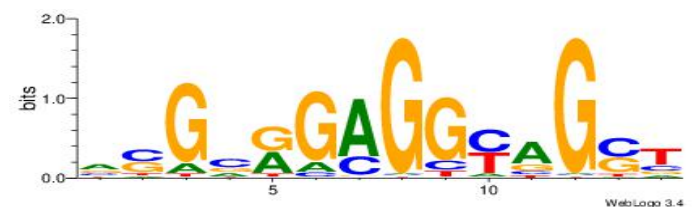


Dataset #: 1 Motif ID: 76 Motif name: C076

Original motif Consensus sequence: ASCTRCCTCYBCSB



Reverse complement motif Consensus sequence: VSGBKGAGGMAGS



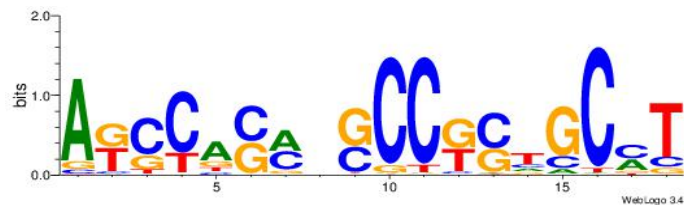
Best Matches for Motif ID 76 (Highest to Lowest)

Dataset #:	1
Motif ID:	93
Motif name:	C093
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:	0.0144167

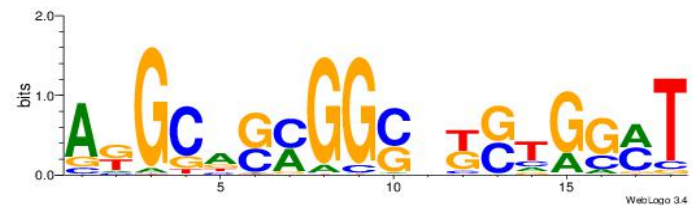
Alignment:

AKCCASMBSCCKSTGCMT
 ----ASCTRCCTCYBCSB

Original motif Consensus sequence: AKCCASMBSCCKSTGCMT



Reverse complement motif Consensus sequence: ARGCASYGGSVYSTGGYT

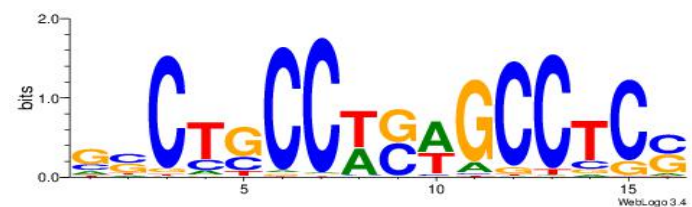
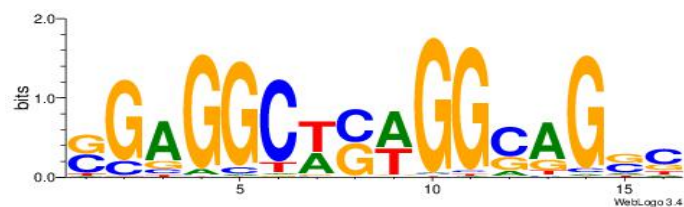


Dataset #:	1
Motif ID:	48
Motif name:	C048
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	3
Number of overlap:	14
Similarity score:	0.01751

Alignment:
 GSCTGCCWSWGCCTCS
 --ASCTRCCTCYBCSB

Original motif Consensus sequence: SGAGGCWSWGGCAGSC

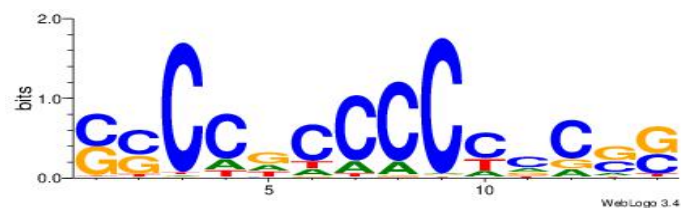
Reverse complement motif Consensus sequence:
 GSCTGCCWSWGCCTCS



Dataset #: 1
 Motif ID: 54
 Motif name: C054
 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: 0.0206235

Alignment:
 SSGGGGGGGHGGSS
 VSGBKGAGGMAGST

Original motif Consensus sequence: SSCDCCCCCCCSS



Reverse complement motif Consensus sequence: SSGGGGGGGHGGSS



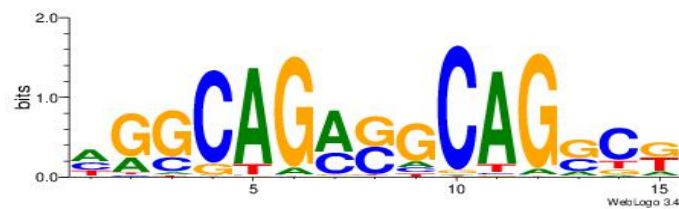
Dataset #: 1
 Motif ID: 75

Motif name:	C075
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	14
Similarity score:	0.0240004

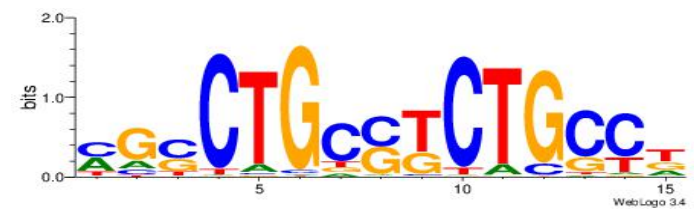
Alignment:

MGGCAGMSGCAGSCK
 -VSGBKGAGGMAGST

Original motif Consensus sequence: MGGCAGMSGCAGSCK



Reverse complement motif Consensus sequence: YGSCTGCSYCTGC



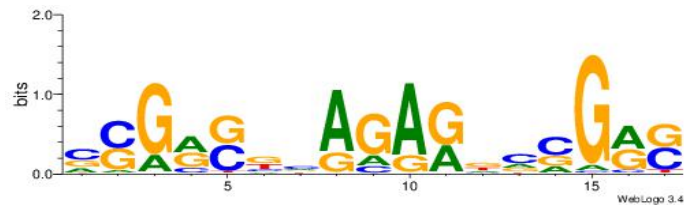
Dataset #:	1
Motif ID:	85
Motif name:	C085
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	4
Number of overlap:	14
Similarity score:	0.0263262

Alignment:

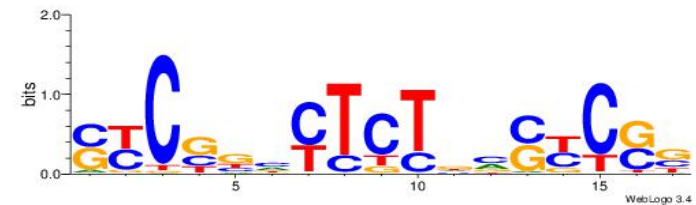
SKCSVHMTCTDBSKCSV

ASCTRCTCYBCSB---

Original motif Consensus sequence: VSGRSBHAGARDVSGRS

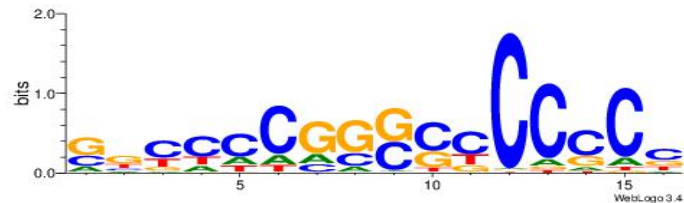


Reverse complement motif Consensus sequence: SKCSVHMTCTDBSKCSV

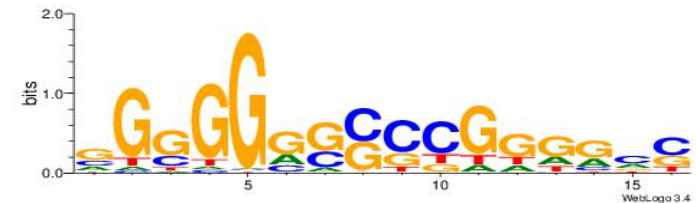


Dataset #: 1 Motif ID: 77 Motif name: C077

Original motif Consensus sequence: SBCCCCGGSSCCCCCB



Reverse complement motif Consensus sequence: BGGGGGSSCCGGGGBS



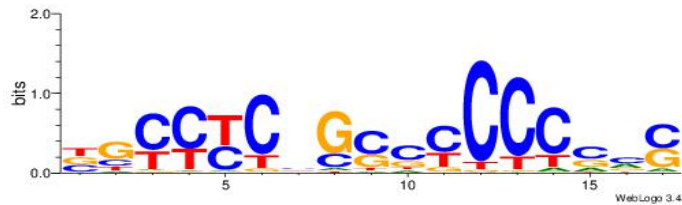
Best Matches for Motif ID 77 (Highest to Lowest)

Dataset #:	1
Motif ID:	22
Motif name:	C022
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif

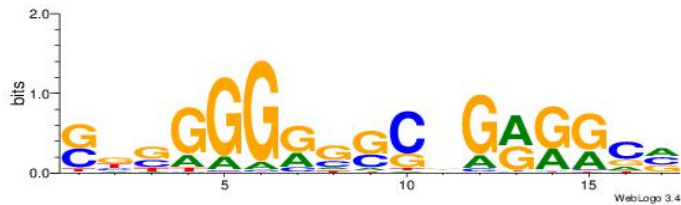
Direction: Backward
Position number: 2
Number of overlap: 16
Similarity score: 0.0139379

Alignment:
BGCCYCBGSCYCCCSVS
SBCCCCGGSSCCCCCB-

Original motif Consensus sequence: BGCCYCBGSCYCCCSVS



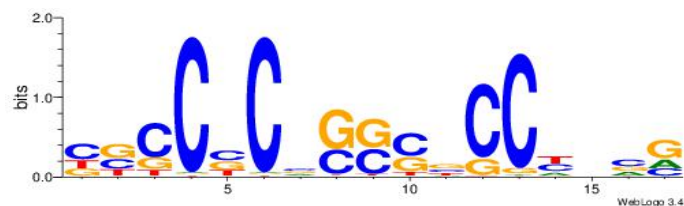
Reverse complement motif Consensus sequence: SVSGGGKGCSCBGMGGCV



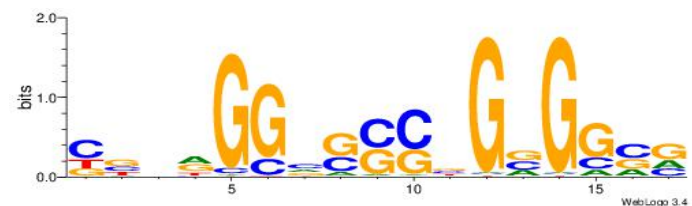
Dataset #: 1
Motif ID: 140
Motif name: C140
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2
Number of overlap: 16
Similarity score: 0.0278254

Alignment:
BSCCBVSSSBCCYHVG
SBCCCCGGSSCCCCCB-

Original motif Consensus sequence: BSCCBCVSSSBCCYHVG



Reverse complement motif Consensus sequence: CVDMGGBSSSVGBGGSB

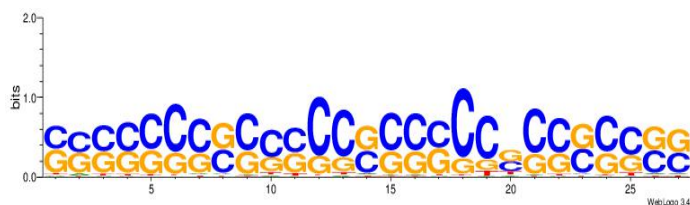


Dataset #: 1
 Motif ID: 4
 Motif name: C004
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 12
 Number of overlap: 16
 Similarity score: 0.028174

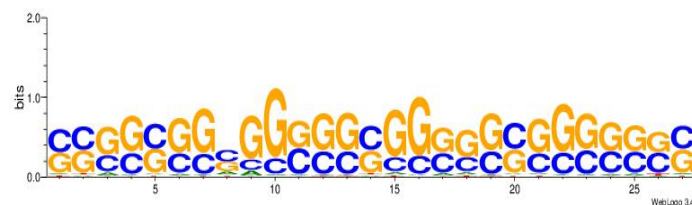
Alignment:

```
SSSSSSGSGGSSSSGSSSSGSSSSS
-----BGGGGSSCCGGGGS
```

Original motif Consensus sequence:
 SSSSSCSSSSCCSSSSCCSCSSSSS



Reverse complement motif Consensus sequence:
 SSSSSGSGGSSSSGSSSSGSSSSS

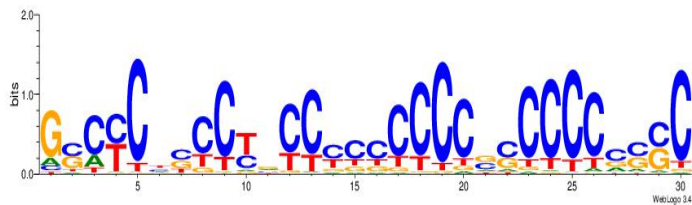


Dataset #: 1
 Motif ID: 3
 Motif name: C003
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 14
 Number of overlap: 16
 Similarity score: 0.029123

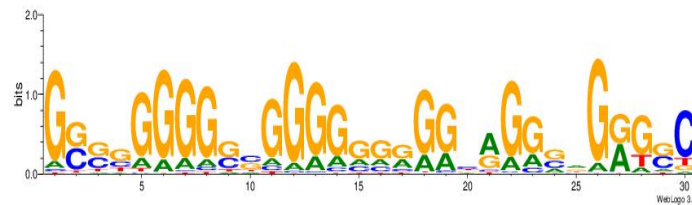
Alignment:

GSSGGGGSSGGGGGKGGVMGGSHGKGSC
 -BGGGGSSCCGGGGBS-----

Original motif Consensus sequence:
 GSCYCHSCCYVCCYCCCCSSCCCCSSC



Reverse complement motif Consensus sequence:
 GSSGGGGSSGGGGGKGGVMGGSHGKGSC

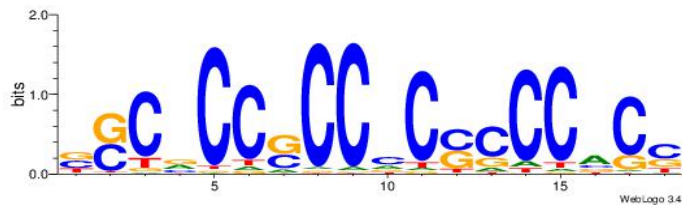


Dataset #: 1
 Motif ID: 20
 Motif name: C020
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3

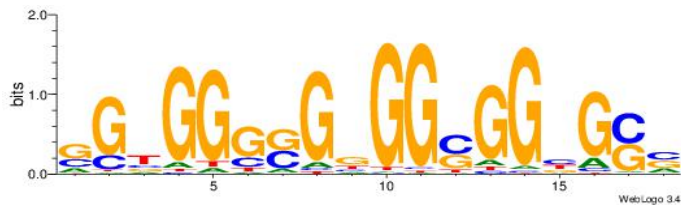
Number of overlap: 16
Similarity score: 0.0454489

Alignment:
BSCVCCSCCVCSCCCACS
--SBCCCCGGSSCCCCCB

Original motif Consensus sequence: BSCVCCSCCVCSCCCACS



Reverse complement motif Consensus sequence: SGTGGGSGVGGSGGVGSB

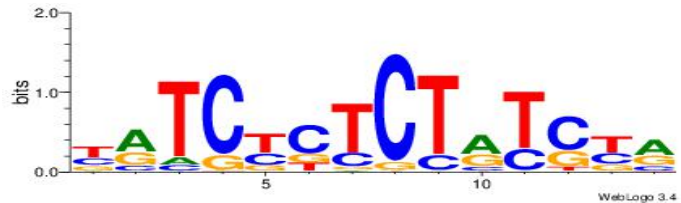


Dataset #: 1 Motif ID: 78 Motif name: C078

Original motif Consensus sequence: YRGAYAGAGRGAYR



Reverse complement motif Consensus sequence: KMTCKCTCTMTCK



Best Matches for Motif ID 78 (Highest to Lowest)

Dataset #: 1
Motif ID: 25
Motif name: C025
Matching format of first motif: Original Motif

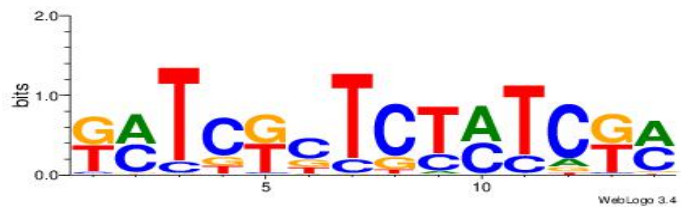
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 14
Similarity score: 0

Alignment:
KMGAKAGAGMGAKM
YRGAYAGAGRGAYR

Original motif Consensus sequence: KMGAKAGAGMGAKM



Reverse complement motif Consensus sequence: RRTCRCCTCTRCR

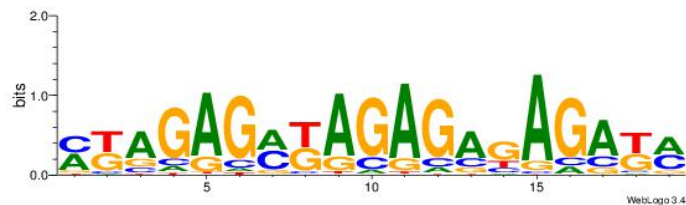


Dataset #: 1
Motif ID: 12
Motif name: C012
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 3
Number of overlap: 14
Similarity score: 0.00828206

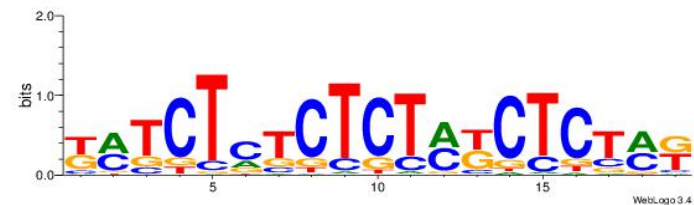
Alignment:

YRTCTCTCTCTRYCTCTRR
--KMTCKCTCTMTCKM---

Original motif Consensus sequence: MKAGAGMKAGAGAGAGAKM



Reverse complement motif Consensus sequence: YRTCTCTCTCTRYCTCTRR

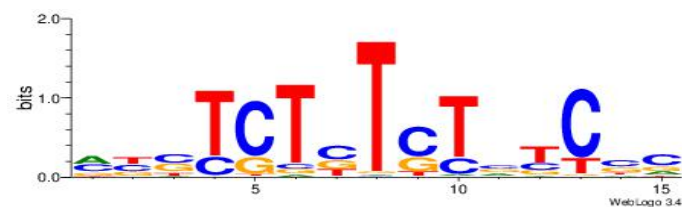
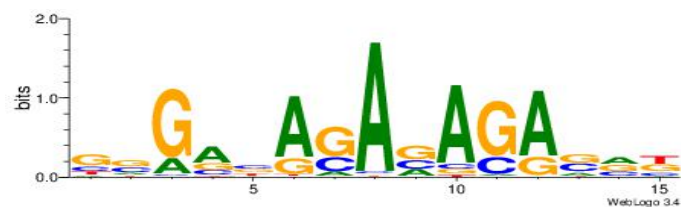


Dataset #:	1
Motif ID:	70
Motif name:	C070
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2
Number of overlap:	14
Similarity score:	0.00930595

Alignment:
GVGABAGAVAGASVK
YRGAYAGARGAYR-

Original motif Consensus sequence: GVGABAGAVAGASVK

Reverse complement motif Consensus sequence: RBSTCTVTCTBTCV

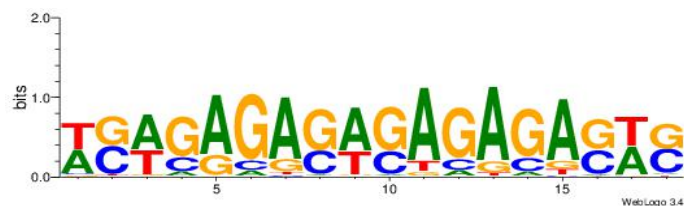


Dataset #: 1
 Motif ID: 17
 Motif name: C017
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 14
 Similarity score: 0.0146835

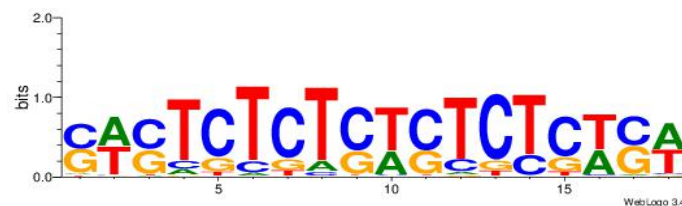
Alignment:

SWSTCTCTSWSTCTCWSW
 ---KMTCKCTCTMTCKM-

Original motif Consensus sequence: WSWGAGASWSAGAGASWS



Reverse complement motif Consensus sequence: SWSTCTCTSWSTCTCWSW



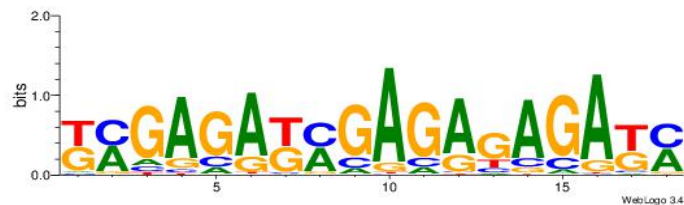
Dataset #: 1

Motif ID: 11
 Motif name: C011
 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: 0.0193986

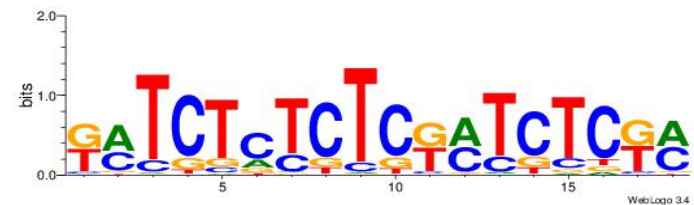
Alignment:

KMGAGAKMGAGAGAGAKM
 ----YRGAYAGAGRGAYR

Original motif Consensus sequence: KMGAGAKMGAGAGAGAKM

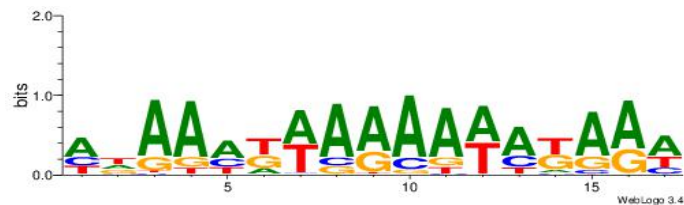


Reverse complement motif Consensus sequence: RRTCTCTCTCRRTCTCRR

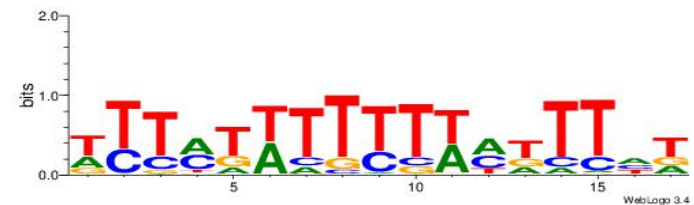


Dataset #: 1 Motif ID: 79 Motif name: C079

Original motif Consensus sequence: ADAAAKWAAAAWAKARW



Reverse complement motif Consensus sequence: WKTRTWTTTTWRTTTDT



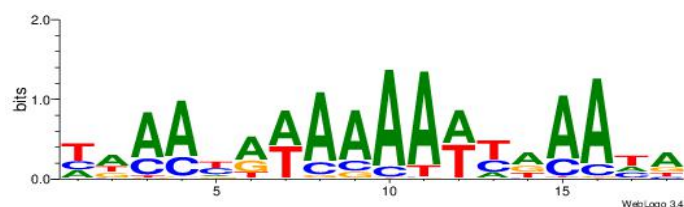
Best Matches for Motif ID 79 (Highest to Lowest)

Dataset #: 1
Motif ID: 24
Motif name: C024
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: 0.0194272

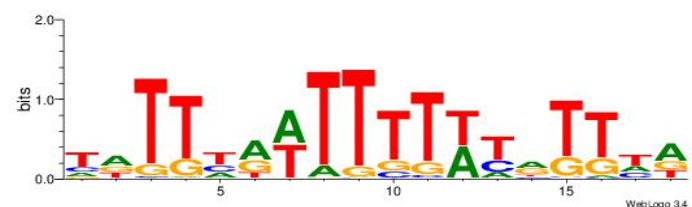
Alignment:

THTTDMWTTTTWKMTTDA
-WKTRTWTTTTWRTTDT

Original motif Consensus sequence: TDAAYRWAAAWYDAAHA



Reverse complement motif Consensus sequence: THTTDMWTTTTWKMTTDA



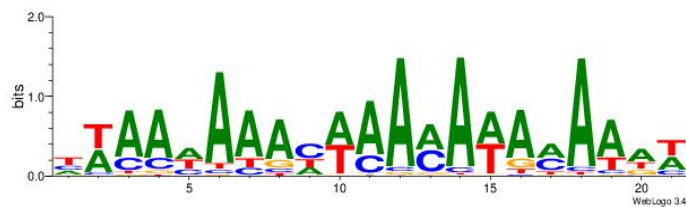
Dataset #: 1
Motif ID: 16
Motif name: C016
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement

Direction: Forward
 Position number: 2
 Number of overlap: 17
 Similarity score: 0.020907

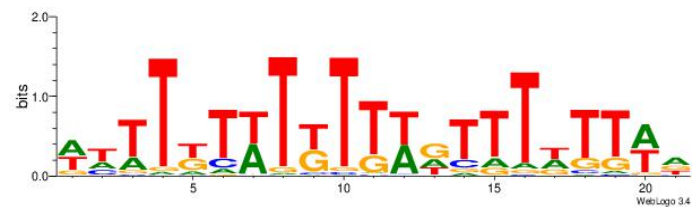
Alignment:

WWTTYTWTYTTWDTTTWTTH
 -WKTRTWTTTTWRITTTDT---

Original motif Consensus sequence: HWAAWAAHWAAMAWAMAAWW



Reverse complement motif Consensus sequence: WWTTYTWTYTTWDTTTWTTH

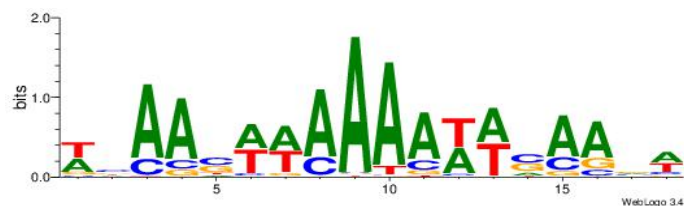


Dataset #: 1
 Motif ID: 97
 Motif name: C097
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 17
 Similarity score: 0.0210687

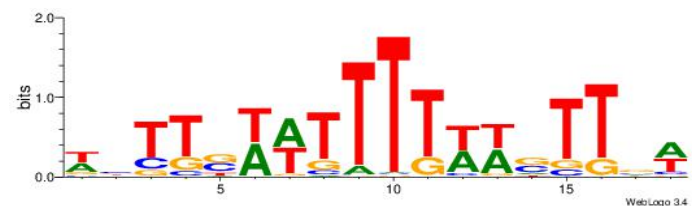
Alignment:

WVTTSWWTTTTWWSTTBW
 -WKTRTWTTTTWRITTTDT

Original motif Consensus sequence: WBAASWWAAAAWWSAAVW



Reverse complement motif Consensus sequence: WTTTSWTTTWWSTTBW

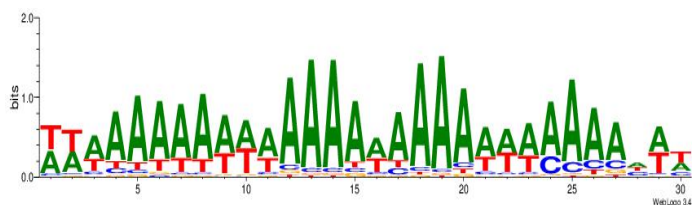


Dataset #: 1
 Motif ID: 1
 Motif name: C001
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 10
 Number of overlap: 17
 Similarity score: 0.0222548

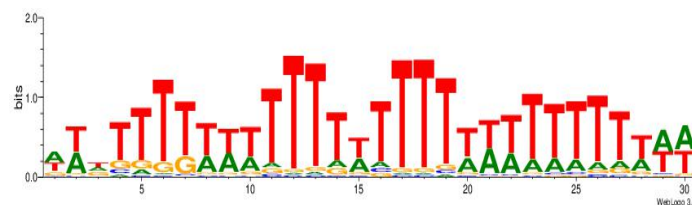
Alignment:

WWHTTTTWTTTTTWTTTTWWTTTTTWW
 -----WKTRTWTTTTWRTTTDT-----

Original motif Consensus sequence:
 WWWAAAAWWAAAAWAAAAWAAAAHWW



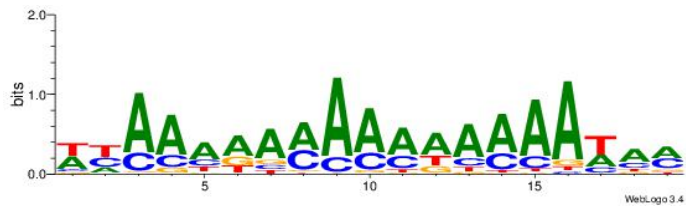
Reverse complement motif Consensus sequence:
 WWHTTTTWTTTTTWTTTTWWTTTTTWW



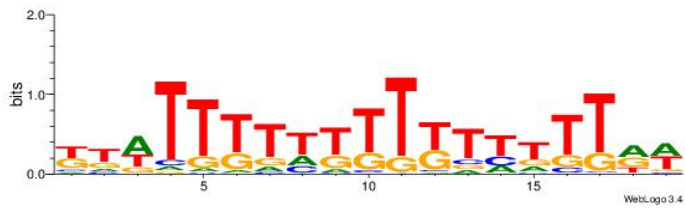
Dataset #: 1
Motif ID: 30
Motif name: C030
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 3
Number of overlap: 17
Similarity score: 0.0272295

Alignment:
YTWTTTTTTTTYTTTTMW
--WKTRTWTTTTWRTTTDT

Original motif Consensus sequence: WYAAAAAIAAAAAAAWAM



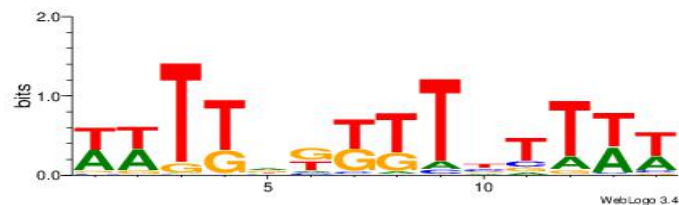
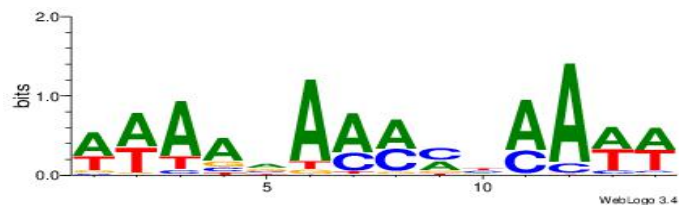
Reverse complement motif Consensus sequence: YTWTTTTTTTTYTTTTMW



Dataset #: 1 Motif ID: 80 Motif name: C080

Original motif Consensus sequence: WWAAVAAMHAAWW

Reverse complement motif Consensus sequence: WWTTHRYTTBTTW



Best Matches for Motif ID 80 (Highest to Lowest)

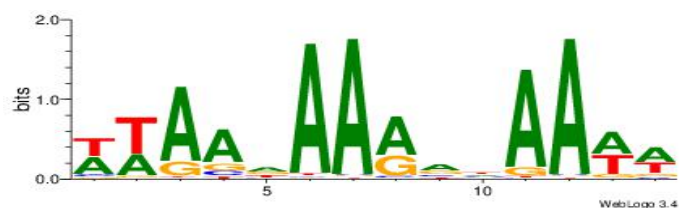
Dataset #: 1
 Motif ID: 131
 Motif name: C131
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0.00242398

Alignment:

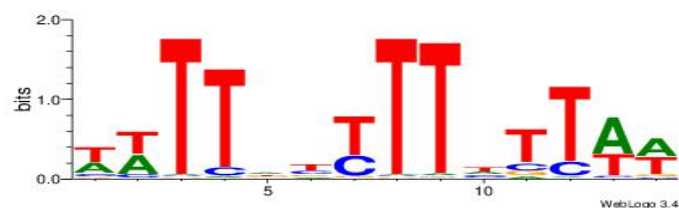
WWAADAARVHAAWW

WWAAVAAMMHAAWW

Original motif Consensus sequence: WWAADAARVHAAWW



Reverse complement motif Consensus sequence: WWTTHBKTTDTTV

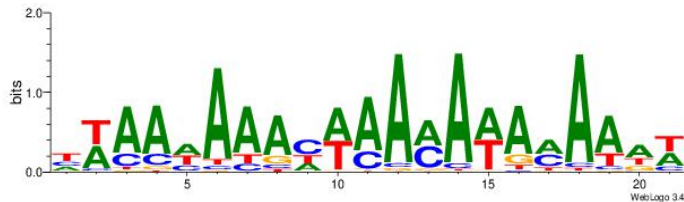


Dataset #: 1

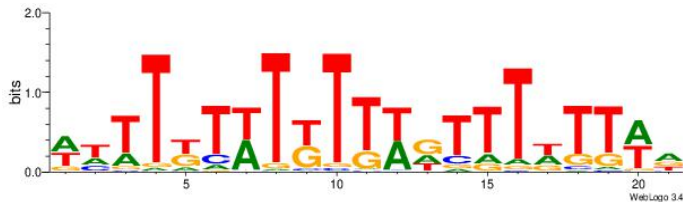
Motif ID: 16
Motif name: C016
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 14
Similarity score: 0.0141088

Alignment:
HWAAWAAAHWAAMAWAMAAWW
WWAAVAAMMHAAWW-----

Original motif Consensus sequence: HWAAWAAAHWAAMAWAMAAWW



Reverse complement motif Consensus sequence: WWTYYTWYTTWDTTTWTTWH

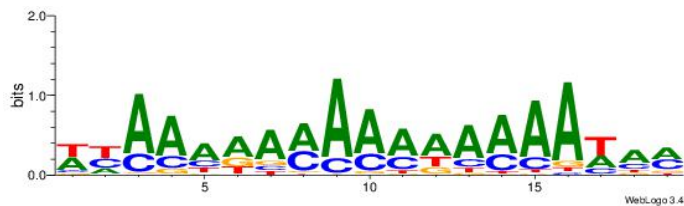


Dataset #: 1
Motif ID: 30
Motif name: C030
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 3
Number of overlap: 14

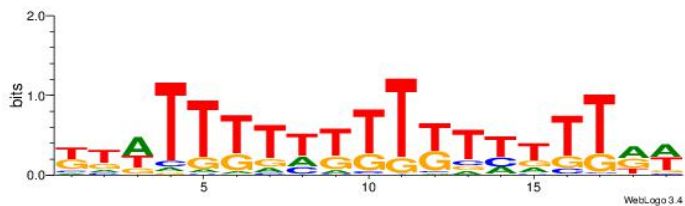
Similarity score: 0.0166572

Alignment:
WYAAAAAMAAAAAAWAM
---WWAAVAAMMHAAWW---

Original motif Consensus sequence: WYAAAAAMAAAAAAWAM



Reverse complement motif Consensus sequence:
YTWTTTTTTTTYTTTTMW

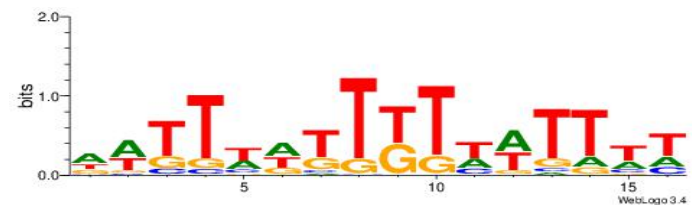
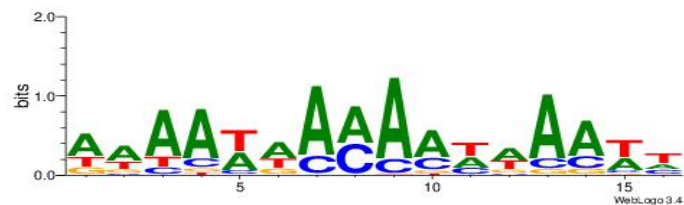


Dataset #: 1
Motif ID: 98
Motif name: C098
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2
Number of overlap: 14
Similarity score: 0.0168591

Alignment:
AAAAWWAMAAWWAAWH
-WWAAVAAMMHAAWW-

Original motif Consensus sequence: AAAAWWAMAAWWAAWH

Reverse complement motif Consensus sequence:
HWTTWWTTYTWTTTT



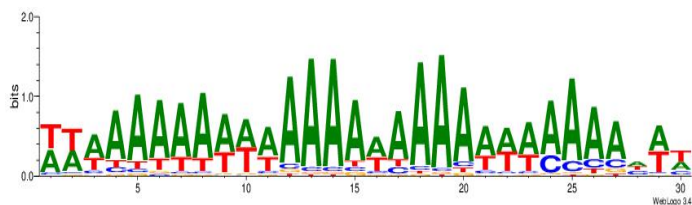
Dataset #: 1
 Motif ID: 1
 Motif name: C001
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 9
 Number of overlap: 14
 Similarity score: 0.0174091

Alignment:

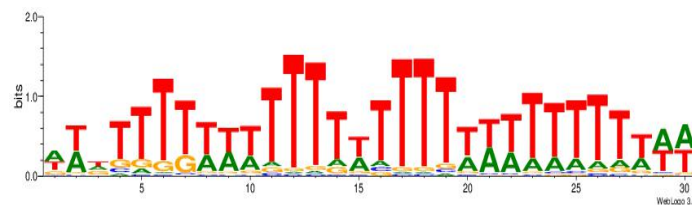
```

WWWAAAAAWWAAAAAWAAAAWWAAAAHWW
-----WWAAVAAMMHAAWW-----
  
```

Original motif Consensus sequence:
 WWWAAAAAWWAAAAAWAAAAWWAAAAHWW

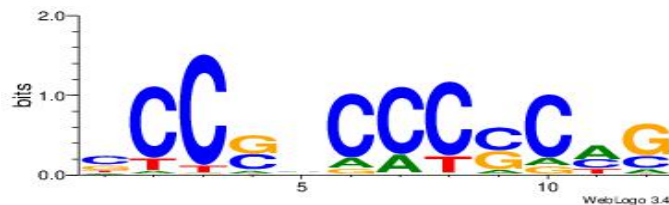


Reverse complement motif Consensus sequence:
 WWHTTTTWWTTTTTWT TTTTWWTTTTTWW

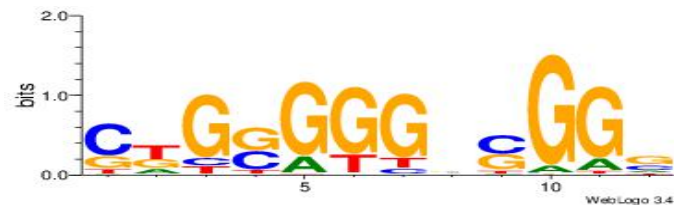


Dataset #: 1 Motif ID: 81 Motif name: C081

Original motif Consensus sequence: BCCSHCCCSCMG



Reverse complement motif Consensus sequence: CYGSGGGHSGGB



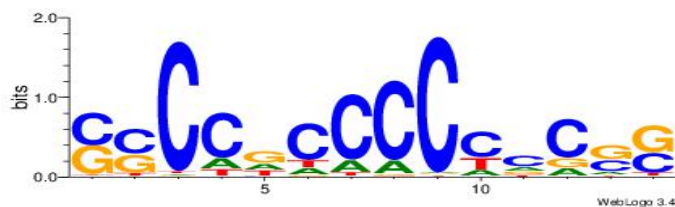
Best Matches for Motif ID 81 (Highest to Lowest)

Dataset #:	1
Motif ID:	54
Motif name:	C054
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:	0.0207001

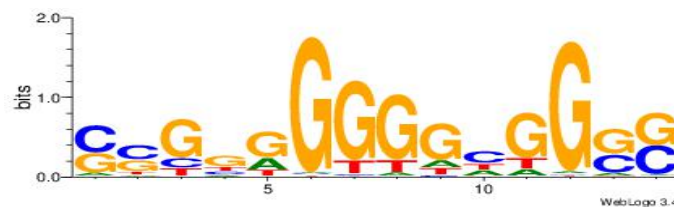
Alignment:

SSCCDCCCCCCCSS
 -BCCSHCCCSCMG-

Original motif Consensus sequence: SSCCDCCCCCCCSS



Reverse complement motif Consensus sequence: SSGGGGGGGHGG

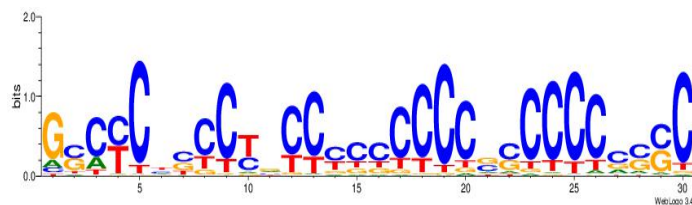


Dataset #: 1
 Motif ID: 3
 Motif name: C003
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 18
 Number of overlap: 12
 Similarity score: 0.0209376

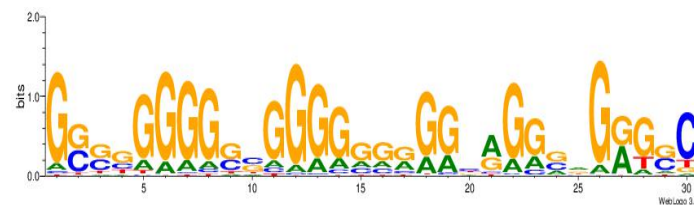
Alignment:

GSCYCHSCCYVCCYCCCCCSCCCCCSSC
 -----BCCSHCCCSCMG--

Original motif Consensus sequence:
 GSCYCHSCCYVCCYCCCCCSCCCCCSSC



Reverse complement motif Consensus sequence:
 GSSGGGGGSSGGGGGKGGVMGGSHGKGC

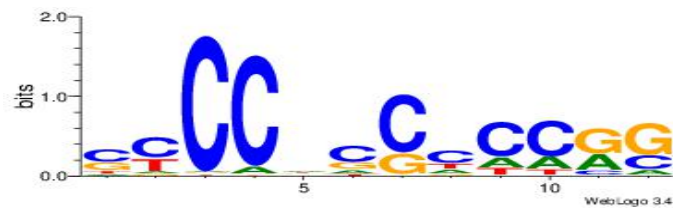


Dataset #: 1
 Motif ID: 59
 Motif name: C059
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1

Number of overlap: 12
Similarity score: 0.0209747

Alignment:
CMGGGGGDGGKS
CYGSGGGHSGGB

Original motif Consensus sequence: SYCCDCCCCCRG



Reverse complement motif Consensus sequence: CMGGGGGDGGKS

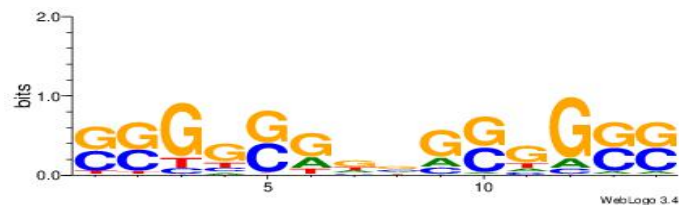
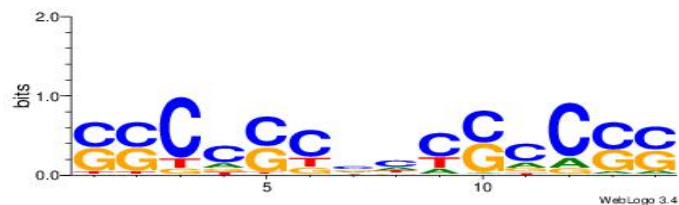


Dataset #: 1
Motif ID: 23
Motif name: C023
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 2
Number of overlap: 12
Similarity score: 0.0227663

Alignment:
SSCCSCBHCSCCSS
-BCCSHCCCSCMG-

Original motif Consensus sequence: SSCCSCBHCSCCSS

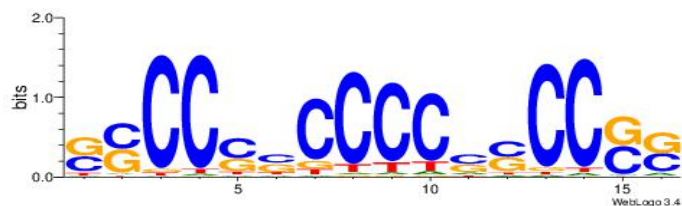
Reverse complement motif Consensus sequence: SSGGSGDBGSGG



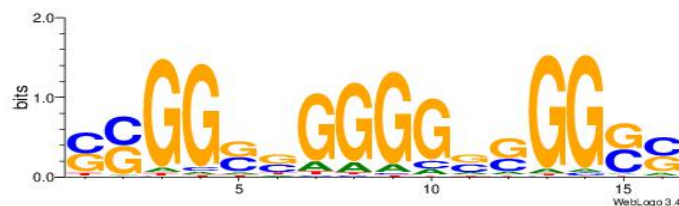
Dataset #: 1
 Motif ID: 8
 Motif name: C008
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 4
 Number of overlap: 12
 Similarity score: 0.0275372

Alignment:
 SSGGSSGGGGSSGGSS
 ---CYGSGGGHSGGB-

Original motif Consensus sequence: SSCCSSCCCCSSCCSS

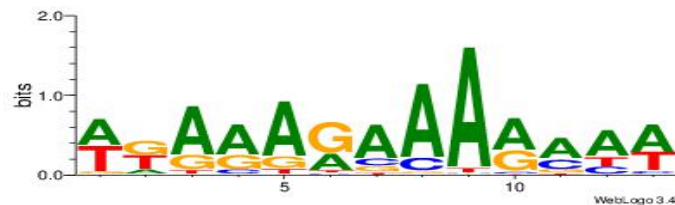


Reverse complement motif Consensus sequence: SSGGSSGGGGSSGGSS

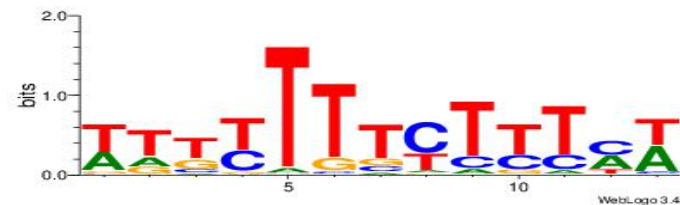


Dataset #: 1 Motif ID: 82 Motif name: C082

Original motif Consensus sequence: WKAAARAAARAAW



Reverse complement motif Consensus sequence: WTTKTTTMTTTYW



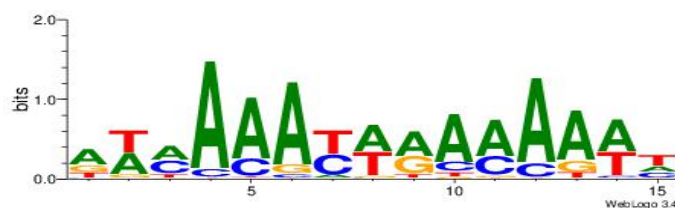
Best Matches for Motif ID 82 (Highest to Lowest)

Dataset #:	1
Motif ID:	56
Motif name:	C056
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	2
Number of overlap:	13
Similarity score:	0.0174406

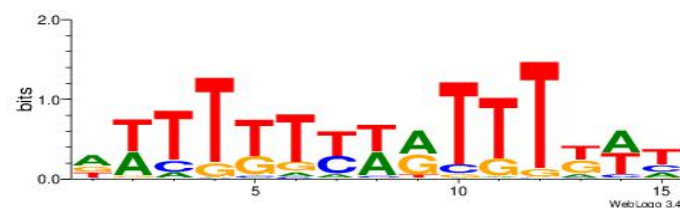
Alignment:

```
HWTTYTKWMTTTYWT
-WTTKTTTMTTTYW-
```

Original motif Consensus sequence: AWMAAAYWRAMAAWH



Reverse complement motif Consensus sequence:
HWTTYTKWMTTTYWT

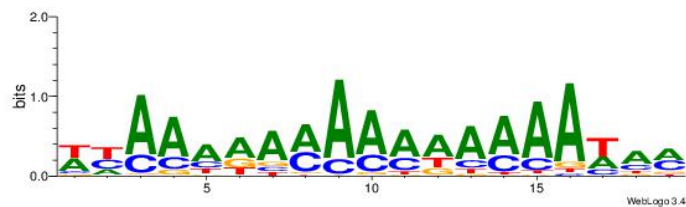


Dataset #: 1
 Motif ID: 30
 Motif name: C030
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 7
 Number of overlap: 13
 Similarity score: 0.018911

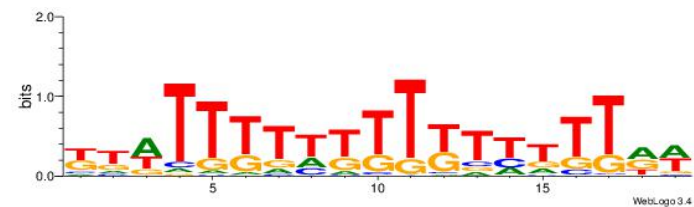
Alignment:

WYAAAAAMAAAAAAWAM
 WKAAARAAARAAW-----

Original motif Consensus sequence: WYAAAAAMAAAAAAWAM



Reverse complement motif Consensus sequence: YTWTTTTTTTTTTTTMW



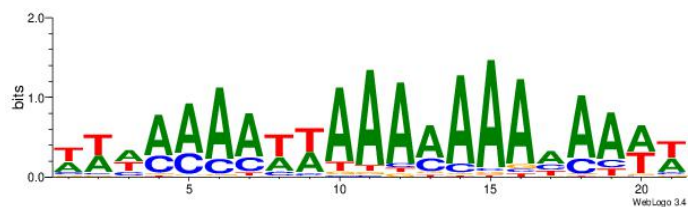
Dataset #: 1
 Motif ID: 10
 Motif name: C010
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2

Number of overlap: 13
Similarity score: 0.0193236

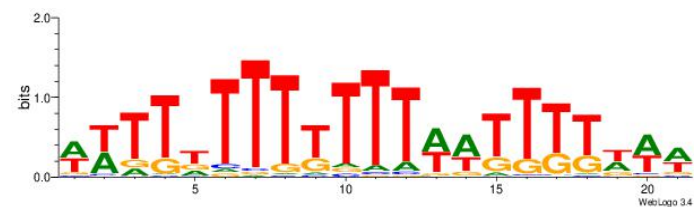
Alignment:

WWWAAAAWWAAAAAAAAAAWW
-----WKAAARAAARA--

Original motif Consensus sequence: WWWAAAAWWAAAAAAAAAAWW



Reverse complement motif Consensus sequence: WWTTTTTTTTTTWWTTTTWWW

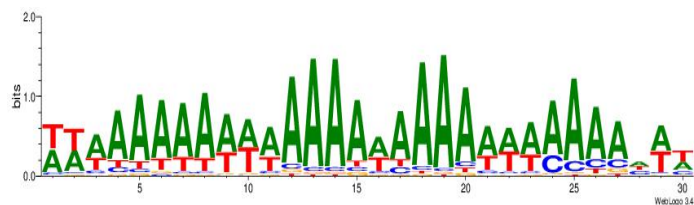


Dataset #: 1
Motif ID: 1
Motif name: C001
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 8
Number of overlap: 13
Similarity score: 0.0203244

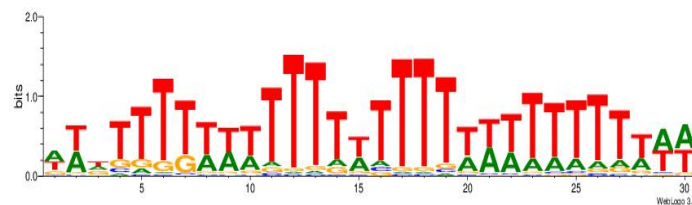
Alignment:

WWHTTTTWWTTTTTWWTTTTTWWTTTTTWW
-----WTTKTTTMTTTYW-----

Original motif Consensus sequence:
WWWAAAAWWAAAAWAAAAWAAAAHWW



Reverse complement motif Consensus sequence:
WWHTTTTWWTTTTWTTTTWTTTTWWW

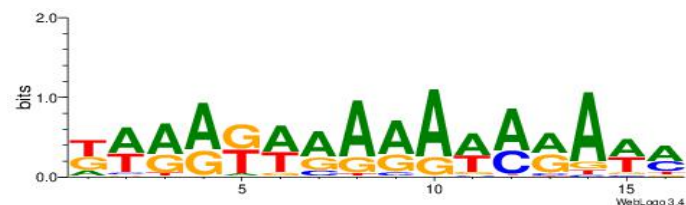


Dataset #: 1
Motif ID: 152
Motif name: C152
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 13
Similarity score: 0.0224829

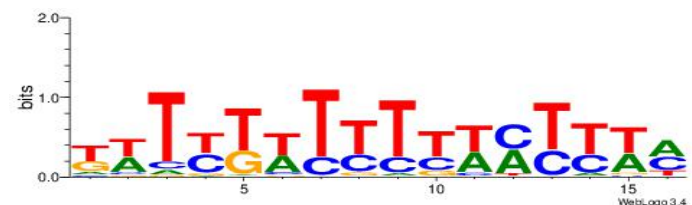
Alignment:

KWRRKWRARAWMRAWM
---WKAAARAAARAAW

Original motif Consensus sequence: KWRRKWRARAWMRAWM

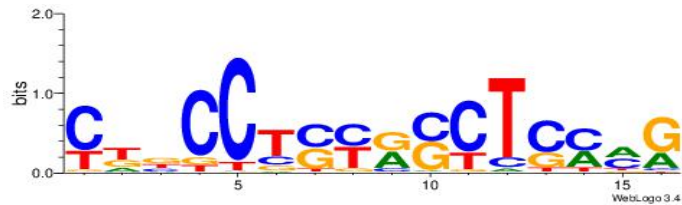


Reverse complement motif Consensus sequence:
YWTKYWTKTKWYKKWR

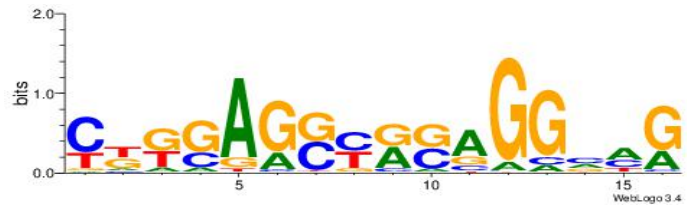


Dataset #: 1 Motif ID: 83 Motif name: C083

Original motif Consensus sequence: CKBCCTSYRSCTCMMG



Reverse complement motif Consensus sequence: CYRGAGSMKSAGGBRG



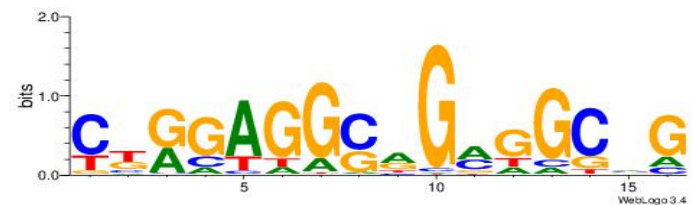
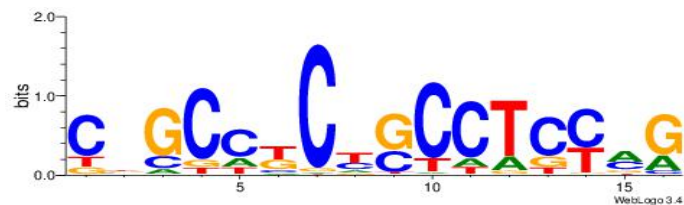
Best Matches for Motif ID 83 (Highest to Lowest)

Dataset #:	1
Motif ID:	50
Motif name:	C050
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	16
Similarity score:	0.0114345

Alignment:
CBGCCCKYSCCTCYMG
CKBCCTSYRSCTCMMG

Original motif Consensus sequence: CBGCCCKYSCCTCYMG

Reverse complement motif Consensus sequence: CYKGAGGSMGRGGCVG

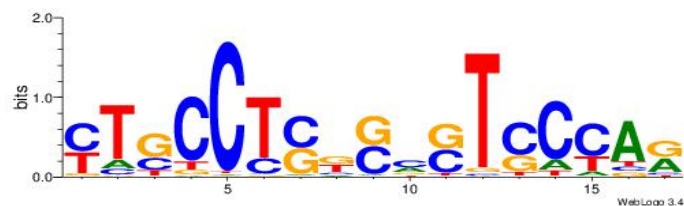


Dataset #: 1
 Motif ID: 101
 Motif name: C101
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 16
 Similarity score: 0.01597

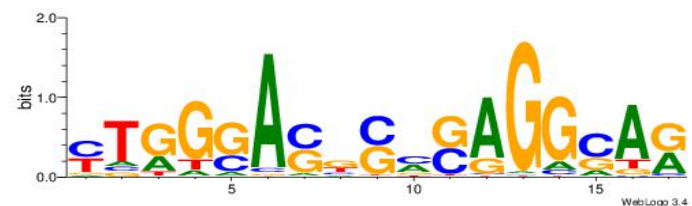
Alignment:

YTSCCTSKSVSTCCCAR
 CKBCCTSYRSCTCMMG-

Original motif Consensus sequence: YTSCCTSKSVSTCCCAR



Reverse complement motif Consensus sequence: MTGGGASVSYSAGGSAK



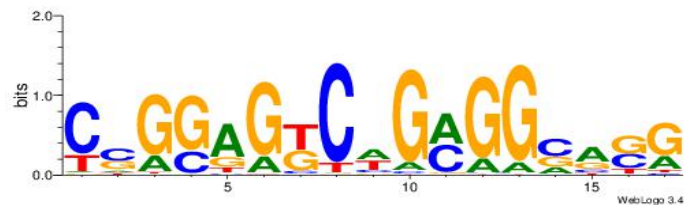
Dataset #: 1

Motif ID: 86
 Motif name: C086
 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: 0.0280972

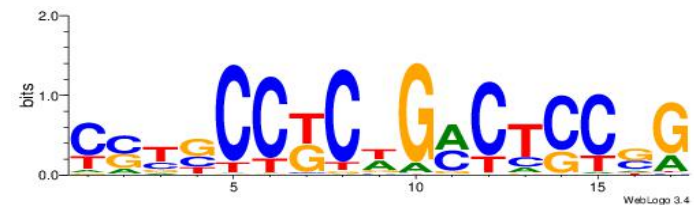
Alignment:

CSTSCCYCWGRCTCCSG
 -CKBCCTSYRSTCMMG

Original motif Consensus sequence: CSGGAGKCWGMGGSASG



Reverse complement motif Consensus sequence: CSTSCCYCWGRCTCCSG

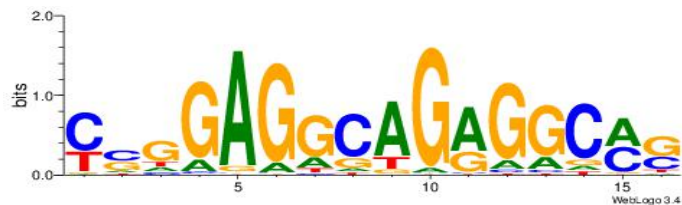


Dataset #: 1
 Motif ID: 14
 Motif name: C014
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 16

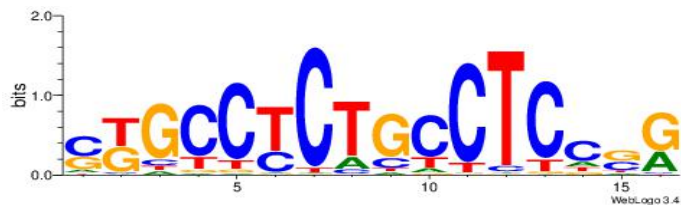
Similarity score: 0.0331373

Alignment:
YSGGAGGCAGAGGCMS
CYRGAGSMKSAGGBRG

Original motif Consensus sequence: YSGGAGGCAGAGGCMS



Reverse complement motif Consensus sequence: SYGCCTCTGCCTCCSK

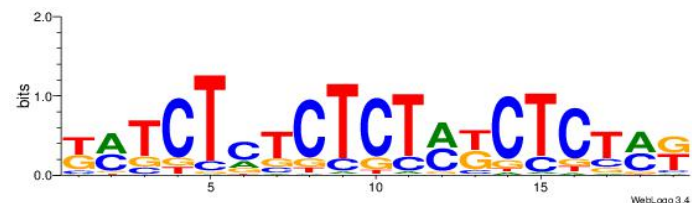
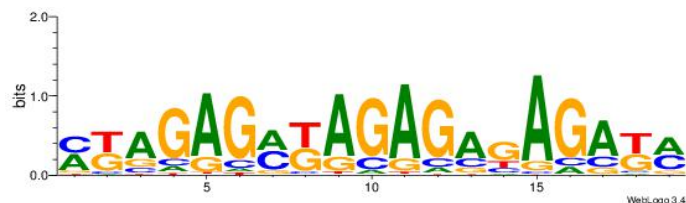


Dataset #: 1
Motif ID: 12
Motif name: C012
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 4
Number of overlap: 16
Similarity score: 0.0363902

Alignment:
MKAGAGMKAGAGAGAGAKM
---CYRGAGSMKSAGGBRG

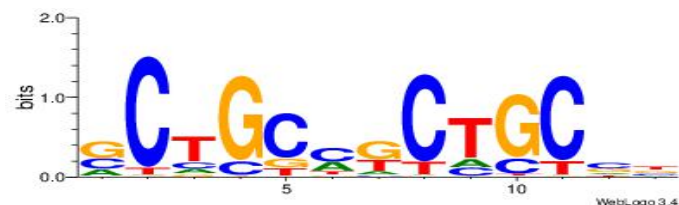
Original motif Consensus sequence: MKAGAGMKAGAGAGAGAKM

Reverse complement motif Consensus sequence: YRTCTCTCTCTRYCTCTRR

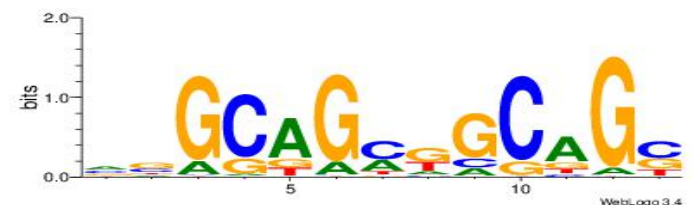


Dataset #: 1 Motif ID: 84 Motif name: C084

Original motif Consensus sequence: SCTGCMKCTGCVB



Reverse complement motif Consensus sequence: VVGCAGYRGCAGS



Best Matches for Motif ID 84 (Highest to Lowest)

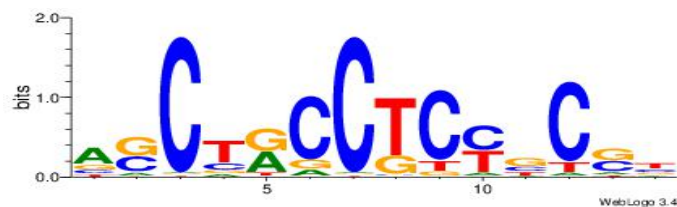
Dataset #:	1
Motif ID:	76
Motif name:	C076
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	13
Similarity score:	0.00787805

Alignment:

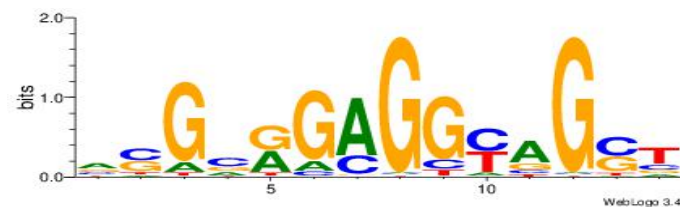
ASCTRCCTCYBCSB

–SCTGCMKCTGCVB

Original motif Consensus sequence: ASCTRCCTCYBCSB



Reverse complement motif Consensus sequence: VSGBKGAGGMAGS

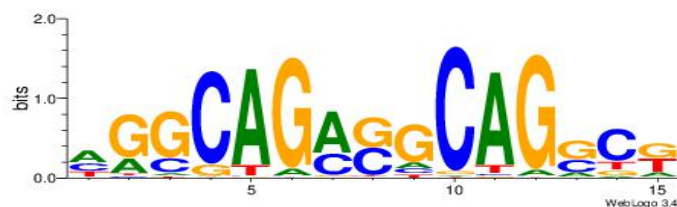


Dataset #: 1
 Motif ID: 75
 Motif name: C075
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 13
 Similarity score: 0.0120992

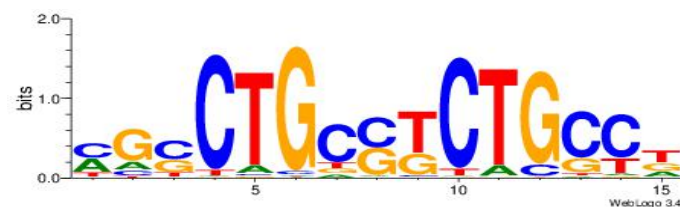
Alignment:

YGSCTGCSYCTGCCY
 SCTGCMKCTGCVB--

Original motif Consensus sequence: MGGCAGMSGCAGSCK



Reverse complement motif Consensus sequence: YGSCTGCSYCTGCC

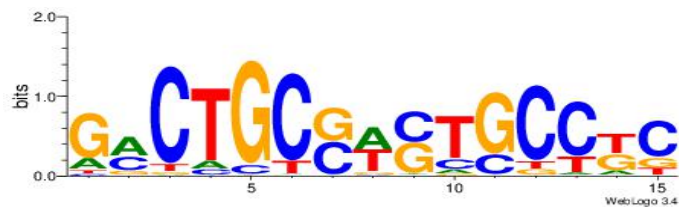


Dataset #: 1
 Motif ID: 118
 Motif name: C118
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 13
 Similarity score: 0.0130639

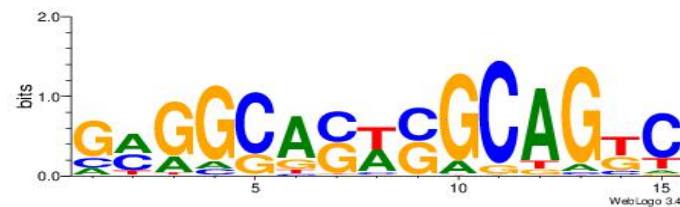
Alignment:

GMCTGCSWSTGCCCKC
 -SCTGCMKCTGCVB-

Original motif Consensus sequence: GMCTGCSWSTGCCCKC



Reverse complement motif Consensus sequence: GRGGCASWSGCAGYC



Dataset #: 1
 Motif ID: 106
 Motif name: C106
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1

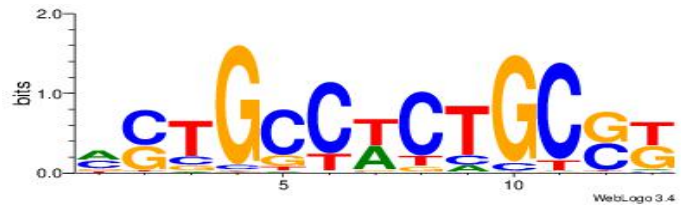
Number of overlap: 13
Similarity score: 0.0148962

Alignment:
RSTGCCWCTGCSY
SCTGCMKCTGCVB

Original motif Consensus sequence: MSGCAGWGGCASK



Reverse complement motif Consensus sequence: RSTGCCWCTGCSY

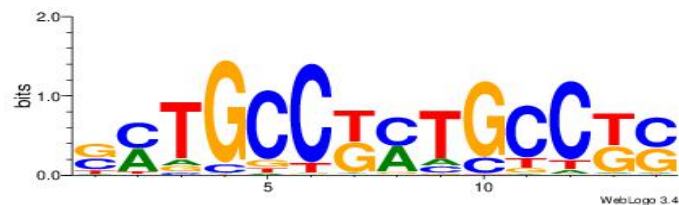
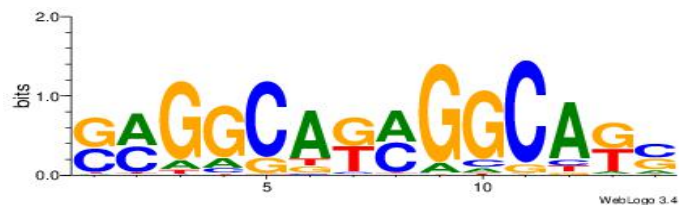


Dataset #: 1
Motif ID: 60
Motif name: C060
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 2
Number of overlap: 13
Similarity score: 0.0166117

Alignment:
SYTGCCYYTGCCYS
-SCTGCMKCTGCVB

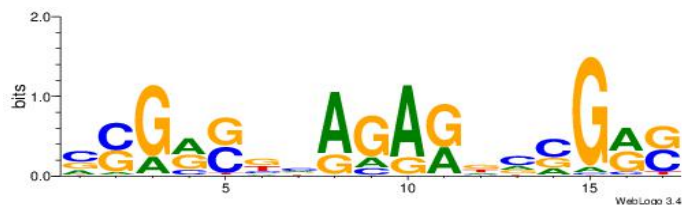
Original motif Consensus sequence: SMGGCAKMGGCAKS

Reverse complement motif Consensus sequence: SYTGCCYYTGCCYS

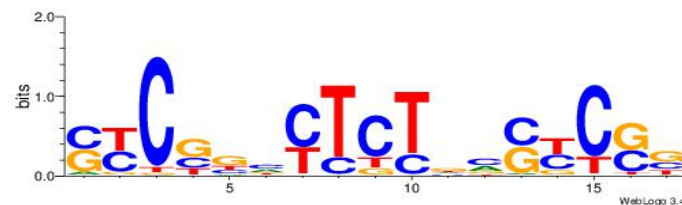


Dataset #: 1 Motif ID: 85 Motif name: C085

Original motif Consensus sequence: VSGRSBHAGARDVSGRS



Reverse complement motif Consensus sequence: SKCSVHMTCTDBSKCSV



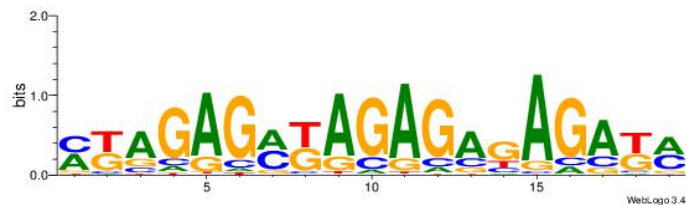
Best Matches for Motif ID 85 (Highest to Lowest)

Dataset #:	1
Motif ID:	12
Motif name:	C012
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	2
Number of overlap:	17
Similarity score:	0.0286515

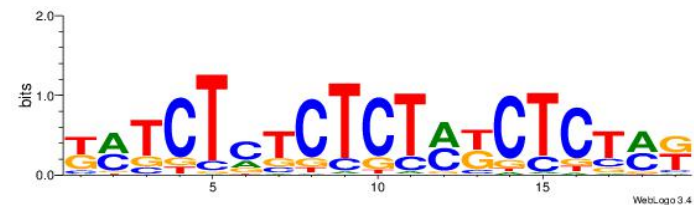
Alignment:

YRTCTCTCTCTRYCTCTRR
-SKCSVHMTCTDBSKCSV-

Original motif Consensus sequence: MKAGAGMKAGAGAGAGAKM



Reverse complement motif Consensus sequence: YRTCTCTCTCTRYCTCTRR

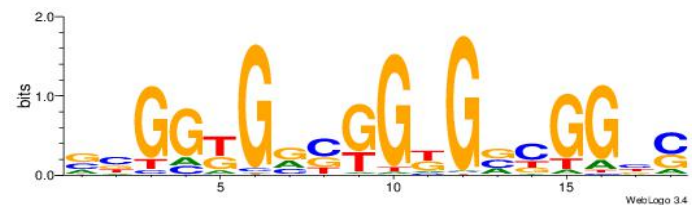
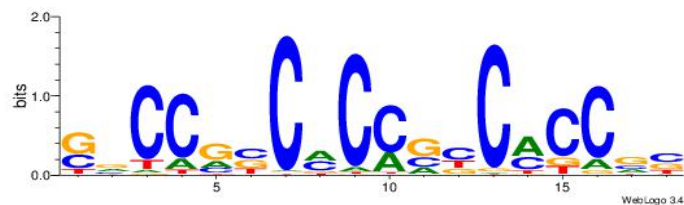


Dataset #:	1
Motif ID:	37
Motif name:	C037
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	17
Similarity score:	0.033047

Alignment:
SVCCGBCMCCSYCMCCVB
-SKCSVHMTCTDBSKCSV

Original motif Consensus sequence: SVCCGBCMCCSYCMCCVB

Reverse complement motif Consensus sequence: BVGGYGKSGGYGBCGGVS

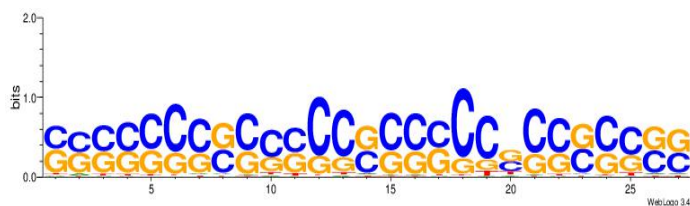


Dataset #: 1
 Motif ID: 4
 Motif name: C004
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 17
 Similarity score: 0.0361207

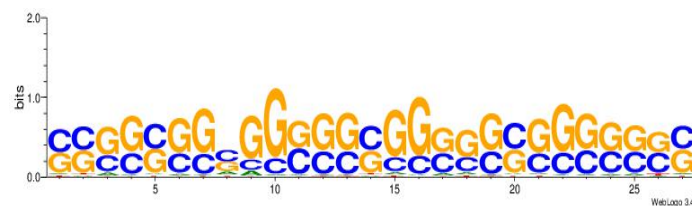
Alignment:

SSSSSCSCSSSSCCSSSSCCSCSSSSSS
 SKCSVHMTCTDBSKCSV-----

Original motif Consensus sequence:
 SSSSSCSCSSSSCCSSSSCCSCSSSSSS



Reverse complement motif Consensus sequence:
 SSSSSGSGGSSSSGGSSSSGSSSSS

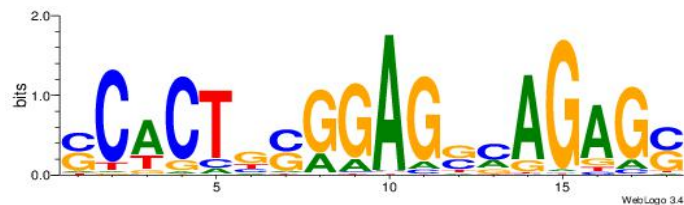


Dataset #: 1

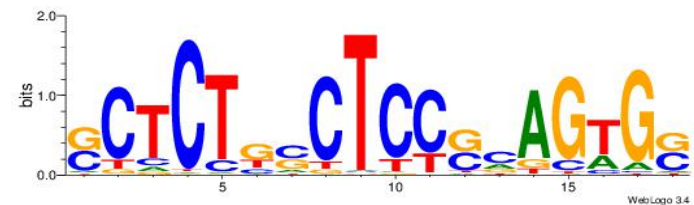
Motif ID: 34
 Motif name: C034
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 17
 Similarity score: 0.0436458

