



MOTIFSIM - MOTIF SIMilarity Detection Tool

Version 2.2

INPUT

Input Parameters

Number of files:	5
Number of top significant motifs:	5
Number of best matches:	5
Similarity cutoff >=	0.75
Matching motif database:	Jaspar Urochordates
Motif tree:	Yes
Combined similar motifs:	Yes
Output file type:	All
Output file format:	All

Input files and motif counts

File name	Count of motifs	Dataset number
DREME_DM230.txt	1	1
MEME_DM230.txt	20	2
PScanChIP_DM230.txt	14	3
RSAT_peak-motifs_DM230.txt	10	4
W-ChIPMotifs_DM230.txt	11	5

RESULTS

Best Matches in Database for Each Motif (Highest to Lowest)

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

Original motif

Consensus sequence: GGCGGGGC



Reverse complement motif

Consensus sequence: GCCCGGCC



Best Matches for Motif ID 1 (Highest to Lowest)

Motif ID:	MA0118.1
Motif name:	Macho-1
Taxon:	Urochordates
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	1
Number of overlap:	8
Similarity score:	0.0156486

Alignment:

VMBCYCCCV

GCCCGGCC-

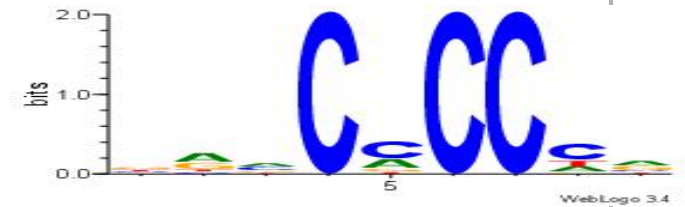
Original motif

Consensus sequence: BGGGKGBYV



Reverse complement motif

Consensus sequence: VMBCYCCCV



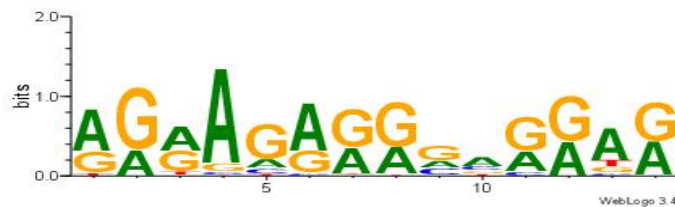
Dataset #: 2

Motif ID: 2

Motif name: Motif 2

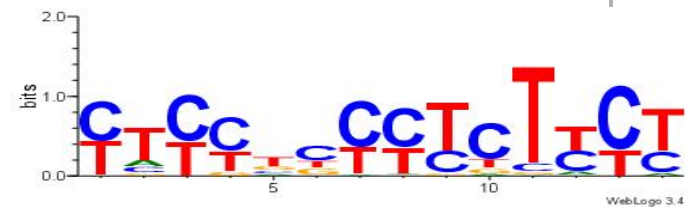
Original motif

Consensus sequence: RGRAGARRGARRAR



Reverse complement motif

Consensus sequence: MTMMTCMMTCTKCK



Best Matches for Motif ID 2 (Highest to Lowest)

Motif ID:	MA0118.1
Motif name:	Macho-1
Taxon:	Urochordates
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	3
Number of overlap:	9
Similarity score:	0.0188162

Alignment:

VMBCYCCCV-----
 --MTMMTCMMTCTKCK

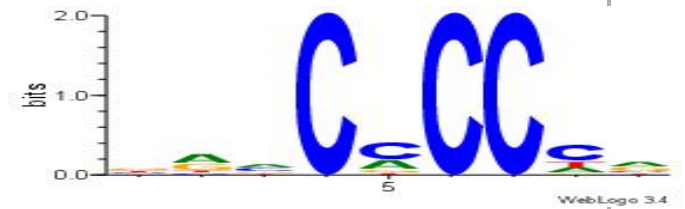
Original motif

Consensus sequence: BGGGKGBYV



Reverse complement motif

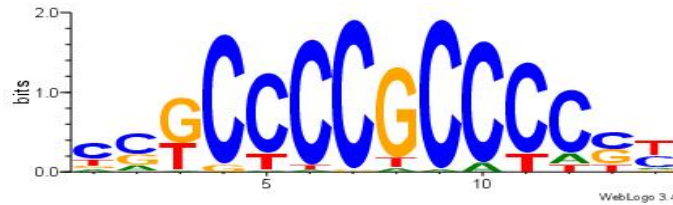
Consensus sequence: VMBCYCCCV



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

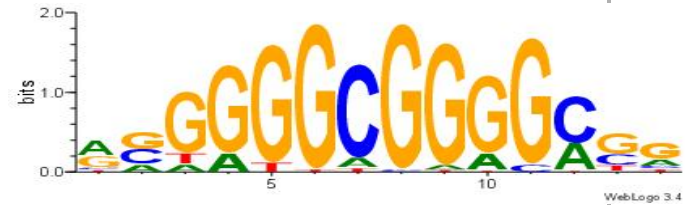
Original motif

Consensus sequence: CSKCCCCGCCCSY



Reverse complement motif

Consensus sequence: MSGGGGCGGGGYSG



Best Matches for Motif ID 7 (Highest to Lowest)

Motif ID:	MA0118.1
Motif name:	Macho-1
Taxon:	Urochordates
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	6
Number of overlap:	9

Similarity score: 0

Alignment:

```
-----BGGGKGBYV  
CSKCCCCGCCCSY-----
```

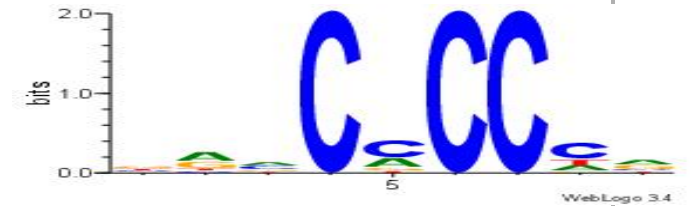
Original motif

Consensus sequence: BGGGKGBYV



Reverse complement motif

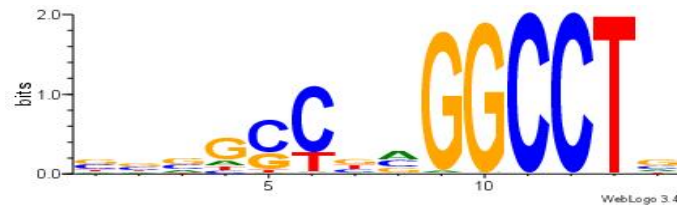
Consensus sequence: VMBCYCCCV



Dataset #: 3 Motif ID: 22 Motif name: Zfx

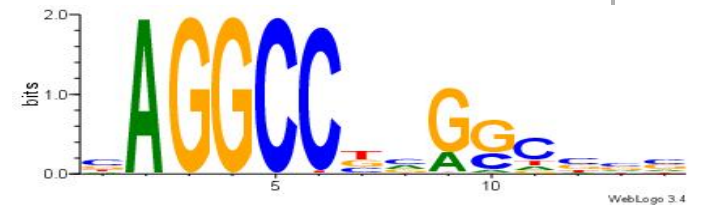
Original motif

Consensus sequence: BBVGCCBVGGCCTV



Reverse complement motif

Consensus sequence: VAGGCCBBGGCVBB



Best Matches for Motif ID 22 (Highest to Lowest)

