



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 \geq	0.75
Matching motif database:	Jaspar Fungi
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)

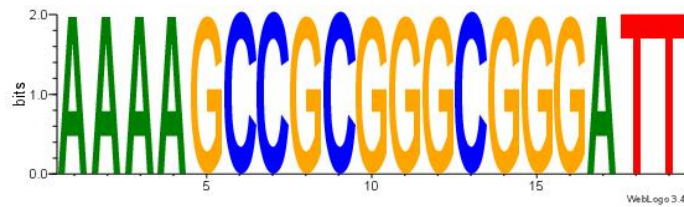
Motif ID:	MA0290.1
Motif name:	DAL81
Taxon:	Fungi
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	11
Number of overlap:	8
Similarity score:	0.0497454

Alignment:

```
AAAAGCCGCGGGCGGGATT  
-----GGCGGGGC-
```

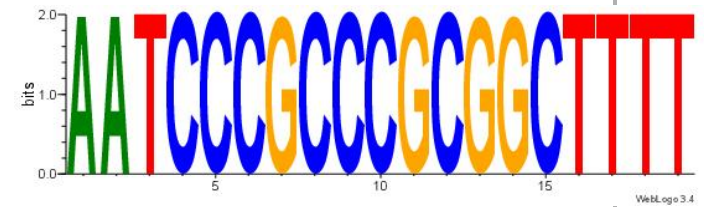
Original motif

Consensus sequence: AAAAGCCGCGGGCGGGATT



Reverse complement motif

Consensus sequence: AATCCCGCCGCGGCTTTT



Motif ID: [MA0283.1](#)
Motif name: CHA4
Taxon: Fungi
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 1
Number of overlap: 8
Similarity score: 0.0552504

Alignment:

GC CGGAGW
GC CGGGGC

Original motif

Consensus sequence: GC CGGAGW



Reverse complement motif

Consensus sequence: WCTCCGCC



Motif ID: [MA0344.1](#)
Motif name: NHP10
Taxon: Fungi
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 1
Number of overlap: 8
Similarity score: 0.0635389

Alignment:
TCCCCGGC
GCCCCGCC

Original motif

Consensus sequence: GCCGGGGA



Reverse complement motif

Consensus sequence: TCCCCGGC

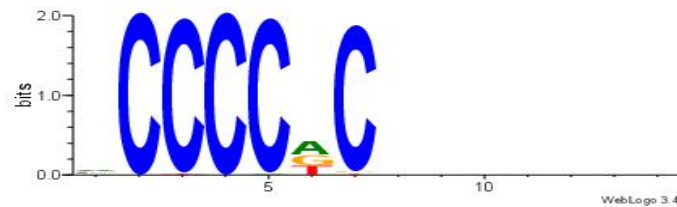


Motif ID: [MA0425.1](#)
Motif name: YGR067C
Taxon: Fungi
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Backward
Position number: 7

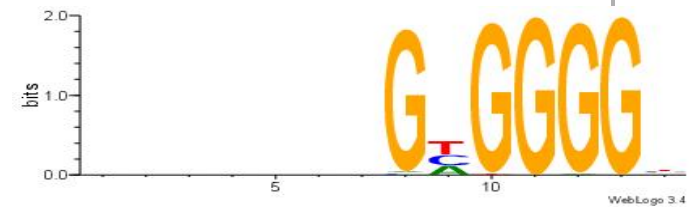
Number of overlap: 8
Similarity score: 0.0654186

Alignment:
VCCCCDCHHHDDBD
GCCCCGCC-----

Original motif
Consensus sequence: VCCCCDCHHHDDBD



Reverse complement motif
Consensus sequence: DBDDHHHGDGGGGG



Motif ID: [MA0431.1](#)
Motif name: TDA9
Taxon: Fungi
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: 0.0668666