Alignment:
 SCACTGSGGAGSMAGAGS
 VSGRSBHAGARDVSGRS-

Original motif Consensus sequence: SCACTGSGGAGSMAGAGS



Reverse complement motif Consensus sequence: SCTCTRSCTCCSCAGTGS

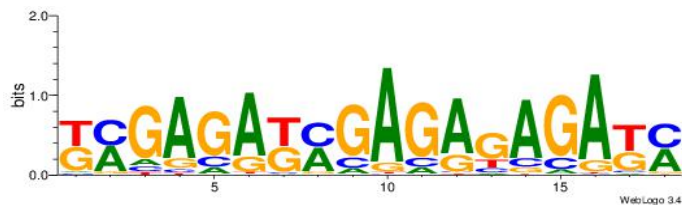


Dataset #: 1
 Motif ID: 11
 Motif name: C011
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 17

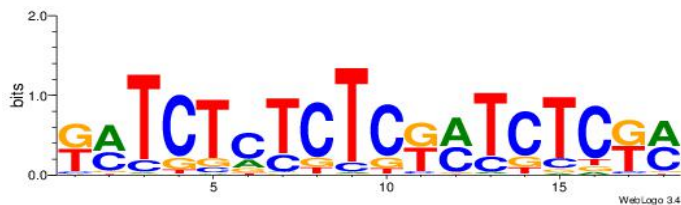
Similarity score: 0.0443201

Alignment:
RRTCTCTCTCRRTCTCRR
-SKCSVHMTCTDBSKCSV

Original motif Consensus sequence: KMGAGAKMGAGAGAGAKM

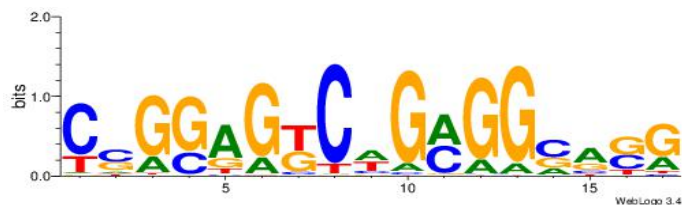


Reverse complement motif Consensus sequence: RRTCTCTCTCRRTCTCRR

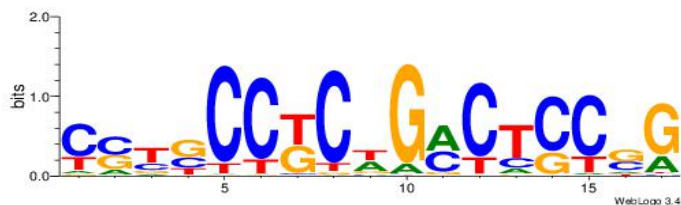


Dataset #: 1 Motif ID: 86 Motif name: C086

Original motif Consensus sequence: CSGGAGKCWGMGGSASG



Reverse complement motif Consensus sequence: CSTSCCYCWGRCTCCSG



Best Matches for Motif ID 86 (Highest to Lowest)

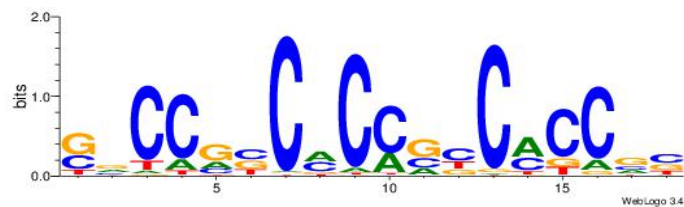
Dataset #: 1
Motif ID: 37
Motif name: C037
Matching format of first motif: Reverse Complement

Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	17
Similarity score:	0.0392191

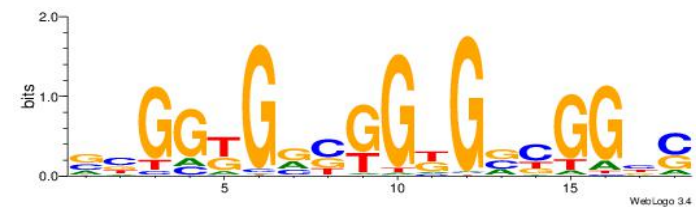
Alignment:

```
SVCCGBCMCCSYCMCCVB
CSTSCCYCWGRCTCCSG-
```

Original motif Consensus sequence: SVCCGBCMCCSYCMCCVB



Reverse complement motif Consensus sequence: BVGGYGKSGGYGBCGGVS

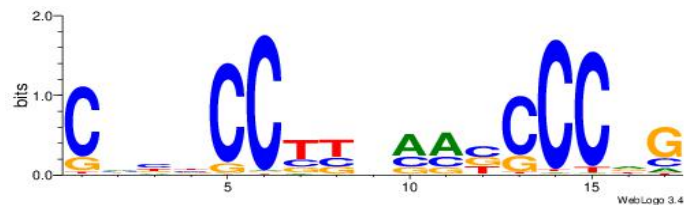


Dataset #:	1
Motif ID:	107
Motif name:	C107
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	17
Similarity score:	0.0441792

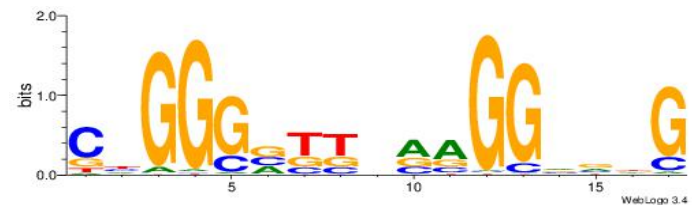
Alignment:

CDGGGBTVMAGGVBHG
CSGGAGKCWGMGGSASG

Original motif Consensus sequence: CHBBCCTYBAABCCCDG



Reverse complement motif Consensus sequence: CDGGGBTVMAGGVBHG



Dataset #:	1
Motif ID:	3
Motif name:	C003
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	3
Number of overlap:	17
Similarity score:	0.047958

Alignment:

GSSGGGGSSGGGGGGKGGVMGGSHGKGSC
-----CSGGAGKCWGMGGSASG--

Original motif Consensus sequence:
GSCYCHSCCYVCCYCCCCCSCCCCCSSC

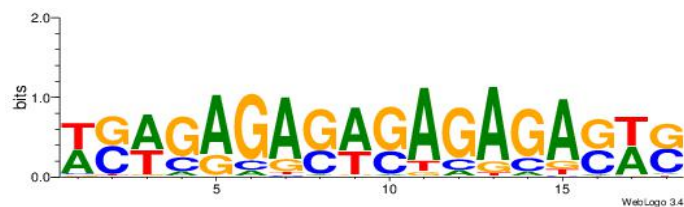
Reverse complement motif Consensus sequence:
GSSGGGGSSGGGGGGKGGVMGGSHGKGSC

Motif ID: 17
 Motif name: C017
 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: 0.0513474

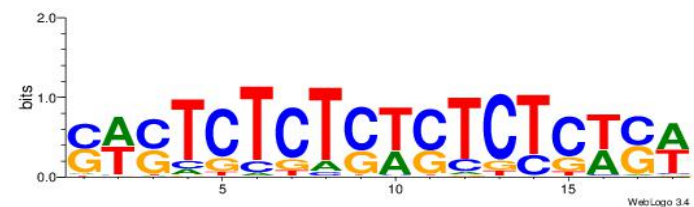
Alignment:

WSWGAGASWSAGAGASWS
 CSGGAGKCGMGGASG-

Original motif Consensus sequence: WSWGAGASWSAGAGASWS

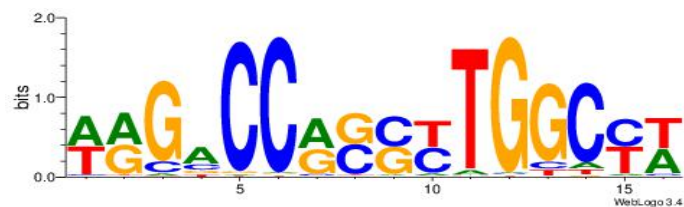


Reverse complement motif Consensus sequence: SWSTCTCTSWSTCTCWSW

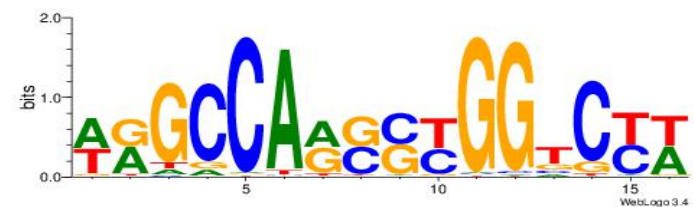


Dataset #: 1 Motif ID: 87 Motif name: C087

Original motif Consensus sequence: WRGACCRSSYTGGCYW



Reverse complement motif Consensus sequence: WKGCCAMSSKGGTCKW



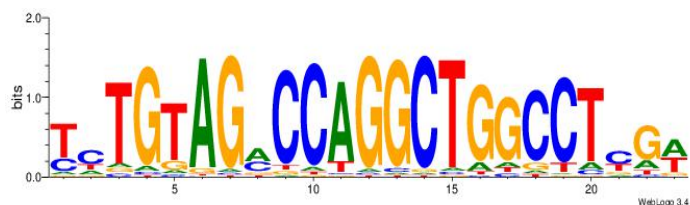
Best Matches for Motif ID 87 (Highest to Lowest)

Dataset #: 1
Motif ID: 5
Motif name: C005
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 5
Number of overlap: 16
Similarity score: 0.0082892

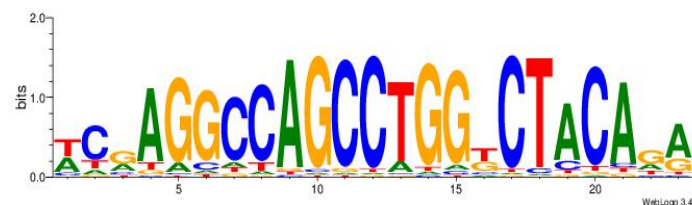
Alignment:

```
TCTGTAGMCCAGGCTGGCCTYGW  
----WRGACCRSSYTGGCYW----
```

Original motif Consensus sequence: TCTGTAGMCCAGGCTGGCCTYGW



Reverse complement motif Consensus sequence:
WCKAGGCCAGCCTGGYCTACAGA



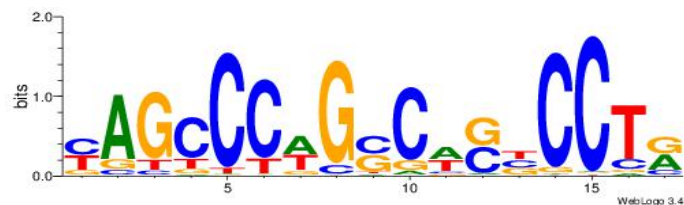
Dataset #: 1
Motif ID: 122
Motif name: C122
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif

Direction: Forward
 Position number: 1
 Number of overlap: 16
 Similarity score: 0.0323948

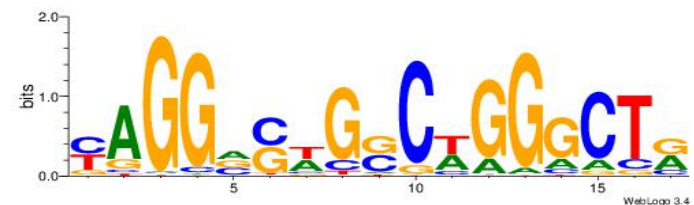
Alignment:

YAGCCCWGSCWSBCCTR
 WRGACCRSSYTGGCYW-

Original motif Consensus sequence: YAGCCCWGSCWSBCCTR



Reverse complement motif Consensus sequence: MAGGVSWGSCWGGGCTK

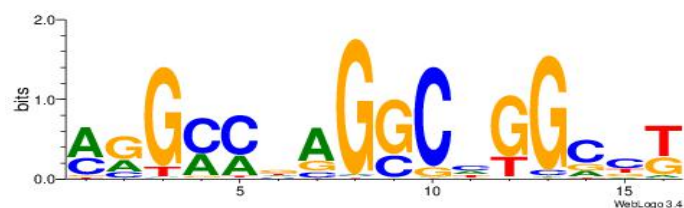


Dataset #: 1
 Motif ID: 61
 Motif name: C061
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 16
 Similarity score: 0.0331199

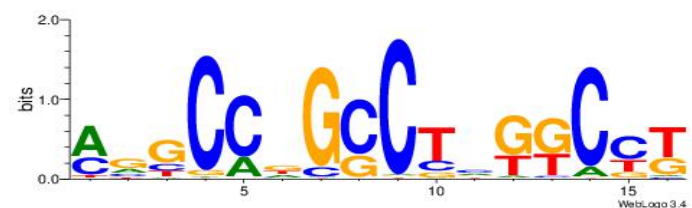
Alignment:

MRGMMBAGGCHGGCCK
 WRGACCRSSYTGGCYW

Original motif Consensus sequence: MRGMMBAGGCHGGCCK



Reverse complement motif Consensus sequence: RGGCCDGCCTBRRCMY

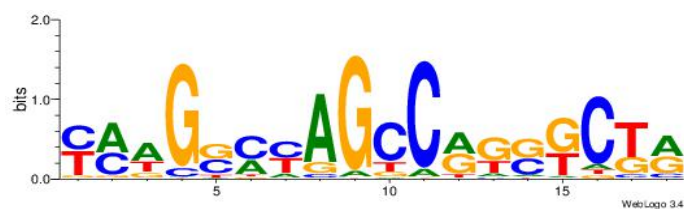


Dataset #: 1
Motif ID: 73
Motif name: C073
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 3
Number of overlap: 16
Similarity score: 0.0403976

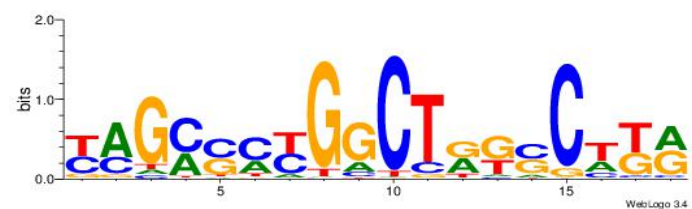
Alignment:

YMWGSMYAGCCRKSKCTR
WKGCCAMSSKGGTCKW--

Original motif Consensus sequence: YMWGSMYAGCCRKSKCTR



Reverse complement motif Consensus sequence: KAGYSYKGGCTKRSCWYK

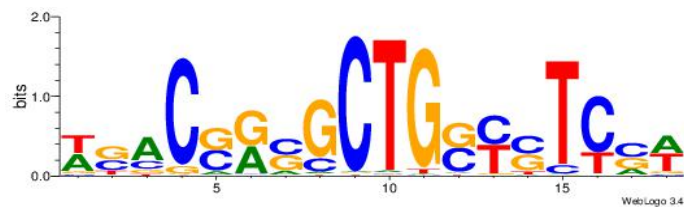


Dataset #: 1
 Motif ID: 124
 Motif name: C124
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 16
 Similarity score: 0.0419895

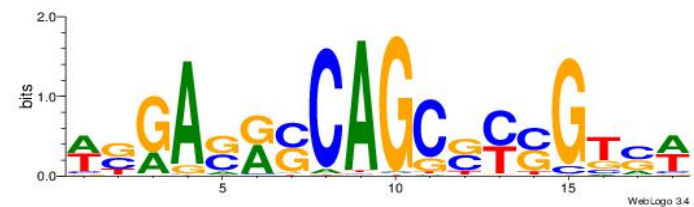
Alignment:

WSACSRSGCTGSYSTCSW
 WKGCCAMSSKGGTCKW--

Original motif Consensus sequence: WSACSRSGCTGSYSTCSW



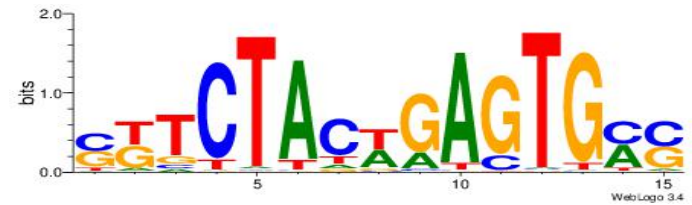
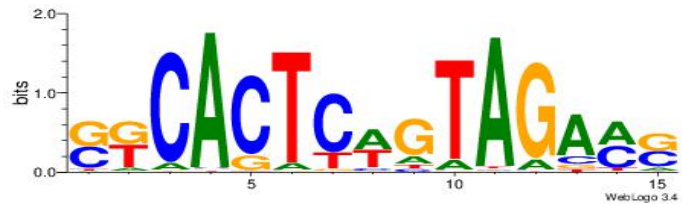
Reverse complement motif Consensus sequence: WSGASKSCAGCSMSGTSW



Dataset #: 1 Motif ID: 88 Motif name: C088

Original motif Consensus sequence: SKACTCWGTAGAMS

Reverse complement motif Consensus sequence: SYTCTACWGAGTG



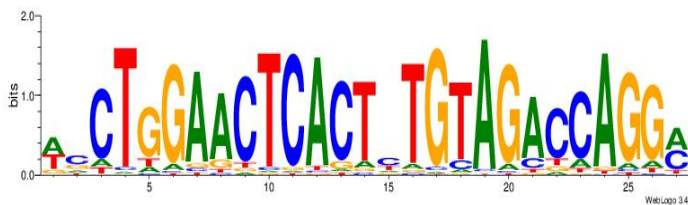
Best Matches for Motif ID 88 (Highest to Lowest)

Dataset #: 1
 Motif ID: 13
 Motif name: C013
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 9
 Number of overlap: 15
 Similarity score: 0

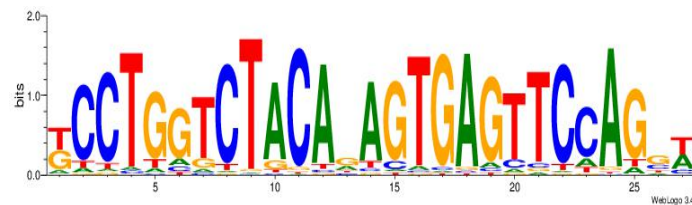
Alignment:

WVCTGGAAC TCACTHTGTAGACCAGGM
 -----SKCACTCWGTAGAMS-----

Original motif Consensus sequence:
 WVCTGGAAC TCACTHTGTAGACCAGGM



Reverse complement motif Consensus sequence:
 YCCTGGTCTACADAGTGAGTTCCAGVW

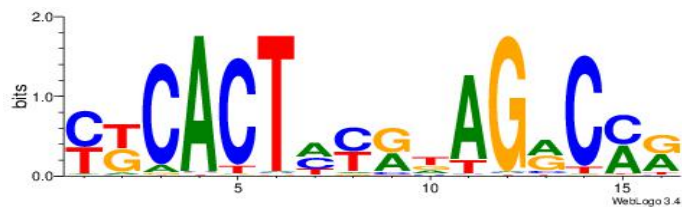


Dataset #: 1
 Motif ID: 89
 Motif name: C089
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 15
 Similarity score: 0.00807426

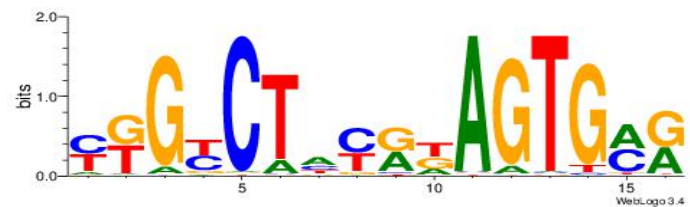
Alignment:

YKCACTMYRDAGRCMR
 SKCACTCWGTAGAMS-

Original motif Consensus sequence: YKCACTMYRDAGRCMR



Reverse complement motif Consensus sequence: MRGKCTDMKYAGTGRK

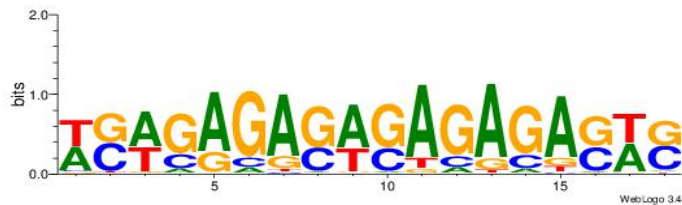


Dataset #: 1
 Motif ID: 17
 Motif name: C017
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3

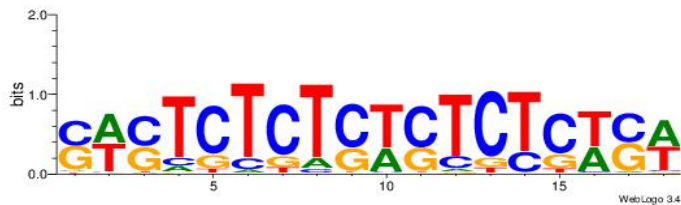
Number of overlap: 15
Similarity score: 0.0441447

Alignment:
WSWGAGASWSAGAGASWS
--SYTCTACWGAGTGYS--

Original motif Consensus sequence: WSWGAGASWSAGAGASWS



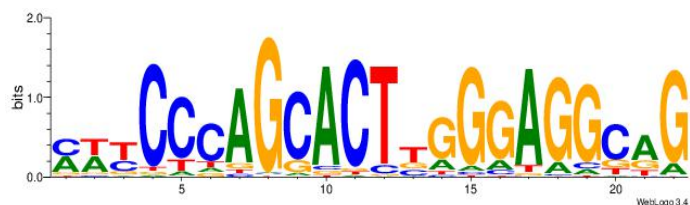
Reverse complement motif Consensus sequence: SWSTCTCTSWSTCTCWSW



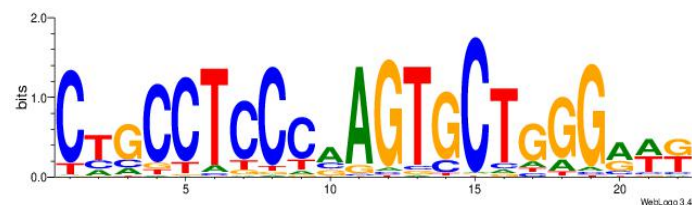
Dataset #: 1
Motif ID: 19
Motif name: C019
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 7
Number of overlap: 15
Similarity score: 0.0452176

Alignment:
MWYCCCAGCACTTGGGAGGCAG
-----SKCACTCWGTAGAMS--

Original motif Consensus sequence: MWYCCCAGCACTTGGGAGGCAG



Reverse complement motif Consensus sequence: CTGCTCCCAAGTGCTGGGMWR

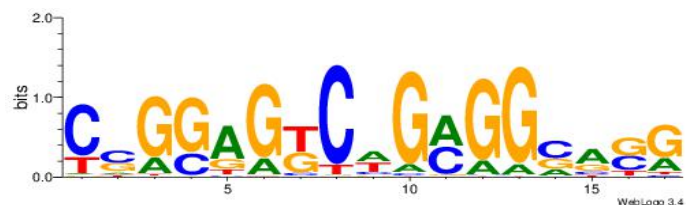


Dataset #: 1
Motif ID: 86
Motif name: C086
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2
Number of overlap: 15
Similarity score: 0.0452921

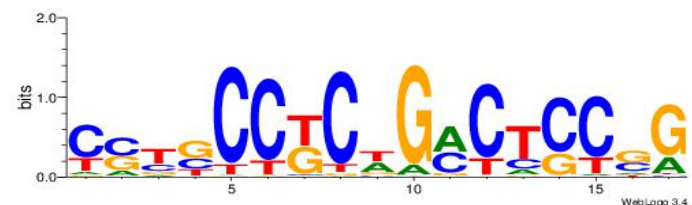
Alignment:

CSGGAGKWCWGMGGSASG
-SKCACTCWGTAGAMS-

Original motif Consensus sequence: CSGGAGKWCWGMGGSASG

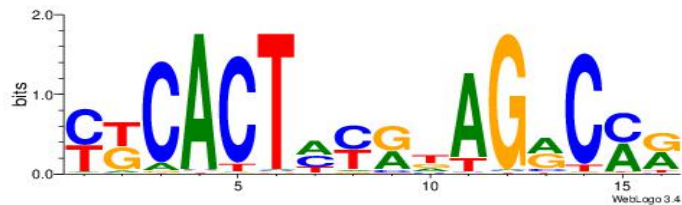


Reverse complement motif Consensus sequence: CSTSCCYCWGRCTCCSG

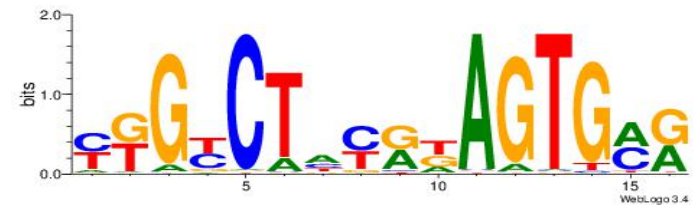


Dataset #: 1 **Motif ID: 89** **Motif name: C089**

Original motif Consensus sequence: YKCACTMYRDAGRCMR



Reverse complement motif Consensus sequence: MRGKCTDMKYAGTGRK



Best Matches for Motif ID 89 (Highest to Lowest)

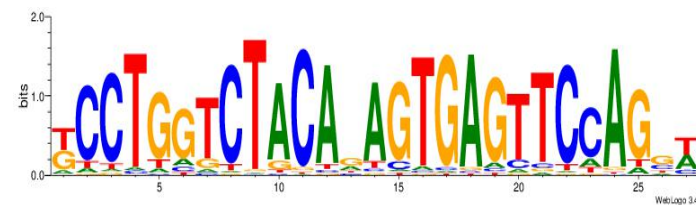
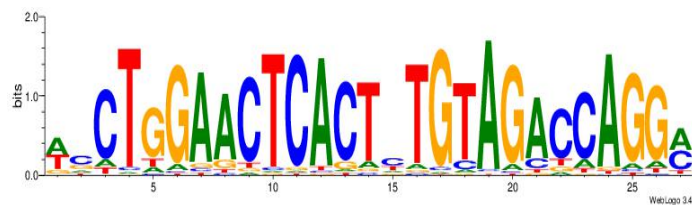
Dataset #:	1
Motif ID:	13
Motif name:	C013
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	9
Number of overlap:	16
Similarity score:	0.00883756

Alignment:

```
WVCTGGAAC TCACTHTGTAGACCAGGM
-----YKCACTMYRDAGRCMR---
```

Original motif Consensus sequence:
WVCTGGAAC TCACTHTGTAGACCAGGM

Reverse complement motif Consensus sequence:
YCCTGGTCTACADAGTGAGTTCCAGVW

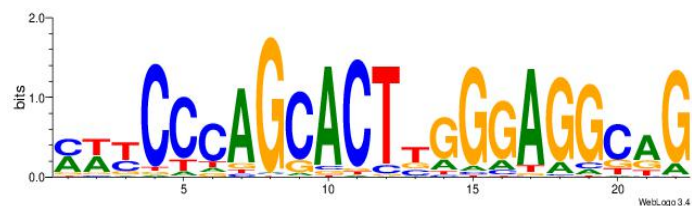


Dataset #: 1
 Motif ID: 19
 Motif name: C019
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 7
 Number of overlap: 16
 Similarity score: 0.0298537

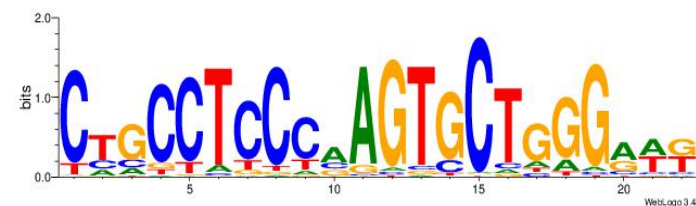
Alignment:

MWYCCCAGCACTTGGGAGGCAG
 -----YKCACTMYRDAGRCMR

Original motif Consensus sequence: MWYCCCAGCACTTGGGAGGCAG



Reverse complement motif Consensus sequence: CTGCCTCCCAAGTGCTGGGMWR

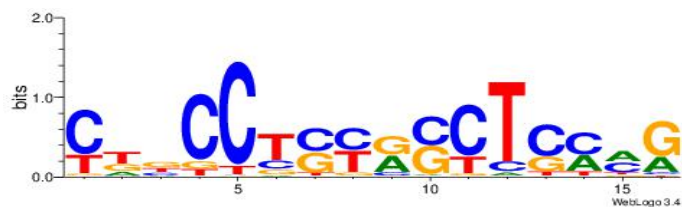


Dataset #: 1

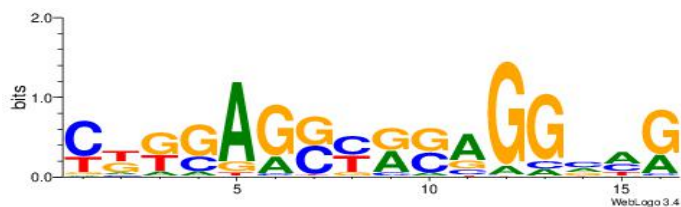
Motif ID: 83
Motif name: C083
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 16
Similarity score: 0.0453026

Alignment:
CKBCCTSYRSCTCMMG
YKCACTMYRDAGRCMR

Original motif Consensus sequence: CKBCCTSYRSCTCMMG



Reverse complement motif Consensus sequence: CYRGAGSMKSAGGBRG

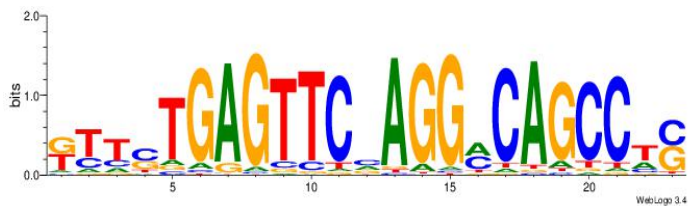


Dataset #: 1
Motif ID: 7
Motif name: C007
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 4
Number of overlap: 16

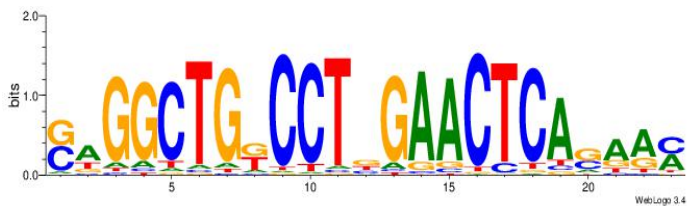
Similarity score: 0.0523729

Alignment:
KTTSTGAGTTCVAGGMCAGCCTS
---YKCACTMYRDAGRCMR----

Original motif Consensus sequence: KTTSTGAGTTCVAGGMCAGCCTS



Reverse complement motif Consensus sequence:
SAGGCTGYCCTVGAAGTCASAAY

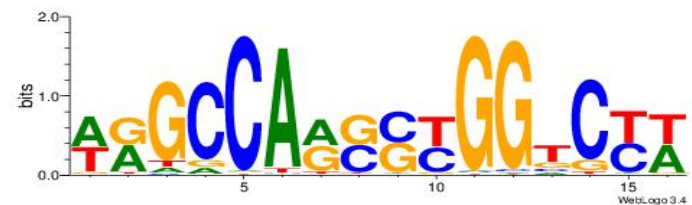
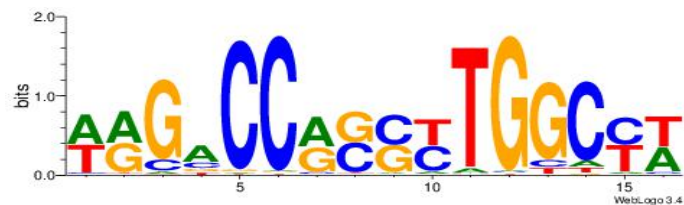


Dataset #: 1
Motif ID: 87
Motif name: C087
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 16
Similarity score: 0.054

Alignment:
WRGACCRSSYTGGCYW
YKCACTMYRDAGRCMR

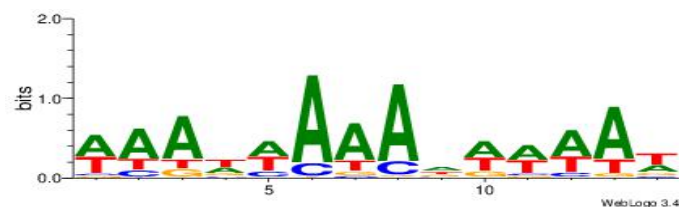
Original motif Consensus sequence: WRGACCRSSYTGGCYW

Reverse complement motif Consensus sequence:
WKGCCAMSSKGGTCKW

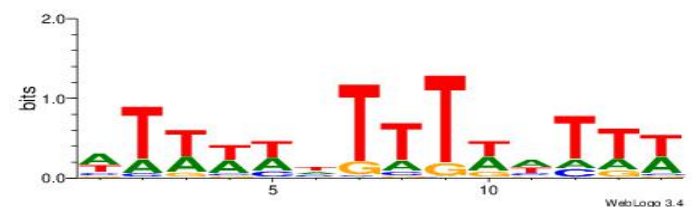


Dataset #: 1 Motif ID: 90 Motif name: C090

Original motif Consensus sequence: WAAWWAAADWWAW



Reverse complement motif Consensus sequence: WTWWWDTTTWWTTW



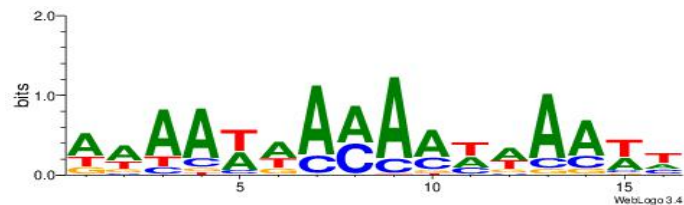
Best Matches for Motif ID 90 (Highest to Lowest)

Dataset #:	1
Motif ID:	98
Motif name:	C098
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:	0.0116821

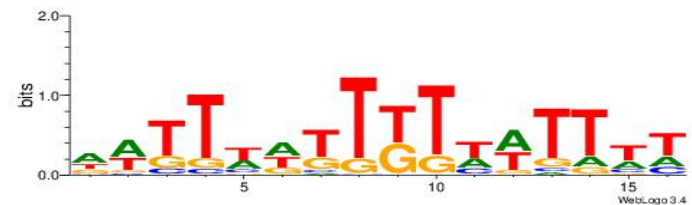
Alignment:

AAAAWWAMAAWWAAWH
 -WAAWWAAADWWWAW-

Original motif Consensus sequence: AAAAWWAMAAWWAAWH



Reverse complement motif Consensus sequence: HWTTWWTTYTWWT TTT

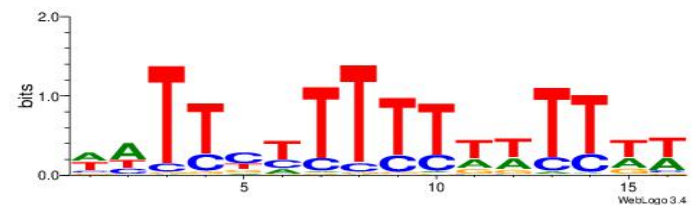
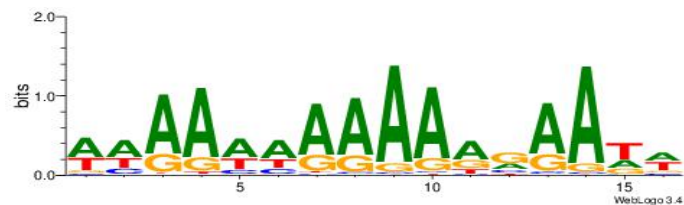


Dataset #:	1
Motif ID:	43
Motif name:	C043
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	14
Similarity score:	0.0235146

Alignment:
 WWAAWAAAAAARAATW
 -WAAWWAAADWWWAW-

Original motif Consensus sequence: WWAAWAAAAAARAATW

Reverse complement motif Consensus sequence: WATTMTTTTTTWTTWW

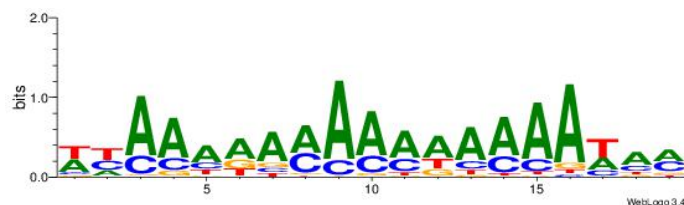


Dataset #: 1
 Motif ID: 30
 Motif name: C030
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 14
 Similarity score: 0.0237672

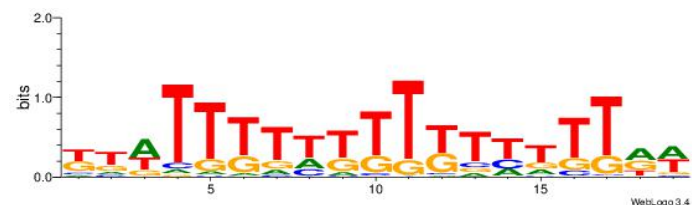
Alignment:

WYAAAAAMAAAAAAWAM
 ---WAAWWAAADWWAW---

Original motif Consensus sequence: WYAAAAAMAAAAAAWAM



Reverse complement motif Consensus sequence: YTWTTTTTTTTTTTTMW



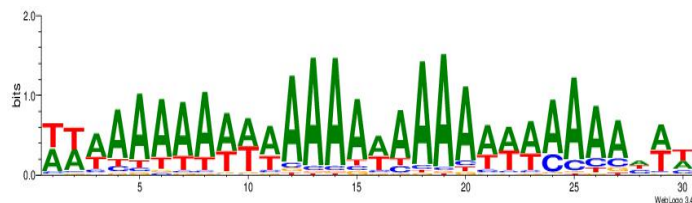
Dataset #: 1

Motif ID: 1
 Motif name: C001
 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: 0.0242608

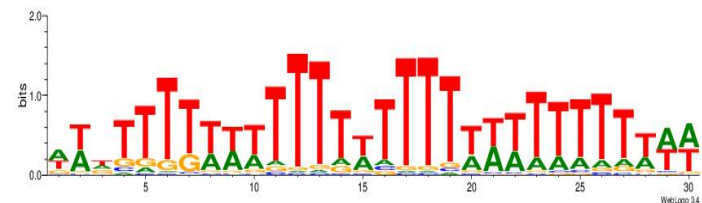
Alignment:

WWWAAAAWWAAAAWAAAAWAAAAHWW
 -----WAAWWAADWWWAW-----

Original motif Consensus sequence:
 WWWAAAAWWAAAAWAAAAWAAAAHWW



Reverse complement motif Consensus sequence:
 WWHTTTTWWTTTTWTTTTWTTTTWWW

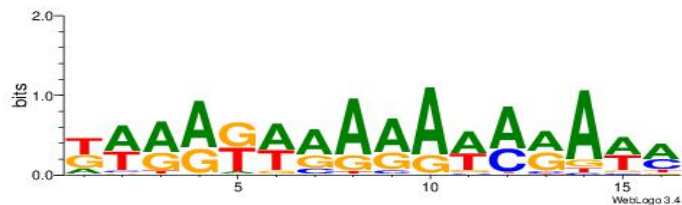


Dataset #: 1
 Motif ID: 152
 Motif name: C152
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 14

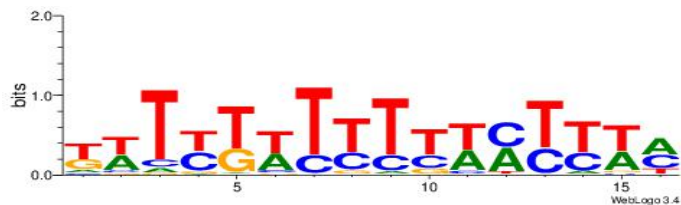
Similarity score: 0.0256107

Alignment:
KWRRKWRARAWMRAWM
-WAAWWAAADWWAW-

Original motif Consensus sequence: KWRRKWRARAWMRAWM

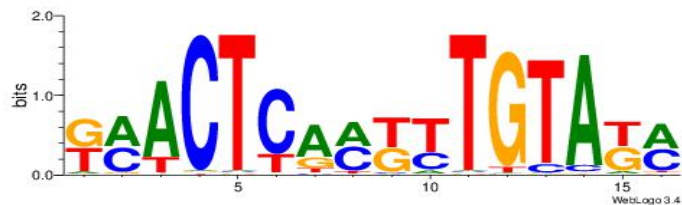


Reverse complement motif Consensus sequence: YWTKYWTKTKWYKKWR

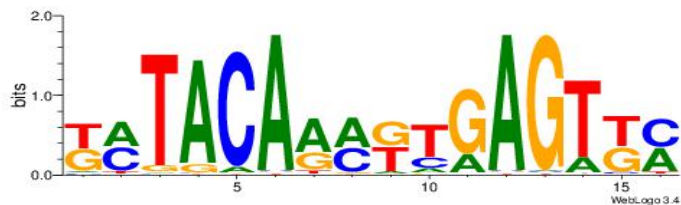


Dataset #: 1 Motif ID: 91 Motif name: C091

Original motif Consensus sequence: KMACTCAMKYTGTAKM



Reverse complement motif Consensus sequence: YRTACAMRYTGAGTYY



Best Matches for Motif ID 91 (Highest to Lowest)

Dataset #:	1
Motif ID:	13
Motif name:	C013
Matching format of first motif:	Original Motif

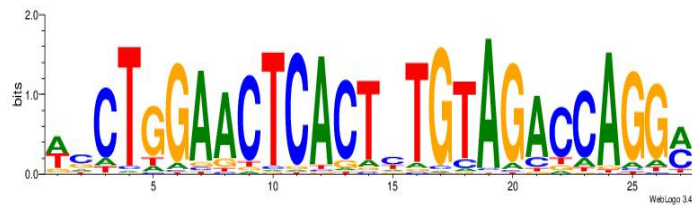
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	6
Number of overlap:	16
Similarity score:	0.00384196

Alignment:

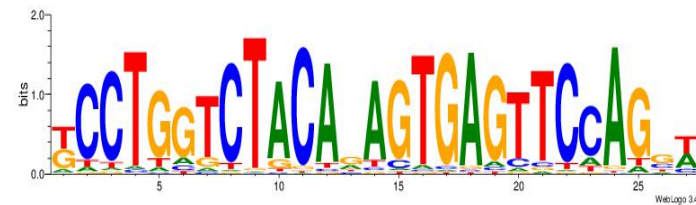
```

WVCTGGAAC TCACTHTGTAGACCAGGM
-----KMACTCAMKYTGTAKM-----
  
```

Original motif Consensus sequence:
WVCTGGAAC TCACTHTGTAGACCAGGM



Reverse complement motif Consensus sequence:
YCCTGGTCTACADAGTGAGTTCCAGVW

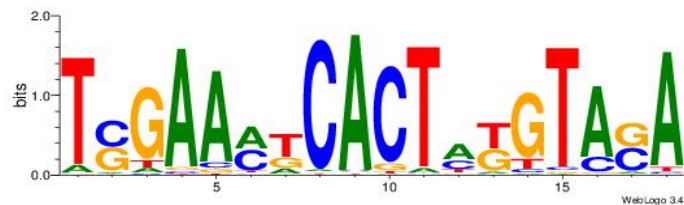


Dataset #:	1
Motif ID:	47
Motif name:	C047
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	16
Similarity score:	0.0310544

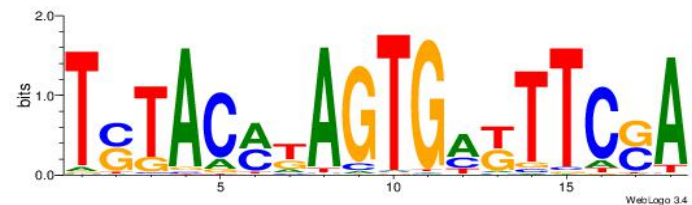
Alignment:

TSGAAMTCACTMKGTASA
 --KMACTCAMKYTGAKM

Original motif Consensus sequence: TSGAAMTCACTMKGTASA



Reverse complement motif Consensus sequence: TSTACRYAGTGAYTTCSA

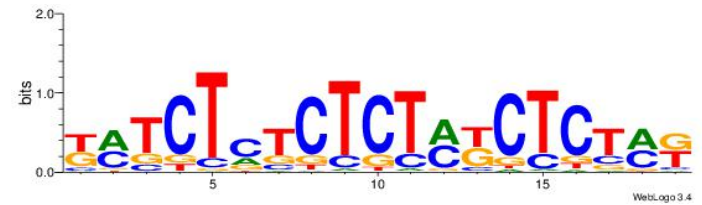
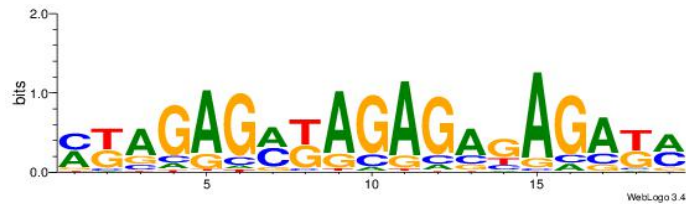


Dataset #:	1
Motif ID:	12
Motif name:	C012
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	4
Number of overlap:	16
Similarity score:	0.0540334

Alignment:
 MKAGAGMKAGAGAGAGAKM
 YRTACAMRYTGAGTYY---

Original motif Consensus sequence: MKAGAGMKAGAGAGAGAKM

Reverse complement motif Consensus sequence: YRTCTCTCTRYCTCTRR

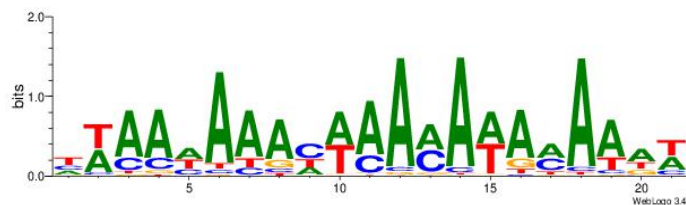


Dataset #: 1
 Motif ID: 16
 Motif name: C016
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 16
 Similarity score: 0.0563449

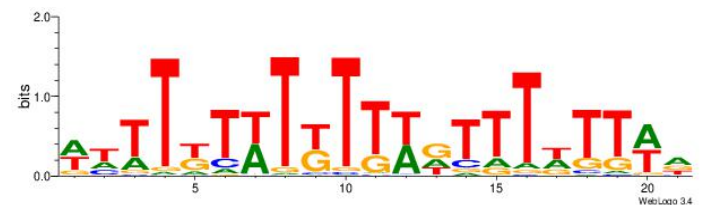
Alignment:

HWAAWAAAHWAAMAWAMAAWW
 -----YRTACAMRYTGAGTTY

Original motif Consensus sequence: HWAAWAAAHWAAMAWAMAAWW



Reverse complement motif Consensus sequence: WWTYYTWYTTWDTTWTWH

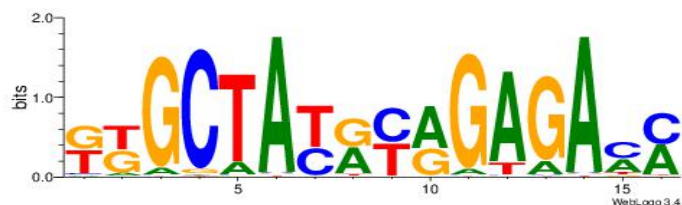


Dataset #: 1

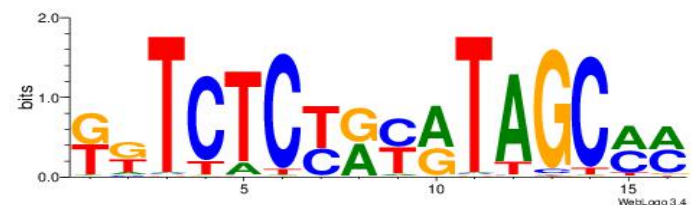
Motif ID: 129
 Motif name: C129
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 16
 Similarity score: 0.0576399

Alignment:
 KKGCTAYRYRGAGAMM
 YRTACAMRYTGAGTYY

Original motif Consensus sequence: KKGCTAYRYRGAGAMM

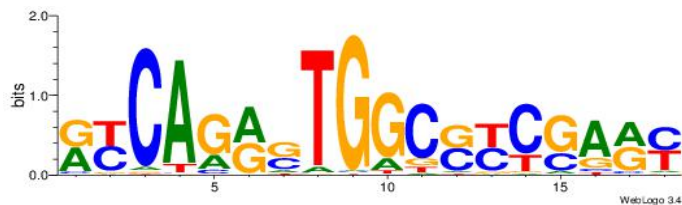


Reverse complement motif Consensus sequence: RRTCTCKKMMTAGCRY

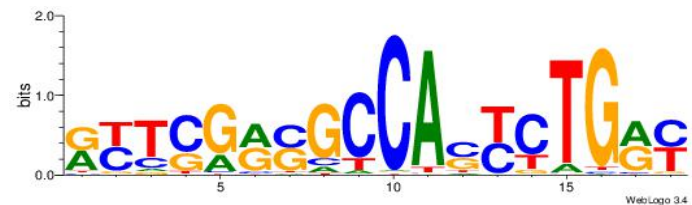


Dataset #: 1 Motif ID: 92 Motif name: C092

Original motif Consensus sequence: RYCAGRSTGGCSYCGARY



Reverse complement motif Consensus sequence: KKTCGMSGCCASKCTGMM



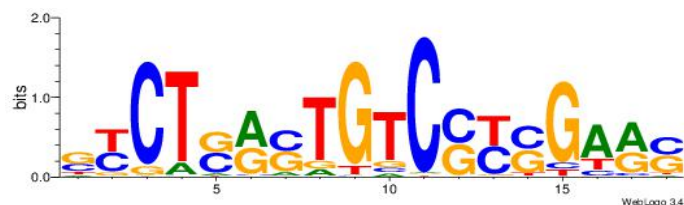
Best Matches for Motif ID 92 (Highest to Lowest)

Dataset #: 1
Motif ID: 128
Motif name: C128
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: 0.0244788

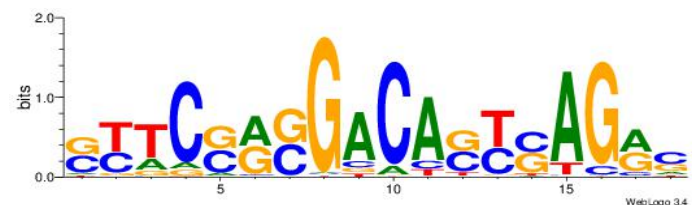
Alignment:

SKTCSMSGACASKSAGMS
KKTCGMSGCCASKCTGMM

Original motif Consensus sequence: SYCTSRSTGTCSYSGARS



Reverse complement motif Consensus sequence: SKTCSMSGACASKSAGMS



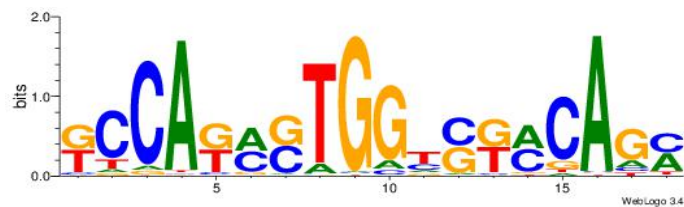
Dataset #: 1
Motif ID: 95
Motif name: C095
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif

Direction: Forward
 Position number: 1
 Number of overlap: 18
 Similarity score: 0.0314384

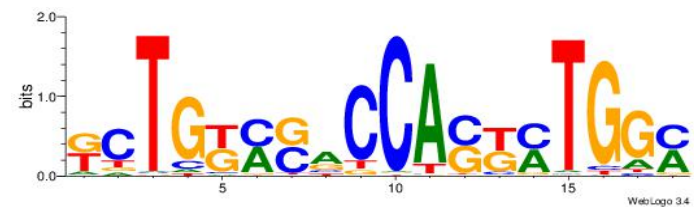
Alignment:

KCCAKMSTGGTSKMCAGM
 RYCAGRSTGGCSYCGARY

Original motif Consensus sequence: KCCAKMSTGGTSKMCAGM



Reverse complement motif Consensus sequence: RCTGYYSACCASYTGGY

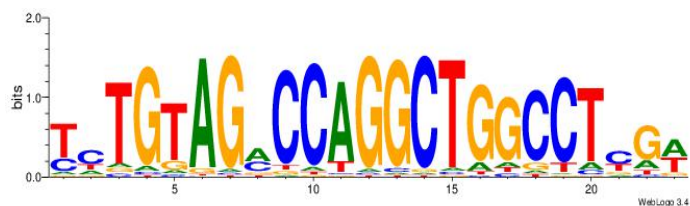


Dataset #: 1
 Motif ID: 5
 Motif name: C005
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 6
 Number of overlap: 18
 Similarity score: 0.0593452

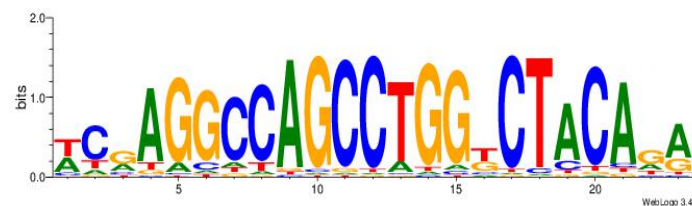
Alignment:

TCTGTAGMCCAGGCTGGCCTYGW
 -----KKTGMSGCCASKCTGMM

Original motif Consensus sequence: TCTGTAGMCCAGGCTGGCCTYGW



Reverse complement motif Consensus sequence: WCKAGGCCAGCCTGGYCTACAGA

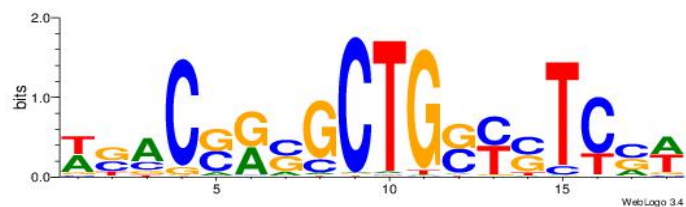


Dataset #: 1
Motif ID: 124
Motif name: C124
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 18
Similarity score: 0.0706106

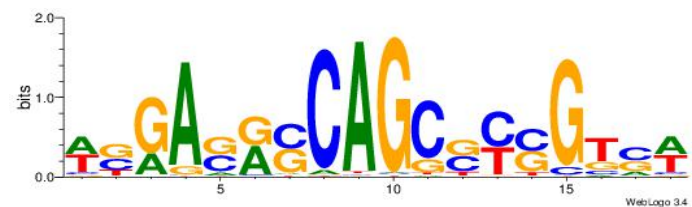
Alignment:

WSACSRSGCTGSYSTCSW
KKTGMSGCCASKCTGMM

Original motif Consensus sequence: WSACSRSGCTGSYSTCSW



Reverse complement motif Consensus sequence: WSGASKCAGCSMSGTSW

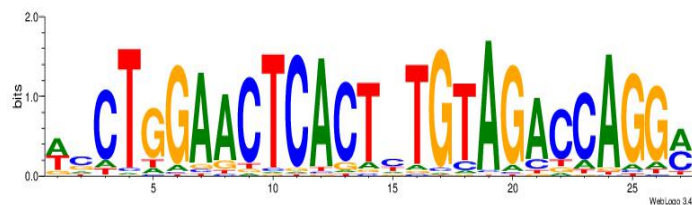


Dataset #: 1
 Motif ID: 13
 Motif name: C013
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 9
 Number of overlap: 18
 Similarity score: 0.0712116

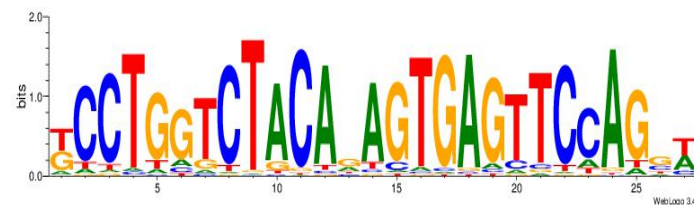
Alignment:

WVCTGGAAC TCACTHTGTAGACCAGGM
 -----KKTCGMSGCCASKCTGMM-

Original motif Consensus sequence:
 WVCTGGAAC TCACTHTGTAGACCAGGM



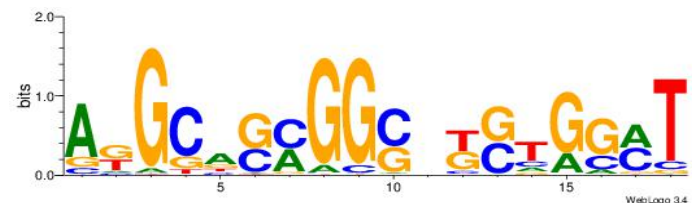
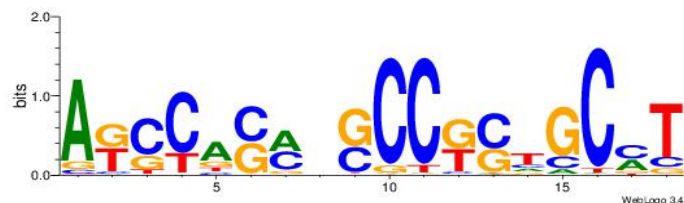
Reverse complement motif Consensus sequence:
 YCCTGGTCTACADAGTGAGTTCCAGVW



Dataset #: 1 Motif ID: 93 Motif name: C093

Original motif Consensus sequence: AKCCASMBSCCKSTGCMT

Reverse complement motif Consensus sequence:
 ARGCASYGGSVYSTGGYT



Best Matches for Motif ID 93 (Highest to Lowest)

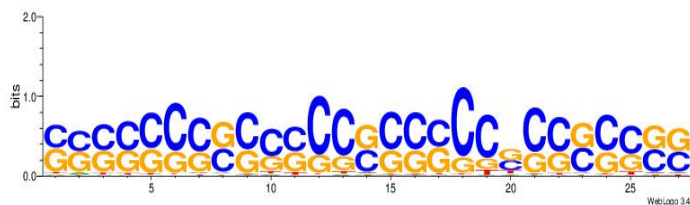
Dataset #: 1
 Motif ID: 4
 Motif name: C004
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 8
 Number of overlap: 18
 Similarity score: 0.0439494

Alignment:

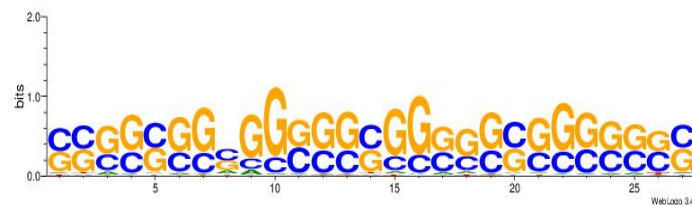
```

SSSSSCSSSSSCSSSSCCSCSSSSSS
--AKCCASMBSCCKSTGCMT-----
  
```

Original motif Consensus sequence:
 SSSSCSSSSSCSSSSCCSCSSSSSS



Reverse complement motif Consensus sequence:
 SSSSSGSGGSSSSGGSSSSSGSSSSS

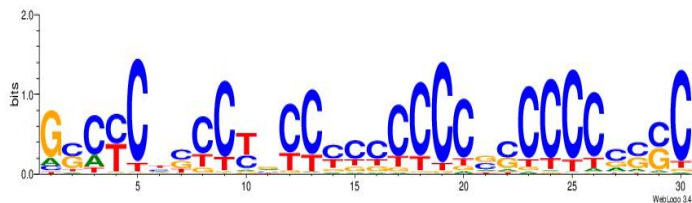


Dataset #: 1
 Motif ID: 3
 Motif name: C003
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 10
 Number of overlap: 18
 Similarity score: 0.0490082

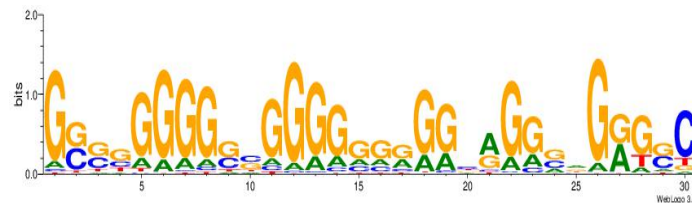
Alignment:

GSSGGGGSSGGGGGKGGVMGGSHGKGSC
 ---ARGCASYGGSVYSTGGYT-----

Original motif Consensus sequence:
 GSCYCHSCCYVCCYCCCCSSCCCCSSC



Reverse complement motif Consensus sequence:
 GSSGGGGSSGGGGGKGGVMGGSHGKGSC

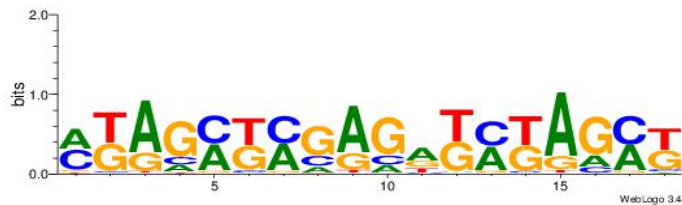


Dataset #: 1
 Motif ID: 36
 Motif name: C036
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1

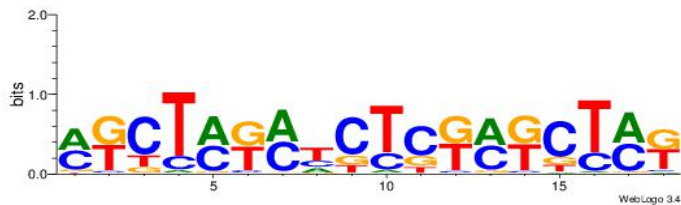
Number of overlap: 18
Similarity score: 0.0639349

Alignment:
RRCRRRTCTCRRRCTRY
AKCCASMBSCCKSTGCMT

Original motif Consensus sequence: MKAGMKMGAGAKMKAGMK



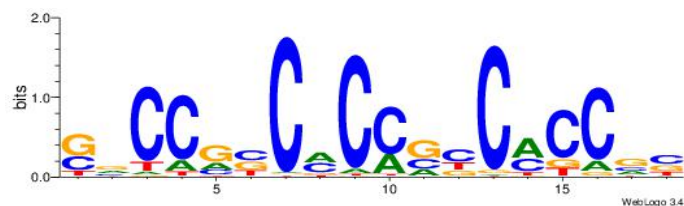
Reverse complement motif Consensus sequence: RRCRRRTCTCRRRCTRY



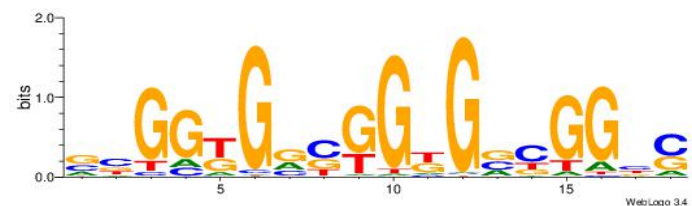
Dataset #: 1
Motif ID: 37
Motif name: C037
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 18
Similarity score: 0.0642642

Alignment:
SVCCGBCMCCSYCMCCVB
AKCCASMBSCCKSTGCMT

Original motif Consensus sequence: SVCCGBCMCCSYCMCCVB



Reverse complement motif Consensus sequence: BVGGYGKSGGYBCGGVS

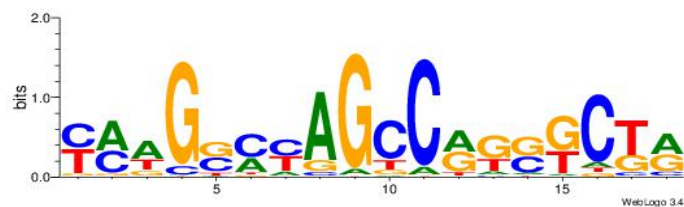


Dataset #: 1
Motif ID: 73
Motif name: C073
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 18
Similarity score: 0.0646787

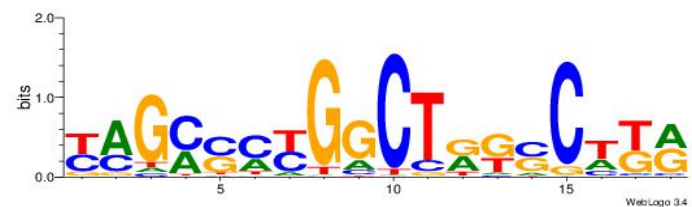
Alignment:

KAGYSYKGGCTKRSCWYK
ARGCASYGGSVYSTGGYT

Original motif Consensus sequence: YMWGSMYAGCCRKSKCTR

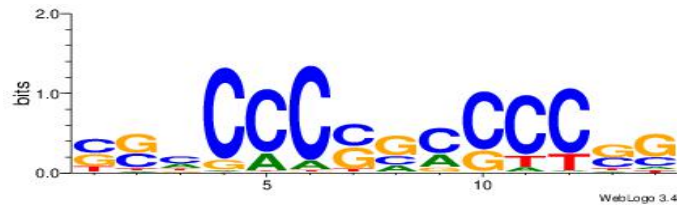


Reverse complement motif Consensus sequence: KAGYSYKGGCTKRSCWYK

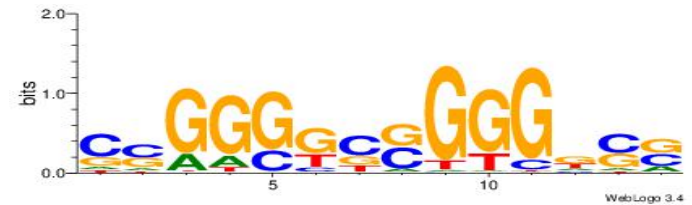


Dataset #: 1 Motif ID: 94 Motif name: C094

Original motif Consensus sequence: SSHCCCSGCCCCSG



Reverse complement motif Consensus sequence: CSGGGGCSGGGD



Best Matches for Motif ID 94 (Highest to Lowest)

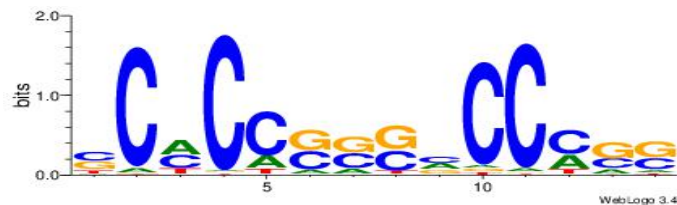
Dataset #:	1
Motif ID:	102
Motif name:	C102
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	14
Similarity score:	0.00913897

Alignment:

SCMCCSSSVCCMSS

SSHCCCSGCCCCSG

Original motif Consensus sequence: SCMCCSSSVCCMSS



Reverse complement motif Consensus sequence: SSRGGVSSSGGYG

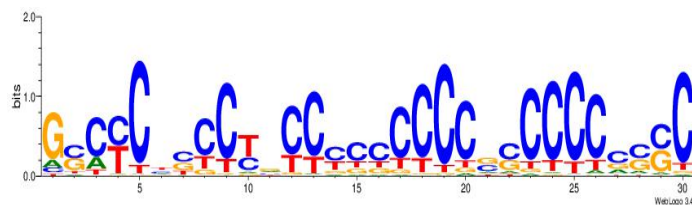


Dataset #: 1
 Motif ID: 3
 Motif name: C003
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 15
 Number of overlap: 14
 Similarity score: 0.010898

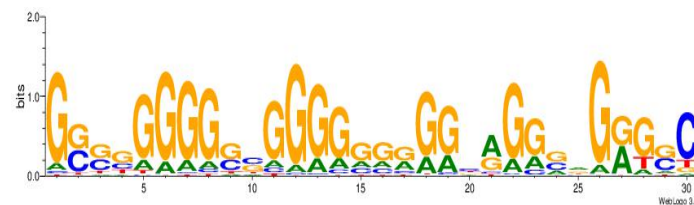
Alignment:

GSSGGGGSSGGGGGKGGVMGGSHGKGC
 --CSGGGCSGGDSS-----

Original motif Consensus sequence:
 GSCYCHSCCYVCCYCCCCSSCCCCSSC



Reverse complement motif Consensus sequence:
 GSSGGGGSSGGGGGKGGVMGGSHGKGC

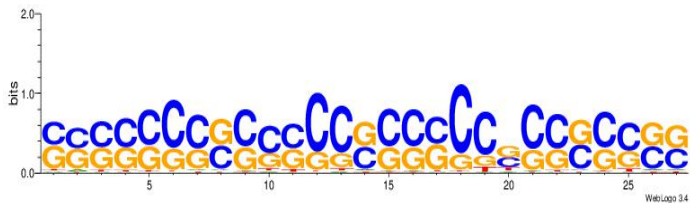


Dataset #: 1
 Motif ID: 4
 Motif name: C004
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward

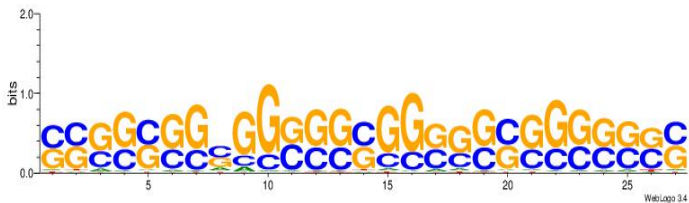
Position number: 8
Number of overlap: 14
Similarity score: 0.0158011

Alignment:
SSSSSSGSGGSSSSGSSSSGSSSSS
-----CSGGGGCSGGGDSS-----

Original motif Consensus sequence:
SSSSSCSSSSCCSSSSCCSCSSSSS



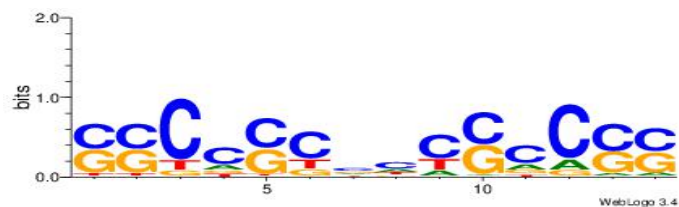
Reverse complement motif Consensus sequence:
SSSSSSGSGGSSSSGSSSSGSSSSS



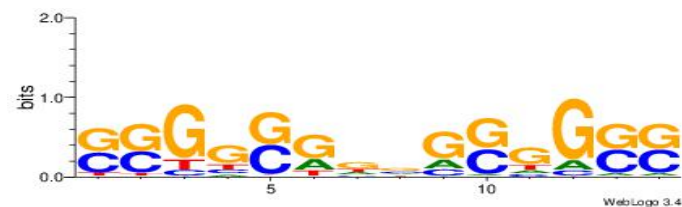
Dataset #: 1
Motif ID: 23
Motif name: C023
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 14
Similarity score: 0.0224328

Alignment:
SSGGSGDBGSGGSS
CSGGGGCSGGGDSS

Original motif Consensus sequence: SSCCSCBHCSCCSS



Reverse complement motif Consensus sequence: SSGGSGDBGSGG

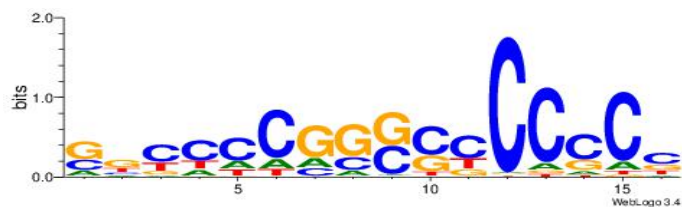


Dataset #: 1
Motif ID: 77
Motif name: C077
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 14
Similarity score: 0.0259051

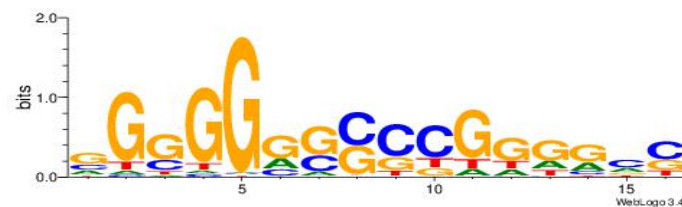
Alignment:

SBCCCCGGSSCCCCCB
SSHCCCSGCCCCSG--

Original motif Consensus sequence: SBCCCCGGSSCCCCCB

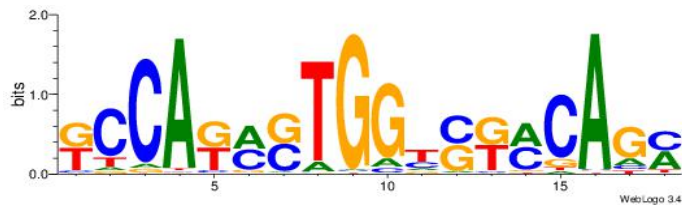


Reverse complement motif Consensus sequence:
BGGGGGSSCCGGGGBS

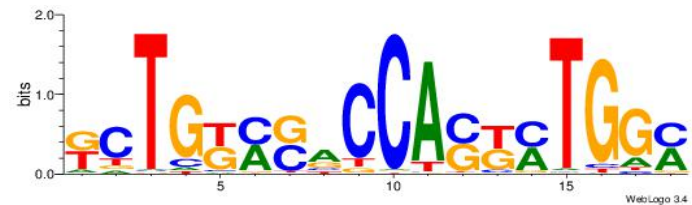


Dataset #: 1 **Motif ID: 95** **Motif name: C095**

Original motif Consensus sequence: KCCAKMSTGGTSKMCAGM



Reverse complement motif Consensus sequence: RCTGYYSACCASYTGGY



Best Matches for Motif ID 95 (Highest to Lowest)

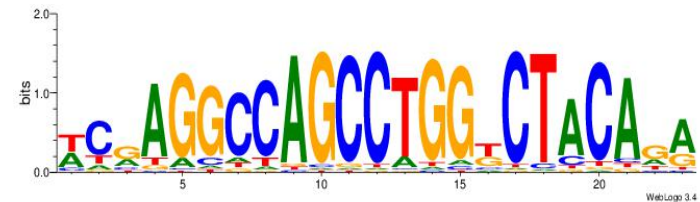
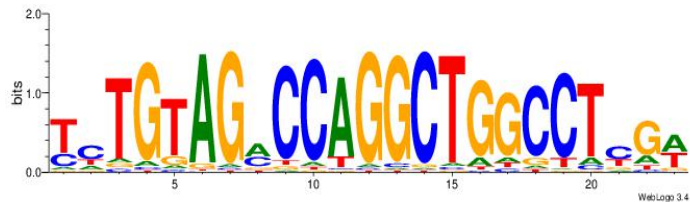
Dataset #:	1
Motif ID:	5
Motif name:	C005
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	18
Similarity score:	0.0148007

Alignment:

```
TCTGTAGMCCAGGCTGGCCTYGW
-----RCTGYYSACCASYTGGY
```

Original motif Consensus sequence: TCTGTAGMCCAGGCTGGCCTYGW

Reverse complement motif Consensus sequence: WCKAGGCCAGCCTGGYCTACAGA

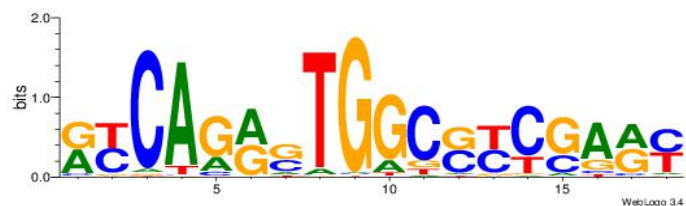


Dataset #: 1
 Motif ID: 92
 Motif name: C092
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 18
 Similarity score: 0.0234986

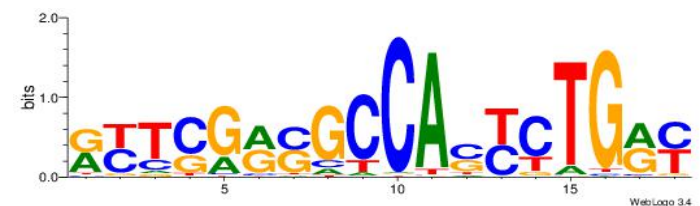
Alignment:

RYCAGRSTGGCSYCGARY
 KCCAKMSTGGTSKMCAGM

Original motif Consensus sequence: RYCAGRSTGGCSYCGARY



Reverse complement motif Consensus sequence: KKTCGMSGCCASKCTGMM



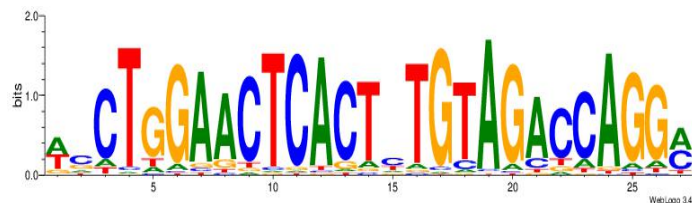
Dataset #: 1

Motif ID: 13
 Motif name: C013
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 9
 Number of overlap: 18
 Similarity score: 0.0466684