Motif ID:	MA0118.1
Motif name:	Macho-1
Taxon:	Urochordates
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif

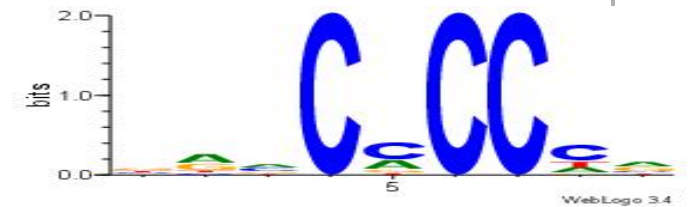
Direction: Backward
 Position number: 6
 Number of overlap: 9
 Similarity score: 0.0164874

Alignment:
 -----VMBCYCCCV
 VAGGCCBBGGCVBB-----

Original motif
 Consensus sequence: BGGGKGBYV



Reverse complement motif
 Consensus sequence: VMBCYCCCV



Dataset #: 3 Motif ID: 23 Motif name: Egr1

Original motif
 Consensus sequence: HGCGTGGGCGK



Reverse complement motif
 Consensus sequence: YGCCCCACGCH



Best Matches for Motif ID 23 (Highest to Lowest)

Motif ID: MA0118.1
 Motif name: Macho-1

Taxon:	Urochordates
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	3
Number of overlap:	9
Similarity score:	0.0535903

Alignment:

```
--BGGGKGBYV
HGCGTGGGCGK--
```

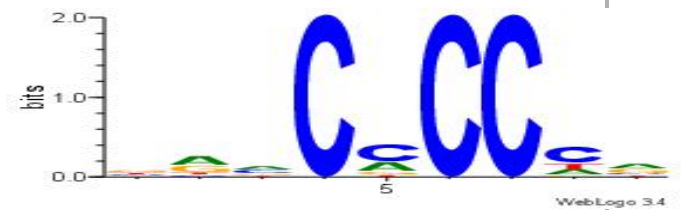
Original motif

Consensus sequence: BGGGKGBYV



Reverse complement motif

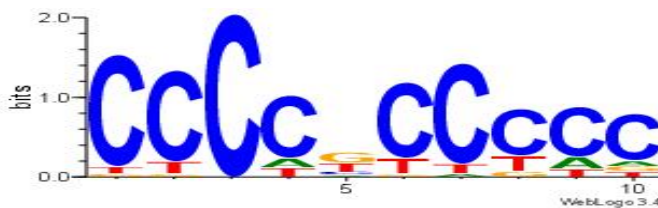
Consensus sequence: VMBCYCCCV



Dataset #: 3 Motif ID: 24 Motif name: SP1

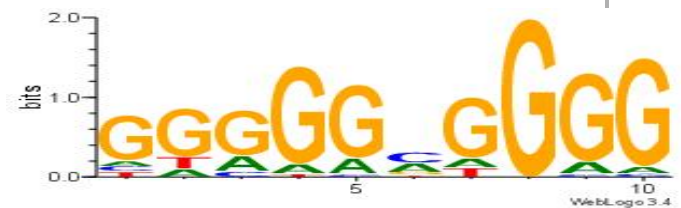
Original motif

Consensus sequence: CCCCKCCCC



Reverse complement motif

Consensus sequence: GGGGGYGGGG



Best Matches for Motif ID 24 (Highest to Lowest)

Motif ID: MA0118.1
Motif name: Macho-1
Taxon: Urochordates
Matching format of first motif: Original Motif
Matching format of second motif: Reverse Complement
Direction: Forward
Position number: 1
Number of overlap: 9
Similarity score: 0.053545

Alignment:

VMBCYCCCV-
CCCCKCCCC

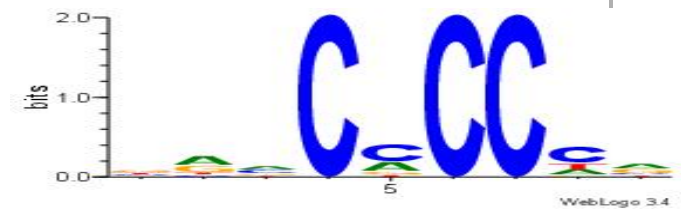
Original motif

Consensus sequence: BGGGKGBYV



Reverse complement motif

Consensus sequence: VMBCYCCCV



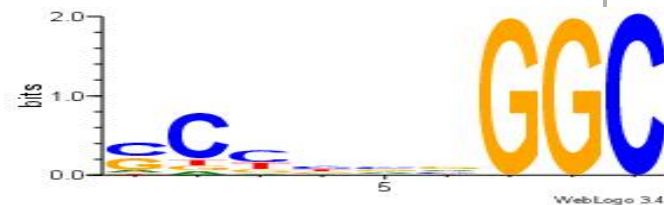
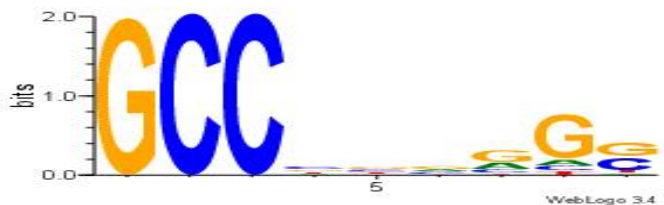
Dataset #: 3 Motif ID: 25 Motif name: TFAP2A

Original motif

Consensus sequence: GCCBBVRGS

Reverse complement motif

Consensus sequence: SCMVBGGC



Best Matches for Motif ID 25 (Highest to Lowest)

Motif ID:	MA0118.1
Motif name:	Macho-1
Taxon:	Urochordates
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	2
Number of overlap:	8
Similarity score:	0.0543002

Alignment:

```
-BGGGKGBYV
SCMVBBGGC-
```

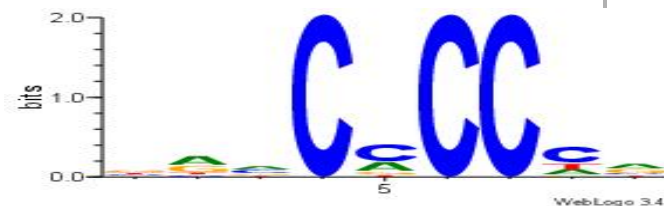
Original motif

Consensus sequence: BGGGKGBYV



Reverse complement motif

Consensus sequence: VMBCYCCCV



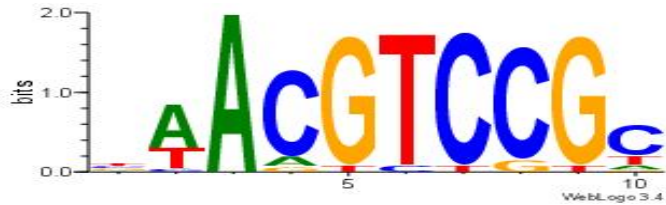
Dataset #: 3

Motif ID: 26

Motif name: MIZF

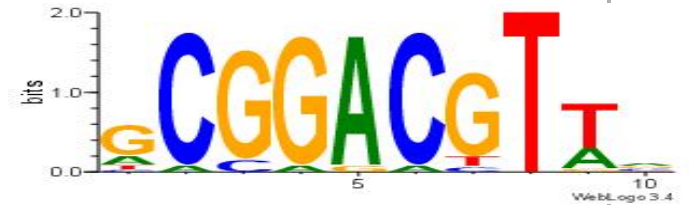
Original motif

Consensus sequence: BAACGTCCGC



Reverse complement motif

Consensus sequence: GCGGACGTTT



Best Matches for Motif ID 26 (Highest to Lowest)