Alignment:
VCCCCDCWH
GCCCCGCC-

Original motif

Reverse complement motif

Consensus sequence: VCCCCDCWH



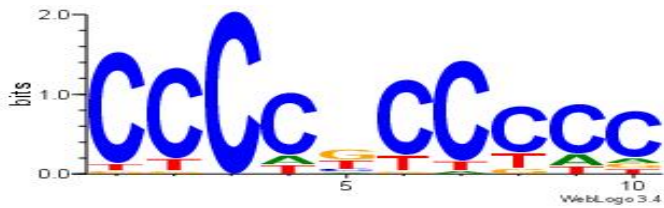
Consensus sequence: DWGHGGGGGB



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

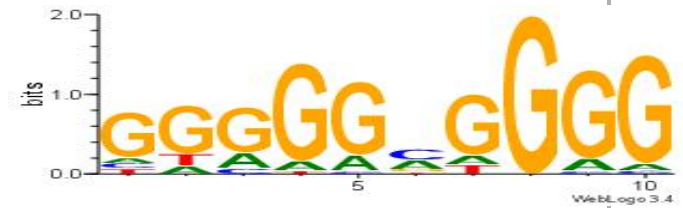
Original motif

Consensus sequence: CCCCKCCCC



Reverse complement motif

Consensus sequence: GGGGYGGGG



Best Matches for Motif ID 24 (Highest to Lowest)

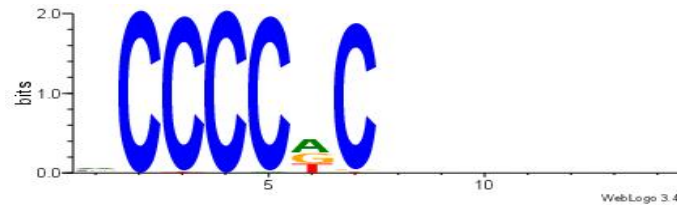
Motif ID:	MA0425.1
Motif name:	YGR067C
Taxon:	Fungi
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Forward
Position number:	2
Number of overlap:	10
Similarity score:	0.0399399

Alignment:

VCCCCDCHHHDDDBD
-CCCCKCCCC---

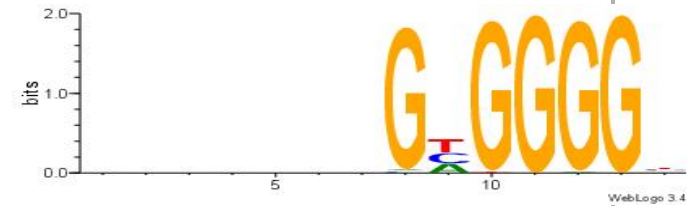
Original motif

Consensus sequence: VCCCCDCHHHDDDBD



Reverse complement motif

Consensus sequence: DBDDHHHGDGGGGG



Motif ID: [MA0323.1](#)
Motif name: IXR1
Taxon: Fungi
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 6
Number of overlap: 10
Similarity score: 0.0418489

Alignment:

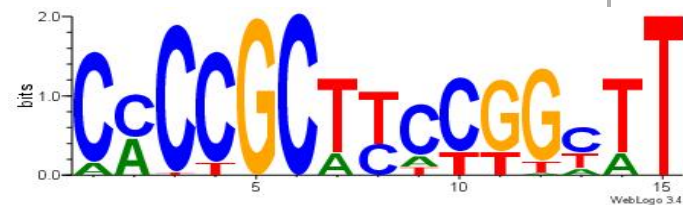
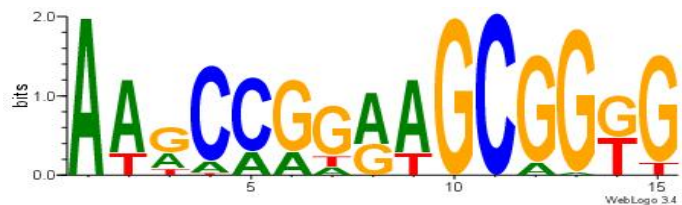
AARCCGGRAGCGGKG
-----GGGGYGGGG

Original motif

Consensus sequence: AARCCGGRAGCGGKG

Reverse complement motif

Consensus sequence: CYCCGCTKCCGGMTT

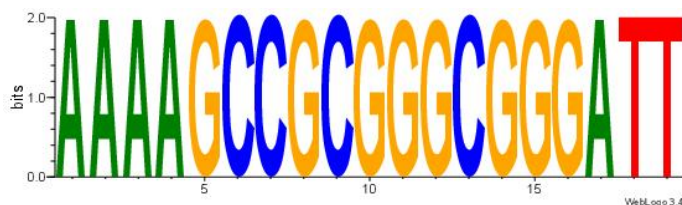


Motif ID: [MA0290.1](#)
 Motif name: DAL81
 Taxon: Fungi
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Backward
 Position number: 8
 Number of overlap: 10
 Similarity score: 0.059697