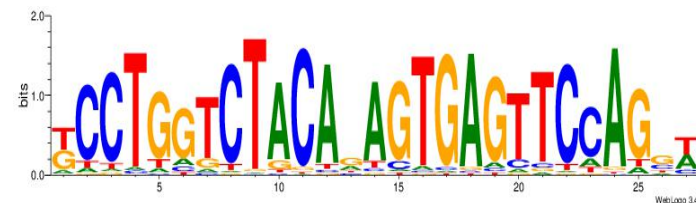
Alignment:

WVCTGGAAC TCACTHTGTAGACCAGGM
 -----RCTGYYSACCASYTTGGY--

Original motif Consensus sequence:
 WVCTGGAAC TCACTHTGTAGACCAGGM



Reverse complement motif Consensus sequence:
 YCCTGGTCTACADAGTGAGTTCCAGVW

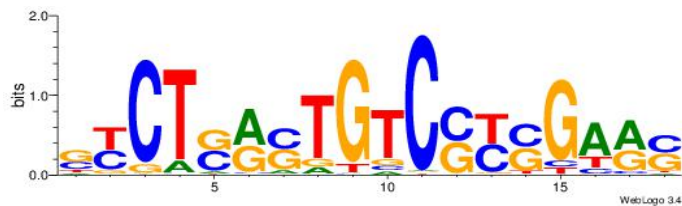


Dataset #: 1
 Motif ID: 128
 Motif name: C128
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 18

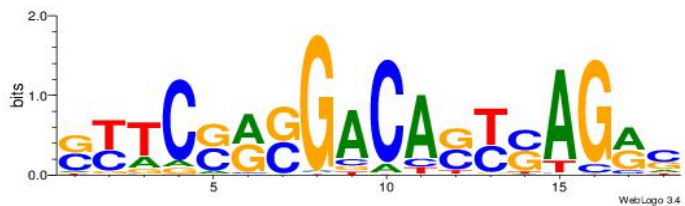
Similarity score: 0.0525333

Alignment:
SYCTSRSTGTCSYSGARS
KCCAKMSTGGTSKMCAGM

Original motif Consensus sequence: SYCTSRSTGTCSYSGARS



Reverse complement motif Consensus sequence: SKTCSMSGACASKSAGMS

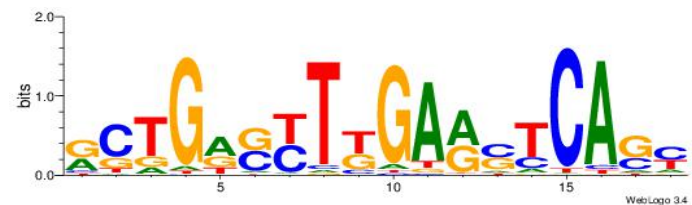
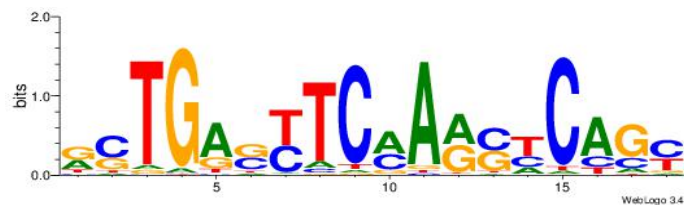


Dataset #: 1
Motif ID: 40
Motif name: C040
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 18
Similarity score: 0.0545308

Alignment:
KCTGMSKTYGAMSTCASM
KCCAKMSTGGTSKMCAGM

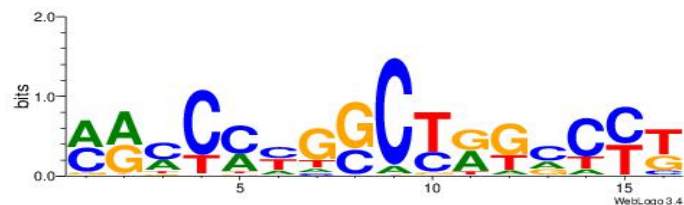
Original motif Consensus sequence: RSTGASYTCMARSYAGY

Reverse complement motif Consensus sequence: KCTGMSKTYGAMSTCASM

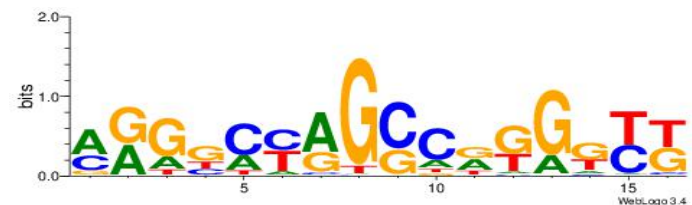


Dataset #: 1 Motif ID: 96 Motif name: C096

Original motif Consensus sequence: MRMCMYGSCYRGCCYK



Reverse complement motif Consensus sequence: RKGCMMGSCCKRGRKY



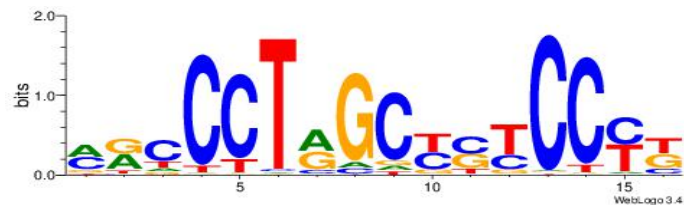
Best Matches for Motif ID 96 (Highest to Lowest)

Dataset #:	1
Motif ID:	121
Motif name:	C121
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	16
Similarity score:	0.00911622

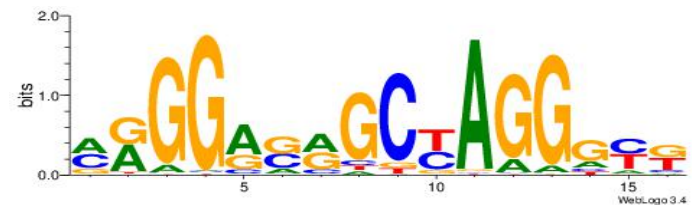
Alignment:

MRCCCTRGCYSTCCYK
MRMCMYGSCYRGCCYK

Original motif Consensus sequence: MRCCCTRGCYSTCCYK



Reverse complement motif Consensus sequence:
RKGGASMGCKAGGGMY



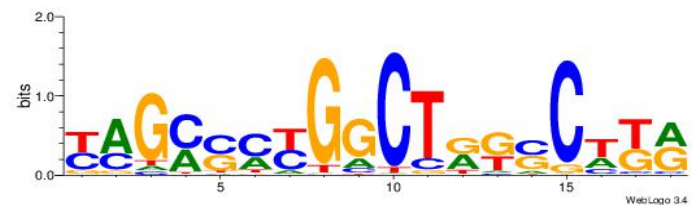
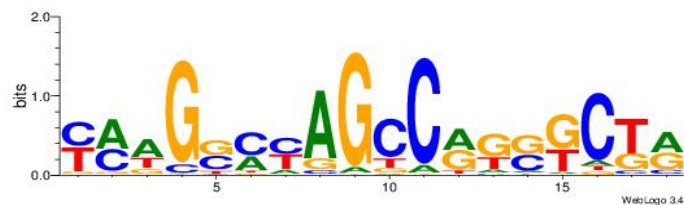
Dataset #:	1
Motif ID:	73
Motif name:	C073
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2
Number of overlap:	16
Similarity score:	0.0193158

Alignment:

YMWGSMYAGCCRKSKCTR
-RKGGCMMGSCKRGRKY-

Original motif Consensus sequence: YMWGSMYAGCCRKSKCTR

Reverse complement motif Consensus sequence:
KAGYSYKGGCTKRSCWYK

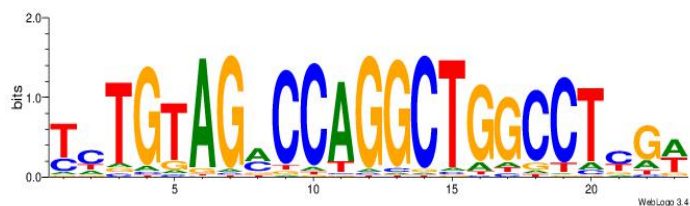


Dataset #: 1
 Motif ID: 5
 Motif name: C005
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 6
 Number of overlap: 16
 Similarity score: 0.0223054

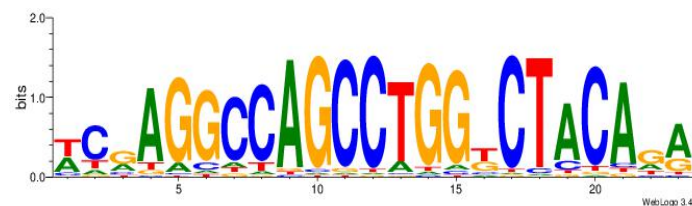
Alignment:

TCTGTAGMCCAGGCTGGCCTYGW
 -----MRMCMYGSCYRGCCYK--

Original motif Consensus sequence: TCTGTAGMCCAGGCTGGCCTYGW



Reverse complement motif Consensus sequence: WCKAGGCCAGCCTGGYCTACAGA



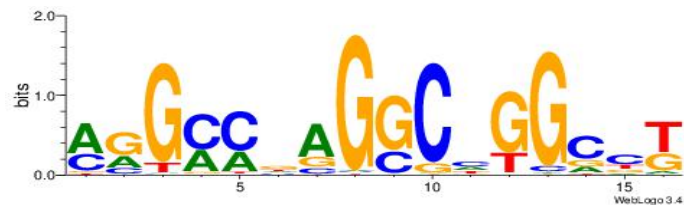
Dataset #: 1

Motif ID: 61
 Motif name: C061
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 16
 Similarity score: 0.026179

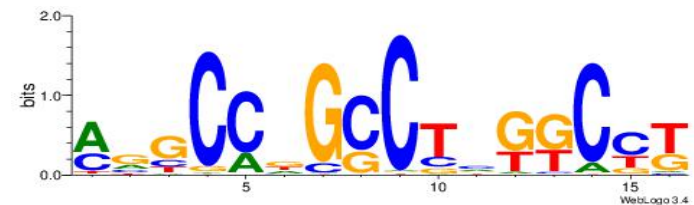
Alignment:

MRGMMBAGGCHGGCCK
 RKGGCMMGSCKRGRKY

Original motif Consensus sequence: MRGMMBAGGCHGGCCK



Reverse complement motif Consensus sequence: RGGCCDGCCTBRRCMY

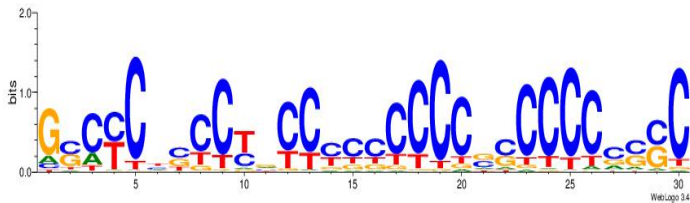


Dataset #: 1
 Motif ID: 3
 Motif name: C003
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 16

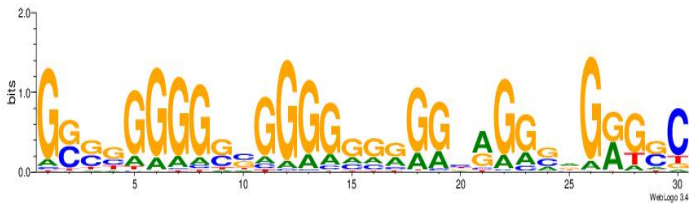
Similarity score: 0.0266849

Alignment:
GSCYCHSCCYVCCYCCCCCSCCCCCSSC
MRMCMYGSCYRGCCYK-----

Original motif Consensus sequence:
GSCYCHSCCYVCCYCCCCCSCCCCCSSC

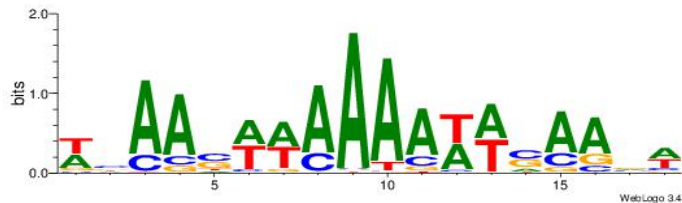


Reverse complement motif Consensus sequence:
GSSGGGGGSSGGGGGGKGGVMGGSHGKGC

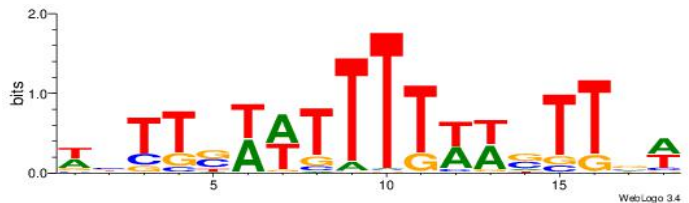


Dataset #: 1 Motif ID: 97 Motif name: C097

Original motif Consensus sequence: WBAASWWAAAWWSAAVW



Reverse complement motif Consensus sequence:
WVTTSWWTTTTWWSTTBW



Best Matches for Motif ID 97 (Highest to Lowest)

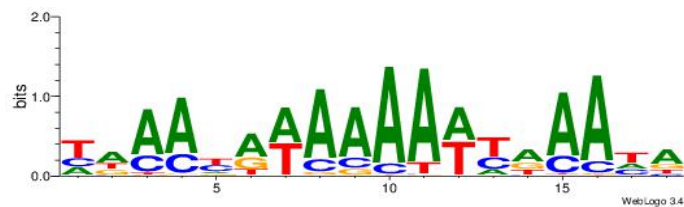
Dataset #:	1
Motif ID:	24
Motif name:	C024
Matching format of first motif:	Reverse Complement

Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 18
Similarity score: 0.00734811

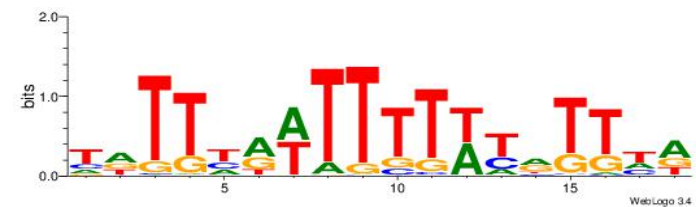
Alignment:

THTTDMWTTTTWKMTTDA
WVTTSWWTTTTWWSTTBW

Original motif Consensus sequence: TDAAYRWAAAAYDAAHA



Reverse complement motif Consensus sequence:
THTTDMWTTTTWKMTTDA

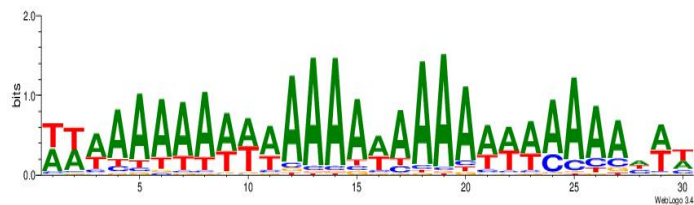


Dataset #: 1
Motif ID: 1
Motif name: C001
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 4
Number of overlap: 18
Similarity score: 0.0172538

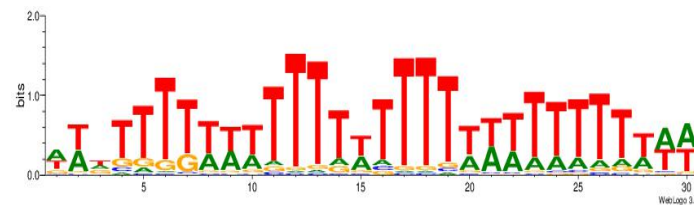
Alignment:

WWWAAAAAWWAAAAAWAAAAWWAAAAHWW
 -----WBAASWWAAAAWWSAAVW----

Original motif Consensus sequence:
 WWWAAAAAWWAAAAAWAAAAWWAAAAHWW



Reverse complement motif Consensus sequence:
 WWHTTTTWWTTTTTWT TTTTWWTTTTTWWW

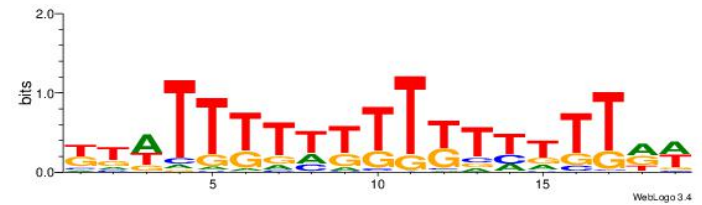


Dataset #: 1
 Motif ID: 30
 Motif name: C030
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 18
 Similarity score: 0.0179689

Alignment:
 WYAAAAAMAAAAAAWAM
 WBAASWWAAAAWWSAAVW-

Original motif Consensus sequence: WYAAAAAMAAAAAAWAM

Reverse complement motif Consensus sequence:
 YTWTTTTTTTTYTTTTMW

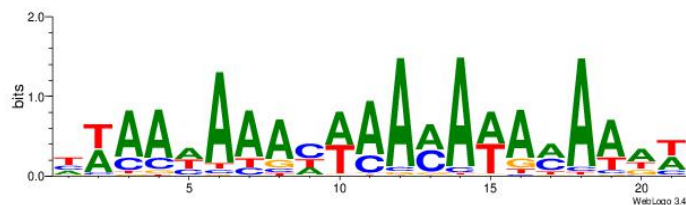


Dataset #:	1
Motif ID:	16
Motif name:	C016
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	18
Similarity score:	0.0187638

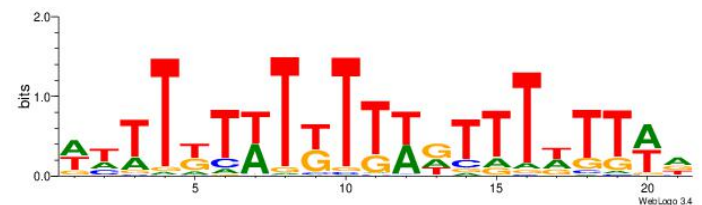
Alignment:

HWAAWAAAHWAAMAWAMAAWW
---WBAAWWAAAWWSAAVW

Original motif Consensus sequence: HWAAWAAHWAAMAWAMAAWW



Reverse complement motif Consensus sequence:
WWTTYTWYTTWDTTWTWH



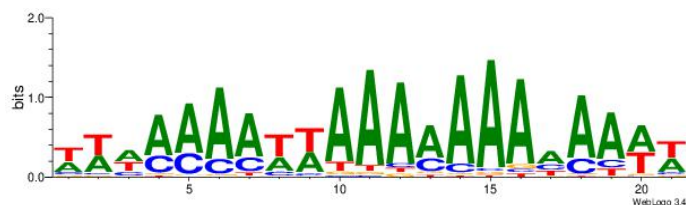
Dataset #: 1

Motif ID: 10
 Motif name: C010
 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: 0.0198187

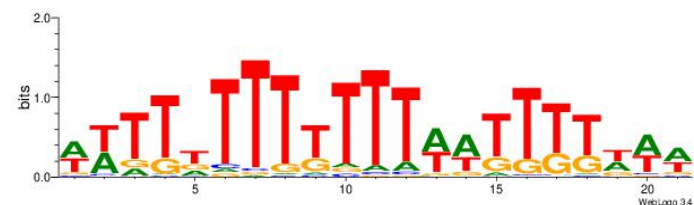
Alignment:

WWWAAAAWWAAAAAAAAAAWW
 --WBAASWWAAAAWWSAAVW-

Original motif Consensus sequence: WWWAAAAWWAAAAAAAAAAWW

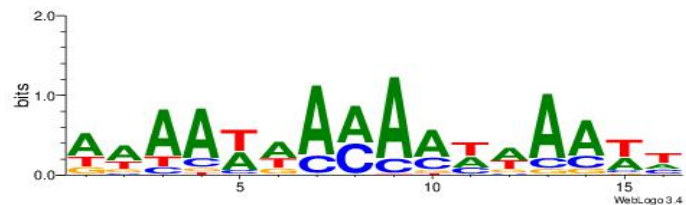


Reverse complement motif Consensus sequence: WWTTTTTTTTTTWWTTTTWWW

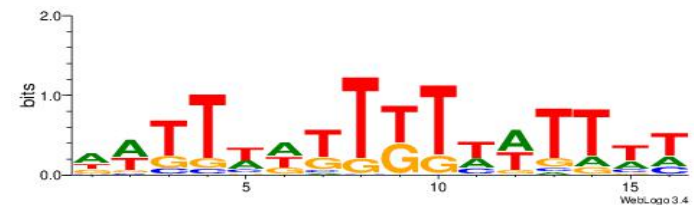


Dataset #: 1 Motif ID: 98 Motif name: C098

Original motif Consensus sequence: AAAWWAMAAWWAAWH



Reverse complement motif Consensus sequence: HWTTWTTTWTWTTTT



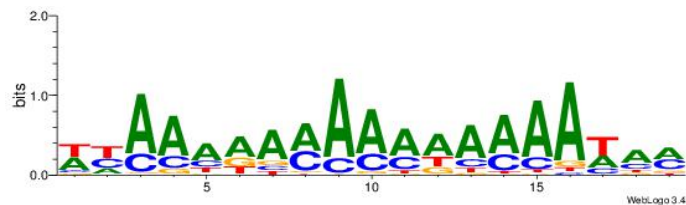
Best Matches for Motif ID 98 (Highest to Lowest)

Dataset #: 1
Motif ID: 30
Motif name: C030
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 4
Number of overlap: 16
Similarity score: 0.0202744

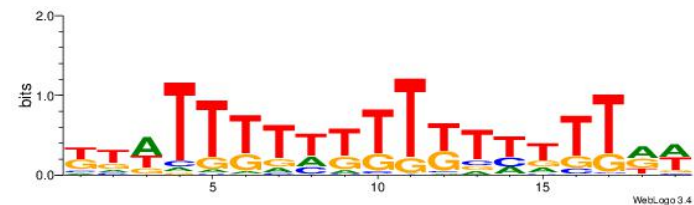
Alignment:

```
YTWTTTTTTTTYTTTTMW  
--HWTTWWTYTWWT
```

Original motif Consensus sequence: WYAAAAAIAAAAAAAWAM



Reverse complement motif Consensus sequence: YTWTTTTTTTTYTTTTMW

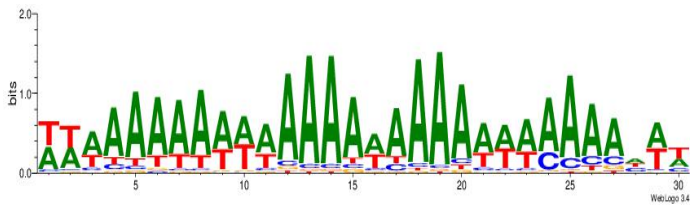


Dataset #: 1
Motif ID: 1
Motif name: C001
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement

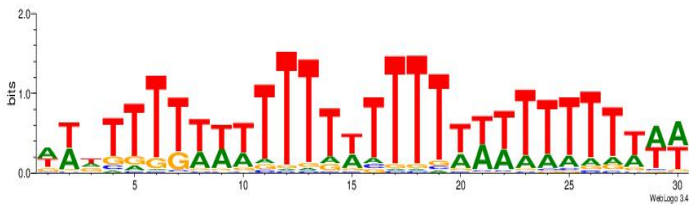
Direction: Backward
Position number: 6
Number of overlap: 16
Similarity score: 0.0239726

Alignment:
WWHTTTTWWTTTWTWTWTWTWTWTWTWT
-----HWTTWWTTYTWWTWTWT-----

Original motif Consensus sequence:
WWWAAAAAWWAAAAWAAAAWAAAAHWW



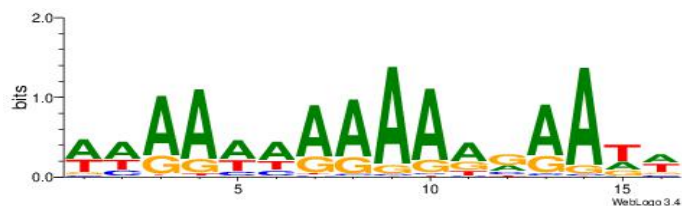
Reverse complement motif Consensus sequence:
WWHTTTTWWTTTWTWTWTWTWTWTWTWT



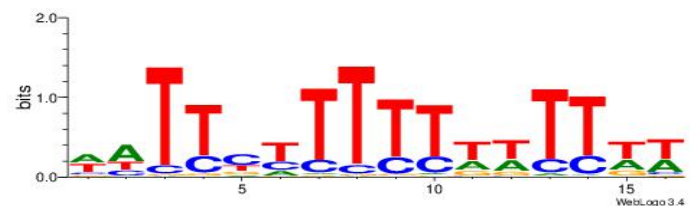
Dataset #: 1
Motif ID: 43
Motif name: C043
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 16
Similarity score: 0.024586

Alignment:
WWAAWAAAAAARAATW
AAAWWAMAAWAAWH

Original motif Consensus sequence: WWAAWAAAAARAATW



Reverse complement motif Consensus sequence: WATTMTTTTTTWTWW

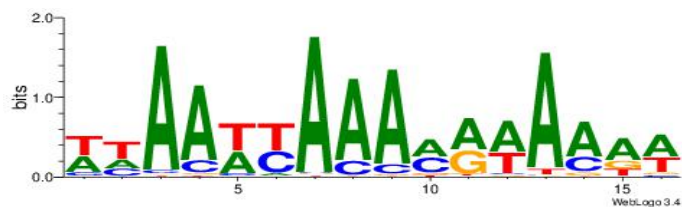


Dataset #: 1
Motif ID: 33
Motif name: C033
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 16
Similarity score: 0.0280152

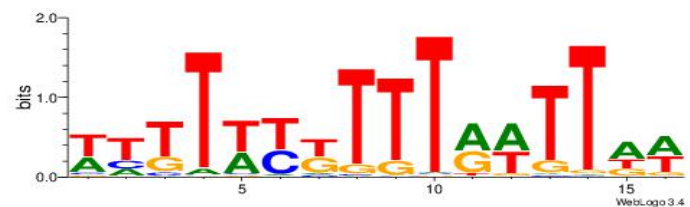
Alignment:

WWAAWYAAAMRWAAAW
AAAAWWAMAAWAAWH

Original motif Consensus sequence: WWAAWYAAAMRWAAAW



Reverse complement motif Consensus sequence: WTTTWKYTTTMTWTTWW

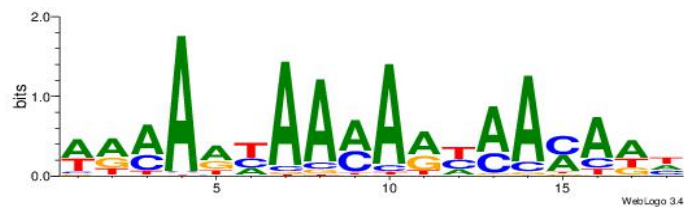


Dataset #: 1
 Motif ID: 57
 Motif name: C057
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 16
 Similarity score: 0.0292107

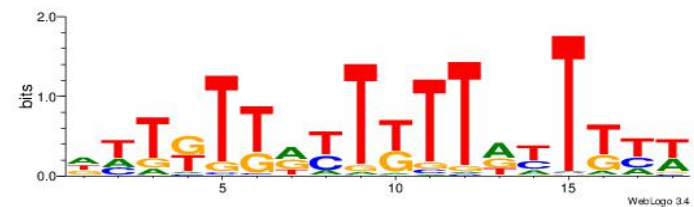
Alignment:

WRMARYAAMARYAAMAWH
 -AAAAWWAMAAWWAH-

Original motif Consensus sequence: WRMARYAAMARYAAMAWH



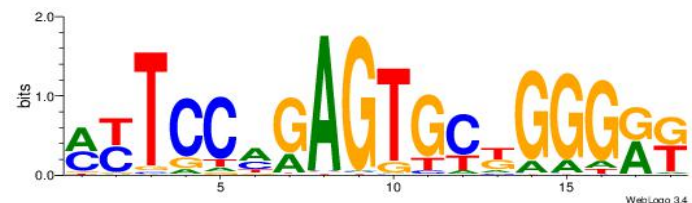
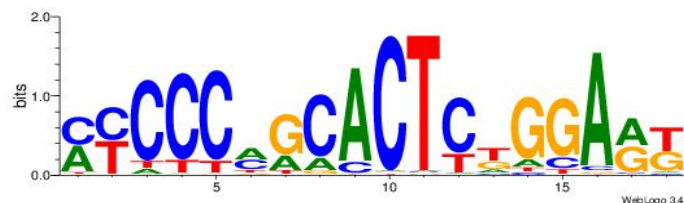
Reverse complement motif Consensus sequence: HWTRTTMKTYTTMKTYKW



Dataset #: 1 Motif ID: 99 Motif name: C099

Original motif Consensus sequence: MYCCMGCACTCKGGARK

Reverse complement motif Consensus sequence: RKTCCRGAGTGCYGGGKR



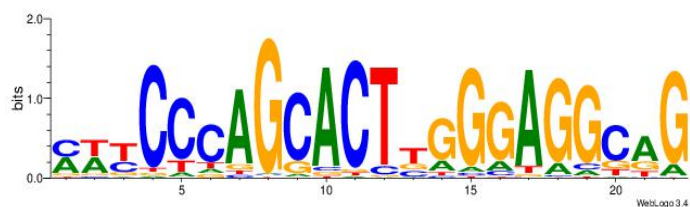
Best Matches for Motif ID 99 (Highest to Lowest)

Dataset #: 1
 Motif ID: 19
 Motif name: C019
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 18
 Similarity score: 0.00861288

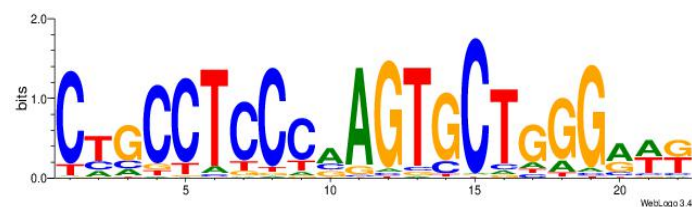
Alignment:

MWYCCCAGCACTTGGGAGGCAG
 -MYCCCMGCACTCKGGARK---

Original motif Consensus sequence: MWYCCCAGCACTTGGGAGGCAG



Reverse complement motif Consensus sequence: CTGCCTCCCAAGTCTGGGMWR

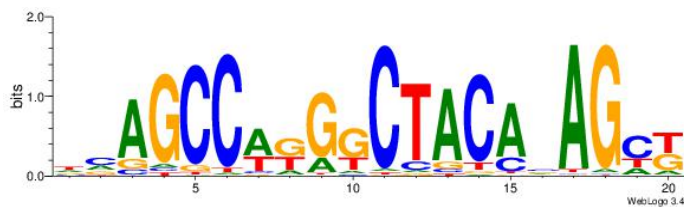


Dataset #: 1
 Motif ID: 15
 Motif name: C015
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 18
 Similarity score: 0.0548981

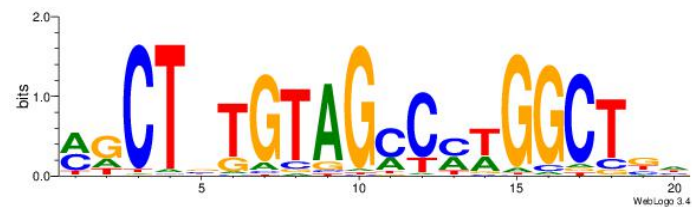
Alignment:

RGCTVTGTAGCCYGGCTVD
 -RKTCCRGAGTGCYGGGKR-

Original motif Consensus sequence: DVAGCCWKGCTACAVAGCK



Reverse complement motif Consensus sequence: RGCTVTGTAGCCYGGCTVD



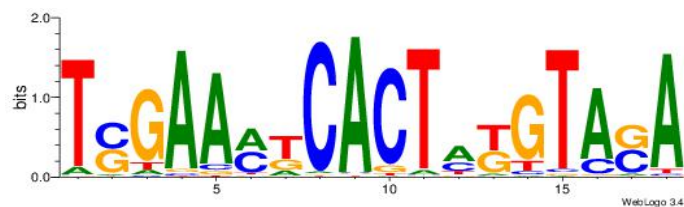
Dataset #: 1
 Motif ID: 47
 Motif name: C047
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1

Number of overlap: 18
Similarity score: 0.0609013

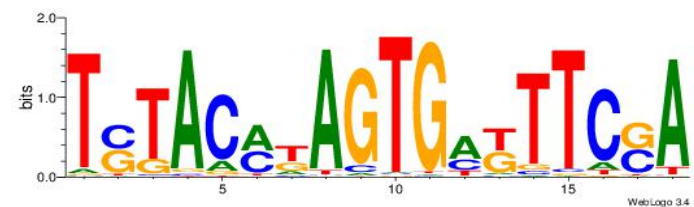
Alignment:

TSTACRYAGTGAYTTCSA
RKTCCRGAGTGCYGGGKR

Original motif Consensus sequence: TSGAAMTCACTMKGTASA



Reverse complement motif Consensus sequence: TSTACRYAGTGAYTTCSA

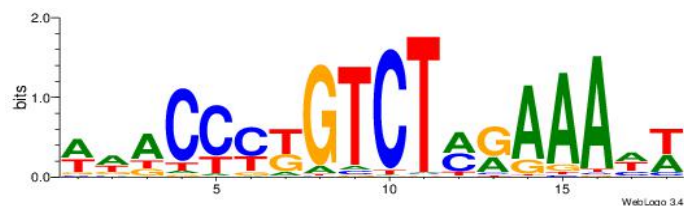


Dataset #: 1
Motif ID: 35
Motif name: C035
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 18
Similarity score: 0.065329

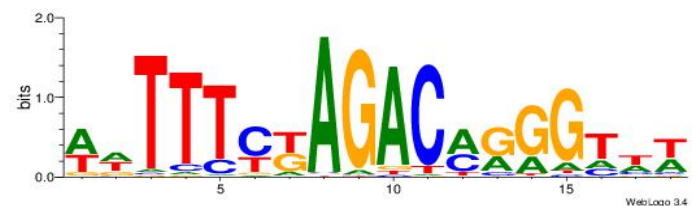
Alignment:

WWACCYKGTCTMRAAAWW
MYCCCMGCACTCKGGARK

Original motif Consensus sequence: WWACCYKGTCTMRAAAWW



Reverse complement motif Consensus sequence: WTTTTMYAGACRKGGTWW

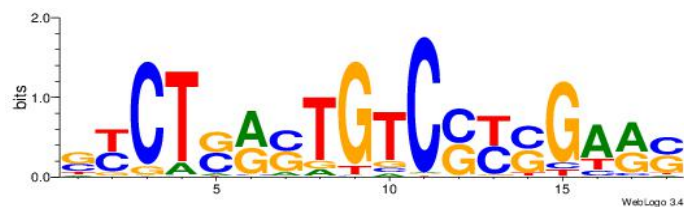


Dataset #: 1
Motif ID: 128
Motif name: C128
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 18
Similarity score: 0.0707153

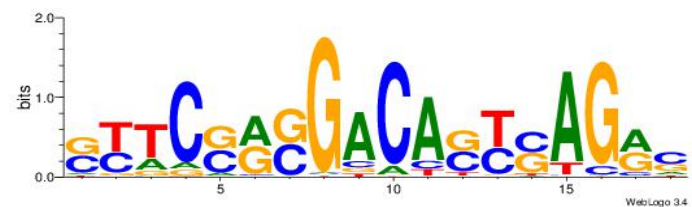
Alignment:

SKTCSMSGACASKSAGMS
MYCCCMGCACTCKGGARK

Original motif Consensus sequence: SYCTSRSTGTCSYSGARS

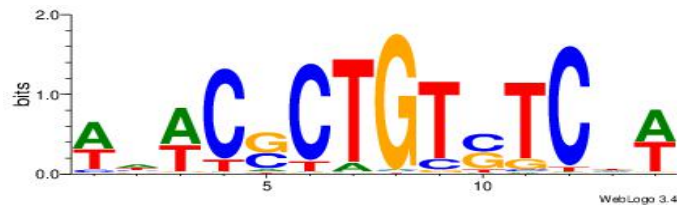


Reverse complement motif Consensus sequence: SKTCSMSGACASKSAGMS



Dataset #: 1 Motif ID: 100 Motif name: C100

Original motif Consensus sequence: WDWCSCTGTSTCHW



Reverse complement motif Consensus sequence: WHGASACAGSGWDW



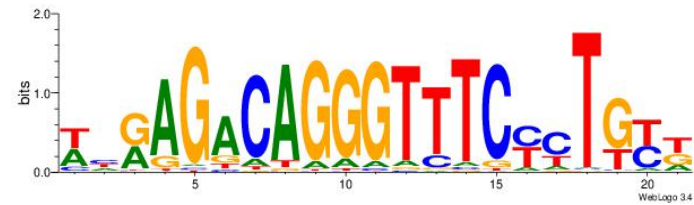
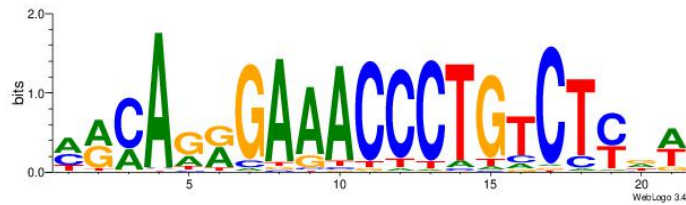
Best Matches for Motif ID 100 (Highest to Lowest)

Dataset #:	1
Motif ID:	27
Motif name:	C027
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

Alignment:
 WHKAGACAGGGTTTCMCTGKY
 WHGASACAGSGWDW-----

Original motif Consensus sequence: MRCAGRGAAACCCTGTCTYDW

Reverse complement motif Consensus sequence: WHKAGACAGGGTTTCMCTGKY

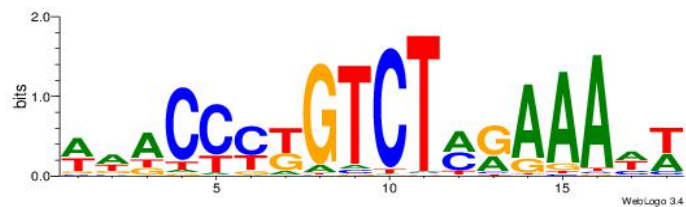


Dataset #: 1
 Motif ID: 35
 Motif name: C035
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 5
 Number of overlap: 14
 Similarity score: 0.0117194

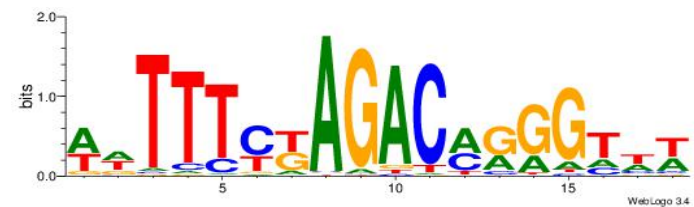
Alignment:

WWACCYKGTCTMRAAAWW
 WDWCSCTGTSTCHW----

Original motif Consensus sequence: WWACCYKGTCTMRAAAWW



Reverse complement motif Consensus sequence: WWTTTYAGACRKGGTWW



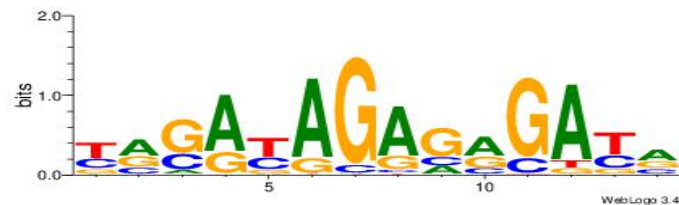
Dataset #: 1

Motif ID: 78
 Motif name: C078
 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: 0.0349672

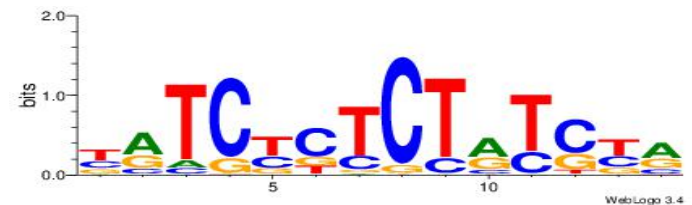
Alignment:

KMTCKCTCTMTCKM
 WDWCSCTGTSTCHW

Original motif Consensus sequence: YRGAYAGAGRGAYR



Reverse complement motif Consensus sequence: KMTCKCTCTMTCK



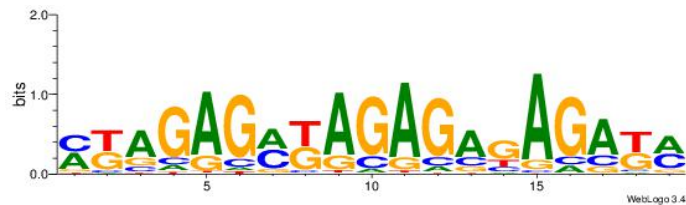
Dataset #: 1
 Motif ID: 12
 Motif name: C012
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 5
 Number of overlap: 14
 Similarity score: 0.0350639

Alignment:

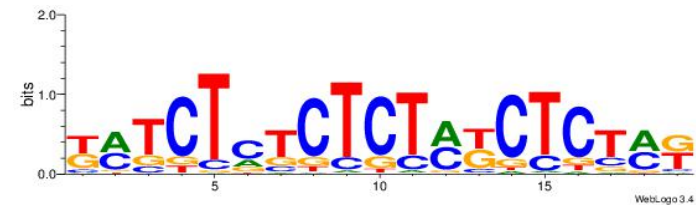
MKAGAGMKAGAGAGAGAKM

----WHGASACAGSGWDW-

Original motif Consensus sequence: MKAGAGMKAGAGAGAGAKM



Reverse complement motif Consensus sequence: YRTCTCTCTCTRYCTCTRR



Dataset #:	1
Motif ID:	25
Motif name:	C025
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:	0.036247

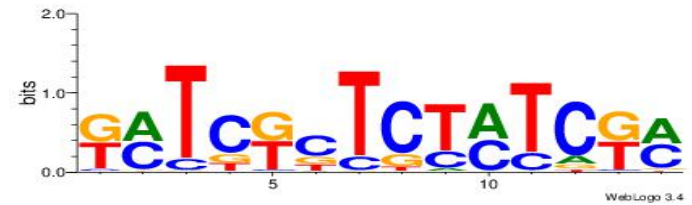
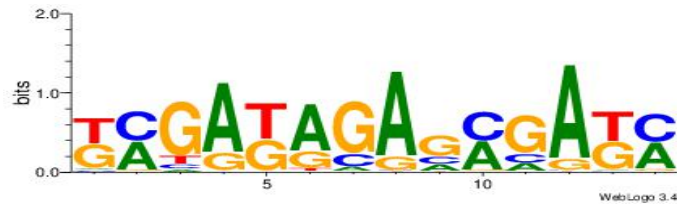
Alignment:

RRTCRCCTCTRTCRR

WDWCSTGTSTCHW

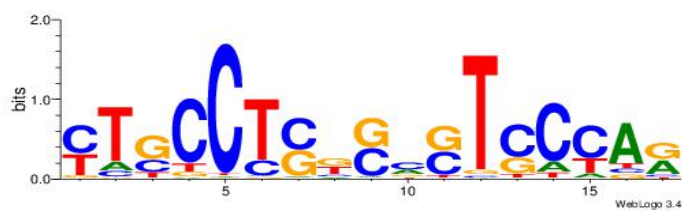
Original motif Consensus sequence: KMGAKAGAGMGAKM

Reverse complement motif Consensus sequence: RRTCRCCTCTRTCRR

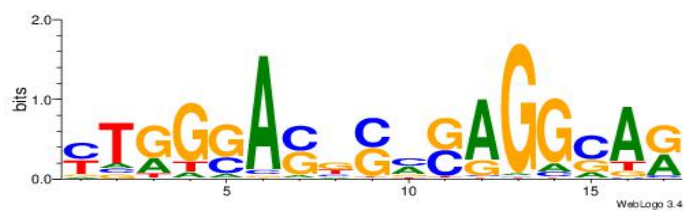


Dataset #: 1 Motif ID: 101 Motif name: C101

Original motif Consensus sequence: YTSCCTSKSVSTCCCAR



Reverse complement motif Consensus sequence: MTGGGASVSYSAGGSAK



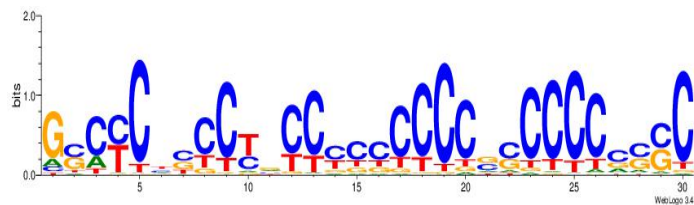
Best Matches for Motif ID 101 (Highest to Lowest)

Dataset #:	1
Motif ID:	3
Motif name:	C003
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	5
Number of overlap:	17
Similarity score:	0.0555244

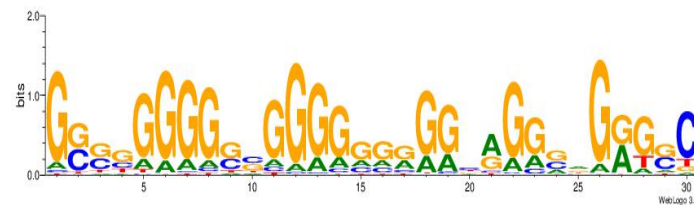
Alignment:

GSCYCHSCCYVCCYCCCCCSCCCCCSSC
 ----YTSCCTSKSVSTCCCAR-----

Original motif Consensus sequence:
 GSCYCHSCCYVCCYCCCCCSCCCCCSSC



Reverse complement motif Consensus sequence:
 GSSGGGGSSGGGGGKGGVMGGSHGKGSC

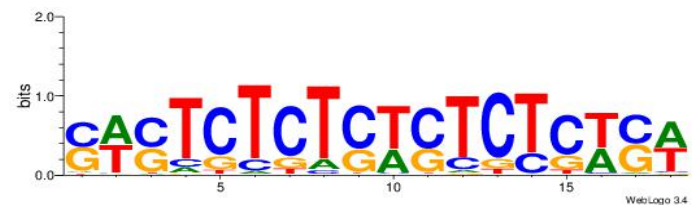
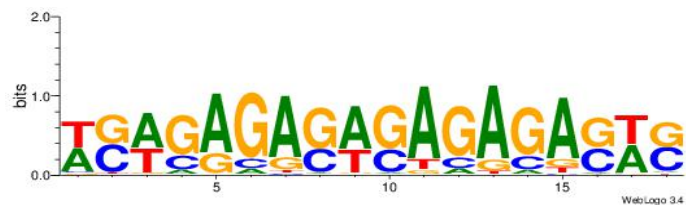


Dataset #:	1
Motif ID:	17
Motif name:	C017
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	17
Similarity score:	0.0606098

Alignment:
 SWSTCTCTSWSTCTCWSW
 -YTSCCTSKSVSTCCCAR

Original motif Consensus sequence: WSWGAGASWSAGAGASWS

Reverse complement motif Consensus sequence:
 SWSTCTCTSWSTCTCWSW

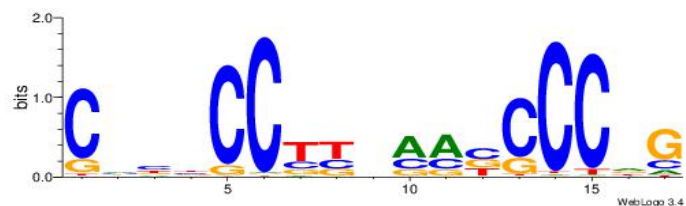


Dataset #: 1
 Motif ID: 107
 Motif name: C107
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 17
 Similarity score: 0.06682

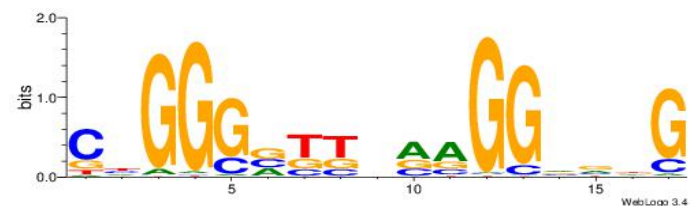
Alignment:

CHBBCCTYBAABCCCDG
 YTSCCTSKSVSTCCCAR

Original motif Consensus sequence: CHBBCCTYBAABCCCDG



Reverse complement motif Consensus sequence: CDGGGBTTVMAGGVBHG



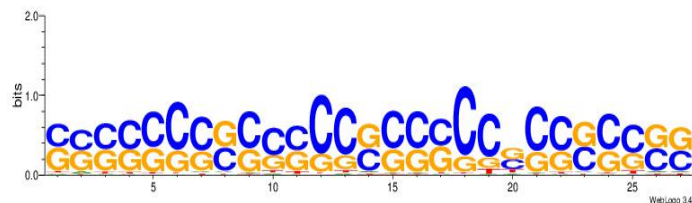
Dataset #: 1

Motif ID: 4
 Motif name: C004
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 17
 Similarity score: 0.0671341

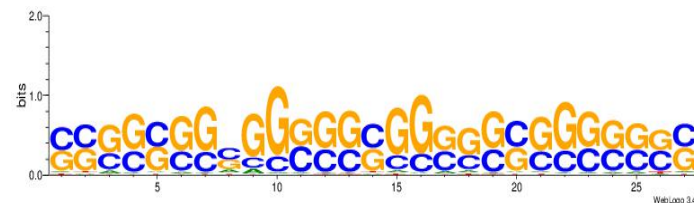
Alignment:

SSSSSCSSSSSCSSSSCCSCSSSSSS
 -----YTSCCTSKSVSTCCCAR--

Original motif Consensus sequence:
 SSSSSCSSSSSCSSSSCCSCSSSSSS



Reverse complement motif Consensus sequence:
 SSSSSSGSGGSSSSSGSSSSSGSSSSS

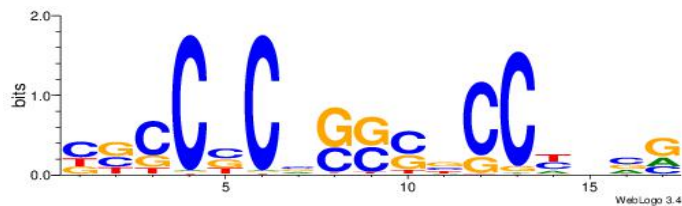


Dataset #: 1
 Motif ID: 140
 Motif name: C140
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 17

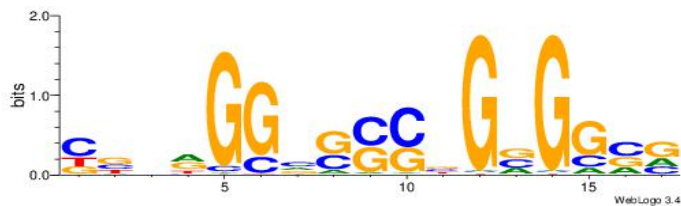
Similarity score: 0.0676017

Alignment:
BSCCBVCSSSBCCYHVG
YTSCCTSKSVSTCCCAR

Original motif Consensus sequence: BSCCBVCSSSBCCYHVG

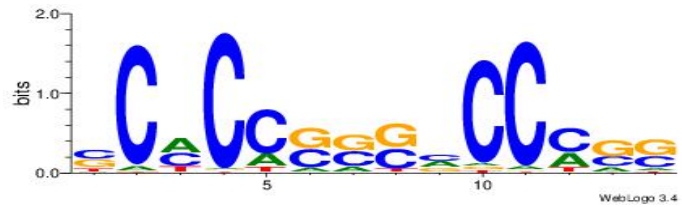


Reverse complement motif Consensus sequence: CVDMGGBSSSVGBGGSB



Dataset #: 1 Motif ID: 102 Motif name: C102

Original motif Consensus sequence: SCMCCSSSVCCMSS



Reverse complement motif Consensus sequence: SSRGGVSSSGGYG



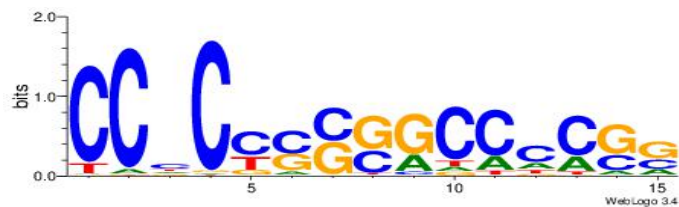
Best Matches for Motif ID 102 (Highest to Lowest)

Dataset #:	1
Motif ID:	112
Motif name:	C112
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif

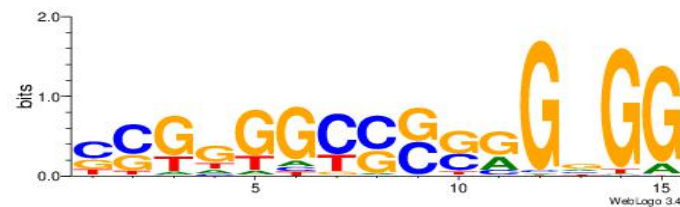
Direction: Backward
 Position number: 2
 Number of overlap: 14
 Similarity score: 0.017662

Alignment:
 CCBCYSSSGCCCCSS
 SCMCCSSSVCCMSS-

Original motif Consensus sequence: CCBCYSSSGCCCCSS



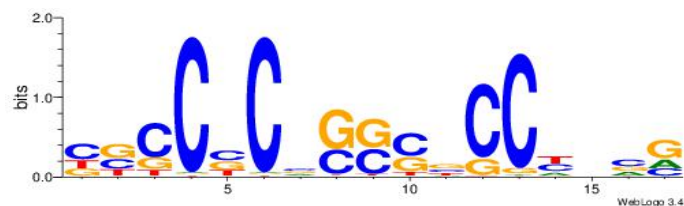
Reverse complement motif Consensus sequence: SSGGGGCSSSKGBGG



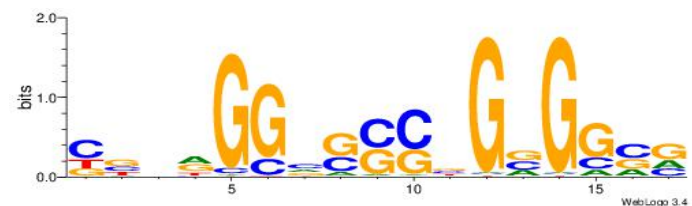
Dataset #: 1
 Motif ID: 140
 Motif name: C140
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 14
 Similarity score: 0.0176967

Alignment:
 BSCCBVCSSSBCCYHVG
 --SCMCCSSSVCCMSS-

Original motif Consensus sequence: BSCCBCVSSSBCCYHVG



Reverse complement motif Consensus sequence: CVDMGGBSSSVGBGGSB

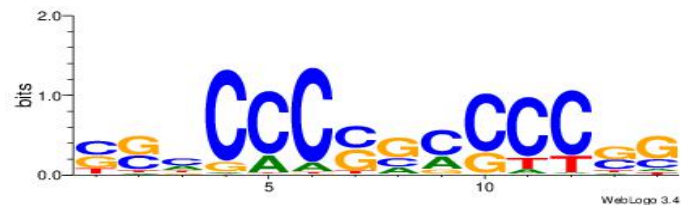


Dataset #: 1
Motif ID: 94
Motif name: C094
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 14
Similarity score: 0.0177805

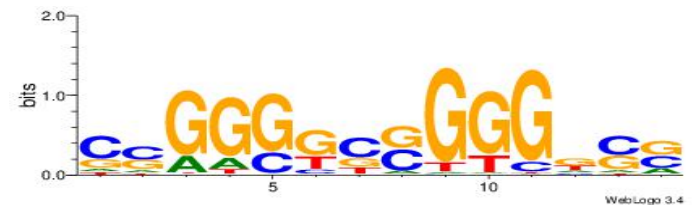
Alignment:

SSHCCCSGCCCCSG
SCMCCSSSVCCMSS

Original motif Consensus sequence: SSHCCCSGCCCCSG



Reverse complement motif Consensus sequence: CSGGGGCSGGGD

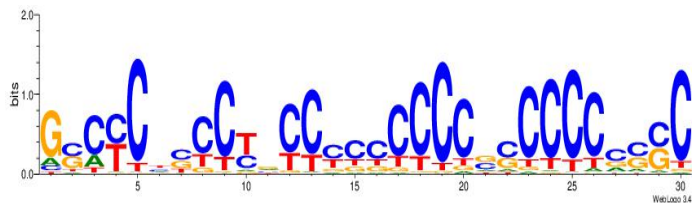


Dataset #: 1
 Motif ID: 3
 Motif name: C003
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 14
 Similarity score: 0.0216318

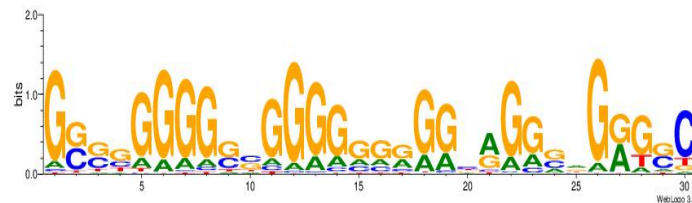
Alignment:

GSCYCHSCCYVCCYCCCCCSCCCCCSSC
 -----SCMCCSSSVCCMSS-

Original motif Consensus sequence:
 GSCYCHSCCYVCCYCCCCCSCCCCCSSC



Reverse complement motif Consensus sequence:
 GSSGGGGGSSGGGGGKGGVMGGSHGKGC

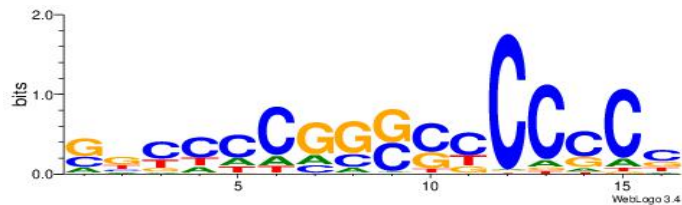


Dataset #: 1
 Motif ID: 77
 Motif name: C077
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2

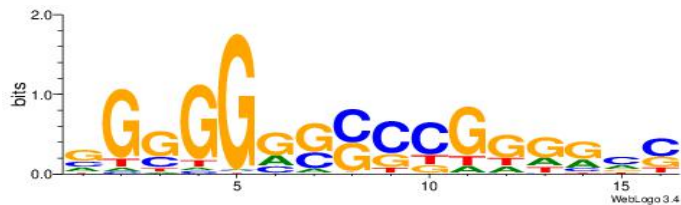
Number of overlap: 14
Similarity score: 0.0320147

Alignment:
SBCCCCGGSSCCCCCB
-SCMCCSSSVCCMSS-

Original motif Consensus sequence: SBCCCCGGSSCCCCCB

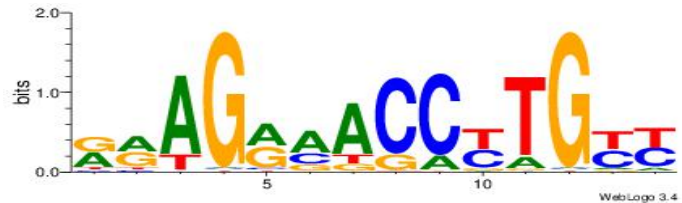


Reverse complement motif Consensus sequence: BGGGGGSSCCGGGGBS



Dataset #: 1 Motif ID: 103 Motif name: C103

Original motif Consensus sequence: RRAGRAACCYTGYY



Reverse complement motif Consensus sequence: MMCAMGGTTKCTH



Best Matches for Motif ID 103 (Highest to Lowest)

Dataset #: 1
Motif ID: 53
Motif name: C053
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:	0.00352554

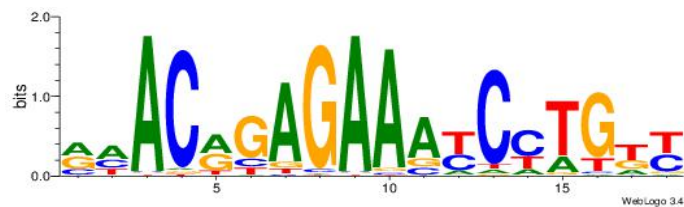
Alignment:

```

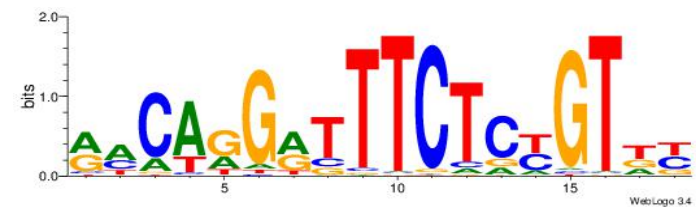
RMACRGAGAAAYCCTGKY
-----RRAGRAACCYTGYY

```

Original motif Consensus sequence: RMACRGAGAAAYCCTGKY



Reverse complement motif Consensus sequence: MRCAGGTTTTCTCKGTYK

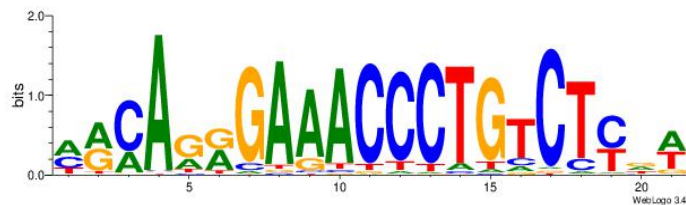


Dataset #:	1
Motif ID:	27
Motif name:	C027
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	4
Number of overlap:	14
Similarity score:	0.01171

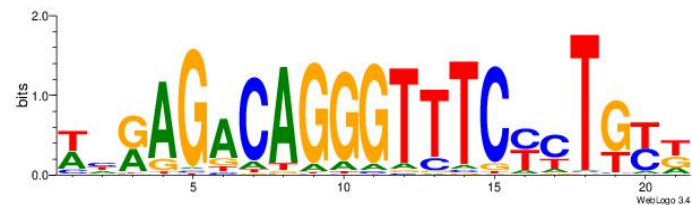
Alignment:

MRCAGRGAAACCCTGTCTYDW
 ---RRAGRAACCYTGYY----

Original motif Consensus sequence: MRCAGRGAAACCCTGTCTYDW



Reverse complement motif Consensus sequence: WHKAGACAGGGTTTCMCTGKY

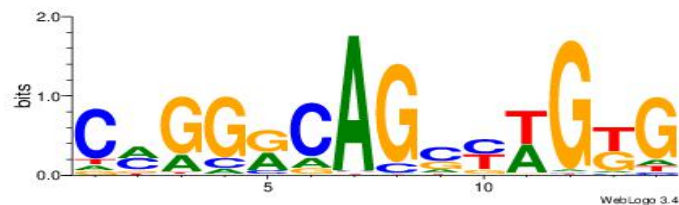
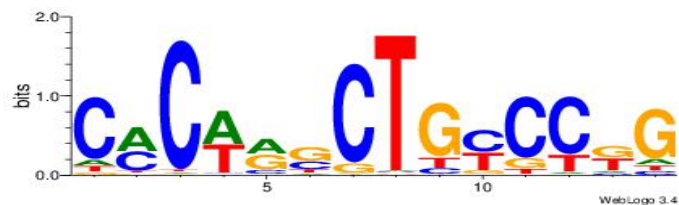


Dataset #:	1
Motif ID:	117
Motif name:	C117
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	14
Similarity score:	0.0352722

Alignment:
 CMCWR SCTGYCCKG
 MMCAMGGTTKCTKM

Original motif Consensus sequence: CMCWR SCTGYCCKG

Reverse complement motif Consensus sequence: CYGGKCAGSKWGY



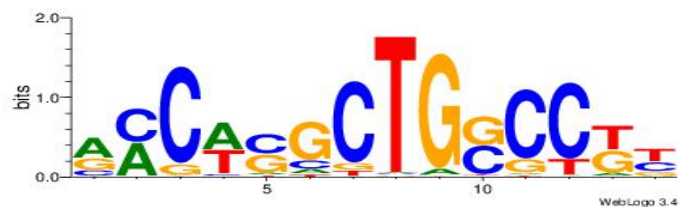
Dataset #: 1
 Motif ID: 109
 Motif name: C109
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0.0358256

Alignment:

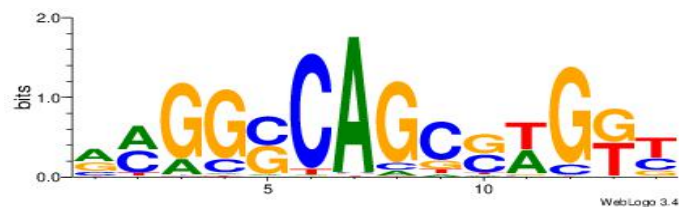
RCWSGCTGSCCKY

MMCAMGGTTKCTKM

Original motif Consensus sequence: RMCWSGCTGSCCKY



Reverse complement motif Consensus sequence: MRGGSCAGCSWG



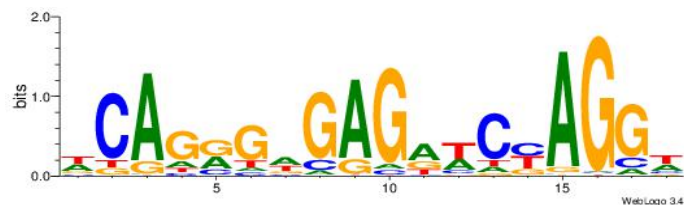
Dataset #: 1
 Motif ID: 132

Motif name: C132
 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: 0.0372435

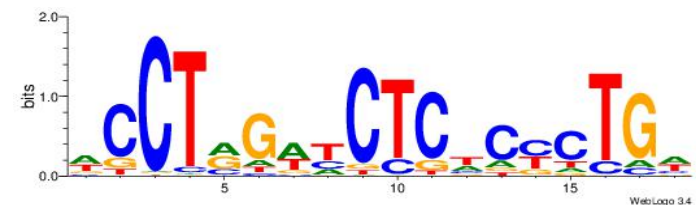
Alignment:

WCAGRGWGAGAWCYAGGW
 ----RRAGRAACCYTGY

Original motif Consensus sequence: WCAGRGWGAGAWCYAGGW

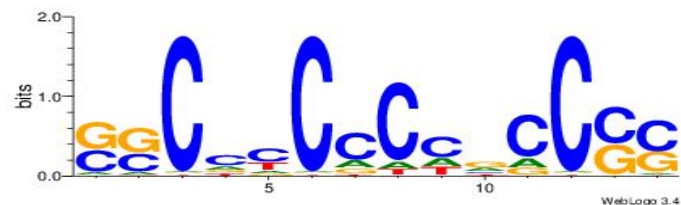


Reverse complement motif Consensus sequence: WCCTKGWTCTCWCMTGW

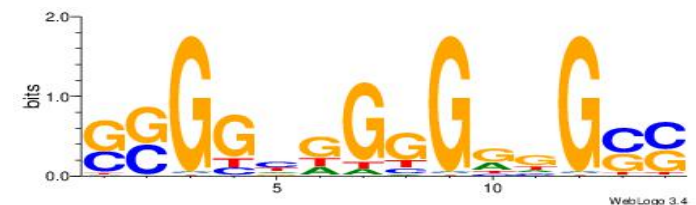


Dataset #: 1 Motif ID: 104 Motif name: C104

Original motif Consensus sequence: SSCYCCCCDCCSS



Reverse complement motif Consensus sequence: SSGHGGGGKGG



Best Matches for Motif ID 104 (Highest to Lowest)

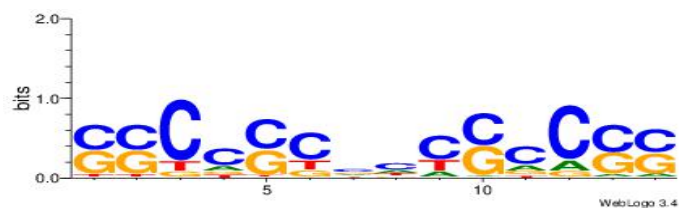
Dataset #: 1
Motif ID: 23
Motif name: C023
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 14
Similarity score: 0.00165547

Alignment:

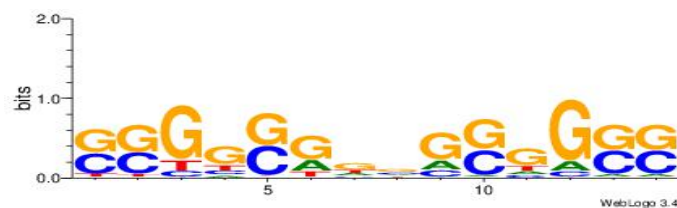
SSGGSGDBGSGGSS

SSGGHGGGKGGSS

Original motif Consensus sequence: SSCCSCBHCSCCSS



Reverse complement motif Consensus sequence: SSGGSGDBGSGGSS

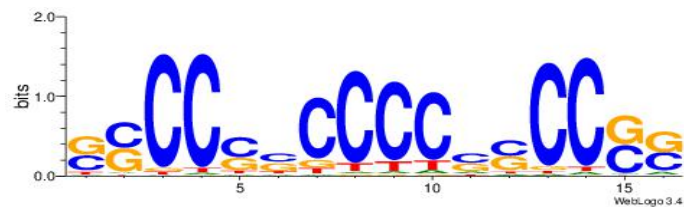


Dataset #: 1
Motif ID: 8
Motif name: C008
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement

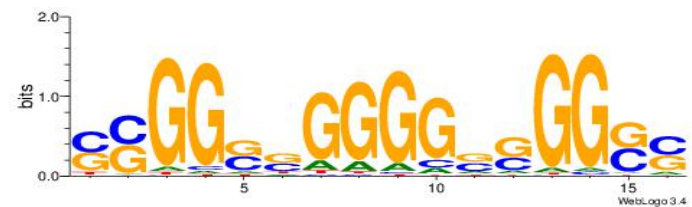
Direction: Forward
 Position number: 2
 Number of overlap: 14
 Similarity score: 0.00956764

Alignment:
 SSGGSSGGGGSSGGSS
 -SSGGHGGGGKGGSS-

Original motif Consensus sequence: SSCSSCCCCSSCCSS



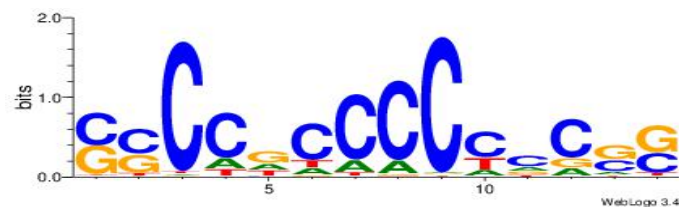
Reverse complement motif Consensus sequence: SSGGSSGGGGSSGGSS



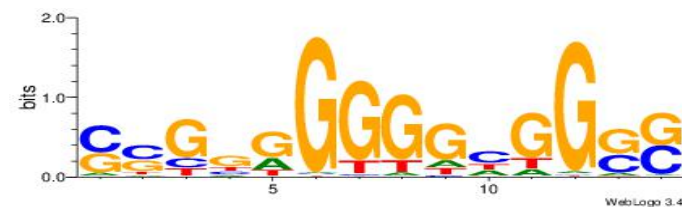
Dataset #: 1
 Motif ID: 54
 Motif name: C054
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0.0123202

Alignment:
 SSCCDCCCCCCCSS
 SSCCYCCCCDCCSS

Original motif Consensus sequence: SSCDCCCCCCSCS



Reverse complement motif Consensus sequence: SSGGGGGGGHGG

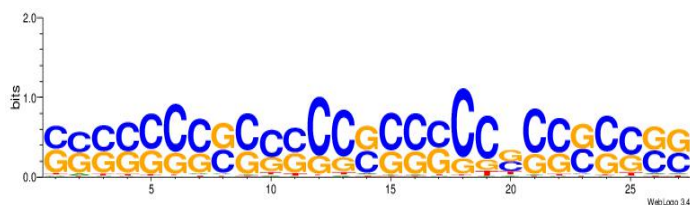


Dataset #: 1
 Motif ID: 4
 Motif name: C004
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 4
 Number of overlap: 14
 Similarity score: 0.0160908

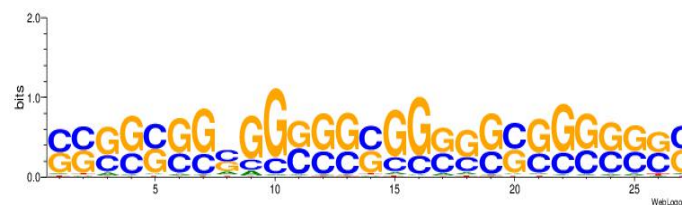
Alignment:

SSSSSSGSGGSSSSGSGSSSSGSSSSS
 ---SSGHHGGGGKGGSS-----

Original motif Consensus sequence: SSSSSCSSSSSCSSSSCCSCSSSSS



Reverse complement motif Consensus sequence: SSSSSGSGGSSSSGSGSSSSGSSSSS

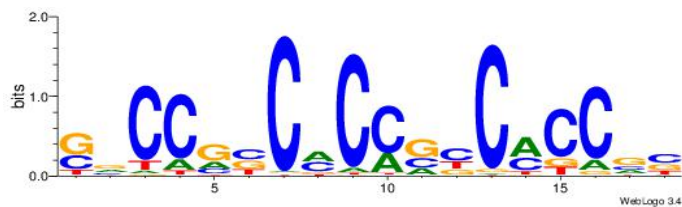


Dataset #: 1
 Motif ID: 37
 Motif name: C037
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 4
 Number of overlap: 14
 Similarity score: 0.0188565

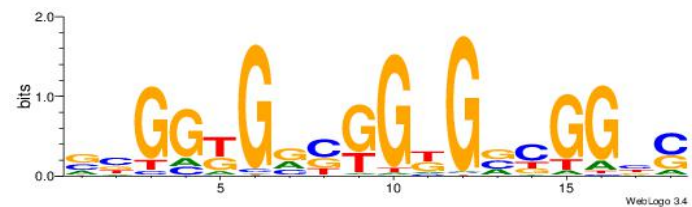
Alignment:

SVCCGBCMCCSYCMCCVB
 -SSCCYCCCCDCCSS---

Original motif Consensus sequence: SVCCGBCMCCSYCMCCVB



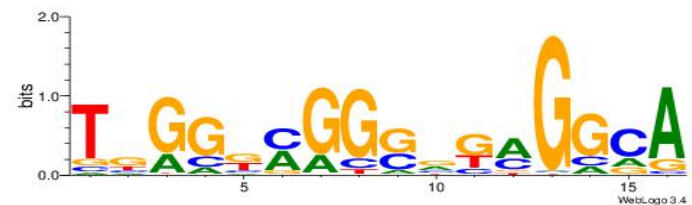
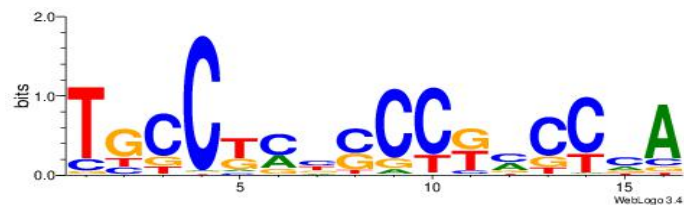
Reverse complement motif Consensus sequence: BVGGYGKSGGYBCGGVS



Dataset #: 1 Motif ID: 105 Motif name: C105

Original motif Consensus sequence: TGCKMBSCCKMCCVA

Reverse complement motif Consensus sequence: TVGGRYGGSBRRGGCA



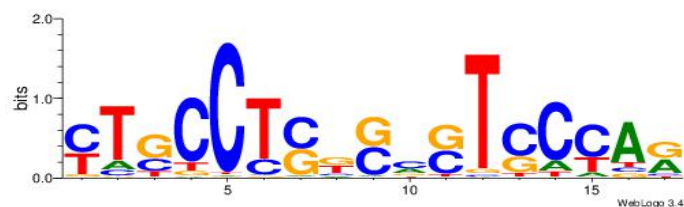
Best Matches for Motif ID 105 (Highest to Lowest)

Dataset #: 1
 Motif ID: 101
 Motif name: C101
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 16
 Similarity score: 0.0216765

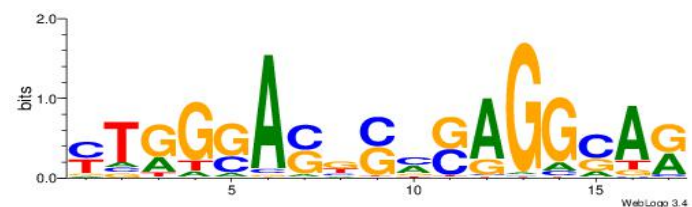
Alignment:

YTSCCTSKSVSTCCCAR
 -TGCKMBSCCKMCCVA

Original motif Consensus sequence: YTSCCTSKSVSTCCCAR



Reverse complement motif Consensus sequence: MTGGGASVSYAGGSAK

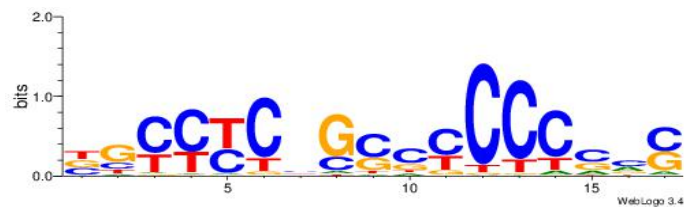


Dataset #: 1
 Motif ID: 22
 Motif name: C022
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 16
 Similarity score: 0.0274458

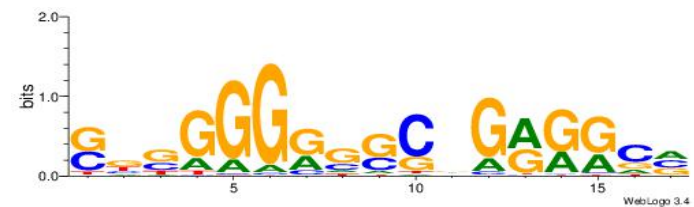
Alignment:

BGCCYCBGSCYCCCSVS
 TGCKMBSCCKMCCVA-

Original motif Consensus sequence: BGCCYCBGSCYCCCSVS



Reverse complement motif Consensus sequence: SVSGGGKGSGBMGGCV

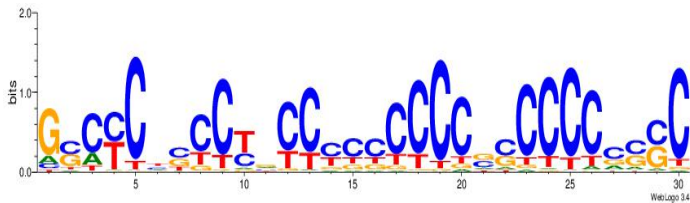


Dataset #: 1
 Motif ID: 3
 Motif name: C003
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 10

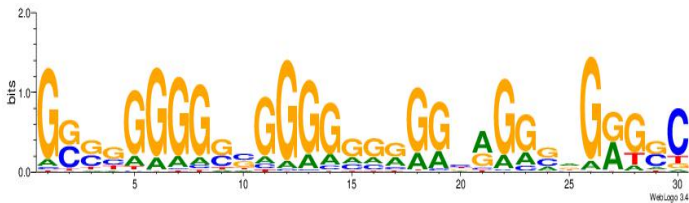
Number of overlap: 16
Similarity score: 0.029655

Alignment:
GSSGGGGSSGGGGGKGGVMGGSHGKGC
-----TVGGRYGGSBRRGGCA-----

Original motif Consensus sequence:
GSCYCHSCCYVCCYCCCCSSCCCCSSC



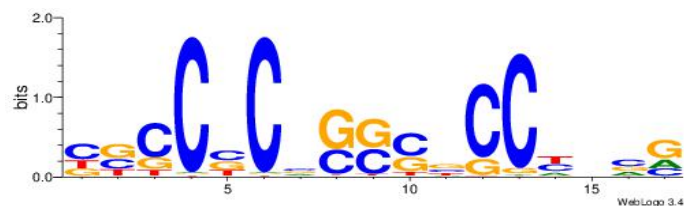
Reverse complement motif Consensus sequence:
GSSGGGGSSGGGGGKGGVMGGSHGKGC



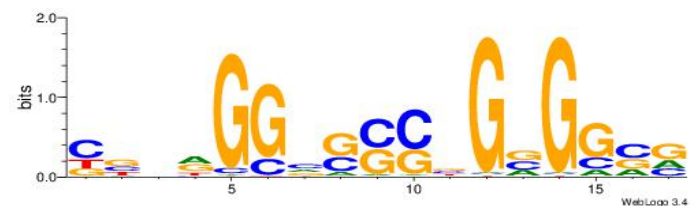
Dataset #: 1
Motif ID: 140
Motif name: C140
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 16
Similarity score: 0.0298105

Alignment:
BSCCBVSSSBCCYHVG
TGCKMBSCCKMCCVA-

Original motif Consensus sequence: BSCCBCVSSSBCCYHVG



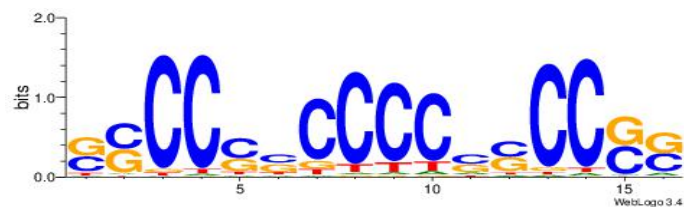
Reverse complement motif Consensus sequence: CVDMGGBSSSVGBGGSB



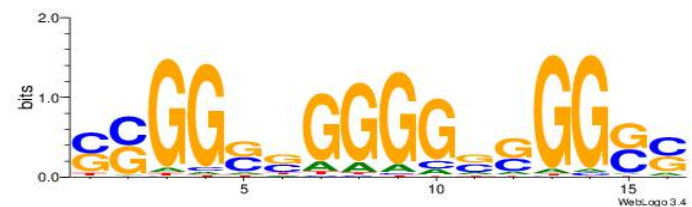
Dataset #: 1
 Motif ID: 8
 Motif name: C008
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 16
 Similarity score: 0.0383734

Alignment:
 SSCCSSCCCCSSCCSS
 TGCCKMBSCCKMCCVA

Original motif Consensus sequence: SSCCSSCCCCSSCCSS



Reverse complement motif Consensus sequence: SSGSSGGGGSSGGSS

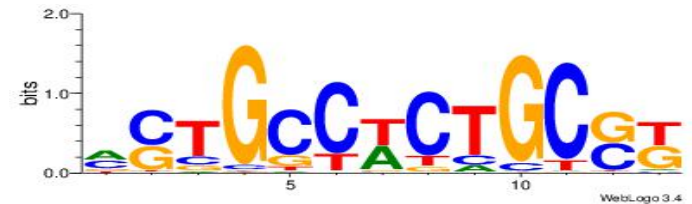


Dataset #: 1 Motif ID: 106 Motif name: C106

Original motif Consensus sequence: MSGCAGWGGCASK



Reverse complement motif Consensus sequence: RSTGCCWCTGCSY

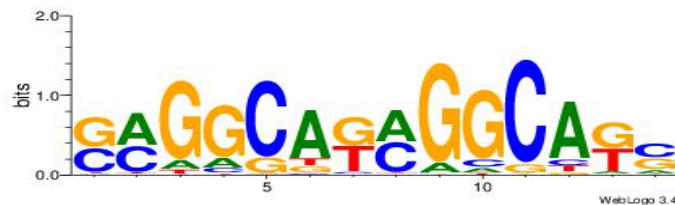


Best Matches for Motif ID 106 (Highest to Lowest)

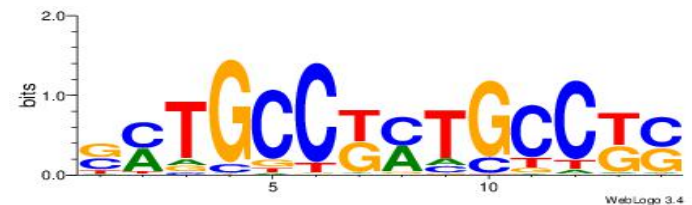
Dataset #:	1
Motif ID:	60
Motif name:	C060
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	2
Number of overlap:	13
Similarity score:	0.00980046

Alignment:
SYTGCCYYTGCCYS
RSTGCCWCTGCSY-

Original motif Consensus sequence: SMGGCAKMGGCAKS



Reverse complement motif Consensus sequence: SYTGCCYYTGCCYS



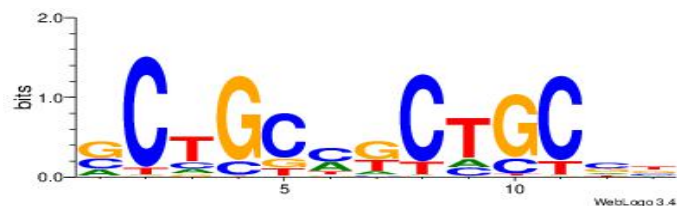
Dataset #: 1
Motif ID: 84
Motif name: C084
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 13
Similarity score: 0.0130594

Alignment:

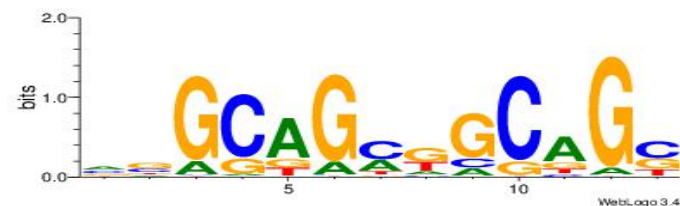
VVGCAGYRGCAGS

MSGCAGWGGCASK

Original motif Consensus sequence: SCTGCMKCTGCVB



Reverse complement motif Consensus sequence: VVGCAGYRGCAGS

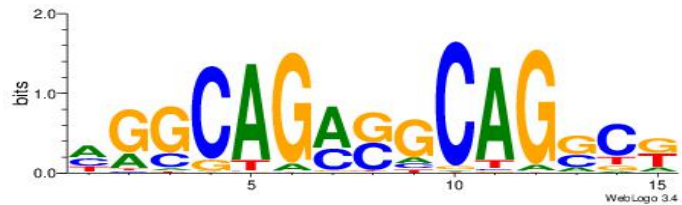


Dataset #: 1
Motif ID: 75
Motif name: C075
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 3

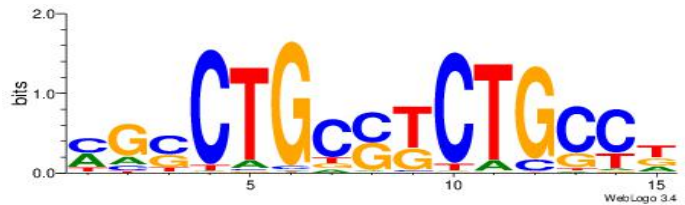
Number of overlap: 13
Similarity score: 0.0158953

Alignment:
YGSCTGCSYCTGCCY
--RSTGCCWCTGCSY

Original motif Consensus sequence: MGGCAGMSGCAGSCK



Reverse complement motif Consensus sequence: YGSCTGCSYCTGCC

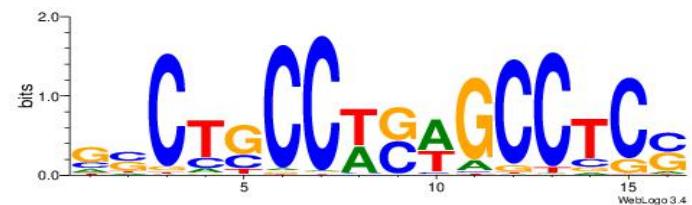
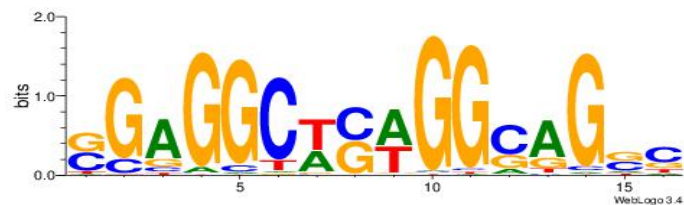


Dataset #: 1
Motif ID: 48
Motif name: C048
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 3
Number of overlap: 13
Similarity score: 0.0219653

Alignment:
GSCTGCCWSWGCCTCS
-RSTGCCWCTGCSY--

Original motif Consensus sequence: SGAGGCWSWGGCAGSC

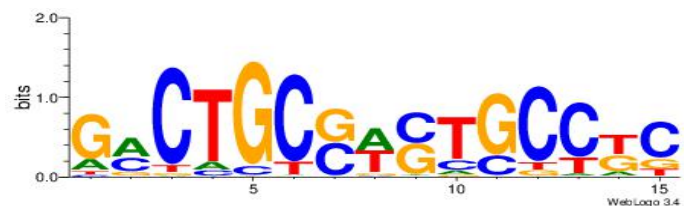
Reverse complement motif Consensus sequence:
GSCTGCCWSWGCCTCS



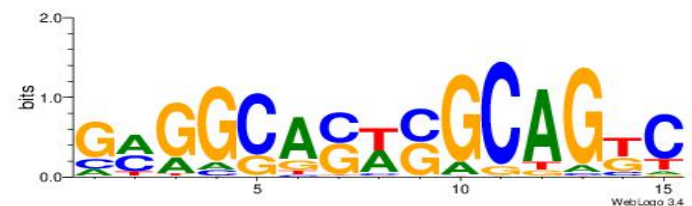
Dataset #: 1
 Motif ID: 118
 Motif name: C118
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 13
 Similarity score: 0.0221158

Alignment:
 GRGGCASWSGCAGYC
 -MSGCAGWGGCASK-

Original motif Consensus sequence: GMCTGCSWSTGCCKC

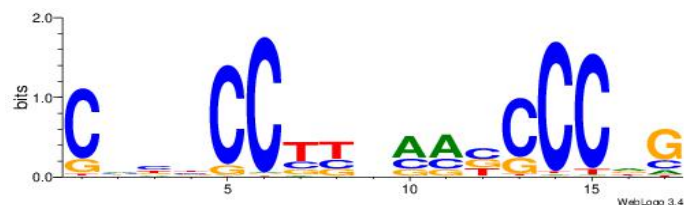


Reverse complement motif Consensus sequence: GRGGCASWSGCAGYC

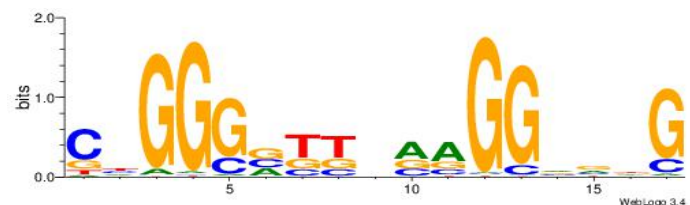


Dataset #: 1 Motif ID: 107 Motif name: C107

Original motif Consensus sequence: CHBBCCTYBAABCCCDG



Reverse complement motif Consensus sequence: CDGGGBTTVMAGGVBHG



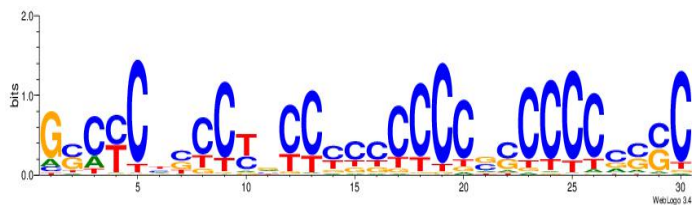
Best Matches for Motif ID 107 (Highest to Lowest)

Dataset #: 1
 Motif ID: 3
 Motif name: C003
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 10
 Number of overlap: 17
 Similarity score: 0.0446524

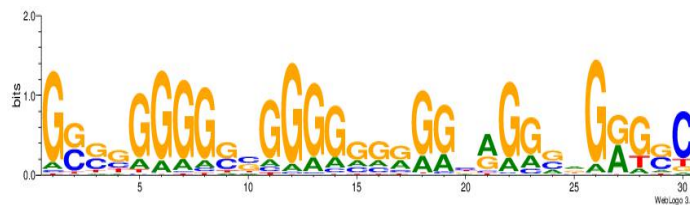
Alignment:

GSCYCHSCCYVCCYCCCCCSCCCCCSSC
 ----CHBBCCTYBAABCCCDG-----

Original motif Consensus sequence:
 GSCYCHSCCYVCCYCCCCCSCCCCCSSC



Reverse complement motif Consensus sequence:
 GSSGGGGGSSGGGGGKGGVMGGSHGKGC

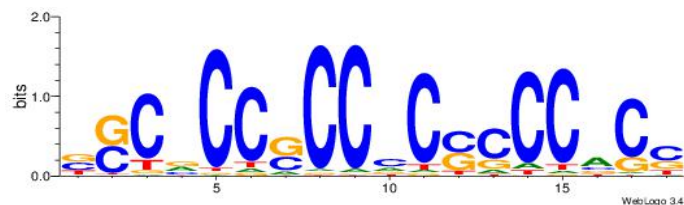


Dataset #: 1
 Motif ID: 20
 Motif name: C020
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 17
 Similarity score: 0.0507615

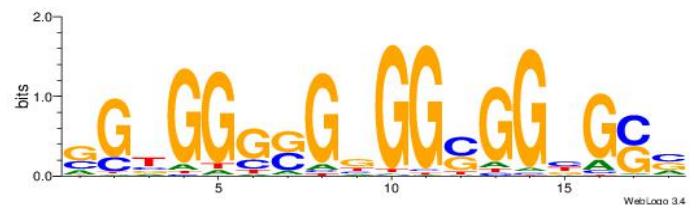
Alignment:

SGTGGGSGVGGSGGVGSB
 -CDGGGBT'TVMAGGV BHG

Original motif Consensus sequence: BSCVCCSCCVSCCCACS



Reverse complement motif Consensus sequence: SGTGGGSGVGGSGGVGSB



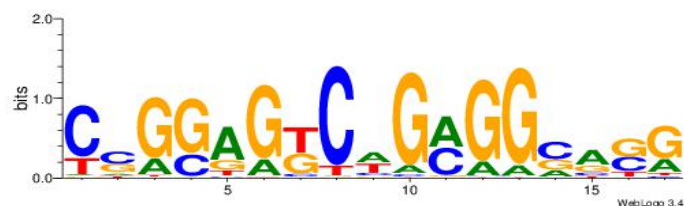
Dataset #: 1
 Motif ID: 86
 Motif name: C086
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward

Position number: 1
Number of overlap: 17
Similarity score: 0.0514928

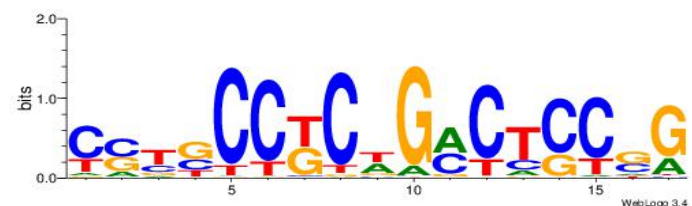
Alignment:

CSTSCCYCWGRCTCCSG
CHBBCCTYBAABCCCDG

Original motif Consensus sequence: CSGGAGKCWGMGGSASG



Reverse complement motif Consensus sequence: CSTSCCYCWGRCTCCSG

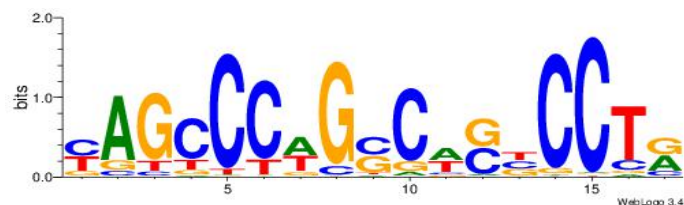


Dataset #: 1
Motif ID: 122
Motif name: C122
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 17
Similarity score: 0.0541557

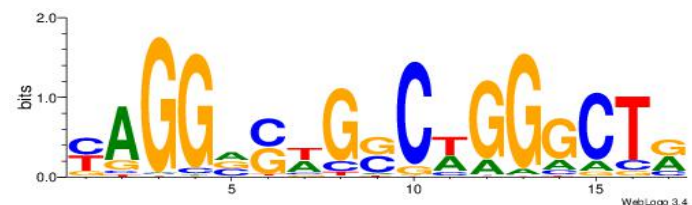
Alignment:

YAGCCWGSBCCTR
CHBBCCTYBAABCCCDG

Original motif Consensus sequence: YAGCCCWGSCWSBCCTR



Reverse complement motif Consensus sequence: MAGGVSWGSCWGGGCTK

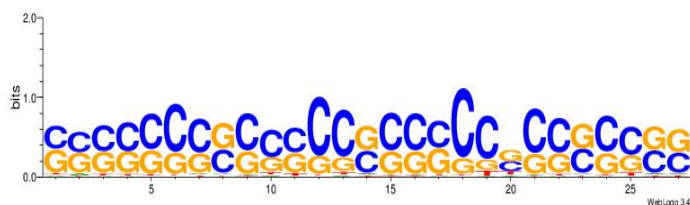


Dataset #: 1
 Motif ID: 4
 Motif name: C004
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 5
 Number of overlap: 17
 Similarity score: 0.0584694

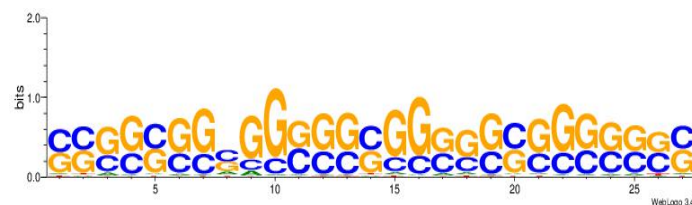
Alignment:

SSSSSCSSSSSCSSSSCCSCSSSSSS
 ----CHBBCCTYBAABCCCDG-----

Original motif Consensus sequence: SSSSSCSSSSSCSSSSCCSCSSSSSS

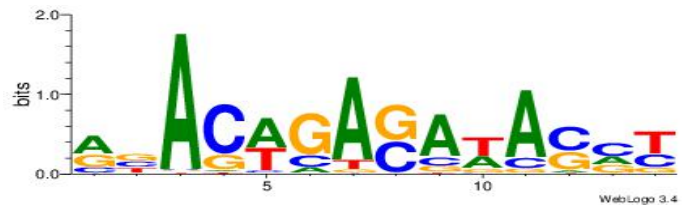


Reverse complement motif Consensus sequence: SSSSSGSGGSSSSGGSSSSSGSSSSS

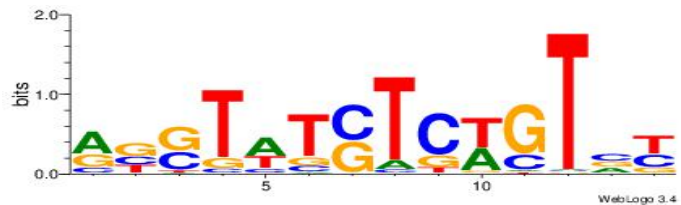


Dataset #: 1 Motif ID: 108 Motif name: C108

Original motif Consensus sequence: RBACWGASAWASVY



Reverse complement motif Consensus sequence: MVSTWTSTCWGTR



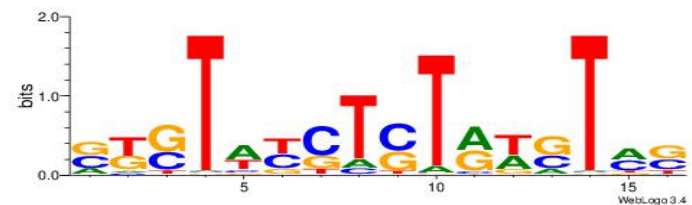
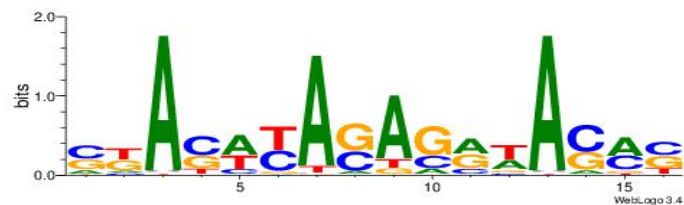
Best Matches for Motif ID 108 (Highest to Lowest)

Dataset #:	1
Motif ID:	125
Motif name:	C125
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:	3.79502e-05

Alignment:
SKASWYASAGRWASMS
--RBACWGASAWASVY

Original motif Consensus sequence: SKASWYASAGRWASMS

Reverse complement motif Consensus sequence:
SYSTWKCTSTMWSTRS



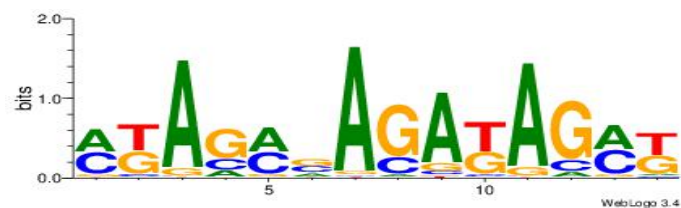
Dataset #: 1
 Motif ID: 21
 Motif name: C021
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0.00124361

Alignment:

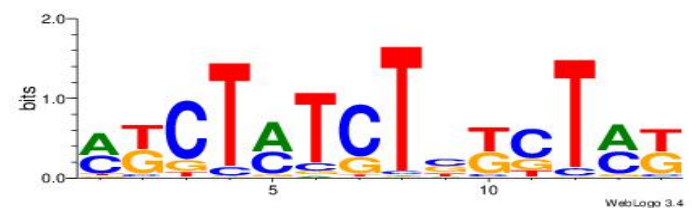
MKAGMVAGAKAGMK

RBACWGASAWASVY

Original motif Consensus sequence: MKAGMVAGAKAGMK



Reverse complement motif Consensus sequence: RYCTRTCTVYCTRY



Dataset #: 1
 Motif ID: 53

Motif name:	C053
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:	0.00887812

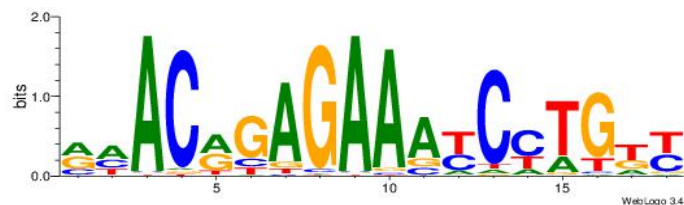
Alignment:

```

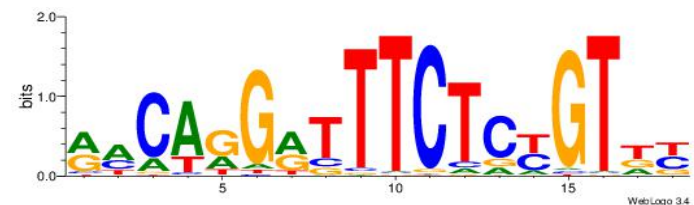
RMACRGAGAAAYCCTGKY
RBACWGASAWASVY----

```

Original motif Consensus sequence: RMACRGAGAAAYCCTGKY



Reverse complement motif Consensus sequence: MRCAGGMTTCTCKGTYK

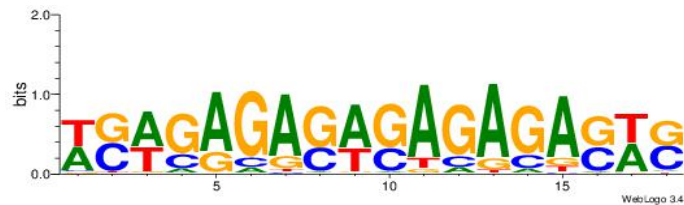


Dataset #:	1
Motif ID:	17
Motif name:	C017
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	5
Number of overlap:	14
Similarity score:	0.0104617

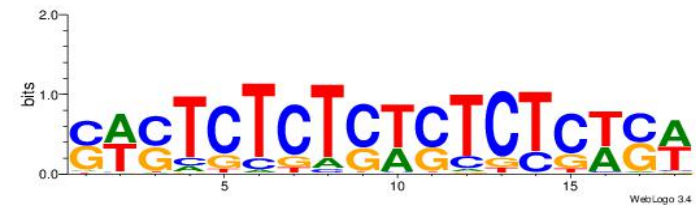
Alignment:

SWSTCTCTSWSTCTCWSW
MVSTWTSTCWGTBK----

Original motif Consensus sequence: WSWGAGASWSAGAGASWS



Reverse complement motif Consensus sequence:
SWSTCTCTSWSTCTCWSW



Dataset #:	1
Motif ID:	70
Motif name:	C070
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	14
Similarity score:	0.0119575

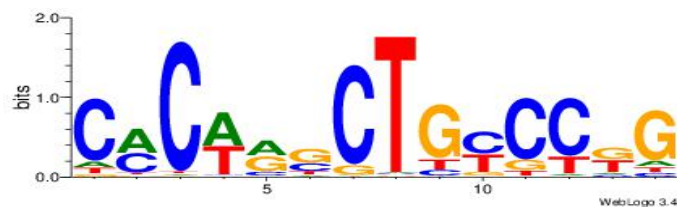
Alignment:

GVGABAGAVAGASVK
-RBACWGASAWASVY

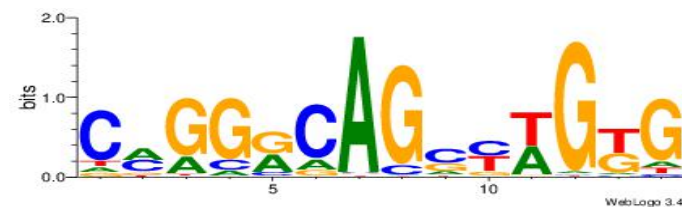
Original motif Consensus sequence: GVGABAGAVAGASVK

Reverse complement motif Consensus sequence: RBSTCTVTCTBTCV

Original motif Consensus sequence: CMCWRCTGYCCKG



Reverse complement motif Consensus sequence: CYGGKCAGSKWG

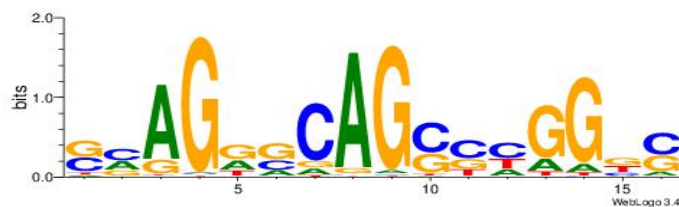


Dataset #: 1
 Motif ID: 39
 Motif name: C039
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 14
 Similarity score: 0.0182618

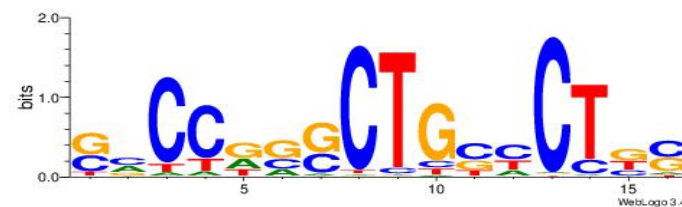
Alignment:

SBCKSSCTGSMCTRS
 -RMCWSGCTGSCCKY-

Original motif Consensus sequence: SMAGRSCAGSSYGGBS



Reverse complement motif Consensus sequence: SBCKSSCTGSMCTRS

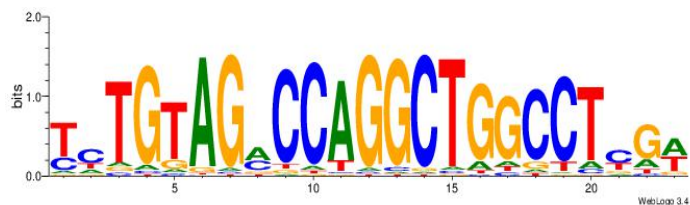


Dataset #: 1
 Motif ID: 5
 Motif name: C005
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 8
 Number of overlap: 14
 Similarity score: 0.0183336

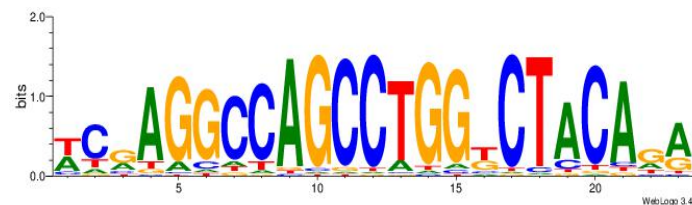
Alignment:

TCTGTAGMCCAGGCTGGCCTYGW
 -----RMCWSGCTGSCCKY--

Original motif Consensus sequence: TCTGTAGMCCAGGCTGGCCTYGW



Reverse complement motif Consensus sequence: WCKAGGCCAGCCTGGYCTACAGA



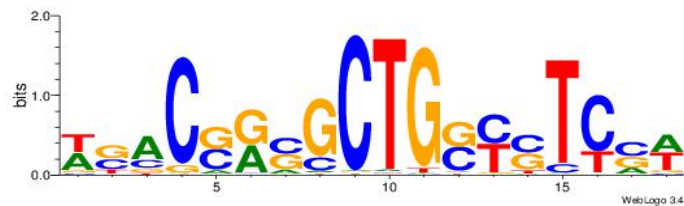
Dataset #: 1
 Motif ID: 124
 Motif name: C124
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3

Number of overlap: 14
Similarity score: 0.0260518

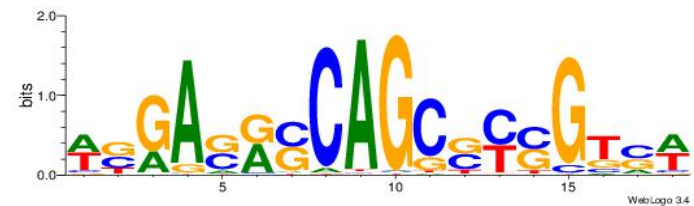
Alignment:

WSACSRSGCTGSYSTCSW
--RMCWSGCTGSCCKY--

Original motif Consensus sequence: WSACSRSGCTGSYSTCSW



Reverse complement motif Consensus sequence: WSGASKSCAGCSMSGTSW

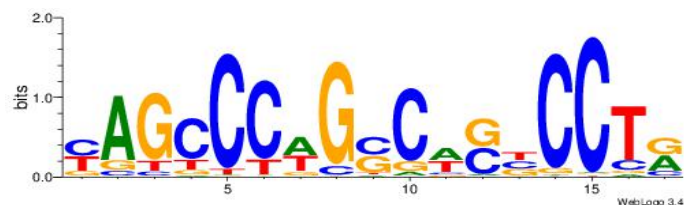


Dataset #: 1
Motif ID: 122
Motif name: C122
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 4
Number of overlap: 14
Similarity score: 0.0339955

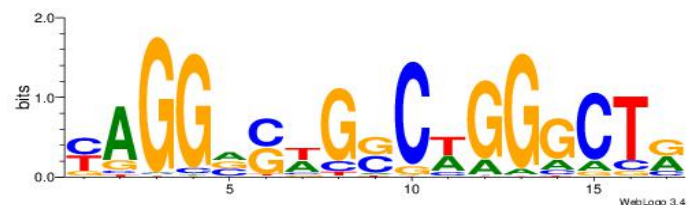
Alignment:

MAGGVSWGSCWGGGCTK
MRGGSCAGCSWGRK---

Original motif Consensus sequence: YAGCCCWGSCWSBCCTR

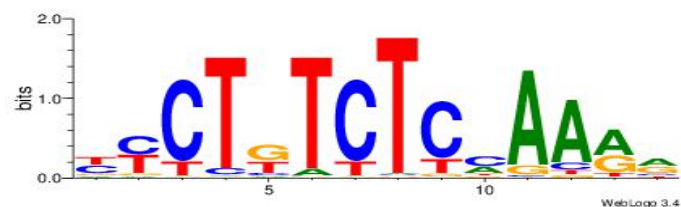


Reverse complement motif Consensus sequence: MAGGVSWGSCWGGGCTK

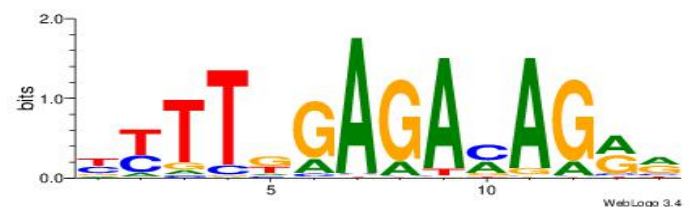


Dataset #: 1 Motif ID: 110 Motif name: C110

Original motif Consensus sequence: YYCTKTCTCMAARR



Reverse complement motif Consensus sequence: KKTTRGAGAYAGK



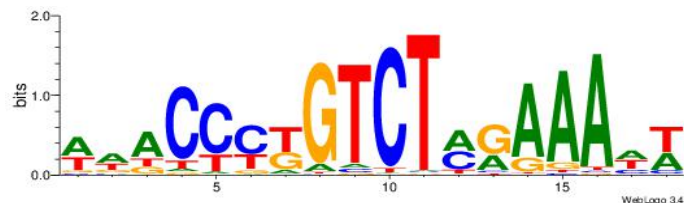
Best Matches for Motif ID 110 (Highest to Lowest)

Dataset #:	1
Motif ID:	35
Motif name:	C035
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:	0.0126083

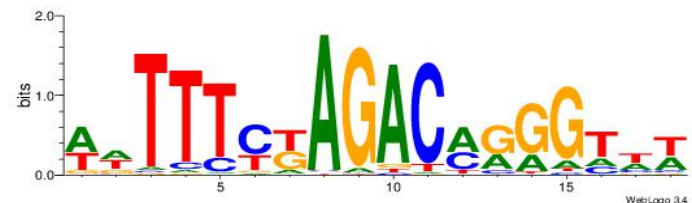
Alignment:

WWACCYKGTCTMRAAAWW
 ---YYCTKTCTCMAARR--

Original motif Consensus sequence: WWACCYKGTCTMRAAAWW



Reverse complement motif Consensus sequence: WWTTTMYAGACRKGGTWW



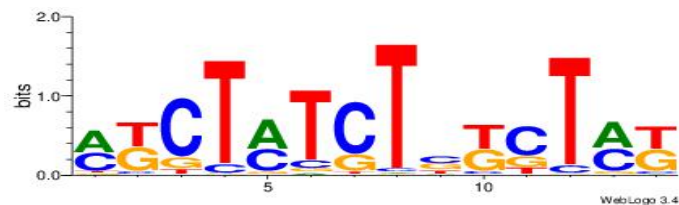
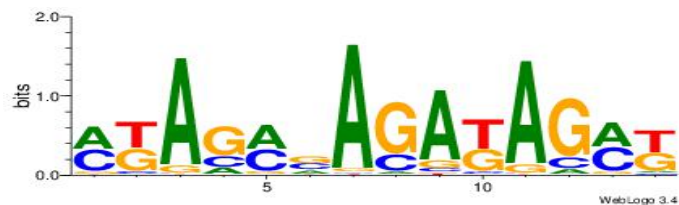
Dataset #:	1
Motif ID:	21
Motif name:	C021
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	14
Similarity score:	0.036224

Alignment:

MKAGMVAGAKAGMK
 KKTTRGAGAYAGKM

Original motif Consensus sequence: MKAGMVAGAKAGMK

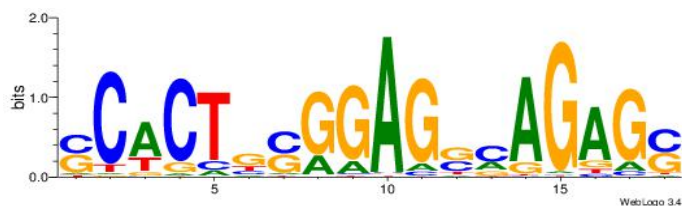
Reverse complement motif Consensus sequence: RYCTRTCTVYCTRY



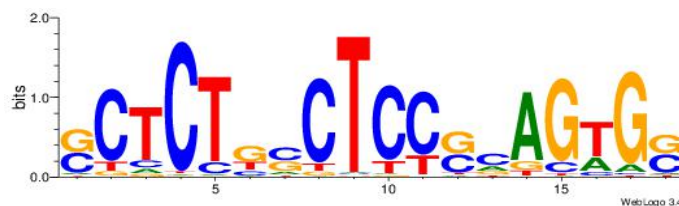
Dataset #: 1
 Motif ID: 34
 Motif name: C034
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 4
 Number of overlap: 14
 Similarity score: 0.0376014

Alignment:
 SCACTGSGGAGSMAGAGS
 -KKTTTRGAGAYAGKM---

Original motif Consensus sequence: SCACTGSGGAGSMAGAGS



Reverse complement motif Consensus sequence: SCTCTRSCTCCSCAGTGS



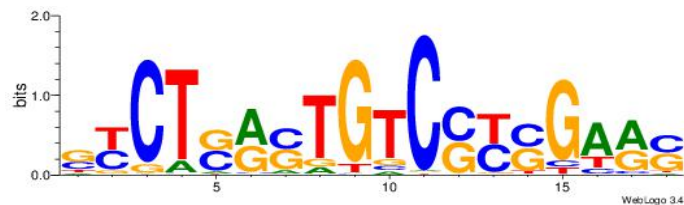
Dataset #: 1

Motif ID: 128
 Motif name: C128
 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: 0.0439701

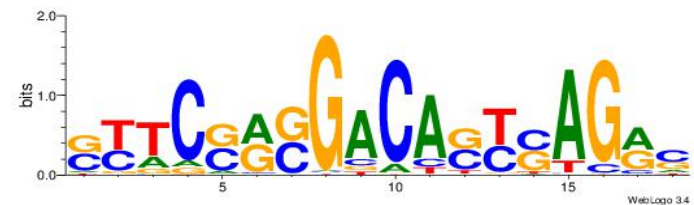
Alignment:

SKTCSMSGACASKSAGMS
 KKTTTRGAGAYAGKM----

Original motif Consensus sequence: SYCTSRSTGTCSYSGARS



Reverse complement motif Consensus sequence: SKTCSMSGACASKSAGMS

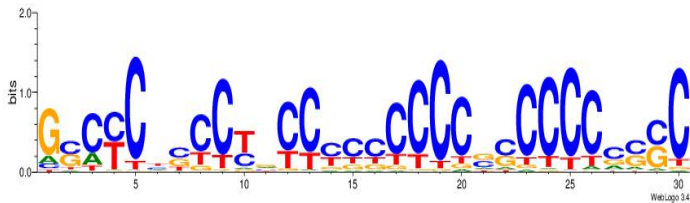


Dataset #: 1
 Motif ID: 3
 Motif name: C003
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 15
 Number of overlap: 14

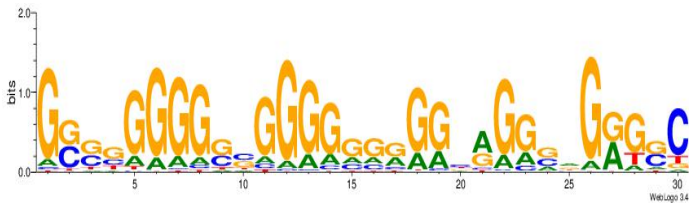
Similarity score: 0.0457893

Alignment:
GSSGGGGSSGGGGGKGGVMGGSHGKGC
-----KKTTRGAGAYAGKM--

Original motif Consensus sequence:
GSCYCHSCCYVCCYCCCCSSCCCCSSC

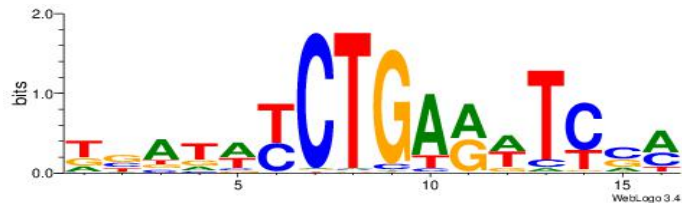


Reverse complement motif Consensus sequence:
GSSGGGGSSGGGGGKGGVMGGSHGKGC

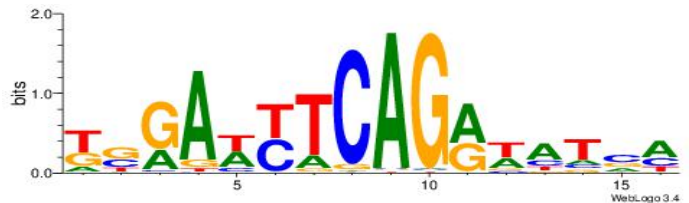


Dataset #: 1 Motif ID: 111 Motif name: C111

Original motif Consensus sequence: TBATWYCTGARWTCSM



Reverse complement motif Consensus sequence:
YSGAWKTCAGMWATBA



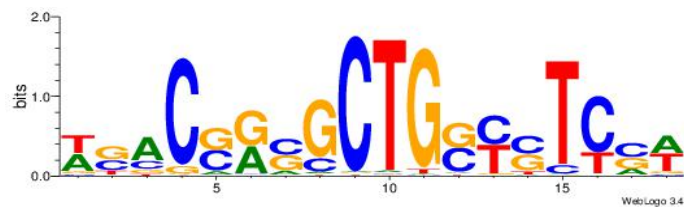
Best Matches for Motif ID 111 (Highest to Lowest)

Dataset #:	1
Motif ID:	124
Motif name:	C124
Matching format of first motif:	Reverse Complement

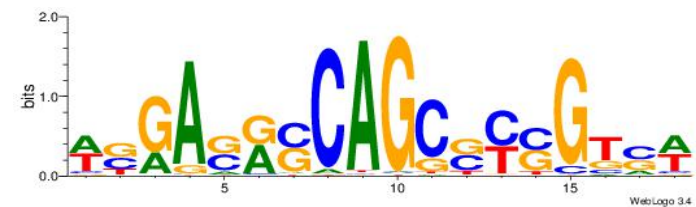
Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 16
 Similarity score: 0.0317368

Alignment:
 WSGASKSCAGCSMSGTSW
 YSGAWKTCAGMWATBA--

Original motif Consensus sequence: WSACSRSGCTGSYSTCSW



Reverse complement motif Consensus sequence: WSGASKSCAGCSMSGTSW

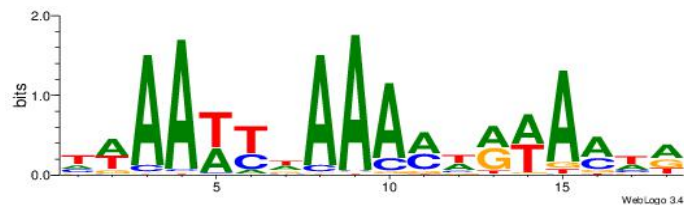


Dataset #: 1
 Motif ID: 32
 Motif name: C032
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 16
 Similarity score: 0.0343652

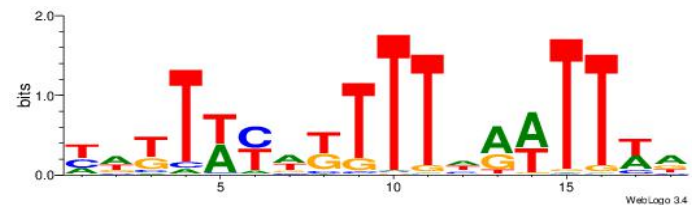
Alignment:

HWAAWYDAAAMWRWAMWR
 --YSGAWKTCAGMWATBA

Original motif Consensus sequence: HWAAWYDAAAMWRWAMWR



Reverse complement motif Consensus sequence: KWYTWKWYTTTDMWTTWH

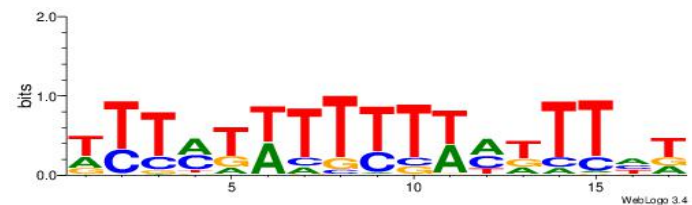
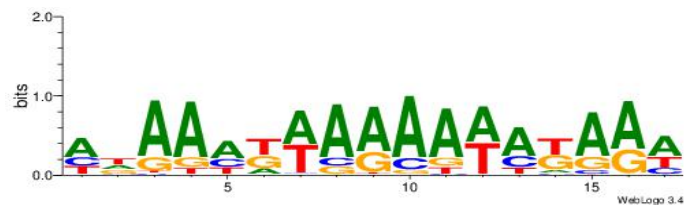


Dataset #:	1
Motif ID:	79
Motif name:	C079
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	16
Similarity score:	0.0379285

Alignment:
 ADAAAKWAAAAWAKARW
 -YSGAWKTCAGMWATBA

Original motif Consensus sequence: ADAAAKWAAAAWAKARW

Reverse complement motif Consensus sequence: WKTRTWTTTTWRTTDT

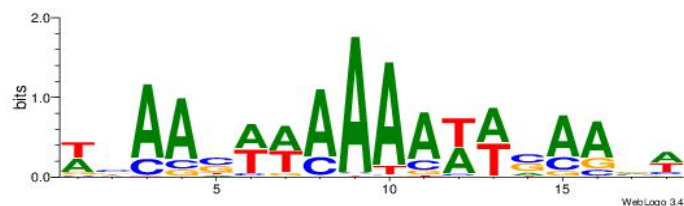


Dataset #: 1
 Motif ID: 97
 Motif name: C097
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 16
 Similarity score: 0.0433488

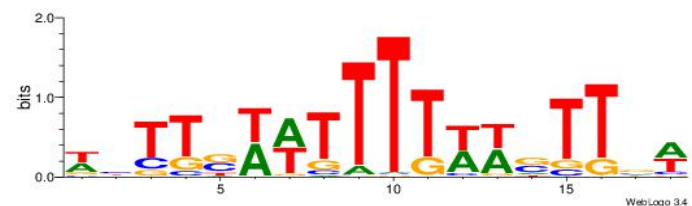
Alignment:

WBAASWWAAA WWSAAVW
 --YSGAWKTCAGMWATBA

Original motif Consensus sequence: WBAASWWAAA WWSAAVW



Reverse complement motif Consensus sequence: WVTTSWWTTT TWWSTTBW



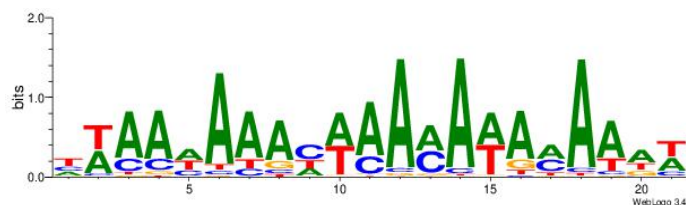
Dataset #: 1

Motif ID: 16
 Motif name: C016
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 4
 Number of overlap: 16
 Similarity score: 0.0454989

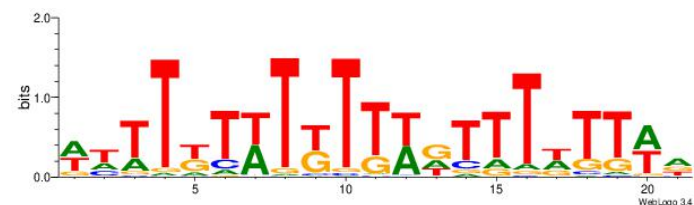
Alignment:

HWAAWAAAHWAAMAWAMAAWW
 --YSGAWKTCAGMWATBA---

Original motif Consensus sequence: HWAAWAAAHWAAMAWAMAAWW

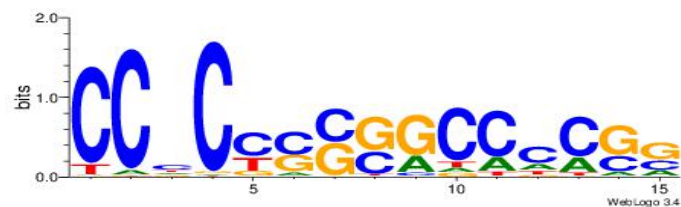


Reverse complement motif Consensus sequence: WWTYYTWYTTWDTTWTWH

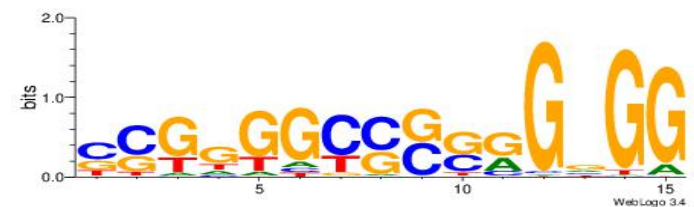


Dataset #: 1 Motif ID: 112 Motif name: C112

Original motif Consensus sequence: CCBCYSSSGCCCCSS



Reverse complement motif Consensus sequence: SSGGGCSSSKGBGG



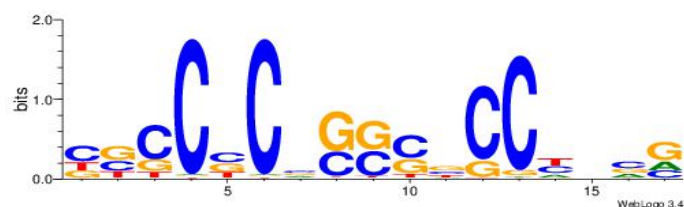
Best Matches for Motif ID 112 (Highest to Lowest)

Dataset #: 1
Motif ID: 140
Motif name: C140
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 15
Similarity score: 0.0255213

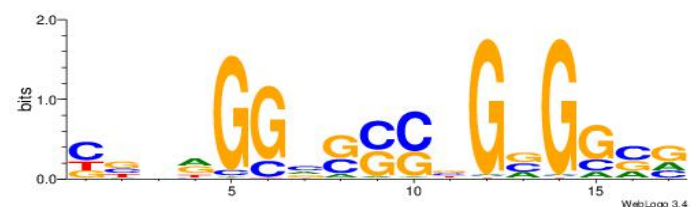
Alignment:

```
BSCCBVCSSSBCCYHVG  
--CCBCYSSSGCCCCSS
```

Original motif Consensus sequence: BSCCBVCSSSBCCYHVG



Reverse complement motif Consensus sequence:
CVDMGGBSSSVGBGGSB

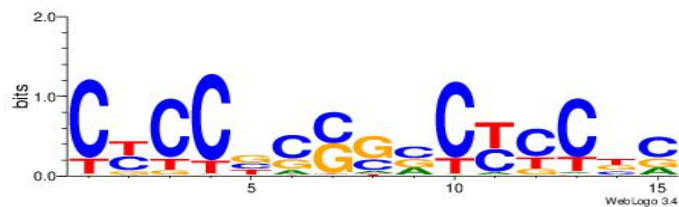


Dataset #: 1
Motif ID: 58
Motif name: C058
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif

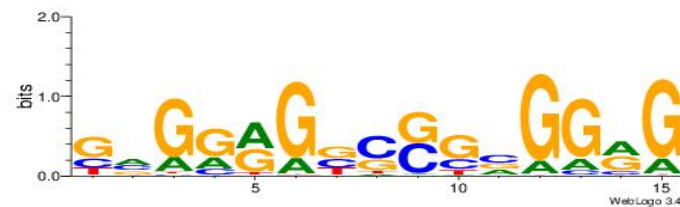
Direction: Backward
 Position number: 1
 Number of overlap: 15
 Similarity score: 0.030544

Alignment:
 CYCCBCSGVCYCCBC
 CCBCYSSSGCCCCSS

Original motif Consensus sequence: CYCCBCSGVCYCCBC



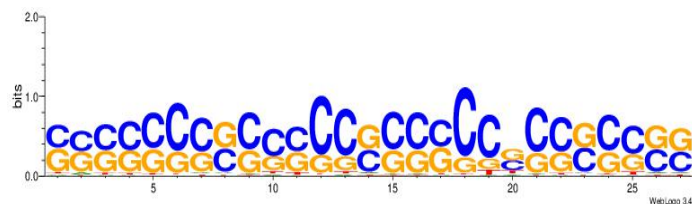
Reverse complement motif Consensus sequence: GVGGMGVCSGBGGMG



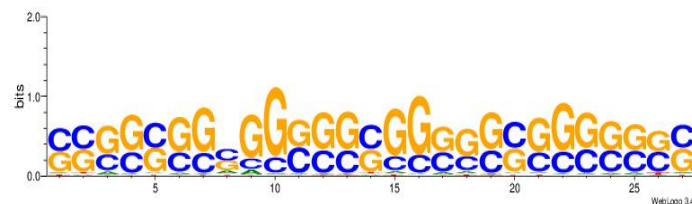
Dataset #: 1
 Motif ID: 4
 Motif name: C004
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 9
 Number of overlap: 15
 Similarity score: 0.0362599

Alignment:
 SSSSSSGSGGSSSSSGSSSSSGSSSSS
 ----SSGGGCSSSKGBGG-----

Original motif Consensus sequence:
SSSSSCSSSSSCSSSSSCSCSSSSSS



Reverse complement motif Consensus sequence:
SSSSSSGSGGSSSSSGGSSSSSGSSSSS

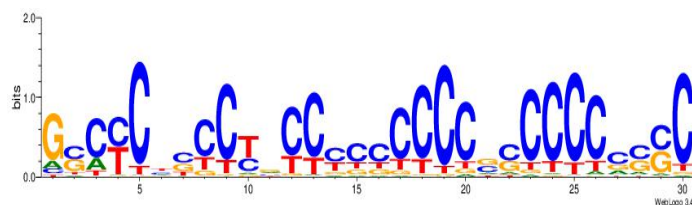


Dataset #: 1
Motif ID: 3
Motif name: C003
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 14
Number of overlap: 15
Similarity score: 0.0409351

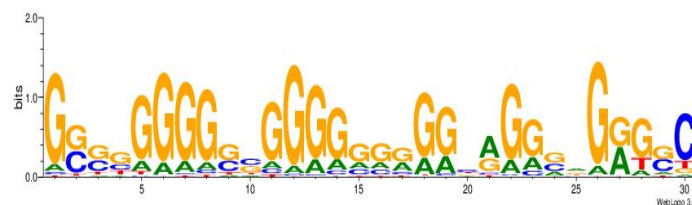
Alignment:

GSSGGGGGSSGGGGGKGGVMGGSHGKGC
--SSGGGCGSSSKGBG-----

Original motif Consensus sequence:
GSCYCHSCCYVCCYCCCCCSCCCCCSSC



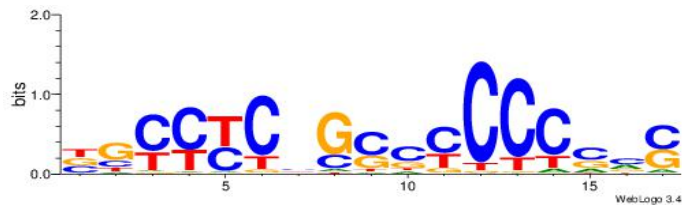
Reverse complement motif Consensus sequence:
GSSGGGGGSSGGGGGKGGVMGGSHGKGC



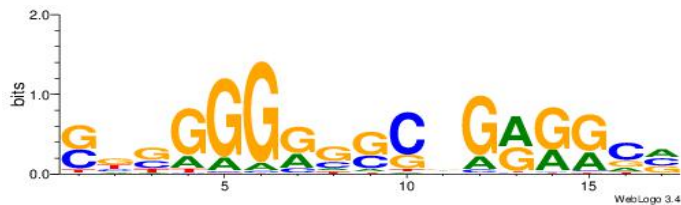
Dataset #: 1
Motif ID: 22
Motif name: C022
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 3
Number of overlap: 15
Similarity score: 0.0453525

Alignment:
BGCCYCBGSCYCCCSVS
--CCBCYSSSGCCCCSS

Original motif Consensus sequence: BGCCYCBGSCYCCCSVS



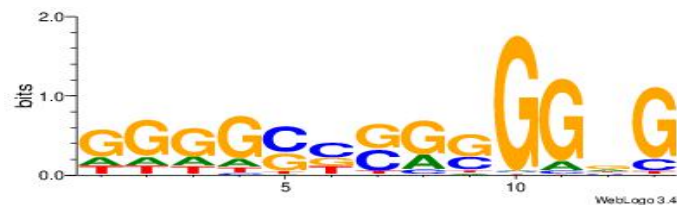
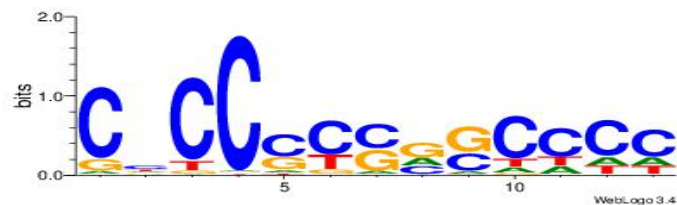
Reverse complement motif Consensus sequence: SVSGGGKGSGBMGGCV



Dataset #: 1 Motif ID: 113 Motif name: C113

Original motif Consensus sequence: CHCCSCSVSCCCC

Reverse complement motif Consensus sequence: GGGGSVSGSGGD



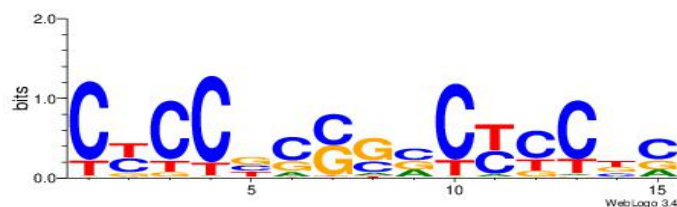
Best Matches for Motif ID 113 (Highest to Lowest)

Dataset #: 1
 Motif ID: 58
 Motif name: C058
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 13
 Similarity score: 0.00967619

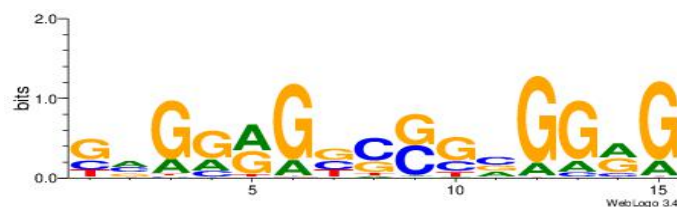
Alignment:

CYCCBCSGVCYCCBC
 CHCCSCSVSCCCC--

Original motif Consensus sequence: CYCCBCSGVCYCCBC



Reverse complement motif Consensus sequence:
 GVGGMGVC SGBGGMG

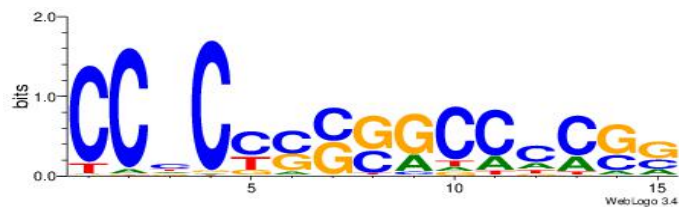


Dataset #: 1
 Motif ID: 112
 Motif name: C112
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 13
 Similarity score: 0.0176733

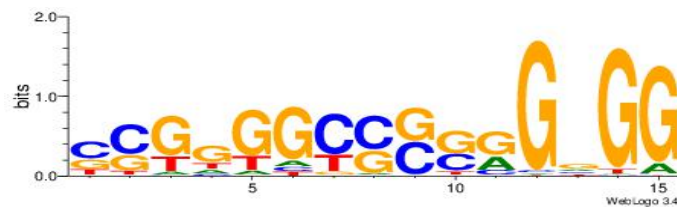
Alignment:

CCBCYSSSGCCCCSS
 CHCCSCSVSCCCC--

Original motif Consensus sequence: CCBCYSSSGCCCCSS



Reverse complement motif Consensus sequence: SSGGGGCSSSKGBGG

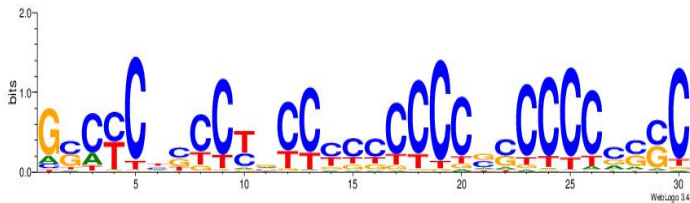


Dataset #: 1
 Motif ID: 3
 Motif name: C003
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 4

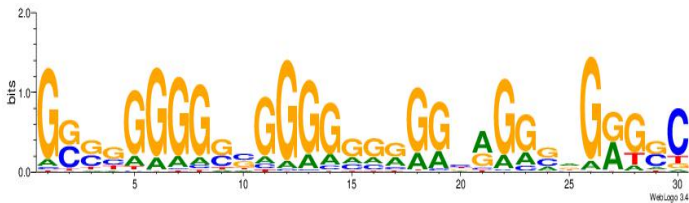
Number of overlap: 13
Similarity score: 0.0208066

Alignment:
GSCYCHSCCYVCCYCCCCCSCCCCCSSC
-----CHCCSCSVSCCCC---

Original motif Consensus sequence:
GSCYCHSCCYVCCYCCCCCSCCCCCSSC



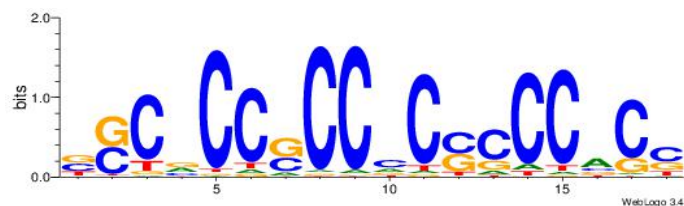
Reverse complement motif Consensus sequence:
GSSGGGGGSSGGGGGKGGVMGGSHGKGSC



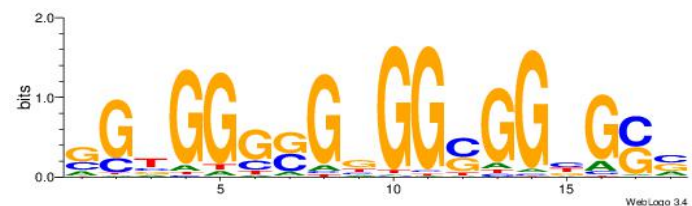
Dataset #: 1
Motif ID: 20
Motif name: C020
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 13
Similarity score: 0.02801

Alignment:
SGTGGGSGVGGSGGVGSB
GGGGSVSGSGGDG-----

Original motif Consensus sequence: BSCVCCSCCVSCCCACS



Reverse complement motif Consensus sequence: SGTGGGSGVGGSGGVGSB

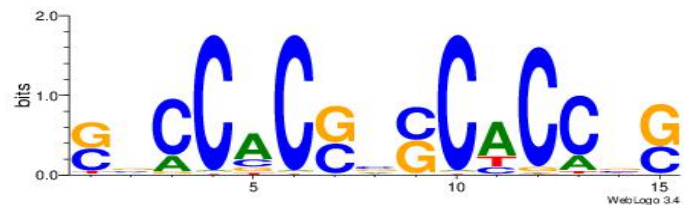


Dataset #: 1
 Motif ID: 71
 Motif name: C071
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 13
 Similarity score: 0.0297711

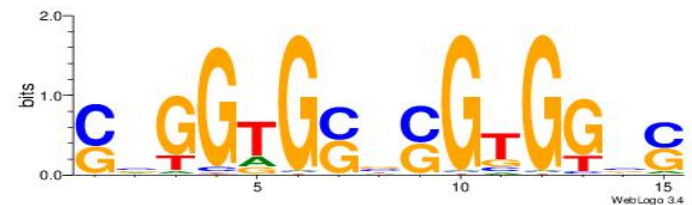
Alignment:

SVCCACSVSCACCBS
 CHCCSCSVSCCC--

Original motif Consensus sequence: SVCCACSVSCACCBS

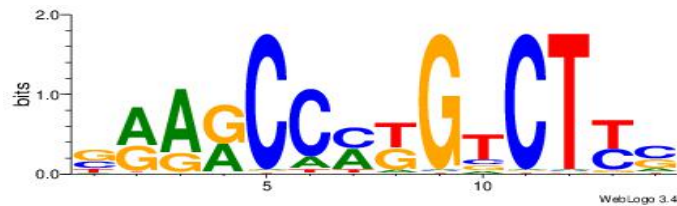


Reverse complement motif Consensus sequence: SBGGTGSVSGTGG

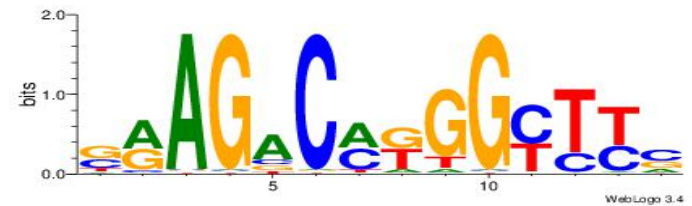


Dataset #: 1 Motif ID: 114 Motif name: C114

Original motif Consensus sequence: SRARCCMKGTCTYS



Reverse complement motif Consensus sequence: SMAGACRRGGMTT



Best Matches for Motif ID 114 (Highest to Lowest)

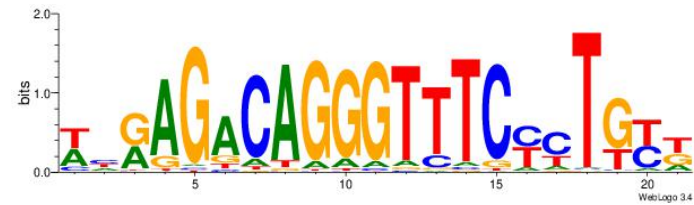
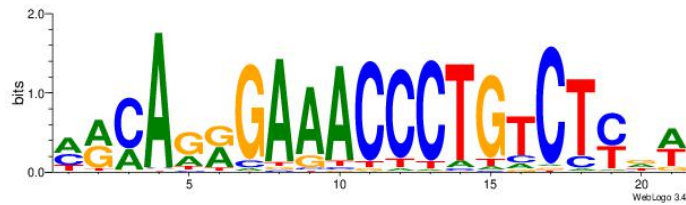
Dataset #:	1
Motif ID:	27
Motif name:	C027
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2
Number of overlap:	14
Similarity score:	0.0171714

Alignment:

```
MRCAGRGAAACCCTGTCTYDW
-----SRARCCMKGTCTYS-
```

Original motif Consensus sequence: MRCAGRGAAACCCTGTCTYDW

Reverse complement motif Consensus sequence: WHKAGACAGGGTTTCMCTGKY

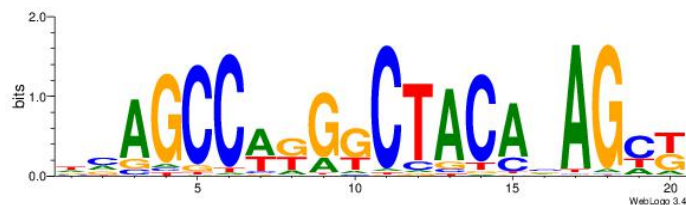


Dataset #: 1
 Motif ID: 15
 Motif name: C015
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0.0317787

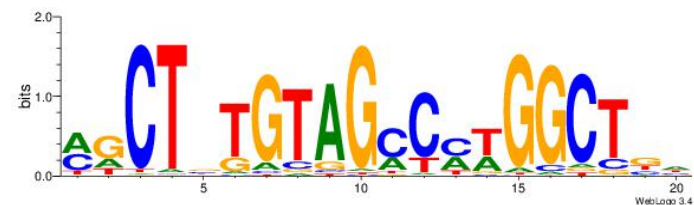
Alignment:

DVAGCCWKGCTACAVAGCK
 SRARCCMKGTCTYS-----

Original motif Consensus sequence: DVAGCCWKGCTACAVAGCK



Reverse complement motif Consensus sequence: RGCTVTGTAGCCYWGCTVD



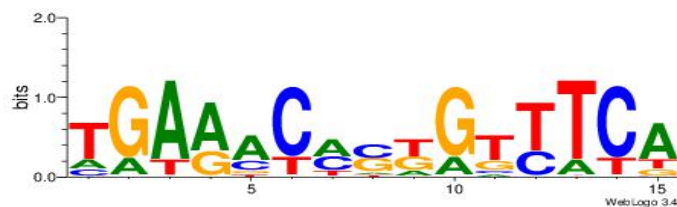
Dataset #: 1

Motif ID: 120
 Motif name: C120
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 14
 Similarity score: 0.0398727

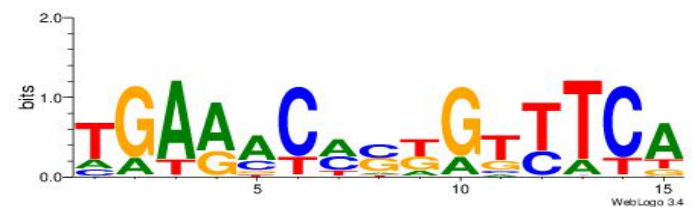
Alignment:

TGAACMSKGTCTCA
 -SRARCCMKGTCTYS

Original motif Consensus sequence: TGAACMSKGTCTCA



Reverse complement motif Consensus sequence: TGAAACRSYGTCT



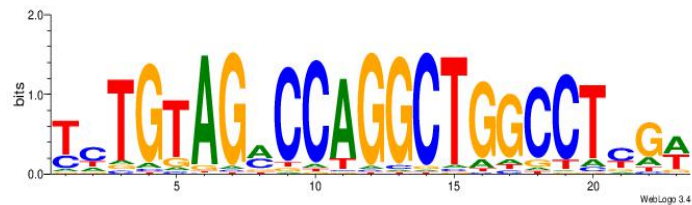
Dataset #: 1
 Motif ID: 5
 Motif name: C005
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 7
 Number of overlap: 14
 Similarity score: 0.0429912

Alignment:

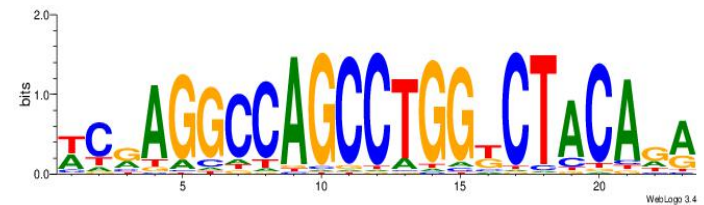
WCKAGGCCAGCCTGGYCTACAGA

---SRARCCMKGCTCTYS-----

Original motif Consensus sequence: TCTGTAGMCCAGGCTGGCCTYGW



Reverse complement motif Consensus sequence: WCKAGGCCAGCCTGGYCTACAGA



Dataset #:	1
Motif ID:	45
Motif name:	C045
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:	0.046959

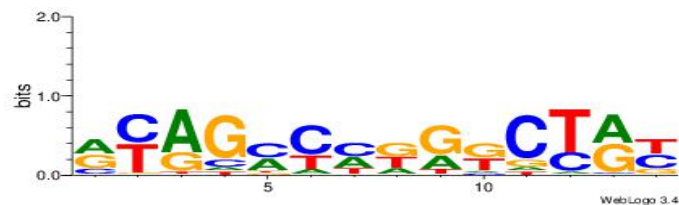
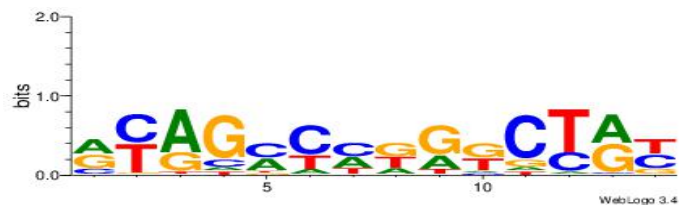
Alignment:

MKAGYCYRGRCTKK

SRARCCMKGCTCTYS

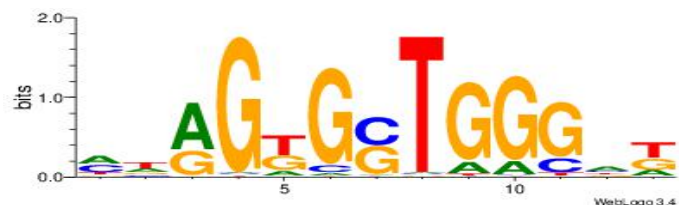
Original motif Consensus sequence: RYAGMCMKGKCTRY