Motif ID:	MA0118.1
Motif name:	Macho-1
Taxon:	Urochordates
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	9
Similarity score:	0

Alignment:

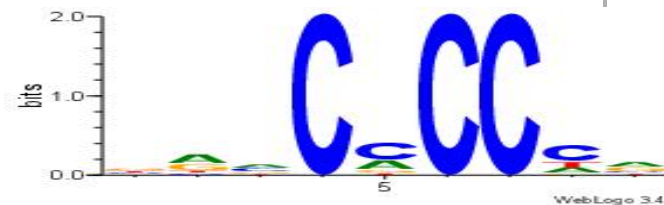
VMBCYCCCV-
-GCGGACGTTT

Original motif

Consensus sequence: BGGGKGBYV

Reverse complement motif

Consensus sequence: VMBCYCCCV



Dataset #: 3 Motif ID: 27 Motif name: Klf4

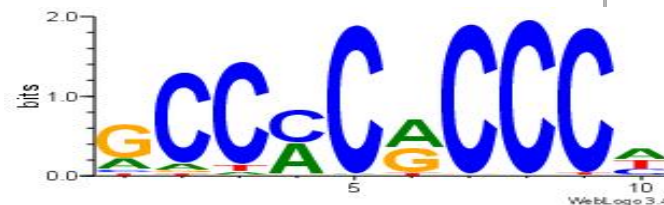
Original motif

Consensus sequence: DGGGYGKGGC



Reverse complement motif

Consensus sequence: GCCYCMCCCD



Best Matches for Motif ID 27 (Highest to Lowest)

Motif ID:	MA0118.1
Motif name:	Macho-1
Taxon:	Urochordates
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	1
Number of overlap:	9
Similarity score:	0

Alignment:

```
-VMBCYCCCV
GCCYCMCCCD
```

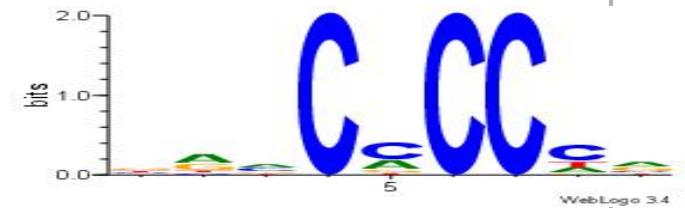
Original motif

Consensus sequence: BGGGKGBYV



Reverse complement motif

Consensus sequence: VMBCYCCCV



Dataset #: 3

Motif ID: 28

Motif name: E2F1

Original motif

Consensus sequence: TTTSGCGC



Reverse complement motif

Consensus sequence: GCGSAAA



Best Matches for Motif ID 28 (Highest to Lowest)

Motif ID:	MA0118.1
Motif name:	Macho-1
Taxon:	Urochordates
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	4
Number of overlap:	6
Similarity score:	0

Alignment:

BGGGKGBYV--

---GCGCSAAA

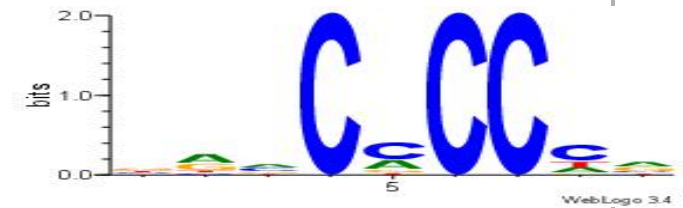
Original motif

Consensus sequence: BGGGKGBYV



Reverse complement motif

Consensus sequence: VMBCYCCCV



Dataset #: 3

Motif ID: 29

Motif name: HIF1AARNT

Original motif

Consensus sequence: VBACGTGV



Reverse complement motif

Consensus sequence: VCACGTBV



Best Matches for Motif ID 29 (Highest to Lowest)

Motif ID:	MA0118.1
Motif name:	Macho-1
Taxon:	Urochordates
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif

Direction: Backward
 Position number: 1
 Number of overlap: 8
 Similarity score: 0.0184683

Alignment:
 BGGGKGBYV
 -VCACGTBV

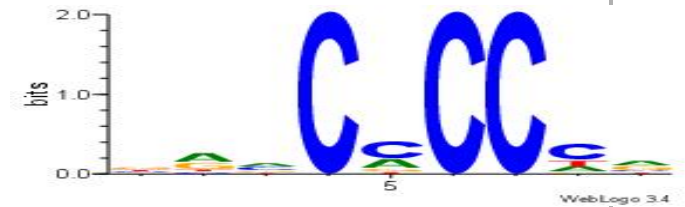
Original motif

Consensus sequence: BGGGKGBYV



Reverse complement motif

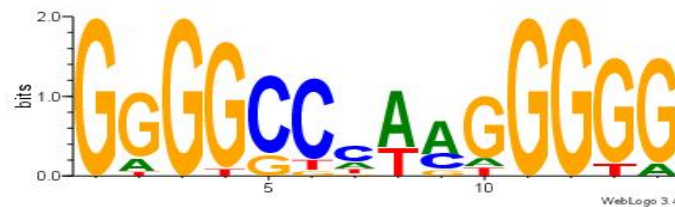
Consensus sequence: VMBCYCCCV



Dataset #: 3 Motif ID: 30 Motif name: PLAG1

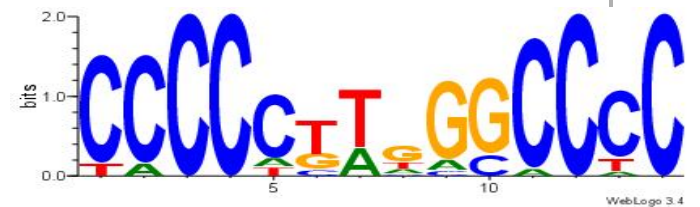
Original motif

Consensus sequence: GGGGCCCAAGGGG



Reverse complement motif

Consensus sequence: CCCCTTGGCCCC



Best Matches for Motif ID 30 (Highest to Lowest)

Motif ID: MA0118.1

Motif name: Macho-1
 Taxon: Urochordates
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 1
 Number of overlap: 9
 Similarity score: 0.0652557