Alignment:
 AATCCCGCCCGGGCTTTT
 --CCCCKCCCC-----

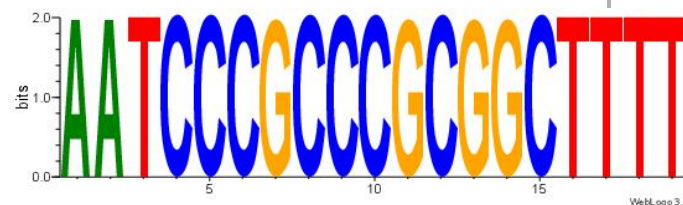
Original motif

Consensus sequence: AAAAGCCGCGGGCGGGATT



Reverse complement motif

Consensus sequence: AATCCCGCCCGGGCTTTT



Motif ID: [MA0395.1](#)

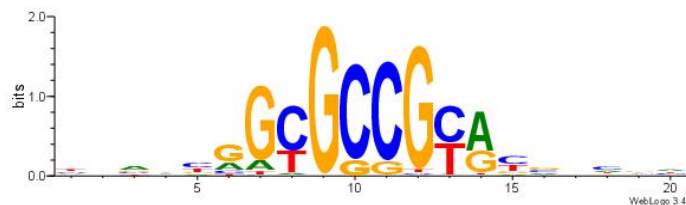
Motif name: STP2
 Taxon: Fungi
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 4
 Number of overlap: 10
 Similarity score: 0.0702654

Alignment:

HBDHVKKKCGGCGCCBHBVH
 ---GGGGYGGG-----

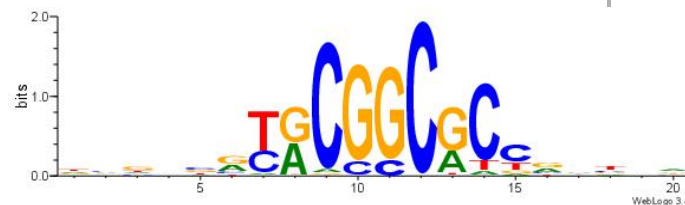
Original motif

Consensus sequence: HVVHBGGCGCCGYRYVHHBH



Reverse complement motif

Consensus sequence: HBDHVKKKCGGCGCCBHBVH



Motif ID: [MA0347.1](#)
 Motif name: NRG1
 Taxon: Fungi
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 10
 Number of overlap: 10

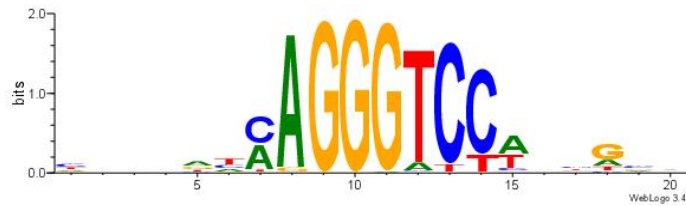
Similarity score: 0.0720885

Alignment:

HHVVDHMAAGGGTCCWDBGVD
-GGGGGYGGGG-----

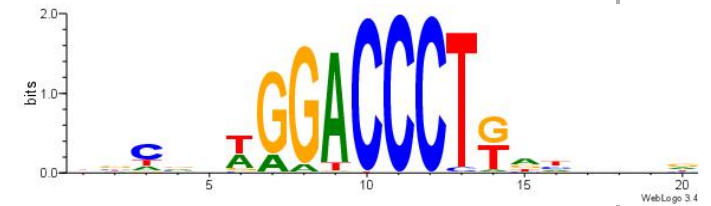
Original motif

Consensus sequence: HHVVDHMAAGGGTCCWDBGVD



Reverse complement motif

Consensus sequence: DVCBDWGGACCCTRHDBHD



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)

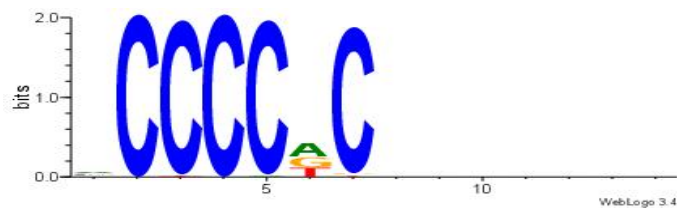
Motif ID: [MA0425.1](#)
Motif name: YGR067C
Taxon: Fungi
Matching format of first motif: Reverse Complement

Matching format of second motif: Original Motif
Direction: Backward
Position number: 5
Number of overlap: 10
Similarity score: 0.0377858