Reverse complement motif Consensus sequence: MKAGYCYRGRCTKK

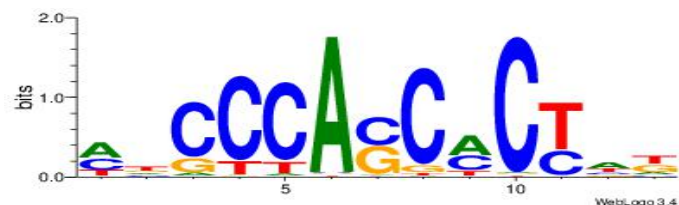


Dataset #: 1 Motif ID: 115 Motif name: C115

Original motif Consensus sequence: MDRGKGSTGGGHK



Reverse complement motif Consensus sequence: RHCCASCRCCKDY



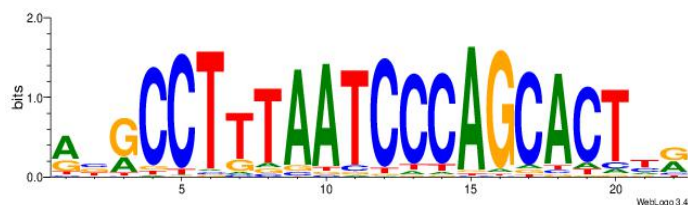
Best Matches for Motif ID 115 (Highest to Lowest)

Dataset #:	1
Motif ID:	9
Motif name:	C009
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	10
Number of overlap:	13
Similarity score:	0

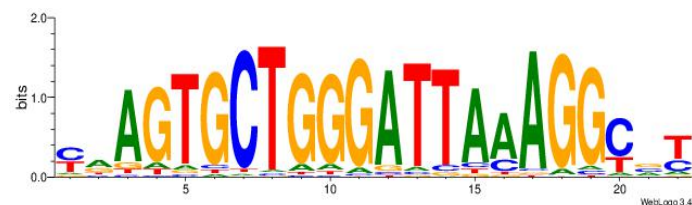
Alignment:

```
ABGCCTTTAATCCCAGCACTHR
RHCCASCRCCKDY-----
```

Original motif Consensus sequence: ABGCCTTTAATCCCAGCACTHR



Reverse complement motif Consensus sequence: MHAGTGCTGGGATTAAAGGCBT

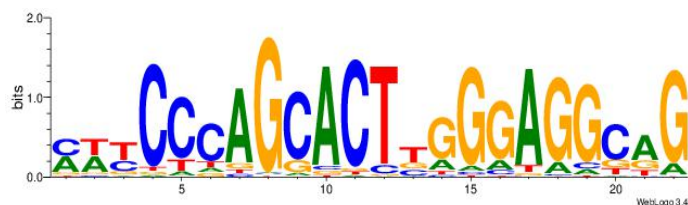


Dataset #: 1
 Motif ID: 19
 Motif name: C019
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 9
 Number of overlap: 13
 Similarity score: 0.00252173

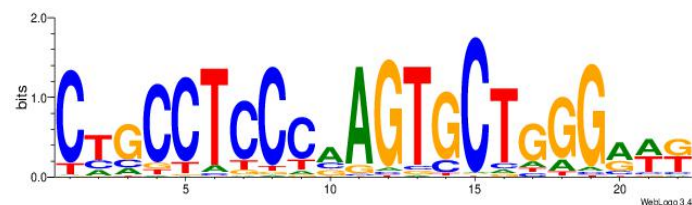
Alignment:

MWYCCCAGCACTTGGGAGGCAG
 -----RHCCASCRCCKDY-

Original motif Consensus sequence: MWYCCCAGCACTTGGGAGGCAG



Reverse complement motif Consensus sequence: CTGCCTCCCAAGTGCTGGGMWR

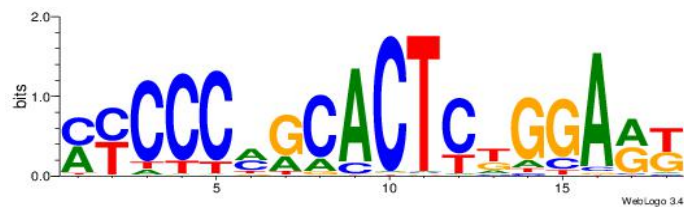


Dataset #: 1
 Motif ID: 99
 Motif name: C099
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 13
 Similarity score: 0.0192508

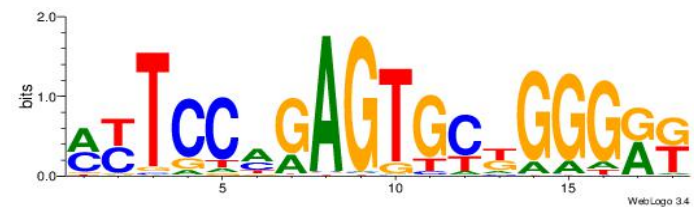
Alignment:

RKTCCRGAGTGCYGGGKR
 MDRGKGSTGGGHK-----

Original motif Consensus sequence: MYCCCMGCACTCKGGARK



Reverse complement motif Consensus sequence: RKTCCRGAGTGCYGGGKR



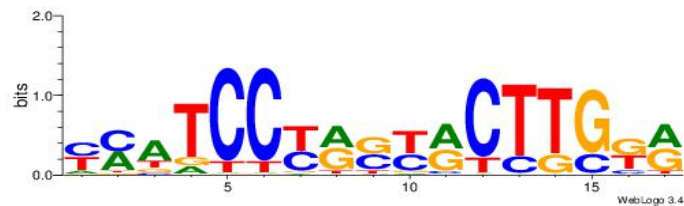
Dataset #: 1
 Motif ID: 141
 Motif name: C141
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3

Number of overlap: 13
Similarity score: 0.0235596

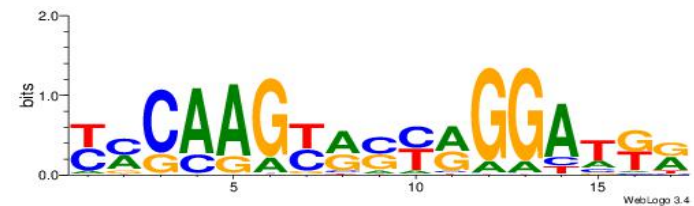
Alignment:

YMATCCYRSYRCTTGKR
--RHCCCASCRCCKDY--

Original motif Consensus sequence: YMATCCYRSYRCTTGKR



Reverse complement motif Consensus sequence: KYCAAGKMSKMGGATRK

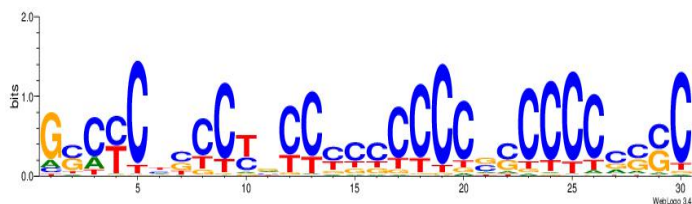


Dataset #: 1
Motif ID: 3
Motif name: C003
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 16
Number of overlap: 13
Similarity score: 0.0285571

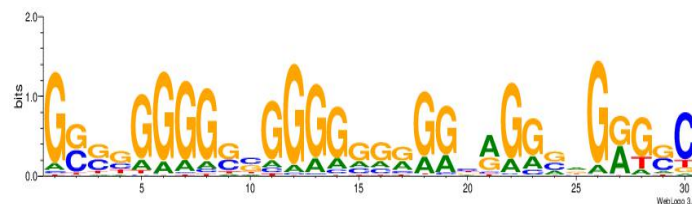
Alignment:

GSCYCHSCCYVCCYCCCCCSCCCCCSSC
--RHCCCASCRCCKDY-----

Original motif Consensus sequence:
GSCYCHSCCYVCCYCCCCSSCCCCSSC

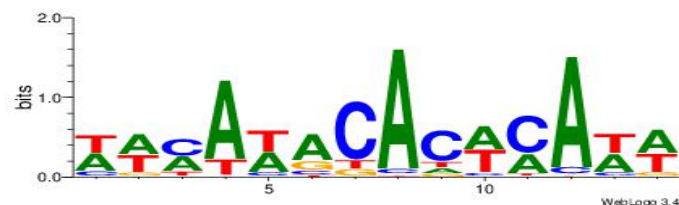


Reverse complement motif Consensus sequence:
GSSGGGGGSSGGGGGGKGGVMGGSHGKGSC

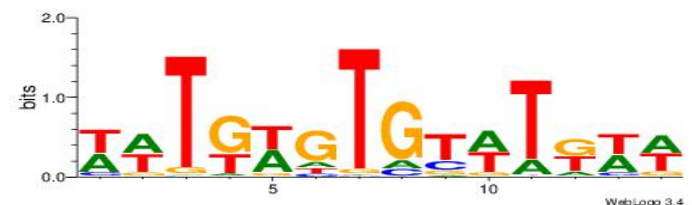


Dataset #: 1 Motif ID: 116 Motif name: C116

Original motif Consensus sequence: WWMAWACACWMAWW



Reverse complement motif Consensus sequence:
WWTRWGTGTWTRWW



Best Matches for Motif ID 116 (Highest to Lowest)

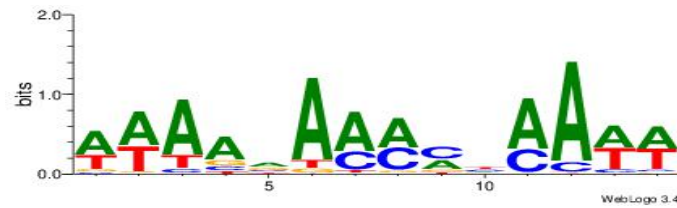
Dataset #:	1
Motif ID:	80
Motif name:	C080
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	14
Similarity score:	0.024005

Alignment:

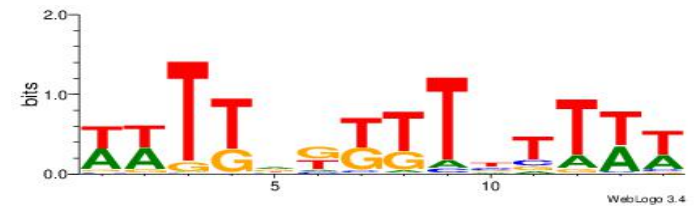
WWAAVAAMMHAAWW

WWMAWACACWMAWW

Original motif Consensus sequence: WWAAVAAMMHAAWW



Reverse complement motif Consensus sequence: WWTTHRYTTBTTW



Dataset #:	1
Motif ID:	16
Motif name:	C016
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:	0.0270168

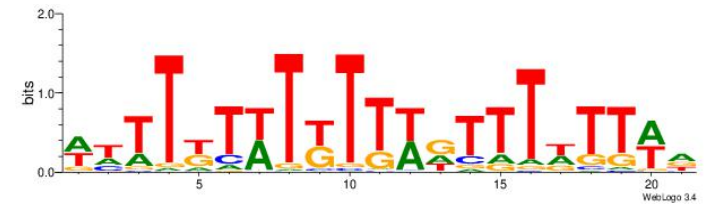
Alignment:

HWAAWAAAHWAAMAWAMAAWW

WWMAWACACWMAWW-----

Original motif Consensus sequence: HWAAWAAAHWAAMAWAMAAWW

Reverse complement motif Consensus sequence:
WWTTYTWYTTWDTTTWTWH



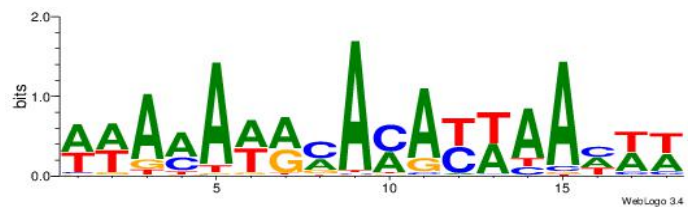
Dataset #:	1
Motif ID:	62
Motif name:	C062
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	14
Similarity score:	0.027254

Alignment:

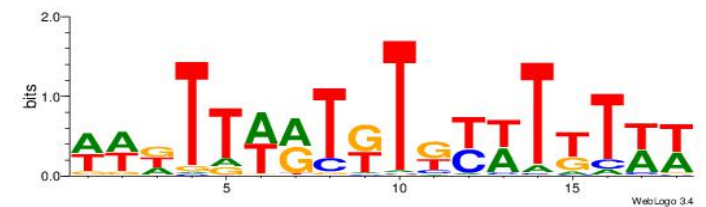
WWAMAWRMAMAYWAAHWW

-WWMAWACACWMAWW---

Original motif Consensus sequence: WWAMAWRMAMAYWAAHWW



Reverse complement motif Consensus sequence:
WWDTTWMTRTRKWYTW



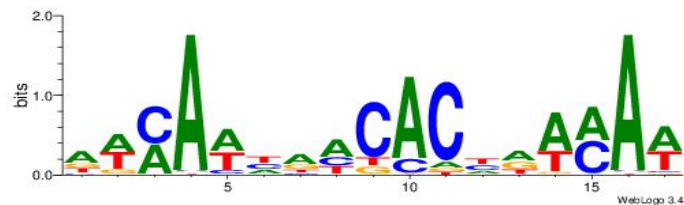
Dataset #: 1

Motif ID: 133
 Motif name: C133
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 4
 Number of overlap: 14
 Similarity score: 0.0314544

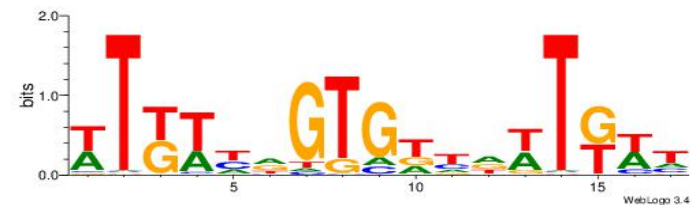
Alignment:

WTYWKHGTGTDHWTRWT
 ---WWTRWGTGTWTRWW

Original motif Consensus sequence: AWMAWHDACACHRWMAW



Reverse complement motif Consensus sequence: WTYWKHGTGTDHWTRWT

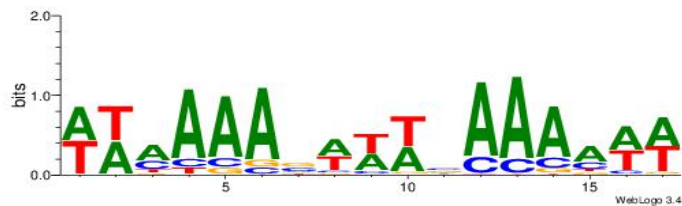


Dataset #: 1
 Motif ID: 139
 Motif name: C139
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 4
 Number of overlap: 14

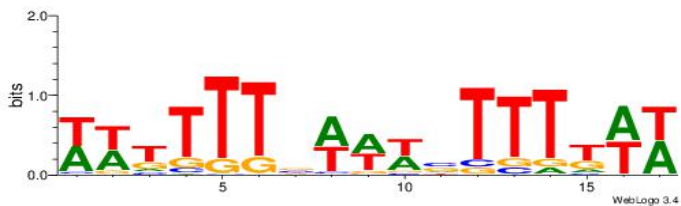
Similarity score: 0.0315898

Alignment:
WWMAAABWWWVAAA
WWMAWACACWMAW---

Original motif Consensus sequence: WWMAAABWWWVAAA

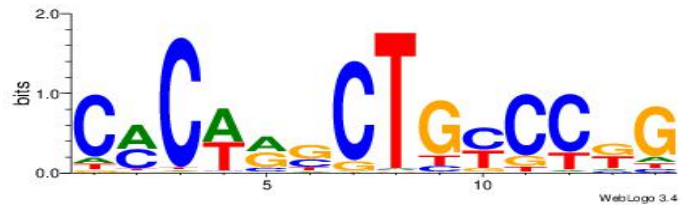


Reverse complement motif Consensus sequence: WWTTTTVWWBTTTYWW



Dataset #: 1 Motif ID: 117 Motif name: C117

Original motif Consensus sequence: CMCWRCTGYCCKG



Reverse complement motif Consensus sequence: CYGGKCAGSKWGW



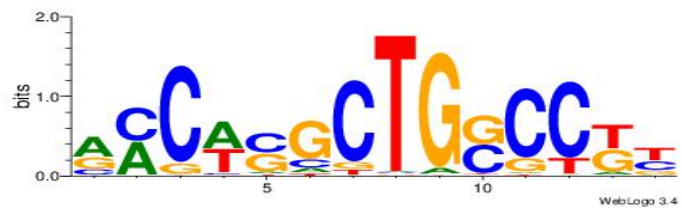
Best Matches for Motif ID 117 (Highest to Lowest)

Dataset #:	1
Motif ID:	109
Motif name:	C109
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: 0.00078041

Alignment:
RMCWSGCTGSCCKY
CMCWR SCTGYCCKG

Original motif Consensus sequence: RMCWSGCTGSCCKY



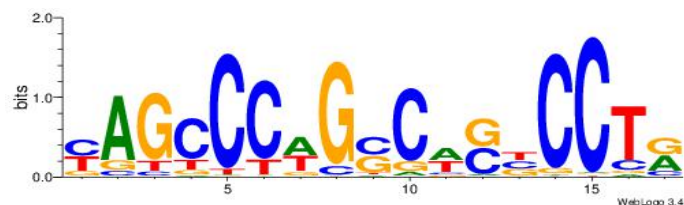
Reverse complement motif Consensus sequence: MRGGSCAGCSWG



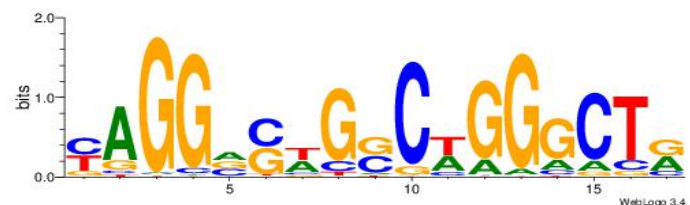
Dataset #: 1
Motif ID: 122
Motif name: C122
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 14
Similarity score: 0.0180152

Alignment:
YAGCCCWGSCWSBCCTR
---CMCWR SCTGYCCKG

Original motif Consensus sequence: YAGCCCWGSCWSBCCTR



Reverse complement motif Consensus sequence: MAGGVSWGSCWGGGCTK



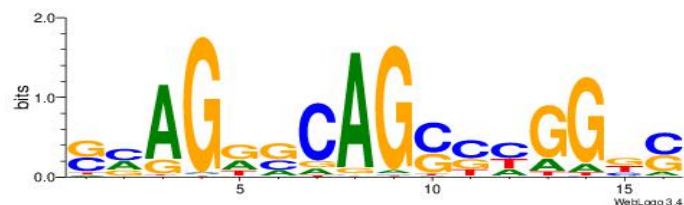
Dataset #: 1
Motif ID: 39
Motif name: C039
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 2
Number of overlap: 14
Similarity score: 0.0207362

Alignment:

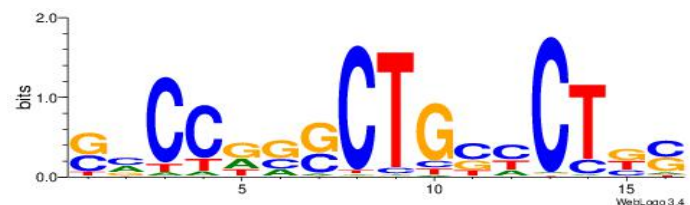
SMAGRSCAGSSYGGBS

-CYGGKCAGSKWGYG-

Original motif Consensus sequence: SMAGRSCAGSSYGGBS



Reverse complement motif Consensus sequence: SBCKSSCTGSMCTRS

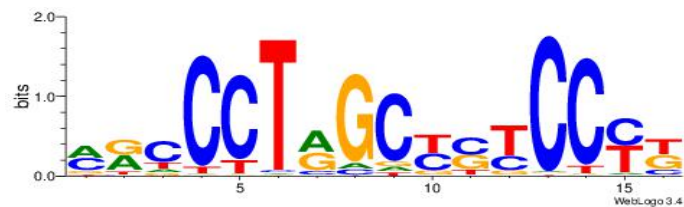


Dataset #: 1
 Motif ID: 121
 Motif name: C121
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 14
 Similarity score: 0.0219721

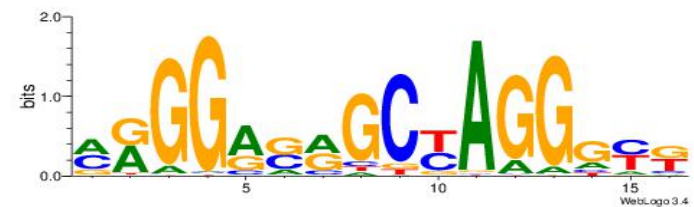
Alignment:

MRCCCTRGCYSTCCYK
 --CMCWR SCTGYCCKG

Original motif Consensus sequence: MRCCCTRGCYSTCCYK



Reverse complement motif Consensus sequence: RKGGASMGCKAGGGM Y

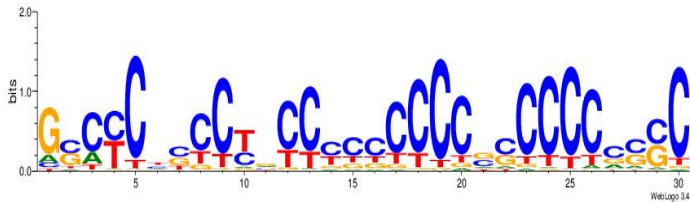


Dataset #: 1
 Motif ID: 3
 Motif name: C003
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3

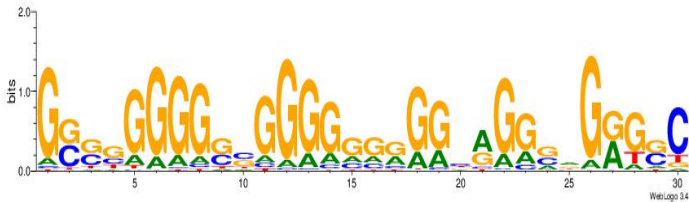
Number of overlap: 14
Similarity score: 0.0258359

Alignment:
GSSGGGGGSSGGGGGKGGVMGGSHGKGSC
-----CYGGKCAGSKWGYG--

Original motif Consensus sequence:
GSCYCHSCCYVCCYCCCCCSCCCCCSSC

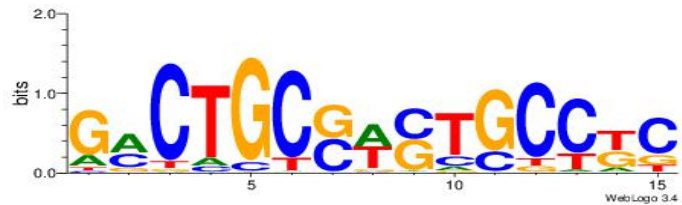


Reverse complement motif Consensus sequence:
GSSGGGGGSSGGGGGKGGVMGGSHGKGSC

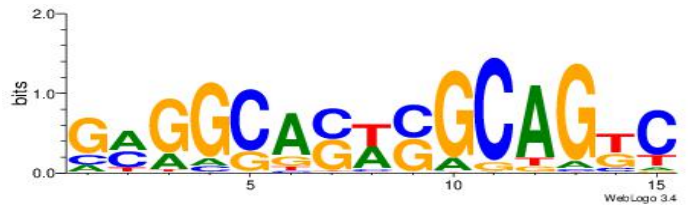


Dataset #: 1 Motif ID: 118 Motif name: C118

Original motif Consensus sequence: GMCTGCSWSTGCCCK



Reverse complement motif Consensus sequence:
GRGGCASWSGCAGYC



Best Matches for Motif ID 118 (Highest to Lowest)

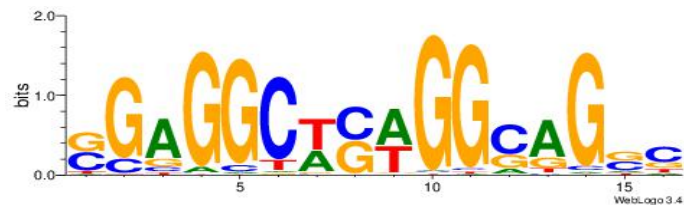
Dataset #: 1
Motif ID: 48
Motif name: C048

Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	15
Similarity score:	0.0102426

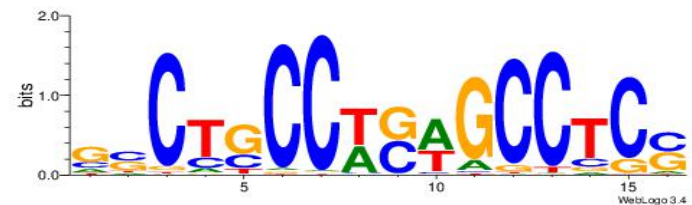
Alignment:

SGAGGCWSWGGCAGSC
GRGGCASWSGCAGYC-

Original motif Consensus sequence: SGAGGCWSWGGCAGSC



Reverse complement motif Consensus sequence: GSCTGCCWSWGCTCS

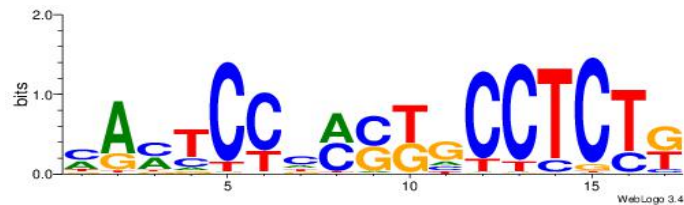


Dataset #:	1
Motif ID:	66
Motif name:	C066
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	15
Similarity score:	0.038962

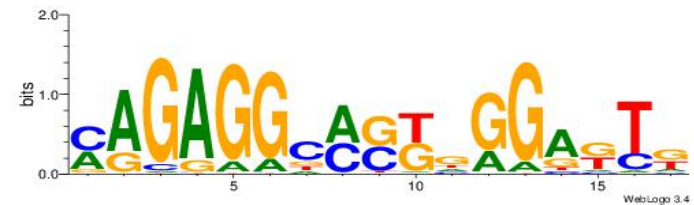
Alignment:

MAMTCCCMSKGCCTCTK
GMCTGCSWSTGCCKC--

Original motif Consensus sequence: MAMTCCCMSKGCCTCTK



Reverse complement motif Consensus sequence:
YAGAGGCRSYGGGARTR



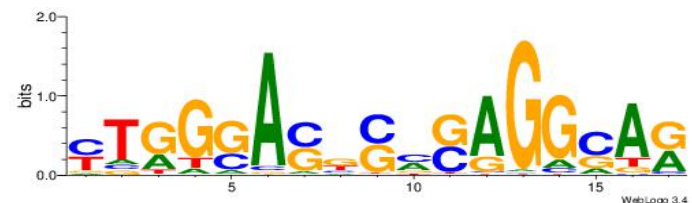
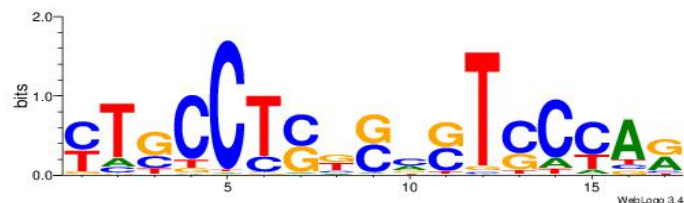
Dataset #:	1
Motif ID:	101
Motif name:	C101
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	15
Similarity score:	0.0391353

Alignment:

YTSCCTSKSVSTCCCAR
--GMCTGCSWSTGCCKC

Original motif Consensus sequence: YTSCCTSKSVSTCCCAR

Reverse complement motif Consensus sequence:
MTGGGASVSYAGGSAK



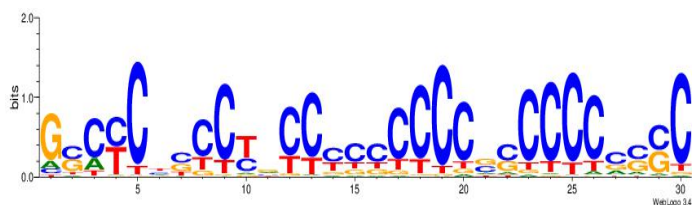
Dataset #: 1
 Motif ID: 3
 Motif name: C003
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 15
 Similarity score: 0.0425686

Alignment:

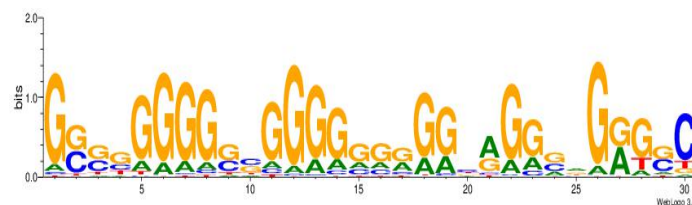
```

GSCYCHSCCYVCCYCCCCCSCCCCCSSC
GMCTGCSWSTGCCKC-----
  
```

Original motif Consensus sequence:
 GSCYCHSCCYVCCYCCCCCSCCCCCSSC



Reverse complement motif Consensus sequence:
 GSSGGGGGSSGGGGGKGGVMGGSHGKGC



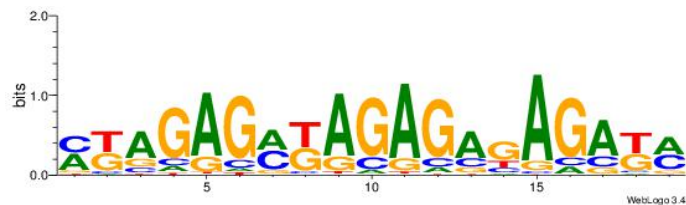
Dataset #: 1

Motif ID: 12
 Motif name: C012
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 15
 Similarity score: 0.0460327

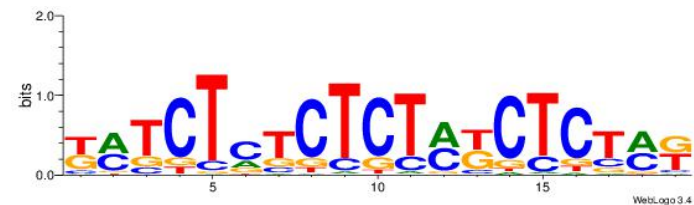
Alignment:

MKAGAGMKAGAGAGAGAKM
 -GRGGCASWSGCAGYC---

Original motif Consensus sequence: MKAGAGMKAGAGAGAGAKM

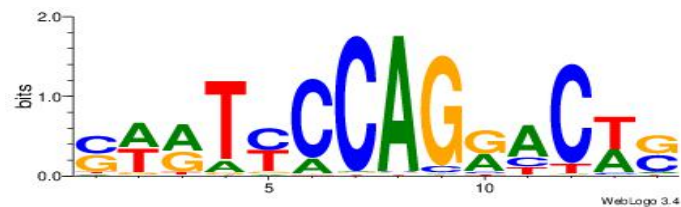


Reverse complement motif Consensus sequence: YRTCTCTCTRYCTCTRR

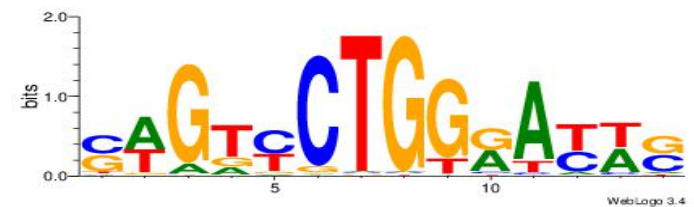


Dataset #: 1 Motif ID: 119 Motif name: C119

Original motif Consensus sequence: SWRTYCCAGRACWS



Reverse complement motif Consensus sequence: SWGTMCTGGKAKV



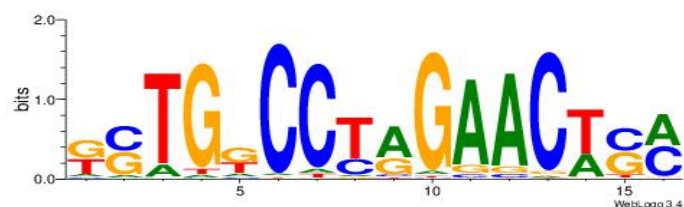
Best Matches for Motif ID 119 (Highest to Lowest)

Dataset #: 1
Motif ID: 46
Motif name: C046
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 2
Number of overlap: 14
Similarity score: 0.0349267

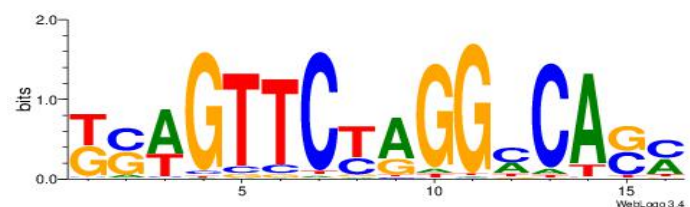
Alignment:

KSTGKCCTRGAAACWSM
-SWRTYCCAGRACWS-

Original motif Consensus sequence: KSTGKCCTRGAAACWSM



Reverse complement motif Consensus sequence: YSWGTTCKAGGYCASY



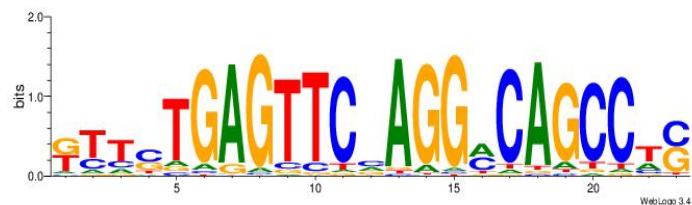
Dataset #: 1
Motif ID: 7
Motif name: C007
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif

Direction: Backward
 Position number: 5
 Number of overlap: 14
 Similarity score: 0.0389643

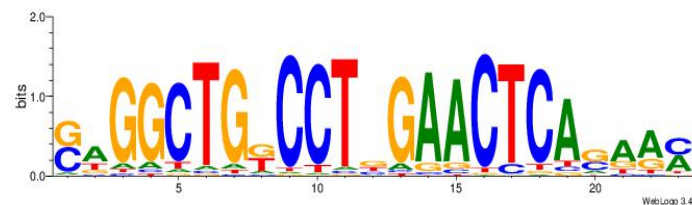
Alignment:

KTTSTGAGTTCVAGGMCAGCCTS
 -----SWRTYCCAGRACWS-----

Original motif Consensus sequence: KTTSTGAGTTCVAGGMCAGCCTS



Reverse complement motif Consensus sequence: SAGGCTGYCCTVGAAGTCASAAY

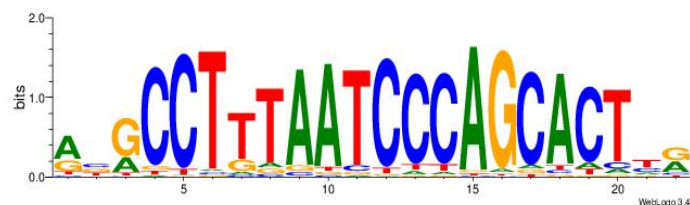


Dataset #: 1
 Motif ID: 9
 Motif name: C009
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 14
 Similarity score: 0.0394017

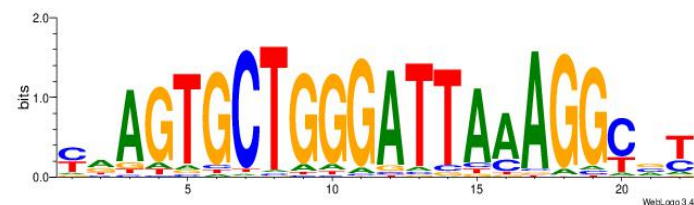
Alignment:

ABGCCTTTAATCCCAGCACTHR
 -----SWRTYCCAGRACWS-----

Original motif Consensus sequence: ABGCCTTTAATCCCAGCACTHR



Reverse complement motif Consensus sequence: MHAGTGCTGGGATTAAAGGCBT

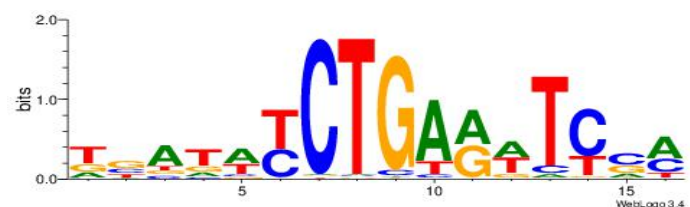


Dataset #: 1
Motif ID: 111
Motif name: C111
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 2
Number of overlap: 14
Similarity score: 0.0500681

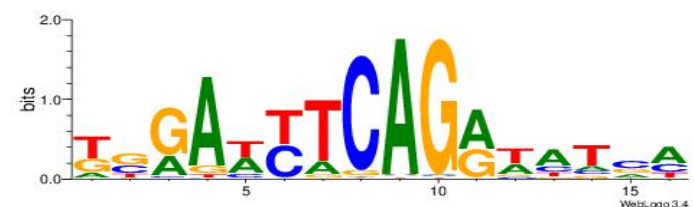
Alignment:

YSGAWKTCAGMWATBA
-SWRTYCCAGRACWS-

Original motif Consensus sequence: TBATWYCTGARWTCSM



Reverse complement motif Consensus sequence: YSGAWKTCAGMWATBA

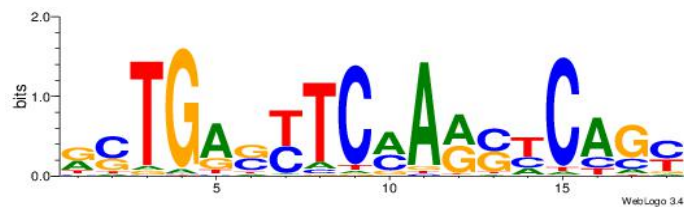


Dataset #: 1
 Motif ID: 40
 Motif name: C040
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 4
 Number of overlap: 14
 Similarity score: 0.0507794

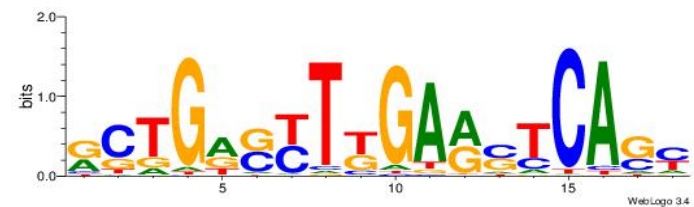
Alignment:

RSTGASYTCMARSYCAGY
 ---SWRTYCCAGRACWS-

Original motif Consensus sequence: RSTGASYTCMARSYCAGY



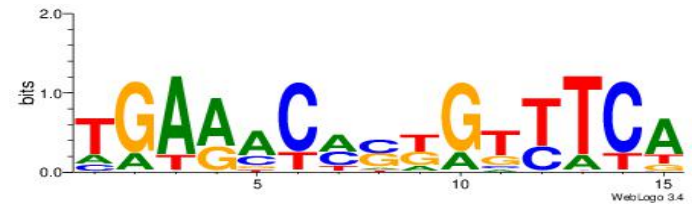
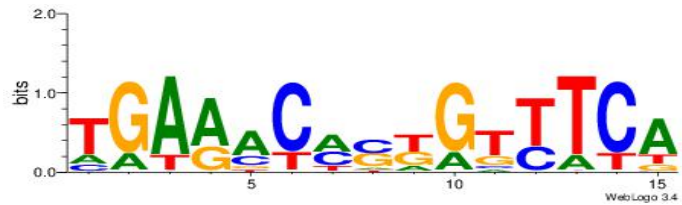
Reverse complement motif Consensus sequence: KCTGMSKTYGAMSTCASM



Dataset #: 1 Motif ID: 120 Motif name: C120

Original motif Consensus sequence: TGARACMSKGYTCA

Reverse complement motif Consensus sequence: TGAMACRSYGTKT



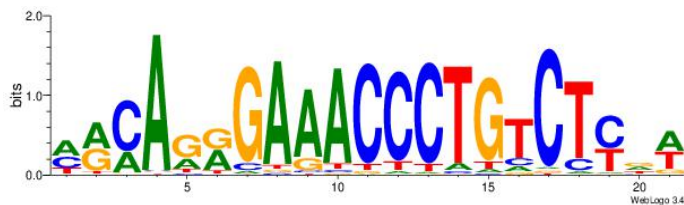
Best Matches for Motif ID 120 (Highest to Lowest)

Dataset #: 1
 Motif ID: 27
 Motif name: C027
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 15
 Similarity score: 0.00903899

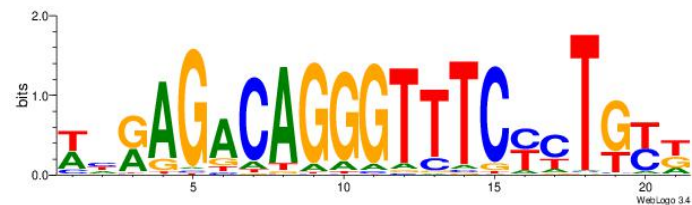
Alignment:

MRCAGRGAAACCCTGTCTYDW
 -----TGARACMSKGTYTCA-

Original motif Consensus sequence: MRCAGRGAAACCCTGTCTYDW



Reverse complement motif Consensus sequence: WHKAGACAGGGTTTCMCTGKY

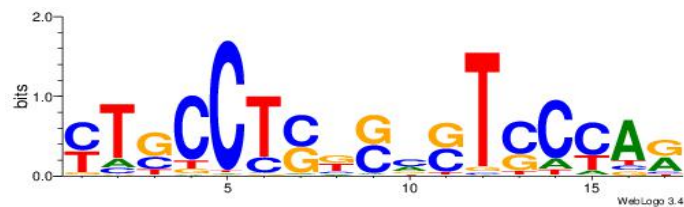


Dataset #: 1
 Motif ID: 101
 Motif name: C101
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 15
 Similarity score: 0.0323346

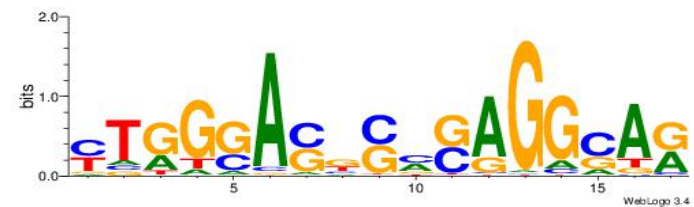
Alignment:

MTGGGASVSYSAGGSAK
 -TGAMACRSYGTKTCA-

Original motif Consensus sequence: YTSCCTSKSVSTCCCAR



Reverse complement motif Consensus sequence: MTGGGASVSYSAGGSAK

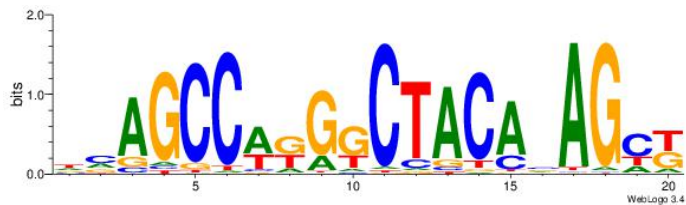


Dataset #: 1
 Motif ID: 15
 Motif name: C015
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1

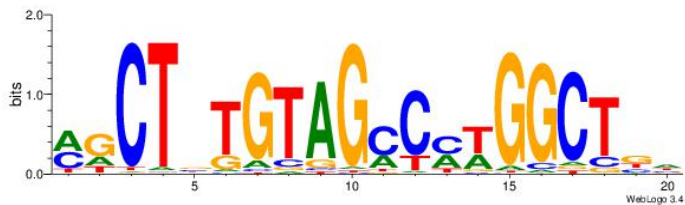
Number of overlap: 15
Similarity score: 0.034022

Alignment:
DVAGCCWKGCTACAVAGCK
TGARACMSKGTYTCA-----

Original motif Consensus sequence: DVAGCCWKGCTACAVAGCK



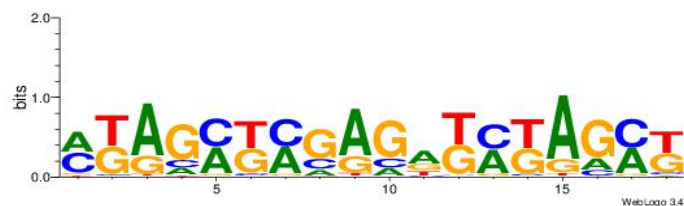
Reverse complement motif Consensus sequence: RGCTVTGTAGCCYWGGCTVD



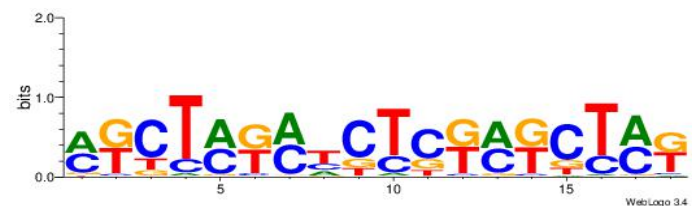
Dataset #: 1
Motif ID: 36
Motif name: C036
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 15
Similarity score: 0.0412488

Alignment:
MKAGMKMGAGAKMKAGMK
TGARACMSKGTYTCA---

Original motif Consensus sequence: MKAGMKMGAGAKMKAGMK



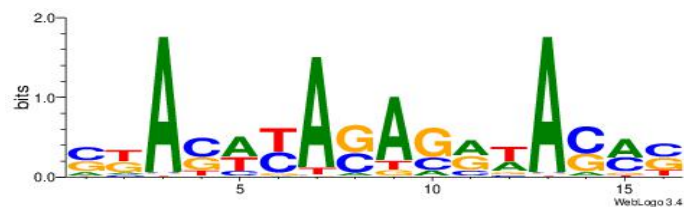
Reverse complement motif Consensus sequence: RRCTRRRTCTCRRRCTRY



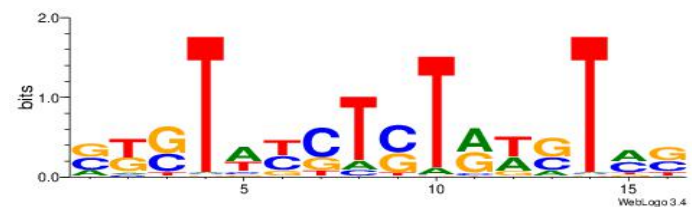
Dataset #: 1
Motif ID: 125
Motif name: C125
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 15
Similarity score: 0.0418412

Alignment:
SKASWYASAGRWASMS
TGARACMSKGTYTCA-

Original motif Consensus sequence: SKASWYASAGRWASMS

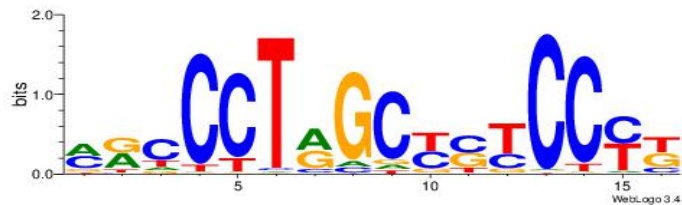


Reverse complement motif Consensus sequence: SYSTWKCTSTMWSTRS

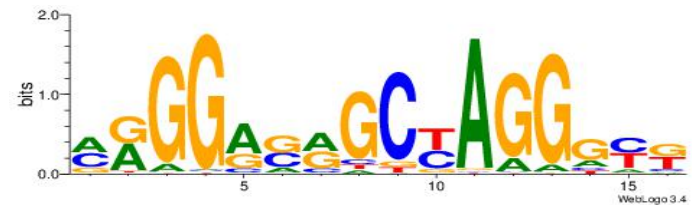


Dataset #: 1 Motif ID: 121 Motif name: C121

Original motif Consensus sequence: MRCCCTRGCYSTCCYK



Reverse complement motif Consensus sequence: RKGGASMGCKAGGGMY



Best Matches for Motif ID 121 (Highest to Lowest)

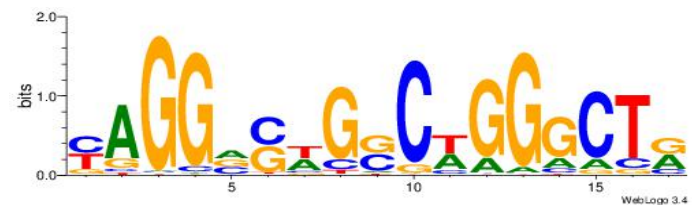
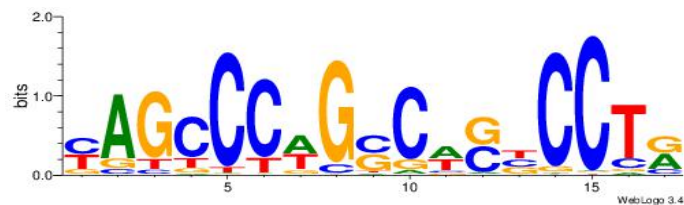
Dataset #:	1
Motif ID:	122
Motif name:	C122
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	16
Similarity score:	0.0165722

Alignment:

```
YAGCCCWGSCWSBCCTR
-MRCCCTRGCYSTCCYK
```

Original motif Consensus sequence: YAGCCCWGSCWSBCCTR

Reverse complement motif Consensus sequence: MAGGVSWGSCWGGGCTK

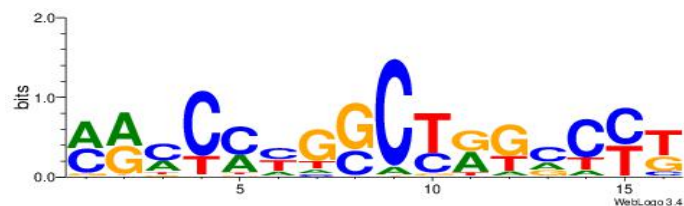


Dataset #: 1
 Motif ID: 96
 Motif name: C096
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 16
 Similarity score: 0.0213031

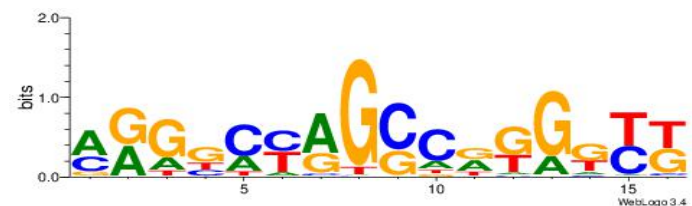
Alignment:

MRMCMYGSCYRGCCYK
 MRCCCTRGCYSTCCYK

Original motif Consensus sequence: MRMCMYGSCYRGCCYK



Reverse complement motif Consensus sequence: RKGGCMMGSCKRGRKY



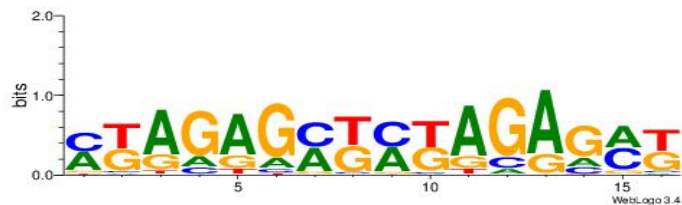
Dataset #: 1

Motif ID:	55
Motif name:	C055
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	16
Similarity score:	0.027157

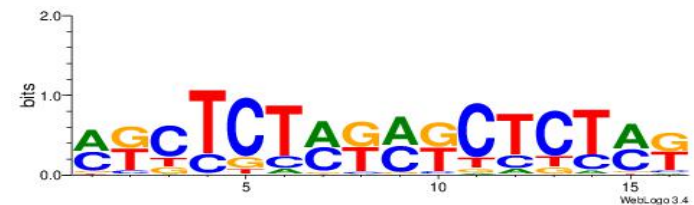
Alignment:

```
RYCTCTRRRRCTCTRR
MRCCCTRGCYSTCCYK
```

Original motif Consensus sequence: MKAGAGMKMKAGAGMK



Reverse complement motif Consensus sequence: RYCTCTRRRRCTCTRR

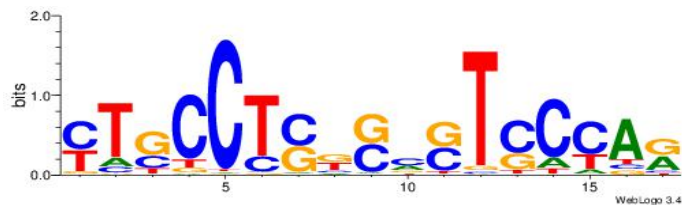


Dataset #:	1
Motif ID:	101
Motif name:	C101
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	2
Number of overlap:	16

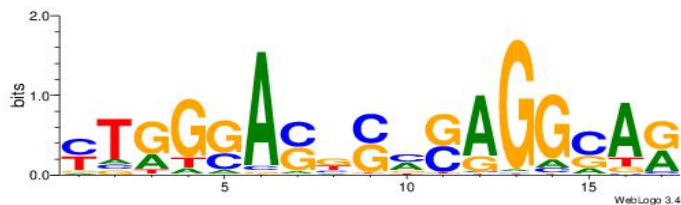
Similarity score: 0.034049

Alignment:
MTGGGASVSYSAGGSAK
-RKGGASMGCKAGGGMY

Original motif Consensus sequence: YTSCCTSKSVSTCCCAR



Reverse complement motif Consensus sequence:
MTGGGASVSYSAGGSAK

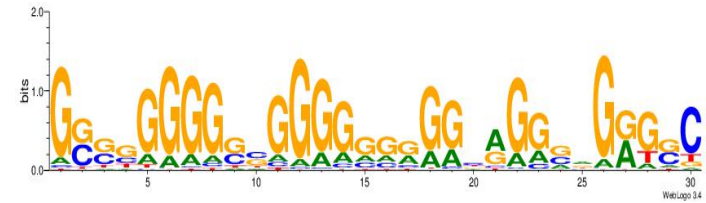


Dataset #: 1
Motif ID: 3
Motif name: C003
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 11
Number of overlap: 16
Similarity score: 0.0360277

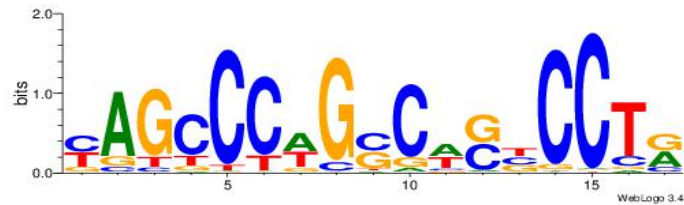
Alignment:
GSCYCHSCCYVCCYCCCCCSCCCCCSSC
----MRCCCTRGCYSTCCYK-----

Original motif Consensus sequence:
GSCYCHSCCYVCCYCCCCCSCCCCCSSC

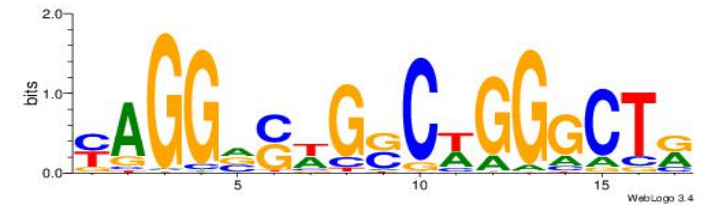
Reverse complement motif Consensus sequence:
GSSGGGGGSSGGGGGKGGVMGGSHGKGSC



Original motif Consensus sequence: YAGCCCWGSCWSBCCTR



Reverse complement motif Consensus sequence:
MAGGVS~~W~~GSCWGGGCTK



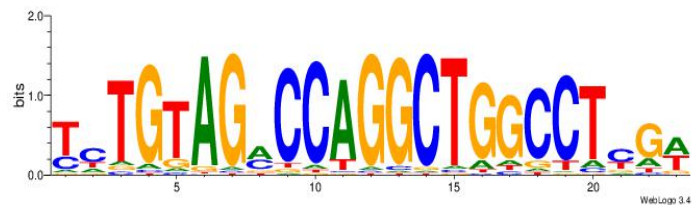
Best Matches for Motif ID 122 (Highest to Lowest)

Dataset #:	1
Motif ID:	5
Motif name:	C005
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	5
Number of overlap:	17
Similarity score:	0.0338286

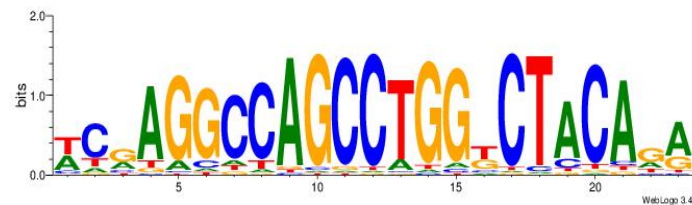
Alignment:

TCTGTAGMCCAGGCTGGCCTYGW
 ----YAGCCCWGSWSBCCTR--

Original motif Consensus sequence: TCTGTAGMCCAGGCTGGCCTYGW



Reverse complement motif Consensus sequence:
 WCKAGGCCAGCCTGGYCTACAGA

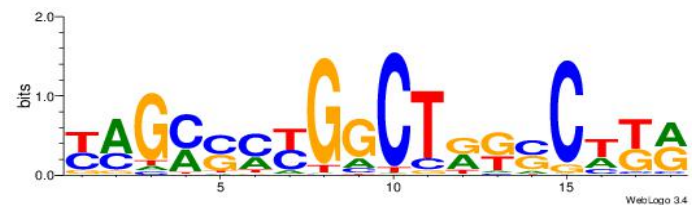
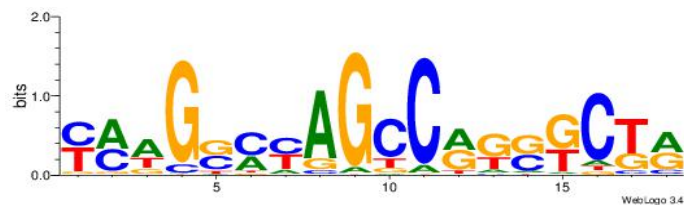


Dataset #:	1
Motif ID:	73
Motif name:	C073
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	2
Number of overlap:	17
Similarity score:	0.0338756

Alignment:
 KAGYSYKGGCTKRSCWYK
 -YAGCCCWGSWSBCCTR

Original motif Consensus sequence: YMWGSMYAGCCRKSKCTR

Reverse complement motif Consensus sequence:
 KAGYSYKGGCTKRSCWYK

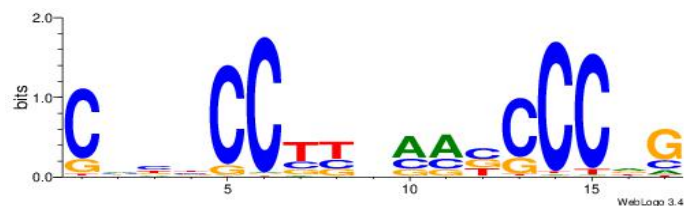


Dataset #: 1
 Motif ID: 107
 Motif name: C107
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 17
 Similarity score: 0.0541557

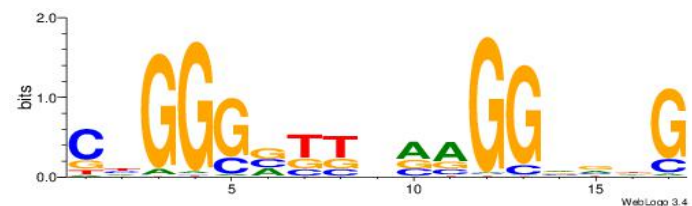
Alignment:

CHBBCCTYBAABCCCDG
 YAGCCCWGSCWSBCCTR

Original motif Consensus sequence: CHBBCCTYBAABCCCDG



Reverse complement motif Consensus sequence: CDGGGBTVMAGGV BHG



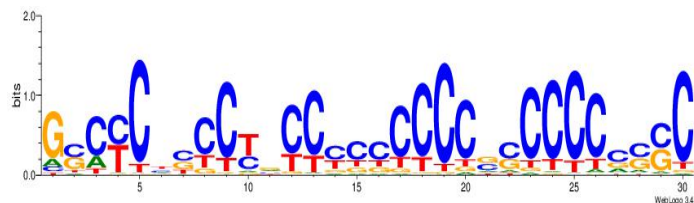
Dataset #: 1

Motif ID: 3
 Motif name: C003
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 4
 Number of overlap: 17
 Similarity score: 0.0606639

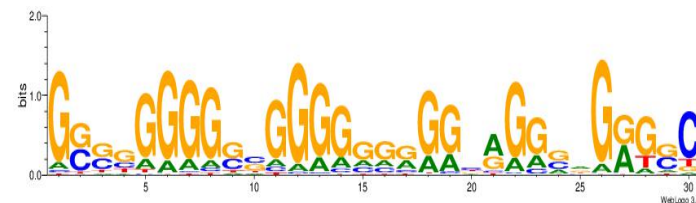
Alignment:

GSSGGGGSSGGGGGKGGVMGGSHGKGC
 -----MAGGVSWGSCWGGGCTK---

Original motif Consensus sequence:
 GSCYCHSCCYVCCYCCCCSSCCCCSSC



Reverse complement motif Consensus sequence:
 GSSGGGGSSGGGGGKGGVMGGSHGKGC

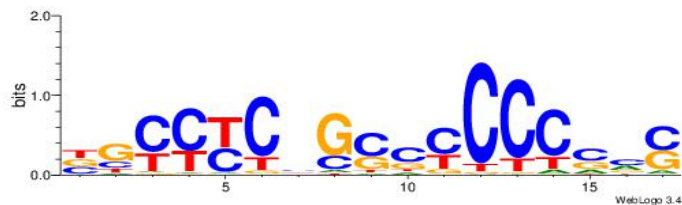


Dataset #: 1
 Motif ID: 22
 Motif name: C022
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 17

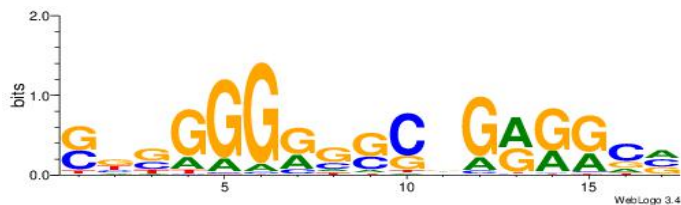
Similarity score: 0.0617615

Alignment:
BGCCYCBGSCYCCCSVS
YAGCCCWGSCWSBCCTR

Original motif Consensus sequence: BGCCYCBGSCYCCCSVS

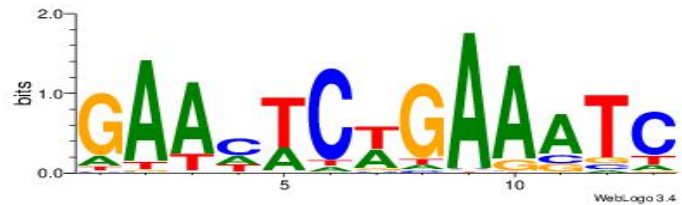


Reverse complement motif Consensus sequence: SVSGGGKGSGBMGGCV

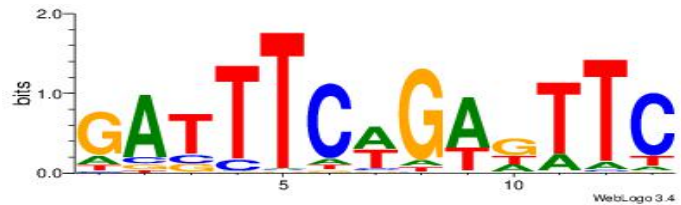


Dataset #: 1 Motif ID: 123 Motif name: C123

Original motif Consensus sequence: GAAMTCWGAAATC



Reverse complement motif Consensus sequence: GATTCWGARTTC



Best Matches for Motif ID 123 (Highest to Lowest)

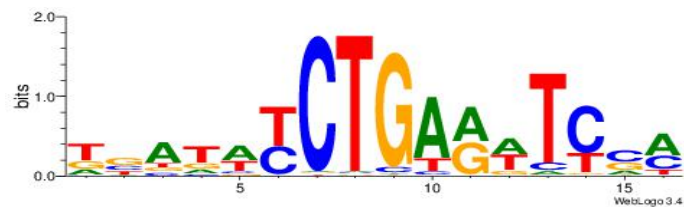
Dataset #:	1
Motif ID:	111
Motif name:	C111
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement

Direction: Backward
 Position number: 3
 Number of overlap: 13
 Similarity score: 0.0136956

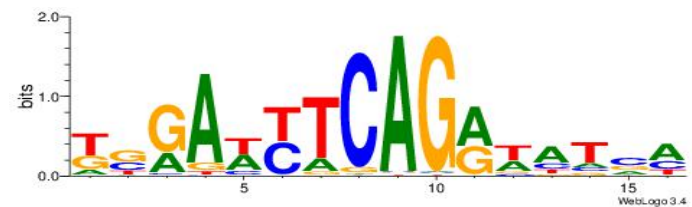
Alignment:

YSGAWKTCAGMWATBA
 -GAAMTCWGAAATC--

Original motif Consensus sequence: TBATWYCTGARWTCSM



Reverse complement motif Consensus sequence: YSGAWKTCAGMWATBA

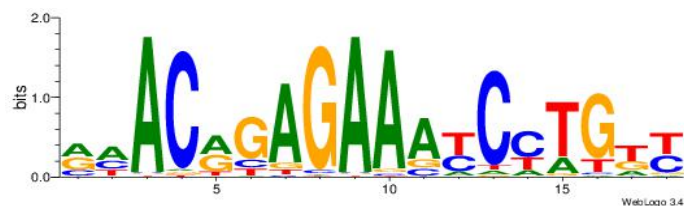


Dataset #: 1
 Motif ID: 53
 Motif name: C053
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 13
 Similarity score: 0.0237752

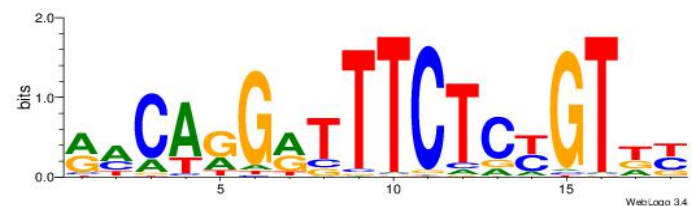
Alignment:

RMACRGAGAAAYCCTGKY
 GAAMTCWGAAATC-----

Original motif Consensus sequence: RMACRGAGAAAYCCTGKY



Reverse complement motif Consensus sequence: MRCAGGMTTCTCKGTYK

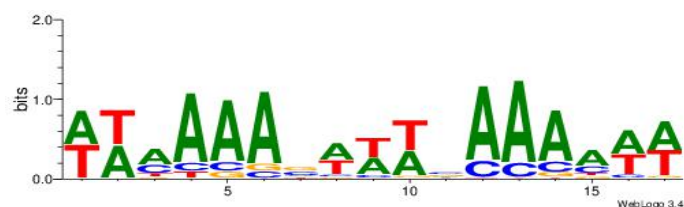


Dataset #: 1
 Motif ID: 139
 Motif name: C139
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 13
 Similarity score: 0.0400487

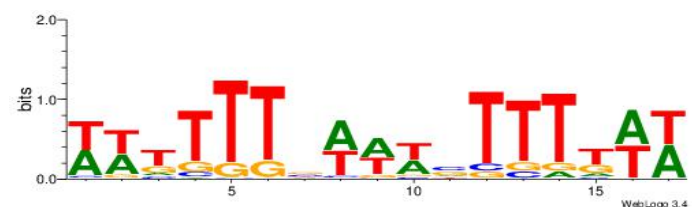
Alignment:

WWMAAABWWWVAAA~~AWW~~
 ---GAAMTCWGAAATC-

Original motif Consensus sequence: WWMAAABWWWVAAA~~AWW~~



Reverse complement motif Consensus sequence: WWTTTTVWWWBTTTYWW

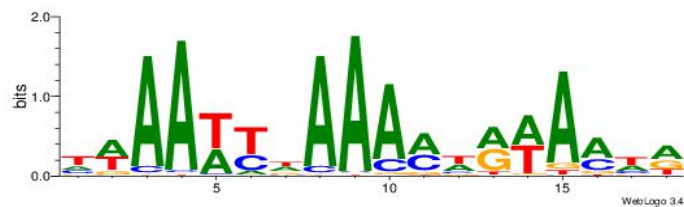


Dataset #: 1
 Motif ID: 32
 Motif name: C032
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 13
 Similarity score: 0.042121

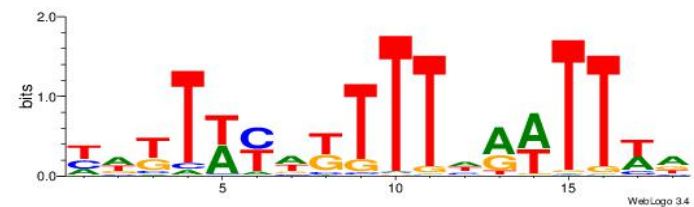
Alignment:

KWYTWKWYTTTDMWTTWH
 -----GATTCWGARTTC

Original motif Consensus sequence: HWAAWYDAAAMWRWAMWR



Reverse complement motif Consensus sequence: KWYTWKWYTTTDMWTTWH

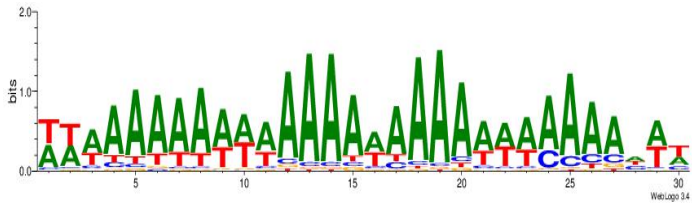


Dataset #: 1
 Motif ID: 1
 Motif name: C001
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 14

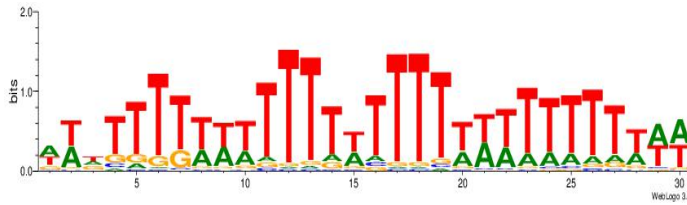
Number of overlap: 13
Similarity score: 0.0457951

Alignment:
WWAAAAAWAAAAWAAAAWAAAAHWW
----GAAMTCWGAAATC-----

Original motif Consensus sequence:
WWAAAAAWAAAAWAAAAWAAAAHWW

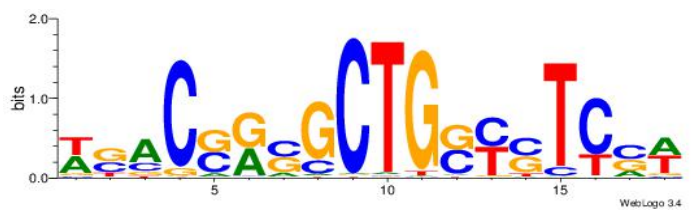


Reverse complement motif Consensus sequence:
WWHTTTTWWTTTTWTTTTWTTTTWWW

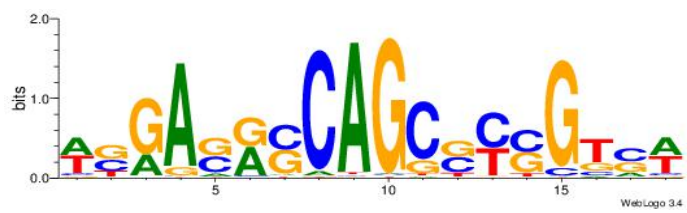


Dataset #: 1 Motif ID: 124 Motif name: C124

Original motif Consensus sequence: WSACSRSGCTGSYSTCSW



Reverse complement motif Consensus sequence:
WSGASKSCAGCSMSGTSW



Best Matches for Motif ID 124 (Highest to Lowest)

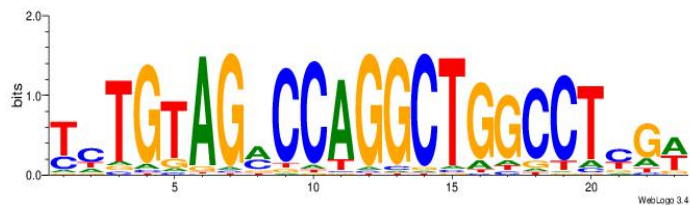
Dataset #: 1
Motif ID: 5
Motif name: C005

Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	6
Number of overlap:	18
Similarity score:	0.0124377

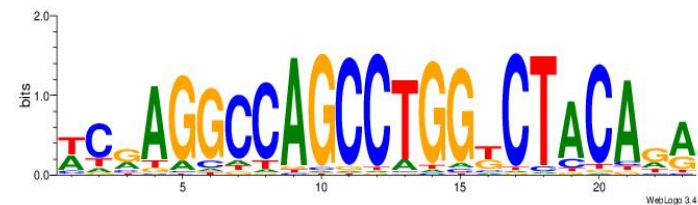
Alignment:

```
TCTGTAGMCCAGGCTGGCCTYGW
-----WSACSRSGCTGSYSTCSW
```

Original motif Consensus sequence: TCTGTAGMCCAGGCTGGCCTYGW



Reverse complement motif Consensus sequence: WCKAGGCCAGCCTGGYCTACAGA

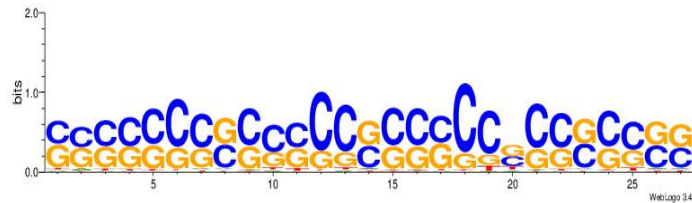


Dataset #:	1
Motif ID:	4
Motif name:	C004
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	10
Number of overlap:	18
Similarity score:	0.0440706

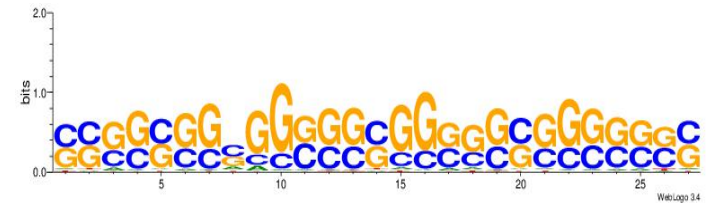
Alignment:

SSSSSCSSSSSCSSSSSCSCSSSSSS
-----WSACSRSGCTGSYSTCSW

Original motif Consensus sequence:
SSSSSCSSSSSCSSSSSCSCSSSSSS



Reverse complement motif Consensus sequence:
SSSSSSGSGGSSSSGSSSSSGSSSSS



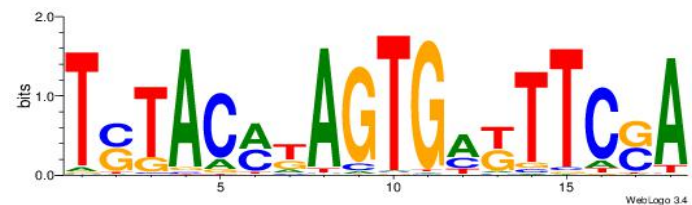
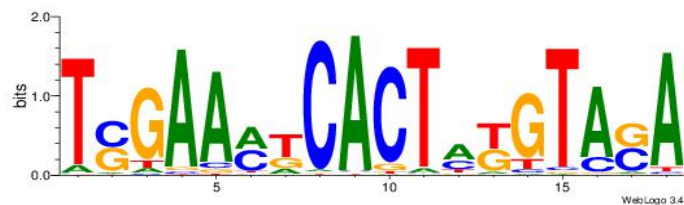
Dataset #:	1
Motif ID:	47
Motif name:	C047
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	18
Similarity score:	0.0480396

Alignment:

TSGAAMTCACTMKGTASA
WSGASKSCAGCSMSGTSW

Original motif Consensus sequence: TSGAAMTCACTMKGTASA

Reverse complement motif Consensus sequence:
TSTACRYAGTGAYTTCSA

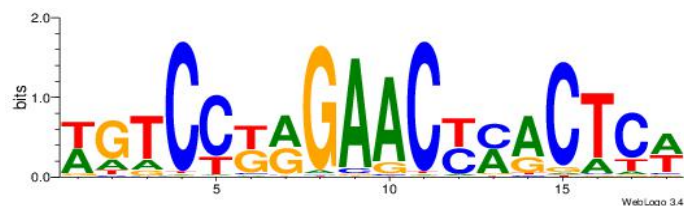


Dataset #: 1
 Motif ID: 42
 Motif name: C042
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 18
 Similarity score: 0.0485766

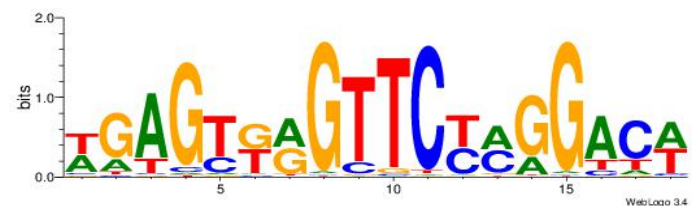
Alignment:

WGAGTRMGTTCKRGGACW
 WSACSRSGCTGSYSTCSW

Original motif Consensus sequence: WGTCKRGAACYMACTCW



Reverse complement motif Consensus sequence: WGAGTRMGTTCKRGGACW



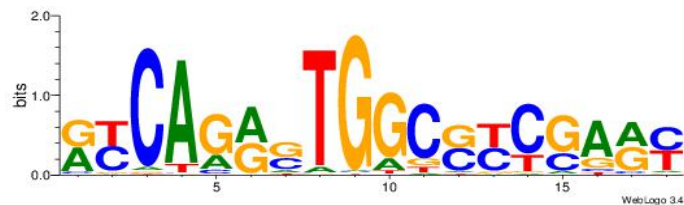
Dataset #: 1

Motif ID: 92
 Motif name: C092
 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: 0.0498144

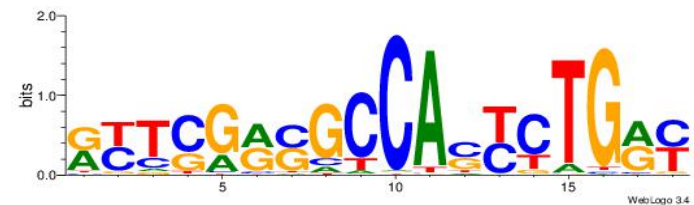
Alignment:

RYCAGRSTGGCSYCGARY
 WSGASKSCAGCSMSGTSW

Original motif Consensus sequence: RYCAGRSTGGCSYCGARY

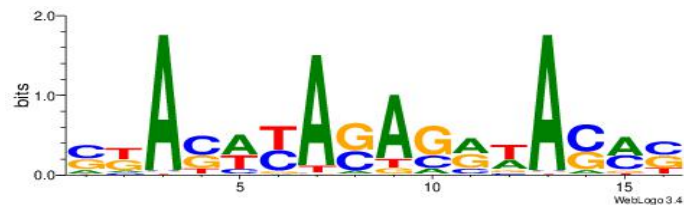


Reverse complement motif Consensus sequence: KKTCGMSGCCASKCTGMM

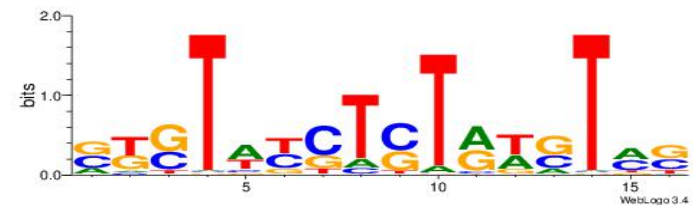


Dataset #: 1 Motif ID: 125 Motif name: C125

Original motif Consensus sequence: SKASWYASAGRWASMS



Reverse complement motif Consensus sequence: SYSTWKCTSTMWSTRS



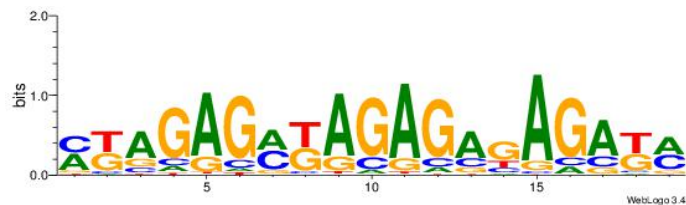
Best Matches for Motif ID 125 (Highest to Lowest)

Dataset #: 1
Motif ID: 12
Motif name: C012
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: 0.0230755

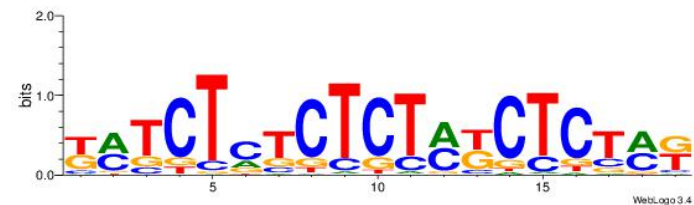
Alignment:

MKAGAGMKAGAGAGAGAKM
--SKASWYASAGRWASMS--

Original motif Consensus sequence: MKAGAGMKAGAGAGAGAKM



Reverse complement motif Consensus sequence:
YRTCTCTCTCTRYCTCTRR

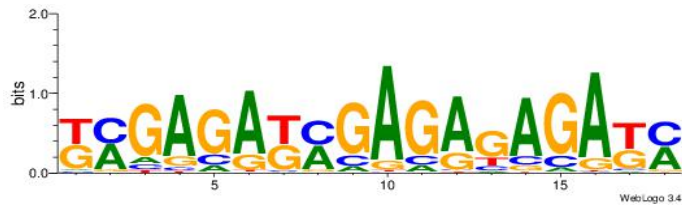


Dataset #: 1
Motif ID: 11
Motif name: C011
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif

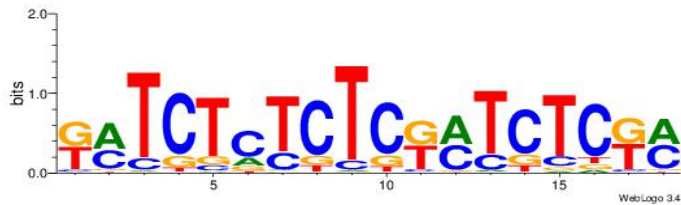
Direction: Backward
Position number: 2
Number of overlap: 16
Similarity score: 0.0308935

Alignment:
KMGAGAKMGAGAGAGAKM
-SKASWYASAGRWASMS-

Original motif Consensus sequence: KMGAGAKMGAGAGAGAKM



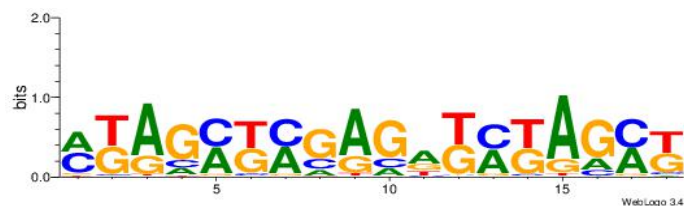
Reverse complement motif Consensus sequence: RRTCTCTCTCRRTCTCRR



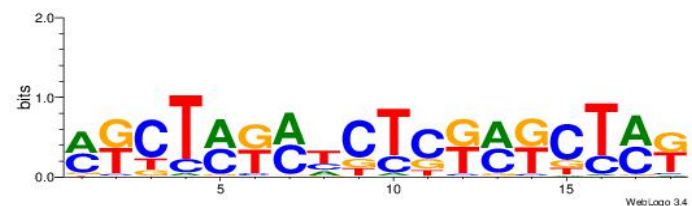
Dataset #: 1
Motif ID: 36
Motif name: C036
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 3
Number of overlap: 16
Similarity score: 0.0309585

Alignment:
MKAGMKMGAGAKMKAGMK
SKASWYASAGRWASMS--

Original motif Consensus sequence: MKAGMKMGAGAKMKAGMK



Reverse complement motif Consensus sequence: RRCTRRRTCTCRRRCTRY

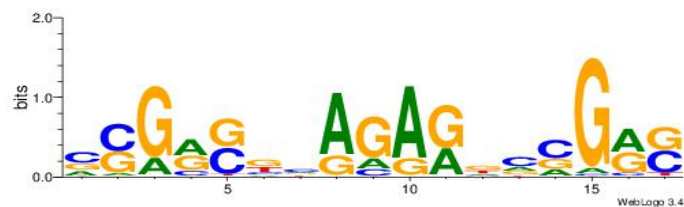


Dataset #: 1
Motif ID: 85
Motif name: C085
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 16
Similarity score: 0.03238

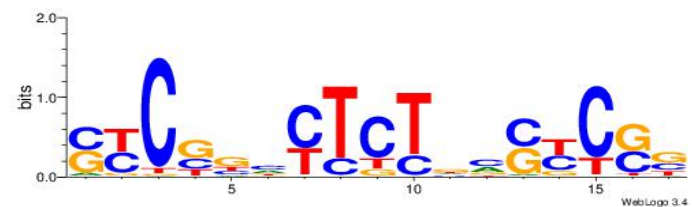
Alignment:

VSGRSBHAGARDVSGRS
-SKASWYASAGRWASMS

Original motif Consensus sequence: VSGRSBHAGARDVSGRS



Reverse complement motif Consensus sequence: SKCSVHMTCTDBSKCSV

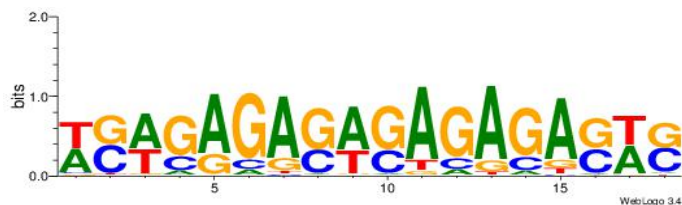


Dataset #: 1
 Motif ID: 17
 Motif name: C017
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 16
 Similarity score: 0.0332023

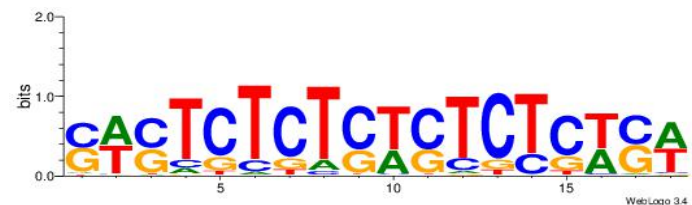
Alignment:

WSWGAGASWSAGAGASWS
 --SKASWYASAGRWASMS

Original motif Consensus sequence: WSWGAGASWSAGAGASWS



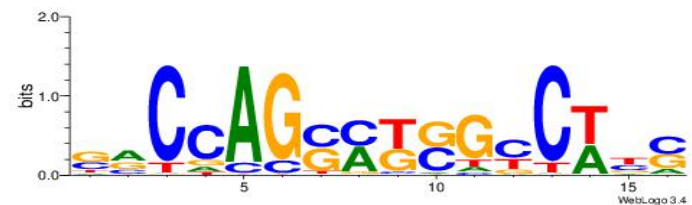
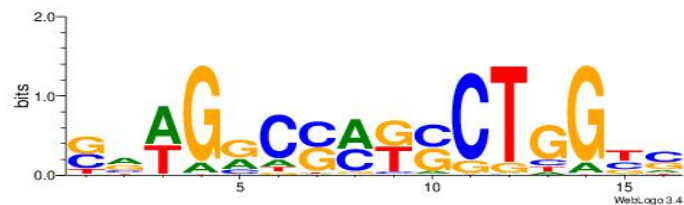
Reverse complement motif Consensus sequence: SWSTCTCTSWSTCTCWSW



Dataset #: 1 Motif ID: 126 Motif name: C126

Original motif Consensus sequence: SVWGRCSMKSCTGGYS

Reverse complement motif Consensus sequence: SMCCAGSYYSGMCWBS



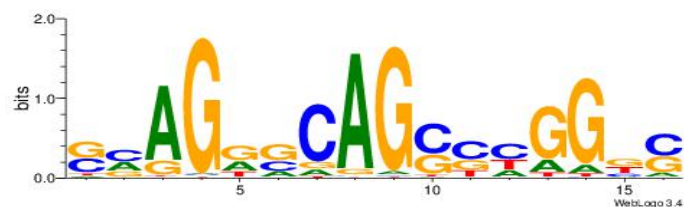
Best Matches for Motif ID 126 (Highest to Lowest)

Dataset #: 1
 Motif ID: 39
 Motif name: C039
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 16
 Similarity score: 0.0111025

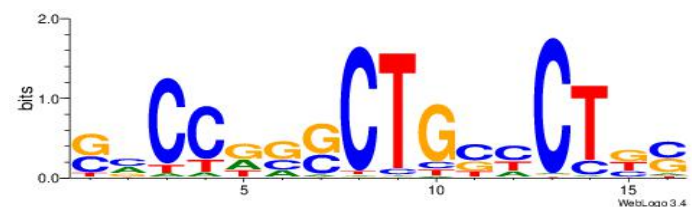
Alignment:

SMAGRSCAGSSYGGBS
 SVWGRCSMKSTGGYS

Original motif Consensus sequence: SMAGRSCAGSSYGGBS



Reverse complement motif Consensus sequence: SBCKSSCTGSMCTRS

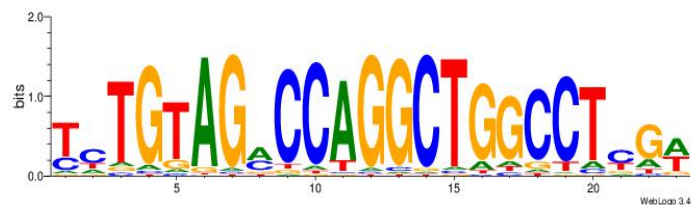


Dataset #: 1
 Motif ID: 5
 Motif name: C005
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 2
 Number of overlap: 16
 Similarity score: 0.0123408

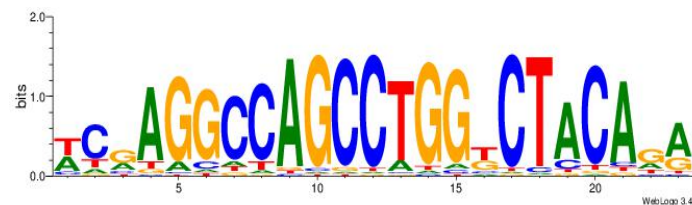
Alignment:

WCKAGGCCAGCCTGGYCTACAGA
 -----SVWGRCSMKSCCTGGYS-

Original motif Consensus sequence: TCTGTAGMCCAGGCTGGCCTYGW



Reverse complement motif Consensus sequence: WCKAGGCCAGCCTGGYCTACAGA

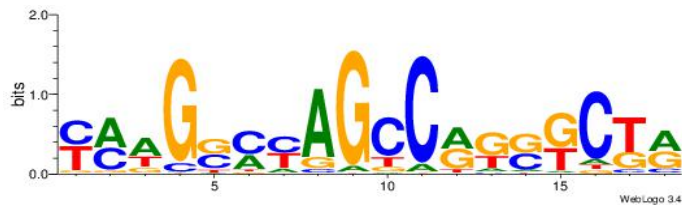


Dataset #: 1
 Motif ID: 73
 Motif name: C073
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3

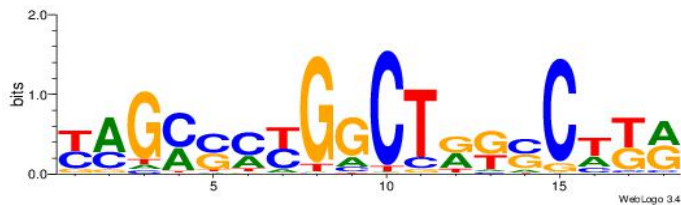
Number of overlap: 16
Similarity score: 0.0292616

Alignment:
YMWGSMYAGCCRKSKCTR
SVWGRCSMKSTGGYS--

Original motif Consensus sequence: YMWGSMYAGCCRKSKCTR



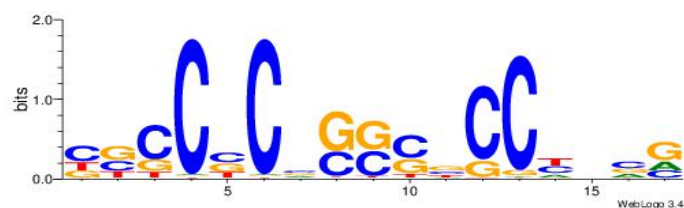
Reverse complement motif Consensus sequence: KAGYSYKGGCTKRSCWYK



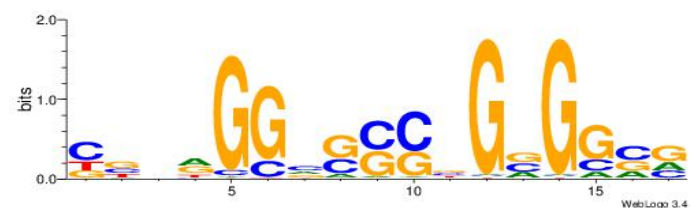
Dataset #: 1
Motif ID: 140
Motif name: C140
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 16
Similarity score: 0.0326058

Alignment:
CVDMGGBSSSVGBGGSB
-SVWGRCSMKSTGGYS

Original motif Consensus sequence: BSCCBVSSSBCCYHVG



Reverse complement motif Consensus sequence: CVDMGGBSSSVGBGGSB

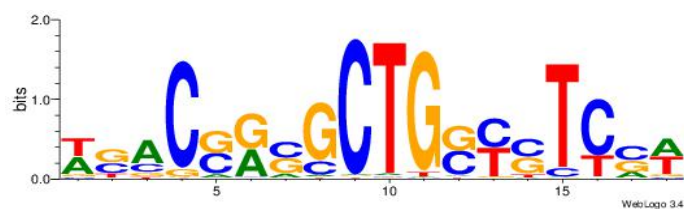


Dataset #: 1
 Motif ID: 124
 Motif name: C124
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 16
 Similarity score: 0.0330425

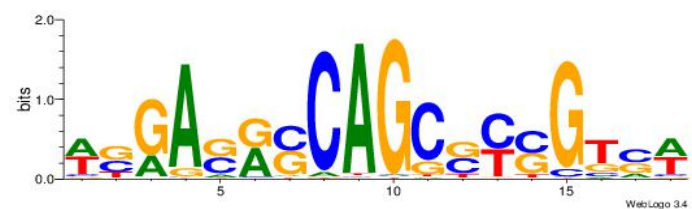
Alignment:

WSGASKSCAGCSMSGTSW
 -SVWGRCSMKCTGGYS-

Original motif Consensus sequence: WSACSRSGCTGSYSTCSW

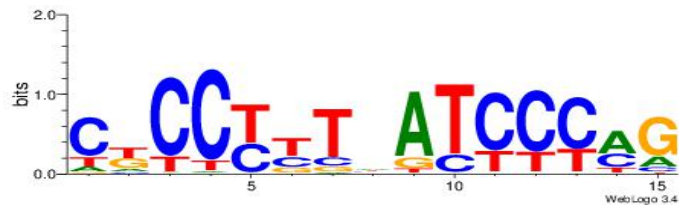


Reverse complement motif Consensus sequence: WSGASKSCAGCSMSGTSW



Dataset #: 1 Motif ID: 127 Motif name: C127

Original motif Consensus sequence: CKCCYYTHATCCCMG



Reverse complement motif Consensus sequence:
CYGGGATHAMMGGRG



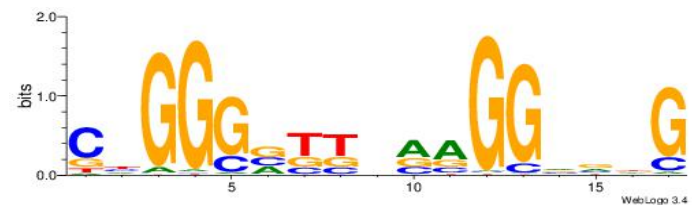
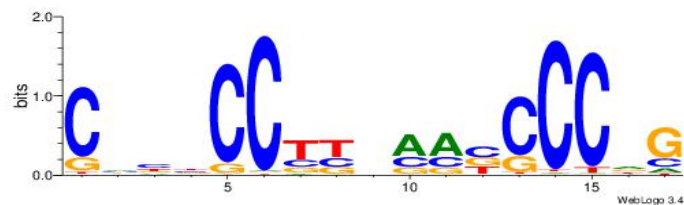
Best Matches for Motif ID 127 (Highest to Lowest)

Dataset #:	1
Motif ID:	107
Motif name:	C107
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	15
Similarity score:	0.0152308

Alignment:
CHBBCCTYBAABCCCDG
--CKCCYYTHATCCCMG

Original motif Consensus sequence: CHBBCCTYBAABCCCDG

Reverse complement motif Consensus sequence:
CDGGGBTTVMAGGVBHG

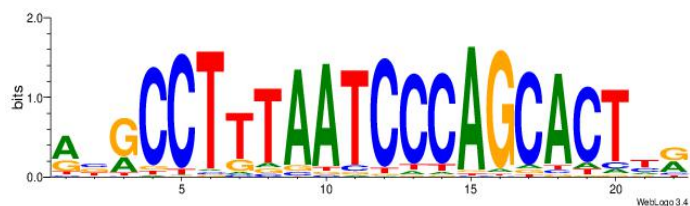


Dataset #: 1
 Motif ID: 9
 Motif name: C009
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 15
 Similarity score: 0.0175228

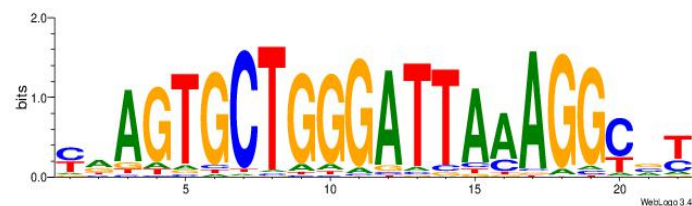
Alignment:

ABGCCTTTAATCCCAGCACTHR
 -CKCCYYTHATCCCMG-----

Original motif Consensus sequence: ABGCCTTTAATCCCAGCACTHR



Reverse complement motif Consensus sequence: MHAGTGCTGGGATTAAAGGCBT

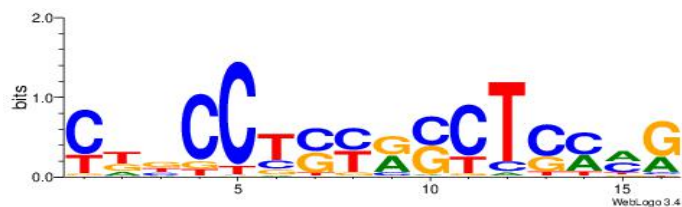


Dataset #: 1

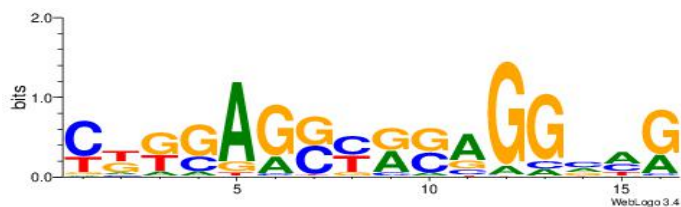
Motif ID: 83
Motif name: C083
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 15
Similarity score: 0.039129

Alignment:
CKBCCTSYRSCTCMMG
-CKCCYYTHATCCCMG

Original motif Consensus sequence: CKBCCTSYRSCTCMMG



Reverse complement motif Consensus sequence: CYRGAGSMKSAGGBRG

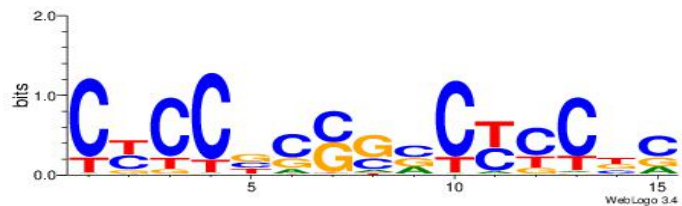


Dataset #: 1
Motif ID: 58
Motif name: C058
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 15

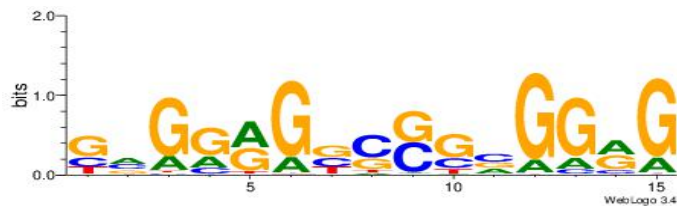
Similarity score: 0.0442699

Alignment:
CYCCBCSGVCYCCBC
CKCCYYTHATCCCMG

Original motif Consensus sequence: CYCCBCSGVCYCCBC



Reverse complement motif Consensus sequence:
GVGGMGVCSGBGGMG

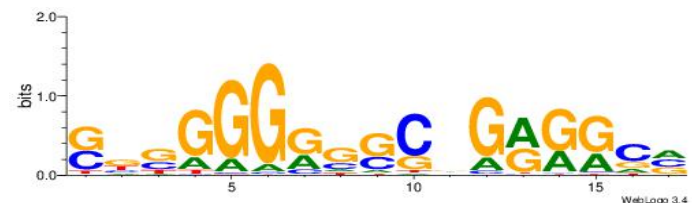
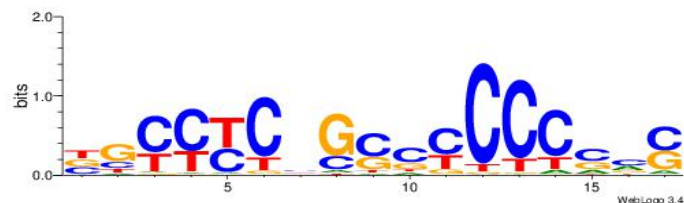


Dataset #: 1
Motif ID: 22
Motif name: C022
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 15
Similarity score: 0.0459854

Alignment:
BGCCYCBGSCYCCCSVS
CKCCYYTHATCCCMG--

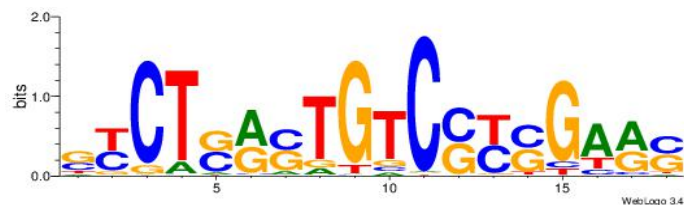
Original motif Consensus sequence: BGCCYCBGSCYCCCSVS

Reverse complement motif Consensus sequence:
SVSGGGKGSGBGMGGCV

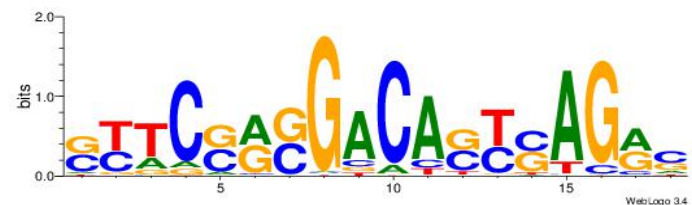


Dataset #: 1 Motif ID: 128 Motif name: C128

Original motif Consensus sequence: SYCTSRSTGTCSYSGARS



Reverse complement motif Consensus sequence: SKTCSMSGACASKSAGMS



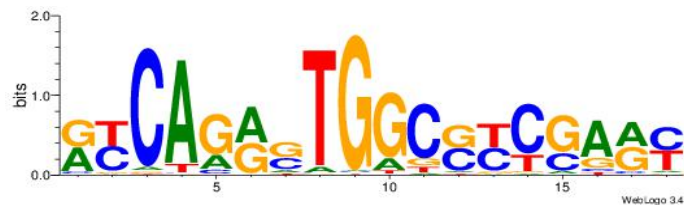
Best Matches for Motif ID 128 (Highest to Lowest)

Dataset #:	1
Motif ID:	92
Motif name:	C092
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:	0.00330143

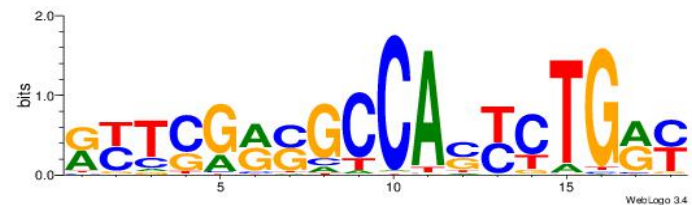
Alignment:

KKTCGMSGCCASKCTGMM
SKTCSMSGACASKSAGMS

Original motif Consensus sequence: RYCAGRSTGGCSYCGARY



Reverse complement motif Consensus sequence:
KKTCGMSGCCASKCTGMM

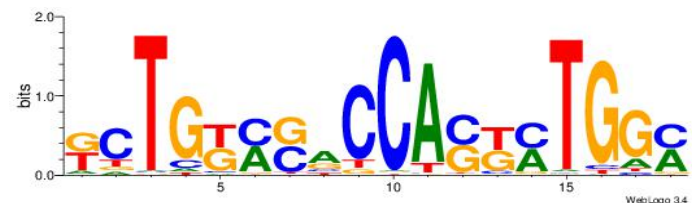
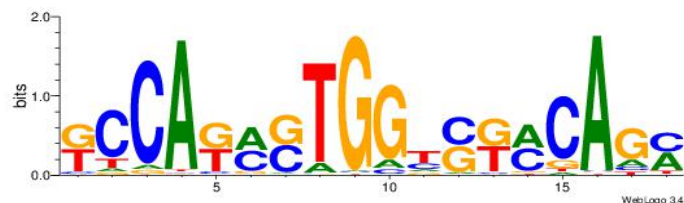


Dataset #:	1
Motif ID:	95
Motif name:	C095
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	18
Similarity score:	0.0392957

Alignment:
KCCAKMSTGGTSKMCAGM
SYCTSRSTGTCSYSGARS

Original motif Consensus sequence: KCCAKMSTGGTSKMCAGM

Reverse complement motif Consensus sequence:
RCTGYYSACCASYTTGGY

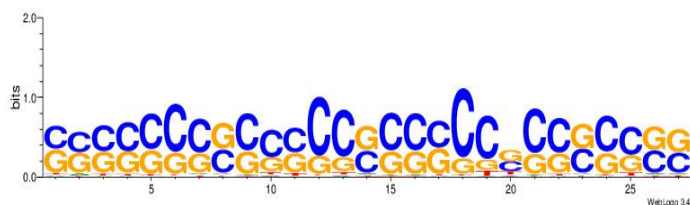


Dataset #: 1
 Motif ID: 4
 Motif name: C004
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 10
 Number of overlap: 18
 Similarity score: 0.0466725

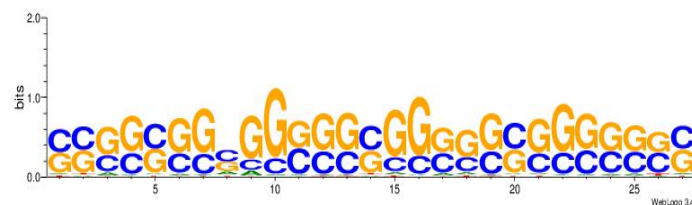
Alignment:

SSSSSSGSGGSSSSSGSSSSSGSSSSS
 -----SYCTSRSTGTCSYSGARS

Original motif Consensus sequence:
 SSSSSCSSSSSCSSSSCCSCSSSSS



Reverse complement motif Consensus sequence:
 SSSSSSGSGGSSSSSGSSSSSGSSSSS



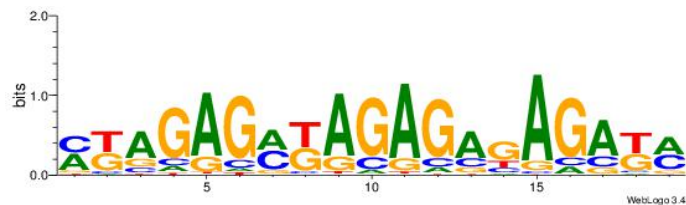
Dataset #: 1

Motif ID: 12
 Motif name: C012
 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: 0.048063

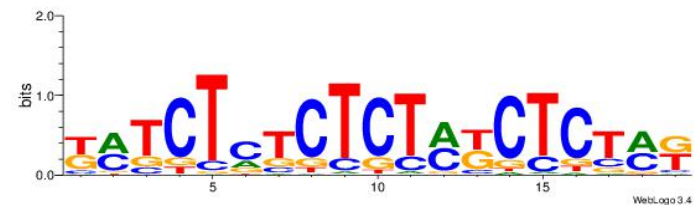
Alignment:

MKAGAGMKAGAGAGAGAKM
 -SKTCSMSGACASKSAGMS

Original motif Consensus sequence: MKAGAGMKAGAGAGAGAKM



Reverse complement motif Consensus sequence: YRTCTCTCTRYCTCTRR



Dataset #: 1
 Motif ID: C020
 Motif name: C020
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 18

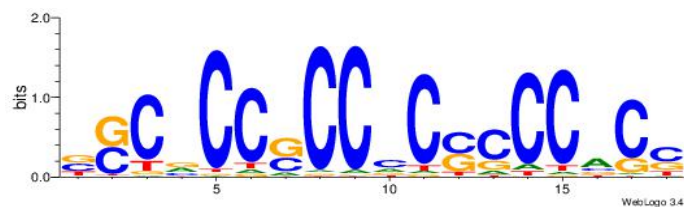
Similarity score: 0.0508385

Alignment:

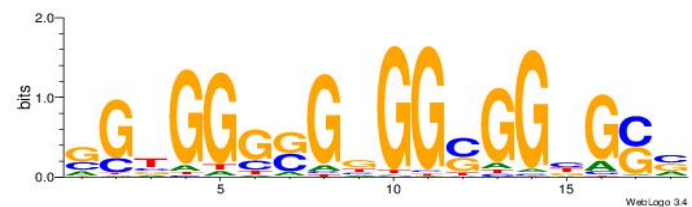
SGTGGGSGVGGSGGVGSB

SKTCSMSGACASKSAGMS

Original motif Consensus sequence: BSCVCCSCCVSCCCACS

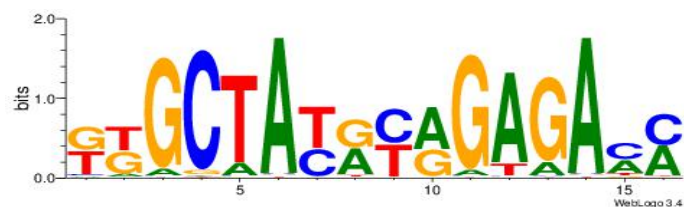


Reverse complement motif Consensus sequence: SGTGGGSGVGGSGGVGSB

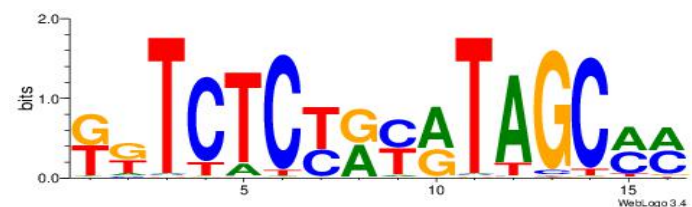


Dataset #: 1 Motif ID: 129 Motif name: C129

Original motif Consensus sequence: KKGCTAYRYRGAGAMM



Reverse complement motif Consensus sequence: RRTCTCKKMMTAGCRY



Best Matches for Motif ID 129 (Highest to Lowest)

Dataset #:	1
Motif ID:	26
Motif name:	C026
Matching format of first motif:	Reverse Complement

Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	16
Similarity score:	0.0373267

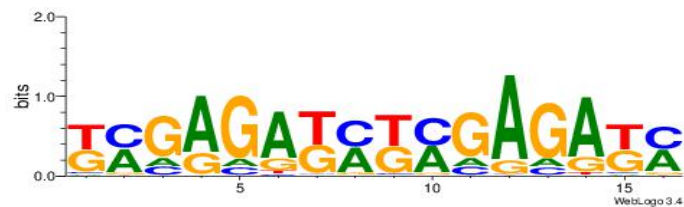
Alignment:

```

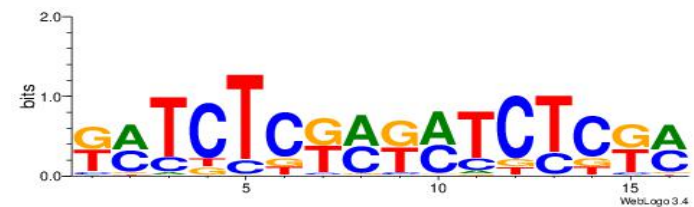
RRTCTCRRRTCTCRR
RRTCTCKMMTAGCRY

```

Original motif Consensus sequence: KMGAGAKMKMGAGAKM



Reverse complement motif Consensus sequence: RRTCTCRRRTCTCRR

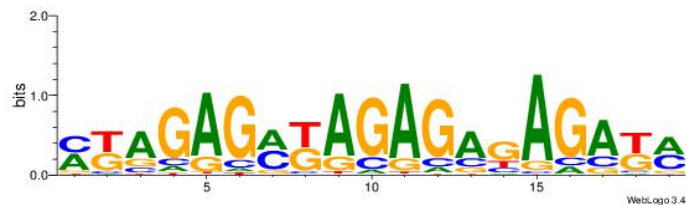


Dataset #:	1
Motif ID:	12
Motif name:	C012
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	4
Number of overlap:	16
Similarity score:	0.0468494

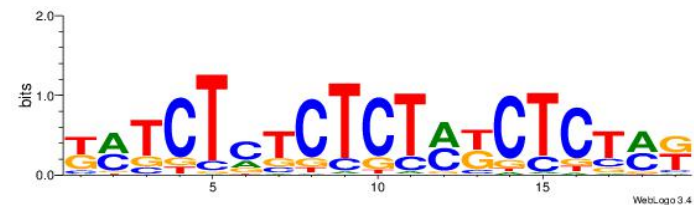
Alignment:

MKAGAGMKAGAGAGAGAKM
 ---KKGCTAYRYRGAGAMM

Original motif Consensus sequence: MKAGAGMKAGAGAGAGAKM



Reverse complement motif Consensus sequence: YRTCTCTCTCTRYCTCTRR

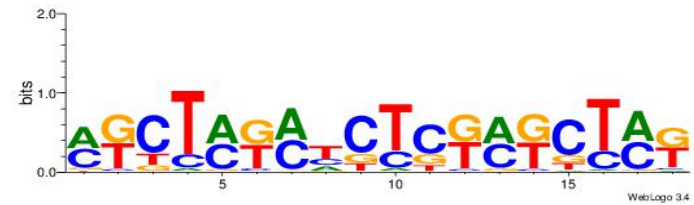
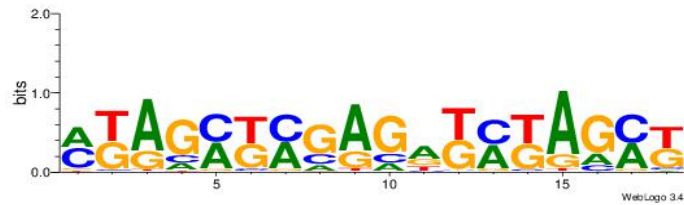


Dataset #:	1
Motif ID:	36
Motif name:	C036
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	16
Similarity score:	0.0517095

Alignment:
 MKAGMKMGAGAKMKAGMK
 -KKGCTAYRYRGAGAMM-

Original motif Consensus sequence: MKAGMKMGAGAKMKAGMK

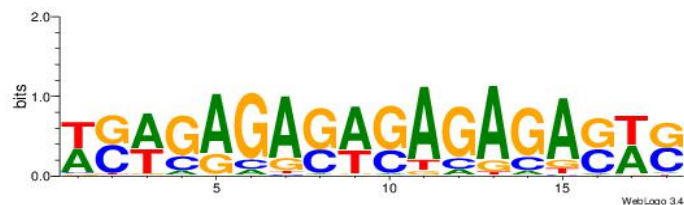
Reverse complement motif Consensus sequence: RRCTRRRTCTCRRRCTRY



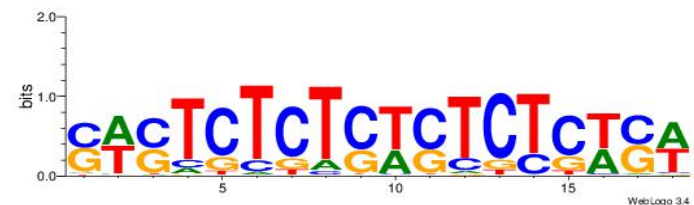
Dataset #: 1
 Motif ID: 17
 Motif name: C017
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 16
 Similarity score: 0.0523389

Alignment:
 SWSTCTCTSWSTCTCWSW
 -RRTCTCKMMTAGCRY-

Original motif Consensus sequence: WSWGAGASWSAGAGASWS



Reverse complement motif Consensus sequence: SWSTCTCTSWSTCTCWSW



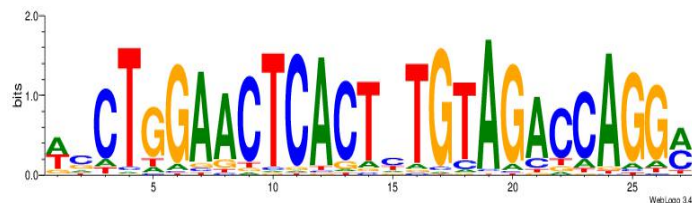
Dataset #: 1

Motif ID: 13
 Motif name: C013
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 8
 Number of overlap: 16
 Similarity score: 0.0523654

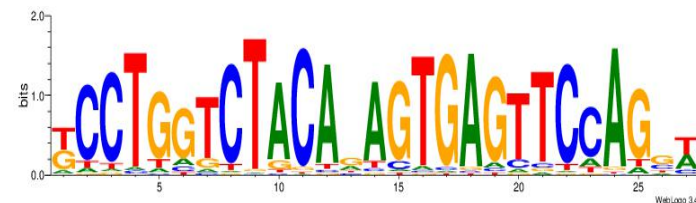
Alignment:

WVCTGGAAC TCACTHTGTAGACCAGGM
 ----RRTCTCKKMMTAGCRY-----

Original motif Consensus sequence:
 WVCTGGAAC TCACTHTGTAGACCAGGM



Reverse complement motif Consensus sequence:
 YCCTGGTCTACADAGTGAGTTCCAGVW

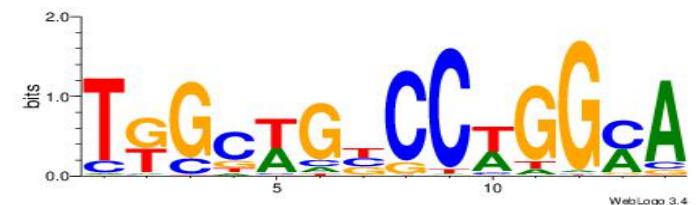


Dataset #: 1 Motif ID: 130 Motif name: C130

Original motif Consensus sequence: TKCCWGGVCWGCMA



Reverse complement motif Consensus sequence: TRGCWGBCCWGG



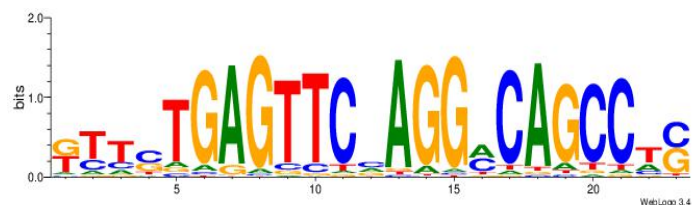
Best Matches for Motif ID 130 (Highest to Lowest)

Dataset #: 1
 Motif ID: 7
 Motif name: C007
 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: 0.00579236

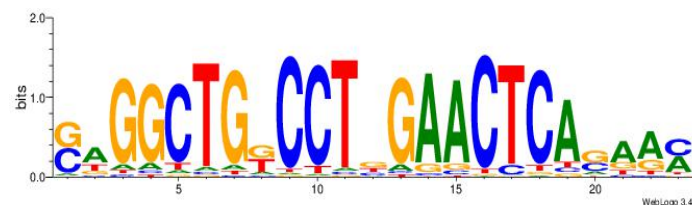
Alignment:

KTTSTGAGTTCVAGGMCAGCCTS
 -----TKCCWGGVCWGCMA-

Original motif Consensus sequence: KTTSTGAGTTCVAGGMCAGCCTS



Reverse complement motif Consensus sequence: SAGGCTGYCCTVGAAGTCASAAY

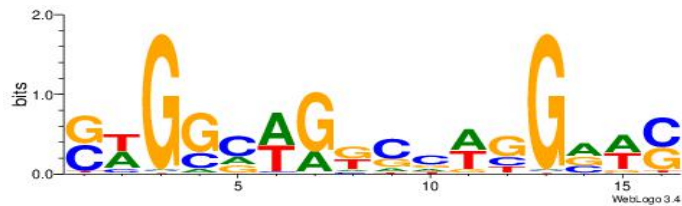


Dataset #: 1
 Motif ID: 151
 Motif name: C151
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement

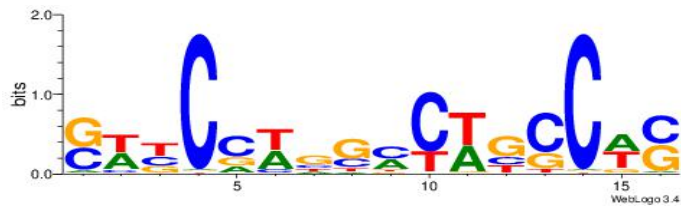
Direction: Forward
Position number: 2
Number of overlap: 14
Similarity score: 0.00882638

Alignment:
SWBCCWGGYCWGCCWS
-TKCCWGGVCWGCMA-

Original motif Consensus sequence: SWGGCWGKCCWGGVWS



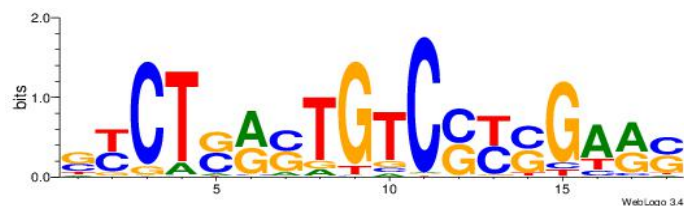
Reverse complement motif Consensus sequence: SWBCCWGGYCWGCCWS



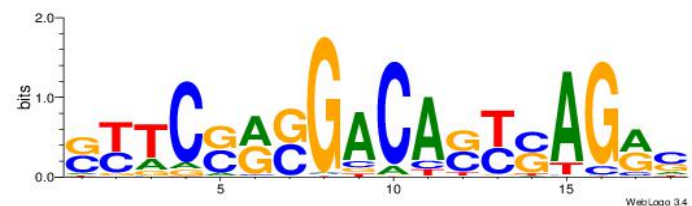
Dataset #: 1
Motif ID: 128
Motif name: C128
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 2
Number of overlap: 14
Similarity score: 0.0249438

Alignment:
SKTCSMSGACASKSAGMS
---TKCCWGGVCWGCMA-

Original motif Consensus sequence: SYCTSRSTGTCSYSGARS



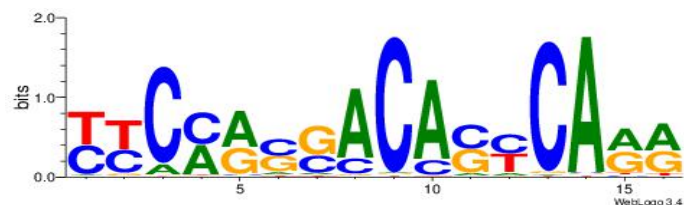
Reverse complement motif Consensus sequence: SKTCSMSGACASKSAGMS



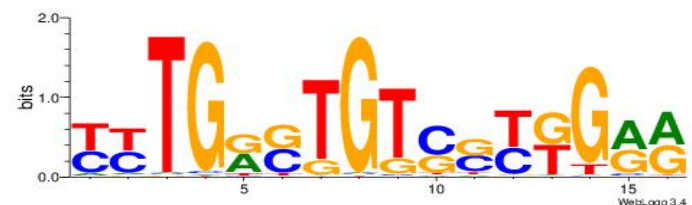
Dataset #: 1
 Motif ID: 150
 Motif name: C150
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0.0273359

Alignment:
 YYCMRSSACASYCARR
 TKCCWGGVCWGCMA--

Original motif Consensus sequence: YYCMRSSACASYCARR



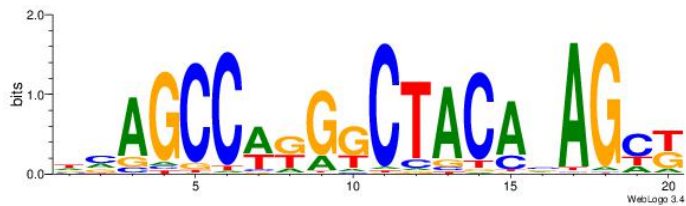
Reverse complement motif Consensus sequence: KKTGKSTGTSSKRGMM



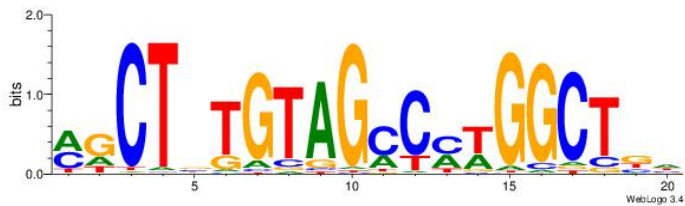
Dataset #: 1
Motif ID: 15
Motif name: C015
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 3
Number of overlap: 14
Similarity score: 0.0315733

Alignment:
DVAGCCWKGCTACAVAGCK
--TKCCWGGVCWGCMA----

Original motif Consensus sequence: DVAGCCWKGCTACAVAGCK



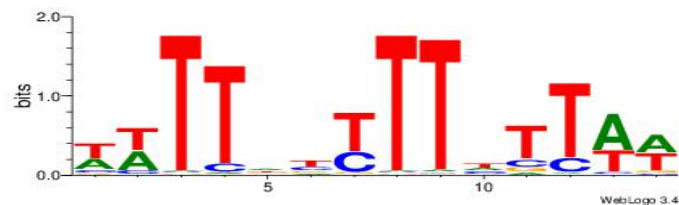
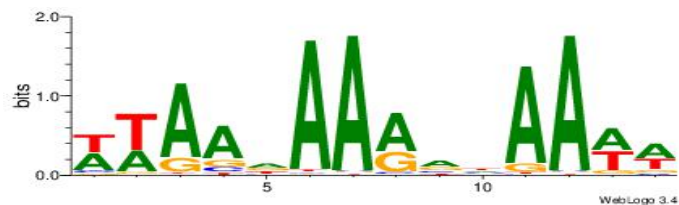
Reverse complement motif Consensus sequence: RGCTVTGTAGCCYWGGCTVD



Dataset #: 1 Motif ID: 131 Motif name: C131

Original motif Consensus sequence: WWAADAARVHAAWW

Reverse complement motif Consensus sequence: WWTTHBKTTDTTV



Best Matches for Motif ID 131 (Highest to Lowest)

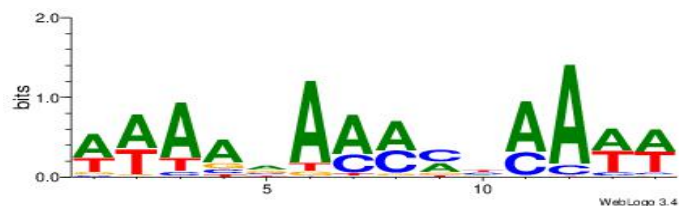
Dataset #: 1
 Motif ID: 80
 Motif name: C080
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0.0182718

Alignment:

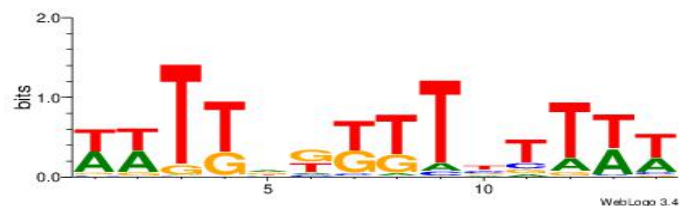
WWAAVAAMMHAAWW

WWAADAARVHAAWW

Original motif Consensus sequence: WWAAVAAMMHAAWW



Reverse complement motif Consensus sequence: WWTTHRYTTBTTW



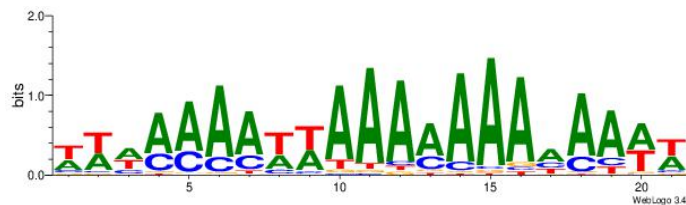
Dataset #: 1

Motif ID: 10
 Motif name: C010
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 8
 Number of overlap: 14
 Similarity score: 0.0270118

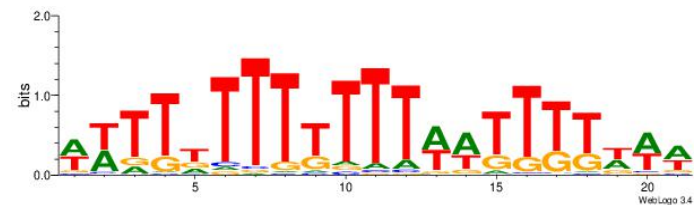
Alignment:

WWTTTTTTTTTTWWTTTTWWW
 WWTTTBKTTDTTWW-----

Original motif Consensus sequence: WWWAAAWWAAAAAAAAAAWW



Reverse complement motif Consensus sequence: WWTTTTTTTTTTWWTTTTWWW

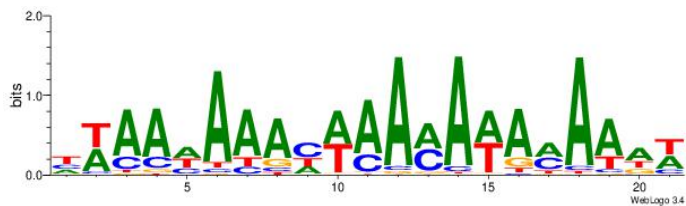


Dataset #: 1
 Motif ID: 16
 Motif name: C016
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 14

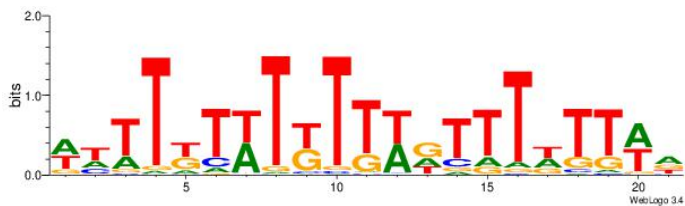
Similarity score: 0.0308734

Alignment:
WWTYYTWYTTWDTTTWTWH
-----WWTTHBKTTDTTWW

Original motif Consensus sequence: HWAAWAAAHWAAMAWAMAAWW



Reverse complement motif Consensus sequence: WWTYYTWYTTWDTTTWTWH

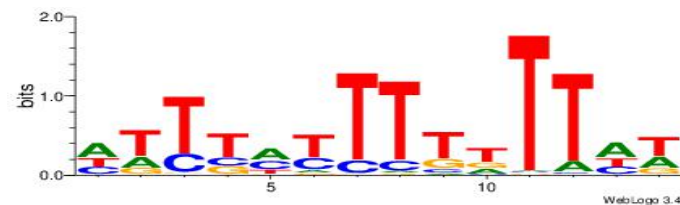


Dataset #: 1
Motif ID: 67
Motif name: C067
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 14
Similarity score: 0.0318891

Alignment:
WDAAAAAARKAAAD
WWAADAARVHAAWW

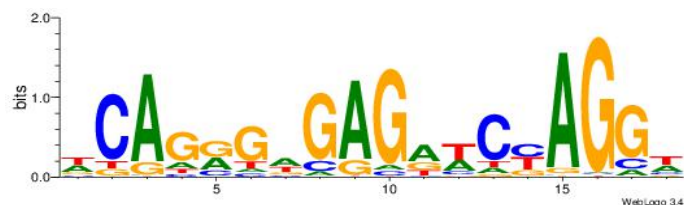
Original motif Consensus sequence: WDAAAAAARKAAAD

Reverse complement motif Consensus sequence: DTTTRKTTTTTTD

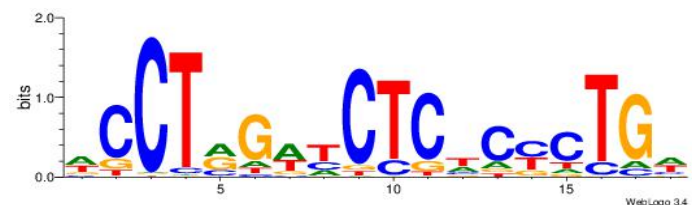


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Original motif Consensus sequence: WCAGRGWGAGAWCYAGGW



Reverse complement motif Consensus sequence: WCCTKGWTCTCWCMTGW



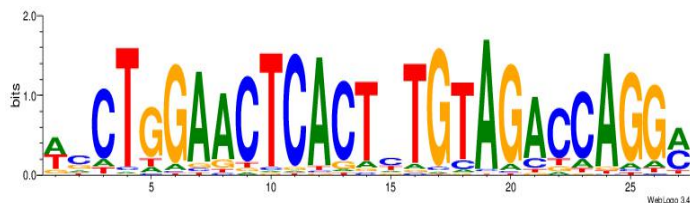
Best Matches for Motif ID 132 (Highest to Lowest)

Dataset #:	1
Motif ID:	13
Motif name:	C013
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	10
Number of overlap:	18
Similarity score:	0.0151683

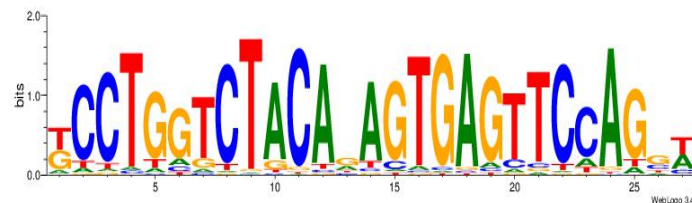
Alignment:

WVCTGGAAC TCACTHTGTAGACCAGGM
 -----WCCTKGWTCTCWCMTGW

Original motif Consensus sequence:
 WVCTGGAAC TCACTHTGTAGACCAGGM



Reverse complement motif Consensus sequence:
 YCCTGGTCTACADAGTGAGTTCCAGVW

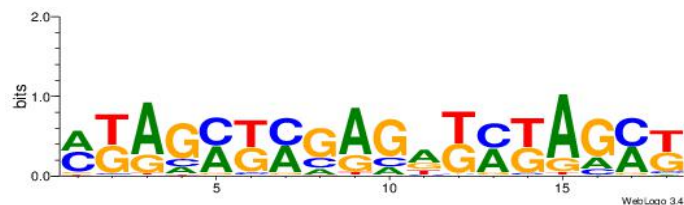


Dataset #: 1
 Motif ID: 36
 Motif name: C036
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 18
 Similarity score: 0.0306284

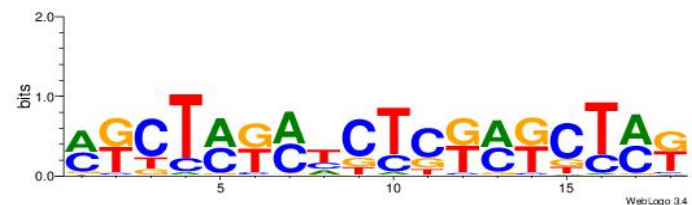
Alignment:

MKAGMKMGAGAKMKAGMK
 WCAGRGWGAGAWCYAGGW

Original motif Consensus sequence: MKAGMKMGAGAKMKAGMK



Reverse complement motif Consensus sequence: RRCTRRRTCTCRRRCTRY



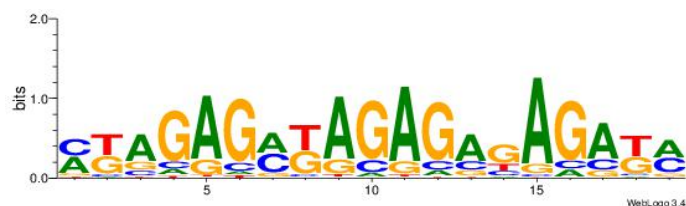
Dataset #: 1
 Motif ID: 12
 Motif name: C012
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward

Position number: 2
Number of overlap: 18
Similarity score: 0.0378139

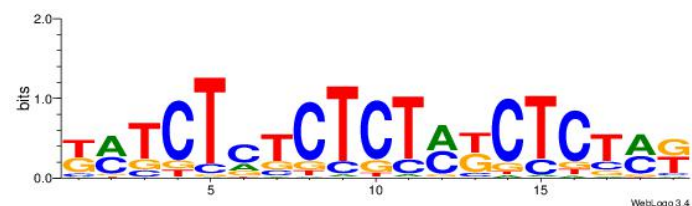
Alignment:

MKAGAGMKAGAGAGAGAKM
WCAGRGWGAGAWCYAGGW-

Original motif Consensus sequence: MKAGAGMKAGAGAGAGAKM



Reverse complement motif Consensus sequence: YRTCTCTCTCTRYCTCTRR

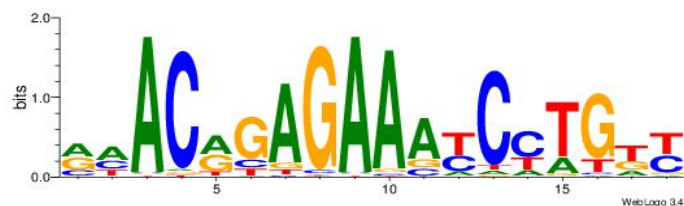


Dataset #: 1
Motif ID: 53
Motif name: C053
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 18
Similarity score: 0.0408936

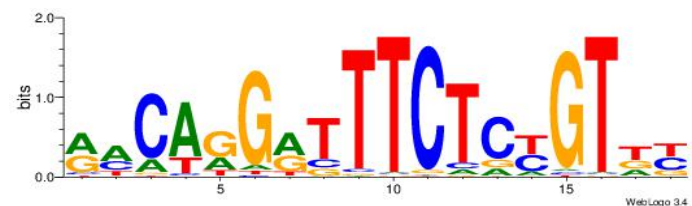
Alignment:

RMACRGAGAAAYCCTGKY
WCAGRGWGAGAWCYAGGW

Original motif Consensus sequence: RMACRGAGAAAYCCTGKY



Reverse complement motif Consensus sequence: MRCAGGMTTCTCKGTYK

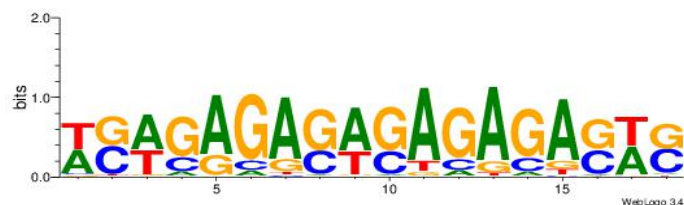


Dataset #: 1
 Motif ID: 17
 Motif name: C017
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 18
 Similarity score: 0.0517011

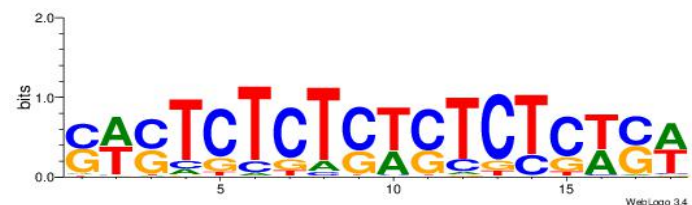
Alignment:

WSWGAGASWSAGAGASWS
 WCAGRGWGAGAWCYAGGW

Original motif Consensus sequence: WSWGAGASWSAGAGASWS

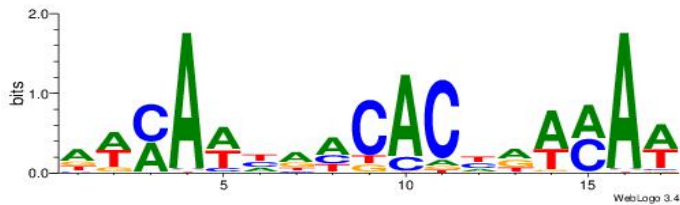


Reverse complement motif Consensus sequence: SWSTCTCTSWSTCTCWSW

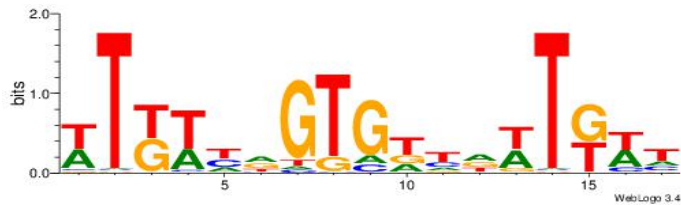


Dataset #: 1 Motif ID: 133 Motif name: C133

Original motif Consensus sequence: AWMAWHDACACHRWMAW



Reverse complement motif Consensus sequence: WTYWKHGTGTDHWTRWT



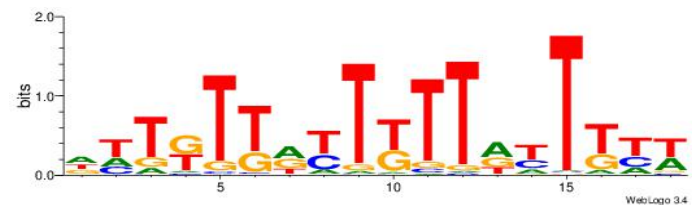
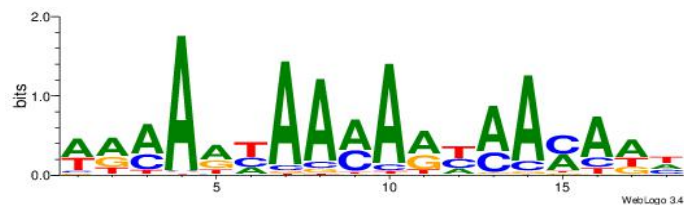
Best Matches for Motif ID 133 (Highest to Lowest)

Dataset #:	1
Motif ID:	57
Motif name:	C057
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:	0.0266447

Alignment:
WRMARYAAMARYAAMAWH
AWMAWHDACACHRWMAW-

Original motif Consensus sequence: WRMARYAAMARYAAMAWH

Reverse complement motif Consensus sequence: HWTRTTMKTYTTMKTYKW

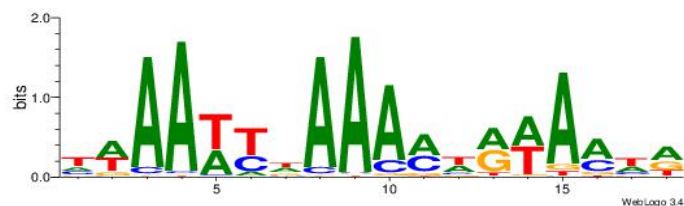


Dataset #: 1
 Motif ID: 32
 Motif name: C032
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 17
 Similarity score: 0.0319281

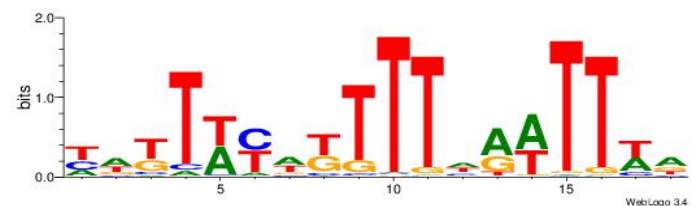
Alignment:

HWAAWYDAAAMWRWAMWR
 AWMAWHDACACHRWMAW-

Original motif Consensus sequence: HWAAWYDAAAMWRWAMWR



Reverse complement motif Consensus sequence: KWYTWKWYTTTDMWTTWH



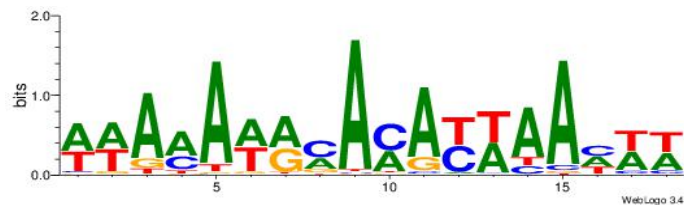
Dataset #: 1

Motif ID: 62
 Motif name: C062
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 17
 Similarity score: 0.0386594

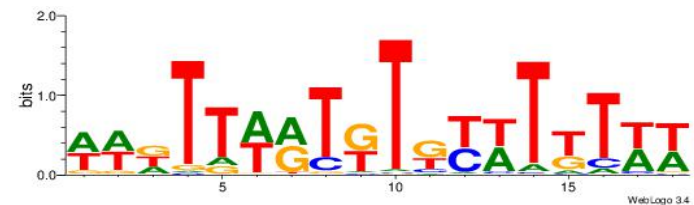
Alignment:

WWAMAWRMAMAYWAAHWW
 -AWMAWHDACACHRWMAW

Original motif Consensus sequence: WWAMAWRMAMAYWAAHWW



Reverse complement motif Consensus sequence: WWDTTWMTRTRKWTYTW

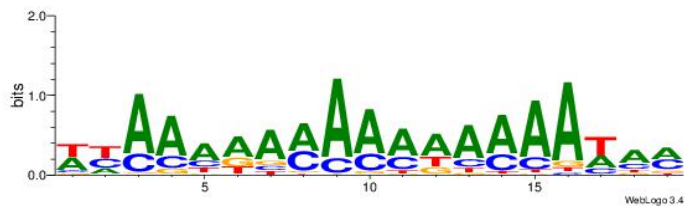


Dataset #: 1
 Motif ID: 30
 Motif name: C030
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 17

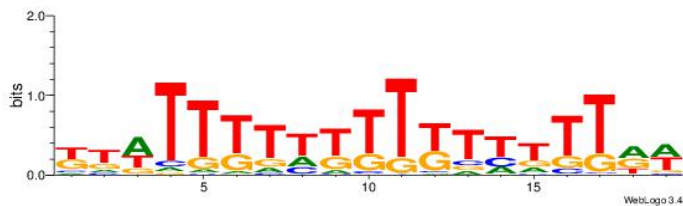
Similarity score: 0.0405967

Alignment:
WYAAAAAMAAAAAAWAM
AWMAWHDACACHRWMAW--

Original motif Consensus sequence: WYAAAAAMAAAAAAWAM



Reverse complement motif Consensus sequence:
YTWTTTTTTTTTTTTMW

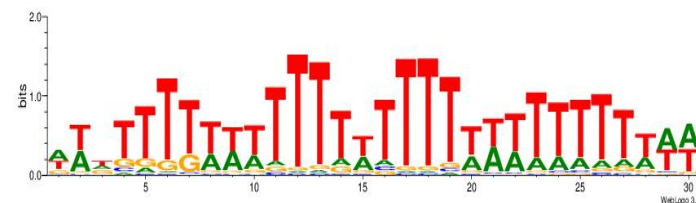
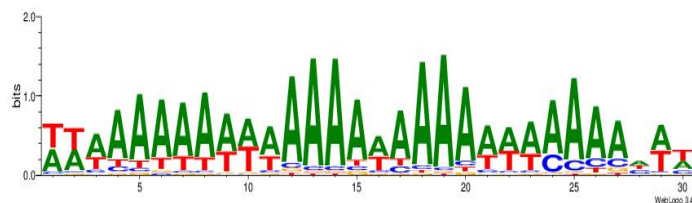


Dataset #: 1
Motif ID: 1
Motif name: C001
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 5
Number of overlap: 17
Similarity score: 0.04166

Alignment:
WWWAAAAAWWAAAAWAAAAWAAAAHWW
-----AWMAWHDACACHRWMAW-----

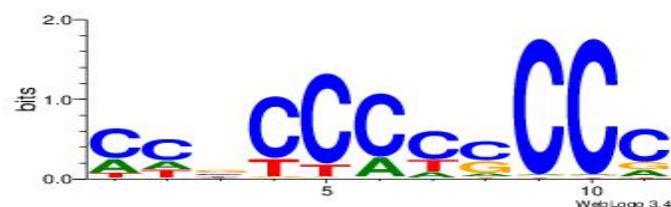
Original motif Consensus sequence:
WWWAAAAAWWAAAAWAAAAWAAAAHWW

Reverse complement motif Consensus sequence:
WWHTTTTWWTTTTTWT TTTTWWTTTTTWW



Dataset #: 1 Motif ID: 134 Motif name: C134

Original motif Consensus sequence: CCBCCCCCCC



Reverse complement motif Consensus sequence: GGGSGGGGBGG



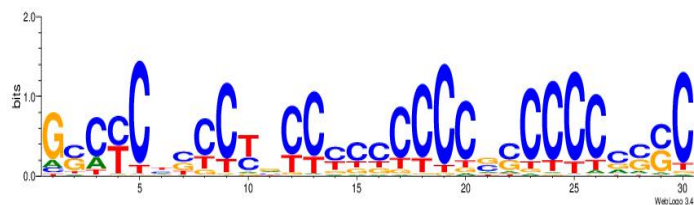
Best Matches for Motif ID 134 (Highest to Lowest)

Dataset #:	1
Motif ID:	3
Motif name:	C003
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	15
Number of overlap:	11
Similarity score:	0.0107438

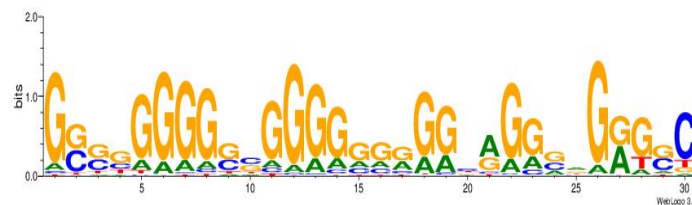
Alignment:

```
GSSGGGGGSSGGGGGKGGVMGGSHGKGC
-----GGGSGGGGBGG-----
```

Original motif Consensus sequence:
GSCYCHSCCYVCCYCCCCCSCCCCCSSC



Reverse complement motif Consensus sequence:
GSSGGGGGSSGGGGGGKGGVMGGSHGKGSC

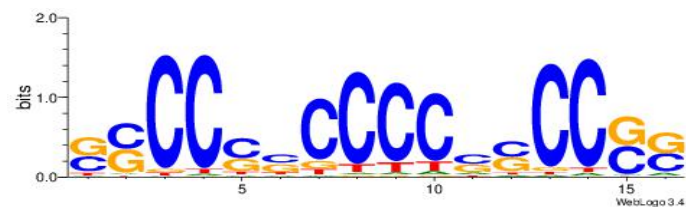


Dataset #: 1
Motif ID: 8
Motif name: C008
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 4
Number of overlap: 11
Similarity score: 0.0135583

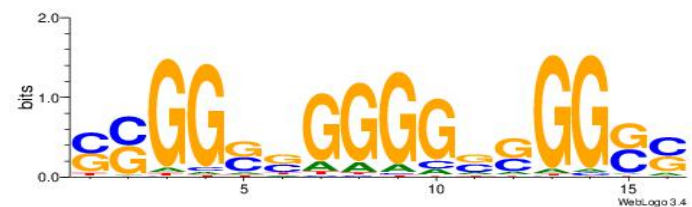
Alignment:

SSCCSSCCCCSSCCSS
---CCBCCCCSCCC---

Original motif Consensus sequence: SSCCSSCCCCSSCCSS



Reverse complement motif Consensus sequence:
SSGSSGGGGSSGGSS

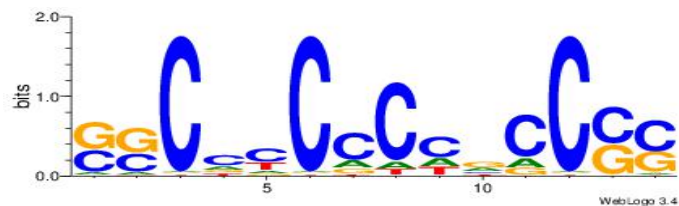


Dataset #: 1
 Motif ID: 104
 Motif name: C104
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 11
 Similarity score: 0.0183091

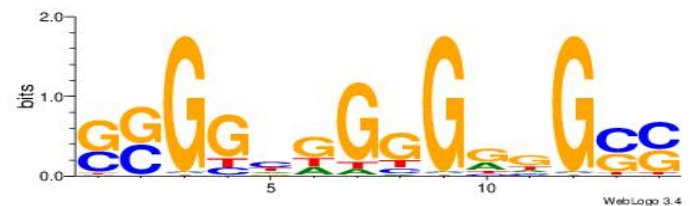
Alignment:

SSCCYCCCCDCCSS
 --CCBCCCCSCCC--

Original motif Consensus sequence: SSCCYCCCCDCCSS



Reverse complement motif Consensus sequence: SSGGHGGGGKGG

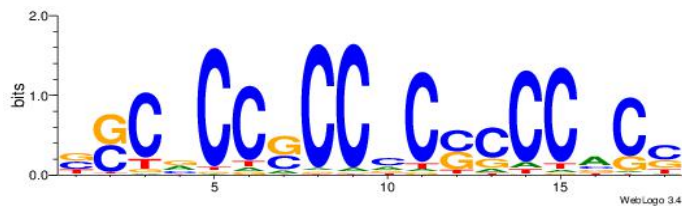


Dataset #: 1
 Motif ID: 20
 Motif name: C020
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 4
 Number of overlap: 11