Alignment:
 BGGGKGBYV-----
 GGGGCCCAAGGGGG

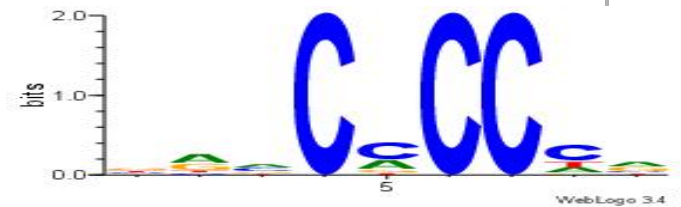
Original motif

Consensus sequence: BGGGKGBYV



Reverse complement motif

Consensus sequence: VMBCYCCCV



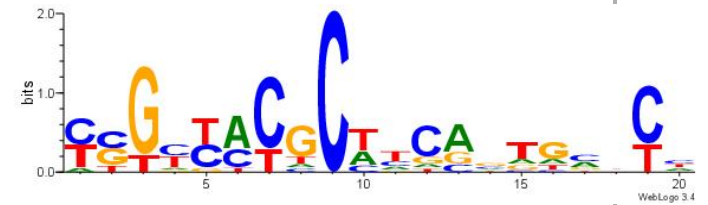
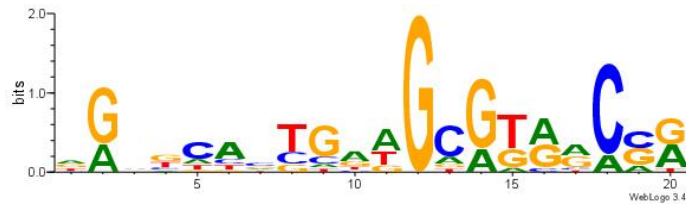
Dataset #: 3 Motif ID: 31 Motif name: Pax5

Original motif

Consensus sequence: DGVBCABTGDWGCGRRCR

Reverse complement motif

Consensus sequence: MSGKKRCGCWDCABTGBBCD



Best Matches for Motif ID 31 (Highest to Lowest)

Motif ID:	MA0118.1
Motif name:	Macho-1
Taxon:	Urochordates
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	4
Number of overlap:	9
Similarity score:	0.0302249

Alignment:

```

-----BGGGKGBYV
DGVBCABTGDWGCGRRCR---
  
```

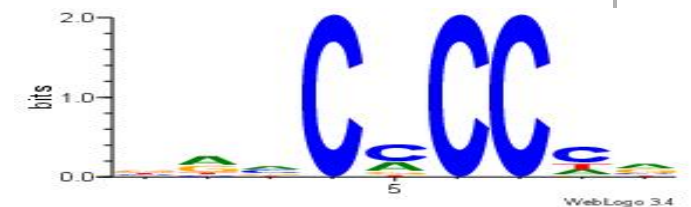
Original motif

Consensus sequence: BGGGKGBYV



Reverse complement motif

Consensus sequence: VMBCYCCCV



Dataset #: 3 Motif ID: 32 Motif name: ArntAhr

Original motif

Consensus sequence: YGCGTG



Reverse complement motif

Consensus sequence: CACGCM



Best Matches for Motif ID 32 (Highest to Lowest)

Motif ID:	MA0118.1
Motif name:	Macho-1
Taxon:	Urochordates
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	1
Number of overlap:	6
Similarity score:	0

Alignment:

BGGGKGBYV

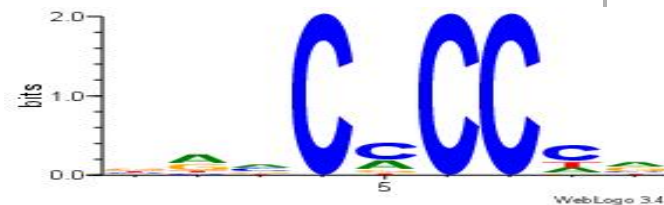
YGCGTG---

Original motif

Consensus sequence: BGGGKGBYV

Reverse complement motif

Consensus sequence: VMBCYCCCV



Dataset #: 3 Motif ID: 33 Motif name: Mycn

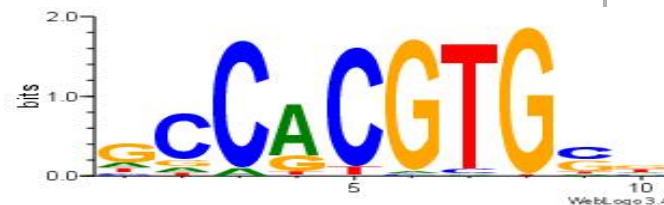
Original motif

Consensus sequence: HSCACGTGGC



Reverse complement motif

Consensus sequence: GCCACGTGSD



Best Matches for Motif ID 33 (Highest to Lowest)

Motif ID:	MA0118.1
Motif name:	Macho-1
Taxon:	Urochordates
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	2
Number of overlap:	8
Similarity score:	0.015945

Alignment:

VMBCYCCCV--
-HSCACGTGGC

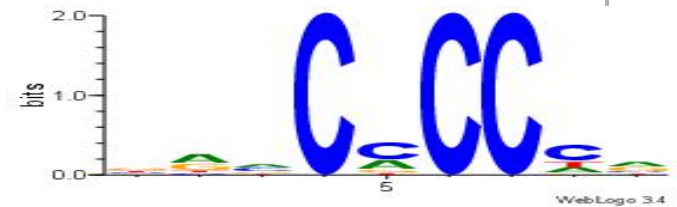
Original motif

Consensus sequence: BGGGKGBYV



Reverse complement motif

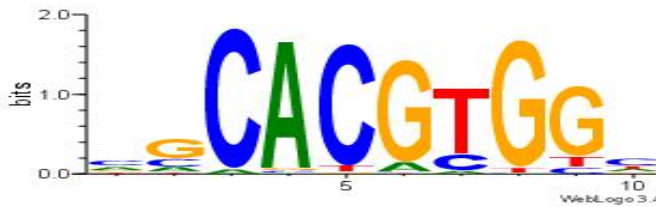
Consensus sequence: VMBCYCCCV



Dataset #: 3 Motif ID: 34 Motif name: Myc

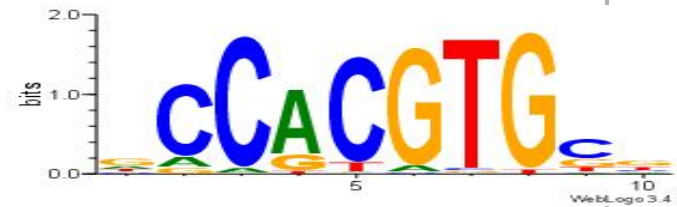
Original motif

Consensus sequence: VGCACGTGGH



Reverse complement motif

Consensus sequence: DCCACGTGCV



Best Matches for Motif ID 34 (Highest to Lowest)

Motif ID:	MA0118.1
Motif name:	Macho-1
Taxon:	Urochordates
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	3
Number of overlap:	8

Similarity score: 0.0249869

Alignment:

BGGGKGBYV--
--VGCACGTGGH

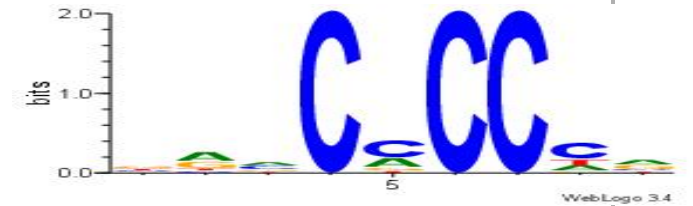
Original motif

Consensus sequence: BGGGKGBYV



Reverse complement motif

Consensus sequence: VMBCYCCCV



Dataset #: 3 Motif ID: 35 Motif name: GABPA

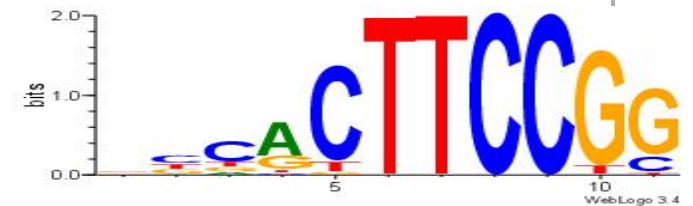
Original motif

Consensus sequence: CCGGAAGTV



Reverse complement motif

Consensus sequence: VVCACTTCCGG



Best Matches for Motif ID 35 (Highest to Lowest)