Alignment:
VCCCCDCHHHDDDBD
GCCYCMCCCD-----

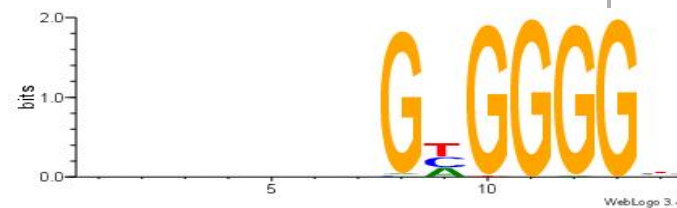
Original motif

Consensus sequence: VCCCCDCHHHDDDBD



Reverse complement motif

Consensus sequence: DBDDHHHGDGGGGG



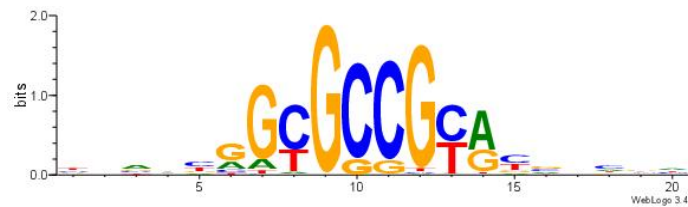
Motif ID: [MA0395.1](#)
Motif name: STP2
Taxon: Fungi
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Backward
Position number: 8
Number of overlap: 10
Similarity score: 0.0479742

Alignment:

HVVHBGGCGCCGYRYVHHBH
---DGGGYGKGGC-----

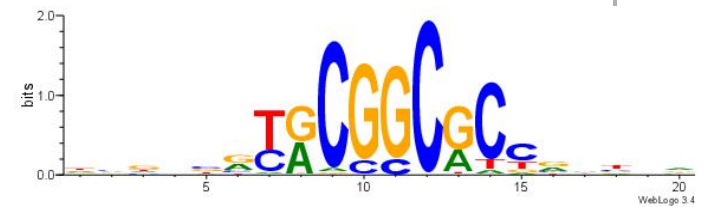
Original motif

Consensus sequence: HVVHBGGCGCCGYRYVHHBH



Reverse complement motif

Consensus sequence: HBDHVKKKCGGCGCCBHBVH

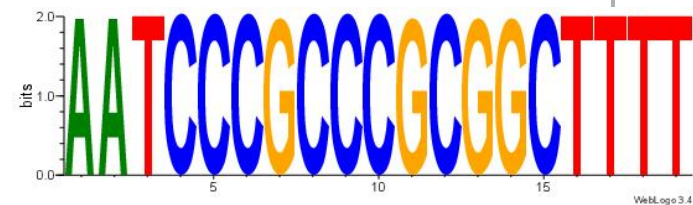
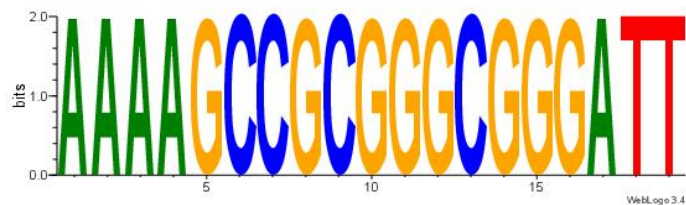


Motif ID: [MA0290.1](#)
Motif name: DAL81
Taxon: Fungi
Matching format of first motif: Original Motif
Matching format of second motif: Original Motif
Direction: Forward
Position number: 9
Number of overlap: 10
Similarity score: 0.0512896

Alignment:
AAAAGCCGCGGGCGGGATT
-----DGGGYGKGGC--

Original motif
Consensus sequence: AAAAGCCGCGGGCGGGATT

Reverse complement motif
Consensus sequence: AATCCCGCCGCGGCTTTT

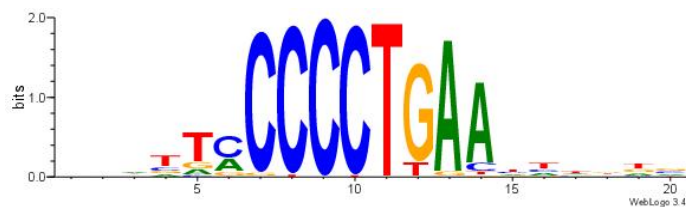


Motif ID: [MA0413.1](#)
 Motif name: USV1
 Taxon: Fungi
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 10
 Number of overlap: 10
 Similarity score: 0.0518653