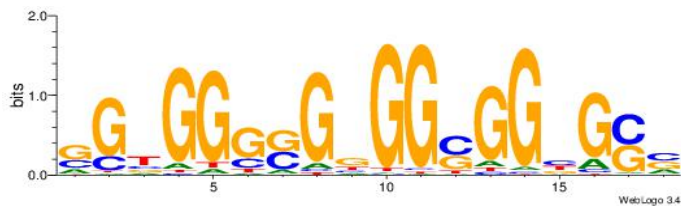
Similarity score: 0.0185182

Alignment:
BSCVCCSCCVSCCCACs
----CCBCCCCSCCC---

Original motif Consensus sequence: BSCVCCSCCVSCCCACs



Reverse complement motif Consensus sequence: SGTGGGSGVGGSGGVGSB

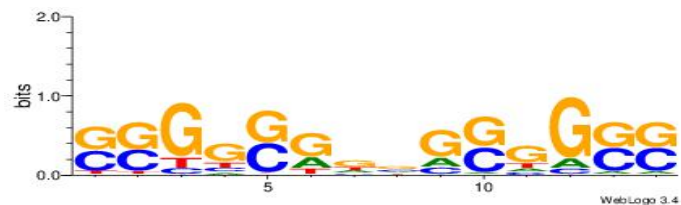
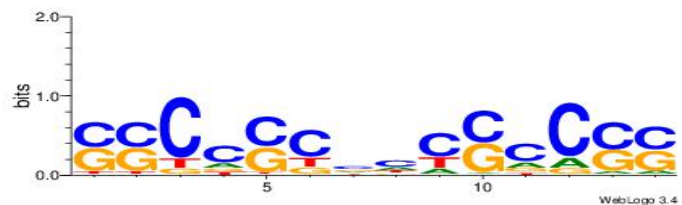


Dataset #: 1
Motif ID: 23
Motif name: C023
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2
Number of overlap: 11
Similarity score: 0.0190337

Alignment:
SSCCSCBHCSCCSS
--CCBCCCCSCCC--

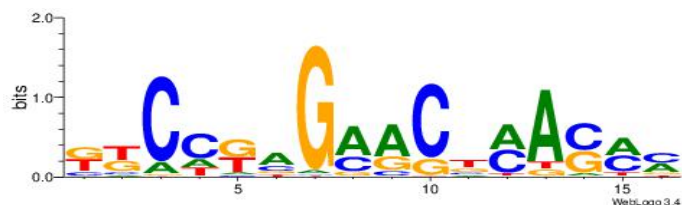
Original motif Consensus sequence: SSCCSCBHCSCCSS

Reverse complement motif Consensus sequence: SSGGSGDBGSGGSG

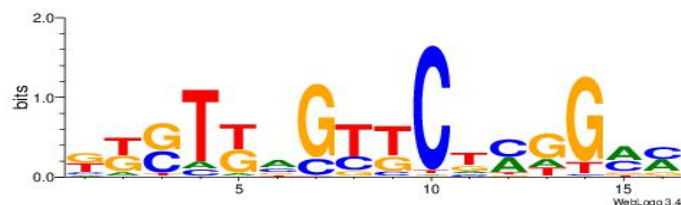


Dataset #: 1 Motif ID: 135 Motif name: C135

Original motif Consensus sequence: KKCKAGMACB MASMM



Reverse complement motif Consensus sequence: RYSTYVGTYCTYGG



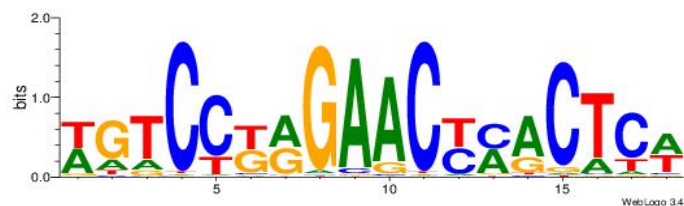
Best Matches for Motif ID 135 (Highest to Lowest)

Dataset #:	1
Motif ID:	42
Motif name:	C042
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:	0.0178338

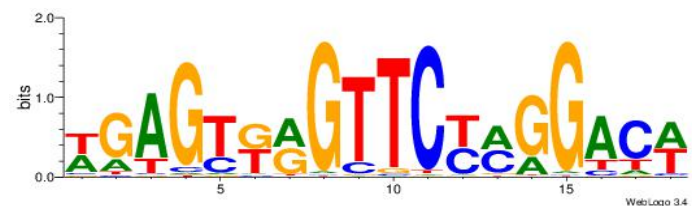
Alignment:

```
WGTCCCKRGAACYMACTCW
-KKCKKAGMACB MASMM-
```

Original motif Consensus sequence: WGTCCKRGAACTCA



Reverse complement motif Consensus sequence: WGAGTRMGTTCKRGGACW

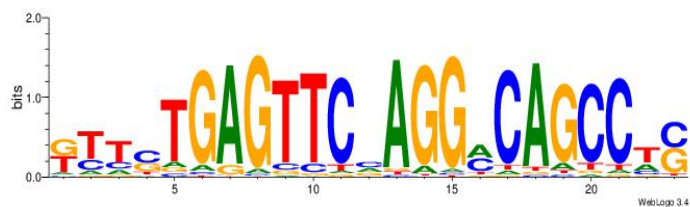


Dataset #: 1
 Motif ID: 7
 Motif name: C007
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 7
 Number of overlap: 16
 Similarity score: 0.0206041

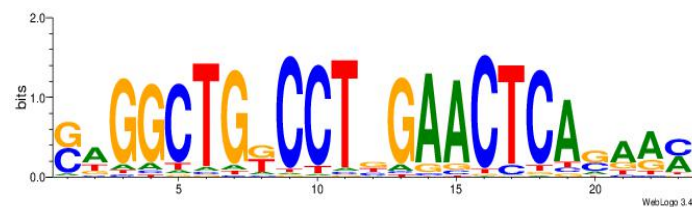
Alignment:

KTTSTGAGTTCVAGGMCAGCCTS
 -----RYSTYVGTYCTYGGRY-

Original motif Consensus sequence: KTTSTGAGTTCVAGGMCAGCCTS



Reverse complement motif Consensus sequence: SAGGCTGYCCTVGAAGTCASAAY

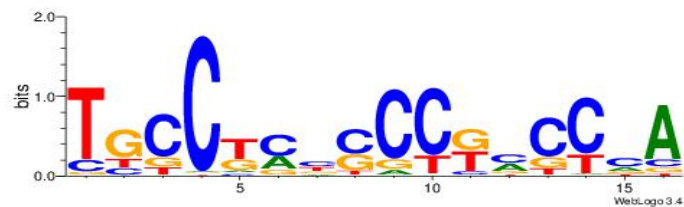


Dataset #: 1
 Motif ID: 105
 Motif name: C105
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 16
 Similarity score: 0.0513991

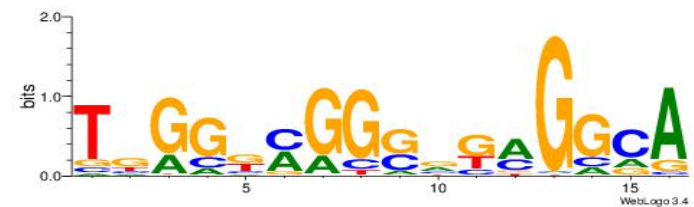
Alignment:

TGCCCKMBSCCKMCCVA
 KKCCCKAGMACBMASMM

Original motif Consensus sequence: TGCCCKMBSCCKMCCVA



Reverse complement motif Consensus sequence: TVGGRYGGSBRRGGCA



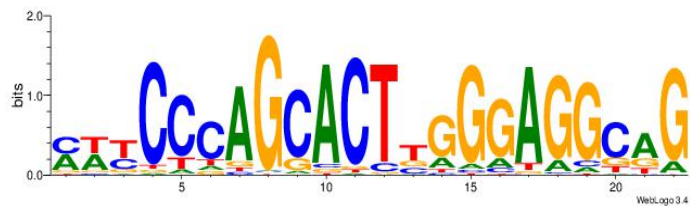
Dataset #: 1
 Motif ID: 19
 Motif name: C019
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2

Number of overlap: 16
Similarity score: 0.0535816

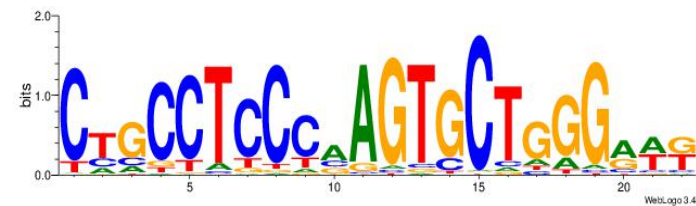
Alignment:

MWYCCCAGCACTTGGGAGGCAG
-KKCKAGMACBMASMM-----

Original motif Consensus sequence: MWYCCCAGCACTTGGGAGGCAG



Reverse complement motif Consensus sequence: CTGCCTCCCAAGTGCTGGGMWR

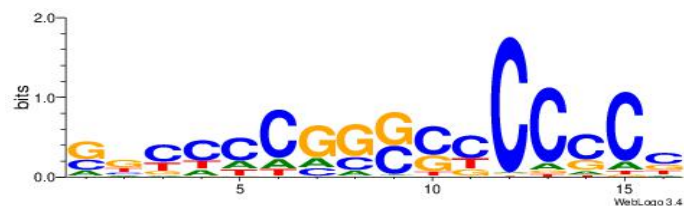


Dataset #: 1
Motif ID: 77
Motif name: C077
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 16
Similarity score: 0.0536029

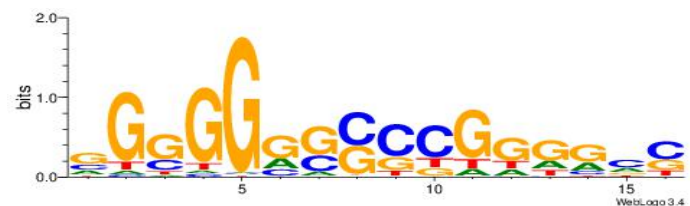
Alignment:

SBCCCCGGSSCCCCCB
KKCKAGMACBMASMM

Original motif Consensus sequence: SBCCCCGGSSCCCCCB

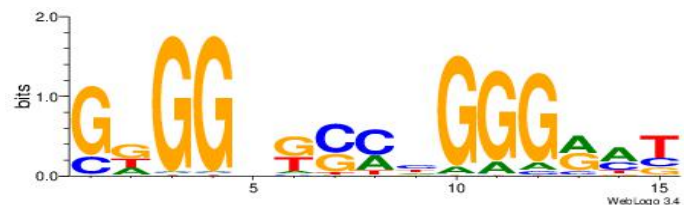


Reverse complement motif Consensus sequence: BGGGGGSSCCGGGGBS

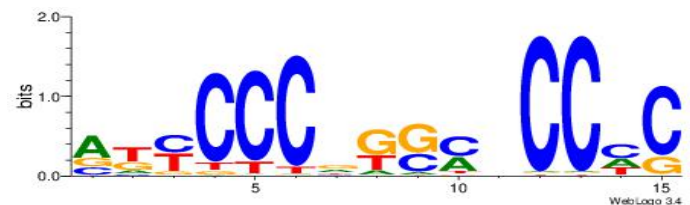


Dataset #: 1 Motif ID: 136 Motif name: C136

Original motif Consensus sequence: GDGGVKSMHGGRMT



Reverse complement motif Consensus sequence: AYKCCCDRSYVCC



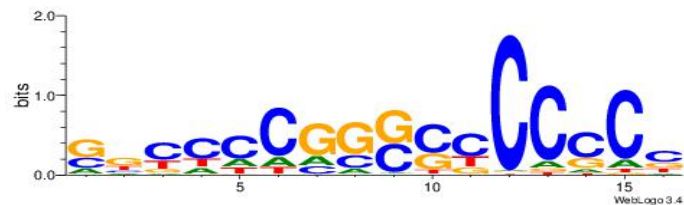
Best Matches for Motif ID 136 (Highest to Lowest)

Dataset #:	1
Motif ID:	77
Motif name:	C077
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	2
Number of overlap:	15
Similarity score:	0.040731

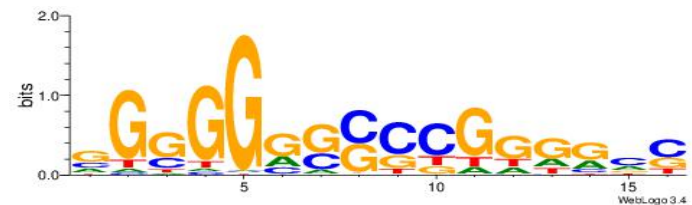
Alignment:

BGGGGSSCCGGGGBS
GDGGVKSMHGGGRMT-

Original motif Consensus sequence: SBCCCCGGSSCCCCCB



Reverse complement motif Consensus sequence:
BGGGGSSCCGGGGBS

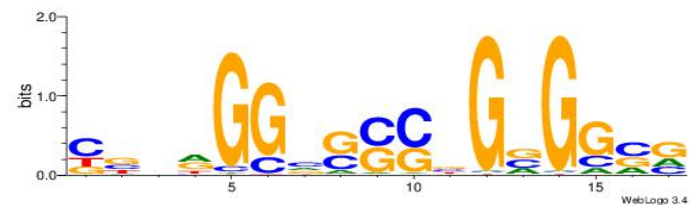
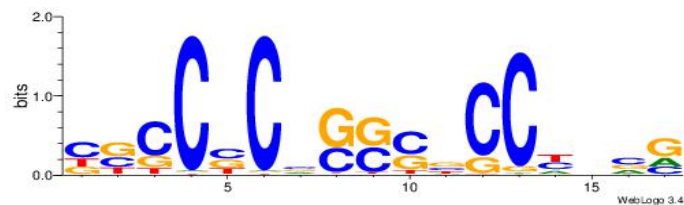


Dataset #:	1
Motif ID:	140
Motif name:	C140
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	3
Number of overlap:	15
Similarity score:	0.0444741

Alignment:
BSCCBVSSSBCCYHVG
AYKCCDRSYVCCHC--

Original motif Consensus sequence: BSCCBVSSSBCCYHVG

Reverse complement motif Consensus sequence:
CVDMGGBSSSVGBGGSB



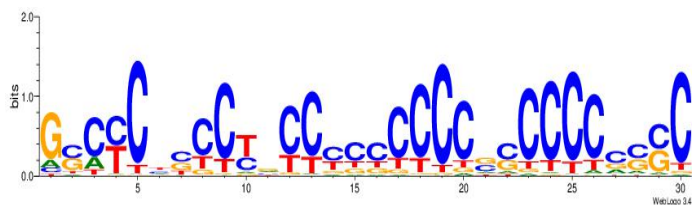
Dataset #: 1
 Motif ID: 3
 Motif name: C003
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 15
 Similarity score: 0.0511206

Alignment:

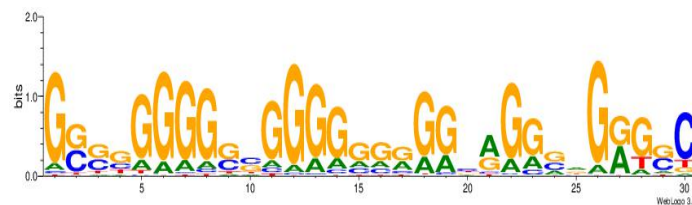
```

GSCYCHSCCYVCCYCCCCCSCCCCCSSC
--AYKCCCDRSYVCCHC-----
  
```

Original motif Consensus sequence:
 GSCYCHSCCYVCCYCCCCCSCCCCCSSC



Reverse complement motif Consensus sequence:
 GSSGGGGSSGGGGGKGGVMGGSHGKGC

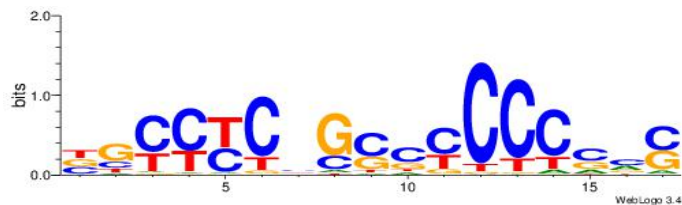


Dataset #: 1

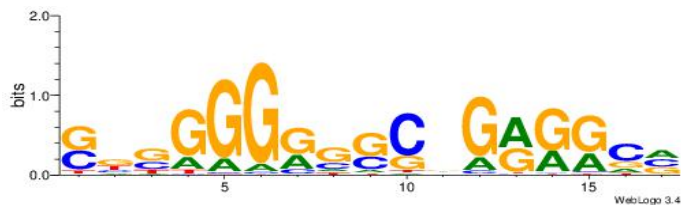
Motif ID: 22
Motif name: C022
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 15
Similarity score: 0.0536142

Alignment:
SVSGGGKGSCBGMGGCV
GDGGVKSMHGGGRMT--

Original motif Consensus sequence: BGCCYCBGSCYCCCSVS



Reverse complement motif Consensus sequence: SVSGGGKGSCBGMGGCV

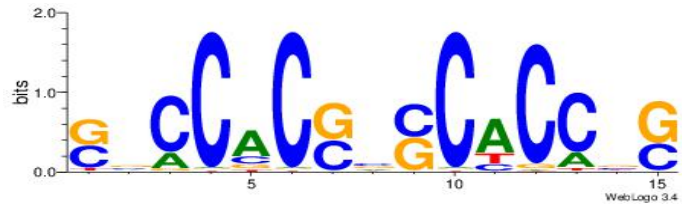


Dataset #: 1
Motif ID: 71
Motif name: C071
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 15

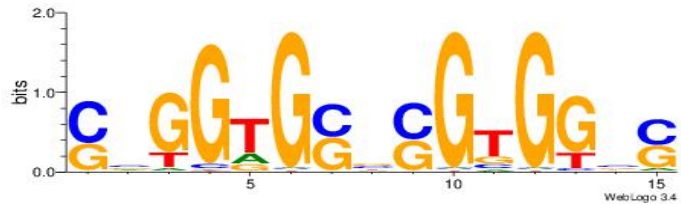
Similarity score: 0.0539648

Alignment:
SVCCACSVSCACCBS
AYKCCCDRSYVCCHC

Original motif Consensus sequence: SVCCACSVSCACCBS

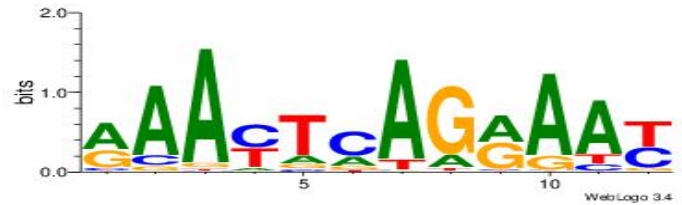


Reverse complement motif Consensus sequence: SBGGTGSVSGTGG

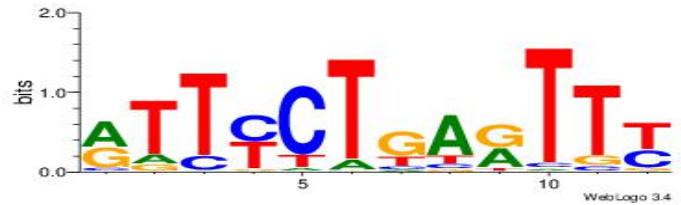


Dataset #: 1 Motif ID: 137 Motif name: C137

Original motif Consensus sequence: RAAITCAGRAAY



Reverse complement motif Consensus sequence: MTTKCTGAKTTK



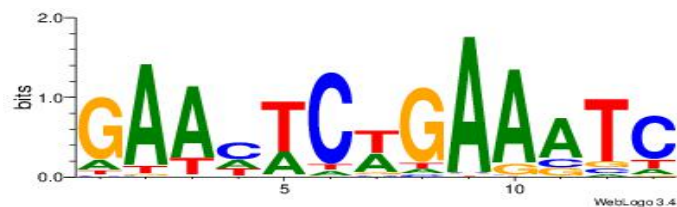
Best Matches for Motif ID 137 (Highest to Lowest)

Dataset #:	1
Motif ID:	123
Motif name:	C123
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward

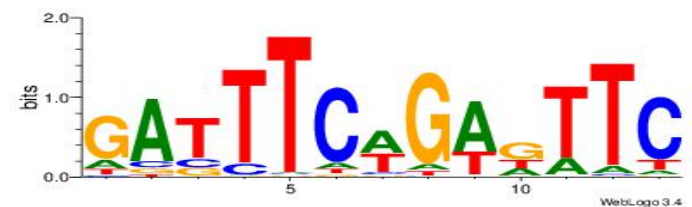
Position number: 1
 Number of overlap: 12
 Similarity score: 0.0147063

Alignment:
 GAAMTCWGAAATC
 RAAATCAGRAAY-

Original motif Consensus sequence: GAAMTCWGAAATC



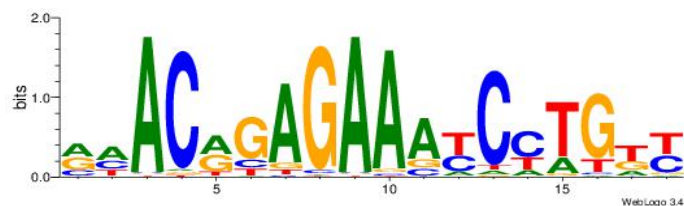
Reverse complement motif Consensus sequence: GATTCWGARTTC



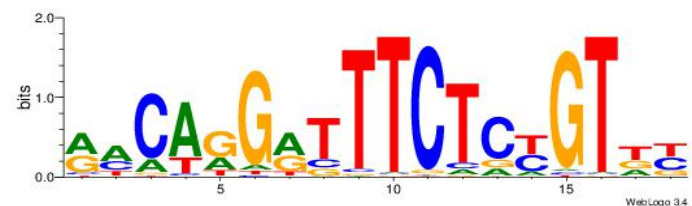
Dataset #: 1
 Motif ID: 53
 Motif name: C053
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 12
 Similarity score: 0.0233558

Alignment:
 MRCAGGTTTTCTCKGTYK
 -----MTTKCTGAKTTK

Original motif Consensus sequence: RMACRGAGAAAYCCTGKY



Reverse complement motif Consensus sequence: MRCAGGMTTCTCKGTYK

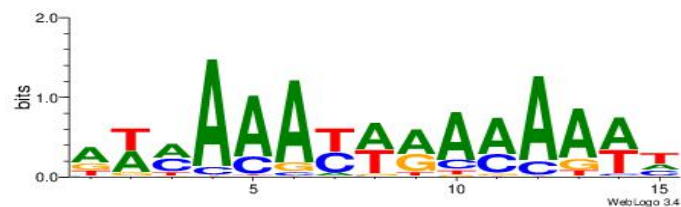


Dataset #: 1
Motif ID: 56
Motif name: C056
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 12
Similarity score: 0.0266873

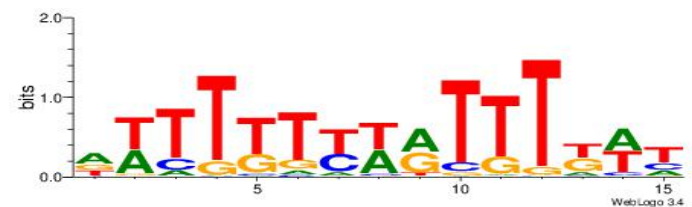
Alignment:

AWMAAAYWRAMAAWH
---RAAYTCAGRAAY

Original motif Consensus sequence: AWMAAAYWRAMAAWH



Reverse complement motif Consensus sequence: HWTTYTKWMTTTYWT

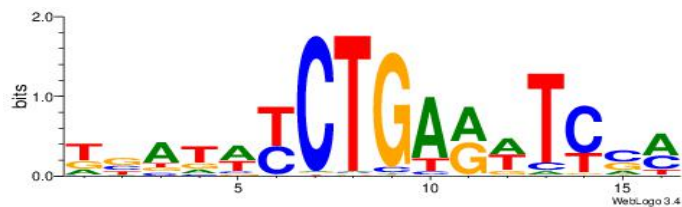


Dataset #: 1
 Motif ID: 111
 Motif name: C111
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 12
 Similarity score: 0.031512

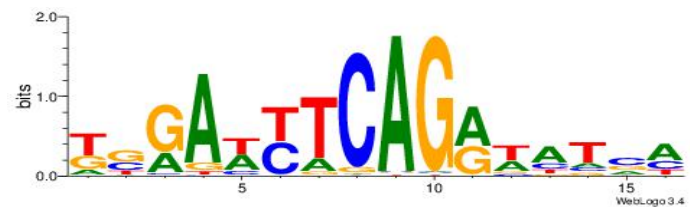
Alignment:

YSGAWKTCAGMWATBA
 --RAAYTCAGRAAY--

Original motif Consensus sequence: TBATWYCTGARWTCSM



Reverse complement motif Consensus sequence: YSGAWKTCAGMWATBA



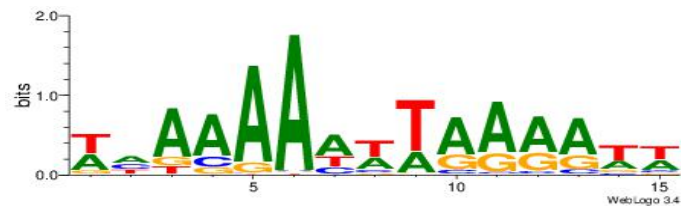
Dataset #: 1
 Motif ID: 142
 Motif name: C142
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1

Number of overlap: 12
Similarity score: 0.0319699

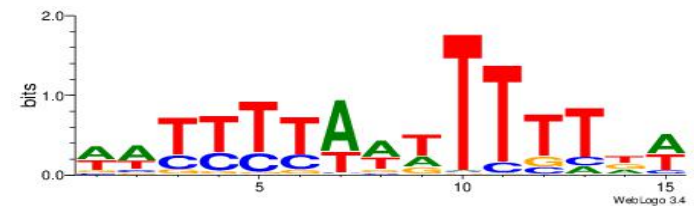
Alignment:

WHAAAAWTAAAWW
---RAAYTCAGRAAY

Original motif Consensus sequence: WHAAAAWTAAAWW

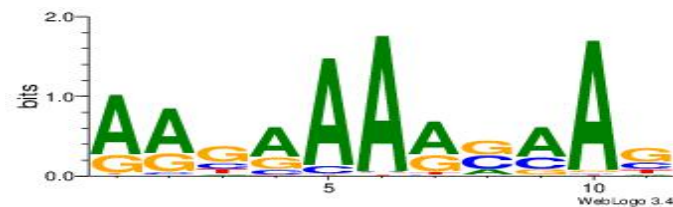


Reverse complement motif Consensus sequence: WTTTTAWTTTTTHW

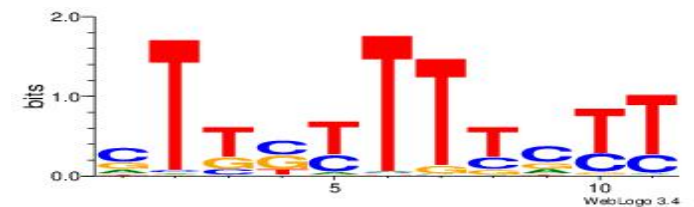


Dataset #: 1 Motif ID: 138 Motif name: C138

Original motif Consensus sequence: AAGAARSAAG



Reverse complement motif Consensus sequence: CTTSKTTTCTT



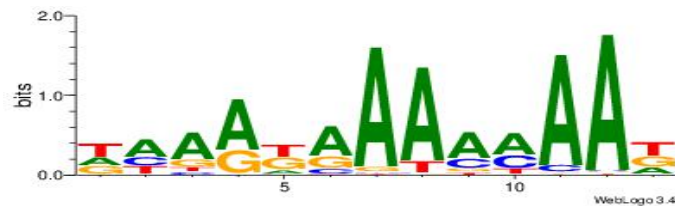
Best Matches for Motif ID 138 (Highest to Lowest)

Dataset #: 1
Motif ID: 64
Motif name: C064
Matching format of first motif: Original Motif

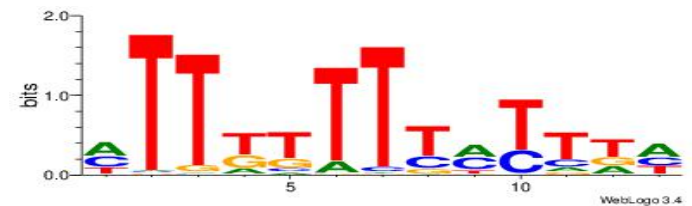
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	3
Number of overlap:	11
Similarity score:	0.00458258

Alignment:
DAAAKAAAAMAAK
--AAGAAARSAAG

Original motif Consensus sequence: DAAAKAAAAMAAK



Reverse complement motif Consensus sequence: RTTYTTTTTRTTTD

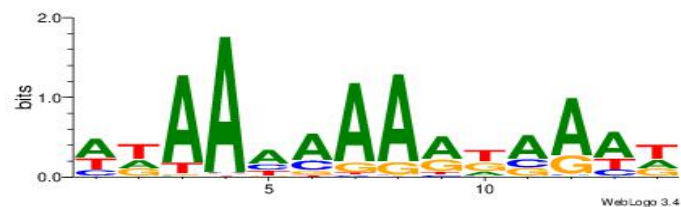


Dataset #:	1
Motif ID:	67
Motif name:	C067
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	3
Number of overlap:	11
Similarity score:	0.0200769

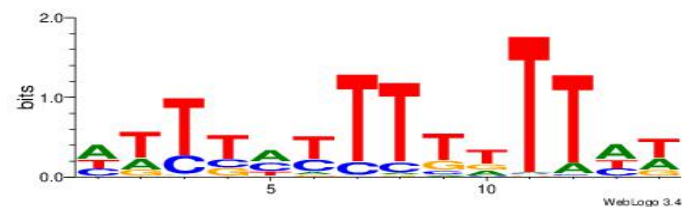
Alignment:

DTTTRKTTTTTDDW
 -CTTSKTTTCTT--

Original motif Consensus sequence: WDAAAAAARKAAAD



Reverse complement motif Consensus sequence: DTTTRKTTTTTDDW



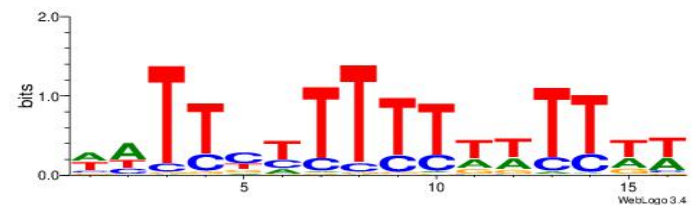
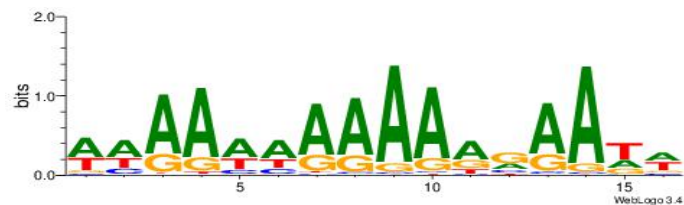
Dataset #:	1
Motif ID:	43
Motif name:	C043
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	2
Number of overlap:	11
Similarity score:	0.0226182

Alignment:

WATTMTTTTTTWTWW
 -CTTSKTTTCTT----

Original motif Consensus sequence: WWAAWAAAAARAATW

Reverse complement motif Consensus sequence:
 WATTMTTTTTTWTWW

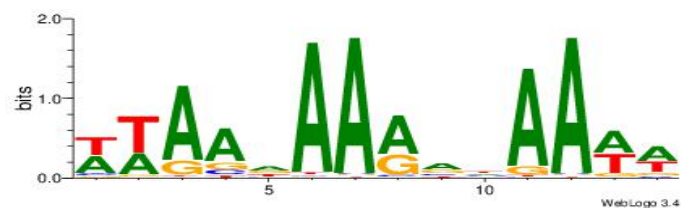


Dataset #: 1
 Motif ID: 131
 Motif name: C131
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 11
 Similarity score: 0.0250941

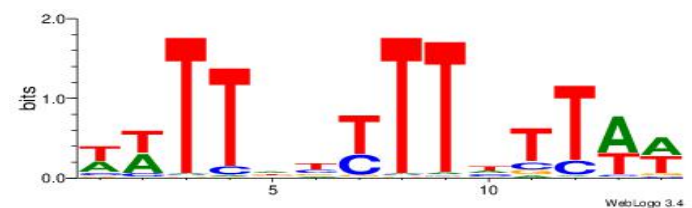
Alignment:

WWAADAARVHAAWW
 --AAGAAARSAAG--

Original motif Consensus sequence: WWAADAARVHAAWW



Reverse complement motif Consensus sequence: WWTTHBKTDDTTV



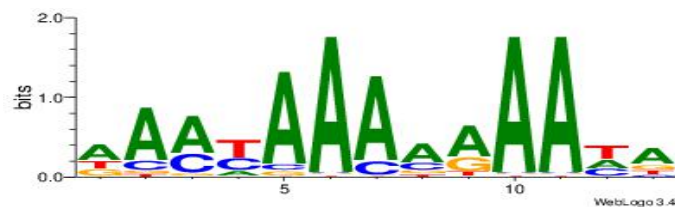
Dataset #: 1
 Motif ID: 18

Motif name: C018
 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: 0.0261093

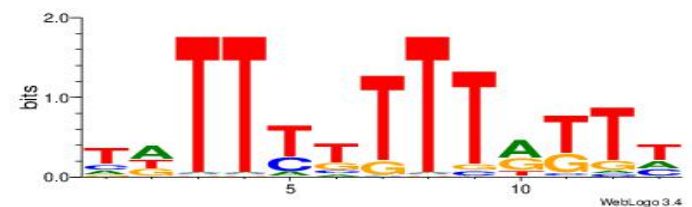
Alignment:

THTTTTTTTMYTT
 -CTTSKTTTCTT-

Original motif Consensus sequence: AAMYAAAAAAHA

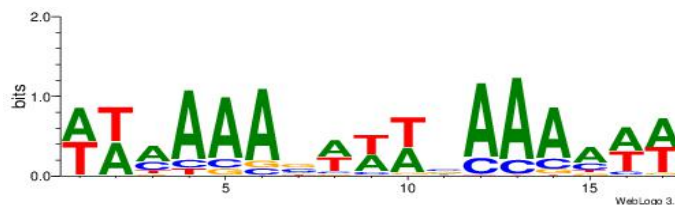


Reverse complement motif Consensus sequence: THTTTTTTTMYTT

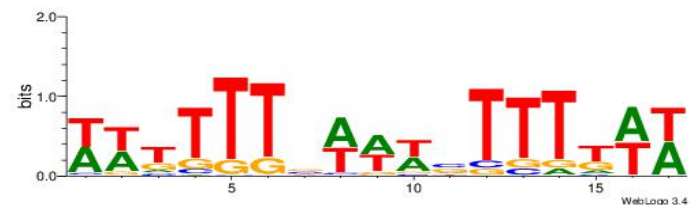


Dataset #: 1 Motif ID: 139 Motif name: C139

Original motif Consensus sequence: WWMAAABWWWVAAAWW



Reverse complement motif Consensus sequence: WWTTTTVWWBTTYWW



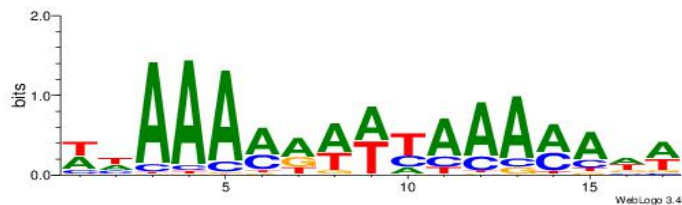
Best Matches for Motif ID 139 (Highest to Lowest)

Dataset #: 1
Motif ID: 31
Motif name: C031
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 17
Similarity score: 0.0155336

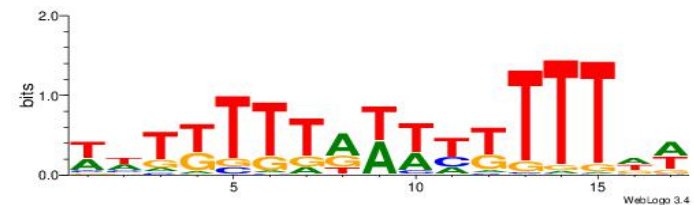
Alignment:

WHAAAMRWWYAAAMAWW
WWMAAABWWWVAAAAWW

Original motif Consensus sequence: WHAAAMRWWYAAAMAWW



Reverse complement motif Consensus sequence: WWTYTTTMWWKYTTTHW

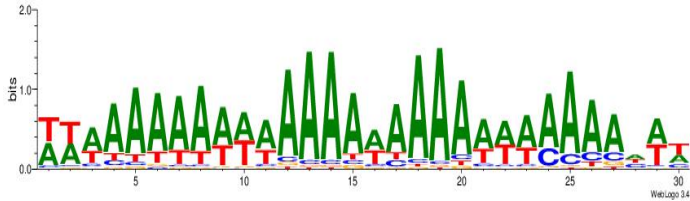


Dataset #: 1
Motif ID: 1
Motif name: C001
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement

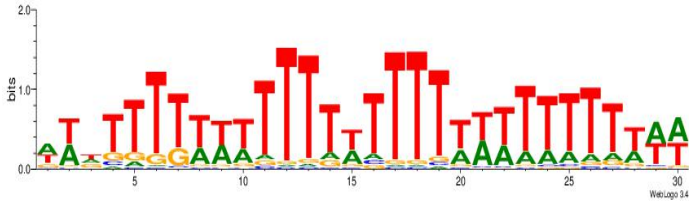
Direction: Backward
Position number: 1
Number of overlap: 17
Similarity score: 0.0179742

Alignment:
WWHTTTTWWTTTTTWWTTTTTWWTTTTTWW
-----WWTTTTVWWBTTTYWW

Original motif Consensus sequence:
WWWAAAAWWAAAAWAAAAWAAAAHWW



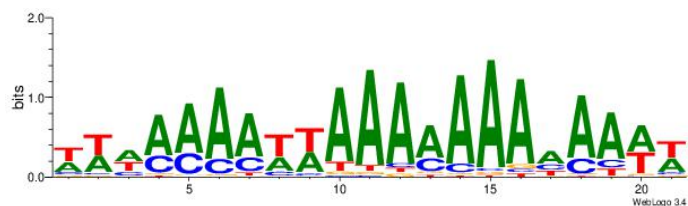
Reverse complement motif Consensus sequence:
WWHTTTTWWTTTTTWWTTTTTWWTTTTTWW



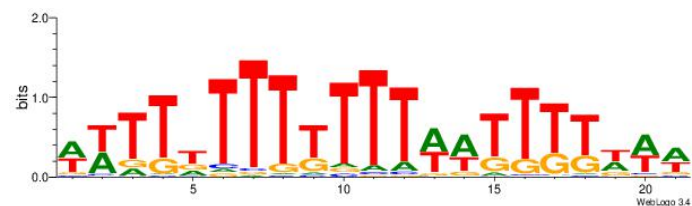
Dataset #: 1
Motif ID: 10
Motif name: C010
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 17
Similarity score: 0.0284807

Alignment:
WWWAAAAWWAAAAAAAAAAWW
WWMAAABWWVAAAWW----

Original motif Consensus sequence: WWWAAAWWAAAAAAAAAAWW



Reverse complement motif Consensus sequence: WWTTTTTTTTTTWWTTTTWWW

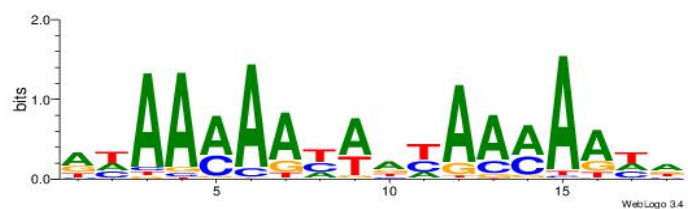


Dataset #: 1
Motif ID: 69
Motif name: C069
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 17
Similarity score: 0.0322212

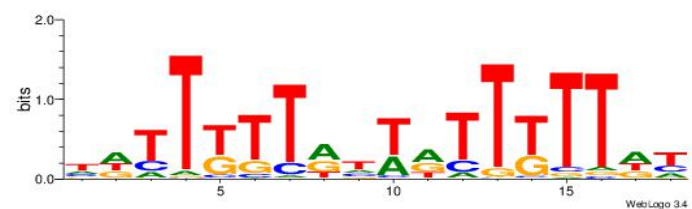
Alignment:

AHAAMAAYWDYAAMAAHD
WWMAAABWWWVAAAAWW-

Original motif Consensus sequence: AHAAMAAYWDYAAMAAHD



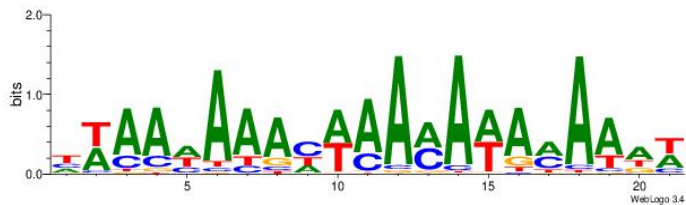
Reverse complement motif Consensus sequence: DHTTYTMDWMTTYTTHT



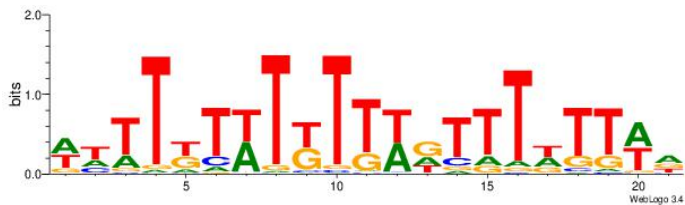
Dataset #: 1
Motif ID: 16
Motif name: C016
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 3
Number of overlap: 17
Similarity score: 0.0367806

Alignment:
HWAAWAAAHWAAMAWAMAAWW
--WWMAAABWWWVAAAAWW--

Original motif Consensus sequence: HWAAWAAAHWAAMAWAMAAWW



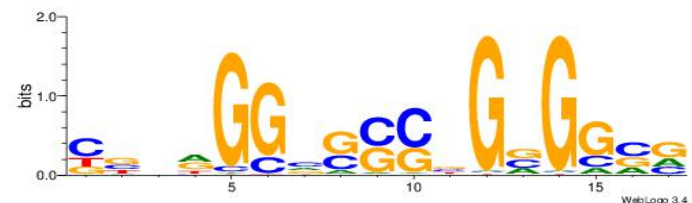
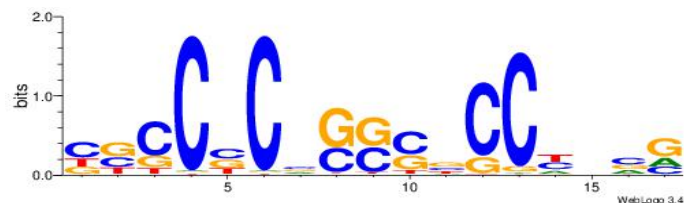
Reverse complement motif Consensus sequence: WWTYYTWYTTWDTTTWTTWH



Dataset #: 1 Motif ID: 140 Motif name: C140

Original motif Consensus sequence: BSCCBVSSSBCCYHVG

Reverse complement motif Consensus sequence: CVDMMGBSSSVGBGGSB



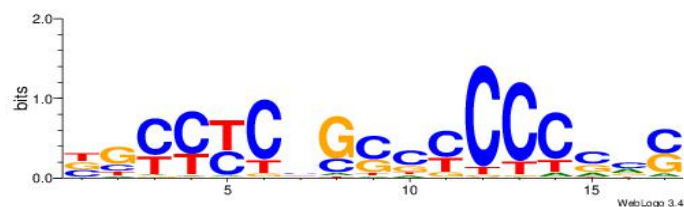
Best Matches for Motif ID 140 (Highest to Lowest)

Dataset #: 1
 Motif ID: 22
 Motif name: C022
 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: 0.00509294

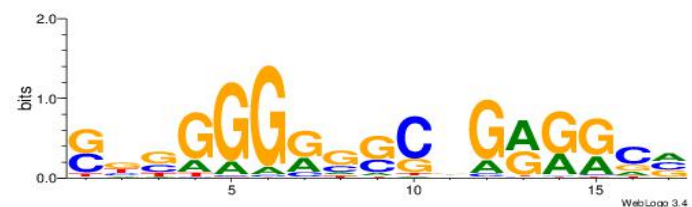
Alignment:

BGCCYCBGSCYCCCSVS
 BSCCBVCSSSBCCYHVG

Original motif Consensus sequence: BGCCYCBGSCYCCCSVS



Reverse complement motif Consensus sequence: SVSGGKGSCBGMGGCV

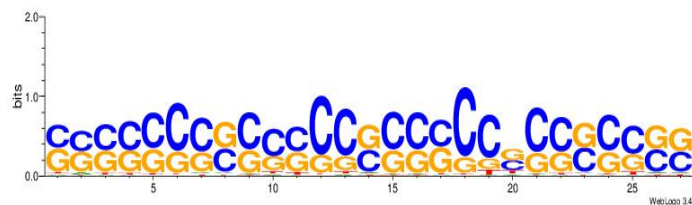


Dataset #: 1
 Motif ID: 4
 Motif name: C004
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 5
 Number of overlap: 17
 Similarity score: 0.00879579

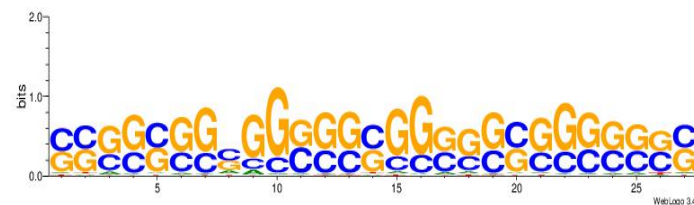
Alignment:

SSSSSSGSGGSSSSGGSSSSSGSSSSS
 ----CVDMGGBSSSVGBGGSB-----

Original motif Consensus sequence:
 SSSSSCSSSSCCSSSSCCSCSSSSSS



Reverse complement motif Consensus sequence:
 SSSSSSGSGGSSSSGGSSSSSGSSSSS

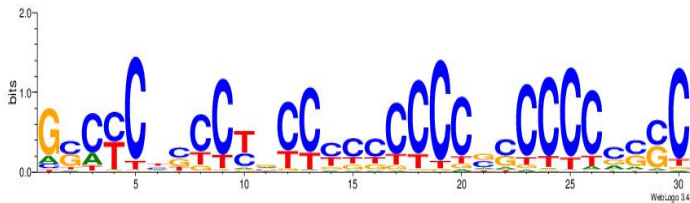


Dataset #: 1
 Motif ID: 3
 Motif name: C003
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 14

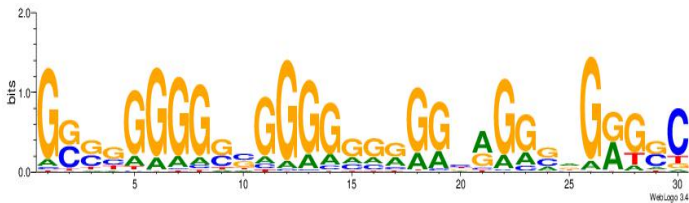
Number of overlap: 17
Similarity score: 0.0228159

Alignment:
GSCYCHSCCYVCCYCCCCCSCCCCCSSC
-----BSCCBVCVSSSBCCYHVG

Original motif Consensus sequence:
GSCYCHSCCYVCCYCCCCCSCCCCCSSC



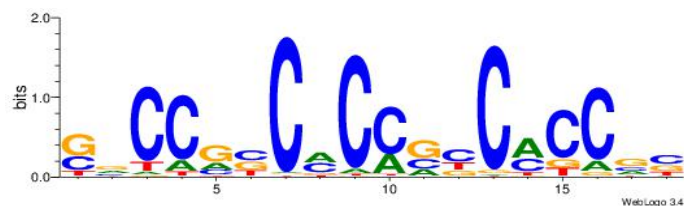
Reverse complement motif Consensus sequence:
GSSGGGGGSSGGGGGKGGVMGGSHGKGSC



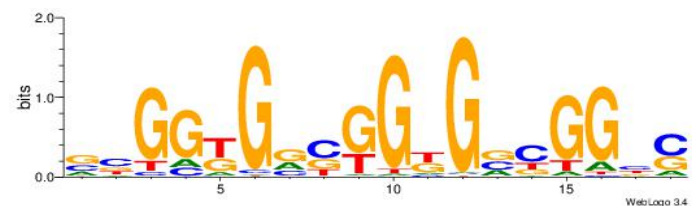
Dataset #: 1
Motif ID: 37
Motif name: C037
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 2
Number of overlap: 17
Similarity score: 0.0353839

Alignment:
BVGGYGKSGGYGBCGGVS
-CVDMGGBSSSVGBGGSB

Original motif Consensus sequence: SVCCGBCMCCSYCMCCVB



Reverse complement motif Consensus sequence: BVGGYGKSGGYGBCGGVS

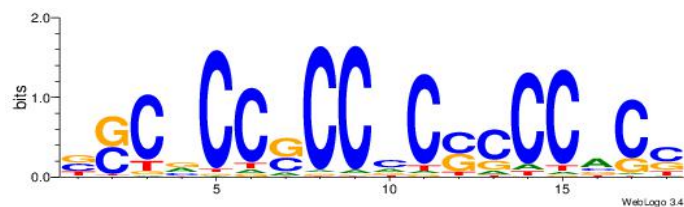


Dataset #: 1
Motif ID: 20
Motif name: C020
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 2
Number of overlap: 17
Similarity score: 0.0426992

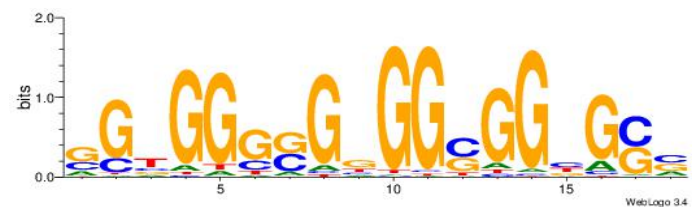
Alignment:

BSCVCCSCCVSCCCACS
-BSCCBVSSSBCCYHVG

Original motif Consensus sequence: BSCVCCSCCVSCCCACS

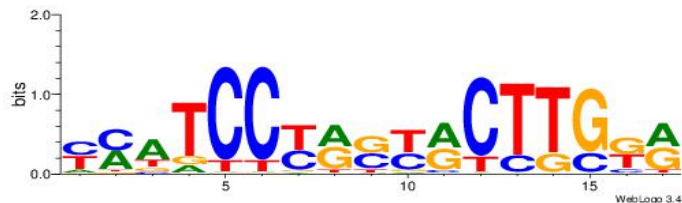


Reverse complement motif Consensus sequence: SGTGGGSGVGGSGGVGSB

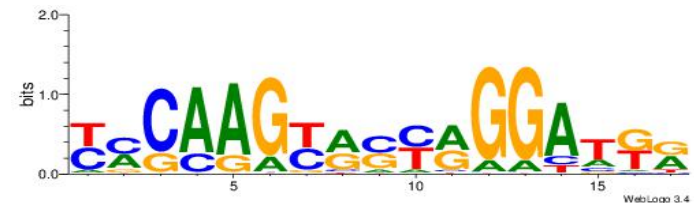


Dataset #: 1 Motif ID: 141 Motif name: C141

Original motif Consensus sequence: YMATCCYRSYRCTTGKR



Reverse complement motif Consensus sequence: KYCAAGKMSKMGGATRK



Best Matches for Motif ID 141 (Highest to Lowest)

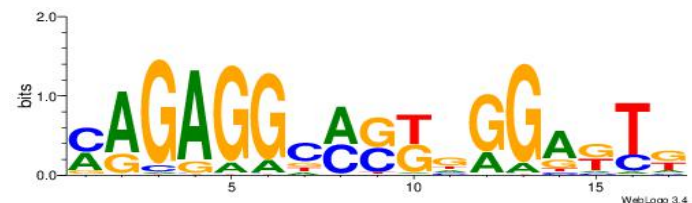
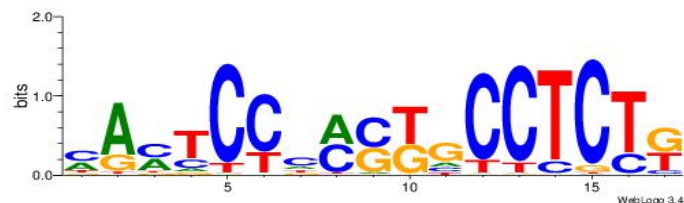
Dataset #:	1
Motif ID:	66
Motif name:	C066
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	17
Similarity score:	0.0228971

Alignment:

MAMTCCCMSKGCCTCTK
YMATCCYRSYRCTTGKR

Original motif Consensus sequence: MAMTCCCMSKGCCTCTK

Reverse complement motif Consensus sequence: YAGAGGCRSYGGGATRK



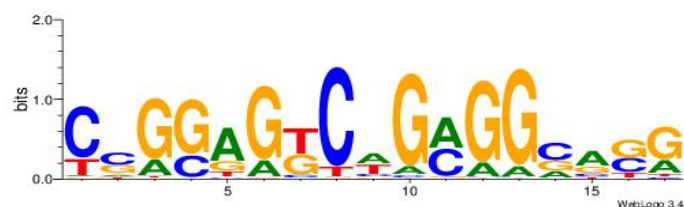
Dataset #: 1
 Motif ID: 86
 Motif name: C086
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 17
 Similarity score: 0.0390911

Alignment:

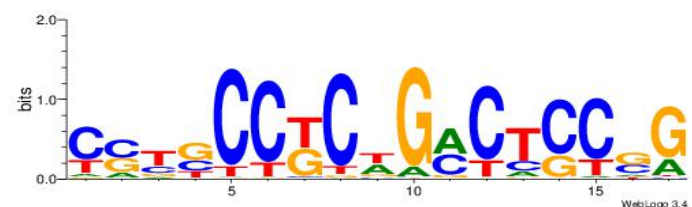
CSTSCCYCWGRCTCCSG

YMATCCYRSYRCTTGKR

Original motif Consensus sequence: CSGGAGKCWGMGGSASG



Reverse complement motif Consensus sequence: CSTSCCYCWGRCTCCSG



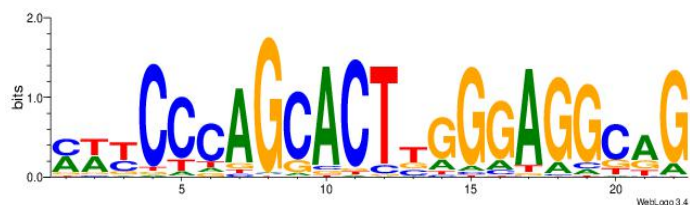
Dataset #: 1

Motif ID: 19
 Motif name: C019
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3
 Number of overlap: 17
 Similarity score: 0.0403604

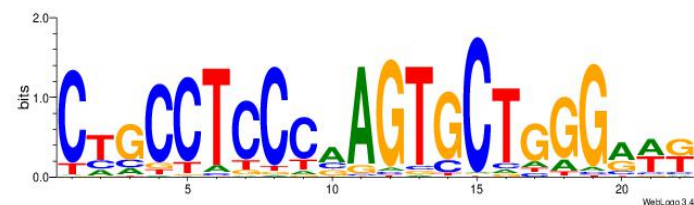
Alignment:

MWYCCCAGCACTTGGGAGGCAG
 ---KYCAAGKMSKMGGATRK--

Original motif Consensus sequence: MWYCCCAGCACTTGGGAGGCAG



Reverse complement motif Consensus sequence: CTGCCTCCCAAGTGCTGGGMWR

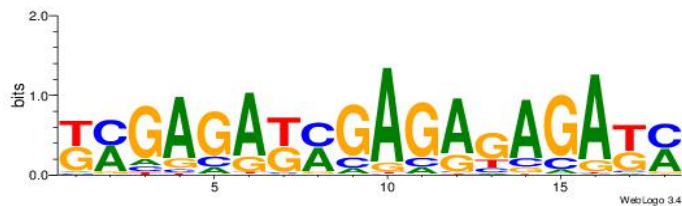


Dataset #: 1
 Motif ID: 11
 Motif name: C011
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 17

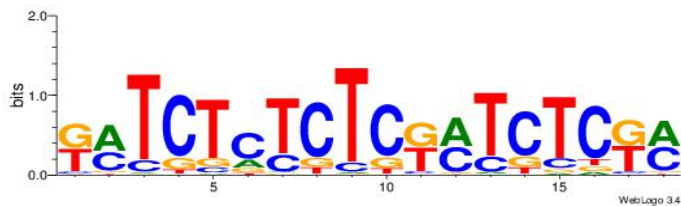
Similarity score: 0.0423875

Alignment:
RRTCTCTCTCRRTCTCRR
YMATCCYRSYRCTTGKR-

Original motif Consensus sequence: KMGAGAKMGAGAGAGAKM



Reverse complement motif Consensus sequence: RRTCTCTCTCRRTCTCRR

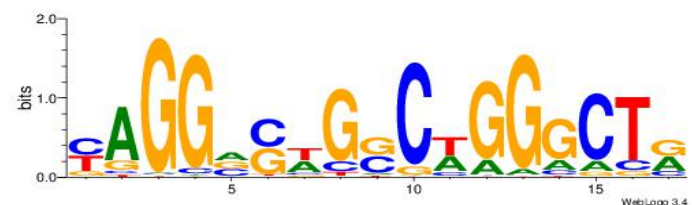
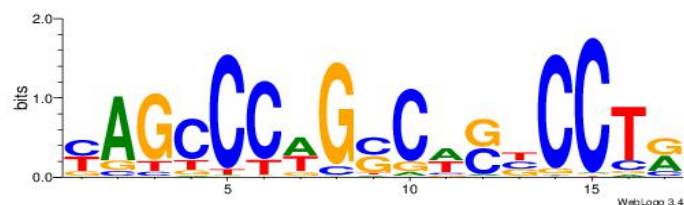


Dataset #: 1
Motif ID: 122
Motif name: C122
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 17
Similarity score: 0.0437955

Alignment:
YAGCCCWGSCWSBCCTR
YMATCCYRSYRCTTGKR

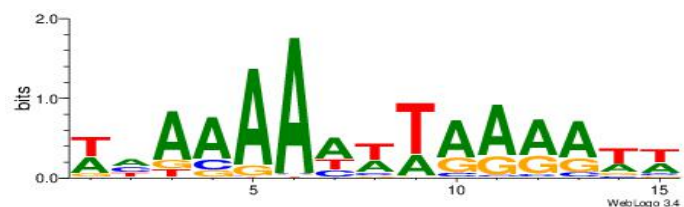
Original motif Consensus sequence: YAGCCCWGSCWSBCCTR

Reverse complement motif Consensus sequence: MAGGVSWGSCWGGGCTK

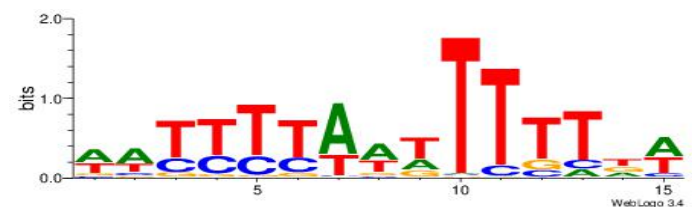


Dataset #: 1 Motif ID: 142 Motif name: C142

Original motif Consensus sequence: WHAAAAWTAAAWW



Reverse complement motif Consensus sequence: WTTTTATTTTTHW



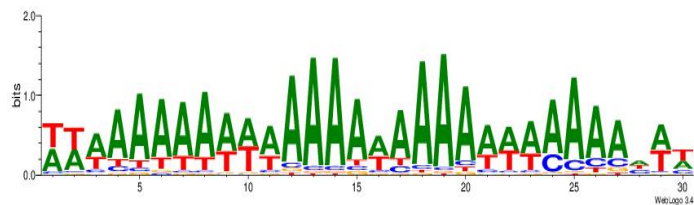
Best Matches for Motif ID 142 (Highest to Lowest)

Dataset #:	1
Motif ID:	1
Motif name:	C001
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	15
Number of overlap:	15
Similarity score:	0.0224897

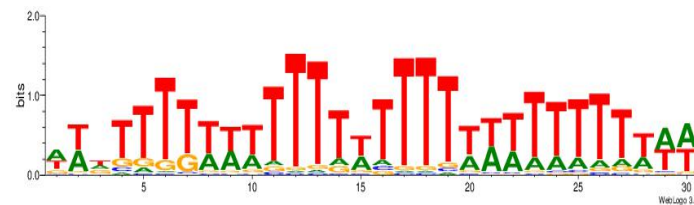
Alignment:

WWWAAAAAWWAAAAAWAAAAWWAAAAHWW
 -----WHAAAAAWTAAAAWW-----

Original motif Consensus sequence:
 WWWAAAAAWWAAAAAWAAAAWWAAAAHWW



Reverse complement motif Consensus sequence:
 WWHTTTTWWTTTTTWT TTTTWWTTTTTWWW

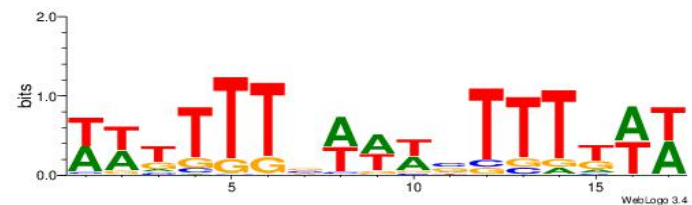


Dataset #:	1
Motif ID:	139
Motif name:	C139
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	15
Similarity score:	0.0287265

Alignment:
 WWMAAABWWWVAAA
 WW-----WHAAAAAWTAAAAWW-----

Original motif Consensus sequence: WWMAAABWWWVAAA

Reverse complement motif Consensus sequence:
 WWTTTTVWWBTTTYWW

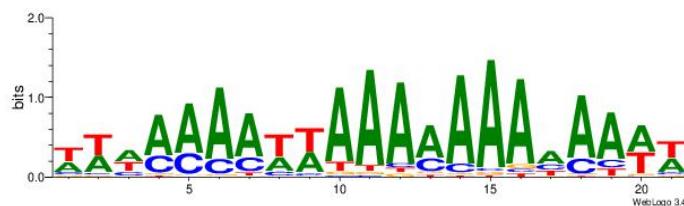


Dataset #:	1
Motif ID:	10
Motif name:	C010
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	7
Number of overlap:	15
Similarity score:	0.0345401

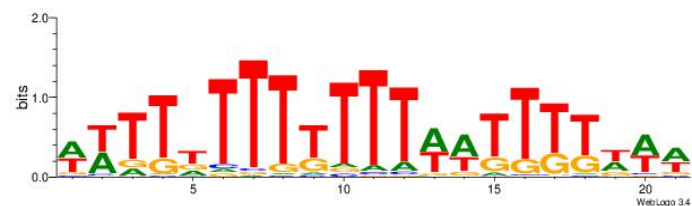
Alignment:

WWTTTTTTTTWWTTTTWWW
-----WTTTTTAWTTTTTHW

Original motif Consensus sequence: WWWAAAWWAAAAAAAAAAWW



Reverse complement motif Consensus sequence:
WWTTTTTTTTTWWTTTWWW

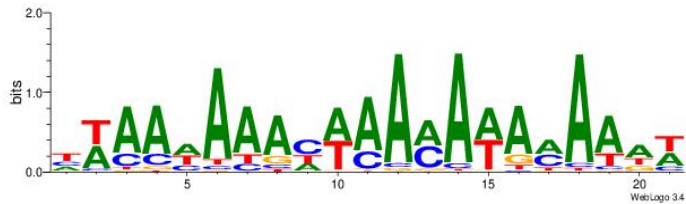


Dataset #: 1

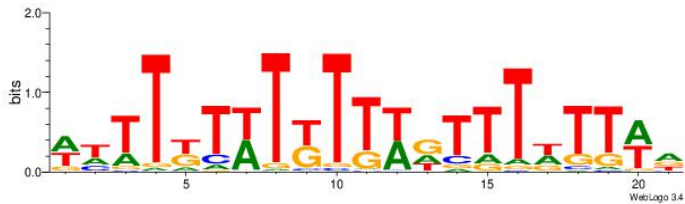
Motif ID: 16
Motif name: C016
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 2
Number of overlap: 15
Similarity score: 0.0359582

Alignment:
HWAAWAAAHWAAMAWAMAAWW
-WHAAAAAWTAAAAWW-----

Original motif Consensus sequence: HWAAWAAAHWAAMAWAMAAWW



Reverse complement motif Consensus sequence: WWTYYTWYTTWDTTWTWH

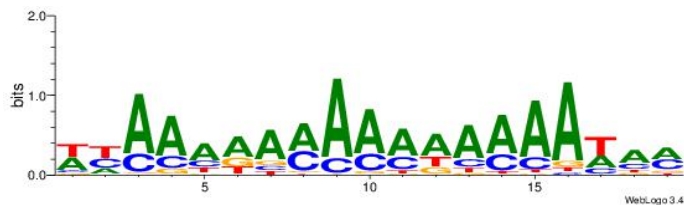


Dataset #: 1
Motif ID: 30
Motif name: C030
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 2
Number of overlap: 15

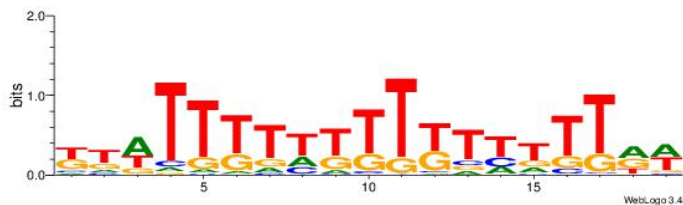
Similarity score: 0.0374284

Alignment:
YTWTTTTTTTTYTTTTMW
-WTTTTAWTTTTTHW---

Original motif Consensus sequence: WYAAAAAAMAAAAAAAWAM

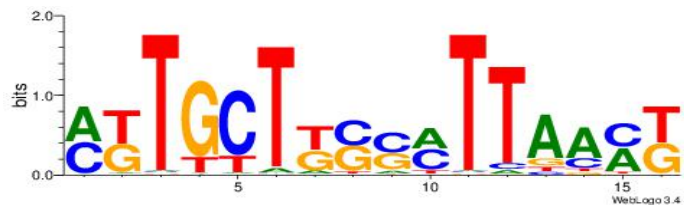


Reverse complement motif Consensus sequence: YTWTTTTTTTTYTTTTMW

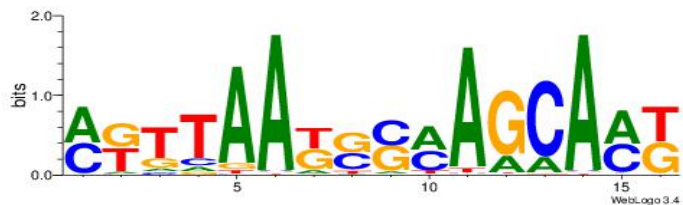


Dataset #: 1 Motif ID: 143 Motif name: C143

Original motif Consensus sequence: MKTGCTKSSMTTAAMK



Reverse complement motif Consensus sequence: RRTTAAYSSRAGCARY



Best Matches for Motif ID 143 (Highest to Lowest)

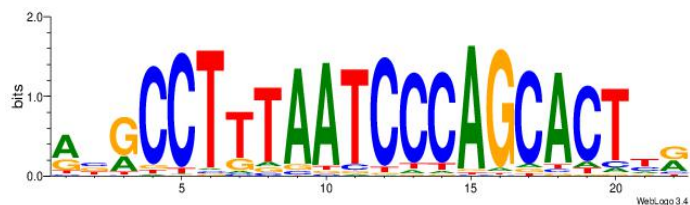
Dataset #:	1
Motif ID:	9
Motif name:	C009
Matching format of first motif:	Reverse Complement

Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	3
Number of overlap:	16
Similarity score:	0.00936417

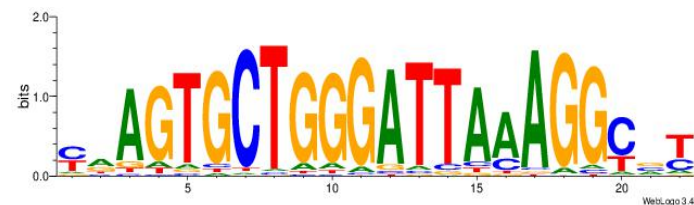
Alignment:

```
ABGCCTTTAATCCCAGCACTHR
--RRTTAAYSSRAGCARY----
```

Original motif Consensus sequence: ABGCCTTTAATCCCAGCACTHR



Reverse complement motif Consensus sequence: MHAGTGCTGGGATTAAAGGCBT

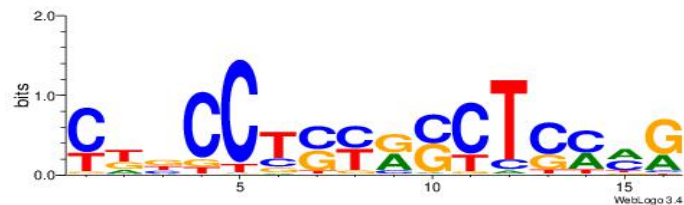


Dataset #:	1
Motif ID:	83
Motif name:	C083
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	16
Similarity score:	0.0450232

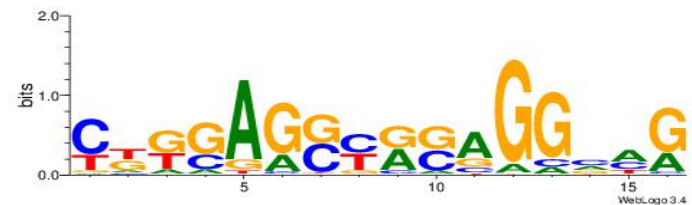
Alignment:

CKBCCTSYRSCTCMMG
MKTGCTKSSMTTAAMK

Original motif Consensus sequence: CKBCCTSYRSCTCMMG



Reverse complement motif Consensus sequence: CYRGAGSMKSAGGBRG



Dataset #:	1
Motif ID:	10
Motif name:	C010
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	16
Similarity score:	0.0471925

Alignment:

WWTTTTTTTTTTWWTTTTWWW
-----MKTGCTKSSMTTAAMK

Original motif Consensus sequence: WWWAAAWWAAAAAAAAAAWW

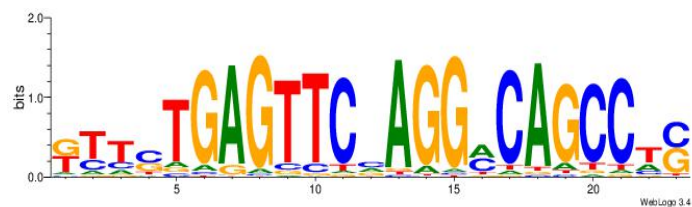
Reverse complement motif Consensus sequence: WWTTTTTTTTTTWWTTTTWWW

Motif ID: 7
 Motif name: C007
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 8
 Number of overlap: 16
 Similarity score: 0.0537183

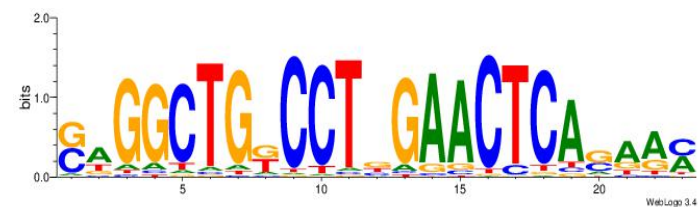
Alignment:

KTTSTGAGTTCVAGGMCAGCCTS
 RRTTAAYSSRAGCARY-----

Original motif Consensus sequence: KTTSTGAGTTCVAGGMCAGCCTS

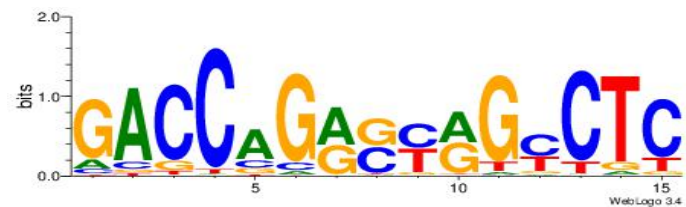


Reverse complement motif Consensus sequence: SAGGCTGYCCTVGAAGTCASAAY

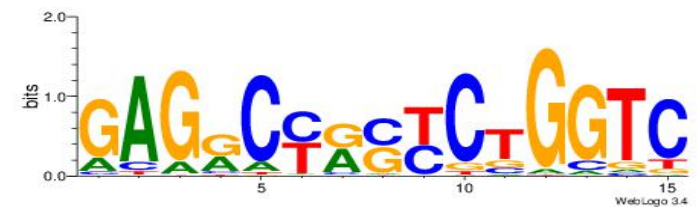


Dataset #: 1 Motif ID: 144 Motif name: C144

Original motif Consensus sequence: GACCAGRSYRGYCTC



Reverse complement motif Consensus sequence: GAGKCKKSKCTGG



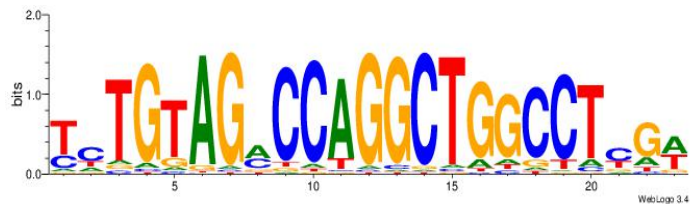
Best Matches for Motif ID 144 (Highest to Lowest)

Dataset #: 1
Motif ID: 5
Motif name: C005
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 3
Number of overlap: 15
Similarity score: 0.0065429

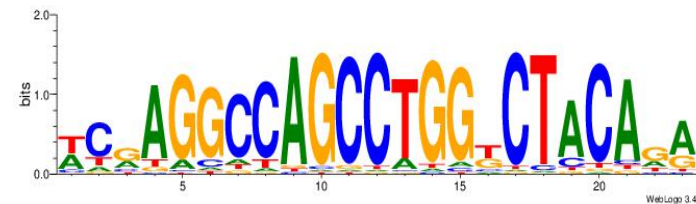
Alignment:

```
TCTGTAGMCCAGGCTGGCCTYGW  
-----GACCAGRSYRGYCTC--
```

Original motif Consensus sequence: TCTGTAGMCCAGGCTGGCCTYGW



Reverse complement motif Consensus sequence:
WCKAGGCCAGCCTGGYCTACAGA

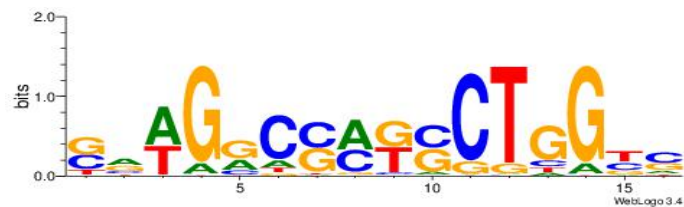


Dataset #: 1
Motif ID: 126
Motif name: C126
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif

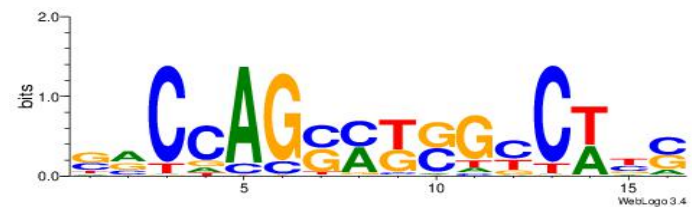
Direction: Forward
 Position number: 1
 Number of overlap: 15
 Similarity score: 0.019929