Motif ID:	MA0118.1
Motif name:	Macho-1
Taxon:	Urochordates
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement

Direction: Forward
Position number: 2
Number of overlap: 9
Similarity score: 0.00567251

Alignment:
VMBCYCCCV--
-VVCACTTCCGG

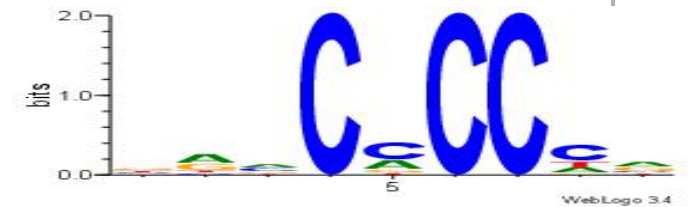
Original motif

Consensus sequence: BGGGKGBYV



Reverse complement motif

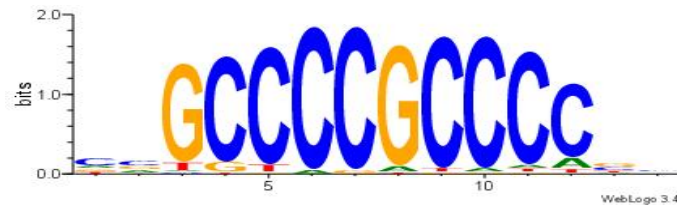
Consensus sequence: VMBCYCCCV



Dataset #: 4 Motif ID: 36 Motif name: csGCCCCGCCCCsc

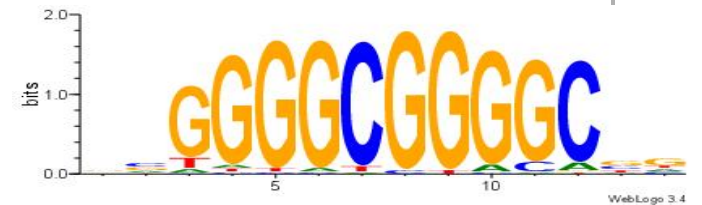
Original motif

Consensus sequence: HVGCCCCGCCCCBB



Reverse complement motif

Consensus sequence: BBGGGGCGGGGCVD



Best Matches for Motif ID 36 (Highest to Lowest)

Motif ID: MA0118.1

Motif name: Macho-1
 Taxon: Urochordates
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 1
 Number of overlap: 9
 Similarity score: 0

Alignment:

VMBCYCCCV-----
 HVGCCCGCCCCBB

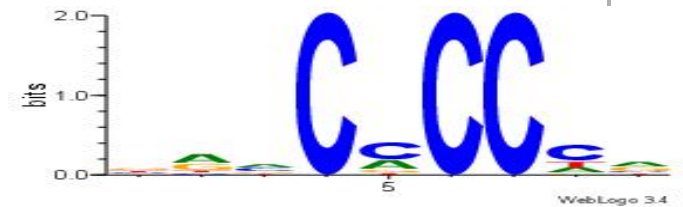
Original motif

Consensus sequence: BGGGKGBYV



Reverse complement motif

Consensus sequence: VMBCYCCCV



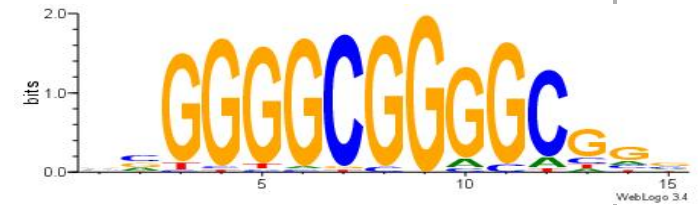
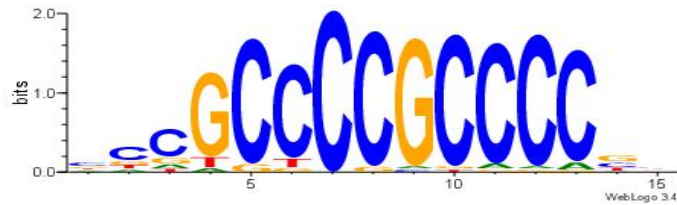
Dataset #: 4 Motif ID: 38 Motif name: cccGCCCGCCCCsb

Original motif

Consensus sequence: BCCGCCCGCCCCBB

Reverse complement motif

Consensus sequence: BBGGGCGGGGCGGB



Best Matches for Motif ID 38 (Highest to Lowest)

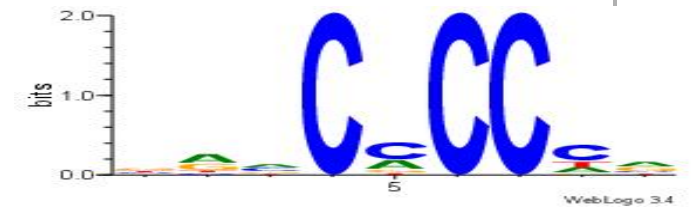
Motif ID: MA0118.1
 Motif name: Macho-1
 Taxon: Urochordates
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 6
 Number of overlap: 9
 Similarity score: 0.00480377

Alignment:
 -----BGGGKGBYV
 BCCGCCCCGCCCCBB-----

Original motif
 Consensus sequence: BGGGKGBYV



Reverse complement motif
 Consensus sequence: VMBCYCCCV



Dataset #: 4 Motif ID: 39 Motif name: kCAGCCAATmr

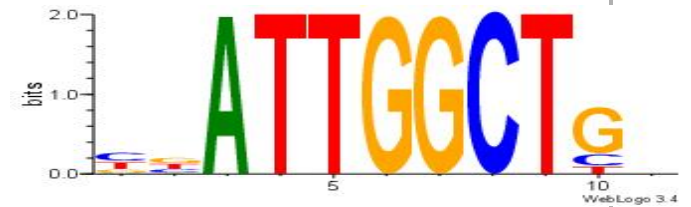
Original motif

Consensus sequence: DCAGCCAATVR



Reverse complement motif

Consensus sequence: MBATTGGCTGH



Best Matches for Motif ID 39 (Highest to Lowest)

Motif ID:	MA0118.1
Motif name:	Macho-1
Taxon:	Urochordates
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	4
Number of overlap:	8
Similarity score:	0.00284489