Alignment:
 DDDTTMCCCCTGAAHHDBDV
 -GCCYCMCCCD-----

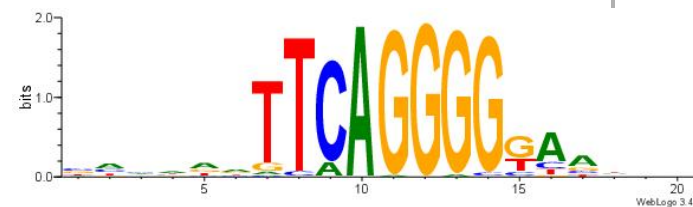
Original motif

Consensus sequence: DDDTTMCCCCTGAAHHDBDV



Reverse complement motif

Consensus sequence: VDBDHHTTCAGGGGRAADDD



Motif ID: [MA0269.1](#)

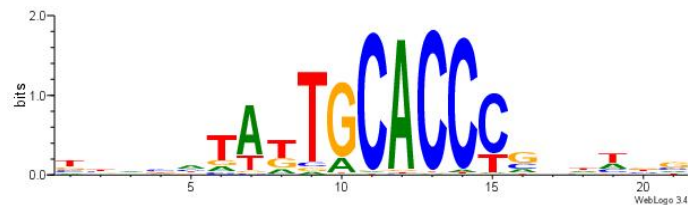
Motif name: AFT1
 Taxon: Fungi
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 6
 Number of overlap: 10
 Similarity score: 0.0608491

Alignment:

VBWDBSGGGTGCARTAHBDVV
 -----DGGGYGKGGC-----

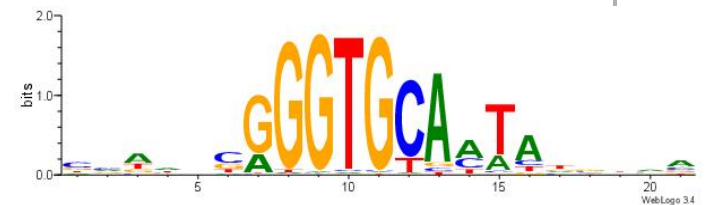
Original motif

Consensus sequence: BBDBHTAKTGCACCCSVDWBV



Reverse complement motif

Consensus sequence: VBWDBSGGGTGCARTAHBDVV



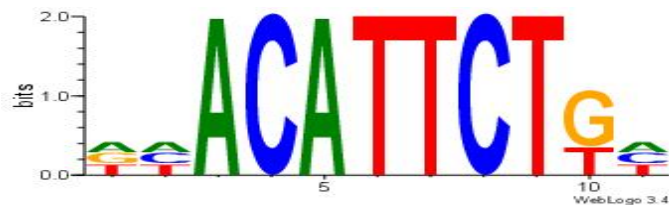
Dataset #: 4 Motif ID: 44 Motif name: dhACATTCTkh

Original motif

Consensus sequence: DHACATTCTGH

Reverse complement motif

Consensus sequence: HCAGAATGTHD



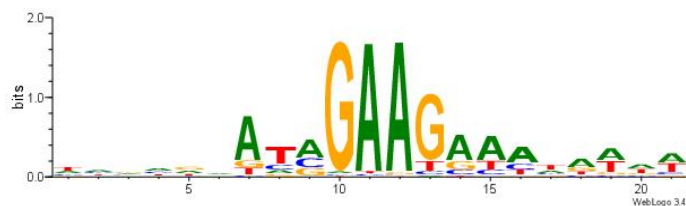
Best Matches for Motif ID 44 (Highest to Lowest)

Motif ID: [MA0377.1](#)
 Motif name: SFL1
 Taxon: Fungi
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Backward
 Position number: 5
 Number of overlap: 11
 Similarity score: 0.0436478

Alignment:
 HHVHDHATMGAAGAAHDWDW
 -----HCAGAATGTHD-----

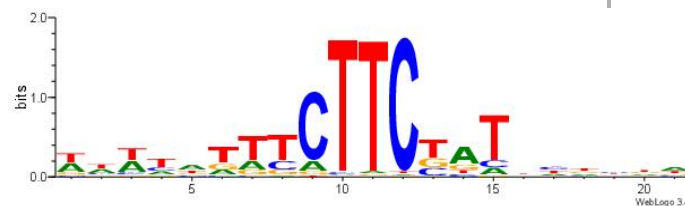
Original motif

Consensus sequence: HHVHDHATMGAAGAAHDWDW



Reverse complement motif

Consensus sequence: WDWDHTTTCTTCYATHHHVHH



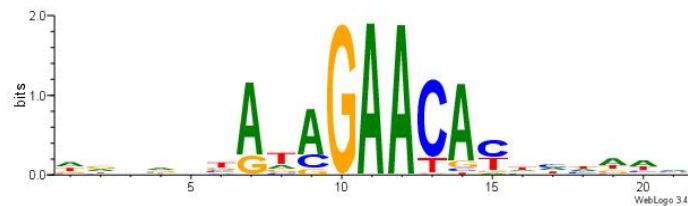
Motif ID: [MA0336.1](#)
 Motif name: MGA1
 Taxon: Fungi
 Matching format of first motif: Reverse Complement
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 7
 Number of overlap: 11
 Similarity score: 0.0439501