Alignment:
 SVWGRCSMKSTGGYS
 GAGKCKKSKCTGGTC-

Original motif Consensus sequence: SVWGRCSMKSTGGYS



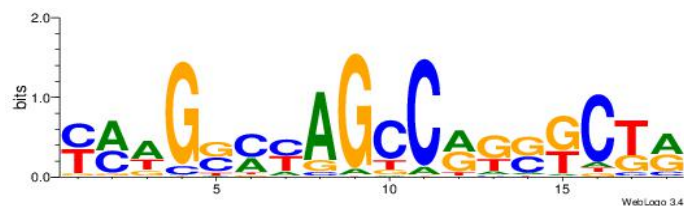
Reverse complement motif Consensus sequence: SMCCAGSYYSGMCWBS



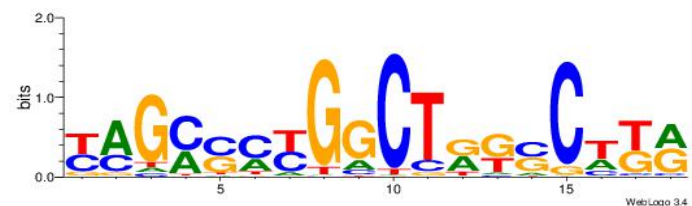
Dataset #: 1
 Motif ID: 73
 Motif name: C073
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 4
 Number of overlap: 15
 Similarity score: 0.033236

Alignment:
 KAGYSYKGGCTKRSCWYK
 GAGKCKKSKCTGGTC---

Original motif Consensus sequence: YMWGSMYAGCCRKSKCTR



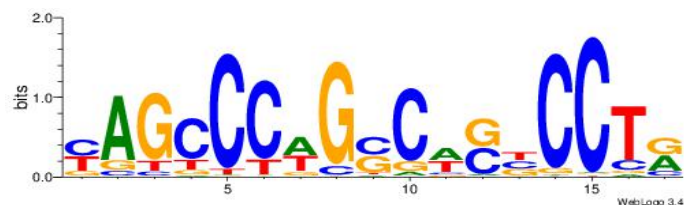
Reverse complement motif Consensus sequence: KAGYSYKGGCTKRSCWYK



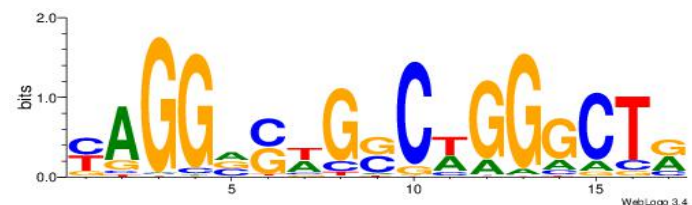
Dataset #: 1
 Motif ID: 122
 Motif name: C122
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 15
 Similarity score: 0.0344934

Alignment:
 MAGGVSWGSCWGGGCTK
 GAGKCKKSKCTGGTC--

Original motif Consensus sequence: YAGCCCWGSCWSBCCTR



Reverse complement motif Consensus sequence: MAGGVSWGSCWGGGCTK

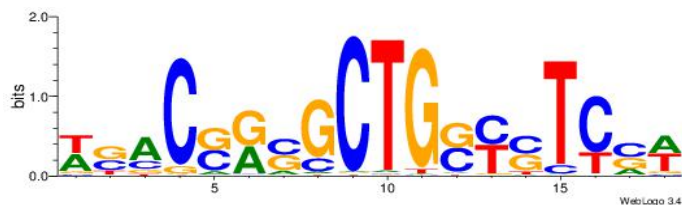


Dataset #: 1
 Motif ID: 124
 Motif name: C124
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 15
 Similarity score: 0.0354076

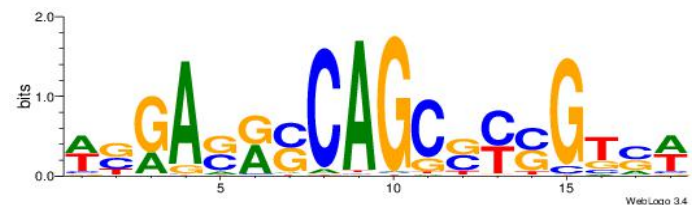
Alignment:

WSACSRSGCTGSYSTCSW
 -GACCAGRSYRGYCTC--

Original motif Consensus sequence: WSACSRSGCTGSYSTCSW



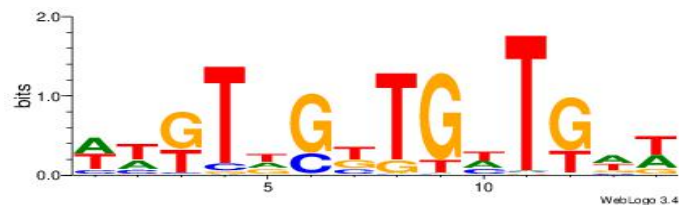
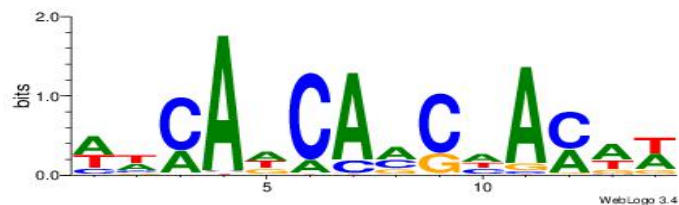
Reverse complement motif Consensus sequence: WSGASKSCAGCSMSGTSW



Dataset #: 1 Motif ID: 145 Motif name: C145

Original motif Consensus sequence: WWCADCAMCHAMWW

Reverse complement motif Consensus sequence: WWRTHGYTGDTGWW



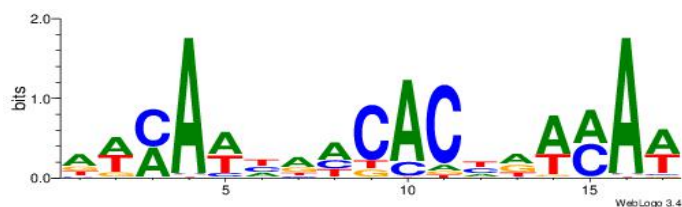
Best Matches for Motif ID 145 (Highest to Lowest)

Dataset #: 1
 Motif ID: 133
 Motif name: C133
 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: 0.0243182

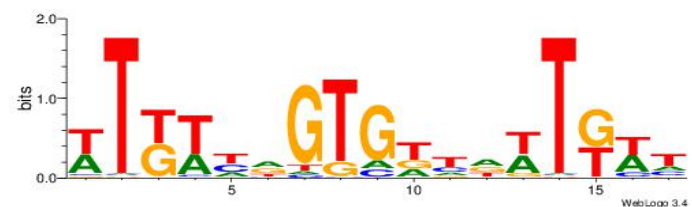
Alignment:

AWMAWHDACACHRWMAW
 WWCADCAMCHAMWW---

Original motif Consensus sequence: AWMAWHDACACHRWMAW



Reverse complement motif Consensus sequence: WT YWKHGTGTDHWTRWT

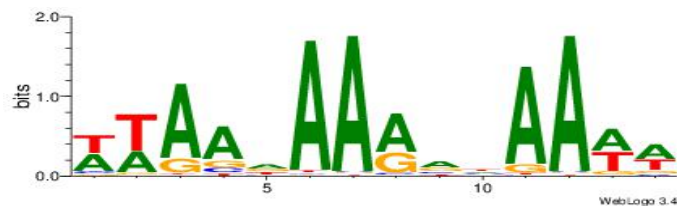


Dataset #: 1
 Motif ID: 131
 Motif name: C131
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0.0271953

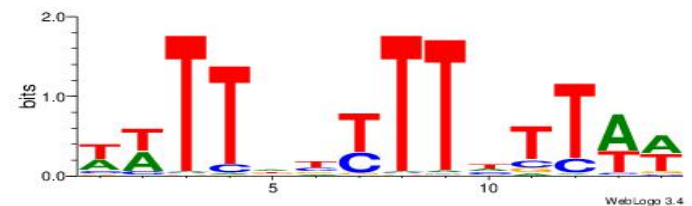
Alignment:

WWAADAARVHAAWW
 WWCADCAMCHAMWW

Original motif Consensus sequence: WWAADAARVHAAWW



Reverse complement motif Consensus sequence: WWTTHBKTTDTTV

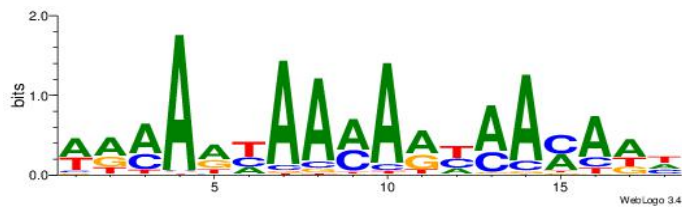


Dataset #: 1
 Motif ID: 57
 Motif name: C057
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 2
 Number of overlap: 14

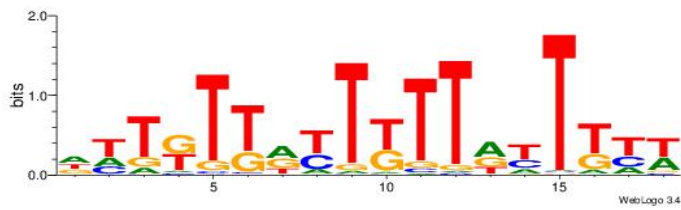
Similarity score: 0.0274615

Alignment:
WRMARYAAMARYAAMAWH
---WWCADCAMCHAMWW--

Original motif Consensus sequence: WRMARYAAMARYAAMAWH



Reverse complement motif Consensus sequence: HWTRTTMKTYTTMKTYKW

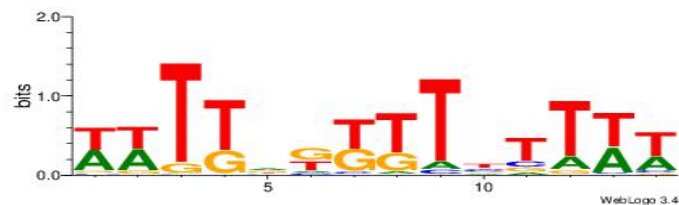
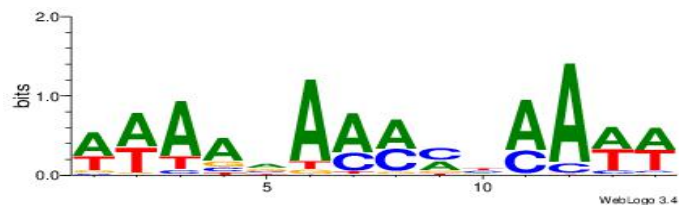


Dataset #: 1
Motif ID: 80
Motif name: C080
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 14
Similarity score: 0.0303459

Alignment:
WWAAVAAMMHAAWW
WWCADCAMCHAMWW

Original motif Consensus sequence: WWAAVAAMMHAAWW

Reverse complement motif Consensus sequence: WWTTHRYTTBTTW



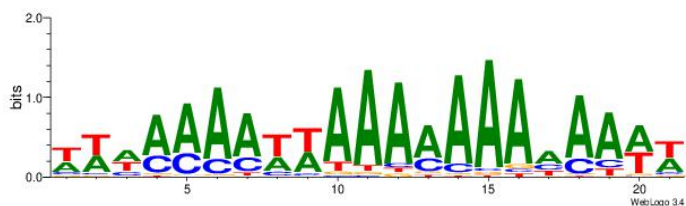
Dataset #: 1
 Motif ID: 10
 Motif name: C010
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0.0314437

Alignment:

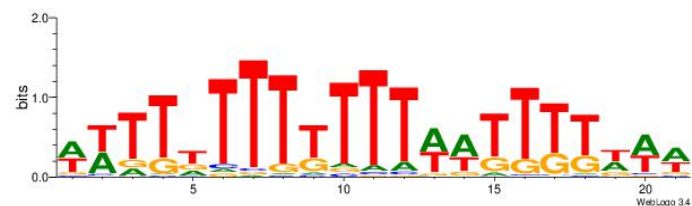
```

WWWAAAAWWAAAAAAAAAAWW
-----WWCADCAMCHAMWW
  
```

Original motif Consensus sequence: WWWAAAAWWAAAAAAAAAAWW

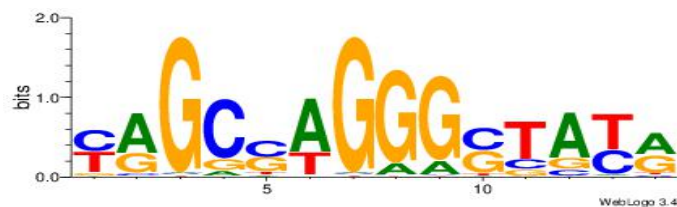


Reverse complement motif Consensus sequence: WWTTTTTTTTTTWWTTTTWWW

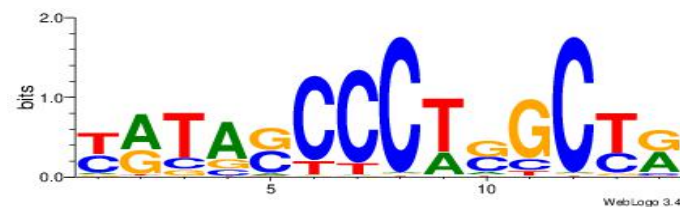


Dataset #: 1 Motif ID: 146 Motif name: C146

Original motif Consensus sequence: YRGCSAGGGSTAYR



Reverse complement motif Consensus sequence: KMTASCCCTSGCK



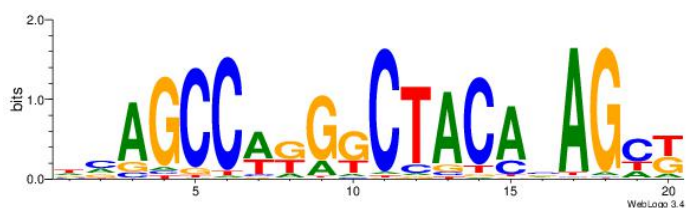
Best Matches for Motif ID 146 (Highest to Lowest)

Dataset #:	1
Motif ID:	15
Motif name:	C015
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	14
Similarity score:	0.0362427

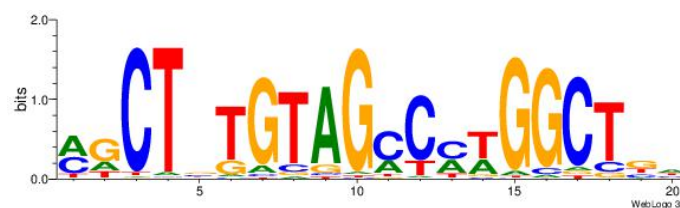
Alignment:

```
DVAGCCWKGCTACAVAGCK
-YRGCSAGGGSTAYR-----
```

Original motif Consensus sequence: DVAGCCWKGCTACAVAGCK



Reverse complement motif Consensus sequence: RGCTVTGTAGCCYWGGCTVD

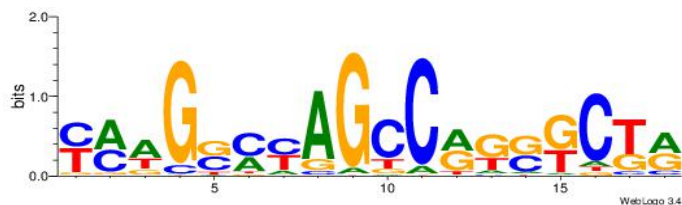


Dataset #: 1
 Motif ID: 73
 Motif name: C073
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0.0492759

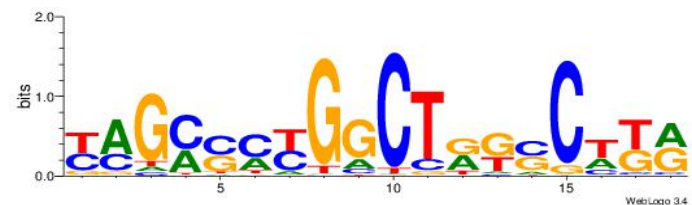
Alignment:

KAGYSYKGGCTKRSCWYK
 ----YRGCSAGGGSTAYR

Original motif Consensus sequence: YMWGSMYAGCCRKSKCTR



Reverse complement motif Consensus sequence: KAGYSYKGGCTKRSCWYK

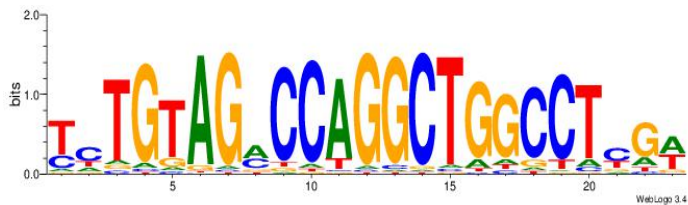


Dataset #: 1
 Motif ID: 5
 Motif name: C005
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 3

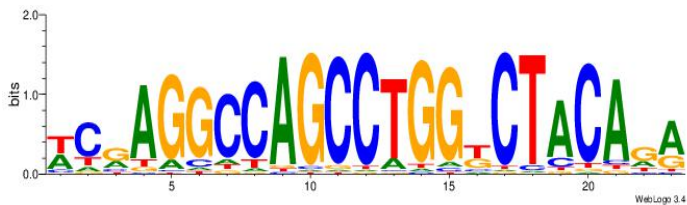
Number of overlap: 14
Similarity score: 0.0495866

Alignment:
TCTGTAGMCCAGGCTGGCCTYGW
-----KMTASCCCTSGCKK--

Original motif Consensus sequence: TCTGTAGMCCAGGCTGGCCTYGW



Reverse complement motif Consensus sequence: WCKAGGCCAGCCTGGYCTACAGA

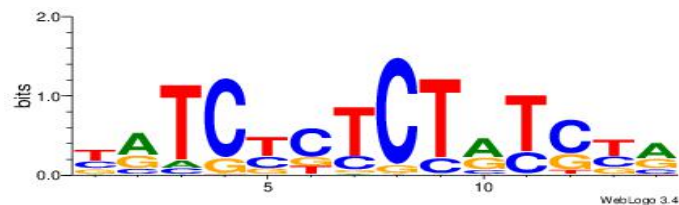


Dataset #: 1
Motif ID: 78
Motif name: C078
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 1
Number of overlap: 14
Similarity score: 0.050766

Alignment:
YRGAYAGAGRGAYR
YRGCSAGGGSTAYR

Original motif Consensus sequence: YRGAYAGAGRGAYR

Reverse complement motif Consensus sequence: KMTCKCTCTMTCK

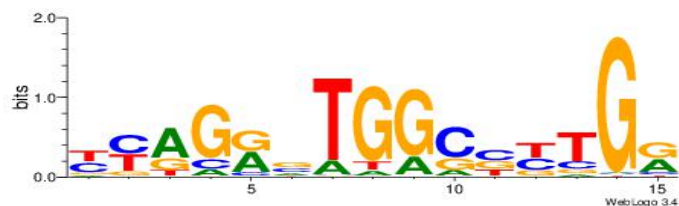


Dataset #: 1
 Motif ID: 153
 Motif name: C153
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 1
 Number of overlap: 14
 Similarity score: 0.0524832

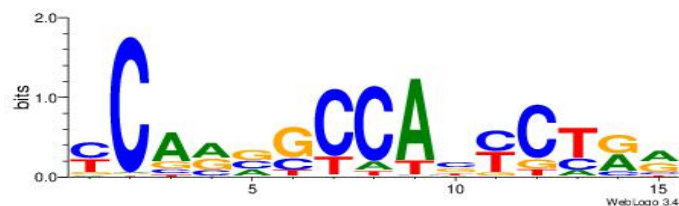
Alignment:

YYAGRVTTGGCBYTGR
 -YRGCSAGGGSTAYR

Original motif Consensus sequence: YYAGRVTTGGCBYTGR

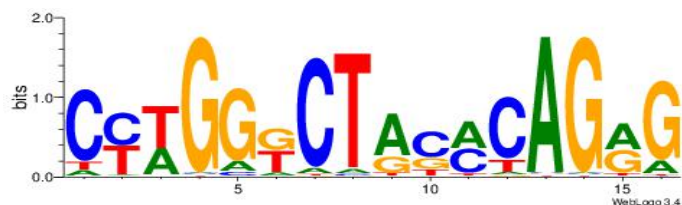


Reverse complement motif Consensus sequence: MCAMBGCCAVMCTKM

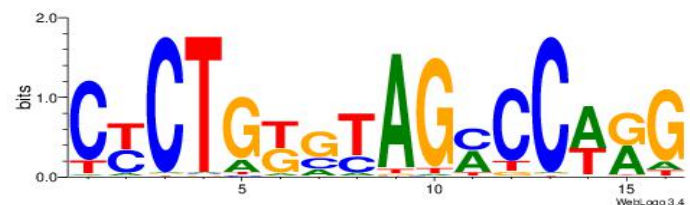


Dataset #: 1 Motif ID: 147 Motif name: C147

Original motif Consensus sequence: CYWGGKCTACMCAGRG



Reverse complement motif Consensus sequence: CKCTGYGTAGYCCWKG



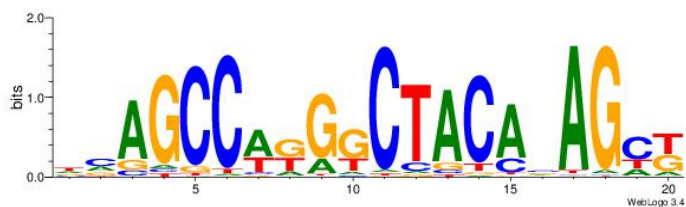
Best Matches for Motif ID 147 (Highest to Lowest)

Dataset #:	1
Motif ID:	15
Motif name:	C015
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	16
Similarity score:	0.0115213

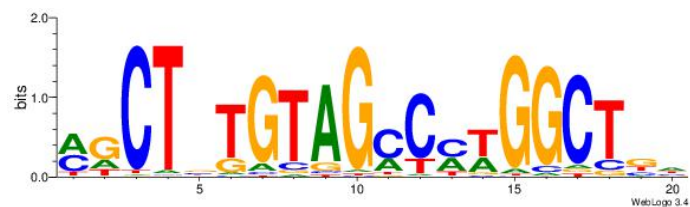
Alignment:

```
RGCTVTGTAGCCYWGGCTVD
CKCTGYGTAGYCCWKG----
```

Original motif Consensus sequence: DVAGCCWKGCTACAVAGCK



Reverse complement motif Consensus sequence: RGCTVTGTAGCCYWGGCTVD

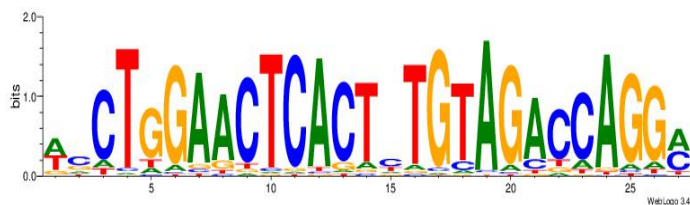


Dataset #: 1
 Motif ID: 13
 Motif name: C013
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 11
 Number of overlap: 16
 Similarity score: 0.0192602

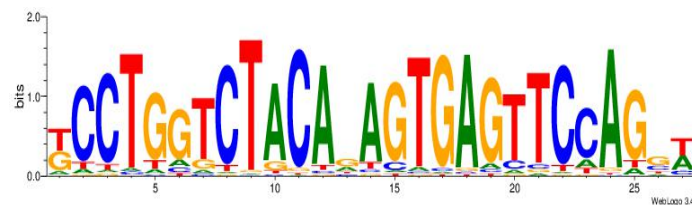
Alignment:

WVCTGGAAC TCACTHTGTAGACCAGGM
 -CKCTGYGTAGYCCWKG-----

Original motif Consensus sequence:
 WVCTGGAAC TCACTHTGTAGACCAGGM



Reverse complement motif Consensus sequence:
 YCCTGGTCTACADAGTGAGTTCCAGVW



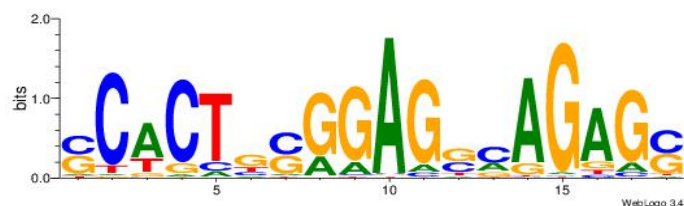
Dataset #: 1
 Motif ID: 34
 Motif name: C034
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward

Position number: 2
 Number of overlap: 16
 Similarity score: 0.044301

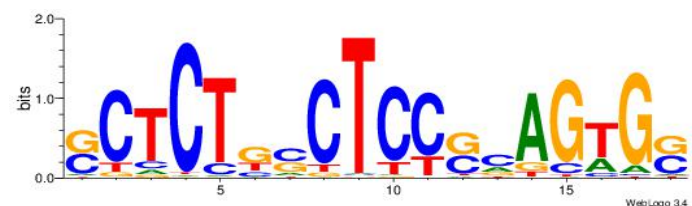
Alignment:

SCACTGSGGAGSMAGAGS
 -CKCTGYGTAGYCCWKG-

Original motif Consensus sequence: SCACTGSGGAGSMAGAGS



Reverse complement motif Consensus sequence: SCTCTRSCTCCSCAGTGS

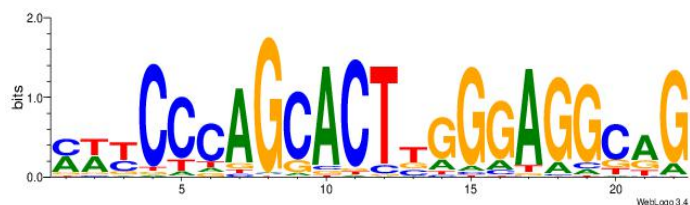


Dataset #: 1
 Motif ID: 19
 Motif name: C019
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 5
 Number of overlap: 16
 Similarity score: 0.0529944

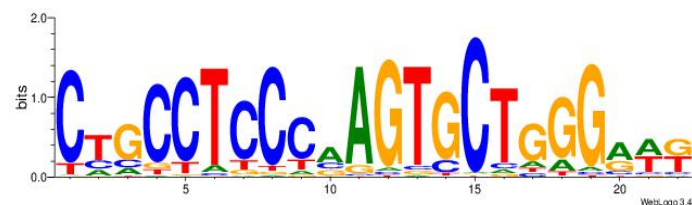
Alignment:

CTGCCTCCCAAGTGCTGGGMWR
 --CKCTGYGTAGYCCWKG----

Original motif Consensus sequence: MWYCCCAGCACTTGGGAGGCAG



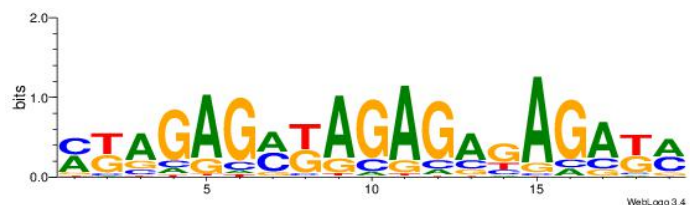
Reverse complement motif Consensus sequence: CTGCCTCCCAAGTGCTGGGMWR



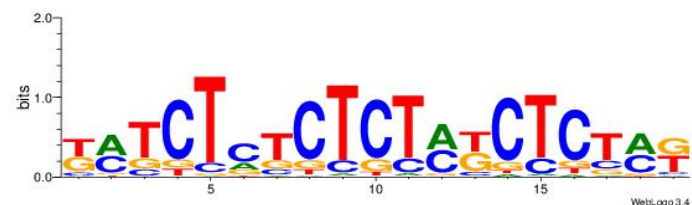
Dataset #: 1
 Motif ID: 12
 Motif name: C012
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 16
 Similarity score: 0.0557861

Alignment:
 MKAGAGMKAGAGAGAGAKM
 CYWGGKCTACMCAGRG---

Original motif Consensus sequence: MKAGAGMKAGAGAGAGAKM

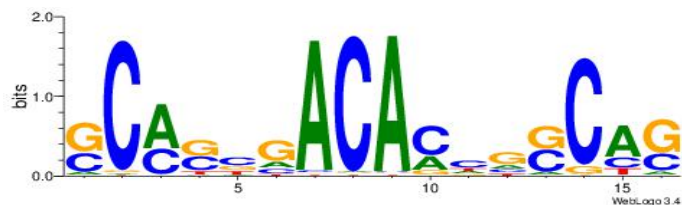


Reverse complement motif Consensus sequence: YRTCTCTCTRYCTCTRR

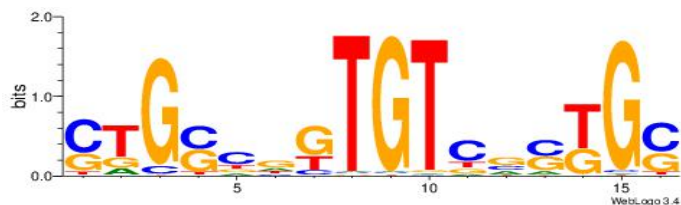


Dataset #: 1 Motif ID: 148 Motif name: C148

Original motif Consensus sequence: SCMSBGACACHGSCAS



Reverse complement motif Consensus sequence: STGSCDGTGTCBSYGS



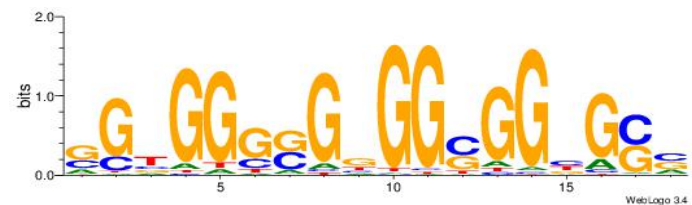
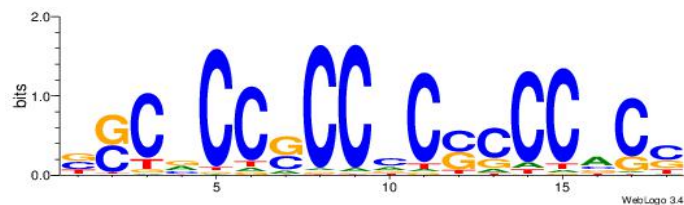
Best Matches for Motif ID 148 (Highest to Lowest)

Dataset #:	1
Motif ID:	20
Motif name:	C020
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:	0.047924

Alignment:
BSCVCCSCCVCSCCCACS
-SCMSBGACACHGSCAS-

Original motif Consensus sequence: BSCVCCSCCVCSCCCACS

Reverse complement motif Consensus sequence: SGTGGGSGVGGSGGVGSB

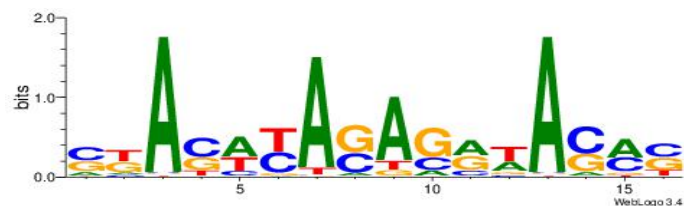


Dataset #: 1
 Motif ID: 125
 Motif name: C125
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 1
 Number of overlap: 16
 Similarity score: 0.0517915

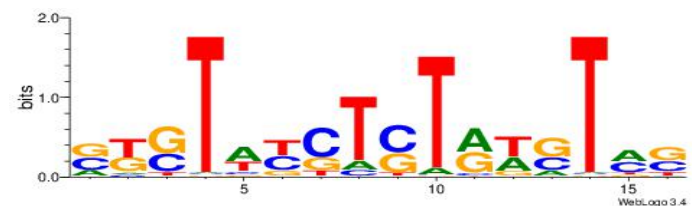
Alignment:

SYSTWKCTSTMWSTRS
 STGSCDGTGTCBSYGS

Original motif Consensus sequence: SKASWYASAGRWASMS



Reverse complement motif Consensus sequence: SYSTWKCTSTMWSTRS



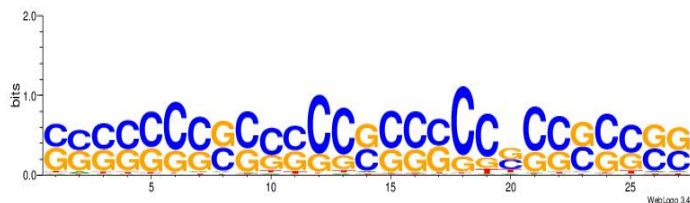
Dataset #: 1

Motif ID: 4
 Motif name: C004
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 5
 Number of overlap: 16
 Similarity score: 0.054196

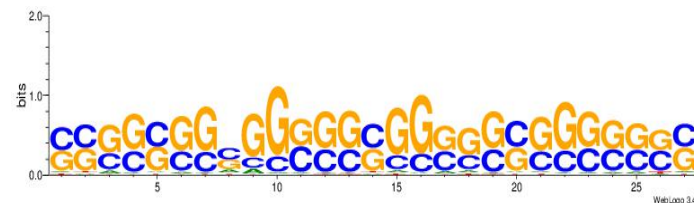
Alignment:

SSSSSCSSSSSCSSSSCCSCSSSSSS
 ----SCMSBGACACHGSCAS-----

Original motif Consensus sequence:
 SSSSSCSSSSSCSSSSCCSCSSSSSS



Reverse complement motif Consensus sequence:
 SSSSSSGSGGSSSSGGSSSSSGSSSSS

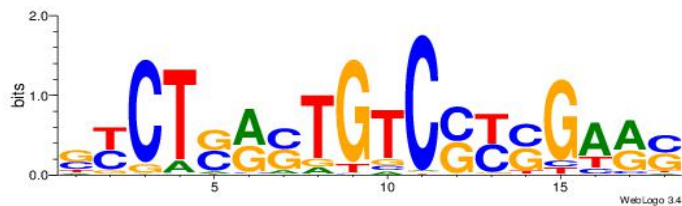


Dataset #: 1
 Motif ID: 128
 Motif name: C128
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 16

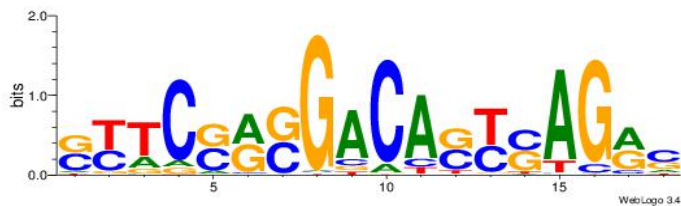
Similarity score: 0.0545529

Alignment:
SKTCSMSGACASKSAGMS
SCMSBGACACHGSCAS--

Original motif Consensus sequence: SYCTSRSTGTCSYSGARS



Reverse complement motif Consensus sequence: SKTCSMSGACASKSAGMS

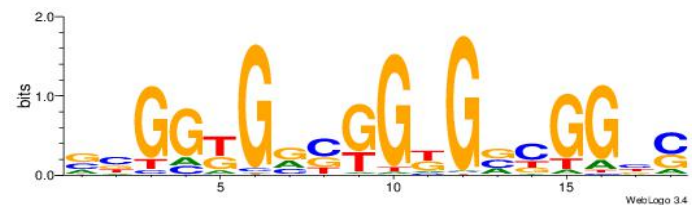
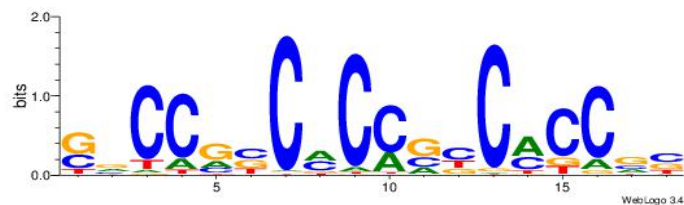


Dataset #: 1
Motif ID: 37
Motif name: C037
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 2
Number of overlap: 16
Similarity score: 0.056153

Alignment:
SVCCGBCMCCSYCMCCVB
-SCMSBGACACHGSCAS-

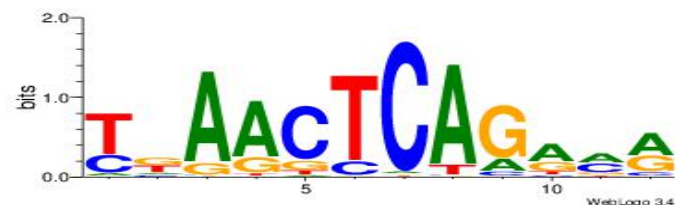
Original motif Consensus sequence: SVCCGBCMCCSYCMCCVB

Reverse complement motif Consensus sequence: BVGGYGKSGGYBCGGVS

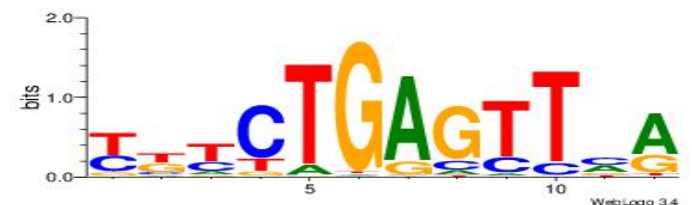


Dataset #: 1 Motif ID: 149 Motif name: C149

Original motif Consensus sequence: TKA⁺ACTCAGRMR



Reverse complement motif Consensus sequence: KYKCTGAGTTYA



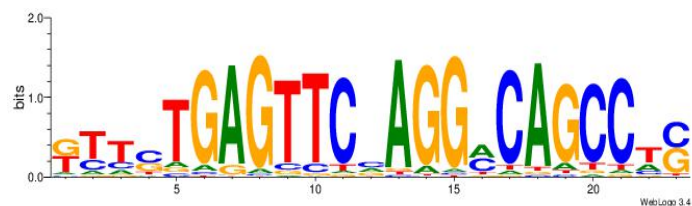
Best Matches for Motif ID 149 (Highest to Lowest)

Dataset #:	1
Motif ID:	7
Motif name:	C007
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:	0.00192863

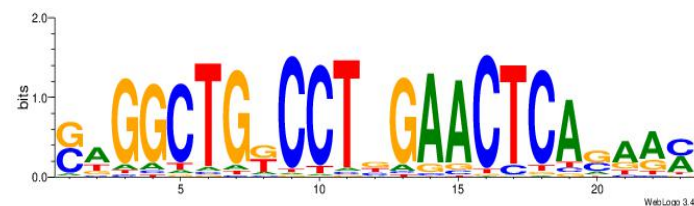
Alignment:

```
SAGGCTGYCCTVGA+ACTCASAAY
TKA+ACTCAGRMR-----
```

Original motif Consensus sequence: KTTSTGAGTTCVAGGMCAGCCTS



Reverse complement motif Consensus sequence: SAGGCTGYCCTVGAAGTCASAAY

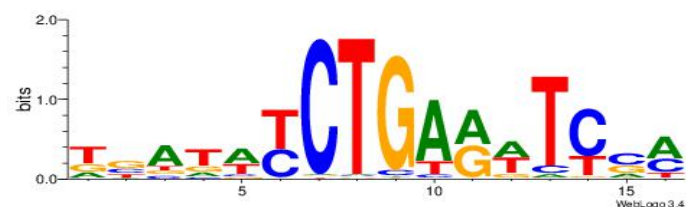


Dataset #: 1
Motif ID: 111
Motif name: C111
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 2
Number of overlap: 12
Similarity score: 0.0163139

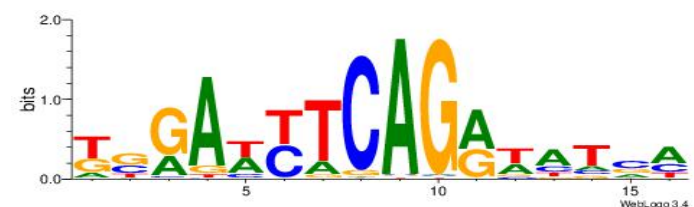
Alignment:

YSGAWKTCAGMWATBA
---TKAACTCAGRMR-

Original motif Consensus sequence: TBATWYCTGARWTCSM



Reverse complement motif Consensus sequence: YSGAWKTCAGMWATBA

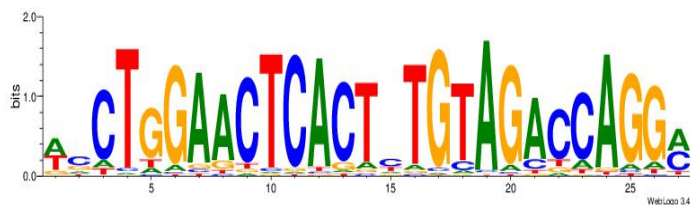


Dataset #: 1
 Motif ID: 13
 Motif name: C013
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 5
 Number of overlap: 12
 Similarity score: 0.0390326

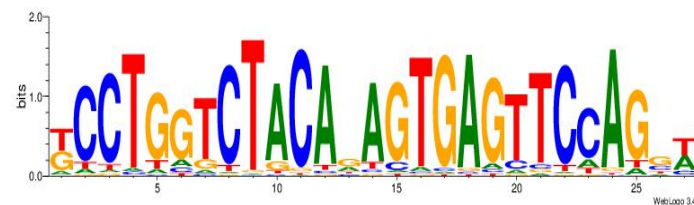
Alignment:

YCCTGGTCTACADAGTGAGTTCCAGVW
 -----KYKCTGAGTTYA-----

Original motif Consensus sequence:
 WVCTGGAAC TCACTHTGTAGACCAGGM



Reverse complement motif Consensus sequence:
 YCCTGGTCTACADAGTGAGTTCCAGVW

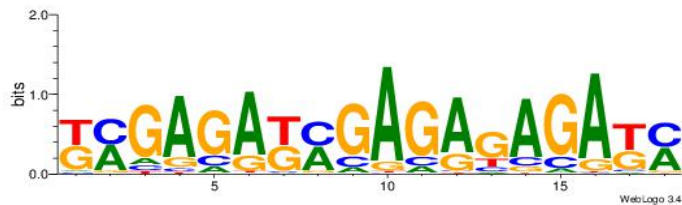


Dataset #: 1
 Motif ID: 11
 Motif name: C011
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 5

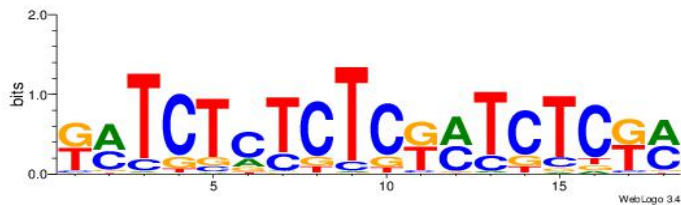
Number of overlap: 12
Similarity score: 0.0416873

Alignment:
RRTCTCTCTCRRTCTCRR
----KYKCTGAGTTYA--

Original motif Consensus sequence: KMGAGAKMGAGAGAGAKM



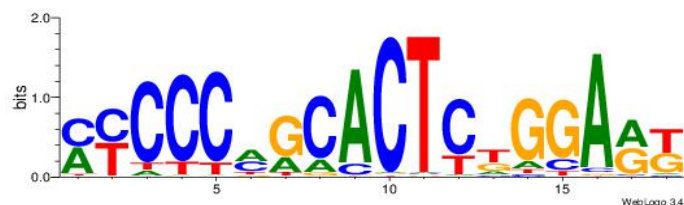
Reverse complement motif Consensus sequence: RRTCTCTCTCRRTCTCRR



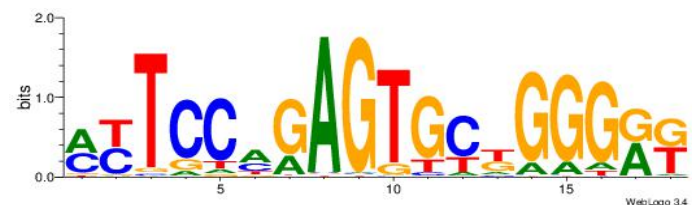
Dataset #: 1
Motif ID: 99
Motif name: C099
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 6
Number of overlap: 12
Similarity score: 0.0437108

Alignment:
MYCCCMGCACTCKGGARK
-----TKAACTCAGRMR-

Original motif Consensus sequence: MYCCCMGCACTCKGGARK

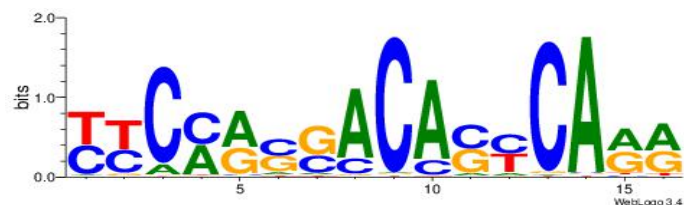


Reverse complement motif Consensus sequence: RKTCCRGAGTGCYGGGKR

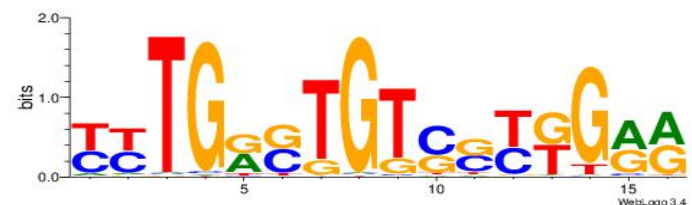


Dataset #: 1 Motif ID: 150 Motif name: C150

Original motif Consensus sequence: YYCMRSSACASYCARR



Reverse complement motif Consensus sequence: KKTGKSTGTSSKRGMM



Best Matches for Motif ID 150 (Highest to Lowest)

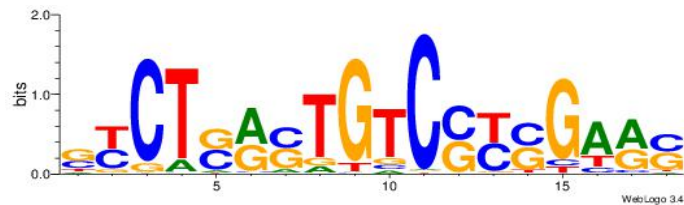
Dataset #:	1
Motif ID:	128
Motif name:	C128
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	16
Similarity score:	0.0371715

Alignment:

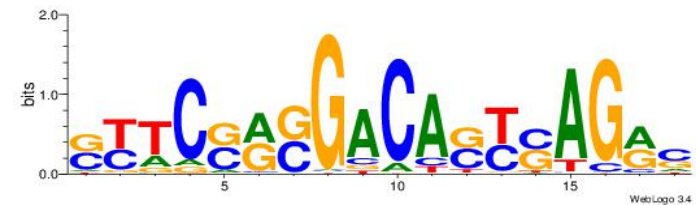
SYCTSRSTGTCSYSGARS

-KKTGKSTGTSSKRGMM-

Original motif Consensus sequence: SYCTSRSTGTCSYSGARS



Reverse complement motif Consensus sequence: SKTCSMSGACASKSAGMS



Dataset #:	1
Motif ID:	28
Motif name:	C028
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	16
Similarity score:	0.0497147

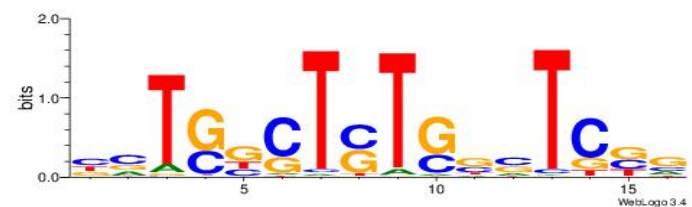
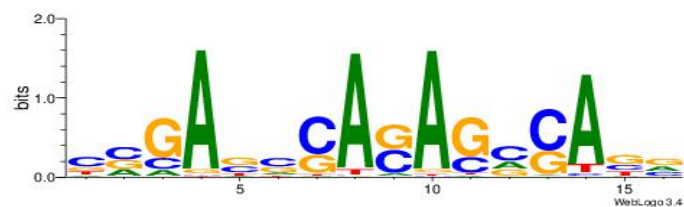
Alignment:

BVGASSCASAGVSABV

YYCMRSSACASYCARR

Original motif Consensus sequence: BVGASSCASAGVSABV

Reverse complement motif Consensus sequence: VBTSVCTSTGSSTCVB

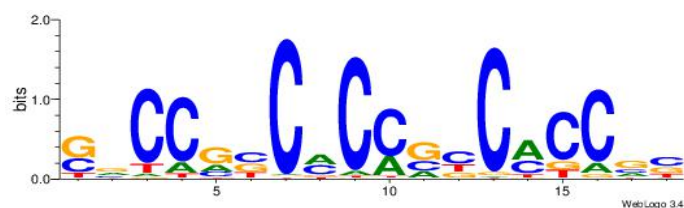


Dataset #:	1
Motif ID:	37
Motif name:	C037
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	16
Similarity score:	0.0545002

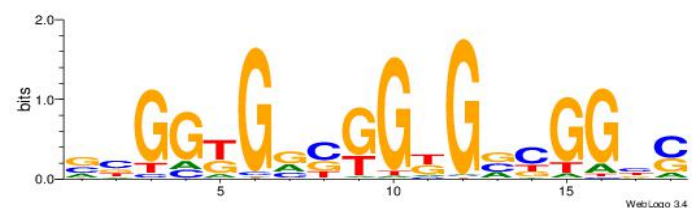
Alignment:

```
BVGGYGKSGGYGBCGGVS
--KKTGKSTGTSSKRGMM
```

Original motif Consensus sequence: SVCCGBCMCCSYCMCCVB



Reverse complement motif Consensus sequence:
BVGGYGKSGGYBCGGVS



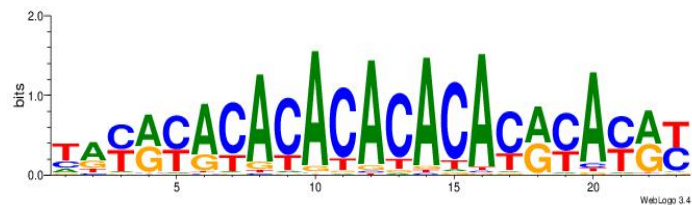
Dataset #: 1

Motif ID: 2
 Motif name: C002
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 8
 Number of overlap: 16
 Similarity score: 0.0550247

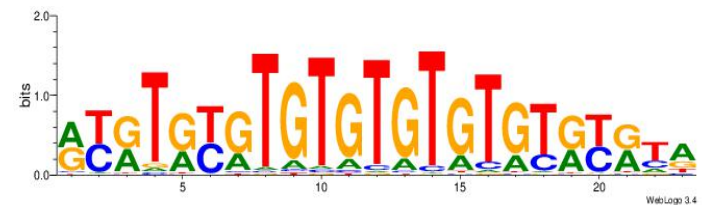
Alignment:

MKKTKKGTGTGTGTGTGTTKKTA
 -----KKTGKSTGTSSKRGMM

Original motif Consensus sequence: TAYRYACACACACACRYAYRY



Reverse complement motif Consensus sequence: MKKTKKGTGTGTGTGTGTTKKTA

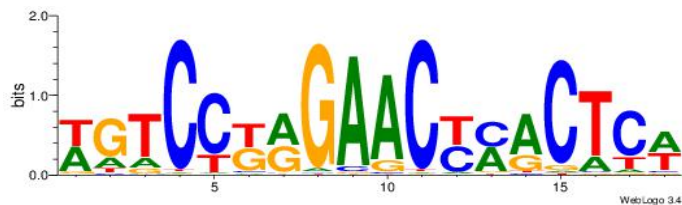


Dataset #: 1
 Motif ID: 42
 Motif name: C042
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 16

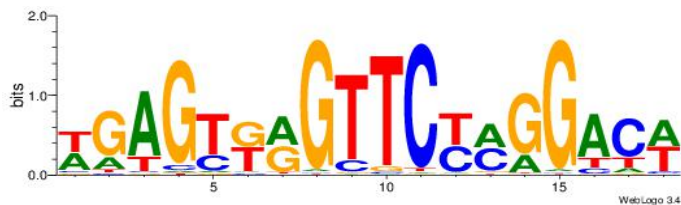
Similarity score: 0.0597653

Alignment:
WGAGTRMGTTCKRGGACW
KKTGKSTGTSSKRGMM--

Original motif Consensus sequence: WGTCCKRGAACTCACTCA

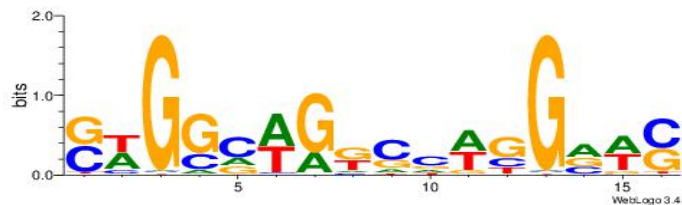


Reverse complement motif Consensus sequence: WGAGTRMGTTCKRGGACW

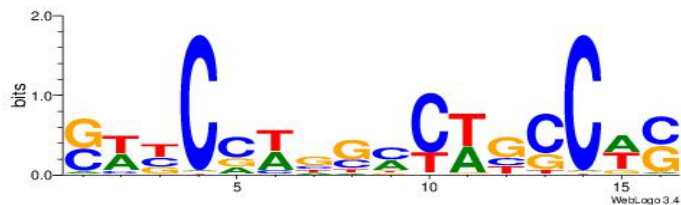


Dataset #: 1 Motif ID: 151 Motif name: C151

Original motif Consensus sequence: SWGGCWGKCCWGGVWS



Reverse complement motif Consensus sequence: SWBCCWGGYCWGCCWS



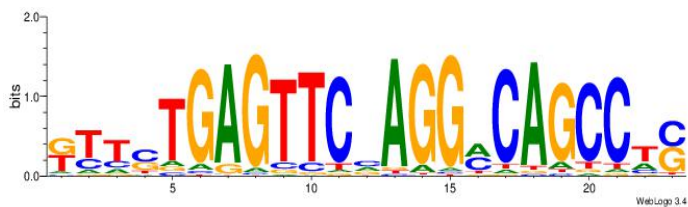
Best Matches for Motif ID 151 (Highest to Lowest)

Dataset #:	1
Motif ID:	7
Motif name:	C007
Matching format of first motif:	Original Motif

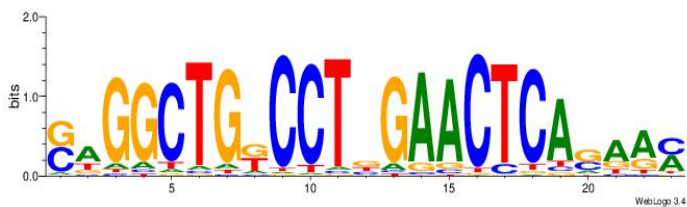
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 8
Number of overlap: 16
Similarity score: 0.0326309

Alignment:
SAGGCTGYCCTVGAAGTCASAAY
-----SWGGCWGKCCWGGVWS

Original motif Consensus sequence: KTTSTGAGTTCVAGGMCAGCCTS



Reverse complement motif Consensus sequence: SAGGCTGYCCTVGAAGTCASAAY

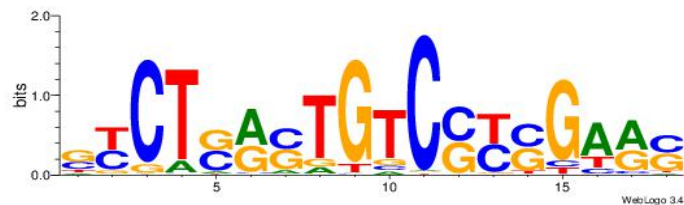


Dataset #: 1
Motif ID: 128
Motif name: C128
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 16
Similarity score: 0.0452604

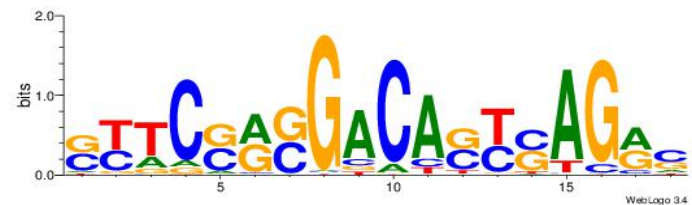
Alignment:

SYCTSRSTGTCSYSGARS
--SWGGCWGKCCWGGVWS

Original motif Consensus sequence: SYCTSRSTGTCSYSGARS



Reverse complement motif Consensus sequence: SKTCSMSGACASKSAGMS

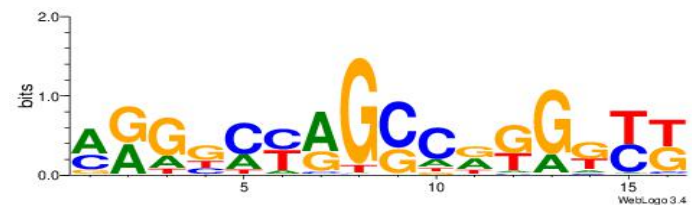
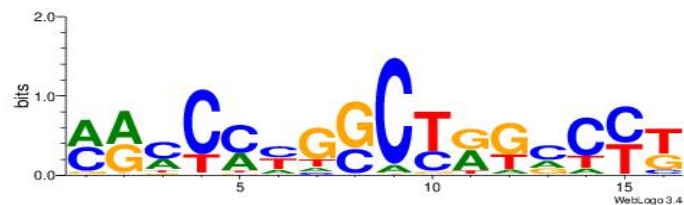


Dataset #:	1
Motif ID:	96
Motif name:	C096
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	16
Similarity score:	0.0486407

Alignment:
MRMCMYGSCYRGCCYK
SWBCCWGGYCWGCCWS

Original motif Consensus sequence: MRMCMYGSCYRGCCYK

Reverse complement motif Consensus sequence: RKGGCMMGSCKRGRKY

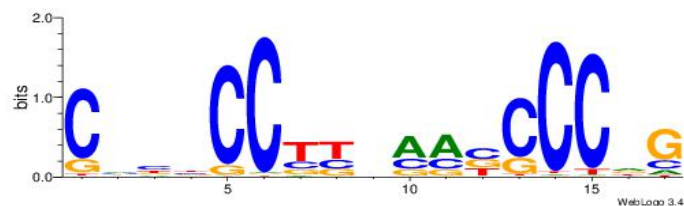


Dataset #: 1
 Motif ID: 107
 Motif name: C107
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 16
 Similarity score: 0.0508318

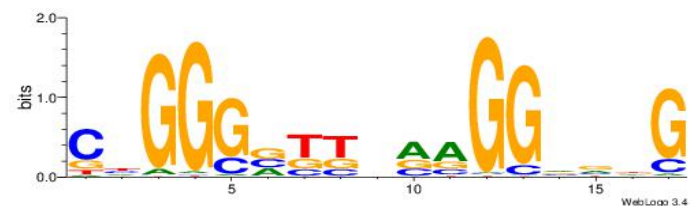
Alignment:

CDGGGBTVMAGGVBHG
 -SWGGCWGKCCWGGVWS

Original motif Consensus sequence: CHBBCCTYBAABCCCDG



Reverse complement motif Consensus sequence: CDGGGBTVMAGGVBHG



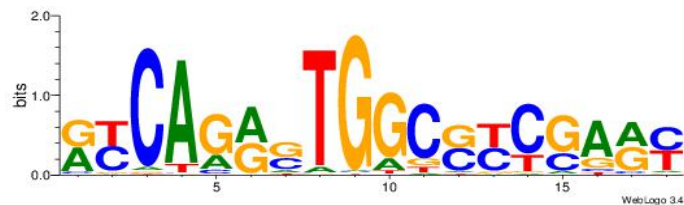
Dataset #: 1

Motif ID: 92
 Motif name: C092
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 3
 Number of overlap: 16
 Similarity score: 0.0536453

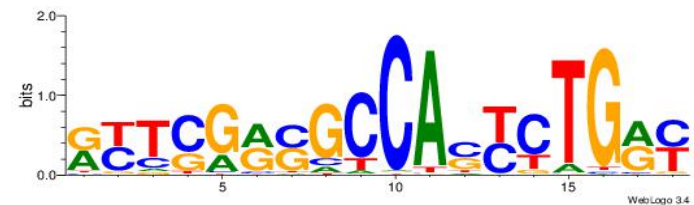
Alignment:

RYCAGRSTGGCSYCGARY
 --SWGGCWGKCCWGGVWS

Original motif Consensus sequence: RYCAGRSTGGCSYCGARY

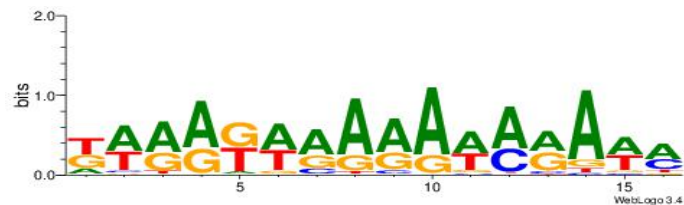


Reverse complement motif Consensus sequence: KKTCGMSGCCASKCTGMM

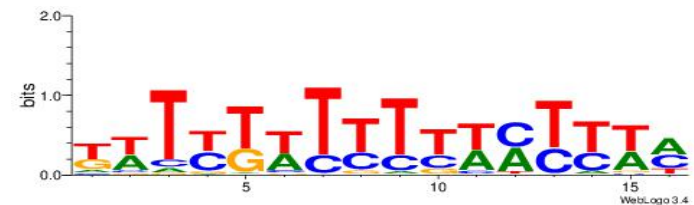


Dataset #: 1 Motif ID: 152 Motif name: C152

Original motif Consensus sequence: KWRRKWRARAWMRAWM



Reverse complement motif Consensus sequence: YWTKYWTKWKWYKKWR



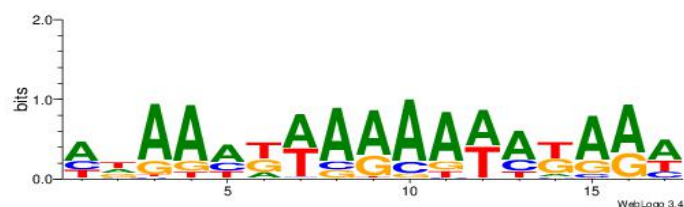
Best Matches for Motif ID 152 (Highest to Lowest)

Dataset #: 1
Motif ID: 79
Motif name: C079
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 16
Similarity score: 0.0113671

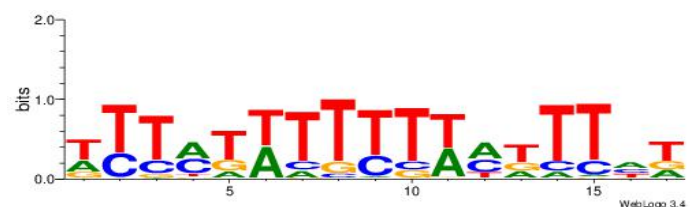
Alignment:

ADAAAKWAAA WAKARW
-KRRRKWRARAWMRAWM

Original motif Consensus sequence: ADAAAKWAAA WAKARW



Reverse complement motif Consensus sequence: WKTRTWTTTTWR TTTDT



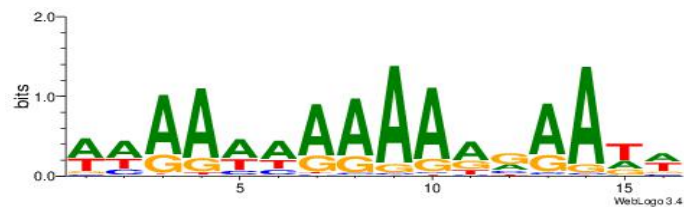
Dataset #: 1
Motif ID: 43
Motif name: C043
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement

Direction: Forward
 Position number: 1
 Number of overlap: 16
 Similarity score: 0.0143924

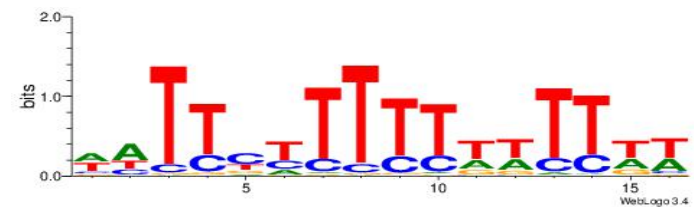
Alignment:

WATTMTTTTTTWTWW
 YWTKYWTKTKWYKKWR

Original motif Consensus sequence: WWAAWAAAAARAATW



Reverse complement motif Consensus sequence: WATTMTTTTTTWTWW

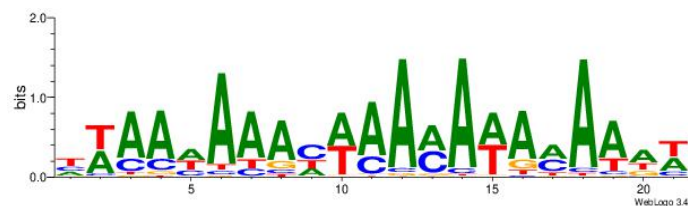


Dataset #: 1
 Motif ID: 16
 Motif name: C016
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2
 Number of overlap: 16
 Similarity score: 0.0283786

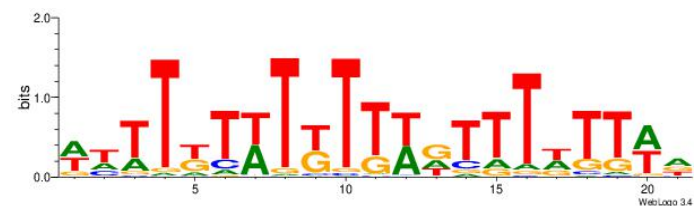
Alignment:

WTTYTWTYTTWDTTTWTWH
 -YWTKYWTKTKWYKKWR----

Original motif Consensus sequence: HWAAWAAHWAAMAWAMAAWW



Reverse complement motif Consensus sequence: WWTYYTWYTTWDTTTTWTTWH

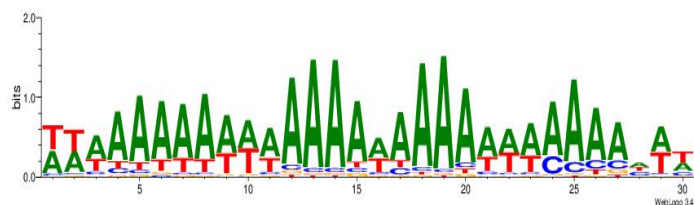


Dataset #: 1
 Motif ID: 1
 Motif name: C001
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 6
 Number of overlap: 16
 Similarity score: 0.0293372

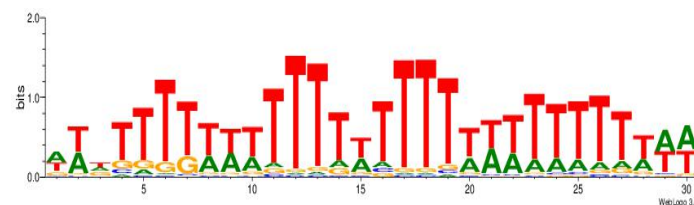
Alignment:

WWWAAAAAWWAAAAAWAAAAWWAAAAHWW
 -----KWRKWRARAWMRAWM-----

Original motif Consensus sequence: WWWAAAAAWWAAAAAWAAAAWWAAAAHWW



Reverse complement motif Consensus sequence: WWHTTTTWWTTTTTWT TTTTWWTTTTTWW

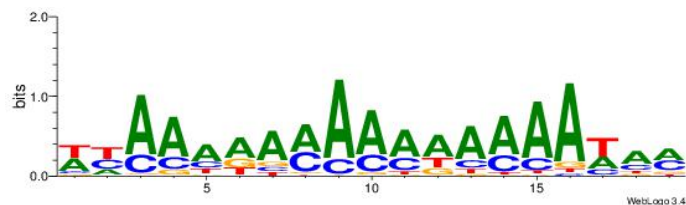


Dataset #: 1
 Motif ID: 30
 Motif name: C030
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 16
 Similarity score: 0.0302673

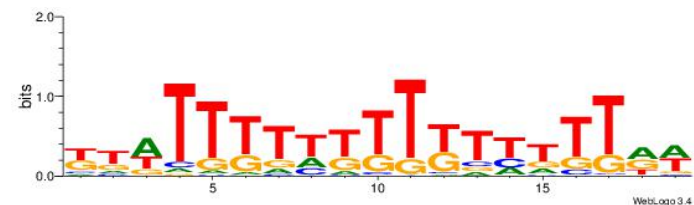
Alignment:

YTWTTTTTTTTYTTTTMW
 -YWTKYWTKTKWYKKWR--

Original motif Consensus sequence: WYAAAAAIAAAAAAAWAM



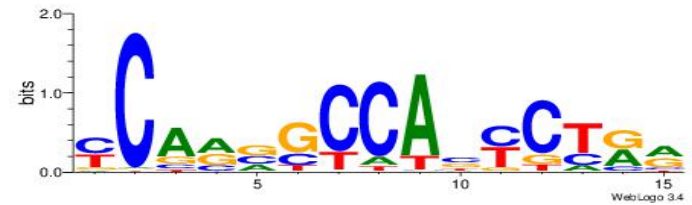
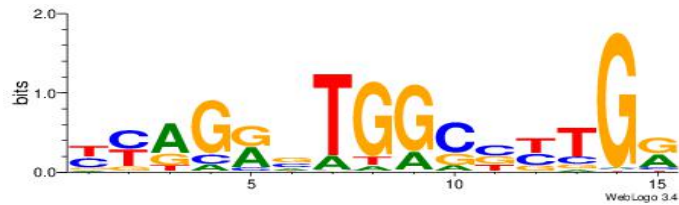
Reverse complement motif Consensus sequence: YTWTTTTTTTTYTTTTMW



Dataset #: 1 Motif ID: 153 Motif name: C153

Original motif Consensus sequence: YYAGRVTTGGCBYTGR

Reverse complement motif Consensus sequence: MCAMBGCCAVMCTKM



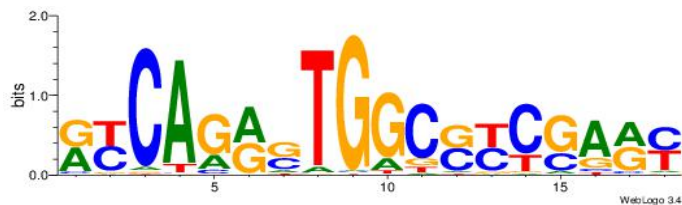
Best Matches for Motif ID 153 (Highest to Lowest)

Dataset #: 1
 Motif ID: 92
 Motif name: C092
 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: 0.00136965

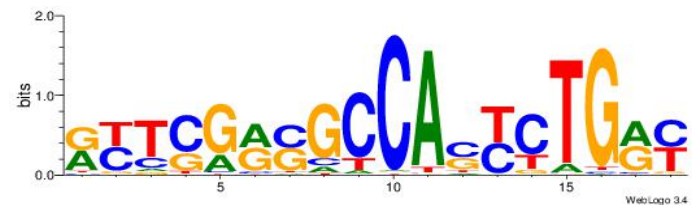
Alignment:

RYCAGRSTGGCSYCGARY
 -YYAGRVTTGGCBYTGR--

Original motif Consensus sequence: RYCAGRSTGGCSYCGARY



Reverse complement motif Consensus sequence: KKTCGMSGCCASKCTGMM

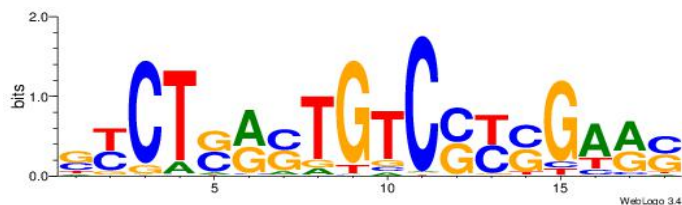


Dataset #: 1
 Motif ID: 128
 Motif name: C128
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 15
 Similarity score: 0.0263267

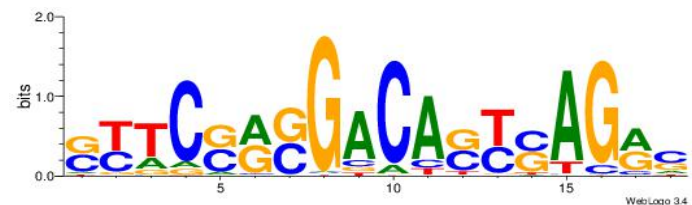
Alignment:

SYCTSRSTGTCSYSGARS
 -YYAGRVTGGCBYTGR--

Original motif Consensus sequence: SYCTSRSTGTCSYSGARS



Reverse complement motif Consensus sequence: SKTCSMSGACASKSAGMS



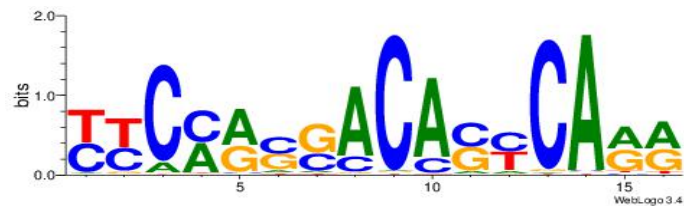
Dataset #: 1
 Motif ID: 150
 Motif name: C150
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 2

Number of overlap: 15
Similarity score: 0.0287525

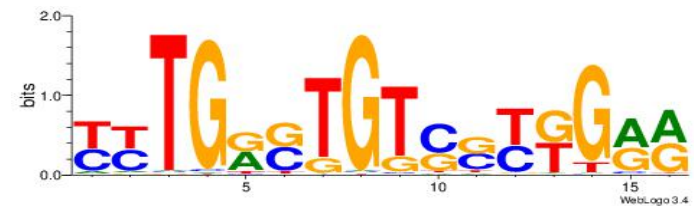
Alignment:

KKTGKSTGTSSKRGMM
-YYAGRVTGGCBYTGR

Original motif Consensus sequence: YYCMRSSACASYCARR



Reverse complement motif Consensus sequence: KKTGKSTGTSSKRGMM

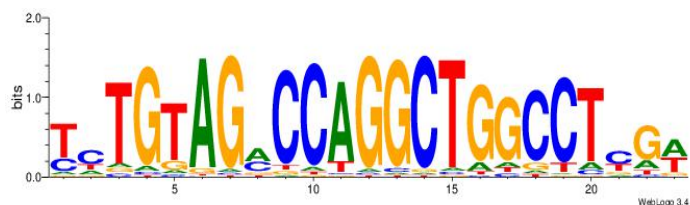


Dataset #: 1
Motif ID: 5
Motif name: C005
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 15
Similarity score: 0.029925

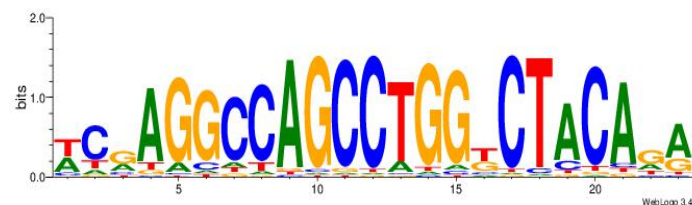
Alignment:

TCTGTAGMCCAGGCTGGCCTYGW
-----YYAGRVTGGCBYTGR

Original motif Consensus sequence: TCTGTAGMCCAGGCTGGCCTYGW



Reverse complement motif Consensus sequence: WCKAGGCCAGCCTGGYCTACAGA



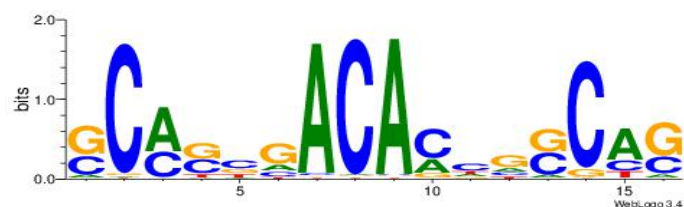
Dataset #: 1
Motif ID: 148
Motif name: C148
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 2
Number of overlap: 15
Similarity score: 0.0327492

Alignment:

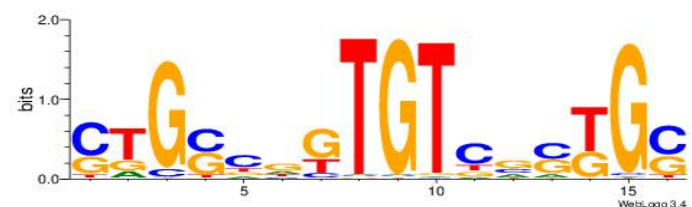
STGSCDGTGTCBSYGS

YYAGRVTGGCBYTGR-

Original motif Consensus sequence: SCMSBGACACHGSCAS



Reverse complement motif Consensus sequence: STGSCDGTGTCBSYGS



Results created by MOTIFSIM on 11-19-2016 22:04:18
Runtime: 1193.59 seconds

MOTIFSIM is written by Ngoc Tam L. Tran
Motif logo generated by [weblogo](#)