Alignment:

```
VMBCYCCCV---  
---MBATTGGCTGH
```

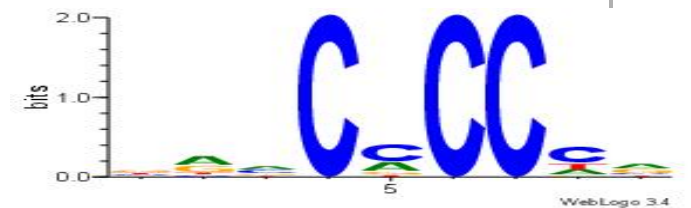
Original motif

Consensus sequence: BGGGKGBYV



Reverse complement motif

Consensus sequence: VMBCYCCCV



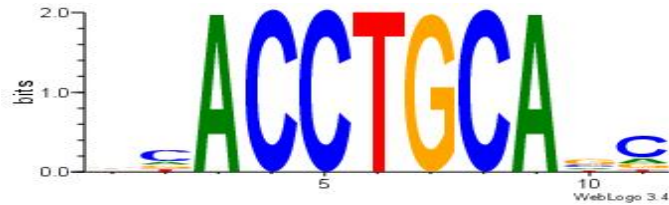
Dataset #: 4

Motif ID: 40

Motif name: kcACCTGCAGc

Original motif

Consensus sequence: BCACCTGCABC



Reverse complement motif

Consensus sequence: GBTGCAGGTGB



Best Matches for Motif ID 40 (Highest to Lowest)

Motif ID:	MA0118.1
Motif name:	Macho-1
Taxon:	Urochordates
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	2
Number of overlap:	9
Similarity score:	0.0223487

Alignment:

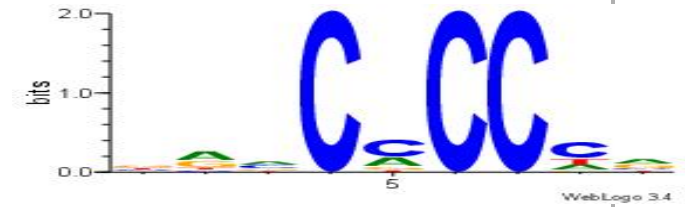
BGGGKGBYV--
-BCACCTGCABC

Original motif

Consensus sequence: BGGGKGBYV

Reverse complement motif

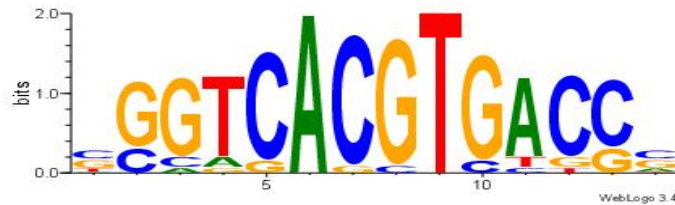
Consensus sequence: VMBCYCCCV



Dataset #: 4 Motif ID: 42 Motif name: sSGTCACGTGACCS

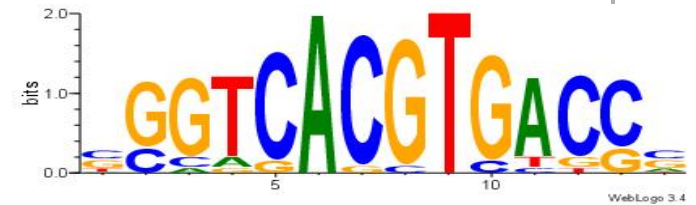
Original motif

Consensus sequence: SGGTCACGTGACCS



Reverse complement motif

Consensus sequence: SGGTCACGTGACCS



Best Matches for Motif ID 42 (Highest to Lowest)

Motif ID:	MA0118.1
Motif name:	Macho-1
Taxon:	Urochordates
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	4
Number of overlap:	6
Similarity score:	0.0205026

Alignment:

BGGGKGBYV-----
---SGGTCACGTGACCS

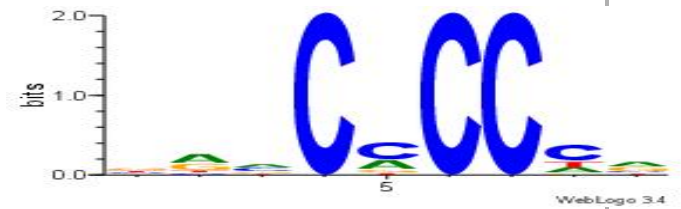
Original motif

Consensus sequence: BGGGKGBYV



Reverse complement motif

Consensus sequence: VMBCYCCCV



Dataset #: 5 Motif ID: 46 Motif name: TFW1

Original motif

Consensus sequence: GTCGCG



Reverse complement motif

Consensus sequence: CGCGAC



Best Matches for Motif ID 46 (Highest to Lowest)

Motif ID:	MA0118.1
Motif name:	Macho-1
Taxon:	Urochordates
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	2

Number of overlap: 6
Similarity score: 0.0274145

Alignment:
VMBCYCCCV
-GTCGCG--

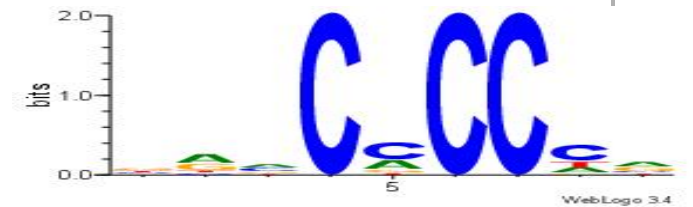
Original motif

Consensus sequence: BGGGKGBYV



Reverse complement motif

Consensus sequence: VMBCYCCCV



Dataset #: 5 Motif ID: 47 Motif name: TFW2

Original motif

Consensus sequence: SCGCGCGG



Reverse complement motif

Consensus sequence: CCGCGCGS



Best Matches for Motif ID 47 (Highest to Lowest)

Motif ID: MA0118.1
Motif name: Macho-1
Taxon: Urochordates

Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 2
 Number of overlap: 7
 Similarity score: 0.00827346

Alignment:
 VMBCYCCCV-
 -CCGCGCGS-

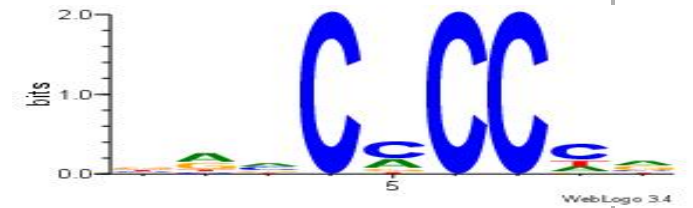
Original motif

Consensus sequence: BGGGKGBYV



Reverse complement motif

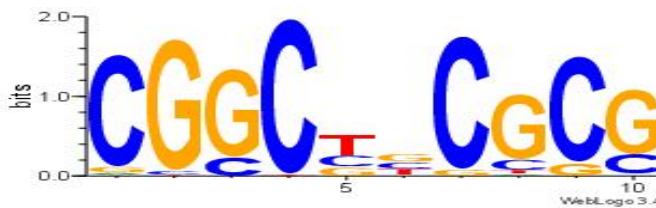
Consensus sequence: VMBCYCCCV



Dataset #: 5 Motif ID: 48 Motif name: TFW3

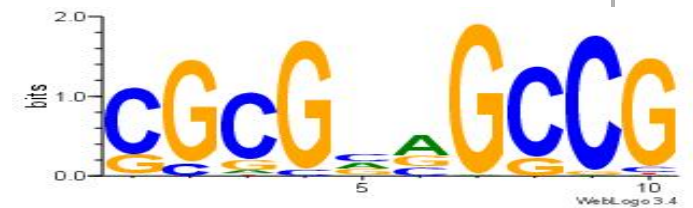
Original motif

Consensus sequence: CGGCYBCGCG



Reverse complement motif

Consensus sequence: CGCGBMGCCG



Best Matches for Motif ID 48 (Highest to Lowest)