Alignment:

DDVVHBATAGAACAYDHHHDHV
 -----HCAGAAATGTHD-----

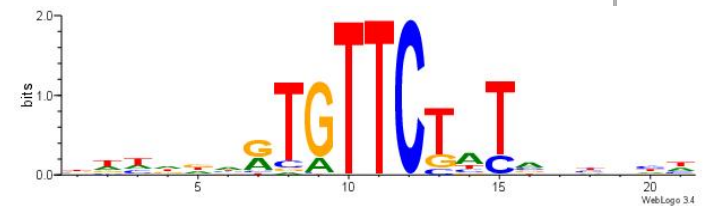
Original motif

Consensus sequence: DDVVHBATAGAACAYDHHHDHV



Reverse complement motif

Consensus sequence: BHDHDDKTGTTCTATVDBVHD



Motif ID: [MA0378.1](#)
 Motif name: SFP1
 Taxon: Fungi
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 6

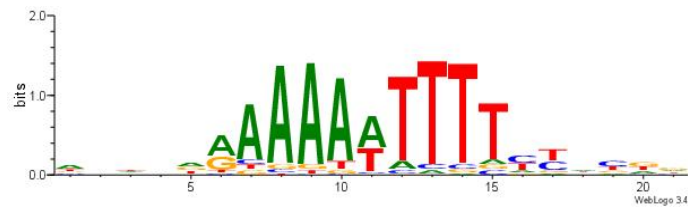
Number of overlap: 11
Similarity score: 0.0443222

Alignment:

DHDDDRAAAWTTTTYYHBDD
-----DHACATTCTGH-----

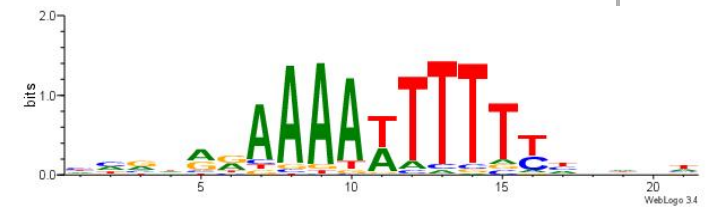
Original motif

Consensus sequence: DHDDDRAAAWTTTTYYHBDD



Reverse complement motif

Consensus sequence: HHBHMKAAAATTTTKDHDHD



Motif ID: [MA0440.1](#)
Motif name: ZAP1
Taxon: Fungi
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 3
Number of overlap: 11
Similarity score: 0.0482357

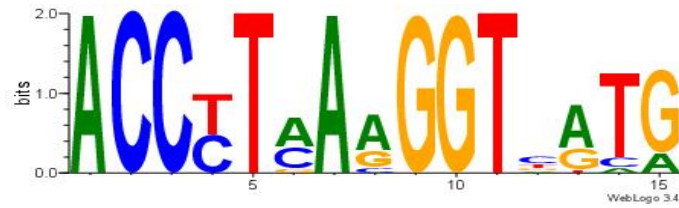
Alignment:

ACCYTMAAGGTBATG
--HCAGAATGTHD--

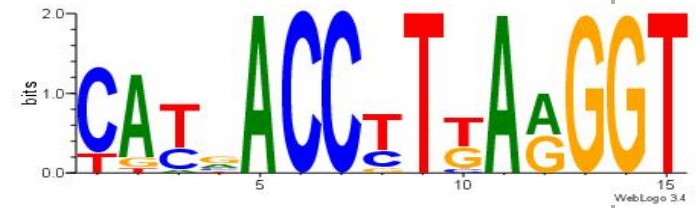
Original motif

Reverse complement motif

Consensus sequence: ACCYTMAAGGTBATG



Consensus sequence: CATBACCTTYAMGGT



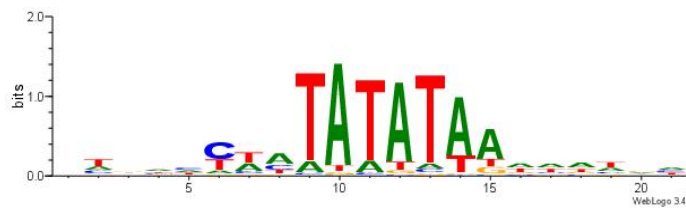
Motif ID: [MA0345.1](#)
Motif name: NHP6A
Taxon: Fungi
Matching format of first motif: Reverse Complement
Matching format of second motif: Original Motif
Direction: Forward
Position number: 5
Number of overlap: 11
Similarity score: 0.0504146

Alignment:

```
VHDHHYWHTATATAADDDHDH  
-----HCAGAATGTHD-----
```

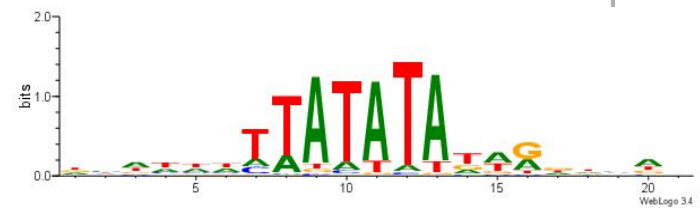
Original motif

Consensus sequence: VHDHHYWHTATATAADDDHDH



Reverse complement motif

Consensus sequence: HHHDDTTATATAHWKDH HHB



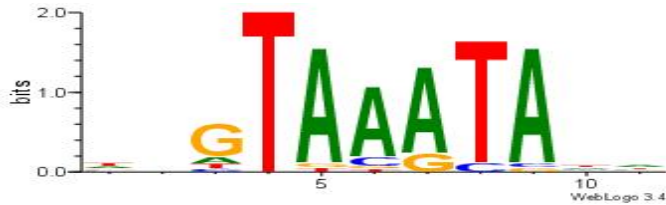
Dataset #: 4

Motif ID: 45

Motif name: wbgTAAATAww

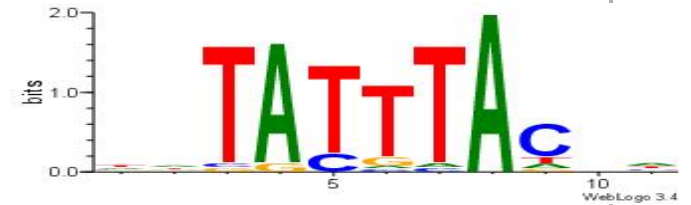
Original motif

Consensus sequence: DBGTAATAHD



Reverse complement motif

Consensus sequence: DHTATTTACBD



Best Matches for Motif ID 45 (Highest to Lowest)

Motif ID:	MA0929.1
Motif name:	NCU00019
Taxon:	Fungi
Matching format of first motif:	Original Motif
Matching format of second motif:	Original Motif
Direction:	Backward
Position number:	1
Number of overlap:	11
Similarity score:	0

Alignment:

DBDGTAAAYAH

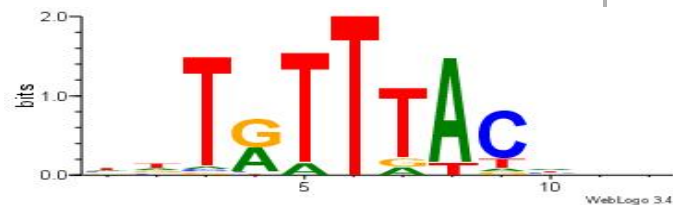
-DBGTAATAHD

Original motif

Consensus sequence: DBDGTAAAYAH

Reverse complement motif

Consensus sequence: BHTKTTTACDD



Motif ID: [MA0345.1](#)
 Motif name: NHP6A
 Taxon: Fungi
 Matching format of first motif: Original Motif
 Matching format of second motif: Reverse Complement
 Direction: Forward
 Position number: 5
 Number of overlap: 11
 Similarity score: 0.0222559

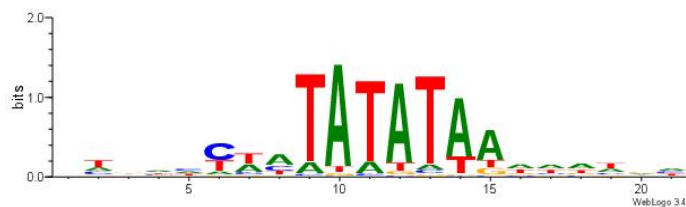
Alignment:

```

HHHDDDTTATATAHWKDH H B
----DBGTAAATAHD-----
  