Motif ID: MA0118.1
 Motif name: Macho-1
 Taxon: Urochordates
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 3
 Number of overlap: 7
 Similarity score: 0.00818027

Alignment:
 ---VMBCYCCCV
 CGGCYBCGCG--

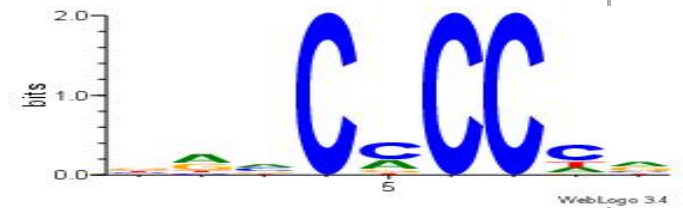
Original motif

Consensus sequence: BGGGKGBYV



Reverse complement motif

Consensus sequence: VMBCYCCCV



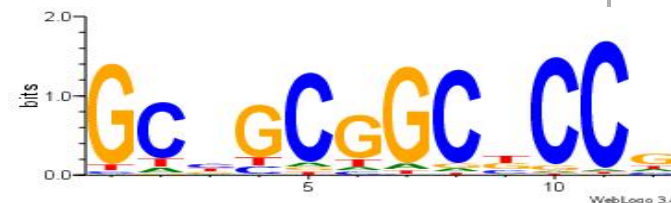
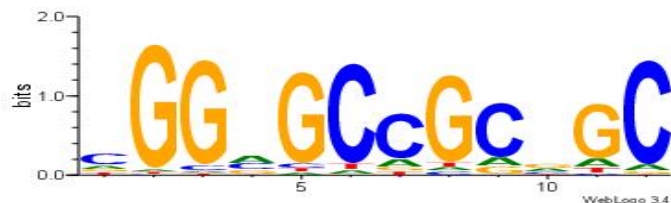
Dataset #: 5 Motif ID: 49 Motif name: TFF1

Original motif

Consensus sequence: CGGVGCCGCVGC

Reverse complement motif

Consensus sequence: GCVGCCGCBCCG



Best Matches for Motif ID 49 (Highest to Lowest)

Motif ID:	MA0118.1
Motif name:	Macho-1
Taxon:	Urochordates
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	3
Number of overlap:	9
Similarity score:	0.0138724

Alignment:

```

---VMBCYCCCV
GCVGCGGCBCCG--
  
```

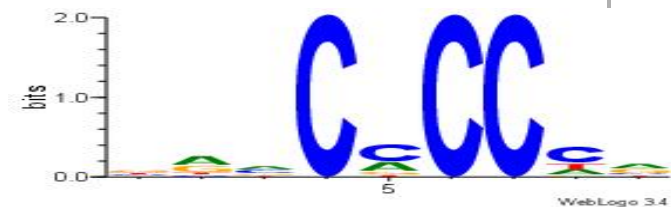
Original motif

Consensus sequence: BGGGKGBYV



Reverse complement motif

Consensus sequence: VMBCYCCCV



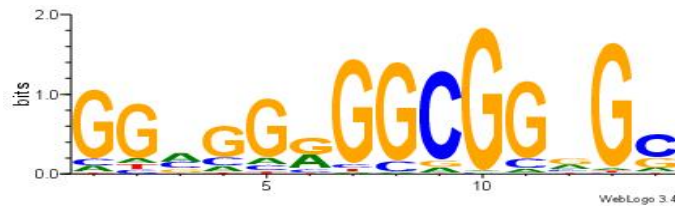
Dataset #: 5

Motif ID: 50

Motif name: TFF11

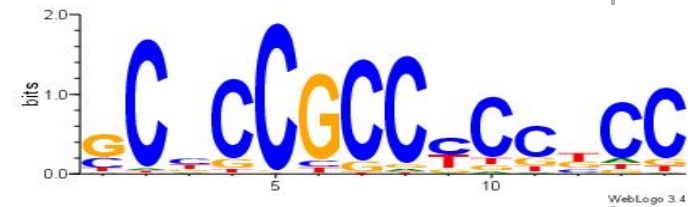
Original motif

Consensus sequence: GGMGGRGGCGGVGC



Reverse complement motif

Consensus sequence: GCVCCGCCMCCYCC



Best Matches for Motif ID 50 (Highest to Lowest)

Motif ID:	MA0118.1
Motif name:	Macho-1
Taxon:	Urochordates
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	2
Number of overlap:	9
Similarity score:	0.00505291

Alignment:

```
VMBCYCCCV-----  
-GCVCCGCCMCCYCC
```

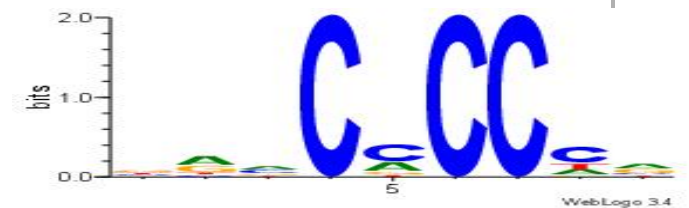
Original motif

Consensus sequence: BGGGKGBYV



Reverse complement motif

Consensus sequence: VMBCYCCCV



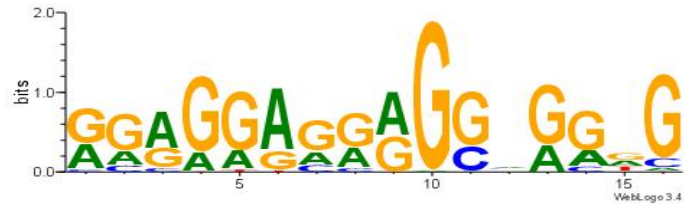
Dataset #: 5

Motif ID: 51

Motif name: TFM2

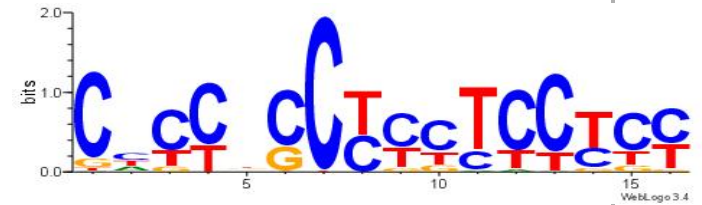
Original motif

Consensus sequence: RGRGGAGRRGGHGGDG



Reverse complement motif

Consensus sequence: CHCCBCKMCTCCKCM



Best Matches for Motif ID 51 (Highest to Lowest)

Motif ID:	MA0118.1
Motif name:	Macho-1
Taxon:	Urochordates
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	8
Number of overlap:	9
Similarity score:	0.0112434

Alignment:

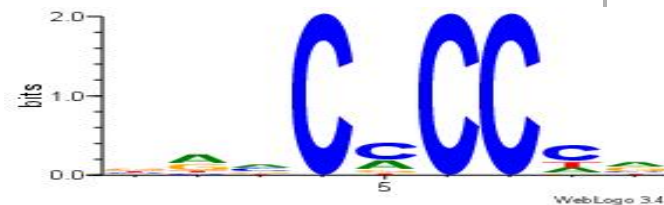
```
-----VMBCYCCCV  
CHCCBCKMCTCCKCM-----
```

Original motif

Consensus sequence: BGGGKGBYV

Reverse complement motif

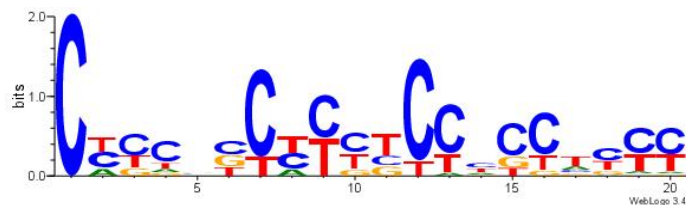
Consensus sequence: VMBCYCCCV



Dataset #: 5 Motif ID: 54 Motif name: TFM12

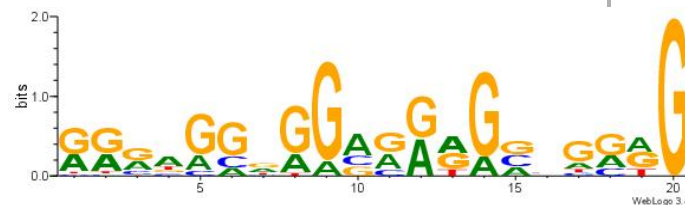
Original motif

Consensus sequence: CYCBBBCYYYTCCHCCTYYY



Reverse complement motif

Consensus sequence: KKKAGGDGGAKKMGBBGKMG



Best Matches for Motif ID 54 (Highest to Lowest)

Motif ID:	MA0118.1
Motif name:	Macho-1
Taxon:	Urochordates
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Forward
Position number:	6
Number of overlap:	9
Similarity score:	0.0107837

Alignment:

```
BGGKGBYV-----
-----CYCBBBCYYYTCCHCCTYYY
```

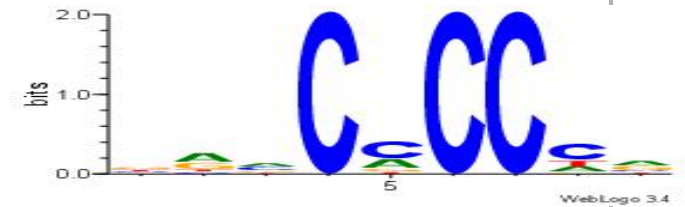
Original motif

Consensus sequence: BGGGKGBYV



Reverse complement motif

Consensus sequence: VMBCYCCCV



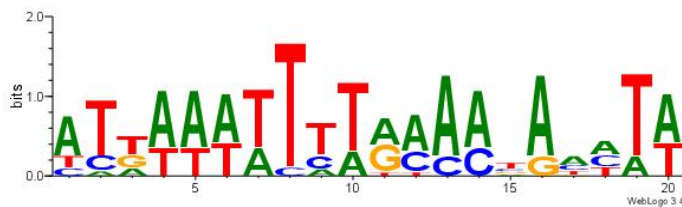
Dataset #: 5

Motif ID: 55

Motif name: TFM13

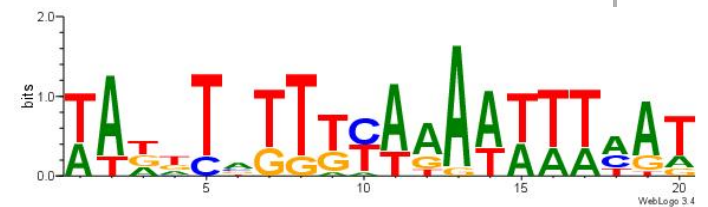
Original motif

Consensus sequence: ATKAAWTTTTTRMAABAHTW



Reverse complement motif

Consensus sequence: WAHHTVTTYKAAAATTRAT



Best Matches for Motif ID 55 (Highest to Lowest)

Motif ID:	MA0118.1
Motif name:	Macho-1
Taxon:	Urochordates
Matching format of first motif:	Original Motif
Matching format of second motif:	Reverse Complement
Direction:	Backward
Position number:	6
Number of overlap:	4
Similarity score:	0

Alignment:

```
-----VMBCYCCCV  
ATKAAWTTTTTRMAABAHHTW-----
```

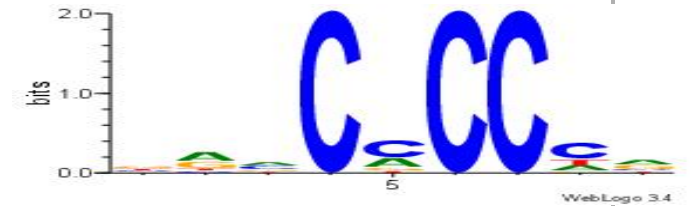
Original motif

Consensus sequence: BGGGKGBYV



Reverse complement motif

Consensus sequence: VMBCYCCCV



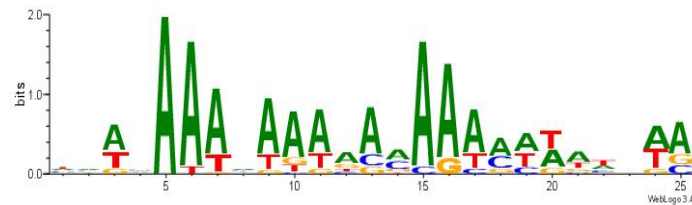
Dataset #: 5

Motif ID: 56

Motif name: TFM11

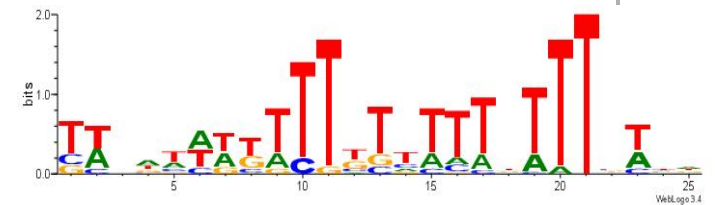
Original motif

Consensus sequence: HDWVAAAHAAAAAMAAAMWWWHBWA



Reverse complement motif

Consensus sequence: TWVHWWYTTTTYTTTTHTTTTWW



Best Matches for Motif ID 56 (Highest to Lowest)

Motif ID:	MA0118.1
Motif name:	Macho-1
Taxon:	Urochordates
Matching format of first motif:	Reverse Complement
Matching format of second motif:	Original Motif

Direction: Forward
Position number: 5
Number of overlap: 5
Similarity score: 0.0192577

Alignment:

BGGGKGBYV-----
----TWVHWWWYTTYTTTTTHTTTVWBH

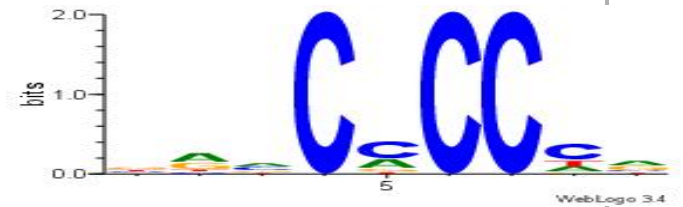
Original motif

Consensus sequence: BGGGKGBYV



Reverse complement motif

Consensus sequence: VMBCYCCCV



Results created by MOTIFSIM on 11-21-2023 10:01:18
Runtime: 65.8356 seconds

MOTIFSIM is written by Ngoc Tam L. Tran
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