```

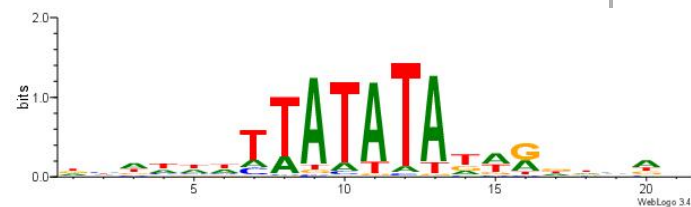
Original motif

Consensus sequence: VHDHHYWHTATATAADDDH D H



Reverse complement motif

Consensus sequence: HHHDDDTTATATAHWKDH H B



Motif ID: [MA0296.1](#)

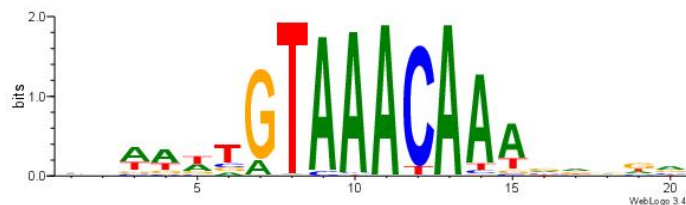
Motif name: FKH1
 Taxon: Fungi
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 5
 Number of overlap: 11
 Similarity score: 0.024745

Alignment:

BDWWWTGTAAACAAVDDD
 ----DBGTAAATAHD-----

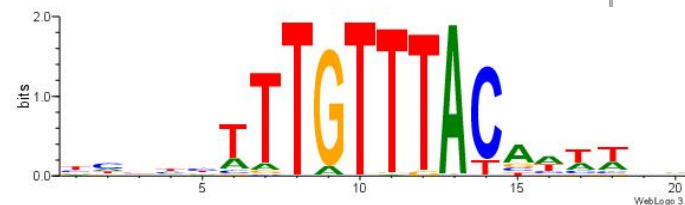
Original motif

Consensus sequence: BDWWWTGTAAACAAVDDD



Reverse complement motif

Consensus sequence: BHHDVTTTGTTTACAWWWHV



Motif ID: [MA0386.1](#)
 Motif name: SPT15
 Taxon: Fungi
 Matching format of first motif: Original Motif
 Matching format of second motif: Original Motif
 Direction: Forward
 Position number: 7
 Number of overlap: 11

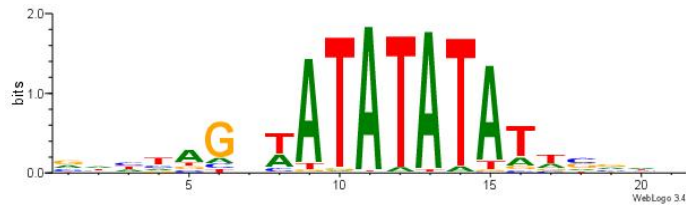
Similarity score: 0.0327275

Alignment:

VHHHAGDWATATATATDSVHD
-----DBGTAATAHD-----

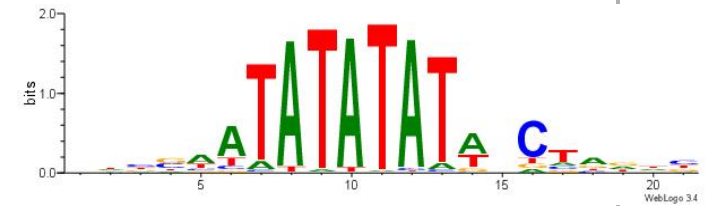
Original motif

Consensus sequence: VHHHAGDWATATATATDSVHD



Reverse complement motif

Consensus sequence: DHVSDATATATATWDCCTHDHV



Motif ID: [MA0346.1](#)
Motif name: NHP6B
Taxon: Fungi
Matching format of first motif: Reverse Complement
Matching format of second motif: Reverse Complement
Direction: Backward
Position number: 4
Number of overlap: 11
Similarity score: 0.0338073

Alignment:

BHKWWWATATATWHHHAHH
-----DHTATTTACBD---

Original motif

Consensus sequence: HHTHHHWATATATWWWRRDDV

Reverse complement motif

Consensus sequence: BHKWWWATATATWHHHAHH



Results created by MOTIFSIM on 02-13-2023 13:18:04

Runtime: 157.253 seconds

MOTIFSIM is written by Ngoc Tam L. Tran

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